

Enterotoxigenic *Escherichia coli* Expression Clone Set, Recombinant in *Escherichia coli*, Plate 6

Catalog No. NR-19795

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Contributor:

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

Manufacturer:

BEI Resources

Product Description:

The Enterotoxigenic *Escherichia coli* (ETEC) expression clone set consists of 14 plates which contain 917 sequence validated clones from *Escherichia coli* (*E. coli*) strains H10407, E24377A and B7A cloned in *E. coli* DH10B-T1 cells. Each open reading frame was constructed in vector [pMCSG7](#) (a pET21 derivative; for routine HTP purification). The sequence was validated by full length sequencing of each clone with greater than 1X coverage and a mutation rate of less than 0.2%. Note: Due to viability issues, all clones may not be available. Please refer to Table 1 for more information on unavailable clones.

Material Provided:

Each inoculated well of the 96-well plate contains approximately 60 µL of *E. coli* culture (strain DH10B-T1) in Luria Bertani (LB) Broth containing 100 µg/mL ampicillin supplemented with 15% glycerol.

Note: Production in the 96-well format has increased risk of cross-contamination between adjacent wells. Individual clones should be purified (e.g. single colony isolation and purification using good microbiological practices) and sequence-verified prior to use. BEI Resources cannot confirm or validate any clone not identified on the plate information table.

Packaging/Storage:

NR-19795 was packaged aseptically in a 96-well plate. The product is provided frozen and should be stored at -80°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

Growth Conditions:

Media:

LB Broth or Agar containing 100 µg/mL ampicillin.

Incubation:

Temperature: *E. coli*, strain DH10B-T1 clones should be

grown at 37°C.

Atmosphere: Aerobic

Propagation:

1. Scrape top of frozen well with a pipette tip and streak onto agar plate.
2. Incubate the plates at 37°C for 18 to 24 hours.

Citation:

Acknowledgment for publications should read “The following reagent was obtained through BEI Resources, NIAID, NIH: Enterotoxigenic *Escherichia coli* Expression Clone Set, Recombinant in *Escherichia coli*, Plate 6, NR-19795.”

Biosafety Level: 2

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. [Biosafety in Microbiological and Biomedical Laboratories](#). 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see www.cdc.gov/biosafety/publications/bmb15/index.htm.

Disclaimers:

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References:

1. Stols, L., et al. "A New Vector for High-Throughput, Ligation-Independent Cloning Encoding a Tobacco Etch Virus Protease Cleavage Site." *Protein Expr. Purif.* 25 (2002): 8-15. PubMed: 12071693.

Table 1: Enterotoxigenic *E. coli* Expression Clone Set, Recombinant in *Escherichia coli*, Plate 6 (EEXAF)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
D000023446	A03	e24_Ch_g141_1_270	xanthine-guanine phosphoribosyltransferase	323	YP_001461426	2
D000023448	A04	EcE24377A_4240_1_1071	outer membrane protein A	1124	YP_001462189	1.597
D000023450	A05	e24_Ch_g150_1_273	outer membrane phosphoprotein E	326	YP_001461429	2
D000023452	A06	EcE24377A_3562_1_1086	Not Available	1139	Not Annotated	1.5751
D000023453	A07	e24_Ch_g302_1_273	outer membrane phosphoprotein E	326	YP_001461429	2
D000023455	A08	EcE24377A_4019_1_1095	membrane protein	1148	YP_001462211	2
D000023457	A09	EcE24377A_0987_1_273	outer membrane phosphoprotein E	326	YP_001461429	2
D000023460	A10	EcE24377A_1698_76_1218	hypothetical protein EcE24377A_1218	1199	YP_001462329	1.4128
D000023461	A11	EcE24377A_4760_1_273	outer membrane phosphoprotein E	326	YP_001461429	2
D000023464	A12	EcE24377A_2214_1_1146	IS3, transposase orfB	1199	YP_001462260	1.2827
D000023465	B01	e24_Ch_g604_1_276	Not Available	329	Not Annotated	2
D000023467	B02	EcE24377A_2166_1_1161	curlin minor subunit	1214	YP_001462273	1.4761
D000023470	B03	e24_Ch_g300_1_279	prophage CP4-57 regulatory protein	332	YP_001461433	2
D000023472	B04	EcE24377A_F0071_1_1164	hypothetical protein EcE24377A_1164	1217	YP_001462276	4.2465
D000023473	B05	e24_Ch_g399_1_279	prophage CP4-57 regulatory protein	332	YP_001461433	2
D000023477	B07	e24_Ch_g406_1_279	prophage CP4-57 regulatory protein	332	YP_001461433	2
D000023481	B09	e24_P35_g35_1_282	SNF2 family helicase	335	YP_001461436	2
D000023485	B11	e24_P74_g44_1_288	hypothetical protein	341	YP_001461442	2
D000023487	B12	EcE24377A_0989_1_1299	isocitrate dehydrogenase	1352	YP_001462405	4.3188
D000023489	C01	e24_Ch_g199_1_294	xanthine dehydrogenase accessory factor	347	YP_001461447	2
D000023491	C02	EcE24377A_3383_1_1392	oligopeptide transporter permease	1445	YP_001462494	4.3716

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
D000023493	C03	e24_Ch_g6_1_297	xanthine dehydrogenase iron-sulfur-binding subunit	350	YP_001461450	2
D000023496	C04	EcE24377A_2649_1_1440	DNA methylase	1493	YP_001462540	3.8754
D000023498	C05	e24_P73_g10_1_300	hypothetical protein	353	YP_001461453	1.2153
D000023500	C06	EcE24377A_C0004_1_1503	outer membrane protein G	1556	YP_001462627	4.4531
D000023502	C07	e24_Ch_g319_1_309	hypothetical protein	362	YP_001461462	2
D000023503	C08	EcE24377A_3971_1_1587	oxidoreductase	1640	YP_001462682	3.0317
D000023506	C09	e24_P74_g14_1_309	hypothetical protein	362	YP_001461462	2
D000023508	C10	e24_P80_g70_1_1629	acetyltransferase	1682	YP_001462722	1.8929
D000023510	C11	e24_P74_g39_1_315	hypothetical protein	368	YP_001461468	2
D000023511	C12	EcE24377A_0300_1_1641	Not Available	1694	Not Annotated	4.778
D000023514	D01	e24_P80_g30_1_318	pyridine nucleotide-disulfide oxidoreductase	371	YP_001461471	1.9919
D000023515	D02	EcE24377A_F0087_1_1743	hypothetical protein	1796	YP_001462826	2.6178
D000023517	D03	EcE24377A_1322_82_399	hypothetical protein	374	YP_001461550	2
D000023520	D04	EcE24377A_1771_1_1773	Not Available	1826	Not Annotated	4.6889
D000023521	D05	EcE24377A_1103_1_321	hypothetical protein	374	YP_001461474	2
D000023525	D07	e24_Ch_g83_1_324	hypothetical protein	377	YP_001461477	1.8753
D000023527	D08	EcE24377A_4641_1_1983	pyrimidine deoxy)nucleoside triphosphate pyrophosphohydro-lase	2036	YP_001463057	3.97
D000023529	D09	e24_Ch_g327_1_327	betaine aldehyde dehydrogenase	380	YP_001461480	2
D000023531	D10	EcE24377A_4401_1_2034	hypothetical protein EcE24377A_2034	2087	YP_001463108	4.3531
D000023533	D11	e24_Ch_g40_1_327	betaine aldehyde dehydrogenase	380	YP_001461480	2
D000023535	D12	EcE24377A_1404_1_2130	L-arabinose transporter permease	2183	YP_001463203	4.7536
D000023537	E01	e24_P73_g3_1_327	betaine aldehyde dehydrogenase	380	YP_001461480	2
D000023539	E02	EcE24377A_3648_1_2166	IS605 family transposase OrfB	2219	YP_001463237	4.7472
D000023541	E03	EcE24377A_D0038_1_327	betaine aldehyde dehydrogenase	380	YP_001461480	1.9868
D000023543	E04	EcE24377A_4868_130_2322	hypothetical protein	2249	YP_001463382	4.6901

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
D000023543	E04	EcE24377A_4868_130_23_22	hypothetical protein	2249	YP_001463382	4.6901
D000023545	E05	e24_P73_g7_1_330	IS1, transposase orfB	383	YP_001461483	1.9948
D000023548	E06	EcE24377A_4160_1_2316	imidazole glycerol phosphate synthase subunit HisF	2369	YP_001463376	-
D000023550	E07	e24_Ch_g213_1_333	LuxR family transcriptional regulator	386	YP_001461486	2
D000023551	E08	EcE24377A_3322_1_2385	fructose-bisphosphate aldolase	2438	YP_001463445	2
D000023553	E09	e24_P74_g53_1_333	LuxR family transcriptional regulator	386	YP_001461486	2
D000023555	E10	EcE24377A_1655_1_2409	von Willebrand factor A	2462	YP_001463466	4.2823
D000023557	E11	EcE24377A_1704_1_333	LuxR family transcriptional regulator	386	YP_001461486	2
D000023559	E12	EcE24377A_0301_97_252_3	alpha-2-macroglobulin	2483	YP_001463575	4.3842
D000023561	F01	e24_Ch_g202_1_336	hypothetical protein	389	YP_001461489	2
D000023565	F03	e24_Ch_g396_1_336	hypothetical protein	389	YP_001461489	2
D000023567	F04	EcE24377A_0142_103_25_98	NUDIX family hydrolase	2552	YP_001463643	4.9694
D000023570	F05	EcE24377A_2695_1_339	hypothetical protein	392	YP_001461550	1.9337
D000023571	F06	EcE24377A_3130_1_2505	nitrate reductase catalytic subunit	2558	YP_001463557	4.6345
D000023573	F07	e24_P6_g3_1_345	sugar ABC transporter periplasmic sugar-binding protein	398	YP_001461498	2
D000023575	F08	EcE24377A_4241_1_2517	transcriptional regulator RcsB	2570	YP_001463568	1.8699
D000023577	F09	e24_Ch_g326_1_348	sugar ABC transporter permease	401	YP_001461501	1.995
D000023580	F10	EcE24377A_D0036_76_26_16	hypothetical protein EcE24377A_2616	2597	YP_001463667	3.1494
D000023582	F11	e24_P35_g48_1_348	sugar ABC transporter permease	401	YP_001461501	1.3766
D000023585	G01	e24_P80_g64_1_354	propionate catabolism operon regulatory protein PrpR	407	YP_001461506	1.5823
D000023587	G02	EcE24377A_3359_106_32_52	hypothetical protein	3203	YP_001464261	2.8882
D000023589	G03	e24_Ch_g602_1_357	methylcitrate synthase	410	YP_001461509	2
D000023591	G04	EcE24377A_1649_1_3768	DNA protecting protein DprA	3821	YP_001464753	2.4593
D000023594	G05	e24_Ch_g517_1_360	cytosine permease	413	YP_001461512	-

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
D000023596	G06	EcE24377A_E0051_178_4098	PTS system mannitol-specific transporter subunit IIABC	3977	YP_001465077	2.4578
D000023597	G07	e24_Ch_g256_1_363	hypothetical protein	416	YP_001461515	2
D000023599	G08	H10407_SANG_p666.0750_1_108	hypothetical protein	161	Not Annotated	2
D000023602	G09	H10407_SANG_CHROM1_092a_130_789	hypothetical protein	716	Not Annotated	2
D000023604	G10	H10407_SANG_p666.0750_109_216	hypothetical protein	164	Not Annotated	2
D000023606	G11	h104_Ch_g211_1_663	hypothetical protein	716	Not Annotated	1.5908
D000023607	G12	H10407_SANG_p948.0360_1_108	hypothetical protein	161	Not Annotated	2
D000023611	H02	H10407_SANG_p948.0360_109_216	hypothetical protein	164	Not Annotated	2
D000023613	H03	H10407_SANG_CHROM3_059_82_753	hypothetical protein	728	Not Annotated	1.9135
D000023615	H04	H10407_SANG_p666.0330_1_111	hypothetical protein	164	Not Annotated	2
D000023617	H05	H10407_SANG_p666.0110_1_675	hypothetical protein	728	Not Annotated	2.8791
D000023619	H06	H10407_SANG_CHROM0_809_67_183	Not Available	173	Not Annotated	n/a
D000023621	H07	H10407_SANG_p948.0880_97_771	hypothetical protein	731	Not Annotated	2
D000023623	H08	H10407_SANG_p948.0690_1_135	hypothetical protein	188	Not Annotated	2