Supplementary Table 3. Genes annotated in the the C227-11 genome.

Gen_id	start_position	end_position	Hit_def	Similar_to	Protein names	Organism
101503	1	630	TY-2482_chromosome	C8TNI9	Putative glucosyl-transferase	Escherichia coli O26:H11 (strain 11368 / EHEC)
89819	2049	778	TY-2482_chromosome	D3GUR0	Putative microcin esterase	Escherichia coli O44:H18 (strain 042 / EAEC)
2665	3638	2658	TY-2482_chromosome	P0CE57	Transposase insH for insertion sequence element IS5R	Escherichia coli (strain K12)
71375	4222	3791	TY-2482_chromosome	D3GUQ8	Putative uncharacterized protein mchS3	Escherichia coli O44:H18 (strain 042 / EAEC)
60152	4623	4381	TY-2482_chromosome	D3GUQ7	Putative uncharacterized protein mchS4	Escherichia coli O44:H18 (strain 042 / EAEC)
71725	5035	5241	TY-2482_chromosome	D3GUQ6	Microcin H47 immunity protein	Escherichia coli O44:H18 (strain 042 / EAEC)
78698	5272	5496	TY-2482_chromosome	D3GUQ5	Microcin H47	Escherichia coli O44:H18 (strain 042 / EAEC)
67590	5771	7318	TY-2482_chromosome	D3GUQ4	Putative microcin H47 biosynthesis protein	Escherichia coli O44:H18 (strain 042 / EAEC)
38267	7347	7796	TY-2482_chromosome	Q83Z99	Putative acyltransferase MchD	Escherichia coli
16317	7952	9223	TY-2482_chromosome	C3VUZ6	McnA	Escherichia coli
104098	9219	11318	TY-2482_chromosome	D3GUQ1	Probable microcin H47 secretion/processing ATP-binding protein (EC 3.4.22.-	Escherichia coli O44:H18 (strain 042 / EAEC)
19086	13002	12320	TY-2482_chromosome	Q6KDB0	McmM protein	Escherichia coli
103701	13560	13105	TY-2482_chromosome	C8TNJ2	Putative membraneprotein	Escherichia coli O26:H11 (strain 11368 / EHEC)
9766	13625	13813	TY-2482_chromosome	A1YN25	Putative uncharacterized protein	Escherichia coli
96521	14018	14524	TY-2482_chromosome	C8UMU7	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
101414	14580	15236	TY-2482_chromosome	B7LG70	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
66387	15260	15565	TY-2482_chromosome	B7LG74	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28466	15519	15794	TY-2482_chromosome	E3PN47	Putative uncharacterized protein	Escherichia coli O78:H11 (strain H10407 / ETEC)
13722	16474	17115	TY-2482_chromosome	Q6WPL3	Putative uncharacterized protein S14	Escherichia coli
92859	17360	20038	TY-2482_chromosome	C8UMV2	Putative UvrD/REP helicase-like protein	Escherichia coli O111:H- (strain 11128 / EHEC)
91886	20550	21779	TY-2482_chromosome	B7LFS5	Immunoglobulin-binding regulator	Escherichia coli (strain 55989 / EAEC)
14374	21915	22609	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli
45719	22628	23468	TY-2482_chromosome	Q9LA20	InsB	Shigella dysenteriae
28540	24952	23657	TY-2482_chromosome	B1LPS0	Anaerobic C4-dicarboxylate transporter, DcuA family	Escherichia coli (strain SMS-3-5 / SECEC)
19288	25737	25021	TY-2482_chromosome	B1EEY8	Aspartate racemase (EC 5.1.1.13)	Escherichia albertii TW07627
10857	26082	27023	TY-2482_chromosome	D8AHZ6	LysR substrate binding domain protein	Escherichia coli MS 116-1
25147	27522	27758	TY-2482_chromosome	Q8FEA4	Putative uncharacterized protein	Escherichia coli O6
34188	27603	27147	TY-2482_chromosome	P59697	Transposase for insertion sequence element IS200	Salmonella typhi
15181	28377	28012	TY-2482_chromosome	D8AHZ3	Conserved domain protein (Fragment)	Escherichia coli MS 116-1
78489	29109	28757	TY-2482_chromosome	D3GX03	Insertion sequence IS100, ATP-binding protein	Escherichia coli O44:H18 (strain 042 / EAEC)
9330	29682	29017	TY-2482_chromosome	Q5I3K9	Aec56	Escherichia coli
23398	31311	29773	TY-2482_chromosome	C1MF88	Protein kinase subdomain-containing protein	Citrobacter sp. 30_2
24509	32932	31298	TY-2482_chromosome	A7MPV8	Putative uncharacterized protein	Enterobacter sakazakii (strain ATCC BAA-894)
28482	33972	32935	TY-2482_chromosome	Q19NM8	TerY3	Escherichia coli O1:K1 / APEC
26172	34698	34060	TY-2482_chromosome	Q19NM7	TerY2	Escherichia coli O1:K1 / APEC
5410	35333	34698	TY-2482_chromosome	P75012	Tellurium resistance protein TerX	Serratia marcescens
25427	36075	35359	TY-2482_chromosome	Q19NM5	TerY1	Escherichia coli O1:K1 / APEC
5409	36925	36461	TY-2482_chromosome	P75010	Tellurium resistance protein terW	Serratia marcescens
111940	38151	36946	TY-2482_chromosome	C6UQE2	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
90392	40233	38165	TY-2482_chromosome	C6UQE3	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
112025	40972	40202	TY-2482_chromosome	C6UQE4	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
115524	42107	40968	TY-2482_chromosome	C6UQE5	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
63751	43184	42120	TY-2482_chromosome	C8UMS5	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
103700	43498	44076	TY-2482_chromosome	C8TNH3	Putative tellurium resistance protein TerZ	Escherichia coli O26:H11 (strain 11368 / EHEC)
107291	44079	45233	TY-2482_chromosome	C8TX27	Putative tellurium resistance protein TerA	Escherichia coli O103:H2 (strain 12009 / EHEC)
111194	45259	45711	TY-2482_chromosome	C8TX26	Putative tellurium resistance protein TerB	Escherichia coli O103:H2 (strain 12009 / EHEC)
100117	45737	46774	TY-2482_chromosome	C8TX25	Putative tellurium resistance protein TerC	Escherichia coli O103:H2 (strain 12009 / EHEC)
29304	47268	48045	TY-2482_chromosome	Q19NL2	TerE	Escherichia coli O1:K1 / APEC
107266	48479	49717	TY-2482_chromosome	C8TX21	Putative tellurium resistance protein TerF	Escherichia coli O103:H2 (strain 12009 / EHEC)
85733	49878	50300	TY-2482_chromosome	C8UCH9	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
104658	51007	51984	TY-2482_chromosome	C8TV65	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
r104	52093	52296	TY-2482_chromosome	ref|NC_010473|:2160347-2160550|-| [gene=isrC] [locus_tag=ECDH10B_2145]		
58183	52317	53099	TY-2482_chromosome	C8TPC9	Adhesin AIDA-I	Escherichia coli O26:H11 (strain 11368 / EHEC)
102145	53074	54345	TY-2482_chromosome	B7LG82	Antigen 43 (Ag43) phase-variable biofilm formation autotransporter; CP4-44 prophage	Escherichia coli (strain 55989 / EAEC)
107744	54456	56852	TY-2482_chromosome	C6UQI7	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
78788	56852	57754	TY-2482_chromosome	C6UZH6	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
104636	57754	58821	TY-2482_chromosome	C6UZH7	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
90293	58850	59638	TY-2482_chromosome	B7L946	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
61054	59657	60064	TY-2482_chromosome	C8TX14	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
71668	60288	61106	TY-2482_chromosome	C8TX13	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
20594	60297	60067	TY-2482_chromosome	D8EDM2	Conserved domain protein	Escherichia coli MS 119-7

26739	61278	61231	TY-2482_chromosome	Q1RA72	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
47869	62401	61445	TY-2482_chromosome	Q5K5L6	Putative uncharacterized protein	Escherichia coli
22614	63009	63588	TY-2482_chromosome	E9TQB2	Conserved domain protein (Fragment)	Escherichia coli MS 60-1
22334	63591	64076	TY-2482_chromosome	Q9X5P0	Putative uncharacterized protein	Escherichia coli
107224	64373	65212	TY-2482_chromosome	C8TNM7	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
r204	65452	65365	TY-2482_chromosome	ref|NC_010473|:1152233-1152320|Ser tRNA| [gene=serX] [locus_tag=ECDH10B_1104]		
31105	65686	66621	TY-2482_chromosome	B7LFE3	Glyoxylate/hydroxypyruvate reductase A (EC 1.1.1.79) (EC 1.1.1.81) (2-ketoacid reductase)	Escherichia coli (strain 55989 / EAEC)
34795	66679	67413	TY-2482_chromosome	B7LFE4	Putative hydrolase ycdX (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
73766	67440	67991	TY-2482_chromosome	B7LFE5	Putative uncharacterized protein ycdY	Escherichia coli (strain 55989 / EAEC)
90422	68048	68584	TY-2482_chromosome	D3H139	Putative membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
90449	69484	68654	TY-2482_chromosome	B7LFE7	Putative outer membrane lipoprotein involved in curli production assembly/transpor	Escherichia coli (strain 55989 / EAEC)
99196	69927	69514	TY-2482_chromosome	B7LFE8	Putative transport/assembly protein for curli synthesis	Escherichia coli (strain 55989 / EAEC)
59174	70341	69955	TY-2482_chromosome	B7LFE9	Putative transport/assembly protein for curli synthesis	Escherichia coli (strain 55989 / EAEC)
87830	70996	70349	TY-2482_chromosome	B7LFF0	DNA-binding transcriptional activator in two-component regulatory system	Escherichia coli (strain 55989 / EAEC)
116158	71656	71411	TY-2482_chromosome	C6UQK8	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
14106	71723	72246	TY-2482_chromosome	E9WD94	Curlin associated protein	Escherichia coli E1520
79086	72246	72698	TY-2482_chromosome	B7LFF2	Cryptic curlin major subunit	Escherichia coli (strain 55989 / EAEC)
72357	72760	73089	TY-2482_chromosome	B7LFF3	Putative curli production protein	Escherichia coli (strain 55989 / EAEC)
93587	73213	73520	TY-2482_chromosome	C8U5K0	Conserved predicted protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
99197	73618	74148	TY-2482_chromosome	B7LFF5	Putative uncharacterized protein ymdB	Escherichia coli (strain 55989 / EAEC)
93780	74153	75571	TY-2482_chromosome	B7LFF6	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
32826	76739	75585	TY-2482_chromosome	B7LFF7	Glucans biosynthesis protein C (EC 2.1.-.-)	Escherichia coli (strain 55989 / EAEC)
32831	77133	78665	TY-2482_chromosome	B7LFG0	Glucans biosynthesis protein G	Escherichia coli (strain 55989 / EAEC)
105396	78661	81201	TY-2482_chromosome	B7LFG1	Glucan biosynthesis: glycosyl transferase	Escherichia coli (strain 55989 / EAEC)
26066	81213	81435	TY-2482_chromosome	Q0TJ23	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
93626	81377	81601	TY-2482_chromosome	B7LFG2	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
81073	81979	81608	TY-2482_chromosome	B7LFG3	Putative uncharacterized protein msyB	Escherichia coli (strain 55989 / EAEC)
32216	83288	82065	TY-2482_chromosome	B7LFG4	Multidrug resistance protein mdtG	Escherichia coli (strain 55989 / EAEC)
113461	84380	83463	TY-2482_chromosome	B7LFG5	Lauryl-acyl carrier protein (ACP)-dependent acyltransferase (EC 2.3.1.-)	Escherichia coli (strain 55989 / EAEC)
34798	84605	85654	TY-2482_chromosome	B7LFG6	UPF0176 protein yceA	Escherichia coli (strain 55989 / EAEC)
99135	86274	85702	TY-2482_chromosome	B7LG46	Protein yceI	Escherichia coli (strain 55989 / EAEC)
59105	86844	86281	TY-2482_chromosome	B7LFZ2	Putative cytochrome b561	Escherichia coli (strain 55989 / EAEC)
32518	88384	87269	TY-2482_chromosome	B7LFZ3	N-methyl-L-tryptophan oxidase (MTOX) (EC 1.5.3.-)	Escherichia coli (strain 55989 / EAEC)
73549	88756	88502	TY-2482_chromosome	B5YVT0	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
87110	89420	89046	TY-2482_chromosome	B7LFZ5	DNA damage-inducible protein I	Escherichia coli (strain 55989 / EAEC)
33197	90408	89365	TY-2482_chromosome	B7LFZ6	Dihydroorotase (DHOase) (EC 3.5.2.3)	Escherichia coli (strain 55989 / EAEC)
77398	91074	90517	TY-2482_chromosome	B7LFZ7	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
77399	91855	91211	TY-2482_chromosome	B7LFZ8	Glutaredoxin 2 (Grx2)	Escherichia coli (strain 55989 / EAEC)
32218	93127	91922	TY-2482_chromosome	B7LFZ9	Multidrug resistance protein mdtH	Escherichia coli (strain 55989 / EAEC)
107800	93363	93944	TY-2482_chromosome	B7LG00	Ribosomal-protein-S5-alanine N-acetyltransferase (EC 2.3.1.128)	Escherichia coli (strain 55989 / EAEC)
75386	94607	95527	TY-2482_chromosome	B7LG02	Putative oxidoreductase with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
81009	95640	97172	TY-2482_chromosome	B7LG03	Putative uncharacterized protein mviN	Escherichia coli (strain 55989 / EAEC)
81010	97631	97218	TY-2482_chromosome	B7LG04	Export chaperone for FlgK and FlgL	Escherichia coli (strain 55989 / EAEC)
101279	97929	97639	TY-2482_chromosome	B7LG05	Anti-sigma factor for FliA (Sigma 28)	Escherichia coli (strain 55989 / EAEC)
72531	98664	98008	TY-2482_chromosome	B7LG06	Assembly protein for flagellar basal-body periplasmic P ring	Escherichia coli (strain 55989 / EAEC)
64904	98819	99232	TY-2482_chromosome	B7LG07	Flagellar component of cell-proximal portion of basal-body rod	Escherichia coli (strain 55989 / EAEC)
95572	99239	99640	TY-2482_chromosome	B7LG08	Flagellar component of cell-proximal portion of basal-body rod	Escherichia coli (strain 55989 / EAEC)
69997	99655	100347	TY-2482_chromosome	B7LG09	Flagellar hook assembly protein	Escherichia coli (strain 55989 / EAEC)
88386	100375	101577	TY-2482_chromosome	B7LG10	Flagellar hook protein	Escherichia coli (strain 55989 / EAEC)
73713	101600	102352	TY-2482_chromosome	B7LG11	Flagellar component of cell-proximal portion of basal-body rod	Escherichia coli (strain 55989 / EAEC)
69395	102527	103306	TY-2482_chromosome	B7LG12	Flagellar component of cell-distal portion of basal-body rod	Escherichia coli (strain 55989 / EAEC)
30971	103362	104057	TY-2482_chromosome	B7LG13	Flagellar L-ring protein (Basal body L-ring protein)	Escherichia coli (strain 55989 / EAEC)
30976	104072	105166	TY-2482_chromosome	B7LG14	Flagellar P-ring protein (Basal body P-ring protein)	Escherichia coli (strain 55989 / EAEC)
88387	105169	106107	TY-2482_chromosome	B7LG15	Muramidase	Escherichia coli (strain 55989 / EAEC)
69394	106176	107816	TY-2482_chromosome	B7LG16	Flagellar hook-filament junction protein 1	Escherichia coli (strain 55989 / EAEC)
59106	107831	108781	TY-2482_chromosome	B7LG17	Flagellar hook-filament junction protein	Escherichia coli (strain 55989 / EAEC)
106502	112166	108984	TY-2482_chromosome	B7LG18	Fused ribonucleaseE: endoribonuclease ; RNA-binding protein ;RNA degradosome binding protein (EC 3.1.4.-	Escherichia coli (strain 55989 / EAEC)
114703	112301	112618	TY-2482_chromosome	C8TPF5	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
109593	112739	113695	TY-2482_chromosome	B7LG19	Pseudouridine synthase (EC 5.4.99.-)	Escherichia coli (strain 55989 / EAEC)
r110	114388	114556	TY-2482_chromosome	ref|NC_010473|:1201257-1201425|-| [gene=sraB] [locus_tag=ECDH10B_1159]		
61974	114433	113813	TY-2482_chromosome	B5YVV6	Maf-like protein yceF 1	Escherichia coli O157:H7 (strain EC4115 / EHEC)
82702	114593	115111	TY-2482_chromosome	B7LG21	Putative uncharacterized protein yceD	Escherichia coli (strain 55989 / EAEC)
33014	115420	116487	TY-2482_chromosome	B7LG23	Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acylt	Escherichia coli (strain 55989 / EAEC)
80265	116558	117508	TY-2482_chromosome	B7LG24	3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl	Escherichia coli (strain 55989 / EAEC)

66385	117527	118453	TY-2482_chromosome	B7LG25	Malonyl-CoA-[acyl-carrier-protein] transacylase (EC 2.3.1.39)	Escherichia coli (strain 55989 / EAEC)
94751	118469	119200	TY-2482_chromosome	B7LG26	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100)	Escherichia coli (strain 55989 / EAEC)
25155	119735	119363	TY-2482_chromosome	Q1RD63	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
99022	119738	120976	TY-2482_chromosome	B7LG28	3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Escherichia coli (strain 55989 / EAEC)
113509	121099	121905	TY-2482_chromosome	B7LG29	4-amino-4-deoxychorismate lyase component of para-aminobenzoate synthase multienzyme complex (EC 4.1.3.38)	Escherichia coli (strain 55989 / EAEC)
97947	121911	122930	TY-2482_chromosome	B7LG30	Putative conserved membrane associated protein	Escherichia coli (strain 55989 / EAEC)
31798	122923	123561	TY-2482_chromosome	B7LG31	Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	Escherichia coli (strain 55989 / EAEC)
65361	123561	124562	TY-2482_chromosome	B7LG32	DNA polymerase III, delta prime subunit (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
83402	124576	125370	TY-2482_chromosome	B7LG33	Putative metallodependent hydrolase	Escherichia coli (strain 55989 / EAEC)
95573	125668	127098	TY-2482_chromosome	B7LG34	Fused glucose-specific PTS enzymes: IIBcomponent ; IIC component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
69924	129350	127164	TY-2482_chromosome	B7LG35	Ferric-rhodotorulic acid outer membrane transporter	Escherichia coli (strain 55989 / EAEC)
114028	129684	130040	TY-2482_chromosome	B7LG36	Purine nucleoside phosphoramidase	Escherichia coli (strain 55989 / EAEC)
81011	130046	130420	TY-2482_chromosome	B7LG37	Putative uncharacterized protein ycfL	Escherichia coli (strain 55989 / EAEC)
72718	130437	131075	TY-2482_chromosome	B7LG38	Putative outer membrane lipoprotein	Escherichia coli (strain 55989 / EAEC)
106367	131059	131880	TY-2482_chromosome	B7LG39	Thiamin kinase (EC 2.7.1.89)	Escherichia coli (strain 55989 / EAEC)
32610	131894	132916	TY-2482_chromosome	B7LG40	Beta-hexosaminidase (EC 3.2.1.52) (Beta-N-acetylhexosaminidase) (N-acetyl-beta-glucosaminidase)	Escherichia coli (strain 55989 / EAEC)
34808	132942	133481	TY-2482_chromosome	B7LG41	UPF0227 protein ycfP	Escherichia coli (strain 55989 / EAEC)
95578	133892	135193	TY-2482_chromosome	B7LG42	Respiratory NADH dehydrogenase 2/cupric reductase (EC 1.16.1.-) (EC 1.6.99.3)	Escherichia coli (strain 55989 / EAEC)
81012	135406	135942	TY-2482_chromosome	B7LG43	Putative uncharacterized protein ycfJ	Escherichia coli (strain 55989 / EAEC)
85660	136717	136010	TY-2482_chromosome	D3H1S7	TetR-family transcriptional regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
64299	136880	137134	TY-2482_chromosome	B7LG45	Putative uncharacterized protein ycfR	Escherichia coli (strain 55989 / EAEC)
77400	138182	137223	TY-2482_chromosome	B7LG47	Putative uncharacterized protein ycfS	Escherichia coli (strain 55989 / EAEC)
59107	141772	138329	TY-2482_chromosome	B7LG48	Transcription-repair coupling factor	Escherichia coli (strain 55989 / EAEC)
104280	142973	141903	TY-2482_chromosome	B7LG49	Putative uncharacterized protein ycfT	Escherichia coli (strain 55989 / EAEC)
73714	143235	144431	TY-2482_chromosome	B7LG50	Outer membrane-specific lipoprotein transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
114029	144427	145125	TY-2482_chromosome	B7LG51	Outer membrane-specific lipoprotein transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
69145	145128	146369	TY-2482_chromosome	B7LG52	Outer membrane-specific lipoprotein transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
32602	146401	147309	TY-2482_chromosome	B7LG53	N-acetyl-D-glucosamine kinase (EC 2.7.1.59) (GlcNAc kinase)	Escherichia coli (strain 55989 / EAEC)
75444	147328	148146	TY-2482_chromosome	B7LG54	Deacetylase of acetyl-CoA synthetase, NAD-dependent	Escherichia coli (strain 55989 / EAEC)
15319	149534	148291	TY-2482_chromosome	D6HVG4	Inner membrane protein ycfZ	Escherichia coli B088
86060	150638	149595	TY-2482_chromosome	B7LG57	Polyamine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
84582	151429	150638	TY-2482_chromosome	B7LG58	Polyamine transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
75731	152283	151429	TY-2482_chromosome	D3H1U1	Spermidine/putrescine ABC transporter, permease protein	Escherichia coli O44:H18 (strain 042 / EAEC)
94667	153403	152270	TY-2482_chromosome	B7LG60	Polyamine transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
102073	153611	154879	TY-2482_chromosome	B7LGW6	Peptidase T	Escherichia coli (strain 55989 / EAEC)
68048	153633	153385	TY-2482_chromosome	B7LG61	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
107801	156149	155031	TY-2482_chromosome	B7LGQ6	Putative uncharacterized protein ycfD	Escherichia coli (strain 55989 / EAEC)
75617	157685	156228	TY-2482_chromosome	B7LGQ7	Sensory histidine kinase in two-compoent regulatory system with PhoP	Escherichia coli (strain 55989 / EAEC)
115814	158356	157688	TY-2482_chromosome	B7LGQ8	DNA-binding response regulator in two-component regulatory system with PhoQ	Escherichia coli (strain 55989 / EAEC)
109823	159894	158527	TY-2482_chromosome	B7LGQ9	Adenylosuccinate lyase (EC 4.3.2.2)	Escherichia coli (strain 55989 / EAEC)
100316	160545	159901	TY-2482_chromosome	D3H1U9	High frequency lysogenization protein hflD	Escherichia coli O44:H18 (strain 042 / EAEC)
102082	161681	160578	TY-2482_chromosome	B7LGR1	tRNA-specific 2-thiouridylase mnmA (EC 2.8.1.-)	Escherichia coli (strain 55989 / EAEC)
80995	162196	161738	TY-2482_chromosome	B7LGR2	Bifunctional thiamin pyrimidine pyrophosphate hydrolase and thiamin pyrophosphate hydrolase	Escherichia coli (strain 55989 / EAEC)
80513	162859	162209	TY-2482_chromosome	B7LGR3	Pseudouridine synthase (EC 5.4.99.-)	Escherichia coli (strain 55989 / EAEC)
25697	164128	162950	TY-2482_chromosome	Q1RD17	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
2781	164707	164387	TY-2482_chromosome	B7LGR5	Anti-adapter protein iraM	Escherichia coli (strain 55989 / EAEC)
66280	165807	165406	TY-2482_chromosome	B7LGR6	Putative uncharacterized protein ycgX	Escherichia coli (strain 55989 / EAEC)
104387	166759	166031	TY-2482_chromosome	B7LGR7	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
59093	168175	166967	TY-2482_chromosome	B7LGR8	Putative cyclic-di-GMP phosphodiesterase; blue-light sensing protein using FAD (BLUF)	Escherichia coli (strain 55989 / EAEC)
80996	168489	168722	TY-2482_chromosome	B7LGR9	Putative uncharacterized protein ycgZ	Escherichia coli (strain 55989 / EAEC)
71422	168768	169037	TY-2482_chromosome	B7LGS0	Putative uncharacterized protein ymgA	Escherichia coli (strain 55989 / EAEC)
78959	169069	169332	TY-2482_chromosome	B7LGS1	Putative uncharacterized protein ymgB	Escherichia coli (strain 55989 / EAEC)
111774	169448	169693	TY-2482_chromosome	B7LGS2	Putative uncharacterized protein ymgC	Escherichia coli (strain 55989 / EAEC)
111718	170028	171548	TY-2482_chromosome	B7LGS3	Putative uncharacterized protein ycgG	Escherichia coli (strain 55989 / EAEC)
111372	171647	171898	TY-2482_chromosome	D3H1W3	Putative membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
99169	172627	174945	TY-2482_chromosome	B7LGS8	Putative Outer membrane autotransporter barrel, putative pectin lyase fold	Escherichia coli (strain 55989 / EAEC)
99173	175334	175008	TY-2482_chromosome	B7LGS9	Putative uncharacterized protein ymgD	Escherichia coli (strain 55989 / EAEC)
35026	175688	175347	TY-2482_chromosome	B7LGT0	UPF0757 protein ymgG	Escherichia coli (strain 55989 / EAEC)
70057	176165	176605	TY-2482_chromosome	B7LGT1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
32409	177246	176983	TY-2482_chromosome	B7LGT2	Cell division topological specificity factor	Escherichia coli (strain 55989 / EAEC)
114073	178062	177253	TY-2482_chromosome	B7LGT3	Membrane ATPase of the MinC-MinD-MinE system	Escherichia coli (strain 55989 / EAEC)
32405	178781	178089	TY-2482_chromosome	B7LGT4	Probable septum site-determining protein minC	Escherichia coli (strain 55989 / EAEC)
9439	178921	179145	TY-2482_chromosome	D6J9E0	Predicted protein	Escherichia coli B354
106529	179301	179666	TY-2482_chromosome	B7LGT5	Putative uncharacterized protein ycgJ	Escherichia coli (strain 55989 / EAEC)

99174	180190	179792	TY-2482_chromosome	B7LGT6	Putative uncharacterized protein ycgK	Escherichia coli (strain 55989 / EAEC)
26609	180219	180417	TY-2482_chromosome	D3QQU1	Putative uncharacterized protein	Escherichia coli O55:H7 (strain CB9615 / EPEC)
34811	180399	180722	TY-2482_chromosome	B7LGT7	UPF0745 protein YcgL	Escherichia coli (strain 55989 / EAEC)
83168	180797	181453	TY-2482_chromosome	B7LGT8	Putative isomerase/hydrolase (EC 3.-.-.-)	Escherichia coli (strain 55989 / EAEC)
18861	181470	181991	TY-2482_chromosome	D8BP59	Putative uncharacterized protein (Fragment)	Escherichia coli MS 200-1
75748	183255	182204	TY-2482_chromosome	B5YXK6	Hemolysin E, chromosomal	Escherichia coli O157:H7 (strain EC4115 / EHEC)
88374	183484	183900	TY-2482_chromosome	B7LGU3	DNA polymerase V, subunit D (EC 3.4.21.-)	Escherichia coli (strain 55989 / EAEC)
61882	183903	185168	TY-2482_chromosome	B7LGU4	DNA polymerase V, subunit C	Escherichia coli (strain 55989 / EAEC)
108639	185753	185220	TY-2482_chromosome	B5YXK9	Disulfide bond formation protein DsbB	Escherichia coli O157:H7 (strain EC4115 / EHEC)
32658	187434	185896	TY-2482_chromosome	B7LGU6	Na(+)/H(+) antiporter nhaB (Sodium/proton antiporter nhaB)	Escherichia coli (strain 55989 / EAEC)
30899	187656	188372	TY-2482_chromosome	B7LGU7	Fatty acid metabolism regulator protein	Escherichia coli (strain 55989 / EAEC)
104971	189959	188430	TY-2482_chromosome	B7LGU8	Putative uncharacterized protein ycgB	Escherichia coli (strain 55989 / EAEC)
30530	190289	191584	TY-2482_chromosome	B7LGU9	D-amino acid dehydrogenase small subunit (EC 1.4.99.1)	Escherichia coli (strain 55989 / EAEC)
91936	191597	192664	TY-2482_chromosome	B7LGV0	Alanine racemase 1 (EC 5.1.1.1)	Escherichia coli (strain 55989 / EAEC)
30441	194789	193056	TY-2482_chromosome	B7LGV1	Cell volume regulation protein A	Escherichia coli (strain 55989 / EAEC)
10220	195784	196506	TY-2482_chromosome	A1YN12	Membrane-bound lytic murein transglycosylase E	Escherichia coli
90220	195798	194887	TY-2482_chromosome	B7LGV2	L,D-carboxypeptidase A (EC 3.4.17.13)	Escherichia coli (strain 55989 / EAEC)
73747	197245	196514	TY-2482_chromosome	B7LGV4	Flagellar brake protein YcgR (Cyclic di-GMP binding protein YcgR)	Escherichia coli (strain 55989 / EAEC)
24501	197769	197503	TY-2482_chromosome	A7ZKW7	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC)
59153	197878	198315	TY-2482_chromosome	B7LGV6	Putative uncharacterized protein ycgY	Escherichia coli (strain 55989 / EAEC)
34312	200094	198400	TY-2482_chromosome	B7LGV7	Periplasmic trehalase (EC 3.2.1.28) (Alpha,alpha-trehalase) (Alpha,alpha-trehalose glucohydrolase	Escherichia coli (strain 55989 / EAEC)
80318	201832	200417	TY-2482_chromosome	B7LGV8	Fused dihydroxyacetone-specific PTS enzymes: HPr component ; EI component	Escherichia coli (strain 55989 / EAEC)
114074	202475	201846	TY-2482_chromosome	B7LGV9	Dihydroxyacetone kinase, C-terminal domain	Escherichia coli (strain 55989 / EAEC)
102913	203556	202489	TY-2482_chromosome	B7LGW0	Dihydroxyacetone kinase, N-terminal domain	Escherichia coli (strain 55989 / EAEC)
91136	203784	205700	TY-2482_chromosome	B7LGW1	DNA-binding transcriptional regulator, dihydroxyacetone metabolism	Escherichia coli (strain 55989 / EAEC)
113399	208670	205806	TY-2482_chromosome	B7LGW2	Putative adhesin; putative autotransporter	Escherichia coli (strain 55989 / EAEC)
110420	210530	209442	TY-2482_chromosome	B7LGW3	Putative GTP-binding protein	Escherichia coli (strain 55989 / EAEC)
33134	211231	210650	TY-2482_chromosome	B7LGW4	Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Escherichia coli (strain 55989 / EAEC)
95613	211509	211784	TY-2482_chromosome	B7LGW5	Putative uncharacterized protein ychH	Escherichia coli (strain 55989 / EAEC)
91215	213521	211845	TY-2482_chromosome	B7LGW7	Putative transporter	Escherichia coli (strain 55989 / EAEC)
72730	214593	213649	TY-2482_chromosome	B7LGW8	Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthase)	Escherichia coli (strain 55989 / EAEC)
31691	215595	214747	TY-2482_chromosome	B7LGW9	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (CMK) (EC 2.7.1.148) (4-(cytidine-5'-diphospho)-2-C-methyl-D-eryt	Escherichia coli (strain 55989 / EAEC)
31920	216218	215598	TY-2482_chromosome	B7LGX0	Outer-membrane lipoprotein lolB	Escherichia coli (strain 55989 / EAEC)
31340	216432	217685	TY-2482_chromosome	B7LGX1	Glutamyl-tRNA reductase (GluTR) (EC 1.2.1.70)	Escherichia coli (strain 55989 / EAEC)
33317	217730	218809	TY-2482_chromosome	B7LGX2	Peptide chain release factor 1 (RF-1)	Escherichia coli (strain 55989 / EAEC)
58397	218812	219642	TY-2482_chromosome	B7LGX3	N5-glutamine methyltransferase, modifies release factors RF-1 and RF-2 (EC 2.1.1.-)	Escherichia coli (strain 55989 / EAEC)
81050	219642	220031	TY-2482_chromosome	B7LGX4	Putative membrane protein; putative component of transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
84610	220038	220844	TY-2482_chromosome	B7LGX5	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
26647	221748	222008	TY-2482_chromosome	Q1RCM2	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
28627	221806	220847	TY-2482_chromosome	Q8FHZ9	Putative uncharacterized protein	Escherichia coli O6
r512	222041	222107	TY-2482_chromosome	ref|NC_010473|:1308787-1308853|-| [gene=rdlA] [locus_tag=ECDH10B_1270]		
12916	222307	222543	TY-2482_chromosome	C1NCG3	Putative uncharacterized protein	Escherichia sp. 1_1_43
r513	222576	222642	TY-2482_chromosome	ref|NC_010473|:1308787-1308853|-| [gene=rdlA] [locus_tag=ECDH10B_1270]		
12917	222842	223078	TY-2482_chromosome	C1NCG3	Putative uncharacterized protein	Escherichia sp. 1_1_43
r514	223116	223178	TY-2482_chromosome	ref|NC_010473|:1308787-1308853|-| [gene=rdlA] [locus_tag=ECDH10B_1270]		
12915	223378	223614	TY-2482_chromosome	C1NCG3	Putative uncharacterized protein	Escherichia sp. 1_1_43
r508	223647	223714	TY-2482_chromosome	ref|NC_010473|:1309857-1309924|-| [gene=rdlC] [locus_tag=ECDH10B_1274]		
91006	225104	224007	TY-2482_chromosome	B7LGX9	Calcium/sodium:proton antiporter	Escherichia coli (strain 55989 / EAEC)
29313	225667	225371	TY-2482_chromosome	A1AAE4	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
102952	225741	226454	TY-2482_chromosome	B7LHL5	Regulatory protein for cation transport	Escherichia coli (strain 55989 / EAEC)
95616	226854	226504	TY-2482_chromosome	B7LHG5	Putative uncharacterized protein ychN	Escherichia coli (strain 55989 / EAEC)
90079	227180	228430	TY-2482_chromosome	B7LHG6	Putative adhesin/invasin	Escherichia coli (strain 55989 / EAEC)
99038	230873	229080	TY-2482_chromosome	B7LHG8	Sensory histidine kinase in two-component regulatory system with NarL	Escherichia coli (strain 55989 / EAEC)
68095	230899	231114	TY-2482_chromosome	D3H2K9	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
91942	231212	232600	TY-2482_chromosome	B7LHG9	Nitrate/nitrite transporter	Escherichia coli (strain 55989 / EAEC)
80266	233119	236859	TY-2482_chromosome	B7LHH0	Nitrate reductase 1, alpha subunit (EC 1.7.99.4)	Escherichia coli (strain 55989 / EAEC)
58534	236859	238394	TY-2482_chromosome	B7LHH1	Nitrate reductase 1, beta (Fe-S) subunit (EC 1.7.99.4)	Escherichia coli (strain 55989 / EAEC)
87625	238394	239101	TY-2482_chromosome	B7LHH2	Molybdenum-cofactor-assembly chaperone subunit (Delta subunit) of nitrate reductase 1 (EC 1.7.99.4)	Escherichia coli (strain 55989 / EAEC)
61654	239104	239778	TY-2482_chromosome	B7LHH3	Nitrate reductase 1, gamma (Cytochrome b(NR)) subunit (EC 1.7.99.4)	Escherichia coli (strain 55989 / EAEC)
27786	239961	240407	TY-2482_chromosome	B7LHH4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
r115	240135	239965	TY-2482_chromosome	ref|NC_010473|:1326530-1326700|-| [gene=rttR] [locus_tag=ECDH10B_1288]		
r233	240227	240143	TY-2482_chromosome	ref|NC_010473|:1327002-1327086|Tyr tRNA| [gene=tyrT] [locus_tag=ECDH10B_1291]		
r232	240346	240262	TY-2482_chromosome	ref|NC_010473|:1327002-1327086|Tyr tRNA| [gene=tyrT] [locus_tag=ECDH10B_1291]		
59010	241348	240509	TY-2482_chromosome	B7LHH5	Formyltetrahydrofolate hydrolase (EC 3.5.1.10)	Escherichia coli (strain 55989 / EAEC)

97279	241877	241401	TY-2482_chromosome	B5YYD8	UPF0225 protein ychJ	Escherichia coli O157:H7 (strain EC4115 / EHEC)
65817	241930	242871	TY-2482_chromosome	B7LHH7	Putative esterase of the alpha-beta hydrolase superfamily	Escherichia coli (strain 55989 / EAEC)
84620	242966	243976	TY-2482_chromosome	B7LHH8	Response regulator of RpoS	Escherichia coli (strain 55989 / EAEC)
94887	244181	245086	TY-2482_chromosome	B7LHH9	Glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	Escherichia coli (strain 55989 / EAEC)
66291	245646	245236	TY-2482_chromosome	B7LHI0	Global nucleic acid-binding transcriptional dual regulator H-NS	Escherichia coli (strain 55989 / EAEC)
100845	246252	246866	TY-2482_chromosome	B7LHI1	Thymidine kinase (EC 2.7.1.21)	Escherichia coli (strain 55989 / EAEC)
6437	248051	247154	TY-2482_chromosome	P30192	Putative uncharacterized protein ychG	Escherichia coli (strain K12)
88433	250850	248178	TY-2482_chromosome	B7LHI5	Fused acetaldehyde-CoA dehydrogenase ; iron-dependent alcohol dehydrogenase ; pyruvate-formate lyase deactivas	Escherichia coli (strain 55989 / EAEC)
94864	251327	251971	TY-2482_chromosome	B7LHI6	Putative uncharacterized protein ychE	Escherichia coli (strain 55989 / EAEC)
13411	252446	252135	TY-2482_chromosome	D6J9L4	Predicted protein	Escherichia coli B354
94577	252712	254340	TY-2482_chromosome	B7LHI8	Oligopeptide transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
81054	254429	255346	TY-2482_chromosome	B7LHI9	Oligopeptide transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
99180	255364	256269	TY-2482_chromosome	B7LHJ0	Oligopeptide transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
98161	256284	257294	TY-2482_chromosome	B7LHJ1	Oligopeptide transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
77437	257294	258295	TY-2482_chromosome	B7LHJ2	Oligopeptide transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
34820	258680	258354	TY-2482_chromosome	B7LHJ3	UPF0263 protein yciU	Escherichia coli (strain 55989 / EAEC)
30345	260175	258718	TY-2482_chromosome	B7LHJ4	Cardiolipin synthase (CL synthase) (EC 2.7.8.-)	Escherichia coli (strain 55989 / EAEC)
64738	260207	260488	TY-2482_chromosome	B7LHJ5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
101053	261799	260549	TY-2482_chromosome	B7LHJ6	Voltage-gated potassium channel	Escherichia coli (strain 55989 / EAEC)
82485	262401	262102	TY-2482_chromosome	D3H2N2	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
69930	262619	263335	TY-2482_chromosome	B7LHJ8	Membrane spanning protein in TonB-ExbB-ExbD complex	Escherichia coli (strain 55989 / EAEC)
91944	263776	263381	TY-2482_chromosome	B7LHJ9	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
31708	264420	263884	TY-2482_chromosome	B7LHK0	Probable intracellular septation protein	Escherichia coli (strain 55989 / EAEC)
34817	265193	264453	TY-2482_chromosome	B7LHK1	UPF0259 membrane protein yciC	Escherichia coli (strain 55989 / EAEC)
72894	265550	266185	TY-2482_chromosome	B7LHK2	Outer membrane protein W	Escherichia coli (strain 55989 / EAEC)
75445	267364	266237	TY-2482_chromosome	B7LHK3	Phage integrase	Escherichia coli (strain 55989 / EAEC)
16442	267590	267268	TY-2482_chromosome	E8IYI4	Excisionase	Escherichia coli O55:H7 str. USDA 5905
66308	270126	267658	TY-2482_chromosome	B7LHK5	Putative exonuclease from phage origin	Escherichia coli (strain 55989 / EAEC)
10582	270189	270791	TY-2482_chromosome	E7JE17	Putative uncharacterized protein	Escherichia coli 1357
20633	270824	271157	TY-2482_chromosome	E1IYN5	Conserved domain protein (Fragment)	Escherichia coli MS 145-7
24668	271090	271353	TY-2482_chromosome	B7LHK9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28408	271695	271348	TY-2482_chromosome	B7LHL0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
114614	271928	271698	TY-2482_chromosome	C8UCK2	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
93012	272563	272147	TY-2482_chromosome	C8TR54	Putative phage repressor protein CI	Escherichia coli O26:H11 (strain 11368 / EHEC)
17356	272571	272894	TY-2482_chromosome	E2QMD4	Regulatory protein	Escherichia coli
86005	272894	273316	TY-2482_chromosome	D3GYH8	Putative prophage protein	Escherichia coli O44:H18 (strain 042 / EAEC)
96893	273327	274301	TY-2482_chromosome	D3GYH7	Putative prophage replication protein	Escherichia coli O44:H18 (strain 042 / EAEC)
17174	274339	274767	TY-2482_chromosome	E1IYP5	Putative uncharacterized protein	Escherichia coli MS 145-7
115645	274924	275607	TY-2482_chromosome	D3H4E4	Putative prophage protein	Escherichia coli O44:H18 (strain 042 / EAEC)
50513	275791	276000	TY-2482_chromosome	E1IYP7	Hok/gef family protein	Escherichia coli MS 145-7
66259	276445	277488	TY-2482_chromosome	B7L8R9	Putative uncharacterized protein ydfU	Escherichia coli (strain 55989 / EAEC)
9564	276518	276048	TY-2482_chromosome	E7IAU7	Putative uncharacterized protein	Escherichia coli LT-68
60754	277504	277875	TY-2482_chromosome	D3H2S1	Crossover junction endodeoxyribonuclease rusA (EC 3.1.22.4)	Escherichia coli O44:H18 (strain 042 / EAEC)
95498	277875	278693	TY-2482_chromosome	B7LER7	Putative antitermination protein Q of prophage	Escherichia coli (strain 55989 / EAEC)
108586	278818	279117	TY-2482_chromosome	C8UNL5	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC)
100726	279271	280317	TY-2482_chromosome	B7LER9	Putative DNA adenine methyltransferase (DNA methylase) from phage origin	Escherichia coli (strain 55989 / EAEC)
r352	280370	280445	TY-2482_chromosome	ref|NC_010473|:2875549-2875624|Ile tRNA| [gene=ileY] [locus_tag=ECDH10B_2820		
95579	280730	281080	TY-2482_chromosome	B7L8R4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28582	281211	281522	TY-2482_chromosome	B7MV04	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
2779	281866	281534	TY-2482_chromosome	B7UQ15	Anti-adapter protein iraM	Escherichia coli O127:H6 (strain E2348/69 / EPEC)
68371	282127	283977	TY-2482_chromosome	B7LES0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
79306	284053	284343	TY-2482_chromosome	D3H2S6	Putative phage lysis protein	Escherichia coli O44:H18 (strain 042 / EAEC)
73644	284351	285154	TY-2482_chromosome	B7LES2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
111796	285200	285730	TY-2482_chromosome	C8U3C5	Lysozyme (EC 3.2.1.17)	Escherichia coli O103:H2 (strain 12009 / EHEC)
113937	285811	286020	TY-2482_chromosome	B7LES5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
102801	286004	286273	TY-2482_chromosome	B7LES6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
29210	286376	286840	TY-2482_chromosome	D3QSD5	Endopeptidase	Escherichia coli O55:H7 (strain CB9615 / EPEC)
23807	287143	287346	TY-2482_chromosome	E3Y9Y5	Putative uncharacterized protein	Shigella flexneri 2a str. 2457T
12060	287803	288204	TY-2482_chromosome	D8EE44	Putative uncharacterized protein	Escherichia coli MS 119-7
27275	288353	289153	TY-2482_chromosome	A1AAK5	Prophage Qin DNA packaging protein NU1-like protein	Escherichia coli O1:K1 / APEC
84565	289086	291053	TY-2482_chromosome	B7L465	Terminase large subunit (Gp2)	Escherichia coli (strain 55989 / EAEC)
88462	291040	291243	TY-2482_chromosome	B7L466	Head stabilization protein (Head protein GP3)	Escherichia coli (strain 55989 / EAEC)
91971	291243	292832	TY-2482_chromosome	B7L467	Portal protein (Head protein Gp4)	Escherichia coli (strain 55989 / EAEC)
115786	292825	294327	TY-2482_chromosome	C8U3B6	Putative head protein/prohead protease	Escherichia coli O103:H2 (strain 12009 / EHEC)

105237	294367	294711	TY-2482_chromosome	D3H3D9	Phage head decoration protein	Escherichia coli O44:H18 (strain 042 / EAEC)
95640	294772	295797	TY-2482_chromosome	B7L470	Major head protein (Head protein gp7)	Escherichia coli (strain 55989 / EAEC)
23542	295852	296217	TY-2482_chromosome	E6B8R1	Uncharacterized 13.5 kDa protein in GP7-GP8 intergenic region	Escherichia coli 3431
26114	296201	296563	TY-2482_chromosome	B7MSC9	Tail attachment protein (Minor capsid protein FII)	Escherichia coli O81 (strain ED1a)
60230	296581	297153	TY-2482_chromosome	D3H3E3	Phage minor tail protein	Escherichia coli O44:H18 (strain 042 / EAEC)
114313	297153	297545	TY-2482_chromosome	C8U3B0	Putative minor tail protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
25167	298983	297652	TY-2482_chromosome	A1AAL5	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
26151	299174	301744	TY-2482_chromosome	B7LEU0	Minor tail protein H	Escherichia coli (strain 55989 / EAEC)
82999	301744	302070	TY-2482_chromosome	C8TUH3	Putative minor tail protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
79403	302734	303516	TY-2482_chromosome	B7LEU3	Putative tail fiber component K of prophage	Escherichia coli (strain 55989 / EAEC)
27266	302777	301980	TY-2482_chromosome	Q1RCC4	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
26121	303417	304055	TY-2482_chromosome	B7ULV9	Predicted tail assembly protein	Escherichia coli O127:H6 (strain E2348/69 / EPEC
24901	304120	304467	TY-2482_chromosome	B7ML65	Putative uncharacterized protein	Escherichia coli O45:K1 (strain S88 / ExPEC)
29091	304537	308013	TY-2482_chromosome	B7LBD5	Host specificity protein J of prophage	Escherichia coli (strain 55989 / EAEC)
98401	308084	308680	TY-2482_chromosome	D3H3F5	Putative prophage-encoded outer membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
13507	308835	311666	TY-2482_chromosome	E6AYR0	Long tail fiber protein p37	Escherichia coli 3431
25987	311669	312250	TY-2482_chromosome	B2U0E5	Tail fiber assembly protein	Shigella boydii serotype 18 (strain CDC 3083-94 / BS512)
100341	312976	312311	TY-2482_chromosome	D3H3F8	Putative phage protein	Escherichia coli O44:H18 (strain 042 / EAEC)
26024	313472	313125	TY-2482_chromosome	A1AAM7	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
73769	314582	314079	TY-2482_chromosome	B7L489	Putative uncharacterized protein yciE	Escherichia coli (strain 55989 / EAEC)
100647	315149	314631	TY-2482_chromosome	B5YZN7	YciF protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
93019	315417	315217	TY-2482_chromosome	D3H3G3	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
34341	316580	315777	TY-2482_chromosome	B7L492	Tryptophan synthase alpha chain (EC 4.2.1.20)	Escherichia coli (strain 55989 / EAEC)
34345	317773	316583	TY-2482_chromosome	B7L493	Tryptophan synthase beta chain (EC 4.2.1.20)	Escherichia coli (strain 55989 / EAEC)
78798	319143	317788	TY-2482_chromosome	B7L494	Fused indole-3-glycerolphosphate synthetase ; N-(5-phosphoribosyl)anthranilate isomerase (EC 4.1.1.48) (EC 5.3.1.24	Escherichia coli (strain 55989 / EAEC)
99115	320778	319150	TY-2482_chromosome	B7L495	Fused glutamine amidotransferase (Component II) of anthranilate synthase ; anthranilate phosphoribosyl transferase	Escherichia coli (strain 55989 / EAEC)
98114	322340	320781	TY-2482_chromosome	B7L496	Component I of anthranilate synthase (EC 4.1.3.27)	Escherichia coli (strain 55989 / EAEC)
62653	322614	323492	TY-2482_chromosome	B7L498	Putative uncharacterized protein yciV	Escherichia coli (strain 55989 / EAEC)
84359	323456	324109	TY-2482_chromosome	B5YZP6	Sua5/YciO/YrdC/YwlC family protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
87165	324186	325082	TY-2482_chromosome	B7L4A0	Pseudouridine synthase (EC 5.4.99.-)	Escherichia coli (strain 55989 / EAEC)
83995	325715	325128	TY-2482_chromosome	B7L4A1	Cob(I)alamin adenolsyltransferase/cobinamide ATP-dependent adenolsyltransferase (EC 2.5.1.-) (EC 2.5.1.17)	Escherichia coli (strain 55989 / EAEC)
111574	326470	325715	TY-2482_chromosome	B7L4A2	Putative oxoacyl-(Acyl carrier protein) reductase	Escherichia coli (strain 55989 / EAEC)
77487	326690	327736	TY-2482_chromosome	B7L4A4	Putative inner membrane peptidase	Escherichia coli (strain 55989 / EAEC)
95649	328026	327778	TY-2482_chromosome	B7L4A5	Putative uncharacterized protein yciN	Escherichia coli (strain 55989 / EAEC)
28027	328071	328280	TY-2482_chromosome	B7L4A6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
58043	328406	331048	TY-2482_chromosome	B7L4A7	DNA topoisomerase (EC 5.99.1.2)	Escherichia coli (strain 55989 / EAEC)
91975	331261	332232	TY-2482_chromosome	B7L4A8	DNA-binding transcriptional dual regulator, O-acetyl-L-serine-binding	Escherichia coli (strain 55989 / EAEC)
75480	332675	332860	TY-2482_chromosome	B7L4B0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
114110	333236	335908	TY-2482_chromosome	B7L4B2	Aconitate hydratase 1 (EC 4.2.1.3)	Escherichia coli (strain 55989 / EAEC)
33397	336565	335978	TY-2482_chromosome	B7L4B3	GTP cyclohydrolase-2 (EC 3.5.4.25) (GTP cyclohydrolase II)	Escherichia coli (strain 55989 / EAEC)
15357	336735	337600	TY-2482_chromosome	E6BMY3	Conserved domain protein	Escherichia coli MS 85-1
78879	337648	337953	TY-2482_chromosome	B7L4B5	Putative uncharacterized protein yciS	Escherichia coli (strain 55989 / EAEC)
84642	337963	339129	TY-2482_chromosome	B7L4B6	Putative uncharacterized protein yciM	Escherichia coli (strain 55989 / EAEC)
110464	339265	340059	TY-2482_chromosome	B5YZR3	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
89944	340062	340385	TY-2482_chromosome	B7L4B8	Putative uncharacterized protein yciH	Escherichia coli (strain 55989 / EAEC)
111728	340732	340517	TY-2482_chromosome	B7L4B9	Lipoprotein	Escherichia coli (strain 55989 / EAEC)
105492	341750	341004	TY-2482_chromosome	B7L4C0	DNA-binding transcriptional repressor, DeoR family	Escherichia coli (strain 55989 / EAEC)
108201	342055	341843	TY-2482_chromosome	B7L4C1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
109507	344145	342163	TY-2482_chromosome	B7L4C2	Modulator of Rnase II stability	Escherichia coli (strain 55989 / EAEC)
33605	346315	344384	TY-2482_chromosome	B7L4C3	Exoribonuclease 2 (EC 3.1.13.1) (Exoribonuclease II) (RNase II) (Ribonuclease II)	Escherichia coli (strain 55989 / EAEC)
76079	347510	346386	TY-2482_chromosome	B7L4C4	Putative amidase or amidotransferase	Escherichia coli (strain 55989 / EAEC)
69037	348443	347658	TY-2482_chromosome	B7L4C5	Enoyl-[acyl-carrier-protein] reductase, NADH-dependent (EC 1.3.1.9)	Escherichia coli (strain 55989 / EAEC)
59050	349166	348816	TY-2482_chromosome	B7L5A7	Putative uncharacterized protein ycjD	Escherichia coli (strain 55989 / EAEC)
90380	350040	349237	TY-2482_chromosome	B7L554	Antimicrobial peptide transporter subunit ; ATP-binding component of ABC superfamily transporte	Escherichia coli (strain 55989 / EAEC)
81039	351034	350045	TY-2482_chromosome	B7L555	Antimicrobial peptide transporter subunit; ATP-binding component of ABC superfamily transporte	Escherichia coli (strain 55989 / EAEC)
62791	351924	351037	TY-2482_chromosome	B7L556	Antimicrobial peptide transporter subunit ; permease component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
91928	352876	351914	TY-2482_chromosome	B7L557	Antimicrobial peptide transporter subunit ; permease component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
110409	354516	352876	TY-2482_chromosome	B7L558	Antimicrobial peptide transporter subunit; periplasmic-binding component of ABC superfamily transporte	Escherichia coli (strain 55989 / EAEC)
114069	355073	354831	TY-2482_chromosome	B7L559	Putative uncharacterized protein ymjA	Escherichia coli (strain 55989 / EAEC)
99147	356592	355210	TY-2482_chromosome	B7L560	Putrescine importer	Escherichia coli (strain 55989 / EAEC)
88419	358313	356898	TY-2482_chromosome	B7L561	Gamma-Glu-putrescine synthase	Escherichia coli (strain 55989 / EAEC)
60234	358513	359286	TY-2482_chromosome	D3H3K5	Gamma-glutamyl-gamma-aminobutyrate hydrolase (EC 3.5.1.-)	Escherichia coli O44:H18 (strain 042 / EAEC)
81049	359316	359870	TY-2482_chromosome	B7L563	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
99149	360148	361632	TY-2482_chromosome	B7L564	Gamma-Glu-gamma-aminobutyraldehyde dehydrogenase, NAD(P)H-dependent (EC 1.2.1.3)	Escherichia coli (strain 55989 / EAEC)

90224	361637	362914	TY-2482_chromosome	B7L565	Gamma-Glu-putrescine oxidase, FAD/NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
80936	362955	364217	TY-2482_chromosome	B7L566	GABA aminotransferase, PLP-dependent (EC 2.6.1.19)	Escherichia coli (strain 55989 / EAEC)
65763	365317	364343	TY-2482_chromosome	B7L567	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
72899	365484	366149	TY-2482_chromosome	B7L568	Regulatory protein for phage-shock-protein operon	Escherichia coli (strain 55989 / EAEC)
73841	366430	366786	TY-2482_chromosome	B7L570	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
29237	366482	366228	TY-2482_chromosome	Q8FHS4	Putative uncharacterized protein	Escherichia coli O6
73637	366798	367016	TY-2482_chromosome	B7L571	Peripheral inner membrane phage-shock protein	Escherichia coli (strain 55989 / EAEC)
76219	367094	367405	TY-2482_chromosome	B7L572	Thiosulfate:cyanide sulfurtransferase (Rhodanese) (EC 2.8.1.1)	Escherichia coli (strain 55989 / EAEC)
91777	367621	369297	TY-2482_chromosome	B7L573	Putative glucosyltransferase	Escherichia coli (strain 55989 / EAEC)
93939	369314	370603	TY-2482_chromosome	B7L574	Putative sugar transporter subunit: periplasmic-binding component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
96978	370627	371505	TY-2482_chromosome	B7L575	Putative sugar transporter subunit: permease component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
86623	371495	372334	TY-2482_chromosome	B7L576	Putative sugar transporter subunit: permease component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
62748	372368	373417	TY-2482_chromosome	B7L577	Putative oxidoreductase, Zn-dependent and NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
66392	373438	374223	TY-2482_chromosome	B7L578	Putative isomerase/epimerase	Escherichia coli (strain 55989 / EAEC)
88878	374236	375288	TY-2482_chromosome	C8TR14	Predicted oxidoreductase, NADH-binding	Escherichia coli O26:H11 (strain 11368 / EHEC)
77349	375288	377552	TY-2482_chromosome	B7L581	Putative glycosyl hydrolase/phosphorylase	Escherichia coli (strain 55989 / EAEC)
84466	377552	378208	TY-2482_chromosome	B7L582	Putative glucose-1-phosphate phosphodismutase, beta-phosphoglucomutase	Escherichia coli (strain 55989 / EAEC)
84484	378225	379304	TY-2482_chromosome	B7L583	Putative sugar transporter subunit: ATP-binding component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
115503	379352	380254	TY-2482_chromosome	B7L584	Outer membrane porin	Escherichia coli (strain 55989 / EAEC)
87709	381366	380371	TY-2482_chromosome	B7L585	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
107980	381521	382915	TY-2482_chromosome	B7L586	Putative uncharacterized protein ycjX	Escherichia coli (strain 55989 / EAEC)
34823	382915	383973	TY-2482_chromosome	B7L587	UPF0283 membrane protein ycjF	Escherichia coli (strain 55989 / EAEC)
72983	384124	385662	TY-2482_chromosome	B7L588	DNA-binding transcriptional dual regulator, tyrosine-binding	Escherichia coli (strain 55989 / EAEC)
102781	386215	385712	TY-2482_chromosome	B7L589	Lipid hydroperoxide peroxidase (EC 1.11.1.-)	Escherichia coli (strain 55989 / EAEC)
115661	386334	387296	TY-2482_chromosome	B7L590	L-Ala-D/L-Glu epimerase	Escherichia coli (strain 55989 / EAEC)
72202	388062	387277	TY-2482_chromosome	B7L591	Murein peptide amidase A	Escherichia coli (strain 55989 / EAEC)
62683	389270	388341	TY-2482_chromosome	B7L593	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
62684	389396	390292	TY-2482_chromosome	B7L594	Putative nucleic acid-binding regulator	Escherichia coli (strain 55989 / EAEC)
110592	390632	392242	TY-2482_chromosome	B7L595	Murein tripeptide (L-ala-gamma-D-glutamyl-meso-DAP) transporter subunit ; periplasmic-binding component of ABC	Escherichia coli (strain 55989 / EAEC)
64808	393327	392299	TY-2482_chromosome	B7L596	Putative uncharacterized protein ynaI	Escherichia coli (strain 55989 / EAEC)
72270	393571	393825	TY-2482_chromosome	B7L597	Putative uncharacterized protein ynaJ	Escherichia coli (strain 55989 / EAEC)
100984	394828	393881	TY-2482_chromosome	B7L598	Stress-induced protein	Escherichia coli (strain 55989 / EAEC)
79806	395732	394983	TY-2482_chromosome	B7L599	DNA-binding transcriptional dual regulator, global regulator of anaerobic growth	Escherichia coli (strain 55989 / EAEC)
91247	396442	395930	TY-2482_chromosome	B7L5A0	O-6-alkylguanine-DNA:cysteine-protein methyltransferase (EC 2.1.1.63)	Escherichia coli (strain 55989 / EAEC)
94279	397979	396456	TY-2482_chromosome	B7L5A1	Para-aminobenzoyl-glutamate transporter	Escherichia coli (strain 55989 / EAEC)
24352	398103	397912	TY-2482_chromosome	B7L5A2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
84568	399461	398019	TY-2482_chromosome	B7L5A3	Putative peptidase, aminobenzoyl-glutamate utilization protein	Escherichia coli (strain 55989 / EAEC)
80943	400771	399464	TY-2482_chromosome	B7L5A4	Putative peptidase, para-aminobenzoyl-glutamate utilization protein (EC 3.5.1.14)	Escherichia coli (strain 55989 / EAEC)
65713	400947	401852	TY-2482_chromosome	B7L5A5	DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
r112	402015	401858	TY-2482_chromosome	ref|NC_010473|:1493072-1493229|-| [gene=isrA] [locus_tag=ECDH10B_1460]		
108074	402185	402745	TY-2482_chromosome	B7L5A6	Putative uncharacterized protein ydaL	Escherichia coli (strain 55989 / EAEC)
87632	404001	402772	TY-2482_chromosome	B7L5A8	Putative diguanylate cyclase, GG[D/E]EF domain signalling protein	Escherichia coli (strain 55989 / EAEC)
35088	404256	405236	TY-2482_chromosome	B7L5A9	Zinc transport protein ZntB	Escherichia coli (strain 55989 / EAEC)
111888	405333	405548	TY-2482_chromosome	D3H4C2	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
91996	405705	405472	TY-2482_chromosome	C6UTJ2	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
69943	405717	407087	TY-2482_chromosome	B7L5B1	ATP-dependent RNA helicase, specific for 23S rRNA	Escherichia coli (strain 55989 / EAEC)
34376	408154	407222	TY-2482_chromosome	B7L5B2	tRNA 2-thiocytidine biosynthesis protein TtcA	Escherichia coli (strain 55989 / EAEC)
71306	408836	408333	TY-2482_chromosome	D3H4I5	Putative universal stress protein	Escherichia coli O44:H18 (strain 042 / EAEC)
95470	410038	408908	TY-2482_chromosome	B7L5B4	Outer membrane pore protein N, non-specific	Escherichia coli (strain 55989 / EAEC)
r193	410266	410374	TY-2482_chromosome	ref|NC_010473|:1525740-1525848|-| [gene=micC] [locus_tag=ECDH10B_1501]		
113463	413929	410408	TY-2482_chromosome	B7L5B5	Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)	Escherichia coli (strain 55989 / EAEC)
115890	414440	414003	TY-2482_chromosome	D3H4I8	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
104978	414888	414469	TY-2482_chromosome	B7L5B7	Heat-inducible protein	Escherichia coli (strain 55989 / EAEC)
91796	415988	415002	TY-2482_chromosome	B7L5B8	Fermentative D-lactate dehydrogenase, NAD-dependent (EC 1.1.1.28)	Escherichia coli (strain 55989 / EAEC)
106438	416196	418832	TY-2482_chromosome	B7L5B9	Putative uncharacterized protein ydbH	Escherichia coli (strain 55989 / EAEC)
95464	419025	419348	TY-2482_chromosome	B7L6A3	Putative uncharacterized protein ydbL	Escherichia coli (strain 55989 / EAEC)
101772	420428	419526	TY-2482_chromosome	B7L6A4	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
84467	420664	422160	TY-2482_chromosome	B7L6A5	Phenylacetaldehyde dehydrogenase (EC 1.2.1.39)	Escherichia coli (strain 55989 / EAEC)
60720	424494	422224	TY-2482_chromosome	B7L6A6	Primary amine oxidase	Escherichia coli (strain 55989 / EAEC)
108561	426787	424745	TY-2482_chromosome	B7L6A7	Fused aldehyde dehydrogenase ; enoyl-CoA hydratase	Escherichia coli (strain 55989 / EAEC)
75439	427072	427998	TY-2482_chromosome	B7L6A8	Putative multicomponent oxygenase/reductase subunit for phenylacetic acid degradation	Escherichia coli (strain 55989 / EAEC)
75288	428013	428297	TY-2482_chromosome	B7L6A9	Putative multicomponent oxygenase/reductase subunit for phenylacetic acid degradation	Escherichia coli (strain 55989 / EAEC)
69940	428309	429052	TY-2482_chromosome	B7L6B0	Putative multicomponent oxygenase/reductase subunit for phenylacetic acid degradation	Escherichia coli (strain 55989 / EAEC)
68638	429070	429564	TY-2482_chromosome	B7L6B1	Putative multicomponent oxygenase/reductase subunit for phenylacetic acid degradation	Escherichia coli (strain 55989 / EAEC)

115414	429575	430642	TY-2482_chromosome	B7L6B2	Subunit of the phenylacetly-CoA oxygenase/reductase	Escherichia coli (strain 55989 / EAEC)
88368	430642	431406	TY-2482_chromosome	B7L6B3	Enoyl-CoA hydratase-isomerase (EC 4.2.1.17)	Escherichia coli (strain 55989 / EAEC)
82453	431409	432194	TY-2482_chromosome	B7L6B4	Acyl-CoA hydratase (EC 4.2.1.17)	Escherichia coli (strain 55989 / EAEC)
108038	432199	433623	TY-2482_chromosome	B7L6B5	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	Escherichia coli (strain 55989 / EAEC)
88245	433616	434035	TY-2482_chromosome	B7L6B6	Phenylacetate pathway hotdog-fold thioesterase	Escherichia coli (strain 55989 / EAEC)
95465	434038	435240	TY-2482_chromosome	B7L6B7	Beta-ketoadipyl CoA thiolase	Escherichia coli (strain 55989 / EAEC)
66393	435270	436580	TY-2482_chromosome	B7L6B8	Phenylacetyl-CoA ligase (EC 6.2.1.30)	Escherichia coli (strain 55989 / EAEC)
114000	436684	437631	TY-2482_chromosome	B7L6B9	DNA-binding transcriptional repressor of phenylacetic acid degradation, aryl-CoA responsive	Escherichia coli (strain 55989 / EAEC)
116098	437616	438203	TY-2482_chromosome	B7L6C0	Putative hexapeptide repeat acetyltransferase	Escherichia coli (strain 55989 / EAEC)
64420	438436	439293	TY-2482_chromosome	B7L6C1	Putative aldo/keto reductase, NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
99053	439360	441663	TY-2482_chromosome	B7L6C2	Putative uncharacterized protein ydbD	Escherichia coli (strain 55989 / EAEC)
102777	441837	442439	TY-2482_chromosome	B7L6C3	Putative uncharacterized protein ynbA	Escherichia coli (strain 55989 / EAEC)
77350	442442	443335	TY-2482_chromosome	B7L6C4	Phosphatidate cytidylyltransferase (EC 2.7.7.41)	Escherichia coli (strain 55989 / EAEC)
66394	443354	445108	TY-2482_chromosome	B7L6C5	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
102778	445125	446414	TY-2482_chromosome	B7L6C6	Putative membrane associated phosphatase	Escherichia coli (strain 55989 / EAEC)
73638	447073	446471	TY-2482_chromosome	B7L6C7	NADH-azoreductase, FMN-dependent (EC 3.1.4.14)	Escherichia coli (strain 55989 / EAEC)
66237	447331	451173	TY-2482_chromosome	B7L6C8	ATP-dependent helicase	Escherichia coli (strain 55989 / EAEC)
104703	451448	452245	TY-2482_chromosome	B7L6C9	Putative uncharacterized protein ydcF	Escherichia coli (strain 55989 / EAEC)
99097	452445	453881	TY-2482_chromosome	B7L6D0	Aldehyde dehydrogenase A, NAD-linked (EC 1.2.1.22)	Escherichia coli (strain 55989 / EAEC)
99107	454927	453929	TY-2482_chromosome	B7L6D1	Glyceraldehyde-3-phosphate dehydrogenase C (EC 1.2.1.12)	Escherichia coli (strain 55989 / EAEC)
88246	455116	455643	TY-2482_chromosome	B7L6D2	Cytochrome b561	Escherichia coli (strain 55989 / EAEC)
26803	456130	456357	TY-2482_chromosome	Q0THZ6	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
99054	456684	458321	TY-2482_chromosome	B7L6D5	Methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor	Escherichia coli (strain 55989 / EAEC)
106433	459285	458365	TY-2482_chromosome	B7L6D6	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
104327	459502	460842	TY-2482_chromosome	B7L6D7	Putative uncharacterized protein ydcJ	Escherichia coli (strain 55989 / EAEC)
20509	461039	460845	TY-2482_chromosome	D7XGD6	Putative uncharacterized protein	Escherichia coli MS 84-1
69024	461100	462722	TY-2482_chromosome	B7L6D8	Glucans biosynthesis protein D	Escherichia coli (strain 55989 / EAEC)
69941	462849	462649	TY-2482_chromosome	B7L6D9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
82638	462865	463086	TY-2482_chromosome	B7L6E0	Putative uncharacterized protein ydcH	Escherichia coli (strain 55989 / EAEC)
59049	463137	463685	TY-2482_chromosome	B7L6E1	Ribosomal-protein-L7/L12-serine acetyltransferase (EC 2.3.1.-)	Escherichia coli (strain 55989 / EAEC)
69942	464663	463686	TY-2482_chromosome	B7L6E2	Putative enzyme	Escherichia coli (strain 55989 / EAEC)
87828	464787	465776	TY-2482_chromosome	B7L6E3	Potassium-tellurite ethidium and proflavin transporter	Escherichia coli (strain 55989 / EAEC)
65364	465776	466366	TY-2482_chromosome	B7L6E4	Putative AdoMet-dependent methyltransferase	Escherichia coli (strain 55989 / EAEC)
64157	466672	467337	TY-2482_chromosome	B7L6E5	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
19467	467844	467361	TY-2482_chromosome	B3IA33	Transposase, family	Escherichia coli E22
84526	467867	469072	TY-2482_chromosome	B7L6E8	Putative transposase	Escherichia coli (strain 55989 / EAEC)
91828	470290	469118	TY-2482_chromosome	B7L6E9	Putative benzoate transporter	Escherichia coli (strain 55989 / EAEC)
99083	470382	470915	TY-2482_chromosome	B7L6F0	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
80909	470991	472949	TY-2482_chromosome	B7L6F1	Putative peptidase (EC 3.4.-.-)	Escherichia coli (strain 55989 / EAEC)
68639	473274	473047	TY-2482_chromosome	B7L6F2	Putative uncharacterized protein yncJ	Escherichia coli (strain 55989 / EAEC)
16809	473456	473647	TY-2482_chromosome	D7XGF3	Putative uncharacterized protein	Escherichia coli MS 84-1
66244	473675	474109	TY-2482_chromosome	B7L6F3	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
62723	474191	475594	TY-2482_chromosome	B7L6F4	Putative DNA-binding transcriptional regulator fused with a domain with PLP-binding moti	Escherichia coli (strain 55989 / EAEC)
61388	475842	476984	TY-2482_chromosome	B7L6F5	Putative spermidine/putrescine transporter subunit ; periplasmic-binding component of ABC superfamily transporte	Escherichia coli (strain 55989 / EAEC)
95502	477005	478015	TY-2482_chromosome	B7L6F6	Putative spermidine/putrescine transporter subunit ; ATP-binding component of ABC superfamily tranporte	Escherichia coli (strain 55989 / EAEC)
80911	478019	478957	TY-2482_chromosome	B7L6F7	Putative spermidine/putrescine transporter subunit ; permease of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
90290	478950	479741	TY-2482_chromosome	B7L6F8	Putative spermidine/putrescine transporter subunit; permease component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
29648	479766	481187	TY-2482_chromosome	B7L6F9	Gamma-aminobutyraldehyde dehydrogenase (EC 1.2.1.19) (1-pyrroline dehydrogenase) (4-aminobutanal dehydroger	Escherichia coli (strain 55989 / EAEC)
62726	481400	482206	TY-2482_chromosome	B7L6G0	Putative acetyltransferase (EC 2.3.1.28)	Escherichia coli (strain 55989 / EAEC)
75883	482551	482739	TY-2482_chromosome	C8TRH0	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
73695	482826	483071	TY-2482_chromosome	B7L6G1	Putative uncharacterized protein ydcX	Escherichia coli (strain 55989 / EAEC)
66225	483160	483390	TY-2482_chromosome	B7L6G2	Putative uncharacterized protein ydcY	Escherichia coli (strain 55989 / EAEC)
106368	483843	483397	TY-2482_chromosome	B7L6G3	Putative uncharacterized protein ydcZ	Escherichia coli (strain 55989 / EAEC)
80945	484539	485573	TY-2482_chromosome	B7L6G5	Putative conserved oxidoreductase, Zn-dependent and NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
79242	484592	483843	TY-2482_chromosome	B7L6G4	Putative acyl-CoA N-acyltransferase	Escherichia coli (strain 55989 / EAEC)
71276	485717	486436	TY-2482_chromosome	D3GRI3	GntR-family transcriptional regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
84530	488577	486478	TY-2482_chromosome	B7L6G7	Putative iron outer membrane receptor	Escherichia coli (strain 55989 / EAEC)
75447	488819	489877	TY-2482_chromosome	B7L6G8	Putative uncharacterized protein yncE	Escherichia coli (strain 55989 / EAEC)
80946	491492	489996	TY-2482_chromosome	B7L6G9	L-asparagine transporter	Escherichia coli (strain 55989 / EAEC)
112507	491759	492373	TY-2482_chromosome	B7L6H0	Putative enzyme with similarity with GST	Escherichia coli (strain 55989 / EAEC)
103657	492452	492661	TY-2482_chromosome	C8UPQ0	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC)
80892	493448	495589	TY-2482_chromosome	B7L7F8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26953	495660	499898	TY-2482_chromosome	B7L7F9	RhsD element protein	Escherichia coli (strain 55989 / EAEC)
66353	499901	500359	TY-2482_chromosome	B7L7G0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)

105191	500623	501411	TY-2482_chromosome	C8UJN2	Putative H repeat-associated protein	Escherichia coli O111:H- (strain 11128 / EHEC
61323	502247	501681	TY-2482_chromosome	B7L7G3	Putative uncharacterized protein yddH	Escherichia coli (strain 55989 / EAEC)
79241	502420	503262	TY-2482_chromosome	B7L7G4	N-hydroxyarylamine O-acetyltransferase (EC 2.3.1.118)	Escherichia coli (strain 55989 / EAEC)
64296	504254	503364	TY-2482_chromosome	B7L7G5	Putative uncharacterized protein yddE	Escherichia coli (strain 55989 / EAEC)
113949	505013	504336	TY-2482_chromosome	B7L7G6	Nitrate reductase 2 (NRZ), gamma subunit (EC 1.7.99.4)	Escherichia coli (strain 55989 / EAEC)
83592	505705	505013	TY-2482_chromosome	B7L7G7	Nitrate reductase 2 (NRZ), delta subunit (Assembly subunit) (EC 1.7.99.4)	Escherichia coli (strain 55989 / EAEC)
65357	507249	505708	TY-2482_chromosome	B7L7G8	Nitrate reductase 2 (NRZ), beta subunit (EC 1.7.99.4)	Escherichia coli (strain 55989 / EAEC)
58434	510986	507249	TY-2482_chromosome	B7L7G9	Nitrate reductase 2 (NRZ), alpha subunit (EC 1.7.99.4)	Escherichia coli (strain 55989 / EAEC)
83810	512456	511071	TY-2482_chromosome	B7L7H0	Nitrate/nitrite transporter	Escherichia coli (strain 55989 / EAEC)
69972	514111	512783	TY-2482_chromosome	B7L7H1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
61736	514425	514138	TY-2482_chromosome	B7L7H2	Outer membrane porin	Escherichia coli (strain 55989 / EAEC)
103098	515565	514687	TY-2482_chromosome	C6UU60	Predicted methyl viologen efflux pump	Escherichia coli O157:H7 (strain TW14359 / EHEC
98323	515797	518841	TY-2482_chromosome	B7L7H4	Formate dehydrogenase-N, alpha subunit, nitrate-inducible (EC 1.2.1.2)	Escherichia coli (strain 55989 / EAEC)
106478	518857	519738	TY-2482_chromosome	B7L7H5	Formate dehydrogenase-N, Fe-S (Beta) subunit, nitrate-inducible	Escherichia coli (strain 55989 / EAEC)
83812	519734	520384	TY-2482_chromosome	B7L7H6	Formate dehydrogenase-N, cytochrome B556 (Gamma) subunit, nitrate-inducible	Escherichia coli (strain 55989 / EAEC)
83390	520800	520441	TY-2482_chromosome	B7L7H7	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
91826	521879	520872	TY-2482_chromosome	B7L7H8	Alcohol dehydrogenase, 1-propanol preferring (EC 1.1.1.1)	Escherichia coli (strain 55989 / EAEC)
32101	523710	522016	TY-2482_chromosome	B7L7H9	NAD-dependent malic enzyme (NAD-ME) (EC 1.1.1.38)	Escherichia coli (strain 55989 / EAEC)
110616	524321	524109	TY-2482_chromosome	B7L7I0	Biofilm-dependent modulation protein	Escherichia coli (strain 55989 / EAEC)
71531	524667	525095	TY-2482_chromosome	B7L7I1	Osmotically inducible, stress-inducible membrane protein	Escherichia coli (strain 55989 / EAEC)
80895	526080	525157	TY-2482_chromosome	B7L7I2	D-ala-D-ala transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
98310	527059	526076	TY-2482_chromosome	B7L7I3	D-ala-D-ala transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
83099	527952	527059	TY-2482_chromosome	B7L7I4	D-ala-D-ala transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
106480	528971	527952	TY-2482_chromosome	B7L7I5	D-ala-D-ala transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
87282	530523	528976	TY-2482_chromosome	B7L7I6	D-ala-D-a la transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
79856	531118	530540	TY-2482_chromosome	B7L7I7	D-ala-D-ala dipeptidase, Zn-dependent (EC 3.4.13.-)	Escherichia coli (strain 55989 / EAEC)
73689	533775	531379	TY-2482_chromosome	B7L7I8	cAMP phosphodiesterase, heme-regulated	Escherichia coli (strain 55989 / EAEC)
76787	535182	533803	TY-2482_chromosome	B7L7I9	Putative diguanylate cyclase YddV	Escherichia coli (strain 55989 / EAEC)
98358	536873	535557	TY-2482_chromosome	B7L7J0	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
65753	538539	537007	TY-2482_chromosome	B7L7J1	Glutamate:gamma-aminobutyric acid antiporter	Escherichia coli (strain 55989 / EAEC)
113951	540095	538698	TY-2482_chromosome	B7L7J2	Glutamate decarboxylase B, PLP-dependent (EC 4.1.1.15)	Escherichia coli (strain 55989 / EAEC)
86220	543252	540460	TY-2482_chromosome	B7L7J3	Putative membrane-associated peptidase	Escherichia coli (strain 55989 / EAEC)
108797	545669	543300	TY-2482_chromosome	B7L7J4	Putative porin protein	Escherichia coli (strain 55989 / EAEC)
110617	547392	545710	TY-2482_chromosome	B7L7J5	Putative multidrug transporter fused subunits of ABC superfamily transporter: permease component; ATP-binding co	Escherichia coli (strain 55989 / EAEC)
75441	548840	547686	TY-2482_chromosome	B7L7J6	Putative uncharacterized protein ydeM	Escherichia coli (strain 55989 / EAEC)
84531	550574	548895	TY-2482_chromosome	B7L7J7	Putative sulfatase (EC 3.1.6.-)	Escherichia coli (strain 55989 / EAEC)
88298	551737	550979	TY-2482_chromosome	B7L7J8	Putative DNA-binding transcriptional acfivator, AraC-type	Escherichia coli (strain 55989 / EAEC)
77380	554536	552260	TY-2482_chromosome	B7L7K0	Putative oxidoreductase; putative molybdoenzyme	Escherichia coli (strain 55989 / EAEC)
106491	555784	554873	TY-2482_chromosome	B7L7K1	Putative fimbrial-like exported adhesin protein	Escherichia coli (strain 55989 / EAEC)
105031	556346	555846	TY-2482_chromosome	B7L7K2	Putative fimbrial-like adhesin exported protein	Escherichia coli (strain 55989 / EAEC)
69973	556889	556362	TY-2482_chromosome	B7L7K3	Putative fimbrial-like adhesin exported protein	Escherichia coli (strain 55989 / EAEC)
110618	559554	556906	TY-2482_chromosome	B7L7K4	Putative fimbrial outer membrane usher protein	Escherichia coli (strain 55989 / EAEC)
91829	560315	559599	TY-2482_chromosome	B7L7K5	Periplasmic chaperone	Escherichia coli (strain 55989 / EAEC)
84571	561251	560643	TY-2482_chromosome	B7L7K6	Putative major fimbrial subunit FmlA	Escherichia coli (strain 55989 / EAEC)
17213	561777	561559	TY-2482_chromosome	D8EA13	Putative uncharacterized protein	Escherichia coli MS 119-7
19033	562145	561924	TY-2482_chromosome	D7ZRJ7	Conserved domain protein	Escherichia coli MS 187-1
80913	563478	562159	TY-2482_chromosome	B7L7K8	Regulator with hipB	Escherichia coli (strain 55989 / EAEC)
43911	563771	563481	TY-2482_chromosome	D7YRT1	Toxin-antitoxin system, antitoxin component, Xre family	Escherichia coli MS 182-1
99084	569374	563956	TY-2482_chromosome	B7L7L0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
68184	571497	569908	TY-2482_chromosome	B7L7L1	Autoinducer AI-2 kinase	Escherichia coli (strain 55989 / EAEC)
115404	572529	571579	TY-2482_chromosome	B7L7L2	DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
78800	572778	574310	TY-2482_chromosome	B7L7L3	Fused AI2 transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
112742	574307	575332	TY-2482_chromosome	B7L7L4	AI2 transporter ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
62127	575335	576324	TY-2482_chromosome	B7L7L5	AI2 transporter ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
61297	576339	577358	TY-2482_chromosome	B7L7L6	AI2 transporter ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
80954	577388	578260	TY-2482_chromosome	B7L7L7	Putative aldolase	Escherichia coli (strain 55989 / EAEC)
69974	578287	578574	TY-2482_chromosome	B7L7L8	Putative uncharacterized protein lsrG	Escherichia coli (strain 55989 / EAEC)
34196	578634	579389	TY-2482_chromosome	B7L7L9	Trans-aconitate 2-methyltransferase (EC 2.1.1.144)	Escherichia coli (strain 55989 / EAEC)
99035	580310	579399	TY-2482_chromosome	B7L7M0	Putative uncharacterized protein yneE	Escherichia coli (strain 55989 / EAEC)
34546	581968	580520	TY-2482_chromosome	B7L7M1	Altronate oxidoreductase (EC 1.1.1.58) (Tagaturonate dehydrogenase) (Tagaturonate reductase)	Escherichia coli (strain 55989 / EAEC)
18417	582277	582116	TY-2482_chromosome	E1HZE7	Diguanylate cyclase domain protein	Escherichia coli MS 78-1
59015	583613	582198	TY-2482_chromosome	B7L7M2	Putative membrane-associated diguanylate cyclase (GGDEF domain)	Escherichia coli (strain 55989 / EAEC)
70103	584111	583755	TY-2482_chromosome	B7L7M3	Putative uncharacterized protein yneG	Escherichia coli (strain 55989 / EAEC)
79327	585037	584114	TY-2482_chromosome	B7L7M4	Putative glutaminase	Escherichia coli (strain 55989 / EAEC)

68192	586489	585104	TY-2482_chromosome	B7L7M5	Putative aldehyde dehydrogenase	Escherichia coli (strain 55989 / EAEC)
101717	586590	587468	TY-2482_chromosome	B7L7M6	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
7874	587549	588659	TY-2482_chromosome	P76150	Uncharacterized protein yneK	Escherichia coli (strain K12)
33971	588812	589999	TY-2482_chromosome	B7L8K7	Probable sugar efflux transporter	Escherichia coli (strain 55989 / EAEC)
62758	590692	590030	TY-2482_chromosome	B7L8K8	Putative wide-spectrum exporter	Escherichia coli (strain 55989 / EAEC)
109704	590904	591335	TY-2482_chromosome	B7L8K9	DNA-binding transcriptional repressor of multiple antibiotic resistance	Escherichia coli (strain 55989 / EAEC)
72621	591358	591738	TY-2482_chromosome	B7L8L0	DNA-binding transcriptional dual activator of multiple antibiotic resistance	Escherichia coli (strain 55989 / EAEC)
91888	591773	591988	TY-2482_chromosome	B7L8L1	Putative uncharacterized protein marB	Escherichia coli (strain 55989 / EAEC)
87778	593493	592051	TY-2482_chromosome	B7L8L2	Putative 6-phospho-beta-glucosidase (EC 3.2.1.86)	Escherichia coli (strain 55989 / EAEC)
86865	595185	593515	TY-2482_chromosome	B7L8L3	Putative carbohydrate-specific outer membrane porin	Escherichia coli (strain 55989 / EAEC)
68709	595555	595244	TY-2482_chromosome	B7L8L4	Putative phosphotransferase system PTS, lactose/cellobiose-specific IIA subunit	Escherichia coli (strain 55989 / EAEC)
88383	596941	595583	TY-2482_chromosome	B7L8L5	Putative phosphotransferase system IIC component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
88385	597328	597020	TY-2482_chromosome	B7L8L6	Putative cellobiose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
83650	597527	598222	TY-2482_chromosome	B7L8L7	Putative DNA-binding transcriptional regulator HTH family	Escherichia coli (strain 55989 / EAEC)
101488	599169	598273	TY-2482_chromosome	B7L8L8	Cysteine and O-acetyl-L-serine efflux system	Escherichia coli (strain 55989 / EAEC)
62759	599364	600548	TY-2482_chromosome	B7L8L9	Putative transporter	Escherichia coli (strain 55989 / EAEC)
61543	601883	600996	TY-2482_chromosome	B7L8M0	Putative uncharacterized protein ydeH	Escherichia coli (strain 55989 / EAEC)
84579	602530	602141	TY-2482_chromosome	B7L8M1	Putative uncharacterized protein ydeI	Escherichia coli (strain 55989 / EAEC)
99134	602806	603321	TY-2482_chromosome	B7L8M2	Putative uncharacterized protein ydeJ	Escherichia coli (strain 55989 / EAEC)
96934	605414	603372	TY-2482_chromosome	B7L8M3	Dipeptidyl carboxypeptidase II (EC 3.4.15.5)	Escherichia coli (strain 55989 / EAEC)
71524	605536	606294	TY-2482_chromosome	D3GSH5	NADP-dependent L-serine/L-allo-threonine dehydrogenase (EC 1.1.1.-)	Escherichia coli O44:H18 (strain 042 / EAEC)
79891	606386	607069	TY-2482_chromosome	B7L8M5	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
28806	607480	607211	TY-2482_chromosome	A1ABC3	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
97574	608949	607492	TY-2482_chromosome	B7L8M7	Putative mannonate dehydrogenase	Escherichia coli (strain 55989 / EAEC)
95566	610321	609041	TY-2482_chromosome	B7L8M8	Putative transporter	Escherichia coli (strain 55989 / EAEC)
111960	611482	610466	TY-2482_chromosome	D3GTE7	Putative dehydrogenase (EC 1.1.1.-)	Escherichia coli O44:H18 (strain 042 / EAEC)
60468	612708	611497	TY-2482_chromosome	B7L5D3	Putative enolase/dehydratase	Escherichia coli (strain 55989 / EAEC)
115116	613249	612917	TY-2482_chromosome	D3GTE9	UPF0060 membrane protein ynfA	Escherichia coli O44:H18 (strain 042 / EAEC)
35032	613375	613713	TY-2482_chromosome	B7L5D5	UPF0482 protein ynfB	Escherichia coli (strain 55989 / EAEC)
96965	613751	614308	TY-2482_chromosome	B7L5D6	Spermidine N1-acetyltransferase (EC 2.3.1.57)	Escherichia coli (strain 55989 / EAEC)
90641	615060	614317	TY-2482_chromosome	B5Z420	Putative membrane protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
43502	615129	615434	TY-2482_chromosome	Q6EWW5	Putative uncharacterized protein Z2573	Escherichia coli
79771	615636	618059	TY-2482_chromosome	B7L5D9	Oxidoreductase subunit	Escherichia coli (strain 55989 / EAEC)
58036	618123	620543	TY-2482_chromosome	B7L5E0	Oxidoreductase subunit	Escherichia coli (strain 55989 / EAEC)
11969	621078	621710	TY-2482_chromosome	Q8KU25	AntB	Escherichia coli
75414	621761	621979	TY-2482_chromosome	C8UMM0	Predicted C4-type zinc finger protein	Escherichia coli O111:H- (strain 11128 / EHEC)
86803	621979	622260	TY-2482_chromosome	C8UML9	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
18615	622250	623083	TY-2482_chromosome	D7JRD8	Putative uncharacterized protein	Escherichia coli FVEC1302
87075	623061	623600	TY-2482_chromosome	C8TPV2	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
21023	623600	624100	TY-2482_chromosome	B3IP95	Valyl-tRNA synthetase	Escherichia coli E110019
114928	632855	624507	TY-2482_chromosome	C8UML1	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
108406	634189	632927	TY-2482_chromosome	C8UML0	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
24735	634451	634203	TY-2482_chromosome	B7MQ07	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
82723	634907	634464	TY-2482_chromosome	C8U7H7	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
104436	635566	634913	TY-2482_chromosome	C6UNY2	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
104991	636059	635661	TY-2482_chromosome	C8U7H9	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
77804	637228	636494	TY-2482_chromosome	C8U7I0	Probable outer membrane Lom	Escherichia coli O103:H2 (strain 12009 / EHEC)
27638	637934	637311	TY-2482_chromosome	B7MQ02	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
89997	638209	637934	TY-2482_chromosome	C8U7I2	Putative outer membrane protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
96492	639492	638227	TY-2482_chromosome	C8UMK2	Predicted tail tip fiber protein	Escherichia coli O111:H- (strain 11128 / EHEC)
110999	641192	639492	TY-2482_chromosome	C6UNY7	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
66843	644230	642326	TY-2482_chromosome	C8UMJ7	Predicted tail fiber protein	Escherichia coli O111:H- (strain 11128 / EHEC)
28509	644877	644230	TY-2482_chromosome	B7MPZ2	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
25278	645500	644880	TY-2482_chromosome	B7MPZ1	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
114405	645885	645427	TY-2482_chromosome	C8UMJ4	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
74425	646325	645939	TY-2482_chromosome	C8U7J1	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
111068	647594	646383	TY-2482_chromosome	C8U7J2	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
27093	648624	647620	TY-2482_chromosome	B7MPY7	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
113735	650926	648785	TY-2482_chromosome	B5YYP6	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
115153	652632	650929	TY-2482_chromosome	C8UMI9	Putative terminase large subunit	Escherichia coli O111:H- (strain 11128 / EHEC)
63362	653428	652616	TY-2482_chromosome	C8U7J6	Putative small subunit terminase	Escherichia coli O103:H2 (strain 12009 / EHEC)
11929	654031	654609	TY-2482_chromosome	Q07682	Transcriptional activator AfrS	Escherichia coli
9898	655151	654696	TY-2482_chromosome	B2N3J6	Bacteriophage lysis protein	Escherichia coli 53638
11418	656240	655490	TY-2482_chromosome	B6ZXG1	Lysozyme (EC 3.2.1.17)	Escherichia coli O157:H7 str. TW1458

64371	656724	656320	TY-2482_chromosome	C6USU0	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
28910	658849	656912	TY-2482_chromosome	B7MPX6	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
47546	658955	659266	TY-2482_chromosome	Q9FBI1	Putative uncharacterized protein	Shigella dysenteriae
90464	660019	659588	TY-2482_chromosome	C6UP10	Antitermination protein Q of bacteriophage BP-933W	Escherichia coli O157:H7 (strain TW14359 / EHEC
115410	660568	660209	TY-2482_chromosome	B7LBN5	Crossover junction endodeoxyribonuclease rusA (EC 3.1.22.4)	Escherichia coli (strain 55989 / EAEC)
70601	660855	660568	TY-2482_chromosome	C8UK75	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC
56695	661477	661070	TY-2482_chromosome	C8TKU1	Putative recombination protein	Escherichia coli O26:H11 (strain 11368 / EHEC
25757	662203	661535	TY-2482_chromosome	B7MPW6	Putative antirepressor protein Ant from prophage	Escherichia coli O81 (strain ED1a)
81620	662589	662914	TY-2482_chromosome	C8TS13	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC
105317	662910	663224	TY-2482_chromosome	C8TS14	Predicted DNA-binding protein	Escherichia coli O26:H11 (strain 11368 / EHEC
9718	663763	663281	TY-2482_chromosome	D6I789	Death on curing protein	Escherichia coli B185
57389	664383	664174	TY-2482_chromosome	Q8X288	Prophage maintenance protein (Putative Gef-like protein encoded by prophage CP-933N) (Putative cell killing protein	Escherichia coli O157:H7
115852	665436	664795	TY-2482_chromosome	C6UV05	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
104599	665828	665436	TY-2482_chromosome	C6USS4	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
96223	666614	665847	TY-2482_chromosome	C8U729	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC
26951	667380	666643	TY-2482_chromosome	B7MPV9	Putative DNA replication protein; Rac prophage	Escherichia coli O81 (strain ED1a)
24685	668469	667390	TY-2482_chromosome	B7MPV8	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
28390	668708	668493	TY-2482_chromosome	B7MPV7	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
27757	669019	668726	TY-2482_chromosome	B7MPV6	Regulatory protein CII from prophage	Escherichia coli O81 (strain ED1a)
71900	669358	669161	TY-2482_chromosome	C6UXV0	Regulatory protein cro	Escherichia coli O157:H7 (strain TW14359 / EHEC
4834	669459	670169	TY-2482_chromosome	P03034	Repressor protein CI	Enterobacteria phage lambda (Bacteriophage lambda)
29096	670219	670758	TY-2482_chromosome	B7MPV3	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
28389	670749	671522	TY-2482_chromosome	B7MPV2	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
100796	672020	672400	TY-2482_chromosome	C8U0Y9	Probable early gene regulator N	Escherichia coli O103:H2 (strain 12009 / EHEC
28731	672404	673117	TY-2482_chromosome	B7MPV0	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
28568	673131	673508	TY-2482_chromosome	B7MPU9	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
26950	673689	673483	TY-2482_chromosome	B7MPU8	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
114798	674146	674364	TY-2482_chromosome	C8TT57	Putative cell division inhibitor protein	Escherichia coli O26:H11 (strain 11368 / EHEC
24556	674451	674834	TY-2482_chromosome	B7MPU6	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
100591	674945	677014	TY-2482_chromosome	C8U8P7	Probable exonuclease	Escherichia coli O103:H2 (strain 12009 / EHEC
38271	677014	677307	TY-2482_chromosome	Q9LA40	Gam	Shigella dysenteriae
37295	677316	678098	TY-2482_chromosome	Q9LA41	Bet	Shigella dysenteriae
111968	678098	678775	TY-2482_chromosome	C6V295	Putative exonuclease encoded by prophage CP-933K	Escherichia coli O157:H7 (strain TW14359 / EHEC
94122	678826	679074	TY-2482_chromosome	C8TPU7	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC
63694	679339	680499	TY-2482_chromosome	C8U2L7	Predicted integrase	Escherichia coli O103:H2 (strain 12009 / EHEC
28489	680851	681942	TY-2482_chromosome	A1ABD5	Oxidoreductase, membrane subunit	Escherichia coli O1:K1 / APEC
64804	681988	682599	TY-2482_chromosome	B7L5E3	Twin-argninine leader-binding protein for DmsA and TorA	Escherichia coli (strain 55989 / EAEC)
30321	682797	684050	TY-2482_chromosome	B7L5E4	Voltage-gated ClC-type chloride channel ClcB	Escherichia coli (strain 55989 / EAEC)
95476	684701	684009	TY-2482_chromosome	B7L5E5	Dethiobiotin synthetase 2 (EC 6.3.3.3) (DTB synthetase 2) (Dethiobiotin synthase 2)	Escherichia coli (strain 55989 / EAEC)
60805	686046	684829	TY-2482_chromosome	B7L5E6	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
65655	687074	686184	TY-2482_chromosome	B7L5E7	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
65305	687181	688431	TY-2482_chromosome	B7L5E8	Putative transporter; MFS type	Escherichia coli (strain 55989 / EAEC)
83084	688831	689163	TY-2482_chromosome	B5Z433	Acid shock protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
65038	689442	690260	TY-2482_chromosome	B7L5F0	Putative exported metallopeptidase	Escherichia coli (strain 55989 / EAEC)
32222	690631	690305	TY-2482_chromosome	B7L5F1	Spermidine export protein mdtI	Escherichia coli (strain 55989 / EAEC)
32226	690983	690621	TY-2482_chromosome	B7L5F2	Spermidine export protein mdtJ	Escherichia coli (strain 55989 / EAEC)
113901	691395	692426	TY-2482_chromosome	B7L5F3	Putative uncharacterized protein ydgG	Escherichia coli (strain 55989 / EAEC)
73651	693842	692457	TY-2482_chromosome	B7L5F4	NAD(P) transhydrogenase subunit beta (EC 1.6.1.2) (Nicotinamide nucleotide transhydrogenase subunit beta)	Escherichia coli (strain 55989 / EAEC)
102782	695385	693856	TY-2482_chromosome	B7L5F5	Pyridine nucleotide transhydrogenase, alpha subunit (EC 1.6.1.2)	Escherichia coli (strain 55989 / EAEC)
68116	695909	696850	TY-2482_chromosome	B7L5F6	Putative uncharacterized protein ydgH	Escherichia coli (strain 55989 / EAEC)
110595	697039	698418	TY-2482_chromosome	B7L5F7	Putative arginine/ornithine antiporter transporter	Escherichia coli (strain 55989 / EAEC)
106446	698458	699177	TY-2482_chromosome	B7L5F8	Dihydrofolate reductase isozyme (EC 1.5.1.3)	Escherichia coli (strain 55989 / EAEC)
72282	699512	699180	TY-2482_chromosome	B7L5F9	Putative uncharacterized protein ydgC	Escherichia coli (strain 55989 / EAEC)
87910	699605	700357	TY-2482_chromosome	D3GTJ4	Two-component response regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
66395	700364	701662	TY-2482_chromosome	B7L5G1	Sensory histidine kinase in two-component regulatory system with RstA	Escherichia coli (strain 55989 / EAEC)
34397	701741	702667	TY-2482_chromosome	B7L5G2	DNA replication terminus site-binding protein (Ter-binding protein)	Escherichia coli (strain 55989 / EAEC)
84498	704070	702670	TY-2482_chromosome	B7L5G3	Fumarate hydratase (Fumarase C),aerobic Class II (EC 4.2.1.2)	Escherichia coli (strain 55989 / EAEC)
113997	705859	704216	TY-2482_chromosome	B7L5G4	Fumarate hydratase (Fumarase A), aerobic Class I (EC 4.2.1.2)	Escherichia coli (strain 55989 / EAEC)
58582	706058	707230	TY-2482_chromosome	B7L5G5	Mannose-6-phosphate isomerase (EC 5.3.1.8)	Escherichia coli (strain 55989 / EAEC)
77353	707334	708839	TY-2482_chromosome	B7L5G6	Putative uncharacterized protein ydgA	Escherichia coli (strain 55989 / EAEC)
99063	710152	708890	TY-2482_chromosome	B7L5G7	Outer membrane porin protein for glucuronides transport	Escherichia coli (strain 55989 / EAEC)
62686	711564	710194	TY-2482_chromosome	B7L5G8	Glucuronide transporter	Escherichia coli (strain 55989 / EAEC)
59051	713372	711564	TY-2482_chromosome	B7L5G9	Beta-D-glucuronidase (EC 3.2.1.31)	Escherichia coli (strain 55989 / EAEC)
99064	714351	713764	TY-2482_chromosome	B7L5H0	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)

110558	715347	714583	TY-2482_chromosome	B7L5H1	7-alpha-hydroxysteroid dehydrogenase, NAD-dependent (EC 1.1.1.159)	Escherichia coli (strain 55989 / EAEC)
58396	716487	715462	TY-2482_chromosome	B7L5H2	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
110008	716662	718251	TY-2482_chromosome	B7L5H3	Fused maltose and glucose-specific PTS enzymes: IIB and IIC components (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
75759	718264	719433	TY-2482_chromosome	B7L5H4	Bifunctional beta-cystathionase, PLP-dependent and regulator of maltose regulon (EC 4.4.1.8)	Escherichia coli (strain 55989 / EAEC)
29715	719540	720538	TY-2482_chromosome	B7L5H5	Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	Escherichia coli (strain 55989 / EAEC)
77355	721616	720579	TY-2482_chromosome	B7L5H6	Putative oxidoreductase	Escherichia coli (strain 55989 / EAEC)
97659	721784	721981	TY-2482_chromosome	B7L5H7	Beta-lactam resistance membrane protein	Escherichia coli (strain 55989 / EAEC)
18118	722073	722333	TY-2482_chromosome	D6JA38	Predicted protein	Escherichia coli B354
83174	722257	722469	TY-2482_chromosome	B7L5H8	Post-transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
113893	722558	722995	TY-2482_chromosome	B7L5H9	Putative uncharacterized protein ydgK	Escherichia coli (strain 55989 / EAEC)
33617	723075	723653	TY-2482_chromosome	B7L5I0	Electron transport complex protein rnfA	Escherichia coli (strain 55989 / EAEC)
33621	723656	724231	TY-2482_chromosome	B7L5I1	Electron transport complex protein rnfB	Escherichia coli (strain 55989 / EAEC)
33625	724227	726446	TY-2482_chromosome	B7L5I2	Electron transport complex protein rnfC	Escherichia coli (strain 55989 / EAEC)
33627	726450	727505	TY-2482_chromosome	B7L5I3	Electron transport complex protein rnfD	Escherichia coli (strain 55989 / EAEC)
91800	727512	728129	TY-2482_chromosome	B7L5I4	Putative oxidoreductase	Escherichia coli (strain 55989 / EAEC)
27834	729130	728423	TY-2482_chromosome	A7ZM93	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
96775	729594	729791	TY-2482_chromosome	D3GUC8	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
76688	730077	731576	TY-2482_chromosome	B7L5I7	Dipeptide and tripeptide permease A	Escherichia coli (strain 55989 / EAEC)
97175	731685	732287	TY-2482_chromosome	B7L5I8	Glutathionine S-transferase (EC 2.5.1.18)	Escherichia coli (strain 55989 / EAEC)
69396	733197	732337	TY-2482_chromosome	B7L5I9	Pyridoxal kinase 2/pyridoxine kinase (EC 2.7.1.35)	Escherichia coli (strain 55989 / EAEC)
34184	734530	733259	TY-2482_chromosome	B7L5J0	Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosine--tRNA ligase) (TyrRS)	Escherichia coli (strain 55989 / EAEC)
32908	735315	734662	TY-2482_chromosome	B7L5J1	Pyridoxine/pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PNP/PMP oxidase) (PNPOx) (Pyridoxal 5'-phosphate synt	Escherichia coli (strain 55989 / EAEC)
66398	735703	735377	TY-2482_chromosome	B7L5J2	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
29780	736910	735804	TY-2482_chromosome	B7L5J3	Anhydro-N-acetylmuramic acid kinase (EC 2.7.1.n1) (AnhMurNAc kinase)	Escherichia coli (strain 55989 / EAEC)
18766	737184	737896	TY-2482_chromosome	E7URP8	Outer membrane lipoprotein pcp	Escherichia coli EC4100B
69949	738333	738566	TY-2482_chromosome	B7L5J6	Putative uncharacterized protein ydhI	Escherichia coli (strain 55989 / EAEC)
65775	738572	739426	TY-2482_chromosome	B7L5J7	Undecaprenyl pyrophosphate phosphatase	Escherichia coli (strain 55989 / EAEC)
93932	739429	741438	TY-2482_chromosome	B7L5J8	Putative uncharacterized protein ydhK	Escherichia coli (strain 55989 / EAEC)
69950	741963	741445	TY-2482_chromosome	B7L5J9	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)	Escherichia coli (strain 55989 / EAEC)
80879	742940	742047	TY-2482_chromosome	B7L5K0	Putative oxidoreductase	Escherichia coli (strain 55989 / EAEC)
113360	743331	743927	TY-2482_chromosome	C8UB70	Predicted DNA-binding transcriptional regulator	Escherichia coli O111:H- (strain 11128 / EHEC)
86062	743399	742992	TY-2482_chromosome	B7L5K1	Putative uncharacterized protein ydhL	Escherichia coli (strain 55989 / EAEC)
79401	743967	745061	TY-2482_chromosome	B7L5K3	N-ethylmaleimide reductase, FMN-linked (EC 1.-.-.-)	Escherichia coli (strain 55989 / EAEC)
110013	745145	745549	TY-2482_chromosome	B7L5K4	Glyoxalase I, Ni-dependent (EC 4.4.1.5)	Escherichia coli (strain 55989 / EAEC)
79174	745655	746299	TY-2482_chromosome	B7L5K5	Ribonuclease T (EC 3.1.13.-) (Exoribonuclease T)	Escherichia coli (strain 55989 / EAEC)
110596	746395	751008	TY-2482_chromosome	B7L5K6	Putative ATP-dependent helicase	Escherichia coli (strain 55989 / EAEC)
62628	751409	751065	TY-2482_chromosome	B7L5K7	Glutaredoxin	Escherichia coli (strain 55989 / EAEC)
77357	751743	752555	TY-2482_chromosome	B7L5K8	Putative exported hydrolase	Escherichia coli (strain 55989 / EAEC)
97066	752686	753264	TY-2482_chromosome	B7L5K9	Superoxide dismutase (EC 1.15.1.1)	Escherichia coli (strain 55989 / EAEC)
69143	754582	753416	TY-2482_chromosome	B7L5L0	Putative efflux protein; MFS family	Escherichia coli (strain 55989 / EAEC)
19029	754924	755145	TY-2482_chromosome	D6JAZ2	Predicted protein	Escherichia coli B354
33159	755136	756158	TY-2482_chromosome	B7L5L1	HTH-type transcriptional repressor purR (Pur regulon repressor) (Purine nucleotide synthesis repressor	Escherichia coli (strain 55989 / EAEC)
76155	757090	756161	TY-2482_chromosome	B7L5L2	Putative DNA-binding transcriptional regulator; LysR-type	Escherichia coli (strain 55989 / EAEC)
72955	757203	758411	TY-2482_chromosome	B7L5L3	Putative transporter; MFS superfamily	Escherichia coli (strain 55989 / EAEC)
60719	758705	759850	TY-2482_chromosome	B7L5L4	Cyclopropane fatty acyl phospholipid synthase (Unsaturated-phospholipid methyltransferase) (EC 2.1.1.79)	Escherichia coli (strain 55989 / EAEC)
73078	760534	759896	TY-2482_chromosome	B7L5L5	Riboflavin synthase, alpha subunit (EC 2.5.1.9)	Escherichia coli (strain 55989 / EAEC)
32230	760749	762119	TY-2482_chromosome	B7L5L6	Multidrug resistance protein mdtK (Multidrug-efflux transporter)	Escherichia coli (strain 55989 / EAEC)
105236	763419	762166	TY-2482_chromosome	B7L5L7	Putative uncharacterized protein ydhQ	Escherichia coli (strain 55989 / EAEC)
r290	763727	763803	TY-2482_chromosome	ref|NC_010473|:1835030-1835106|Val tRNA| [gene=valV] [locus_tag=ECDH10B_1799]		
r288	763808	763884	TY-2482_chromosome	ref|NC_010473|:1835111-1835187|Val tRNA| [gene=valW] [locus_tag=ECDH10B_1800]		
27254	763840	764265	TY-2482_chromosome	Q1RBD0	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
59000	764423	766024	TY-2482_chromosome	B7L5L9	Putative uncharacterized protein ydhS	Escherichia coli (strain 55989 / EAEC)
78947	766851	766042	TY-2482_chromosome	B7L5M0	Putative uncharacterized protein ydhT	Escherichia coli (strain 55989 / EAEC)
114152	767640	766858	TY-2482_chromosome	B7L5M1	Putative cytochrome b subunit of a reductase	Escherichia coli (strain 55989 / EAEC)
22209	769016	767640	TY-2482_chromosome	E6AKY5	4Fe-4S binding domain protein	Escherichia coli MS 16-3
93664	771122	769023	TY-2482_chromosome	B7L5M5	Putative ferredoxin:oxidoreductase subunit	Escherichia coli (strain 55989 / EAEC)
105041	771769	771146	TY-2482_chromosome	B7L5M6	Putative 4Fe-4S ferridoxin-type subunit of oxidoreductase	Escherichia coli (strain 55989 / EAEC)
86356	772434	772228	TY-2482_chromosome	B7L5M7	Putative uncharacterized protein ydhZ	Escherichia coli (strain 55989 / EAEC)
65256	772991	774400	TY-2482_chromosome	B7L5M8	Pyruvate kinase (EC 2.7.1.40)	Escherichia coli (strain 55989 / EAEC)
105042	774714	774947	TY-2482_chromosome	B7L5M9	Murein lipoprotein	Escherichia coli (strain 55989 / EAEC)
98995	776018	775017	TY-2482_chromosome	B7L5N0	Putative uncharacterized protein ynhG	Escherichia coli (strain 55989 / EAEC)
34054	776583	776170	TY-2482_chromosome	B7L5N1	Cysteine desulfuration protein sufE	Escherichia coli (strain 55989 / EAEC)
34060	777816	776599	TY-2482_chromosome	B7L5N2	Cysteine desulfurase (EC 2.8.1.7) (Selenocysteine beta-lyase) (SCL) (Selenocysteine lyase) (EC 4.4.1.16) (Selenocystein	Escherichia coli (strain 55989 / EAEC)
59001	779084	777816	TY-2482_chromosome	B7L5N3	Component of SufBCD complex	Escherichia coli (strain 55989 / EAEC)

106356	779805	779062	TY-2482_chromosome	B7L5N4	Component of SufBCD complex, ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
91007	781302	779818	TY-2482_chromosome	B7L5N5	Component of SufBCD complex	Escherichia coli (strain 55989 / EAEC)
101838	781679	781314	TY-2482_chromosome	B7L5N6	Fe-S cluster assembly protein	Escherichia coli (strain 55989 / EAEC)
r507	782073	782006	TY-2482_chromosome	ref|NC_010473|:1853308-1853375|-| [gene=rydB] [locus_tag=ECDH10B_1819		
61885	782926	782519	TY-2482_chromosome	B7L5N8	Putative esterase (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
64822	785979	782926	TY-2482_chromosome	B7L5N9	Putative conserved FAD-linked oxidoreductase	Escherichia coli (strain 55989 / EAEC)
68713	786368	787477	TY-2482_chromosome	B7L5P0	Putative uncharacterized protein ydiK	Escherichia coli (strain 55989 / EAEC)
r195	787666	787770	TY-2482_chromosome	ref|NC_010473|:1858967-1859071|-| [gene=rprA] [locus_tag=ECDH10B_1824		
85818	787882	788262	TY-2482_chromosome	D3GUI0	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
91769	788365	789576	TY-2482_chromosome	B7L5P2	Putative transporter; MFS superfamily	Escherichia coli (strain 55989 / EAEC)
99000	789806	791068	TY-2482_chromosome	B7L5P3	Putative transporter	Escherichia coli (strain 55989 / EAEC)
34834	791083	791946	TY-2482_chromosome	B7L5P4	Quinate/shikimate dehydrogenase (EC 1.1.1.282) (NAD-dependent shikimate 5-dehydrogenase 2)	Escherichia coli (strain 55989 / EAEC)
29904	791980	792735	TY-2482_chromosome	B7L5P5	3-dehydroquinate dehydratase (3-dehydroquinase) (EC 4.2.1.10) (Type I DHQase)	Escherichia coli (strain 55989 / EAEC)
94818	792882	794474	TY-2482_chromosome	B7L5P6	Short chain acyl-CoA transferase: fused alpha subunit ; beta subunit	Escherichia coli (strain 55989 / EAEC)
71650	794491	795639	TY-2482_chromosome	B7L5P7	Putative acyl-CoA dehydrogenase	Escherichia coli (strain 55989 / EAEC)
80381	796596	795688	TY-2482_chromosome	B7L5P8	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
115792	796813	797673	TY-2482_chromosome	D3GUI8	Putative electron transfer flavoprotein beta subunit	Escherichia coli O44:H18 (strain 042 / EAEC)
111474	797696	798631	TY-2482_chromosome	B7L6H1	Putative electron transfer flavoprotein subunit, FAD-binding	Escherichia coli (strain 55989 / EAEC)
106486	798690	799976	TY-2482_chromosome	B7L6H2	Putative oxidoreductase subunit with FAD/NAD(P)-binding domain	Escherichia coli (strain 55989 / EAEC)
77378	799976	800266	TY-2482_chromosome	B7L6H3	Putative 4Fe-4S ferredoxin-type oxidoreductase subunit	Escherichia coli (strain 55989 / EAEC)
69904	800272	801969	TY-2482_chromosome	B7L6H4	Short chain acyl-CoA synthetase, anaerobic	Escherichia coli (strain 55989 / EAEC)
109629	804407	802032	TY-2482_chromosome	B7L6H5	Phosphoenolpyruvate synthase (EC 2.7.9.2)	Escherichia coli (strain 55989 / EAEC)
34831	804740	805570	TY-2482_chromosome	B7L6H6	Putative phosphotransferase ydiA (EC 2.7.-.-)	Escherichia coli (strain 55989 / EAEC)
95518	805730	806773	TY-2482_chromosome	B7L6H7	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate syntha	Escherichia coli (strain 55989 / EAEC)
73436	806881	807096	TY-2482_chromosome	B5YPZ3	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
34836	808539	807106	TY-2482_chromosome	B7L6H9	UPF0061 protein ydiU	Escherichia coli (strain 55989 / EAEC)
71942	809315	808605	TY-2482_chromosome	B7L6I0	Putative uncharacterized protein ydiV	Escherichia coli (strain 55989 / EAEC)
106489	810026	809565	TY-2482_chromosome	B7L6I1	Putative peptidase lipoprotein	Escherichia coli (strain 55989 / EAEC)
30173	810853	810107	TY-2482_chromosome	B7L6I2	Vitamin B12 import ATP-binding protein BtuD (EC 3.6.3.33) (Vitamin B12-transporting ATPase	Escherichia coli (strain 55989 / EAEC)
102809	811404	810856	TY-2482_chromosome	B7L6I3	Glutathione peroxidase	Escherichia coli (strain 55989 / EAEC)
30164	812447	811470	TY-2482_chromosome	B7L6I4	Vitamin B12 import system permease protein BtuC	Escherichia coli (strain 55989 / EAEC)
28093	813032	812640	TY-2482_chromosome	D3QUK6	Putative uncharacterized protein	Escherichia coli O55:H7 (strain CB9615 / EPEC)
28352	814167	813046	TY-2482_chromosome	B2U362	Integrase	Shigella boydii serotype 18 (strain CDC 3083-94 / BS512)
103479	814378	814070	TY-2482_chromosome	C8TSI7	Putative repressor protein C	Escherichia coli O26:H11 (strain 11368 / EHEC)
96932	814470	814745	TY-2482_chromosome	C8U9T4	Predicted DNA-binding protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
28723	814763	815098	TY-2482_chromosome	B7US54	Predicted protein	Escherichia coli O127:H6 (strain E2348/69 / EPEC)
28724	815052	815396	TY-2482_chromosome	B7L7W7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
103480	815411	815650	TY-2482_chromosome	C8TSJ1	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
24619	816162	816362	TY-2482_chromosome	D2TSK5	Hypothetical prophage protein	Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4
91787	816305	816604	TY-2482_chromosome	B7L7X0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
106231	816604	816900	TY-2482_chromosome	B5YRR7	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
9681	816915	817529	TY-2482_chromosome	B3Y106	Predicted protein	Escherichia coli O111:H-
101065	817529	817915	TY-2482_chromosome	C8TTF9	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
75545	818005	820752	TY-2482_chromosome	B7L7X2	Putative phage replication protein	Escherichia coli (strain 55989 / EAEC)
116075	820832	821788	TY-2482_chromosome	B7L7X3	Plasmid segregation protein parM (Protein stbA) (ParA locus 36 kDa protein)	Escherichia coli (strain 55989 / EAEC)
27641	821796	822107	TY-2482_chromosome	B7L7X4	Putative stability/partitioning protein phage encoded (Putative plasmid partition protein) (Modular protein	Escherichia coli (strain 55989 / EAEC)
28371	822130	822558	TY-2482_chromosome	B7L7X5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
84441	822542	822823	TY-2482_chromosome	B7L7X6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
27139	823235	822852	TY-2482_chromosome	B7L7X7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73603	824384	823341	TY-2482_chromosome	B7L7X8	Portal capsid protein Q (GpQ)	Escherichia coli (strain 55989 / EAEC)
70107	826135	824387	TY-2482_chromosome	B7L7X9	Terminase, ATPase subunit (GpP)	Escherichia coli (strain 55989 / EAEC)
28019	826257	827123	TY-2482_chromosome	B7L7Y0	Capsid scaffolding protein O	Escherichia coli (strain 55989 / EAEC)
94311	827150	828199	TY-2482_chromosome	B7L7Y2	Major capsid protein (GpN)	Escherichia coli (strain 55989 / EAEC)
115199	828248	829045	TY-2482_chromosome	C8TSK3	Putative terminase small subunit	Escherichia coli O26:H11 (strain 11368 / EHEC)
112395	829150	829641	TY-2482_chromosome	C8TSK4	Putative capsid completion protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
29536	829628	830167	TY-2482_chromosome	B7L7Y5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
24669	830412	830960	TY-2482_chromosome	B7L7Y8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25009	831102	832979	TY-2482_chromosome	B7L7Y9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
78251	833457	834098	TY-2482_chromosome	C8UBF1	Predicted tail completion protein	Escherichia coli O111:H- (strain 11128 / EHEC
59606	834098	834676	TY-2482_chromosome	C8TTH7	Putative baseplate assembly protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
64803	834676	835023	TY-2482_chromosome	B7L7Z3	Baseplate assembly protein W	Escherichia coli (strain 55989 / EAEC)
68751	835030	835923	TY-2482_chromosome	C8TTH9	Putative baseplate assembly protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
69408	835919	836446	TY-2482_chromosome	C8UBF5	Putative phage tail protein	Escherichia coli O111:H- (strain 11128 / EHEC
82394	836452	838581	TY-2482_chromosome	C8TTI1	Probable side tail fiber protein	Escherichia coli O26:H11 (strain 11368 / EHEC)

101496	838584	839159	TY-2482_chromosome	C8UR26	Putative tail fiber assembly protein	Escherichia coli O111:H- (strain 11128 / EHEC
18343	839811	839209	TY-2482_chromosome	E7HLF3	Bacterial transferase hexapeptide family protein	Escherichia coli EPECa14
60807	840429	839938	TY-2482_chromosome	B7L7Z9	Putative tail fiber protein	Escherichia coli (strain 55989 / EAEC)
61887	843252	840439	TY-2482_chromosome	B7L800	Putative tail protein (Modular protein)	Escherichia coli (strain 55989 / EAEC)
86279	843466	843233	TY-2482_chromosome	C8TSM0	Putative tail protein	Escherichia coli O26:H11 (strain 11368 / EHEC
100155	843759	843397	TY-2482_chromosome	C8U9X1	Putative tail protein	Escherichia coli O103:H2 (strain 12009 / EHEC
59829	844326	843817	TY-2482_chromosome	C8UBG3	Putative tail tube protein	Escherichia coli O111:H- (strain 11128 / EHEC
107862	845510	844329	TY-2482_chromosome	B7L804	Major tail sheath protein FI	Escherichia coli (strain 55989 / EAEC)
26265	845536	846774	TY-2482_chromosome	B7L805	Gene late control D protein	Escherichia coli (strain 55989 / EAEC)
2662	848293	849273	TY-2482_chromosome	P0CE57	Transposase insH for insertion sequence element IS5R	Escherichia coli (strain K12)
93414	849470	849727	TY-2482_chromosome	C8U9X6	Predicted regulatory protein	Escherichia coli O103:H2 (strain 12009 / EHEC
27253	849989	849730	TY-2482_chromosome	Q1RE18	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
31599	850662	850366	TY-2482_chromosome	B7L6I5	Integration host factor subunit alpha (IHF-alpha)	Escherichia coli (strain 55989 / EAEC)
113960	853054	850670	TY-2482_chromosome	B7L6I6	Phenylalanine tRNA synthetase, beta subunit (EC 6.1.1.20)	Escherichia coli (strain 55989 / EAEC)
34101	854052	853072	TY-2482_chromosome	B7L6I7	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase alpha chain) (PheRS)	Escherichia coli (strain 55989 / EAEC)
33492	854858	854505	TY-2482_chromosome	B7L6I9	50S ribosomal protein L20	Escherichia coli (strain 55989 / EAEC)
25514	854980	855588	TY-2482_chromosome	A1ABQ1	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
34175	857679	855754	TY-2482_chromosome	B7L6J2	Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase) (ThrRS)	Escherichia coli (strain 55989 / EAEC)
110179	858203	860098	TY-2482_chromosome	Q8XE25	Putative uncharacterized protein	Escherichia coli O157:H7
73696	861195	860440	TY-2482_chromosome	B7L6J5	Putative uncharacterized protein ydiY	Escherichia coli (strain 55989 / EAEC)
110583	861482	862408	TY-2482_chromosome	B7L6J6	6-phosphofructokinase II (EC 2.7.1.11)	Escherichia coli (strain 55989 / EAEC)
26007	862817	862443	TY-2482_chromosome	Q1RB71	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
91865	862908	863765	TY-2482_chromosome	B7L6J8	Putative phosphotransferase/kinase	Escherichia coli (strain 55989 / EAEC)
90297	864345	863812	TY-2482_chromosome	B7L6J9	Putative uncharacterized protein yniB	Escherichia coli (strain 55989 / EAEC)
66226	864492	865157	TY-2482_chromosome	B7L6K0	Putative phosphoglycolate phosphatase	Escherichia coli (strain 55989 / EAEC)
82315	865311	865910	TY-2482_chromosome	D3GVE1	Putative membrane-bound metal-dependent hydrolase	Escherichia coli O44:H18 (strain 042 / EAEC)
100912	866046	867434	TY-2482_chromosome	B7L6K2	Putative cation-acid symporter	Escherichia coli (strain 55989 / EAEC)
17952	867668	867444	TY-2482_chromosome	D8E437	Conserved domain protein	Escherichia coli MS 119-7
2663	867700	868680	TY-2482_chromosome	P0CE57	Transposase insH for insertion sequence element IS5R	Escherichia coli (strain K12)
70410	869455	868724	TY-2482_chromosome	C6UW71	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
98983	869995	869735	TY-2482_chromosome	B7L6K5	Cell division activator CedA	Escherichia coli (strain 55989 / EAEC)
81109	870178	872436	TY-2482_chromosome	B7L6K6	Catalase (EC 1.11.1.6)	Escherichia coli (strain 55989 / EAEC)
30291	873244	872489	TY-2482_chromosome	B7L6K7	UPF0249 protein ChbG	Escherichia coli (strain 55989 / EAEC)
73824	874609	873260	TY-2482_chromosome	B7L6K8	Cryptic phospho-beta-glucosidase, NAD(P)-binding (EC 3.2.1.86)	Escherichia coli (strain 55989 / EAEC)
77515	875556	874717	TY-2482_chromosome	B7L6K9	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
88482	875914	875567	TY-2482_chromosome	B7L6L0	N,N'-diacetylchitobiose-specific enzyme IIA component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
106343	877323	875968	TY-2482_chromosome	B7L6L1	N,N'-diacetylchitobiose-specific enzyme IIC component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
77516	877728	877411	TY-2482_chromosome	B7L6L2	N,N'-diacetylchitobiose-specific enzyme IIB component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
24991	878009	877752	TY-2482_chromosome	Q1RB56	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
82451	878365	878030	TY-2482_chromosome	B7L6L3	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
32595	878567	879391	TY-2482_chromosome	B7L6L4	NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Escherichia coli (strain 55989 / EAEC)
95376	879624	880508	TY-2482_chromosome	B7L6L5	Endonuclease of nucleotide excision repair (EC 3.1.25.-)	Escherichia coli (strain 55989 / EAEC)
20446	879702	879481	TY-2482_chromosome	D8AB29	Putative uncharacterized protein	Escherichia coli MS 21-1
101588	881109	880474	TY-2482_chromosome	D3GVF5	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
64178	881734	881252	TY-2482_chromosome	B7L6L7	Envelope stress induced periplasmic protein	Escherichia coli (strain 55989 / EAEC)
30013	883032	882067	TY-2482_chromosome	B7L6L8	Succinylglutamate desuccinylase (EC 3.5.1.96)	Escherichia coli (strain 55989 / EAEC)
29950	884368	883028	TY-2482_chromosome	B7L6L9	N-succinylarginine dihydrolase (EC 3.5.3.23)	Escherichia coli (strain 55989 / EAEC)
29979	885843	884368	TY-2482_chromosome	B7L6M0	N-succinylglutamate 5-semialdehyde dehydrogenase (EC 1.2.1.71) (Succinylglutamic semialdehyde dehydrogenase) (S	Escherichia coli (strain 55989 / EAEC)
29946	886874	885843	TY-2482_chromosome	B7L6M1	Arginine N-succinyltransferase (AST) (EC 2.3.1.109) (AOST)	Escherichia coli (strain 55989 / EAEC)
29954	888091	886874	TY-2482_chromosome	B7L6M2	Succinylornithine transaminase (EC 2.6.1.81) (Succinylornithine aminotransferase)	Escherichia coli (strain 55989 / EAEC)
114142	888537	889340	TY-2482_chromosome	B7L6M3	Exonuclease III (EC 3.1.11.2)	Escherichia coli (strain 55989 / EAEC)
89490	889462	890217	TY-2482_chromosome	D3GVG3	Putative membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
114001	890225	890899	TY-2482_chromosome	B7L6M5	Putative uncharacterized protein ydjY	Escherichia coli (strain 55989 / EAEC)
75222	890916	891620	TY-2482_chromosome	B7L6M6	Putative uncharacterized protein ydjZ	Escherichia coli (strain 55989 / EAEC)
66239	891623	892168	TY-2482_chromosome	B7L6M7	Putative uncharacterized protein ynjA	Escherichia coli (strain 55989 / EAEC)
108279	892181	893344	TY-2482_chromosome	B7L6M8	Putative uncharacterized protein ynjB	Escherichia coli (strain 55989 / EAEC)
68376	893365	894852	TY-2482_chromosome	B7L6M9	Fused putative transporter subunits of ABC superfamily: membrane components	Escherichia coli (strain 55989 / EAEC)
59200	894855	895505	TY-2482_chromosome	B7L6N0	Putative sulfate/thiosulfate transporter subunit: ATP-binding component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
68115	895575	896879	TY-2482_chromosome	B7L6N1	Putative exported thiosulfate sulfur transferase / thiosulfate binding protein	Escherichia coli (strain 55989 / EAEC)
100570	897511	896894	TY-2482_chromosome	C8TSS4	Predicted phosphatidyl transferase, inner membrane protein	Escherichia coli O26:H11 (strain 11368 / EHEC
76055	897598	898002	TY-2482_chromosome	B7L6N3	Pyrimidine (Deoxy)nucleoside triphosphate pyrophosphohydrolase (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
85280	898243	897974	TY-2482_chromosome	C8TSS6	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC
81110	898479	899819	TY-2482_chromosome	B7L6N4	Glutamate dehydrogenase, NADP-specific (EC 1.4.1.4)	Escherichia coli (strain 55989 / EAEC)
106441	900979	899942	TY-2482_chromosome	B7L6N5	Putative uncharacterized protein ynjI	Escherichia coli (strain 55989 / EAEC)

114002	903116	901110	TY-2482_chromosome	B7L6N6	DNA topoisomerase (EC 5.99.1.2)	Escherichia coli (strain 55989 / EAEC)
65774	904164	903124	TY-2482_chromosome	B7L6N7	Selenide, water dikinase (EC 2.7.9.3) (Selenium donor protein) (Selenophosphate synthase)	Escherichia coli (strain 55989 / EAEC)
68716	904847	904284	TY-2482_chromosome	D3GVH9	Putative nitroreductase	Escherichia coli O44:H18 (strain 042 / EAEC)
91765	904993	906846	TY-2482_chromosome	B7L6P1	Protease IV (Signal peptide peptidase) (EC 3.4.-.-)	Escherichia coli (strain 55989 / EAEC)
106345	907016	908029	TY-2482_chromosome	B7L6P2	Cytoplasmic L-asparaginase I (EC 3.5.1.1)	Escherichia coli (strain 55989 / EAEC)
114143	908043	908681	TY-2482_chromosome	B7L6P3	Nicotinamidase/pyrazinamidase (EC 3.5.1.-) (EC 3.5.1.19)	Escherichia coli (strain 55989 / EAEC)
81111	910135	908780	TY-2482_chromosome	B7L6P4	Putative transporter; MFS superfamily	Escherichia coli (strain 55989 / EAEC)
91859	911010	910255	TY-2482_chromosome	B7L6P5	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
102694	912127	911150	TY-2482_chromosome	B7L6P6	Putative oxidoreductase; similar to aldo/keto reductase	Escherichia coli (strain 55989 / EAEC)
102696	913084	912140	TY-2482_chromosome	B7L6P7	Putative sugar kinase	Escherichia coli (strain 55989 / EAEC)
87132	913925	913092	TY-2482_chromosome	B7L6P8	Putative aldolase	Escherichia coli (strain 55989 / EAEC)
66327	914923	913949	TY-2482_chromosome	B7L6P9	Putative iditol dehydrogenase (EC 1.1.1.14)	Escherichia coli (strain 55989 / EAEC)
91766	916385	915009	TY-2482_chromosome	B7L6Q0	Putative transporter; MFS superfamily	Escherichia coli (strain 55989 / EAEC)
98984	917488	916415	TY-2482_chromosome	B7L6Q1	Putative oxidoreductase, Zn-dependent and NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
106346	918130	917861	TY-2482_chromosome	B7L6Q2	Putative uncharacterized protein yeaC	Escherichia coli (strain 55989 / EAEC)
32498	918585	918175	TY-2482_chromosome	B7L6Q3	Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) (Peptide-methionine (R)-S-oxide reductase)	Escherichia coli (strain 55989 / EAEC)
65527	918927	919919	TY-2482_chromosome	B7L6Q4	Glyceraldehyde-3-phosphate dehydrogenase A (EC 1.2.1.12)	Escherichia coli (strain 55989 / EAEC)
97400	919985	920887	TY-2482_chromosome	D3GVJ4	Putative aldose 1-epimerase	Escherichia coli O44:H18 (strain 042 / EAEC)
77517	921795	920944	TY-2482_chromosome	B7L6Q6	Putative oxidoreductase	Escherichia coli (strain 55989 / EAEC)
94277	922631	921888	TY-2482_chromosome	B7L6Q7	Scaffolding protein for murein synthesizing machinery	Escherichia coli (strain 55989 / EAEC)
72201	923067	924998	TY-2482_chromosome	B7L6Q8	Putative uncharacterized protein yeaG	Escherichia coli (strain 55989 / EAEC)
34839	925114	926394	TY-2482_chromosome	B7L6Q9	UPF0229 protein yeaH	Escherichia coli (strain 55989 / EAEC)
98307	926544	928016	TY-2482_chromosome	B7L6R0	Putative diguanylate cyclase	Escherichia coli (strain 55989 / EAEC)
84570	928200	929687	TY-2482_chromosome	B7L6R1	Putative diguanylate cyclase	Escherichia coli (strain 55989 / EAEC)
77518	929733	930233	TY-2482_chromosome	B7L6R2	Putative uncharacterized protein yeaK	Escherichia coli (strain 55989 / EAEC)
21577	930330	930515	TY-2482_chromosome	D8B8Y4	Putative uncharacterized protein	Escherichia coli MS 175-1
65750	931739	930921	TY-2482_chromosome	B7L6R5	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
102697	931836	933014	TY-2482_chromosome	B7L6R6	Putative transporter; MFS superfamily	Escherichia coli (strain 55989 / EAEC)
98987	933072	933416	TY-2482_chromosome	B7L6R7	Putative uncharacterized protein yeaO	Escherichia coli (strain 55989 / EAEC)
98988	933695	933444	TY-2482_chromosome	B7L6R8	Putative uncharacterized protein yoaF	Escherichia coli (strain 55989 / EAEC)
66332	933878	934900	TY-2482_chromosome	B7L6R9	Putative diguanylate cyclase	Escherichia coli (strain 55989 / EAEC)
59201	935418	935173	TY-2482_chromosome	B7L6S0	Putative uncharacterized protein yeaQ	Escherichia coli (strain 55989 / EAEC)
82503	935615	935433	TY-2482_chromosome	B7L6S1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
87771	936853	935648	TY-2482_chromosome	B7L6S2	Putative transposase	Escherichia coli (strain 55989 / EAEC)
27078	936876	937820	TY-2482_chromosome	A7ZMR8	Transposase, IS605 family	Escherichia coli O139:H28 (strain E24377A / ETEC
82452	938670	938035	TY-2482_chromosome	B7L6S6	Putative neutral amino-acid efflux system	Escherichia coli (strain 55989 / EAEC)
73826	939720	938800	TY-2482_chromosome	B7L6S7	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
114144	939823	940905	TY-2482_chromosome	B7L6S8	Putative tartrate dehydrogenase	Escherichia coli (strain 55989 / EAEC)
114146	941324	942766	TY-2482_chromosome	B7L6S9	Putative transporter	Escherichia coli (strain 55989 / EAEC)
67972	942801	943922	TY-2482_chromosome	B7L6T0	Putative 2Fe-2S cluster-containing dioxygenase subunit	Escherichia coli (strain 55989 / EAEC)
104336	943981	944943	TY-2482_chromosome	B7L6T1	Putative dioxygenase subunit	Escherichia coli (strain 55989 / EAEC)
69038	946127	945003	TY-2482_chromosome	B7L6T2	Ribonuclease D (EC 3.1.26.3)	Escherichia coli (strain 55989 / EAEC)
87059	947882	946200	TY-2482_chromosome	B7L6T3	Acyl-CoA synthetase (Long-chain-fatty-acid--CoA ligase) (EC 6.2.1.3)	Escherichia coli (strain 55989 / EAEC)
76153	948668	948090	TY-2482_chromosome	B7L6T4	Putative outer membrane-associated lipoprotein	Escherichia coli (strain 55989 / EAEC)
114150	949403	948711	TY-2482_chromosome	B7L6T5	Putative peptidase	Escherichia coli (strain 55989 / EAEC)
99041	951371	949464	TY-2482_chromosome	B7L6T6	Putative ATP-dependent helicase	Escherichia coli (strain 55989 / EAEC)
26504	951790	951407	TY-2482_chromosome	A7ZMT0	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
93521	952210	952566	TY-2482_chromosome	B7L6T8	Putative uncharacterized protein yoaC	Escherichia coli (strain 55989 / EAEC)
102761	952942	954300	TY-2482_chromosome	B7L6U0	Aminodeoxychorismate synthase, subunit I (EC 2.6.1.85)	Escherichia coli (strain 55989 / EAEC)
32736	954307	954882	TY-2482_chromosome	B7L6U1	Uncharacterized Nudix hydrolase nudL (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
76159	955069	956430	TY-2482_chromosome	B7L6U2	L-serine deaminase I (EC 4.3.1.17)	Escherichia coli (strain 55989 / EAEC)
72218	956564	958159	TY-2482_chromosome	B7L6U3	Putative cyclic di-GMP phosphodiesterase	Escherichia coli (strain 55989 / EAEC)
66389	959722	958169	TY-2482_chromosome	B7L6U4	Putative membrane protein fused with conserved domain	Escherichia coli (strain 55989 / EAEC)
111011	959919	959713	TY-2482_chromosome	C8UBR5	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC
106406	960185	961153	TY-2482_chromosome	B7L6U5	Fused mannose-specific PTS enzymes: IIA component ; IIB component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
17120	960214	960023	TY-2482_chromosome	D7X960	Conserved domain protein	Escherichia coli MS 198-1
83334	961219	962016	TY-2482_chromosome	B7L6U6	Mannose-specific enzyme IIC component of PTS	Escherichia coli (strain 55989 / EAEC)
77293	962023	962880	TY-2482_chromosome	B7L6U7	Mannose-specific enzyme IID component of PTS	Escherichia coli (strain 55989 / EAEC)
35037	962938	963393	TY-2482_chromosome	B7L6U8	UPF0266 membrane protein yobD	Escherichia coli (strain 55989 / EAEC)
27418	963583	963825	TY-2482_chromosome	B7L6U9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
34849	963825	964388	TY-2482_chromosome	B7L6V0	UPF0059 membrane protein yebN	Escherichia coli (strain 55989 / EAEC)
99042	965197	964391	TY-2482_chromosome	B7L6V1	23S rRNA m1G745 methyltransferase (EC 2.1.1.51)	Escherichia coli (strain 55989 / EAEC)
24490	965690	965936	TY-2482_chromosome	A1ABZ1	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
27255	966651	966346	TY-2482_chromosome	Q1RAW4	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)

81126	967062	967298	TY-2482_chromosome	B7L6V6	Putative uncharacterized protein yobH	Escherichia coli (strain 55989 / EAEC)
114568	968235	967447	TY-2482_chromosome	C8UBS7	Predicted DNA-binding transcriptional regulator	Escherichia coli O111:H- (strain 11128 / EHEC)
91782	968412	969782	TY-2482_chromosome	B7L7N0	Putative transporter; MFS superfamily	Escherichia coli (strain 55989 / EAEC)
31561	970712	969834	TY-2482_chromosome	B7L7N1	Protease HtpX (EC 3.4.24.-) (Heat shock protein HtpX)	Escherichia coli (strain 55989 / EAEC)
73601	972952	970907	TY-2482_chromosome	B7L7N2	Carboxy-terminal protease for penicillin-binding protein 3 (EC 3.4.21.102	Escherichia coli (strain 55989 / EAEC)
33081	973670	972975	TY-2482_chromosome	B7L7N3	ProP effector	Escherichia coli (strain 55989 / EAEC)
110541	974318	973770	TY-2482_chromosome	B7L7N4	Putative uncharacterized protein yebR	Escherichia coli (strain 55989 / EAEC)
66356	974394	975674	TY-2482_chromosome	B7L7N5	Putative uncharacterized protein yebS	Escherichia coli (strain 55989 / EAEC)
116094	975646	978276	TY-2482_chromosome	B7L7N6	Putative uncharacterized protein yebT	Escherichia coli (strain 55989 / EAEC)
33796	978359	979795	TY-2482_chromosome	B7L7N7	Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.178) (16S rRNA m5C1407 methyltransferase) (rRNA (cyto	Escherichia coli (strain 55989 / EAEC)
81122	979916	980149	TY-2482_chromosome	B7L7N8	Putative uncharacterized protein yebV	Escherichia coli (strain 55989 / EAEC)
86871	980173	980445	TY-2482_chromosome	B7L7N9	Putative uncharacterized protein yebW	Escherichia coli (strain 55989 / EAEC)
75966	981105	980452	TY-2482_chromosome	B7L7P0	Serine/threonine-specific protein phosphatase 1 (EC 3.1.3.16)	Escherichia coli (strain 55989 / EAEC)
r101	981202	981450	TY-2482_chromosome	ref|NC_010473|:2011661-2011909|-| [gene=ryeA] [locus_tag=ECDH10B_1978]		
90136	981842	981504	TY-2482_chromosome	B7L7P2	Putative uncharacterized protein yebY	Escherichia coli (strain 55989 / EAEC)
91783	982727	981858	TY-2482_chromosome	B7L7P3	Putative uncharacterized protein yebZ	Escherichia coli (strain 55989 / EAEC)
59011	983105	982734	TY-2482_chromosome	B7L7P4	Putative uncharacterized protein yobA	Escherichia coli (strain 55989 / EAEC)
90073	983244	983471	TY-2482_chromosome	B7L7P5	DNA polymerase III, theta subunit (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
84439	983576	984229	TY-2482_chromosome	B7L7P6	Putative uncharacterized protein yobB	Escherichia coli (strain 55989 / EAEC)
77573	984256	984915	TY-2482_chromosome	B7L7P7	DNA exonuclease X (EC 3.1.11.-)	Escherichia coli (strain 55989 / EAEC)
90081	986975	984918	TY-2482_chromosome	B7L7P8	Protease II (EC 3.4.21.83)	Escherichia coli (strain 55989 / EAEC)
95425	987843	987187	TY-2482_chromosome	B7L7P9	Putative uncharacterized protein yebE	Escherichia coli (strain 55989 / EAEC)
12478	988050	988253	TY-2482_chromosome	D6JAC7	Predicted protein	Escherichia coli B354
81123	988538	988173	TY-2482_chromosome	B7L7Q0	Protein yebF	Escherichia coli (strain 55989 / EAEC)
66358	988883	988596	TY-2482_chromosome	B7L7Q1	Putative uncharacterized protein yebG	Escherichia coli (strain 55989 / EAEC)
72735	989017	990192	TY-2482_chromosome	B7L7Q2	Phosphoribosylglycinamide formyltransferase 2 (EC 2.7.2.1)	Escherichia coli (strain 55989 / EAEC)
88204	990892	990254	TY-2482_chromosome	B7L7Q3	Multifunctional 2-keto-3-deoxygluconate 6-phosphate aldolase and 2-keto-4-hydroxyglutarate aldolase and oxaloace	Escherichia coli (strain 55989 / EAEC)
83699	992740	990932	TY-2482_chromosome	B7L7Q4	6-phosphogluconate dehydratase (EC 4.2.1.12)	Escherichia coli (strain 55989 / EAEC)
83457	994450	992978	TY-2482_chromosome	B7L7Q5	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	Escherichia coli (strain 55989 / EAEC)
66240	994788	995654	TY-2482_chromosome	B7L7Q6	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
70104	995785	997224	TY-2482_chromosome	B7L7Q7	Pyruvate kinase (EC 2.7.1.40)	Escherichia coli (strain 55989 / EAEC)
61651	998329	997361	TY-2482_chromosome	B7L7Q8	Myristoyl-acyl carrier protein (ACP)-dependent acyltransferase (EC 2.3.1.-)	Escherichia coli (strain 55989 / EAEC)
91784	999771	998452	TY-2482_chromosome	B7L7Q9	Putative metallopeptidase	Escherichia coli (strain 55989 / EAEC)
104789	1000719	999790	TY-2482_chromosome	B7L7R0	Zinc transporter subunit: periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
111835	1000798	1001550	TY-2482_chromosome	B7L7R1	Zinc transporter subunit: ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
111636	1001550	1002332	TY-2482_chromosome	B7L7R2	Zinc transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
33872	1003492	1002485	TY-2482_chromosome	B7L7R3	Holliday junction ATP-dependent DNA helicase ruvB (EC 3.6.4.12)	Escherichia coli (strain 55989 / EAEC)
33868	1004112	1003504	TY-2482_chromosome	B7L7R4	Holliday junction ATP-dependent DNA helicase ruvA (EC 3.6.4.12)	Escherichia coli (strain 55989 / EAEC)
17220	1004288	1004986	TY-2482_chromosome	B3Y0L8	Predicted protein	Escherichia coli O111:H-
33876	1005512	1004994	TY-2482_chromosome	B7L7R6	Crossover junction endodeoxyribonuclease ruvC (EC 3.1.22.4) (Holliday junction nuclease ruvC) (Holliday junction res	Escherichia coli (strain 55989 / EAEC)
97940	1006287	1005550	TY-2482_chromosome	B7L7R7	UPF0082 protein yeeN 1	Escherichia coli (strain 55989 / EAEC)
77341	1006759	1006319	TY-2482_chromosome	B7L7R8	dATP pyrophosphohydrolase (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
34091	1008533	1006764	TY-2482_chromosome	B7L7R9	Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase) (AspRS)	Escherichia coli (strain 55989 / EAEC)
71884	1008843	1009406	TY-2482_chromosome	B7L7S0	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
101333	1009764	1010009	TY-2482_chromosome	C6V226	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC)
24728	1011246	1010554	TY-2482_chromosome	B7LEU8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28034	1012706	1011171	TY-2482_chromosome	B7LEU7	Putative tail fiber protein (Modular protein)	Escherichia coli (strain 55989 / EAEC)
98402	1013457	1012861	TY-2482_chromosome	D3H3F5	Putative prophage-encoded outer membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
64239	1016920	1013528	TY-2482_chromosome	B7L8N6	Host specificity protein J	Escherichia coli (strain 55989 / EAEC)
93092	1017652	1016984	TY-2482_chromosome	D3GSI6	Phage tail assembly protein	Escherichia coli O44:H18 (strain 042 / EAEC)
27267	1018292	1019095	TY-2482_chromosome	Q1RCC4	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
79402	1018335	1017553	TY-2482_chromosome	B7LEU3	Putative tail fiber component K of prophage	Escherichia coli (strain 55989 / EAEC)
111771	1019325	1018999	TY-2482_chromosome	B7LBD1	Minor tail protein M	Escherichia coli (strain 55989 / EAEC)
105592	1021934	1019325	TY-2482_chromosome	C8UEI9	Putative tail length tape measure protein	Escherichia coli O111:H- (strain 11128 / EHEC)
25168	1022113	1023447	TY-2482_chromosome	A1AAL5	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
114314	1023946	1023554	TY-2482_chromosome	C8U3B0	Putative minor tail protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
60231	1024518	1023946	TY-2482_chromosome	D3H3E3	Phage minor tail protein	Escherichia coli O44:H18 (strain 042 / EAEC)
84631	1024886	1024536	TY-2482_chromosome	B7L472	Tail attachment protein (Minor capsid protein FII)	Escherichia coli (strain 55989 / EAEC)
59176	1025310	1024882	TY-2482_chromosome	B7L471	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
95639	1026342	1025317	TY-2482_chromosome	B7L470	Major head protein (Head protein gp7)	Escherichia coli (strain 55989 / EAEC)
105238	1026747	1026403	TY-2482_chromosome	D3H3D9	Phage head decoration protein	Escherichia coli O44:H18 (strain 042 / EAEC)
90026	1028289	1026787	TY-2482_chromosome	B7L468	Head-tail preconnector protein GP5	Escherichia coli (strain 55989 / EAEC)
107063	1029871	1028282	TY-2482_chromosome	C8TUI5	Putative portal protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
111505	1030074	1029871	TY-2482_chromosome	C8TKW0	Head-tail joining protein	Escherichia coli O26:H11 (strain 11368 / EHEC)

84566	1032028	1030061	TY-2482_chromosome	B7L465	Terminase large subunit (Gp2)	Escherichia coli (strain 55989 / EAEC)
27274	1032746	1031961	TY-2482_chromosome	A1AAK5	Prophage Qin DNA packaging protein NU1-like protein	Escherichia coli O1:K1 / APEC
29487	1034183	1033713	TY-2482_chromosome	B7N3K3	Endopeptidase (Lysis protein) from bacteriophage origin (EC 3.4.-.-)	Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC)
24557	1034401	1034183	TY-2482_chromosome	B7MPY1	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
17934	1034541	1034329	TY-2482_chromosome	D6IMM0	Predicted protein	Escherichia coli FVEC1412
59063	1035198	1034668	TY-2482_chromosome	B7LES4	Lysozyme (EC 3.2.1.17)	Escherichia coli (strain 55989 / EAEC)
29118	1035327	1035638	TY-2482_chromosome	B7LES3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25586	1036457	1035654	TY-2482_chromosome	B7LES2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
79307	1036755	1036465	TY-2482_chromosome	D3H2S6	Putative phage lysis protein	Escherichia coli O44:H18 (strain 042 / EAEC)
28911	1038711	1036831	TY-2482_chromosome	B7MPX6	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
28583	1039137	1038847	TY-2482_chromosome	B7MV04	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
r354	1039423	1039348	TY-2482_chromosome	ref|NC_010473|:2875549-2875624|Ile tRNA| [gene=ileY] [locus_tag=ECDH10B_2820		
110860	1040522	1039467	TY-2482_chromosome	C6USM2	Putative DNA adenine methyltransferase encoded by prophage CP-933O	Escherichia coli O157:H7 (strain TW14359 / EHEC
27487	1040910	1040677	TY-2482_chromosome	B7NVG6	Putative uncharacterized protein	Escherichia coli O7:K1 (strain IAI39 / ExPEC)
11019	1041142	1042065	TY-2482_chromosome	B3HVA3	Putative uncharacterized protein	Escherichia coli F11
9406	1042055	1042600	TY-2482_chromosome	B3IDN1	Putative uncharacterized protein	Escherichia coli E22
9386	1042957	1042619	TY-2482_chromosome	B3HVA5	Antitermination protein Q	Escherichia coli F11
108737	1043964	1042978	TY-2482_chromosome	C8TVZ3	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
24937	1044787	1043975	TY-2482_chromosome	D3QMI3	KilA-N domain family	Escherichia coli O55:H7 (strain CB9615 / EPEC)
28121	1045345	1044953	TY-2482_chromosome	D3QMI2	Crossover junction endodeoxyribonuclease rusA (EC 3.1.22.4)	Escherichia coli O55:H7 (strain CB9615 / EPEC)
103835	1046318	1045668	TY-2482_chromosome	C8U2N1	Putative DNA methylase	Escherichia coli O103:H2 (strain 12009 / EHEC)
100128	1046806	1046321	TY-2482_chromosome	C8U2N0	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
28222	1047666	1046812	TY-2482_chromosome	B7MND7	Replication protein from phage origin	Escherichia coli O45:K1 (strain S88 / ExPEC)
86176	1047848	1047627	TY-2482_chromosome	C8TW00	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
13597	1049038	1047848	TY-2482_chromosome	B3WIT4	Putative antirepressor	Escherichia coli B171
21556	1049625	1049038	TY-2482_chromosome	D6HVI9	YmfL protein	Escherichia coli B088
105454	1049845	1049588	TY-2482_chromosome	C8UKW3	Putative antirepressor protein Cro	Escherichia coli O111:H- (strain 11128 / EHEC
109607	1049943	1050632	TY-2482_chromosome	C8UKW2	Putative repressor protein CI	Escherichia coli O111:H- (strain 11128 / EHEC
26492	1051064	1050735	TY-2482_chromosome	Q1R2C0	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
100062	1051107	1051697	TY-2482_chromosome	C8TW05	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
7029	1051766	1052587	TY-2482_chromosome	P76513	Uncharacterized protein yfdQ	Escherichia coli (strain K12)
78016	1052718	1053251	TY-2482_chromosome	C8TW07	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
7032	1053245	1053604	TY-2482_chromosome	P76515	Uncharacterized protein yfdS	Escherichia coli (strain K12)
59493	1053604	1053804	TY-2482_chromosome	C8U7N2	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
81711	1053800	1054036	TY-2482_chromosome	C8U7N3	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
14555	1054036	1054581	TY-2482_chromosome	E7UPB9	Phage EaA protein	Escherichia coli EC4100B
87074	1054547	1055098	TY-2482_chromosome	C8TPV2	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
15631	1055098	1055853	TY-2482_chromosome	B3WUG8	Upf89.5	Escherichia coli B171
29071	1055941	1056180	TY-2482_chromosome	B2TYH9	Hypothetical bacteriophage protein	Shigella boydii serotype 18 (strain CDC 3083-94 / BS512)
29266	1056342	1056575	TY-2482_chromosome	B6I1E3	Putative phage excisionase	Escherichia coli (strain SE11)
24981	1056622	1057941	TY-2482_chromosome	B7MPT9	Phage integrase	Escherichia coli O81 (strain ED1a)
27722	1057926	1059141	TY-2482_chromosome	E1RYP9	Putative uncharacterized protein	Escherichia coli (strain UM146)
30349	1059185	1059925	TY-2482_chromosome	B7L7S3	tRNA (cmo5U34)-methyltransferase (EC 2.1.1.-)	Escherichia coli (strain 55989 / EAEC)
30353	1059925	1060893	TY-2482_chromosome	B7L7S4	tRNA (mo5U34)-methyltransferase (EC 2.1.1.-)	Escherichia coli (strain 55989 / EAEC)
114176	1063491	1061065	TY-2482_chromosome	B7L7S5	Trimethylamine N-oxide reductase system III, catalytic subunit (EC 1.6.6.9)	Escherichia coli (strain 55989 / EAEC)
64743	1064616	1063519	TY-2482_chromosome	B7L7S6	TMAO reductase III (TorYZ), cytochrome c-type subunit	Escherichia coli (strain 55989 / EAEC)
30435	1065750	1065007	TY-2482_chromosome	B7L7S7	Copper homeostasis protein CutC	Escherichia coli (strain 55989 / EAEC)
84440	1066330	1065767	TY-2482_chromosome	B7L7S8	Putative metal-binding enzyme	Escherichia coli (strain 55989 / EAEC)
34167	1066546	1068276	TY-2482_chromosome	B7L7S9	Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS)	Escherichia coli (strain 55989 / EAEC)
20981	1068435	1068941	TY-2482_chromosome	D6HY23	YecT protein	Escherichia coli B088
59016	1069456	1069067	TY-2482_chromosome	B7L7T1	Putative uncharacterized protein flhE	Escherichia coli (strain 55989 / EAEC)
77574	1071534	1069459	TY-2482_chromosome	B7L7T2	Putative flagellar export pore protein	Escherichia coli (strain 55989 / EAEC)
101874	1072675	1071530	TY-2482_chromosome	B7L7T3	Flagellar export pore protein	Escherichia coli (strain 55989 / EAEC)
61187	1073521	1072880	TY-2482_chromosome	B7L7T4	Chemotaxis regulator, protein phosphatase for CheY	Escherichia coli (strain 55989 / EAEC)
70106	1073921	1073535	TY-2482_chromosome	B7L7T5	Chemotaxis regulator transmitting signal to flagellar motor component	Escherichia coli (strain 55989 / EAEC)
99111	1074985	1073939	TY-2482_chromosome	B7L7T6	Fused chemotaxis regulator ; protein-glutamate methylesterase in two-component regulatory system with CheA (EC	Escherichia coli (strain 55989 / EAEC)
71432	1075848	1074991	TY-2482_chromosome	B7L7T7	Chemotaxis regulator, protein-glutamate methyltransferase (EC 2.1.1.80)	Escherichia coli (strain 55989 / EAEC)
106392	1077468	1075870	TY-2482_chromosome	B7L7T8	Methyl-accepting protein IV	Escherichia coli (strain 55989 / EAEC)
114182	1079175	1077517	TY-2482_chromosome	B7L7T9	Methyl-accepting chemotaxis protein II	Escherichia coli (strain 55989 / EAEC)
75158	1079823	1079323	TY-2482_chromosome	B7L7U0	Purine-binding chemotaxis protein	Escherichia coli (strain 55989 / EAEC)
99112	1081808	1079847	TY-2482_chromosome	B7L7U1	Fused chemotactic sensory histidine kinase in two-component regulatory system with CheB and CheY: sensory histidi	Escherichia coli (strain 55989 / EAEC)
82339	1082739	1081816	TY-2482_chromosome	B7L7U2	Protein that enables flagellar motor rotation	Escherichia coli (strain 55989 / EAEC)
97166	1083623	1082739	TY-2482_chromosome	B7L7U3	Proton conductor component of flagella motor	Escherichia coli (strain 55989 / EAEC)
83333	1084328	1083753	TY-2482_chromosome	B7L7U4	DNA-binding transcriptional dual regulator with FlhD	Escherichia coli (strain 55989 / EAEC)

30981	1084690	1084334	TY-2482_chromosome	B7L7U5	Flagellar transcriptional regulator FlhD	Escherichia coli (strain 55989 / EAEC)
99036	1085460	1085885	TY-2482_chromosome	B7L7U6	Universal stress protein	Escherichia coli (strain 55989 / EAEC)
87924	1087319	1085898	TY-2482_chromosome	B7L7U7	Trehalose-6-phosphate synthase (EC 2.4.1.15)	Escherichia coli (strain 55989 / EAEC)
24408	1088151	1087297	TY-2482_chromosome	A1AC54	Trehalose-6-phosphate phosphatase	Escherichia coli O1:K1 / APEC
77336	1089250	1088264	TY-2482_chromosome	B7L7U9	Fused L-arabinose transporter subunits of ABC superfamily: membrane components	Escherichia coli (strain 55989 / EAEC)
114187	1090776	1089265	TY-2482_chromosome	B7L7V0	Fused L-arabinose transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
73602	1091835	1090849	TY-2482_chromosome	B7L7V1	L-arabinose transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
28109	1092160	1091924	TY-2482_chromosome	Q0TGT5	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
78960	1092632	1093132	TY-2482_chromosome	B7L7V2	Putative ferritin-like protein	Escherichia coli (strain 55989 / EAEC)
8589	1093217	1093486	TY-2482_chromosome	C3T592	Putative uncharacterized protein	Escherichia coli
r111	1093705	1093546	TY-2482_chromosome	ref|NC_010473|:2076871-2077030|-| [gene=isrB] [locus_tag=ECDH10B_2044]		
115184	1093929	1094249	TY-2482_chromosome	B7L7V5	Putative uncharacterized protein yecR	Escherichia coli (strain 55989 / EAEC)
97167	1094424	1094918	TY-2482_chromosome	B7L7V6	Ferritin iron storage protein (Cytoplasmic)	Escherichia coli (strain 55989 / EAEC)
95415	1095198	1094962	TY-2482_chromosome	B7L7V7	Putative uncharacterized protein yecH	Escherichia coli (strain 55989 / EAEC)
83556	1095388	1096596	TY-2482_chromosome	B7L7V8	Tyrosine transporter	Escherichia coli (strain 55989 / EAEC)
59017	1097326	1096664	TY-2482_chromosome	B7L7V9	Putative uncharacterized protein yecA	Escherichia coli (strain 55989 / EAEC)
r226	1097608	1097522	TY-2482_chromosome	ref|NC_010473|:2080847-2080933|Leu tRNA| [gene=leuZ] [locus_tag=ECDH10B_2050]		
r506	1097694	1097621	TY-2482_chromosome	ref|NC_010473|:2080946-2081019|Cys tRNA| [gene=cysT] [locus_tag=ECDH10B_2051]		
r310	1097824	1097749	TY-2482_chromosome	ref|NC_010473|:4490968-4491043|Gly tRNA| [gene=glyY] [locus_tag=ECDH10B_4360]		
76399	1098524	1097979	TY-2482_chromosome	B7L807	Phosphatidylglycerophosphate synthetase (EC 2.7.8.5)	Escherichia coli (strain 55989 / EAEC)
34542	1100413	1098584	TY-2482_chromosome	B7L8S5	UvrABC system protein C (Protein uvrC) (Excinuclease ABC subunit C)	Escherichia coli (strain 55989 / EAEC)
77404	1101066	1100413	TY-2482_chromosome	B7L8S6	DNA-binding response regulator in two-component regulatory system with BarA	Escherichia coli (strain 55989 / EAEC)
115679	1101525	1101746	TY-2482_chromosome	B7L8S8	Putative uncharacterized protein yecF	Escherichia coli (strain 55989 / EAEC)
109719	1102539	1101820	TY-2482_chromosome	B7L8S9	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
102865	1103521	1102772	TY-2482_chromosome	B7L8T0	Putative transporter subunit: ATP-binding component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
104585	1104186	1103521	TY-2482_chromosome	B7L8T1	Putative transporter subunit: permease component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
30573	1105187	1104204	TY-2482_chromosome	B7L8T2	D-cysteine desulfhydrase (EC 4.4.1.15)	Escherichia coli (strain 55989 / EAEC)
91897	1106092	1105295	TY-2482_chromosome	B7L8T3	Cystine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
96838	1106767	1106183	TY-2482_chromosome	D3GXH3	FliZ protein	Escherichia coli O44:H18 (strain 042 / EAEC)
69999	1107496	1106780	TY-2482_chromosome	B7L8T5	RNA polymerase sigma factor	Escherichia coli (strain 55989 / EAEC)
105040	1107950	1107663	TY-2482_chromosome	B7L8T6	Flagellin	Escherichia coli (strain 55989 / EAEC)
105039	1108675	1107926	TY-2482_chromosome	B7L8T6	Flagellin	Escherichia coli (strain 55989 / EAEC)
75155	1108923	1110335	TY-2482_chromosome	B7L8T7	Putative Flagellar hook-associated protein 2 (HAP2) (Filament cap protein) (Flagellar cap protein	Escherichia coli (strain 55989 / EAEC)
88390	1110354	1110761	TY-2482_chromosome	B7L8T8	Flagellar protein potentiates polymerization	Escherichia coli (strain 55989 / EAEC)
30992	1110764	1111126	TY-2482_chromosome	B7L8T9	Flagellar protein FliT	Escherichia coli (strain 55989 / EAEC)
102886	1111207	1112691	TY-2482_chromosome	B7L8U0	Cytoplasmic alpha-amylase (EC 3.2.1.1)	Escherichia coli (strain 55989 / EAEC)
78968	1113141	1112731	TY-2482_chromosome	B7L8U1	Putative uncharacterized protein yedD	Escherichia coli (strain 55989 / EAEC)
86355	1113328	1114530	TY-2482_chromosome	B7L8U2	Putative uncharacterized protein yedE	Escherichia coli (strain 55989 / EAEC)
110382	1114530	1114760	TY-2482_chromosome	B7L8U3	Putative uncharacterized protein yedF	Escherichia coli (strain 55989 / EAEC)
15356	1114872	1115366	TY-2482_chromosome	E6BEB6	Gifsy-2 prophage YedK	Escherichia coli MS 85-1
114041	1115558	1116124	TY-2482_chromosome	B7L8U5	Putative transposase ORF A, IS609 family	Escherichia coli (strain 55989 / EAEC)
110429	1117081	1116287	TY-2482_chromosome	B7L8U6	Putative DNA-binding transcriptional regulator; DLP12 prophage	Escherichia coli (strain 55989 / EAEC)
73755	1117642	1117094	TY-2482_chromosome	B7L8U7	Putative kinase inhibitor; DLP12 prophage	Escherichia coli (strain 55989 / EAEC)
13066	1118243	1118557	TY-2482_chromosome	E9UHF9	Conserved domain protein	Escherichia coli MS 57-2
59169	1118323	1117814	TY-2482_chromosome	B7L8U8	Putative multidrug resistance protein; DLP12 prophage	Escherichia coli (strain 55989 / EAEC)
30986	1118801	1118490	TY-2482_chromosome	B7L8U9	Flagellar hook-basal body complex protein FliE	Escherichia coli (strain 55989 / EAEC)
98080	1119016	1120671	TY-2482_chromosome	B7L8V0	Flagellar basal-body MS-ring and collar protein	Escherichia coli (strain 55989 / EAEC)
90951	1120667	1121659	TY-2482_chromosome	B7L8V1	Flagellar motor switching and energizing component	Escherichia coli (strain 55989 / EAEC)
79321	1121655	1122338	TY-2482_chromosome	B7L8V2	Flagellar biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
76640	1122341	1123711	TY-2482_chromosome	B7L8V3	Flagellum-specific ATP synthase (EC 3.6.3.14)	Escherichia coli (strain 55989 / EAEC)
113091	1123733	1124173	TY-2482_chromosome	B7L8V4	Flagellar protein	Escherichia coli (strain 55989 / EAEC)
110430	1124173	1125297	TY-2482_chromosome	B7L8V5	Flagellar hook-length control protein	Escherichia coli (strain 55989 / EAEC)
71643	1125405	1125866	TY-2482_chromosome	B7L8V6	Flagellar biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
98237	1125874	1126875	TY-2482_chromosome	B7L8V7	Flagellar motor switching and energizing component	Escherichia coli (strain 55989 / EAEC)
59171	1126875	1127285	TY-2482_chromosome	B7L8V8	Flagellar motor switching and energizing component	Escherichia coli (strain 55989 / EAEC)
99113	1127291	1127653	TY-2482_chromosome	B7L8V9	Flagellar biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
95619	1127656	1128390	TY-2482_chromosome	B7L8W0	Flagellar biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
98605	1128403	1128669	TY-2482_chromosome	B7L8W1	Flagellar biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
62056	1128681	1129463	TY-2482_chromosome	B7L8W2	Flagellar biosynthetic protein fliR	Escherichia coli (strain 55989 / EAEC)
84622	1129756	1130376	TY-2482_chromosome	B7L8W3	DNA-binding transcriptional activator, co-regulator with RcsB	Escherichia coli (strain 55989 / EAEC)
27947	1130502	1130774	TY-2482_chromosome	A1ACA1	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
24989	1131104	1130757	TY-2482_chromosome	Q1RAI7	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
r225	1131147	1131061	TY-2482_chromosome	ref|NC_010473|:2114259-2114345|-| [gene=dsrA] [locus_tag=ECDH10B_2096]		
34854	1133852	1132026	TY-2482_chromosome	Q8Z5R0	Cellulose synthesis regulatory protein	Salmonella typhi

82338	1135201	1134287	TY-2482_chromosome	B7L8X1	Putative uncharacterized protein yedI	Escherichia coli (strain 55989 / EAEC)
72423	1135374	1136291	TY-2482_chromosome	B7L8X2	Putative uncharacterized protein yedA	Escherichia coli (strain 55989 / EAEC)
77454	1136753	1136286	TY-2482_chromosome	B7L8X3	DNA mismatch endonuclease of very short patch repair (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
66293	1138152	1136737	TY-2482_chromosome	B7L8X4	Cytosine-specific methyltransferase (EC 2.1.1.37)	Escherichia coli (strain 55989 / EAEC)
63987	1138950	1138222	TY-2482_chromosome	D3GXL0	Putative phosphohydrolase	Escherichia coli O44:H18 (strain 042 / EAEC)
112152	1139319	1138957	TY-2482_chromosome	B7L8X6	Putative uncharacterized protein yedR	Escherichia coli (strain 55989 / EAEC)
28096	1139412	1139663	TY-2482_chromosome	E4PAJ7	Putative uncharacterized protein	Escherichia coli O83:H1 (strain NRG 857C / AIEC)
28732	1139815	1140941	TY-2482_chromosome	B7MWF2	Outer membrane protein F (Porin ompF)	Escherichia coli O81 (strain ED1a)
17824	1140996	1141343	TY-2482_chromosome	E9XVB1	Transposase (Fragment)	Escherichia coli TW10509
115338	1142417	1141269	TY-2482_chromosome	D3GUS1	Transposase InsI for insertion sequence element IS30b/c/d	Escherichia coli O44:H18 (strain 042 / EAEC)
64171	1142491	1143372	TY-2482_chromosome	B7LDT8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
14869	1143679	1143437	TY-2482_chromosome	D8AVP8	Putative uncharacterized protein	Escherichia coli MS 116-1
14367	1144578	1143884	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli
31326	1144664	1145512	TY-2482_chromosome	B7L8Y4	Chaperone protein hchA (Hsp31)	Escherichia coli (strain 55989 / EAEC)
95621	1146971	1145616	TY-2482_chromosome	B7L8Y5	Sensory kinase in two-component regulatory system with YedW	Escherichia coli (strain 55989 / EAEC)
63988	1147690	1146974	TY-2482_chromosome	D3GXL6	Two-component response regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
102922	1147775	1148185	TY-2482_chromosome	B7L8Y7	5-hydroxyisourate hydrolase	Escherichia coli (strain 55989 / EAEC)
34855	1148297	1149298	TY-2482_chromosome	B7L8Y8	Sulfoxide reductase catalytic subunit yedY (EC 1.8.-.-)	Escherichia coli (strain 55989 / EAEC)
34859	1149302	1149934	TY-2482_chromosome	B7L8Y9	Sulfoxide reductase heme-binding subunit yedZ (Flavocytochrome yedZ)	Escherichia coli (strain 55989 / EAEC)
79322	1150194	1150841	TY-2482_chromosome	B7L8Z0	Putative uncharacterized protein yodA	Escherichia coli (strain 55989 / EAEC)
16855	1150880	1151206	TY-2482_chromosome	E2QNG5	Putative uncharacterized protein	Escherichia coli
r200	1151603	1151514	TY-2482_chromosome	ref|NC_010473|:2132500-2132589|Ser tRNA| [gene=serU] [locus_tag=ECDH10B_2118]		
78944	1151658	1152491	TY-2482_chromosome	D3GYI6	Protein mtfA (Mlc titration factor A)	Escherichia coli O44:H18 (strain 042 / EAEC)
r399	1152595	1152670	TY-2482_chromosome	ref|NC_010473|:2151292-2151367|Asn tRNA| [gene=asnV] [locus_tag=ECDH10B_2133]		
81060	1152832	1154091	TY-2482_chromosome	B7L8Z2	Integrase	Escherichia coli (strain 55989 / EAEC)
114003	1155592	1154291	TY-2482_chromosome	B7L8Z3	Salicylate synthase	Escherichia coli (strain 55989 / EAEC)
69391	1157023	1155623	TY-2482_chromosome	B7L8Z4	Putative permease of yersiniabactin-iron transporter YbtX	Escherichia coli (strain 55989 / EAEC)
62801	1160484	1158685	TY-2482_chromosome	B7L8Z6	Permease and ATP-binding protein of yersiniabactin-iron ABC transporter YbtP	Escherichia coli (strain 55989 / EAEC)
88438	1160651	1161607	TY-2482_chromosome	B7L8Z7	AraC type regulator of yersiniabactin gene cluster (HPI)	Escherichia coli (strain 55989 / EAEC)
82912	1161783	1167905	TY-2482_chromosome	B7L8Z8	High-molecular-weight nonribosomal peptide/polyketide synthetase 2 (HMWP2)	Escherichia coli (strain 55989 / EAEC)
77456	1167996	1177484	TY-2482_chromosome	B7L8Z9	High-molecular-weight nonribosomal peptide/polyketide synthetase 1 (HMWP1)	Escherichia coli (strain 55989 / EAEC)
95625	1177424	1178581	TY-2482_chromosome	B7L900	Thiazolinyl-S-HMWP1 reductase YbtU	Escherichia coli (strain 55989 / EAEC)
115995	1178581	1179381	TY-2482_chromosome	B7L901	Putative thioesterase YbtT	Escherichia coli (strain 55989 / EAEC)
114004	1179388	1180962	TY-2482_chromosome	B7L902	Salicyl-AMP ligase YbtE	Escherichia coli (strain 55989 / EAEC)
86971	1181096	1183114	TY-2482_chromosome	B7L903	Yersiniabactin/pesticin outer membrane receptor (IRPC)	Escherichia coli (strain 55989 / EAEC)
19693	1183774	1184514	TY-2482_chromosome	E6B2Q6	Uncharacterized yeeJ domain protein	Escherichia coli 3431
19320	1184444	1186950	TY-2482_chromosome	F1ZIR7	Putative uncharacterized protein	Escherichia coli STEC_7v
83598	1188103	1189416	TY-2482_chromosome	B7L909	Shikimate transporter	Escherichia coli (strain 55989 / EAEC)
114088	1189521	1190972	TY-2482_chromosome	B7L910	AMP nucleosidase (EC 3.2.2.4)	Escherichia coli (strain 55989 / EAEC)
114089	1191318	1192031	TY-2482_chromosome	B7L911	UPF0082 protein yeeN 2	Escherichia coli (strain 55989 / EAEC)
29322	1192374	1192093	TY-2482_chromosome	A1ACI3	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
r402	1192561	1192486	TY-2482_chromosome	ref|NC_010473|:2151292-2151367|Asn tRNA| [gene=asnV] [locus_tag=ECDH10B_2133]		
112766	1194302	1192665	TY-2482_chromosome	B7L912	Putative Na+-driven multidrug efflux system	Escherichia coli (strain 55989 / EAEC)
r400	1194310	1194385	TY-2482_chromosome	ref|NC_010473|:2151292-2151367|Asn tRNA| [gene=asnV] [locus_tag=ECDH10B_2133]		
95626	1195373	1194426	TY-2482_chromosome	B7L913	DNA-binding transcriptional activator of cysteine biosynthesis	Escherichia coli (strain 55989 / EAEC)
61810	1196392	1195478	TY-2482_chromosome	B7L914	DNA-binding transcriptional dual regulator of nitrogen assimilation	Escherichia coli (strain 55989 / EAEC)
r401	1196719	1196794	TY-2482_chromosome	ref|NC_010473|:2151292-2151367|Asn tRNA| [gene=asnV] [locus_tag=ECDH10B_2133]		
76517	1197782	1196853	TY-2482_chromosome	B7L915	Putative uncharacterized protein erfK	Escherichia coli (strain 55989 / EAEC)
30371	1198926	1197850	TY-2482_chromosome	B7L916	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (NN:DBI PRT) (EC 2.4.2.21) (N(1)-alpha-pho	Escherichia coli (strain 55989 / EAEC)
30368	1199681	1198941	TY-2482_chromosome	B7L917	Cobalamin synthase (EC 2.-.-.-)	Escherichia coli (strain 55989 / EAEC)
75287	1200223	1199681	TY-2482_chromosome	B7L918	Bifunctional cobinamide kinase and cobinamide phosphate guanylyltransferase	Escherichia coli (strain 55989 / EAEC)
20921	1200852	1200617	TY-2482_chromosome	D8CLM5	Conserved domain protein	Escherichia coli MS 185-1
9353	1201798	1202144	TY-2482_chromosome	Q6EZC1	L0015-like protein	Escherichia coli
71526	1202286	1203497	TY-2482_chromosome	B7L922	Putative carbohydrate kinase (EC 2.7.1.15)	Escherichia coli (strain 55989 / EAEC)
112254	1203514	1204269	TY-2482_chromosome	B7L923	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
15666	1204329	1205291	TY-2482_chromosome	C2DPG0	Membrane protein	Escherichia coli 83972
99192	1205297	1206328	TY-2482_chromosome	B7L926	Putative phosphotriesterase-related protein (EC 3.1.8.1)	Escherichia coli (strain 55989 / EAEC)
71619	1206699	1206374	TY-2482_chromosome	D3GYL6	Gamma-glutamyltranspeptidase (Fragment)	Escherichia coli O44:H18 (strain 042 / EAEC)
91847	1208362	1206986	TY-2482_chromosome	B7L930	Putative transposase, ISL3 family	Escherichia coli (strain 55989 / EAEC)
77472	1209143	1208649	TY-2482_chromosome	B7L931	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26506	1209411	1210277	TY-2482_chromosome	A7ZVI3	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC)
91957	1209451	1209047	TY-2482_chromosome	B7L932	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
19075	1210748	1210432	TY-2482_chromosome	E9TFH8	Putative uncharacterized protein	Escherichia coli MS 117-3
26050	1211074	1211421	TY-2482_chromosome	Q0TGB3	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)

64210	1211600	1212004	TY-2482_chromosome	B7L934	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
64752	1211628	1211395	TY-2482_chromosome	C8U534	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
75581	1211947	1212700	TY-2482_chromosome	C8TTS1	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
81070	1213131	1213388	TY-2482_chromosome	B7L936	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104857	1215197	1213665	TY-2482_chromosome	B7L938	Putative transposase ORF 1, IS66 family	Escherichia coli (strain 55989 / EAEC)
77474	1215594	1215250	TY-2482_chromosome	B7L939	Putative transposase ORF 2, IS66 family	Escherichia coli (strain 55989 / EAEC)
18624	1215974	1215594	TY-2482_chromosome	D8AYZ0	Transposase	Escherichia coli MS 175-1
11094	1216020	1216335	TY-2482_chromosome	D8APM5	Conserved domain protein	Escherichia coli MS 116-1
22710	1216531	1216325	TY-2482_chromosome	D7ZIU0	Putative uncharacterized protein	Escherichia coli MS 69-1
27111	1216960	1216568	TY-2482_chromosome	Q0TGA2	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
104404	1217530	1218690	TY-2482_chromosome	B7L940	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104656	1218660	1219645	TY-2482_chromosome	C8TV65	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
90075	1219866	1222259	TY-2482_chromosome	B7L943	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
69909	1222259	1223161	TY-2482_chromosome	B7L944	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
86491	1223161	1224228	TY-2482_chromosome	B7L945	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
90292	1224259	1225047	TY-2482_chromosome	B7L946	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
79178	1225066	1225473	TY-2482_chromosome	B7L947	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
20593	1225709	1225476	TY-2482_chromosome	D8EDM2	Conserved domain protein	Escherichia coli MS 119-7
26662	1226545	1225706	TY-2482_chromosome	B2TXM8	Putative uncharacterized protein	Shigella boydii serotype 18 (strain CDC 3083-94 / BS512)
47872	1227559	1226588	TY-2482_chromosome	Q5K5L6	Putative uncharacterized protein	Escherichia coli
22615	1228180	1228756	TY-2482_chromosome	E9TQB2	Conserved domain protein (Fragment)	Escherichia coli MS 60-1
21993	1228759	1229073	TY-2482_chromosome	D7YLU2	Conserved domain protein	Escherichia coli MS 182-1
7929	1229391	1229744	TY-2482_chromosome	Q1RA65	Uncharacterized protein yoeF	Escherichia coli (strain UTI89 / UPEC)
60812	1230243	1229851	TY-2482_chromosome	B7L9N3	Putative uncharacterized protein yeeX	Escherichia coli (strain 55989 / EAEC)
97818	1230882	1230352	TY-2482_chromosome	C8U552	Conserved predicted inner membrane protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
115754	1231942	1230965	TY-2482_chromosome	B7LF78	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
11025	1232686	1232009	TY-2482_chromosome	B3WPJ5	Inner membrane protein YeeA	Escherichia coli B171
23469	1233384	1232887	TY-2482_chromosome	D8B6I8	Bacterial transcription activator, effector binding domain protein (Fragment	Escherichia coli MS 175-1
60863	1234642	1233479	TY-2482_chromosome	B7L9N6	D-alanyl-D-alanine carboxypeptidase (Penicillin-binding protein 6b) (EC 3.4.16.4	Escherichia coli (strain 55989 / EAEC)
88388	1234851	1236275	TY-2482_chromosome	B7L9N7	Exonuclease I (EC 3.1.11.1)	Escherichia coli (strain 55989 / EAEC)
88389	1236548	1236324	TY-2482_chromosome	B7L9N8	Putative uncharacterized protein yeeD	Escherichia coli (strain 55989 / EAEC)
79565	1237620	1236565	TY-2482_chromosome	B7L9N9	Putative uncharacterized protein yeeE	Escherichia coli (strain 55989 / EAEC)
115224	1239157	1237802	TY-2482_chromosome	B7L9P0	Putative amino-acid/amine transporter	Escherichia coli (strain 55989 / EAEC)
91891	1240353	1239427	TY-2482_chromosome	B7L9P1	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
66367	1241223	1240402	TY-2482_chromosome	B7L9P2	Putative epimerase, with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
69998	1241560	1241309	TY-2482_chromosome	B7L9P3	Toxin of the YoeB-YefM toxin-antitoxin system	Escherichia coli (strain 55989 / EAEC)
73408	1241835	1241560	TY-2482_chromosome	A1ACN0	Antitoxin of the YoeB-YefM toxin-antitoxin system	Escherichia coli O1:K1 / APEC
31381	1242288	1243184	TY-2482_chromosome	B7L9P6	ATP phosphoribosyltransferase (ATP-PRT) (ATP-PRTase) (EC 2.4.2.17)	Escherichia coli (strain 55989 / EAEC)
79888	1243193	1244494	TY-2482_chromosome	B7L9P7	Histidinol dehydrogenase (HDH) (EC 1.1.1.23)	Escherichia coli (strain 55989 / EAEC)
31399	1244494	1245561	TY-2482_chromosome	B7L9P8	Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase)	Escherichia coli (strain 55989 / EAEC)
105393	1245564	1246628	TY-2482_chromosome	B7L9P9	Fused histidinol-phosphatase ; imidazoleglycerol-phosphate dehydratase (EC 3.1.3.15) (EC 4.2.1.19)	Escherichia coli (strain 55989 / EAEC)
68710	1246631	1247218	TY-2482_chromosome	B7L9Q0	Imidazole glycerol phosphate synthase, glutamine amidotransferase subunit with HisF (EC 2.4.2.-)	Escherichia coli (strain 55989 / EAEC)
31387	1247221	1247955	TY-2482_chromosome	B7L9Q1	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase (EC 5.3.1.1	Escherichia coli (strain 55989 / EAEC)
31393	1247940	1248713	TY-2482_chromosome	B7L9Q2	Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP synthase cyclase subunit) (IGP synthase subunit	Escherichia coli (strain 55989 / EAEC)
81014	1248710	1249318	TY-2482_chromosome	B7L9Q3	Fused phosphoribosyl-AMP cyclohydrolase ; phosphoribosyl-ATP pyrophosphatase (EC 3.5.4.19) (EC 3.6.1.31	Escherichia coli (strain 55989 / EAEC)
66258	1250399	1249422	TY-2482_chromosome	B7L9Q4	Regulator of length of O-antigen component of lipopolysaccharide chains	Escherichia coli (strain 55989 / EAEC)
114040	1251709	1250546	TY-2482_chromosome	B7L9Q5	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	Escherichia coli (strain 55989 / EAEC)
81015	1253363	1251960	TY-2482_chromosome	B7L9Q6	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Escherichia coli (strain 55989 / EAEC)
108192	1254302	1253487	TY-2482_chromosome	B7L9Q7	Glycosyl transferase, putative	Escherichia coli (strain 55989 / EAEC)
115408	1255610	1254318	TY-2482_chromosome	B7L9Q8	Wzx	Escherichia coli (strain 55989 / EAEC)
71810	1256815	1255595	TY-2482_chromosome	B7L9Q9	WbwB	Escherichia coli (strain 55989 / EAEC)
19996	1257933	1256824	TY-2482_chromosome	Q93NP8	Wzy	Escherichia coli
102860	1258880	1257933	TY-2482_chromosome	B7L9R0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104459	1260128	1258968	TY-2482_chromosome	B7L9R1	NnaA	Escherichia coli (strain 55989 / EAEC)
66267	1261390	1260128	TY-2482_chromosome	B7L9R2	NnaC (EC 2.7.7.43)	Escherichia coli (strain 55989 / EAEC)
106402	1262436	1261399	TY-2482_chromosome	B7L9R3	NnaB (EC 2.5.1.57)	Escherichia coli (strain 55989 / EAEC)
67967	1263061	1262444	TY-2482_chromosome	B7L9R4	WckD	Escherichia coli (strain 55989 / EAEC)
94999	1264315	1263425	TY-2482_chromosome	B7L9R5	Putative subunit with GalU	Escherichia coli (strain 55989 / EAEC)
116017	1265553	1264561	TY-2482_chromosome	B7L9R6	UDP-N-acetylglucosamine 4-epimerase (UDP-GlcNAc 4-epimerase) (EC 5.1.3.7)	Escherichia coli (strain 55989 / EAEC)
106403	1267105	1265714	TY-2482_chromosome	B7L9R7	Putative colanic acid biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
64475	1268336	1267119	TY-2482_chromosome	B7L9R8	Putative glycosyl transferase	Escherichia coli (strain 55989 / EAEC)
66268	1269613	1268336	TY-2482_chromosome	B7L9R9	Putative pyruvyl transferase	Escherichia coli (strain 55989 / EAEC)
16010	1269893	1269624	TY-2482_chromosome	E1I6L3	Putative uncharacterized protein	Escherichia coli MS 78-1
82363	1271376	1269901	TY-2482_chromosome	B7L9S0	Colanic acid exporter	Escherichia coli (strain 55989 / EAEC)

114046	1272772	1271381	TY-2482_chromosome	B7L9S1	Putative UDP-sugar lipid carrier transferase	Escherichia coli (strain 55989 / EAEC)
84535	1274197	1272830	TY-2482_chromosome	B7L9S2	Phosphomannomutase (EC 5.4.2.8)	Escherichia coli (strain 55989 / EAEC)
60970	1276090	1274657	TY-2482_chromosome	B7L9S3	Mannose-1-phosphate guanyltransferase (EC 2.7.7.22)	Escherichia coli (strain 55989 / EAEC)
108497	1277316	1276096	TY-2482_chromosome	B7L9S4	Putative glycosyl transferase	Escherichia coli (strain 55989 / EAEC)
67752	1277792	1277316	TY-2482_chromosome	B7L9S5	GDP-mannose mannosyl hydrolase (EC 1.1.1.271)	Escherichia coli (strain 55989 / EAEC)
105113	1278760	1277798	TY-2482_chromosome	B7L9S6	Bifunctional GDP-fucose synthetase: GDP-4-dehydro-6-deoxy-D-mannose epimerase and GDP-4-dehydro-6-L-deoxyga	Escherichia coli (strain 55989 / EAEC)
113176	1279884	1278766	TY-2482_chromosome	B7L9S7	GDP-D-mannose dehydratase, NAD(P)-binding (EC 4.2.1.47)	Escherichia coli (strain 55989 / EAEC)
73309	1280459	1279914	TY-2482_chromosome	B7L9S8	Putative glycose-acyl transferase	Escherichia coli (strain 55989 / EAEC)
102841	1281221	1280478	TY-2482_chromosome	B7L9S9	Putative glycosyl transferase	Escherichia coli (strain 55989 / EAEC)
86059	1282449	1281235	TY-2482_chromosome	B7L9T0	Putative colanic acid polymerase	Escherichia coli (strain 55989 / EAEC)
99114	1283641	1282427	TY-2482_chromosome	B7L9T1	Putative glycosyl transferase	Escherichia coli (strain 55989 / EAEC)
88392	1284126	1283641	TY-2482_chromosome	B7L9T2	Putative acyl transferase	Escherichia coli (strain 55989 / EAEC)
89942	1284968	1284132	TY-2482_chromosome	B7L9T3	Putative glycosyl transferase	Escherichia coli (strain 55989 / EAEC)
95580	1287308	1285149	TY-2482_chromosome	B7L9T4	Protein-tyrosine kinase (EC 2.7.10.2)	Escherichia coli (strain 55989 / EAEC)
70013	1287754	1287314	TY-2482_chromosome	B7L9T5	Protein-tyrosine phosphatase (EC 3.1.3.48)	Escherichia coli (strain 55989 / EAEC)
95582	1288899	1287763	TY-2482_chromosome	B7L9T6	Lipoprotein required for capsular polysaccharide translocation through the outer membrane	Escherichia coli (strain 55989 / EAEC)
88393	1289558	1291138	TY-2482_chromosome	B7L9T7	Fused putative membrane protein ; putative membrane protein	Escherichia coli (strain 55989 / EAEC)
108635	1293268	1291418	TY-2482_chromosome	B7L9T8	Putative inner membrane protein involved in outer membrane protein assembly	Escherichia coli (strain 55989 / EAEC)
30557	1293871	1293293	TY-2482_chromosome	B7L9T9	Deoxycytidine triphosphate deaminase (dCTP deaminase) (EC 3.5.4.13)	Escherichia coli (strain 55989 / EAEC)
110392	1294604	1293966	TY-2482_chromosome	B7L9U0	Uridine kinase (EC 2.7.1.48) (Cytidine monophosphokinase) (Uridine monophosphokinase)	Escherichia coli (strain 55989 / EAEC)
112782	1294922	1298236	TY-2482_chromosome	B7L9U1	Putative diguanylate cyclase, GGDEF domain signalling protein	Escherichia coli (strain 55989 / EAEC)
105170	1299135	1298281	TY-2482_chromosome	B7L9U2	3-methyl-adenine DNA glycosylase II (EC 3.2.2.21)	Escherichia coli (strain 55989 / EAEC)
68173	1299269	1300618	TY-2482_chromosome	B7L9U3	Putative chaperone	Escherichia coli (strain 55989 / EAEC)
112012	1302582	1300636	TY-2482_chromosome	B7L9U4	Putative uncharacterized protein yegI	Escherichia coli (strain 55989 / EAEC)
91905	1303331	1302573	TY-2482_chromosome	B7L9U5	Putative uncharacterized protein yegK	Escherichia coli (strain 55989 / EAEC)
106513	1303987	1303331	TY-2482_chromosome	B7L9U6	Putative uncharacterized protein yegL	Escherichia coli (strain 55989 / EAEC)
r116	1304134	1304282	TY-2482_chromosome	ref|NC_010473|:2242307-2242455|-| [gene=ryeC] [locus_tag=ECDH10B_2224		
r118	1304469	1304611	TY-2482_chromosome	ref|NC_010473|:2242642-2242784|-| [gene=ryeD] [locus_tag=ECDH10B_2225		
r119	1304797	1304939	TY-2482_chromosome	ref|NC_010473|:2242642-2242784|-| [gene=ryeD] [locus_tag=ECDH10B_2225		
32124	1305203	1306447	TY-2482_chromosome	B7L9U7	Multidrug resistance protein mdtA (Multidrug transporter mdtA)	Escherichia coli (strain 55989 / EAEC)
32134	1306450	1309569	TY-2482_chromosome	B7L9U8	Multidrug resistance protein MdtB (Multidrug transporter MdtB)	Escherichia coli (strain 55989 / EAEC)
32166	1309573	1312647	TY-2482_chromosome	B7L9U9	Multidrug resistance protein MdtC (Multidrug transporter MdtC)	Escherichia coli (strain 55989 / EAEC)
32198	1312651	1314063	TY-2482_chromosome	B7L9V0	Putative multidrug resistance protein mdtD	Escherichia coli (strain 55989 / EAEC)
110393	1314063	1315463	TY-2482_chromosome	B7L9V1	Sensory histidine kinase in two-component regulatory system with BaeR	Escherichia coli (strain 55989 / EAEC)
59122	1315463	1316182	TY-2482_chromosome	B7L9V2	DNA-binding response regulator in two-component regulatory system with BaeS	Escherichia coli (strain 55989 / EAEC)
90219	1316376	1316705	TY-2482_chromosome	B7L9V3	Putative uncharacterized protein yegP	Escherichia coli (strain 55989 / EAEC)
76832	1316917	1317210	TY-2482_chromosome	B7L9V4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
79461	1317215	1317508	TY-2482_chromosome	B7L9V5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
101214	1317614	1318972	TY-2482_chromosome	B7L9V6	Putative peptidase	Escherichia coli (strain 55989 / EAEC)
r227	1319058	1319143	TY-2482_chromosome	ref|NC_010473|:2256144-2256229|-| [gene=ryeE] [locus_tag=ECDH10B_2234		
107696	1319682	1319260	TY-2482_chromosome	D3GZE6	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
34887	1320037	1320933	TY-2482_chromosome	B7L9V9	Probable lipid kinase YegS (EC 2.7.1.-)	Escherichia coli (strain 55989 / EAEC)
83802	1321797	1321021	TY-2482_chromosome	B7L9W0	Galactitol utilization operon repressor	Escherichia coli (strain 55989 / EAEC)
102893	1322937	1321900	TY-2482_chromosome	B7L9W1	Galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding (EC 1.1.1.251)	Escherichia coli (strain 55989 / EAEC)
77412	1324340	1322988	TY-2482_chromosome	B7L9W2	Galactitol-specific enzyme IIC component of PTS	Escherichia coli (strain 55989 / EAEC)
101548	1324628	1324347	TY-2482_chromosome	B7L9W3	Galactitol-specific enzyme IIB component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
108566	1325111	1324662	TY-2482_chromosome	B7L9W4	Galactitol-specific enzyme IIA component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
106591	1326378	1325124	TY-2482_chromosome	C6V1J1	D-tagatose-1,6-bisphosphate aldolase subunit gatZ	Escherichia coli O157:H7 (strain TW14359 / EHEC
31074	1327261	1326410	TY-2482_chromosome	B7L9W7	D-tagatose-1,6-bisphosphate aldolase subunit GatY (TBPA) (TagBP aldolase) (EC 4.1.2.40) (D-tagatose-bisphosphate a	Escherichia coli (strain 55989 / EAEC)
80956	1328623	1327574	TY-2482_chromosome	B7L9W8	Fructose-bisphosphate aldolase class I (EC 4.1.2.13)	Escherichia coli (strain 55989 / EAEC)
102225	1328880	1330154	TY-2482_chromosome	B7L9W9	Putative hydrophilic substrate transporter; MFS superfamily	Escherichia coli (strain 55989 / EAEC)
59127	1330154	1331155	TY-2482_chromosome	B7L9X0	Putative (Phospho)hydrolase	Escherichia coli (strain 55989 / EAEC)
91906	1331155	1332117	TY-2482_chromosome	B7L9X1	Putative kinase	Escherichia coli (strain 55989 / EAEC)
98180	1332840	1332097	TY-2482_chromosome	B7L9X2	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
18219	1333738	1332895	TY-2482_chromosome	E7IBA7	Glycosyl hydrolases family 25 family protein	Escherichia coli LT-68
78969	1334575	1333778	TY-2482_chromosome	B7L9X4	Bifunctional hydroxy-methylpyrimidine kinase and hydroxy-phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7	Escherichia coli (strain 55989 / EAEC)
34260	1335360	1334575	TY-2482_chromosome	B7L9X5	Hydroxyethylthiazole kinase (EC 2.7.1.50) (4-methyl-5-beta-hydroxyethylthiazole kinase) (TH kinase) (Thz kinase)	Escherichia coli (strain 55989 / EAEC)
16995	1335391	1335594	TY-2482_chromosome	E1I695	Putative uncharacterized protein	Escherichia coli MS 78-1
82977	1335855	1335586	TY-2482_chromosome	B7L9X6	Putative uncharacterized protein yohL	Escherichia coli (strain 55989 / EAEC)
99141	1335976	1336797	TY-2482_chromosome	B7L9X7	Nickel and cobalt resistance	Escherichia coli (strain 55989 / EAEC)
102896	1336839	1337354	TY-2482_chromosome	B7L9X8	Putative uncharacterized protein yohN	Escherichia coli (strain 55989 / EAEC)
110652	1338473	1337442	TY-2482_chromosome	B7L9X9	Putative exported fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
62664	1340969	1338492	TY-2482_chromosome	B7L9Y0	Putative uncharacterized protein yehB	Escherichia coli (strain 55989 / EAEC)
6882	1341692	1340988	TY-2482_chromosome	P33342	Uncharacterized fimbrial chaperone yehC	Escherichia coli (strain K12)

99142	1342282	1341743	TY-2482_chromosome	B7L9Y3	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
90223	1342856	1342578	TY-2482_chromosome	B7L9Y4	Putative uncharacterized protein yehE	Escherichia coli (strain 55989 / EAEC)
93254	1344228	1343122	TY-2482_chromosome	B7L9Y5	Antiporter inner membrane protein	Escherichia coli (strain 55989 / EAEC)
34153	1344360	1346390	TY-2482_chromosome	B7L9Y6	Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase) (MetRS)	Escherichia coli (strain 55989 / EAEC)
100430	1346534	1350325	TY-2482_chromosome	D3GZY0	Putative nucleic acid binding protein (Putative regulator)	Escherichia coli O44:H18 (strain 042 / EAEC)
88988	1350332	1353967	TY-2482_chromosome	C8U658	Conserved predicted protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
6887	1354031	1354345	TY-2482_chromosome	P33347	Uncharacterized protein yehK	Escherichia coli (strain K12)
106062	1355588	1356673	TY-2482_chromosome	C8UD52	Predicted transporter subunit	Escherichia coli O111:H- (strain 11128 / EHEC)
99764	1356687	1358963	TY-2482_chromosome	C8U663	Conserved predicted protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
99724	1358959	1360092	TY-2482_chromosome	C6V1M4	Conserved protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
114876	1360092	1362089	TY-2482_chromosome	C8TU47	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
79002	1362205	1362675	TY-2482_chromosome	D3GZY8	Putative exported protein	Escherichia coli O44:H18 (strain 042 / EAEC)
17081	1363246	1362722	TY-2482_chromosome	D6IBS4	YehS protein	Escherichia coli B185
73595	1363955	1363239	TY-2482_chromosome	B7L9Z1	Response regulator in two-component system with YehU	Escherichia coli (strain 55989 / EAEC)
104324	1365637	1363955	TY-2482_chromosome	B7L9Z2	Sensory kinase in two-component system with YehT	Escherichia coli (strain 55989 / EAEC)
86186	1365859	1366587	TY-2482_chromosome	B7L9Z3	DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
17741	1366778	1366590	TY-2482_chromosome	D7YJB0	Conserved domain protein	Escherichia coli MS 182-1
84581	1367469	1366741	TY-2482_chromosome	B7L9Z5	Putative transporter subunit: permease component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
93782	1368400	1367477	TY-2482_chromosome	B7L9Z6	Putative transporter subunit: ATP-binding component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
81020	1369550	1368396	TY-2482_chromosome	B7L9Z7	Putative transporter subunit: permease component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
75964	1370474	1369560	TY-2482_chromosome	B7L9Z8	Putative transporter subunit: periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
91851	1372982	1370688	TY-2482_chromosome	B7L9Z9	Beta-D-glucoside glucohydrolase, periplasmic (EC 3.2.1.21)	Escherichia coli (strain 55989 / EAEC)
83904	1373178	1374890	TY-2482_chromosome	B7LA00	D-lactate dehydrogenase, FAD-binding, NADH independent (EC 1.1.1.28)	Escherichia coli (strain 55989 / EAEC)
81121	1375863	1374934	TY-2482_chromosome	B7LA01	D-alanyl-D-alanine endopeptidase (EC 3.4.24.-)	Escherichia coli (strain 55989 / EAEC)
111904	1376648	1376040	TY-2482_chromosome	B5YW61	Putative membrane protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
101384	1376758	1377369	TY-2482_chromosome	D3H001	Putative membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
102897	1378263	1377505	TY-2482_chromosome	B7LA04	Putative oxidoreductase with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
91253	1379404	1378319	TY-2482_chromosome	B7LA05	Putative uncharacterized protein yohG	Escherichia coli (strain 55989 / EAEC)
97353	1380069	1380398	TY-2482_chromosome	C6V2L9	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
93255	1381379	1380435	TY-2482_chromosome	B7LA06	tRNA-dihydrouridine synthase (EC 1.-.-.-)	Escherichia coli (strain 55989 / EAEC)
35043	1381618	1382013	TY-2482_chromosome	B7LA07	UPF0299 membrane protein yohJ	Escherichia coli (strain 55989 / EAEC)
94817	1382013	1382705	TY-2482_chromosome	B7LA08	Putative uncharacterized protein yohK	Escherichia coli (strain 55989 / EAEC)
30270	1382838	1383719	TY-2482_chromosome	B7LA09	Cytidine deaminase (EC 3.5.4.5) (Cytidine aminohydrolase) (CDA)	Escherichia coli (strain 55989 / EAEC)
90366	1383872	1384588	TY-2482_chromosome	B7LA10	Putative uncharacterized protein sanA	Escherichia coli (strain 55989 / EAEC)
115300	1384594	1384830	TY-2482_chromosome	B7LAG5	Putative uncharacterized protein yeiS	Escherichia coli (strain 55989 / EAEC)
110498	1385152	1386387	TY-2482_chromosome	B7LAG6	Putative Fe-S cluster containing oxidoreductase subunit	Escherichia coli (strain 55989 / EAEC)
66297	1386413	1387616	TY-2482_chromosome	B7LAG7	Putative oxidoreductase subunit	Escherichia coli (strain 55989 / EAEC)
87288	1388700	1387693	TY-2482_chromosome	B7LAG8	Methyl-galactoside transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
77489	1390236	1388719	TY-2482_chromosome	B7LAG9	Fused methyl-galactoside transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
59187	1391295	1390300	TY-2482_chromosome	B7LAH0	Methyl-galactoside transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
95651	1392605	1392805	TY-2482_chromosome	B7LAH2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
81089	1392615	1391578	TY-2482_chromosome	B7LAH1	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
65066	1393914	1392760	TY-2482_chromosome	B7LAH3	Putative uncharacterized protein yeiB	Escherichia coli (strain 55989 / EAEC)
31085	1394599	1393934	TY-2482_chromosome	B7LAH4	GTP cyclohydrolase 1 (EC 3.5.4.16) (GTP cyclohydrolase I) (GTP-CH-I)	Escherichia coli (strain 55989 / EAEC)
102946	1394857	1395690	TY-2482_chromosome	B7LAH6	S-formylglutathione hydrolase (EC 3.1.2.12)	Escherichia coli (strain 55989 / EAEC)
66298	1397716	1395728	TY-2482_chromosome	B7LAH7	Ferric iron-catecholate outer membrane transporter	Escherichia coli (strain 55989 / EAEC)
106548	1397912	1397712	TY-2482_chromosome	B7LAH8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
75548	1399478	1398012	TY-2482_chromosome	B7LAH9	Lysine transporter	Escherichia coli (strain 55989 / EAEC)
15748	1399644	1399465	TY-2482_chromosome	D7JPX3	Predicted protein	Escherichia coli FVEC1302
79987	1400564	1399686	TY-2482_chromosome	B7LAI0	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
66366	1400663	1401709	TY-2482_chromosome	B7LAI1	Putative uncharacterized protein yeiH	Escherichia coli (strain 55989 / EAEC)
30761	1401786	1402640	TY-2482_chromosome	B7LAI2	Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV	Escherichia coli (strain 55989 / EAEC)
80547	1402647	1403732	TY-2482_chromosome	B7LAI3	Putative kinase	Escherichia coli (strain 55989 / EAEC)
95652	1405041	1403794	TY-2482_chromosome	B7LAI4	Putative sodium/proton nucleoside transporter	Escherichia coli (strain 55989 / EAEC)
33414	1406082	1405144	TY-2482_chromosome	B7LAI5	Pyrimidine-specific ribonucleoside hydrolase rihB (EC 3.2.2.8) (Cytidine/uridine-specific hydrolase	Escherichia coli (strain 55989 / EAEC)
83495	1406212	1406907	TY-2482_chromosome	B5YWV4	Regulatory protein Nsr	Escherichia coli O157:H7 (strain EC4115 / EHEC)
61803	1408228	1406981	TY-2482_chromosome	B7LAI7	Putative sodium/proton nucleoside transporter	Escherichia coli (strain 55989 / EAEC)
64365	1409260	1408325	TY-2482_chromosome	B7LAI8	Pseudouridine-5'-phosphate glycosidase (PsiMP glycosidase) (EC 3.2.-.-)	Escherichia coli (strain 55989 / EAEC)
58125	1410189	1409251	TY-2482_chromosome	B7LAI9	Putative kinase	Escherichia coli (strain 55989 / EAEC)
79465	1412304	1410616	TY-2482_chromosome	B7LAJ0	Fused fructose-specific PTS enzymes: IIBcomponent ; IIC components	Escherichia coli (strain 55989 / EAEC)
61082	1413259	1412324	TY-2482_chromosome	B7LAJ1	Fructose-1-phosphate kinase (EC 2.7.1.56)	Escherichia coli (strain 55989 / EAEC)
86966	1414389	1413262	TY-2482_chromosome	B7LAJ2	Fused fructose-specific PTS enzymes: IIA component ; HPr component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
58070	1414757	1415935	TY-2482_chromosome	B7LAJ3	Lactose/glucose efflux system	Escherichia coli (strain 55989 / EAEC)
22067	1416089	1416913	TY-2482_chromosome	D7YNX5	Elongation factor P	Escherichia coli MS 182-1

95655	1417139	1418602	TY-2482_chromosome	B7LAJ6	Putative sugar dehydrogenase, NAD-dependent	Escherichia coli (strain 55989 / EAEC)
86218	1418723	1419706	TY-2482_chromosome	B7LAJ7	Putative enzyme	Escherichia coli (strain 55989 / EAEC)
62833	1419748	1420458	TY-2482_chromosome	B7LAJ8	Undecaprenyl pyrophosphate phosphatase	Escherichia coli (strain 55989 / EAEC)
110503	1420873	1421436	TY-2482_chromosome	B7LAJ9	Putative peptidase, outer membrane lipoprotein	Escherichia coli (strain 55989 / EAEC)
108821	1421620	1423173	TY-2482_chromosome	B7LAK0	Putative uncharacterized protein rtn	Escherichia coli (strain 55989 / EAEC)
73809	1423258	1425069	TY-2482_chromosome	B7LAK1	Putative oligopeptide transporter subunit ; periplasmic-binding component of ABC superfamily transporte	Escherichia coli (strain 55989 / EAEC)
95658	1425073	1426164	TY-2482_chromosome	B7LAK2	Putative oligopeptide transporter subunit; permease component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
111575	1426167	1427189	TY-2482_chromosome	B7LAK3	Putative oligopeptide transporter subunit ; permease component of ABC superfamily transporter	Escherichia coli (strain 55989 / EAEC)
88341	1427194	1428780	TY-2482_chromosome	B7LAK4	Putative fused oligopeptide transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
77384	1429131	1428790	TY-2482_chromosome	B7LAK5	Putative uncharacterized protein yejG	Escherichia coli (strain 55989 / EAEC)
61806	1430654	1429467	TY-2482_chromosome	B7LAK6	Bicyclomycin/multidrug efflux system	Escherichia coli (strain 55989 / EAEC)
83984	1431377	1430685	TY-2482_chromosome	B7LAK7	Pseudouridine synthase (EC 5.4.99.-)	Escherichia coli (strain 55989 / EAEC)
108828	1431526	1433283	TY-2482_chromosome	B7LAK8	Putative nucleic acid ATP-dependent helicase	Escherichia coli (strain 55989 / EAEC)
25835	1433827	1433399	TY-2482_chromosome	Q1R9N3	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
32642	1434841	1433837	TY-2482_chromosome	B7LAL0	Nucleoid-associated protein YejK	Escherichia coli (strain 55989 / EAEC)
34893	1435023	1435247	TY-2482_chromosome	B7LAL1	UPF0352 protein yejL	Escherichia coli (strain 55989 / EAEC)
75116	1435270	1437027	TY-2482_chromosome	B7LAL2	Putative hydrolase, inner membrane-associated	Escherichia coli (strain 55989 / EAEC)
r287	1437105	1437181	TY-2482_chromosome	ref|NC_010473|:2375221-2375297|Pro tRNA| [gene=proL] [locus_tag=ECDH10B_2347		
113390	1439875	1437287	TY-2482_chromosome	B5YWY3	Putative autotransporter, IS5K-containing	Escherichia coli O157:H7 (strain EC4115 / EHEC)
12995	1440163	1439909	TY-2482_chromosome	E2QP58	Putative uncharacterized protein	Escherichia coli
95661	1440195	1440839	TY-2482_chromosome	B7LAL6	DNA-binding response regulator in two-component regulatory system with NarQ or NarX	Escherichia coli (strain 55989 / EAEC)
84643	1441929	1440880	TY-2482_chromosome	B7LAL7	Heme lyase, CcmH subunit	Escherichia coli (strain 55989 / EAEC)
27221	1442483	1441856	TY-2482_chromosome	Q0TFP6	Thiol:disulfide interchange protein DsbE	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
66368	1444423	1442483	TY-2482_chromosome	B7LAL9	Heme lyase, CcmF subunit	Escherichia coli (strain 55989 / EAEC)
30266	1444899	1444423	TY-2482_chromosome	B7LAM0	Cytochrome c-type biogenesis protein CcmE (Cytochrome c maturation protein E) (Heme chaperone CcmE	Escherichia coli (strain 55989 / EAEC)
106549	1445105	1444899	TY-2482_chromosome	B7LAM1	Cytochrome c biogenesis protein	Escherichia coli (strain 55989 / EAEC)
109427	1445839	1445105	TY-2482_chromosome	B7LAM2	Heme exporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
114119	1446543	1445884	TY-2482_chromosome	B7LAM3	Heme exporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
94570	1447163	1446543	TY-2482_chromosome	B7LAM4	Heme exporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
94571	1447778	1447179	TY-2482_chromosome	B7LAM5	Nitrate reductase, cytochrome c-type,periplasmic	Escherichia coli (strain 55989 / EAEC)
61545	1449097	1448237	TY-2482_chromosome	B7LAM7	Ferredoxin-type protein essential for electron transfer from ubiquinol to periplasmic nitrate reductase (NapAB	Escherichia coli (strain 55989 / EAEC)
69911	1449779	1449087	TY-2482_chromosome	B7LAM8	Ferredoxin-type protein essential for electron transfer from ubiquinol to periplasmic nitrate reductase (NapAB	Escherichia coli (strain 55989 / EAEC)
32630	1452272	1449789	TY-2482_chromosome	B7LAM9	Periplasmic nitrate reductase (EC 1.7.99.4)	Escherichia coli (strain 55989 / EAEC)
65362	1452532	1452272	TY-2482_chromosome	B7LAN0	Assembly protein for periplasmic nitrate reductase	Escherichia coli (strain 55989 / EAEC)
87785	1453016	1452525	TY-2482_chromosome	B7LAN1	Ferredoxin-type protein, putative role in electron transfer to periplasmic nitrate reductase (NapA	Escherichia coli (strain 55989 / EAEC)
24044	1453125	1453336	TY-2482_chromosome	E0IY94	Putative uncharacterized protein yojO	Escherichia coli (strain ATCC 9637 / CCM 2024 / DSM 1116 / NCIMB
30721	1453424	1453909	TY-2482_chromosome	B7LAN3	Ecotin	Escherichia coli (strain 55989 / EAEC)
32463	1455707	1454064	TY-2482_chromosome	B7LAN4	Probable malate:quinone oxidoreductase (EC 1.1.5.4) (MQO) (Malate dehydrogenase [quinone])	Escherichia coli (strain 55989 / EAEC)
91979	1457568	1455928	TY-2482_chromosome	B7LAN5	Fused multidrug transport subunits of ABC superfamily transporter: permease component/ATP-binding component	Escherichia coli (strain 55989 / EAEC)
113406	1458294	1457647	TY-2482_chromosome	B7LAN6	Oxidative demethylase of N1-methyladenine or N3-methylcytosine DNA lesions	Escherichia coli (strain 55989 / EAEC)
84644	1459358	1458297	TY-2482_chromosome	B7LAN7	Fused DNA-binding transcriptional dual regulator ; O6-methylguanine-DNA methyltransferase (EC 2.1.1.63)	Escherichia coli (strain 55989 / EAEC)
110653	1460487	1459435	TY-2482_chromosome	B7LAN8	Putative thiamine biosynthesis lipoprotein; defective assembly or repair of ThiH Fe-S cluster	Escherichia coli (strain 55989 / EAEC)
62632	1461702	1460602	TY-2482_chromosome	B7LAN9	Outer membrane porin protein C	Escherichia coli (strain 55989 / EAEC)
11425	1461983	1462207	TY-2482_chromosome	D6JCB6	Putative uncharacterized protein	Escherichia coli B354
r199	1462037	1462129	TY-2482_chromosome	ref|NC_010473|:2402094-2402186|-| [gene=micF] [locus_tag=ECDH10B_2373		
62834	1462441	1465110	TY-2482_chromosome	B7LAP0	Phosphotransfer intermediate protein in two-component regulatory system with RcsBC	Escherichia coli (strain 55989 / EAEC)
81095	1465130	1465777	TY-2482_chromosome	B7LAP1	DNA-binding response regulator in two-component regulatory system with RcsC and YojN	Escherichia coli (strain 55989 / EAEC)
107975	1468781	1465983	TY-2482_chromosome	B7LAP2	Hybrid sensory kinase in two-component regulatory system with RcsB and YojN	Escherichia coli (strain 55989 / EAEC)
104390	1469880	1469107	TY-2482_chromosome	B7LAP3	Putative uncharacterized protein yfaP	Escherichia coli (strain 55989 / EAEC)
99212	1471534	1469888	TY-2482_chromosome	B7LAP4	Putative uncharacterized protein yfaQ	Escherichia coli (strain 55989 / EAEC)
81096	1476154	1471538	TY-2482_chromosome	B7LAP5	Putative large extracellular alpha-helical protein	Escherichia coli (strain 55989 / EAEC)
88363	1476696	1476076	TY-2482_chromosome	B7LAP6	Putative uncharacterized protein yfaT	Escherichia coli (strain 55989 / EAEC)
73676	1478381	1476696	TY-2482_chromosome	B7LAP7	Putative uncharacterized protein yfaA	Escherichia coli (strain 55989 / EAEC)
91980	1481157	1478533	TY-2482_chromosome	B7LAP8	DNA gyrase (Type II topoisomerase), subunit A (EC 5.99.1.3)	Escherichia coli (strain 55989 / EAEC)
5655	1481304	1482023	TY-2482_chromosome	B7LAP9	3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64) (3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase)	Escherichia coli (strain 55989 / EAEC)
98483	1485888	1482157	TY-2482_chromosome	B7LAQ0	Adhesin	Escherichia coli (strain 55989 / EAEC)
66302	1486584	1488866	TY-2482_chromosome	B7LAQ1	Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Escherichia coli (strain 55989 / EAEC)
14754	1486585	1486316	TY-2482_chromosome	B3HLS5	Conserved domain protein	Escherichia coli F11
97332	1488958	1490085	TY-2482_chromosome	B7LAQ2	Ribonucleoside diphosphate reductase 1, beta subunit, ferritin-like (EC 1.17.4.1	Escherichia coli (strain 55989 / EAEC)
64128	1490088	1490339	TY-2482_chromosome	B7LAQ3	Putative 2Fe-2S cluster-containing protein; putative oxidoreductase subunit	Escherichia coli (strain 55989 / EAEC)
115996	1491046	1490399	TY-2482_chromosome	B7LAQ4	Putative uncharacterized protein inaA	Escherichia coli (strain 55989 / EAEC)
2664	1492283	1491303	TY-2482_chromosome	P0CE57	Transposase insH for insertion sequence element IS5R	Escherichia coli (strain K12)
94400	1492425	1492664	TY-2482_chromosome	B5YX24	Conserved domain protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
115658	1493785	1492712	TY-2482_chromosome	B7LAQ7	Periplasmic glycerophosphodiester phosphodiesterase (EC 3.1.4.46)	Escherichia coli (strain 55989 / EAEC)

95663	1495148	1493793	TY-2482_chromosome	B7LAQ8	sn-glycerol-3-phosphate transporter	Escherichia coli (strain 55989 / EAEC)
24500	1495199	1495393	TY-2482_chromosome	A7ZP61	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
110654	1495421	1497046	TY-2482_chromosome	B7LAQ9	sn-glycerol-3-phosphate dehydrogenase (Anaerobic) , large subunit, FAD/NAD(P)-binding (EC 1.1.99.5	Escherichia coli (strain 55989 / EAEC)
31156	1497039	1498295	TY-2482_chromosome	B7LAR0	Anaerobic glycerol-3-phosphate dehydrogenase subunit B (Anaerobic G-3-P dehydrogenase subunit B) (Anaerobic G3	Escherichia coli (strain 55989 / EAEC)
87833	1498295	1499482	TY-2482_chromosome	B7LAR1	sn-glycerol-3-phosphate dehydrogenase (Anaerobic) , small subunit (EC 1.1.99.5)	Escherichia coli (strain 55989 / EAEC)
99213	1499679	1500578	TY-2482_chromosome	B7LAR2	Putative uncharacterized protein yfaD	Escherichia coli (strain 55989 / EAEC)
24844	1501134	1500625	TY-2482_chromosome	A7ZP66	HpcH/HpaI aldolase/citrate lyase family protein	Escherichia coli O139:H28 (strain E24377A / ETEC
30302	1502349	1501150	TY-2482_chromosome	B7LAR4	CinA-like protein	Escherichia coli (strain 55989 / EAEC)
95407	1502991	1502452	TY-2482_chromosome	B7LAR5	Putative outer membrane porin protein	Escherichia coli (strain 55989 / EAEC)
32732	1503270	1503692	TY-2482_chromosome	B7LAR6	Nucleoside triphosphatase nudI (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
192	1504357	1503737	TY-2482_chromosome	Q31YK5	Lipopolysaccharide core heptose(II)-phosphate phosphatase (EC 3.1.3.-)	Shigella boydii serotype 4 (strain Sb227)
29865	1504644	1505780	TY-2482_chromosome	B7LAR8	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase (EC 2.6.1.87) (UDP-(beta-L-threo-pentapyranosyl-	Escherichia coli (strain 55989 / EAEC)
29873	1505787	1506752	TY-2482_chromosome	B7LAR9	Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase (EC 2.7.8.30) (Undecaprenyl-phosphate Ara4	Escherichia coli (strain 55989 / EAEC)
29859	1506755	1508734	TY-2482_chromosome	B7LAS0	Bifunctional polymyxin resistance protein ArnA [Includes: UDP-4-amino-4-deoxy-L-arabinose formyltransferase (EC 2.	Escherichia coli (strain 55989 / EAEC)
29877	1508734	1509621	TY-2482_chromosome	B7LAS1	Probable 4-deoxy-4-formamido-L-arabinose-phosphoundecaprenol deformylase ArnD (EC 3.5.1.n3	Escherichia coli (strain 55989 / EAEC)
29887	1509624	1511273	TY-2482_chromosome	B7LAS2	Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase (EC 2.4.2.43) (4-amino-4-deoxy-	Escherichia coli (strain 55989 / EAEC)
12392	1511326	1511991	TY-2482_chromosome	D6I9J9	Polymyxin resistance protein PmrM	Escherichia coli B185
114120	1512254	1511991	TY-2482_chromosome	B7LAS5	Polymyxin resistance protein B	Escherichia coli (strain 55989 / EAEC)
73677	1513719	1512367	TY-2482_chromosome	B7LAS6	O-succinylbenzoate-CoA ligase (EC 6.2.1.26)	Escherichia coli (strain 55989 / EAEC)
32239	1514678	1513719	TY-2482_chromosome	B7LAS7	o-succinylbenzoate synthase (OSB synthase) (OSBS) (EC 4.2.1.113) (4-(2'-carboxyphenyl)-4-oxybutyric acid synthase) (	Escherichia coli (strain 55989 / EAEC)
59188	1515535	1514681	TY-2482_chromosome	B7LAS8	Dihydroxynaphthoic acid synthetase (EC 4.1.3.36)	Escherichia coli (strain 55989 / EAEC)
32247	1516308	1515553	TY-2482_chromosome	B7LAS9	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase (SHCHC synthase) (EC 4.2.99.20)	Escherichia coli (strain 55989 / EAEC)
32243	1517975	1516308	TY-2482_chromosome	B7LAT0	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase (SEPHCHC synthase) (EC 2.2.1.9) (Menaqui	Escherichia coli (strain 55989 / EAEC)
58504	1519359	1518067	TY-2482_chromosome	B7LAT1	Isochorismate synthase 2 (EC 5.4.4.2)	Escherichia coli (strain 55989 / EAEC)
100764	1519743	1519441	TY-2482_chromosome	B7LAT2	Putative uncharacterized protein elaB	Escherichia coli (strain 55989 / EAEC)
73757	1520259	1519801	TY-2482_chromosome	B7LAT3	Putative acyltransferase with acyl-CoA N-acyltransferase domain	Escherichia coli (strain 55989 / EAEC)
33259	1520324	1521238	TY-2482_chromosome	B7LAT4	Ribonuclease BN (RNase BN) (EC 3.1.-.-) (Ribonuclease Z homolog) (RNase Z homolog	Escherichia coli (strain 55989 / EAEC)
89902	1521429	1522647	TY-2482_chromosome	B7LAT5	Putative enzyme	Escherichia coli (strain 55989 / EAEC)
9511	1523092	1523319	TY-2482_chromosome	D7ZXR9	Putative uncharacterized protein	Escherichia coli MS 187-1
75322	1523295	1523642	TY-2482_chromosome	B7LAT6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
93292	1523771	1524271	TY-2482_chromosome	B7LAT7	Putative uncharacterized protein yfbM	Escherichia coli (strain 55989 / EAEC)
32771	1525798	1524344	TY-2482_chromosome	B7LAT8	NADH-quinone oxidoreductase subunit N (EC 1.6.99.5) (NADH dehydrogenase I subunit N) (NDH-1 subunit N	Escherichia coli (strain 55989 / EAEC)
77459	1527334	1525808	TY-2482_chromosome	B7LAT9	NADH:ubiquinone oxidoreductase, membrane subunit M	Escherichia coli (strain 55989 / EAEC)
95633	1529339	1527501	TY-2482_chromosome	B7LAU0	NADH:ubiquinone oxidoreductase, membrane subunit L	Escherichia coli (strain 55989 / EAEC)
32767	1529638	1529339	TY-2482_chromosome	B7LAU1	NADH-quinone oxidoreductase subunit K (EC 1.6.99.5) (NADH dehydrogenase I subunit K) (NDH-1 subunit K	Escherichia coli (strain 55989 / EAEC)
116131	1530189	1529638	TY-2482_chromosome	B7LAU2	NADH:ubiquinone oxidoreductase, membrane subunit J	Escherichia coli (strain 55989 / EAEC)
97124	1530743	1530204	TY-2482_chromosome	B7LAU3	NADH-quinone oxidoreductase subunit I (EC 1.6.99.5) (NADH dehydrogenase I subunit I) (NDH-1 subunit I)	Escherichia coli (strain 55989 / EAEC)
32761	1531735	1530761	TY-2482_chromosome	B7LAU4	NADH-quinone oxidoreductase subunit H (EC 1.6.99.5) (NADH dehydrogenase I subunit H) (NDH-1 subunit H	Escherichia coli (strain 55989 / EAEC)
88439	1534464	1531735	TY-2482_chromosome	B7LAU5	NADH-quinone oxidoreductase (EC 1.6.99.5)	Escherichia coli (strain 55989 / EAEC)
94274	1535848	1534514	TY-2482_chromosome	B7LAU6	NADH:ubiquinone oxidoreductase, chain F (EC 1.6.5.3)	Escherichia coli (strain 55989 / EAEC)
73758	1536345	1535848	TY-2482_chromosome	B7LAU7	NADH:ubiquinone oxidoreductase, chain E (EC 1.6.5.3)	Escherichia coli (strain 55989 / EAEC)
32746	1538150	1536351	TY-2482_chromosome	B7LAU8	NADH-quinone oxidoreductase subunit C/D (EC 1.6.99.5) (NADH dehydrogenase I subunit C/D) (NDH-1 subunit C/D	Escherichia coli (strain 55989 / EAEC)
32742	1538906	1538247	TY-2482_chromosome	B7LBP8	NADH-quinone oxidoreductase subunit B (EC 1.6.99.5) (NADH dehydrogenase I subunit B) (NDH-1 subunit B	Escherichia coli (strain 55989 / EAEC)
86873	1539365	1538925	TY-2482_chromosome	B7LBE2	NADH-quinone oxidoreductase subunit (EC 1.6.99.5)	Escherichia coli (strain 55989 / EAEC)
28545	1539820	1539515	TY-2482_chromosome	A1ADD7	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
98082	1540934	1539999	TY-2482_chromosome	B7LBE3	DNA-binding transcriptional repressor of flagellar, motility and chemotaxis genes	Escherichia coli (strain 55989 / EAEC)
19111	1541174	1541425	TY-2482_chromosome	D6JCI7	Predicted protein	Escherichia coli B354
88481	1541854	1543068	TY-2482_chromosome	B7LBE4	Putative aminotransferase	Escherichia coli (strain 55989 / EAEC)
34897	1543155	1543751	TY-2482_chromosome	B7LBE5	UPF0207 protein yfbR	Escherichia coli (strain 55989 / EAEC)
95366	1545645	1543816	TY-2482_chromosome	B7LBE6	Putative transporter	Escherichia coli (strain 55989 / EAEC)
91627	1546382	1545735	TY-2482_chromosome	B5YXT3	Sugar-phosphatase, YfbT (EC 3.1.3.23)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
34900	1546935	1546396	TY-2482_chromosome	B7LBE8	UPF0304 protein yfbU	Escherichia coli (strain 55989 / EAEC)
34903	1547473	1547021	TY-2482_chromosome	B7LBE9	UPF0208 membrane protein yfbV	Escherichia coli (strain 55989 / EAEC)
59194	1547811	1549010	TY-2482_chromosome	B7LBF0	Acetate kinase A and propionate kinase 2 (EC 2.7.2.-) (EC 2.7.2.1)	Escherichia coli (strain 55989 / EAEC)
62841	1549088	1551229	TY-2482_chromosome	B7LBF1	Phosphate acetyltransferase (EC 2.3.1.8) (Phosphotransacetylase)	Escherichia coli (strain 55989 / EAEC)
113183	1551422	1552939	TY-2482_chromosome	B7LBF2	Putative uncharacterized protein yfcC	Escherichia coli (strain 55989 / EAEC)
104335	1553517	1552978	TY-2482_chromosome	B7LBF3	Putative NUDIX hydrolase	Escherichia coli (strain 55989 / EAEC)
58642	1554129	1553578	TY-2482_chromosome	B7LBF4	Putative phosphatase	Escherichia coli (strain 55989 / EAEC)
82642	1554826	1554185	TY-2482_chromosome	B7LBF5	Putative enzyme	Escherichia coli (strain 55989 / EAEC)
95368	1554962	1555606	TY-2482_chromosome	B7LBF6	Putative S-transferase	Escherichia coli (strain 55989 / EAEC)
102676	1555666	1556025	TY-2482_chromosome	B7LBF7	D-erythro-7,8-dihydroneopterin triphosphate 2'-epimerase and dihydroneopterin aldolase	Escherichia coli (strain 55989 / EAEC)
57964	1556049	1556939	TY-2482_chromosome	B7LBF8	Putative uncharacterized protein yfcH	Escherichia coli (strain 55989 / EAEC)
108273	1557892	1556993	TY-2482_chromosome	B7LBF9	Putative transposase	Escherichia coli (strain 55989 / EAEC)
102677	1558862	1558092	TY-2482_chromosome	B7LBG0	Histidine/lysine/arginine/ornithine transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)

70088	1559586	1558873	TY-2482_chromosome	B7LBG1	Histidine/lysine/arginine/ornithine transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
95370	1560269	1559586	TY-2482_chromosome	B7LBG2	Histidine/lysine/arginine/ornithine transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
106338	1561141	1560362	TY-2482_chromosome	B7LBG3	Histidine/lysine/arginine/ornithine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
78781	1562144	1561365	TY-2482_chromosome	B7LBG4	Lysine/arginine/ornithine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
110515	1562979	1562413	TY-2482_chromosome	B7LBG5	3-octaprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.-)	Escherichia coli (strain 55989 / EAEC)
70089	1564591	1563077	TY-2482_chromosome	B7LBG6	Amidophosphoribosyltransferase (ATase) (EC 2.4.2.14) (Glutamine phosphoribosylpyrophosphate amidotransferase)	Escherichia coli (strain 55989 / EAEC)
112245	1565116	1564631	TY-2482_chromosome	B7LBG7	Membrane protein required for colicin V production	Escherichia coli (strain 55989 / EAEC)
95372	1566037	1565378	TY-2482_chromosome	B7LBG8	Putative uncharacterized protein dedD	Escherichia coli (strain 55989 / EAEC)
114135	1567295	1566030	TY-2482_chromosome	B7LBG9	Bifunctional folylpolyglutamate synthase and dihydrofolate synthase (EC 6.3.2.12) (EC 6.3.2.17)	Escherichia coli (strain 55989 / EAEC)
76390	1568279	1567368	TY-2482_chromosome	B7LBH0	Acetyl-CoA carboxylase, beta (Carboxyltranferase) subunit (EC 6.4.1.2)	Escherichia coli (strain 55989 / EAEC)
75221	1569094	1568438	TY-2482_chromosome	B7LBH1	Putative uncharacterized protein dedA	Escherichia coli (strain 55989 / EAEC)
34359	1569989	1569180	TY-2482_chromosome	B7LBH2	tRNA pseudouridine synthase A (EC 5.4.99.12) (tRNA pseudouridine(38-40) synthase) (tRNA pseudouridylate synthase	Escherichia coli (strain 55989 / EAEC)
79805	1571002	1569992	TY-2482_chromosome	B7LBH3	Putative semialdehyde dehydrogenase	Escherichia coli (strain 55989 / EAEC)
32904	1572204	1571071	TY-2482_chromosome	B7LBH4	Erythronate-4-phosphate dehydrogenase (EC 1.1.1.290)	Escherichia coli (strain 55989 / EAEC)
59196	1572303	1573295	TY-2482_chromosome	B7LBH5	Flagella control of anti-sigma factor FlgM secretion into the periplasm	Escherichia coli (strain 55989 / EAEC)
87707	1574473	1573298	TY-2482_chromosome	B7LBH6	UPF0226 membrane protein EC55989_2566	Escherichia coli (strain 55989 / EAEC)
108036	1575977	1574760	TY-2482_chromosome	B7LBH7	3-oxoacyl-[acyl-carrier-protein] synthase I (EC 2.3.1.41)	Escherichia coli (strain 55989 / EAEC)
81106	1576136	1578139	TY-2482_chromosome	B7LBH8	tRNA 5-methylaminomethyl-2-thiouridine biosynthesis bifunctional protein mnmC (tRNA mnm(5)s(2)U biosynthesis b	Escherichia coli (strain 55989 / EAEC)
86829	1578541	1578266	TY-2482_chromosome	B7LBH9	Putative uncharacterized protein yfcL	Escherichia coli (strain 55989 / EAEC)
102692	1579123	1578578	TY-2482_chromosome	B7LBI0	Putative uncharacterized protein yfcM	Escherichia coli (strain 55989 / EAEC)
77513	1579932	1579126	TY-2482_chromosome	B7LBI1	Putative uncharacterized protein yfcA	Escherichia coli (strain 55989 / EAEC)
32251	1580756	1579935	TY-2482_chromosome	B7LBI2	Penicillin-insensitive murein endopeptidase (EC 3.4.24.-) (D-alanyl-D-alanine-endopeptidase) (DD-endopeptidase	Escherichia coli (strain 55989 / EAEC)
29900	1581845	1580763	TY-2482_chromosome	B7LBI3	Chorismate synthase (EC 4.2.3.5) (5-enolpyruvylshikimate-3-phosphate phospholyase)	Escherichia coli (strain 55989 / EAEC)
69914	1582812	1581883	TY-2482_chromosome	B7LBI4	N5-glutamine methyltransferase (EC 2.1.1.-)	Escherichia coli (strain 55989 / EAEC)
34910	1582978	1583526	TY-2482_chromosome	B7LBI5	UPF0115 protein yfcN	Escherichia coli (strain 55989 / EAEC)
115753	1584703	1583726	TY-2482_chromosome	B7LF78	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
70090	1585802	1584933	TY-2482_chromosome	B7LBI7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
71431	1586313	1585792	TY-2482_chromosome	B7LBI8	Putative fimbrial protein (Adhesin)	Escherichia coli (strain 55989 / EAEC)
86961	1586780	1586313	TY-2482_chromosome	B7LBI9	Putative fimbrial protein	Escherichia coli (strain 55989 / EAEC)
59197	1587391	1586780	TY-2482_chromosome	B7LBJ0	Putative minor fimbrial subunit	Escherichia coli (strain 55989 / EAEC)
81107	1588052	1587303	TY-2482_chromosome	B7LBJ1	Putative periplasmic pilus exported chaperone	Escherichia coli (strain 55989 / EAEC)
101575	1590714	1588075	TY-2482_chromosome	B7LBJ2	Putative outer membrane usher protein yfcU	Escherichia coli (strain 55989 / EAEC)
73815	1591359	1590799	TY-2482_chromosome	B7LBJ3	Putative fimbrial-like adhesin exported protein	Escherichia coli (strain 55989 / EAEC)
87154	1592519	1592037	TY-2482_chromosome	B7LBJ4	Phosphohistidine phosphatase (EC 3.1.3.-)	Escherichia coli (strain 55989 / EAEC)
30886	1594866	1592725	TY-2482_chromosome	B7LBJ5	Fatty acid oxidation complex subunit alpha [Includes: Enoyl-CoA hydratase/3-hydroxybutyryl-CoA epimerase (EC 4.2.1	Escherichia coli (strain 55989 / EAEC)
30870	1596176	1594869	TY-2482_chromosome	B7LBJ6	3-ketoacyl-CoA thiolase (EC 2.3.1.16) (ACSs) (Acetyl-CoA acyltransferase) (Acyl-CoA ligase) (Beta-ketothiolase) (Fatty a	Escherichia coli (strain 55989 / EAEC)
62135	1596640	1596359	TY-2482_chromosome	B7LBJ7	Putative uncharacterized protein yfcZ	Escherichia coli (strain 55989 / EAEC)
10548	1596976	1596728	TY-2482_chromosome	D6JCN8	Predicted protein	Escherichia coli B354
70091	1597006	1598349	TY-2482_chromosome	B7LBJ8	Long-chain fatty acid outer membrane transporter	Escherichia coli (strain 55989 / EAEC)
80958	1598718	1599773	TY-2482_chromosome	B7LBJ9	Putative uncharacterized protein yfdF	Escherichia coli (strain 55989 / EAEC)
59198	1600713	1599961	TY-2482_chromosome	B7LBK0	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
98177	1601007	1601936	TY-2482_chromosome	B7LBK2	Putative uncharacterized protein yfdC	Escherichia coli (strain 55989 / EAEC)
r478	1602015	1602089	TY-2482_chromosome	ref|NC_010473|:2556096-2556170|Arg tRNA| [gene=argW] [locus_tag=ECDH10B_2511]		
108643	1602251	1603405	TY-2482_chromosome	B7LBK3	Putative prophage CPS-53 integrase; CPS-53 (KpLE1) prophage	Escherichia coli (strain 55989 / EAEC)
27670	1603625	1605544	TY-2482_chromosome	B7LBK4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
29117	1607597	1605621	TY-2482_chromosome	B7LBK5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104786	1608576	1607701	TY-2482_chromosome	B5YWP4	Antirepressor protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
8215	1609055	1609303	TY-2482_chromosome	A5VW59	Phage regulatory protein	Enterobacteria phage CUS-3
9449	1609303	1609614	TY-2482_chromosome	D7X4T9	Putative uncharacterized protein	Escherichia coli MS 198-1
79643	1609607	1610125	TY-2482_chromosome	C8TUZ6	Predicted lipoprotein	Escherichia coli O26:H11 (strain 11368 / EHEC)
25402	1611990	1610146	TY-2482_chromosome	B7LTY2	DNA transfer protein from phage	Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-7
10419	1613453	1611990	TY-2482_chromosome	E7SY70	Phage DNA transfer protein	Shigella boydii ATCC 9905
111659	1614155	1613466	TY-2482_chromosome	C8TUZ9	Putative DNA transfer protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
115409	1614616	1614161	TY-2482_chromosome	B7LBL6	Head assembly protein	Escherichia coli (strain 55989 / EAEC)
107146	1615461	1614616	TY-2482_chromosome	C8TV01	Putative head DNA stabilization protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
86942	1616879	1615464	TY-2482_chromosome	B7LBL8	Packaged DNA stabilization protein from phage	Escherichia coli (strain 55989 / EAEC)
108495	1617370	1616891	TY-2482_chromosome	B7LBL9	Putative packaged DNA stabilization protein p27	Escherichia coli (strain 55989 / EAEC)
29522	1618844	1617576	TY-2482_chromosome	B7LBM1	Major head protein (P24) (Major coat protein)	Escherichia coli (strain 55989 / EAEC)
102693	1619740	1618859	TY-2482_chromosome	B7LBM2	Putative scaffold protein	Escherichia coli (strain 55989 / EAEC)
106342	1621952	1619757	TY-2482_chromosome	B7LBM3	Portal protein p19	Escherichia coli (strain 55989 / EAEC)
59199	1623295	1621886	TY-2482_chromosome	B7LBM4	Terminase large subunit	Escherichia coli (strain 55989 / EAEC)
8189	1623732	1623295	TY-2482_chromosome	A5VW76	Phage terminase small subunit	Enterobacteria phage CUS-3
67964	1623977	1623738	TY-2482_chromosome	B7LBM6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
14372	1624794	1624100	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli

28811	1625519	1626151	TY-2482_chromosome	B7LBQ5	DNA single-strand annealing protein; essential recombination function protein Er	Escherichia coli (strain 55989 / EAEC)
80882	1626064	1626534	TY-2482_chromosome	B7LBQ6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73656	1626561	1626854	TY-2482_chromosome	B7LBQ7	Anti-RecBCD protein 2	Escherichia coli (strain 55989 / EAEC)
8199	1626868	1627155	TY-2482_chromosome	Q716F1	Gene 24 protein	Enterobacteria phage Sf6 (Shigella flexneri bacteriophage VI) (Bacter
24263	1627319	1627987	TY-2482_chromosome	B7LBQ9	Putative EA22-like protein; similarities with EA22 from lambda (Modular protein involved in blocking host replication	Escherichia coli (strain 55989 / EAEC)
25073	1628163	1628348	TY-2482_chromosome	B7LBR0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
59056	1628353	1628559	TY-2482_chromosome	B7LBR1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
27445	1628559	1629185	TY-2482_chromosome	B7LBR2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
16183	1629244	1629480	TY-2482_chromosome	E9U5T6	Conserved domain protein	Escherichia coli MS 57-2
79480	1629596	1629793	TY-2482_chromosome	B7LBR3	Response regulator inhibitor for tor operon	Escherichia coli (strain 55989 / EAEC)
77364	1631573	1630329	TY-2482_chromosome	B7LBR4	Sucrose transport protein (Sucrose permease) (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
5005	1632559	1631648	TY-2482_chromosome	P40713	Fructokinase (EC 2.7.1.4)	Escherichia coli
66211	1632766	1634205	TY-2482_chromosome	B7LBR6	Sucrose-6-phosphate hydrolase (Beta-fructofuranosidase) (Sucrase) (Invertase) (EC 3.2.1.26)	Escherichia coli (strain 55989 / EAEC)
58046	1635397	1634219	TY-2482_chromosome	B7LBR7	Sucrose operon repressor (Csc operon regulatory protein)	Escherichia coli (strain 55989 / EAEC)
9988	1635442	1635657	TY-2482_chromosome	E6A6E9	GntP family permease (Fragment)	Escherichia coli MS 153-1
33903	1635678	1637003	TY-2482_chromosome	B7LBR9	D-serine dehydratase (EC 4.3.1.18) (D-serine deaminase) (DSD)	Escherichia coli (strain 55989 / EAEC)
88252	1638652	1637117	TY-2482_chromosome	B7LBS0	Putative multidrug efflux system	Escherichia coli (strain 55989 / EAEC)
108499	1639815	1638655	TY-2482_chromosome	B7LBS1	EmrKY-TolC multidrug resistance efflux pump, membrane fusion protein componen	Escherichia coli (strain 55989 / EAEC)
69953	1640231	1640842	TY-2482_chromosome	B7LBS2	DNA-binding response regulator in two-component regulatory system with EvgS	Escherichia coli (strain 55989 / EAEC)
112172	1640850	1644440	TY-2482_chromosome	B7LBS3	Hybrid sensory histidine kinase in two-component regulatory system with EvgA	Escherichia coli (strain 55989 / EAEC)
79015	1645644	1644502	TY-2482_chromosome	B7LBS4	Putative acyl-CoA-transferase, NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
72044	1646662	1645721	TY-2482_chromosome	B7LBS5	Putative transporter	Escherichia coli (strain 55989 / EAEC)
79857	1648426	1646735	TY-2482_chromosome	B7LBS6	Putative oxalyl-CoA decarboxylase	Escherichia coli (strain 55989 / EAEC)
30915	1649730	1648483	TY-2482_chromosome	B7LBS7	Formyl-coenzyme A transferase (Formyl-CoA transferase) (EC 2.8.3.16)	Escherichia coli (strain 55989 / EAEC)
94053	1650875	1650246	TY-2482_chromosome	B7LCC6	Putative uncharacterized protein yfdX	Escherichia coli (strain 55989 / EAEC)
88373	1651171	1651443	TY-2482_chromosome	B7LCC7	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
111473	1651765	1651526	TY-2482_chromosome	B7LCC8	Putative uncharacterized protein yfdY	Escherichia coli (strain 55989 / EAEC)
87786	1652118	1653035	TY-2482_chromosome	B7LCD0	Palmitoleoyl-acyl carrier protein (ACP)-dependent acyltransferase	Escherichia coli (strain 55989 / EAEC)
59012	1654768	1653533	TY-2482_chromosome	B7LCD1	Putative aminotransferase, PLP-dependent	Escherichia coli (strain 55989 / EAEC)
13971	1654888	1655193	TY-2482_chromosome	E1J8V4	Conserved domain protein	Escherichia coli MS 124-1
62622	1655145	1656839	TY-2482_chromosome	B7LCD2	Putative sensory kinase in two-component system with YpdB	Escherichia coli (strain 55989 / EAEC)
102728	1656857	1657588	TY-2482_chromosome	B7LCD3	Putative response regulator in two-component system with YpdA	Escherichia coli (strain 55989 / EAEC)
101623	1657604	1658458	TY-2482_chromosome	B7LCD4	Putative DNA-binding protein	Escherichia coli (strain 55989 / EAEC)
105752	1660959	1658467	TY-2482_chromosome	B7LCD5	Putative fused PTS enzymes (Multiphosphoryl transfer protein): Hpr component ; enzyme I component ; enzyme IIA c	Escherichia coli (strain 55989 / EAEC)
99026	1662021	1660987	TY-2482_chromosome	B7LCD6	Broad substrate metalloaminopeptidase	Escherichia coli (strain 55989 / EAEC)
73596	1663106	1662024	TY-2482_chromosome	B7LCD7	Xaa-Pro and Met-Xaa peptidase	Escherichia coli (strain 55989 / EAEC)
84431	1664368	1663124	TY-2482_chromosome	B7LCD8	Putative enzyme IIC component of PTS	Escherichia coli (strain 55989 / EAEC)
64407	1664716	1664393	TY-2482_chromosome	B7LCD9	Putative enzyme IIB component of PTS	Escherichia coli (strain 55989 / EAEC)
31128	1665900	1664938	TY-2482_chromosome	B7LCE0	Glucokinase (EC 2.7.1.2) (Glucose kinase)	Escherichia coli (strain 55989 / EAEC)
34914	1666104	1667357	TY-2482_chromosome	B7LCE1	Putative ion-transport protein yfeO	Escherichia coli (strain 55989 / EAEC)
115747	1667475	1667798	TY-2482_chromosome	B7LCE2	Putative uncharacterized protein ypeC	Escherichia coli (strain 55989 / EAEC)
32436	1669180	1667945	TY-2482_chromosome	B7LCE3	Manganese transport protein mntH	Escherichia coli (strain 55989 / EAEC)
98077	1669516	1670715	TY-2482_chromosome	B7LCE4	Nucleoside (Except guanosine) transporter	Escherichia coli (strain 55989 / EAEC)
109631	1672957	1670771	TY-2482_chromosome	B7LCE5	Putative diguanylate cyclase	Escherichia coli (strain 55989 / EAEC)
r386	1673240	1673165	TY-2482_chromosome	ref|NC_010473|:2607943-2608018|Ala tRNA| [gene=alaW] [locus_tag=ECDH10B_2561		
r385	1673355	1673280	TY-2482_chromosome	ref|NC_010473|:2607943-2608018|Ala tRNA| [gene=alaW] [locus_tag=ECDH10B_2561		
75125	1673576	1673932	TY-2482_chromosome	C8UDX7	Predicted DNA-binding transcriptional regulator	Escherichia coli O111:H- (strain 11128 / EHEC)
100849	1673937	1674326	TY-2482_chromosome	B7LCE7	Putative nucleic acid-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
81118	1675796	1674384	TY-2482_chromosome	B7LCE8	Glutamyl-tRNA synthetase (EC 6.1.1.17)	Escherichia coli (strain 55989 / EAEC)
r364	1676055	1676130	TY-2482_chromosome	ref|NC_010473|:2610960-2611035|Val tRNA| [gene=valY] [locus_tag=ECDH10B_2567		
r365	1676175	1676250	TY-2482_chromosome	ref|NC_010473|:2610960-2611035|Val tRNA| [gene=valY] [locus_tag=ECDH10B_2567		
r370	1676295	1676371	TY-2482_chromosome	ref|NC_010473|:2610960-2611035|Val tRNA| [gene=valY] [locus_tag=ECDH10B_2567		
r366	1676416	1676491	TY-2482_chromosome	ref|NC_010473|:2610960-2611035|Val tRNA| [gene=valY] [locus_tag=ECDH10B_2567		
r367	1676538	1676613	TY-2482_chromosome	ref|NC_010473|:2610960-2611035|Val tRNA| [gene=valY] [locus_tag=ECDH10B_2567		
r363	1676618	1676691	TY-2482_chromosome	ref|NC_010473|:2611040-2611115|Lys tRNA| [gene=lysV] [locus_tag=ECDH10B_2568		
95417	1677684	1676803	TY-2482_chromosome	B7LCE9	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
94865	1679192	1677939	TY-2482_chromosome	B7LCF0	Xanthosine transporter	Escherichia coli (strain 55989 / EAEC)
59013	1680085	1679255	TY-2482_chromosome	B7LCF1	Purine nucleoside phosphorylase II (EC 2.4.2.1)	Escherichia coli (strain 55989 / EAEC)
104402	1680334	1681095	TY-2482_chromosome	B7LCF2	Putative outer membrane protein	Escherichia coli (strain 55989 / EAEC)
94309	1682063	1681140	TY-2482_chromosome	B7LCF3	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
68637	1682153	1683148	TY-2482_chromosome	B7LCF4	Putative sodium/bile acid symporter family (MazG-like)	Escherichia coli (strain 55989 / EAEC)
70101	1683366	1683151	TY-2482_chromosome	B7LCF5	Putative uncharacterized protein ypeB	Escherichia coli (strain 55989 / EAEC)
30657	1685383	1683371	TY-2482_chromosome	B7LCF6	DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+])	Escherichia coli (strain 55989 / EAEC)
35082	1686440	1685457	TY-2482_chromosome	B7LCF7	Cell division protein ZipA homolog	Escherichia coli (strain 55989 / EAEC)

30527	1686670	1687428	TY-2482_chromosome	B7LCF8	Protein CysZ	Escherichia coli (strain 55989 / EAEC)
72856	1687616	1688584	TY-2482_chromosome	B7LCF9	Cysteine synthase (EC 2.5.1.47)	Escherichia coli (strain 55989 / EAEC)
4309	1688971	1689225	TY-2482_chromosome	Q83QP3	Multiphosphoryl transfer protein (MTP) [Includes: Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Ph	Shigella flexneri
75433	1689273	1690997	TY-2482_chromosome	B7LCG1	PEP-protein phosphotransferase of PTS system (Enzyme I) (EC 2.7.3.9)	Escherichia coli (strain 55989 / EAEC)
112091	1691041	1691547	TY-2482_chromosome	B7LCG2	Glucose-specific enzyme IIA component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
32914	1692443	1691595	TY-2482_chromosome	B7LCG3	Pyridoxine kinase (EC 2.7.1.35) (PN/PL/PM kinase) (Pyridoxal kinase) (Pyridoxamine kinase) (Vitamin B6 kinase)	Escherichia coli (strain 55989 / EAEC)
73597	1692548	1692913	TY-2482_chromosome	B7LCG4	Putative uncharacterized protein yfeK	Escherichia coli (strain 55989 / EAEC)
99028	1693830	1692922	TY-2482_chromosome	B7LCG5	Cysteine synthase (EC 2.5.1.47)	Escherichia coli (strain 55989 / EAEC)
100604	1695061	1693967	TY-2482_chromosome	B7LCG6	Sulfate/thiosulfate transporter subunit ; ATP-binding component of ABC superfamily (EC 3.6.3.25	Escherichia coli (strain 55989 / EAEC)
73598	1695926	1695054	TY-2482_chromosome	B7LCG7	Sulfate/thiosulfate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
114172	1696759	1695929	TY-2482_chromosome	B7LCG8	Sulfate/thiosulfate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
99030	1697775	1696762	TY-2482_chromosome	B7LCG9	Thiosulfate transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
77568	1698737	1697949	TY-2482_chromosome	B7LCH0	Putative oxidoredutase, sulfate metabolism protein	Escherichia coli (strain 55989 / EAEC)
32565	1699723	1698869	TY-2482_chromosome	B7LCH1	HTH-type transcriptional regulator murR (MurPQ operon repressor)	Escherichia coli (strain 55989 / EAEC)
32561	1699887	1700780	TY-2482_chromosome	B7LCH2	N-acetylmuramic acid 6-phosphate etherase (MurNAc-6-P etherase) (EC 4.2.1.n1) (N-acetylmuramic acid 6-phosphate	Escherichia coli (strain 55989 / EAEC)
90504	1700787	1702208	TY-2482_chromosome	B7LCH3	Putative fused PTS enzymes: IIB component ; IIC component	Escherichia coli (strain 55989 / EAEC)
77351	1702216	1703517	TY-2482_chromosome	B7LCH4	UPF0214 protein yfeW	Escherichia coli (strain 55989 / EAEC)
108850	1704502	1703579	TY-2482_chromosome	D3H2T1	Putative peroxidase	Escherichia coli O44:H18 (strain 042 / EAEC)
115180	1705146	1704574	TY-2482_chromosome	B7LCH6	Putative uncharacterized protein yfeY	Escherichia coli (strain 55989 / EAEC)
64298	1705656	1705210	TY-2482_chromosome	B7LCH7	Putative uncharacterized protein yfeZ	Escherichia coli (strain 55989 / EAEC)
25642	1706179	1705646	TY-2482_chromosome	D3QM21	Acetyltransferase ypeA	Escherichia coli O55:H7 (strain CB9615 / EPEC)
110584	1706282	1707148	TY-2482_chromosome	B7LCH9	N-acetylmuramoyl-l-alanine amidase I (EC 3.5.1.28)	Escherichia coli (strain 55989 / EAEC)
113142	1707155	1708051	TY-2482_chromosome	C8UE11	Coproporphyrinogen-III oxidase, aerobic (Coprogen oxidase) (Coproporphyrinogenase) (EC 1.3.3.3)	Escherichia coli O111:H- (strain 11128 / EHEC
91799	1709112	1708063	TY-2482_chromosome	B7LCI1	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
90369	1709658	1709161	TY-2482_chromosome	B7LCI2	Putative ethanolaminosome structural protein with putative role in ethanolamine utilization	Escherichia coli (strain 55989 / EAEC)
104487	1710330	1709674	TY-2482_chromosome	B7LCI3	Putative carboxysome-related structural protein with putative role in ethanolamine utilization	Escherichia coli (strain 55989 / EAEC)
30812	1711227	1710343	TY-2482_chromosome	B7LCI4	Ethanolamine ammonia-lyase light chain (EC 4.3.1.7) (Ethanolamine ammonia-lyase small subunit	Escherichia coli (strain 55989 / EAEC)
93256	1712609	1711251	TY-2482_chromosome	B7LCI5	Ethanolamine ammonia-lyase, large subunit, heavy chain (EC 4.3.1.7)	Escherichia coli (strain 55989 / EAEC)
106434	1714024	1712624	TY-2482_chromosome	B7LCI6	Reactivating factor for ethanolamine ammonia lyase	Escherichia coli (strain 55989 / EAEC)
62743	1715247	1714024	TY-2482_chromosome	B7LCI7	Putative ethanolamine transporter	Escherichia coli (strain 55989 / EAEC)
10612	1715563	1715312	TY-2482_chromosome	D7Y0Y7	Putative uncharacterized protein	Escherichia coli MS 115-1
84477	1716751	1715567	TY-2482_chromosome	B7LCI8	Putative alcohol dehydrogenase in ethanolamine utilization; ethanolaminosome	Escherichia coli (strain 55989 / EAEC)
73639	1717577	1716744	TY-2482_chromosome	B7LCI9	Putative chaperonin, ethanolamine utilization protein	Escherichia coli (strain 55989 / EAEC)
102779	1718991	1717591	TY-2482_chromosome	B7LCJ0	Putative aldehyde dehydrogenase, ethanolamine utilization protein	Escherichia coli (strain 55989 / EAEC)
57347	1719690	1719006	TY-2482_chromosome	Q8Z4T7	Putative ethanolamine utilization protein EutN	Salmonella typhi
80067	1720745	1719732	TY-2482_chromosome	B7LCJ3	Putative phosphotransacetylase subunit	Escherichia coli (strain 55989 / EAEC)
110587	1721545	1720745	TY-2482_chromosome	B7LCJ4	Putative cobalamin adenosyltransferase in ethanolamine utilization	Escherichia coli (strain 55989 / EAEC)
112156	1722243	1721545	TY-2482_chromosome	B7LCJ5	Putative uncharacterized protein eutQ	Escherichia coli (strain 55989 / EAEC)
79247	1722697	1722221	TY-2482_chromosome	B7LCJ6	Putative nucleoside triphosphate hydrolase domain protein	Escherichia coli (strain 55989 / EAEC)
86221	1723045	1722713	TY-2482_chromosome	B7LCJ7	Putative carboxysome-like ethanolaminosome structural protein with putative role in ethanol utilization	Escherichia coli (strain 55989 / EAEC)
110081	1725617	1723341	TY-2482_chromosome	B7LCJ8	Putative fused malic enzyme oxidoreductase ; putative phosphotransacetylase (EC 1.1.1.40) (EC 2.3.1.8)	Escherichia coli (strain 55989 / EAEC)
102313	1725906	1726853	TY-2482_chromosome	B7LCJ9	Transaldolase 2 (EC 2.2.1.2)	Escherichia coli (strain 55989 / EAEC)
62680	1726876	1728876	TY-2482_chromosome	B7LCK0	Transketolase 2, thiamin-binding (EC 2.2.1.1)	Escherichia coli (strain 55989 / EAEC)
28641	1729918	1730175	TY-2482_chromosome	Q1R8R2	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
108762	1730018	1728978	TY-2482_chromosome	B7LCK1	Putative uncharacterized protein ypfG	Escherichia coli (strain 55989 / EAEC)
84481	1730719	1730147	TY-2482_chromosome	B7LCK2	Putative NUDIX hydrolase	Escherichia coli (strain 55989 / EAEC)
110124	1732766	1730790	TY-2482_chromosome	B7LCK3	Fused putative oxidoreductase: FeS binding subunit ; NAD/FAD-binding subunit	Escherichia coli (strain 55989 / EAEC)
84482	1732972	1734669	TY-2482_chromosome	B7LCK4	Sensory histidine kinase in two-component regulatory system with NarP (NarL)	Escherichia coli (strain 55989 / EAEC)
101266	1734836	1737946	TY-2482_chromosome	B7LCK5	Aminoglycoside/multidrug efflux system	Escherichia coli (strain 55989 / EAEC)
12038	1737953	1738246	TY-2482_chromosome	D7ZI85	Conserved domain protein (Fragment)	Escherichia coli MS 69-1
112968	1738488	1738841	TY-2482_chromosome	B7LCK6	Putative uncharacterized protein yffB	Escherichia coli (strain 55989 / EAEC)
30547	1738848	1739972	TY-2482_chromosome	B7LCK7	Succinyl-diaminopimelate desuccinylase (SDAP desuccinylase) (EC 3.5.1.18) (N-succinyl-LL-2,6-diaminoheptanedioate	Escherichia coli (strain 55989 / EAEC)
35047	1740003	1740200	TY-2482_chromosome	B7LCK8	UPF0370 protein ypfN	Escherichia coli (strain 55989 / EAEC)
60689	1741011	1740316	TY-2482_chromosome	B7LCK9	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
62682	1743100	1741088	TY-2482_chromosome	B7LCL0	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
99059	1743978	1743118	TY-2482_chromosome	B7LCL1	Putative uncharacterized protein ypfJ	Escherichia coli (strain 55989 / EAEC)
90516	1744523	1744128	TY-2482_chromosome	B7LCL2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
82425	1744789	1744526	TY-2482_chromosome	B7LCL3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
33147	1745618	1744908	TY-2482_chromosome	B7LCL4	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)	Escherichia coli (strain 55989 / EAEC)
24478	1745669	1745917	TY-2482_chromosome	Q32D89	Putative uncharacterized protein	Shigella dysenteriae serotype 1 (strain Sd197)
68177	1746865	1745834	TY-2482_chromosome	B7LCL5	Lipoprotein	Escherichia coli (strain 55989 / EAEC)
30536	1747760	1746885	TY-2482_chromosome	B7LCL6	Dihydrodipicolinate synthase (DHDPS) (EC 4.2.1.52)	Escherichia coli (strain 55989 / EAEC)
9019	1747840	1748475	TY-2482_chromosome	C3T0C3	Transcriptional regulation of gcv operon	Escherichia coli
97769	1748478	1748945	TY-2482_chromosome	B7LCL8	Thiol peroxidase, thioredoxin-dependent (EC 1.11.1.-) (EC 1.11.1.7)	Escherichia coli (strain 55989 / EAEC)

110588	1749201	1749815	TY-2482_chromosome	B7LCL9	Hydrogenase 4, 4Fe-4S subunit	Escherichia coli (strain 55989 / EAEC)
86136	1749818	1751833	TY-2482_chromosome	B7LCM0	Hydrogenase 4, membrane subunit	Escherichia coli (strain 55989 / EAEC)
100022	1751847	1752791	TY-2482_chromosome	C8UE52	Hydrogenase 4, membrane subunit HyfC	Escherichia coli O111:H- (strain 11128 / EHEC)
91696	1752811	1754246	TY-2482_chromosome	B5Z021	Hydrogenase-4 component D	Escherichia coli O157:H7 (strain EC4115 / EHEC)
112146	1754261	1754908	TY-2482_chromosome	B7LCM5	Hydrogenase 4, membrane subunit	Escherichia coli (strain 55989 / EAEC)
77305	1754916	1756493	TY-2482_chromosome	B7LCM6	Hydrogenase 4, membrane subunit	Escherichia coli (strain 55989 / EAEC)
90696	1756534	1758198	TY-2482_chromosome	B7LCM7	Hydrogenase 4, subunit	Escherichia coli (strain 55989 / EAEC)
110590	1758211	1758747	TY-2482_chromosome	B7LCM8	Hydrogenase 4, Fe-S subunit	Escherichia coli (strain 55989 / EAEC)
88247	1758747	1759502	TY-2482_chromosome	B7LCM9	Hydrogenase 4, Fe-S subunit	Escherichia coli (strain 55989 / EAEC)
90517	1759498	1759908	TY-2482_chromosome	B7LCN0	Putative processing element hydrogenase 4	Escherichia coli (strain 55989 / EAEC)
113903	1759941	1761950	TY-2482_chromosome	B7LCN1	DNA-binding transcriptional activator, formate sensing	Escherichia coli (strain 55989 / EAEC)
76686	1761975	1762703	TY-2482_chromosome	B7LCN2	Putative formate transporter	Escherichia coli (strain 55989 / EAEC)
75618	1763921	1762863	TY-2482_chromosome	B7LCN3	Putative permease	Escherichia coli (strain 55989 / EAEC)
84500	1764134	1765594	TY-2482_chromosome	B7LCN4	Putative peptidase	Escherichia coli (strain 55989 / EAEC)
91407	1765618	1765974	TY-2482_chromosome	B7LCN5	Putative oxidoreductase	Escherichia coli (strain 55989 / EAEC)
107305	1766861	1766118	TY-2482_chromosome	C8U815	DnaA-homolog protein hda	Escherichia coli O103:H2 (strain 12009 / EHEC)
110597	1768200	1766914	TY-2482_chromosome	B7LCN7	Uracil transporter	Escherichia coli (strain 55989 / EAEC)
34520	1768912	1768289	TY-2482_chromosome	B7LCN8	Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Escherichia coli (strain 55989 / EAEC)
33143	1769237	1770271	TY-2482_chromosome	B7LCN9	Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole sy	Escherichia coli (strain 55989 / EAEC)
71652	1770274	1770909	TY-2482_chromosome	B7LCP0	Phosphoribosylglycinamide formyltransferase 1 (EC 2.1.2.2)	Escherichia coli (strain 55989 / EAEC)
88249	1771083	1773146	TY-2482_chromosome	B7LCP1	Polyphosphate kinase (EC 2.7.4.1)	Escherichia coli (strain 55989 / EAEC)
116070	1773154	1774692	TY-2482_chromosome	B7LCP2	Exopolyphosphatase (EC 3.6.1.11)	Escherichia coli (strain 55989 / EAEC)
101280	1776977	1774737	TY-2482_chromosome	B7LCP3	Putative uncharacterized protein yfgF	Escherichia coli (strain 55989 / EAEC)
91801	1777484	1777197	TY-2482_chromosome	B7LCP4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
90587	1777831	1778346	TY-2482_chromosome	C6UQQ6	Predicted outer membrane lipoprotein	Escherichia coli O157:H7 (strain TW14359 / EHEC)
80881	1778365	1778901	TY-2482_chromosome	B7LCP6	Putative uncharacterized protein yfgI	Escherichia coli (strain 55989 / EAEC)
31308	1780574	1779000	TY-2482_chromosome	B7LCP7	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Escherichia coli (strain 55989 / EAEC)
87883	1782109	1780646	TY-2482_chromosome	B7LCP8	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Escherichia coli (strain 55989 / EAEC)
30820	1782271	1783638	TY-2482_chromosome	B7LCP9	Exodeoxyribonuclease 7 large subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII large subunit) (Exonuclease VII large su	Escherichia coli (strain 55989 / EAEC)
115901	1783853	1783641	TY-2482_chromosome	B7LCQ0	Putative uncharacterized protein yfgJ	Escherichia coli (strain 55989 / EAEC)
30599	1785394	1783925	TY-2482_chromosome	B7LCQ1	GTPase Der (GTP-binding protein EngA)	Escherichia coli (strain 55989 / EAEC)
69951	1786690	1785515	TY-2482_chromosome	B7LCQ2	Protein assembly complex, lipoprotein component	Escherichia coli (strain 55989 / EAEC)
95478	1787321	1786704	TY-2482_chromosome	B7LCQ3	Putative uncharacterized protein yfgM	Escherichia coli (strain 55989 / EAEC)
34115	1788613	1787342	TY-2482_chromosome	B7LCQ4	Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase) (HisRS)	Escherichia coli (strain 55989 / EAEC)
31700	1789842	1788727	TY-2482_chromosome	B7LDA7	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (EC 1.17.7.1) (1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphat	Escherichia coli (strain 55989 / EAEC)
33656	1790882	1789872	TY-2482_chromosome	B7LDA8	Cytoskeleton protein rodZ	Escherichia coli (strain 55989 / EAEC)
33586	1792321	1791170	TY-2482_chromosome	B7LDA9	Ribosomal RNA large subunit methyltransferase N (EC 2.1.1.192) (23S rRNA m2A2503 methyltransferase)	Escherichia coli (strain 55989 / EAEC)
71858	1792438	1792962	TY-2482_chromosome	D3H3M8	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
102768	1795363	1793054	TY-2482_chromosome	B7LDB1	Fused transglycosylase ; transpeptidase (EC 2.4.1.-) (EC 3.4.-.-)	Escherichia coli (strain 55989 / EAEC)
69935	1800325	1795367	TY-2482_chromosome	B7LDB2	Putative uncharacterized protein yfhM	Escherichia coli (strain 55989 / EAEC)
115877	1800532	1801374	TY-2482_chromosome	C8TVL6	3-mercaptopyruvate sulfurtransferase	Escherichia coli O26:H11 (strain 11368 / EHEC)
r102	1801567	1801871	TY-2482_chromosome	ref|NC_010473|:2743642-2743945|-| [gene=ryfA] [locus_tag=ECDH10B_2688]		
61111	1802646	1801873	TY-2482_chromosome	B7LDB4	Rhodanase-like enzyme, sulfur transfer from thiosulfate	Escherichia coli (strain 55989 / EAEC)
32926	1804071	1802791	TY-2482_chromosome	B7LDB5	Peptidase B (EC 3.4.11.23) (Aminopeptidase B)	Escherichia coli (strain 55989 / EAEC)
66384	1804449	1804252	TY-2482_chromosome	B7LDB6	Putative uncharacterized protein yfhJ	Escherichia coli (strain 55989 / EAEC)
99046	1804796	1804464	TY-2482_chromosome	B7LDB7	[2Fe-2S] ferredoxin	Escherichia coli (strain 55989 / EAEC)
31528	1806648	1804801	TY-2482_chromosome	B7LDB8	Chaperone protein hscA (Hsc66)	Escherichia coli (strain 55989 / EAEC)
31540	1807180	1806668	TY-2482_chromosome	B7LDB9	Co-chaperone protein hscB (Hsc20)	Escherichia coli (strain 55989 / EAEC)
26416	1807535	1808014	TY-2482_chromosome	Q8FF43	Putative uncharacterized protein	Escherichia coli O6
91674	1807605	1807279	TY-2482_chromosome	B5Z102	Iron-binding protein iscA (Iron-sulfur cluster assembly protein)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
31684	1809244	1808033	TY-2482_chromosome	B7LDC2	Cysteine desulfurase (EC 2.8.1.7)	Escherichia coli (strain 55989 / EAEC)
31680	1809844	1809359	TY-2482_chromosome	B7LDC3	HTH-type transcriptional regulator iscR	Escherichia coli (strain 55989 / EAEC)
106416	1810854	1810117	TY-2482_chromosome	B7LDC4	Putative methyltransferase	Escherichia coli (strain 55989 / EAEC)
116014	1810973	1811773	TY-2482_chromosome	B7LDC5	Inositol monophosphatase (EC 3.1.3.25)	Escherichia coli (strain 55989 / EAEC)
80268	1811894	1812772	TY-2482_chromosome	B7LDC6	Putative peptidase	Escherichia coli (strain 55989 / EAEC)
64179	1812966	1814243	TY-2482_chromosome	B7LDC7	Stationary phase inducible protein	Escherichia coli (strain 55989 / EAEC)
81120	1815377	1814241	TY-2482_chromosome	B7LDC8	Putative 3-phenylpropionic transporter	Escherichia coli (strain 55989 / EAEC)
84458	1816427	1815540	TY-2482_chromosome	B7LDC9	DNA-binding transcriptional activator of 3-phenylpropionic acid catabolism	Escherichia coli (strain 55989 / EAEC)
73632	1816563	1817921	TY-2482_chromosome	B7LDD0	3-phenylpropionate dioxygenase, large (Alpha) subunit (EC 1.14.12.19)	Escherichia coli (strain 55989 / EAEC)
31324	1817921	1818436	TY-2482_chromosome	B7LDD1	3-phenylpropionate/cinnamic acid dioxygenase subunit beta (EC 1.14.12.19) (Digoxigenin subunit beta	Escherichia coli (strain 55989 / EAEC)
112872	1818439	1818756	TY-2482_chromosome	B7LDD2	3-phenylpropionate dioxygenase, putative ferredoxin subunit	Escherichia coli (strain 55989 / EAEC)
31320	1818756	1819565	TY-2482_chromosome	B7LDD3	3-phenylpropionate-dihydrodiol/cinnamic acid-dihydrodiol dehydrogenase (EC 1.3.1.n1) (2,3-dihydroxy-2,3-dihydrop	Escherichia coli (strain 55989 / EAEC)
31322	1819578	1820777	TY-2482_chromosome	B7LDD4	3-phenylpropionate/cinnamic acid dioxygenase ferredoxin--NAD(+) reductase component (EC 1.18.1.3) (Digoxigenin s	Escherichia coli (strain 55989 / EAEC)
86802	1820832	1821296	TY-2482_chromosome	C8UEB1	Predicted inner membrane protein	Escherichia coli O111:H- (strain 11128 / EHEC)

62662	1822219	1821350	TY-2482_chromosome	B7LDD6	Putative uncharacterized protein yphB	Escherichia coli (strain 55989 / EAEC)
71529	1823292	1822234	TY-2482_chromosome	B7LDD7	Putative oxidoreductase, Zn-dependent and NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
65182	1824356	1823361	TY-2482_chromosome	B7LDD8	Putative sugar transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
79472	1825892	1824384	TY-2482_chromosome	B7LDD9	Fused putative sugar transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
99048	1826898	1825918	TY-2482_chromosome	B7LDE0	Putative sugar transporter subunit: periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
94159	1830276	1826998	TY-2482_chromosome	B7LDE1	Putative uncharacterized protein yphG	Escherichia coli (strain 55989 / EAEC)
73633	1830394	1831584	TY-2482_chromosome	B7LDE2	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
31181	1832904	1831654	TY-2482_chromosome	B7LDE3	Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Escherichia coli (strain 55989 / EAEC)
110577	1833232	1834419	TY-2482_chromosome	B7LDE4	Fused nitric oxide dioxygenase ; dihydropteridine reductase 2 (EC 1.14.12.1) (EC 1.5.1.34)	Escherichia coli (strain 55989 / EAEC)
58436	1834805	1834470	TY-2482_chromosome	B7LDE5	Regulatory protein P-II for glutamine synthetase	Escherichia coli (strain 55989 / EAEC)
114160	1836200	1834869	TY-2482_chromosome	B7LDE6	Putative DNA-binding response regulator in two-component system	Escherichia coli (strain 55989 / EAEC)
104716	1836903	1836193	TY-2482_chromosome	B7LDE7	Putative uncharacterized protein yfhG	Escherichia coli (strain 55989 / EAEC)
67746	1838495	1837071	TY-2482_chromosome	B7LDE8	Putative sensory kinase in two-component system	Escherichia coli (strain 55989 / EAEC)
r117	1838737	1838589	TY-2482_chromosome	ref|NC_010473|:2780979-2781127|-| [gene=sroF] [locus_tag=ECDH10B_2724]		
59046	1842958	1839074	TY-2482_chromosome	B7LDE9	Phosphoribosylformyl-glycineamide synthetase (EC 6.3.5.3)	Escherichia coli (strain 55989 / EAEC)
113888	1843354	1844769	TY-2482_chromosome	B7LDF0	Putative transglycosylase	Escherichia coli (strain 55989 / EAEC)
101265	1845305	1844772	TY-2482_chromosome	B7LDF1	tRNA-specific adenosine deaminase (EC 3.5.4.-)	Escherichia coli (strain 55989 / EAEC)
67935	1845965	1845333	TY-2482_chromosome	B7LDF2	Putative uncharacterized protein yfhB	Escherichia coli (strain 55989 / EAEC)
96742	1846102	1847019	TY-2482_chromosome	D3H3S1	RpiR-family transcriptional regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
91675	1847054	1847335	TY-2482_chromosome	B5Z135	4Fe-4S binding domain protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
29698	1848412	1848035	TY-2482_chromosome	B7LDF6	Holo-[acyl-carrier-protein] synthase (Holo-ACP synthase) (EC 2.7.8.7) (4'-phosphopantetheinyl transferase AcpS)	Escherichia coli (strain 55989 / EAEC)
101718	1849143	1848415	TY-2482_chromosome	B7LDF7	Pyridoxine 5'-phosphate synthase (PNP synthase) (EC 2.6.99.2)	Escherichia coli (strain 55989 / EAEC)
73634	1849883	1849158	TY-2482_chromosome	B7LDF8	DNA repair protein recO (Recombination protein O)	Escherichia coli (strain 55989 / EAEC)
30782	1850800	1849898	TY-2482_chromosome	B7LDF9	GTPase Era	Escherichia coli (strain 55989 / EAEC)
33613	1851477	1850800	TY-2482_chromosome	B7LDG0	Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III) (RNase III)	Escherichia coli (strain 55989 / EAEC)
69558	1852724	1851753	TY-2482_chromosome	B7LDG1	Signal peptidase I (EC 3.4.21.89)	Escherichia coli (strain 55989 / EAEC)
31846	1854539	1852743	TY-2482_chromosome	B7LDG2	Elongation factor 4 (EF-4) (EC 3.6.5.n1) (Ribosomal back-translocase LepA)	Escherichia coli (strain 55989 / EAEC)
64244	1855216	1854740	TY-2482_chromosome	B7LDG3	RseC protein involved in reduction of the SoxR iron-sulfur cluster	Escherichia coli (strain 55989 / EAEC)
71559	1856169	1855216	TY-2482_chromosome	B7LDG4	Anti-sigma factor	Escherichia coli (strain 55989 / EAEC)
95445	1856819	1856172	TY-2482_chromosome	B7LDG5	Anti-sigma factor	Escherichia coli (strain 55989 / EAEC)
61735	1857427	1856855	TY-2482_chromosome	B7LDG6	RNA polymerase sigma factor	Escherichia coli (strain 55989 / EAEC)
87204	1857835	1859454	TY-2482_chromosome	B7LDG7	Quinolinate synthase, L-aspartate oxidase (B protein) subunit (EC 1.4.3.16)	Escherichia coli (strain 55989 / EAEC)
34336	1860179	1859445	TY-2482_chromosome	B7LDG8	tRNA (adenine-N(6)-)-methyltransferase (EC 2.1.1.55) (tRNA m6A37 methyltransferase)	Escherichia coli (strain 55989 / EAEC)
97335	1860311	1861642	TY-2482_chromosome	B7LDG9	ATP-dependent RNA helicase (EC 2.7.7.-)	Escherichia coli (strain 55989 / EAEC)
80383	1862780	1861857	TY-2482_chromosome	B5Z151	Transcriptional regulator, LysR family	Escherichia coli O157:H7 (strain EC4115 / EHEC)
64826	1862838	1863422	TY-2482_chromosome	B7LDH1	Neutral amino-acid efflux system	Escherichia coli (strain 55989 / EAEC)
31220	1863863	1863483	TY-2482_chromosome	B7LDH2	Autonomous glycyl radical cofactor	Escherichia coli (strain 55989 / EAEC)
34510	1864168	1864854	TY-2482_chromosome	B7LDH3	Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	Escherichia coli (strain 55989 / EAEC)
95526	1865942	1864908	TY-2482_chromosome	B7LDH4	Putative methyltransferase	Escherichia coli (strain 55989 / EAEC)
72622	1866149	1866565	TY-2482_chromosome	B7LDH6	Thioredoxin	Escherichia coli (strain 55989 / EAEC)
115096	1866586	1867332	TY-2482_chromosome	D3H3U5	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
72134	1867367	1870024	TY-2482_chromosome	B7LDH8	Fused acyl-CoA synthetase: NAD(P)-binding subunit ; ATP-binding subunit (EC 6.2.1.13)	Escherichia coli (strain 55989 / EAEC)
67971	1870141	1871493	TY-2482_chromosome	B7LDH9	Phosphatidylserine synthase (CDP-diacylglycerol-serine O-phosphatidyltransferase) (EC 2.7.8.8)	Escherichia coli (strain 55989 / EAEC)
66040	1871521	1871862	TY-2482_chromosome	B5Z160	Putative lipoprotein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
94823	1873160	1871865	TY-2482_chromosome	B7LDI1	Alpha-ketoglutarate transporter	Escherichia coli (strain 55989 / EAEC)
25406	1873415	1873718	TY-2482_chromosome	Q1RFY5	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
r128	1873603	1873484	TY-2482_chromosome	ref|NC_010473|:4043643-4043762|5S ribosomal RNA| [gene=rrfC] [locus_tag=ECDH10B_3948		
22415	1873922	1874278	TY-2482_chromosome	C1HUN0	Prolipoprotein diacylglyceryl transferase (Fragment)	Escherichia sp. 3_2_53FAA
20476	1874282	1874734	TY-2482_chromosome	C1HUN1	Cell wall-associated hydrolase (Fragment)	Escherichia sp. 3_2_53FAA
13799	1874811	1875014	TY-2482_chromosome	C1HUN3	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
24093	1876072	1876374	TY-2482_chromosome	Q1R3T8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
r4	1876600	1873697	TY-2482_chromosome	ref|NC_010473|:4307762-4310665|23S ribosomal RNA| [gene=rrlE] [locus_tag=ECDH10B_4198		
r320	1876869	1876794	TY-2482_chromosome	ref|NC_010473|:4307493-4307568|Glu tRNA| [gene=gltV] [locus_tag=ECDH10B_4197]		
25827	1877461	1877144	TY-2482_chromosome	Q57H85	ORF16-lacZ fusion protein	Salmonella choleraesuis
11304	1878436	1878669	TY-2482_chromosome	E9WNY3	Putative uncharacterized protein	Escherichia coli E1520
r54	1878582	1877041	TY-2482_chromosome	ref|NC_010473|:3522988-3524529|16S ribosomal RNA| [gene=rrsD] [locus_tag=ECDH10B_3453		
95446	1881599	1879029	TY-2482_chromosome	B7LDI2	Protein disaggregation chaperone	Escherichia coli (strain 55989 / EAEC)
113203	1882460	1881732	TY-2482_chromosome	B7LDI3	Putative uncharacterized protein yfiH	Escherichia coli (strain 55989 / EAEC)
72849	1883437	1882460	TY-2482_chromosome	B7LDI4	Pseudouridine synthase (EC 5.4.99.-)	Escherichia coli (strain 55989 / EAEC)
73140	1883572	1884306	TY-2482_chromosome	B7LDI5	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
25508	1885035	1884502	TY-2482_chromosome	Q1R8C8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
77324	1885171	1886328	TY-2482_chromosome	B7LDI8	Fused chorismate mutase P ; prephenate dehydratase (EC 4.2.1.51) (EC 5.4.99.5)	Escherichia coli (strain 55989 / EAEC)
111582	1887495	1886377	TY-2482_chromosome	B7LDI9	T-protein	Escherichia coli (strain 55989 / EAEC)
58643	1888576	1887509	TY-2482_chromosome	B7LDJ0	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate syntha	Escherichia coli (strain 55989 / EAEC)

24356	1888657	1889148	TY-2482_chromosome	B7NRQ4	Putative uncharacterized protein	Escherichia coli O7:K1 (strain IAI39 / ExPEC)
68820	1889301	1889816	TY-2482_chromosome	B7LDJ2	Putative uncharacterized protein yfiR	Escherichia coli (strain 55989 / EAEC)
80875	1889809	1891032	TY-2482_chromosome	B7LDJ3	Putative diguanylate cyclase	Escherichia coli (strain 55989 / EAEC)
84460	1891051	1891530	TY-2482_chromosome	B7LDJ4	Putative outer membrane lipoprotein	Escherichia coli (strain 55989 / EAEC)
33484	1891957	1891613	TY-2482_chromosome	B7LDJ5	50S ribosomal protein L19	Escherichia coli (strain 55989 / EAEC)
34329	1892766	1892002	TY-2482_chromosome	B7LDJ6	tRNA (guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (M1G-methyltransferase) (tRNA [GM37] methyltransferase)	Escherichia coli (strain 55989 / EAEC)
4732	1893354	1892800	TY-2482_chromosome	Q31XD7	Ribosome maturation factor rimM	Shigella boydii serotype 4 (strain Sb227)
33720	1893612	1893367	TY-2482_chromosome	B7LDJ8	30S ribosomal protein S16	Escherichia coli (strain 55989 / EAEC)
80319	1895110	1893752	TY-2482_chromosome	B7LDJ9	Signal Recognition Particle (SRP) component with 4.5S RNA (Ffs)	Escherichia coli (strain 55989 / EAEC)
110579	1895202	1896065	TY-2482_chromosome	B7LDK0	Putative uncharacterized protein ypjD	Escherichia coli (strain 55989 / EAEC)
75694	1896179	1897372	TY-2482_chromosome	B7LDK1	Putative uncharacterized protein yfjD	Escherichia coli (strain 55989 / EAEC)
24372	1897397	1898146	TY-2482_chromosome	A1AEE4	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
33054	1898146	1899021	TY-2482_chromosome	B7LDK3	Probable inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATP NAD kinase) (EC 2.7.1.23)	Escherichia coli (strain 55989 / EAEC)
62663	1899110	1900768	TY-2482_chromosome	B7LDK4	Recombination and repair protein	Escherichia coli (strain 55989 / EAEC)
93869	1900920	1901258	TY-2482_chromosome	B7LDK5	Small membrane lipoprotein	Escherichia coli (strain 55989 / EAEC)
36018	1901631	1901326	TY-2482_chromosome	Q5CCH1	Putative uncharacterized protein	Escherichia coli
80876	1902079	1901606	TY-2482_chromosome	B7LDK7	Putative uncharacterized protein yfjG	Escherichia coli (strain 55989 / EAEC)
34009	1902211	1902690	TY-2482_chromosome	B7LDK8	SsrA-binding protein (Small protein B)	Escherichia coli (strain 55989 / EAEC)
r99	1902908	1903270	TY-2482_chromosome	ref|NC_010473|:2845380-2845742|-| [gene=ssrA] [locus_tag=ECDH10B_2787)		
27853	1903476	1904714	TY-2482_chromosome	B7LDK9	Integrase; CP4-57 prophage	Escherichia coli (strain 55989 / EAEC)
26236	1908602	1904859	TY-2482_chromosome	B7LDL0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26309	1909070	1912918	TY-2482_chromosome	B7LDL1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26572	1912967	1913710	TY-2482_chromosome	B7LDL2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28941	1915028	1914150	TY-2482_chromosome	B7LDL5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
90459	1915547	1915843	TY-2482_chromosome	B7LDL6	Putative GTP-binding factor from putative CP4-like prophage	Escherichia coli (strain 55989 / EAEC)
77325	1915867	1916211	TY-2482_chromosome	B7LDL7	Transposase ORF A, IS3 family	Escherichia coli (strain 55989 / EAEC)
59964	1916334	1917077	TY-2482_chromosome	C8TWQ4	Predicted IS602 transposase OrfB	Escherichia coli O103:H2 (strain 12009 / EHEC)
24914	1917649	1917053	TY-2482_chromosome	B7LDL9	Putative outer membrane protein	Escherichia coli (strain 55989 / EAEC)
29102	1917833	1918302	TY-2482_chromosome	B7M996	Putative uncharacterized protein	Escherichia coli O8 (strain IAI1)
75652	1919804	1918435	TY-2482_chromosome	C6URJ2	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
r350	1920630	1920555	TY-2482_chromosome	ref|NC_010473|:2875549-2875624|Ile tRNA| [gene=ileY] [locus_tag=ECDH10B_2820)		
29380	1920648	1920322	TY-2482_chromosome	B7LDM3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
94631	1921190	1923440	TY-2482_chromosome	D3H4R8	Alpha-amylase	Escherichia coli O44:H18 (strain 042 / EAEC)
30419	1923779	1924753	TY-2482_chromosome	B7LDM7	Protein CsiD	Escherichia coli (strain 55989 / EAEC)
115660	1924776	1926041	TY-2482_chromosome	B7LDM8	Putative enzyme	Escherichia coli (strain 55989 / EAEC)
64577	1926067	1927512	TY-2482_chromosome	B7LDM9	Succinate-semialdehyde dehydrogenase I, NADP-dependent (EC 1.2.1.16)	Escherichia coli (strain 55989 / EAEC)
86943	1927529	1928806	TY-2482_chromosome	B7LDN0	4-aminobutyrate aminotransferase, PLP-dependent (EC 2.6.1.19)	Escherichia coli (strain 55989 / EAEC)
110543	1929120	1930517	TY-2482_chromosome	B7LE81	Gamma-aminobutyrate transporter	Escherichia coli (strain 55989 / EAEC)
87752	1930523	1931200	TY-2482_chromosome	D3H4S4	GntR-family transcriptional regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
83657	1931653	1931207	TY-2482_chromosome	B7LE82	Putative uncharacterized protein ygaU	Escherichia coli (strain 55989 / EAEC)
28854	1931725	1931907	TY-2482_chromosome	Q1R837	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
102734	1932078	1932374	TY-2482_chromosome	B7LE84	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
71866	1932387	1932908	TY-2482_chromosome	B7LE85	Putative uncharacterized protein ygaP	Escherichia coli (strain 55989 / EAEC)
73609	1933362	1932961	TY-2482_chromosome	B7LE86	DNA binding protein, nucleoid-associated	Escherichia coli (strain 55989 / EAEC)
97334	1934030	1934476	TY-2482_chromosome	B7LE87	Putative uncharacterized protein ygaW	Escherichia coli (strain 55989 / EAEC)
108496	1934860	1934519	TY-2482_chromosome	B7LE88	Putative uncharacterized protein ygaC	Escherichia coli (strain 55989 / EAEC)
101586	1935000	1935338	TY-2482_chromosome	B7LE89	Putative uncharacterized protein ygaM	Escherichia coli (strain 55989 / EAEC)
88316	1935589	1935831	TY-2482_chromosome	B7LE90	Glutaredoxin-like protein	Escherichia coli (strain 55989 / EAEC)
32710	1935831	1936238	TY-2482_chromosome	B7LE91	Protein nrdI	Escherichia coli (strain 55989 / EAEC)
60868	1936214	1938355	TY-2482_chromosome	B7LE92	Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Escherichia coli (strain 55989 / EAEC)
59018	1938368	1939324	TY-2482_chromosome	B7LE93	Ribonucleoside-diphosphate reductase 2, beta subunit, ferritin-like (EC 1.17.4.1	Escherichia coli (strain 55989 / EAEC)
27781	1939445	1939675	TY-2482_chromosome	Q0TEJ8	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
102735	1939682	1940881	TY-2482_chromosome	B7LE94	Glycine betaine transporter subunit ; ATP-binding compoent of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
106398	1940877	1941938	TY-2482_chromosome	B7LE95	Glycine betaine transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
73611	1941998	1942987	TY-2482_chromosome	B7LE96	Glycine betaine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
87439	1943182	1944363	TY-2482_chromosome	B7LE97	Putative transport protein (OusB-like)	Escherichia coli (strain 55989 / EAEC)
88206	1944490	1945224	TY-2482_chromosome	B7LE99	Putative transporter	Escherichia coli (strain 55989 / EAEC)
83289	1945217	1945549	TY-2482_chromosome	B7LE98	Putative uncharacterized protein ygaH	Escherichia coli (strain 55989 / EAEC)
105627	1945643	1946170	TY-2482_chromosome	B7LEA0	DNA-binding transcriptional repressor of microcin B17 synthesis and multidrug efflux	Escherichia coli (strain 55989 / EAEC)
101133	1946300	1947469	TY-2482_chromosome	B7LEA2	Multidrug efflux system	Escherichia coli (strain 55989 / EAEC)
91262	1947489	1949024	TY-2482_chromosome	B7LEA3	Multidrug efflux system protein	Escherichia coli (strain 55989 / EAEC)
3005	1949606	1949094	TY-2482_chromosome	B7LEA1	S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein luxS	Escherichia coli (strain 55989 / EAEC)
r477	1949674	1949748	TY-2482_chromosome	ref|NC_010473|:2905365-2905439|-| [gene=sraD] [locus_tag=ECDH10B_2855)		
31251	1951312	1949759	TY-2482_chromosome	B7LEA4	Glutamate--cysteine ligase (EC 6.3.2.2) (Gamma-ECS) (GCS) (Gamma-glutamylcysteine synthetase)	Escherichia coli (strain 55989 / EAEC)

112155	1951813	1951388	TY-2482_chromosome	B7LEA5	Putative uncharacterized protein yqaA	Escherichia coli (strain 55989 / EAEC)
76051	1952376	1951813	TY-2482_chromosome	B7LEA6	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
22845	1952687	1952409	TY-2482_chromosome	D7Z1T1	Conserved domain protein (Fragment)	Escherichia coli MS 45-1
r274	1952733	1952657	TY-2482_chromosome	ref|NC_010473|:2909037-2909113|Arg tRNA| [gene=argV] [locus_tag=ECDH10B_2862		
r273	1952873	1952797	TY-2482_chromosome	ref|NC_010473|:2909037-2909113|Arg tRNA| [gene=argV] [locus_tag=ECDH10B_2862		
r272	1953013	1952937	TY-2482_chromosome	ref|NC_010473|:2909037-2909113|Arg tRNA| [gene=argV] [locus_tag=ECDH10B_2862		
r271	1953155	1953079	TY-2482_chromosome	ref|NC_010473|:2909037-2909113|Arg tRNA| [gene=argV] [locus_tag=ECDH10B_2862		
r270	1953296	1953220	TY-2482_chromosome	ref|NC_010473|:2909037-2909113|Arg tRNA| [gene=argV] [locus_tag=ECDH10B_2862		
49649	1953359	1953726	TY-2482_chromosome	Q83SY0	Putative uncharacterized protein	Salmonella typhi
r269	1953436	1953360	TY-2482_chromosome	ref|NC_010473|:2909037-2909113|Arg tRNA| [gene=argV] [locus_tag=ECDH10B_2862		
r198	1953532	1953440	TY-2482_chromosome	ref|NC_010473|:2909117-2909209|Ser tRNA| [gene=serV] [locus_tag=ECDH10B_2863		
99024	1956898	1954271	TY-2482_chromosome	B7LEA8	Alanyl-tRNA synthetase (EC 6.1.1.7)	Escherichia coli (strain 55989 / EAEC)
33311	1957526	1957029	TY-2482_chromosome	B7LEB0	Regulatory protein recX	Escherichia coli (strain 55989 / EAEC)
33296	1958830	1957772	TY-2482_chromosome	B7LEB1	Protein RecA (Recombinase A)	Escherichia coli (strain 55989 / EAEC)
90841	1959407	1958913	TY-2482_chromosome	B7LEA9	Putative uncharacterized protein ygaD	Escherichia coli (strain 55989 / EAEC)
59019	1960637	1959555	TY-2482_chromosome	B7LEB2	Membrane-bound lytic murein transglycosylase B (EC 3.2.1.-)	Escherichia coli (strain 55989 / EAEC)
91789	1960893	1961453	TY-2482_chromosome	B7LEB3	Glucitol/sorbitol-specific enzyme IIC component of PTS	Escherichia coli (strain 55989 / EAEC)
72281	1961453	1962409	TY-2482_chromosome	B7LEB4	Glucitol/sorbitol-specific enzyme IIB component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
58074	1962423	1962791	TY-2482_chromosome	B7LEB5	Glucitol/sorbitol-specific enzyme IIA component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
73612	1962798	1963574	TY-2482_chromosome	B7LEB6	Sorbitol-6-phosphate dehydrogenase (EC 1.1.1.140)	Escherichia coli (strain 55989 / EAEC)
86689	1963682	1964038	TY-2482_chromosome	B7LEB7	DNA-binding transcriptional activator of glucitol operor	Escherichia coli (strain 55989 / EAEC)
76595	1964108	1964878	TY-2482_chromosome	B7LEB8	DNA-bindng transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
114197	1964874	1965836	TY-2482_chromosome	B7LEB9	Putative phosphosugar-binding protein	Escherichia coli (strain 55989 / EAEC)
32668	1967350	1965839	TY-2482_chromosome	B7LEC0	Anaerobic nitric oxide reductase transcription regulator norF	Escherichia coli (strain 55989 / EAEC)
105314	1967537	1968973	TY-2482_chromosome	B7LEC1	Rubredoxin	Escherichia coli (strain 55989 / EAEC)
32702	1968973	1970103	TY-2482_chromosome	B7LEC2	Nitric oxide reductase FlRd-NAD(+) reductase (EC 1.18.1.-) (Flavorubredoxin reductase) (FlRd-reductase) (FlavoRb red	Escherichia coli (strain 55989 / EAEC)
62625	1972584	1970335	TY-2482_chromosome	B7LEC3	Carbamoyl phosphate phosphatase and maturation protein for [NiFe] hydrogenases	Escherichia coli (strain 55989 / EAEC)
114199	1973264	1972740	TY-2482_chromosome	B7LEC4	Formate dehydrogenase-H, [4Fe-4S] ferredoxin subunit	Escherichia coli (strain 55989 / EAEC)
80962	1974426	1973416	TY-2482_chromosome	B7LEC5	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
83907	1974683	1976137	TY-2482_chromosome	B7LEC6	Fused cellobiose/arbutin/salicin-specific PTS enzymes: IIB component ; IIC component (EC 2.7.1.69	Escherichia coli (strain 55989 / EAEC)
97936	1976149	1977570	TY-2482_chromosome	B7LEC7	Cryptic 6-phospho-beta-glucosidase (EC 3.2.1.86)	Escherichia coli (strain 55989 / EAEC)
115752	1978721	1977744	TY-2482_chromosome	B7LF78	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
102758	1979451	1978969	TY-2482_chromosome	B7LEC9	Putative HTH-type transcriptional regulator ygjM	Escherichia coli (strain 55989 / EAEC)
91790	1980229	1979459	TY-2482_chromosome	B7LED0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
105433	1980724	1980257	TY-2482_chromosome	B7LED1	Protease involved in processing C-terminal end of HycE (EC 3.4.-.-)	Escherichia coli (strain 55989 / EAEC)
94003	1981127	1980720	TY-2482_chromosome	B7LED2	Protein required for maturation of hydrogenase 3	Escherichia coli (strain 55989 / EAEC)
85937	1981891	1981127	TY-2482_chromosome	D3GRQ1	Formate hydrogenlyase subunit 7	Escherichia coli O44:H18 (strain 042 / EAEC)
110551	1982433	1981894	TY-2482_chromosome	B7LED4	Formate hydrogenlyase complex iron-sulfur protein (EC 1.12.7.2)	Escherichia coli (strain 55989 / EAEC)
102308	1984152	1982446	TY-2482_chromosome	B7LED5	Hydrogenase 3, large subunit (EC 1.12.7.2)	Escherichia coli (strain 55989 / EAEC)
116096	1985093	1984173	TY-2482_chromosome	B7LED6	Hydrogenase 3, membrane subunit	Escherichia coli (strain 55989 / EAEC)
66362	1986922	1985099	TY-2482_chromosome	B7LED7	Hydrogenase 3, membrane subunit	Escherichia coli (strain 55989 / EAEC)
114203	1987530	1986922	TY-2482_chromosome	B7LED8	Hydrogenase 3, Fe-S subunit (EC 1.12.7.2)	Escherichia coli (strain 55989 / EAEC)
114207	1988116	1987658	TY-2482_chromosome	B7LED9	Regulator of the transcriptional regulator FhlA	Escherichia coli (strain 55989 / EAEC)
68925	1988315	1988674	TY-2482_chromosome	B5Z389	Probable hydrogenase nickel incorporation protein hypA 1	Escherichia coli O157:H7 (strain EC4115 / EHEC)
83728	1988681	1989550	TY-2482_chromosome	B7LEE1	GTP hydrolase involved in nickel liganding into hydrogenases	Escherichia coli (strain 55989 / EAEC)
84083	1989544	1989813	TY-2482_chromosome	B7LEE2	Protein required for maturation of hydrogenases 1 and 3	Escherichia coli (strain 55989 / EAEC)
95431	1989816	1990934	TY-2482_chromosome	B7LEE3	Protein required for maturation of hydrogenases	Escherichia coli (strain 55989 / EAEC)
62163	1990976	1991941	TY-2482_chromosome	B7LEE4	Carbamoyl phosphate phosphatase, hydrogenase 3 maturation protein	Escherichia coli (strain 55989 / EAEC)
95451	1992018	1994093	TY-2482_chromosome	B7LEE5	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
66364	1994486	1994136	TY-2482_chromosome	B7LEE6	Putative uncharacterized protein ygbA	Escherichia coli (strain 55989 / EAEC)
11135	1994543	1994773	TY-2482_chromosome	D7YDC0	Conserved domain protein	Escherichia coli MS 182-1
32579	1994773	1997331	TY-2482_chromosome	B7LEE7	DNA mismatch repair protein mutS	Escherichia coli (strain 55989 / EAEC)
64912	1997440	1998093	TY-2482_chromosome	B7LEE8	Serine/threonine-specific protein phosphatase 2 (EC 3.1.3.16)	Escherichia coli (strain 55989 / EAEC)
73200	1998944	1998150	TY-2482_chromosome	B7LEE9	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
84445	1999110	2000015	TY-2482_chromosome	B7LEF0	Putative dehydrogenase, with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
112425	2000015	2001274	TY-2482_chromosome	B7LEF1	Putative uncharacterized protein ygbK	Escherichia coli (strain 55989 / EAEC)
82979	2001274	2001909	TY-2482_chromosome	B7LEF2	Putative class II aldolase	Escherichia coli (strain 55989 / EAEC)
77289	2001917	2002690	TY-2482_chromosome	B7LEF3	Putative uncharacterized protein ygbM	Escherichia coli (strain 55989 / EAEC)
84447	2002782	2004143	TY-2482_chromosome	B7LEF4	Putative transporter	Escherichia coli (strain 55989 / EAEC)
105114	2004422	2004189	TY-2482_chromosome	B7LEF5	Conserved putative non-oxidative reversible hydroxyarylic acid decarboxylase	Escherichia coli (strain 55989 / EAEC)
69896	2005860	2004436	TY-2482_chromosome	B7LEF6	Conserved putative non-oxidative hydroxyarylic acid decarboxylase activity	Escherichia coli (strain 55989 / EAEC)
90688	2006453	2005863	TY-2482_chromosome	B7LEF7	Conserved putative non-oxidative reversible hydroxyarylic acid decarboxylase	Escherichia coli (strain 55989 / EAEC)
98369	2006600	2007004	TY-2482_chromosome	C8TFY8	Transcriptional regulator	Escherichia coli O26:H11 (strain 11368 / EHEC)
113036	2008120	2007131	TY-2482_chromosome	B7LEF8	RNA polymerase sigma factor	Escherichia coli (strain 55989 / EAEC)

69898	2009322	2008186	TY-2482_chromosome	B7LEG0	Outer membrane lipoprotein	Escherichia coli (strain 55989 / EAEC)
33005	2010088	2009465	TY-2482_chromosome	B7LEG1	Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77) (L-isoaspartyl protein carboxyl methyltransferase) (Protein L	Escherichia coli (strain 55989 / EAEC)
34076	2010843	2010085	TY-2482_chromosome	B7LEG2	Multifunctional protein surE [Includes: 5'/3'-nucleotidase (EC 3.1.3.5) (EC 3.1.3.6) (Nucleoside monophosphate phosp	Escherichia coli (strain 55989 / EAEC)
34367	2011873	2010827	TY-2482_chromosome	B7LEG3	tRNA pseudouridine synthase D (EC 5.4.99.27) (tRNA pseudouridine(13) synthase) (tRNA pseudouridylate synthase D)	Escherichia coli (strain 55989 / EAEC)
31695	2012349	2011873	TY-2482_chromosome	B7LEG4	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (MECDP-synthase) (MECPS) (EC 4.6.1.12)	Escherichia coli (strain 55989 / EAEC)
31687	2013059	2012352	TY-2482_chromosome	B7LEG5	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60) (4-diphosphocytidyl-2C-methyl-D-erythritol sy	Escherichia coli (strain 55989 / EAEC)
31030	2013389	2013081	TY-2482_chromosome	B7LEG6	Cell division protein ftsB homolog	Escherichia coli (strain 55989 / EAEC)
108567	2013906	2013586	TY-2482_chromosome	B7LEG7	Putative uncharacterized protein ygbE	Escherichia coli (strain 55989 / EAEC)
30499	2014561	2013959	TY-2482_chromosome	B7LEG8	Adenylyl-sulfate kinase (EC 2.7.1.25) (APS kinase) (ATP adenosine-5'-phosphosulfate 3'-phosphotransferase) (Adenosi	Escherichia coli (strain 55989 / EAEC)
30522	2015988	2014564	TY-2482_chromosome	B7LEG9	Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) (ATP-sulfurylase large subunit) (Sulfate adenylate transferase) (SAT)	Escherichia coli (strain 55989 / EAEC)
30503	2016898	2015993	TY-2482_chromosome	B7LEH0	Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4) (ATP-sulfurylase small subunit) (Sulfate adenylate transferase) (SAT	Escherichia coli (strain 55989 / EAEC)
97174	2017150	2018184	TY-2482_chromosome	B7LEH1	Aminopeptidase in alkaline phosphatase isozyme conversion (EC 3.4.11.-)	Escherichia coli (strain 55989 / EAEC)
84454	2018748	2018458	TY-2482_chromosome	B7LEH2	Putative uncharacterized protein ygbF	Escherichia coli (strain 55989 / EAEC)
106407	2019668	2018751	TY-2482_chromosome	B7LEH3	Putative uncharacterized protein ygbT	Escherichia coli (strain 55989 / EAEC)
94569	2020453	2019668	TY-2482_chromosome	B7LEH4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
87181	2022109	2021057	TY-2482_chromosome	B7LEH6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
65363	2022657	2022124	TY-2482_chromosome	B7LEH7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73199	2024285	2022657	TY-2482_chromosome	B7LEH8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73259	2027013	2024317	TY-2482_chromosome	B7LEH9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
5323	2028479	2027370	TY-2482_chromosome	P11901	Transposase for insertion sequence element IS421	Escherichia coli
71234	2028844	2028559	TY-2482_chromosome	D3QPV9	Small toxic membrane polypeptide	Escherichia coli O55:H7 (strain CB9615 / EPEC)
30511	2029707	2028976	TY-2482_chromosome	B7LEI1	Phosphoadenosine phosphosulfate reductase (EC 1.8.4.8) (3'-phosphoadenylylsulfate reductase) (PAPS reductase, thi	Escherichia coli (strain 55989 / EAEC)
30514	2031493	2029784	TY-2482_chromosome	B7LEI2	Sulfite reductase [NADPH] hemoprotein beta-component (SiR-HP) (SiRHP) (EC 1.8.1.2)	Escherichia coli (strain 55989 / EAEC)
62627	2033292	2031496	TY-2482_chromosome	B7LEI3	Sulfite reductase [NADPH] flavoprotein alpha-component (SiR-FP) (EC 1.8.1.2)	Escherichia coli (strain 55989 / EAEC)
84507	2033608	2033970	TY-2482_chromosome	B7LEI4	6-pyruvoyl tetrahydrobiopterin synthase (PTPS)	Escherichia coli (strain 55989 / EAEC)
66216	2034051	2035319	TY-2482_chromosome	B7LEI5	Putative oxidoreductase with FAD/NAD(P)-binding domain	Escherichia coli (strain 55989 / EAEC)
111775	2035313	2035570	TY-2482_chromosome	B7LEI6	Putative 4Fe-4S cluster-containing protein	Escherichia coli (strain 55989 / EAEC)
101197	2035590	2036162	TY-2482_chromosome	B7LEI8	Putative anti-terminator regulatory protein	Escherichia coli (strain 55989 / EAEC)
86875	2037173	2036316	TY-2482_chromosome	B7LEI7	Putative flavoprotein	Escherichia coli (strain 55989 / EAEC)
75115	2037949	2037173	TY-2482_chromosome	B7LEI9	Putative flavoprotein	Escherichia coli (strain 55989 / EAEC)
80469	2039264	2037930	TY-2482_chromosome	B7LEJ0	Putative transporter	Escherichia coli (strain 55989 / EAEC)
73679	2040812	2039361	TY-2482_chromosome	B7LEJ1	Putative FAD containing dehydrogenase	Escherichia coli (strain 55989 / EAEC)
96757	2041742	2040885	TY-2482_chromosome	D3GRV6	Putative short chain dehydrogenase (EC 1.1.1.69)	Escherichia coli O44:H18 (strain 042 / EAEC)
79777	2041986	2043260	TY-2482_chromosome	B7LEJ3	Putative transporter	Escherichia coli (strain 55989 / EAEC)
97770	2043290	2044765	TY-2482_chromosome	B7LEJ4	Putative kinase	Escherichia coli (strain 55989 / EAEC)
14517	2045408	2045986	TY-2482_chromosome	E7J7X4	Putative uncharacterized protein	Escherichia coli 1357
64994	2046995	2046327	TY-2482_chromosome	B7LEJ5	Putative uncharacterized protein ygcF	Escherichia coli (strain 55989 / EAEC)
108004	2047288	2048157	TY-2482_chromosome	C8TG25	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
28163	2048175	2049401	TY-2482_chromosome	Q8FEG8	Putative uncharacterized protein	Escherichia coli O6
33212	2051243	2049609	TY-2482_chromosome	B7LEK0	CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Escherichia coli (strain 55989 / EAEC)
102799	2052262	2051474	TY-2482_chromosome	B7LEK1	Nucleoside triphosphate pyrophosphohydrolase	Escherichia coli (strain 55989 / EAEC)
27425	2052585	2052944	TY-2482_chromosome	Q1R7R0	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
62712	2052668	2052336	TY-2482_chromosome	B7LEJ9	Toxin of the ChpA-ChpR toxin-antitoxin system, endoribonuclease	Escherichia coli (strain 55989 / EAEC)
79892	2055228	2052997	TY-2482_chromosome	B7LEK2	(P)ppGpp synthetase I/GTP pyrophosphokinase (EC 2.7.6.5)	Escherichia coli (strain 55989 / EAEC)
113404	2056577	2055279	TY-2482_chromosome	B7LEK4	23S rRNA (Uracil-5)-methyltransferase (EC 2.1.1.-)	Escherichia coli (strain 55989 / EAEC)
111303	2056634	2059387	TY-2482_chromosome	C8UAB8	Hybrid sensory histidine kinase BarY, in two-component regulatory system with UvrY	Escherichia coli O103:H2 (strain 12009 / EHEC)
102829	2060962	2059625	TY-2482_chromosome	B7LEW6	(D)-glucarate dehydratase 1 (EC 4.2.1.40)	Escherichia coli (strain 55989 / EAEC)
108354	2062323	2060986	TY-2482_chromosome	C8TG35	Putative (D)-glucarate dehydratase 2 GudX	Escherichia coli O26:H11 (strain 11368 / EHEC)
73682	2063677	2062328	TY-2482_chromosome	B7LEW9	Putative D-glucarate transporter	Escherichia coli (strain 55989 / EAEC)
95555	2064561	2064115	TY-2482_chromosome	B7LEX0	Putative flavoprotein	Escherichia coli (strain 55989 / EAEC)
86063	2065361	2064582	TY-2482_chromosome	B7LEX1	Pseudouridine synthase (EC 5.4.99.-)	Escherichia coli (strain 55989 / EAEC)
102831	2065690	2065364	TY-2482_chromosome	B7LEW7	Putative uncharacterized protein yqcC	Escherichia coli (strain 55989 / EAEC)
r100	2066092	2065733	TY-2482_chromosome	ref|NC_010473|:3016056-3016415|-| [gene=csrB] [locus_tag=ECDH10B_2961]		
34087	2066857	2066315	TY-2482_chromosome	B7LEX3	Protein syd	Escherichia coli (strain 55989 / EAEC)
33237	2066925	2067770	TY-2482_chromosome	B7LEX4	NADPH-dependent 7-cyano-7-deazaguanine reductase (EC 1.7.1.13) (7-cyano-7-carbaguanine reductase) (NADPH-dep	Escherichia coli (strain 55989 / EAEC)
59067	2067885	2069246	TY-2482_chromosome	B7LEX5	Putative uncharacterized protein ygdH	Escherichia coli (strain 55989 / EAEC)
110609	2069806	2071092	TY-2482_chromosome	B7LEX2	Putative serine transporter	Escherichia coli (strain 55989 / EAEC)
106507	2071153	2072517	TY-2482_chromosome	B7LEX7	L-serine deaminase II (EC 4.3.1.17)	Escherichia coli (strain 55989 / EAEC)
87081	2072542	2073384	TY-2482_chromosome	C8UAD0	Protein Xni	Escherichia coli O103:H2 (strain 12009 / EHEC)
102887	2074593	2073445	TY-2482_chromosome	B7LEX9	L-1,2-propanediol oxidoreductase (EC 1.1.1.77)	Escherichia coli (strain 55989 / EAEC)
94275	2075265	2074621	TY-2482_chromosome	B7LEX8	L-fuculose-1-phosphate aldolase (EC 4.1.2.17)	Escherichia coli (strain 55989 / EAEC)
106510	2075812	2077125	TY-2482_chromosome	B7LEY1	L-fucose transporter	Escherichia coli (strain 55989 / EAEC)
31038	2077161	2078933	TY-2482_chromosome	B7LEY2	L-fucose isomerase (EC 5.3.1.25) (6-deoxy-L-galactose isomerase) (FucIase)	Escherichia coli (strain 55989 / EAEC)
95556	2079015	2080460	TY-2482_chromosome	B7LEY0	L-fuculokinase (EC 2.7.1.51)	Escherichia coli (strain 55989 / EAEC)

31042	2080465	2080884	TY-2482_chromosome	B7LEY4	L-fucose mutarotase (EC 5.1.3.n2) (Fucose 1-epimerase) (Type-2 mutarotase)	Escherichia coli (strain 55989 / EAEC)
77301	2080945	2081673	TY-2482_chromosome	B7LEY5	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
33581	2082820	2081723	TY-2482_chromosome	B7LEY3	Ribosomal RNA large subunit methyltransferase M (EC 2.1.1.-) (23S rRNA 2'-O-ribose methyltransferase rlmM)	Escherichia coli (strain 55989 / EAEC)
115349	2083208	2082816	TY-2482_chromosome	B7LEY7	Putative uncharacterized protein ygdD	Escherichia coli (strain 55989 / EAEC)
102891	2084144	2083230	TY-2482_chromosome	B7LEY8	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
r107	2084273	2084478	TY-2482_chromosome	ref|NC_010473|:3034596-3034793|-| [gene=gcvB] [locus_tag=ECDH10B_2978		
24255	2084439	2084752	TY-2482_chromosome	B7N743	Putative uncharacterized protein	Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC)
81016	2084914	2086116	TY-2482_chromosome	B7LEZ0	Cysteine sulfinate desulfinase (EC 4.4.1.-)	Escherichia coli (strain 55989 / EAEC)
99140	2086119	2086559	TY-2482_chromosome	B7LEY6	Putative Fe-S metabolism protein (SufE-like)	Escherichia coli (strain 55989 / EAEC)
82588	2087419	2086616	TY-2482_chromosome	B7LEZ2	Putative uncharacterized protein ygdL	Escherichia coli (strain 55989 / EAEC)
73717	2088593	2087499	TY-2482_chromosome	B7LEZ1	Membrane-bound lytic murein transglycosylase A (EC 3.2.1.-)	Escherichia coli (strain 55989 / EAEC)
r257	2088802	2088878	TY-2482_chromosome	ref|NC_010473|:3039499-3039575|Met tRNA| [gene=metV] [locus_tag=ECDH10B_2986		
r258	2088912	2088988	TY-2482_chromosome	ref|NC_010473|:3039499-3039575|Met tRNA| [gene=metV] [locus_tag=ECDH10B_2986		
r259	2089021	2089097	TY-2482_chromosome	ref|NC_010473|:3039499-3039575|Met tRNA| [gene=metV] [locus_tag=ECDH10B_2986		
68865	2090424	2089174	TY-2482_chromosome	B7LEZ4	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	Escherichia coli (strain 55989 / EAEC)
97768	2090656	2091984	TY-2482_chromosome	B7LEZ5	Fused acetylglutamate kinase homolog (Inactive) ; amino acid N-acetyltransferase (EC 2.3.1.1)	Escherichia coli (strain 55989 / EAEC)
113400	2093875	2092052	TY-2482_chromosome	B7LEZ6	Exonuclease V (RecBCD complex), alpha chain (EC 3.1.11.5)	Escherichia coli (strain 55989 / EAEC)
88317	2097417	2093878	TY-2482_chromosome	B7LEZ3	Exonuclease V (RecBCD complex), beta subunit (EC 3.1.11.5)	Escherichia coli (strain 55989 / EAEC)
73646	2100298	2097413	TY-2482_chromosome	B7LEZ8	Protease III (EC 3.4.24.55)	Escherichia coli (strain 55989 / EAEC)
69294	2103842	2100477	TY-2482_chromosome	B7LEZ9	Exonuclease V (RecBCD complex), gamma chain (EC 3.1.11.5)	Escherichia coli (strain 55989 / EAEC)
73645	2104178	2103858	TY-2482_chromosome	B7LEZ7	Prepilin peptidase-dependent protein C	Escherichia coli (strain 55989 / EAEC)
68129	2104570	2104166	TY-2482_chromosome	B7LF01	Putative uncharacterized protein ygdB	Escherichia coli (strain 55989 / EAEC)
24207	2105370	2104570	TY-2482_chromosome	A1AF37	Prepilin peptidase dependent protein B	Escherichia coli O1:K1 / APEC
26388	2105580	2105780	TY-2482_chromosome	Q0TE06	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
34414	2106570	2105779	TY-2482_chromosome	B7LF04	Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Escherichia coli (strain 55989 / EAEC)
31881	2107452	2106580	TY-2482_chromosome	B7LF05	Prolipoprotein diacylglyceryl transferase (EC 2.4.99.-)	Escherichia coli (strain 55989 / EAEC)
93617	2109849	2107606	TY-2482_chromosome	B7LF06	Fused PTS enzyme: PEP-protein phosphotransferase (Enzyme I) ; GAF domain containing protein (EC 2.7.3.9	Escherichia coli (strain 55989 / EAEC)
33682	2110392	2109865	TY-2482_chromosome	B7LF07	RNA pyrophosphohydrolase (EC 3.6.1.-) ((Di)nucleoside polyphosphate hydrolase)	Escherichia coli (strain 55989 / EAEC)
28802	2110704	2110895	TY-2482_chromosome	E4P678	Putative uncharacterized protein	Escherichia coli O83:H1 (strain NRG 857C / AIEC)
32571	2111077	2111763	TY-2482_chromosome	B7LF08	DNA mismatch repair protein mutH (Methyl-directed mismatch repair protein)	Escherichia coli (strain 55989 / EAEC)
100761	2111835	2112545	TY-2482_chromosome	B7LF09	Putative uncharacterized protein ygdQ	Escherichia coli (strain 55989 / EAEC)
26491	2112907	2112623	TY-2482_chromosome	Q1R7H9	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
102892	2113012	2114049	TY-2482_chromosome	B7LF11	Putative oxidoreductase, NADP(H)-dependent aldo-keto reductase	Escherichia coli (strain 55989 / EAEC)
31950	2115277	2114087	TY-2482_chromosome	B7LF12	Lysophospholipid transporter lplT	Escherichia coli (strain 55989 / EAEC)
29638	2117429	2115273	TY-2482_chromosome	B7LF13	Bifunctional protein aas [Includes: 2-acylglycerophosphoethanolamine acyltransferase (EC 2.3.1.40) (2-acyl-GPE acylt	Escherichia coli (strain 55989 / EAEC)
13165	2117526	2117819	TY-2482_chromosome	E6AX10	Conserved domain protein (Fragment)	Escherichia coli MS 16-3
r202	2117604	2117517	TY-2482_chromosome	ref|NC_010473|:3067994-3068081|-| [gene=rygA] [locus_tag=ECDH10B_3007		
25148	2117720	2117932	TY-2482_chromosome	Q8FEA4	Putative uncharacterized protein	Escherichia coli O6
r349	2117801	2117726	TY-2482_chromosome	ref|NC_010473|:3068202-3068277|-| [gene=rygB] [locus_tag=ECDH10B_3008		
87765	2118015	2119043	TY-2482_chromosome	B7LF02	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
113401	2120315	2119056	TY-2482_chromosome	B7LF15	Diaminopimelate decarboxylase (EC 4.1.1.20)	Escherichia coli (strain 55989 / EAEC)
106512	2120437	2121369	TY-2482_chromosome	B7LF16	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
109503	2122051	2121362	TY-2482_chromosome	B7LF17	Putative racemase	Escherichia coli (strain 55989 / EAEC)
77405	2123598	2122183	TY-2482_chromosome	B7LF18	Arabinose transporter	Escherichia coli (strain 55989 / EAEC)
76827	2124722	2123964	TY-2482_chromosome	B7LF19	2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)	Escherichia coli (strain 55989 / EAEC)
31753	2125588	2124755	TY-2482_chromosome	B7LF20	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17) (5-keto-4-deoxyuronate isomerase) (DKI isomer	Escherichia coli (strain 55989 / EAEC)
77408	2127056	2125878	TY-2482_chromosome	B7LF21	Acetyl-CoA acetyltransferase (EC 2.3.1.9)	Escherichia coli (strain 55989 / EAEC)
91900	2127311	2128537	TY-2482_chromosome	B7LF14	Putative transporter	Escherichia coli (strain 55989 / EAEC)
88391	2129000	2129629	TY-2482_chromosome	B7LF23	Putative uncharacterized protein yqeH	Escherichia coli (strain 55989 / EAEC)
69922	2129966	2130772	TY-2482_chromosome	B7LF22	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
105106	2130768	2131247	TY-2482_chromosome	B7LF25	Putative uncharacterized protein yqeJ	Escherichia coli (strain 55989 / EAEC)
95557	2131824	2131402	TY-2482_chromosome	B7LF26	Putative uncharacterized protein yqeK	Escherichia coli (strain 55989 / EAEC)
90642	2132018	2132452	TY-2482_chromosome	B7LF24	Putative uncharacterized protein ygeF	Escherichia coli (strain 55989 / EAEC)
81018	2132733	2133221	TY-2482_chromosome	B7LF28	Putative chaperone	Escherichia coli (strain 55989 / EAEC)
83456	2133559	2134932	TY-2482_chromosome	B7LF27	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
97064	2135103	2135318	TY-2482_chromosome	B7LF30	Putative uncharacterized protein ygeI	Escherichia coli (strain 55989 / EAEC)
88510	2135404	2135877	TY-2482_chromosome	B7LF31	Putative peptidoglycan-binding-like protein	Escherichia coli (strain 55989 / EAEC)
67624	2136557	2135928	TY-2482_chromosome	D3GSV2	Putative two-component response regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
114045	2137209	2136781	TY-2482_chromosome	B7LF33	Putative uncharacterized protein ygeM	Escherichia coli (strain 55989 / EAEC)
81019	2138007	2137429	TY-2482_chromosome	B7LF35	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
64177	2138757	2138026	TY-2482_chromosome	B7LF36	Putative Type III secretion system lipoprotein EprK	Escherichia coli (strain 55989 / EAEC)
91753	2139085	2138757	TY-2482_chromosome	B5Z4H9	Type III secretion apparatus protein EprJ	Escherichia coli O157:H7 (strain EC4115 / EHEC)
100416	2139345	2139108	TY-2482_chromosome	D3GSV7	Type III secretion system protein	Escherichia coli O44:H18 (strain 042 / EAEC)
73718	2140549	2139362	TY-2482_chromosome	B7LF39	Putative Type III secretion EprH protein	Escherichia coli (strain 55989 / EAEC)

110384	2140798	2141295	TY-2482_chromosome	B7LF38	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
76046	2141300	2141590	TY-2482_chromosome	B7LF41	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
107896	2142764	2141658	TY-2482_chromosome	B5Z4I3	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
94306	2143540	2142776	TY-2482_chromosome	B7LF43	Putative Type III secretion protein EpaR	Escherichia coli (strain 55989 / EAEC)
109703	2143802	2143545	TY-2482_chromosome	B5Z4I4	Type III secretion apparatus protein EpaQ	Escherichia coli O157:H7 (strain EC4115 / EHEC)
110385	2144477	2143815	TY-2482_chromosome	B7LF47	Putative type III secretion system protein EpaP	Escherichia coli (strain 55989 / EAEC)
15584	2145414	2144395	TY-2482_chromosome	Q3SBB5	EpaO	Escherichia coli
112170	2147198	2145549	TY-2482_chromosome	B7LF50	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
r499	2147463	2147390	TY-2482_chromosome	ref|NC_010473|:3090876-3090949|Gly tRNA| [gene=glyU] [locus_tag=ECDH10B_3039]		
109400	2148297	2147545	TY-2482_chromosome	B7LF51	Tetratricopeptide repeat transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
14388	2148485	2148297	TY-2482_chromosome	E6BGA4	Formate dehydrogenase accessory protein FdhD	Escherichia coli MS 85-1
115566	2148751	2151006	TY-2482_chromosome	B7LF45	Xanthine dehydrogenase, molybdenum binding subunit	Escherichia coli (strain 55989 / EAEC)
66261	2151020	2151895	TY-2482_chromosome	B7LF53	Xanthine dehydrogenase, FAD-binding subunit	Escherichia coli (strain 55989 / EAEC)
70012	2151895	2152371	TY-2482_chromosome	B7LF54	Xanthine dehydrogenase, Fe-S binding subunit	Escherichia coli (strain 55989 / EAEC)
70000	2154192	2152417	TY-2482_chromosome	B7LF52	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
65429	2154668	2155855	TY-2482_chromosome	B7LF55	Putative uncharacterized protein ygeW	Escherichia coli (strain 55989 / EAEC)
91903	2155916	2157109	TY-2482_chromosome	B7LF57	2,3-diaminopropionate ammonia-lyase (EC 4.3.1.15)	Escherichia coli (strain 55989 / EAEC)
110388	2157170	2158378	TY-2482_chromosome	B7LF58	Putative peptidase	Escherichia coli (strain 55989 / EAEC)
32998	2158434	2159816	TY-2482_chromosome	B7LF59	D-phenylhydantoinase (EC 3.5.2.-) (Hydantoin-utilizing enzyme hyuA)	Escherichia coli (strain 55989 / EAEC)
110389	2159867	2160796	TY-2482_chromosome	B7LF60	Amino acid (Carbamate) kinase (EC 2.7.2.2)	Escherichia coli (strain 55989 / EAEC)
105493	2162465	2160843	TY-2482_chromosome	B7LF61	Putative uncharacterized protein yqeB	Escherichia coli (strain 55989 / EAEC)
110387	2163283	2162516	TY-2482_chromosome	B7LF56	Putative uncharacterized protein yqeC	Escherichia coli (strain 55989 / EAEC)
87558	2163386	2163961	TY-2482_chromosome	B7LF63	Putative uncharacterized protein ygfJ	Escherichia coli (strain 55989 / EAEC)
105945	2164286	2167381	TY-2482_chromosome	B7LF64	Putative oxidoreductase, Fe-S subunit	Escherichia coli (strain 55989 / EAEC)
73719	2167387	2168712	TY-2482_chromosome	B7LF62	Putative chlorohydrolase/aminohydrolase	Escherichia coli (strain 55989 / EAEC)
91904	2168766	2169542	TY-2482_chromosome	B7LF66	Putative oxidoreductase	Escherichia coli (strain 55989 / EAEC)
102832	2169542	2172409	TY-2482_chromosome	B7LF67	Fused putative xanthine/hypoxanthine oxidase: molybdopterin-binding subunit ; Fe-S binding subunit	Escherichia coli (strain 55989 / EAEC)
91867	2172577	2173974	TY-2482_chromosome	B7LF65	Putative transporter	Escherichia coli (strain 55989 / EAEC)
73721	2173992	2175308	TY-2482_chromosome	B7LF69	Guanine deaminase (EC 3.5.4.3)	Escherichia coli (strain 55989 / EAEC)
96955	2175347	2176711	TY-2482_chromosome	B7LF70	Putative transporter	Escherichia coli (strain 55989 / EAEC)
66262	2177238	2176753	TY-2482_chromosome	B7LF68	Putative oxidoreductase, 4Fe-4S ferredoxin-type subunit	Escherichia coli (strain 55989 / EAEC)
102899	2179157	2177241	TY-2482_chromosome	B7LF72	Fused putative oxidoreductase: Fe-S subunit ; nucleotide-binding subunit	Escherichia coli (strain 55989 / EAEC)
76352	2179593	2181038	TY-2482_chromosome	B7LF73	Transporter	Escherichia coli (strain 55989 / EAEC)
115744	2181291	2181836	TY-2482_chromosome	B7LF71	Isopentenyl-diphosphate Delta-isomerase 1 (IPP isomerase 1) (EC 5.3.3.2) (IPP:DMAPP isomerase 1) (Isopentenyl pyro	Escherichia coli (strain 55989 / EAEC)
77414	2183399	2181885	TY-2482_chromosome	B7LF75	Lysyl-tRNA synthetase 1 (EC 6.1.1.6) (Lysine--tRNA ligase 1)	Escherichia coli (strain 55989 / EAEC)
33325	2184507	2183412	TY-2482_chromosome	B7LF76	Peptide chain release factor 2 (RF-2)	Escherichia coli (strain 55989 / EAEC)
62708	2186331	2184601	TY-2482_chromosome	B7LF77	SsDNA exonuclease, 5'--> 3'-specific (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
111580	2187047	2186340	TY-2482_chromosome	B7LF74	Protein disulfide isomerase II (EC 5.3.4.1)	Escherichia coli (strain 55989 / EAEC)
81021	2187968	2187075	TY-2482_chromosome	B7LF79	Site-specific tyrosine recombinase	Escherichia coli (strain 55989 / EAEC)
98018	2188080	2188598	TY-2482_chromosome	B7LF80	Flavodoxin 2	Escherichia coli (strain 55989 / EAEC)
114049	2189048	2188644	TY-2482_chromosome	B7LF81	Putative uncharacterized protein ygfX	Escherichia coli (strain 55989 / EAEC)
81023	2189295	2189032	TY-2482_chromosome	B7LF82	Putative uncharacterized protein ygfY	Escherichia coli (strain 55989 / EAEC)
34929	2189538	2190515	TY-2482_chromosome	B7LF83	tRNA-modifying protein ygfZ	Escherichia coli (strain 55989 / EAEC)
40516	2191285	2190599	TY-2482_chromosome	D8A3I5	Channel protein, hemolysin III family protein	Escherichia coli MS 21-1
35054	2191730	2191422	TY-2482_chromosome	B7LF85	UPF0267 protein yqfB	Escherichia coli (strain 55989 / EAEC)
114050	2191769	2193205	TY-2482_chromosome	B7LF86	6-phospho-beta-glucosidase A (EC 3.2.1.86)	Escherichia coli (strain 55989 / EAEC)
79013	2194008	2193268	TY-2482_chromosome	B7LF88	Putative NAD(P)-binding oxidoreductase with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
31097	2197142	2194272	TY-2482_chromosome	B7LF89	Glycine dehydrogenase [decarboxylating] (EC 1.4.4.2) (Glycine cleavage system P-protein) (Glycine decarboxylase)	Escherichia coli (strain 55989 / EAEC)
31093	2197650	2197264	TY-2482_chromosome	B7LF90	Glycine cleavage system H protein	Escherichia coli (strain 55989 / EAEC)
31101	2198768	2197677	TY-2482_chromosome	B7LF91	Aminomethyltransferase (EC 2.1.2.10) (Glycine cleavage system T protein)	Escherichia coli (strain 55989 / EAEC)
66269	2200418	2199219	TY-2482_chromosome	B7LF87	Putative oxidoreductase with FAD/NAD(P)-binding domain	Escherichia coli (strain 55989 / EAEC)
90460	2201619	2200444	TY-2482_chromosome	B7LF93	2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD(P)-binding (EC 1.14.-.-)	Escherichia coli (strain 55989 / EAEC)
77314	2202941	2201619	TY-2482_chromosome	B7LF92	Proline aminopeptidase P II (EC 3.4.11.9)	Escherichia coli (strain 55989 / EAEC)
74940	2203551	2202970	TY-2482_chromosome	D3GTS3	UPF0149 protein ygfB	Escherichia coli O44:H18 (strain 042 / EAEC)
18887	2203576	2203761	TY-2482_chromosome	D6JEQ2	Predicted protein	Escherichia coli B354
35075	2203713	2204039	TY-2482_chromosome	B7LFG9	Cell division protein ZapA (Z ring-associated protein ZapA)	Escherichia coli (strain 55989 / EAEC)
r106	2204084	2204266	TY-2482_chromosome	ref|NC_010473|:3147875-3148057|-| [gene=ssrS] [locus_tag=ECDH10B_3085]		
26194	2204144	2204887	TY-2482_chromosome	A8A452	5,10-methenyltetrahydrofolate synthetase (EC 6.3.3.2)	Escherichia coli O9:H4 (strain HS)
r122	2204916	2205066	TY-2482_chromosome	ref|NC_010473|:3148707-3148857|-| [gene=rygC] [locus_tag=ECDH10B_3087]		
20821	2205275	2205066	TY-2482_chromosome	E1I1F6	Putative uncharacterized protein (Fragment)	Escherichia coli MS 78-1
r123	2205308	2205455	TY-2482_chromosome	ref|NC_010473|:3148707-3148857|-| [gene=rygC] [locus_tag=ECDH10B_3087]		
94916	2206903	2205674	TY-2482_chromosome	B7LFG7	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	Escherichia coli (strain 55989 / EAEC)
4838	2207854	2207162	TY-2482_chromosome	A1AFA2	Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A) (PRI)	Escherichia coli O1:K1 / APEC
17763	2208108	2207908	TY-2482_chromosome	D7YB63	Conserved domain protein	Escherichia coli MS 115-1

31583	2208201	2209091	TY-2482_chromosome	B7LFH3	Chromosome initiation inhibitor (OriC replication inhibitor	Escherichia coli (strain 55989 / EAEC)
98513	2209298	2211439	TY-2482_chromosome	B5YQB0	Methylmalonyl-CoA mutase (EC 5.4.99.2)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
91837	2211435	2212427	TY-2482_chromosome	B7LFH1	Membrane ATPase/protein kinase	Escherichia coli (strain 55989 / EAEC)
99198	2212441	2213223	TY-2482_chromosome	B7LFH7	Methylmalonyl-CoA decarboxylase, biotin-independent (EC 4.1.1.41)	Escherichia coli (strain 55989 / EAEC)
114102	2213250	2214725	TY-2482_chromosome	B7LFH6	Propionyl-CoA:succinate-CoA transferase (EC 2.8.3.-)	Escherichia coli (strain 55989 / EAEC)
14393	2215621	2214673	TY-2482_chromosome	E9WIW1	LysR family bacterial regulatory helix-turn-helix protein	Escherichia coli E1520
70065	2216528	2215791	TY-2482_chromosome	B7LFI0	Putative uncharacterized protein yggE	Escherichia coli (strain 55989 / EAEC)
62818	2217256	2216624	TY-2482_chromosome	B7LFH8	Arginine exporter protein ArgO	Escherichia coli (strain 55989 / EAEC)
95635	2218255	2217398	TY-2482_chromosome	B7LFI2	Mechanosensitive channel	Escherichia coli (strain 55989 / EAEC)
76398	2219692	2218616	TY-2482_chromosome	B7LFI1	Fructose-bisphosphate aldolase, class II (EC 4.1.2.13)	Escherichia coli (strain 55989 / EAEC)
81074	2221070	2219910	TY-2482_chromosome	B7LFI4	Phosphoglycerate kinase (EC 2.7.2.3)	Escherichia coli (strain 55989 / EAEC)
30708	2222139	2221123	TY-2482_chromosome	B7LFI3	D-erythrose-4-phosphate dehydrogenase (E4PDH) (EC 1.2.1.72)	Escherichia coli (strain 55989 / EAEC)
59186	2222511	2222939	TY-2482_chromosome	B7LFI6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
62819	2222866	2223540	TY-2482_chromosome	B7LFI5	Putative ABC-type transport system	Escherichia coli (strain 55989 / EAEC)
91838	2223544	2224248	TY-2482_chromosome	B7LFI8	Putative ABC-type transport system	Escherichia coli (strain 55989 / EAEC)
64739	2224233	2224913	TY-2482_chromosome	B7LFI9	Putative ATP-binding protein of ABC transport system	Escherichia coli (strain 55989 / EAEC)
84641	2224877	2225584	TY-2482_chromosome	B7LFI7	Putative ATP-binding protein of ABC transport system	Escherichia coli (strain 55989 / EAEC)
99207	2226272	2225562	TY-2482_chromosome	B7LFJ1	Putative uncharacterized protein yggC	Escherichia coli (strain 55989 / EAEC)
62747	2226778	2226272	TY-2482_chromosome	B7LFJ2	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
114111	2227765	2226803	TY-2482_chromosome	B7LFJ0	Putative hexoseP phosphatase	Escherichia coli (strain 55989 / EAEC)
111640	2229039	2227765	TY-2482_chromosome	B7LFJ4	Putative dehydrogenase	Escherichia coli (strain 55989 / EAEC)
57979	2230442	2229057	TY-2482_chromosome	B7LFJ5	Fused mannitol-specific PTS enzymes: IIB component ; IIC component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
105098	2230913	2230473	TY-2482_chromosome	B7LFJ3	Putative mannitol-specific enzyme IIA component of PTS	Escherichia coli (strain 55989 / EAEC)
101495	2231174	2230926	TY-2482_chromosome	D3GTU6	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
102943	2233218	2231230	TY-2482_chromosome	B7LFJ7	Transketolase 1, thiamin-binding (EC 2.2.1.1)	Escherichia coli (strain 55989 / EAEC)
108413	2233370	2234251	TY-2482_chromosome	D3GTU8	Putative peptidase	Escherichia coli O44:H18 (strain 042 / EAEC)
20414	2234307	2235320	TY-2482_chromosome	Q47649	ORF1; putative	Escherichia coli
72279	2236247	2235519	TY-2482_chromosome	B7LFJ9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
102016	2238369	2236396	TY-2482_chromosome	B7LFK0	Biosynthetic arginine decarboxylase (ADC) (EC 4.1.1.19)	Escherichia coli (strain 55989 / EAEC)
110495	2238645	2238857	TY-2482_chromosome	B7LFK3	Putative uncharacterized protein yqgC	Escherichia coli (strain 55989 / EAEC)
62823	2239108	2238860	TY-2482_chromosome	B7LFK1	Putative uncharacterized protein yqgD	Escherichia coli (strain 55989 / EAEC)
32279	2239164	2240315	TY-2482_chromosome	B7LFK4	S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Escherichia coli (strain 55989 / EAEC)
19949	2240341	2240592	TY-2482_chromosome	D7YXP3	Putative uncharacterized protein (Fragment)	Escherichia coli MS 45-1
101626	2240754	2242145	TY-2482_chromosome	B7LFK6	D-galactose transporter	Escherichia coli (strain 55989 / EAEC)
115403	2242174	2242719	TY-2482_chromosome	B5YQE2	Protein sprT	Escherichia coli O157:H7 (strain EC4115 / EHEC)
87119	2242817	2243521	TY-2482_chromosome	B7LFK5	DNA-specific endonuclease I (EC 3.1.21.1)	Escherichia coli (strain 55989 / EAEC)
87561	2243604	2244332	TY-2482_chromosome	B7LFK9	Putative uncharacterized protein yggJ	Escherichia coli (strain 55989 / EAEC)
91302	2244348	2245295	TY-2482_chromosome	B7LFL0	Glutathione synthetase (EC 6.3.2.3)	Escherichia coli (strain 55989 / EAEC)
35057	2245407	2245967	TY-2482_chromosome	B7LFL1	UPF0301 protein yqgE	Escherichia coli (strain 55989 / EAEC)
33880	2245970	2246383	TY-2482_chromosome	B7LFL2	Putative Holliday junction resolvase (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
109824	2247542	2246565	TY-2482_chromosome	B7LFK8	Transporter	Escherichia coli (strain 55989 / EAEC)
69519	2247560	2248261	TY-2482_chromosome	B7LFL4	Putative enzyme	Escherichia coli (strain 55989 / EAEC)
95650	2248282	2248845	TY-2482_chromosome	B7LFL5	Putative uncharacterized protein yggT	Escherichia coli (strain 55989 / EAEC)
34933	2248845	2249132	TY-2482_chromosome	B7LFL6	UPF0235 protein yggU	Escherichia coli (strain 55989 / EAEC)
98117	2249143	2249733	TY-2482_chromosome	B7LFL7	Nucleoside-triphosphatase rdgB (EC 3.6.1.15) (Nucleoside triphosphate phosphohydrolase)	Escherichia coli (strain 55989 / EAEC)
68946	2249729	2250862	TY-2482_chromosome	B7LFL8	Putative oxidoreductase	Escherichia coli (strain 55989 / EAEC)
62824	2252027	2251023	TY-2482_chromosome	B7LFL3	Putative uncharacterized protein yggM	Escherichia coli (strain 55989 / EAEC)
102945	2253190	2252147	TY-2482_chromosome	B7LFM0	Periplasmic L-asparaginase II (EC 3.5.1.1)	Escherichia coli (strain 55989 / EAEC)
88465	2254085	2253369	TY-2482_chromosome	B7LFL9	Putative uncharacterized protein yggN	Escherichia coli (strain 55989 / EAEC)
104494	2254595	2254272	TY-2482_chromosome	B7LFM2	Putative uncharacterized protein yggL	Escherichia coli (strain 55989 / EAEC)
110496	2255314	2254598	TY-2482_chromosome	B7LFM3	tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA(m7G46)-methyltransferase)	Escherichia coli (strain 55989 / EAEC)
65595	2255475	2256524	TY-2482_chromosome	B7LFM4	Adenine DNA glycosylase (EC 3.2.2.-)	Escherichia coli (strain 55989 / EAEC)
16406	2256555	2256864	TY-2482_chromosome	E7HG43	Bacterial Fe(2+) trafficking family protein	Escherichia coli EPECa14
32413	2256895	2257971	TY-2482_chromosome	B7LFM1	Membrane-bound lytic murein transglycosylase C (EC 3.2.1.-) (Murein hydrolase C)	Escherichia coli (strain 55989 / EAEC)
73791	2258176	2259429	TY-2482_chromosome	B7LFM7	Nucleoside transporter	Escherichia coli (strain 55989 / EAEC)
116133	2261617	2259485	TY-2482_chromosome	B7LFM6	Ornithine decarboxylase, constitutive (EC 4.1.1.17)	Escherichia coli (strain 55989 / EAEC)
24688	2261900	2261700	TY-2482_chromosome	Q1R759	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
81080	2262015	2262719	TY-2482_chromosome	B7LFM9	Putative uncharacterized protein yqgA	Escherichia coli (strain 55989 / EAEC)
61103	2262789	2263034	TY-2482_chromosome	B7LBZ3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
r318	2262828	2262903	TY-2482_chromosome	ref|NC_010473|:4460936-4461011|Phe tRNA| [gene=pheU] [locus_tag=ECDH10B_4327		
81081	2263101	2264360	TY-2482_chromosome	B7LFN0	Prophage integrase	Escherichia coli (strain 55989 / EAEC)
14366	2264776	2265470	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli
9387	2265584	2265874	TY-2482_chromosome	B3Y1G8	Predicted protein	Escherichia coli O111:H-
84564	2266936	2266346	TY-2482_chromosome	B7LFN2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)

26997	2267133	2266867	TY-2482_chromosome	B7LFM8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
27356	2267329	2270193	TY-2482_chromosome	B7LFN4	Helicase	Escherichia coli (strain 55989 / EAEC)
83096	2270198	2271199	TY-2482_chromosome	B7LFN3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
110497	2271212	2273596	TY-2482_chromosome	B7LFN6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
82510	2273609	2275234	TY-2482_chromosome	B7LFN7	DNA methylase N-4/N-6 (EC 2.1.1.72)	Escherichia coli (strain 55989 / EAEC)
62825	2275240	2278107	TY-2482_chromosome	B7LFN5	Putative PstII restriction-modification enzyme Res subunit	Escherichia coli (strain 55989 / EAEC)
24347	2278199	2278489	TY-2482_chromosome	B7LFN8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73794	2278526	2278909	TY-2482_chromosome	B7LFN9	Transposase ORF A, IS3 family	Escherichia coli (strain 55989 / EAEC)
56696	2279983	2278835	TY-2482_chromosome	B7LEP8	IS30 transposase; KpLE2 phage-like element	Escherichia coli (strain 55989 / EAEC)
23302	2280048	2280536	TY-2482_chromosome	Q6Q6S9	Transposase	Escherichia coli
8448	2281060	2280755	TY-2482_chromosome	P71290	Orf58 protein	Escherichia coli
52535	2281131	2282651	TY-2482_chromosome	B7LBU5	Putative reverse transcriptase-like protein from putative prophage or plasmid (EC 2.7.7.49)	Escherichia coli (strain 55989 / EAEC)
26334	2282729	2283226	TY-2482_chromosome	Q327G0	IS629 ORF2	Shigella dysenteriae serotype 1 (strain Sd197)
55299	2283382	2287497	TY-2482_chromosome	B7LBW0	Serine protease pic (ShMu)	Escherichia coli (strain 55989 / EAEC)
10661	2287905	2287597	TY-2482_chromosome	B3IA48	Transposase	Escherichia coli E22
43232	2288601	2287935	TY-2482_chromosome	Q5K5W0	Putative uncharacterized protein	Escherichia coli
93002	2288791	2289051	TY-2482_chromosome	D3GV17	Transposase	Escherichia coli O44:H18 (strain 042 / EAEC)
73799	2289085	2290695	TY-2482_chromosome	B7LFP0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
8412	2291489	2290887	TY-2482_chromosome	B3I233	Integrase, catalytic region	Escherichia coli E22
105044	2292566	2291436	TY-2482_chromosome	B7LX19	Putative transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
108663	2292615	2292812	TY-2482_chromosome	B7LBX6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
90581	2293496	2293092	TY-2482_chromosome	D3GV13	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
108257	2295035	2293884	TY-2482_chromosome	D3GV12	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
101211	2295497	2295145	TY-2482_chromosome	B7LWW5	Transposase ORF A, IS629	Escherichia coli (strain 55989 / EAEC)
101247	2296080	2295517	TY-2482_chromosome	D3GV09	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
86915	2296922	2296670	TY-2482_chromosome	D3GV08	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
26335	2298326	2297829	TY-2482_chromosome	Q327G0	IS629 ORF2	Shigella dysenteriae serotype 1 (strain Sd197)
52536	2299924	2298404	TY-2482_chromosome	B7LBU5	Putative reverse transcriptase-like protein from putative prophage or plasmid (EC 2.7.7.49)	Escherichia coli (strain 55989 / EAEC)
8447	2299995	2300300	TY-2482_chromosome	P71290	Orf58 protein	Escherichia coli
16056	2300218	2300586	TY-2482_chromosome	Q9S110	Orf57 protein	Escherichia coli
27674	2301089	2300519	TY-2482_chromosome	B7LFP9	Transposase ORF B, IS629	Escherichia coli (strain 55989 / EAEC)
29410	2304066	2301520	TY-2482_chromosome	B7LFQ0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26998	2307483	2304073	TY-2482_chromosome	B7LFP6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
27175	2308082	2307483	TY-2482_chromosome	B7LFQ2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25270	2308381	2308070	TY-2482_chromosome	B7LFQ1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26577	2309839	2308412	TY-2482_chromosome	B7LFQ4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
24593	2310394	2309843	TY-2482_chromosome	B7LFQ5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
29396	2311475	2310402	TY-2482_chromosome	B7LFQ6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
24689	2311784	2311482	TY-2482_chromosome	B7LFQ7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
29191	2312255	2311791	TY-2482_chromosome	B7LFQ3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
24162	2314248	2312269	TY-2482_chromosome	B7LFQ9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28502	2315220	2314264	TY-2482_chromosome	B7LFR0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
27814	2316986	2315187	TY-2482_chromosome	B7LFR1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28039	2317401	2316982	TY-2482_chromosome	B7LFR2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25651	2317917	2317414	TY-2482_chromosome	B7LFR3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
67799	2319405	2317930	TY-2482_chromosome	B7LFQ8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
102853	2319884	2319411	TY-2482_chromosome	B7LFR5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
7598	2320280	2321307	TY-2482_chromosome	P16943	Insertion element IS630 uncharacterized 39 kDa protein (ISO-IS200 39 kDa protein)	Shigella sonnei
25710	2321904	2321422	TY-2482_chromosome	B7LFS0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
20585	2321982	2322591	TY-2482_chromosome	D8EKF9	Integrase core domain protein	Escherichia coli MS 107-1
69991	2322948	2322628	TY-2482_chromosome	B7LFS4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
89972	2323658	2323017	TY-2482_chromosome	B7LFS2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
62717	2323987	2323682	TY-2482_chromosome	B7LFS6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
101309	2324614	2324312	TY-2482_chromosome	D3GUY0	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
73647	2326466	2324682	TY-2482_chromosome	B7LFT1	Putative UvrD/REP helicase	Escherichia coli (strain 55989 / EAEC)
24351	2327826	2326663	TY-2482_chromosome	B7LFT2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25236	2329367	2328009	TY-2482_chromosome	B7LG71	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25915	2329910	2329392	TY-2482_chromosome	B7LG72	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28465	2330686	2330414	TY-2482_chromosome	E3PN47	Putative uncharacterized protein	Escherichia coli O78:H11 (strain H10407 / ETEC)
66386	2330945	2330640	TY-2482_chromosome	B7LG74	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
101413	2331625	2330969	TY-2482_chromosome	B7LG70	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28816	2332371	2331901	TY-2482_chromosome	B7LG76	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
106515	2332696	2332310	TY-2482_chromosome	B7LG75	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
97486	2333427	2332861	TY-2482_chromosome	B7LG78	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)

25603	2333877	2333677	TY-2482_chromosome	B7LG80	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
68254	2334337	2334047	TY-2482_chromosome	Q0TDJ8	Putative hemolysin expression modulating protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
71239	2334883	2335158	TY-2482_chromosome	D3GU29	Putative phage-related regulatory protein	Escherichia coli O44:H18 (strain 042 / EAEC)
86266	2335220	2335816	TY-2482_chromosome	B7LG83	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
105223	2335895	2336155	TY-2482_chromosome	D3GU27	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
21539	2336333	2336148	TY-2482_chromosome	D8AG23	Putative uncharacterized protein	Escherichia coli MS 21-1
27417	2337314	2338330	TY-2482_chromosome	B7LG85	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104659	2338311	2339312	TY-2482_chromosome	C8TV65	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
102141	2339643	2342765	TY-2482_chromosome	B7LG82	Antigen 43 (Ag43) phase-variable biofilm formation autotransporter; CP4-44 prophage	Escherichia coli (strain 55989 / EAEC)
86965	2342883	2345402	TY-2482_chromosome	B7LG88	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
79239	2345481	2345933	TY-2482_chromosome	B7LG89	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
78892	2346015	2346245	TY-2482_chromosome	B7LG87	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
106469	2346348	2347163	TY-2482_chromosome	B7LG91	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
47870	2348421	2347465	TY-2482_chromosome	Q5K5L6	Putative uncharacterized protein	Escherichia coli
22617	2349072	2349218	TY-2482_chromosome	E9TQB2	Conserved domain protein (Fragment)	Escherichia coli MS 60-1
81024	2349140	2349619	TY-2482_chromosome	B7LG96	Toxin of the YeeV-YeeU toxin-antitoxin system	Escherichia coli (strain 55989 / EAEC)
107832	2349619	2350038	TY-2482_chromosome	B7LG97	Putative uncharacterized protein yeeW	Escherichia coli (strain 55989 / EAEC)
62718	2350126	2350965	TY-2482_chromosome	B7LG90	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
81029	2351785	2351252	TY-2482_chromosome	B7LG99	Putative secretion pathway M-type protein, membrane anchored	Escherichia coli (strain 55989 / EAEC)
105909	2352965	2351790	TY-2482_chromosome	B7LGA0	Putative secretion pathway protein, L-type protein	Escherichia coli (strain 55989 / EAEC)
66388	2353939	2352965	TY-2482_chromosome	B7LGA1	Putative type II secretion protein (GspK-like)	Escherichia coli (strain 55989 / EAEC)
95593	2354541	2353945	TY-2482_chromosome	B7LG98	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
88397	2354909	2354541	TY-2482_chromosome	B7LGA2	Putative type II secretion protein (GspI-like)	Escherichia coli (strain 55989 / EAEC)
81030	2355469	2354909	TY-2482_chromosome	B7LGA4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
61881	2355955	2355476	TY-2482_chromosome	B7LGA5	Putative general secretion pathway protein G (EpsG-like)	Escherichia coli (strain 55989 / EAEC)
29089	2357168	2355948	TY-2482_chromosome	B7LGA3	General secretion pathway protein F	Escherichia coli (strain 55989 / EAEC)
59128	2358661	2357171	TY-2482_chromosome	B7LGA7	General secretion pathway protein E	Escherichia coli (strain 55989 / EAEC)
25795	2360721	2358664	TY-2482_chromosome	B7LGA8	General secretion pathway protein D	Escherichia coli (strain 55989 / EAEC)
76836	2361710	2360754	TY-2482_chromosome	B7LGA9	Putative secretion pathway protein, C-type protein	Escherichia coli (strain 55989 / EAEC)
88398	2362138	2361731	TY-2482_chromosome	B7LGA6	Putative uncharacterized protein yghG	Escherichia coli (strain 55989 / EAEC)
99143	2363013	2362207	TY-2482_chromosome	B7LGB1	Bifunctional prepilin leader peptidase and methylase	Escherichia coli (strain 55989 / EAEC)
90197	2367784	2363156	TY-2482_chromosome	B7LGB2	Inner membrane lipoprotein	Escherichia coli (strain 55989 / EAEC)
29173	2367917	2368221	TY-2482_chromosome	A7ZRK1	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC)
110401	2369934	2368255	TY-2482_chromosome	B7LGB4	Glycolate transporter	Escherichia coli (strain 55989 / EAEC)
84601	2372461	2370293	TY-2482_chromosome	B7LGB5	Malate synthase G (EC 2.3.3.9)	Escherichia coli (strain 55989 / EAEC)
89747	2372887	2372486	TY-2482_chromosome	B7LGB3	Putative uncharacterized protein glcG	Escherichia coli (strain 55989 / EAEC)
59131	2374115	2372895	TY-2482_chromosome	B7LGB7	Glycolate oxidase iron-sulfur subunit	Escherichia coli (strain 55989 / EAEC)
114054	2375178	2374129	TY-2482_chromosome	B7LGB8	Glycolate oxidase FAD binding subunit	Escherichia coli (strain 55989 / EAEC)
113271	2376677	2375181	TY-2482_chromosome	B7LGB9	Glycolate oxidase subunit, FAD-linked	Escherichia coli (strain 55989 / EAEC)
102272	2376928	2377689	TY-2482_chromosome	C8UFR4	DNA-binding transcriptional dual regulator, glycolate-binding	Escherichia coli O111:H- (strain 11128 / EHEC)
111568	2378841	2377702	TY-2482_chromosome	D3GVN3	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
60460	2379212	2380930	TY-2482_chromosome	D3GVN4	AMP-binding protein	Escherichia coli O44:H18 (strain 042 / EAEC)
114486	2380930	2381841	TY-2482_chromosome	C8UFR7	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC)
97111	2381876	2382121	TY-2482_chromosome	D3GVN6	Putative acyl carrier protein	Escherichia coli O44:H18 (strain 042 / EAEC)
87055	2382124	2383293	TY-2482_chromosome	B7LGC4	Putative 8-amino-7-oxononanoate synthase (EC 2.3.1.47)	Escherichia coli (strain 55989 / EAEC)
84602	2384491	2383334	TY-2482_chromosome	B7LGC5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
105107	2385477	2384410	TY-2482_chromosome	B7LGC0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
106519	2386071	2385511	TY-2482_chromosome	B7LGC7	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
82589	2386904	2386083	TY-2482_chromosome	B7LGC8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
60565	2388253	2386907	TY-2482_chromosome	B7LGC9	Putative membrane protein, conserved protein	Escherichia coli (strain 55989 / EAEC)
96959	2389057	2388302	TY-2482_chromosome	B7LGC6	Putative uncharacterized protein yghR	Escherichia coli (strain 55989 / EAEC)
116072	2389802	2389092	TY-2482_chromosome	B7LGD1	Putative uncharacterized protein yghS	Escherichia coli (strain 55989 / EAEC)
81031	2389976	2390665	TY-2482_chromosome	B7LGD0	Putative uncharacterized protein yghT	Escherichia coli (strain 55989 / EAEC)
73723	2392216	2390720	TY-2482_chromosome	B7LGD2	Phosphate transporter	Escherichia coli (strain 55989 / EAEC)
78791	2394367	2392511	TY-2482_chromosome	B7LGD4	Fused glutathionylspermidine amidase ; glutathionylspermidine synthetase (EC 3.5.1.78) (EC 6.3.1.8)	Escherichia coli (strain 55989 / EAEC)
64736	2394572	2395435	TY-2482_chromosome	B7LGD5	S-transferase (EC 2.5.1.18)	Escherichia coli (strain 55989 / EAEC)
115750	2395738	2396715	TY-2482_chromosome	B7LF78	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
13891	2395821	2395432	TY-2482_chromosome	D8EBP7	Putative uncharacterized protein (Fragment)	Escherichia coli MS 119-7
66273	2397088	2396843	TY-2482_chromosome	B7LGD3	Hydrogenase 2 accessory protein	Escherichia coli (strain 55989 / EAEC)
112877	2397442	2397104	TY-2482_chromosome	B7LGD8	Probable hydrogenase nickel incorporation protein hypA 2	Escherichia coli (strain 55989 / EAEC)
76445	2397923	2397438	TY-2482_chromosome	B7LGD9	Hydrogenase 2-specific chaperone	Escherichia coli (strain 55989 / EAEC)
84584	2398410	2397919	TY-2482_chromosome	B7LGE0	Maturation element for hydrogenase 2	Escherichia coli (strain 55989 / EAEC)
105096	2400113	2398413	TY-2482_chromosome	B7LGD7	Hydrogenase 2, large subunit (EC 1.12.7.2)	Escherichia coli (strain 55989 / EAEC)
66365	2401288	2400113	TY-2482_chromosome	B7LGE2	Hydrogenase 2 cytochrome b type component	Escherichia coli (strain 55989 / EAEC)

70016	2402264	2401281	TY-2482_chromosome	B7LGE3	Hydrogenase 2 4Fe-4S ferredoxin-type component	Escherichia coli (strain 55989 / EAEC)
91910	2403385	2402270	TY-2482_chromosome	B7LGE4	Hydrogenase 2, small subunit (EC 1.12.7.2)	Escherichia coli (strain 55989 / EAEC)
104322	2403577	2403395	TY-2482_chromosome	B7LGE5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
93446	2403861	2403577	TY-2482_chromosome	B7LGE6	Putative uncharacterized protein yghW	Escherichia coli (strain 55989 / EAEC)
64575	2404906	2403983	TY-2482_chromosome	B7LGE7	Putative enzyme (EC 3.1.1.45)	Escherichia coli (strain 55989 / EAEC)
95558	2405024	2406061	TY-2482_chromosome	B7LGE1	Aldo-keto reductase	Escherichia coli (strain 55989 / EAEC)
35060	2406598	2406107	TY-2482_chromosome	B7LGE9	UPF0114 protein yqhA	Escherichia coli (strain 55989 / EAEC)
95594	2406789	2407670	TY-2482_chromosome	B7LGF0	Putative glutathionylspermidine synthase, with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
115657	2408137	2407715	TY-2482_chromosome	B7LGF1	Membrane spanning protein in TonB-ExbB-ExbD complex	Escherichia coli (strain 55989 / EAEC)
66274	2408878	2408147	TY-2482_chromosome	B7LGF2	Membrane spanning protein in TonB-ExbB-ExbD complex	Escherichia coli (strain 55989 / EAEC)
95596	2409130	2410314	TY-2482_chromosome	B7LGF4	Cystathionine beta-lyase, PLP-dependent (EC 4.4.1.8)	Escherichia coli (strain 55989 / EAEC)
62770	2410457	2411113	TY-2482_chromosome	B7LGF5	Putative uncharacterized protein yghB	Escherichia coli (strain 55989 / EAEC)
62769	2412112	2411159	TY-2482_chromosome	B7LGE8	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
61043	2412249	2413409	TY-2482_chromosome	B7LGF6	Alcohol dehydrogenase, NAD(P)-dependent	Escherichia coli (strain 55989 / EAEC)
84585	2413517	2414341	TY-2482_chromosome	B7LGF8	2,5-diketo-D-gluconate reductase A (EC 1.1.1.274)	Escherichia coli (strain 55989 / EAEC)
84452	2414544	2415467	TY-2482_chromosome	B7LGF7	Putative uncharacterized protein yqhG	Escherichia coli (strain 55989 / EAEC)
97570	2415521	2415775	TY-2482_chromosome	B7LGG0	Putative outer membrane lipoprotein	Escherichia coli (strain 55989 / EAEC)
79769	2418040	2415824	TY-2482_chromosome	B7LGG1	UPF0313 protein ygiQ	Escherichia coli (strain 55989 / EAEC)
95598	2419563	2418154	TY-2482_chromosome	B7LGF9	Repressor protein for FtsI	Escherichia coli (strain 55989 / EAEC)
77366	2420375	2419641	TY-2482_chromosome	B7LGG3	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)	Escherichia coli (strain 55989 / EAEC)
77416	2422866	2420611	TY-2482_chromosome	B7LGG5	DNA topoisomerase IV, subunit A (EC 5.99.1.-)	Escherichia coli (strain 55989 / EAEC)
74939	2422962	2423171	TY-2482_chromosome	D3GVS6	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
13886	2423412	2423197	TY-2482_chromosome	D7YH50	Putative uncharacterized protein	Escherichia coli MS 182-1
81034	2423894	2423415	TY-2482_chromosome	B7LGG6	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
72776	2424339	2423950	TY-2482_chromosome	B7LGG7	Putative uncharacterized protein ygiW	Escherichia coli (strain 55989 / EAEC)
64814	2424491	2425147	TY-2482_chromosome	B7LGG8	DNA-binding response regulator in two-component regulatory system with QseC	Escherichia coli (strain 55989 / EAEC)
111586	2425147	2426493	TY-2482_chromosome	B7LGG9	Sensory histidine kinase in two-component regulatory system with QseB	Escherichia coli (strain 55989 / EAEC)
66275	2426874	2426545	TY-2482_chromosome	B7LGG2	Putative uncharacterized protein ygiZ	Escherichia coli (strain 55989 / EAEC)
99144	2427193	2427771	TY-2482_chromosome	B7LGH1	NADPH quinone reductase (EC 1.6.99.6)	Escherichia coli (strain 55989 / EAEC)
110403	2427805	2428116	TY-2482_chromosome	B7LGH2	Quinol monooxygenase	Escherichia coli (strain 55989 / EAEC)
81035	2430059	2428170	TY-2482_chromosome	B7LGH0	DNA topoisomerase IV, subunit B (EC 5.99.1.-)	Escherichia coli (strain 55989 / EAEC)
71755	2430669	2430091	TY-2482_chromosome	B7LGH4	Putative esterase	Escherichia coli (strain 55989 / EAEC)
90016	2431496	2430672	TY-2482_chromosome	B7LGH3	Cyclic 3',5'-adenosine monophosphate phosphodiesterase (EC 3.1.4.17)	Escherichia coli (strain 55989 / EAEC)
62773	2431943	2431524	TY-2482_chromosome	B7LGH6	Putative dehydrogenase	Escherichia coli (strain 55989 / EAEC)
69342	2432573	2431947	TY-2482_chromosome	B7LGH7	ADP-ribose pyrophosphatase (EC 3.6.1.13)	Escherichia coli (strain 55989 / EAEC)
62772	2432778	2434256	TY-2482_chromosome	B7LGH5	Transport channel	Escherichia coli (strain 55989 / EAEC)
116161	2434407	2435075	TY-2482_chromosome	C8TWX3	UPF0441 protein ygiB	Escherichia coli O103:H2 (strain 12009 / EHEC)
93515	2435084	2436241	TY-2482_chromosome	B7LGI0	Putative enzyme	Escherichia coli (strain 55989 / EAEC)
59132	2437097	2436285	TY-2482_chromosome	B7LGH8	Putative dioxygenase	Escherichia coli (strain 55989 / EAEC)
35109	2437213	2437983	TY-2482_chromosome	B7LGI2	Zinc transporter ZupT	Escherichia coli (strain 55989 / EAEC)
66276	2438238	2438047	TY-2482_chromosome	B7LGI3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
33401	2439128	2438478	TY-2482_chromosome	B7LGI1	3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase) (EC 4.1.99.12)	Escherichia coli (strain 55989 / EAEC)
96544	2439442	2439789	TY-2482_chromosome	D3GVV8	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
88399	2440075	2440623	TY-2482_chromosome	B7LGI6	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
107850	2440677	2443187	TY-2482_chromosome	B7LGI4	Outer membrane usher protein	Escherichia coli (strain 55989 / EAEC)
84604	2443206	2443952	TY-2482_chromosome	B7LGY1	Periplasmic pilin chaperone	Escherichia coli (strain 55989 / EAEC)
70059	2443957	2445018	TY-2482_chromosome	B7LGY2	Putative uncharacterized protein yqiI	Escherichia coli (strain 55989 / EAEC)
31122	2445264	2445067	TY-2482_chromosome	B7LGY3	Glycogen synthesis protein glgS	Escherichia coli (strain 55989 / EAEC)
84611	2445533	2446159	TY-2482_chromosome	B7LGY5	Putative uncharacterized protein yqiJ	Escherichia coli (strain 55989 / EAEC)
67743	2446189	2447847	TY-2482_chromosome	B7LGY6	Putative uncharacterized protein yqiK	Escherichia coli (strain 55989 / EAEC)
28120	2447869	2448198	TY-2482_chromosome	D3QRZ7	Putative uncharacterized protein	Escherichia coli O55:H7 (strain CB9615 / EPEC)
28119	2448185	2448574	TY-2482_chromosome	D3QRZ7	Putative uncharacterized protein	Escherichia coli O55:H7 (strain CB9615 / EPEC)
r113	2448223	2448074	TY-2482_chromosome	ref|NC_010473|:3290518-3290667|-| [gene=rygD] [locus_tag=ECDH10B_3226]		
r114	2448599	2448451	TY-2482_chromosome	ref|NC_010473|:3290518-3290667|-| [gene=rygD] [locus_tag=ECDH10B_3226]		
31413	2450077	2448647	TY-2482_chromosome	B7LGY7	Bifunctional protein hldE [Includes: D-beta-D-heptose 7-phosphate kinase (EC 2.7.1.-) (D-beta-D-heptose 7-phospho	Escherichia coli (strain 55989 / EAEC)
64406	2452965	2450128	TY-2482_chromosome	B7LGY4	Glutamate-ammonia-ligase adenylyltransferase (EC 2.7.7.42) (Glutamine-synthase adenylyltransferase) ([Glutamate--	Escherichia coli (strain 55989 / EAEC)
87776	2454289	2452991	TY-2482_chromosome	B7LGY8	Putative adenylate cyclase	Escherichia coli (strain 55989 / EAEC)
68711	2454531	2455148	TY-2482_chromosome	B7LGZ0	Putative signal transduction protein (SH3 domain)	Escherichia coli (strain 55989 / EAEC)
20613	2454537	2454298	TY-2482_chromosome	D8E4T8	Putative uncharacterized protein	Escherichia coli MS 119-7
30255	2455215	2456450	TY-2482_chromosome	B7LGZ2	Multifunctional CCA protein [Includes: CCA-adding enzyme (EC 2.7.7.72) (CCA tRNA nucleotidyltransferase) (tRNA CC	Escherichia coli (strain 55989 / EAEC)
34514	2457437	2456619	TY-2482_chromosome	B7LGZ1	Undecaprenyl-diphosphatase (EC 3.6.1.27) (Bacitracin resistance protein) (Undecaprenyl pyrophosphate phosphatas	Escherichia coli (strain 55989 / EAEC)
69186	2457896	2457531	TY-2482_chromosome	B7LGZ4	Bifunctioal dihydroneopterin aldolase ; dihydroneopterin triphosphate 2'-epimerase (EC 4.1.2.25	Escherichia coli (strain 55989 / EAEC)
33018	2458001	2458615	TY-2482_chromosome	B7LGZ5	Glycerol-3-phosphate acyltransferase (G3P acyltransferase) (GPAT) (EC 2.3.1.15) (EC 2.3.1.n5) (Lysophosphatidic acid	Escherichia coli (strain 55989 / EAEC)
57951	2459563	2458634	TY-2482_chromosome	B7LGZ3	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)

87362	2459770	2460678	TY-2482_chromosome	B7LGZ7	L-tartrate dehydratase, alpha subunit (EC 4.2.1.32)	Escherichia coli (strain 55989 / EAEC)
83550	2460678	2461280	TY-2482_chromosome	B7LGZ8	L-tartrate dehydratase, beta subunit (EC 4.2.1.32)	Escherichia coli (strain 55989 / EAEC)
69231	2461332	2462792	TY-2482_chromosome	B7LGZ6	Putative tartrate:succinate antiporter	Escherichia coli (strain 55989 / EAEC)
31089	2463851	2462841	TY-2482_chromosome	B7LGZ9	Probable tRNA threonylcarbamoyladenosine biosynthesis protein Gcp (t(6)A37 threonylcarbamoyladenosine biosynth	Escherichia coli (strain 55989 / EAEC)
33740	2464088	2464300	TY-2482_chromosome	B7LH01	30S ribosomal protein S21	Escherichia coli (strain 55989 / EAEC)
27812	2464146	2463863	TY-2482_chromosome	Q1R6R6	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
79985	2464414	2466156	TY-2482_chromosome	B7LH02	DNA primase (EC 2.7.7.-)	Escherichia coli (strain 55989 / EAEC)
73759	2466354	2468192	TY-2482_chromosome	B7LH00	RNA polymerase sigma factor	Escherichia coli (strain 55989 / EAEC)
32522	2468779	2468276	TY-2482_chromosome	B7LH04	G/U mismatch-specific DNA glycosylase (EC 3.2.2.28) (Double-strand-specific uracil glycosylase) (Mismatch-specific ur	Escherichia coli (strain 55989 / EAEC)
r345	2468904	2468979	TY-2482_chromosome	ref|NC_010473|:3311365-3311440|Ile tRNA| [gene=ileX] [locus_tag=ECDH10B_3244]		
68501	2469797	2469036	TY-2482_chromosome	B7LH05	Putative siderophore interacting protein	Escherichia coli (strain 55989 / EAEC)
114091	2470074	2470694	TY-2482_chromosome	B7LH06	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
114092	2472371	2470854	TY-2482_chromosome	B7LH07	Fused signal transducer for aerotaxis sensory component ; methyl accepting chemotaxis component	Escherichia coli (strain 55989 / EAEC)
13204	2472647	2472850	TY-2482_chromosome	D6JEV2	Predicted protein	Escherichia coli B354
32866	2472789	2474165	TY-2482_chromosome	B7LH08	Putrescine aminotransferase (EC 2.6.1.82) (Putrescine--2-oxoglutaric acid transaminase) (PAT) (PATase)	Escherichia coli (strain 55989 / EAEC)
26426	2474152	2474559	TY-2482_chromosome	A1AFZ4	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
90687	2474761	2475741	TY-2482_chromosome	B7LH10	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
102837	2475928	2479017	TY-2482_chromosome	B7LH11	Cryptic beta-D-galactosidase, alpha subunit (EC 3.2.1.23)	Escherichia coli (strain 55989 / EAEC)
80970	2479017	2479463	TY-2482_chromosome	B7LH12	Cryptic beta-D-galactosidase, beta subunit	Escherichia coli (strain 55989 / EAEC)
86216	2479529	2480959	TY-2482_chromosome	B7LH09	Putative transporter	Escherichia coli (strain 55989 / EAEC)
75843	2481096	2482163	TY-2482_chromosome	B7LH14	Putative uncharacterized protein ygjJ	Escherichia coli (strain 55989 / EAEC)
72035	2482183	2484531	TY-2482_chromosome	B7LH15	Putative glycosyl hydrolase	Escherichia coli (strain 55989 / EAEC)
21905	2484581	2484805	TY-2482_chromosome	D7YDG0	Conserved domain protein	Escherichia coli MS 182-1
70063	2484860	2486875	TY-2482_chromosome	B7LH13	2,4-dienoyl-CoA reductase, NADH and FMN-linked (EC 1.3.1.34)	Escherichia coli (strain 55989 / EAEC)
46286	2487348	2486926	TY-2482_chromosome	E6ARB5	Toxin-antitoxin system, antitoxin component, Xre family	Escherichia coli MS 16-3
59172	2488746	2487613	TY-2482_chromosome	B7LH19	Ribosomal RNA large subunit methyltransferase G (EC 2.1.1.174) (23S rRNA m2G1835 methyltransferase) (rRNA (guar	Escherichia coli (strain 55989 / EAEC)
68412	2488795	2489331	TY-2482_chromosome	D3GWQ3	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
77367	2489411	2490091	TY-2482_chromosome	B7LH21	Putative thioredoxin-like	Escherichia coli (strain 55989 / EAEC)
59094	2490155	2491156	TY-2482_chromosome	B7LH22	Putative NAD(P)-binding dehydrogenase	Escherichia coli (strain 55989 / EAEC)
r105	2491236	2491423	TY-2482_chromosome	ref|NC_010473|:3334141-3334328|-| [gene=sraF] [locus_tag=ECDH10B_3263]		
75757	2491442	2492404	TY-2482_chromosome	B7LH23	Putative uncharacterized protein alx	Escherichia coli (strain 55989 / EAEC)
61041	2492806	2494047	TY-2482_chromosome	B7LH24	Sodium:serine/threonine symporter	Escherichia coli (strain 55989 / EAEC)
79012	2494606	2494058	TY-2482_chromosome	B7LH25	Putative uncharacterized protein ygjV	Escherichia coli (strain 55989 / EAEC)
88210	2496176	2494692	TY-2482_chromosome	B7LH26	Altronate hydrolase (EC 4.2.1.7)	Escherichia coli (strain 55989 / EAEC)
34549	2497603	2496194	TY-2482_chromosome	B7LH20	Uronate isomerase (EC 5.3.1.12) (Glucuronate isomerase) (Uronic isomerase)	Escherichia coli (strain 55989 / EAEC)
80425	2497966	2499381	TY-2482_chromosome	B7LH28	Hexuronate transporter	Escherichia coli (strain 55989 / EAEC)
68284	2500560	2499475	TY-2482_chromosome	B7LH29	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
84623	2503259	2500560	TY-2482_chromosome	B7LH30	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
108498	2503833	2503336	TY-2482_chromosome	B7LH27	Putative adhesin major subunit pilin	Escherichia coli (strain 55989 / EAEC)
91946	2504579	2503866	TY-2482_chromosome	B7LH32	Putative fimbrial protein	Escherichia coli (strain 55989 / EAEC)
98638	2504875	2505648	TY-2482_chromosome	B7LH33	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
86687	2505996	2506655	TY-2482_chromosome	B7LH34	Putative uncharacterized protein yqjA	Escherichia coli (strain 55989 / EAEC)
62809	2506662	2507042	TY-2482_chromosome	B7LH35	Putative uncharacterized protein yqjB	Escherichia coli (strain 55989 / EAEC)
108535	2507177	2507557	TY-2482_chromosome	D3GWR6	Putative exported protein	Escherichia coli O44:H18 (strain 042 / EAEC)
99186	2507598	2507900	TY-2482_chromosome	B7LH37	Putative uncharacterized protein yqjD	Escherichia coli (strain 55989 / EAEC)
101574	2507906	2508307	TY-2482_chromosome	B7LH36	Putative uncharacterized protein yqjE	Escherichia coli (strain 55989 / EAEC)
101135	2508300	2508596	TY-2482_chromosome	B7LH39	Putative uncharacterized protein yqjK	Escherichia coli (strain 55989 / EAEC)
78723	2508695	2509174	TY-2482_chromosome	D3GWS0	Putative membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
60962	2509247	2510230	TY-2482_chromosome	B7LH38	S-transferase	Escherichia coli (strain 55989 / EAEC)
59089	2510526	2510888	TY-2482_chromosome	B7LH42	Putative uncharacterized protein yhaH	Escherichia coli (strain 55989 / EAEC)
14371	2511001	2511695	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli
109981	2512638	2511745	TY-2482_chromosome	B7LH41	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
88440	2512743	2513441	TY-2482_chromosome	B7LH45	Putative pirin-related protein	Escherichia coli (strain 55989 / EAEC)
34941	2515002	2513695	TY-2482_chromosome	B7LH44	UPF0597 protein yhaM	Escherichia coli (strain 55989 / EAEC)
91779	2516298	2515033	TY-2482_chromosome	B7LH48	Putative transporter	Escherichia coli (strain 55989 / EAEC)
62810	2518000	2516639	TY-2482_chromosome	B7LH49	L-serine dehydratase 3 (EC 4.3.1.17)	Escherichia coli (strain 55989 / EAEC)
106544	2518461	2518075	TY-2482_chromosome	B7LH50	L-PSP (MRNA) endoribonuclease	Escherichia coli (strain 55989 / EAEC)
73762	2520769	2518478	TY-2482_chromosome	B7LH51	Pyruvate formate-lyase 4/2-ketobutyrate formate-lyase (EC 2.3.1.54)	Escherichia coli (strain 55989 / EAEC)
102839	2522023	2520806	TY-2482_chromosome	B7LH47	Propionate kinase/acetate kinase C, anaerobic (EC 2.7.2.-) (EC 2.7.2.1)	Escherichia coli (strain 55989 / EAEC)
34213	2523368	2522040	TY-2482_chromosome	B7LH53	Threonine/serine transporter TdcC (H(+)/threonine-serine symporter)	Escherichia coli (strain 55989 / EAEC)
81068	2524379	2523393	TY-2482_chromosome	B7LH54	Catabolic threonine dehydratase, PLP-dependent (EC 4.3.1.19)	Escherichia coli (strain 55989 / EAEC)
91300	2525416	2524481	TY-2482_chromosome	B7LH55	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
104629	2525593	2525946	TY-2482_chromosome	B7LH56	Threonine dehydratase operon activator protein	Escherichia coli (strain 55989 / EAEC)
111581	2526205	2526741	TY-2482_chromosome	B7LH52	Putative uncharacterized protein yhaB	Escherichia coli (strain 55989 / EAEC)

106474	2526766	2527950	TY-2482_chromosome	B7LH57	Putative uncharacterized protein yhaC	Escherichia coli (strain 55989 / EAEC)
115751	2528291	2529268	TY-2482_chromosome	B7LF78	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
27818	2529684	2530211	TY-2482_chromosome	A1AG32	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
r98	2530109	2529733	TY-2482_chromosome	ref|NC_010473|:3365983-3366359|-| [gene=rnpB] [locus_tag=ECDH10B_3296]		
105295	2531368	2530145	TY-2482_chromosome	B7LH60	Glycerate kinase I (EC 2.7.1.31)	Escherichia coli (strain 55989 / EAEC)
99187	2532274	2531387	TY-2482_chromosome	B7LH61	Tartronate semialdehyde reductase (EC 1.1.1.60)	Escherichia coli (strain 55989 / EAEC)
31071	2533074	2532307	TY-2482_chromosome	B7LH62	5-keto-4-deoxy-D-glucarate aldolase (KDGluc aldolase) (KDGlucA) (EC 4.1.2.20) (2-dehydro-3-deoxy-D-glucarate aldol	Escherichia coli (strain 55989 / EAEC)
88442	2534424	2533093	TY-2482_chromosome	B7LH59	Putative (D)-galactarate transporter	Escherichia coli (strain 55989 / EAEC)
106546	2534798	2536366	TY-2482_chromosome	B7LH63	(D)-galactarate dehydrogenase (EC 4.2.1.42)	Escherichia coli (strain 55989 / EAEC)
38571	2536464	2536850	TY-2482_chromosome	D7ZZI1	Toxin-antitoxin system, antitoxin component, AbrB family	Escherichia coli MS 187-1
79499	2536853	2537314	TY-2482_chromosome	B7LH64	Putative uncharacterized protein yhaV	Escherichia coli (strain 55989 / EAEC)
66304	2538181	2537375	TY-2482_chromosome	B7LH66	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
31728	2538430	2539707	TY-2482_chromosome	B7LH67	D-tagatose-1,6-bisphosphate aldolase subunit kbaZ	Escherichia coli (strain 55989 / EAEC)
21379	2539697	2540203	TY-2482_chromosome	Q9KIQ4	AgaV	Escherichia coli
88447	2540217	2540993	TY-2482_chromosome	B7LH70	Putative enzyme IIC component of PTS	Escherichia coli (strain 55989 / EAEC)
84624	2540980	2541861	TY-2482_chromosome	B7LH71	Putative hexose/hexosamine family PTS permease IID component	Escherichia coli (strain 55989 / EAEC)
91947	2541882	2542313	TY-2482_chromosome	B7LH68	Putative phosphotransferase system enzyme subunit (N-acetyl-galactosamine / galactosamine PTS system enzyme IIA	Escherichia coli (strain 55989 / EAEC)
61975	2542292	2543443	TY-2482_chromosome	B7LH73	N-acetylglucosamine-6-phosphate deacetylase (GlcNAc 6-P deacetylase) (EC 3.5.1.25)	Escherichia coli (strain 55989 / EAEC)
99191	2543796	2544947	TY-2482_chromosome	B7LH74	Tagatose-6-phosphate ketose/aldose isomerase	Escherichia coli (strain 55989 / EAEC)
31722	2544963	2545820	TY-2482_chromosome	B7LH72	D-tagatose-1,6-bisphosphate aldolase subunit KbaY (TBPA) (TagBP aldolase) (EC 4.1.2.40) (D-tagatose-bisphosphate a	Escherichia coli (strain 55989 / EAEC)
109588	2545990	2546463	TY-2482_chromosome	B7LH76	N-acetylgalactosamine-specific enzyme IIB component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
113962	2546505	2547305	TY-2482_chromosome	B7LH77	N-acetylgalactosamine-specific enzyme IIC component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
114097	2547298	2548086	TY-2482_chromosome	B7LH75	N-acetylgalactosamine-specific enzyme IID component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
110646	2548090	2548842	TY-2482_chromosome	B7LH79	Galactosamine-6-phosphate isomerase	Escherichia coli (strain 55989 / EAEC)
60803	2549245	2549826	TY-2482_chromosome	B7LH78	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
91950	2549909	2550601	TY-2482_chromosome	B7LH81	Periplasmic pilin chaperone (LpfB-like)	Escherichia coli (strain 55989 / EAEC)
77461	2550634	2553147	TY-2482_chromosome	B7LH82	Putative outer membrane protein	Escherichia coli (strain 55989 / EAEC)
88449	2553161	2554249	TY-2482_chromosome	B7LH80	Putative fimbrial-like adhesin protein (LpfD-like)	Escherichia coli (strain 55989 / EAEC)
62813	2555155	2554298	TY-2482_chromosome	B7LH84	Ribosomal RNA small subunit methyltransferase I (EC 2.1.1.198) (16S rRNA 2'-O-ribose C1402 methyltransferase) (rRN	Escherichia coli (strain 55989 / EAEC)
97600	2555219	2557252	TY-2482_chromosome	B7LH85	Putative uncharacterized protein yraM	Escherichia coli (strain 55989 / EAEC)
35063	2557213	2557605	TY-2482_chromosome	B7LH86	UPF0102 protein yraN	Escherichia coli (strain 55989 / EAEC)
30613	2557628	2558215	TY-2482_chromosome	B7LH87	DnaA initiator-associating protein diaA	Escherichia coli (strain 55989 / EAEC)
88450	2558228	2558800	TY-2482_chromosome	B7LH83	Putative uncharacterized protein ecfH	Escherichia coli (strain 55989 / EAEC)
64127	2559957	2558920	TY-2482_chromosome	B7LH89	Putative permease	Escherichia coli (strain 55989 / EAEC)
94273	2560710	2560033	TY-2482_chromosome	D3GXP1	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
62814	2560793	2561308	TY-2482_chromosome	B7LH91	Putative intracellular protease	Escherichia coli (strain 55989 / EAEC)
34949	2561734	2561294	TY-2482_chromosome	B7LH88	UPF0306 protein yhbP	Escherichia coli (strain 55989 / EAEC)
34952	2561785	2562084	TY-2482_chromosome	B7LH93	UPF0213 protein yhbQ	Escherichia coli (strain 55989 / EAEC)
84627	2562577	2562077	TY-2482_chromosome	B7LH94	Putative acyltransferase with acyl-CoA N-acyltransferase domain	Escherichia coli (strain 55989 / EAEC)
91839	2563095	2562574	TY-2482_chromosome	B7LH95	Putative lipid carrier protein	Escherichia coli (strain 55989 / EAEC)
113403	2563304	2564296	TY-2482_chromosome	B7LH96	Peptidase (Collagenase-like)	Escherichia coli (strain 55989 / EAEC)
82580	2564290	2565183	TY-2482_chromosome	D3GXP8	Putative peptidase	Escherichia coli O44:H18 (strain 042 / EAEC)
61761	2565392	2566396	TY-2482_chromosome	B7LH98	Putative enzyme	Escherichia coli (strain 55989 / EAEC)
112779	2567761	2566520	TY-2482_chromosome	B7LH97	Tryptophan transporter of high affinity	Escherichia coli (strain 55989 / EAEC)
101202	2569804	2567918	TY-2482_chromosome	B7LHA0	ATP-dependent RNA helicase	Escherichia coli (strain 55989 / EAEC)
88305	2570868	2569987	TY-2482_chromosome	B7LHA1	Lipoprotein	Escherichia coli (strain 55989 / EAEC)
33026	2573112	2570980	TY-2482_chromosome	B7LH99	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase)	Escherichia coli (strain 55989 / EAEC)
r108	2573169	2573342	TY-2482_chromosome	ref|NC_010473|:3406992-3407165|-| [gene=sraG] [locus_tag=ECDH10B_3338]		
33716	2573628	2573362	TY-2482_chromosome	B7LGI7	30S ribosomal protein S15	Escherichia coli (strain 55989 / EAEC)
77505	2574721	2573780	TY-2482_chromosome	B7LHN1	tRNA pseudouridine synthase B (EC 5.4.99.-) (tRNA pseudouridine 55 synthase) (tRNA pseudouridylate synthase) (tRN	Escherichia coli (strain 55989 / EAEC)
83488	2575149	2574724	TY-2482_chromosome	D3GXQ8	Ribosome-binding factor A	Escherichia coli O44:H18 (strain 042 / EAEC)
31591	2577958	2575289	TY-2482_chromosome	B7LHN3	Translation initiation factor IF-2	Escherichia coli (strain 55989 / EAEC)
77504	2579470	2577986	TY-2482_chromosome	B7LHN0	Transcription termination/antitermination L factor	Escherichia coli (strain 55989 / EAEC)
27213	2580076	2579501	TY-2482_chromosome	E6WIP2	Ribosome maturation factor rimP	Pantoea sp. (strain At-9b)
r260	2580233	2580157	TY-2482_chromosome	ref|NC_010473|:3039499-3039575|Met tRNA| [gene=metV] [locus_tag=ECDH10B_2986]		
29942	2580581	2581921	TY-2482_chromosome	B7LHN6	Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate ligase)	Escherichia coli (strain 55989 / EAEC)
97070	2583557	2581935	TY-2482_chromosome	B7LHN7	Putative hydrolase, inner membrane	Escherichia coli (strain 55989 / EAEC)
93158	2583951	2583730	TY-2482_chromosome	D3GXR4	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
r224	2584100	2584014	TY-2482_chromosome	ref|NC_010473|:3417839-3417925|Leu tRNA| [gene=leuU] [locus_tag=ECDH10B_3348]		
58035	2584447	2584118	TY-2482_chromosome	B7LHN4	Preprotein translocase membrane subunit	Escherichia coli (strain 55989 / EAEC)
31132	2586012	2584678	TY-2482_chromosome	B7LHN9	Phosphoglucosamine mutase (EC 5.4.2.10)	Escherichia coli (strain 55989 / EAEC)
93378	2586853	2586008	TY-2482_chromosome	B7LHN8	7,8-dihydropteroate synthase (EC 2.5.1.15)	Escherichia coli (strain 55989 / EAEC)
114127	2588877	2586946	TY-2482_chromosome	B7LHP1	ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Escherichia coli (strain 55989 / EAEC)
33561	2589606	2588980	TY-2482_chromosome	B7LHP2	Ribosomal RNA large subunit methyltransferase E (EC 2.1.1.166) (23S rRNA Um2552 methyltransferase) (rRNA (uridin	Escherichia coli (strain 55989 / EAEC)

29219	2589964	2589665	TY-2482_chromosome	A1AG83	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
102186	2590657	2590184	TY-2482_chromosome	B7LHP0	Transcription elongation factor greA 1 (Transcript cleavage factor greA 1)	Escherichia coli (strain 55989 / EAEC)
114128	2590905	2592335	TY-2482_chromosome	B7LHP4	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)	Escherichia coli (strain 55989 / EAEC)
32781	2593550	2592381	TY-2482_chromosome	B7LHP6	GTPase obg (GTP-binding protein obg)	Escherichia coli (strain 55989 / EAEC)
86967	2594531	2593569	TY-2482_chromosome	B7LHP7	Putative uncharacterized protein yhbE	Escherichia coli (strain 55989 / EAEC)
97396	2594885	2595451	TY-2482_chromosome	D3GXS5	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
33514	2594915	2594661	TY-2482_chromosome	B7LHP5	50S ribosomal protein L27	Escherichia coli (strain 55989 / EAEC)
70077	2595506	2596474	TY-2482_chromosome	B7LHQ0	Octaprenyl diphosphate synthase (EC 2.5.1.-)	Escherichia coli (strain 55989 / EAEC)
61466	2596705	2596980	TY-2482_chromosome	B7LHQ1	DNA-binding transcriptional activator of maltose metabolism	Escherichia coli (strain 55989 / EAEC)
32535	2598290	2597034	TY-2482_chromosome	B7LHP8	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosam	Escherichia coli (strain 55989 / EAEC)
25688	2598411	2598749	TY-2482_chromosome	A7ZS88	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
61290	2599052	2598762	TY-2482_chromosome	B7LHQ2	Putative uncharacterized protein yrbB	Escherichia coli (strain 55989 / EAEC)
114129	2599687	2599055	TY-2482_chromosome	B7LHQ5	Toluene transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
88475	2600257	2599709	TY-2482_chromosome	B7LHQ6	Toluene transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
69402	2601044	2600265	TY-2482_chromosome	B7LHQ4	Toluene transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
90375	2601861	2601055	TY-2482_chromosome	B7LHQ8	Toluene transporter subunit: ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
65821	2602071	2603045	TY-2482_chromosome	B7LHQ7	Putative calcium/sodium:proton antiporter	Escherichia coli (strain 55989 / EAEC)
114130	2603062	2604045	TY-2482_chromosome	B7LHR0	D-arabinose 5-phosphate isomerase (EC 5.3.1.13)	Escherichia coli (strain 55989 / EAEC)
91778	2604069	2604632	TY-2482_chromosome	B7LHR1	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)	Escherichia coli (strain 55989 / EAEC)
62837	2604632	2605204	TY-2482_chromosome	B7LHR2	Putative uncharacterized protein yrbK	Escherichia coli (strain 55989 / EAEC)
98980	2605176	2605730	TY-2482_chromosome	B7LHR3	Putative lipopolysaccharide transport protein A: periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
100718	2605740	2606462	TY-2482_chromosome	B7LHR4	Putative lipopolysaccharide transport protein B: ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
62624	2606513	2607943	TY-2482_chromosome	B7LHR5	RNA polymerase, sigma 54 (Sigma N) factor	Escherichia coli (strain 55989 / EAEC)
84652	2607969	2608253	TY-2482_chromosome	B7LHR6	Ribosome-associated, sigma 54 modulation protein	Escherichia coli (strain 55989 / EAEC)
76277	2608374	2608862	TY-2482_chromosome	B7LHR7	Sugar-specific enzyme IIA component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
34946	2608911	2609762	TY-2482_chromosome	B7LHQ9	UPF0042 nucleotide-binding protein yhbJ	Escherichia coli (strain 55989 / EAEC)
102953	2609762	2610031	TY-2482_chromosome	B7LHR9	Phosphohistidinoprotein-hexose phosphotransferase component of N-regulated PTS system (Npr)	Escherichia coli (strain 55989 / EAEC)
95374	2610247	2610876	TY-2482_chromosome	B7LHS0	Putative uncharacterized protein yrbL	Escherichia coli (strain 55989 / EAEC)
32506	2611604	2610879	TY-2482_chromosome	B7LHS1	Monofunctional biosynthetic peptidoglycan transglycosylase (Monofunctional TGase) (EC 2.4.2.-)	Escherichia coli (strain 55989 / EAEC)
110514	2612254	2611604	TY-2482_chromosome	B7LHR8	Isoprenoid biosynthesis protein with amidotransferase-like domain	Escherichia coli (strain 55989 / EAEC)
r192	2612372	2612479	TY-2482_chromosome	ref|NC_010473|:3446344-3446451|-| [gene=ryhA] [locus_tag=ECDH10B_3384]		
114136	2614820	2612487	TY-2482_chromosome	B7LHS3	Hybrid sensory histidine kinase in two-component regulatory system with ArcA	Escherichia coli (strain 55989 / EAEC)
66323	2615845	2614919	TY-2482_chromosome	B7LHS4	Putative Fe-S oxidoreductase	Escherichia coli (strain 55989 / EAEC)
16758	2615864	2616052	TY-2482_chromosome	D6JFL7	Putative uncharacterized protein	Escherichia coli B354
84606	2616427	2620977	TY-2482_chromosome	B7LHS5	Glutamate synthase, large subunit (EC 1.4.1.13)	Escherichia coli (strain 55989 / EAEC)
21557	2616473	2616240	TY-2482_chromosome	D7Z4E7	Conserved domain protein	Escherichia coli MS 45-1
80997	2620993	2622408	TY-2482_chromosome	B7LHS6	Glutamate synthase, 4Fe-4S protein, small subunit (EC 1.4.1.13)	Escherichia coli (strain 55989 / EAEC)
18579	2622595	2623071	TY-2482_chromosome	C5W9G1	Predicted protein	Escherichia coli (strain B / BL21)
98982	2623055	2623393	TY-2482_chromosome	B7LHS7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
70092	2623936	2623475	TY-2482_chromosome	B7LHS9	Putative uncharacterized protein yhcH	Escherichia coli (strain 55989 / EAEC)
32620	2624808	2623936	TY-2482_chromosome	B7LHT0	N-acetylmannosamine kinase (EC 2.7.1.60) (ManNAc kinase) (N-acetyl-D-mannosamine kinase)	Escherichia coli (strain 55989 / EAEC)
110517	2625494	2624808	TY-2482_chromosome	B7LHT1	Putative N-acetylmannosamine-6-phosphate 2-epimerase 1 (EC 5.1.3.9) (ManNAc-6-P epimerase 1)	Escherichia coli (strain 55989 / EAEC)
3498	2627032	2625545	TY-2482_chromosome	B7LHS8	Putative sialic acid transporter (Sialic acid permease)	Escherichia coli (strain 55989 / EAEC)
32614	2628034	2627144	TY-2482_chromosome	B7LHT3	N-acetylneuraminate lyase (EC 4.1.3.3) (N-acetylneuraminate pyruvate-lyase) (N-acetylneuraminic acid aldolase) (Sial	Escherichia coli (strain 55989 / EAEC)
32624	2628947	2628159	TY-2482_chromosome	B7LHT2	Transcriptional regulator nanR	Escherichia coli (strain 55989 / EAEC)
66324	2629375	2630739	TY-2482_chromosome	B7LHT5	Putative transporter	Escherichia coli (strain 55989 / EAEC)
90135	2631282	2630788	TY-2482_chromosome	B7LHT6	ClpXP protease specificity-enhancing factor	Escherichia coli (strain 55989 / EAEC)
27256	2631868	2632074	TY-2482_chromosome	Q0TCN7	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
95375	2631926	2631291	TY-2482_chromosome	B7LHT4	Stringent starvation protein A	Escherichia coli (strain 55989 / EAEC)
33770	2632713	2632324	TY-2482_chromosome	B7LHT8	30S ribosomal protein S9	Escherichia coli (strain 55989 / EAEC)
33460	2633157	2632732	TY-2482_chromosome	B7LHT9	50S ribosomal protein L13	Escherichia coli (strain 55989 / EAEC)
68128	2634503	2633379	TY-2482_chromosome	B7LHU0	Putative uncharacterized protein yhcM	Escherichia coli (strain 55989 / EAEC)
112086	2634697	2635092	TY-2482_chromosome	B7LHU1	Putative cytochrome d ubiquinol oxidase subunit III (EC 1.10.3.-)	Escherichia coli (strain 55989 / EAEC)
83538	2635249	2636613	TY-2482_chromosome	B7LHU2	Serine endoprotease, periplasmic (EC 3.4.21.-)	Escherichia coli (strain 55989 / EAEC)
65164	2636706	2637770	TY-2482_chromosome	B7LHU3	Serine endoprotease, periplasmic (EC 3.4.21.-)	Escherichia coli (strain 55989 / EAEC)
32120	2638774	2637839	TY-2482_chromosome	B7LHU4	Malate dehydrogenase (EC 1.1.1.37)	Escherichia coli (strain 55989 / EAEC)
29840	2639209	2639676	TY-2482_chromosome	B7LHT7	Arginine repressor	Escherichia coli (strain 55989 / EAEC)
98912	2639993	2640304	TY-2482_chromosome	B5YSW4	Protein YcfR	Escherichia coli O157:H7 (strain EC4115 / EHEC)
72280	2640635	2640366	TY-2482_chromosome	B7LHU7	Putative barnase inhibitor	Escherichia coli (strain 55989 / EAEC)
29632	2642694	2640730	TY-2482_chromosome	B7LHU8	p-hydroxybenzoic acid efflux pump subunit AaeB (pHBA efflux pump protein B	Escherichia coli (strain 55989 / EAEC)
29624	2643632	2642703	TY-2482_chromosome	B7LHU9	p-hydroxybenzoic acid efflux pump subunit AaeA (pHBA efflux pump protein A)	Escherichia coli (strain 55989 / EAEC)
78945	2643912	2643643	TY-2482_chromosome	B5YSW8	Protein AaeX	Escherichia coli O157:H7 (strain EC4115 / EHEC)
105292	2644026	2644952	TY-2482_chromosome	B7LHV1	DNA-binding transcriptional regulator, efflux system	Escherichia coli (strain 55989 / EAEC)
97069	2646528	2645086	TY-2482_chromosome	B7LHV2	Putative peptidase	Escherichia coli (strain 55989 / EAEC)

98442	2650484	2646687	TY-2482_chromosome	B7LHU5	Putative uncharacterized protein yhdP	Escherichia coli (strain 55989 / EAEC)
93621	2652021	2650555	TY-2482_chromosome	B7LHV4	Ribonuclease G (EC 3.1.4.-)	Escherichia coli (strain 55989 / EAEC)
102146	2652604	2652014	TY-2482_chromosome	B7LHV5	Maf-like protein yceF 2	Escherichia coli (strain 55989 / EAEC)
62749	2653101	2652616	TY-2482_chromosome	B7LHV6	Cell wall structural complex MreBCD transmembrane component MreD	Escherichia coli (strain 55989 / EAEC)
77383	2654204	2653104	TY-2482_chromosome	B7LHV8	Cell wall structural complex MreBCD transmembrane component MreC	Escherichia coli (strain 55989 / EAEC)
16187	2655282	2655470	TY-2482_chromosome	D7X6F8	Putative uncharacterized protein	Escherichia coli MS 198-1
87233	2655313	2654273	TY-2482_chromosome	B7LHV9	Cell wall structural complex MreBCD, actin-like component MreB	Escherichia coli (strain 55989 / EAEC)
95609	2655421	2655606	TY-2482_chromosome	B7LHW0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
69105	2657558	2655621	TY-2482_chromosome	B7LHW1	Inner membrane associated factor modulating specific RNAseE dependent RNA degradation pathways	Escherichia coli (strain 55989 / EAEC)
73735	2657710	2658681	TY-2482_chromosome	B7LHV3	Putative oxidoreductase, Zn-dependent and NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
60337	2658867	2659254	TY-2482_chromosome	D3GXL9	Sulfoxide reductase heme-binding subunit yedZ (Flavocytochrome yedZ)	Escherichia coli O44:H18 (strain 042 / EAEC)
21053	2659501	2659686	TY-2482_chromosome	Q53295	Orf 5' of BCCP protein (Fragment)	Escherichia coli
98584	2659662	2660129	TY-2482_chromosome	B7LHW3	Acetyl CoA carboxylase, BCCP subunit	Escherichia coli (strain 55989 / EAEC)
69557	2660143	2661489	TY-2482_chromosome	B7LHW4	Acetyl-CoA carboxylase, biotin carboxylase subunit (EC 6.3.4.14)	Escherichia coli (strain 55989 / EAEC)
102912	2661601	2661840	TY-2482_chromosome	B7LHW5	Putative uncharacterized protein yhdT	Escherichia coli (strain 55989 / EAEC)
59148	2661833	2663281	TY-2482_chromosome	B7LHW2	Pantothenate:sodium symporter	Escherichia coli (strain 55989 / EAEC)
33069	2663296	2664174	TY-2482_chromosome	B7LHW6	Ribosomal protein L11 methyltransferase (L11 Mtase) (EC 2.1.1.-)	Escherichia coli (strain 55989 / EAEC)
80317	2664506	2665468	TY-2482_chromosome	B7LHW7	tRNA-dihydrouridine synthase (EC 1.-.-.-)	Escherichia coli (strain 55989 / EAEC)
30945	2665497	2665790	TY-2482_chromosome	B7LHW8	DNA-binding protein fis	Escherichia coli (strain 55989 / EAEC)
97491	2665879	2666760	TY-2482_chromosome	B7LHW9	Methyltransferase (EC 2.1.1.72)	Escherichia coli (strain 55989 / EAEC)
62795	2667691	2667032	TY-2482_chromosome	B7LHX1	DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
71554	2668090	2669244	TY-2482_chromosome	B7LHX3	Cytoplasmic membrane lipoprotein	Escherichia coli (strain 55989 / EAEC)
20922	2668101	2667871	TY-2482_chromosome	D6JFR7	Putative uncharacterized protein	Escherichia coli B354
99159	2669259	2672360	TY-2482_chromosome	B7LHX4	Multidrug efflux system protein	Escherichia coli (strain 55989 / EAEC)
75543	2672616	2672834	TY-2482_chromosome	B7LHX2	Putative uncharacterized protein yhdV	Escherichia coli (strain 55989 / EAEC)
95610	2673376	2674290	TY-2482_chromosome	B7LHX7	Amino-acid transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
95562	2674361	2675539	TY-2482_chromosome	B7LHX8	Amino-acid transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
90296	2675552	2676652	TY-2482_chromosome	B7LHX5	Amino-acid transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
70033	2676663	2677418	TY-2482_chromosome	B7LHY0	Amino-acid transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
46800	2677629	2678106	TY-2482_chromosome	Q8CLX4	Putative uncharacterized protein	Yersinia pestis
r141	2677769	2677650	TY-2482_chromosome	ref|NC_010473|:3519190-3519309|5S ribosomal RNA| [gene=rrfF] [locus_tag=ECDH10B_3447		
r343	2677882	2677807	TY-2482_chromosome	ref|NC_010473|:3519347-3519422|Thr tRNA| [gene=thrV] [locus_tag=ECDH10B_3448		
r125	2678014	2677895	TY-2482_chromosome	ref|NC_010473|:4043643-4043762|5S ribosomal RNA| [gene=rrfC] [locus_tag=ECDH10B_3948		
22418	2678333	2678689	TY-2482_chromosome	C1HUN0	Prolipoprotein diacylglyceryl transferase (Fragment)	Escherichia sp. 3_2_53FAA
20477	2678693	2679145	TY-2482_chromosome	C1HUN1	Cell wall-associated hydrolase (Fragment)	Escherichia sp. 3_2_53FAA
13801	2679222	2679425	TY-2482_chromosome	C1HUN3	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
24099	2680483	2680785	TY-2482_chromosome	Q1R3T8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
r0	2681011	2678108	TY-2482_chromosome	ref|NC_010473|:4307762-4310665|23S ribosomal RNA| [gene=rrlE] [locus_tag=ECDH10B_4198		
r319	2681280	2681205	TY-2482_chromosome	ref|NC_010473|:4307493-4307568|Glu tRNA| [gene=gltV] [locus_tag=ECDH10B_4197		
25824	2681786	2681469	TY-2482_chromosome	Q57H85	ORF16-lacZ fusion protein	Salmonella choleraesuis
11307	2682761	2682994	TY-2482_chromosome	E9WNY3	Putative uncharacterized protein	Escherichia coli E1520
r49	2682907	2681366	TY-2482_chromosome	ref|NC_010473|:3522988-3524529|16S ribosomal RNA| [gene=rrsD] [locus_tag=ECDH10B_3453		
63605	2683088	2683930	TY-2482_chromosome	C6UV66	Conserved protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
59149	2684166	2683912	TY-2482_chromosome	B7LHY2	Putative uncharacterized protein yrdB	Escherichia coli (strain 55989 / EAEC)
29908	2684981	2684166	TY-2482_chromosome	B7LHX9	Shikimate dehydrogenase (EC 1.1.1.25)	Escherichia coli (strain 55989 / EAEC)
71941	2685558	2684989	TY-2482_chromosome	B7LHY4	Putative ribosome maturation factor	Escherichia coli (strain 55989 / EAEC)
71642	2686105	2685566	TY-2482_chromosome	B7LHY5	Putative DNA topoisomerase	Escherichia coli (strain 55989 / EAEC)
33960	2686607	2686137	TY-2482_chromosome	B7LHY6	Protein smg	Escherichia coli (strain 55989 / EAEC)
114070	2687703	2686582	TY-2482_chromosome	B7LHY7	Putative uncharacterized protein smf	Escherichia coli (strain 55989 / EAEC)
30583	2687833	2688339	TY-2482_chromosome	B7LHY3	Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Escherichia coli (strain 55989 / EAEC)
30995	2688357	2689301	TY-2482_chromosome	B7LHY8	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	Escherichia coli (strain 55989 / EAEC)
33788	2689350	2690636	TY-2482_chromosome	B7LHZ0	Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.176) (16S rRNA m5C967 methyltransferase) (rRNA (cytosi	Escherichia coli (strain 55989 / EAEC)
84598	2690661	2692034	TY-2482_chromosome	B7LHY9	NAD-binding component of TrK potassium transporter	Escherichia coli (strain 55989 / EAEC)
32490	2692167	2692574	TY-2482_chromosome	B7LHZ2	Large-conductance mechanosensitive channel	Escherichia coli (strain 55989 / EAEC)
66279	2692792	2692577	TY-2482_chromosome	B7LHZ3	Putative uncharacterized protein yhdL	Escherichia coli (strain 55989 / EAEC)
82984	2693273	2692851	TY-2482_chromosome	B7LHZ4	DNA-binding transcriptional activator in response to Zn(II)	Escherichia coli (strain 55989 / EAEC)
111553	2693652	2693287	TY-2482_chromosome	B7LHZ1	Putative uncharacterized protein yhdN	Escherichia coli (strain 55989 / EAEC)
33476	2694142	2693762	TY-2482_chromosome	B7LHZ6	50S ribosomal protein L17	Escherichia coli (strain 55989 / EAEC)
73736	2695172	2694186	TY-2482_chromosome	B7LHZ7	RNA polymerase, alpha subunit (EC 2.7.7.6)	Escherichia coli (strain 55989 / EAEC)
33752	2695818	2695201	TY-2482_chromosome	B7LHZ8	30S ribosomal protein S4	Escherichia coli (strain 55989 / EAEC)
33703	2696241	2695855	TY-2482_chromosome	B7LHZ9	30S ribosomal protein S11	Escherichia coli (strain 55989 / EAEC)
87058	2696614	2696261	TY-2482_chromosome	B7LHZ5	30S ribosomal protein S13	Escherichia coli (strain 55989 / EAEC)
82797	2698240	2696912	TY-2482_chromosome	B7LI01	Preprotein translocase subunit secY	Escherichia coli (strain 55989 / EAEC)
33468	2698682	2698251	TY-2482_chromosome	B7LI02	50S ribosomal protein L15	Escherichia coli (strain 55989 / EAEC)

24325	2698839	2699387	TY-2482_chromosome	A8AQJ7	Putative uncharacterized protein	Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)
27579	2699441	2700061	TY-2482_chromosome	Q1R625	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
86217	2701027	2700725	TY-2482_chromosome	B7L4J6	30S ribosomal protein S14	Escherichia coli (strain 55989 / EAEC)
33543	2701581	2701045	TY-2482_chromosome	B7L4J7	50S ribosomal protein L5	Escherichia coli (strain 55989 / EAEC)
24482	2701792	2702343	TY-2482_chromosome	Q1R618	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
33724	2702711	2702460	TY-2482_chromosome	B7L4K0	30S ribosomal protein S17	Escherichia coli (strain 55989 / EAEC)
33472	2703312	2702905	TY-2482_chromosome	B7L4K2	50S ribosomal protein L16	Escherichia coli (strain 55989 / EAEC)
33748	2704026	2703328	TY-2482_chromosome	B7L4K3	30S ribosomal protein S3	Escherichia coli (strain 55989 / EAEC)
26886	2704026	2704430	TY-2482_chromosome	A8AQL1	Putative uncharacterized protein	Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)
24854	2704539	2705576	TY-2482_chromosome	A7MPI1	Putative uncharacterized protein	Enterobacter sakazakii (strain ATCC BAA-894)
24419	2706359	2707057	TY-2482_chromosome	Q1R603	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
33539	2706429	2705827	TY-2482_chromosome	B7L4K8	50S ribosomal protein L4	Escherichia coli (strain 55989 / EAEC)
33699	2707413	2707105	TY-2482_chromosome	B7L4L0	30S ribosomal protein S10	Escherichia coli (strain 55989 / EAEC)
60618	2707792	2708256	TY-2482_chromosome	B7L4L2	Putative bifunctional prepilin peptidase HopD: leader peptidase; methyl transferase (General Secretory Pathway)	Escherichia coli (strain 55989 / EAEC)
106335	2708732	2708259	TY-2482_chromosome	B7L4L3	Bacterioferritin	Escherichia coli (strain 55989 / EAEC)
70076	2708999	2708808	TY-2482_chromosome	B7L4L4	Bacterioferritin-associated ferredoxin	Escherichia coli (strain 55989 / EAEC)
114540	2710366	2709185	TY-2482_chromosome	C6UVB2	Elongation factor Tu 1 (EF-Tu 1)	Escherichia coli O157:H7 (strain TW14359 / EHEC
30726	2712551	2710440	TY-2482_chromosome	B7L4L1	Elongation factor G (EF-G)	Escherichia coli (strain 55989 / EAEC)
4881	2713118	2712582	TY-2482_chromosome	C4ZUJ6	30S ribosomal protein S7	Escherichia coli (strain K12 / MC4100 / BW2952)
27474	2713131	2713589	TY-2482_chromosome	A7MKJ1	Putative uncharacterized protein	Enterobacter sakazakii (strain ATCC BAA-894)
34384	2714002	2713718	TY-2482_chromosome	B7L4L8	Protein tusB (tRNA 2-thiouridine synthesizing protein B)	Escherichia coli (strain 55989 / EAEC)
34387	2714369	2714013	TY-2482_chromosome	B7L4L9	Protein tusC (tRNA 2-thiouridine synthesizing protein C)	Escherichia coli (strain 55989 / EAEC)
34391	2714755	2714372	TY-2482_chromosome	B7L4M1	Sulfurtransferase tusD (EC 2.8.1.-) (tRNA 2-thiouridine synthesizing protein D)	Escherichia coli (strain 55989 / EAEC)
64746	2715477	2714758	TY-2482_chromosome	B7L4M2	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
73811	2716456	2715647	TY-2482_chromosome	B7L4M3	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Escherichia coli (strain 55989 / EAEC)
33957	2716677	2716892	TY-2482_chromosome	B7L4M4	Protein slyX	Escherichia coli (strain 55989 / EAEC)
59192	2717534	2716947	TY-2482_chromosome	B7L4M0	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Escherichia coli (strain 55989 / EAEC)
106336	2717829	2717632	TY-2482_chromosome	B7L4M6	Putative uncharacterized protein yheV	Escherichia coli (strain 55989 / EAEC)
31757	2719644	2717842	TY-2482_chromosome	B7L4M7	Glutathione-regulated potassium-efflux system protein kefB (K(+)/H(+) antiporter) (NEM-activatable K(+)/H(+) antipo	Escherichia coli (strain 55989 / EAEC)
31781	2720198	2719647	TY-2482_chromosome	B7L4M8	Glutathione-regulated potassium-efflux system ancillary protein kefG	Escherichia coli (strain 55989 / EAEC)
104793	2720326	2722236	TY-2482_chromosome	B7L4M9	Fused putative transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
93665	2722239	2723258	TY-2482_chromosome	B7L4M5	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
34956	2723255	2723470	TY-2482_chromosome	B7L4N1	UPF0270 protein yheU	Escherichia coli (strain 55989 / EAEC)
62836	2723527	2724393	TY-2482_chromosome	B7L4N2	Phosphoribulokinase (EC 2.7.1.19)	Escherichia coli (strain 55989 / EAEC)
61319	2724855	2724454	TY-2482_chromosome	B7L4N3	Putative uncharacterized protein yhfA	Escherichia coli (strain 55989 / EAEC)
86271	2724935	2725147	TY-2482_chromosome	B7L4N4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
65285	2725157	2725786	TY-2482_chromosome	B7L4N0	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
65034	2725828	2727927	TY-2482_chromosome	B7L4N6	Putative uncharacterized protein yhfK	Escherichia coli (strain 55989 / EAEC)
88423	2729217	2728000	TY-2482_chromosome	B7L4N7	Bifunctional acetylornithine aminotransferase and succinyldiaminopimelate aminotransferase (EC 2.6.1.11) (EC 2.6.1.	Escherichia coli (strain 55989 / EAEC)
83697	2729866	2729306	TY-2482_chromosome	B7L4N8	Aminodeoxychorismate synthase, subunit II (EC 2.6.1.85)	Escherichia coli (strain 55989 / EAEC)
93623	2730500	2729901	TY-2482_chromosome	B7L4N5	Stationary-phase protein, cell division	Escherichia coli (strain 55989 / EAEC)
114075	2731334	2730765	TY-2482_chromosome	B7L4P1	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Escherichia coli (strain 55989 / EAEC)
34371	2731605	2732783	TY-2482_chromosome	B7L4N9	Protein tsgA	Escherichia coli (strain 55989 / EAEC)
109875	2733048	2735588	TY-2482_chromosome	B7L4P3	Nitrite reductase, large subunit, NAD(P) H-binding (EC 1.7.1.4)	Escherichia coli (strain 55989 / EAEC)
87370	2735588	2735911	TY-2482_chromosome	B7L4P4	Nitrite reductase, NAD(P)H-binding, small subunit (EC 1.7.1.4)	Escherichia coli (strain 55989 / EAEC)
114077	2736041	2736844	TY-2482_chromosome	B7L4P5	Nitrite transporter	Escherichia coli (strain 55989 / EAEC)
30507	2736866	2738236	TY-2482_chromosome	B7L4P2	Siroheme synthase [Includes: Uroporphyrinogen-III C-methyltransferase (Urogen III methylase) (EC 2.1.1.107) (SUMT)	Escherichia coli (strain 55989 / EAEC)
68500	2738948	2740282	TY-2482_chromosome	B7L4P8	Putative fructoselysine transporter	Escherichia coli (strain 55989 / EAEC)
73748	2740306	2741325	TY-2482_chromosome	B7L4P9	Fructoselysine-6-P-deglycase	Escherichia coli (strain 55989 / EAEC)
82553	2741378	2742205	TY-2482_chromosome	B7L4Q0	Fructoselysine 3-epimerase	Escherichia coli (strain 55989 / EAEC)
65163	2742205	2742987	TY-2482_chromosome	B7L4P6	Fructoselysine 6-kinase (EC 2.7.1.-)	Escherichia coli (strain 55989 / EAEC)
80367	2743024	2743818	TY-2482_chromosome	B5YTT2	GntR-family transcriptional regulator FrlR	Escherichia coli O157:H7 (strain EC4115 / EHEC)
96940	2745058	2743976	TY-2482_chromosome	B7L4Q3	Putative uncharacterized protein yhfS	Escherichia coli (strain 55989 / EAEC)
87925	2746374	2745073	TY-2482_chromosome	B7L4Q4	Putative uncharacterized protein yhfT	Escherichia coli (strain 55989 / EAEC)
106530	2746739	2746389	TY-2482_chromosome	B7L4Q5	Putative uncharacterized protein yhfU	Escherichia coli (strain 55989 / EAEC)
102914	2747628	2746753	TY-2482_chromosome	B7L4Q1	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
93225	2748851	2747628	TY-2482_chromosome	B7L4Q7	Putative mutase (EC 5.4.2.7)	Escherichia coli (strain 55989 / EAEC)
67742	2750014	2748854	TY-2482_chromosome	B7L4Q8	Putative amino acid racemase	Escherichia coli (strain 55989 / EAEC)
108420	2750460	2750101	TY-2482_chromosome	B7L4Q9	Putative uncharacterized protein yhfY	Escherichia coli (strain 55989 / EAEC)
71357	2751382	2750480	TY-2482_chromosome	B7L4Q6	Putative uncharacterized protein yhfZ	Escherichia coli (strain 55989 / EAEC)
91938	2752655	2751654	TY-2482_chromosome	B7L4R1	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	Escherichia coli (strain 55989 / EAEC)
72269	2753406	2752651	TY-2482_chromosome	B7L4R0	Phosphoglycolate phosphatase (EC 3.1.3.18)	Escherichia coli (strain 55989 / EAEC)
113881	2754076	2753402	TY-2482_chromosome	B7L4R3	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Escherichia coli (strain 55989 / EAEC)
76594	2754930	2754097	TY-2482_chromosome	B7L4R4	DNA adenine methylase (EC 2.1.1.72)	Escherichia coli (strain 55989 / EAEC)

89943	2756323	2755040	TY-2482_chromosome	B7L4R2	Putative uncharacterized protein damX	Escherichia coli (strain 55989 / EAEC)
29896	2757503	2756418	TY-2482_chromosome	B7L4R5	3-dehydroquinate synthase (EC 4.2.3.4)	Escherichia coli (strain 55989 / EAEC)
8816	2758282	2757563	TY-2482_chromosome	C3SQ92	Shikimate kinase I	Escherichia coli
115341	2759720	2758485	TY-2482_chromosome	B7L4R8	Fimbrial transporter	Escherichia coli (strain 55989 / EAEC)
25669	2760015	2759635	TY-2482_chromosome	D3QTK9	Putative uncharacterized protein hofP	Escherichia coli O55:H7 (strain CB9615 / EPEC)
25668	2760466	2760029	TY-2482_chromosome	D3QTK9	Putative uncharacterized protein hofP	Escherichia coli O55:H7 (strain CB9615 / EPEC)
75847	2760989	2760453	TY-2482_chromosome	B7L4S1	Putative fimbrial assembly protein (PilN-like)	Escherichia coli (strain 55989 / EAEC)
62797	2761768	2760992	TY-2482_chromosome	B7L4S2	Putative pilus assembly protein	Escherichia coli (strain 55989 / EAEC)
71737	2761888	2764437	TY-2482_chromosome	B7L4S0	Fused penicillin-binding protein 1a: murein transglycosylase ; murein transpeptidase (EC 2.4.1.-) (EC 3.4.-.-	Escherichia coli (strain 55989 / EAEC)
86188	2765168	2764611	TY-2482_chromosome	B7L4S4	ADP-ribose diphosphatase (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
105240	2765488	2767620	TY-2482_chromosome	B7L4S5	Intracellular growth attenuator protein	Escherichia coli (strain 55989 / EAEC)
111367	2767643	2768353	TY-2482_chromosome	D3GZL7	Putative hydrolase	Escherichia coli O44:H18 (strain 042 / EAEC)
81051	2768367	2768765	TY-2482_chromosome	B7L4S3	Ribosome-associated heat shock protein Hsp15	Escherichia coli (strain 55989 / EAEC)
108265	2768787	2769668	TY-2482_chromosome	B5YTV0	33 kDa chaperonin (Heat shock protein 33 homolog)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
99117	2771530	2769809	TY-2482_chromosome	B7L4S9	Putative uncharacterized protein yhgE	Escherichia coli (strain 55989 / EAEC)
32891	2771909	2773528	TY-2482_chromosome	B7L4T1	Phosphoenolpyruvate carboxykinase [ATP] (PEP carboxykinase) (PEPCK) (EC 4.1.1.49) (Phosphoenolpyruvate carboxyl	Escherichia coli (strain 55989 / EAEC)
81102	2773648	2773962	TY-2482_chromosome	B7L4T2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
62839	2774024	2774317	TY-2482_chromosome	B7L4T3	Putative HTH-type transcriptional regulator yiaG	Escherichia coli (strain 55989 / EAEC)
90514	2775702	2774353	TY-2482_chromosome	B7L4T4	Sensory histidine kinase in two-component regulatory system with OmpR	Escherichia coli (strain 55989 / EAEC)
77326	2776418	2775702	TY-2482_chromosome	B7L4S7	DNA-binding response regulator in two-component regulatory system with EnvZ	Escherichia coli (strain 55989 / EAEC)
98586	2776646	2777119	TY-2482_chromosome	B7L4T6	Transcription elongation factor greA 2 (Transcript cleavage factor greA 2)	Escherichia coli (strain 55989 / EAEC)
25510	2776693	2776511	TY-2482_chromosome	Q1R5M9	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
91763	2777219	2779537	TY-2482_chromosome	B7L4T7	Transcriptional accessory protein	Escherichia coli (strain 55989 / EAEC)
81103	2779978	2780202	TY-2482_chromosome	B7L4T5	Ferrous iron transporter, protein A	Escherichia coli (strain 55989 / EAEC)
95365	2780222	2782588	TY-2482_chromosome	B7L4T8	Fused ferrous iron transporter, protein B: GTP-binding protein ; membrane protein	Escherichia coli (strain 55989 / EAEC)
1669	2782591	2782824	TY-2482_chromosome	B7L4U0	Ferrous iron transport protein C	Escherichia coli (strain 55989 / EAEC)
82497	2783030	2783905	TY-2482_chromosome	B7L4U1	Putative transposase	Escherichia coli (strain 55989 / EAEC)
22887	2783057	2782833	TY-2482_chromosome	D8BVW7	Putative uncharacterized protein	Escherichia coli MS 196-1
113122	2784682	2785425	TY-2482_chromosome	B5YTW4	Protein GntX	Escherichia coli O157:H7 (strain EC4115 / EHEC)
30144	2784707	2783940	TY-2482_chromosome	B7L4T9	Carboxylesterase BioH (EC 3.1.1.1) (Biotin synthesis protein BioH)	Escherichia coli (strain 55989 / EAEC)
32652	2785487	2786059	TY-2482_chromosome	B7L4U4	Fe/S biogenesis protein nfuA	Escherichia coli (strain 55989 / EAEC)
90730	2786423	2787736	TY-2482_chromosome	B7L4U2	Gluconate transporter, high-affinity GNT I system	Escherichia coli (strain 55989 / EAEC)
58073	2789868	2787787	TY-2482_chromosome	B7L4U5	4-alpha-glucanotransferase (Amylomaltase) (EC 2.4.1.25)	Escherichia coli (strain 55989 / EAEC)
94051	2792271	2789881	TY-2482_chromosome	B7L4U7	Phosphorylase (EC 2.4.1.1)	Escherichia coli (strain 55989 / EAEC)
32097	2792883	2795585	TY-2482_chromosome	B7L4U8	HTH-type transcriptional regulator malT (ATP-dependent transcriptional activator malT)	Escherichia coli (strain 55989 / EAEC)
33812	2796647	2795634	TY-2482_chromosome	B7L4U9	RNA 3'-terminal phosphate cyclase (RNA cyclase) (RNA-3'-phosphate cyclase) (EC 6.5.1.4)	Escherichia coli (strain 55989 / EAEC)
110655	2797877	2796654	TY-2482_chromosome	B7L4U6	Putative uncharacterized protein rtcB	Escherichia coli (strain 55989 / EAEC)
66314	2798066	2799661	TY-2482_chromosome	B7L4V1	Sigma 54-dependent transcriptional regulator of rtcBA expression	Escherichia coli (strain 55989 / EAEC)
58044	2800404	2799649	TY-2482_chromosome	B7L4V2	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
31164	2801251	2800424	TY-2482_chromosome	B7L4V0	Rhomboid protease glpG (EC 3.4.21.105) (Intramembrane serine protease)	Escherichia coli (strain 55989 / EAEC)
31160	2801622	2801299	TY-2482_chromosome	B7L4V4	Thiosulfate sulfurtransferase glpE (EC 2.8.1.1)	Escherichia coli (strain 55989 / EAEC)
115906	2801812	2803314	TY-2482_chromosome	B7L4V5	sn-glycerol-3-phosphate dehydrogenase, aerobic, FAD/NAD(P)-binding (EC 1.1.99.5)	Escherichia coli (strain 55989 / EAEC)
111523	2803974	2803372	TY-2482_chromosome	B7L4V6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
72424	2804744	2803980	TY-2482_chromosome	B7L4V3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
82986	2805457	2804750	TY-2482_chromosome	B7L4V8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73823	2806990	2805476	TY-2482_chromosome	B7L4V9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
88477	2809553	2807109	TY-2482_chromosome	B7L4V7	Phosphorylase (EC 2.4.1.1)	Escherichia coli (strain 55989 / EAEC)
31112	2811005	2809575	TY-2482_chromosome	B7L4W1	Glycogen synthase (EC 2.4.1.21) (Starch [bacterial glycogen] synthase)	Escherichia coli (strain 55989 / EAEC)
31118	2812300	2811008	TY-2482_chromosome	B7L4W0	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADPGlc PPase) (ADP-glucos	Escherichia coli (strain 55989 / EAEC)
31124	2814291	2812321	TY-2482_chromosome	B7L4W3	Glycogen debranching enzyme (EC 3.2.1.-) (Glycogen operon protein GlgX)	Escherichia coli (strain 55989 / EAEC)
77512	2816474	2814291	TY-2482_chromosome	B7L4W4	1,4-alpha-glucan-branching enzyme (EC 2.4.1.18) (1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-transferase) (Gly	Escherichia coli (strain 55989 / EAEC)
98176	2817850	2816750	TY-2482_chromosome	B7L4W2	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	Escherichia coli (strain 55989 / EAEC)
98981	2818043	2818633	TY-2482_chromosome	B7L4W6	Putative antibiotic transporter	Escherichia coli (strain 55989 / EAEC)
105822	2820033	2818696	TY-2482_chromosome	B7L4W7	Gluconate transporter, low affinity GNT 1 system	Escherichia coli (strain 55989 / EAEC)
24639	2820091	2820720	TY-2482_chromosome	Q8FCR0	Putative uncharacterized protein	Escherichia coli O6
95408	2821698	2820706	TY-2482_chromosome	B7L4W9	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
81104	2822617	2821925	TY-2482_chromosome	B7L4X0	Putative uncharacterized protein yhhW	Escherichia coli (strain 55989 / EAEC)
112084	2823777	2822743	TY-2482_chromosome	B7L4X1	Putative oxidoreductase with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
r197	2823987	2823894	TY-2482_chromosome	ref|NC_010473|:3676691-3676784|-| [gene=ryhB] [locus_tag=ECDH10B_3614]		
75220	2824109	2824594	TY-2482_chromosome	B7L4X2	Putative acetyltransferase	Escherichia coli (strain 55989 / EAEC)
115350	2824834	2826009	TY-2482_chromosome	B7L4W8	Putative uncharacterized protein yhhZ	Escherichia coli (strain 55989 / EAEC)
60695	2826009	2826500	TY-2482_chromosome	B7L4X4	Putative uncharacterized protein yrhA	Escherichia coli (strain 55989 / EAEC)
97697	2826953	2827234	TY-2482_chromosome	B7L4X6	Putative uncharacterized protein yrhB	Escherichia coli (strain 55989 / EAEC)
94307	2829017	2827278	TY-2482_chromosome	B7L4X7	Gamma-glutamyltranspeptidase (EC 2.3.2.2)	Escherichia coli (strain 55989 / EAEC)

79471	2829137	2829574	TY-2482_chromosome	B7L4X3	Putative uncharacterized protein yhhA	Escherichia coli (strain 55989 / EAEC)
107861	2830307	2829567	TY-2482_chromosome	B7L5Q2	Glycerophosphodiester phosphodiesterase, cytosolic (EC 3.1.4.46)	Escherichia coli (strain 55989 / EAEC)
79846	2831374	2830307	TY-2482_chromosome	B7L5Q3	Glycerol-3-phosphate transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
81113	2832221	2831379	TY-2482_chromosome	B7L5Q4	Glycerol-3-phosphate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
81114	2833105	2832221	TY-2482_chromosome	B7L5Q5	Glycerol-3-phosphate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
95390	2834519	2833206	TY-2482_chromosome	B7L5Q6	Glycerol-3-phosphate transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
88489	2835628	2834918	TY-2482_chromosome	B7L5Q7	Leucine/isoleucine/valine transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
66339	2836397	2835633	TY-2482_chromosome	B7L5Q8	Leucine/isoleucine/valine transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
72216	2837671	2836397	TY-2482_chromosome	B7L5Q9	Leucine/isoleucine/valine transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
59003	2838594	2837671	TY-2482_chromosome	B7L5Q1	Leucine/isoleucine/valine transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
13536	2839718	2838590	TY-2482_chromosome	E9VUM2	Receptor family protein ligand binding protein	Escherichia coli H263
91771	2840175	2840555	TY-2482_chromosome	B7L5R2	Putative uncharacterized protein yhhK	Escherichia coli (strain 55989 / EAEC)
66354	2841860	2840760	TY-2482_chromosome	B7L5R3	Leucine/isoleucine/valine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
91380	2842985	2842134	TY-2482_chromosome	B7L5R4	RNA polymerase sigma factor	Escherichia coli (strain 55989 / EAEC)
58580	2844288	2843233	TY-2482_chromosome	B7L5R5	Transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
65823	2844949	2844284	TY-2482_chromosome	B7L5R6	Transporter subunit: ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
72854	2846445	2844955	TY-2482_chromosome	B7L5R0	Putative uncharacterized protein ftsY	Escherichia coli (strain 55989 / EAEC)
73591	2846595	2847188	TY-2482_chromosome	B7L5R8	Putative methyltransferase	Escherichia coli (strain 55989 / EAEC)
64576	2847812	2847456	TY-2482_chromosome	B7L5R7	Putative uncharacterized protein yhhM	Escherichia coli (strain 55989 / EAEC)
62609	2847953	2848576	TY-2482_chromosome	B7L5S0	Putative uncharacterized protein yhhN	Escherichia coli (strain 55989 / EAEC)
102701	2848653	2850848	TY-2482_chromosome	B7L5S2	Zinc, cobalt and lead efflux system (EC 3.6.3.3) (EC 3.6.3.5)	Escherichia coli (strain 55989 / EAEC)
29314	2850914	2851213	TY-2482_chromosome	A1AH06	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
88490	2851419	2852081	TY-2482_chromosome	B7L5S4	Putative uncharacterized protein yhhQ	Escherichia coli (strain 55989 / EAEC)
107907	2852115	2852711	TY-2482_chromosome	C8TJR1	Periplasmic protein DcrB	Escherichia coli O26:H11 (strain 11368 / EHEC)
105312	2853935	2852721	TY-2482_chromosome	B7L5S6	UPF0226 membrane protein EC55989_3881	Escherichia coli (strain 55989 / EAEC)
104972	2854067	2855113	TY-2482_chromosome	B7L5S3	Putative uncharacterized protein yhhT	Escherichia coli (strain 55989 / EAEC)
60804	2855171	2855755	TY-2482_chromosome	B7L5S7	Holo-(Acyl carrier protein) synthase 2 (EC 2.7.8.7)	Escherichia coli (strain 55989 / EAEC)
72844	2855869	2857440	TY-2482_chromosome	B7L5S8	Nickel transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
69455	2857443	2858384	TY-2482_chromosome	B7L5T0	Nickel transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
109921	2858384	2859214	TY-2482_chromosome	B7L5T1	Nickel transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
83996	2859217	2859978	TY-2482_chromosome	B7L5T2	Nickel transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
99003	2859978	2860781	TY-2482_chromosome	B7L5S9	Nickel transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
32662	2860790	2861188	TY-2482_chromosome	B7L5T4	Nickel-responsive regulator	Escherichia coli (strain 55989 / EAEC)
81115	2861670	2861314	TY-2482_chromosome	B7L5T5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
101408	2861942	2861670	TY-2482_chromosome	C6UWI3	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
79172	2863125	2862004	TY-2482_chromosome	B7L5T6	Putative transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
62610	2865860	2863128	TY-2482_chromosome	B7L5T7	Fused ribosome-associated ATPase: ATP-binding protein ; ATP-binding protein ; putative membrane protein	Escherichia coli (strain 55989 / EAEC)
111554	2866924	2865860	TY-2482_chromosome	B7L5T3	Putative HlyD family secretion protein	Escherichia coli (strain 55989 / EAEC)
110441	2868911	2867293	TY-2482_chromosome	B5YUR9	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
108836	2870815	2869176	TY-2482_chromosome	D3H0S6	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
59004	2871182	2872231	TY-2482_chromosome	B7L5U4	Putative uncharacterized protein yhiM	Escherichia coli (strain 55989 / EAEC)
89973	2873361	2872897	TY-2482_chromosome	B7L5U5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
77360	2874946	2873549	TY-2482_chromosome	B7L5U2	Putative sensor protein pcoS (EC 2.7.13.3)	Escherichia coli (strain 55989 / EAEC)
113040	2875629	2874946	TY-2482_chromosome	B7L5U7	Transcriptional regulatory protein pcoR	Escherichia coli (strain 55989 / EAEC)
95527	2876607	2875681	TY-2482_chromosome	B7L5U8	Copper resistance protein D	Escherichia coli (strain 55989 / EAEC)
113999	2876992	2876615	TY-2482_chromosome	B7L5U9	Copper resistance protein C	Escherichia coli (strain 55989 / EAEC)
99016	2877931	2877035	TY-2482_chromosome	B7L5V0	Copper resistance protein B	Escherichia coli (strain 55989 / EAEC)
91860	2879751	2877931	TY-2482_chromosome	B7L5V1	Copper resistance protein A	Escherichia coli (strain 55989 / EAEC)
115258	2879980	2880426	TY-2482_chromosome	B7L5U6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
61648	2880718	2881452	TY-2482_chromosome	B7L5V2	Putative peptidase	Escherichia coli (strain 55989 / EAEC)
28644	2881686	2881492	TY-2482_chromosome	A4Y217	Putative uncharacterized protein	Shewanella putrefaciens (strain CN-32 / ATCC BAA-453)
66340	2884174	2881730	TY-2482_chromosome	B7L5V4	Putative cation-transporting P-type ATPase	Escherichia coli (strain 55989 / EAEC)
105109	2884747	2884304	TY-2482_chromosome	B7L5V5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
72036	2887974	2884831	TY-2482_chromosome	B7L5V6	Copper/silver efflux system, membrane component	Escherichia coli (strain 55989 / EAEC)
115310	2889277	2887988	TY-2482_chromosome	B7L5V7	Putative membrane fusion protein silB	Escherichia coli (strain 55989 / EAEC)
88491	2889744	2889394	TY-2482_chromosome	B7L5V3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
110520	2891460	2889775	TY-2482_chromosome	B7L5V8	Putative outer membrane lipoprotein silC	Escherichia coli (strain 55989 / EAEC)
91861	2892020	2893498	TY-2482_chromosome	B7L5W2	Putative sensory histidine kinase in two-component regulatory system with SilR, senses silver ions (EC 2.7.13.3)	Escherichia coli (strain 55989 / EAEC)
29209	2893629	2894174	TY-2482_chromosome	B7L5W1	Silver-binding protein SilE	Escherichia coli (strain 55989 / EAEC)
26999	2894325	2894672	TY-2482_chromosome	B7L5W0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
114155	2896730	2894847	TY-2482_chromosome	B7L5W4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
66235	2897563	2897237	TY-2482_chromosome	B7L5W5	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
24392	2898812	2897889	TY-2482_chromosome	B7L5W6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26175	2900389	2898827	TY-2482_chromosome	Q19NI3	TnsD	Escherichia coli O1:K1 / APEC

24985	2901869	2900424	TY-2482_chromosome	B7L5W7	Tn7-like transposition protein TnsC	Escherichia coli (strain 55989 / EAEC)
25716	2903992	2901872	TY-2482_chromosome	B7L5X1	Tn7-like transposition protein TnsB	Escherichia coli (strain 55989 / EAEC)
28472	2904821	2903982	TY-2482_chromosome	B7L5X0	Tn7-like transposase TnsA	Escherichia coli (strain 55989 / EAEC)
98121	2906166	2904967	TY-2482_chromosome	B7L5X3	Putative oxidoreductase with FAD/NAD(P)-binding domain	Escherichia coli (strain 55989 / EAEC)
86968	2906398	2907894	TY-2482_chromosome	B7L5X2	Phosphate transporter, low-affinity	Escherichia coli (strain 55989 / EAEC)
34528	2908303	2907971	TY-2482_chromosome	B7L5X4	Universal stress protein B	Escherichia coli (strain 55989 / EAEC)
82985	2908694	2909125	TY-2482_chromosome	B7L5X5	Universal stress global response regulator	Escherichia coli (strain 55989 / EAEC)
90816	2909446	2910912	TY-2482_chromosome	B7L5X7	Dipeptide and tripeptide permease B	Escherichia coli (strain 55989 / EAEC)
34962	2911716	2910967	TY-2482_chromosome	B7L5X8	UPF0341 protein yhiQ	Escherichia coli (strain 55989 / EAEC)
28525	2913766	2911727	TY-2482_chromosome	B7L5X6	Oligopeptidase A (EC 3.4.24.70)	Escherichia coli (strain 55989 / EAEC)
78948	2913969	2914808	TY-2482_chromosome	B7L5Y0	Putative DNA (Exogenous) processing protein	Escherichia coli (strain 55989 / EAEC)
58487	2914883	2916232	TY-2482_chromosome	B7L5Y1	Glutathione oxidoreductase (EC 1.8.1.7)	Escherichia coli (strain 55989 / EAEC)
98020	2917112	2917462	TY-2482_chromosome	B7L5Y4	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
59005	2917519	2918805	TY-2482_chromosome	B7L5Y2	Arsenite/antimonite transporter	Escherichia coli (strain 55989 / EAEC)
102723	2918821	2919243	TY-2482_chromosome	B7L5Y6	Arsenate reductase (EC 1.20.4.1)	Escherichia coli (strain 55989 / EAEC)
65830	2919676	2919383	TY-2482_chromosome	B7L5Y7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
110647	2919771	2920793	TY-2482_chromosome	B7L5Y5	Putative membrane protein	Escherichia coli (strain 55989 / EAEC)
76050	2921376	2922518	TY-2482_chromosome	B7L5Y9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
29286	2922680	2923408	TY-2482_chromosome	Q0SZF7	Outer membrane protein induced after carbon starvation	Shigella flexneri serotype 5b (strain 8401)
94410	2923567	2924094	TY-2482_chromosome	B7L5Z1	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
77110	2924798	2924142	TY-2482_chromosome	B5YVF1	Putative Mg2+ transporter-C (MgtC) family protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
112343	2925188	2924853	TY-2482_chromosome	C8TJU6	Acid-resistance protein HdeB	Escherichia coli O26:H11 (strain 11368 / EHEC)
106360	2925624	2925295	TY-2482_chromosome	B7L5Z4	Stress response protein acid-resistance protein	Escherichia coli (strain 55989 / EAEC)
66344	2925879	2926448	TY-2482_chromosome	B7L5Z3	Acid-resistance membrane protein	Escherichia coli (strain 55989 / EAEC)
114156	2927250	2927774	TY-2482_chromosome	B7L5Z6	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
12437	2928056	2927730	TY-2482_chromosome	D7Z0Y0	Putative uncharacterized protein	Escherichia coli MS 45-1
66345	2928116	2929270	TY-2482_chromosome	B7L5Z7	Multidrug resistance efflux transporter	Escherichia coli (strain 55989 / EAEC)
95528	2929298	2932408	TY-2482_chromosome	B7L5Z5	Multidrug transporter, RpoS-dependent	Escherichia coli (strain 55989 / EAEC)
91144	2933502	2932777	TY-2482_chromosome	B7L5Z9	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
r194	2933748	2933852	TY-2482_chromosome	ref|NC_010473|:3760632-3760736|-| [gene=gadY] [locus_tag=ECDH10B_3692]		
79986	2934694	2933873	TY-2482_chromosome	B7L600	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
101131	2936464	2935067	TY-2482_chromosome	B7L5Z8	Glutamate decarboxylase A, PLP-dependent (EC 4.1.1.15)	Escherichia coli (strain 55989 / EAEC)
81116	2938072	2936678	TY-2482_chromosome	B7L601	Cytochrome C peroxidase (Cpp-like) (EC 1.11.1.5)	Escherichia coli (strain 55989 / EAEC)
34316	2938477	2940123	TY-2482_chromosome	B7L603	Cytoplasmic trehalase (EC 3.2.1.28) (Alpha,alpha-trehalase) (Alpha,alpha-trehalose glucohydrolase)	Escherichia coli (strain 55989 / EAEC)
88236	2940779	2940180	TY-2482_chromosome	B7L604	Putative DNA-binding response regulator in two-component regulatory system	Escherichia coli (strain 55989 / EAEC)
88237	2941227	2942195	TY-2482_chromosome	B7L605	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
102769	2942247	2943257	TY-2482_chromosome	B7L606	Putative uncharacterized protein yhjD	Escherichia coli (strain 55989 / EAEC)
110569	2943671	2944990	TY-2482_chromosome	B7L607	Putative transporter	Escherichia coli (strain 55989 / EAEC)
57187	2946387	2945230	TY-2482_chromosome	Q8Z283	Putative membrane protein	Salmonella typhi
115738	2947343	2946354	TY-2482_chromosome	B7L602	Putative outer membrane biogenesis protein	Escherichia coli (strain 55989 / EAEC)
95436	2948165	2947401	TY-2482_chromosome	B7L609	EAL domain containing protein involved in flagellar function	Escherichia coli (strain 55989 / EAEC)
75478	2948392	2948168	TY-2482_chromosome	B5YVH2	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
90368	2948397	2949323	TY-2482_chromosome	B7L608	Ketodeoxygluconokinase (EC 2.7.1.45)	Escherichia coli (strain 55989 / EAEC)
106414	2950918	2949425	TY-2482_chromosome	B7L611	Putative zinc-dependent peptidase	Escherichia coli (strain 55989 / EAEC)
30561	2952425	2951142	TY-2482_chromosome	B7L612	C4-dicarboxylate transport protein	Escherichia coli (strain 55989 / EAEC)
73358	2954536	2952545	TY-2482_chromosome	Q8Z288	Putative uncharacterized protein STY4188	Salmonella typhi
68625	2958151	2954681	TY-2482_chromosome	B7L615	Cellulose synthase subunit	Escherichia coli (strain 55989 / EAEC)
73631	2959239	2958136	TY-2482_chromosome	B7L614	Endo-1,4-D-glucanase (EC 3.2.1.4)	Escherichia coli (strain 55989 / EAEC)
84429	2961585	2959249	TY-2482_chromosome	B7L617	Regulator of cellulose synthase, cyclic di-GMP binding	Escherichia coli (strain 55989 / EAEC)
101719	2964214	2961599	TY-2482_chromosome	B7L616	Cellulose synthase, catalytic subunit (EC 2.4.1.12)	Escherichia coli (strain 55989 / EAEC)
62230	2964963	2964214	TY-2482_chromosome	B7L619	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
75623	2965163	2964978	TY-2482_chromosome	B7L620	Putative uncharacterized protein yhjR	Escherichia coli (strain 55989 / EAEC)
102770	2965436	2967005	TY-2482_chromosome	B7L621	Putative protease involved in cellulose biosynthesis	Escherichia coli (strain 55989 / EAEC)
110575	2967005	2967193	TY-2482_chromosome	B7L618	Putative uncharacterized protein bcsF	Escherichia coli (strain 55989 / EAEC)
102771	2967193	2968869	TY-2482_chromosome	B7L623	Putative endoglucanase involved in cellulose biosynthesis	Escherichia coli (strain 55989 / EAEC)
18062	2969031	2969423	TY-2482_chromosome	D8E601	Conserved domain protein	Escherichia coli MS 119-7
18061	2969514	2969906	TY-2482_chromosome	D8E601	Conserved domain protein	Escherichia coli MS 119-7
18060	2969997	2970389	TY-2482_chromosome	D8E601	Conserved domain protein	Escherichia coli MS 119-7
18063	2970485	2970811	TY-2482_chromosome	D8E601	Conserved domain protein	Escherichia coli MS 119-7
65875	2970990	2972258	TY-2482_chromosome	B7L627	Transporter	Escherichia coli (strain 55989 / EAEC)
113184	2973295	2972294	TY-2482_chromosome	B7L622	Dipeptide transporter ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
69009	2974275	2973295	TY-2482_chromosome	B7L629	Dipeptide transporter ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
75200	2975188	2974289	TY-2482_chromosome	B7L630	Dipeptide transporter ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
22821	2976180	2976392	TY-2482_chromosome	E9TED3	Conserved domain protein	Escherichia coli MS 117-3

95437	2976217	2975201	TY-2482_chromosome	B7L631	Dipeptide transporter; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
113883	2977975	2976371	TY-2482_chromosome	B7L632	Dipeptide transporter ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
r251	2978795	2978719	TY-2482_chromosome	ref|NC_010473|:3804216-3804292|Pro tRNA| [gene=proK] [locus_tag=ECDH10B_3724		
28861	2978836	2978330	TY-2482_chromosome	Q1R551	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
86690	2980578	2978890	TY-2482_chromosome	B7L764	Putative metal dependent hydrolase	Escherichia coli (strain 55989 / EAEC)
111836	2981355	2980834	TY-2482_chromosome	B7L6V8	LpfE protein	Escherichia coli (strain 55989 / EAEC)
26266	2982416	2981364	TY-2482_chromosome	B7L6V7	LpfD protein	Escherichia coli (strain 55989 / EAEC)
116178	2984901	2982409	TY-2482_chromosome	C8TJB8	Predicted outer membrane export usher protein SfmD	Escherichia coli O26:H11 (strain 11368 / EHEC)
115989	2985668	2984985	TY-2482_chromosome	B7L6W1	Chaperone protein lpfB	Escherichia coli (strain 55989 / EAEC)
104326	2986276	2985755	TY-2482_chromosome	B7L6W2	Long polar fimbria protein A	Escherichia coli (strain 55989 / EAEC)
88209	2987847	2986603	TY-2482_chromosome	B7L6V9	Putative transporter	Escherichia coli (strain 55989 / EAEC)
27557	2988722	2989447	TY-2482_chromosome	A1AH92	3-methyl-adenine DNA glycosylase I, constitutive	Escherichia coli O1:K1 / APEC
101664	2988729	2988034	TY-2482_chromosome	B7L6W3	Putative uncharacterized protein yhjY	Escherichia coli (strain 55989 / EAEC)
110562	2989447	2989884	TY-2482_chromosome	B7L6W6	Putative acyltransferase with acyl-CoA N-acyltransferase domain	Escherichia coli (strain 55989 / EAEC)
87440	2992135	2989859	TY-2482_chromosome	B7L6W4	Biotin sulfoxide reductase (EC 1.-.-.-)	Escherichia coli (strain 55989 / EAEC)
59042	2992342	2992998	TY-2482_chromosome	B7L6W8	Putative outer membrane lipoprotien	Escherichia coli (strain 55989 / EAEC)
31108	2993105	2994076	TY-2482_chromosome	B7L6W9	Glyoxylate/hydroxypyruvate reductase B (EC 1.1.1.79) (EC 1.1.1.81)	Escherichia coli (strain 55989 / EAEC)
110563	2994839	2994132	TY-2482_chromosome	B7L6X0	Putative uncharacterized protein yiaF	Escherichia coli (strain 55989 / EAEC)
106409	2995273	2995560	TY-2482_chromosome	B7L6W7	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
25170	2996203	2995784	TY-2482_chromosome	A1AH99	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
83391	2996456	2996163	TY-2482_chromosome	E8YB84	Hok/gef cell toxic protein	Escherichia coli (strain ATCC 55124 / KO11)
34111	2998791	2996725	TY-2482_chromosome	B7L6X3	Glycyl-tRNA synthetase beta subunit (EC 6.1.1.14) (Glycine--tRNA ligase beta subunit) (GlyRS)	Escherichia coli (strain 55989 / EAEC)
34107	2999712	2998804	TY-2482_chromosome	B7L6X1	Glycyl-tRNA synthetase alpha subunit (EC 6.1.1.14) (Glycine--tRNA ligase alpha subunit) (GlyRS)	Escherichia coli (strain 55989 / EAEC)
110565	3000106	2999810	TY-2482_chromosome	B7L6X5	Putative uncharacterized protein ysaB	Escherichia coli (strain 55989 / EAEC)
108565	3000281	3001273	TY-2482_chromosome	B7L6X6	Putative uncharacterized protein yiaH	Escherichia coli (strain 55989 / EAEC)
71944	3001755	3001321	TY-2482_chromosome	B7L6X4	Putative uncharacterized protein yiaA	Escherichia coli (strain 55989 / EAEC)
71879	3002142	3001804	TY-2482_chromosome	B7L6X8	Putative uncharacterized protein yiaB	Escherichia coli (strain 55989 / EAEC)
111717	3003765	3002314	TY-2482_chromosome	B7L6X7	Xylulokinase (EC 2.7.1.-) (EC 2.7.1.17)	Escherichia coli (strain 55989 / EAEC)
34615	3005207	3003840	TY-2482_chromosome	B7L6Y0	Xylose isomerase (EC 5.3.1.5)	Escherichia coli (strain 55989 / EAEC)
73627	3005573	3006562	TY-2482_chromosome	B7L6Y1	D-xylose transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
61657	3006643	3008181	TY-2482_chromosome	B7L6Y2	Fused D-xylose transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
84006	3008162	3009340	TY-2482_chromosome	B7L6X9	D-xylose transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
25092	3009255	3009428	TY-2482_chromosome	B7L6Y4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
112822	3009421	3010596	TY-2482_chromosome	B7L6Y5	DNA-binding transcriptional activator, xylose-binding	Escherichia coli (strain 55989 / EAEC)
81129	3011619	3010798	TY-2482_chromosome	B7L6Y3	Putative uncharacterized protein bax	Escherichia coli (strain 55989 / EAEC)
90763	3011939	3013965	TY-2482_chromosome	B7L6Y6	Alpha-amylase (EC 3.2.1.1)	Escherichia coli (strain 55989 / EAEC)
91792	3014146	3015396	TY-2482_chromosome	B7L6Y7	Valine-pyruvate aminotransferase (EC 2.6.1.66)	Escherichia coli (strain 55989 / EAEC)
81130	3016024	3015554	TY-2482_chromosome	B7L6Y9	Putative hydrogenase, 4Fe-4S ferredoxin-type component	Escherichia coli (strain 55989 / EAEC)
102765	3016974	3016129	TY-2482_chromosome	B7L6Z0	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
30633	3017175	3018170	TY-2482_chromosome	B7L6Z1	2,3-diketo-L-gulonate reductase (2,3-DKG reductase) (EC 1.1.1.130) (3-dehydro-L-gulonate 2-dehydrogenase	Escherichia coli (strain 55989 / EAEC)
112772	3018185	3018649	TY-2482_chromosome	B7L6Y8	Putative uncharacterized protein yiaL	Escherichia coli (strain 55989 / EAEC)
99044	3018770	3019240	TY-2482_chromosome	B7L6Z3	Transporter	Escherichia coli (strain 55989 / EAEC)
99045	3019246	3020520	TY-2482_chromosome	B7L6Z4	Transporter	Escherichia coli (strain 55989 / EAEC)
72665	3020536	3021519	TY-2482_chromosome	B7L6Z5	Transporter	Escherichia coli (strain 55989 / EAEC)
65304	3021526	3023019	TY-2482_chromosome	B7L6Z2	L-xylulose kinase (EC 2.7.1.53)	Escherichia coli (strain 55989 / EAEC)
88216	3023019	3023678	TY-2482_chromosome	B7L6Z7	3-keto-L-gulonate 6-phosphate decarboxylase (EC 4.1.2.-)	Escherichia coli (strain 55989 / EAEC)
96075	3023641	3024531	TY-2482_chromosome	C8TZI5	Predicted L-xylulose 5-phosphate 3-epimerase	Escherichia coli O103:H2 (strain 12009 / EHEC)
98487	3024528	3025220	TY-2482_chromosome	B7L6Z9	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)	Escherichia coli (strain 55989 / EAEC)
77315	3026358	3025621	TY-2482_chromosome	B7L700	Putative uncharacterized protein yiaT	Escherichia coli (strain 55989 / EAEC)
62649	3026482	3027453	TY-2482_chromosome	B7L701	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
72427	3028589	3027456	TY-2482_chromosome	B7L6Z8	Membrane fusion protein (MFP) component of efflux pump, signal anchor	Escherichia coli (strain 55989 / EAEC)
73628	3028918	3028598	TY-2482_chromosome	B7L703	Putative uncharacterized protein yiaW	Escherichia coli (strain 55989 / EAEC)
27169	3029032	3029241	TY-2482_chromosome	B7L702	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
88218	3031001	3029466	TY-2482_chromosome	B7L705	Aldehyde dehydrogenase B (EC 1.2.1.22)	Escherichia coli (strain 55989 / EAEC)
113964	3032317	3031169	TY-2482_chromosome	B7L706	Fe-containing alcohol dehydrogenase (EC 1.1.1.1)	Escherichia coli (strain 55989 / EAEC)
106442	3034351	3032510	TY-2482_chromosome	B7L704	Selenocysteinyl-tRNA-specific translation factor	Escherichia coli (strain 55989 / EAEC)
33918	3035739	3034351	TY-2482_chromosome	B7L708	L-seryl-tRNA(Sec) selenium transferase (EC 2.9.1.1) (Selenocysteine synthase) (Sec synthase) (Selenocysteinyl-tRNA(S	Escherichia coli (strain 55989 / EAEC)
82509	3036445	3035840	TY-2482_chromosome	B7L709	Putative glutathione S-transferase	Escherichia coli (strain 55989 / EAEC)
94463	3036674	3040636	TY-2482_chromosome	B7L711	RhsB element core protein RshB	Escherichia coli (strain 55989 / EAEC)
61083	3040881	3041261	TY-2482_chromosome	B7L707	Putative uncharacterized protein yhhH	Escherichia coli (strain 55989 / EAEC)
104355	3041369	3042208	TY-2482_chromosome	C8TME0	Lyase containing HEAT-repeat	Escherichia coli O26:H11 (strain 11368 / EHEC)
97127	3042253	3043194	TY-2482_chromosome	B7L717	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
67795	3043209	3043667	TY-2482_chromosome	B7L718	Putative uncharacterized protein yibG	Escherichia coli (strain 55989 / EAEC)
28311	3043837	3044285	TY-2482_chromosome	Q3YVV7	RhsB protein in rhs element	Shigella sonnei (strain Ss046)

12957	3044317	3044806	TY-2482_chromosome	D7Z8X7	Putative uncharacterized protein	Escherichia coli MS 69-1
67912	3046405	3045272	TY-2482_chromosome	B7L715	Putative uncharacterized protein yibH	Escherichia coli (strain 55989 / EAEC)
66380	3046770	3046411	TY-2482_chromosome	B7L721	Putative uncharacterized protein yibI	Escherichia coli (strain 55989 / EAEC)
102766	3047307	3049217	TY-2482_chromosome	B7L722	Fused mannitol-specific PTS enzymes: IIA components ; IIB components ; IIC components (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
32510	3049450	3050595	TY-2482_chromosome	B7L723	Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Escherichia coli (strain 55989 / EAEC)
88421	3050598	3051182	TY-2482_chromosome	B7L720	DNA-binding repressor	Escherichia coli (strain 55989 / EAEC)
73630	3051406	3051200	TY-2482_chromosome	B7L724	Putative uncharacterized protein yibT	Escherichia coli (strain 55989 / EAEC)
29243	3051984	3051610	TY-2482_chromosome	A7ZTF2	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
95435	3052597	3053277	TY-2482_chromosome	B7L727	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104455	3053324	3058171	TY-2482_chromosome	B7L728	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
112878	3058543	3060195	TY-2482_chromosome	B7L729	L-lactate permease	Escherichia coli (strain 55989 / EAEC)
66242	3060198	3060971	TY-2482_chromosome	B7L730	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
31909	3060971	3062158	TY-2482_chromosome	B7L725	L-lactate dehydrogenase [cytochrome] (EC 1.1.2.3)	Escherichia coli (strain 55989 / EAEC)
77317	3062347	3062817	TY-2482_chromosome	B7L732	tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmL (EC 2.1.1.-)	Escherichia coli (strain 55989 / EAEC)
106410	3063694	3062876	TY-2482_chromosome	B7L731	Serine acetyltransferase (EC 2.3.1.30)	Escherichia coli (strain 55989 / EAEC)
31196	3064793	3063777	TY-2482_chromosome	B7L734	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydroger	Escherichia coli (strain 55989 / EAEC)
33910	3065260	3064796	TY-2482_chromosome	B7L735	Protein-export protein secB	Escherichia coli (strain 55989 / EAEC)
66382	3065574	3065326	TY-2482_chromosome	B7L736	Glutaredoxin 3	Escherichia coli (strain 55989 / EAEC)
100625	3066147	3065719	TY-2482_chromosome	B7L733	Putative rhodanese-related sulfurtransferase	Escherichia coli (strain 55989 / EAEC)
28729	3066171	3066365	TY-2482_chromosome	B6I3J1	Putative uncharacterized protein	Escherichia coli (strain SE11)
58492	3066392	3067933	TY-2482_chromosome	B7L738	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (BPG-independent PGAM) (Phosphoglyceromutase)	Escherichia coli (strain 55989 / EAEC)
112506	3067970	3069226	TY-2482_chromosome	B7L739	Protease with a role in cell division	Escherichia coli (strain 55989 / EAEC)
77340	3069233	3070189	TY-2482_chromosome	B7L737	Putative polysaccharide deacetylase	Escherichia coli (strain 55989 / EAEC)
86344	3071213	3070182	TY-2482_chromosome	B7L741	Putative glycosyl transferase	Escherichia coli (strain 55989 / EAEC)
26859	3071443	3072465	TY-2482_chromosome	Q1R4X5	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
90138	3073683	3072490	TY-2482_chromosome	B7L740	Glycine C-acetyltransferase (EC 2.3.1.29)	Escherichia coli (strain 55989 / EAEC)
104462	3074815	3073961	TY-2482_chromosome	B7L743	Putative uncharacterized protein htrL	Escherichia coli (strain 55989 / EAEC)
31409	3075119	3076048	TY-2482_chromosome	B7L745	ADP-L-glycero-D-manno-heptose-6-epimerase (EC 5.1.3.20) (ADP-L-glycero-beta-D-manno-heptose-6-epimerase) (AD	Escherichia coli (strain 55989 / EAEC)
98118	3076061	3077104	TY-2482_chromosome	B7L746	ADP-heptose:LPS heptosyltransferase II (EC 2.-.-.-)	Escherichia coli (strain 55989 / EAEC)
113882	3077111	3078100	TY-2482_chromosome	B7L744	ADP-heptose:LPS heptosyl transferase I (EC 2.-.-.-)	Escherichia coli (strain 55989 / EAEC)
59043	3078100	3079305	TY-2482_chromosome	B7L748	O-antigen ligase	Escherichia coli (strain 55989 / EAEC)
86018	3080486	3079347	TY-2482_chromosome	B7L749	Lipopolysaccharide 1, 2-N-acetylglucosaminetransferase (EC 2.4.1.56)	Escherichia coli (strain 55989 / EAEC)
110566	3081508	3080498	TY-2482_chromosome	B7L750	Lipopolysaccharide 1,2-glucosyltransferase (EC 2.4.1.58)	Escherichia coli (strain 55989 / EAEC)
81135	3082240	3081536	TY-2482_chromosome	B7L751	Lipopolysaccharide core biosynthesis protein rfaY	Escherichia coli (strain 55989 / EAEC)
91793	3083273	3082269	TY-2482_chromosome	B7L752	Lipopolysaccharide 1,3-galactosyltransferase (EC 2.4.1.44)	Escherichia coli (strain 55989 / EAEC)
59044	3084122	3083319	TY-2482_chromosome	B7L753	Kinase that phosphorylates core heptose of lipopolysaccharide	Escherichia coli (strain 55989 / EAEC)
104337	3085230	3084109	TY-2482_chromosome	B7L754	Glucosyltransferase I (EC 2.4.1.-)	Escherichia coli (strain 55989 / EAEC)
77318	3086285	3085230	TY-2482_chromosome	B7L755	Lipopolysaccharide core biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
89810	3086698	3087972	TY-2482_chromosome	B7L756	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	Escherichia coli (strain 55989 / EAEC)
30361	3087983	3088459	TY-2482_chromosome	B7L747	Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate	Escherichia coli (strain 55989 / EAEC)
31010	3089310	3088504	TY-2482_chromosome	B7L758	Formamidopyrimidine-DNA glycosylase (Fapy-DNA glycosylase) (EC 3.2.2.23) (DNA-(apurinic or apyrimidinic site) lyas	Escherichia coli (strain 55989 / EAEC)
24824	3089324	3089596	TY-2482_chromosome	Q1R4V7	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
33518	3089832	3089599	TY-2482_chromosome	B7L760	50S ribosomal protein L28	Escherichia coli (strain 55989 / EAEC)
34967	3090717	3090052	TY-2482_chromosome	B7L757	UPF0758 protein yicR	Escherichia coli (strain 55989 / EAEC)
106411	3090889	3092106	TY-2482_chromosome	B7L762	Fused 4'-phosphopantothenoylcysteine decarboxylase ; phosphopantothenoylcysteine synthetase, FMN-binding (EC	Escherichia coli (strain 55989 / EAEC)
30699	3092087	3092542	TY-2482_chromosome	B5YWD8	Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) (EC 3.6.1.23) (dUTP pyrophosphatase)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
33944	3092652	3093245	TY-2482_chromosome	B7L761	HTH-type protein slmA	Escherichia coli (strain 55989 / EAEC)
33205	3093926	3093288	TY-2482_chromosome	B7L766	Orotate phosphoribosyltransferase (OPRT) (OPRTase) (EC 2.4.2.10)	Escherichia coli (strain 55989 / EAEC)
23896	3094640	3094819	TY-2482_chromosome	E3XS42	Putative uncharacterized protein	Escherichia coli 2362-75
60971	3094732	3093995	TY-2482_chromosome	B7L767	Ribonuclease PH (RNase PH) (EC 2.7.7.56) (tRNA nucleotidyltransferase)	Escherichia coli (strain 55989 / EAEC)
66383	3094835	3095695	TY-2482_chromosome	B7L765	Putative uncharacterized protein yicC	Escherichia coli (strain 55989 / EAEC)
60870	3095907	3096740	TY-2482_chromosome	B7L769	DNA-damage-inducible protein	Escherichia coli (strain 55989 / EAEC)
108568	3097035	3097649	TY-2482_chromosome	B7L770	Putative uncharacterized protein yicG	Escherichia coli (strain 55989 / EAEC)
15076	3099246	3099536	TY-2482_chromosome	D7XWY5	Conserved domain protein	Escherichia coli MS 84-1
31886	3099331	3097652	TY-2482_chromosome	B7L771	DNA ligase B (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+] B)	Escherichia coli (strain 55989 / EAEC)
76561	3099589	3100209	TY-2482_chromosome	B7L768	Guanylate kinase (EC 2.7.4.8)	Escherichia coli (strain 55989 / EAEC)
33678	3100267	3100539	TY-2482_chromosome	B7L773	DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit)	Escherichia coli (strain 55989 / EAEC)
87485	3100561	3102666	TY-2482_chromosome	B7L774	Bifunctional (P)ppGpp synthetase II and guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase (EC 2.7.6.5) (EC	Escherichia coli (strain 55989 / EAEC)
58438	3102676	3103362	TY-2482_chromosome	B7L775	tRNA (Guanosine-2'-O-)-methyltransferase	Escherichia coli (strain 55989 / EAEC)
106412	3103371	3105449	TY-2482_chromosome	B7L772	ATP-dependent DNA helicase (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
112871	3106823	3105621	TY-2482_chromosome	B7L777	Glutamate transporter	Escherichia coli (strain 55989 / EAEC)
98438	3107103	3108491	TY-2482_chromosome	B7L778	Putative transporter	Escherichia coli (strain 55989 / EAEC)
115563	3108615	3110321	TY-2482_chromosome	B7L776	Putative uncharacterized protein yicH	Escherichia coli (strain 55989 / EAEC)
71757	3112695	3110380	TY-2482_chromosome	B7L780	Putative alpha-glucosidase (EC 3.2.1.20)	Escherichia coli (strain 55989 / EAEC)

110613	3114087	3112708	TY-2482_chromosome	B7L781	Putative transporter	Escherichia coli (strain 55989 / EAEC)
r196	3114380	3114474	TY-2482_chromosome	ref|NC_010473|:3931829-3931923|Sec tRNA| [gene=selC] [locus_tag=ECDH10B_3840]		
19976	3114534	3114181	TY-2482_chromosome	D8CB43	Conserved domain protein	Escherichia coli MS 185-1
77112	3114696	3115955	TY-2482_chromosome	B5YWF9	Integrase	Escherichia coli O157:H7 (strain EC4115 / EHEC)
14370	3116774	3116080	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli
35853	3119960	3116967	TY-2482_chromosome	Q4MUS7	Transposase (Transposase X)	Bacillus cereus G9241
94624	3120493	3119936	TY-2482_chromosome	D3H359	Transposon Tn21 resolvase	Escherichia coli O44:H18 (strain 042 / EAEC)
15083	3121233	3120622	TY-2482_chromosome	C7S9T2	Transposon Tn21 modulator protein	Escherichia coli
20211	3122142	3122813	TY-2482_chromosome	C7S9T5	Dihydrofolate reductase type VII	Escherichia coli
104135	3122185	3121175	TY-2482_chromosome	D3H361	Integrase	Escherichia coli O44:H18 (strain 042 / EAEC)
19395	3123010	3123390	TY-2482_chromosome	Q3I3P0	ORF3-QacEdelta1 fusion protein	Escherichia coli
60552	3123387	3124163	TY-2482_chromosome	D3H364	Dihydropteroate synthase type-1 (EC 2.5.1.15)	Escherichia coli O44:H18 (strain 042 / EAEC)
53350	3124904	3124203	TY-2482_chromosome	Q7AQT7	Putative transposase	Salmonella typhi
66979	3125352	3124954	TY-2482_chromosome	C8UQP4	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC
105703	3125826	3126080	TY-2482_chromosome	C8UQP5	TEM-1 beta-lactamase	Escherichia coli O111:H- (strain 11128 / EHEC
105702	3125831	3125505	TY-2482_chromosome	C8UQP5	TEM-1 beta-lactamase	Escherichia coli O111:H- (strain 11128 / EHEC
66980	3126233	3126631	TY-2482_chromosome	C8UQP4	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC
53351	3126681	3127382	TY-2482_chromosome	Q7AQT7	Putative transposase	Salmonella typhi
13974	3128042	3128989	TY-2482_chromosome	E3PYS5	Replication protein C	Escherichia coli
82442	3129300	3130112	TY-2482_chromosome	C8UQP1	Sulfonamide-resistant dihydropteroate synthase	Escherichia coli O111:H- (strain 11128 / EHEC
11978	3130176	3131105	TY-2482_chromosome	A8SPZ5	StrA	Escherichia coli
53349	3132580	3131879	TY-2482_chromosome	Q7AQT7	Putative transposase	Salmonella typhi
79314	3133931	3132630	TY-2482_chromosome	D3H369	Putative transposase	Escherichia coli O44:H18 (strain 042 / EAEC)
25657	3134854	3133973	TY-2482_chromosome	Q5J458	Urf2	Salmonella choleraesuis
115809	3135269	3134910	TY-2482_chromosome	D3H372	MerR-family transcriptional regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
113578	3136981	3135290	TY-2482_chromosome	Q935L3	Putative mercuric reductase (EC 1.16.1.1)	Salmonella typhi
8580	3137494	3137036	TY-2482_chromosome	Q0ZKU6	Mercuric resistance protein MerC (Mercury resistance operon transport protein MerC) (Putative uncharacterized pro	Escherichia coli
96677	3137766	3137494	TY-2482_chromosome	D3H375	Mercuric ion transport protein	Escherichia coli O44:H18 (strain 042 / EAEC)
105131	3138130	3137783	TY-2482_chromosome	C8UQM9	Mercuric ion transport protein MerT	Escherichia coli O111:H- (strain 11128 / EHEC
96933	3138202	3138633	TY-2482_chromosome	C8UQM8	Mercuric resistance operon regulatory protein MerR	Escherichia coli O111:H- (strain 11128 / EHEC
5322	3140116	3139007	TY-2482_chromosome	P11901	Transposase for insertion sequence element IS421	Escherichia coli
111823	3140911	3140579	TY-2482_chromosome	D3H379	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
15990	3140964	3141227	TY-2482_chromosome	E5FD82	Relaxase (Fragment)	Klebsiella pneumoniae
72641	3141912	3141265	TY-2482_chromosome	D3H381	Tetracycline repressor	Escherichia coli O44:H18 (strain 042 / EAEC)
91293	3142018	3143214	TY-2482_chromosome	D3H382	Tetracycline resistance protein	Escherichia coli O44:H18 (strain 042 / EAEC)
8470	3144160	3143252	TY-2482_chromosome	Q6SJ76	PecM (PecM-like protein) (Protein pecM)	Escherichia coli
79315	3144837	3144097	TY-2482_chromosome	D3H369	Putative transposase	Escherichia coli O44:H18 (strain 042 / EAEC)
107872	3145618	3145351	TY-2482_chromosome	B7LG76	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
12861	3145940	3145557	TY-2482_chromosome	Q5I3K5	Aec60	Escherichia coli
25378	3146672	3146106	TY-2482_chromosome	D2NGS8	Putative uncharacterized protein	Escherichia coli O150:H5 (strain SE15)
68255	3147708	3147419	TY-2482_chromosome	Q0TDJ8	Putative hemolysin expression modulating protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
115826	3148140	3148538	TY-2482_chromosome	B7LDW1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
75582	3148481	3149235	TY-2482_chromosome	C8TTS1	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC
12378	3149872	3150217	TY-2482_chromosome	E9YZX6	IstB ATP binding protein	Escherichia coli M863
52691	3151826	3152695	TY-2482_chromosome	C8TWJ4	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC
104657	3152695	3153666	TY-2482_chromosome	C8TV65	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC
105928	3153931	3156885	TY-2482_chromosome	C8TNL5	Putative AidA-I adhesin-like protein	Escherichia coli O26:H11 (strain 11368 / EHEC
14427	3156923	3157114	TY-2482_chromosome	B3Y1R9	Predicted protein	Escherichia coli O111:H-
56483	3157272	3158087	TY-2482_chromosome	C8TWJ8	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC
26740	3158259	3158212	TY-2482_chromosome	Q1RA72	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
47868	3159382	3158426	TY-2482_chromosome	Q5K5L6	Putative uncharacterized protein	Escherichia coli
68099	3159733	3160215	TY-2482_chromosome	D3GX48	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
108195	3160151	3160639	TY-2482_chromosome	B7MN77	Toxin of the YeeV-YeeU toxin-antitoxin system	Escherichia coli O45:K1 (strain S88 / ExPEC)
61212	3160639	3161124	TY-2482_chromosome	B7LBT9	Putative uncharacterized protein yeeW	Escherichia coli (strain 55989 / EAEC)
24594	3161429	3162271	TY-2482_chromosome	B7MSL6	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
106475	3163067	3164248	TY-2482_chromosome	B7L779	Putative sugar efflux system	Escherichia coli (strain 55989 / EAEC)
97644	3164362	3165282	TY-2482_chromosome	B7L784	Putative uncharacterized protein yicL	Escherichia coli (strain 55989 / EAEC)
95499	3166107	3165292	TY-2482_chromosome	B7L785	Cytoplasmic membrane lipoprotein-28	Escherichia coli (strain 55989 / EAEC)
61188	3166329	3166619	TY-2482_chromosome	B7L783	Putative uncharacterized protein yicS	Escherichia coli (strain 55989 / EAEC)
95501	3168012	3166666	TY-2482_chromosome	B7L787	Transporter	Escherichia coli (strain 55989 / EAEC)
93061	3168537	3168061	TY-2482_chromosome	D3H2G2	Putative exported protein	Escherichia coli O44:H18 (strain 042 / EAEC)
91816	3169897	3168566	TY-2482_chromosome	B7L788	Putative xanthine/uracil permease	Escherichia coli (strain 55989 / EAEC)
29718	3170072	3171835	TY-2482_chromosome	B7L789	Adenine deaminase (Adenase) (Adenine aminase) (EC 3.5.4.2)	Escherichia coli (strain 55989 / EAEC)
91820	3173274	3171886	TY-2482_chromosome	B7L790	Hexose phosphate transporter	Escherichia coli (strain 55989 / EAEC)

65818	3174731	3173415	TY-2482_chromosome	B7L809	Membrane protein regulates uhpT expression	Escherichia coli (strain 55989 / EAEC)
78880	3176243	3174744	TY-2482_chromosome	B7L808	Sensory histidine kinase in two-component regulatory sytem with UhpA	Escherichia coli (strain 55989 / EAEC)
105874	3176833	3176246	TY-2482_chromosome	B7L811	DNA-binding response regulator in two-component regulatory system wtih UhpB	Escherichia coli (strain 55989 / EAEC)
68611	3177198	3176911	TY-2482_chromosome	B7L812	Acetolactate synthase I, small subunit (EC 2.2.1.6)	Escherichia coli (strain 55989 / EAEC)
66359	3178874	3179368	TY-2482_chromosome	B7L810	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
95479	3178890	3177205	TY-2482_chromosome	B7L813	Acetolactate synthase (EC 2.2.1.6)	Escherichia coli (strain 55989 / EAEC)
22726	3179789	3180124	TY-2482_chromosome	E1HWK4	Putative uncharacterized protein (Fragment)	Escherichia coli MS 78-1
20994	3179874	3179518	TY-2482_chromosome	E1JD58	Conserved domain protein	Escherichia coli MS 124-1
91303	3180167	3181348	TY-2482_chromosome	B7L816	Multidrug efflux system protein	Escherichia coli (strain 55989 / EAEC)
68117	3181856	3181362	TY-2482_chromosome	B7L817	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
112331	3182215	3181856	TY-2482_chromosome	B7L819	Putative uncharacterized protein yidG	Escherichia coli (strain 55989 / EAEC)
102784	3182552	3182208	TY-2482_chromosome	B7L820	Putative uncharacterized protein yidH	Escherichia coli (strain 55989 / EAEC)
68183	3182661	3183107	TY-2482_chromosome	B7L818	Putative uncharacterized protein yidI	Escherichia coli (strain 55989 / EAEC)
59054	3184650	3183160	TY-2482_chromosome	B7L822	Putative sulfatase/phosphatase	Escherichia coli (strain 55989 / EAEC)
73653	3186362	3184650	TY-2482_chromosome	B7L823	Transporter	Escherichia coli (strain 55989 / EAEC)
69952	3186499	3187419	TY-2482_chromosome	B7L821	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
60525	3187643	3187422	TY-2482_chromosome	C6UYS2	Putative 6-phospho-beta-glucosidase	Escherichia coli O157:H7 (strain TW14359 / EHEC)
114658	3188233	3187598	TY-2482_chromosome	C8TLC9	Predicted 6-phospho-beta-glucosidase, NAD(P)-binding	Escherichia coli O26:H11 (strain 11368 / EHEC)
65259	3190110	3188236	TY-2482_chromosome	B7L827	Putative PTS system alpha-glucoside-specific EIICB component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
105678	3190145	3190858	TY-2482_chromosome	B7L828	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
34973	3192519	3190861	TY-2482_chromosome	B7L824	Putative transport protein YidE	Escherichia coli (strain 55989 / EAEC)
97046	3193150	3192719	TY-2482_chromosome	D3H311	Small heat shock protein ibpB (16 kDa heat shock protein B)	Escherichia coli O44:H18 (strain 042 / EAEC)
71216	3193675	3193259	TY-2482_chromosome	D3H312	Small heat shock protein ibpA (16 kDa heat shock protein A)	Escherichia coli O44:H18 (strain 042 / EAEC)
88259	3193975	3194304	TY-2482_chromosome	B7L832	Putative uncharacterized protein yidQ	Escherichia coli (strain 55989 / EAEC)
61042	3195523	3194312	TY-2482_chromosome	B7L833	Putative uncharacterized protein yidR	Escherichia coli (strain 55989 / EAEC)
79099	3195624	3196685	TY-2482_chromosome	B7L829	Putative oxidoreductase with FAD/NAD(P)-binding domain	Escherichia coli (strain 55989 / EAEC)
112773	3197977	3196688	TY-2482_chromosome	B7L834	D-galactonate transporter	Escherichia coli (strain 55989 / EAEC)
30603	3199245	3198100	TY-2482_chromosome	B7L836	D-galactonate dehydratase (GalD) (EC 4.2.1.6)	Escherichia coli (strain 55989 / EAEC)
95489	3199859	3199245	TY-2482_chromosome	B7L835	2-oxo-3-deoxygalactonate 6-phosphate aldolase (EC 4.1.2.21)	Escherichia coli (strain 55989 / EAEC)
84502	3200721	3199846	TY-2482_chromosome	B7L838	2-oxo-3-deoxygalactonate kinase (EC 2.7.1.58)	Escherichia coli (strain 55989 / EAEC)
102786	3201407	3200721	TY-2482_chromosome	B7L837	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
91811	3201685	3202338	TY-2482_chromosome	B7L840	Putative lipoprotein C	Escherichia coli (strain 55989 / EAEC)
99068	3203199	3202390	TY-2482_chromosome	B7L841	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
9020	3203721	3203317	TY-2482_chromosome	C3SLN7	DNA gyrase subunit B GyrB	Escherichia coli
110602	3206366	3203955	TY-2482_chromosome	B7L843	DNA gyrase subunit B (EC 5.99.1.3)	Escherichia coli (strain 55989 / EAEC)
33300	3207468	3206398	TY-2482_chromosome	B7L842	DNA replication and repair protein recF	Escherichia coli (strain 55989 / EAEC)
91219	3208568	3207471	TY-2482_chromosome	B7L845	DNA polymerase III, beta subunit (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
30639	3209976	3208576	TY-2482_chromosome	B7L846	Chromosomal replication initiator protein DnaA	Escherichia coli (strain 55989 / EAEC)
113874	3210470	3210273	TY-2482_chromosome	B5YXA5	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
33647	3210740	3211096	TY-2482_chromosome	B7L844	Ribonuclease P protein component (RNase P protein) (RNaseP protein) (EC 3.1.26.5) (Protein C5	Escherichia coli (strain 55989 / EAEC)
34971	3211063	3211317	TY-2482_chromosome	B7L848	UPF0161 protein yidD	Escherichia coli (strain 55989 / EAEC)
32845	3211323	3212966	TY-2482_chromosome	B7L849	Inner membrane protein oxaA	Escherichia coli (strain 55989 / EAEC)
32426	3213075	3214436	TY-2482_chromosome	B7L851	tRNA modification GTPase mnmE (EC 3.6.-.-)	Escherichia coli (strain 55989 / EAEC)
34284	3214977	3216389	TY-2482_chromosome	B7L853	Tryptophanase (EC 4.1.99.1) (L-tryptophan indole-lyase) (TNase)	Escherichia coli (strain 55989 / EAEC)
84503	3216483	3217727	TY-2482_chromosome	B7L854	Tryptophan transporter of low affinity	Escherichia coli (strain 55989 / EAEC)
32234	3217863	3219035	TY-2482_chromosome	B7L855	Multidrug resistance protein mdtL	Escherichia coli (strain 55989 / EAEC)
34977	3219013	3219969	TY-2482_chromosome	B7L852	HTH-type transcriptional regulator yidZ	Escherichia coli (strain 55989 / EAEC)
88339	3220117	3220875	TY-2482_chromosome	B7L857	Putative phosphopantetheinyl transferase	Escherichia coli (strain 55989 / EAEC)
113926	3220900	3221463	TY-2482_chromosome	B7L858	Chromate reductase, Class I, flavoprotein	Escherichia coli (strain 55989 / EAEC)
102787	3222857	3221523	TY-2482_chromosome	B7L859	Putative uncharacterized protein yieG	Escherichia coli (strain 55989 / EAEC)
80468	3223024	3223686	TY-2482_chromosome	B7L856	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
69958	3223756	3224226	TY-2482_chromosome	B7L861	Putative uncharacterized protein yieI	Escherichia coli (strain 55989 / EAEC)
101196	3224278	3224862	TY-2482_chromosome	B7L862	Putative uncharacterized protein cbrC	Escherichia coli (strain 55989 / EAEC)
75160	3225649	3224930	TY-2482_chromosome	B7L863	Putative 6-phosphogluconolactonase	Escherichia coli (strain 55989 / EAEC)
84506	3226860	3225667	TY-2482_chromosome	B7L864	Putative xylanase	Escherichia coli (strain 55989 / EAEC)
66213	3228476	3226863	TY-2482_chromosome	B7L860	Carbohydrate-specific outer membrane porin, cryptic	Escherichia coli (strain 55989 / EAEC)
65530	3229956	3228565	TY-2482_chromosome	B7L866	Cryptic phospho-beta-glucosidase B (EC 3.2.1.86)	Escherichia coli (strain 55989 / EAEC)
94401	3231852	3229978	TY-2482_chromosome	B7L867	Fused beta-glucoside-specific PTS enzymes: IIA component ; IIB component ; IIC component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
61267	3232822	3231989	TY-2482_chromosome	C8UJB0	Transcriptional antiterminator of the bgl operon	Escherichia coli O111:H- (strain 11128 / EHEC)
102791	3233833	3233111	TY-2482_chromosome	B7L870	Negative regulator of PhoR/PhoB two-component regulator	Escherichia coli (strain 55989 / EAEC)
86550	3234621	3233851	TY-2482_chromosome	B7L868	Phosphate transporter subunit ; ATP-binding component of ABC superfamily (EC 3.6.3.27)	Escherichia coli (strain 55989 / EAEC)
93933	3235602	3234715	TY-2482_chromosome	B7L872	Phosphate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
110582	3236561	3235605	TY-2482_chromosome	B7L873	Phosphate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
61104	3237688	3236651	TY-2482_chromosome	B7L874	Phosphate transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)

75755	3239009	3237939	TY-2482_chromosome	B7L871	Putative fimbrial protein LpfD; putative adhesin	Escherichia coli (strain 55989 / EAEC)
71653	3241542	3239023	TY-2482_chromosome	B7L876	Putative fimbrial usher	Escherichia coli (strain 55989 / EAEC)
113927	3242298	3241570	TY-2482_chromosome	B7L877	Putative fimbrial chaperone protein	Escherichia coli (strain 55989 / EAEC)
79173	3242918	3242349	TY-2482_chromosome	B7L875	Putative major fimbrial subunit	Escherichia coli (strain 55989 / EAEC)
76402	3245049	3243223	TY-2482_chromosome	B7L879	L-glutamine:D-fructose-6-phosphate aminotransferase (EC 2.6.1.16)	Escherichia coli (strain 55989 / EAEC)
31138	3246581	3245214	TY-2482_chromosome	B7L878	Bifunctional protein glmU [Includes: UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (N-acetylglucosamine	Escherichia coli (strain 55989 / EAEC)
27840	3246827	3247372	TY-2482_chromosome	A1AHR3	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
30047	3248754	3247375	TY-2482_chromosome	B7L882	ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Escherichia coli (strain 55989 / EAEC)
30066	3249644	3248784	TY-2482_chromosome	B7L880	ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Escherichia coli (strain 55989 / EAEC)
30043	3251236	3249698	TY-2482_chromosome	B7L884	ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Escherichia coli (strain 55989 / EAEC)
25708	3251423	3252157	TY-2482_chromosome	Q1R4J7	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
30070	3252568	3252332	TY-2482_chromosome	B7L883	ATP synthase subunit c (ATP synthase F(0) sector subunit c) (F-type ATPase subunit c) (F-ATPase subunit c) (Lipid-bind	Escherichia coli (strain 55989 / EAEC)
30039	3253430	3252618	TY-2482_chromosome	B7L888	ATP synthase subunit a (ATP synthase F0 sector subunit a) (F-ATPase subunit 6)	Escherichia coli (strain 55989 / EAEC)
78666	3253819	3253442	TY-2482_chromosome	B7L887	ATP synthase, membrane-bound accesory subunit (EC 3.6.3.14)	Escherichia coli (strain 55989 / EAEC)
33799	3255059	3254439	TY-2482_chromosome	B7L890	Ribosomal RNA small subunit methyltransferase G (EC 2.1.1.170) (16S rRNA 7-methylguanosine methyltransferase) (1	Escherichia coli (strain 55989 / EAEC)
32430	3257012	3255126	TY-2482_chromosome	B7L889	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A	Escherichia coli (strain 55989 / EAEC)
62702	3257834	3257394	TY-2482_chromosome	B7L892	FMN-binding protein MioC	Escherichia coli (strain 55989 / EAEC)
80883	3258382	3257927	TY-2482_chromosome	B7L893	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
29937	3258534	3259523	TY-2482_chromosome	B7L891	Aspartate--ammonia ligase (EC 6.3.1.1) (Asparagine synthetase A)	Escherichia coli (strain 55989 / EAEC)
34560	3260982	3259534	TY-2482_chromosome	B7L895	Protein viaA (VWA domain protein interacting with AAA ATPase)	Escherichia coli (strain 55989 / EAEC)
33251	3262472	3260979	TY-2482_chromosome	B7L896	ATPase ravA (EC 3.6.3.-) (Regulatory ATPase variant A)	Escherichia coli (strain 55989 / EAEC)
31802	3262695	3264560	TY-2482_chromosome	B7L897	Low affinity potassium transport system protein kup (Kup system potassium uptake protein)	Escherichia coli (strain 55989 / EAEC)
4541	3264730	3265146	TY-2482_chromosome	B7L894	D-ribose pyranase (EC 5.5.1.n1)	Escherichia coli (strain 55989 / EAEC)
99069	3265157	3266659	TY-2482_chromosome	B7L899	Fused D-ribose transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
91147	3266667	3267629	TY-2482_chromosome	B7L8A0	D-ribose transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
75969	3267657	3268544	TY-2482_chromosome	B7L8A1	D-ribose transporter subunit ; periplasmic-binding compoent of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
112232	3268658	3269599	TY-2482_chromosome	B5YY10	Ribokinase (EC 2.7.1.15)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
95490	3269606	3270595	TY-2482_chromosome	B7L8A3	DNA-binding transcriptional repressor of ribose metabolism	Escherichia coli (strain 55989 / EAEC)
73664	3271991	3270567	TY-2482_chromosome	B7L8A4	Multidrug or homocysteine efflux system	Escherichia coli (strain 55989 / EAEC)
69343	3272706	3272017	TY-2482_chromosome	B7L898	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
r50	3273187	3274728	TY-2482_chromosome	ref|NC_010473|:3522988-3524529|16S ribosomal RNA| [gene=rrsD] [locus_tag=ECDH10B_3453		
11306	3273333	3273100	TY-2482_chromosome	E9WNY3	Putative uncharacterized protein	Escherichia coli E1520
25825	3274308	3274625	TY-2482_chromosome	Q57H85	ORF16-lacZ fusion protein	Salmonella choleraesuis
r240	3274797	3274873	TY-2482_chromosome	ref|NC_010473|:4134084-4134160|Ile tRNA| [gene=ileT] [locus_tag=ECDH10B_4041]		
r326	3274916	3274991	TY-2482_chromosome	ref|NC_010473|:4134203-4134278|Ala tRNA| [gene=alaT] [locus_tag=ECDH10B_4042		
r1	3275175	3278078	TY-2482_chromosome	ref|NC_010473|:4307762-4310665|23S ribosomal RNA| [gene=rrlE] [locus_tag=ECDH10B_4198		
24098	3275703	3275401	TY-2482_chromosome	Q1R3T8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
13800	3276964	3276761	TY-2482_chromosome	C1HUN3	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
20480	3277493	3277041	TY-2482_chromosome	C1HUN1	Cell wall-associated hydrolase (Fragment)	Escherichia sp. 3_2_53FAA
22417	3277853	3277497	TY-2482_chromosome	C1HUN0	Prolipoprotein diacylglyceryl transferase (Fragment)	Escherichia sp. 3_2_53FAA
r126	3278171	3278290	TY-2482_chromosome	ref|NC_010473|:4043643-4043762|5S ribosomal RNA| [gene=rrfC] [locus_tag=ECDH10B_3948		
25407	3278332	3278057	TY-2482_chromosome	Q1RFY5	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
r248	3278343	3278419	TY-2482_chromosome	ref|NC_010473|:4043815-4043891|Asp tRNA| [gene=aspT] [locus_tag=ECDH10B_3949]		
45708	3278420	3278298	TY-2482_chromosome	Q8CLS5	Putative uncharacterized protein	Yersinia pestis
r333	3278428	3278503	TY-2482_chromosome	ref|NC_010473|:4043900-4043975|Trp tRNA| [gene=trpT] [locus_tag=ECDH10B_3950		
31336	3279438	3278602	TY-2482_chromosome	B7L8A6	HTH-type transcriptional regulator hdfR (H-NS-dependent flhDC regulator)	Escherichia coli (strain 55989 / EAEC)
36831	3279476	3279892	TY-2482_chromosome	Q8D1L6	Putative uncharacterized protein	Yersinia pestis
98640	3281470	3279923	TY-2482_chromosome	B7L8A8	Putative bifunctional enzyme and transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
102074	3282031	3283674	TY-2482_chromosome	B7L8B0	Acetolactate synthase (EC 2.2.1.6)	Escherichia coli (strain 55989 / EAEC)
86107	3283674	3283934	TY-2482_chromosome	B7L8A7	Acetolactate synthase II, small subunit (EC 2.2.1.6)	Escherichia coli (strain 55989 / EAEC)
61467	3283957	3284883	TY-2482_chromosome	B7L8B1	Branched-chain amino-acid aminotransferase (EC 2.6.1.42)	Escherichia coli (strain 55989 / EAEC)
31611	3284951	3286798	TY-2482_chromosome	B7L8B3	Dihydroxy-acid dehydratase (DAD) (EC 4.2.1.9)	Escherichia coli (strain 55989 / EAEC)
94665	3286804	3288345	TY-2482_chromosome	B7L8B4	Threonine deaminase (EC 4.3.1.19)	Escherichia coli (strain 55989 / EAEC)
76446	3289293	3288403	TY-2482_chromosome	B7L8B2	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
31607	3289443	3290915	TY-2482_chromosome	B7L8B5	Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydroxylacil redu	Escherichia coli (strain 55989 / EAEC)
18801	3291330	3291008	TY-2482_chromosome	E9WNG1	Ppic-type ppiase domain-containing protein	Escherichia coli E1520
108829	3291976	3291488	TY-2482_chromosome	B7L8B8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
59110	3292151	3294169	TY-2482_chromosome	B7L8B9	DNA helicase and single-stranded DNA-dependent ATPase (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
31212	3295703	3294222	TY-2482_chromosome	B7L8C0	Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase (EC 3.6.1.40) (Guanosine pentaphosphate phosphohydro	Escherichia coli (strain 55989 / EAEC)
33372	3297102	3295840	TY-2482_chromosome	B7L8B6	ATP-dependent RNA helicase rhlB (EC 3.6.4.13)	Escherichia coli (strain 55989 / EAEC)
28326	3297619	3297230	TY-2482_chromosome	A1AHV1	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
110604	3297889	3299145	TY-2482_chromosome	B7L8C4	Transcription termination factor Rho (EC 3.6.4.-) (ATP-dependent helicase Rho)	Escherichia coli (strain 55989 / EAEC)
61115	3299158	3299373	TY-2482_chromosome	B7L8C1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
112330	3299388	3300488	TY-2482_chromosome	B7L8C6	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase (EC 2.4.1.-)	Escherichia coli (strain 55989 / EAEC)

104495	3300503	3301546	TY-2482_chromosome	B7L8C7	Entobacterial Common Antigen (ECA) polysaccharide chain length modulation protein	Escherichia coli (strain 55989 / EAEC)
65286	3301605	3302732	TY-2482_chromosome	B7L8C8	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)	Escherichia coli (strain 55989 / EAEC)
106452	3302732	3303991	TY-2482_chromosome	B7L8C5	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase (EC 1.1.1.-)	Escherichia coli (strain 55989 / EAEC)
113931	3303994	3305058	TY-2482_chromosome	B7L8D0	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Escherichia coli (strain 55989 / EAEC)
113932	3305080	3305958	TY-2482_chromosome	B7L8D1	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	Escherichia coli (strain 55989 / EAEC)
102792	3305939	3306610	TY-2482_chromosome	B7L8C9	TDP-fucosamine acetyltransferase	Escherichia coli (strain 55989 / EAEC)
68623	3306618	3307745	TY-2482_chromosome	B7L8D3	TDP-4-oxo-6-deoxy-D-glucose transaminase (EC 2.6.1.-)	Escherichia coli (strain 55989 / EAEC)
115289	3307750	3308997	TY-2482_chromosome	B7L8D4	O-antigen translocase	Escherichia coli (strain 55989 / EAEC)
34572	3308997	3310073	TY-2482_chromosome	B7L8D5	4-alpha-L-fucosyltransferase (EC 2.4.1.-) (TDP-Fuc4NAc:lipid II Fuc4NAc transferase) (Fuc4NAc transferase)	Escherichia coli (strain 55989 / EAEC)
34590	3310073	3311422	TY-2482_chromosome	B7L952	Putative ECA polymerase	Escherichia coli (strain 55989 / EAEC)
34576	3311428	3312165	TY-2482_chromosome	B7L953	Probable UDP-N-acetyl-D-mannosaminuronic acid transferase (UDP-ManNAcA transferase) (EC 2.4.1.-)	Escherichia coli (strain 55989 / EAEC)
78657	3312359	3313741	TY-2482_chromosome	B7L954	Putative amino acid transporter	Escherichia coli (strain 55989 / EAEC)
r247	3313847	3313923	TY-2482_chromosome	ref|NC_010473|:4079318-4079394|Arg tRNA| [gene=argX] [locus_tag=ECDH10B_3986]		
r246	3313981	3314057	TY-2482_chromosome	ref|NC_010473|:4079452-4079528|His tRNA| [gene=hisR] [locus_tag=ECDH10B_3987]		
r210	3314078	3314164	TY-2482_chromosome	ref|NC_010473|:4650800-4650886|Leu tRNA| [gene=leuQ] [locus_tag=ECDH10B_4527]		
r245	3314207	3314283	TY-2482_chromosome	ref|NC_010473|:4079678-4079754|Pro tRNA| [gene=proM] [locus_tag=ECDH10B_3989		
97848	3314430	3315662	TY-2482_chromosome	B7L956	Regulator of arylsulfatase activity	Escherichia coli (strain 55989 / EAEC)
r109	3316335	3316506	TY-2482_chromosome	ref|NC_010473|:4083375-4083546|-| [gene=ryiA] [locus_tag=ECDH10B_3992]		
68832	3317785	3316592	TY-2482_chromosome	B7L958	Putative protoheme IX synthesis protein	Escherichia coli (strain 55989 / EAEC)
70064	3318999	3317791	TY-2482_chromosome	B7L955	Putative uroporphyrinogen III methylase (EC 2.1.1.107)	Escherichia coli (strain 55989 / EAEC)
81071	3319761	3319024	TY-2482_chromosome	B7L960	Uroporphyrinogen III synthase (EC 4.2.1.75)	Escherichia coli (strain 55989 / EAEC)
106311	3320714	3319761	TY-2482_chromosome	B5YY51	Porphobilinogen deaminase (PBG) (EC 2.5.1.61) (Hydroxymethylbilane synthase) (Pre-uroporphyrinogen synthase)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
11112	3321058	3320855	TY-2482_chromosome	D7XDC1	Conserved domain protein	Escherichia coli MS 198-1
81072	3321086	3323629	TY-2482_chromosome	B7L961	Adenylate cyclase (EC 4.6.1.1)	Escherichia coli (strain 55989 / EAEC)
66294	3325365	3324043	TY-2482_chromosome	B7L964	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
75198	3326870	3325365	TY-2482_chromosome	B7L965	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
83231	3327762	3327211	TY-2482_chromosome	B7L966	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104405	3328112	3328312	TY-2482_chromosome	B7L962	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
30551	3328352	3329173	TY-2482_chromosome	B7L969	Diaminopimelate epimerase (DAP epimerase) (EC 5.1.1.7)	Escherichia coli (strain 55989 / EAEC)
79240	3329173	3329877	TY-2482_chromosome	B7L970	Putative uncharacterized protein yigA	Escherichia coli (strain 55989 / EAEC)
34595	3329877	3330770	TY-2482_chromosome	B7L968	Tyrosine recombinase xerC	Escherichia coli (strain 55989 / EAEC)
75157	3330773	3331486	TY-2482_chromosome	B7L971	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
90810	3331573	3333732	TY-2482_chromosome	B7L973	DNA-dependent ATPase I and helicase II (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
102935	3334646	3333885	TY-2482_chromosome	B7L974	Putative uncharacterized protein yigE	Escherichia coli (strain 55989 / EAEC)
99194	3335016	3335963	TY-2482_chromosome	B7L972	Magnesium/nickel/cobalt transporter	Escherichia coli (strain 55989 / EAEC)
99195	3336499	3336011	TY-2482_chromosome	B7L976	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
83652	3337350	3336499	TY-2482_chromosome	B7L977	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
80955	3337474	3337674	TY-2482_chromosome	B7L975	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
78201	3338088	3337705	TY-2482_chromosome	C6UZV7	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
77482	3338260	3338619	TY-2482_chromosome	B7L981	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
94915	3339556	3338672	TY-2482_chromosome	B7L982	Putative chloramphenicol resistance permease	Escherichia coli (strain 55989 / EAEC)
76208	3340093	3339611	TY-2482_chromosome	D3H4V8	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
59173	3340240	3341106	TY-2482_chromosome	B7L984	Outer membrane phospholipase A (EC 3.1.1.32)	Escherichia coli (strain 55989 / EAEC)
114100	3341242	3343068	TY-2482_chromosome	B7L985	ATP-dependent DNA helicase (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
97423	3343135	3343752	TY-2482_chromosome	B7L983	Threonine efflux system	Escherichia coli (strain 55989 / EAEC)
111496	3344437	3343820	TY-2482_chromosome	B7L987	Neutral amino-acid efflux system	Escherichia coli (strain 55989 / EAEC)
77511	3344548	3345567	TY-2482_chromosome	B7L988	Lysophospholipase L(2) (EC 3.1.1.5)	Escherichia coli (strain 55989 / EAEC)
108425	3345578	3346375	TY-2482_chromosome	B7L986	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
94229	3348194	3347244	TY-2482_chromosome	B7L991	DNA-binding transcriptional activator, homocysteine-binding	Escherichia coli (strain 55989 / EAEC)
84403	3348312	3350570	TY-2482_chromosome	B7L992	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent met	Escherichia coli (strain 55989 / EAEC)
91761	3351427	3350615	TY-2482_chromosome	B7L989	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
59193	3351689	3352447	TY-2482_chromosome	B7L994	Uridine phosphorylase (EC 2.4.2.3)	Escherichia coli (strain 55989 / EAEC)
66311	3352591	3354015	TY-2482_chromosome	B7L995	Recombination limiting protein	Escherichia coli (strain 55989 / EAEC)
34433	3354113	3354865	TY-2482_chromosome	B7L996	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE (EC 2.1.1.163) (EC 2.1.1.201) (2-methoxy-6-polypreny	Escherichia coli (strain 55989 / EAEC)
79171	3354882	3355484	TY-2482_chromosome	B7L993	Putative uncharacterized protein yigP	Escherichia coli (strain 55989 / EAEC)
34421	3355484	3357121	TY-2482_chromosome	B7L998	Probable ubiquinone biosynthesis protein UbiB	Escherichia coli (strain 55989 / EAEC)
61977	3357203	3357469	TY-2482_chromosome	B7L997	Sec-independent protein translocase protein tatA/E homolog 2	Escherichia coli (strain 55989 / EAEC)
73814	3357476	3357988	TY-2482_chromosome	B7L9A0	TatABCE protein translocation system subunit	Escherichia coli (strain 55989 / EAEC)
102675	3357994	3358767	TY-2482_chromosome	B7L9A1	TatABCE protein translocation system subunit	Escherichia coli (strain 55989 / EAEC)
64109	3358800	3359591	TY-2482_chromosome	B5YY88	Deoxyribonuclease TatD (EC 3.1.21.-)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
70087	3360079	3359594	TY-2482_chromosome	B7L9A3	DNA-binding transcriptional antiterminator	Escherichia coli (strain 55989 / EAEC)
81098	3360246	3361736	TY-2482_chromosome	B7L9A4	3-octaprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.-) (Polyprenyl p-hydroxybenzoate decarboxylase)	Escherichia coli (strain 55989 / EAEC)
84404	3361785	3362483	TY-2482_chromosome	B7L999	Flavin reductase (EC 1.5.1.29)	Escherichia coli (strain 55989 / EAEC)
101925	3363841	3362681	TY-2482_chromosome	B7L9A6	3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Acetyl-CoA acyltransferase) (Beta-ketothiolase) (Fatty acid oxidation complex s	Escherichia coli (strain 55989 / EAEC)

30856	3366040	3363854	TY-2482_chromosome	B7L9A7	Fatty acid oxidation complex subunit alpha [Includes: Enoyl-CoA hydratase/Delta(3)-cis-Delta(2)-trans-enoyl-CoA ison	Escherichia coli (strain 55989 / EAEC)
32938	3366230	3367558	TY-2482_chromosome	B7L9A5	Xaa-Pro dipeptidase (X-Pro dipeptidase) (EC 3.4.13.9) (Imidodipeptidase) (Proline dipeptidase) (Prolidase	Escherichia coli (strain 55989 / EAEC)
114132	3367561	3368172	TY-2482_chromosome	B7L9A8	Putative elongation factor	Escherichia coli (strain 55989 / EAEC)
114133	3368214	3369662	TY-2482_chromosome	B7L9A9	Potassium transporter	Escherichia coli (strain 55989 / EAEC)
71430	3369677	3370219	TY-2482_chromosome	B7L9B1	Protoporphyrin oxidase, flavoprotein (EC 1.3.3.4)	Escherichia coli (strain 55989 / EAEC)
r51	3370600	3372141	TY-2482_chromosome	ref|NC_010473|:3522988-3524529|16S ribosomal RNA| [gene=rrsD] [locus_tag=ECDH10B_3453		
11305	3370746	3370513	TY-2482_chromosome	E9WNY3	Putative uncharacterized protein	Escherichia coli E1520
25826	3371721	3372038	TY-2482_chromosome	Q57H85	ORF16-lacZ fusion protein	Salmonella choleraesuis
r241	3372210	3372286	TY-2482_chromosome	ref|NC_010473|:4134084-4134160|Ile tRNA| [gene=ileT] [locus_tag=ECDH10B_4041		
r327	3372329	3372404	TY-2482_chromosome	ref|NC_010473|:4134203-4134278|Ala tRNA| [gene=alaT] [locus_tag=ECDH10B_4042		
r3	3372588	3375491	TY-2482_chromosome	ref|NC_010473|:4307762-4310665|23S ribosomal RNA| [gene=rrlE] [locus_tag=ECDH10B_4198		
24097	3373116	3372814	TY-2482_chromosome	Q1R3T8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
13803	3374377	3374174	TY-2482_chromosome	C1HUN3	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
20479	3374906	3374454	TY-2482_chromosome	C1HUN1	Cell wall-associated hydrolase (Fragment)	Escherichia sp. 3_2_53FAA
22416	3375266	3374910	TY-2482_chromosome	C1HUN0	Prolipoprotein diacylglyceryl transferase (Fragment)	Escherichia sp. 3_2_53FAA
r127	3375585	3375704	TY-2482_chromosome	ref|NC_010473|:4043643-4043762|5S ribosomal RNA| [gene=rrfC] [locus_tag=ECDH10B_3948		
27250	3375761	3375470	TY-2482_chromosome	Q1R8D8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
89007	3376334	3375810	TY-2482_chromosome	C8UKB4	Molybdopterin-guanine dinucleotide biosynthesis protein B	Escherichia coli O111:H- (strain 11128 / EHEC
90952	3376900	3376319	TY-2482_chromosome	B7L9B3	Molybdopterin-guanine dinucleotide biosynthesis protein A	Escherichia coli (strain 55989 / EAEC)
66312	3376970	3377236	TY-2482_chromosome	B7L9B4	Putative uncharacterized protein yihD	Escherichia coli (strain 55989 / EAEC)
88377	3377316	3378299	TY-2482_chromosome	B7L9B0	Putative kinase	Escherichia coli (strain 55989 / EAEC)
60861	3378319	3378942	TY-2482_chromosome	B7L9B6	Thiol:disulfide interchange protein DsbA	Escherichia coli (strain 55989 / EAEC)
114008	3379100	3380527	TY-2482_chromosome	B7L9B7	Putative uncharacterized protein yihF	Escherichia coli (strain 55989 / EAEC)
67805	3381503	3380574	TY-2482_chromosome	B7L9B8	Putative endonuclease	Escherichia coli (strain 55989 / EAEC)
81100	3381867	3384650	TY-2482_chromosome	B7L9B5	Fused DNA polymerase I 5'->3' exonuclease ; 3'->5' polymerase ; 3'->5' exonuclease (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
r191	3384801	3384909	TY-2482_chromosome	ref|NC_010473|:4146842-4146950|-| [gene=spf] [locus_tag=ECDH10B_4053		
1418	3385685	3385038	TY-2482_chromosome	A1AI47	Probable GTP-binding protein EngB	Escherichia coli O1:K1 / APEC
r103	3385938	3386182	TY-2482_chromosome	ref|NC_010473|:4147979-4148223|-| [gene=csrC] [locus_tag=ECDH10B_4055		
26222	3385939	3385706	TY-2482_chromosome	B6I4K2	Putative uncharacterized protein	Escherichia coli (strain SE11)
34992	3386249	3386755	TY-2482_chromosome	B7L9B9	Der GTPase-activating protein YihI	Escherichia coli (strain 55989 / EAEC)
83656	3386947	3388317	TY-2482_chromosome	B7L9C1	Coproporphyrinogen III oxidase, SAM and NAD(P)H dependent, oxygen-independent	Escherichia coli (strain 55989 / EAEC)
72623	3390141	3388735	TY-2482_chromosome	B7L9C2	Fused DNA-binding response regulator in two-component regulatory system with GlnL: response regulator ; sigma54	Escherichia coli (strain 55989 / EAEC)
95363	3391202	3390156	TY-2482_chromosome	B7L9C3	Sensory histidine kinase in two-component regulatory system with GlnG	Escherichia coli (strain 55989 / EAEC)
81101	3392897	3391491	TY-2482_chromosome	B7L9C4	Glutamine synthetase (EC 6.3.1.2)	Escherichia coli (strain 55989 / EAEC)
65751	3393270	3395090	TY-2482_chromosome	B7L9C6	GTP-binding protein	Escherichia coli (strain 55989 / EAEC)
27109	3393298	3392879	TY-2482_chromosome	B5BJ09	Putative cytoplasmic protein	Salmonella paratyphi A (strain AKU_12601)
69226	3395310	3396017	TY-2482_chromosome	B7L9C7	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
108560	3396028	3397005	TY-2482_chromosome	B7L9C5	Putative sugar phosphate isomerase	Escherichia coli (strain 55989 / EAEC)
58640	3397110	3398372	TY-2482_chromosome	B7L9C9	Putative transporter	Escherichia coli (strain 55989 / EAEC)
62125	3399274	3398489	TY-2482_chromosome	B7L9C8	Putative DEOR-type transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
61733	3400182	3401258	TY-2482_chromosome	B7L9D2	Putative oxidoreductase with NAD(P)-binding Rossmann-fold domain, putative 3-hydroxyisobutyrate dehydrogenase	Escherichia coli (strain 55989 / EAEC)
68467	3400249	3399317	TY-2482_chromosome	B7L9D1	Putative sugar kinase (EC 2.7.1.-)	Escherichia coli (strain 55989 / EAEC)
75621	3401286	3402170	TY-2482_chromosome	B7L9D0	Putative aldolase yihT (EC 4.1.2.40)	Escherichia coli (strain 55989 / EAEC)
61379	3402206	3403213	TY-2482_chromosome	B7L9D4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
106337	3403286	3404716	TY-2482_chromosome	B7L9D5	Putative transporter	Escherichia coli (strain 55989 / EAEC)
95536	3404818	3406164	TY-2482_chromosome	B7L9D3	Putative transport protein (Shikimate homolog)	Escherichia coli (strain 55989 / EAEC)
88476	3406100	3407041	TY-2482_chromosome	B7L9D7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
93027	3407164	3407781	TY-2482_chromosome	D3H517	Phosphatase (EC 3.1.3.-)	Escherichia coli O44:H18 (strain 042 / EAEC)
34997	3407778	3408647	TY-2482_chromosome	B7L9D9	UPF0761 membrane protein yihY	Escherichia coli (strain 55989 / EAEC)
30680	3408647	3409081	TY-2482_chromosome	B7L9D6	D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
87788	3409081	3410067	TY-2482_chromosome	B7L9E1	Putative acetyltransferase	Escherichia coli (strain 55989 / EAEC)
62838	3411117	3410137	TY-2482_chromosome	B7L9E2	Putative lipase	Escherichia coli (strain 55989 / EAEC)
66313	3411271	3411579	TY-2482_chromosome	B7L9E0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
112987	3411583	3411870	TY-2482_chromosome	B7L9E4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
67631	3412432	3412674	TY-2482_chromosome	D3H522	CopG-family DNA-binding protein	Escherichia coli O44:H18 (strain 042 / EAEC)
45251	3412897	3413136	TY-2482_chromosome	D8ET41	Toxin-antitoxin system protein	Escherichia coli MS 107-1
30923	3414398	3413472	TY-2482_chromosome	B7L9E7	Protein FdhE	Escherichia coli (strain 55989 / EAEC)
102232	3415030	3414398	TY-2482_chromosome	B7L9E8	Formate dehydrogenase-O, cytochrome b556 subunit	Escherichia coli (strain 55989 / EAEC)
76036	3415929	3415030	TY-2482_chromosome	B7L9E9	Formate dehydrogenase-O, Fe-S subunit	Escherichia coli (strain 55989 / EAEC)
110656	3418992	3415945	TY-2482_chromosome	B7L9E5	Formate dehydrogenase-O, large subunit (EC 1.2.1.2)	Escherichia coli (strain 55989 / EAEC)
30919	3419186	3420016	TY-2482_chromosome	B7L9F1	Protein FdhD	Escherichia coli (strain 55989 / EAEC)
73708	3420172	3421209	TY-2482_chromosome	B7L9F2	Putative uncharacterized protein yiiG	Escherichia coli (strain 55989 / EAEC)
89945	3423010	3421265	TY-2482_chromosome	B7L9F0	Putative regulator	Escherichia coli (strain 55989 / EAEC)
86183	3424080	3423013	TY-2482_chromosome	B7L9F4	Putative endo-1,4-beta-glucanase	Escherichia coli (strain 55989 / EAEC)

91878	3425521	3424073	TY-2482_chromosome	B7L9F5	Fused putative PTS enzymes: IIB component ; IIC component	Escherichia coli (strain 55989 / EAEC)
76835	3425978	3425535	TY-2482_chromosome	B7L9F6	Enzyme IIA component of PTS	Escherichia coli (strain 55989 / EAEC)
33353	3426605	3426294	TY-2482_chromosome	B7L9F7	L-rhamnose mutarotase (EC 5.1.3.n3) (Rhamnose 1-epimerase) (Type-3 mutarotase)	Escherichia coli (strain 55989 / EAEC)
33349	3427439	3426618	TY-2482_chromosome	B7L9F8	Rhamnulose-1-phosphate aldolase (EC 4.1.2.19)	Escherichia coli (strain 55989 / EAEC)
33341	3428940	3427684	TY-2482_chromosome	B7L9F3	L-rhamnose isomerase (EC 5.3.1.14)	Escherichia coli (strain 55989 / EAEC)
33345	3430406	3428940	TY-2482_chromosome	B7L9G0	Rhamnulokinase (EC 2.7.1.5) (Rhamnulose kinase)	Escherichia coli (strain 55989 / EAEC)
33361	3430694	3431527	TY-2482_chromosome	B7L9G1	HTH-type transcriptional activator rhaS (L-rhamnose operon regulatory protein rhaS	Escherichia coli (strain 55989 / EAEC)
109867	3431514	3432449	TY-2482_chromosome	B7L9G2	DNA-binding transcriptional activator, L-rhamnose-binding	Escherichia coli (strain 55989 / EAEC)
33369	3433483	3432452	TY-2482_chromosome	B7L9F9	L-rhamnose-proton symporter (L-rhamnose-H(+) transport protein)	Escherichia coli (strain 55989 / EAEC)
75078	3433762	3434385	TY-2482_chromosome	D3GRW3	Superoxide dismutase (EC 1.15.1.1)	Escherichia coli O44:H18 (strain 042 / EAEC)
113479	3434648	3435628	TY-2482_chromosome	C6V0W7	2-keto-3-deoxygluconate permease (KDG permease)	Escherichia coli O157:H7 (strain TW14359 / EHEC
72130	3435750	3436451	TY-2482_chromosome	D3GRW5	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
75448	3437933	3436563	TY-2482_chromosome	B7L9G7	Sensory histidine kinase in two-component regulatory system with CpxR	Escherichia coli (strain 55989 / EAEC)
84572	3438628	3437933	TY-2482_chromosome	B7L9G3	DNA-binding response regulator in two-component regulatory system with CpxA	Escherichia coli (strain 55989 / EAEC)
73668	3438778	3439275	TY-2482_chromosome	B7L8D2	Periplasmic protein combats stress	Escherichia coli (strain 55989 / EAEC)
30939	3439427	3440326	TY-2482_chromosome	B7LA12	Ferrous-iron efflux pump FieF	Escherichia coli (strain 55989 / EAEC)
31713	3440510	3441469	TY-2482_chromosome	B7LA13	6-phosphofructokinase (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Escherichia coli (strain 55989 / EAEC)
19005	3441512	3441728	TY-2482_chromosome	E1IUI5	Putative uncharacterized protein	Escherichia coli MS 145-7
91907	3441792	3442778	TY-2482_chromosome	B7LA14	Sulfate transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
30275	3442888	3443640	TY-2482_chromosome	B7LA15	CDP-diacylglycerol pyrophosphatase (EC 3.6.1.26) (CDP-diacylglycerol phosphatidylhydrolase) (CDP-diglyceride hydro	Escherichia coli (strain 55989 / EAEC)
94822	3444465	3443701	TY-2482_chromosome	B7LA16	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Escherichia coli (strain 55989 / EAEC)
95585	3445172	3444576	TY-2482_chromosome	B7LA11	Putative uncharacterized protein yiiQ	Escherichia coli (strain 55989 / EAEC)
104788	3445273	3445710	TY-2482_chromosome	B7LA18	Putative uncharacterized protein yiiR	Escherichia coli (strain 55989 / EAEC)
91909	3445925	3446221	TY-2482_chromosome	B7LA19	Putative uncharacterized protein yiiS	Escherichia coli (strain 55989 / EAEC)
114048	3446251	3446676	TY-2482_chromosome	B7LA20	Stress-induced protein	Escherichia coli (strain 55989 / EAEC)
86941	3447430	3446687	TY-2482_chromosome	B7LA17	Ferredoxin-NADP reductase (EC 1.18.1.2)	Escherichia coli (strain 55989 / EAEC)
69400	3448537	3447530	TY-2482_chromosome	B7LA22	Fructose 1,6-bisphosphatase II (EC 3.1.3.11)	Escherichia coli (strain 55989 / EAEC)
31168	3450181	3448676	TY-2482_chromosome	B7LA23	Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase) (GK)	Escherichia coli (strain 55989 / EAEC)
113402	3451049	3450207	TY-2482_chromosome	B7LA24	Glycerol facilitator	Escherichia coli (strain 55989 / EAEC)
35079	3451475	3451717	TY-2482_chromosome	B7LA21	Cell division protein ZapB	Escherichia coli (strain 55989 / EAEC)
28643	3451862	3452365	TY-2482_chromosome	A1AIA4	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
87762	3453321	3452386	TY-2482_chromosome	B5YZ70	1,4-dihydroxy-2-naphthoate octaprenyltransferase (EC 2.5.1.-)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
31547	3454707	3453379	TY-2482_chromosome	B7LA28	ATP-dependent protease ATPase subunit HslU (Heat shock protein HslU) (Unfoldase HslU)	Escherichia coli (strain 55989 / EAEC)
31551	3455247	3454720	TY-2482_chromosome	B7LA29	ATP-dependent protease subunit HslV (EC 3.4.25.2) (Heat shock protein HslV)	Escherichia coli (strain 55989 / EAEC)
62741	3456299	3455343	TY-2482_chromosome	B7LA30	Essential cell division protein	Escherichia coli (strain 55989 / EAEC)
91255	3457416	3456394	TY-2482_chromosome	B7LA31	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
88401	3459770	3457575	TY-2482_chromosome	B7LA32	Primosome factor n' (Replication factor Y)	Escherichia coli (strain 55989 / EAEC)
33529	3459973	3460182	TY-2482_chromosome	B7LA33	50S ribosomal protein L31	Escherichia coli (strain 55989 / EAEC)
59133	3460345	3464526	TY-2482_chromosome	B7LA34	RhsB element core protein RshB	Escherichia coli (strain 55989 / EAEC)
95743	3464531	3464764	TY-2482_chromosome	C6V0Z8	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
75128	3465538	3465828	TY-2482_chromosome	C8UKJ8	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC
14258	3465615	3464826	TY-2482_chromosome	Q0H058	IS1N transposase	Escherichia coli
97634	3466367	3465763	TY-2482_chromosome	B5YZ79	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
32275	3466744	3466430	TY-2482_chromosome	B7LA39	Met repressor (Met regulon regulatory protein metJ)	Escherichia coli (strain 55989 / EAEC)
64140	3467021	3468178	TY-2482_chromosome	B7LA40	Cystathionine gamma-synthase, PLP-dependent (EC 2.5.1.48)	Escherichia coli (strain 55989 / EAEC)
102906	3468184	3470613	TY-2482_chromosome	B7LA41	Fused aspartokinase II ; homoserine dehydrogenase II (EC 1.1.1.3) (EC 2.7.2.4)	Escherichia coli (strain 55989 / EAEC)
105528	3470965	3471852	TY-2482_chromosome	B7LA42	Methylenetetrahydrofolate reductase (EC 1.5.1.20)	Escherichia coli (strain 55989 / EAEC)
73624	3472184	3474361	TY-2482_chromosome	B7LA43	Catalase-peroxidase (CP) (EC 1.11.1.6) (EC 1.11.1.7) (Peroxidase/catalase)	Escherichia coli (strain 55989 / EAEC)
94189	3474425	3475360	TY-2482_chromosome	D3GS01	Putative membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
77567	3476007	3475393	TY-2482_chromosome	B7LA45	Putative uncharacterized protein yijF	Escherichia coli (strain 55989 / EAEC)
68512	3477385	3476285	TY-2482_chromosome	B7LA46	Glycerol dehydrogenase, NAD (EC 1.1.1.6)	Escherichia coli (strain 55989 / EAEC)
83730	3478058	3477399	TY-2482_chromosome	B7LA47	Probable fructose-6-phosphate aldolase 2 (EC 4.1.2.-)	Escherichia coli (strain 55989 / EAEC)
114010	3480571	3478073	TY-2482_chromosome	B7LA48	Fused putative PTS enzymes: Hpr component ; enzyme I component ; enzyme IIA component (EC 2.7.1.69) (EC 2.7.3.	Escherichia coli (strain 55989 / EAEC)
91912	3480880	3481956	TY-2482_chromosome	B7LA49	Enzyme IIC component of PTS	Escherichia coli (strain 55989 / EAEC)
95546	3481974	3482291	TY-2482_chromosome	B7LA44	Putative enzyme IIB component of PTS	Escherichia coli (strain 55989 / EAEC)
62677	3482345	3484639	TY-2482_chromosome	B7LA51	Putative formate acetyltransferase 2 (Pyruvate formate lyase II)	Escherichia coli (strain 55989 / EAEC)
76833	3484608	3485483	TY-2482_chromosome	B7LA52	Pyruvate formate lyase II activase	Escherichia coli (strain 55989 / EAEC)
84587	3485488	3485826	TY-2482_chromosome	B7LA53	Enzyme IIB component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
59113	3486667	3485819	TY-2482_chromosome	B7LA50	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
86963	3488615	3486885	TY-2482_chromosome	B7LA55	Putative uncharacterized protein yijP	Escherichia coli (strain 55989 / EAEC)
30241	3491449	3488801	TY-2482_chromosome	B7LA56	Phosphoenolpyruvate carboxylase (PEPC) (PEPCase) (EC 4.1.1.31)	Escherichia coli (strain 55989 / EAEC)
29834	3492952	3491804	TY-2482_chromosome	B7LA57	Acetylornithine deacetylase (AO) (Acetylornithinase) (EC 3.5.1.16) (N-acetylornithinase) (NAO)	Escherichia coli (strain 55989 / EAEC)
65421	3493106	3494107	TY-2482_chromosome	B7LA58	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acetyl-glutamate semialdehyde dehydrogena	Escherichia coli (strain 55989 / EAEC)
94763	3494118	3494891	TY-2482_chromosome	C6V122	Acetylglutamate kinase (EC 2.7.2.8) (N-acetyl-L-glutamate 5-phosphotransferase) (NAG kinase)	Escherichia coli O157:H7 (strain TW14359 / EHEC

29855	3494955	3496325	TY-2482_chromosome	B7LA60	Argininosuccinate lyase (ASAL) (EC 4.3.2.1) (Arginosuccinase)	Escherichia coli (strain 55989 / EAEC)
62629	3496826	3498037	TY-2482_chromosome	B7LA61	Putative enolase/dehydratase	Escherichia coli (strain 55989 / EAEC)
114055	3498107	3499387	TY-2482_chromosome	B7LA59	Putative transporter	Escherichia coli (strain 55989 / EAEC)
r190	3499545	3499436	TY-2482_chromosome	ref|NC_010473|:4256005-4256114|-| [gene=oxyS] [locus_tag=ECDH10B_4149]		
99032	3499641	3500555	TY-2482_chromosome	B7LA63	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
34027	3501941	3500544	TY-2482_chromosome	B7LA64	Soluble pyridine nucleotide transhydrogenase (STH) (EC 1.6.1.1) (NAD(P)(+) transhydrogenase [B-specific]	Escherichia coli (strain 55989 / EAEC)
70017	3502218	3502919	TY-2482_chromosome	B7LA62	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
102908	3502922	3503278	TY-2482_chromosome	B7LA66	Putative uncharacterized protein yijD	Escherichia coli (strain 55989 / EAEC)
34323	3504421	3503324	TY-2482_chromosome	B7LA67	tRNA (uracil-5-)-methyltransferase (EC 2.1.1.35) (tRNA(M-5-U54)-methyltransferase) (RUMT)	Escherichia coli (strain 55989 / EAEC)
110404	3504790	3506631	TY-2482_chromosome	B7LA68	Vitamin B12/cobalamin outer membrane transporter	Escherichia coli (strain 55989 / EAEC)
32558	3506579	3507433	TY-2482_chromosome	B7LA65	Glutamate racemase (EC 5.1.1.3)	Escherichia coli (strain 55989 / EAEC)
r52	3507810	3509351	TY-2482_chromosome	ref|NC_010473|:3522988-3524529|16S ribosomal RNA| [gene=rrsD] [locus_tag=ECDH10B_3453		
11303	3507956	3507723	TY-2482_chromosome	E9WNY3	Putative uncharacterized protein	Escherichia coli E1520
25828	3508931	3509248	TY-2482_chromosome	Q57H85	ORF16-lacZ fusion protein	Salmonella choleraesuis
r242	3509420	3509496	TY-2482_chromosome	ref|NC_010473|:4134084-4134160|Ile tRNA| [gene=ileT] [locus_tag=ECDH10B_4041]		
r328	3509539	3509614	TY-2482_chromosome	ref|NC_010473|:4134203-4134278|Ala tRNA| [gene=alaT] [locus_tag=ECDH10B_4042]		
r5	3509798	3512701	TY-2482_chromosome	ref|NC_010473|:4307762-4310665|23S ribosomal RNA| [gene=rrlE] [locus_tag=ECDH10B_4198		
24096	3510326	3510024	TY-2482_chromosome	Q1R3T8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
13798	3511587	3511384	TY-2482_chromosome	C1HUN3	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
20475	3512116	3511664	TY-2482_chromosome	C1HUN1	Cell wall-associated hydrolase (Fragment)	Escherichia sp. 3_2_53FAA
22414	3512476	3512120	TY-2482_chromosome	C1HUN0	Prolipoprotein diacylglyceryl transferase (Fragment)	Escherichia sp. 3_2_53FAA
r129	3512795	3512914	TY-2482_chromosome	ref|NC_010473|:4043643-4043762|5S ribosomal RNA| [gene=rrfC] [locus_tag=ECDH10B_3948		
19524	3513082	3512759	TY-2482_chromosome	C5WBP6	Ybl209	Escherichia coli (strain B / BL21)
76152	3513215	3514240	TY-2482_chromosome	B7LA70	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158) (UDP-N-acetylmuramate dehydrogenase)	Escherichia coli (strain 55989 / EAEC)
99145	3514240	3515202	TY-2482_chromosome	B7LA71	Bifunctional biotin-[acetylCoA carboxylase] holoenzyme synthetase and DNA-binding transcriptional repressor, bio-5'	Escherichia coli (strain 55989 / EAEC)
80784	3516167	3516358	TY-2482_chromosome	B5Z075	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
30358	3516184	3515237	TY-2482_chromosome	B7LA72	Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase)	Escherichia coli (strain 55989 / EAEC)
r323	3516546	3516621	TY-2482_chromosome	ref|NC_010473|:4273107-4273182|Thr tRNA| [gene=thrU] [locus_tag=ECDH10B_4164		
r229	3516630	3516714	TY-2482_chromosome	ref|NC_010473|:4273191-4273275|Tyr tRNA| [gene=tyrU] [locus_tag=ECDH10B_4165]		
r476	3516831	3516905	TY-2482_chromosome	ref|NC_010473|:4273392-4273466|Gly tRNA| [gene=glyT] [locus_tag=ECDH10B_4166]		
r321	3516912	3516987	TY-2482_chromosome	ref|NC_010473|:4273473-4273548|Thr tRNA| [gene=thrT] [locus_tag=ECDH10B_4167		
61645	3517102	3518283	TY-2482_chromosome	B7LA73	Elongation factor Tu 2 (EF-Tu 2)	Escherichia coli (strain 55989 / EAEC)
61969	3518516	3518896	TY-2482_chromosome	B7LA69	Preprotein translocase membrane subunit	Escherichia coli (strain 55989 / EAEC)
113097	3518901	3519443	TY-2482_chromosome	B7LA75	Transcription antitermination protein nusG	Escherichia coli (strain 55989 / EAEC)
25342	3520552	3519554	TY-2482_chromosome	A1AIF6	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
16023	3520864	3520673	TY-2482_chromosome	D6JHU1	Putative uncharacterized protein (Fragment)	Escherichia coli B354
33452	3521154	3521648	TY-2482_chromosome	B7LA78	50S ribosomal protein L10	Escherichia coli (strain 55989 / EAEC)
24697	3522209	3521706	TY-2482_chromosome	E1PAV1	50S ribosomal protein L7/L12	Escherichia coli OR:K5:H- (strain ABU 83972)
33667	3522403	3526428	TY-2482_chromosome	B7LA80	DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcr	Escherichia coli (strain 55989 / EAEC)
62124	3526508	3530728	TY-2482_chromosome	B7LA76	DNA-directed RNA polymerase (EC 2.7.7.6)	Escherichia coli (strain 55989 / EAEC)
70018	3530944	3531480	TY-2482_chromosome	B7LA82	Heat shock protein	Escherichia coli (strain 55989 / EAEC)
91916	3533026	3531896	TY-2482_chromosome	B7LA83	Thiamin biosynthesis ThiGH complex subunit	Escherichia coli (strain 55989 / EAEC)
82508	3533838	3533026	TY-2482_chromosome	B5Z086	Thiazole synthase (EC 4.-.-.-)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
99146	3533995	3533798	TY-2482_chromosome	B7LA81	Sulphur carrier protein	Escherichia coli (strain 55989 / EAEC)
91917	3534734	3533982	TY-2482_chromosome	B7LA86	Thiamin (Thiazole moiety) biosynthesis protein (EC 2.7.7.-)	Escherichia coli (strain 55989 / EAEC)
72895	3535362	3534730	TY-2482_chromosome	B7LA87	Thiamine-phosphate pyrophosphorylase (TMP pyrophosphorylase) (TMP-PPase) (EC 2.5.1.3) (Thiamine-phosphate sy	Escherichia coli (strain 55989 / EAEC)
34244	3537257	3535365	TY-2482_chromosome	B7LA88	Phosphomethylpyrimidine synthase (EC 4.-.-.-) (Hydroxymethylpyrimidine phosphate synthase) (HMP-P synthase) (HN	Escherichia coli (strain 55989 / EAEC)
33774	3537966	3537493	TY-2482_chromosome	B7LA89	Regulator of sigma D	Escherichia coli (strain 55989 / EAEC)
32727	3538061	3538831	TY-2482_chromosome	B7LA85	NADH pyrophosphatase (EC 3.6.1.22)	Escherichia coli (strain 55989 / EAEC)
30569	3538874	3539935	TY-2482_chromosome	B7LA91	Uroporphyrinogen decarboxylase (UPD) (URO-D) (EC 4.1.1.37)	Escherichia coli (strain 55989 / EAEC)
32647	3539948	3540616	TY-2482_chromosome	B7LA92	Endonuclease V (EC 3.1.21.7) (Deoxyinosine 3'endonuclease) (Deoxyribonuclease V) (DNase V)	Escherichia coli (strain 55989 / EAEC)
95600	3540662	3541249	TY-2482_chromosome	B7LA93	Putative uncharacterized protein yjaG	Escherichia coli (strain 55989 / EAEC)
62775	3541439	3541708	TY-2482_chromosome	B7LA94	HU, DNA-binding transcriptional regulator, alpha subunit	Escherichia coli (strain 55989 / EAEC)
115730	3541718	3542416	TY-2482_chromosome	D3GSY0	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
25327	3542987	3542424	TY-2482_chromosome	B2TWI9	Zinc resistance-associated protein	Shigella boydii serotype 18 (strain CDC 3083-94 / BS512)
79101	3543084	3544457	TY-2482_chromosome	B7LAV0	Sensory histidine kinase in two-component regulatory system with ZraR	Escherichia coli (strain 55989 / EAEC)
102923	3544457	3545779	TY-2482_chromosome	B7LAU9	Fused DNA-binding response regulator in two-component regulatory system with ZraS: response regulator ; sigma54	Escherichia coli (strain 55989 / EAEC)
62808	3547068	3545782	TY-2482_chromosome	B7LAV2	Phosphoribosylglycinamide synthetase phosphoribosylamine-glycine ligase (EC 6.3.4.13)	Escherichia coli (strain 55989 / EAEC)
33151	3548669	3547083	TY-2482_chromosome	B7LAV3	Bifunctional purine biosynthesis protein purH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransfera	Escherichia coli (strain 55989 / EAEC)
11538	3548945	3548745	TY-2482_chromosome	D6JHW4	Putative uncharacterized protein	Escherichia coli B354
r53	3549284	3550825	TY-2482_chromosome	ref|NC_010473|:3522988-3524529|16S ribosomal RNA| [gene=rrsD] [locus_tag=ECDH10B_3453		
11302	3549430	3549197	TY-2482_chromosome	E9WNY3	Putative uncharacterized protein	Escherichia coli E1520
25829	3550405	3550722	TY-2482_chromosome	Q57H85	ORF16-lacZ fusion protein	Salmonella choleraesuis
r243	3550894	3550970	TY-2482_chromosome	ref|NC_010473|:4134084-4134160|Ile tRNA| [gene=ileT] [locus_tag=ECDH10B_4041]		

r329	3551013	3551088	TY-2482_chromosome	ref|NC_010473|:4134203-4134278|Ala tRNA| [gene=alaT] [locus_tag=ECDH10B_4042		
r6	3551272	3554175	TY-2482_chromosome	ref|NC_010473|:4307762-4310665|23S ribosomal RNA| [gene=rrlE] [locus_tag=ECDH10B_4198		
24095	3551800	3551498	TY-2482_chromosome	Q1R3T8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
13804	3553061	3552858	TY-2482_chromosome	C1HUN3	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
20474	3553590	3553138	TY-2482_chromosome	C1HUN1	Cell wall-associated hydrolase (Fragment)	Escherichia sp. 3_2_53FAA
22413	3553950	3553594	TY-2482_chromosome	C1HUN0	Prolipoprotein diacylglyceryl transferase (Fragment)	Escherichia sp. 3_2_53FAA
r130	3554269	3554388	TY-2482_chromosome	ref|NC_010473|:4043643-4043762|5S ribosomal RNA| [gene=rrfC] [locus_tag=ECDH10B_3948		
27249	3554478	3554154	TY-2482_chromosome	Q1R8D8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
77460	3554947	3554507	TY-2482_chromosome	B7LAV4	Putative acetyltransferase	Escherichia coli (strain 55989 / EAEC)
32266	3555104	3556030	TY-2482_chromosome	B7LAV1	Homoserine O-succinyltransferase (EC 2.3.1.46) (Homoserine O-transsuccinylase) (HTS)	Escherichia coli (strain 55989 / EAEC)
72896	3556302	3557900	TY-2482_chromosome	B7LAV5	Malate synthase (EC 2.3.3.9)	Escherichia coli (strain 55989 / EAEC)
102915	3557933	3559234	TY-2482_chromosome	B7LAV7	Isocitrate lyase (EC 4.1.3.1)	Escherichia coli (strain 55989 / EAEC)
27951	3559306	3559539	TY-2482_chromosome	A7ZUM9	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
29686	3559518	3561251	TY-2482_chromosome	B7LAV8	Isocitrate dehydrogenase kinase/phosphatase (IDH kinase/phosphatase) (IDHK/P) (EC 2.7.11.5) (EC 3.1.3.-)	Escherichia coli (strain 55989 / EAEC)
116140	3562797	3561226	TY-2482_chromosome	C8UKR4	T3SS effector-like protein EspL-homolog	Escherichia coli O111:H- (strain 11128 / EHEC
87831	3563938	3563117	TY-2482_chromosome	B7LAV9	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
101837	3564138	3567818	TY-2482_chromosome	B7LAW1	Homocysteine-N5-methyltetrahydrofolate transmethylase, B12-dependent (EC 2.1.1.13)	Escherichia coli (strain 55989 / EAEC)
64098	3568041	3569669	TY-2482_chromosome	B7LAW2	Putative transporter	Escherichia coli (strain 55989 / EAEC)
32934	3570452	3569766	TY-2482_chromosome	B7LAW3	Peptidase E (EC 3.4.13.21) (Alpha-aspartyl dipeptidase) (Asp-specific dipeptidase) (Dipeptidase E)	Escherichia coli (strain 55989 / EAEC)
94907	3570664	3571533	TY-2482_chromosome	B7LAW0	Pseudouridine synthase (EC 5.4.99.-)	Escherichia coli (strain 55989 / EAEC)
110422	3571809	3571540	TY-2482_chromosome	B7LAW5	Putative uncharacterized protein yjbD	Escherichia coli (strain 55989 / EAEC)
21516	3572327	3572133	TY-2482_chromosome	D8EA79	Putative uncharacterized protein	Escherichia coli MS 119-7
112313	3572338	3573462	TY-2482_chromosome	B7LAW6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
110423	3573462	3574259	TY-2482_chromosome	B7LAW7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73749	3575230	3574301	TY-2482_chromosome	B7LAW4	Putative zeta toxin; poison-antidote element	Escherichia coli (strain 55989 / EAEC)
114078	3576718	3575372	TY-2482_chromosome	B7LAW9	Aspartokinase (EC 2.7.2.4)	Escherichia coli (strain 55989 / EAEC)
31059	3577243	3578889	TY-2482_chromosome	B7LAX0	Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PH	Escherichia coli (strain 55989 / EAEC)
24900	3579518	3579231	TY-2482_chromosome	B7MRF8	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
72276	3579603	3580238	TY-2482_chromosome	B7LAX2	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
110424	3580238	3580972	TY-2482_chromosome	B7LAW8	Putative uncharacterized protein yjbG	Escherichia coli (strain 55989 / EAEC)
114014	3580975	3583068	TY-2482_chromosome	B7LAX4	Putative porin	Escherichia coli (strain 55989 / EAEC)
68714	3583396	3583121	TY-2482_chromosome	B7LAX6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
33102	3583666	3584073	TY-2482_chromosome	B7LAX3	Protein psiE	Escherichia coli (strain 55989 / EAEC)
80070	3585595	3584123	TY-2482_chromosome	B7LAX8	D-xylose transporter	Escherichia coli (strain 55989 / EAEC)
97490	3586857	3585970	TY-2482_chromosome	B7LAX9	Maltose transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
107974	3588416	3586875	TY-2482_chromosome	B7LAX7	Maltose transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
106531	3589760	3588573	TY-2482_chromosome	B7LAY1	Maltose transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
68595	3590125	3591237	TY-2482_chromosome	B7LAY2	Fused maltose transport subunit, ATP-binding component of ABC superfamily ; regulatory protein	Escherichia coli (strain 55989 / EAEC)
31816	3591312	3592649	TY-2482_chromosome	B7LAY3	Maltoporin (Maltose-inducible porin)	Escherichia coli (strain 55989 / EAEC)
67705	3592804	3593721	TY-2482_chromosome	B7LAY4	Maltose regulon periplasmic protein	Escherichia coli (strain 55989 / EAEC)
70060	3594205	3595530	TY-2482_chromosome	B7LAY0	Putative uncharacterized protein yjbI	Escherichia coli (strain 55989 / EAEC)
34425	3595756	3596250	TY-2482_chromosome	B7LAY7	Chorismate--pyruvate lyase (CL) (CPL) (EC 4.1.3.40)	Escherichia coli (strain 55989 / EAEC)
34417	3596266	3597135	TY-2482_chromosome	B7LAY8	4-hydroxybenzoate octaprenyltransferase (EC 2.5.1.-) (4-HB polyprenyltransferase)	Escherichia coli (strain 55989 / EAEC)
33009	3599716	3597296	TY-2482_chromosome	B7LAY9	Glycerol-3-phosphate acyltransferase (GPAT) (EC 2.3.1.15)	Escherichia coli (strain 55989 / EAEC)
60467	3599887	3600252	TY-2482_chromosome	B7LAY6	Diacylglycerol kinase (EC 2.7.1.107)	Escherichia coli (strain 55989 / EAEC)
31873	3600365	3600970	TY-2482_chromosome	B7LAZ0	LexA repressor (EC 3.4.21.88)	Escherichia coli (strain 55989 / EAEC)
84612	3600992	3602389	TY-2482_chromosome	B7LAZ2	DNA-damage-inducible SOS response protein	Escherichia coli (strain 55989 / EAEC)
71280	3602482	3602694	TY-2482_chromosome	D3GT26	Putative general stress response protein	Escherichia coli O44:H18 (strain 042 / EAEC)
66282	3603254	3602742	TY-2482_chromosome	B7LAZ1	DNA-binding transcriptional repressor, Zn(II)-binding	Escherichia coli (strain 55989 / EAEC)
20878	3603572	3604560	TY-2482_chromosome	D6I3T6	YjbM protein	Escherichia coli B088
112870	3604927	3605961	TY-2482_chromosome	B7LAZ7	tRNA-dihydrouridine synthase (EC 1.-.-.-)	Escherichia coli (strain 55989 / EAEC)
80273	3605888	3606337	TY-2482_chromosome	B7LAZ8	Putative uncharacterized protein yjbO	Escherichia coli (strain 55989 / EAEC)
73750	3607489	3606509	TY-2482_chromosome	B7LAZ9	Quinone oxidoreductase, NADPH-dependent (EC 1.6.5.5)	Escherichia coli (strain 55989 / EAEC)
95547	3607572	3608984	TY-2482_chromosome	B7LB00	Replicative DNA helicase (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
76396	3609040	3610116	TY-2482_chromosome	B7LB01	Alanine racemase 2 (EC 5.1.1.1)	Escherichia coli (strain 55989 / EAEC)
106532	3610372	3611562	TY-2482_chromosome	B7LAZ6	Tyrosine aminotransferase, tyrosine-repressible, PLP-dependent (EC 2.6.1.57)	Escherichia coli (strain 55989 / EAEC)
75619	3612329	3611790	TY-2482_chromosome	B7LB03	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28638	3612452	3613402	TY-2482_chromosome	Q0SXS2	Diadenosine tetraphosphatase	Shigella flexneri serotype 5b (strain 8401)
106534	3613516	3613929	TY-2482_chromosome	B7LB05	Putative uncharacterized protein yjbQ	Escherichia coli (strain 55989 / EAEC)
93928	3613936	3614289	TY-2482_chromosome	B7LB06	Putative uncharacterized protein yjbR	Escherichia coli (strain 55989 / EAEC)
61544	3617149	3614330	TY-2482_chromosome	B7LB07	ATPase and DNA damage recognition protein of nucleotide excision repair excinuclease UvrABC	Escherichia coli (strain 55989 / EAEC)
91268	3617403	3617936	TY-2482_chromosome	B7LB08	Single-stranded DNA-binding protein	Escherichia coli (strain 55989 / EAEC)
71515	3618418	3618041	TY-2482_chromosome	D3GT41	Putative membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
76063	3618749	3620332	TY-2482_chromosome	B7LB02	Putative signal transduction protein (EAL domain containing protein)	Escherichia coli (strain 55989 / EAEC)

88430	3620661	3620341	TY-2482_chromosome	B7LB11	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
67933	3620747	3621208	TY-2482_chromosome	B7LB12	DNA-binding transcriptional dual regulator, Fe-S center for redox-sensing	Escherichia coli (strain 55989 / EAEC)
60279	3621198	3621461	TY-2482_chromosome	D3GT45	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
r120	3621344	3621205	TY-2482_chromosome	ref|NC_010473|:4375646-4375785|-| [gene=ryjA] [locus_tag=ECDH10B_4253]		
27742	3621641	3621853	TY-2482_chromosome	Q8FAZ7	Putative uncharacterized protein	Escherichia coli O6
28572	3621720	3621505	TY-2482_chromosome	B6I5T1	Putative uncharacterized protein	Escherichia coli (strain SE11)
66284	3621757	3623103	TY-2482_chromosome	B7LB13	Putative permease	Escherichia coli (strain 55989 / EAEC)
110426	3623257	3624903	TY-2482_chromosome	B7LB10	Putative cation/proton antiporter	Escherichia coli (strain 55989 / EAEC)
69912	3626352	3625063	TY-2482_chromosome	B7LB15	Putative uncharacterized protein yjcF	Escherichia coli (strain 55989 / EAEC)
29710	3628179	3626533	TY-2482_chromosome	B7LB16	Cation/acetate symporter ActP (Acetate permease) (Acetate transporter ActP)	Escherichia coli (strain 55989 / EAEC)
115166	3628490	3628179	TY-2482_chromosome	B7LB17	Putative uncharacterized protein yjcH	Escherichia coli (strain 55989 / EAEC)
68037	3630648	3628693	TY-2482_chromosome	B7LB14	Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-activating enzyme)	Escherichia coli (strain 55989 / EAEC)
32718	3631040	3632521	TY-2482_chromosome	B7LB19	Cytochrome c-552 (EC 1.7.2.2) (Ammonia-forming cytochrome c nitrite reductase) (Cytochrome c nitrite reductase	Escherichia coli (strain 55989 / EAEC)
87879	3632569	3633132	TY-2482_chromosome	B7LB20	Nitrite reductase, formate-dependent, penta-heme cytochrome c (EC 1.7.2.2)	Escherichia coli (strain 55989 / EAEC)
80514	3633132	3633800	TY-2482_chromosome	B7LB21	Formate-dependent nitrite reductase, 4Fe4S subunit	Escherichia coli (strain 55989 / EAEC)
66288	3633800	3634753	TY-2482_chromosome	B7LB18	Formate-dependent nitrite reductase, membrane subunit	Escherichia coli (strain 55989 / EAEC)
59155	3634836	3636491	TY-2482_chromosome	B7LB23	Heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfE	Escherichia coli (strain 55989 / EAEC)
87160	3636487	3636867	TY-2482_chromosome	B7LB22	Heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfF	Escherichia coli (strain 55989 / EAEC)
77432	3636867	3637460	TY-2482_chromosome	B7LB25	Heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfG	Escherichia coli (strain 55989 / EAEC)
91849	3637805	3639115	TY-2482_chromosome	B7LB26	Glutamate/aspartate:proton symporter	Escherichia coli (strain 55989 / EAEC)
101200	3639885	3639199	TY-2482_chromosome	B7LB27	Putative uncharacterized protein yjcO	Escherichia coli (strain 55989 / EAEC)
102916	3642126	3639982	TY-2482_chromosome	B7LB28	Formate dehydrogenase-H, selenopolypeptide subunit (EC 1.2.1.2)	Escherichia coli (strain 55989 / EAEC)
94505	3643790	3642327	TY-2482_chromosome	B7LB29	Outer membrane factor of efflux pump	Escherichia coli (strain 55989 / EAEC)
93995	3645838	3643790	TY-2482_chromosome	B7LB24	Multidrug efflux system component	Escherichia coli (strain 55989 / EAEC)
64142	3646869	3645841	TY-2482_chromosome	B7LB31	Membrane fusion protein of efflux pump	Escherichia coli (strain 55989 / EAEC)
104528	3647163	3646891	TY-2482_chromosome	C8TMX3	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
62799	3649357	3647375	TY-2482_chromosome	B7LB32	Putative alkyl sulfatase	Escherichia coli (strain 55989 / EAEC)
111905	3649610	3649924	TY-2482_chromosome	B7LB30	Putative ribose-5-phosphate isomerase B (RpiB-like)	Escherichia coli (strain 55989 / EAEC)
21587	3650485	3650105	TY-2482_chromosome	D7XTI2	Putative uncharacterized protein	Escherichia coli MS 84-1
115994	3651230	3650475	TY-2482_chromosome	B7LB33	Carbon-phosphorus lyase complex accessory protein	Escherichia coli (strain 55989 / EAEC)
111726	3651666	3651235	TY-2482_chromosome	B7LB36	Putative acyltransferase with acyl-CoA N-acyltransferase domain	Escherichia coli (strain 55989 / EAEC)
99176	3652210	3651656	TY-2482_chromosome	B7LB37	Ribose 1,5-bisphosphokinase	Escherichia coli (strain 55989 / EAEC)
110428	3653346	3652213	TY-2482_chromosome	B7LB38	Carbon-phosphorus lyase complex subunit	Escherichia coli (strain 55989 / EAEC)
93097	3654065	3653346	TY-2482_chromosome	D3GTX6	Phosphonates transport ATP-binding protein	Escherichia coli O44:H18 (strain 042 / EAEC)
82799	3654958	3654203	TY-2482_chromosome	B7LB40	Carbon-phosphorus lyase complex subunit	Escherichia coli (strain 55989 / EAEC)
102919	3655800	3654958	TY-2482_chromosome	B7LB39	Carbon-phosphorus lyase complex subunit	Escherichia coli (strain 55989 / EAEC)
116093	3656857	3655796	TY-2482_chromosome	B7LB42	Carbon-phosphorus lyase complex subunit	Escherichia coli (strain 55989 / EAEC)
77434	3657890	3657441	TY-2482_chromosome	B7LB44	Carbon-phosphorus lyase complex subunit	Escherichia coli (strain 55989 / EAEC)
105873	3658616	3657894	TY-2482_chromosome	B7LB45	Putative DNA-binding transcriptional regulator of phosphonate uptake and biodegradation	Escherichia coli (strain 55989 / EAEC)
110634	3659479	3658640	TY-2482_chromosome	B7LB41	Phosphonates transport system, permease protein	Escherichia coli (strain 55989 / EAEC)
67753	3660538	3659525	TY-2482_chromosome	B7LB46	Phosphonate/organophosphate ester transporter subunit ; periplasmic binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
79008	3661351	3660566	TY-2482_chromosome	B7LB48	Phosphonate/organophosphate ester transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
69913	3661927	3661487	TY-2482_chromosome	B7LB49	Putative uncharacterized protein phnB	Escherichia coli (strain 55989 / EAEC)
84613	3662569	3662090	TY-2482_chromosome	B7LB50	Putative alkylphosphonate uptake protein in phosphonate metabolism	Escherichia coli (strain 55989 / EAEC)
65067	3662824	3665049	TY-2482_chromosome	B7LB47	Putative uncharacterized protein yjdA	Escherichia coli (strain 55989 / EAEC)
90017	3665049	3665924	TY-2482_chromosome	B7LB52	Putative uncharacterized protein yjcZ	Escherichia coli (strain 55989 / EAEC)
59158	3666191	3667690	TY-2482_chromosome	B7LB53	Proline/glycine betaine transporter	Escherichia coli (strain 55989 / EAEC)
90372	3668961	3667873	TY-2482_chromosome	B7LB54	Sensory histidine kinase in two-component regulatory system with BasR	Escherichia coli (strain 55989 / EAEC)
112314	3669639	3668974	TY-2482_chromosome	B7LB51	DNA-binding response regulator in two-component regulatory system with BasS	Escherichia coli (strain 55989 / EAEC)
93919	3671279	3669639	TY-2482_chromosome	B7LB56	Putative metal dependent hydrolase	Escherichia coli (strain 55989 / EAEC)
83286	3672720	3671386	TY-2482_chromosome	B7LB57	Arginine/agmatine antiporter	Escherichia coli (strain 55989 / EAEC)
65872	3673663	3672860	TY-2482_chromosome	B7LB58	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
113894	3676258	3673991	TY-2482_chromosome	B7LB59	Biodegradative arginine decarboxylase (EC 4.1.1.19)	Escherichia coli (strain 55989 / EAEC)
12974	3677361	3677552	TY-2482_chromosome	D7YA75	Putative uncharacterized protein	Escherichia coli MS 115-1
109872	3677362	3676457	TY-2482_chromosome	B7LB60	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
62638	3677645	3678997	TY-2482_chromosome	B7LB55	Alpha-galactosidase, NAD(P)-binding (EC 3.2.1.22)	Escherichia coli (strain 55989 / EAEC)
94574	3679115	3680521	TY-2482_chromosome	B7LB62	Melibiose:sodium symporter	Escherichia coli (strain 55989 / EAEC)
106540	3681292	3680666	TY-2482_chromosome	B7LB63	Putative uncharacterized protein yjdF	Escherichia coli (strain 55989 / EAEC)
105748	3683061	3681418	TY-2482_chromosome	B7LB64	Anaerobic class I fumarate hydratase (Fumarase B) (EC 4.2.1.2)	Escherichia coli (strain 55989 / EAEC)
91939	3684479	3683142	TY-2482_chromosome	B7LB65	C4-dicarboxylate antiporter	Escherichia coli (strain 55989 / EAEC)
84430	3685769	3685053	TY-2482_chromosome	B7LB66	DNA-binding response regulator in two-component regulatory system with DcuS	Escherichia coli (strain 55989 / EAEC)
94663	3687397	3685769	TY-2482_chromosome	B7LB67	Sensory histidine kinase in two-component regulatory system with DcuR, regulator of anaerobic fumarate respiration	Escherichia coli (strain 55989 / EAEC)
90195	3687578	3687805	TY-2482_chromosome	B7LB61	Putative uncharacterized protein yjdI	Escherichia coli (strain 55989 / EAEC)
28165	3688244	3687852	TY-2482_chromosome	Q1R3D4	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)

69954	3688319	3688612	TY-2482_chromosome	B7LBS9	Putative uncharacterized protein yjdK	Escherichia coli (strain 55989 / EAEC)
105827	3690452	3688938	TY-2482_chromosome	B7LBT1	Lysyl-tRNA synthetase 2 (EC 6.1.1.6) (Lysine--tRNA ligase 2)	Escherichia coli (strain 55989 / EAEC)
61888	3692146	3690692	TY-2482_chromosome	B7LBT2	Putative transporter	Escherichia coli (strain 55989 / EAEC)
108125	3694352	3692208	TY-2482_chromosome	B7LBT3	Lysine decarboxylase 1 (EC 4.1.1.18)	Escherichia coli (strain 55989 / EAEC)
61112	3695766	3694435	TY-2482_chromosome	B7LBT4	Putative lysine/cadaverine transporter	Escherichia coli (strain 55989 / EAEC)
99065	3697670	3696135	TY-2482_chromosome	B7LBT5	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
11087	3697957	3698280	TY-2482_chromosome	D7ZE65	Putative uncharacterized protein	Escherichia coli MS 69-1
110636	3699261	3698422	TY-2482_chromosome	B7LBT7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
61211	3700051	3699566	TY-2482_chromosome	B7LBT9	Putative uncharacterized protein yeeW	Escherichia coli (strain 55989 / EAEC)
64463	3700530	3700051	TY-2482_chromosome	B7LBU0	Toxin of the YeeV-YeeU toxin-antitoxin system	Escherichia coli (strain 55989 / EAEC)
22616	3700598	3700452	TY-2482_chromosome	E9TQB2	Conserved domain protein (Fragment)	Escherichia coli MS 60-1
61291	3702583	3701732	TY-2482_chromosome	B7LBT6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
95589	3702958	3703528	TY-2482_chromosome	B7LFP9	Transposase ORF B, IS629	Escherichia coli (strain 55989 / EAEC)
16055	3703829	3703461	TY-2482_chromosome	Q9S110	Orf57 protein	Escherichia coli
8446	3704052	3703747	TY-2482_chromosome	P71290	Orf58 protein	Escherichia coli
52537	3704123	3705643	TY-2482_chromosome	B7LBU5	Putative reverse transcriptase-like protein from putative prophage or plasmid (EC 2.7.7.49)	Escherichia coli (strain 55989 / EAEC)
26336	3705721	3706218	TY-2482_chromosome	Q327G0	IS629 ORF2	Shigella dysenteriae serotype 1 (strain Sd197)
113975	3706374	3710489	TY-2482_chromosome	B7LBY5	Serine protease pet (Plasmid-encoded toxin pet) (EC 3.4.21.72)	Escherichia coli (strain 55989 / EAEC)
10660	3710897	3710589	TY-2482_chromosome	B3IA48	Transposase	Escherichia coli E22
43233	3711566	3710927	TY-2482_chromosome	Q5K5W0	Putative uncharacterized protein	Escherichia coli
29385	3711654	3712775	TY-2482_chromosome	B7LBW1	Transposase	Escherichia coli (strain 55989 / EAEC)
26337	3714068	3714463	TY-2482_chromosome	Q327G0	IS629 ORF2	Shigella dysenteriae serotype 1 (strain Sd197)
16965	3714080	3713556	TY-2482_chromosome	D7JSS3	Predicted protein	Escherichia coli FVEC1302
28475	3715636	3714497	TY-2482_chromosome	B7LBV5	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
108664	3715685	3715882	TY-2482_chromosome	B7LBX6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
95485	3716069	3715875	TY-2482_chromosome	B7LBV3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
29384	3716376	3717299	TY-2482_chromosome	B7LBU8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
102235	3718445	3717255	TY-2482_chromosome	B7LBV1	Putative membrane transport protein, major facilitator superfamily	Escherichia coli (strain 55989 / EAEC)
86629	3718518	3720302	TY-2482_chromosome	B7LBV0	Aerobactin siderophore biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
78881	3720306	3721250	TY-2482_chromosome	B7LBU9	Aerobactin siderophore biosynthesis protein, N(6)-hydroxylysine acetylase	Escherichia coli (strain 55989 / EAEC)
82602	3721253	3722992	TY-2482_chromosome	B7LBU4	Aerobactin siderophore biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
88257	3722992	3724326	TY-2482_chromosome	B7LBU7	L-lysine 6-monooxygenase (Lysine N(6)-hydroxylase) (EC 1.14.13.59)	Escherichia coli (strain 55989 / EAEC)
28380	3724251	3726527	TY-2482_chromosome	B7LBU6	Ferric aerobactin receptor	Escherichia coli (strain 55989 / EAEC)
26333	3727420	3726923	TY-2482_chromosome	Q327G0	IS629 ORF2	Shigella dysenteriae serotype 1 (strain Sd197)
52529	3729018	3727498	TY-2482_chromosome	B7LB68	Putative reverse transcriptase-like protein from putative prophage or plasmid (EC 2.7.7.49) (Reverse transcriptase-lik	Escherichia coli (strain 55989 / EAEC)
8449	3729089	3729394	TY-2482_chromosome	P71290	Orf58 protein	Escherichia coli
16057	3729312	3729680	TY-2482_chromosome	Q9S110	Orf57 protein	Escherichia coli
95588	3730183	3729613	TY-2482_chromosome	B7LFP9	Transposase ORF B, IS629	Escherichia coli (strain 55989 / EAEC)
114469	3730692	3730444	TY-2482_chromosome	C8UCI0	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
73657	3731114	3730692	TY-2482_chromosome	B7LBY1	Putative transposase OrfA from plasmid origin	Escherichia coli (strain 55989 / EAEC)
75558	3732256	3731345	TY-2482_chromosome	B7LBY2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
113920	3733023	3732346	TY-2482_chromosome	B7LBY3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
108655	3733358	3734818	TY-2482_chromosome	B7LBX6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
113973	3739498	3735644	TY-2482_chromosome	B7LBY5	Serine protease pet (Plasmid-encoded toxin pet) (EC 3.4.21.72)	Escherichia coli (strain 55989 / EAEC)
27995	3740848	3741264	TY-2482_chromosome	B6ICP6	Truncated transposase	Escherichia coli (strain SE11)
36036	3740863	3739862	TY-2482_chromosome	C1J8M7	TraF	Escherichia coli
104315	3741629	3741267	TY-2482_chromosome	B7LBV5	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
16881	3741827	3741563	TY-2482_chromosome	E3Y4T4	Integrase core domain protein	Shigella flexneri 2a str. 2457T
86874	3745485	3741972	TY-2482_chromosome	B7LBY9	Putative superfamily I DNA helicase	Escherichia coli (strain 55989 / EAEC)
115829	3745574	3745834	TY-2482_chromosome	B7LBZ1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
68615	3747200	3745941	TY-2482_chromosome	B7LBZ2	Prophage integrase	Escherichia coli (strain 55989 / EAEC)
r317	3747473	3747398	TY-2482_chromosome	ref|NC_010473|:4460936-4461011|Phe tRNA| [gene=pheU] [locus_tag=ECDH10B_4327		
24375	3747512	3747267	TY-2482_chromosome	B7LBZ3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
103983	3748179	3747583	TY-2482_chromosome	D3GV37	Putative transcriptional regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
98238	3749889	3748195	TY-2482_chromosome	B7LBZ0	Thiol:disulfide interchange protein DsbD (EC 1.8.1.8) (Protein-disulfide reductase	Escherichia coli (strain 55989 / EAEC)
30431	3750203	3749868	TY-2482_chromosome	B7LBZ6	Divalent-cation tolerance protein CutA	Escherichia coli (strain 55989 / EAEC)
62697	3751620	3750322	TY-2482_chromosome	B7LBZ7	C4-dicarboxylate antiporter	Escherichia coli (strain 55989 / EAEC)
27929	3751720	3753168	TY-2482_chromosome	Q8FAM6	Putative uncharacterized protein	Escherichia coli O6
82601	3753511	3753984	TY-2482_chromosome	B7LBZ5	Inner membrane protein	Escherichia coli (strain 55989 / EAEC)
107831	3755259	3754006	TY-2482_chromosome	B7LC00	Transporter	Escherichia coli (strain 55989 / EAEC)
25662	3755725	3755405	TY-2482_chromosome	A1AJ50	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
30287	3755872	3757515	TY-2482_chromosome	B7LC02	60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Escherichia coli (strain 55989 / EAEC)
99066	3757656	3758006	TY-2482_chromosome	B7LBZ9	Putative uncharacterized protein yjeI	Escherichia coli (strain 55989 / EAEC)
99067	3759081	3758215	TY-2482_chromosome	B7LC04	Putative uncharacterized protein yjeJ	Escherichia coli (strain 55989 / EAEC)

62700	3760499	3759474	TY-2482_chromosome	B7LC05	Putative lysine aminomutase	Escherichia coli (strain 55989 / EAEC)
30738	3760541	3761104	TY-2482_chromosome	B7LC03	Elongation factor P (EF-P)	Escherichia coli (strain 55989 / EAEC)
29325	3761630	3761382	TY-2482_chromosome	A7ZV20	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
110601	3761716	3762030	TY-2482_chromosome	B7LC09	Multidrug efflux system protein	Escherichia coli (strain 55989 / EAEC)
59057	3762563	3762033	TY-2482_chromosome	B7LC10	Outer membrane lipoprotein (Lipocalin)	Escherichia coli (strain 55989 / EAEC)
88258	3763785	3762655	TY-2482_chromosome	B7LC06	Beta-lactamase/D-alanine carboxypeptidase (EC 3.5.2.6)	Escherichia coli (strain 55989 / EAEC)
31020	3764195	3763839	TY-2482_chromosome	B7LC12	Fumarate reductase subunit D (Fumarate reductase 13 kDa hydrophobic protein)	Escherichia coli (strain 55989 / EAEC)
31016	3764601	3764209	TY-2482_chromosome	B7LC13	Fumarate reductase subunit C (Fumarate reductase 15 kDa hydrophobic protein)	Escherichia coli (strain 55989 / EAEC)
69498	3765346	3764615	TY-2482_chromosome	B7LC11	Fumarate reductase (Anaerobic), Fe-S subunit (EC 1.3.99.1)	Escherichia coli (strain 55989 / EAEC)
113923	3767147	3765342	TY-2482_chromosome	B7LC15	Fumarate reductase (Anaerobic) catalytic and NAD/flavoprotein subunit (EC 1.3.99.1)	Escherichia coli (strain 55989 / EAEC)
35004	3767472	3768446	TY-2482_chromosome	B7LC16	Uncharacterized protein YjeA	Escherichia coli (strain 55989 / EAEC)
107732	3768668	3770167	TY-2482_chromosome	B7LC17	Putative transporter	Escherichia coli (strain 55989 / EAEC)
66372	3770222	3770533	TY-2482_chromosome	B7LC14	Putative uncharacterized protein yjeN	Escherichia coli (strain 55989 / EAEC)
60808	3770533	3770844	TY-2482_chromosome	B7LC19	Putative uncharacterized protein yjeO	Escherichia coli (strain 55989 / EAEC)
77303	3774199	3770879	TY-2482_chromosome	B7LC20	Putative mechanosensitive channel	Escherichia coli (strain 55989 / EAEC)
33098	3775189	3774224	TY-2482_chromosome	B7LC21	Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65) [Cleaved into: Phosphatidylserine decarboxylase alpha ch	Escherichia coli (strain 55989 / EAEC)
33780	3776338	3775289	TY-2482_chromosome	B7LC22	Putative ribosome biogenesis GTPase RsgA (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
61322	3776433	3776975	TY-2482_chromosome	B7LC23	Oligoribonuclease (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
r308	3777189	3777264	TY-2482_chromosome	ref|NC_010473|:4490968-4491043|Gly tRNA| [gene=glyY] [locus_tag=ECDH10B_4360]		
r309	3777301	3777376	TY-2482_chromosome	ref|NC_010473|:4490968-4491043|Gly tRNA| [gene=glyY] [locus_tag=ECDH10B_4360]		
26501	3777469	3777203	TY-2482_chromosome	A1AJ71	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
77369	3778784	3780328	TY-2482_chromosome	B7LC25	Putative carbohydrate kinase	Escherichia coli (strain 55989 / EAEC)
62701	3778785	3777649	TY-2482_chromosome	B7LC18	Putative Fe-S electron transport protein	Escherichia coli (strain 55989 / EAEC)
110381	3780303	3780761	TY-2482_chromosome	B7LC27	ATPase with strong ADP affinity	Escherichia coli (strain 55989 / EAEC)
64293	3780783	3782117	TY-2482_chromosome	B7LC28	N-acetylmuramoyl-l-alanine amidase II (EC 3.5.1.28)	Escherichia coli (strain 55989 / EAEC)
32575	3782130	3783974	TY-2482_chromosome	B7LC24	DNA mismatch repair protein mutL	Escherichia coli (strain 55989 / EAEC)
32391	3783970	3784917	TY-2482_chromosome	B7LC30	tRNA dimethylallyltransferase (EC 2.5.1.75) (Dimethylallyl diphosphate:tRNA dimethylallyltransferase) (DMAPP:tRNA	Escherichia coli (strain 55989 / EAEC)
31360	3785006	3785311	TY-2482_chromosome	B7LC31	Protein hfq (HF-1) (Host factor-I protein) (HF-I)	Escherichia coli (strain 55989 / EAEC)
84422	3785391	3786668	TY-2482_chromosome	B7LC32	Putative GTPase	Escherichia coli (strain 55989 / EAEC)
106453	3786757	3788013	TY-2482_chromosome	B7LC29	Modulator for HflB protease specific for phage lambda cII repressor	Escherichia coli (strain 55989 / EAEC)
59006	3788019	3789020	TY-2482_chromosome	B7LC34	Modulator for HflB protease specific for phage lambda cII repressor	Escherichia coli (strain 55989 / EAEC)
81117	3789105	3789299	TY-2482_chromosome	B7LC35	Putative uncharacterized protein yjeT	Escherichia coli (strain 55989 / EAEC)
33155	3789406	3790701	TY-2482_chromosome	B7LC36	Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Escherichia coli (strain 55989 / EAEC)
32721	3790909	3791331	TY-2482_chromosome	B7LC37	HTH-type transcriptional repressor nsrR	Escherichia coli (strain 55989 / EAEC)
99124	3791373	3793811	TY-2482_chromosome	B7LC38	Exoribonuclease R, RNase R (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
62618	3793994	3794722	TY-2482_chromosome	B7LC33	23S rRNA (Gm2251)-methyltransferase (EC 2.1.1.-)	Escherichia coli (strain 55989 / EAEC)
106361	3794852	3795250	TY-2482_chromosome	B7LC40	Putative uncharacterized protein yjfI	Escherichia coli (strain 55989 / EAEC)
97333	3795272	3795967	TY-2482_chromosome	B7LC41	Putative transcriptional regulator effector protein	Escherichia coli (strain 55989 / EAEC)
110581	3796021	3796677	TY-2482_chromosome	B7LC42	Putative uncharacterized protein yjfK	Escherichia coli (strain 55989 / EAEC)
77536	3796698	3797093	TY-2482_chromosome	B7LC43	Putative uncharacterized protein yjfL	Escherichia coli (strain 55989 / EAEC)
108849	3797106	3797741	TY-2482_chromosome	B7LC39	Putative uncharacterized protein yjfM	Escherichia coli (strain 55989 / EAEC)
60764	3797747	3798907	TY-2482_chromosome	B7LC46	Putative synthetase/amidase	Escherichia coli (strain 55989 / EAEC)
102724	3798994	3800616	TY-2482_chromosome	B7LC47	Isovaleryl CoA dehydrogenase	Escherichia coli (strain 55989 / EAEC)
113859	3801023	3800739	TY-2482_chromosome	B5Z2J4	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
66349	3801489	3801163	TY-2482_chromosome	B7LC49	Putative uncharacterized protein yjfO	Escherichia coli (strain 55989 / EAEC)
84536	3801671	3802417	TY-2482_chromosome	B7LC50	Putative hydrolase	Escherichia coli (strain 55989 / EAEC)
34507	3803172	3802420	TY-2482_chromosome	B7LC45	HTH-type transcriptional regulator ulaR	Escherichia coli (strain 55989 / EAEC)
34504	3804344	3803283	TY-2482_chromosome	B7LC52	Probable L-ascorbate-6-phosphate lactonase ulaG (EC 3.1.1.-) (L-ascorbate utilization protein G)	Escherichia coli (strain 55989 / EAEC)
71882	3804699	3806093	TY-2482_chromosome	B7LC53	L-ascorbate-specific enzyme IIC component of PTS	Escherichia coli (strain 55989 / EAEC)
97171	3806427	3806888	TY-2482_chromosome	B7LC51	L-ascorbate-specific enzyme IIA component of PTS (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
24843	3806428	3806096	TY-2482_chromosome	A1AJ99	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
34489	3807565	3808416	TY-2482_chromosome	B7LCQ7	L-ribulose-5-phosphate 3-epimerase ulaE (EC 5.1.3.22) (L-ascorbate utilization protein E) (L-xylulose-5-phosphate 3-ep	Escherichia coli (strain 55989 / EAEC)
27102	3807579	3806914	TY-2482_chromosome	A7ZV67	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
34495	3808419	3809102	TY-2482_chromosome	B7LCQ8	L-ribulose-5-phosphate 4-epimerase UlaF (EC 5.1.3.4) (L-ascorbate utilization protein F) (Phosphoribulose isomerase	Escherichia coli (strain 55989 / EAEC)
106447	3809250	3809798	TY-2482_chromosome	B7LCQ9	Putative Inner membrane protein yagU	Escherichia coli (strain 55989 / EAEC)
107874	3810151	3809879	TY-2482_chromosome	B7LCR0	Putative uncharacterized protein yjfY	Escherichia coli (strain 55989 / EAEC)
33758	3810478	3810870	TY-2482_chromosome	B7LCQ6	30S ribosomal protein S6	Escherichia coli (strain 55989 / EAEC)
33066	3810880	3811191	TY-2482_chromosome	B7LCR2	Primosomal replication protein n	Escherichia coli (strain 55989 / EAEC)
33728	3811199	3811423	TY-2482_chromosome	B7LCR3	30S ribosomal protein S18	Escherichia coli (strain 55989 / EAEC)
25506	3811929	3811444	TY-2482_chromosome	Q8FAI4	Putative uncharacterized protein	Escherichia coli O6
97577	3812782	3811991	TY-2482_chromosome	B7LCR5	Putative uncharacterized protein yjfZ	Escherichia coli (strain 55989 / EAEC)
111678	3813821	3813225	TY-2482_chromosome	C8ULY2	Putative IS609 transposase TnpA	Escherichia coli O111:H- (strain 11128 / EHEC)
84537	3813844	3815049	TY-2482_chromosome	B7LCR8	Putative transposase	Escherichia coli (strain 55989 / EAEC)
97257	3815825	3815190	TY-2482_chromosome	C8TP27	Predicted cell envelope opacity-associated protein	Escherichia coli O26:H11 (strain 11368 / EHEC)

12919	3815900	3816661	TY-2482_chromosome	C1NBA6	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (Fragment)	Escherichia sp. 1_1_43
62689	3816973	3818382	TY-2482_chromosome	B7LCS1	D-alanine/D-serine/glycine transporter	Escherichia coli (strain 55989 / EAEC)
35071	3819092	3818433	TY-2482_chromosome	B7LCS2	Iron-sulfur cluster repair protein YtfE	Escherichia coli (strain 55989 / EAEC)
62704	3820174	3819203	TY-2482_chromosome	B7LCS3	Putative uncharacterized protein ytfF	Escherichia coli (strain 55989 / EAEC)
115820	3821133	3820276	TY-2482_chromosome	B7LCS4	NAD(P)H:quinone oxidoreductase	Escherichia coli (strain 55989 / EAEC)
106449	3823674	3821734	TY-2482_chromosome	B7LCS6	2':3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16)	Escherichia coli (strain 55989 / EAEC)
90695	3823864	3824601	TY-2482_chromosome	B7LCS0	PAPS (Adenosine 3'-phosphate 5'-phosphosulfate) 3'(2'),5'-bisphosphate nucleotidase	Escherichia coli (strain 55989 / EAEC)
91805	3825151	3824597	TY-2482_chromosome	B7LCS8	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
53806	3825410	3825679	TY-2482_chromosome	Q8Z151	Putative uncharacterized protein ytfK	Salmonella typhi
88250	3827087	3825747	TY-2482_chromosome	B7LCT0	Putative uncharacterized protein ytfL	Escherichia coli (strain 55989 / EAEC)
32494	3828048	3827413	TY-2482_chromosome	B7LCT1	Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methion	Escherichia coli (strain 55989 / EAEC)
86343	3828254	3829984	TY-2482_chromosome	B7LCS7	Putative uncharacterized protein ytfM	Escherichia coli (strain 55989 / EAEC)
94005	3829984	3833760	TY-2482_chromosome	B7LCT3	Putative uncharacterized protein ytfN	Escherichia coli (strain 55989 / EAEC)
102783	3833766	3834104	TY-2482_chromosome	B7LCT4	Putative uncharacterized protein ytfP	Escherichia coli (strain 55989 / EAEC)
62599	3834313	3834567	TY-2482_chromosome	B5Z3I0	PemI protein 2	Escherichia coli O157:H7 (strain EC4115 / EHEC)
82505	3834564	3834911	TY-2482_chromosome	B7LCT2	Toxin of the ChpB-ChpS toxin-antitoxin system	Escherichia coli (strain 55989 / EAEC)
114159	3835524	3834997	TY-2482_chromosome	B7LCT7	Inorganic pyrophosphatase (EC 3.6.1.1)	Escherichia coli (strain 55989 / EAEC)
110599	3835834	3836787	TY-2482_chromosome	B7LCT8	Putative sugar transporter subunit: periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
97649	3837100	3838599	TY-2482_chromosome	B7LCT9	Putative sugar transporter subunit: ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
98354	3838616	3839635	TY-2482_chromosome	B7LCT6	Putative sugar transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
91248	3839625	3840617	TY-2482_chromosome	B7LCU0	Putative sugar transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
88509	3841651	3840656	TY-2482_chromosome	B7LCU2	Fructose-1,6-bisphosphatase class 1 (FBPase class 1) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase	Escherichia coli (strain 55989 / EAEC)
59053	3841827	3843197	TY-2482_chromosome	B7LCU3	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-)	Escherichia coli (strain 55989 / EAEC)
35015	3843902	3843354	TY-2482_chromosome	B7LCU1	UPF0307 protein yjgA	Escherichia coli (strain 55989 / EAEC)
71362	3843996	3845345	TY-2482_chromosome	B7LCU4	Peptidase required for the maturation and secretion of the antibiotic peptide MccB17	Escherichia coli (strain 55989 / EAEC)
90441	3845531	3845914	TY-2482_chromosome	B7LCU6	Soluble cytochrome b562	Escherichia coli (strain 55989 / EAEC)
76802	3846426	3845965	TY-2482_chromosome	B7LCU7	Anaerobic ribonucleoside-triphosphate reductase-activating protein (EC 1.97.1.-)	Escherichia coli (strain 55989 / EAEC)
72429	3848722	3846587	TY-2482_chromosome	B7LCU8	Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Escherichia coli (strain 55989 / EAEC)
73652	3850780	3849128	TY-2482_chromosome	B7LCU5	Trehalose-6-P hydrolase (EC 3.2.1.93)	Escherichia coli (strain 55989 / EAEC)
66400	3852251	3850833	TY-2482_chromosome	B7LCV0	Fused trehalose(Maltose)-specific PTS enzyme: IIB component ; IIC component	Escherichia coli (strain 55989 / EAEC)
80321	3853317	3852373	TY-2482_chromosome	B7LCV1	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
65430	3853696	3856389	TY-2482_chromosome	B7LCV2	Magnesium transporter (EC 3.6.3.1)	Escherichia coli (strain 55989 / EAEC)
115749	3857600	3856623	TY-2482_chromosome	B7LF78	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
29492	3857970	3858431	TY-2482_chromosome	Q1R311	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
33218	3858797	3858339	TY-2482_chromosome	B7LCV5	Aspartate carbamoyltransferase regulatory chain	Escherichia coli (strain 55989 / EAEC)
33193	3859745	3858813	TY-2482_chromosome	B7LCV3	Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase) (ATCase)	Escherichia coli (strain 55989 / EAEC)
21955	3859863	3860192	TY-2482_chromosome	Q79D60	ORF_o110	Escherichia coli
90526	3859940	3859752	TY-2482_chromosome	C6UP50	PyrBI operon leader peptide	Escherichia coli O157:H7 (strain TW14359 / EHEC
64827	3860559	3860167	TY-2482_chromosome	B7LCV8	Putative mRNA endoribonuclease	Escherichia coli (strain 55989 / EAEC)
110600	3861403	3860693	TY-2482_chromosome	B7LCV9	Putative oxidoreductase with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
66404	3861474	3862064	TY-2482_chromosome	B7LCV6	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
110561	3862212	3862661	TY-2482_chromosome	B7LCW1	Putative uncharacterized protein yjgK	Escherichia coli (strain 55989 / EAEC)
101286	3862787	3864345	TY-2482_chromosome	C8TP74	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
29447	3864324	3864374	TY-2482_chromosome	C5W5U6	Predicted protein	Escherichia coli (strain B / BL21)
32841	3865453	3864452	TY-2482_chromosome	B7LCW4	Ornithine carbamoyltransferase (OTCase) (EC 2.1.3.3)	Escherichia coli (strain 55989 / EAEC)
111498	3865615	3866028	TY-2482_chromosome	B7LCW5	Putative uncharacterized protein yjgD	Escherichia coli (strain 55989 / EAEC)
95377	3866580	3866080	TY-2482_chromosome	B7LCW6	Putative acetyltransferase	Escherichia coli (strain 55989 / EAEC)
106347	3866773	3867966	TY-2482_chromosome	B7LCW7	Putative uncharacterized protein yjgN	Escherichia coli (strain 55989 / EAEC)
76355	3870880	3868028	TY-2482_chromosome	B7LCW8	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase)	Escherichia coli (strain 55989 / EAEC)
57429	3871362	3870883	TY-2482_chromosome	Q8Z117	DNA polymerase III, chi subunit	Salmonella typhi
29771	3872968	3871460	TY-2482_chromosome	B7LCX0	Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (EC 3.4.11.10) (Leucyl aminopeptidase	Escherichia coli (strain 55989 / EAEC)
64129	3873235	3874332	TY-2482_chromosome	B7LCX1	Putative uncharacterized protein yjgP	Escherichia coli (strain 55989 / EAEC)
59202	3874335	3875414	TY-2482_chromosome	B7LCX2	Putative uncharacterized protein yjgQ	Escherichia coli (strain 55989 / EAEC)
112154	3877038	3875539	TY-2482_chromosome	B7LCX3	Putative ATPase	Escherichia coli (strain 55989 / EAEC)
102698	3878114	3877119	TY-2482_chromosome	B7LCW9	DNA-binding transcriptional repressor, 5-gluconate-binding	Escherichia coli (strain 55989 / EAEC)
66333	3879500	3878184	TY-2482_chromosome	B7LCX5	L-idonate and D-gluconate transporter	Escherichia coli (strain 55989 / EAEC)
77519	3880329	3879568	TY-2482_chromosome	B7LCX6	5-keto-D-gluconate-5-reductase (EC 1.1.1.69)	Escherichia coli (strain 55989 / EAEC)
96962	3881384	3880356	TY-2482_chromosome	B7LCX7	L-idonate 5-dehydrogenase, NAD-binding (EC 1.1.1.264)	Escherichia coli (strain 55989 / EAEC)
73829	3881601	3882161	TY-2482_chromosome	B7LCX4	D-gluconate kinase, thermosensitive (EC 2.7.1.12)	Escherichia coli (strain 55989 / EAEC)
71867	3883187	3882171	TY-2482_chromosome	B7LCX9	Putative alcohol dehydrogenase, Zn-dependent and NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
r228	3883383	3883467	TY-2482_chromosome	ref|NC_010473|:4596236-4596320|Leu tRNA| [gene=leuX] [locus_tag=ECDH10B_4463]		
110519	3883468	3883265	TY-2482_chromosome	B7LCY0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73635	3884624	3883620	TY-2482_chromosome	B7LDP4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
97591	3886152	3884536	TY-2482_chromosome	B7LDP5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)

64740	3887496	3886165	TY-2482_chromosome	B7LDP6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
24262	3887779	3887456	TY-2482_chromosome	B7LDP1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
28953	3888986	3888117	TY-2482_chromosome	B7LDP8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
10354	3889674	3889234	TY-2482_chromosome	E5ZR87	Conserved domain protein	Escherichia coli MS 110-3
14369	3890362	3889668	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli
99088	3891282	3891575	TY-2482_chromosome	B7LDQ2	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
102810	3891728	3891904	TY-2482_chromosome	B7LDQ3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
102811	3892148	3892324	TY-2482_chromosome	B7LDQ3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25098	3892288	3892464	TY-2482_chromosome	B7LDQ4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
59068	3892628	3893701	TY-2482_chromosome	B7LDQ7	Putative Filamentation induced by cAMP protein Fic	Escherichia coli (strain 55989 / EAEC)
28915	3894384	3893758	TY-2482_chromosome	B7LDQ8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
14375	3894426	3895120	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli
88299	3896119	3895298	TY-2482_chromosome	B7LDQ5	Putative Transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
109633	3896246	3897838	TY-2482_chromosome	B7LDR2	PTS system, glucose-specific enzyme II, ABC component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
102812	3897841	3898527	TY-2482_chromosome	B7LDR3	Putative N-acetylmannosamine-6-phosphate 2-epimerase 2 (EC 5.1.3.9) (ManNAc-6-P epimerase 2)	Escherichia coli (strain 55989 / EAEC)
83169	3898591	3898803	TY-2482_chromosome	B7LDR4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
89975	3898785	3899003	TY-2482_chromosome	B7LDR5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
9560	3898904	3899209	TY-2482_chromosome	E5ZNX5	Putative uncharacterized protein	Escherichia coli MS 110-3
18905	3899580	3900001	TY-2482_chromosome	B3IA39	Truncated transposase	Escherichia coli E22
24006	3900648	3900094	TY-2482_chromosome	B7UHC5	Transposase of ISEc13 of IS110 family (Transposase of ISEc21)	Escherichia coli O127:H6 (strain E2348/69 / EPEC
69975	3901807	3900779	TY-2482_chromosome	B7LDS0	Putative Transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
101549	3902078	3902518	TY-2482_chromosome	B7LDS1	Putative PTS system, specific IIA component	Escherichia coli (strain 55989 / EAEC)
108075	3902537	3902821	TY-2482_chromosome	B7LDS2	Putative PTS system, specific IIB component	Escherichia coli (strain 55989 / EAEC)
84532	3902837	3904090	TY-2482_chromosome	B7LDR9	Putative PTS system, Specific IIC component	Escherichia coli (strain 55989 / EAEC)
88300	3904594	3904343	TY-2482_chromosome	B7LDS3	Putative transposase ORF1, IS3 family	Escherichia coli (strain 55989 / EAEC)
62706	3906029	3905019	TY-2482_chromosome	B7LDS6	Deoxyribose specific mutarotase	Escherichia coli (strain 55989 / EAEC)
95521	3907357	3906044	TY-2482_chromosome	B7LDS7	Putative L-fucose permease	Escherichia coli (strain 55989 / EAEC)
73698	3908332	3907388	TY-2482_chromosome	B7LDS8	Deoxyribokinase (EC 2.7.1.15)	Escherichia coli (strain 55989 / EAEC)
65831	3908608	3909390	TY-2482_chromosome	B7LDS4	Putative transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
101113	3909645	3909398	TY-2482_chromosome	D3GWZ4	Putative acetolactate synthase isozyme I small subunit (EC 2.2.1.6) (Fragment)	Escherichia coli O44:H18 (strain 042 / EAEC)
23390	3909821	3909624	TY-2482_chromosome	C1HR96	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
27559	3910175	3910498	TY-2482_chromosome	Q8FKR7	Putative uncharacterized protein	Escherichia coli O6
75970	3912190	3910580	TY-2482_chromosome	B7LDT2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
57843	3912571	3912224	TY-2482_chromosome	B7LB70	Putative uncharacterized protein (Transposase)	Escherichia coli (strain 55989 / EAEC)
84646	3912993	3912571	TY-2482_chromosome	B7LX21	Transposase	Escherichia coli (strain 55989 / EAEC)
100491	3913084	3913380	TY-2482_chromosome	D3GX00	Putative alcohol dehydrogenase (Fragment)	Escherichia coli O44:H18 (strain 042 / EAEC)
105382	3914124	3913444	TY-2482_chromosome	B7LDT4	Putative HTH regulator, TetR family	Escherichia coli (strain 55989 / EAEC)
20824	3915503	3914164	TY-2482_chromosome	E9WYU6	Putative uncharacterized protein	Escherichia coli E482
62213	3917686	3915686	TY-2482_chromosome	B7LDT5	Betaine-carnitine-choline transporter family member BetU	Escherichia coli (strain 55989 / EAEC)
64167	3918973	3917837	TY-2482_chromosome	B7LDT8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
94859	3920098	3919157	TY-2482_chromosome	B7LDT9	Lipid A biosynthesis (KDO)2-(Lauroyl)-lipid IVA acyltransferase 2 (EC 2.3.1.-)	Escherichia coli (strain 55989 / EAEC)
88302	3921113	3920166	TY-2482_chromosome	B7LDU0	Regulator of virG protein	Escherichia coli (strain 55989 / EAEC)
62707	3922206	3921121	TY-2482_chromosome	B7LDT7	Glycosyl transferase	Escherichia coli (strain 55989 / EAEC)
9336	3923051	3922212	TY-2482_chromosome	Q9X692	Shf	Escherichia coli
23299	3923237	3924017	TY-2482_chromosome	Q6Q6S9	Transposase	Escherichia coli
8445	3924541	3924236	TY-2482_chromosome	P71290	Orf58 protein	Escherichia coli
52538	3924612	3926132	TY-2482_chromosome	B7LBU5	Putative reverse transcriptase-like protein from putative prophage or plasmid (EC 2.7.7.49)	Escherichia coli (strain 55989 / EAEC)
23996	3926150	3926700	TY-2482_chromosome	Q0T2D8	IS911 ORF2	Shigella flexneri serotype 5b (strain 8401)
75632	3926630	3927040	TY-2482_chromosome	B7LDU8	Putative uncharacterized protein yjhV	Escherichia coli (strain 55989 / EAEC)
101396	3928368	3927604	TY-2482_chromosome	B7LDU9	Iron-dicitrate transporter subunit ; ATP-binding component of ABC superfamily; KpLE2 phage-like elemen	Escherichia coli (strain 55989 / EAEC)
80925	3929325	3928372	TY-2482_chromosome	B7LDV1	Iron-dicitrate transporter subunit ; membrane component of ABC superfamily; KpLE2 phage-like elemen	Escherichia coli (strain 55989 / EAEC)
108142	3930320	3929325	TY-2482_chromosome	B7LDV0	Iron-dicitrate transporter subunit ; membrane component of ABC superfamily; KpLE2 phage-like elemen	Escherichia coli (strain 55989 / EAEC)
95524	3931219	3930320	TY-2482_chromosome	B7LDV3	Iron-dicitrate transporter subunit ; periplasmic-binding component of ABC superfamily; KpLE2 phage-like elemen	Escherichia coli (strain 55989 / EAEC)
99136	3933588	3931267	TY-2482_chromosome	B7LDV4	Ferric citrate outer membrane transporter; KpLE2 phage-like element	Escherichia coli (strain 55989 / EAEC)
113961	3934628	3933678	TY-2482_chromosome	B7LDV5	Transmembrane signal transducer for ferric citrate transport; KpLE2 phage-like element	Escherichia coli (strain 55989 / EAEC)
77382	3935146	3934628	TY-2482_chromosome	B7LDV2	RNA polymerase sigma factor	Escherichia coli (strain 55989 / EAEC)
17709	3935519	3935830	TY-2482_chromosome	D8A8G4	Conserved domain protein	Escherichia coli MS 21-1
14737	3936028	3936318	TY-2482_chromosome	B3Y1Q0	Predicted protein	Escherichia coli O111:H-
26395	3936693	3936487	TY-2482_chromosome	B7LDV7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
99138	3937057	3938427	TY-2482_chromosome	B7LDV8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
105017	3940054	3938672	TY-2482_chromosome	B7LDV9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26478	3940676	3940107	TY-2482_chromosome	Q8XC14	Putative IS encoded protein encoded within prophage CP-933C	Escherichia coli O157:H7
16051	3941183	3940950	TY-2482_chromosome	B3Y1Q5	Predicted protein	Escherichia coli O111:H-
59090	3941704	3941186	TY-2482_chromosome	B7LDW2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)

26505	3941972	3942838	TY-2482_chromosome	A7ZVI3	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC)
62727	3942012	3941608	TY-2482_chromosome	B7LDW3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25317	3943359	3943081	TY-2482_chromosome	E3PBJ5	Putative uncharacterized protein	Escherichia coli O78:H11 (strain H10407 / ETEC)
26051	3943821	3944082	TY-2482_chromosome	Q0TGB3	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
115825	3944265	3944663	TY-2482_chromosome	B7LDW1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
80960	3944319	3944056	TY-2482_chromosome	B7LDW6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
75580	3944606	3945360	TY-2482_chromosome	C8TTS1	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
108424	3945535	3945729	TY-2482_chromosome	B7LDW9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
12327	3946431	3946219	TY-2482_chromosome	C1HRB5	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
26703	3946564	3947238	TY-2482_chromosome	B7LDX0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
14373	3947949	3947255	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli
65597	3949691	3948351	TY-2482_chromosome	B7LDX4	Fructuronate transporter	Escherichia coli (strain 55989 / EAEC)
73701	3949771	3950076	TY-2482_chromosome	B7LDX5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
34553	3950031	3951212	TY-2482_chromosome	B7LDX2	Mannonate dehydratase (EC 4.2.1.8) (D-mannonate hydrolase)	Escherichia coli (strain 55989 / EAEC)
99090	3951296	3952753	TY-2482_chromosome	B7LDX7	D-mannonate oxidoreductase, NAD-binding (EC 1.1.1.57)	Escherichia coli (strain 55989 / EAEC)
69978	3952971	3953741	TY-2482_chromosome	B7LDX8	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
27950	3952972	3952781	TY-2482_chromosome	A8A849	Putative uncharacterized protein	Escherichia coli O9:H4 (strain HS)
108076	3954715	3953888	TY-2482_chromosome	B7LDX9	Putative uncharacterized protein yjiC	Escherichia coli (strain 55989 / EAEC)
31668	3955387	3955776	TY-2482_chromosome	B7LDX6	Anti-adapter protein iraD	Escherichia coli (strain 55989 / EAEC)
69980	3956683	3955775	TY-2482_chromosome	B7LDY2	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
58042	3957920	3956751	TY-2482_chromosome	B7LDY3	Isoaspartyl dipeptidase (EC 3.4.19.5)	Escherichia coli (strain 55989 / EAEC)
60871	3958394	3957936	TY-2482_chromosome	B7LDY4	Putative uncharacterized protein yjiG	Escherichia coli (strain 55989 / EAEC)
111249	3959086	3958394	TY-2482_chromosome	D3GXY1	Putative transporter	Escherichia coli O44:H18 (strain 042 / EAEC)
31795	3959324	3959875	TY-2482_chromosome	B7LDY6	Probable RNA 2'-phosphotransferase (EC 2.7.1.-)	Escherichia coli (strain 55989 / EAEC)
91835	3961069	3959894	TY-2482_chromosome	B7LDY5	Putative uncharacterized protein yjiJ	Escherichia coli (strain 55989 / EAEC)
112309	3962108	3961140	TY-2482_chromosome	C8U0T1	Putative uncharacterized protein yjiK	Escherichia coli O103:H2 (strain 12009 / EHEC)
93942	3962319	3962065	TY-2482_chromosome	B7LDZ0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
100632	3963083	3962319	TY-2482_chromosome	B7LDY8	ATPase, activator of (R)-hydroxyglutaryl-CoA dehydratase	Escherichia coli (strain 55989 / EAEC)
66227	3964244	3963096	TY-2482_chromosome	B7LDZ2	Putative 2-hydroxyglutaryl-CoA dehydratase (HgdB-like)	Escherichia coli (strain 55989 / EAEC)
106492	3965667	3964363	TY-2482_chromosome	B7LDZ3	Putative uncharacterized protein yjiN	Escherichia coli (strain 55989 / EAEC)
69345	3966913	3965684	TY-2482_chromosome	B7LDZ1	Multidrug efflux system protein	Escherichia coli (strain 55989 / EAEC)
19868	3967171	3967380	TY-2482_chromosome	E9TKV9	Conserved domain protein	Escherichia coli MS 117-3
69982	3967380	3968333	TY-2482_chromosome	B7LDZ5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
105407	3969478	3968582	TY-2482_chromosome	C6UPC5	Fused predicted DNA-binding transcriptional regulator, predicted aminotransferase	Escherichia coli O157:H7 (strain TW14359 / EHEC)
94819	3969938	3969459	TY-2482_chromosome	B7LDZ4	Fused putative DNA-binding transcriptional regulator ; putative aminotransferase	Escherichia coli (strain 55989 / EAEC)
16654	3970376	3972466	TY-2482_chromosome	Q659X8	Conserved protein	Escherichia coli
64099	3972914	3972519	TY-2482_chromosome	B7LQL5	Endoribonuclease symE (EC 3.1.-.-)	Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-7
26571	3974814	3973081	TY-2482_chromosome	B7LE00	Type I restriction enzyme EcoAI specificity protein (S protein) (S.EcoAI)	Escherichia coli (strain 55989 / EAEC)
60563	3976319	3974817	TY-2482_chromosome	B7LE01	Type I restriction enzyme EcoEI M protein (M.EcoEI) (EC 2.1.1.72)	Escherichia coli (strain 55989 / EAEC)
73840	3978782	3976353	TY-2482_chromosome	B7LE02	Type I restriction enzyme EcoAI R protein (R.EcoAI) (EC 3.1.21.3)	Escherichia coli (strain 55989 / EAEC)
115148	3979039	3980709	TY-2482_chromosome	B7LE03	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104631	3981737	3980784	TY-2482_chromosome	B7LDZ9	Putative GTPase	Escherichia coli (strain 55989 / EAEC)
98989	3982077	3981751	TY-2482_chromosome	B7LE04	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
58245	3984232	3982085	TY-2482_chromosome	B7LE05	Putative uncharacterized protein yjiY	Escherichia coli (strain 55989 / EAEC)
88483	3984609	3986270	TY-2482_chromosome	B7LE07	Methyl-accepting chemotaxis protein I, serine sensor receptor	Escherichia coli (strain 55989 / EAEC)
77525	3987683	3986325	TY-2482_chromosome	B7LE06	Putative transporter	Escherichia coli (strain 55989 / EAEC)
62844	3988812	3987901	TY-2482_chromosome	B7LE08	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
78893	3988951	3989970	TY-2482_chromosome	B7LE09	Putative oxidoreductase, Zn-dependent and NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
32823	3992405	3990117	TY-2482_chromosome	B7LE10	Phosphoglycerol transferase I (EC 2.7.8.20) (Phosphatidylglycerol--membrane-oligosaccharide glycerophosphotransfe	Escherichia coli (strain 55989 / EAEC)
68532	3993156	3992662	TY-2482_chromosome	C8UN70	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC)
75556	3993939	3993205	TY-2482_chromosome	B7LE12	DNA biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
30654	3994481	3993945	TY-2482_chromosome	B7LEK9	Primosomal protein 1 (Primosomal protein I)	Escherichia coli (strain 55989 / EAEC)
110605	3995076	3994591	TY-2482_chromosome	B7LEL0	UPF0442 protein yjjB	Escherichia coli (strain 55989 / EAEC)
86133	3995885	3995055	TY-2482_chromosome	D3GY05	Putative membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)
98400	3996443	3997165	TY-2482_chromosome	B7LEL2	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
90840	3997126	3997800	TY-2482_chromosome	B5Z4P9	Transcriptional regulator, LuxR family	Escherichia coli O157:H7 (strain EC4115 / EHEC)
99077	3998629	3997844	TY-2482_chromosome	B7LEL4	Ferric iron reductase involved in ferric hydroximate transport	Escherichia coli (strain 55989 / EAEC)
88276	3998659	3999003	TY-2482_chromosome	B7LEL5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
r209	3999131	3999045	TY-2482_chromosome	ref|NC_010473|:4650800-4650886|Leu tRNA| [gene=leuQ] [locus_tag=ECDH10B_4527]		
r212	3999252	3999166	TY-2482_chromosome	ref|NC_010473|:4650685-4650771|Leu tRNA| [gene=leuP] [locus_tag=ECDH10B_4526]		
r208	3999367	3999281	TY-2482_chromosome	ref|NC_010473|:4650800-4650886|Leu tRNA| [gene=leuQ] [locus_tag=ECDH10B_4527]		
33792	4000707	3999679	TY-2482_chromosome	B7LEL6	Ribosomal RNA small subunit methyltransferase C (EC 2.1.1.172) (16S rRNA m2G1207 methyltransferase) (rRNA (guar	Escherichia coli (strain 55989 / EAEC)
75440	4000810	4001220	TY-2482_chromosome	B7LEL7	DNA polymerase III, psi subunit (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
102800	4001192	4001635	TY-2482_chromosome	B7LEL8	Acetylase for 30S ribosomal subunit protein S18 (EC 2.3.1.128)	Escherichia coli (strain 55989 / EAEC)

29324	4003647	4002160 TY-2482_chromosome	A7ZVR4	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
25412	4005062	4004373 TY-2482_chromosome	A7ZVR6	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
69959	4005418	4006488 TY-2482_chromosome	B7LEM3	Putative esterase	Escherichia coli (strain 55989 / EAEC)
59060	4006488	4007267 TY-2482_chromosome	B7LEM4	Putative DNase	Escherichia coli (strain 55989 / EAEC)
113934	4008363	4007503 TY-2482_chromosome	B7LEM5	Putative pyruvate formate lyase activating enzyme	Escherichia coli (strain 55989 / EAEC)
66219	4009885	4008338 TY-2482_chromosome	B7LEM6	Putative uncharacterized protein yjjI	Escherichia coli (strain 55989 / EAEC)
30592	4010143	4010919 TY-2482_chromosome	B7LEM7	Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboald	Escherichia coli (strain 55989 / EAEC)
34400	4011000	4012319 TY-2482_chromosome	B7LEM8	Thymidine phosphorylase (EC 2.4.2.4) (TdRPase)	Escherichia coli (strain 55989 / EAEC)
30587	4012374	4013594 TY-2482_chromosome	B7LEM9	Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Escherichia coli (strain 55989 / EAEC)
30595	4013677	4014393 TY-2482_chromosome	B7LEN0	Purine nucleoside phosphorylase deoD-type (PNP) (EC 2.4.2.1)	Escherichia coli (strain 55989 / EAEC)
85935	4014820	4014560 TY-2482_chromosome	D3GY25	Putative transcriptional regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
31947	4015868	4014855 TY-2482_chromosome	B7LEN2	Lipoate-protein ligase A (EC 2.7.7.63) (Lipoate--protein ligase)	Escherichia coli (strain 55989 / EAEC)
69960	4016540	4015899 TY-2482_chromosome	B7LEN3	Putative uncharacterized protein ytjB	Escherichia coli (strain 55989 / EAEC)
62713	4016646	4017611 TY-2482_chromosome	B7LEN4	3-phosphoserine phosphatase (EC 3.1.3.3)	Escherichia coli (strain 55989 / EAEC)
105531	4017663	4019042 TY-2482_chromosome	B7LEN5	DNA repair protein radA	Escherichia coli (strain 55989 / EAEC)
62714	4019066	4020295 TY-2482_chromosome	B7LEN6	Bifunctional DNA-binding transcriptional repressor and NMN adenylyltransferase	Escherichia coli (strain 55989 / EAEC)
115290	4022272	4020608 TY-2482_chromosome	B7LEN7	Fused putative transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
101829	4022483	4024417 TY-2482_chromosome	B7LEN8	Lytic murein transglycosylase, soluble (EC 3.2.1.-)	Escherichia coli (strain 55989 / EAEC)
34356	4024510	4024833 TY-2482_chromosome	B7LEN9	Trp operon repressor	Escherichia coli (strain 55989 / EAEC)
65303	4025399	4024881 TY-2482_chromosome	B5Z4S6	UPF0244 protein yjjX	Escherichia coli O157:H7 (strain EC4115 / EHEC)
31206	4025442	4026086 TY-2482_chromosome	B7LEP1	Probable phosphoglycerate mutase gpmB (EC 5.4.2.1) (PGAM) (Phosphoglyceromutase)	Escherichia coli (strain 55989 / EAEC)
59061	4026955	4026089 TY-2482_chromosome	B7LEP2	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
100906	4027166	4027636 TY-2482_chromosome	B7LEP3	Putative uncharacterized protein creA	Escherichia coli (strain 55989 / EAEC)
71433	4027652	4028338 TY-2482_chromosome	B7LEP4	DNA-binding response regulator in two-component regulatory system with CreC	Escherichia coli (strain 55989 / EAEC)
105016	4028341	4029762 TY-2482_chromosome	B7LEP5	Sensory histidine kinase in two-component regulatory system with CreB or PhoB, regulator of the CreBC regulon	Escherichia coli (strain 55989 / EAEC)
105239	4029823	4031172 TY-2482_chromosome	B7LEP6	Inner membrane protein	Escherichia coli (strain 55989 / EAEC)
69559	4031951	4031238 TY-2482_chromosome	B7LEP7	DNA-binding response regulator in two-component regulatory system with ArcB or CpxA	Escherichia coli (strain 55989 / EAEC)
61509	4032587	4033270 TY-2482_chromosome	B7LEP9	rRNA methyltransferase	Escherichia coli (strain 55989 / EAEC)
99208	4033633	4036092 TY-2482_chromosome	B7L4C7	Fused aspartokinase I ; homoserine dehydrogenase I (EC 1.1.1.3) (EC 2.7.2.4)	Escherichia coli (strain 55989 / EAEC)
31787	4036097	4037026 TY-2482_chromosome	B7L4C8	Homoserine kinase (HK) (HSK) (EC 2.7.1.39)	Escherichia coli (strain 55989 / EAEC)
98175	4037030	4038313 TY-2482_chromosome	B7L4C9	Threonine synthase (EC 4.2.3.1)	Escherichia coli (strain 55989 / EAEC)
27095	4039017	4038609 TY-2482_chromosome	A7ZVW4	Putative uncharacterized protein	Escherichia coli O9:H4 (strain HS)
34703	4039756	4038983 TY-2482_chromosome	B7L4D1	UPF0246 protein yaaA	Escherichia coli (strain 55989 / EAEC)
99211	4041256	4039829 TY-2482_chromosome	B7L4D2	Putative amino acid sodium/proton transporter	Escherichia coli (strain 55989 / EAEC)
105394	4041535	4042485 TY-2482_chromosome	B7L4D3	Transaldolase 1 (EC 2.2.1.2)	Escherichia coli (strain 55989 / EAEC)
62835	4042603	4043187 TY-2482_chromosome	B7L4D4	Molybdochelatase MogA, involved in Moco biosynthesis	Escherichia coli (strain 55989 / EAEC)
60613	4043791	4043228 TY-2482_chromosome	B7L4D5	Putative uncharacterized protein yaaH	Escherichia coli (strain 55989 / EAEC)
93929	4044653	4043943 TY-2482_chromosome	B7L4D6	Heat shock protein	Escherichia coli (strain 55989 / EAEC)
34706	4045083	4044682 TY-2482_chromosome	B7L4D7	UPF0412 protein yaaI	Escherichia coli (strain 55989 / EAEC)
88470	4045460	4047373 TY-2482_chromosome	B7L4D8	Chaperone Hsp70, co-chaperone with DnaJ	Escherichia coli (strain 55989 / EAEC)
30644	4047465	4048592 TY-2482_chromosome	B7L4D9	Chaperone protein DnaJ	Escherichia coli (strain 55989 / EAEC)
46902	4048941	4048702 TY-2482_chromosome	D6I4R4	Regulatory protein mokC	Escherichia coli B088
102950	4049437	4050600 TY-2482_chromosome	B7L4E0	Sodium-proton antiporter	Escherichia coli (strain 55989 / EAEC)
87364	4050663	4051565 TY-2482_chromosome	B7L4E1	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
90141	4052566	4051610 TY-2482_chromosome	B7L4E2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
74863	4053910	4052582 TY-2482_chromosome	D3H3A6	Fimbrial outer membrane usher protein	Escherichia coli O44:H18 (strain 042 / EAEC)
13230	4055577	4054106 TY-2482_chromosome	E9YZ54	Putative uncharacterized protein	Escherichia coli M863
25773	4055974	4056306 TY-2482_chromosome	Q1RGI0	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
66307	4056427	4056642 TY-2482_chromosome	B7L4E6	Putative uncharacterized protein yaaY	Escherichia coli (strain 55989 / EAEC)
101775	4056653	4057591 TY-2482_chromosome	B7L4E7	Bifunctional riboflavin kinase and FAD synthetase (EC 2.7.1.26) (EC 2.7.7.2)	Escherichia coli (strain 55989 / EAEC)
34119	4057637	4060450 TY-2482_chromosome	B7L4E8	Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase) (IleRS)	Escherichia coli (strain 55989 / EAEC)
31986	4060453	4060944 TY-2482_chromosome	B7L4E9	Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal peptidase) (Signal peptidase II) (SPase II	Escherichia coli (strain 55989 / EAEC)
91776	4061035	4061481 TY-2482_chromosome	B7L4F0	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Escherichia coli (strain 55989 / EAEC)
31704	4061486	4062433 TY-2482_chromosome	B7L4F1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)	Escherichia coli (strain 55989 / EAEC)
33420	4062502	4063413 TY-2482_chromosome	B7L4F2	Non-specific ribonucleoside hydrolase rihC (EC 3.2.-.-) (Purine/pyrimidine ribonucleoside hydrolase	Escherichia coli (strain 55989 / EAEC)
30540	4063583	4064401 TY-2482_chromosome	B7L4F3	Dihydrodipicolinate reductase (DHPR) (EC 1.3.1.26)	Escherichia coli (strain 55989 / EAEC)
68039	4064860	4066005 TY-2482_chromosome	B7L4F4	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)	Escherichia coli (strain 55989 / EAEC)
75845	4066026	4069244 TY-2482_chromosome	B7L4F5	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)	Escherichia coli (strain 55989 / EAEC)
8273	4069403	4069900 TY-2482_chromosome	C3TRD2	Transcriptional regulator of cai operon	Escherichia coli
90137	4069473	4069258 TY-2482_chromosome	B7L4F6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
30223	4070579	4069992 TY-2482_chromosome	B7L4F8	Carnitine operon protein CaiE	Escherichia coli (strain 55989 / EAEC)
59190	4071478	4070588 TY-2482_chromosome	B7L4F9	Crotonobetainyl CoA hydratase (EC 4.2.1.-)	Escherichia coli (strain 55989 / EAEC)
30207	4073032	4071482 TY-2482_chromosome	B7L4G0	Probable crotonobetaine/carnitine-CoA ligase (EC 6.2.1.-)	Escherichia coli (strain 55989 / EAEC)
30204	4074323	4073109 TY-2482_chromosome	B7L4G1	Crotonobetainyl-CoA:carnitine CoA-transferase (EC 2.8.3.-)	Escherichia coli (strain 55989 / EAEC)

30198	4075594	4074455	TY-2482_chromosome	B7L4G2	Crotonobetainyl-CoA dehydrogenase (EC 1.3.99.-) (Crotonobetainyl-CoA reductase)	Escherichia coli (strain 55989 / EAEC)
30229	4077139	4075628	TY-2482_chromosome	B7L4G3	L-carnitine/gamma-butyrobetaine antiporter	Escherichia coli (strain 55989 / EAEC)
62448	4077550	4078380	TY-2482_chromosome	B5YYD5	Protein FixA	Escherichia coli O157:H7 (strain EC4115 / EHEC)
30953	4078398	4079336	TY-2482_chromosome	B7L4G5	Protein fixB	Escherichia coli (strain 55989 / EAEC)
61108	4079390	4080673	TY-2482_chromosome	B7L4G6	Putative oxidoreductase with FAD/NAD(P)-binding domain (EC 1.5.5.1)	Escherichia coli (strain 55989 / EAEC)
115677	4080673	4080957	TY-2482_chromosome	B7L4G7	Putative 4Fe-4S ferredoxin	Escherichia coli (strain 55989 / EAEC)
109706	4081019	4082347	TY-2482_chromosome	B7L4G8	Putative transporter	Escherichia coli (strain 55989 / EAEC)
31778	4082458	4082985	TY-2482_chromosome	B7L4G9	Glutathione-regulated potassium-efflux system ancillary protein kefF	Escherichia coli (strain 55989 / EAEC)
31766	4082981	4084840	TY-2482_chromosome	B7L4H0	Glutathione-regulated potassium-efflux system protein kefC (K(+)/H(+) antiporter)	Escherichia coli (strain 55989 / EAEC)
58941	4084924	4085511	TY-2482_chromosome	B5YZ84	Dihydrofolate reductase (EC 1.5.1.3)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
29788	4086434	4085595	TY-2482_chromosome	B7L4H2	Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41) (Ap4A hydrolase) (Diadenosine 5',5'''-P1,P4-tetraphosp	Escherichia coli (strain 55989 / EAEC)
29784	4086818	4086444	TY-2482_chromosome	B7L4H3	Protein ApaG	Escherichia coli (strain 55989 / EAEC)
33784	4087642	4086824	TY-2482_chromosome	B7L4H4	Ribosomal RNA small subunit methyltransferase A (EC 2.1.1.182) (16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6)	Escherichia coli (strain 55989 / EAEC)
32901	4088628	4087642	TY-2482_chromosome	B7L4H5	4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262) (4-(phosphohydroxy)-L-threonine dehydrogenase	Escherichia coli (strain 55989 / EAEC)
65526	4089914	4088631	TY-2482_chromosome	B7L4H6	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	Escherichia coli (strain 55989 / EAEC)
82364	4092321	4089970	TY-2482_chromosome	B7L4H7	LPS-assembly protein lptD (Organic solvent tolerance protein)	Escherichia coli (strain 55989 / EAEC)
114126	4092576	4093388	TY-2482_chromosome	B7L4H8	DnaJ-like protein, membrane anchored	Escherichia coli (strain 55989 / EAEC)
69452	4094167	4093511	TY-2482_chromosome	B7L4H9	Pseudouridine synthase (EC 5.4.99.-)	Escherichia coli (strain 55989 / EAEC)
33241	4097085	4094182	TY-2482_chromosome	B7L4I0	RNA polymerase-associated protein rapA (EC 3.6.4.-) (ATP-dependent helicase hepA)	Escherichia coli (strain 55989 / EAEC)
69900	4099601	4097253	TY-2482_chromosome	B7L4I1	DNA polymerase (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
69901	4100371	4099679	TY-2482_chromosome	B7L4I2	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)	Escherichia coli (strain 55989 / EAEC)
29797	4102042	4100543	TY-2482_chromosome	B7L4I3	L-arabinose isomerase (EC 5.3.1.4)	Escherichia coli (strain 55989 / EAEC)
29801	4103753	4102056	TY-2482_chromosome	B7L4I4	Ribulokinase (EC 2.7.1.16)	Escherichia coli (strain 55989 / EAEC)
24616	4103875	4104096	TY-2482_chromosome	D2NB21	Putative uncharacterized protein	Escherichia coli O150:H5 (strain SE15)
58786	4104041	4104967	TY-2482_chromosome	B5YZA0	Arabinose operon regulatory protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
82424	4105056	4105817	TY-2482_chromosome	B7L4I6	Putative uncharacterized protein yabI	Escherichia coli (strain 55989 / EAEC)
110505	4106632	4105937	TY-2482_chromosome	B7L4I7	Thiamin transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
81097	4108226	4106619	TY-2482_chromosome	B7L4I8	Fused thiamin transporter subunits of ABC superfamily: membrane components	Escherichia coli (strain 55989 / EAEC)
102851	4109185	4108205	TY-2482_chromosome	B7L4I9	Thiamin transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
62654	4111004	4109352	TY-2482_chromosome	B7L4J0	DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
109915	4111326	4112501	TY-2482_chromosome	B7L4J1	Broad specificity sugar efflux system	Escherichia coli (strain 55989 / EAEC)
31868	4113158	4112556	TY-2482_chromosome	B7L4J2	3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) (Alpha-IPM isomerase) (IPMI) (Isopropylmalate isomerase)	Escherichia coli (strain 55989 / EAEC)
31864	4114569	4113172	TY-2482_chromosome	B7L4J3	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) (Alpha-IPM isomerase) (IPMI) (Isopropylmalate isomerase)	Escherichia coli (strain 55989 / EAEC)
95564	4115663	4114575	TY-2482_chromosome	B7LFU4	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	Escherichia coli (strain 55989 / EAEC)
31856	4117234	4115666	TY-2482_chromosome	B7LFU5	2-isopropylmalate synthase (EC 2.3.3.13) (Alpha-IPM synthase) (Alpha-isopropylmalate synthase)	Escherichia coli (strain 55989 / EAEC)
62751	4118073	4119014	TY-2482_chromosome	B7LFU7	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
94238	4119335	4121056	TY-2482_chromosome	B7LFU8	Acetolactate synthase (EC 2.2.1.6)	Escherichia coli (strain 55989 / EAEC)
106249	4121032	4121550	TY-2482_chromosome	B5YZB5	Acetolactate synthase, small subunit, isozyme III (EC 2.2.1.6)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
62212	4121733	4122734	TY-2482_chromosome	B7LFV0	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
11223	4122903	4123103	TY-2482_chromosome	E6A074	Putative uncharacterized protein	Escherichia coli MS 110-3
32469	4123339	4123794	TY-2482_chromosome	B7LFV1	Protein MraZ	Escherichia coli (strain 55989 / EAEC)
33803	4123799	4124737	TY-2482_chromosome	B7LFV2	Ribosomal RNA small subunit methyltransferase H (EC 2.1.1.199) (16S rRNA m(4)C1402 methyltransferase) (rRNA (cyt	Escherichia coli (strain 55989 / EAEC)
101774	4124737	4125099	TY-2482_chromosome	B7LFV3	Membrane bound cell division protein at septum containing leucine zipper motif	Escherichia coli (strain 55989 / EAEC)
106500	4125118	4126881	TY-2482_chromosome	B7LFV4	Transpeptidase involved in septal peptidoglycan synthesis (Penicillin-binding protein 3)	Escherichia coli (strain 55989 / EAEC)
87357	4126871	4128355	TY-2482_chromosome	B7LFV5	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:meso-diaminopimelate ligase (EC 6.3.2.13)	Escherichia coli (strain 55989 / EAEC)
113181	4128355	4129710	TY-2482_chromosome	B7LFV6	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10)	Escherichia coli (strain 55989 / EAEC)
32465	4129707	4130786	TY-2482_chromosome	B7LFV7	Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) (UDP-MurNAc-pentapeptide phosphotransferase	Escherichia coli (strain 55989 / EAEC)
76273	4130792	4132105	TY-2482_chromosome	B7LFV8	UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmura	Escherichia coli (strain 55989 / EAEC)
83497	4132108	4133349	TY-2482_chromosome	B7LFV9	Integral membrane protein involved in stabilizing FstZ ring during cell division	Escherichia coli (strain 55989 / EAEC)
32554	4133349	4134413	TY-2482_chromosome	B7LFW0	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine tran	Escherichia coli (strain 55989 / EAEC)
32542	4134470	4135942	TY-2482_chromosome	B7LFW1	UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Escherichia coli (strain 55989 / EAEC)
64361	4135938	4136855	TY-2482_chromosome	B7LFW2	D-alanine--D-alanine ligase 1 (EC 6.3.2.4) (D-Ala-D-Ala ligase 1) (D-alanylalanine synthetase 1)	Escherichia coli (strain 55989 / EAEC)
73600	4136860	4137687	TY-2482_chromosome	B7LFW3	Membrane anchored protein involved in growth of wall at septum	Escherichia coli (strain 55989 / EAEC)
72952	4137687	4138946	TY-2482_chromosome	B7LFW4	ATP-binding cell division protein involved in recruitment of FtsK to Z ring	Escherichia coli (strain 55989 / EAEC)
61757	4139010	4140158	TY-2482_chromosome	B7LFW5	Cell division protein ftsZ	Escherichia coli (strain 55989 / EAEC)
31972	4140262	4141176	TY-2482_chromosome	B7LFW6	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (EC 3.5.1.-) (UDP-3-O-acyl-GlcNAc deacetylase)	Escherichia coli (strain 55989 / EAEC)
98915	4141335	4141919	TY-2482_chromosome	B5YZD3	Secretion monitor protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
21928	4141405	4141154	TY-2482_chromosome	D6J5V7	Predicted protein	Escherichia coli B354
33906	4141984	4144686	TY-2482_chromosome	B7LFW8	Protein translocase subunit secA	Escherichia coli (strain 55989 / EAEC)
110666	4144749	4145135	TY-2482_chromosome	B7LFW9	Nucleoside triphosphate pyrophosphohydrolase, marked preference for dGTP (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
106971	4145435	4145241	TY-2482_chromosome	C8TGN2	UPF0243 zinc-binding protein yacG	Escherichia coli O26:H11 (strain 11368 / EHEC)
34709	4146188	4145448	TY-2482_chromosome	B7LFX0	UPF0289 protein yacF	Escherichia coli (strain 55989 / EAEC)
62162	4146808	4146191	TY-2482_chromosome	B7LFX1	Dephospho-CoA kinase (EC 2.7.1.24)	Escherichia coli (strain 55989 / EAEC)
31312	4147033	4148073	TY-2482_chromosome	B7LFX2	GMP reductase (EC 1.7.1.7) (Guanosine 5'-monophosphate oxidoreductase) (Guanosine monophosphate reductase)	Escherichia coli (strain 55989 / EAEC)

82640	4149313	4148114	TY-2482_chromosome	B7LFX3	Assembly protein in type IV pilin biogenesis, transmembrane protein	Escherichia coli (strain 55989 / EAEC)
78965	4150688	4149306	TY-2482_chromosome	B7LFX4	Putative uncharacterized protein hofB	Escherichia coli (strain 55989 / EAEC)
66257	4151138	4150701	TY-2482_chromosome	B7LFX5	Putative major pilin subunit	Escherichia coli (strain 55989 / EAEC)
11564	4151160	4151381	TY-2482_chromosome	D6J5W8	Putative uncharacterized protein	Escherichia coli B354
109506	4152234	4151344	TY-2482_chromosome	B7LFX6	Quinolinate phosphoribosyltransferase (EC 2.4.2.19)	Escherichia coli (strain 55989 / EAEC)
78958	4152322	4152870	TY-2482_chromosome	B7LFX7	N-acetyl-anhydromuranmyl-L-alanine amidase (EC 3.5.1.28)	Escherichia coli (strain 55989 / EAEC)
99132	4152870	4153721	TY-2482_chromosome	B7LFX8	Putative uncharacterized protein ampE	Escherichia coli (strain 55989 / EAEC)
86051	4155140	4153770	TY-2482_chromosome	B7LFX9	Aromatic amino acid transporter	Escherichia coli (strain 55989 / EAEC)
62760	4155681	4156442	TY-2482_chromosome	B7LFY0	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
87695	4156606	4159266	TY-2482_chromosome	B7LFY1	Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	Escherichia coli (strain 55989 / EAEC)
81007	4159284	4161173	TY-2482_chromosome	B7LFY2	Pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2 (EC 2.3.1.12)	Escherichia coli (strain 55989 / EAEC)
59100	4161501	4162922	TY-2482_chromosome	B7LFY3	Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Escherichia coli (strain 55989 / EAEC)
116191	4164753	4162999	TY-2482_chromosome	B7LFY4	Putative uncharacterized protein yacH	Escherichia coli (strain 55989 / EAEC)
113338	4165108	4167702	TY-2482_chromosome	B7LFY5	Aconitate hydratase 2 (EC 4.2.1.3)	Escherichia coli (strain 55989 / EAEC)
34713	4167881	4168240	TY-2482_chromosome	B7LFY6	UPF0231 protein yacL	Escherichia coli (strain 55989 / EAEC)
33991	4169075	4168284	TY-2482_chromosome	B7LFY7	S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SAMDC) (EC 4.1.1.50) [Cleaved into: S-adenosylmethi	Escherichia coli (strain 55989 / EAEC)
33995	4169957	4169094	TY-2482_chromosome	B7LFY8	Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) (PAPT) (SPDSY)	Escherichia coli (strain 55989 / EAEC)
114026	4170576	4172123	TY-2482_chromosome	B7LFZ0	Multicopper oxidase (Laccase)	Escherichia coli (strain 55989 / EAEC)
95545	4170581	4170066	TY-2482_chromosome	B7LFY9	Putative uncharacterized protein yacC	Escherichia coli (strain 55989 / EAEC)
69996	4174563	4172176	TY-2482_chromosome	B7LFZ1	Glucose dehydrogenase (EC 1.1.5.2)	Escherichia coli (strain 55989 / EAEC)
106528	4174769	4175302	TY-2482_chromosome	B7LGP1	Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	Escherichia coli (strain 55989 / EAEC)
79100	4176008	4175349	TY-2482_chromosome	B7LGI8	Carbonic anhydrase (EC 4.2.1.1)	Escherichia coli (strain 55989 / EAEC)
106521	4176117	4177040	TY-2482_chromosome	B7LGI9	Putative transporter subunit: ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
61210	4177040	4177807	TY-2482_chromosome	B7LGJ0	Putative transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
71421	4177915	4178352	TY-2482_chromosome	B7LGJ1	Putative PTS Enzyme IIA	Escherichia coli (strain 55989 / EAEC)
88320	4178419	4179645	TY-2482_chromosome	B7LGJ2	Putative exported polysaccharide deacetylase	Escherichia coli (strain 55989 / EAEC)
32858	4180032	4179655	TY-2482_chromosome	B7LGJ3	Aspartate 1-decarboxylase (EC 4.1.1.11) (Aspartate alpha-decarboxylase) [Cleaved into: Aspartate 1-decarboxylase be	Escherichia coli (strain 55989 / EAEC)
70050	4180306	4181205	TY-2482_chromosome	B7LGJ4	Putative transposase	Escherichia coli (strain 55989 / EAEC)
32854	4182133	4181285	TY-2482_chromosome	B7LGJ5	Pantothenate synthetase (PS) (EC 6.3.2.1) (Pantoate--beta-alanine ligase) (Pantoate-activating enzyme)	Escherichia coli (strain 55989 / EAEC)
32850	4182939	4182148	TY-2482_chromosome	B7LGJ6	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (Ketopantoate hydroxymethyltransferase) (KPHMT	Escherichia coli (strain 55989 / EAEC)
90198	4184326	4183055	TY-2482_chromosome	B7LGJ7	Putative exported protein, putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
110419	4184975	4184382	TY-2482_chromosome	B7LGJ8	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
106524	4185604	4185005	TY-2482_chromosome	B7LGJ9	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
94123	4186188	4185622	TY-2482_chromosome	B7LGK0	Putative fimbrial-like adhesin exported protein	Escherichia coli (strain 55989 / EAEC)
68441	4188769	4186169	TY-2482_chromosome	Q8Z9C7	Outer membrane usher protein HtrE	Salmonella typhi
108562	4189580	4188843	TY-2482_chromosome	B7LGK2	Periplasmic pilin chaperone	Escherichia coli (strain 55989 / EAEC)
114071	4190269	4189688	TY-2482_chromosome	B7LGK3	Putative fimbrial-like adhesin exported protein	Escherichia coli (strain 55989 / EAEC)
62136	4191118	4190642	TY-2482_chromosome	B7LGK4	2-amino-4-hydroxy-6-hydroxymethyldihyropteridine pyrophosphokinase (EC 2.7.6.3)	Escherichia coli (strain 55989 / EAEC)
91406	4192533	4191118	TY-2482_chromosome	B7LGK5	Poly(A) polymerase I (EC 2.7.7.19)	Escherichia coli (strain 55989 / EAEC)
102835	4193498	4192575	TY-2482_chromosome	B7LGK6	Glutamyl-Q tRNA(Asp) synthetase (Glu-Q-RSs) (EC 6.1.1.-)	Escherichia coli (strain 55989 / EAEC)
11257	4193990	4193468	TY-2482_chromosome	E7IEQ9	DnaK transcriptional regulator DksA	Escherichia coli LT-68
33931	4194872	4194171	TY-2482_chromosome	B7LGK8	Sugar fermentation stimulation protein A	Escherichia coli (strain 55989 / EAEC)
73737	4195491	4197917	TY-2482_chromosome	B7LGL0	ATP-dependent (RNA) helicase	Escherichia coli (strain 55989 / EAEC)
106525	4198116	4200647	TY-2482_chromosome	B7LGL1	Fused glycosyl transferase ; transpeptidase (EC 2.4.1.129) (EC 3.4.-.-)	Escherichia coli (strain 55989 / EAEC)
73739	4200870	4203110	TY-2482_chromosome	B7LGL2	Ferrichrome outer membrane transporter	Escherichia coli (strain 55989 / EAEC)
75960	4203164	4203958	TY-2482_chromosome	B7LGL3	Iron-hydroxamate transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
70056	4203961	4204848	TY-2482_chromosome	B7LGL4	Iron-hydroxamate transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
106527	4204848	4206827	TY-2482_chromosome	B7LGL5	Fused iron-hydroxamate transporter subunits of ABC superfamily: membrane components	Escherichia coli (strain 55989 / EAEC)
31232	4208145	4206868	TY-2482_chromosome	B7LGL6	Glutamate-1-semialdehyde 2,1-aminomutase (GSA) (EC 5.4.3.8) (Glutamate-1-semialdehyde aminotransferase) (GSA-	Escherichia coli (strain 55989 / EAEC)
30317	4208370	4209788	TY-2482_chromosome	B7LGL7	H(+)/Cl(-) exchange transporter ClcA	Escherichia coli (strain 55989 / EAEC)
30787	4209873	4210214	TY-2482_chromosome	B7LGL8	Iron--sulfur cluster insertion protein erpA	Escherichia coli (strain 55989 / EAEC)
84608	4210887	4210267	TY-2482_chromosome	B7LGL9	Putative uncharacterized protein yadS	Escherichia coli (strain 55989 / EAEC)
73740	4211725	4210928	TY-2482_chromosome	B7LGM0	Vitamin B12 transporter subunit: periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
32514	4212416	4211721	TY-2482_chromosome	B7LGM1	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase (MTA/SAH nucleosidase) (MTAN) (EC 3.2.2.9) (5'-met	Escherichia coli (strain 55989 / EAEC)
30606	4212500	4214014	TY-2482_chromosome	B7LGM2	Deoxyguanosinetriphosphate triphosphohydrolase (dGTP triphosphohydrolase) (dGTPase) (EC 3.1.5.1)	Escherichia coli (strain 55989 / EAEC)
109926	4214147	4215568	TY-2482_chromosome	B7LGM3	Serine endoprotease (Protease Do), membrane-associated (EC 3.4.21.-)	Escherichia coli (strain 55989 / EAEC)
60679	4215726	4216880	TY-2482_chromosome	B7LGM4	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
34716	4217358	4216975	TY-2482_chromosome	B7LGM5	UPF0325 protein yaeH	Escherichia coli (strain 55989 / EAEC)
88508	4218497	4217676	TY-2482_chromosome	B7LGM6	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) (Tetrahydrodipicolinate N-succinylt	Escherichia coli (strain 55989 / EAEC)
31145	4221200	4218531	TY-2482_chromosome	B7LGM7	[Protein-PII] uridylyltransferase (PII uridylyl-transferase) (EC 2.7.7.59) (UTase) (Uridylyl-removing enzyme)	Escherichia coli (strain 55989 / EAEC)
84609	4222056	4221265	TY-2482_chromosome	B7LGM8	Methionine aminopeptidase (EC 3.4.11.18)	Escherichia coli (strain 55989 / EAEC)
r121	4222262	4222397	TY-2482_chromosome	ref|NC_010473|:163816-163951|-| [gene=tff] [locus_tag=ECDH10B_0148]		
24429	4222277	4222059	TY-2482_chromosome	B7LGM9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
33744	4222424	4223146	TY-2482_chromosome	B7LGN0	30S ribosomal protein S2	Escherichia coli (strain 55989 / EAEC)

27173	4224153	4223104	TY-2482_chromosome	A1A7L4	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
105623	4224405	4225127	TY-2482_chromosome	B7LGN2	Uridylate kinase (EC 2.7.4.-)	Escherichia coli (strain 55989 / EAEC)
33691	4225422	4225976	TY-2482_chromosome	B7LGN3	Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Escherichia coli (strain 55989 / EAEC)
93720	4226071	4227264	TY-2482_chromosome	B7LGN4	1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXP reductoisomerase) (EC 1.1.1.267) (1-deoxyxylulose-5-phospł	Escherichia coli (strain 55989 / EAEC)
66241	4227453	4228211	TY-2482_chromosome	B7LGN5	Undecaprenyl pyrophosphate synthase (EC 2.5.1.31)	Escherichia coli (strain 55989 / EAEC)
90025	4228227	4229081	TY-2482_chromosome	B7LGN6	Phosphatidate cytidylyltransferase (EC 2.7.7.41)	Escherichia coli (strain 55989 / EAEC)
114072	4229096	4230445	TY-2482_chromosome	B7LGN7	Zinc metallopeptidase (EC 3.4.24.-)	Escherichia coli (strain 55989 / EAEC)
34722	4230478	4232907	TY-2482_chromosome	B7LGN8	Outer membrane protein assembly factor yaeT	Escherichia coli (strain 55989 / EAEC)
102147	4233032	4233514	TY-2482_chromosome	B7LGN9	Periplasmic chaperone	Escherichia coli (strain 55989 / EAEC)
57950	4233521	4234543	TY-2482_chromosome	B7LGP0	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-)	Escherichia coli (strain 55989 / EAEC)
9284	4234579	4235103	TY-2482_chromosome	Q14F34	FabZ (Fragment)	Escherichia coli
31964	4235110	4235895	TY-2482_chromosome	B7LGP3	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase (UDP-N-acetylglucosamine acyltransferase) (I	Escherichia coli (strain 55989 / EAEC)
31968	4235898	4237043	TY-2482_chromosome	B7LGP4	Lipid-A-disaccharide synthase (EC 2.4.1.182)	Escherichia coli (strain 55989 / EAEC)
33639	4237043	4237636	TY-2482_chromosome	B7LGP5	Ribonuclease HII (RNase HII) (EC 3.1.26.4)	Escherichia coli (strain 55989 / EAEC)
59151	4237676	4241155	TY-2482_chromosome	B7LGP6	DNA polymerase III alpha subunit (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
29678	4241171	4242127	TY-2482_chromosome	B7LGP7	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (ACCase subunit alpha) (Acetyl-CoA carboxylase ca	Escherichia coli (strain 55989 / EAEC)
73741	4242229	4244367	TY-2482_chromosome	B7LGP8	Lysine decarboxylase 2, constitutive (EC 4.1.1.18)	Escherichia coli (strain 55989 / EAEC)
88422	4244427	4244813	TY-2482_chromosome	B7LGP9	Putative S-C lyase	Escherichia coli (strain 55989 / EAEC)
95612	4244881	4246176	TY-2482_chromosome	B7LGQ0	tRNA(Ile)-lysidine synthase (EC 6.3.4.-) (tRNA(Ile)-2-lysyl-cytidine synthase) (tRNA(Ile)-lysidine synthetase)	Escherichia coli (strain 55989 / EAEC)
113720	4246488	4246231	TY-2482_chromosome	B5Z0G8	Rof protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
34719	4246675	4246478	TY-2482_chromosome	B7LGQ2	UPF0253 protein yaeP	Escherichia coli (strain 55989 / EAEC)
105030	4246841	4247383	TY-2482_chromosome	B7LGQ3	Putative uncharacterized protein yaeQ	Escherichia coli (strain 55989 / EAEC)
115299	4247383	4247802	TY-2482_chromosome	B7LGQ4	Putative uncharacterized protein yaeJ	Escherichia coli (strain 55989 / EAEC)
69928	4247819	4248526	TY-2482_chromosome	B7LGQ5	Lipoprotein involved with copper homeostasis and adhesion	Escherichia coli (strain 55989 / EAEC)
115755	4248779	4249756	TY-2482_chromosome	B7LF78	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
17378	4250786	4250208	TY-2482_chromosome	E7H755	YaeF	Escherichia coli EPECa14
34159	4252557	4250842	TY-2482_chromosome	B7LHA4	Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (ProRS)	Escherichia coli (strain 55989 / EAEC)
70073	4253376	4252672	TY-2482_chromosome	B7LHA5	Putative uncharacterized protein yaeB	Escherichia coli (strain 55989 / EAEC)
112383	4253777	4253376	TY-2482_chromosome	B7LHA6	Putative uncharacterized protein rcsF	Escherichia coli (strain 55989 / EAEC)
91355	4254710	4253898	TY-2482_chromosome	B7LHA7	DL-methionine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
72138	4255403	4254753	TY-2482_chromosome	B7LHA8	DL-methionine transporter subunit ; membrane component protein of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
73770	4256427	4255399	TY-2482_chromosome	B7LHA9	DL-methionine transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
95434	4256615	4257184	TY-2482_chromosome	B7LHB0	D,D-heptose 1,7-bisphosphate phosphatase	Escherichia coli (strain 55989 / EAEC)
r55	4257551	4259092	TY-2482_chromosome	ref|NC_010473|:3522988-3524529|16S ribosomal RNA| [gene=rrsD] [locus_tag=ECDH10B_3453		
11308	4257697	4257464	TY-2482_chromosome	E9WNY3	Putative uncharacterized protein	Escherichia coli E1520
25830	4258672	4258989	TY-2482_chromosome	Q57H85	ORF16-lacZ fusion protein	Salmonella choleraesuis
r244	4259161	4259237	TY-2482_chromosome	ref|NC_010473|:4134084-4134160|Ile tRNA| [gene=ileT] [locus_tag=ECDH10B_4041		
r330	4259280	4259355	TY-2482_chromosome	ref|NC_010473|:4134203-4134278|Ala tRNA| [gene=alaT] [locus_tag=ECDH10B_4042		
r2	4259539	4262442	TY-2482_chromosome	ref|NC_010473|:4307762-4310665|23S ribosomal RNA| [gene=rrlE] [locus_tag=ECDH10B_4198		
24094	4260067	4259765	TY-2482_chromosome	Q1R3T8	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
13802	4261328	4261125	TY-2482_chromosome	C1HUN3	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
20478	4261857	4261405	TY-2482_chromosome	C1HUN1	Cell wall-associated hydrolase (Fragment)	Escherichia sp. 3_2_53FAA
22412	4262217	4261861	TY-2482_chromosome	C1HUN0	Prolipoprotein diacylglyceryl transferase (Fragment)	Escherichia sp. 3_2_53FAA
r131	4262536	4262655	TY-2482_chromosome	ref|NC_010473|:4043643-4043762|5S ribosomal RNA| [gene=rrfC] [locus_tag=ECDH10B_3948		
29585	4262760	4263032	TY-2482_chromosome	B7LHB1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
r249	4262847	4262923	TY-2482_chromosome	ref|NC_010473|:4043815-4043891|Asp tRNA| [gene=aspT] [locus_tag=ECDH10B_3949		
88306	4263085	4263885	TY-2482_chromosome	B7LHB2	2,5-diketo-D-gluconate reductase B (EC 1.1.1.274)	Escherichia coli (strain 55989 / EAEC)
113545	4264799	4263888	TY-2482_chromosome	B7LHB4	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
34726	4265040	4265837	TY-2482_chromosome	B7LHB5	UPF0294 protein yafD	Escherichia coli (strain 55989 / EAEC)
102940	4265918	4266685	TY-2482_chromosome	B7LHB6	Putative S-adenosyl-L-methionine-dependent methyltransferase	Escherichia coli (strain 55989 / EAEC)
70102	4268094	4266739	TY-2482_chromosome	B7LHB7	Membrane-bound lytic murein transglycosylase D (EC 3.2.1.-)	Escherichia coli (strain 55989 / EAEC)
31152	4268921	4268169	TY-2482_chromosome	B7LHB8	Hydroxyacylglutathione hydrolase (EC 3.1.2.6) (Glyoxalase II) (Glx II)	Escherichia coli (strain 55989 / EAEC)
102941	4268955	4269674	TY-2482_chromosome	B7LHB9	Putative S-adenosyl-L-methionine-dependent methyltransferase	Escherichia coli (strain 55989 / EAEC)
113262	4270197	4270934	TY-2482_chromosome	D3GS43	DNA polymerase III epsilon subunit	Escherichia coli O44:H18 (strain 042 / EAEC)
15676	4270252	4269677	TY-2482_chromosome	C4X416	Ribonuclease H (RNase H) (EC 3.1.26.4)	Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044
r250	4271070	4271146	TY-2482_chromosome	ref|NC_010473|:4043815-4043891|Asp tRNA| [gene=aspT] [locus_tag=ECDH10B_3949		
27948	4271153	4270842	TY-2482_chromosome	A1A7Q7	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
97065	4271473	4272255	TY-2482_chromosome	B7LHC2	Putative aminopeptidase	Escherichia coli (strain 55989 / EAEC)
90311	4272874	4272398	TY-2482_chromosome	C8THN8	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
27355	4273813	4272887	TY-2482_chromosome	B7LHC3	Inner membrane protein yafU	Escherichia coli (strain 55989 / EAEC)
60680	4274324	4273845	TY-2482_chromosome	B7LHC4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
70074	4275790	4274351	TY-2482_chromosome	B7LHC5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26996	4279235	4275714	TY-2482_chromosome	B7LHC6	IcmF-like protein	Escherichia coli (strain 55989 / EAEC)
78665	4280735	4279257	TY-2482_chromosome	B7LHC7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)

67968	4281417	4280677	TY-2482_chromosome	B7LHC8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
84614	4284287	4281417	TY-2482_chromosome	B7LHC9	Putative ATP-dependent Clp proteinase Aec27 ATP-binding chain, with chaperone activity	Escherichia coli (strain 55989 / EAEC)
94063	4284943	4284185	TY-2482_chromosome	B7LHD0	Putative membrane protein Aec26	Escherichia coli (strain 55989 / EAEC)
59164	4286279	4284951	TY-2482_chromosome	B7LHD1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
82641	4286806	4286285	TY-2482_chromosome	B7LHD2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
59165	4288104	4286806	TY-2482_chromosome	B7LHD3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
116130	4289196	4288111	TY-2482_chromosome	B7LHD4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
99178	4291004	4289157	TY-2482_chromosome	B7LHD5	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
94129	4291421	4291011	TY-2482_chromosome	B7LHD6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
79168	4292903	4291431	TY-2482_chromosome	B7LHD7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
60762	4293178	4292957	TY-2482_chromosome	B7LHD8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
97331	4293713	4293216	TY-2482_chromosome	B7LHD9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
75547	4294410	4294925	TY-2482_chromosome	B7LHE1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73752	4295138	4297276	TY-2482_chromosome	B7LHE2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
17606	4297355	4300568	TY-2482_chromosome	B3IHE6	Protein RhsA	Escherichia coli E110019
77435	4301002	4301481	TY-2482_chromosome	B7LHE5	Putative uncharacterized protein ydcD	Escherichia coli (strain 55989 / EAEC)
110629	4301665	4302408	TY-2482_chromosome	B7LHE6	Putative uncharacterized protein yncI	Escherichia coli (strain 55989 / EAEC)
111491	4302969	4304027	TY-2482_chromosome	B7LHE8	Putative transposase	Escherichia coli (strain 55989 / EAEC)
64821	4304842	4304075	TY-2482_chromosome	B7LHF0	Putative C-N hydrolase family amidase	Escherichia coli (strain 55989 / EAEC)
79011	4304996	4305466	TY-2482_chromosome	B7LHF1	Inhibitor of vertebrate C-lysozyme	Escherichia coli (strain 55989 / EAEC)
93374	4307956	4305515	TY-2482_chromosome	B7LHF2	Acyl coenzyme A dehydrogenase (EC 1.3.99.3)	Escherichia coli (strain 55989 / EAEC)
25515	4308034	4308771	TY-2482_chromosome	A1A7T5	Phosphoheptose isomerase	Escherichia coli O1:K1 / APEC
62800	4308980	4309744	TY-2482_chromosome	B7LHF4	Putative glutamine amidotransferases class-II	Escherichia coli (strain 55989 / EAEC)
84619	4310458	4309721	TY-2482_chromosome	B7LHF5	Putative uncharacterized protein yafK	Escherichia coli (strain 55989 / EAEC)
59166	4310892	4310617	TY-2482_chromosome	B7LHF6	Toxin of the YafQ-DinJ toxin-antitoxin system	Escherichia coli (strain 55989 / EAEC)
77436	4311155	4310898	TY-2482_chromosome	B7LHF7	Antitoxin of YafQ-DinJ toxin-antitoxin system	Escherichia coli (strain 55989 / EAEC)
75906	4311341	4312111	TY-2482_chromosome	C8THQ7	Predicted lipoprotein and C40 family peptidase	Escherichia coli O26:H11 (strain 11368 / EHEC)
105527	4312527	4312174	TY-2482_chromosome	B7LHF9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
81053	4312819	4312523	TY-2482_chromosome	B7LHG0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
95560	4314642	4312906	TY-2482_chromosome	B7LHG1	Flagellar system protein	Escherichia coli (strain 55989 / EAEC)
99033	4315443	4316495	TY-2482_chromosome	B7LHG3	DNA polymerase IV (Pol IV) (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
106963	4316495	4316944	TY-2482_chromosome	C8UI55	Predicted acyltransferase	Escherichia coli O111:H- (strain 11128 / EHEC)
101643	4317166	4318329	TY-2482_chromosome	B7L3Y7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25847	4318245	4318940	TY-2482_chromosome	A1A7U7	Peptide chain release factor-like protein	Escherichia coli O1:K1 / APEC
88400	4320457	4319003	TY-2482_chromosome	B7L3Y9	Aminoacyl-histidine dipeptidase (Peptidase D) (EC 3.4.13.3)	Escherichia coli (strain 55989 / EAEC)
34607	4320718	4321173	TY-2482_chromosome	B7L3Z0	Xanthine phosphoribosyltransferase (EC 2.4.2.22) (Xanthine-guanine phosphoribosyltransferase) (XGPRT)	Escherichia coli (strain 55989 / EAEC)
31024	4321268	4322509	TY-2482_chromosome	B7L3Z1	Esterase frsA (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
30410	4322570	4322968	TY-2482_chromosome	B7L3Z2	Sigma factor-binding protein crl	Escherichia coli (strain 55989 / EAEC)
87433	4324065	4323013	TY-2482_chromosome	B7L3Z3	Outer membrane phosphoporin protein E	Escherichia coli (strain 55989 / EAEC)
33077	4324353	4325453	TY-2482_chromosome	B7L3Z4	Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl kinase) (GK)	Escherichia coli (strain 55989 / EAEC)
33073	4325468	4326718	TY-2482_chromosome	B7L3Z5	Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-ga	Escherichia coli (strain 55989 / EAEC)
r468	4326836	4326911	TY-2482_chromosome	ref|NC_010473|:236199-236274|Thr tRNA| [gene=thrW] [locus_tag=ECDH10B_0226]		
13276	4327284	4326973	TY-2482_chromosome	D6J782	Predicted protein	Escherichia coli B354
23364	4328793	4328239	TY-2482_chromosome	B3HAL5	Transposon Tn21 resolvase	Escherichia coli B7A
17111	4330792	4331457	TY-2482_chromosome	E2WYY1	Putative uncharacterized protein	Escherichia coli 1827-70
22803	4331470	4331736	TY-2482_chromosome	E9V5S4	Putative uncharacterized protein	Escherichia coli H252
21579	4331837	4332217	TY-2482_chromosome	D7ZST0	Conserved domain protein	Escherichia coli MS 187-1
14317	4332236	4332478	TY-2482_chromosome	B3HAK9	ABC transporter ATPase component	Escherichia coli B7A
12484	4332481	4332777	TY-2482_chromosome	B3HAK8	Putative uncharacterized protein	Escherichia coli B7A
15659	4333973	4334353	TY-2482_chromosome	B3HAK3	Putative uncharacterized protein	Escherichia coli B7A
18561	4334371	4335399	TY-2482_chromosome	B3HAK2	Putative uncharacterized protein	Escherichia coli B7A
90110	4335786	4337624	TY-2482_chromosome	C8THX6	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
22613	4337675	4338349	TY-2482_chromosome	E9TCE4	Putative uncharacterized protein	Escherichia coli MS 117-3
115462	4339710	4338436	TY-2482_chromosome	C8THX8	Putative integrase	Escherichia coli O26:H11 (strain 11368 / EHEC)
102843	4340038	4341249	TY-2482_chromosome	B7L3Z6	Putative prophage CPS-53 integrase	Escherichia coli (strain 55989 / EAEC)
29409	4341375	4342175	TY-2482_chromosome	B7L3Z7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
27689	4342373	4342567	TY-2482_chromosome	B7L3Z8	Phage transcriptional regulator, AlpA	Escherichia coli (strain 55989 / EAEC)
26580	4342649	4343446	TY-2482_chromosome	B7L3Z9	AntA/AntB antirepressor	Escherichia coli (strain 55989 / EAEC)
28044	4343442	4345025	TY-2482_chromosome	B7L400	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
24286	4345021	4345383	TY-2482_chromosome	B7L402	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
24586	4345379	4345576	TY-2482_chromosome	B7L403	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
26614	4345584	4345871	TY-2482_chromosome	B7L404	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
29566	4345871	4348000	TY-2482_chromosome	B7L405	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25604	4348462	4349016	TY-2482_chromosome	B7L406	Activator of ProP osmoprotectant transporter	Escherichia coli (strain 55989 / EAEC)

25783	4349016	4349300	TY-2482_chromosome	B7L407	Protein perC (Protein bfpW)	Escherichia coli (strain 55989 / EAEC)
25901	4349438	4350577	TY-2482_chromosome	B7L408	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
24755	4350645	4350965	TY-2482_chromosome	B7L409	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
29590	4351411	4351680	TY-2482_chromosome	B7L410	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
91966	4351765	4352307	TY-2482_chromosome	B7L411	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
27690	4352914	4353906	TY-2482_chromosome	B7L412	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
24353	4353902	4354879	TY-2482_chromosome	B7L413	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
23740	4355264	4355764	TY-2482_chromosome	P71299	Putative uncharacterized protein	Escherichia coli
62821	4356687	4355734	TY-2482_chromosome	B7L415	Putative uncharacterized protein yagQ	Escherichia coli (strain 55989 / EAEC)
102936	4358895	4356700	TY-2482_chromosome	B7L416	Putative oxidoreductase with molybdenum-binding domain	Escherichia coli (strain 55989 / EAEC)
60499	4359848	4358895	TY-2482_chromosome	B7L417	Putative oxidoreductase with FAD-binding domain	Escherichia coli (strain 55989 / EAEC)
72954	4360534	4359848	TY-2482_chromosome	B7L418	Putative oxidoreductase, 2Fe-2S subunit	Escherichia coli (strain 55989 / EAEC)
90373	4360952	4361563	TY-2482_chromosome	B7L419	Putative uncharacterized protein yagU	Escherichia coli (strain 55989 / EAEC)
16686	4361571	4361816	TY-2482_chromosome	B3XF80	Putative uncharacterized protein	Escherichia coli 101-1
97566	4362143	4361817	TY-2482_chromosome	C8U1Y0	Predicted ferredoxin	Escherichia coli O103:H2 (strain 12009 / EHEC)
115824	4363166	4362459	TY-2482_chromosome	B7L420	Putative uncharacterized protein yagV	Escherichia coli (strain 55989 / EAEC)
114104	4364778	4363138	TY-2482_chromosome	B7L421	Putative surface or exported protein	Escherichia coli (strain 55989 / EAEC)
90196	4367293	4364771	TY-2482_chromosome	B7L422	Putative uncharacterized protein yagX	Escherichia coli (strain 55989 / EAEC)
32111	4367987	4367322	TY-2482_chromosome	B7L423	Uncharacterized protein matC	Escherichia coli (strain 55989 / EAEC)
104630	4368632	4368048	TY-2482_chromosome	B7L424	E. coli common pilus (ECP)	Escherichia coli (strain 55989 / EAEC)
32108	4369297	4368710	TY-2482_chromosome	B7L425	Probable HTH-type transcriptional regulator matA homolog	Escherichia coli (strain 55989 / EAEC)
62822	4370072	4370296	TY-2482_chromosome	B7L426	Putative uncharacterized protein ykgL	Escherichia coli (strain 55989 / EAEC)
33526	4370737	4370477	TY-2482_chromosome	B7L427	50S ribosomal protein L31 type B	Escherichia coli (strain 55989 / EAEC)
85927	4371023	4370794	TY-2482_chromosome	D3GT81	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
21503	4372312	4374381	TY-2482_chromosome	D6JDQ4	Predicted protein (Fragment)	Escherichia coli B354
65133	4377582	4376695	TY-2482_chromosome	B7L429	Putatve transcriptional regulator ykgA	Escherichia coli (strain 55989 / EAEC)
8547	4378715	4378981	TY-2482_chromosome	C3TNJ2	Putative uncharacterized protein	Escherichia coli
102939	4378732	4378142	TY-2482_chromosome	B7L430	Putative uncharacterized protein ykgB	Escherichia coli (strain 55989 / EAEC)
83551	4380414	4379092	TY-2482_chromosome	B7L432	Putative pyridine nucleotide-disulfide oxidoreductase	Escherichia coli (strain 55989 / EAEC)
87363	4380640	4381491	TY-2482_chromosome	B7L433	Putative AraC-type DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
86867	4382021	4382737	TY-2482_chromosome	B7L434	Putative hydroxyacid oxidoreductase (Fe-S centre)	Escherichia coli (strain 55989 / EAEC)
94276	4382751	4384175	TY-2482_chromosome	B7L435	Putative oxidoreductase subunit with NAD(P)-binding domain and ferridoxin-like domain	Escherichia coli (strain 55989 / EAEC)
72426	4384171	4384863	TY-2482_chromosome	B7L436	Putative uncharacterized protein ykgG	Escherichia coli (strain 55989 / EAEC)
86999	4385033	4384824	TY-2482_chromosome	C8TI04	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
77484	4385137	4384943	TY-2482_chromosome	B7L437	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
88461	4385777	4385115	TY-2482_chromosome	B7L438	Putative uncharacterized protein ykgH	Escherichia coli (strain 55989 / EAEC)
30079	4387660	4385993	TY-2482_chromosome	B7L439	Choline dehydrogenase (CDH) (CHD) (EC 1.1.99.1)	Escherichia coli (strain 55989 / EAEC)
30082	4389146	4387677	TY-2482_chromosome	B7L441	Betaine aldehyde dehydrogenase (BADH) (EC 1.2.1.8)	Escherichia coli (strain 55989 / EAEC)
29480	4389664	4389876	TY-2482_chromosome	Q0TKV8	Putative uncharacterized protein	Escherichia coli O6:K15:H31 (strain 536 / UPEC)
30112	4389747	4389163	TY-2482_chromosome	B7L442	HTH-type transcriptional regulator BetI	Escherichia coli (strain 55989 / EAEC)
91967	4389876	4391906	TY-2482_chromosome	B7L443	Choline transporter of high affinity	Escherichia coli (strain 55989 / EAEC)
110489	4392416	4396462	TY-2482_chromosome	B7L444	Putative beta-barrel outer membrane protein, similar to AidA-I adhesin-like protein	Escherichia coli (strain 55989 / EAEC)
67706	4396607	4397692	TY-2482_chromosome	B7L445	Cyclic di-GMP phosphodiesterase	Escherichia coli (strain 55989 / EAEC)
98233	4398669	4397740	TY-2482_chromosome	B7L446	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
67744	4399258	4398764	TY-2482_chromosome	B7L447	Putative uncharacterized protein yahC	Escherichia coli (strain 55989 / EAEC)
104478	4399335	4399565	TY-2482_chromosome	D3GTA7	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
70066	4399516	4400118	TY-2482_chromosome	B7L448	Putative uncharacterized protein yahD	Escherichia coli (strain 55989 / EAEC)
101274	4400161	4401021	TY-2482_chromosome	B7L449	Putative uncharacterized protein yahE	Escherichia coli (strain 55989 / EAEC)
97417	4401014	4402558	TY-2482_chromosome	B7L450	Putative enzyme with acyl-CoA domain	Escherichia coli (strain 55989 / EAEC)
114208	4402561	4403976	TY-2482_chromosome	B7L451	Putative uncharacterized protein yahG	Escherichia coli (strain 55989 / EAEC)
70067	4404122	4405069	TY-2482_chromosome	B7L452	Putative carbamate kinase (EC 2.7.2.-)	Escherichia coli (strain 55989 / EAEC)
73768	4405082	4406461	TY-2482_chromosome	B7L453	Putative deaminase/amidohydrolase with metallo-dependent hydrolase domain	Escherichia coli (strain 55989 / EAEC)
114105	4406733	4407170	TY-2482_chromosome	B7L454	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
72278	4407424	4408407	TY-2482_chromosome	B7L455	Putative periplasmic binding protein, substrate ribose (Sugar-binding protein), ABC-type transport system	Escherichia coli (strain 55989 / EAEC)
112322	4408444	4409940	TY-2482_chromosome	B7L4X8	Putative ATP-binding component of ABC sugar transport system (EC 3.6.3.17)	Escherichia coli (strain 55989 / EAEC)
99126	4409936	4410904	TY-2482_chromosome	B7L4X9	Putative permease component of sugar ABC transport system	Escherichia coli (strain 55989 / EAEC)
101840	4410874	4411857	TY-2482_chromosome	B7L4Y0	Putative permease component of sugar ABC transport system	Escherichia coli (strain 55989 / EAEC)
88479	4411947	4412993	TY-2482_chromosome	B7L4Y1	Putative oxidoreductase, Zn-dependent and NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
114134	4413239	4414051	TY-2482_chromosome	B7L4Y2	Putative uncharacterized protein yahL	Escherichia coli (strain 55989 / EAEC)
82916	4414466	4414708	TY-2482_chromosome	B7L4Y3	Putative uncharacterized protein yahM	Escherichia coli (strain 55989 / EAEC)
62840	4415399	4414731	TY-2482_chromosome	B7L4Y4	Neutral amino-acid efflux system	Escherichia coli (strain 55989 / EAEC)
91764	4415546	4415818	TY-2482_chromosome	B7L4Y5	Putative uncharacterized protein yahO	Escherichia coli (strain 55989 / EAEC)
70020	4417508	4415925	TY-2482_chromosome	B7L4Y6	DNA-binding transcriptional activator	Escherichia coli (strain 55989 / EAEC)
88414	4417746	4418633	TY-2482_chromosome	B7L4Y7	2-methylisocitrate lyase (EC 4.1.3.30)	Escherichia coli (strain 55989 / EAEC)

114065	4418681	4419847	TY-2482_chromosome	B7L4Y8	2-methylcitrate synthase (EC 2.3.3.1)	Escherichia coli (strain 55989 / EAEC)
84592	4419884	4421332	TY-2482_chromosome	B7L4Y9	2-methylcitrate dehydratase (EC 4.2.1.79)	Escherichia coli (strain 55989 / EAEC)
98231	4421375	4423258	TY-2482_chromosome	B7L4Z0	Propionyl-CoA synthetase (EC 6.2.1.17)	Escherichia coli (strain 55989 / EAEC)
106523	4423687	4424943	TY-2482_chromosome	B7L4Z2	Cytosine transporter	Escherichia coli (strain 55989 / EAEC)
88415	4424936	4426216	TY-2482_chromosome	B7L4Z3	Cytosine deaminase (EC 3.5.4.1)	Escherichia coli (strain 55989 / EAEC)
76826	4427158	4426262	TY-2482_chromosome	B7L4Z4	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
97121	4427268	4427924	TY-2482_chromosome	B7L4Z5	Carbonic anhydrase (EC 4.2.1.1)	Escherichia coli (strain 55989 / EAEC)
30457	4427958	4428425	TY-2482_chromosome	B7L4Z6	Cyanate hydratase (Cyanase) (EC 4.2.1.104) (Cyanate hydrolase) (Cyanate lyase)	Escherichia coli (strain 55989 / EAEC)
90957	4428461	4429612	TY-2482_chromosome	B7L4Z7	Putative cyanate transporter	Escherichia coli (strain 55989 / EAEC)
82473	4430380	4429721	TY-2482_chromosome	D3GTD3	Galactoside O-acetyltransferase (EC 2.3.1.18)	Escherichia coli O44:H18 (strain 042 / EAEC)
106435	4431648	4430398	TY-2482_chromosome	B7L4Z9	Lactose/galactose transporter	Escherichia coli (strain 55989 / EAEC)
73727	4434774	4431703	TY-2482_chromosome	B7L500	Beta-galactosidase (Beta-gal) (EC 3.2.1.23) (Lactase)	Escherichia coli (strain 55989 / EAEC)
102861	4435979	4434900	TY-2482_chromosome	B7L501	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
65822	4437003	4436059	TY-2482_chromosome	B7L502	DNA-binding transcriptional activator, 3HPP-binding	Escherichia coli (strain 55989 / EAEC)
32383	4437080	4438741	TY-2482_chromosome	B7L503	3-(3-hydroxy-phenyl)propionate/3-hydroxycinnamic acid hydroxylase (3-HCI hydroxylase) (3-HPP hydroxylase) (EC 1.1	Escherichia coli (strain 55989 / EAEC)
32385	4438746	4439687	TY-2482_chromosome	B7L504	2,3-dihydroxyphenylpropionate/2,3-dihydroxicinnamic acid 1,2-dioxygenase (EC 1.13.11.16	Escherichia coli (strain 55989 / EAEC)
32387	4439693	4440571	TY-2482_chromosome	B7L505	2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxononatrienedioate hydrolase (EC 3.7.1.n1) (2-hydroxy-6-ketonona-	Escherichia coli (strain 55989 / EAEC)
32388	4440584	4441390	TY-2482_chromosome	B7L506	2-keto-4-pentenoate hydratase (EC 4.2.1.80) (2-hydroxypentadienoic acid hydratase)	Escherichia coli (strain 55989 / EAEC)
29684	4441390	4442337	TY-2482_chromosome	B7L507	Acetaldehyde dehydrogenase (EC 1.2.1.10) (Acetaldehyde dehydrogenase [acetylating])	Escherichia coli (strain 55989 / EAEC)
31522	4442337	4443347	TY-2482_chromosome	B7L508	4-hydroxy-2-oxovalerate aldolase (HOA) (EC 4.1.3.39) (4-hydroxy-2-keto-pentanoic acid aldolase) (4-hydroxy-2-oxope	Escherichia coli (strain 55989 / EAEC)
91267	4443526	4444734	TY-2482_chromosome	B7L509	Hydroxy-aromatic acid transporter	Escherichia coli (strain 55989 / EAEC)
64243	4444839	4445375	TY-2482_chromosome	B7L510	Nucleoprotein/polynucleotide-associated enzyme	Escherichia coli (strain 55989 / EAEC)
88416	4446438	4445608	TY-2482_chromosome	B7L512	S-formylglutathione hydrolase	Escherichia coli (strain 55989 / EAEC)
94226	4447640	4446534	TY-2482_chromosome	B7L513	Alcohol dehydrogenase class III/glutathione-dependent formaldehyde dehydrogenase (EC 1.1.1.1) (EC 1.1.1.284)	Escherichia coli (strain 55989 / EAEC)
27137	4447720	4448019	TY-2482_chromosome	Q1RFI5	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
106437	4448909	4448139	TY-2482_chromosome	B7L515	Putative uncharacterized protein yaiO	Escherichia coli (strain 55989 / EAEC)
77430	4450666	4449473	TY-2482_chromosome	B7L517	Putative membrane-associated glycosyltransferase	Escherichia coli (strain 55989 / EAEC)
73729	4451347	4450679	TY-2482_chromosome	B7L518	Putative uncharacterized protein yaiS	Escherichia coli (strain 55989 / EAEC)
27730	4451812	4451600	TY-2482_chromosome	E3PET9	Putative uncharacterized protein	Escherichia coli O78:H11 (strain H10407 / ETEC)
110154	4451963	4452922	TY-2482_chromosome	B7L519	Taurine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
62780	4452938	4453702	TY-2482_chromosome	B7L520	Taurine transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
29264	4454257	4454526	TY-2482_chromosome	B7NJD4	Taurine dioxygenase, 2-oxoglutarate-dependent (EC 1.14.11.17)	Escherichia coli O7:K1 (strain IAI39 / ExPEC)
29265	4454592	4455374	TY-2482_chromosome	B7NJD4	Taurine dioxygenase, 2-oxoglutarate-dependent (EC 1.14.11.17)	Escherichia coli O7:K1 (strain IAI39 / ExPEC)
75695	4456457	4455486	TY-2482_chromosome	B7L523	Delta-aminolevulinic acid dehydratase (EC 4.2.1.24)	Escherichia coli (strain 55989 / EAEC)
27642	4456896	4456630	TY-2482_chromosome	B6HZH1	Putative uncharacterized protein	Escherichia coli (strain SE11)
76743	4456981	4459866	TY-2482_chromosome	B7L524	Putative flagellin structural protein; putative exported protein	Escherichia coli (strain 55989 / EAEC)
88418	4459912	4460577	TY-2482_chromosome	B7L525	Putative uncharacterized protein yaiV	Escherichia coli (strain 55989 / EAEC)
107983	4461738	4460584	TY-2482_chromosome	B7L526	Beta-lactamase/D-alanine carboxypeptidase (EC 3.4.17.8) (EC 3.5.2.6)	Escherichia coli (strain 55989 / EAEC)
102910	4461876	4462067	TY-2482_chromosome	B7L527	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
88367	4462090	4463307	TY-2482_chromosome	B7L528	Transporter involved in cell envelope modification	Escherichia coli (strain 55989 / EAEC)
101587	4463323	4464414	TY-2482_chromosome	B7L529	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
72275	4464784	4464479	TY-2482_chromosome	B7L530	Putative uncharacterized protein yaiY	Escherichia coli (strain 55989 / EAEC)
95602	4464912	4465253	TY-2482_chromosome	B7L531	Putative uncharacterized protein yaiZ	Escherichia coli (strain 55989 / EAEC)
111587	4466374	4465283	TY-2482_chromosome	B7L532	D-alanine--D-alanine ligase 2 (EC 6.3.2.4) (D-Ala-D-Ala ligase 2) (D-alanylalanine synthetase 2)	Escherichia coli (strain 55989 / EAEC)
29090	4466452	4466652	TY-2482_chromosome	B7L533	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
31674	4466837	4467094	TY-2482_chromosome	B7L534	Anti-adapter protein iraP	Escherichia coli (strain 55989 / EAEC)
10195	4466937	4466689	TY-2482_chromosome	P71314	Putative uncharacterized protein	Escherichia coli
115538	4467198	4468610	TY-2482_chromosome	C8U269	Bacterial alkaline phosphatase PhoA	Escherichia coli O103:H2 (strain 12009 / EHEC)
102911	4468732	4469049	TY-2482_chromosome	B7L539	Phosphate starvation-inducible protein	Escherichia coli (strain 55989 / EAEC)
91919	4469154	4470266	TY-2482_chromosome	B7L540	Putative diguanylate cyclase	Escherichia coli (strain 55989 / EAEC)
77431	4471095	4470289	TY-2482_chromosome	B7L541	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	Escherichia coli (strain 55989 / EAEC)
50325	4471095	4471670	TY-2482_chromosome	D8CGU2	Toxin-antitoxin system, toxin component, PIN family	Escherichia coli MS 185-1
29920	4471856	4472377	TY-2482_chromosome	B7L543	Shikimate kinase 2 (SK 2) (EC 2.7.1.71)	Escherichia coli (strain 55989 / EAEC)
27765	4472699	4472373	TY-2482_chromosome	Q1RFF5	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
66277	4472879	4473553	TY-2482_chromosome	B7L545	Putative uncharacterized protein aroM	Escherichia coli (strain 55989 / EAEC)
34740	4473628	4473909	TY-2482_chromosome	B7L546	UPF0345 protein yaiE	Escherichia coli (strain 55989 / EAEC)
103022	4474092	4474532	TY-2482_chromosome	C6UZ26	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
33291	4475524	4474616	TY-2482_chromosome	B7L548	Recombination-associated protein rdgC	Escherichia coli (strain 55989 / EAEC)
81037	4475649	4476554	TY-2482_chromosome	B7L549	Manno(Fructo)kinase (EC 2.7.1.4)	Escherichia coli (strain 55989 / EAEC)
114067	4477884	4476703	TY-2482_chromosome	B7L550	Putative major facilitator class transporter	Escherichia coli (strain 55989 / EAEC)
102234	4481153	4478013	TY-2482_chromosome	B7L551	Exonuclease, dsDNA, ATP-dependent	Escherichia coli (strain 55989 / EAEC)
79770	4482352	4481153	TY-2482_chromosome	B7L552	Exonuclease, dsDNA, ATP-dependent	Escherichia coli (strain 55989 / EAEC)
91920	4482542	4483228	TY-2482_chromosome	B7L553	DNA-binding response regulator in two-component regulatory system with PhoR (Or CreC)	Escherichia coli (strain 55989 / EAEC)
87881	4483289	4484581	TY-2482_chromosome	B7L688	Sensory histidine kinase in two-component regulatory system with PhoB (EC 2.7.3.-)	Escherichia coli (strain 55989 / EAEC)

80272	4484991	4486307 TY-2482_chromosome	B7L634	Branched chain amino acid transporter (LIV-II)	Escherichia coli (strain 55989 / EAEC)
96941	4486386	4487756 TY-2482_chromosome	B7L635	Proline transporter	Escherichia coli (strain 55989 / EAEC)
95444	4487915	4489729 TY-2482_chromosome	B7L636	Maltodextrin glucosidase (EC 3.2.1.20)	Escherichia coli (strain 55989 / EAEC)
29694	4490318	4489740 TY-2482_chromosome	B7L637	Acyl carrier protein phosphodiesterase (ACP phosphodiesterase) (EC 3.1.4.14)	Escherichia coli (strain 55989 / EAEC)
33229	4490411	4491478 TY-2482_chromosome	B7L638	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.-) (Queuosine biosynthesis protein queA)	Escherichia coli (strain 55989 / EAEC)
34240	4491537	4492661 TY-2482_chromosome	B7L639	Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (Guanine insertion enzyme) (tRNA-guanine transglycosylase)	Escherichia coli (strain 55989 / EAEC)
109594	4492687	4493016 TY-2482_chromosome	B7L640	SecYEG protein translocase auxillary subunit	Escherichia coli (strain 55989 / EAEC)
110576	4493047	4494891 TY-2482_chromosome	B7L641	SecYEG protein translocase auxillary subunit	Escherichia coli (strain 55989 / EAEC)
91146	4494905	4495873 TY-2482_chromosome	B7L642	SecYEG protein translocase auxillary subunit	Escherichia coli (strain 55989 / EAEC)
82639	4496005	4496349 TY-2482_chromosome	B7L643	Putative uncharacterized protein yajD	Escherichia coli (strain 55989 / EAEC)
101060	4497413	4496532 TY-2482_chromosome	B7L644	Nucleoside channel, receptor of phage T6 and colicin K	Escherichia coli (strain 55989 / EAEC)
67591	4498251	4497715 TY-2482_chromosome	C8TJ02	Predicted lipoprotein	Escherichia coli O26:H11 (strain 11368 / EHEC)
32714	4498402	4498848 TY-2482_chromosome	B7L647	Transcriptional repressor NrdR	Escherichia coli (strain 55989 / EAEC)
76401	4498855	4499955 TY-2482_chromosome	B7L648	Fused diaminohydroxyphosphoribosylaminopyrimidine deaminase; 5-amino-6-(5-phosphoribosylamino) uracil reduct	Escherichia coli (strain 55989 / EAEC)
27272	4499951	4500514 TY-2482_chromosome	A1A885	6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase) (Lumazine synthase) (EC 2.5.1.9) (Riboflavin synthase beta (	Escherichia coli O1:K1 / APEC
62661	4501034	4502008 TY-2482_chromosome	B7L651	Thiamin-monophosphate kinase (EC 2.7.4.16)	Escherichia coli (strain 55989 / EAEC)
24208	4501040	4500510 TY-2482_chromosome	A1A886	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
86621	4501989	4502504 TY-2482_chromosome	B7L652	Phosphatidylglycerophosphatase A (EC 3.1.3.27)	Escherichia coli (strain 55989 / EAEC)
84455	4503535	4502564 TY-2482_chromosome	B7L653	Aldoketo-oxidoreductase, NADP-binding	Escherichia coli (strain 55989 / EAEC)
30704	4505452	4503593 TY-2482_chromosome	B7L654	1-deoxy-D-xylulose-5-phosphate synthase (EC 2.2.1.7) (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS	Escherichia coli (strain 55989 / EAEC)
100775	4506376	4505480 TY-2482_chromosome	B7L655	Geranyltranstransferase (EC 2.5.1.1) (EC 2.5.1.10)	Escherichia coli (strain 55989 / EAEC)
30824	4506618	4506379 TY-2482_chromosome	B7L656	Exodeoxyribonuclease 7 small subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII small subunit) (Exonuclease VII small s	Escherichia coli (strain 55989 / EAEC)
34254	4506824	4508269 TY-2482_chromosome	B7L657	tRNA sulfurtransferase (EC 2.8.1.4) (Sulfur carrier protein ThiS sulfurtransferase) (Thiamine biosynthesis protein thiI) (	Escherichia coli (strain 55989 / EAEC)
76515	4508916	4508329 TY-2482_chromosome	B7L658	Putative uncharacterized protein yajL	Escherichia coli (strain 55989 / EAEC)
69936	4509790	4508882 TY-2482_chromosome	B7L659	2-dehydropantoate reductase, NADPH-specific (EC 1.1.1.169)	Escherichia coli (strain 55989 / EAEC)
34747	4509958	4510446 TY-2482_chromosome	B7L660	UPF0234 protein yajQ	Escherichia coli (strain 55989 / EAEC)
106415	4511941	4510580 TY-2482_chromosome	B7L661	Putative transporter, major facilitator family	Escherichia coli (strain 55989 / EAEC)
71752	4512289	4513281 TY-2482_chromosome	B7L662	Putative zinc-dependent hydrolase	Escherichia coli (strain 55989 / EAEC)
59045	4513882	4513343 TY-2482_chromosome	B7L663	Putative acetyltransferase	Escherichia coli (strain 55989 / EAEC)
83665	4514243	4513869 TY-2482_chromosome	B7L664	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
95243	4515297	4514365 TY-2482_chromosome	B5Z3T4	Protoheme IX farnesyltransferase (EC 2.5.1.-)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
102776	4515593	4515267 TY-2482_chromosome	B7L666	Cytochrome o ubiquinol oxidase subunit IV (EC 1.10.3.-)	Escherichia coli (strain 55989 / EAEC)
79108	4516207	4515596 TY-2482_chromosome	B7L667	Cytochrome o ubiquinol oxidase subunit III (EC 1.10.3.-)	Escherichia coli (strain 55989 / EAEC)
65258	4518188	4516200 TY-2482_chromosome	B7L668	Cytochrome o ubiquinol oxidase subunit I (EC 1.10.3.-)	Escherichia coli (strain 55989 / EAEC)
95463	4519157	4518213 TY-2482_chromosome	B7L669	Cytochrome o ubiquinol oxidase subunit II (EC 1.10.3.-)	Escherichia coli (strain 55989 / EAEC)
80944	4521092	4519620 TY-2482_chromosome	B7L670	Muropeptide transporter	Escherichia coli (strain 55989 / EAEC)
96979	4521714	4521139 TY-2482_chromosome	B7L671	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
80878	4522019	4522333 TY-2482_chromosome	B7L672	Regulator of penicillin binding proteins and beta lactamase transcription (Morphogene	Escherichia coli (strain 55989 / EAEC)
34278	4522680	4523975 TY-2482_chromosome	B7L673	Trigger factor (TF)	Escherichia coli (strain 55989 / EAEC)
24357	4522685	4522266 TY-2482_chromosome	Q1RFA2	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
88240	4524224	4524844 TY-2482_chromosome	B7L674	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Escherichia coli (strain 55989 / EAEC)
20508	4524946	4524749 TY-2482_chromosome	E0QWE8	Putative uncharacterized protein	Escherichia coli NC101
30341	4524973	4526244 TY-2482_chromosome	B7L675	ATP-dependent Clp protease ATP-binding subunit ClpX	Escherichia coli (strain 55989 / EAEC)
95563	4526435	4528786 TY-2482_chromosome	B7L676	DNA-binding ATP-dependent protease La (EC 3.4.21.53)	Escherichia coli (strain 55989 / EAEC)
101828	4528998	4529267 TY-2482_chromosome	B7L677	HU, DNA-binding transcriptional regulator, beta subunit	Escherichia coli (strain 55989 / EAEC)
64180	4529462	4531330 TY-2482_chromosome	B7L678	Peptidyl-prolyl cis-trans isomerase (Rotamase D) (EC 5.2.1.8)	Escherichia coli (strain 55989 / EAEC)
59041	4531484	4531852 TY-2482_chromosome	B7L679	Putative uncharacterized protein ybaV	Escherichia coli (strain 55989 / EAEC)
91797	4531949	4532344 TY-2482_chromosome	B7L680	Putative uncharacterized protein ybaW	Escherichia coli (strain 55989 / EAEC)
33233	4533094	4532402 TY-2482_chromosome	B7L681	7-cyano-7-deazaguanine synthase (EC 6.3.-.-) (7-cyano-7-carbaguanine synthase) (PreQ(0) synthase) (Queuosine bios	Escherichia coli (strain 55989 / EAEC)
106439	4534859	4533162 TY-2482_chromosome	B7L682	Putative uncharacterized protein ybaE	Escherichia coli (strain 55989 / EAEC)
112659	4534947	4535774 TY-2482_chromosome	D3GV76	HMP-PP phosphatase (EC 3.6.1.-)	Escherichia coli O44:H18 (strain 042 / EAEC)
58124	4535702	4536385 TY-2482_chromosome	B7L684	Putative DNA-binding transcriptional regulator (Lrp-like)	Escherichia coli (strain 55989 / EAEC)
112246	4536418	4538187 TY-2482_chromosome	B7L685	Putative fused ATPase and permease component of metabolite transporter	Escherichia coli (strain 55989 / EAEC)
79593	4538183	4539961 TY-2482_chromosome	B7L686	Putative fused ATPase and permease component of metabolite ABC transporter	Escherichia coli (strain 55989 / EAEC)
105529	4540145	4540480 TY-2482_chromosome	B7L687	Nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB	Escherichia coli (strain 55989 / EAEC)
90842	4540513	4541796 TY-2482_chromosome	B7L689	Ammonium transporter	Escherichia coli (strain 55989 / EAEC)
106422	4542708	4541851 TY-2482_chromosome	B7L690	Acyl-CoA thioesterase II (EC 3.1.2.-)	Escherichia coli (strain 55989 / EAEC)
94004	4542926	4543495 TY-2482_chromosome	B7L691	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
25782	4543822	4544157 TY-2482_chromosome	B7MDX7	Putative uncharacterized protein	Escherichia coli O45:K1 (strain S88 / ExPEC)
91798	4543918	4543532 TY-2482_chromosome	B7L692	Putative methylated DNA-protein cysteine alkyltransferase	Escherichia coli (strain 55989 / EAEC)
r189	4543995	4544108 TY-2482_chromosome	ref|NC_010473|:415003-415116|-| [gene=ffs] [locus_tag=ECDH10B_0411]		
82978	4544219	4544569 TY-2482_chromosome	B7L693	Putative uncharacterized protein ybaA	Escherichia coli (strain 55989 / EAEC)
60963	4546164	4544617 TY-2482_chromosome	B7L694	Putative uncharacterized protein ylaB	Escherichia coli (strain 55989 / EAEC)
94030	4546837	4546331 TY-2482_chromosome	D3GV87	Putative membrane protein	Escherichia coli O44:H18 (strain 042 / EAEC)

86624	4547465	4546917	TY-2482_chromosome	B7L696	Maltose O-acetyltransferase (EC 2.3.1.79)	Escherichia coli (strain 55989 / EAEC)
75159	4548100	4547639	TY-2482_chromosome	B7L697	Modulator of gene expression, with H-NS	Escherichia coli (strain 55989 / EAEC)
106423	4551949	4548803	TY-2482_chromosome	B7L699	Multidrug efflux system protein	Escherichia coli (strain 55989 / EAEC)
88241	4553165	4551975	TY-2482_chromosome	B7L6A0	Multidrug efflux system	Escherichia coli (strain 55989 / EAEC)
106431	4553307	4553951	TY-2482_chromosome	B7L6A1	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
78704	4554082	4557441	TY-2482_chromosome	B7L7E3	Putative uncharacterized protein kefA	Escherichia coli (strain 55989 / EAEC)
73654	4558358	4557834	TY-2482_chromosome	B7L792	Primosomal replication protein N''	Escherichia coli (strain 55989 / EAEC)
100846	4558428	4558802	TY-2482_chromosome	B7L793	Putative uncharacterized protein ybaN	Escherichia coli (strain 55989 / EAEC)
29793	4558958	4559506	TY-2482_chromosome	B7L794	Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Escherichia coli (strain 55989 / EAEC)
73688	4559638	4561566	TY-2482_chromosome	B7L795	DNA polymerase III/DNA elongation factor III, tau and gamma subunits (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
33307	4561951	4562553	TY-2482_chromosome	B7L797	Recombination protein recR	Escherichia coli (strain 55989 / EAEC)
11675	4561975	4561601	TY-2482_chromosome	P77122	Putative uncharacterized protein	Escherichia coli
90518	4562666	4564537	TY-2482_chromosome	B7L798	Chaperone protein htpG (Heat shock protein htpG) (High temperature protein G)	Escherichia coli (strain 55989 / EAEC)
109630	4564661	4565362	TY-2482_chromosome	B5Z3Y5	Adenylate kinase (AK) (EC 2.7.4.3) (ATP-AMP transphosphorylase)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
31351	4565601	4566560	TY-2482_chromosome	B7L7A0	Ferrochelatase (EC 4.99.1.1) (Heme synthase) (Protoheme ferro-lyase)	Escherichia coli (strain 55989 / EAEC)
29726	4567519	4566563	TY-2482_chromosome	B7L7A1	Acetyl esterase (EC 3.1.1.-)	Escherichia coli (strain 55989 / EAEC)
66223	4567671	4568972	TY-2482_chromosome	B7L7A2	Inosine/guanosine kinase (EC 2.7.1.73)	Escherichia coli (strain 55989 / EAEC)
75629	4570784	4569111	TY-2482_chromosome	B7L7A3	Putative monovalent cation:proton antiporter (CPA2 family)	Escherichia coli (strain 55989 / EAEC)
66224	4572242	4571025	TY-2482_chromosome	B7L7A4	Fosmidomycin efflux system, member of the major facilitator superfamily	Escherichia coli (strain 55989 / EAEC)
88284	4572460	4574109	TY-2482_chromosome	B7L7A5	Bifunctional UDP-sugar hydrolase and 5'-nucleotidase (EC 3.6.1.45)	Escherichia coli (strain 55989 / EAEC)
80889	4574628	4574152	TY-2482_chromosome	B7L7A6	Putative uncharacterized protein ybaK	Escherichia coli (strain 55989 / EAEC)
r239	4574750	4574833	TY-2482_chromosome	ref|NC_010473|:445759-445842|-| [gene=sroB] [locus_tag=ECDH10B_0438]		
99110	4575626	4574835	TY-2482_chromosome	B7L7A7	Putative uncharacterized protein ybaP	Escherichia coli (strain 55989 / EAEC)
113673	4575710	4576102	TY-2482_chromosome	B6I0D3	Putative uncharacterized protein	Escherichia coli (strain SE11)
113942	4578723	4576222	TY-2482_chromosome	B7L7A9	Copper transporter (EC 3.6.3.4)	Escherichia coli (strain 55989 / EAEC)
112252	4578985	4579914	TY-2482_chromosome	B7L7B0	Glutaminase 1 (EC 3.5.1.2)	Escherichia coli (strain 55989 / EAEC)
64367	4579920	4581209	TY-2482_chromosome	B7L7B1	Putative nitrogen-containing metabolite transporter	Escherichia coli (strain 55989 / EAEC)
113946	4581337	4581741	TY-2482_chromosome	B7L7B2	DNA-binding transcriptional activator of copper-responsive regulon genes	Escherichia coli (strain 55989 / EAEC)
6154	4582203	4581748	TY-2482_chromosome	P0AAS3	Inner membrane protein ybbJ	Escherichia coli (strain K12)
75760	4583117	4582203	TY-2482_chromosome	B7L7B4	Putative protease, membrane anchored	Escherichia coli (strain 55989 / EAEC)
99082	4583263	4583937	TY-2482_chromosome	B7L7B5	Putative transporter subunit: ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
105269	4583927	4584703	TY-2482_chromosome	B7L7B6	Putative permease of an ABC transporter	Escherichia coli (strain 55989 / EAEC)
85651	4585659	4584772	TY-2482_chromosome	D3GVD0	Thioredoxin-like protein	Escherichia coli O44:H18 (strain 042 / EAEC)
113947	4586493	4585687	TY-2482_chromosome	B7L7B8	Putative oxidoreductase with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
84510	4587077	4587760	TY-2482_chromosome	B7L7C0	Putative transporter subunit: ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
115743	4587109	4586486	TY-2482_chromosome	B7L7B9	Multifunctional acyl-CoA thioesterase I and protease I and lysophospholipase L1 (EC 3.1.1.5) (EC 3.1.2.-	Escherichia coli (strain 55989 / EAEC)
88285	4587760	4590171	TY-2482_chromosome	B7L7C1	Putative ABC transporter permease	Escherichia coli (strain 55989 / EAEC)
88327	4590604	4594890	TY-2482_chromosome	B7L7C2	RhsD element protein	Escherichia coli (strain 55989 / EAEC)
68377	4594933	4595298	TY-2482_chromosome	B7L7C5	Putative uncharacterized protein ybbC	Escherichia coli (strain 55989 / EAEC)
84517	4595301	4596008	TY-2482_chromosome	B7L7C6	Putative uncharacterized protein ylbH	Escherichia coli (strain 55989 / EAEC)
88337	4595992	4596480	TY-2482_chromosome	B7L7C7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
64166	4596983	4596771	TY-2482_chromosome	B7L7C8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
79109	4597404	4596973	TY-2482_chromosome	B7L7C9	Putative regulator with homeodomain-like DNA binding domain	Escherichia coli (strain 55989 / EAEC)
33924	4598578	4597487	TY-2482_chromosome	B7L7D0	tRNA 2-selenouridine synthase (EC 2.9.1.-) (Selenophosphate-dependent tRNA 2-selenouridine synthase)	Escherichia coli (strain 55989 / EAEC)
87201	4599573	4598650	TY-2482_chromosome	B7L7D1	Putative DNA-binding transcriptional activator of the allD operon	Escherichia coli (strain 55989 / EAEC)
29748	4599803	4600282	TY-2482_chromosome	B7L7D2	Ureidoglycolate hydrolase (EC 3.5.3.19)	Escherichia coli (strain 55989 / EAEC)
113476	4600363	4601175	TY-2482_chromosome	B7L7D3	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
87696	4601268	4603046	TY-2482_chromosome	B7L7D4	Glyoxylate carboligase (EC 4.1.1.47)	Escherichia coli (strain 55989 / EAEC)
80890	4603062	4603835	TY-2482_chromosome	B7L7D5	Hydroxypyruvate isomerase (EC 5.3.1.22)	Escherichia coli (strain 55989 / EAEC)
98356	4603938	4604813	TY-2482_chromosome	B7L7D6	Tartronate semialdehyde reductase, NADH-dependent (EC 1.1.1.60)	Escherichia coli (strain 55989 / EAEC)
113269	4604985	4606436	TY-2482_chromosome	B7L7D7	Allantoin or uracil transporter	Escherichia coli (strain 55989 / EAEC)
29750	4606499	4607857	TY-2482_chromosome	B7L7D8	Allantoinase (EC 3.5.2.5) (Allantoin-utilizing enzyme)	Escherichia coli (strain 55989 / EAEC)
104403	4607917	4609215	TY-2482_chromosome	B7L7D9	Putative uracil/xanthine transporter	Escherichia coli (strain 55989 / EAEC)
102005	4609240	4610382	TY-2482_chromosome	B7L7E0	Glycerate kinase II (EC 2.7.1.31)	Escherichia coli (strain 55989 / EAEC)
88286	4611299	4610517	TY-2482_chromosome	B7L7E1	Putative uncharacterized protein ylbA	Escherichia coli (strain 55989 / EAEC)
83442	4612545	4611313	TY-2482_chromosome	B7L7E2	Allantoate amidohydrolase (EC 3.5.3.4)	Escherichia coli (strain 55989 / EAEC)
68051	4613616	4612570	TY-2482_chromosome	B7L7E4	Ureidoglycolate dehydrogenase (EC 1.1.1.154)	Escherichia coli (strain 55989 / EAEC)
98398	4613933	4615597	TY-2482_chromosome	B7L7E5	Putative acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
102806	4615610	4616866	TY-2482_chromosome	B7L7E6	Putative uncharacterized protein ylbE	Escherichia coli (strain 55989 / EAEC)
93937	4616880	4617692	TY-2482_chromosome	B7L7E7	Putative uncharacterized protein ylbF	Escherichia coli (strain 55989 / EAEC)
91823	4617692	4618582	TY-2482_chromosome	B7L7E8	Putative carbamate kinase	Escherichia coli (strain 55989 / EAEC)
21396	4618776	4618492	TY-2482_chromosome	P77130	Putative uncharacterized protein	Escherichia coli
105270	4619847	4618783	TY-2482_chromosome	B7L7E9	N5-carboxyaminoimidazole ribonucleotide synthase (EC 4.1.1.21)	Escherichia coli (strain 55989 / EAEC)
113948	4620353	4619847	TY-2482_chromosome	B7L7F0	N5-carboxyaminoimidazole ribonucleotide mutase (EC 4.1.1.21)	Escherichia coli (strain 55989 / EAEC)

14246	4621184	4621867	TY-2482_chromosome	P77131	Putative uncharacterized protein	Escherichia coli
31978	4621193	4620474	TY-2482_chromosome	B7L7F1	UDP-2,3-diacylglucosamine hydrolase (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
34082	4621864	4623246	TY-2482_chromosome	B7L7F3	Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase) (CysRS)	Escherichia coli (strain 55989 / EAEC)
88287	4623806	4623288	TY-2482_chromosome	B7L7F4	Putative uncharacterized protein ybcI	Escherichia coli (strain 55989 / EAEC)
29254	4623892	4624146	TY-2482_chromosome	Q1RF06	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
31006	4624994	4624131	TY-2482_chromosome	B7L7F6	Bifunctional protein FolD [Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolat	Escherichia coli (strain 55989 / EAEC)
112087	4625475	4626014	TY-2482_chromosome	B7L7F7	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
90508	4626237	4626926	TY-2482_chromosome	B7L8D6	Pilin chaperone, periplasmic	Escherichia coli (strain 55989 / EAEC)
88260	4626960	4629566	TY-2482_chromosome	B7L8D7	Putative outer membrane export usher protein	Escherichia coli (strain 55989 / EAEC)
110649	4629612	4630586	TY-2482_chromosome	B7L8D8	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
112178	4630600	4631112	TY-2482_chromosome	B7L8D9	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
58505	4631750	4631121	TY-2482_chromosome	B7L8E0	DNA-binding transcriptional regulator, isolated component of a two-component regulator system	Escherichia coli (strain 55989 / EAEC)
r296	4631993	4632069	TY-2482_chromosome	ref|NC_010473|:503278-503354|Arg tRNA| [gene=argU] [locus_tag=ECDH10B_0492]		
88271	4632876	4632118	TY-2482_chromosome	B7L8E2	DNA-binding transcriptional activator of porin biosynthesis	Escherichia coli (strain 55989 / EAEC)
10187	4632933	4633142	TY-2482_chromosome	P77089	Putative uncharacterized protein	Escherichia coli
100983	4633949	4633062	TY-2482_chromosome	B7L8E3	Putative uncharacterized protein ybcH	Escherichia coli (strain 55989 / EAEC)
111641	4636922	4633953	TY-2482_chromosome	B7L8E4	Bacteriophage N4 receptor, outer membrane subunit	Escherichia coli (strain 55989 / EAEC)
79470	4639146	4636912	TY-2482_chromosome	B7L8E5	Bacteriophage N4 receptor, inner membrane subunit	Escherichia coli (strain 55989 / EAEC)
73669	4640551	4639418	TY-2482_chromosome	B7L8E6	Putative transposase	Escherichia coli (strain 55989 / EAEC)
90143	4640966	4640658	TY-2482_chromosome	B7L8E7	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73675	4641332	4641084	TY-2482_chromosome	B7L8E8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
65474	4646191	4641332	TY-2482_chromosome	B7L8E9	Rhs core protein with extension	Escherichia coli (strain 55989 / EAEC)
91812	4646672	4646214	TY-2482_chromosome	B7L8F0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
91840	4648601	4646703	TY-2482_chromosome	B7L8F1	Putative Rhs element Vgr protein	Escherichia coli (strain 55989 / EAEC)
83403	4650798	4649341	TY-2482_chromosome	B7L8F2	Sensory histidine kinase in two-component regulatory system with CusR, senses copper ions	Escherichia coli (strain 55989 / EAEC)
83541	4651459	4650779	TY-2482_chromosome	B7L8F3	DNA-binding response regulator in two-component regulatory system with CusS	Escherichia coli (strain 55989 / EAEC)
79766	4651616	4652995	TY-2482_chromosome	B7L8F4	Copper/silver efflux system, outer membrane component	Escherichia coli (strain 55989 / EAEC)
86185	4653022	4653351	TY-2482_chromosome	B7L8F5	Periplasmic copper-binding protein	Escherichia coli (strain 55989 / EAEC)
75615	4653370	4654590	TY-2482_chromosome	B7L8F6	Copper/silver efflux system, membrane fusion protein	Escherichia coli (strain 55989 / EAEC)
114018	4654605	4657745	TY-2482_chromosome	B7L8F7	Copper/silver efflux system, membrane component	Escherichia coli (strain 55989 / EAEC)
76038	4657850	4659223	TY-2482_chromosome	B7L8F8	Phenylalanine transporter	Escherichia coli (strain 55989 / EAEC)
61037	4660541	4659297	TY-2482_chromosome	B7L8F9	Putative membrane protein; putative channel	Escherichia coli (strain 55989 / EAEC)
93727	4661302	4660652	TY-2482_chromosome	B7L8G0	Dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive (EC 1.5.1.34)	Escherichia coli (strain 55989 / EAEC)
28022	4661884	4661399	TY-2482_chromosome	B7N9I3	Putative uncharacterized protein ybdF	Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC)
93377	4662077	4661832	TY-2482_chromosome	B7L8G2	Putative uncharacterized protein ybdJ	Escherichia coli (strain 55989 / EAEC)
30182	4663261	4662146	TY-2482_chromosome	B7L8G3	Carboxylate-amine ligase YbdK (EC 6.3.-.-)	Escherichia coli (strain 55989 / EAEC)
25028	4663734	4663468	TY-2482_chromosome	A1A8L3	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
5324	4663932	4665041	TY-2482_chromosome	P11901	Transposase for insertion sequence element IS421	Escherichia coli
63961	4665410	4665704	TY-2482_chromosome	D2NE71	Putative uncharacterized protein	Escherichia coli O150:H5 (strain SE15)
5321	4667012	4665903	TY-2482_chromosome	P11901	Transposase for insertion sequence element IS421	Escherichia coli
60849	4667921	4667181	TY-2482_chromosome	D3GWC2	4'-phosphopantetheinyl transferase (Enterobactin synthetase component D) (EC 2.7.8.-)	Escherichia coli O44:H18 (strain 042 / EAEC)
21530	4670206	4670478	TY-2482_chromosome	D8E8Y6	Conserved domain protein	Escherichia coli MS 119-7
77394	4670213	4667976	TY-2482_chromosome	B7L8G6	Iron-enterobactin outer membrane transporter	Escherichia coli (strain 55989 / EAEC)
82545	4670534	4671655	TY-2482_chromosome	B7L8G7	Enterobactin/ferric enterobactin esterase	Escherichia coli (strain 55989 / EAEC)
75382	4671661	4671876	TY-2482_chromosome	B7L8G8	Putative uncharacterized protein ybdZ	Escherichia coli (strain 55989 / EAEC)
73710	4671876	4675754	TY-2482_chromosome	B7L8G9	Enterobactin synthase multienzyme complex component, ATP-dependent (EC 2.7.7.-)	Escherichia coli (strain 55989 / EAEC)
100907	4675973	4677103	TY-2482_chromosome	B7L8H0	Regulator of length of O-antigen component of lipopolysaccharide chains	Escherichia coli (strain 55989 / EAEC)
62754	4677918	4677106	TY-2482_chromosome	B7L8H1	Iron-enterobactin transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
68190	4678907	4677918	TY-2482_chromosome	B7L8H2	Iron-enterobactin transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
100772	4679908	4678907	TY-2482_chromosome	B7L8H3	Iron-enterobactin transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
30777	4680019	4681266	TY-2482_chromosome	B7L8H4	Enterobactin exporter EntS	Escherichia coli (strain 55989 / EAEC)
93354	4682229	4681276	TY-2482_chromosome	B7L8H5	Iron-enterobactin transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
68945	4682604	4683776	TY-2482_chromosome	B7L8H6	Isochorismate synthase 1 (EC 5.4.4.2)	Escherichia coli (strain 55989 / EAEC)
83226	4683789	4685396	TY-2482_chromosome	B7L8H7	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex (EC 2.7.7.58)	Escherichia coli (strain 55989 / EAEC)
91330	4685413	4686267	TY-2482_chromosome	B7L8H8	Isochorismatase (EC 3.3.2.1)	Escherichia coli (strain 55989 / EAEC)
97846	4686270	4687013	TY-2482_chromosome	B7L8H9	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28)	Escherichia coli (strain 55989 / EAEC)
112831	4687019	4687429	TY-2482_chromosome	B7L8I0	Putative esterase (EC 3.1.-.-)	Escherichia coli (strain 55989 / EAEC)
69992	4687613	4689715	TY-2482_chromosome	B7L8I1	Carbon starvation protein	Escherichia coli (strain 55989 / EAEC)
64176	4689900	4690094	TY-2482_chromosome	B7L8I2	Putative uncharacterized protein ybdD	Escherichia coli (strain 55989 / EAEC)
81004	4691195	4690110	TY-2482_chromosome	B7L8I3	Putative oxidoreductase (EC 1.1.1.-)	Escherichia coli (strain 55989 / EAEC)
76077	4691304	4692461	TY-2482_chromosome	B7L8I4	Methionine aminotransferase, PLP-dependent (EC 2.6.1.-)	Escherichia coli (strain 55989 / EAEC)
73712	4693094	4692468	TY-2482_chromosome	B7L8I5	Immunoglobulin-binding regulator	Escherichia coli (strain 55989 / EAEC)
83905	4694287	4693070	TY-2482_chromosome	B7L8I6	Immunoglobulin-binding regulator	Escherichia coli (strain 55989 / EAEC)
76345	4695336	4694437	TY-2482_chromosome	B7L8I7	Putative DNA-binding transcriptional regulator, LysR-type	Escherichia coli (strain 55989 / EAEC)

77572	4696291	4695548	TY-2482_chromosome	B7L8I8	Periplasmic disulfide isomerase/thiol-disulphide oxidase (EC 5.3.4.1)	Escherichia coli (strain 55989 / EAEC)
91889	4696663	4697223	TY-2482_chromosome	B7L8I9	Alkyl hydroperoxide reductase, C22 subunit (EC 1.11.1.15)	Escherichia coli (strain 55989 / EAEC)
98016	4697355	4698917	TY-2482_chromosome	B7L8J0	Alkyl hydroperoxide reductase, F52a subunit, FAD/NAD(P)-binding (EC 1.11.1.15)	Escherichia coli (strain 55989 / EAEC)
60678	4699469	4699044	TY-2482_chromosome	B7L8J1	Universal stress protein UP12	Escherichia coli (strain 55989 / EAEC)
62757	4699690	4700925	TY-2482_chromosome	B7L8J2	Putative oxidoreductase, Zn-dependent and NAD(P)-binding	Escherichia coli (strain 55989 / EAEC)
8599	4701009	4701467	TY-2482_chromosome	C3TJV7	Putative uncharacterized protein	Escherichia coli
107924	4702623	4701802	TY-2482_chromosome	D3GX75	Ribonuclease I	Escherichia coli O44:H18 (strain 042 / EAEC)
88380	4704182	4702722	TY-2482_chromosome	B7L8J5	Citrate:succinate antiporter	Escherichia coli (strain 55989 / EAEC)
30314	4705111	4704236	TY-2482_chromosome	B7L8J6	2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase (2-(5''-triphosphoribosyl)-3'-dephospho-CoA synthase) (	Escherichia coli (strain 55989 / EAEC)
27577	4705605	4706996	TY-2482_chromosome	Q1REU7	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
30315	4705637	4705089	TY-2482_chromosome	B7L8J7	Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61) (Apo-ACP nucleodityltransferase	Escherichia coli (strain 55989 / EAEC)
29236	4707175	4708218	TY-2482_chromosome	Q1REU5	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
84003	4709458	4708403	TY-2482_chromosome	B7L8K1	Citrate lyase synthetase (EC 6.2.1.22)	Escherichia coli (strain 55989 / EAEC)
60463	4709838	4711493	TY-2482_chromosome	B7L8K2	Sensory histidine kinase in two-component regulatory system with citB	Escherichia coli (strain 55989 / EAEC)
101547	4711465	4712142	TY-2482_chromosome	B7L8K3	DNA-binding response regulator in two-component regulatory system with citA	Escherichia coli (strain 55989 / EAEC)
109556	4713571	4712189	TY-2482_chromosome	B7L8K4	Anaerobic C4-dicarboxylate transport	Escherichia coli (strain 55989 / EAEC)
15063	4713931	4713713	TY-2482_chromosome	D7ZY80	Conserved domain protein	Escherichia coli MS 187-1
106366	4714160	4714717	TY-2482_chromosome	B7L9L5	Palmitoyl transferase for Lipid A (EC 2.3.1.-)	Escherichia coli (strain 55989 / EAEC)
36534	4714865	4715101	TY-2482_chromosome	Q8D127	Cold shock protein (Putative cold shock protein)	Yersinia pestis
30407	4715541	4715161	TY-2482_chromosome	B7L9G9	Protein CrcB homolog	Escherichia coli (strain 55989 / EAEC)
86278	4715634	4716419	TY-2482_chromosome	C8UJU2	Predicted amidase	Escherichia coli O111:H- (strain 11128 / EHEC)
113180	4716551	4716751	TY-2482_chromosome	B7L9H1	Sec-independent protein translocase protein tatA/E homolog 1	Escherichia coli (strain 55989 / EAEC)
31889	4717820	4716858	TY-2482_chromosome	B7L9H2	Lipoyl synthase (EC 2.8.1.8) (Lip-syn) (LS) (Lipoate synthase) (Lipoic acid synthase) (Sulfur insertion protein lipA	Escherichia coli (strain 55989 / EAEC)
97925	4718982	4718032	TY-2482_chromosome	B7L9H3	Putative DNA-binding transcriptional regulator, LysR-type	Escherichia coli (strain 55989 / EAEC)
110097	4719882	4719244	TY-2482_chromosome	C6V152	Octanoyltransferase (EC 2.3.1.181) (Lipoate-protein ligase B) (Lipoyl/octanoyl transferase) (Octanoyl-[acyl-carrier-pro	Escherichia coli O157:H7 (strain TW14359 / EHEC
34755	4720246	4719986	TY-2482_chromosome	B7L9H5	UPF0250 protein ybeD	Escherichia coli (strain 55989 / EAEC)
88512	4721568	4720360	TY-2482_chromosome	B7L9H6	D-alanyl-D-alanine carboxypeptidase (Penicillin-binding protein 5) (EC 3.4.16.4	Escherichia coli (strain 55989 / EAEC)
59095	4722795	4721710	TY-2482_chromosome	B7L9H7	Minor lipoprotein	Escherichia coli (strain 55989 / EAEC)
58394	4723918	4722809	TY-2482_chromosome	B7L9H8	Cell wall shape-determining protein	Escherichia coli (strain 55989 / EAEC)
88378	4725822	4723924	TY-2482_chromosome	B7L9H9	Transpeptidase involved in peptidoglycan synthesis (Penicillin-binding protein 2)	Escherichia coli (strain 55989 / EAEC)
33571	4726320	4725856	TY-2482_chromosome	B7L9I0	Ribosomal RNA large subunit methyltransferase H (EC 2.1.1.-) (23S rRNA m3Psi1915 methyltransferase) (rRNA (pseud	Escherichia coli (strain 55989 / EAEC)
83597	4726641	4726327	TY-2482_chromosome	B7L9I1	Putative uncharacterized protein ybeB	Escherichia coli (strain 55989 / EAEC)
15973	4726655	4726942	TY-2482_chromosome	P77108	Putative uncharacterized protein	Escherichia coli
80471	4727512	4726904	TY-2482_chromosome	B7L9I2	Putative phosphatase with phosphoglycerate mutase domain	Escherichia coli (strain 55989 / EAEC)
76395	4728177	4727539	TY-2482_chromosome	B7L9I3	Probable nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18) (Deamido-NAD(+) diphosphorylase) (Deamido-NAD(	Escherichia coli (strain 55989 / EAEC)
88340	4729210	4728182	TY-2482_chromosome	B7L9I4	DNA polymerase III, delta subunit (EC 2.7.7.7)	Escherichia coli (strain 55989 / EAEC)
31960	4729791	4729213	TY-2482_chromosome	B7L9I5	LPS-assembly lipoprotein lptE	Escherichia coli (strain 55989 / EAEC)
34129	4732388	4729809	TY-2482_chromosome	B7L9I6	Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)	Escherichia coli (strain 55989 / EAEC)
100715	4732623	4733102	TY-2482_chromosome	B7L9I7	Putative uncharacterized protein ybeL	Escherichia coli (strain 55989 / EAEC)
62750	4734152	4733178	TY-2482_chromosome	B7L9I8	Putative uncharacterized protein ybeQ	Escherichia coli (strain 55989 / EAEC)
66245	4734316	4735020	TY-2482_chromosome	B7L9I9	Putative uncharacterized protein ybeR	Escherichia coli (strain 55989 / EAEC)
90501	4735020	4736444	TY-2482_chromosome	B7L9J0	Putative DnaJ-class chaperone	Escherichia coli (strain 55989 / EAEC)
82605	4737011	4736460	TY-2482_chromosome	B7L9J1	Putative uncharacterized protein ybeT	Escherichia coli (strain 55989 / EAEC)
80974	4737112	4737816	TY-2482_chromosome	B7L9J2	Putative uncharacterized protein ybeU	Escherichia coli (strain 55989 / EAEC)
110650	4737816	4739264	TY-2482_chromosome	B7L9J3	Hsc56 co-chaperone of HscC	Escherichia coli (strain 55989 / EAEC)
115924	4740997	4739330	TY-2482_chromosome	C8TKH1	Hsp70 family chaperone Hsc62	Escherichia coli O26:H11 (strain 11368 / EHEC)
33405	4742016	4741084	TY-2482_chromosome	B7L9J7	Pyrimidine-specific ribonucleoside hydrolase rihA (EC 3.2.-.-) (Cytidine/uridine-specific hydrolase	Escherichia coli (strain 55989 / EAEC)
80976	4742859	4742137	TY-2482_chromosome	B7L9J8	Glutamate and aspartate transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
66247	4743533	4742862	TY-2482_chromosome	B7L9J9	Glutamate and aspartate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
69989	4744273	4743536	TY-2482_chromosome	B7L9K0	Glutamate and aspartate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
80992	4745351	4744446	TY-2482_chromosome	B7L9K1	Glutamate and aspartate transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
114309	4745806	4747679	TY-2482_chromosome	C8U318	Rhomboid family protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
15678	4747651	4747857	TY-2482_chromosome	C5W100	Ybl25	Escherichia coli (strain B / BL21)
73258	4749298	4747763	TY-2482_chromosome	B7L9K4	Apolipoprotein N-acyltransferase (EC 2.3.1.-)	Escherichia coli (strain 55989 / EAEC)
68290	4750201	4749326	TY-2482_chromosome	B7L9K5	Putative uncharacterized protein ybeX	Escherichia coli (strain 55989 / EAEC)
33695	4750758	4750294	TY-2482_chromosome	B7L9K6	Probable rRNA maturation factor YbeY	Escherichia coli (strain 55989 / EAEC)
84577	4751834	4750758	TY-2482_chromosome	B7L9K7	Putative enzyme with nucleoside triphosphate hydrolase domain	Escherichia coli (strain 55989 / EAEC)
32397	4753372	4751951	TY-2482_chromosome	B7L9K8	(Dimethylallyl)adenosine tRNA methylthiotransferase miaB (EC 2.-.-.-) (tRNA-i(6)A37 methylthiotransferase)	Escherichia coli (strain 55989 / EAEC)
91883	4753518	4754690	TY-2482_chromosome	B7L9K9	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol oxygenase (EC 1.14.13.-)	Escherichia coli (strain 55989 / EAEC)
28642	4754844	4755122	TY-2482_chromosome	A1A8T1	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
r488	4754921	4754847	TY-2482_chromosome	ref|NC_010473|:748357-748431|Gln tRNA| [gene=glnV] [locus_tag=ECDH10B_0733]		
r487	4755033	4754959	TY-2482_chromosome	ref|NC_010473|:748357-748431|Gln tRNA| [gene=glnV] [locus_tag=ECDH10B_0733]		
r293	4755158	4755082	TY-2482_chromosome	ref|NC_010473|:748872-748948|Met tRNA| [gene=metT] [locus_tag=ECDH10B_0738]		
r480	4755248	4755174	TY-2482_chromosome	ref|NC_010473|:748680-748754|Gln tRNA| [gene=glnU] [locus_tag=ECDH10B_0736]		

24649	4755282	4755528	TY-2482_chromosome	A1A8T2	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
r479	4755357	4755283	TY-2482_chromosome	ref|NC_010473|:748680-748754|Gln tRNA| [gene=glnU] [locus_tag=ECDH10B_0736		
r238	4755465	4755381	TY-2482_chromosome	ref|NC_010473|:748778-748862|Leu tRNA| [gene=leuW] [locus_tag=ECDH10B_0737		
r292	4755550	4755474	TY-2482_chromosome	ref|NC_010473|:748872-748948|Met tRNA| [gene=metT] [locus_tag=ECDH10B_0738		
18655	4755594	4755785	TY-2482_chromosome	D8ENZ6	Conserved domain protein	Escherichia coli MS 107-1
95542	4757595	4755934	TY-2482_chromosome	B7L9L0	Asparagine synthetase B (EC 6.3.5.4)	Escherichia coli (strain 55989 / EAEC)
16063	4757830	4757552	TY-2482_chromosome	D8C3Y4	Conserved domain protein	Escherichia coli MS 196-1
71648	4758604	4757855	TY-2482_chromosome	B7L9L1	NMP phosphatase	Escherichia coli (strain 55989 / EAEC)
113968	4759872	4758655	TY-2482_chromosome	B7L9L2	DNA-binding transcriptional dual regulator, repressor of N-acetylglucosamine	Escherichia coli (strain 55989 / EAEC)
87877	4761029	4759884	TY-2482_chromosome	B7L9L3	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	Escherichia coli (strain 55989 / EAEC)
32598	4761889	4761092	TY-2482_chromosome	B7L9L4	Glucosamine-6-phosphate deaminase (EC 3.5.99.6) (GlcN6P deaminase) (GNPDA) (Glucosamine-6-phosphate isomera	Escherichia coli (strain 55989 / EAEC)
110658	4762222	4764165	TY-2482_chromosome	B7L9L6	Fused N-acetyl glucosamine specific PTS enzymes: IIC component ; IIB component ; IIA component (EC 2.7.1.69)	Escherichia coli (strain 55989 / EAEC)
34163	4764371	4766032	TY-2482_chromosome	B7L9L7	Glutaminyl-tRNA synthetase (EC 6.1.1.18) (Glutamine--tRNA ligase) (GlnRS)	Escherichia coli (strain 55989 / EAEC)
99025	4766481	4767884	TY-2482_chromosome	B7L9L8	Putative outer membrane porin	Escherichia coli (strain 55989 / EAEC)
75614	4767937	4768260	TY-2482_chromosome	B7L9L9	Putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
86265	4768793	4768350	TY-2482_chromosome	B7L9M0	DNA-binding transcriptional dual regulator of siderophore biosynthesis and transpor	Escherichia coli (strain 55989 / EAEC)
59096	4768838	4769089	TY-2482_chromosome	B7L9M1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
61721	4769729	4769085	TY-2482_chromosome	D3GXD6	Flavodoxin 1	Escherichia coli O44:H18 (strain 042 / EAEC)
106113	4770114	4769755	TY-2482_chromosome	B5YQM9	Ribbon-helix-helix protein, CopG family	Escherichia coli O157:H7 (strain EC4115 / EHEC)
86050	4770949	4770188	TY-2482_chromosome	B7L9M4	Putative esterase	Escherichia coli (strain 55989 / EAEC)
69562	4770999	4771676	TY-2482_chromosome	D3GXD9	Negative modulator of initiation of replication	Escherichia coli O44:H18 (strain 042 / EAEC)
109385	4771705	4773342	TY-2482_chromosome	B7L9M6	Phosphoglucomutase (EC 5.4.2.2)	Escherichia coli (strain 55989 / EAEC)
71418	4774720	4773404	TY-2482_chromosome	B7L9M7	Putrescine/proton symporter: putrescine/ornithine antiporter	Escherichia coli (strain 55989 / EAEC)
90444	4776915	4774720	TY-2482_chromosome	B7L9M8	Ornithine decarboxylase isozyme, inducible (EC 4.1.1.17)	Escherichia coli (strain 55989 / EAEC)
114783	4778282	4777608	TY-2482_chromosome	C8UJZ6	DNA-binding response regulator KdpE in two-component regulatory system with KdpD	Escherichia coli O111:H- (strain 11128 / EHEC
84591	4780963	4778282	TY-2482_chromosome	B7LAF0	Fused sensory histidine kinase in two-component regulatory system with KdpE: signal sensing protein ; sensory histid	Escherichia coli (strain 55989 / EAEC)
30035	4781528	4780959	TY-2482_chromosome	B7LAA3	Potassium-transporting ATPase C chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] C chain) (Pota	Escherichia coli (strain 55989 / EAEC)
30021	4783585	4781540	TY-2482_chromosome	B7LAA4	Potassium-transporting ATPase B chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] B chain) (Pota	Escherichia coli (strain 55989 / EAEC)
30017	4785281	4783611	TY-2482_chromosome	B7LAA5	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Pota	Escherichia coli (strain 55989 / EAEC)
28283	4785484	4785284	TY-2482_chromosome	B7MFW4	Potassium ion accessory transporter subunit	Escherichia coli O45:K1 (strain S88 / ExPEC)
95416	4785683	4785886	TY-2482_chromosome	B7LAA6	Putative uncharacterized protein ybfA	Escherichia coli (strain 55989 / EAEC)
88402	4786132	4790322	TY-2482_chromosome	B7LAA7	RhsC element core protein RshC	Escherichia coli (strain 55989 / EAEC)
83260	4790325	4790648	TY-2482_chromosome	B7LAA8	Putative uncharacterized protein ybfB	Escherichia coli (strain 55989 / EAEC)
104707	4790769	4792199	TY-2482_chromosome	B7LAA9	Putative uncharacterized protein ybfO	Escherichia coli (strain 55989 / EAEC)
77335	4792199	4792765	TY-2482_chromosome	B7LAB0	Putative uncharacterized protein ybfC	Escherichia coli (strain 55989 / EAEC)
6227	4792994	4793245	TY-2482_chromosome	Q2EEQ8	Putative defective transposase ybfQ	Escherichia coli (strain K12)
105190	4793374	4794288	TY-2482_chromosome	C8UJN2	Putative H repeat-associated protein	Escherichia coli O111:H- (strain 11128 / EHEC
68712	4794283	4794789	TY-2482_chromosome	B7LAB3	Putative uncharacterized protein ybgA	Escherichia coli (strain 55989 / EAEC)
65033	4794789	4796204	TY-2482_chromosome	B7LAB4	Deoxyribodipyrimidine photolyase, FAD-binding (EC 4.1.99.3)	Escherichia coli (strain 55989 / EAEC)
114060	4797730	4796252	TY-2482_chromosome	B7LAB5	Dipeptide permease D	Escherichia coli (strain 55989 / EAEC)
81002	4798001	4798741	TY-2482_chromosome	B7LAB6	Putative uncharacterized protein ybgI	Escherichia coli (strain 55989 / EAEC)
84082	4799417	4800346	TY-2482_chromosome	B7LAB8	Putative hydrolase subunit	Escherichia coli (strain 55989 / EAEC)
34759	4800339	4801070	TY-2482_chromosome	B7LAB9	UPF0271 protein ybgL	Escherichia coli (strain 55989 / EAEC)
30765	4801109	4801897	TY-2482_chromosome	B7LAC0	Endonuclease 8 (DNA glycosylase/AP lyase Nei) (EC 3.2.2.-) (EC 4.2.99.18) (DNA-(apurinic or apyrimidinic site) lyase N	Escherichia coli (strain 55989 / EAEC)
75195	4802943	4801900	TY-2482_chromosome	B7LAC1	Putative membrane protein	Escherichia coli (strain 55989 / EAEC)
112359	4803778	4803098	TY-2482_chromosome	C8UK15	Predicted fimbrial-like adhesin protein	Escherichia coli O111:H- (strain 11128 / EHEC
14368	4804477	4803783	TY-2482_chromosome	E1U309	Transposase InsAB'	Escherichia coli
77418	4804805	4804509	TY-2482_chromosome	B7LAC4	Putative uncharacterized protein ybgQ	Escherichia coli (strain 55989 / EAEC)
102909	4805380	4804817	TY-2482_chromosome	B7LAC5	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
17042	4807035	4807223	TY-2482_chromosome	D6HU93	Citrate synthase	Escherichia coli B088
84588	4807053	4805773	TY-2482_chromosome	B7LAC6	Citrate synthase (EC 2.3.3.1)	Escherichia coli (strain 55989 / EAEC)
14234	4807729	4807493	TY-2482_chromosome	D6J831	Putative uncharacterized protein	Escherichia coli B354
79944	4807747	4808148	TY-2482_chromosome	B5YQQ9	Succinate dehydrogenase, cytochrome b556 subunit	Escherichia coli O157:H7 (strain EC4115 / EHEC)
80957	4808145	4808489	TY-2482_chromosome	B7LAC9	Succinate dehydrogenase, membrane subunit, binds cytochrome b556	Escherichia coli (strain 55989 / EAEC)
94861	4808492	4810255	TY-2482_chromosome	B7LAD0	Succinate dehydrogenase, flavoprotein subunit (EC 1.3.99.1)	Escherichia coli (strain 55989 / EAEC)
88412	4810274	4810987	TY-2482_chromosome	B7LAD1	Succinate dehydrogenase, FeS subunit (EC 1.3.99.1)	Escherichia coli (strain 55989 / EAEC)
70019	4811191	4813989	TY-2482_chromosome	B7LAD2	2-oxoglutarate decarboxylase, thiamin-requiring (EC 1.2.4.2)	Escherichia coli (strain 55989 / EAEC)
90955	4814007	4815221	TY-2482_chromosome	B7LAD3	Dihydrolipoyltranssuccinase (EC 2.3.1.61)	Escherichia coli (strain 55989 / EAEC)
34050	4815318	4816481	TY-2482_chromosome	B7LAD4	Succinyl-CoA ligase [ADP-forming] subunit beta (EC 6.2.1.5) (Succinyl-CoA synthetase subunit beta) (SCS-beta)	Escherichia coli (strain 55989 / EAEC)
114064	4816484	4817350	TY-2482_chromosome	B7LAD5	Succinyl-CoA ligase [ADP-forming] subunit alpha (EC 6.2.1.5)	Escherichia coli (strain 55989 / EAEC)
59144	4818179	4817460	TY-2482_chromosome	B7LAD6	DNA-binding transcriptional dual regulator, fatty-acyl-binding	Escherichia coli (strain 55989 / EAEC)
61798	4818288	4820261	TY-2482_chromosome	B7LAD7	Fused 2-O-a-mannosyl-D-glycerate specific PTS enzymes: IIA component ; IIB component ; IIC component (EC 2.7.1.6	Escherichia coli (strain 55989 / EAEC)
64300	4820282	4822912	TY-2482_chromosome	B7LAD8	Alpha-mannosidase	Escherichia coli (strain 55989 / EAEC)
101386	4822940	4823164	TY-2482_chromosome	B7LAD9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)

68612	4823762	4825327	TY-2482_chromosome	B7LAE0	Cytochrome d terminal oxidase, subunit I (EC 1.9.3.-)	Escherichia coli (strain 55989 / EAEC)
110406	4825346	4826482	TY-2482_chromosome	B7LAE1	Cytochrome d terminal oxidase, subunit II (EC 1.9.3.-)	Escherichia coli (strain 55989 / EAEC)
62778	4826613	4826903	TY-2482_chromosome	B7LAE2	Putative uncharacterized protein ybgE	Escherichia coli (strain 55989 / EAEC)
91135	4827056	4827457	TY-2482_chromosome	B7LAE3	Acyl-CoA thioesterase	Escherichia coli (strain 55989 / EAEC)
113337	4827457	4828146	TY-2482_chromosome	B7LAE4	Membrane spanning protein in TolA-TolQ-TolR complex	Escherichia coli (strain 55989 / EAEC)
84590	4828153	4828578	TY-2482_chromosome	B7LAE5	Membrane spanning protein in TolA-TolQ-TolR complex	Escherichia coli (strain 55989 / EAEC)
61691	4828646	4829908	TY-2482_chromosome	B7LAE6	Membrane anchored protein in TolA-TolQ-TolR complex	Escherichia coli (strain 55989 / EAEC)
34286	4830044	4831333	TY-2482_chromosome	B7LAE7	Protein tolB	Escherichia coli (strain 55989 / EAEC)
59146	4831902	4832690	TY-2482_chromosome	B7LAE9	Putative RNA binding protein	Escherichia coli (strain 55989 / EAEC)
24199	4831922	4831308	TY-2482_chromosome	Q1REI4	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
r357	4832858	4832933	TY-2482_chromosome	ref|NC_010473|:2611040-2611115|Lys tRNA| [gene=lysV] [locus_tag=ECDH10B_2568]		
r368	4832969	4833044	TY-2482_chromosome	ref|NC_010473|:2610960-2611035|Val tRNA| [gene=valY] [locus_tag=ECDH10B_2567]		
r358	4833048	4833123	TY-2482_chromosome	ref|NC_010473|:2611040-2611115|Lys tRNA| [gene=lysV] [locus_tag=ECDH10B_2568]		
r369	4833273	4833348	TY-2482_chromosome	ref|NC_010473|:2610960-2611035|Val tRNA| [gene=valY] [locus_tag=ECDH10B_2567]		
r359	4833353	4833428	TY-2482_chromosome	ref|NC_010473|:2611040-2611115|Lys tRNA| [gene=lysV] [locus_tag=ECDH10B_2568]		
r360	4833575	4833650	TY-2482_chromosome	ref|NC_010473|:2611040-2611115|Lys tRNA| [gene=lysV] [locus_tag=ECDH10B_2568]		
r361	4833684	4833759	TY-2482_chromosome	ref|NC_010473|:2611040-2611115|Lys tRNA| [gene=lysV] [locus_tag=ECDH10B_2568]		
r362	4833793	4833868	TY-2482_chromosome	ref|NC_010473|:2611040-2611115|Lys tRNA| [gene=lysV] [locus_tag=ECDH10B_2568]		
32583	4834117	4835157	TY-2482_chromosome	B7LAF1	Quinolinate synthase A (EC 2.5.1.72)	Escherichia coli (strain 55989 / EAEC)
62779	4835198	4835914	TY-2482_chromosome	B7LAF2	Nicotinamide mononucleotide transporter	Escherichia coli (strain 55989 / EAEC)
112171	4836855	4835917	TY-2482_chromosome	B7LAF3	Zinc transporter zitB	Escherichia coli (strain 55989 / EAEC)
71363	4837349	4836972	TY-2482_chromosome	B7LAF4	Putative uncharacterized protein ybgS	Escherichia coli (strain 55989 / EAEC)
19551	4837662	4837438	TY-2482_chromosome	D6J868	Predicted protein	Escherichia coli B354
58501	4837665	4838714	TY-2482_chromosome	B7LAF5	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate syntha	Escherichia coli (strain 55989 / EAEC)
31202	4839627	4838878	TY-2482_chromosome	B7LAF6	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromut	Escherichia coli (strain 55989 / EAEC)
59150	4840872	4839835	TY-2482_chromosome	B7LAF7	Galactose-1-epimerase (Mutarotase) (EC 5.1.3.3)	Escherichia coli (strain 55989 / EAEC)
31063	4842014	4840869	TY-2482_chromosome	B7LAF8	Galactokinase (EC 2.7.1.6) (Galactose kinase)	Escherichia coli (strain 55989 / EAEC)
79759	4843064	4842021	TY-2482_chromosome	B7LAF9	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)	Escherichia coli (strain 55989 / EAEC)
70049	4844090	4843077	TY-2482_chromosome	B7LAG0	UDP-galactose-4-epimerase (EC 5.1.3.2)	Escherichia coli (strain 55989 / EAEC)
60690	4845823	4844354	TY-2482_chromosome	B7LAG1	Fused molybdate transporter subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
80380	4846679	4845894	TY-2482_chromosome	B7LAG3	DNA-binding transcriptional dual regulator	Escherichia coli (strain 55989 / EAEC)
62639	4847124	4847894	TY-2482_chromosome	B7LB71	Molybdate transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
114080	4847897	4848583	TY-2482_chromosome	B7LB72	Molybdate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
65534	4848589	4849644	TY-2482_chromosome	B7LB73	Molybdate transporter subunit ; ATP-binding component of ABC superfamily (EC 3.6.3.29	Escherichia coli (strain 55989 / EAEC)
75836	4850568	4849651	TY-2482_chromosome	B5YRG4	Phosphatase YbhA (EC 3.1.3.11)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
29620	4850621	4851613	TY-2482_chromosome	B7LB75	6-phosphogluconolactonase (6-P-gluconolactonase) (EC 3.1.1.31)	Escherichia coli (strain 55989 / EAEC)
102014	4852610	4851660	TY-2482_chromosome	B5YRG6	Transcriptional regulator, LysR family	Escherichia coli O157:H7 (strain EC4115 / EHEC)
114678	4852794	4853843	TY-2482_chromosome	C8TKR7	Conserved predicted protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
105675	4853922	4855352	TY-2482_chromosome	B7LB80	Putative anion transporter	Escherichia coli (strain 55989 / EAEC)
99177	4855538	4857796	TY-2482_chromosome	B7LB81	Putative enzyme	Escherichia coli (strain 55989 / EAEC)
86548	4859316	4858036	TY-2482_chromosome	B7LB82	Pectin methylesterase	Escherichia coli (strain 55989 / EAEC)
86868	4860521	4859454	TY-2482_chromosome	B7LB83	Integrase from phage	Escherichia coli (strain 55989 / EAEC)
104617	4860717	4860502	TY-2482_chromosome	C8TKS2	Putative excisionase	Escherichia coli O26:H11 (strain 11368 / EHEC)
103519	4861167	4861766	TY-2482_chromosome	C6V292	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
109515	4862201	4861983	TY-2482_chromosome	B7LB85	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73751	4862611	4862303	TY-2482_chromosome	B7LB86	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
68291	4863615	4862938	TY-2482_chromosome	B7LB88	Exonuclease from phage origin	Escherichia coli (strain 55989 / EAEC)
102920	4864397	4863615	TY-2482_chromosome	B7LB89	Recombination protein bet from phage origin	Escherichia coli (strain 55989 / EAEC)
5783	4864774	4864406	TY-2482_chromosome	P03702	Host-nuclease inhibitor protein gam	Enterobacteria phage lambda (Bacteriophage lambda)
16835	4865194	4864778	TY-2482_chromosome	E2QKN0	Prophage Kil protein	Escherichia coli
25260	4866331	4865582	TY-2482_chromosome	B7LB92	Regulatory protein CI from bacteriophage origin	Escherichia coli (strain 55989 / EAEC)
88431	4866374	4866601	TY-2482_chromosome	B7LB93	Cro	Escherichia coli (strain 55989 / EAEC)
86556	4866674	4867210	TY-2482_chromosome	B7LB94	Regulatory protein CII (Modular protein) from bacteriophage origin; putative coiled-coi	Escherichia coli (strain 55989 / EAEC)
81052	4867210	4868226	TY-2482_chromosome	B7LB95	Replication protein O frm phage origin	Escherichia coli (strain 55989 / EAEC)
86488	4868226	4868924	TY-2482_chromosome	B7LB96	Putative replication protein P of bacteriophage	Escherichia coli (strain 55989 / EAEC)
102842	4868924	4869223	TY-2482_chromosome	B7LB97	Ren protein from phage origin	Escherichia coli (strain 55989 / EAEC)
59170	4869216	4869512	TY-2482_chromosome	B7L8U8	Putative multidrug resistance protein; DLP12 prophage	Escherichia coli (strain 55989 / EAEC)
71939	4869472	4870263	TY-2482_chromosome	B7LB99	Putative site-specific invertase; DLP12 prophage	Escherichia coli (strain 55989 / EAEC)
23859	4870378	4870698	TY-2482_chromosome	E1IVP2	Conserved domain protein	Escherichia coli MS 145-7
100717	4870936	4871442	TY-2482_chromosome	B7LBA2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
91934	4871640	4872092	TY-2482_chromosome	B7LBA3	Putative uncharacterized protein ybcN	Escherichia coli (strain 55989 / EAEC)
70031	4872258	4872545	TY-2482_chromosome	B7LBA5	Putative uncharacterized protein ybcO	Escherichia coli (strain 55989 / EAEC)
106816	4872545	4872903	TY-2482_chromosome	C6V1R1	Crossover junction endodeoxyribonuclease rusA (EC 3.1.22.4)	Escherichia coli O157:H7 (strain TW14359 / EHEC
95603	4873129	4873509	TY-2482_chromosome	B7LBA7	Putative antitermination protein Q homolog; DLP12 prophage	Escherichia coli (strain 55989 / EAEC)

77343	4874783	4873704	TY-2482_chromosome	B7LBA8	Outer membrane porin; DLP12 prophage	Escherichia coli (strain 55989 / EAEC)
9871	4874993	4875259	TY-2482_chromosome	D8C8F3	Conserved domain protein	Escherichia coli MS 185-1
24756	4875327	4875584	TY-2482_chromosome	D3QKQ6	Putative uncharacterized protein essD	Escherichia coli O55:H7 (strain CB9615 / EPEC)
97168	4875587	4876081	TY-2482_chromosome	B7LBB0	Lysozyme (EC 3.2.1.17)	Escherichia coli (strain 55989 / EAEC)
20563	4876081	4876638	TY-2482_chromosome	D8ACV6	Bacteriophage lysis protein	Escherichia coli MS 21-1
86349	4876723	4877241	TY-2482_chromosome	B7LBB2	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104489	4878019	4877597	TY-2482_chromosome	B7LBB3	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
12241	4878056	4878319	TY-2482_chromosome	D7Y1Y3	Conserved domain protein	Escherichia coli MS 115-1
23824	4878567	4878313	TY-2482_chromosome	D7XQE2	Conserved domain protein	Escherichia coli MS 84-1
62640	4878683	4879225	TY-2482_chromosome	B7LBB5	DNA packaging protein; DLP12 prophage	Escherichia coli (strain 55989 / EAEC)
29393	4879203	4880861	TY-2482_chromosome	B7LBB6	Terminase large subunit from bacteriophage origin	Escherichia coli (strain 55989 / EAEC)
78739	4881124	4881327	TY-2482_chromosome	B7LBB8	Head-to-tail joining protein W (GpW) from bacteriophage origin	Escherichia coli (strain 55989 / EAEC)
58242	4881327	4882925	TY-2482_chromosome	B7LBB9	Portal protein; minor capsid protein	Escherichia coli (strain 55989 / EAEC)
60802	4884232	4884567	TY-2482_chromosome	B7LBC1	Head decoration protein from bacteriophage origin	Escherichia coli (strain 55989 / EAEC)
95606	4884599	4885648	TY-2482_chromosome	B7LBC2	Major head coat protein from bacteriophage origin	Escherichia coli (strain 55989 / EAEC)
84593	4885654	4886085	TY-2482_chromosome	B7LBC3	DNA packaging protein from bacteriophage origin	Escherichia coli (strain 55989 / EAEC)
95987	4886100	4886471	TY-2482_chromosome	C8TJG4	Putative minor capsid protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
64417	4886465	4887040	TY-2482_chromosome	B7LBC5	Minor tail protein Z (GpZ)	Escherichia coli (strain 55989 / EAEC)
76047	4887040	4887432	TY-2482_chromosome	B7LBC6	Minor tail protein U	Escherichia coli (strain 55989 / EAEC)
112081	4887413	4888180	TY-2482_chromosome	B7LBC7	Major tail protein V	Escherichia coli (strain 55989 / EAEC)
84594	4889030	4891588	TY-2482_chromosome	B7LBD0	Minor tail protein H	Escherichia coli (strain 55989 / EAEC)
111772	4891588	4891914	TY-2482_chromosome	B7LBD1	Minor tail protein M	Escherichia coli (strain 55989 / EAEC)
14543	4891917	4893361	TY-2482_chromosome	E8HW87	Tail fiber component K (Fragment)	Escherichia coli O157:H- str. H 2687
94156	4893262	4893930	TY-2482_chromosome	B7LBD4	Tail assembly protein I	Escherichia coli (strain 55989 / EAEC)
28045	4893991	4895823	TY-2482_chromosome	B7MSE1	Host specificity protein J from prophage	Escherichia coli O81 (strain ED1a)
100645	4895778	4897694	TY-2482_chromosome	C8U2R4	Putative host specificity protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
94528	4897738	4898364	TY-2482_chromosome	C8TVW5	Putative outer membrane Lom	Escherichia coli O26:H11 (strain 11368 / EHEC)
12764	4898432	4899061	TY-2482_chromosome	E8HC23	Putative membrane protein of prophage CP-933X	Escherichia coli O157:H7 str. G5101
89847	4899437	4901695	TY-2482_chromosome	B7LBD7	Putative tail fiber protein	Escherichia coli (strain 55989 / EAEC)
86159	4901698	4902279	TY-2482_chromosome	B7LBD8	Putative tail fibre chaperone; Qin prophage	Escherichia coli (strain 55989 / EAEC)
87198	4903687	4902359	TY-2482_chromosome	B7LBD9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
73593	4904909	4904436	TY-2482_chromosome	B7LC55	Putative UPF0098 class protein	Escherichia coli (strain 55989 / EAEC)
105427	4906257	4904971	TY-2482_chromosome	B7LC56	7,8-diaminopelargonic acid synthase, PLP-dependent (EC 2.6.1.62)	Escherichia coli (strain 55989 / EAEC)
30120	4906344	4907381	TY-2482_chromosome	B7LC57	Biotin synthase (EC 2.8.1.6)	Escherichia coli (strain 55989 / EAEC)
30132	4907381	4908532	TY-2482_chromosome	B7LC58	8-amino-7-oxononanoate synthase (AONS) (EC 2.3.1.47) (7-keto-8-amino-pelargonic acid synthase) (7-KAP synthase)	Escherichia coli (strain 55989 / EAEC)
112493	4908522	4909274	TY-2482_chromosome	B7LC59	Putative methltransferase, enzyme of biotin synthesis	Escherichia coli (strain 55989 / EAEC)
102725	4909270	4909944	TY-2482_chromosome	B7LC60	Dethiobiotin synthetase 1 (EC 6.3.3.3) (DTB synthetase 1) (Dethiobiotin synthase 1)	Escherichia coli (strain 55989 / EAEC)
34538	4910526	4912544	TY-2482_chromosome	B7LC61	UvrABC system protein B (Protein uvrB) (Excinuclease ABC subunit B)	Escherichia coli (strain 55989 / EAEC)
79102	4913647	4912742	TY-2482_chromosome	B7LC62	Putative transferase with NAD(P)-binding Rossmann-fold domain; UPF0052 family	Escherichia coli (strain 55989 / EAEC)
32442	4914044	4915030	TY-2482_chromosome	B7LC63	Molybdenum cofactor biosynthesis protein A	Escherichia coli (strain 55989 / EAEC)
84423	4915055	4915564	TY-2482_chromosome	B7LC64	Molybdopterin biosynthesis protein B	Escherichia coli (strain 55989 / EAEC)
32446	4915570	4916052	TY-2482_chromosome	B7LC65	Molybdenum cofactor biosynthesis protein C	Escherichia coli (strain 55989 / EAEC)
61650	4916048	4916290	TY-2482_chromosome	B7LC66	Molybdopterin synthase, small subunit	Escherichia coli (strain 55989 / EAEC)
93624	4916295	4916744	TY-2482_chromosome	B7LC67	Molybdopterin synthase, large subunit	Escherichia coli (strain 55989 / EAEC)
65073	4916884	4917585	TY-2482_chromosome	B7LC68	Putative uncharacterized protein ybhL	Escherichia coli (strain 55989 / EAEC)
95401	4917733	4918434	TY-2482_chromosome	B7LC69	Putative integral membrane protein	Escherichia coli (strain 55989 / EAEC)
77537	4918507	4919217	TY-2482_chromosome	B7LC70	Putative uncharacterized protein ybhM	Escherichia coli (strain 55989 / EAEC)
77538	4920212	4919259	TY-2482_chromosome	B7LC71	Putative uncharacterized protein ybhN	Escherichia coli (strain 55989 / EAEC)
84424	4921453	4920215	TY-2482_chromosome	B7LC72	Cardiolipin synthase 2 (EC 2.7.8.-)	Escherichia coli (strain 55989 / EAEC)
108650	4922211	4921453	TY-2482_chromosome	B7LC73	Putative metal-dependent hydrolase	Escherichia coli (strain 55989 / EAEC)
93866	4922344	4922751	TY-2482_chromosome	B7LC74	Putative uncharacterized protein ybhQ	Escherichia coli (strain 55989 / EAEC)
61320	4923822	4922719	TY-2482_chromosome	B7LC75	Putative transporter subunit: permease component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
110537	4924966	4923836	TY-2482_chromosome	B7LC76	Putative transporter subunit: permease component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
75689	4926695	4924962	TY-2482_chromosome	B7LC77	Putative transporter fused subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
34763	4927686	4926691	TY-2482_chromosome	B7LC78	UPF0194 membrane protein ybhG	Escherichia coli (strain 55989 / EAEC)
80546	4928369	4927689	TY-2482_chromosome	D3GZ40	TetR-family transcriptional regulator	Escherichia coli O44:H18 (strain 042 / EAEC)
95419	4928586	4929947	TY-2482_chromosome	B7LC80	RNA helicase	Escherichia coli (strain 55989 / EAEC)
98606	4930664	4930185	TY-2482_chromosome	B7LC81	Putative uncharacterized protein ybiA	Escherichia coli (strain 55989 / EAEC)
69915	4930784	4932931	TY-2482_chromosome	B7LC82	ATP-dependent DNA helicase	Escherichia coli (strain 55989 / EAEC)
69916	4932962	4933921	TY-2482_chromosome	B7LC83	Putative transferase/phosphorylase	Escherichia coli (strain 55989 / EAEC)
66350	4934065	4935147	TY-2482_chromosome	B7LC84	Putative hydroxyacid dehydrogenase	Escherichia coli (strain 55989 / EAEC)
66352	4935639	4935382	TY-2482_chromosome	B7LC85	Putative uncharacterized protein ybiJ	Escherichia coli (strain 55989 / EAEC)
108528	4936259	4935885	TY-2482_chromosome	C6V2G3	Conserved protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
34769	4936921	4936247	TY-2482_chromosome	B7LC87	PKHD-type hydroxylase ybiX (EC 1.14.11.-)	Escherichia coli (strain 55989 / EAEC)

18934	4939207	4939452	TY-2482_chromosome	D8EK43	Conserved domain protein	Escherichia coli MS 107-1
71558	4939245	4936966	TY-2482_chromosome	B7LC88	Putative TonB-dependent iron outer membrane transporter	Escherichia coli (strain 55989 / EAEC)
110540	4939914	4939513	TY-2482_chromosome	B7LC89	Putative uncharacterized protein ybiM	Escherichia coli (strain 55989 / EAEC)
33565	4940046	4940969	TY-2482_chromosome	B7LC90	Ribosomal RNA large subunit methyltransferase F (EC 2.1.1.181) (23S rRNA mA1618 methyltransferase) (rRNA adenin	Escherichia coli (strain 55989 / EAEC)
91852	4943194	4940972	TY-2482_chromosome	B7LC91	Putative membrane protein	Escherichia coli (strain 55989 / EAEC)
60696	4944033	4943314	TY-2482_chromosome	B7LC92	Glutamine transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
68294	4944689	4944033	TY-2482_chromosome	B7LC93	Glutamine transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
105750	4945574	4944831	TY-2482_chromosome	B7LC94	Glutamine transporter subunit ; periplasmic binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
17903	4945692	4945504	TY-2482_chromosome	C1HG03	Putative uncharacterized protein	Escherichia sp. 3_2_53FAA
17904	4945913	4945623	TY-2482_chromosome	E2QIH9	Putative uncharacterized protein	Escherichia coli
30665	4946481	4945981	TY-2482_chromosome	B7LC95	DNA protection during starvation protein (EC 1.16.-.-)	Escherichia coli (strain 55989 / EAEC)
64209	4947679	4946783	TY-2482_chromosome	B5YSA5	Threonine/homoserine efflux transporter RhtA	Escherichia coli O157:H7 (strain EC4115 / EHEC)
62619	4948020	4948532	TY-2482_chromosome	B7LC97	Outer membrane protein	Escherichia coli (strain 55989 / EAEC)
114158	4950167	4948587	TY-2482_chromosome	B7LC98	Putative enzyme, UPF0141 family, inner membrane	Escherichia coli (strain 55989 / EAEC)
7828	4950241	4950507	TY-2482_chromosome	P75786	Putative uncharacterized protein yliL	Escherichia coli (strain K12)
r201	4950610	4950522	TY-2482_chromosome	ref|NC_010473|:906103-906191|-| [gene=rybA] [locus_tag=ECDH10B_0885]		
115999	4950753	4951217	TY-2482_chromosome	B7LC99	DNA-binding transcriptional regulator of mntH	Escherichia coli (strain 55989 / EAEC)
62620	4951217	4952332	TY-2482_chromosome	B7LCA0	Putative transporter	Escherichia coli (strain 55989 / EAEC)
84425	4953314	4952397	TY-2482_chromosome	B7LCA1	Putative uncharacterized protein ybiS	Escherichia coli (strain 55989 / EAEC)
106362	4953533	4955122	TY-2482_chromosome	B7LCA2	Putative transporter fused subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
115756	4955404	4956381	TY-2482_chromosome	B7LF78	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
83173	4957905	4956643	TY-2482_chromosome	B7LCA4	Putative uncharacterized protein ybiU	Escherichia coli (strain 55989 / EAEC)
97172	4958872	4958060	TY-2482_chromosome	B7LCA5	Type II HAD phosphatase	Escherichia coli (strain 55989 / EAEC)
68816	4961450	4959021	TY-2482_chromosome	B7LCA6	Putative glycyl radical cofactor protein	Escherichia coli (strain 55989 / EAEC)
113977	4962382	4961459	TY-2482_chromosome	B7LCA7	Putative AdoMet-dependent glycyl radical activating enzyme	Escherichia coli (strain 55989 / EAEC)
58202	4962486	4963145	TY-2482_chromosome	B7LCA8	Probable fructose-6-phosphate aldolase 1 (EC 4.1.2.-)	Escherichia coli (strain 55989 / EAEC)
69392	4963985	4963239	TY-2482_chromosome	B7LCA9	Molybdopterin synthase sulfurylase	Escherichia coli (strain 55989 / EAEC)
73139	4965220	4963988	TY-2482_chromosome	B7LCB0	Molybdopterin biosynthesis protein	Escherichia coli (strain 55989 / EAEC)
88507	4965424	4966386	TY-2482_chromosome	B7LCB1	Isoaspartyl dipeptidase with L-asparaginase activity (EC 3.5.1.-)	Escherichia coli (strain 55989 / EAEC)
77539	4966409	4968244	TY-2482_chromosome	B7LCB2	Putative peptide transport fused subunits of ABC superfamily: ATP-binding components	Escherichia coli (strain 55989 / EAEC)
113979	4968267	4969802	TY-2482_chromosome	B7LCB3	Putative peptide transporter subunit: periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
93997	4969823	4970740	TY-2482_chromosome	B7LCB4	Putative peptide transporter permease subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
112486	4970746	4971654	TY-2482_chromosome	B7LCB5	Putative peptide transporter permease subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
62621	4971835	4974180	TY-2482_chromosome	B7LCB6	Putative uncharacterized protein yliE	Escherichia coli (strain 55989 / EAEC)
109514	4974191	4975516	TY-2482_chromosome	B7LCB7	Putative diguanylate cyclase	Escherichia coli (strain 55989 / EAEC)
33438	4976891	4975569	TY-2482_chromosome	B7LCB8	Ribosomal protein S12 methylthiotransferase RimO (S12 MTTase) (S12 methylthiotransferase) (EC 2.-.-.-) (Ribosome r	Escherichia coli (strain 55989 / EAEC)
116000	4977104	4977484	TY-2482_chromosome	B7LCB9	Biofilm regulator	Escherichia coli (strain 55989 / EAEC)
83762	4977598	4978710	TY-2482_chromosome	B7LCC0	PQQ-dependent aldose sugar dehydrogenase (Asd) (EC 1.1.5.-) (EC 1.1.5.2)	Escherichia coli (strain 55989 / EAEC)
101201	4979336	4978713	TY-2482_chromosome	B7LCC1	Putative glutathione S-transferase	Escherichia coli (strain 55989 / EAEC)
59007	4979583	4980782	TY-2482_chromosome	B7LCC2	D-alanyl-D-alanine carboxypeptidase (Penicillin-binding protein 6a) (EC 3.4.16.4	Escherichia coli (strain 55989 / EAEC)
91853	4981590	4980835	TY-2482_chromosome	B7LCC3	DNA-binding transcriptional repressor	Escherichia coli (strain 55989 / EAEC)
99021	4982244	4981651	TY-2482_chromosome	B7LCC4	Undecaprenyl pyrophosphate phosphatase	Escherichia coli (strain 55989 / EAEC)
72897	4982529	4983758	TY-2482_chromosome	B7LCC5	Multidrug efflux system protein	Escherichia coli (strain 55989 / EAEC)
102705	4984086	4983805	TY-2482_chromosome	B7LD36	Putative uncharacterized protein ybjH	Escherichia coli (strain 55989 / EAEC)
115997	4984987	4984175	TY-2482_chromosome	B7LD37	Putative phosphatase (EC 3.1.3.-)	Escherichia coli (strain 55989 / EAEC)
76549	4986195	4984990	TY-2482_chromosome	B7LD38	Putative transporter	Escherichia coli (strain 55989 / EAEC)
114153	4986279	4986812	TY-2482_chromosome	B7LD39	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
r418	4986910	4986832	TY-2482_chromosome	ref|NC_010473|:941127-941205|-| [gene=rybB] [locus_tag=ECDH10B_0916]		
34771	4988675	4986993	TY-2482_chromosome	B7LD40	Putative transport protein YbjL	Escherichia coli (strain 55989 / EAEC)
70097	4988945	4989319	TY-2482_chromosome	B7LD41	Putative uncharacterized protein ybjM	Escherichia coli (strain 55989 / EAEC)
94230	4989609	4989355	TY-2482_chromosome	B7LD42	Glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a)	Escherichia coli (strain 55989 / EAEC)
101282	4989769	4990053	TY-2482_chromosome	B7LD43	Putative uncharacterized protein ybjC	Escherichia coli (strain 55989 / EAEC)
88505	4990040	4990759	TY-2482_chromosome	B7LD44	Nitroreductase A, NADPH-dependent, FMN-dependent	Escherichia coli (strain 55989 / EAEC)
33429	4990823	4991722	TY-2482_chromosome	B7LD45	Ribosomal protein S6 modification protein	Escherichia coli (strain 55989 / EAEC)
95391	4991813	4992286	TY-2482_chromosome	B7LD46	Putative uncharacterized protein ybjN	Escherichia coli (strain 55989 / EAEC)
97125	4992641	4993750	TY-2482_chromosome	B7LD47	Putrescine transporter subunit: periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
84541	4993848	4994978	TY-2482_chromosome	B7LD48	Putrescine transporter subunit: ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
111197	4994991	4995941	TY-2482_chromosome	C8UL80	Putrescine transporter subunit PotH	Escherichia coli O111:H- (strain 11128 / EHEC)
77532	4995941	4996783	TY-2482_chromosome	B7LD50	Putrescine transporter subunit: membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
84405	4996846	4997331	TY-2482_chromosome	B7LD51	Putative uncharacterized protein ybjO	Escherichia coli (strain 55989 / EAEC)
33829	4997375	4998499	TY-2482_chromosome	B7LD52	23S rRNA (uracil-5-)-methyltransferase RumB (EC 2.1.1.189) (23S rRNA(M-5-U747)-methyltransferase	Escherichia coli (strain 55989 / EAEC)
100765	4999408	4998680	TY-2482_chromosome	B7LD53	Arginine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
71411	5000368	4999703	TY-2482_chromosome	B7LD54	Arginine transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
84406	5001084	5000371	TY-2482_chromosome	B7LD55	Arginine transporter subunit ;membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)

84408	5001822	5001094	TY-2482_chromosome	B7LD56	Arginine transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
102708	5002568	5001843	TY-2482_chromosome	B7LD57	Arginine transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
77307	5003301	5002789	TY-2482_chromosome	B7LD58	Putative uncharacterized protein ybjP	Escherichia coli (strain 55989 / EAEC)
34777	5003427	5003747	TY-2482_chromosome	B7LD59	UPF0145 protein ybjQ	Escherichia coli (strain 55989 / EAEC)
110523	5003747	5004574	TY-2482_chromosome	B7LD60	Putative cell wall amidase and lipoprotein	Escherichia coli (strain 55989 / EAEC)
62615	5005587	5004577	TY-2482_chromosome	B7LD61	Putative NAD(P)H-binding oxidoreductase with NAD(P)-binding Rossmann-fold domain	Escherichia coli (strain 55989 / EAEC)
73592	5007116	5005689	TY-2482_chromosome	B7LD62	Putative uncharacterized protein ybjT	Escherichia coli (strain 55989 / EAEC)
108194	5008128	5007130	TY-2482_chromosome	B7LD63	L-allo-threonine aldolase, PLP-dependent (EC 4.1.2.5)	Escherichia coli (strain 55989 / EAEC)
115284	5009883	5008168	TY-2482_chromosome	B7LD64	Pyruvate dehydrogenase (Pyruvate oxidase), thiamin-dependent, FAD-binding (EC 1.2.2.2)	Escherichia coli (strain 55989 / EAEC)
100913	5010984	5010019	TY-2482_chromosome	B7LD65	HCP oxidoreductase, NADH-dependent	Escherichia coli (strain 55989 / EAEC)
31328	5012648	5010999	TY-2482_chromosome	B7LD66	Hydroxylamine reductase (EC 1.7.-.-) (Hybrid-cluster protein) (HCP)	Escherichia coli (strain 55989 / EAEC)
102722	5013691	5012795	TY-2482_chromosome	B7LD67	Putative transporter	Escherichia coli (strain 55989 / EAEC)
97354	5014126	5013842	TY-2482_chromosome	C6V2L9	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
65654	5014881	5014189	TY-2482_chromosome	B7LD68	Aquaporin Z	Escherichia coli (strain 55989 / EAEC)
99020	5015307	5016962	TY-2482_chromosome	B7LD69	Putative uncharacterized protein ybjD	Escherichia coli (strain 55989 / EAEC)
84412	5017954	5016965	TY-2482_chromosome	B7LD70	Putative uncharacterized protein ybjX	Escherichia coli (strain 55989 / EAEC)
104323	5018069	5019181	TY-2482_chromosome	B7LD71	Macrolide transporter subunit, membrane fusion protein (MFP) component	Escherichia coli (strain 55989 / EAEC)
95392	5019181	5021124	TY-2482_chromosome	B7LD72	Fused macrolide transporter subunits of ABC superfamily: ATP-binding component ; membrane componen	Escherichia coli (strain 55989 / EAEC)
27507	5021582	5021301	TY-2482_chromosome	Q1RE42	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
30337	5021747	5022064	TY-2482_chromosome	B7LD74	ATP-dependent Clp protease adapter protein ClpS	Escherichia coli (strain 55989 / EAEC)
84432	5022098	5024371	TY-2482_chromosome	B7LD75	ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine protease, chaperone activity	Escherichia coli (strain 55989 / EAEC)
26588	5024674	5024914	TY-2482_chromosome	C5W2A2	Ybl54	Escherichia coli (strain B / BL21)
20819	5024692	5024456	TY-2482_chromosome	D8EAE3	Conserved domain protein	Escherichia coli MS 119-7
r203	5024805	5024718	TY-2482_chromosome	ref|NC_010473|:1152233-1152320|Ser tRNA| [gene=serX] [locus_tag=ECDH10B_1104		
109504	5025277	5025062	TY-2482_chromosome	B7LD76	Translation initiation factor IF-1	Escherichia coli (strain 55989 / EAEC)
31877	5026266	5025565	TY-2482_chromosome	B7LD77	Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6) (L/F-transferase) (Leucyltransferase) (Phenyalanyltransfer	Escherichia coli (strain 55989 / EAEC)
84414	5028029	5026311	TY-2482_chromosome	B7LD78	Fused cysteine transporter subunits of ABC superfamily: membrane component ; ATP-binding component	Escherichia coli (strain 55989 / EAEC)
76056	5029796	5028033	TY-2482_chromosome	B7LD79	Fused cysteine transporter subunits of ABC superfamily: membrane component ; ATP-binding component	Escherichia coli (strain 55989 / EAEC)
91773	5030884	5029922	TY-2482_chromosome	B7LD80	Thioredoxin reductase (EC 1.8.1.9)	Escherichia coli (strain 55989 / EAEC)
20900	5031429	5031993	TY-2482_chromosome	E9VK05	AsnC family protein	Escherichia coli H263
106948	5032058	5034307	TY-2482_chromosome	C8U4H0	DNA-binding membrane protein FtsK	Escherichia coli O103:H2 (strain 12009 / EHEC)
102187	5034287	5036005	TY-2482_chromosome	B7LD82	DNA-binding membrane protein required for chromosome resolution and partitioning	Escherichia coli (strain 55989 / EAEC)
87336	5036160	5036771	TY-2482_chromosome	B7LD83	Outer-membrane lipoprotein carrier protein	Escherichia coli (strain 55989 / EAEC)
114154	5036785	5038125	TY-2482_chromosome	B7LD84	Recombination protein	Escherichia coli (strain 55989 / EAEC)
34171	5038219	5039508	TY-2482_chromosome	B7LD85	Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase)	Escherichia coli (strain 55989 / EAEC)
113984	5039750	5042191	TY-2482_chromosome	B7LD86	Dimethyl sulfoxide reductase, anaerobic, subunit A (EC 1.8.99.-)	Escherichia coli (strain 55989 / EAEC)
27511	5043305	5042403	TY-2482_chromosome	A7ZJW5	Putative uncharacterized protein	Escherichia coli O139:H28 (strain E24377A / ETEC
24823	5044508	5043726	TY-2482_chromosome	Q1RDV9	Protein YcaC	Escherichia coli (strain UTI89 / UPEC)
34780	5044663	5045808	TY-2482_chromosome	B7LD90	Uncharacterized MFS-type transporter ycaD	Escherichia coli (strain 55989 / EAEC)
62705	5046021	5047496	TY-2482_chromosome	B7LD91	Putative transporter	Escherichia coli (strain 55989 / EAEC)
61468	5048408	5047503	TY-2482_chromosome	B7LD92	Putative DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
115659	5048508	5049095	TY-2482_chromosome	B7LD93	Putative NAD(P)H oxidoreductase (EC 1.6.99.-)	Escherichia coli (strain 55989 / EAEC)
109818	5049920	5049183	TY-2482_chromosome	B7LD94	Pyruvate formate lyase activating enzyme 1 (EC 1.97.1.4)	Escherichia coli (strain 55989 / EAEC)
94407	5052394	5050115	TY-2482_chromosome	B7LD95	Pyruvate formate lyase I (EC 2.3.1.54)	Escherichia coli (strain 55989 / EAEC)
106357	5053306	5052452	TY-2482_chromosome	B7LD96	Formate transporter	Escherichia coli (strain 55989 / EAEC)
59112	5055471	5053714	TY-2482_chromosome	B7LD97	Putative uncharacterized protein ycaO	Escherichia coli (strain 55989 / EAEC)
106359	5055601	5056290	TY-2482_chromosome	B7LD98	Putative uncharacterized protein ycaP	Escherichia coli (strain 55989 / EAEC)
33927	5056492	5057577	TY-2482_chromosome	B7LD99	Phosphoserine aminotransferase (EC 2.6.1.52) (Phosphohydroxythreonine aminotransferase) (PSAT)	Escherichia coli (strain 55989 / EAEC)
29891	5057651	5058931	TY-2482_chromosome	B7LDA0	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP sy	Escherichia coli (strain 55989 / EAEC)
66117	5059079	5059864	TY-2482_chromosome	B5YT43	Peptidase, M48B family (EC 3.4.24.-)	Escherichia coli O157:H7 (strain EC4115 / EHEC)
31732	5060040	5060720	TY-2482_chromosome	B7LDA2	Cytidylate kinase (CK) (EC 2.7.4.14) (Cytidine monophosphate kinase) (CMP kinase)	Escherichia coli (strain 55989 / EAEC)
62617	5060834	5062504	TY-2482_chromosome	B7LDA3	30S ribosomal subunit protein S1	Escherichia coli (strain 55989 / EAEC)
29034	5062984	5062679	TY-2482_chromosome	A1A9I9	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
68040	5063158	5065419	TY-2482_chromosome	B7LDA5	Putative uncharacterized protein ycaI	Escherichia coli (strain 55989 / EAEC)
110524	5065459	5067204	TY-2482_chromosome	B7LDA6	Fused lipid transporter subunits of ABC superfamily: membrane component ; ATP-binding componen	Escherichia coli (strain 55989 / EAEC)
31982	5067204	5068187	TY-2482_chromosome	B7LE13	Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130) (Lipid A 4'-kinase)	Escherichia coli (strain 55989 / EAEC)
66338	5068227	5069456	TY-2482_chromosome	B7LE14	Putative uncharacterized protein ycaQ	Escherichia coli (strain 55989 / EAEC)
21153	5069690	5070530	TY-2482_chromosome	E7H9E7	3-deoxy-D-manno-octulosonate cytidylyltransferase (EC 2.7.7.38)	Escherichia coli EPECa14
28193	5069785	5069519	TY-2482_chromosome	A1A9J4	Putative uncharacterized protein	Escherichia coli O1:K1 / APEC
88488	5070590	5071480	TY-2482_chromosome	B7LE17	Putative uncharacterized protein ycbJ	Escherichia coli (strain 55989 / EAEC)
61038	5072239	5071463	TY-2482_chromosome	B7LE18	Putative uncharacterized protein ycbC	Escherichia coli (strain 55989 / EAEC)
64366	5072375	5073157	TY-2482_chromosome	B7LE20	Putative AdoMet-dependent methyltransferase	Escherichia coli (strain 55989 / EAEC)
32531	5073157	5074476	TY-2482_chromosome	B7LE21	Chromosome partition protein mukF	Escherichia coli (strain 55989 / EAEC)
108418	5074433	5075161	TY-2482_chromosome	B5YT57	Chromosome partition protein mukE	Escherichia coli O157:H7 (strain EC4115 / EHEC)

32525	5075164	5079621	TY-2482_chromosome	B7LE23	Chromosome partition protein mukB (Structural maintenance of chromosome-related protein	Escherichia coli (strain 55989 / EAEC)
114151	5079885	5081729	TY-2482_chromosome	B7LE24	Putative exported enzyme	Escherichia coli (strain 55989 / EAEC)
62845	5081913	5082458	TY-2482_chromosome	B7LE25	Putative uncharacterized protein ycbK	Escherichia coli (strain 55989 / EAEC)
86489	5082488	5083132	TY-2482_chromosome	B7LE26	Putative metal-binding hydrolase	Escherichia coli (strain 55989 / EAEC)
54167	5084357	5083380	TY-2482_chromosome	B7L511	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
13282	5085813	5086011	TY-2482_chromosome	E7H9D3	Putative uncharacterized protein	Escherichia coli EPECa14
83097	5085826	5084639	TY-2482_chromosome	B7LE28	Aspartate aminotransferase, PLP-dependent (EC 2.6.1.1)	Escherichia coli (strain 55989 / EAEC)
106348	5087099	5086014	TY-2482_chromosome	B7LE29	Outer membrane porin 1a (Ia;b;F)	Escherichia coli (strain 55989 / EAEC)
105311	5089101	5087704	TY-2482_chromosome	B7LE30	Asparaginyl-tRNA synthetase (EC 6.1.1.22) (Asparagine--tRNA ligase)	Escherichia coli (strain 55989 / EAEC)
33022	5090472	5089273	TY-2482_chromosome	B7LE31	Nicotinate phosphoribosyltransferase (NAPRTase) (EC 2.4.2.11)	Escherichia coli (strain 55989 / EAEC)
87777	5090738	5093347	TY-2482_chromosome	B7LE32	Aminopeptidase N (EC 3.4.11.2)	Escherichia coli (strain 55989 / EAEC)
13921	5093564	5093334	TY-2482_chromosome	D8ESU4	Conserved domain protein	Escherichia coli MS 107-1
71869	5094324	5093560	TY-2482_chromosome	B7LE33	Alkanesulfonate transporter subunit ; ATP-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
93930	5095112	5094324	TY-2482_chromosome	B7LE34	Alkanesulfonate transporter subunit ; membrane component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
34024	5096268	5095126	TY-2482_chromosome	B7LE35	Alkanesulfonate monooxygenase (EC 1.14.14.5) (FMNH2-dependent aliphatic sulfonate monooxygenase)	Escherichia coli (strain 55989 / EAEC)
113995	5097224	5096268	TY-2482_chromosome	B7LE36	Alkanesulfonate transporter subunit ; periplasmic-binding component of ABC superfamily	Escherichia coli (strain 55989 / EAEC)
112384	5097792	5097220	TY-2482_chromosome	B7LE37	NAD(P)H-dependent FMN reductase (EC 1.5.1.29)	Escherichia coli (strain 55989 / EAEC)
107985	5098139	5098687	TY-2482_chromosome	B7LE38	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
98990	5098773	5099471	TY-2482_chromosome	B7LE39	Putative periplasmic pilin chaperone	Escherichia coli (strain 55989 / EAEC)
95379	5099499	5102096	TY-2482_chromosome	B7LE40	Putative outer membrane export usher protein	Escherichia coli (strain 55989 / EAEC)
59204	5102090	5103157	TY-2482_chromosome	B7LE41	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
66360	5103172	5103711	TY-2482_chromosome	B7LE42	Putative fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
82590	5103722	5104234	TY-2482_chromosome	B7LE43	Putative exported fimbrial-like adhesin protein	Escherichia coli (strain 55989 / EAEC)
91788	5104230	5104937	TY-2482_chromosome	B7LE44	Putative periplasmic pilin chaperone	Escherichia coli (strain 55989 / EAEC)
33201	5105051	5106058	TY-2482_chromosome	B7LE45	Dihydroorotate dehydrogenase (quinone) (EC 1.3.5.2) (DHOdehase) (DHOD) (DHODase) (Dihydroorotate oxidase)	Escherichia coli (strain 55989 / EAEC)
86830	5106235	5106774	TY-2482_chromosome	B7LE46	Putative uncharacterized protein ycbW	Escherichia coli (strain 55989 / EAEC)
64297	5107883	5106777	TY-2482_chromosome	B7LE47	Putative 2Fe-2S cluster-containing protein	Escherichia coli (strain 55989 / EAEC)
75438	5108127	5110232	TY-2482_chromosome	B7LE48	Ribosomal RNA large subunit methyltransferase L (EC 2.1.1.173) (23S rRNA m2G2445 methyltransferase) (rRNA (guan	Escherichia coli (strain 55989 / EAEC)
73604	5110246	5112150	TY-2482_chromosome	B7LE49	Fused ATP-binding subunits of ABC superfamily protein involved in precise excision of transposons	Escherichia coli (strain 55989 / EAEC)
69892	5112283	5113533	TY-2482_chromosome	B7LE50	Paraquat-inducible membrane protein A	Escherichia coli (strain 55989 / EAEC)
90018	5113541	5115178	TY-2482_chromosome	B7LE51	Paraquat-inducible protein B	Escherichia coli (strain 55989 / EAEC)
93507	5115178	5115738	TY-2482_chromosome	C8ULH5	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC)
115609	5115981	5116175	TY-2482_chromosome	C6UNL9	Ribosome modulation factor	Escherichia coli O157:H7 (strain TW14359 / EHEC)
73608	5118581	5116824	TY-2482_chromosome	B7LE55	Putative ATP-dependent protease	Escherichia coli (strain 55989 / EAEC)
34785	5118767	5119216	TY-2482_chromosome	B7LE56	UPF0268 protein ycbG	Escherichia coli (strain 55989 / EAEC)
84443	5120335	5119298	TY-2482_chromosome	B7LE57	Outer membrane protein A (3a;II*;G;d)	Escherichia coli (strain 55989 / EAEC)
82881	5120490	5120705	TY-2482_chromosome	D3H0I0	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
34070	5121201	5120695	TY-2482_chromosome	B7LE58	Cell division inhibitor sulA	Escherichia coli (strain 55989 / EAEC)
104625	5121420	5122046	TY-2482_chromosome	B7LE59	Putative uncharacterized protein yccR	Escherichia coli (strain 55989 / EAEC)
106463	5124165	5122015	TY-2482_chromosome	B7LE60	Putative uncharacterized protein yccS	Escherichia coli (strain 55989 / EAEC)
82658	5124630	5124187	TY-2482_chromosome	C8U5C5	Conserved predicted inner membrane protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
82504	5124753	5126804	TY-2482_chromosome	B7LE62	DNA helicase IV (EC 3.6.1.-)	Escherichia coli (strain 55989 / EAEC)
32379	5127297	5126842	TY-2482_chromosome	B7LE63	Methylglyoxal synthase (MGS) (EC 4.2.3.3)	Escherichia coli (strain 55989 / EAEC)
34790	5128055	5127396	TY-2482_chromosome	B7LE64	UPF0319 protein yccT	Escherichia coli (strain 55989 / EAEC)
60532	5128228	5128638	TY-2482_chromosome	B7LE65	Putative CoA-binding protein	Escherichia coli (strain 55989 / EAEC)
29160	5128610	5129002	TY-2482_chromosome	Q1RDP7	Putative uncharacterized protein	Escherichia coli (strain UTI89 / UPEC)
66361	5130133	5130621	TY-2482_chromosome	B7LE68	Acylphosphatase (EC 3.6.1.7)	Escherichia coli (strain 55989 / EAEC)
68041	5130164	5129064	TY-2482_chromosome	B7LE67	Putative AdoMet-dependent methyltransferase, UPF0064 family	Escherichia coli (strain 55989 / EAEC)
84444	5130950	5130624	TY-2482_chromosome	B7LE69	Subunit of enzyme for 2-thio modification of mnm5s2U of tRNA anticodon U	Escherichia coli (strain 55989 / EAEC)
60813	5131700	5131044	TY-2482_chromosome	B7LE70	Putative uncharacterized protein yccA	Escherichia coli (strain 55989 / EAEC)
r205	5131994	5131907	TY-2482_chromosome	ref|NC_010473|:1084776-1084863|Ser tRNA| [gene=serT] [locus_tag=ECDH10B_1041		
113938	5132421	5133536	TY-2482_chromosome	B7LEU9	Hydrogenase 1, small subunit (EC 1.12.99.6)	Escherichia coli (strain 55989 / EAEC)
113940	5133536	5135326	TY-2482_chromosome	B7LEV1	Hydrogenase 1, large subunit (EC 1.12.99.6)	Escherichia coli (strain 55989 / EAEC)
66220	5135348	5136052	TY-2482_chromosome	B7LEV2	Hydrogenase 1, b-type cytochrome subunit	Escherichia coli (strain 55989 / EAEC)
110606	5136052	5136636	TY-2482_chromosome	B7LEV3	Protein involved in processing of HyaA and HyaB proteins	Escherichia coli (strain 55989 / EAEC)
99078	5136636	5137031	TY-2482_chromosome	B7LEV4	Protein involved in processing of HyaA and HyaB proteins	Escherichia coli (strain 55989 / EAEC)
59092	5137031	5137885	TY-2482_chromosome	B7LEV5	Protein involved in nickel incorporation into hydrogenase-1 proteins	Escherichia coli (strain 55989 / EAEC)
110607	5138022	5139563	TY-2482_chromosome	B7LEV6	Cytochrome bd-II oxidase, subunit I (EC 1.10.3.-)	Escherichia coli (strain 55989 / EAEC)
113038	5139578	5140711	TY-2482_chromosome	B7LEV7	Cytochrome bd-II oxidase, subunit II (EC 1.10.3.-)	Escherichia coli (strain 55989 / EAEC)
94057	5140899	5142194	TY-2482_chromosome	B7LEV8	Phosphoanhydride phosphorylase (EC 3.1.3.2) (EC 3.1.3.26)	Escherichia coli (strain 55989 / EAEC)
90953	5144492	5142315	TY-2482_chromosome	B7LEV9	Cryptic autophosphorylating protein tyrosine kinase Etk (EC 2.7.10.2)	Escherichia coli (strain 55989 / EAEC)
66378	5144958	5144515	TY-2482_chromosome	B7LEW0	Phosphotyrosine-protein phosphatase	Escherichia coli (strain 55989 / EAEC)
73680	5146085	5144949	TY-2482_chromosome	B7LEW1	Putative exopolysaccharide export protein	Escherichia coli (strain 55989 / EAEC)
84508	5148227	5146134	TY-2482_chromosome	B7LEW2	Putative uncharacterized protein ymcA	Escherichia coli (strain 55989 / EAEC)

112021	5148973	5148230	TY-2482_chromosome	B7LEW3	Putative uncharacterized protein ymcB	Escherichia coli (strain 55989 / EAEC)
88281	5149614	5148973	TY-2482_chromosome	B7LEW4	Putative outer membrane lipoprotein	Escherichia coli (strain 55989 / EAEC)
100722	5150026	5149724	TY-2482_chromosome	B7LF95	Putative uncharacterized protein ymcD	Escherichia coli (strain 55989 / EAEC)
95591	5150680	5150471	TY-2482_chromosome	B7LF96	Stress protein, member of the CspA-family	Escherichia coli (strain 55989 / EAEC)
61255	5150966	5151175	TY-2482_chromosome	B7LF99	DNA-binding transcriptional regulator	Escherichia coli (strain 55989 / EAEC)
21555	5151117	5151374	TY-2482_chromosome	D6I8Q5	Cold shock protein	Escherichia coli B185
100638	5151352	5151579	TY-2482_chromosome	C8TPT1	Sfa protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
71943	5152867	5151797	TY-2482_chromosome	B7LFA1	Putative 4Fe-4S membrane protein	Escherichia coli (strain 55989 / EAEC)
112157	5155683	5152942	TY-2482_chromosome	B7LFA2	Hybrid sensory histidine kinase in two-component regulatory system with TorR	Escherichia coli (strain 55989 / EAEC)
95592	5155766	5156791	TY-2482_chromosome	B7LFA3	Periplasmic sensory protein associated with the TorRS two-component regulatory system	Escherichia coli (strain 55989 / EAEC)
93661	5157459	5156770	TY-2482_chromosome	B7LFA4	DNA-binding response regulator in two-component regulatory system with TorS	Escherichia coli (strain 55989 / EAEC)
61463	5157589	5158758	TY-2482_chromosome	B7LFA5	Trimethylamine N-oxide (TMAO) reductase I, cytochrome c-type subunit	Escherichia coli (strain 55989 / EAEC)
79799	5158761	5161304	TY-2482_chromosome	B7LFA6	Trimethylamine N-oxide (TMAO) reductase I, catalytic subunit (EC 1.6.6.9)	Escherichia coli (strain 55989 / EAEC)
34301	5161304	5161900	TY-2482_chromosome	B7LFA7	Chaperone protein torD	Escherichia coli (strain 55989 / EAEC)
30252	5162301	5161999	TY-2482_chromosome	B7LFA8	Chaperone modulatory protein CbpM	Escherichia coli (strain 55989 / EAEC)
30249	5163221	5162304	TY-2482_chromosome	B7LFA9	Curved DNA-binding protein	Escherichia coli (strain 55989 / EAEC)
93938	5163554	5164738	TY-2482_chromosome	B7LFB0	Putative uncharacterized protein yccE	Escherichia coli (strain 55989 / EAEC)
116012	5165030	5166268	TY-2482_chromosome	B7LFB1	Glucose-1-phosphatase/inositol phosphatase (EC 3.1.3.10)	Escherichia coli (strain 55989 / EAEC)
62763	5166536	5166312	TY-2482_chromosome	B7LFB2	Putative uncharacterized protein yccJ	Escherichia coli (strain 55989 / EAEC)
34580	5167150	5166560	TY-2482_chromosome	B7LFB3	Flavoprotein wrbA (Trp repressor-binding protein)	Escherichia coli (strain 55989 / EAEC)
24980	5168466	5167135	TY-2482_chromosome	B7MPT9	Phage integrase	Escherichia coli O81 (strain ED1a)
104812	5168779	5168498	TY-2482_chromosome	C8TPU6	Excisionase	Escherichia coli O26:H11 (strain 11368 / EHEC)
94121	5169076	5168828	TY-2482_chromosome	C8TPU7	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
105066	5169444	5169067	TY-2482_chromosome	C8TPU8	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
75817	5169794	5169444	TY-2482_chromosome	C8TPU9	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
72342	5170042	5169833	TY-2482_chromosome	C8U7P4	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
81824	5170628	5170005	TY-2482_chromosome	C6UPU4	Adenine methylase	Escherichia coli O157:H7 (strain TW14359 / EHEC
68249	5171056	5170628	TY-2482_chromosome	C8U7P2	Probable regulatory protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
84994	5171750	5171115	TY-2482_chromosome	C8U7P1	Probable antirepressor	Escherichia coli O103:H2 (strain 12009 / EHEC)
11545	5171752	5172138	TY-2482_chromosome	E1J6T9	Putative uncharacterized protein	Escherichia coli MS 124-1
71346	5173002	5172109	TY-2482_chromosome	C8TPV1	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
25386	5173238	5173008	TY-2482_chromosome	B7MXC9	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
92887	5173605	5173201	TY-2482_chromosome	C8TPV5	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
107384	5174135	5173605	TY-2482_chromosome	C8TPV6	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
82307	5174873	5174433	TY-2482_chromosome	C8U7N0	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
108764	5175771	5174953	TY-2482_chromosome	C8U7M9	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
108168	5176182	5175838	TY-2482_chromosome	C8U7M8	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
93557	5176844	5176260	TY-2482_chromosome	C8U7M7	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
72117	5177533	5176847	TY-2482_chromosome	C8U7M6	Putative exonuclease	Escherichia coli O103:H2 (strain 12009 / EHEC)
69096	5178480	5177533	TY-2482_chromosome	C8U7M5	Predicted DNA recombination protein Bet	Escherichia coli O103:H2 (strain 12009 / EHEC)
107846	5178778	5178500	TY-2482_chromosome	C8U7M4	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
70440	5179080	5178802	TY-2482_chromosome	C8U7M3	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
67094	5179304	5179095	TY-2482_chromosome	C8U7M2	Putative host killing protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
8210	5180049	5179378	TY-2482_chromosome	E7DYR2	Putative uncharacterized protein	Enterobacteria phage VT2phi_272
14195	5180205	5180396	TY-2482_chromosome	B3AW45	Putative uncharacterized protein	Escherichia coli O157:H7 str. EC4486
9389	5181078	5180308	TY-2482_chromosome	B6ZXE1	Phage regulatory protein, Rha family	Escherichia coli O157:H7 str. TW14588
24477	5182660	5181710	TY-2482_chromosome	Q32F72	Type II site-specific deoxyribonuclease	Shigella dysenteriae serotype 1 (strain Sd197)
25819	5184126	5182660	TY-2482_chromosome	Q32F73	Site-specific DNA-methyltransferase	Shigella dysenteriae serotype 1 (strain Sd197)
24189	5184934	5184224	TY-2482_chromosome	Q32F74	Repressor protein CI	Shigella dysenteriae serotype 1 (strain Sd197)
8203	5185030	5185230	TY-2482_chromosome	E7DYT8	Cro antirepressor	Enterobacteria phage VT2phi_272
112477	5185264	5185554	TY-2482_chromosome	C8U7L4	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
97437	5185765	5186139	TY-2482_chromosome	C8U7L3	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
63386	5186136	5187653	TY-2482_chromosome	C8U7L2	Predicted helicase	Escherichia coli O103:H2 (strain 12009 / EHEC)
79355	5187646	5188614	TY-2482_chromosome	C8U7L1	Predicted DNA primase	Escherichia coli O103:H2 (strain 12009 / EHEC)
67184	5188617	5189063	TY-2482_chromosome	C8U7L0	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
79511	5189074	5189634	TY-2482_chromosome	C8U7K9	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
3587	5189634	5189825	TY-2482_chromosome	O48428	Protein ninH	Enterobacteria phage H19B (Bacteriophage H19B)
107087	5189821	5190252	TY-2482_chromosome	C8U7K8	Putative late gene regulator Q	Escherichia coli O103:H2 (strain 12009 / EHEC)
r353	5190697	5190772	TY-2482_chromosome	ref|NC_010473|:2875549-2875624|Ile tRNA| [gene=ileY] [locus_tag=ECDH10B_2820		
45329	5190956	5191995	TY-2482_chromosome	B3BQ93	Shiga toxin subunit A (EC 3.2.2.22)	Escherichia coli O157:H7 str. EC869
112258	5192010	5192276	TY-2482_chromosome	C6UP08	Shiga toxin II subunit B	Escherichia coli O157:H7 (strain TW14359 / EHEC
29255	5192732	5194699	TY-2482_chromosome	B7MRX3	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
92049	5194885	5195301	TY-2482_chromosome	C6V1Q5	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
11417	5195382	5196132	TY-2482_chromosome	B6ZXG1	Lysozyme (EC 3.2.1.17)	Escherichia coli O157:H7 str. TW14588

115832	5196409	5196975	TY-2482_chromosome	C6UP04	Putative antirepressor protein Ant	Escherichia coli O157:H7 (strain TW14359 / EHEC
20564	5197139	5197753	TY-2482_chromosome	D8ACV6	Bacteriophage lysis protein	Escherichia coli MS 21-1
98132	5197770	5198318	TY-2482_chromosome	C8U7J7	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
114926	5198340	5198555	TY-2482_chromosome	C8UMI7	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC)
74717	5198614	5199417	TY-2482_chromosome	C8UMI8	Putative small subunit terminase	Escherichia coli O111:H- (strain 11128 / EHEC)
115152	5199401	5201104	TY-2482_chromosome	C8UMI9	Putative terminase large subunit	Escherichia coli O111:H- (strain 11128 / EHEC)
113734	5201107	5203248	TY-2482_chromosome	B5YYP6	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
115696	5203409	5204413	TY-2482_chromosome	C8UMJ1	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
111067	5204440	5205651	TY-2482_chromosome	C8U7J2	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
107336	5205710	5206096	TY-2482_chromosome	C8UMJ3	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
114404	5206149	5206607	TY-2482_chromosome	C8UMJ4	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
95298	5206594	5207154	TY-2482_chromosome	B5YYN8	Putative uncharacterized protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
96207	5207157	5207804	TY-2482_chromosome	C8U7I8	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
104816	5207804	5209993	TY-2482_chromosome	C8U7I7	Predicted tail fiber protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
111000	5210763	5212451	TY-2482_chromosome	C6UNY7	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
96491	5212451	5213716	TY-2482_chromosome	C8UMK2	Predicted tail tip fiber protein	Escherichia coli O111:H- (strain 11128 / EHEC)
61137	5213734	5214009	TY-2482_chromosome	C8UMK3	Predicted outer membrane protein	Escherichia coli O111:H- (strain 11128 / EHEC)
97449	5214018	5214632	TY-2482_chromosome	C6UNY5	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
96493	5214726	5215457	TY-2482_chromosome	C8UMK5	Putative outer membrane protein Lom	Escherichia coli O111:H- (strain 11128 / EHEC)
63484	5215890	5216288	TY-2482_chromosome	C6UNY3	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
75856	5216385	5217038	TY-2482_chromosome	C8UMK7	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
71004	5217044	5217487	TY-2482_chromosome	C8UMK8	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
114330	5217500	5217748	TY-2482_chromosome	C8U7H6	Putative uncharacterized protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
108405	5217762	5219024	TY-2482_chromosome	C8UML0	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
114927	5219097	5227475	TY-2482_chromosome	C8UML1	Putative uncharacterized protein	Escherichia coli O111:H- (strain 11128 / EHEC)
114653	5227816	5228184	TY-2482_chromosome	C8TNB3	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
110399	5228391	5228618	TY-2482_chromosome	B7LFB4	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
91004	5230138	5228813	TY-2482_chromosome	B7LFB6	Pyrimidine transporter	Escherichia coli (strain 55989 / EAEC)
4944	5230734	5230162	TY-2482_chromosome	A1A9R2	NAD(P)H-flavin reductase RutF (EC 1.5.1.29) (FMN reductase) (NAD(P)H:flavin oxidoreductase)	Escherichia coli O1:K1 / APEC
33859	5231254	5230667	TY-2482_chromosome	B7LFB8	Probable malonic semialdehyde reductase RutE (EC 1.1.1.298)	Escherichia coli (strain 55989 / EAEC)
33856	5232064	5231267	TY-2482_chromosome	B7LFB9	Putative aminoacrylate hydrolase RutD (EC 3.5.1.-) (Aminohydrolase)	Escherichia coli (strain 55989 / EAEC)
17218	5232486	5232075	TY-2482_chromosome	E1J245	Pyrimidine utilization protein	Escherichia coli MS 124-1
4940	5233204	5232473	TY-2482_chromosome	D3QPK4	Peroxyureidoacrylate/ureidoacrylate amidohydrolase RutB (EC 3.5.1.n4) (Ureidoacrylate amidohydrolase	Escherichia coli O55:H7 (strain CB9615 / EPEC)
33837	5234310	5233165	TY-2482_chromosome	B7LFC2	Pyrimidine monooxygenase RutA (EC 1.14.14.n1)	Escherichia coli (strain 55989 / EAEC)
91965	5234541	5235176	TY-2482_chromosome	B7LFC3	DNA-binding transcriptional regulator of the alternative pyrimidine degradation pathway	Escherichia coli (strain 55989 / EAEC)
88451	5239181	5235222	TY-2482_chromosome	B7LFC4	Fused DNA-binding transcriptional regulator ; proline dehydrogenase ; pyrroline-5-carboxylate dehydrogenase (EC 1.5	Escherichia coli (strain 55989 / EAEC)
9440	5239236	5239442	TY-2482_chromosome	D6IM82	Predicted protein	Escherichia coli FVEC1412
77483	5239604	5241109	TY-2482_chromosome	B7LFC5	Proline:sodium symporter	Escherichia coli (strain 55989 / EAEC)
9789	5241618	5241301	TY-2482_chromosome	D8EB88	Conserved domain protein	Escherichia coli MS 119-7
113182	5241645	5242481	TY-2482_chromosome	B7LFC6	Ferrous iron permease	Escherichia coli (strain 55989 / EAEC)
111837	5242542	5243666	TY-2482_chromosome	B7LFC7	Ferrous iron transport binding protein	Escherichia coli (strain 55989 / EAEC)
58493	5243675	5244943	TY-2482_chromosome	B7LFC8	Heme-binding periplasmic protein involved in iron transport; Tat-dependent exported	Escherichia coli (strain 55989 / EAEC)
17881	5245210	5244867	TY-2482_chromosome	E6ANA4	Conserved domain protein	Escherichia coli MS 16-3
62816	5245430	5246350	TY-2482_chromosome	B7LFD0	Putative phosphate starvation-inducible protein with ATPase activity	Escherichia coli (strain 55989 / EAEC)
97425	5246816	5246406	TY-2482_chromosome	B7LFD1	Putative inner membrane protein associated with biofilm formation	Escherichia coli (strain 55989 / EAEC)
84628	5248143	5246821	TY-2482_chromosome	B7LFD2	Putative glycosyl transferase associated with biofilm formation	Escherichia coli (strain 55989 / EAEC)
104389	5250154	5248139	TY-2482_chromosome	B7LFD3	Putative polysaccharide deacetylase associated with biofilm formation; putative lipoprotein	Escherichia coli (strain 55989 / EAEC)
62709	5252586	5250166	TY-2482_chromosome	B7LFD4	Putative outer membrane protein associated with biofilm formation	Escherichia coli (strain 55989 / EAEC)
79946	5253101	5254528	TY-2482_chromosome	B5YU69	Diguanylate cyclase (GGDEF) domain protein	Escherichia coli O157:H7 (strain EC4115 / EHEC)
56371	5255438	5254575	TY-2482_chromosome	B7LA99	IS3 element protein InsF (Transposase ORF B, IS3)	Escherichia coli (strain 55989 / EAEC)
115259	5255743	5255438	TY-2482_chromosome	B7LFE0	IS3 element protein InsE	Escherichia coli (strain 55989 / EAEC)
91989	5255801	5256325	TY-2482_chromosome	C6UQ95	Acyl transferase	Escherichia coli O157:H7 (strain TW14359 / EHEC
107984	5256325	5257308	TY-2482_chromosome	B7LFE2	Putative uncharacterized protein ycdU	Escherichia coli (strain 55989 / EAEC)
107350	5257678	5258892	TY-2482_chromosome	C8UMN7	Putative integrase	Escherichia coli O111:H- (strain 11128 / EHEC)
25590	5260594	5259068	TY-2482_chromosome	B7UP05	Predicted protein	Escherichia coli O127:H6 (strain E2348/69 / EPEC
11356	5260865	5260569	TY-2482_chromosome	E6B380	Prophage CP4-57 regulatory protein alpA	Escherichia coli 3431
28660	5260954	5262786	TY-2482_chromosome	B1LKM5	Putative uncharacterized protein	Escherichia coli (strain SMS-3-5 / SECEC)
68234	5264125	5264685	TY-2482_chromosome	C8TX59	Conserved predicted protein	Escherichia coli O103:H2 (strain 12009 / EHEC)
96441	5264843	5267200	TY-2482_chromosome	C8UMP3	Putative helicase	Escherichia coli O111:H- (strain 11128 / EHEC)
26933	5267460	5267224	TY-2482_chromosome	B7MQ88	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
111612	5268912	5267479	TY-2482_chromosome	D3GX28	Transposase	Escherichia coli O44:H18 (strain 042 / EAEC)
14010	5269130	5268912	TY-2482_chromosome	E5ZNV7	IS66 family element, transposase	Escherichia coli MS 110-3
56255	5269900	5269499	TY-2482_chromosome	C8TKW2	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
107367	5270362	5270141	TY-2482_chromosome	C8UMT3	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC)

69955	5272686	5270599	TY-2482_chromosome	B7LBX4	Putative Iha adhesin (receptor)	Escherichia coli (strain 55989 / EAEC)
23433	5272843	5273025	TY-2482_chromosome	D7ZBG8	Putative uncharacterized protein	Escherichia coli MS 69-1
9573	5273466	5273735	TY-2482_chromosome	E6B1S6	Putative uncharacterized protein	Escherichia coli 3431
9741	5273660	5274354	TY-2482_chromosome	Q5I3M9	Aec34	Escherichia coli
85489	5274991	5275324	TY-2482_chromosome	C6UQF6	Predicted protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
26935	5276307	5277093	TY-2482_chromosome	B7N312	Putative uncharacterized protein	Escherichia coli O81 (strain ED1a)
107273	5276320	5276129	TY-2482_chromosome	C8UMT8	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC
90480	5277222	5277413	TY-2482_chromosome	C8UMU1	Conserved predicted protein	Escherichia coli O111:H- (strain 11128 / EHEC
23688	5277833	5277374	TY-2482_chromosome	Q8VR34	Putative uncharacterized protein	Escherichia coli
18468	5278409	5278900	TY-2482_chromosome	Q712Q2	MchA protein	Escherichia coli
5108	1145	21	TY-2482_pTY1	P09748	Shufflon protein B'	Escherichia coli
8462	1801	1148	TY-2482_pTY1	Q6JB05	PilU (Prepilin peptidase)	Escherichia coli
8474	2346	1789	TY-2482_pTY1	Q6JB04	IncI1 conjugal transfer transglycosylase protein PilT (PilT) (Putative transglycosylase PilT)	Escherichia coli
15758	2970	2359	TY-2482_pTY1	D9Z518	PilS	Escherichia coli
8472	4072	2990	TY-2482_pTY1	Q6JB02	IncI1 conjugal transfer protein PilR (Integral membrane protein) (PilR)	Escherichia coli
8491	5638	4088	TY-2482_pTY1	Q6JB01	IncI1 conjugal transfer protein PilQ (Nucleotide-binding protein) (PilQ	Escherichia coli
8727	6101	5652	TY-2482_pTY1	Q6JB00	IncI1 conjugal transfer pilus biogenesis protein PilP (PilP) (PilP protein)	Escherichia coli
8480	7383	6091	TY-2482_pTY1	Q6JAZ9	IncI1 conjugal transfer protein PilO (PilO) (PilO protein)	Escherichia coli
8729	9058	7379	TY-2482_pTY1	C7SA78	IncI1 conjugal transfer protein PilN (Lipoprotein)	Escherichia coli
8903	9509	9075	TY-2482_pTY1	Q6JAZ7	IncI1 conjugal transfer protein PilM (PilM) (PilM protein)	Escherichia coli
22434	10576	9512	TY-2482_pTY1	C7SA80	Lipoprotein	Escherichia coli
11548	11498	10908	TY-2482_pTY1	C7SA81	PilK	Escherichia coli
20190	11922	11626	TY-2482_pTY1	E9LMM5	IncI1 conjugal transfer protein TraC	Escherichia coli
8946	12732	12052	TY-2482_pTY1	Q6JAZ2	IncI1 conjugal transfer protein TraC (TraC) (TraC protein)	Escherichia coli
19421	13519	12929	TY-2482_pTY1	Q6JAZ1	TraB	Escherichia coli
8340	14248	13964	TY-2482_pTY1	E2E9F3	IncI1 conjugal transfer protein TraA (TraA)	Escherichia coli
13423	14429	14169	TY-2482_pTY1	Q2VNV1	Putative uncharacterized protein	Escherichia coli
13919	14903	15106	TY-2482_pTY1	D7XWR3	Putative uncharacterized protein	Escherichia coli MS 84-1
63642	15402	16430	TY-2482_pTY1	C8TW44	Putative replication initiation protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
12244	15426	15109	TY-2482_pTY1	E1JE00	Putative uncharacterized protein	Escherichia coli MS 124-1
11329	17278	16994	TY-2482_pTY1	E9LLT7	Putative replication protein RepA4	Escherichia coli
9434	18012	17506	TY-2482_pTY1	C7S9Z5	YafA	Escherichia coli
36692	18670	18071	TY-2482_pTY1	Q68JD7	YafB	Escherichia coli
14954	18849	18628	TY-2482_pTY1	E6AXF5	Conserved domain protein	Escherichia coli MS 16-3
14773	18933	20366	TY-2482_pTY1	C7S9Z7	YagA	Escherichia coli
27424	20378	20599	TY-2482_pTY1	D3QYQ9	Putative uncharacterized protein	Escherichia coli O55:H7 (strain CB9615 / EPEC)
5486	23652	20860	TY-2482_pTY1	P03008	Transposase for transposon Tn3	Escherichia coli
8409	23666	23995	TY-2482_pTY1	A5JTS3	ORF477 (Putative uncharacterized protein) (Fragment)	Proteus mirabilis
36068	24920	24048	TY-2482_pTY1	Q6BBP7	Beta-lactamase (Beta-lactamase CTX-M-3) (CTX-M-3 extended-spectrum beta-lactamase) (Extended-spectrum class A	Escherichia coli
8615	26441	25179	TY-2482_pTY1	D9Z5B6	TnpA	Escherichia coli
28725	26915	27556	TY-2482_pTY1	B7LWU0	Transposon Tn3 resolvase	Escherichia coli (strain 55989 / EAEC)
8888	26997	26623	TY-2482_pTY1	C7S9E2	Transposase for transposon Tn3 (Truncated TnpA)	Escherichia coli
105700	27742	28599	TY-2482_pTY1	C8UQP5	TEM-1 beta-lactamase	Escherichia coli O111:H- (strain 11128 / EHEC
36929	29796	29173	TY-2482_pTY1	C1J8J6	Cobyrinic acid a,c-diamide synthase (Putative partition-related protein)	Escherichia coli
50805	31271	30003	TY-2482_pTY1	Q8Z1G9	UV protection protein	Salmonella typhi
35141	31708	31274	TY-2482_pTY1	Q6EMF3	ImpA (ImpA UV protection protein) (UV protection and mutation protein) (UV protection protein UmuD	Escherichia coli
40799	32115	31708	TY-2482_pTY1	C1J8J3	Putative uncharacterized protein	Escherichia coli
9032	32183	33271	TY-2482_pTY1	D9Z555	YccB	Escherichia coli
107813	33659	34339	TY-2482_pTY1	C8TW60	Putative adenine DNA methyltransferase	Escherichia coli O26:H11 (strain 11368 / EHEC)
9358	34452	35009	TY-2482_pTY1	Q0E851	W0054	Escherichia coli
108627	35058	35831	TY-2482_pTY1	C6V3G9	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
28859	36606	37139	TY-2482_pTY1	A7ZH45	Putative DNA methylase	Escherichia coli O139:H28 (strain E24377A / ETEC
21958	36637	36140	TY-2482_pTY1	C7S9L2	Putative uncharacterized protein	Escherichia coli
16306	37896	38099	TY-2482_pTY1	E1JFK5	Putative uncharacterized protein	Escherichia coli MS 124-1
15080	37978	37230	TY-2482_pTY1	E9LLW4	Putative uncharacterized protein	Escherichia coli
35325	38099	38623	TY-2482_pTY1	C1J8I1	Single-stranded DNA-binding protein	Escherichia coli
101989	38970	40931	TY-2482_pTY1	D3H5D8	ParB-like nuclease	Escherichia coli O44:H18 (strain 042 / EAEC)
18727	40986	41420	TY-2482_pTY1	E0WGX5	Plasmid SOS inhibition protein	Escherichia coli
36030	41420	42136	TY-2482_pTY1	C1J8T1	Plasmid SOS inhibition protein PsiA (PsiA) (PsiA protein)	Escherichia coli
36653	42136	42729	TY-2482_pTY1	C1J8T0	Putative uncharacterized protein (YgaA)	Escherichia coli
18581	42804	43691	TY-2482_pTY1	C7SA25	YgbA-ard	Escherichia coli
41714	44084	44854	TY-2482_pTY1	C1J8S7	Putative uncharacterized protein	Escherichia coli
49483	44858	45214	TY-2482_pTY1	C1J8H1	Putative uncharacterized protein	Escherichia coli
36932	45319	45780	TY-2482_pTY1	C1J8S5	Conserved hypothetical plasmid protein (Putative uncharacterized protein)	Escherichia coli

19423	45780	46691	TY-2482_pTY1	Q68J76	YdgA	Escherichia coli
85997	46723	46959	TY-2482_pTY1	C8TW70	Putative uncharacterized protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
35255	47244	46996	TY-2482_pTY1	C1J8S2	Putative uncharacterized protein ygeA (YgeA)	Escherichia coli
24542	47819	47306	TY-2482_pTY1	B6IC38	Putative uncharacterized protein	Escherichia coli (strain SE11)
19743	47821	48669	TY-2482_pTY1	Q68J80	YdiA	Escherichia coli
8574	49100	48762	TY-2482_pTY1	D9Z504	YggA	Escherichia coli
8415	49328	49657	TY-2482_pTY1	C7SA35	Plasmid mobilization protein (Plasmid relaxome component protein NikA)	Escherichia coli
97151	49671	52367	TY-2482_pTY1	C8TW76	Putative plasmid conjugation system NikB protein	Escherichia coli O26:H11 (strain 11368 / EHEC)
35836	54698	52410	TY-2482_pTY1	Q68J84	Conjugal transfer protein (TrbC)	Escherichia coli
9474	55767	54694	TY-2482_pTY1	D9Z502	TrbB	Escherichia coli
16955	56988	55783	TY-2482_pTY1	C7SA39	TrbA protein	Escherichia coli
23795	58272	57346	TY-2482_pTY1	C7SA40	FinQ	Escherichia coli
11048	58610	58891	TY-2482_pTY1	C7SA41	Post-segregation killing protein	Escherichia coli
17705	59524	59817	TY-2482_pTY1	D8EU26	Putative uncharacterized protein	Escherichia coli MS 107-1
28586	60127	59888	TY-2482_pTY1	B6IC49	Putative uncharacterized protein	Escherichia coli (strain SE11)
11328	61165	60554	TY-2482_pTY1	E9LLN8	Surface exclusion protein ExcA	Escherichia coli
18849	63478	61244	TY-2482_pTY1	B3AEC6	Integral membrane protein	Escherichia coli O157:H7 str. EC4401
12474	64090	63509	TY-2482_pTY1	C7SA45	TraX protein	Escherichia coli
14774	65321	64122	TY-2482_pTY1	C7SA46	TraW protein	Escherichia coli
20548	65914	65291	TY-2482_pTY1	D9Z526	TraV	Escherichia coli
36778	68946	65905	TY-2482_pTY1	Q68JA2	TraU	Escherichia coli
8633	69836	69039	TY-2482_pTY1	C7SA49	IncI1 conjugal transfer protein TraT (TraT protein)	Escherichia coli
23932	70008	69823	TY-2482_pTY1	C7SA50	TraS protein	Escherichia coli
8628	70476	70075	TY-2482_pTY1	C7SA51	TraR (TraR protein)	Escherichia coli
8493	71054	70530	TY-2482_pTY1	C7SA52	IncI1 conjugal transfer protein TraQ (TraQ protein)	Escherichia coli
16313	71758	71057	TY-2482_pTY1	C7SA53	TraP protein	Escherichia coli
14775	73047	71761	TY-2482_pTY1	C7SA54	TraO protein	Escherichia coli
9436	74033	73053	TY-2482_pTY1	C7SA55	TraN protein	Escherichia coli
9039	74736	74047	TY-2482_pTY1	C7SA56	IncI1 conjugal transfer protein TraM (TraM protein)	Escherichia coli
8614	75080	74736	TY-2482_pTY1	C7SA57	IncI1 conjugal transfer protein TraL (TraL) (TraL protein)	Escherichia coli
17670	78862	75101	TY-2482_pTY1	C7SA58	SogL protein	Escherichia coli
8673	79863	78955	TY-2482_pTY1	E9LLQ3	Putative uncharacterized protein	Escherichia coli
16751	80953	79808	TY-2482_pTY1	C7SA62	TraJ protein	Escherichia coli
12436	81768	80953	TY-2482_pTY1	Q68JB5	TraI	Escherichia coli
8414	82223	81768	TY-2482_pTY1	Q68JB6	IncI1 conjugal transfer protein TraH (TraH) (TraH protein)	Escherichia coli
15456	83202	82621	TY-2482_pTY1	E9LM08	IncI1 conjugal transfer protein TraG	Escherichia coli
13732	84464	83265	TY-2482_pTY1	Q68JB8	TraF	Escherichia coli
10587	85374	84553	TY-2482_pTY1	Q68JB9	TraE	Escherichia coli
5107	86678	86986	TY-2482_pTY1	P09747	Shufflon protein B	Escherichia coli
4552	86679	85528	TY-2482_pTY1	P10487	Shufflon-specific DNA recombinase	Escherichia coli
10369	87223	87527	TY-2482_pTY1	E6BU42	Shufflon protein C	Escherichia coli MS 85-1
12944	87302	86994	TY-2482_pTY1	D8EU43	Putative uncharacterized protein	Escherichia coli MS 107-1
5113	87790	87530	TY-2482_pTY1	P09750	Shufflon protein C'	Escherichia coli
9705	88058	88447	TY-2482_pTY1	E9Y7H3	Shufflon protein A (Fragment)	Escherichia coli H489
5115	88134	87790	TY-2482_pTY1	P09751	Shufflon protein D'	Escherichia coli
5105	88695	88450	TY-2482_pTY1	P09746	Shufflon protein A'	Escherichia coli
14295	2	328	TY-2482_pTY2	Q4E6D2	Transposase (IS4 family)	Wolbachia endosymbiont of Drosophila simulans
14394	606	1514	TY-2482_pTY2	E9Z073	Transposase	Escherichia coli M863
26934	2164	1763	TY-2482_pTY2	B7LWW4	Transposase ORF A, IS1	Escherichia coli (strain 55989 / EAEC)
83458	3062	2268	TY-2482_pTY2	B7LWW2	Putative transcriptional activator aggR (AAF-III) regulatory protein	Escherichia coli (strain 55989 / EAEC)
18305	3600	3233	TY-2482_pTY2	E7JSW2	Integrase core domain protein	Escherichia coli RN587/1
27677	4028	4598	TY-2482_pTY2	B7LFP9	Transposase ORF B, IS629	Escherichia coli (strain 55989 / EAEC)
16059	4899	4531	TY-2482_pTY2	Q9S110	Orf57 protein	Escherichia coli
8444	5122	4817	TY-2482_pTY2	P71290	Orf58 protein	Escherichia coli
52540	5193	5498	TY-2482_pTY2	B7LBU5	Putative reverse transcriptase-like protein from putative prophage or plasmid (EC 2.7.7.49)	Escherichia coli (strain 55989 / EAEC)
16058	6008	5574	TY-2482_pTY2	Q9S110	Orf57 protein	Escherichia coli
8443	6231	5926	TY-2482_pTY2	P71290	Orf58 protein	Escherichia coli
52527	6302	7822	TY-2482_pTY2	B7LB68	Putative reverse transcriptase-like protein from putative prophage or plasmid (EC 2.7.7.49) (Reverse transcriptase-lik	Escherichia coli (strain 55989 / EAEC)
26332	7900	8397	TY-2482_pTY2	Q327G0	IS629 ORF2	Shigella dysenteriae serotype 1 (strain Sd197)
26240	8942	8595	TY-2482_pTY2	B7LWW0	14 kDa aggregative adherence fimbriae I protein (Modular protein)	Escherichia coli (strain 55989 / EAEC)
2658	9296	10276	TY-2482_pTY2	P0CE57	Transposase insH for insertion sequence element IS5R	Escherichia coli (strain K12)
83352	10498	10737	TY-2482_pTY2	E1PC79	Putative secreted autotransporter toxin sat	Escherichia coli OR:K5:H- (strain ABU 83972)
26069	10854	11069	TY-2482_pTY2	B7LWV8	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
7600	11255	12280	TY-2482_pTY2	P16943	Insertion element IS630 uncharacterized 39 kDa protein (ISO-IS200 39 kDa protein)	Shigella sonnei

20460	12594	14385	TY-2482_pTY2	B3HJU4	Serine proteAse eata (EC 3.4.21.-)	Escherichia coli B7A
26239	14596	14363	TY-2482_pTY2	B7LWV1	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
25401	14987	14742	TY-2482_pTY2	B7LWV0	Transposase ORF A, IS629	Escherichia coli (strain 55989 / EAEC)
88207	15334	16494	TY-2482_pTY2	B7LWU9	AatP permease	Escherichia coli (strain 55989 / EAEC)
81125	16494	17729	TY-2482_pTY2	B7LWU8	AatA outermembrane protein	Escherichia coli (strain 55989 / EAEC)
73706	17629	18447	TY-2482_pTY2	B7LWU7	AatB	Escherichia coli (strain 55989 / EAEC)
72382	18443	19069	TY-2482_pTY2	B7LWU6	AatC ATB binding protein of ABC transporter (EC 3.6.3.28)	Escherichia coli (strain 55989 / EAEC)
67969	19089	20297	TY-2482_pTY2	B7LWU5	AatD	Escherichia coli (strain 55989 / EAEC)
28478	21275	22405	TY-2482_pTY2	B7LBV5	Transposase, IS110 family	Escherichia coli (strain 55989 / EAEC)
73796	24086	22521	TY-2482_pTY2	B7LFP0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
56541	24467	24120	TY-2482_pTY2	B7LA97	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
57887	24901	24467	TY-2482_pTY2	B7LA98	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
93542	24997	25194	TY-2482_pTY2	C6UQD7	Putative uncharacterized protein	Escherichia coli O157:H7 (strain TW14359 / EHEC
55302	29586	25495	TY-2482_pTY2	B7LBW0	Serine protease pic (ShMu)	Escherichia coli (strain 55989 / EAEC)
24349	30533	29898	TY-2482_pTY2	A7ZH69	Resolvase domain protein	Escherichia coli O139:H28 (strain E24377A / ETEC
90454	31115	31978	TY-2482_pTY2	B7LX00	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
15087	32294	32145	TY-2482_pTY2	D6IDD7	X polypeptide	Escherichia coli B185
73678	32880	32281	TY-2482_pTY2	B7LWZ9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
69599	33211	33591	TY-2482_pTY2	D3H5C8	Conjugative transfer protein	Escherichia coli O44:H18 (strain 042 / EAEC)
26017	33728	34255	TY-2482_pTY2	B7LWZ7	Protein traJ	Escherichia coli (strain 55989 / EAEC)
14377	34938	34255	TY-2482_pTY2	E1U309	Transposase InsAB'	Escherichia coli
113449	34979	39662	TY-2482_pTY2	D3H556	DNA helicase I (EC 3.6.1.-)	Escherichia coli O44:H18 (strain 042 / EAEC)
84453	40486	41043	TY-2482_pTY2	B7LWY8	Fertility inhibition protein (Conjugal transfer repressor)	Escherichia coli (strain 55989 / EAEC)
57886	41272	41706	TY-2482_pTY2	B7LA98	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
92994	41706	41999	TY-2482_pTY2	D3GV17	Transposase	Escherichia coli O44:H18 (strain 042 / EAEC)
108668	41950	42261	TY-2482_pTY2	B7LBX6	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
104768	43889	42321	TY-2482_pTY2	D3H551	Transposase	Escherichia coli O44:H18 (strain 042 / EAEC)
82235	44256	43912	TY-2482_pTY2	D3H552	Transposase	Escherichia coli O44:H18 (strain 042 / EAEC)
86545	44933	44259	TY-2482_pTY2	D3H553	Transposase	Escherichia coli O44:H18 (strain 042 / EAEC)
9931	45002	45250	TY-2482_pTY2	Q84A18	Putative uncharacterized protein orf7	Escherichia coli
2659	46644	45664	TY-2482_pTY2	P0CE57	Transposase insH for insertion sequence element IS5R	Escherichia coli (strain K12)
35456	46922	47173	TY-2482_pTY2	Q79RI5	Negative regulator of repA1 expression (RepA2) (Replication protein) (Replication regulatory protein RepA2	Escherichia coli
78128	47481	47666	TY-2482_pTY2	C8URD0	Replication initiation protein RepA1	Escherichia coli O111:H- (strain 11128 / EHEC
78129	47629	48306	TY-2482_pTY2	C8URD0	Replication initiation protein RepA1	Escherichia coli O111:H- (strain 11128 / EHEC
7991	48672	49052	TY-2482_pTY2	P03848	Uncharacterized protein repA4	Escherichia coli
62626	49217	49498	TY-2482_pTY2	B7LWY0	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
77292	49501	49773	TY-2482_pTY2	B7LWX9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
8675	49782	50024	TY-2482_pTY2	D9Z536	IPF_393	Escherichia coli
14303	50270	49986	TY-2482_pTY2	B1VCJ6	ORF 153 Hypothetical protein	Escherichia coli
73622	50759	51496	TY-2482_pTY2	B7LWX4	Site-specific recombinase	Escherichia coli (strain 55989 / EAEC)
101487	52755	51781	TY-2482_pTY2	B7LWX3	RepFIB replication protein A	Escherichia coli (strain 55989 / EAEC)
15680	53553	53068	TY-2482_pTY2	C8CGL3	Putative uncharacterized protein	Escherichia coli
8629	54052	54810	TY-2482_pTY2	D9Z540	VagD	Escherichia coli
15238	54804	55199	TY-2482_pTY2	D8EV54	Putative uncharacterized protein	Escherichia coli MS 107-1
107875	55269	55544	TY-2482_pTY2	B7LX17	Protein ccdA (Protein letA) (Protein H) (LynA) (Modular protein)	Escherichia coli (strain 55989 / EAEC)
77373	55522	55851	TY-2482_pTY2	B7LX16	Cytotoxic protein ccdB (Protein letB) (Protein G) (LynB)	Escherichia coli (strain 55989 / EAEC)
116015	55855	56658	TY-2482_pTY2	B7LX15	Putative resolvase (Protein D)	Escherichia coli (strain 55989 / EAEC)
104191	56807	57481	TY-2482_pTY2	D3H584	Putative uncharacterized protein	Escherichia coli O44:H18 (strain 042 / EAEC)
13306	57571	57876	TY-2482_pTY2	Q9Z4E6	YegA protein	Salmonella typhimurium
15380	58239	59270	TY-2482_pTY2	E9LLV1	Plasmid partitioning and stability protein StbA	Escherichia coli
22906	59266	59679	TY-2482_pTY2	Q3ZU22	Plasmid stability protein	Escherichia coli
36047	60958	59687	TY-2482_pTY2	C1J8J5	DNA polymerase V subunit UmuC (UV protection protein)	Escherichia coli
10165	61398	60961	TY-2482_pTY2	A1YLB7	ImpA	Escherichia coli
20443	61422	62030	TY-2482_pTY2	A1YLB6	Putative resolvase	Escherichia coli
13396	62440	62219	TY-2482_pTY2	Q3L7G2	Putative uncharacterized protein	Escherichia coli
178	62882	63637	TY-2482_pTY2	P46004	Chaperone protein AggD	Escherichia coli
25242	63654	66179	TY-2482_pTY2	B7LX07	Outer membrane usher protein Agg3C	Escherichia coli (strain 55989 / EAEC)
14674	66734	67234	TY-2482_pTY2	O87745	AggA457 protein	Escherichia coli
14185	67374	67691	TY-2482_pTY2	E9XTW5	Integrase core domain-containing protein	Escherichia coli TW10509
37864	67968	67666	TY-2482_pTY2	F2W481	ISL3 family transposase	Escherichia coli
26474	68195	68752	TY-2482_pTY2	Q8XC14	Putative IS encoded protein encoded within prophage CP-933O	Escherichia coli O157:H7
104870	68805	70340	TY-2482_pTY2	B7L938	Putative transposase ORF 1, IS66 family	Escherichia coli (strain 55989 / EAEC)
16883	70481	70994	TY-2482_pTY2	E3Y4T4	Integrase core domain protein	Shigella flexneri 2a str. 2457T
15950	71380	70931	TY-2482_pTY2	E9Z010	Putative uncharacterized protein	Escherichia coli M863

14071	71859	71362	TY-2482_pTY2	E9Z008	Transposase	Escherichia coli M863
24986	72172	71990	TY-2482_pTY2	B7LWX0	Putative tail fiber protein	Escherichia coli (strain 55989 / EAEC)
77291	72295	73320	TY-2482_pTY2	B7LWW9	Putative uncharacterized protein	Escherichia coli (strain 55989 / EAEC)
29189	73327	73863	TY-2482_pTY2	B7LWW8	Isopentenyl-diphosphate Delta-isomerase 2 (IPP isomerase 2) (EC 5.3.3.2) (IPP:DMAPP isomerase 2) (Isopentenyl pyr	Escherichia coli (strain 55989 / EAEC)
24071	74681	75328	TY-2482_pTY2	B1LJZ9	IS5 transposase	Escherichia coli (strain SMS-3-5 / SECEC)
36208	523	996	TY-2482_pTY3	O07102	Plasmid replication protein (RepA)	Escherichia coli
18920	1549	1029	TY-2482_pTY3	A0A1K7	Probable replication protein	Escherichia coli

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