

Enterotoxigenic *Escherichia coli* Expression Clone Set, Recombinant in *Escherichia coli*, Plate 5

Catalog No. NR-19794

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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* (EPEC) expression clone set consists of approximately 900 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, using ligation independent cloning, in vector [pMCSG7](#) (a pET21 derivative that contains an N-terminal 6xHis tag; for routine HTP purification). The sequence was validated by full length sequencing of each clone (using 5' and 3' primers; TACTTCCAATCCAATGCG and TTATCCCACTCCAATG, respectively) with greater than 1X coverage and a mutation rate of less than 0.2%. Please refer to Table 1 for more information on the available 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-19794 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 5, NR-19794."

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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Ligation-Independent Cloning Encoding a Tobacco Etch Virus Protease Cleavage Site." *Protein Expr. Purif.* 25 (2002): 8-15. PubMed: 12071693.

References:

1. Stols, L., et al. "A New Vector for High-Throughput,

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Table 1: Enterotoxigenic *E. coli* Expression Clone Set, Recombinant in *E. coli*, Plate 5 (EEXAE)

Clone	Well	Locus ID	Description	ORF Length	Protein Accession Number ¹	Average Depth of Coverage
D000023257	A03	e24_Ch_g626_1_207	D,D-heptose 1,7-bisphosphate phosphatase	260	YP_001461371	2
D000023259	A04	EcE24377A_2242_1_558	hypothetical protein EcE24377A_0558	611	YP_001461707	3.2308
D000023261	A05	e24_P35_g2_1_207	D,D-heptose 1,7-bisphosphate phosphatase	260	YP_001461371	2
D000023263	A06	e24_P73_g70_1_567	hypothetical protein	620	YP_001461715	3.4839
D000023265	A07	EcE24377A_1310_1_207	D,D-heptose 1,7-bisphosphate phosphatase	260	YP_001461371	2
D000023267	A08	EcE24377A_4243_1_570	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase	623	YP_001461717	2
D000023269	A09	e24_Ch_g374_1_210	hypothetical protein	263	NA	2
D000023271	A10	EcE24377A_0303_1_585	hypothetical protein EcE24377A_0585	638	YP_001461729	4.2386
D000023273	A11	e24_Ch_g165_1_213	2,5-diketo-D-gluconate reductase B	266	YP_001461372	3.3057
D000023275	A12	e24_P74_g5_1_594	phenylalanine transporter	647	YP_001461738	2
D000023277	B01	e24_Ch_g627_1_213	2,5-diketo-D-gluconate reductase B	266	YP_001461372	2
D000023279	B02	EcE24377A_0140_1_600	carboxylate-amine ligase	653	YP_001461744	2
D000023281	B03	e24_Ch_g29_1_216	membrane-bound lytic murein transglycosylase D	269	YP_001461376	2
D000023283	B04	EcE24377A_3406_181_780	hypothetical protein EcE24377A_0780	656	YP_001461907	1.75
D000023285	B05	e24_Ch_g566_1_216	membrane-bound lytic murein transglycosylase D	269	YP_001461376	-
D000023287	B06	EcE24377A_4105_67_681	glutamate/aspartate ABC transporter permease	671	YP_001461823	1.9821
D000023289	B07	EcE24377A_1486_1_216	membrane-bound lytic murein transglycosylase D	269	YP_001461376	2
D000023291	B08	EcE24377A_4398_73_690	(dimethylallyl)adenosine tRNA methyltransferase	674	YP_001461833	2

Clone	Well	Locus ID	Description	ORF Length	Protein Accession Number ¹	Average Depth of Coverage
D000023293	B09	e24_P73_g47_1_219	ribonuclease H	272	YP_001461380	2
D000023297	B11	e24_Ch_g617_1_225	hypothetical protein	278	YP_001461384	2
D000023299	B12	e24_Ch_g484_1_633	ribonuclease I	686	YP_001461776	2
D000023302	C01	e24_Ch_g653_1_225	hypothetical protein	278	YP_001461384	2
D000023303	C02	e24_P35_g45_1_642	sensor histidine kinase	695	YP_001461784	1.5669
D000023305	C03	e24_P80_g38_1_225	hypothetical protein	278	YP_001461384	2
D000023308	C04	EcE24377A_D0037_73_714	hypothetical protein EcE24377A_0714	698	YP_001461850	3.5244
D000023310	C05	e24_P35_g33_1_228	hypothetical protein	281	YP_001461387	1.9929
D000023311	C06	EcE24377A_1286_1_654	DNA-binding transcriptional regulator	707	YP_001461796	2
D000023313	C07	e24_P35_g42_160_387	hypothetical protein	284	YP_001461539	2
D000023316	C08	EcE24377A_1408_1_681	glutamate/aspartate ABC transporter permease	734	YP_001461823	1.9305
D000023317	C09	e24_P73_g39_1_228	hypothetical protein	281	YP_001461387	2
D000023319	C10	EcE24377A_0676_1_705	PTS system N-acetyl glucosamine specific transporter subunit II	758	YP_001461840	2
D000023321	C11	e24_P74_g62_1_228	hypothetical protein	281	YP_001461387	2.1779
D000023324	C12	EcE24377A_3905_1_708	hypothetical protein EcE24377A_0708	761	YP_001461844	1.958
D000023326	D01	e24_Ch_g63_1_231	ATP-dependent chaperone protein	284	YP_001461390	-
D000023327	D02	EcE24377A_F0020_91_807	protein KiL	773	YP_001461934	1.9974
D000023329	D03	e24_P5_g9_1_231	ATP-dependent chaperone protein	284	YP_001461390	2
D000023331	D04	EcE24377A_3280_1_729	hypothetical protein EcE24377A_0729	782	YP_001461865	1.3465
D000023333	D05	e24_Ch_g471_1_234	type VI secretion lipoprotein	287	YP_001461393	2
D000023336	D06	EcE24377A_1270_1_741	hypothetical protein	794	NA	3.3791
D000023338	D07	e24_P73_g53_1_234	type VI secretion lipoprotein	287	YP_001461393	2
D000023339	D08	EcE24377A_E0029_1_747	type II citrate synthase	800	YP_001461880	1.25
D000023341	D09	EcE24377A_0302_433_666	DNA polymerase III subunit delta	290	YP_001461808	1.831
D000023343	D10	EcE24377A_1269_1_762	cytochrome d ubiquinol oxidase, subunit II	815	YP_001461894	4.1789
D000023346	D11	e24_Ch_g1_1_237	hypothetical protein	290	YP_001461396	2

Clone	Well	Locus ID	Description	ORF Length	Protein Accession Number ¹	Average Depth of Coverage
D000023347	D12	EcE24377A_3961_1_762	cytochrome d ubiquinol oxidase, subunit II	815	YP_001461894	1.9031
D000023349	E01	e24_P35_g4_1_237	hypothetical protein	290	YP_001461396	2
D000023351	E02	EcE24377A_1451_1_789	hypothetical protein EcE24377A_0789	842	YP_001461916	3.6992
D000023353	E03	e24_P80_g16_1_237	hypothetical protein	290	YP_001461396	1.2414
D000023356	E04	EcE24377A_1884_1_810	hypothetical protein	863	NA	1.949
D000023357	E05	e24_Ch_g114_1_243	hypothetical protein	296	YP_001461402	2
D000023360	E06	EcE24377A_4855_1_819	hypothetical protein EcE24377A_0819	872	YP_001461944	1.6743
D000023361	E07	e24_Ch_g313_1_243	hypothetical protein	296	YP_001461402	2
D000023363	E08	EcE24377A_E0060_1_819	hypothetical protein EcE24377A_0819	872	YP_001461944	4.1022
D000023365	E09	e24_Ch_g321_1_243	hypothetical protein	296	YP_001461402	2
D000023367	E10	EcE24377A_0380_1_831	phage DNA packaging protein	884	YP_001461956	1.9276
D000023369	E11	e24_Ch_g308_1_246	Rhs protein	299	YP_001461405	2
D000023371	E12	EcE24377A_1699_1_831	phage DNA packaging protein	884	YP_001461956	1.8462
D000023374	F01	e24_Ch_g476_1_246	Rhs protein	299	YP_001461405	2
D000023375	F02	EcE24377A_1437_1_837	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	890	YP_001461962	2
D000023377	F03	e24_Ch_g483_1_246	Rhs protein	299	YP_001461405	-
D000023380	F04	EcE24377A_1974_1_837	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	890	YP_001461962	1.9449
D000023384	F06	EcE24377A_4338_1_846	molybdenum cofactor biosynthesis protein	899	YP_001461971	1.4327
D000023386	F07	e24_Ch_g93_1_249	hypothetical protein	302	NA	2
D000023389	F09	EcE24377A_1444_1_249	hypothetical protein	302	NA	2
D000023391	F10	EcE24377A_4885_1_867	glycosyl transferase family protein	920	YP_001461992	3.4315
D000023394	F11	e24_Ch_g76_1_252	C-lysozyme inhibitor	305	YP_001461408	1.9869
D000023394	F11	e24_Ch_g76_1_252	C-lysozyme inhibitor	305	YP_001461408	1.9869
D000023395	F12	EcE24377A_1039_1_912	undecaprenyl pyrophosphate phosphatase	965	YP_001462037	1.6964
D000023397	G01	e24_P73_g5_1_252	C-lysozyme inhibitor	305	YP_001461408	2

Clone	Well	Locus ID	Description	ORF Length	Protein Accession Number ¹	Average Depth of Coverage
D000023399	G02	EcE24377A_2243_1_921	glutaredoxin	974	YP_001462046	3.9466
D000023401	G03	e24_Ch_g439_1_255	hypothetical protein	308	YP_001461411	2
D000023404	G04	EcE24377A_4571_1_924	ribosomal protein S6 modification protein	977	YP_001462049	3.042
D000023406	G05	e24_Ch_g663_1_255	hypothetical protein	308	YP_001461411	1.9805
D000023407	G06	EcE24377A_2916_1_942	NAD dependent epimerase/dehydratase	995	YP_001462067	1.7246
D000023409	G07	e24_Ch_g92_1_255	hypothetical protein	308	YP_001461411	1.9026
D000023411	G08	EcE24377A_4869_1_951	macrolide transporter subunit	1004	YP_001462076	3.0867
D000023413	G09	e24_P73_g54_1_255	hypothetical protein	308	YP_001461411	2
D000023415	G10	EcE24377A_2913_1_984	hypothetical protein EcE24377A_0984	1037	YP_001462107	2.9122
D000023417	G11	e24_P80_g52_1_258	hypothetical protein	311	YP_001461414	3.2219
D000023419	G12	EcE24377A_2197_67_1071	outer membrane protein A	1061	YP_001462189	1.5231
D000023421	H01	e24_Ch_g384_1_261	NlpC/P60 family protein	314	YP_001461416	2
D000023424	H02	e24_P80_g1_1_1011	hypothetical protein	1064	YP_001462131	2.7222
D000023425	H03	e24_P73_g64_1_261	NlpC/P60 family protein	314	YP_001461416	1.6879
D000023427	H04	EcE24377A_D0035_67_1089	hydrogenase 1 b-type cytochrome subunit	1079	YP_001462205	3.9713
D000023429	H05	e24_P35_g10_1_267	hypothetical protein EcE24377A_0267	320	YP_001461423	-
D000023431	H06	EcE24377A_2433_1_1026	metallo-beta-lactamase	1079	YP_001462146	1.3114
D000023433	H07	e24_P35_g24_1_267	hypothetical protein EcE24377A_0267	320	YP_001461423	2
D000023436	H08	EcE24377A_2223_1_1032	hypothetical protein	1085	NA	4.4525
D000023437	H09	e24_P73_g50_1_267	hypothetical protein EcE24377A_0267	320	YP_001461423	2
D000023439	H10	EcE24377A_D0051_1_1065	paraquat-inducible protein A	1118	YP_001462183	4.7737
D000023441	H11	EcE24377A_1340_1_267	hypothetical protein EcE24377A_0267	320	YP_001461423	2.2219

¹NA – Not Available