

Enterotoxigenic *Escherichia coli* Expression Clone Set, Recombinant in *Escherichia coli*, Plates 1-14

Catalog No. NR-19439

Table 1: Enterotoxigenic *E. coli* Expression Clone Set, Plate 1 (EEXAA), NR-19790¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000022503	A02	EcB7A_2419_1_105	metal binding protein	161	-	2
D000022505	A03	b7a_C91_g4_1_339	hypothetical protein	395	-	2
D000022508	A04	b7a_C32_g1_1_111	hypothetical protein	167	-	2
D000022511	A06	b7a_C219_g1_1_114	-	167	-	2
D000022513	A07	b7a_C107_g5_1_345	-	398	-	2
D000022519	A10	EcB7A_2090_1_135	-	188	-	2
D000022521	A11	b7a_C127_g3_1_354	-	407	-	2
D000022524	A12	EcB7A_1787_1_156	hypothetical protein	209	-	2
D000022525	B01	b7a_C2_g16_1_354	hypothetical protein	407	-	2
D000022527	B02	EcB7A_2338_1_159	hypothetical protein	212	-	2
D000022529	B03	b7a_C12_g60_1_360	-	416	-	2
D000022531	B04	EcB7A_1866_1_174	hypothetical protein	227	-	2
D000022534	B05	b7a_C123_g2_1_360	-	413	-	2
D000022535	B06	EcB7A_1063_1_177	hypothetical protein	230	-	2
D000022541	B09	b7a_C25_g9_1_369	type 1 fimbrial protein	422	-	2
D000022543	B10	b7a_C10_g4_1_198	transcriptional activator	254	-	2
D000022547	B12	b7a_C142_g2_1_198	-	254	-	2
D000022549	C01	b7a_C16_g3_1_375	hypothetical protein	428	-	2
D000022556	C04	b7a_C38_g2_1_198	leu operon leader peptide	254	-	2
D000022572	C12	EcB7A_3130_1_198	hypothetical protein	251	-	2
D000022577	D03	b7a_C12_g42_1_393	-	449	-	2
D000022580	D04	b7a_C3_g8_1_201	hypothetical protein	254	-	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000022584	D06	b7a_C30_g5_1_201	activating enzyme	254	-	2
D000022585	D07	b7a_C233_g1_1_396	-	449	-	2
D000022591	D10	b7a_C1_g21_1_204	gamma-glutamylputrescine synthetase	260	-	2
D000022593	D11	EcB7A_4206_67_468	fimbrial subunit protein	458	-	2
D000022596	D12	b7a_C197_g1_1_204	transporter	260	-	2
D000022597	E01	EcB7A_0578_2155_2559	tail protein	461	-	2
D000022600	E02	b7a_C75_g5_1_204	-	260	-	2
D000022603	E04	b7a_C9_g8_1_204	type III secretion system protein	257	-	2
D000022607	E06	b7a_C98_g5_1_204	-	260	-	2
D000022612	E08	b7a_C219_g2_1_207	putative transposase	260	-	2
D000022613	E09	EcB7A_1642_67_483	-	473	-	2
D000022620	E12	b7a_C26_g3_1_207	fimbrial-like protein	260	-	2
D000022621	F01	EcB7A_1674_1_435	-	488	-	2
D000022623	F02	b7a_C34_g8_1_207	phage protein	263	-	2
D000022627	F04	b7a_C75_g22_1_207	transposase	263	-	2
D000022630	F05	b7a_C38_g3_1_444	2-isopropylmalate synthase	500	-	2
D000022632	F06	b7a_C76_g2_1_207	hypothetical protein	260	-	2
D000022633	F07	EcB7A_0414_67_510	hypothetical protein	500	-	2
D000022635	F08	b7a_C76_g4_1_207	hypothetical protein	263	-	2
D000022639	F10	b7a_C1_g17_1_210	Periplasmic murine protein-binding protein	266	-	2
D000022641	F11	EcB7A_1796_1_453	hypothetical protein	506	-	2
D000022643	F12	b7a_C1_g25_1_210	hypothetical protein	266	-	2
D000022646	G01	EcB7A_1634_1_456	-	509	-	2
D000022647	G02	b7a_C27_g9_1_210	aspartate carbamoyl-transferase	266	-	2
D000022653	G05	EcB7A_4650_1_459	inner membrane protein	512	-	2
D000022655	G06	b7a_C30_g8_1_213	hypothetical protein	269	-	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000022658	G07	b7a_C142_g8_148_609	-	518	-	2
D000022659	G08	EcB7A_4878_1_213	hypothetical protein	266	-	2
D000022661	G09	b7a_C125_g2_1_465	hypothetical protein	518	-	3.1160542
D000022664	G10	b7a_C1_g14_1_216	small toxic polypeptide	272	-	2
D000022666	G11	b7a_C62_g3_1_471	hypothetical protein	524	-	-
D000022671	H02	EcB7A_0403_1_216	lipoprotein	269	-	2
D000022676	H04	b7a_C158_g1_1_219	-	272	-	2
D000022677	H05	EcB7A_3345_1_483	hypothetical protein	536	-	2
D000022682	H07	EcB7A_3108_1_486	D-alanyl-D-alanine-carboxypeptidase	542	-	2
D000022684	H08	b7a_C18_g1_1_219	hypothetical protein	275	-	2
D000022690	H11	EcB7A_3787_76_573	lipopolysaccharide periplasmic protein	554	-	2

Table 2: Enterotoxigenic *E. coli* Expression Clone Set, Plate 2 (EEXAB), NR-19791¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000022693	A03	EcB7A_2312_1_501	sulfurtransferase	554	ZP_03028426	2
D000022695	A04	EcB7A_C4_g18_1_219	inner membrane ABC transporter permease	275	ZP_03026866	2
D000022697	A05	EcB7A_3089_79_579	phage minor tail protein	557	ZP_03028415	2
D000022699	A06	EcB7A_C21_g20_1_222	transcriptional regulator, LysR family	275	ZP_03026868	2
D000022702	A07	EcB7A_4230_1_510	hydrogenase-1 operon protein HyaF	563	ZP_03028367	2
D000022713	B01	EcB7A_4207_1_522	cold shock DNA-binding protein	575	ZP_03028394	2
D000022715	B02	EcB7A_C22_g4_1_225	acetyl-CoA acetyltransferase	281	ZP_03026966	2
D000022717	B03	EcB7A_3133_1_525	TMAO reductase system sensor TorS	578	ZP_03028393	2
D000022719	B04	EcB7A_C64_g1_1_225	acetyl-CoA acetyltransferase	281	ZP_03026966	2
D000022721	B05	EcB7A_3464_211_735	cupin family protein	581	ZP_03030135	2
D000022726	B07	EcB7A_C4_g13_1_528	Eaa protein	584	ZP_03028396	2
D000022727	B08	EcB7A_C12_g27_1_231	30S ribosomal protein, S22 family	284	ZP_03026832	2
D000022729	B09	EcB7A_C4_g21_1_531	Eaa protein	587	ZP_03028420	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000022732	B10	EcB7A_C50_g5_1_231	30S ribosomal protein, S22 family	287	ZP_03026832	2
D000022735	B12	EcB7A_C67_g3_1_231	30S ribosomal protein, S22 family	287	ZP_03026832	2
D000022738	C01	EcB7A_5025_1_540	putative repressor protein	596	ZP_03028391	2
D000022743	C04	EcB7A_C31_g10_1_234	addiction module antidote protein, HigA family	290	ZP_03026890	2
D000022747	C06	EcB7A_C75_g15_1_234	addiction module antidote protein, HigA family	287	ZP_03026890	2
D000022751	C08	EcB7A_2479_433_666	glucarate permease	290	ZP_03030338	2
D000022754	C09	EcB7A_4896_94_648	fucose operon protein FucU	611	ZP_03030333	2
D000022755	C10	EcB7A_C51_g6_1_237	hypothetical protein	293	-	2
D000022757	C11	EcB7A_0195_1_561	bacteriophage lysis protein	614	ZP_03028378	2
D000022759	C12	EcB7A_C1_g18_1_240	outer membrane porin	296	ZP_03027016	2
D000022763	D02	EcB7A_C75_g19_1_240	outer membrane porin	296	ZP_03027016	2
D000022767	D04	EcB7A_2999_1_240	outer membrane porin	293	ZP_03027016	2
D000022769	D05	EcB7A_C183_g1_1_579	phage minor tail protein	635	ZP_03028415	2
D000022774	D07	EcB7A_3481_1_579	phage minor tail protein	632	ZP_03028415	2
D000022776	D08	EcB7A_C12_g45_1_243	nitrate reductase 2, alpha subunit	296	ZP_03026854	2
D000022777	D09	EcB7A_2323_1_582	hypothetical protein	638	-	2
D000022781	D11	EcB7A_2478_1_585	CDP-diacylglycerol--serine O-phosphatidyltransferase	638	ZP_03029772	2
D000022791	E04	EcB7A_C15_g13_1_246	respiratory nitrate reductase 2, gamma subunit	302	ZP_03027034	2
D000022794	E05	EcB7A_0048_1_600	sigma-E factor regulatory protein RseC	653	ZP_03029763	2
D000022795	E06	EcB7A_C19_g5_1_246	respiratory nitrate reductase 2, gamma subunit	299	ZP_03027034	2
D000022799	E08	EcB7A_C53_g7_1_246	respiratory nitrate reductase 2, gamma subunit	302	ZP_03027034	2
D000022801	E09	EcB7A_4185_1_612	tRNA-specific adenosine deaminase	665	ZP_03029780	2
D000022803	E10	EcB7A_C148_g4_1_249	flavin reductase domain protein	305	ZP_03026861	2
D000022805	E11	EcB7A_5152_1_615	hypothetical protein	671	-	2
D000022807	E12	EcB7A_C5_g4_1_249	flavin reductase domain protein	305	ZP_03026861	2
D000022809	F01	EcB7A_0415_1_618	putative lipoprotein	671	ZP_03029792	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000022811	F02	EcB7A_C67_g8_1_249	flavin reductase domain protein	302	ZP_03026861	2
D000022815	F04	EcB7A_2078_1_249	flavin reductase domain protein	302	ZP_03026861	2
D000022817	F05	EcB7A_3291_1_621	impA-related N-terminal domain	674	ZP_03030396	2
D000022819	F06	EcB7A_3128_1_252	regulatory protein	305	ZP_03030973	2
D000022823	F08	EcB7A_C12_g43_1_255	hypothetical protein	311	-	2
D000022827	F10	EcB7A_C145_g4_1_255	hypothetical protein	308	-	2
D000022829	F11	EcB7A_3341_1_654	exodeoxyribonuclease-g	707	ZP_03030330	2
D000022831	F12	EcB7A_C52_g4_1_255	hypothetical protein	308	-	2
D000022835	G02	EcB7A_C54_g4_1_255	hypothetical protein	311	-	2
D000022839	G04	EcB7A_C88_g3_1_255	hypothetical protein	311	-	2
D000022843	G06	EcB7A_C98_g2_1_255	-	311	-	2
D000022847	G08	EcB7A_C21_g1_1_258	conserved hypothetical protein	314	ZP_03027014	2
D000022852	G10	EcB7A_C2_g11_1_261	conserved hypothetical protein	314	ZP_03026973	2
D000022854	G11	EcB7A_3716_1_708	conserved hypothetical protein	761	ZP_03029124	1.9961
D000022855	G12	EcB7A_C22_g8_1_261	conserved hypothetical protein	314	ZP_03026973	2
D000022859	H02	EcB7A_5153_1_261	conserved hypothetical protein	314	ZP_03026973	2
D000022861	H03	EcB7A_0575_1_717	maltose O-acetyltransferase	770	ZP_03029322	1.9935
D000022863	H04	EcB7A_C127_g8_1_264	oxidoreductase, zinc-binding dehydrogenase family	320	ZP_03026895	2
D000022868	H06	EcB7A_C15_g3_1_264	oxidoreductase, zinc-binding dehydrogenase family	320	ZP_03026895	2
D000022870	H07	EcB7A_0823_1_729	tRNA (5-ethylaminomethyl-2-thiouridylate)-methyltransferase	782	ZP_03030119	1.991
D000022871	H08	EcB7A_1478_1_264	oxidoreductase, zinc-binding dehydrogenase family	320	ZP_03026895	2
D000022875	H10	EcB7A_4205_1_264	oxidoreductase, zinc-binding dehydrogenase family	317	ZP_03026895	2

Table 3: Enterotoxigenic *E. coli* Expression Clone Set, Plate 3 (EEXAC), NR-19792¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000022881	A03	EcB7A_4173_1_738	spermidine/putrescine ABC transporter, permease protein	791	ZP_03030123	4.1985

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000022883	A04	b7a_C12_g47_1_267	conserved hypothetical protein	323	ZP_03026927	3.2632
D000022886	A05	EcB7A_2311_1_756	conserved hypothetical protein	812	ZP_03030117	4.0333
D000022905	B03	EcB7A_1010_1_846	conserved hypothetical protein	899	ZP_03029740	4.0567
D000022908	B04	b7a_C257_g1_1_273	ABC transporter, periplasmic substrate-binding protein	329	ZP_03026948	3.2006
D000022909	B05	EcB7A_4183_1_846	conserved hypothetical protein	899	ZP_03029740	3.4461
D000022911	B06	b7a_C35_g3_1_273	ABC transporter, periplasmic substrate-binding protein	326	ZP_03026948	3.227
D000022913	B07	EcB7A_2518_1_852	membrane-bound lytic murein transglycosylase C	905	ZP_03029730	4.0652
D000022915	B08	b7a_C116_g3_1_276	hypothetical protein EcB7A_0276	329	ZP_03026897	3.2188
D000022918	B09	EcB7A_4155_1_858	gp59	911	ZP_03027307	3.3787
D000022924	B12	b7a_C4_g15_1_276	hypothetical protein EcB7A_0276	329	ZP_03026897	3.2492
D000022927	C02	EcB7A_3401_1_276	hypothetical protein EcB7A_0276	329	ZP_03026897	3.2249
D000022931	C04	b7a_C12_g51_1_279	DNA-binding protein	335	ZP_03026827	3.2388
D000022934	C05	EcB7A_1776_1_951	transcriptional regulator	1004	ZP_03027967	3.8297
D000022936	C06	b7a_C148_g2_1_279	DNA-binding protein	332	ZP_03026827	2.2199
D000022939	C08	b7a_C214_g1_1_282	hypothetical protein	338	-	3.2189
D000022946	C11	EcB7A_4052_1_975	TDP-D-fucosamine acetyltransferase	1028	ZP_03027928	3.6449
D000022954	D03	EcB7A_4584_67_1071	YciL domain protein	1061	ZP_03028458	4.5146
D000022956	D04	EcB7A_0562_1_291	periplasmic glucan biosynthesis protein	344	ZP_03026825	3.2297
D000022960	D06	EcB7A_1229_1_291	periplasmic glucan biosynthesis protein	344	ZP_03026825	3.2238
D000022962	D07	EcB7A_0742_1_1047	conserved hypothetical protein	1100	ZP_03028468	4.0036
D000022964	D08	EcB7A_2520_1_291	periplasmic glucan biosynthesis protein	344	ZP_03026825	3.2209
D000022968	D10	EcB7A_4284_1_291	periplasmic glucan biosynthesis protein	344	ZP_03026825	2.2209
D000022970	D11	EcB7A_0777_1_1074	conserved hypothetical protein	1127	ZP_03028468	4.5102
D000022971	D12	b7a_C7_g2_1_294	methyl-accepting chemotaxis protein III	347	ZP_03026842	3.1988
D000022976	E02	b7a_C91_g5_1_294	methyl-accepting chemotaxis protein III	347	ZP_03026842	2.1902

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000022982	E05	EcB7A_1637_88_1200	hydrogenase-2 operon protein	1169	ZP_03029351	3.9196
D000022983	E06	b7a_C44_g12_1_297	nickel-dependent hydrogenase, b-type cytochrome subunit	350	ZP_03026962	3.2343
D000022986	E07	EcB7A_4904_1_1113	putative invasion gene expression up-regulator	1166	ZP_03028490	4.5575
D000022989	E09	EcB7A_4733_76_1200	hydrogenase-2 operon protein	1181	ZP_03029351	4.5651
D000022991	E10	b7a_C91_g8_1_297	nickel-dependent hydrogenase, b-type cytochrome subunit	350	ZP_03026962	3.1914
D000022998	F01	EcB7A_4973_1_1188	oxidoreductase, short chain dehydrogenase/reductase family	1241	ZP_03029384	3.3779
D000023007	F06	b7a_C99_g5_1_300	conserved hypothetical protein	356	ZP_03026936	3.2045
D000023010	F07	EcB7A_3342_679_1899	hypothetical protein EcB7A_1899	1277	ZP_03027102	4.2968
D000023014	F09	EcB7A_4179_1_1269	hypothetical protein EcB7A_1269	1322	ZP_03028583	4.1619
D000023018	F11	EcB7A_1790_160_1482	conserved hypothetical protein	1379	ZP_03027283	3.0218
D000023019	F12	EcB7A_0520_1_303	PAP2 family protein	356	ZP_03026903	3.1601
D000023022	G01	EcB7A_3145_1_1398	conserved hypothetical protein	1451	ZP_03028926	3.4431
D000023024	G02	EcB7A_5042_898_1200	hydrogenase-2 operon protein	359	ZP_03029351	3.2006
D000023028	G04	b7a_C133_g2_70_375	hypothetical protein	362	-	3.2072
D000023032	G06	b7a_C225_g1_1_306	CDP-alcohol phosphatidyltransferase family protein	362	ZP_03026839	3.2017
D000023035	G08	b7a_C1_g30_1_309	phenylacetic acid degradation protein	365	ZP_03026857	3.2192
D000023038	G09	EcB7A_2481_1_1569	efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	1622	ZP_03027200	4.5037
D000023043	G12	b7a_C6_g2_1_312	beta-ketoacyl-CoA thiolase	368	ZP_03026937	3.2174
D000023046	H01	EcB7A_3462_1156_2838	catabolite gene activator	1739	ZP_03030187	4.4756
D000023048	H02	b7a_C116_g2_1_315	enoyl-CoA hydratase	371	ZP_03026981	3.1995
D000023050	H03	EcB7A_3144_1_1746	flagellar hook capping protein	1799	ZP_03030259	4.1668
D000023052	H04	b7a_C12_g46_1_315	enoyl-CoA hydratase	371	ZP_03026981	2.2318
D000023055	H06	b7a_C25_g2_1_315	enoyl-CoA hydratase	371	ZP_03026981	3.2075
D000023060	H08	b7a_C53_g8_1_315	enoyl-CoA hydratase	371	ZP_03026981	3.221

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023064	H10	EcB7A_4236_1_321	phenylacetyl-CoA oxygenase, alpha subunit	377	ZP_03026919	3.1963

Table 4: Enterotoxigenic *E. coli* Expression Clone Set, Plate 4 (EEXAD), NR-19793¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023071	A04	EcB7A_1218_1_324	copper amine oxidase	377	ZP_03026875	2
D000023075	A06	b7a_C75_g20_1_327	conserved hypothetical protein	383	ZP_03026845	2
D000023080	A08	b7a_C12_g3_1_330	D-lactate dehydrogenase	383	ZP_03026912	2
D000023083	A10	b7a_C6_g7_1_330	D-lactate dehydrogenase	386	ZP_03026912	2
D000023088	A12	b7a_C12_g37_1_333	pyruvate-flavodoxin oxidoreductase	386	ZP_03026992	2
D000023091	B02	b7a_C6_g13_1_333	pyruvate-flavodoxin oxidoreductase	389	ZP_03026992	2
D000023093	B03	b7a_C140_g1_1_336	universal stress protein F	392	ZP_03027029	2
D000023097	B05	EcE24377A_0549_1_90	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	143	YP_001461258	2
D000023100	B06	e24_Ch_g277_1_366	cyanate transporter	419	YP_001461518	2
D000023101	B07	EcE24377A_1495_1_96	cell division protein	149	YP_001461264	2
D000023103	B08	e24_P80_g23_1_369	lac repressor	422	YP_001461521	2.6019
D000023105	B09	EcE24377A_3163_1_96	cell division protein	149	YP_001461264	2
D000023107	B10	e24_Ch_g209_1_375	acetaldehyde dehydrogenase	428	YP_001461527	2
D000023109	B11	EcE24377A_2812_1_114	acriflavine resistance protein D	167	ZP_03029459	3.2108
D000023113	C01	EcE24377A_1316_1_117	hydrolase, NUDIX family	170	ZP_03029433	2
D000023115	C02	EcE24377A_1226_1_375	acetaldehyde dehydrogenase	428	YP_001461527	2
D000023117	C03	EcE24377A_3459_1_126	glucose dehydrogenase	179	YP_001461292	2
D000023120	C04	e24_P73_g51_1_384	acyltransferase	437	YP_001461536	2
D000023121	C05	e24_P74_g51_88_216	membrane-bound lytic murein transglycosylase D	185	YP_001461376	2
D000023123	C06	EcE24377A_2919_1_384	acyltransferase	437	YP_001461536	2
D000023126	C07	EcE24377A_3711_1_132	polysaccharide deacetylase	185	YP_001461298	2
D000023127	C08	EcE24377A_1276_1_390	-	443	-	2
D000023129	C09	EcE24377A_1483_1_141	hypothetical protein EcE24377A_0141	194	YP_001461307	2
D000023131	C10	EcE24377A_3170_1_390	hypothetical protein	443	-	2
D000023134	C11	EcE24377A_1115_1_147	poly(A) polymerase	200	YP_001461313	2.6735

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023135	C12	e24_P35_g12_1_399	hypothetical protein EcE24377A_0399	452	YP_001461550	2
D000023137	D01	EcE24377A_3646_1_153	penicillin-binding protein 1b	206	YP_001461319	2
D000023140	D02	EcE24377A_3357_1_399	hypothetical protein EcE24377A_0399	452	YP_001461550	2
D000023141	D03	EcE24377A_4848_1_159	glutamate-1-semialdehyde aminotransferase	212	YP_001461325	2
D000023144	D04	e24_P73_g83_1_405	hypothetical protein EcE24377A_0405	458	YP_001461556	2
D000023145	D05	EcE24377A_4974_1_159	glutamate-1-semialdehyde aminotransferase	212	YP_001461325	2
D000023147	D06	EcE24377A_4197_1_405	hypothetical protein EcE24377A_0405	458	YP_001461556	2
D000023149	D07	EcE24377A_2643_1_168	hypothetical protein EcE24377A_0168	221	YP_001461334	2
D000023153	D09	EcE24377A_F0028_1_168	hypothetical protein EcE24377A_0168	221	YP_001461334	2
D000023155	D10	e24_Ch_g142_1_414	hypothetical protein	467	YP_001461565	2
D000023157	D11	EcE24377A_1913_1_174	elongation factor Ts	227	YP_001461339	2
D000023159	D12	e24_Ch_g22_1_417	hypothetical protein	470	YP_001461568	2
D000023161	E01	EcE24377A_3753_1_174	elongation factor Ts	227	YP_001461339	2
D000023163	E02	e24_P6_g8_1_420	recombination associated protein	473	YP_001461571	2
D000023165	E03	EcE24377A_1458_1_177	1-deoxy-D-xylulose 5-phosphate reductoisomerase	230	YP_001461342	2
D000023167	E04	e24_Ch_g90_1_423	MFS transport protein	476	YP_001461574	2
D000023169	E05	e24_P80_g26_1_186	lipid-A-disaccharide synthase	239	YP_001461351	2
D000023171	E06	EcE24377A_3258_1_429	hypothetical protein EcE24377A_0429	482	YP_001461580	2
D000023173	E07	EcE24377A_2920_1_186	lipid-A-disaccharide synthase	239	YP_001461351	2
D000023175	E08	e24_Ch_g436_1_435	S-adenosylmethionine-tRNA ribosyltransferase-isomerase	488	YP_001461586	2
D000023175	E08	e24_Ch_g436_1_435	S-adenosylmethionine-tRNA ribosyltransferase-isomerase	488	YP_001461586	2
D000023177	E09	EcE24377A_4922_1_192	tRNA(Ile)-lysidine synthetase	245	YP_001461357	2
D000023179	E10	EcE24377A_D0052_1_435	S-adenosylmethionine-tRNA ribosyltransferase-isomerase	488	YP_001461586	2
D000023181	E11	e24_Ch_g301_235_426	hypothetical protein	248	YP_001461577	2
D000023183	E12	EcE24377A_2914_1_438	preprotein translocase subunit	491	YP_001461589	2
D000023185	F01	EcE24377A_1449_1_195	hypothetical protein EcE24377A_0195	248	YP_001461360	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023187	F02	e24_P35_g6_1_447	transcription anti-termination protein	500	YP_001461598	3.152
D000023189	F03	e24_Ch_g193_1_198	IS621, transposase	251	YP_001461363	2
D000023191	F04	EcE24377A_1244_1_459	major facilitator transporter	512	YP_001461610	2
D000023193	F05	e24_Ch_g317_1_198	IS621, transposase	251	YP_001461363	2
D000023195	F06	e24_P73_g69_1_462	hypothetical protein EcE24377A_0462	515	YP_001461613	2
D000023197	F07	e24_Ch_g606_1_198	IS621, transposase	251	YP_001461363	2
D000023199	F08	e24_Ch_g468_1_477	peptidyl-prolyl cis-trans isomerase	530	YP_001461628	2
D000023201	F09	e24_Ch_g80_1_198	IS621, transposase	251	YP_001461363	2
D000023203	F10	e24_P80_g51_1_486	nitrogen regulatory protein P-II 2	539	YP_001461637	2
D000023208	F12	EcE24377A_2630_1_501	hypothetical protein EcE24377A_0501	554	YP_001461652	2
D000023209	G01	e24_P73_g34_1_198	IS621, transposase	251	YP_001461363	2
D000023211	G02	e24_Ch_g492_1_513	adenylate kinase	566	YP_001461663	2
D000023213	G03	e24_P73_g42_1_198	IS621, transposase	251	YP_001461363	2
D000023215	G04	EcE24377A_2395_1_516	inosine-guanosine kinase	569	YP_001461666	2
D000023217	G05	e24_Ch_g273_1_201	prolyl-tRNA synthetase	254	YP_001461365	2
D000023219	G06	e24_Ch_g212_1_519	bifunctional UDP-sugar hydrolase/5'-nucleotidase periplasmic	572	YP_001461669	2
D000023221	G07	e24_Ch_g474_1_201	prolyl-tRNA synthetase	254	YP_001461365	2
D000023223	G08	e24_P73_g6_1_519	bifunctional UDP-sugar hydrolase/5'-nucleotidase periplasmic	572	YP_001461669	2
D000023225	G09	e24_Ch_g497_1_201	prolyl-tRNA synthetase	254	YP_001461365	2
D000023229	G11	e24_Ch_g668_1_201	prolyl-tRNA synthetase	254	YP_001461365	2
D000023234	H01	e24_P5_g2_1_201	prolyl-tRNA synthetase	254	YP_001461365	2
D000023236	H02	EcE24377A_2219_1_534	ABC transporter ATP-binding protein	587	YP_001461684	1.7513
D000023237	H03	e24_P6_g12_1_201	prolyl-tRNA synthetase	254	YP_001461365	2
D000023241	H05	e24_Ch_g254_1_204	DL-methionine transporter substrate-binding subunit	257	YP_001461368	2
D000023245	H07	e24_Ch_g453_1_207	D,D-heptose 1,7-bisphosphate phosphatase	260	YP_001461371	2
D000023248	H08	EcE24377A_3672_1_543	DNA-binding transcriptional repressor AIIR	596	YP_001461692	2
D000023250	H09	e24_Ch_g496_1_207	D,D-heptose 1,7-bisphosphate phosphatase	260	YP_001461371	2
D000023252	H10	e24_Ch_g325_1_546	2-hydroxy-3-oxopropionate reductase	599	YP_001461695	2.2237

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023254	H11	e24_Ch_g524_1_207	D,D-heptose 1,7-bisphosphate phosphatase	260	YP_001461371	NA

Table 5: Enterotoxigenic *E. coli* Expression Clone Set, Plate 5 (EEXAE), NR-19794¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	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	-	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 trans-glycosylase 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 trans-glycosylase D	269	YP_001461376	-
D000023287	B06	EcE24377A_4105_67_681	glutamate/aspartate ABC transporter permease	671	YP_001461823	1.9821

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023289	B07	EcE24377A_1486_1_216	membrane-bound lytic murein trans-glycosylase D	269	YP_001461376	2
D000023291	B08	EcE24377A_4398_73_690	(dimethylallyl) adenosine tRNA methylthio-transferase	674	YP_001461833	2
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	-	3.3791
D000023338	D07	e24_P73_g53_1_234	type VI secretion lipoprotein	287	YP_001461393	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023339	D08	EcE24377A_E0029_1_747	type II citrate synthase	800	YP_001461880	1.25
D000023341	D09	EcE24377A_0302_433_66 6	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
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	-	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	-	2
D000023389	F09	EcE24377A_1444_1_249	hypothetical protein	302	-	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
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
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_107 1	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_10 89	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	-	4.4525
D000023437	H09	e24_P73_g50_1_267	hypothetical protein EcE24377A_0267	320	YP_001461423	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023439	H10	EcE24377A_D0051_1_106 5	paraquat-inducible protein A	1118	YP_001462183	4.7737
D000023441	H11	EcE24377A_1340_1_267	hypothetical protein EcE24377A_0267	320	YP_001461423	2.2219

Table 6: Enterotoxigenic *E. coli* Expression Clone Set, Plate 6 (EEXAF), NR-19795¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023446	A03	e24_Ch_g141_1_270	xanthine-guanine phosphoribosyl-transferase	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	-	1139	-	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_121 8	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	-	329	-	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_116 4	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

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
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
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	-	1694	-	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	-	1826	-	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

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023535	D12	EcE24377A_1404_1_2130	L-arabinose trans- porter 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_23 22	hypothetical protein	2249	YP_001463382	4.6901
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 trans- criptional 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 trans- criptional 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 peri-plasmic 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

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
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	-
D000023596	G06	EcE24377A_E0051_178_4_098	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	-	2
D000023602	G09	H10407_SANG_CHROM1_092a_130_789	hypothetical protein	716	-	2
D000023604	G10	H10407_SANG_p666.0750_109_216	hypothetical protein	164	-	2
D000023606	G11	h104_Ch_g211_1_663	hypothetical protein	716	-	1.5908
D000023607	G12	H10407_SANG_p948.0360_1_108	hypothetical protein	161	-	2
D000023611	H02	H10407_SANG_p948.0360_109_216	hypothetical protein	164	-	2
D000023613	H03	H10407_SANG_CHROM3_059_82_753	hypothetical protein	728	-	1.9135
D000023615	H04	H10407_SANG_p666.0330_1_111	hypothetical protein	164	-	2
D000023617	H05	H10407_SANG_p666.0110_1_675	hypothetical protein	728	-	2.8791
D000023619	H06	H10407_SANG_CHROM0_809_67_183	-	173	-	n/a
D000023621	H07	H10407_SANG_p948.0880_97_771	hypothetical protein	731	-	2
D000023623	H08	H10407_SANG_p948.0690_1_135	hypothetical protein	188	-	2

Table 7: Enterotoxigenic *E. coli* Expression Clone Set, Plate 7 (EEXAG), NR-19796¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023631	A02	H10407_SANG_CHROM0_453_1_147	hypothetical protein	200	-	2
D000023634	A03	H10407_SANG_CHROM1_754_73_756	putative exported protein	740	-	1.4784

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023636	A04	H10407_SANG_CHROM3_920_148_315	putative transmembrane HD family hydrolase	224	-	2
D000023638	A05	H10407_SANG_CHROM2_853_1_684	putative alpha-amylase precursor, pseudogene	737	-	1.9701
D000023639	A06	H10407_SANG_CHROM1_074_1_171	hypothetical protein	224	-	2
D000023641	A07	H10407_SANG_CHROM0_414_82_771	hypothetical protein	746	-	1.9853
D000023643	A08	H10407_SANG_CHROM1_490_1_171	hypothetical protein	224	-	2
D000023645	A09	H10407_SANG_CHROM1_140_1_693	basal-body rod modification protein FlgD	746	-	1.9705
D000023647	A10	H10407_SANG_CHROM1_361_1_177	hypothetical protein	230	-	2
D000023649	A11	H10407_SANG_CHROM4_720_1_693	minor tail protein	746	-	1.9062
D000023651	A12	H10407_SANG_CHROM4_732_1_177	putative membrane protein	230	-	2
D000023653	B01	H10407_SANG_CHROM0_830_1_696	putative phage minor tail protein	749	-	1.8905
D000023655	B02	H10407_SANG_CHROM1_676_1_180	outer membrane lipoprotein	233	-	2
D000023658	B03	H10407_SANG_CHROM1_238_1_696	putative minor tail protein L	749	-	3.4486
D000023659	B04	H10407_SANG_p948.0910_1_180	<i>Escherichia coli</i> strain ETEC 27D CexE (cexE) gene	233	-	2
D000023662	B05	H10407_SANG_CHROM4_528_1_696	hypothetical protein	749	-	1.2951
D000023664	B06	H10407_SANG_p948.0910_181_360	-	236	-	2
D000023665	B07	H10407_SANG_CHROM2_531_148_849	hypothetical protein	758	-	1.8971
D000023667	B08	H10407_SANG_p666.0650_1_186	hypothetical protein	239	-	2
D000023669	B09	H10407_SANG_CHROM0_677_1_705	hypothetical protein	758	-	1.9908
D000023671	B10	H10407_SANG_p666.0650_187_372	hypothetical protein	242	-	2
D000023673	B11	H10407_SANG_CHROM3_135_1_705	-	758	-	2
D000023675	B12	H10407_SANG_p666.0020_1_189	hypothetical protein	242	-	2
D000023677	C01	H10407_SANG_CHROM0_551_1_708	-	761	-	2
D000023679	C02	H10407_SANG_CHROM1_960_1_192	hypothetical protein	245	-	2
D000023681	C03	H10407_SANG_CHROM1_011_1_711	fimbrial precursor	764	-	1.945

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023683	C04	h104_Ch_g354_1_198	putative restriction endonuclease	251	-	2
D000023686	C05	H10407_SANG_CHROM0_228_91_810	copper resistance protein A precursor	776	-	1.9497
D000023687	C06	H10407_SANG_CHROM2_744_208_405	putative phage protein	254	-	2
D000023690	C07	H10407_SANG_CHROM2_241_97_816	putative glycosyl hydrolase	776	-	1.8634
D000023691	C08	h104_P666_g28_1_201	hypothetical protein	254	-	2
D000023694	C09	H10407_SANG_CHROM0_226_1_735	putative peptidase	788	-	1.7411
D000023695	C10	h104_Ch_g642_1_204	LacI-family transcriptional regulator	257	-	2
D000023697	C11	H10407_SANG_CHROM0_327_1_735	putative prophage protein	788	-	1.9023
D000023699	C12	h104_P666_g20_1_204	hypothetical protein	257	-	2
D000023701	D01	H10407_SANG_CHROM4_715_1_738	phage major tail protein	791	-	1.9279
D000023703	D02	H10407_SANG_CHROM2_638_1_204	hypothetical phage protein	257	-	2
D000023705	D03	H10407_SANG_CHROM0_314_1_741	predicted AraC family DNA-binding transcriptional activator	794	CBI99818	1.8778
D000023708	D04	h104_Ch_g644_1_207	-	260	-	2
D000023710	D05	H10407_SANG_CHROM3_095_1_741	predicted NAD(P)-binding oxidoreductase with NAD(P)-binding Rossmann-fold domain	794	CBJ02597	1.3753
D000023711	D06	h104_Ch_g660_1_207	integral membrane protein	260	CBJ02717	2
D000023713	D07	H10407_SANG_CHROM2_198_1_744	putative colanic acid biosynthesis glycosyl transferase	797	CBJ01701	4.1493
D000023715	D08	h104_P52_g6_1_210	hypothetical protein	263	-	2
D000023717	D09	H10407_SANG_CHROM3_813_79_822	putative endo-beta-N-acetylglucosaminidase	800	CBJ03316	1.3625
D000023719	D10	H10407_SANG_CHROM1_277_1_210	hypothetical protein	263	-	2
D000023721	D11	H10407_SANG_CHROM2_730_1_750	putative phage related protein	803	-	1.8929
D000023725	E01	H10407_SANG_CHROM2_398_1_756	-	809	-	2
D000023727	E02	H10407_SANG_CHROM1_382_277_489	phosphatidylglycerophosphate B	269	CBJ00885	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023731	E04	h104_Ch_g519_1_216	-	269	-	1.9926
D000023733	E05	H10407_SANG_CHROM4_424_1_759	-	812	-	2
D000023735	E06	h104_Ch_g810_1_216	hypothetical protein	269	-	2
D000023737	E07	H10407_SANG_CHROM0_977_1_762	putative membrane-associated peptidase	815	CBJ00485	2.8931
D000023740	E08	H10407_SANG_CHROM1_387_1_216	osmotically inducible lipoprotein B	269	CBJ00890	2
D000023741	E09	H10407_SANG_CHROM0_248_1_765	putative amidotransferase	818	-	1.879
D000023743	E10	H10407_SANG_CHROM3_020_1_216	possible lipoprotein	269	CBJ02522	2
D000023745	E11	H10407_SANG_CHROM1_234_1_768	hypothetical protein	821	-	1.8502
D000023749	F01	H10407_SANG_CHROM1_271b_1_768	hypothetical protein	821	-	1.8709
D000023752	F02	H10407_SANG_CHROM3_543_1_216	large-conductance mechanosensitive channel	269	CBJ03043	2
D000023753	F03	H10407_SANG_CHROM3_057_1_768	hypothetical protein	821	-	1.3788
D000023756	F04	h104_Ch_g879_1_222	putative acetyltransferase	275	CBJ03663	2
D000023759	F06	H10407_SANG_CHROM1_543_67_288	putative outer membrane porin protein	278	CBJ01047	2
D000023762	F07	H10407_SANG_CHROM2_359_1_774	putative exported protein	827	-	1.9601
D000023763	F08	h104_Ch_g213_1_225	-	278	-	-
D000023766	F09	H10407_SANG_CHROM4_646_193_966	putative exported protein	830	-	1.8217
D000023768	F10	h104_Ch_g402_1_225	-	278	-	1.9928
D000023769	F11	H10407_SANG_CHROM1_679_79_855	HlyD-family secretion protein	833	CBJ01183	1.6122
D000023772	F12	H10407_SANG_CHROM2_999_1_225	putative lipoprotein	278	CBJ02501	2
D000023773	G01	H10407_SANG_CHROM1_143_1_780	flagellar basal-body rod protein FlgG	833	CBJ00651	1.8535
D000023776	G02	h104_Ch_g210_1_228	-	281	-	2
D000023777	G03	H10407_SANG_CHROM0_567_1_783	hypothetical protein	836	-	1.8983
D000023779	G04	h104_Ch_g646_1_228	-	281	-	2
D000023781	G05	H10407_SANG_CHROM2_966_1_783	putative short chain dehydrogenase	836	CBJ02466	1.8959
D000023783	G06	h104_P666_g19_1_228	hypothetical protein	281	-	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023785	G07	H10407_SANG_CHROM3 942_1_783	-	836	-	-
D000023787	G08	H10407_SANG_CHROM1 196_1_231	putative prophage protein	284	CBJ00703	-
D000023789	G09	H10407_SANG_CHROM2 847_1_789	hypothetical protein	842	-	3.7399
D000023792	G10	H10407_SANG_CHROM2 622_1_231	putative transmembrane anchored protein	284	CBJ02128	-
D000023793	G11	H10407_SANG_CHROM0 163_1_792	methionine aminopeptidase	845	CBI99664	1.8213
D000023795	G12	h104_Ch_g265_1_234	predicted transposase, pseudogene	287	-	2
D000023797	H01	H10407_SANG_CHROM0 464_70_882	nucleoside-specific channel-forming protein	869	CBI99969	1.8113
D000023799	H02	H10407_SANG_CHROM0 351_433_666	putative fimbrial protein	290	CBI99856	3.2457
D000023801	H03	H10407_SANG_CHROM1 690_1_813	putative exported protein	866	-	1.888
D000023803	H04	H10407_SANG_CHROM0 360_1_234	putative exported protein	287	-	2
D000023805	H05	H10407_SANG_CHROM2 618_1_813	phage tail-fibre protein	866	CBJ02124	1.4781
D000023807	H06	H10407_SANG_CHROM1 109_1_234	putative fimbrial protein	287	CBJ00616	1.9861
D000023811	H08	H10407_SANG_CHROM1 710_1_234	-	287	-	2
D000023813	H09	H10407_SANG_CHROM3 576_1_813	probable general secretion pathway protein D precursor	866	CBJ03078	4.0382

Table 8: Enterotoxigenic *E. coli* Expression Clone Set, Plate 8 (EEXAH), NR-19797¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023819	A02	H10407_SANG_CHROM4 281_1_240	hypothetical protein	293	-	2
D000023821	A03	H10407_SANG_p948.0560 _1_816	hypothetical protein	869	-	1.9574
D000023823	A04	h104_Ch_g54_1_243	hypothetical protein	296	-	1.8615
D000023825	A05	H10407_SANG_CHROM0 056_1_819	hypothetical protein	872	-	1.9163
D000023827	A06	h104_Ch_g637_1_243	hypothetical protein	296	-	2
D000023829	A07	H10407_SANG_CHROM1 632_1_819	putative protease	872	CBJ01135	1.9278
D000023831	A08	H10407_SANG_CHROM2 010_1_243	putative phage P2 gpv family protein	296	CBJ01513	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023833	A09	H10407_SANG_CHROM2_468_1_819	hypothetical protein	872	-	1.9037
D000023835	A10	h104_Ch_g650_1_246	hypothetical protein	299	-	2
D000023837	A11	H10407_SANG_p52.0003_1_822	hypothetical protein	875	-	1.7657
D000023840	A12	h104_P948_g17_1_246	hypothetical protein	299	-	2
D000023841	B01	H10407_SANG_CHROM0_232_1_825	putative transposase	878	CBI99731	1.8314
D000023843	B02	H10407_SANG_CHROM0_608_1_246	putative membrane protein	299	CBJ00114	2
D000023845	B03	H10407_SANG_CHROM0_308_1_825	putative tail fiber/collar phage protein	878	CBI99812	1.9066
D000023847	B04	H10407_SANG_CHROM1_827_1_246	putative transglycosylase associated protein	299	CBJ01331	1.9632
D000023849	B05	H10407_SANG_CHROM1_246_1_834	putative phage tail protein	887	CBJ00750	3.4848
D000023851	B06	h104_Ch_g1038_1_249	KpLE2 phage-like element; predicted frameshift suppressor	302	CBJ04129	2
D000023854	B07	H10407_SANG_CHROM2_008_1_834	phage-related tail fiber protein, pseudogene	887	-	4.0507
D000023855	B08	h104_Ch_g146_1_249	-	302	-	1.7781
D000023857	B09	H10407_SANG_CHROM3_502_97_930	p-hydroxybenzoic acid efflux pump subunit A	890	CBJ03003	1.8955
D000023859	B10	h104_Ch_g542_1_249	putative phage DNA polymerase	302	CBJ02271	2
D000023862	B11	H10407_SANG_p948.1100_1_837	hypothetical protein	890	-	2.4456
D000023865	C01	H10407_SANG_CHROM3_869_139_993	UDP-D-glucose:(galactosyl) lipopolysaccharide glucosyltransferase	911	CBJ03376	1.8946
D000023868	C02	h104_Ch_g200_1_255	hypothetical protein	308	-	2
D000023869	C03	H10407_SANG_CHROM2_580_1_861	putative peptidase	914	CBJ02084	1.3195
D000023872	C04	h104_Ch_g635_1_255	iron(III) dicitrate transport system,ATP-binding protein	308	CBJ02666	2
D000023873	C05	H10407_SANG_CHROM2_784_91_954	sigma-E factor regulatory protein	920	CBJ02288	1.9315
D000023876	C06	H10407_SANG_CHROM1_177_1_255	putative exported protein	308	CBJ00684	2
D000023877	C07	H10407_SANG_CHROM3_904_1_864	virulence associated protein	917	CBJ03411	2.6172

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023879	C08	H10407_SANG_CHROM3_995_1_255	ribonuclease P protein component	308	CBJ03498	1.9935
D000023881	C09	H10407_SANG_CHROM3_904_865_1731	virulence associated protein	923	CBJ03411	1.8884
D000023883	C10	h104_Ch_g96_1_258	putative RHS repeat protein	311	CBJ00101	2
D000023885	C11	H10407_SANG_CHROM4_099_1_867	phospholipase A1 (detergent resistant phospholipase A)	920	CBJ03603	1.787
D000023887	C12	H10407_SANG_CHROM0_275_1_258	conserved hypothetical protein	311	CBI99775	2
D000023889	D01	H10407_SANG_CHROM1_638_70_942	putative exported protein	929	CBJ01141	1.8213
D000023892	D02	H10407_SANG_CHROM0_869_1_258	putative exported protein	311	CBJ00378	2
D000023893	D03	H10407_SANG_CHROM2_770_1_882	hypothetical protein	935	-	1.5561
D000023895	D04	H10407_SANG_CHROM0_873_1_258	putative exported protein	311	CBJ00382	1.9132
D000023899	D06	H10407_SANG_CHROM2_018_1_258	DNA-binding transcriptional regulator prophage remnant	311	CBJ01521	1.9453
D000023901	D07	H10407_SANG_CHROM3_430_1_882	TPR repeat lipoprotein	935	CBJ02931	1.9251
D000023903	D08	H10407_SANG_CHROM3_158_1_258	transposase	311	CBJ02659	1.9775
D000023907	D10	H10407_SANG_p666.0790_1_258	hypothetical protein	311	-	2
D000023913	E01	H10407_SANG_CHROM4_632_1_900	minor component of type 1 fimbriae	953	CBJ04141	1.7681
D000023915	E02	H10407_SANG_CHROM1_674_67_327	putative lipoprotein	317	CBJ01178	2
D000023917	E03	H10407_SANG_CHROM1_571_1_912	fimbrial adhesin	965	CBJ01075	2.9461
D000023921	E05	H10407_SANG_CHROM3_638_373_1284	DamX protein	968	CBJ03140	1.813
D000023923	E06	H10407_SANG_CHROM0_259_1_264	hypothetical protein	317	CBI99759	1.9937
D000023925	E07	H10407_SANG_CHROM0_862_79_996	ABC transporter, permease protein	974	CBJ00369	1.8634
D000023927	E08	H10407_SANG_CHROM1_453_1_264	conserved hypothetical protein	317	CBJ00956	2
D000023929	E09	H10407_SANG_CHROM0_825_1_927	conserved hypothetical protein	980	CBJ00335	1.8214
D000023931	E10	H10407_SANG_CHROM1_578_1_264	putative HipB DNA-binding transcriptional regulator	317	CBJ01082	2
D000023933	E11	H10407_SANG_CHROM2_771_1_927	putative phage protein	980	CBJ02275	1.702
D000023935	E12	H10407_SANG_CHROM3_299_1_264	putative IS element protein	317	CBJ02799	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023937	F01	H10407_SANG_CHROM1 432_1_930	conserved hypothetical protein	983	CBJ00935	1.708
D000023939	F02	h104_Ch_g1031_1_267	isppu9, transposase	320	CBJ04127	1.9938
D000023943	F04	h104_Ch_g1062_271_537	Phage DNA packaging protein	323	CBJ04209	1.7988
D000023945	F05	H10407_SANG_p666.0570 _1_936	-	989	-	1.6545
D000023948	F06	h104_Ch_g306_1_267	putative electron transfer flavoprotein beta subunit	320	CBJ01234	1.9094
D000023950	F07	H10407_SANG_CHROM2 301_1_939	conserved hypothetical protein	992	CBJ01804	1.7964
D000023952	F08	h104_Ch_g420_1_267	putative flippase (Putative export protein)	320	CBJ01692	1.9
D000023953	F09	H10407_SANG_CHROM2 746_1_939	putative phage protein	992	CBJ02249	1.7651
D000023956	F10	H10407_SANG_p948.0600 _1_267	-	320	-	1.9938
D000023958	F11	H10407_SANG_CHROM4 319_1_939	putative phage O protein	992	CBI99778	4.125
D000023959	F12	h104_Ch_g353_1_270	conserved hypothetical protein	323	CBJ01446	2
D000023962	G01	H10407_SANG_CHROM2 599_520_1461	putative peptidase	998	CBJ02103	1.6202
D000023963	G02	H10407_SANG_CHROM2 799_1_270	conserved hypothetical protein	323	CBJ02303	2
D000023965	G03	H10407_SANG_CHROM2 058_127_1071	cellulose synthesis regulatory protein (signal transduction protein)	1001	CBJ01561	3.4276
D000023967	G04	H10407_SANG_CHROM2 823_70_339	putative outer membrane assembly lipoprotein	326	CBJ02327	1.9448
D000023970	G05	H10407_SANG_CHROM3 161_1_951	RNA polymerase sigma factor	1004	CBJ02660	1.7799
D000023972	G06	H10407_SANG_CHROM2 855_1_270	putative alpha-amylase precursor, pseudogene	323	-	2
D000023973	G07	H10407_SANG_CHROM1 542_1_954	putative LRR repeat protein	1007	CBJ01046	2.9722
D000023975	G08	H10407_SANG_CHROM0 776A_1_273	transposase	326	CBJ00281	1.7883
D000023977	G09	H10407_SANG_CHROM2 180_1_957	putative UDP-D-galactose:(glucosyl) lipopolysaccharide-1,6-D-galactosyl-transferase	1010	CBJ01682	3.303
D000023980	G10	H10407_SANG_CHROM0 852_1_273	insertion element is1 protein InsA	326	CBJ00361	1.9939
D000023982	G11	H10407_SANG_CHROM4 520_301_1257	HflK protein	1013	CBJ04029	1.617

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000023983	G12	H10407_SANG_CHROM1 122A_1_273	-	326	-	3.2055
D000023986	H01	H10407_SANG_p666.0550 1_960	-	1013	-	3.1718
D000023988	H02	H10407_SANG_CHROM4 446_1_273	transposase	326	CBJ00629	2
D000023989	H03	H10407_SANG_CHROM2 246_70_1032	putative fimbrial adhesin	1019	CBJ01750	1.7174
D000023991	H04	H10407_SANG_p666.0620 1_273	putative insertion element	326	-	3.2178
D000023994	H05	H10407_SANG_CHROM1 523_94_1059	possible exported protein	1022	CBJ01027	3.2466
D000023995	H06	H10407_SANG_CHROM3 258_1_276	conserved hypothetical protein	329	CBJ02759	1.8841
D000023997	H07	H10407_SANG_CHROM4 509_1_966	phosphatidylserine decarboxylase proenzyme	1019	CBJ04018	1.6889
D000023999	H08	h104_Ch_g980_1_279	conserved hypothetical protein	332	-	2
D000024001	H09	H10407_SANG_CHROM2 407_1_969	putative peptidase	1022	CBJ01911	1.6781
D000024003	H10	H10407_SANG_CHROM2 113_1_279	hypothetical protein	332	CBJ01615	2

Table 9: Enterotoxigenic *E. coli* Expression Clone Set, Plate 9 (EEXAI), NR-19798¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024007	A02	H10407_SANG_CHROM2 250_1_279	putative exported protein	332	CBJ01754	2
D000024009	A03	H10407_SANG_CHROM0 673_1_975	conserved hypothetical protein	1028	CBJ00180	1.5856
D000024011	A04	H10407_SANG_CHROM3 792b_1_279	putative lipase 1 precursor (triacylglycerol lipase), pseudogene	332	PSEUDO:CBJ032 94	2
D000024013	A05	H10407_SANG_CHROM4 621_1_978	putative prophage protein	1031	CBJ04130	2.9699
D000024015	A06	H10407_SANG_CHROM3 272_1_285	conserved hypothetical protein	338	CBJ02773	2
D000024018	A07	H10407_SANG_CHROM3 372_1_984	putative glutathione S- transferase	1037	CBJ02872	1.5796
D000024019	A08	H10407_SANG_CHROM1 136_1_291	negative regulator of flagellin synthesis (anti-sigma factor)	344	CBJ00644	2
D000024022	A09	H10407_SANG_CHROM0 264_67_1053	outer membrane pore protein E	1043	CBI99764	1.6222
D000024023	A10	H10407_SANG_CHROM3 386_1_294	tdc operon trans- criptional activator	347	CBJ02886	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024027	A12	h104_Ch_g1026_1_300	KpLE2 phage-like element; predicted protein	353	CBJ04122	2
D000024029	B01	H10407_SANG_CHROM0_330_1_990	putative DNA transfer protein	1043	CBI99834	1.4708
D000024032	B02	h104_Ch_g520_1_300	putative transmembrane anchored protein	353	CBJ02128	2
D000024035	B04	H10407_SANG_CHROM1_286_610_909	haemolysin/cytolysin A	356	CBJ00789	2
D000024040	B06	H10407_SANG_CHROM1_056_1_303	predicted transmembrane protein	356	CBJ00565	2
D000024042	B07	H10407_SANG_CHROM2_372_79_1074	glycerophosphoryl diester phosphodiesterase	1052	CBJ01876	1.5504
D000024043	B08	H10407_SANG_CHROM2_481_1_306	lipoprotein	359	CBJ01985	2
D000024046	B09	H10407_SANG_CHROM2_737_982_1986	putative lytic transglycosylase, catalytic	1061	CBJ02242	1.6098
D000024047	B10	H10407_SANG_CHROM4_518_1_306	host factor-I protein (HF-I)	359	CBJ04027	2
D000024050	B11	h104_Ch_g978_1_1011	conserved hypothetical protein	1064	CBJ03965	4.657
D000024051	B12	H10407_SANG_CHROM0_328_1_309	putative prophage protein	362	CBI99830	2
D000024053	C01	H10407_SANG_CHROM2_673_1_1011	putative regulatory protein	1064	CBJ02179	1.4981
D000024055	C02	H10407_SANG_CHROM2_646_1_312	hypothetical phage protein	365	CBJ02151	2
D000024059	C04	h104_Ch_g639_1_315	putative lipoprotein	368	CBJ02668	2
D000024062	C05	H10407_SANG_CHROM3_903_661_1671	predicted hydrolase	1067	CBJ03410	4.7657
D000024065	C07	H10407_SANG_CHROM1_272_1_1014	putative AidA-I adhesin-like protein, pseudogene	1067	PSEUDO:CBJ00776	1.4864
D000024068	C08	H10407_SANG_CHROM1_282_82_399	putative exported protein	374	CBJ00785	2
D000024069	C09	H10407_SANG_CHROM0_997_70_1086	outer membrane protein F	1073	CBJ00505	3.8639
D000024071	C10	H10407_SANG_CHROM4_332_1_318	hypothetical phage protein	371	CBJ03838	2
D000024073	C11	H10407_SANG_CHROM2_892_67_1083	membrane-bound lytic transglycosylase B	1073	CBJ02392	1.3868
D000024075	C12	H10407_SANG_CHROM1_934_1_321	conserved hypothetical protein	374	CBJ01439	2
D000024078	D01	H10407_SANG_CHROM0_806_73_1095	outer membrane porin protein	1079	CBJ00316	1.5273
D000024079	D02	h104_Ch_g804_1_324	integrase	377	CBJ03406	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024081	D03	H10407_SANG_CHROM2 349_67_1101	outer membrane protein C	1091	CBJ01853	1.4308
D000024083	D04	H10407_SANG_CHROM2 520_67_390	conserved hypothetical protein	380	CBJ02024	2
D000024085	D05	H10407_SANG_CHROM2 944_1_1035	-	1088	-	-
D000024090	D07	H10407_SANG_CHROM1 649_226_1263	putative exported protein	1094	CBJ01152	1.4369
D000024091	D08	H10407_SANG_CHROM0 347_1_327	conserved hypothetical protein	380	CBI99852	2
D000024093	D09	H10407_SANG_CHROM3 275_1_1038	putative aldo/keto reductase	1091	CBJ02775	1.4519
D000024095	D10	H10407_SANG_CHROM3 239_82_408	type II secretion system lipoprotein	383	CBJ02739	2
D000024098	D11	H10407_SANG_CHROM2 066_67_1113	outer membrane protein	1103	CBJ01569	4.6872
D000024103	E02	H10407_SANG_CHROM1 224_1_330	head decoration protein (major capsid protein)	383	CBJ04213	3.1958
D000024106	E03	H10407_SANG_CHROM2 487_106_1161	EmrKY-TolC multidrug resistance efflux pump, membrane fusion protein component	1112	CBJ01991	1.3534
D000024107	E04	H10407_SANG_CHROM2 223_1_330	conserved hypothetical protein	383	CBJ01726	2
D000024111	E06	H10407_SANG_CHROM4 707_1_330	putative head-DNA stabilization phage protein	383	CBJ00729	3.2063
D000024113	E07	H10407_SANG_CHROM2 734_1_1062	putative phage related protein	1115	CBJ02239	1.4942
D000024115	E08	h104_Ch_g641_1_333	LacI-family transcriptional regulator	386	CBJ02686	2
D000024118	E09	H10407_SANG_CHROM3 319_1_1062	conserved hypothetical protein	1115	CBJ02819	1.5381
D000024119	E10	h104_Ch_g820_1_333	putative radC-like protein	386	CBJ03451	2
D000024122	E11	H10407_SANG_CHROM1 052_73_1137	phosphotyrosine-protein phosphatase	1121	CBJ00560	1.4451
D000024123	E12	H10407_SANG_CHROM0 277_1_336	hypothetical phage protein	389	CBJ03823	3.1979
D000024126	F01	H10407_SANG_CHROM1 451_67_1131	outer membrane protein N (porin)	1121	CBJ00954	1.4362
D000024127	F02	H10407_SANG_CHROM4 318_1_336	e14 prophage; predicted DNA-binding transcriptional regulator	389	CBI99776	3.1414
D000024129	F03	H10407_SANG_CHROM2 205_73_1137	putative polysaccharide export protein	1121	CBJ01708	1.4567
D000024131	F04	h104_Ch_g652_1_342	-	395	-	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024133	F05	H10407_SANG_CHROM4 168_1_1068	predicted endo-1,4- beta-glucanase	1121	CBJ03673	3.8519
D000024136	F06	H10407_SANG_CHROM0 152_1_342	conserved hypothetical protein	395	CBI99653	2
D000024138	F07	H10407_SANG_CHROM3 153_1_1077	-	1130	-	2
D000024139	F08	H10407_SANG_CHROM2 318_1_342	conserved hypothetical protein	395	CBJ01822	2
D000024141	F09	H10407_SANG_CHROM0 882_502_1581	putative membrane protein	1136	CBJ00391	1.4076
D000024143	F10	H10407_SANG_CHROM3 915_1_345	putative trans- membrane protein	398	CBJ03422	2
D000024146	F11	H10407_SANG_CHROM2 504_1_1083	aminopeptidase	1136	CBJ02008	4.6056
D000024147	F12	H10407_SANG_CHROM1 974_1_348	conserved hypothetical protein	401	CBJ01477	2
D000024151	G02	h104_Ch_g912_1_351	50S ribosomal subunit protein L7/L12	404	CBJ03750	2
D000024153	G03	H10407_SANG_CHROM0 661_1_1086	rare lipoprotein A	1139	CBJ00168	1.4276
D000024155	G04	H10407_SANG_CHROM2 729_1_351	putative phage related protein	404	CBJ02234	2
D000024157	G05	H10407_SANG_CHROM3 412_1_1089	predicted fimbrial-like adhesin prot	1142	CBJ02913	1.3862
D000024159	G06	H10407_SANG_CHROM4 491_1_351	putative lipoprotein	404	CBJ04000	2
D000024161	G07	H10407_SANG_CHROM3 003_1_1095	membrane-bound lytic murein transglycosylase A	1148	CBJ02505	4.5218
D000024163	G08	h104_Ch_g945_1_354	-	407	-	2
D000024165	G09	H10407_SANG_CHROM3 777_1_1104	cellulose synthase operon protein C (TPR-repeat- containing protein)	1157	CBJ03277	1.3319
D000024167	G10	h104_P948_g14_1_357	-	410	-	2
D000024169	G11	H10407_SANG_CHROM4 622_1_1104	putative exported protein	1157	CBJ04131	1.2904
D000024171	G12	h104_P948_g8_1_357	-	410	-	2
D000024174	H01	H10407_SANG_CHROM2 669_70_1176	putative dehydrogenase	1163	CBJ02175	1.2846
D000024175	H02	H10407_SANG_CHROM2 047_106_462	flagellar protein FliL	413	CBJ01550	2
D000024177	H03	H10407_SANG_CHROM4 612_1_1113	putative sulfatase	1166	CBJ04121	3.7161
D000024179	H04	h104_Ch_g1065_1_360	Phage DNA packaging protein	413	CBJ04209	2
D000024182	H05	H10407_SANG_CHROM2 203_163_1278	tyrosine-protein kinase	1172	CBJ01706	1.4283
D000024184	H06	H10407_SANG_CHROM2 625_1_363	hypothetical phage protein	416	CBJ02131	2

D000024186	H07	H10407_SANG_CHROM0 515_70_1191	acriflavin resistance protein A precursor	1178	CBJ00019	1.4329
D000024188	H08	H10407_SANG_CHROM2 809_1_363	putative lipoprotein	416	CBJ02313	2
D000024190	H09	H10407_SANG_CHROM1 836_1_1125	ribonuclease D	1178	CBJ01340	1.3591
D000024191	H10	H10407_SANG_p666.0340 1_363	-	416	-	2
D000024193	H11	H10407_SANG_p948.0890 _76_1200	-	1181	-	1.2752

Table 10: Enterotoxigenic *E. coli* Expression Clone Set, Plate 10 (EEXAJ), NR-19799¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024195	A02	H10407_SANG_CHROM1 281_1_366	conserved hypothetical protein	419	CBJ00784	2
D000024197	A03	H10407_SANG_CHROM3 439_490_1623	putative membrane- associated sulfatase	1190	CBJ02940	1.4310924 37
D000024200	A04	H10407_SANG_CHROM3 367_1_366	putative exported protein	419	CBJ02867	2
D000024203	A06	H10407_SANG_CHROM3 694_70_438	conserved hypothetical protein	425	CBJ03195	2
D000024206	A07	H10407_SANG_CHROM2 933_1_1137	-	1190	-	3
D000024207	A08	H10407_SANG_CHROM3 907_1_372	heat resistant agglutinin 1	425	CBJ03414	2
D000024211	A10	H10407_SANG_CHROM3 907_373_744	heat resistant agglutinin 1	425	CBJ03414	2
D000024213	A11	H10407_SANG_CHROM1 567_1_1155	putative arylsulfatase- activating protein	1208	CBJ01071	4.4147350 99
D000024215	A12	H10407_SANG_CHROM3 582_1_375	putative general secretion pathway protein H precursor (protein transport protein HofH)	428	CBJ03082	2
D000024217	B01	H10407_SANG_CHROM3 856_103_1257	putative peptidase	1211	CBJ03363	1.3443435 18
D000024220	B02	H10407_SANG_CHROM0 757_1_378	putative exported protein	431	CBJ00265	3.1666666 67
D000024222	B03	H10407_SANG_CHROM2 217_79_1245	multidrug resistance protein	1223	CBJ01720	1.4186426 82
D000024223	B04	H10407_SANG_CHROM2 836_1_384	putative lipoprotein	437	CBJ02340	2
D000024226	B05	H10407_SANG_CHROM4 641_1_1170	isoaspartyl dipeptidase	1223	CBJ04150	1.4603434 18
D000024227	B06	H10407_SANG_CHROM4 328_1_384	phage membrane protein	437	CBJ03834	2
D000024229	B07	H10407_SANG_CHROM1 946_1_1176	putative restriction endonuclease	1229	CBJ01451	1.4296175 75
D000024231	B08	H10407_SANG_CHROM3 168_1_387	putative lipoprotein	440	CBJ02668	2
D000024233	B09	H10407_SANG_CHROM3 690_1_1176	conserved protein	1229	CBJ03192	1.3702196 91

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024235	B10	H10407_SANG_p666.0660_1_387	-	440	-	2
D000024237	B11	H10407_SANG_CHROM3_389_1_1185	conserved hypothetical protein	1238	CBJ02889	1.282714055
D000024241	C01	H10407_SANG_CHROM4_010_1_1194	predicted xylanase	1247	CBJ03514	1.349639134
D000024243	C02	h104_Ch_g55_1_390	-	443	-	2
D000024246	C03	H10407_SANG_CHROM2_728_1_1197	putative phage related protein	1250	CBJ02232	1.4112
D000024247	C04	H10407_SANG_CHROM1_213_1_390	putative phage protein	443	CBJ00718	2
D000024249	C05	H10407_SANG_CHROM1_889_121_1320	putative peptidoglycan-binding peptidase	1256	CBJ01394	1.362261147
D000024252	C06	H10407_SANG_CHROM1_997_1_390	putative phage tail X family protein	443	CBJ01498	2
D000024253	C07	H10407_SANG_CHROM1_141_1_1206	flagellar hook protein FlgE	1259	CBJ00649	1.260524226
D000024255	C08	H10407_SANG_CHROM2_839_1_390	conserved hypothetical protein	443	CBJ02343	2
D000024258	C09	H10407_SANG_CHROM3_066_1_1209	putative peptidase	1262	CBJ02568	1.375594295
D000024259	C10	H10407_SANG_CHROM0_821_1_393	putative phage protein	446	CBJ00331	2
D000024261	C11	H10407_SANG_CHROM3_751_1_1221	conserved hypothetical protein	1274	CBJ03252	1.238618524
D000024263	C12	H10407_SANG_CHROM3_988_1_396	conserved hypothetical protein	449	CBJ03492	2
D000024266	D01	H10407_SANG_CHROM4_223_511_1731	putative membrane protein	1277	CBJ03728	1.294440094
D000024267	D02	h104_Ch_g1030_1_399	isppu9, transposase	452	CBJ04127	2
D000024270	D03	H10407_SANG_CHROM0_126_1_1227	putative polysaccharide deacetylase	1280	CBI99627	1.37265625
D000024271	D04	h104_Ch_g533_1_399	-	452	-	2
D000024273	D05	H10407_SANG_CHROM3_185_1_1227	putative short chain dehydrogenase	1280	CBJ02684	1.20625
D000024275	D06	H10407_SANG_CHROM0_321_1_399	putative prophage protein	452	CBI99823	2
D000024278	D07	H10407_SANG_CHROM1_699_1_1254	conserved hypothetical protein	1307	CBJ01203	3.725325172
D000024279	D08	H10407_SANG_CHROM0_012_1_402	conserved hypothetical protein	455	CBI99513	2
D000024282	D09	H10407_SANG_CHROM2_479_88_1344	long-chain fatty acid transport protein	1313	CBJ01983	1.324447829
D000024283	D10	H10407_SANG_CHROM1_972_1_402	putative phage protein	455	CBJ01475	2
D000024286	D11	H10407_SANG_CHROM4_291_79_1338	maltoporin (maltose-inducible porin)	1316	CBJ03797	4.382218845
D000024290	E01	H10407_SANG_CHROM4_515_76_1335	N-acetylmuramoyl-L-alanine amidase	1316	CBJ04024	1.260638298

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024292	E02	H10407_SANG_CHROM3 796_253_657	putative outer membrane protein	461	CBJ03298	2
D000024293	E03	H10407_SANG_CHROM0 779_1_1281	acyl-CoA thioester hydrolase	1334	CBJ00288	4.1851574 21
D000024295	E04	H10407_SANG_CHROM4 718_2173_2577	hypothetical protein	461	-	1.7093275 49
D000024297	E05	H10407_SANG_CHROM4 376_1_1290	pentapeptide repeat protein	1343	CBJ03883	4.4475055 85
D000024300	E06	H10407_SANG_CHROM1 810_1_411	peptide methionine sulfoxide reductase	464	CBJ01314	2
D000024301	E07	H10407_SANG_CHROM0 750_1_1296	protein tola	1349	CBJ00258	4.0630096 37
D000024303	E08	H10407_SANG_CHROM1 103_1_414	curli production assembly/transport component	467	CBJ00611	2
D000024306	E09	H10407_SANG_CHROM2 841_1_1302	putative tyrosine recombinase	1355	CBJ02344	1.2966789 67
D000024307	E10	H10407_SANG_CHROM1 135_1_414	flagella synthesis protein FlgN	467	CBJ00643	2
D000024311	E12	H10407_SANG_CHROM1 287_1_417	SOS mutagenesis and repair protein	470	CBJ00791	2
D000024314	F01	H10407_SANG_CHROM3 101_1_1323	hypothetical protein	1376	-	1.1729651 16
D000024315	F02	H10407_SANG_CHROM4 262_1_417	zinc resistance-associated protein	470	CBJ03767	2
D000024317	F03	H10407_SANG_CHROM4 464_160_1482	conserved hypothetical protein	1379	CBJ03973	4.3168963 02
D000024319	F04	H10407_SANG_CHROM2 745_1_423	putative phage protein	476	CBJ02249	2
D000024322	F05	H10407_SANG_CHROM0 698_79_1404	putative exported protein	1379	CBJ00205	3.9528643 94
D000024324	F06	H10407_SANG_CHROM3 036_1_423	conserved hypothetical protein	476	CBJ02538	2
D000024326	F07	H10407_SANG_CHROM4 122_1_1329	hypothetical protein	1382	-	4.3907380 61
D000024327	F08	H10407_SANG_CHROM0 881_88_513	outer membrane protein X	482	CBJ00390	2
D000024331	F10	H10407_SANG_CHROM2 969_1_426	conserved hypothetical protein	482	-	1.8464730 29
D000024333	F11	H10407_SANG_CHROM0 201_1_1356	membrane-bound lytic murein transglycosylase D precursor	1409	CBI99702	4.2640170 33
D000024335	F12	H10407_SANG_CHROM0 237_1_432	putative copper-binding protein PcoE precursor	485	CBI99737	2
D000024337	G01	H10407_SANG_CHROM3 175_1_1356	hypothetical protein	1409	-	3.6195883 61
D000024340	G02	H10407_SANG_CHROM2 633_1_435	hypothetical phage protein	488	CBJ02139	2
D000024341	G03	H10407_SANG_CHROM3 495_1_1365	protease	1418	CBJ02996	4.3596614 95

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024344	G04	H10407_SANG_CHROM0104_1_438	prepilin peptidase dependent protein D precursor	491	CBI99605	2
D000024346	G05	H10407_SANG_CHROM2033_1_1410	putative flagellar hook-associated protein 2	1463	CBJ01536	3.56937799
D000024347	G06	H10407_SANG_CHROM0932_76_513	probable lipoprotein	494	CBJ00441	2
D000024350	G07	H10407_SANG_CHROM0157_1_1422	putative protease Do precursor	1475	CBI99658	4.315254237
D000024351	G08	H10407_SANG_CHROM2739_1_438	putative phage related protein	491	CBJ02244	2
D000024353	G09	H10407_SANG_CHROM2907_1_1422	6-phospho-beta-glucosidase	1475	CBJ02407	4.181694915
D000024355	G10	h104_Ch_g66_1_444	methylisocitrate lyase	497	CBI99893	1.327967807
D000024357	G11	H10407_SANG_CHROM3094_1_1437	6-phospho-beta-glucosidase	1490	CBJ02596	4.059731544
D000024359	G12	H10407_SANG_CHROM0227_1_447	probable copper-binding protein PcoE precursor	500	CBI99727	2
D000024364	H02	H10407_SANG_CHROM1013_67_513	fimbrial protein	503	CBJ00522	2
D000024366	H03	h104_Ch_g511_1_1452	hypothetical protein	1505	CBJ02120	4.176079734
D000024367	H04	H10407_SANG_CHROM1867_118_564	putative membrane protein	503	CBJ01371	2
D000024370	H05	H10407_SANG_CHROM0260_1_1455	aminoacyl-histidine dipeptidase	1508	CBI99760	3.553050398
D000024372	H06	H10407_SANG_CHROM0752_70_519	peptidoglycan-associated lipoprotein	506	CBJ00260	2
D000024374	H07	H10407_SANG_CHROM2032_1_1461	putative flagellin	1514	CBJ01535	4.266182299
D000024376	H08	H10407_SANG_CHROM1106_1_453	minor curlin subunit	506	CBJ00614	2
D000024378	H09	H10407_SANG_CHROM2088_1_1467	putative invasins/adhesin protein	1520	CBJ01591	4.157236842
D000024379	H10	H10407_SANG_CHROM1107_1_453	major curlin subunit	506	CBJ00615	2

Table 11: Enterotoxigenic *E. coli* Expression Clone Set, Plate 11 (EEXAK), NR-19800¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024383	A02	H10407_SANG_CHROM3219_1_453	putative exported protein	506	CBJ02718	2
D000024385	A03	H10407_SANG_CHROM1716_1_1485	component of SufB-SufC-SufD cysteine desulfurase activator complex	1538	CBJ01220	4.1749

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024387	A04	H10407_SANG_CHROM4 460_1_453	conserved hypothetical protein	506	CBJ03969	2
D000024392	A06	H10407_SANG_CHROM3 458_94_549	putative organic solvent tolerance protein	512	CBJ02959	2
D000024395	A08	H10407_SANG_CHROM0 301_70_528	conserved hypothetical exported protein	515	CBI99805	2
D000024397	A09	h104_Ch_g372_1_1488	putative flagellar hook-associated protein 2	1541	CBJ01536	4.0247
D000024399	A10	H10407_SANG_CHROM0 596_1_459	conserved hypothetical protein	512	CBJ00102	2
D000024401	A11	H10407_SANG_CHROM3 773_1_1494	putative protease	1547	CBJ03274	3.735
D000024405	B01	H10407_SANG_CHROM4 606_1_1509	cytosol aminopeptidase	1562	CBJ04115	4.9802
D000024407	B02	H10407_SANG_CHROM1 573_79_537	putative fimbrial FimF precursor	515	CBJ01077	2
D000024409	B03	H10407_SANG_CHROM1 021_115_1638	paraquat-inducible protein B	1580	CBJ00530	5.0354
D000024411	B04	H10407_SANG_CHROM1 175_76_537	putative exported protein	518	CBJ00682	2
D000024413	B05	H10407_SANG_CHROM4 011_76_1614	carbohydrate-specific outer membrane porin, cryptic	1595	CBJ03515	5.015
D000024415	B06	H10407_SANG_CHROM2 384_76_540	putative exported protein	521	CBJ01888	2
D000024418	B07	H10407_SANG_p58.0005_1_1596	-	1649	-	4.51
D000024419	B08	H10407_SANG_CHROM2 089_1_474	putative invasins	527	CBJ01592	2
D000024421	B09	H10407_SANG_CHROM3 737_1_1605	conserved hypothetical protein	1658	CBJ03238	4.4047
D000024424	B10	H10407_SANG_CHROM2 125_1_474	conserved hypothetical protein	527	CBJ01628	2.1518
D000024425	B11	H10407_SANG_CHROM2 176_1_1620	putative polysaccharide biosynthesis protein	1673	CBJ01677	4.8201
D000024427	B12	H10407_SANG_CHROM3 947_1_474	-	527	-	2
D000024429	C01	H10407_SANG_CHROM3 736_1_1620	conserved hypothetical protein	1673	CBJ03237	4.5111
D000024431	C02	h104_Ch_g663_1_477	integral membrane protein	530	CBJ02717	2
D000024433	C03	H10407_SANG_CHROM3 896_79_1707	putative exported protein	1685	CBJ03403	4.9027
D000024435	C04	H10407_SANG_CHROM2 312_88_564	lipoprotein	533	CBJ01816	2
D000024438	C05	H10407_SANG_CHROM0 082_130_1764	peptidoglycan synthetase	1691	CBI99583	3.8729
D000024439	C06	H10407_SANG_CHROM2 848_1_480	conserved hypothetical protein	533	CBJ02352	1.3715

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024444	C08	H10407_SANG_CHROM0 651_76_558	subunit of palmitoyl transferase for Lipid A	539	CBJ00158	1.4453
D000024447	C10	H10407_SANG_CHROM1 576_1_483	putative outer membrane usher protein FimD precursor, pseudogene	536	PSEUDO:CBJ01080	2
D000024449	C11	H10407_SANG_CHROM4 080_1_1662	putative arylsulphatase, pseudogene	1715	PSEUDO:CBJ03584	4.1313
D000024451	C12	H10407_SANG_CHROM3 417_91_573	putative phospholipid-binding protein	539	CBJ02918	2
D000024453	D01	H10407_SANG_CHROM1 568_1_1680	putative sulfatase	1733	CBJ01072	4.8246
D000024455	D02	H10407_SANG_CHROM3 945_1_483	putative antirestriction protein	536	CBJ03450	2
D000024459	D04	H10407_SANG_p948.0490 1_483	-	536	-	2
D000024461	D05	H10407_SANG_CHROM2 406_1_1725	putative lipoprotein	1778	CBJ01910	4.8363
D000024463	D06	H10407_SANG_CHROM2 470_1_486	putative minor fimbrial subunit StfG	539	CBJ01973	2
D000024467	D08	h104_Ch_g207_1_489	putative minor capsid protein	542	CBJ04212	3.131
D000024469	D09	H10407_SANG_CHROM1 482_1_1755	conserved hypothetical protein	1808	CBJ00985	4.7373
D000024471	D10	H10407_SANG_CHROM3 038_1_489	type III secretion-associated chaperone	542	CBJ02540	2
D000024473	D11	H10407_SANG_CHROM2 489_1798_3591	putative hybrid sensory histidine kinase in two-component regulatory system	1850	CBJ01993	4.4497
D000024476	D12	H10407_SANG_CHROM1 076_1_492	putative flavin reductase (pyrimidine utilization protein F)	545	CBJ00585	2
D000024479	E02	H10407_SANG_CHROM2 342_1_492	NapD protein	545	CBJ01845	2
D000024481	E03	H10407_SANG_CHROM1 651_1_1809	glucuronide permease	1862	CBJ01153	4.6407
D000024483	E04	H10407_SANG_CHROM3 827_1_492	putative MltA-interacting MipA family protein precursor	545	CBJ03330	2
D000024485	E05	H10407_SANG_p948.0120 1_1809	-	1862	-	4.5951
D000024487	E06	H10407_SANG_CHROM4 662_1_492	putative glycoprotein/receptor	545	CBJ04171	2
D000024489	E07	H10407_SANG_CHROM2 314_1_1812	ABC transporter, substrate-binding protein	1865	CBJ01818	4.5174

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024491	E08	H10407_SANG_CHROM3 752_70_564	outer membrane lipoprotein	551	CBJ03253	2
D000024493	E09	H10407_SANG_CHROM0 456_1_1815	maltodextrin glucosidase	1868	CBI99961	4.3169
D000024495	E10	H10407_SANG_CHROM3 464_76_573	putative organic solvent tolerance protein	554	CBJ02965	2
D000024500	E12	H10407_SANG_CHROM1 838_79_579	putative lipoprotein	557	CBJ01342	2
D000024503	F02	H10407_SANG_CHROM2 471_1_510	putative minor fimbrial subunit StfF	563	CBJ01974	2
D000024505	F03	H10407_SANG_CHROM4 661_385_2289	phosphoglycerol transferase I (phosphatidylglycerol --membrane-oligosaccharide glycerophosphotransferase)	1961	CBJ04170	4.3422
D000024508	F04	H10407_SANG_p948.0400 1_510	-	563	-	2
D000024509	F05	H10407_SANG_CHROM4 747_1_1935	-	1988	-	2
D000024511	F06	H10407_SANG_CHROM0 587_1_513	fimbrial protein	566	CBJ00093	2
D000024516	F08	H10407_SANG_CHROM2 610_1_516	putative lipoprotein	569	CBJ02114	2
D000024520	F10	H10407_SANG_CHROM3 326_1_516	conserved hypothetical protein	569	CBJ02826	2
D000024521	F11	H10407_SANG_CHROM2 086_1_2019	pesticin/yersiniabactin TonB-dependent receptor	2072	CBJ01589	4.4773
D000024523	F12	H10407_SANG_CHROM1 197_1_522	putative prophage repressor	575	CBJ00704	2
D000024525	G01	H10407_SANG_CHROM4 284_76_2094	putative lipoprotein	2075	CBJ03790	4.1711
D000024527	G02	H10407_SANG_CHROM0 834_73_597	putative prophage-encoded outer membrane protein	581	CBJ00344	2
D000024531	G04	H10407_SANG_CHROM1 242_73_597	putative trans-membrane protein	581	CBJ00746	2
D000024535	G06	H10407_SANG_p666.0170 1_525	-	581	-	2
D000024539	G08	H10407_SANG_CHROM4 630_1_528	minor component of type 1 fimbriae	581	CBJ04139	2
D000024541	G09	H10407_SANG_p948.0020 1_2046	-	2099	-	4.99
D000024543	G10	H10407_SANG_CHROM4 369_1_534	single-stranded binding protein	587	CBJ03875	2
D000024546	G11	H10407_SANG_p948.0020 2047_4092	-	2102	-	4.8915
D000024548	G12	H10407_SANG_CHROM0 465_1_537	putative lipoprotein	590	CBI99970	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024551	H02	H10407_SANG_CHROM1_006_1_537	predicted fimbrial-like adhesin protein	590	CBJ00514	2
D000024555	H04	H10407_SANG_CHROM0_582_1_540	fimbrial protein (type-1A pilin)	593	CBJ00088	2
D000024559	H06	H10407_SANG_CHROM1_012_1_540	fimbrial protein	593	CBJ00521	2
D000024564	H08	H10407_SANG_CHROM1_313_82_621	outer-membrane lipoprotein	596	CBJ00815	2
D000024568	H10	H10407_SANG_CHROM2_627_1_540	hypothetical phage protein	593	CBJ02133	1.4418
D000024569	H11	H10407_SANG_CHROM0_146_106_2241	ferrichrome-iron TonB-dependent receptor	2192	CBI99647	4.5169

Table 12: Enterotoxigenic *E. coli* Expression Clone Set, Plate 12 (EEXAL), NR-19801¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024575	A04	H10407_SANG_CHROM4_307_1_540	hypothetical phage protein	593	CBJ03813	3.2305
D000024578	A05	H10407_SANG_CHROM0_872_103_2280	hypothetical protein	2234	-	-
D000024581	A07	H10407_SANG_CHROM3_162_115_2322	iron(III) dicitrate TonB-dependent receptor	2264	CBJ02662	2.4109
D000024583	A08	H10407_SANG_p948.0420_541_1080	hypothetical protein	596	-	3.2737
D000024587	A10	H10407_SANG_CHROM0_304_1_546	bacteriophage v tail protein	599	CBJ03856	4.2597
D000024595	B02	H10407_SANG_CHROM4_626_1_546	fimbrial protein	599	CBJ04135	3.2424
D000024597	B03	H10407_SANG_p948.0110_1_2307	hypothetical protein	2360	-	3.2126
D000024599	B04	H10407_SANG_CHROM1_403_1_555	transcriptional regulator of the polyamine metabolism genes	608	CBJ00906	3.2619
D000024601	B05	H10407_SANG_p948.0110_2308_4617	hypothetical protein	2366	-	5.8438
D000024603	B06	H10407_SANG_CHROM2_041_796_1350	flagellar M-ring protein	611	CBJ01544	4.2488
D000024605	B07	H10407_SANG_CHROM0_172_76_2430	hypothetical protein	2408	-	2
D000024607	B08	H10407_SANG_CHROM2_474_1_561	putative fimbria A protein precursor	614	CBJ01978	4.2553
D000024610	B09	H10407_SANG_CHROM2_005_1_2355	probable tail fiber protein (gph)	2408	CBJ01508	-
D000024611	B10	H10407_SANG_CHROM4_356_1_561	phage invertase	614	CBJ03862	4.2377
D000024617	C01	H10407_SANG_CHROM3_411_121_2514	putative outer membrane usher protein LpfC precursor	2450	CBJ02912	3.4698

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024619	C02	H10407_SANG_CHROM0 134_1_567	predicted fimbrial-like adhesin protein	620	CBI99635	4.2508
D000024624	C04	H10407_SANG_CHROM2 450_88_660	putative peptidoglycan-binding protein	629	CBJ01955	4.248
D000024627	C06	H10407_SANG_CHROM2 545_1_573	putative lipoprotein	626	CBJ02049	4.246
D000024631	C08	H10407_SANG_CHROM3 309_1_573	conserved hypothetical protein	626	CBJ02808	4.2396
D000024635	C10	H10407_SANG_CHROM2 073_73_648	putative exported protein	632	CBJ01576	4.2294
D000024639	C12	H10407_SANG_CHROM1 558_1_579	D-alanyl-D-alanine dipeptidase	632	CBJ01062	4.2452
D000024642	D01	H10407_SANG_CHROM1 008_94_2598	fimbrial outer membrane usher protein	2561	CBJ00516	4.261
D000024643	D02	H10407_SANG_CHROM1 691_1_579	superoxide dismutase [Fe]	632	CBJ01195	4.2215
D000024647	D04	H10407_SANG_CHROM2 001_1_579	putative tail completion phage protein	632	CBJ01503	2.9446
D000024649	D05	H10407_SANG_CHROM2 626_1_2508	hypothetical phage protein	2561	CBJ02131	3.8524
D000024651	D06	H10407_SANG_CHROM3 181_1_582	putative membrane protein	635	CBJ02680	3.5307
D000024654	D07	H10407_SANG_CHROM4 629_121_2634	fimbrial outer membrane usher protein	2570	CBJ04138	3.7283
D000024656	D08	H10407_SANG_CHROM0 352_1_585	putative fimbrial protein	638	CBI99857	4.2273
D000024660	D10	H10407_SANG_CHROM1 137_73_657	flagellar basal body P-ring protein	641	CBJ00645	4.2543
D000024661	D11	H10407_SANG_CHROM1 456_91_2637	putative exported protein	2603	CBJ00959	4.4867
D000024666	E01	H10407_SANG_CHROM2 473_88_2643	putative outer membrane fimbrial usher protein	2612	CBJ01977	-
D000024668	E02	H10407_SANG_CHROM0 132_1_594	predicted fimbrial-like adhesin protein	647	CBI99633	4.2287
D000024669	E03	H10407_SANG_CHROM0 135_1_2595	fimbrial outer membrane usher protein	2648	CBI99636	3.625
D000024672	E04	H10407_SANG_CHROM1 073_1_594	flavoprotein	647	CBJ00582	4.2303
D000024676	E06	H10407_SANG_CHROM2 854_1_594	putative alpha-amylase precursor, pseudogene	647	PSEUDO:CBJ02355	4.2427
D000024677	E07	H10407_SANG_CHROM0 427_1_2610	hypothetical protein	2663	-	2
D000024679	E08	H10407_SANG_CHROM4 155_1_597	phosphatase	650	CBJ03660	3.2462
D000024683	E10	H10407_SANG_CHROM0 309_1_600	putative tail fiber/collar phage protein	653	CBI99812	3.2205
D000024685	E11	H10407_SANG_CHROM2 119_160_2844	putative adhesin autotransporter	2741	CBJ01621	2.0921

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024689	F01	H10407_SANG_CHROM3_590_1_2691	putative glycosyl hydrolase, possible endochitinase	2744	CBJ03091	3.9796
D000024691	F02	H10407_SANG_CHROM0_133_1_603	predicted fimbrial-like adhesin protein	656	CBI99634	4.2141
D000024693	F03	H10407_SANG_CHROM1_564_88_2793	probable zinc protease	2762	CBJ01068	3.3049
D000024695	F04	H10407_SANG_CHROM0_374_1_603	ankyrin repeat protein	656	CBI99879	4.2009
D000024697	F05	H10407_SANG_CHROM1_306_142_2865	autotransporter (putative adhesin)	2780	CBJ00808	3.7737
D000024699	F06	H10407_SANG_CHROM2_630_1_603	hypothetical phage protein	656	CBJ02136	4.218
D000024703	F08	H10407_SANG_CHROM2_831_1_603	conserved hypothetical protein	656	CBJ02335	4.0046
D000024707	F10	H10407_SANG_p948.0080_1_603	transposase	656	CBJ00179	4.2546
D000024709	F11	H10407_SANG_CHROM0_591_82_2970	hypothetical protein	2945	-	-
D000024711	F12	H10407_SANG_p948.0080_604_1206	hypothetical protein	656	-	4.2135
D000024721	G05	H10407_SANG_CHROM0_400_1_3072	beta-galactosidase	3125	CBI99905	4.4309
D000024723	G06	H10407_SANG_CHROM1_014_94_708	fimbrial chaperone	671	CBJ00523	4.2126
D000024727	G08	H10407_SANG_CHROM1_980_1_615	conserved hypothetical protein	668	CBJ01483	4.2402
D000024729	G09	H10407_SANG_CHROM0_595_1027_4251	hypothetical protein	3281	-	2
D000024731	G10	H10407_SANG_CHROM4_144_73_690	porin	674	CBJ03649	3.5402

Table 13: Enterotoxigenic *E. coli* Expression Clone Set, Plate 13 (EEXAM), NR-19802¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024759	A02	EcB7A_2521	hypothetical protein EcB7A_2521	170	ZP_03031456	2
D000024761	A03	EcB7A_3485	endolysin	443	ZP_03030498	2
D000024763	A04	EcB7A_5260	hypothetical protein EcB7A_5260	170	ZP_03031430	2
D000024767	A06	b7a_C127_g1	putative transposase	260	CBJ01632	2
D000024769	A07	b7a_C12_g21	hypothetical protein	467	-	2
D000024771	A08	EcB7A_5176	hypothetical protein EcB7A_5176	260	ZP_03030884	2
D000024773	A09	EcB7A_5357	protein stbB	473	ZP_03031338	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024778	A11	b7a_C114_g3	conserved hypothetical protein	479	-	2
D000024782	B01	EcB7A_2545	conserved hypothetical protein	482	ZP_03029994	2
D000024783	B02	b7a_C155_g6	hypothetical protein	305	-	2
D000024785	B03	EcB7A_1649	PilM	488	ZP_03028091	2
D000024793	B07	b7a_C267_g1	putative pinE invertase/site-specific DNA recombinase [<i>Escherichia coli</i> ETEC H10407]	662	CBI99815	2
D000024796	B08	b7a_C75_g11	hypothetical protein	353	-	2
D000024797	B09	EcB7A_3472	hypothetical protein EcB7A_3472	713	ZP_03030157	2
D000024800	B10	b7a_C98_g1	putative transposase TnpA protein [<i>Escherichia coli</i> ETEC H10407]	371	CBI99738	3.216802168
D000024801	B11	b7a_C53_g5	putative phage protein [<i>Escherichia coli</i> ETEC H10407]	719	CBJ00752	2
D000024803	B12	EcB7A_2390	glycosyl hydrolase [<i>Escherichia coli</i> E24377A]	377	YP_001463450	3.217506631
D000024807	C02	b7a_C6_g8	hypothetical protein	386	-	2
D000024809	C03	EcB7A_4053	conserved hypothetical protein	758	ZP_03030453	2
D000024811	C04	b7a_C6_g14	hypothetical protein	389	-	2
D000024814	C05	EcB7A_3479	baseplate assembly protein J	947	ZP_03030499	1.488912355
D000024815	C06	b7a_C12_g38	hypothetical protein	404	-	1.440594059
D000024817	C07	EcB7A_0626	baseplate assembly protein GpJ	959	ZP_03031402	1.689259645
D000024820	C08	b7a_C34_g10	hypothetical protein	410	-	2
D000024821	C09	EcB7A_5246	conserved hypothetical protein	1121	ZP_03031253	4.801962533
D000024823	C10	b7a_C67_g6	hypothetical protein	425	-	2
D000024829	D01	EcB7A_4240	hypothetical protein	1466	-	3.660300136
D000024831	D02	EcB7A_4632	conserved hypothetical protein	428	ZP_03030837	2
D000024835	D04	b7a_C2_g15	hypothetical protein	443	-	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024839	D06	EcE24377A_0671	hypothetical protein EcE24377A_0671	224	YP_001461813	2
D000024841	D07	e24_Ch_g249	conserved hypothetical protein	464	ABV21012	2.574514039
D000024843	D08	e24_P73_g43	hypothetical protein	251	-	2
D000024845	D09	EcE24377A_C0017	hypothetical protein	479	-	2
D000024847	D10	e24_P74_g36	hypothetical protein	287	-	2.61971831
D000024849	D11	e24_Ch_g188	hypothetical protein	599	-	2
D000024855	E02	e24_P35_g22	hypothetical protein	308	-	2
D000024857	E03	EcE24377A_0675	hypothetical protein EcE24377A_0675	605	YP_001461817	1.995041322
D000024859	E04	e24_P80_g33	hypothetical protein	308	-	2
D000024862	E05	e24_Ch_g115	conserved hypothetical protein	632	ABV20431	2
D000024863	E06	e24_P74_g37	hypothetical protein	347	-	2
D000024865	E07	EcE24377A_F0035	hypothetical protein	677	-	2
D000024867	E08	e24_P73_g80	hypothetical protein	350	-	1.865714286
D000024869	E09	EcE24377A_0673	hypothetical protein EcE24377A_0673	758	YP_001461815	2
D000024871	E10	e24_P74_g55	hypothetical protein	359	-	1.708609272
D000024873	E11	EcE24377A_0299	hypothetical protein EcE24377A_0299	761	YP_001461452	2
D000024875	E12	e24_Ch_g108	phage regulatory protein	368	ABV20548	2
D000024879	F02	e24_P74_g34	hypothetical protein	377	-	1.840848806
D000024881	F03	EcE24377A_F0072	hypothetical protein	824	-	1.996359223
D000024883	F04	e24_P35_g23	hypothetical protein	401	-	1.643391521
D000024885	F05	EcE24377A_F0046	polysaccharide deacetylase family protein	872	ABV20269	1.969036697
D000024887	F06	EcE24377A_E0037	hypothetical protein	401	-	2
D000024889	F07	EcE24377A_2216	baseplate assembly protein J	941	YP_001463284	3.060573858
D000024891	F08	e24_P80_g12	hypothetical protein	404	-	2
D000024894	F09	EcE24377A_F0009	hypothetical protein	995	-	1.715577889
D000024896	F10	e24_P74_g26	hypothetical protein	425	-	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024898	F11	EcE24377A_2927	hypothetical protein EcE24377A_2927	1043	YP_001463961	1.448705657
D000024899	F12	EcE24377A_1278	hypothetical protein EcE24377A_1278	428	YP_001462385	2
D000024902	G01	e24_P80_g2	hypothetical protein	1064	-	2.675213675
D000024905	G03	EcE24377A_3135	ImpA-related N-terminal domain-containing protein	1427	YP_001464150	4.156271899
D000024907	G04	e24_Ch_g151	hypothetical protein EcE24377A_1254	440	-	1.652272727
D000024909	G05	H10407_SANG_p948.1000	hypothetical protein	194	-	2
D000024911	G06	H10407_SANG_CHROM0216	putative copper/silver-binding protein SilE precursor	599	CBI99716	2
D000024913	G07	H10407_SANG_p948.0540	hypothetical protein	233	-	2
D000024916	G08	H10407_SANG_CHROM4314	hypothetical phage protein	599	CBJ03820	1.949916528
D000024917	G09	H10407_SANG_p948.1040	hypothetical protein	242	-	3.272727273
D000024920	G10	H10407_SANG_CHROM0311	putative pinE invertase/site-specific DNA recombinase	605	CBI99815	2.828150573
D000024922	G11	H10407_SANG_CHROM1247	dna-invertase	245	CBJ00751	1.971428571
D000024923	G12	H10407_SANG_CHROM0676	putative exported protein	605	CBJ00183	2
D000024925	H01	H10407_SANG_CHROM2721	putative DNA-invertase from lambdoid prophage e14	266	CBJ02227	2
D000024927	H02	H10407_SANG_p948.0850	hypothetical protein	617	-	2.539708266
D000024929	H03	h104_P666_g13	hypothetical protein	275	-	2.483636364
D000024931	H04	H10407_SANG_CHROM1248	hypothetical protein	635	-	2
D000024933	H05	H10407_SANG_p666.0100	hypothetical protein	284	-	2
D000024937	H07	H10407_SANG_CHROM2846	putative DNA-invertase from prophage	293	CBJ02350	2
D000024939	H08	H10407_SANG_CHROM3045_1_627	type III secretion system protein	680	CBJ02547	2
D000024941	H09	H10407_SANG_CHROM1978	conserved hypothetical protein	296	CBJ01480	2
D000024943	H10	H10407_SANG_CHROM3214_103_735	conserved hypothetical protein	689	CBJ02712	1.928882438
D000024945	H11	h104_P666_g14	hypothetical protein	311	-	1.774919614

Table 14: Enterotoxigenic *E. coli* Expression Clone Set, Plate 14 (EEXAN), NR-19803¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000024948	A02	H10407_SANG_p666.0310_94_726	hypothetical protein	689	-	2
D000024949	A03	H10407_SANG_p666.0400	hypothetical protein	347	-	2
D000024951	A04	H10407_SANG_CHROM4_531_1_636	conserved hypothetical protein	689	CBJ04040	1.9071
D000024955	A06	H10407_SANG_CHROM4_559_1_636	putative transcriptional regulator	689	CBJ04067	2
D000024957	A07	H10407_SANG_CHROM2_129	hypothetical protein	377	-	3.1989
D000024961	A09	H10407_SANG_p948.0050	hypothetical protein	377	-	2
D000024963	A10	H10407_SANG_CHROM4_623_73_714	probable N-acetylneuraminic acid outer membrane porin	698	CBJ04132	2
D000024966	A11	H10407_SANG_p948.0170	hypothetical protein	377	-	2
D000024967	A12	H10407_SANG_p948.0510	hypothetical protein	698	-	1.7006
D000024969	B01	H10407_SANG_p948.0240	hypothetical protein	377	-	2
D000024973	B03	H10407_SANG_p948.0310	hypothetical protein	377	-	2
D000024976	B04	H10407_SANG_CHROM0_674	conserved hypothetical protein	758	CBJ00181	2
D000024977	B05	H10407_SANG_p948.0370	hypothetical protein	377	-	2
D000024979	B06	H10407_SANG_CHROM0_348	putative fimbrial protein	761	CBI99853	1.9882
D000024982	B07	H10407_SANG_p948.0580	hypothetical protein	377	-	2
D000024983	B08	H10407_SANG_p948.0430	hypothetical protein	842	-	3.3972
D000024986	B09	H10407_SANG_p948.0950	hypothetical protein	377	-	2
D000024988	B10	h104_P52_g1	hypothetical protein	875	-	1.9143
D000024989	B11	H10407_SANG_p948.1110	hypothetical protein	377	-	3.1995
D000024991	B12	H10407_SANG_CHROM2_003	putative baseplate J family protein	947	CBJ01506	1.6705
D000024994	C01	H10407_SANG_CHROM2_722	putative DNA-invertase from lambdoid prophage e14	404	CBJ02227	2
D000024995	C02	H10407_SANG_CHROM1_199	conserved hypothetical protein	1121	CBJ00706	1.5272
D000024998	C03	H10407_SANG_p666.0560	hypothetical protein	404	-	2
D000024999	C04	H10407_SANG_p948.0900	hypothetical protein	1187	-	1.4912

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
D000025001	C05	h104_Ch_g563	putative DNA-invertase from prophage	419	CBJ02350	2
D000025003	C06	H10407_SANG_CHROM3_182	putative beta-ketoacyl synthase	1220	CBJ02682	4.441
D000025005	C07	h104_Ch_g564	putative DNA-invertase from prophage	419	CBJ02350	2
D000025007	C08	H10407_SANG_p666.0870	hypothetical protein	1625	-	4.6326
D000025009	C09	H10407_SANG_CHROM1_215	putative phage endolysin	428	CBJ00720	2
D000025011	C10	H10407_SANG_CHROM2_085	yersiniabactin siderophore biosynthetic protein	1628	CBJ01588	4.6087
D000025015	C12	H10407_SANG_CHROM1_990	putative phage portal protein, pbsx family	1784	CBJ01492	4.3997
D000025018	D01	H10407_SANG_CHROM1_194	putative transmembrane protein, pseudogene	539	PSEUDO:CBJ00701	2
D000025022	D03	H10407_SANG_p666.0380	hypothetical protein	560	-	2
D000025023	D04	H10407_SANG_CHROM3_506_91_3798	possible exported protein	3764	CBJ03007	2.5696
D000025025	D05	H10407_SANG_CHROM2_845_106_4572	adhesin autotransporter	4523	CBJ02349	2.5094
D000025027	D06	H10407_SANG_CHROM3_241_85_4557	accessory colonization factor	4529	CBJ02741	3.5308
D000025031	D08	H10407_SANG_CHROM2_081	phosphoribosylglycine amide synthetase	6158	CBJ03770	1

¹All information on these tables was provided by J. Craig Venter Institute at the time of deposition

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