

Investigation of Wza in Erythromycin Sensitivity of *Escherichia coli* K30 E69 by Genetic Complementation

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SUPPLEMENTAL MATERIAL

Escherichia coli K30 capsule biosynthesis cluster, partial sequence
Sequence ID: [AF104912.3](#) Length: 16109 Number of Matches: 1

Range 1: 1888 to 3292 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
2595 bits(1405)	0.0	1405/1405(100%)	0/1405(0%)	Plus/Minus
Query 1	ACGGCAGATATTTCTGTGCAGATCACTAAAAATGAATCAACATTAGTTGGCCATCTC			60
Sbjct 3292	ACGGCAGATATTTCTGTGCAGATCACTAAAAATGAATCAACATTAGTTGGCCATCTC			3233
Query 61	TTAATGTATCGTACTGTTCCGTGATATCATGAACACCTGATATGTAGGTACGAGCTGT			120
Sbjct 3232	TTAATGTATCGTACTGTTCCGTGATATCATGAACACCTGATATGTAGGTACGAGCTGT			3173
Query 121	GATATAACACGATTCCAACGAACAAGAGGTGCAGTGGTTACATATAACAATGTCAAAAGGT			180
Sbjct 3172	GATATAACACGATTCCAACGAACAAGAGGTGCAGTGGTTACATATAACAATGTCAAAAGGT			3113
Query 181	TGTAGTTGAAATTTCTGTACCTAAGACCATGGCTGAAGCATCTGAGCATTCAATTGATAT			240
Sbjct 3112	TGTAGTTGAAATTTCTGTACCTAAGACCATGGCTGAAGCATCTGAGCATTCAATTGATAT			3053
Query 241	ATATCTGCTATTTTTCTGTGCTTATCACCTTTAACTGACGTACAACAATATCCCTGTA			300
Sbjct 3052	ATATCTGCTATTTTTCTGTGCTTATCACCTTTAACTGACGTACAACAATATCCCTGTA			2993
Query 301	GCATCGCTCATTCTTGAGAAATACCTCAGCATTACCAAGCGCTCTGCAAGGGTCATA			360
Sbjct 2992	GCATCGCTCATTCTTGAGAAATACCTCAGCATTACCAAGCGCTCTGCAAGGGTCATA			2933
Query 361	CCGCTGCGGTCCATTTCAATGTACTTTGCTTACCAGCTCTCCCATGACAAATACTTTG			420
Sbjct 2932	CCGCTGCGGTCCATTTCAATGTACTTTGCTTACCAGCTCTCCCATGACAAATACTTTG			2873
Query 421	AGATCATCATTACTTGGAAATGAATAATATATGCCATGGTATAAATAATGATCTGGGTT			480
Sbjct 2872	AGATCATCATTACTTGGAAATGAATAATATATGCCATGGTATAAATAATGATCTGGGTT			2813
Query 481	AGATCTCCTTTCTGCATTAGTGATATAAATGAAATCTTTGTATCTTTACCGTTATGAGTA			540
Sbjct 2812	AGATCTCCTTTCTGCATTAGTGATATAAATGAAATCTTTGTATCTTTACCGTTATGAGTA			2753
Query 541	AGAACCAACGTTTCTCCAGTCAGCATCAGCGCAAGCCCCCTGCCGATGATAGCATCC			600
Sbjct 2752	AGAACCAACGTTTCTCCAGTCAGCATCAGCGCAAGCCCCCTGCCGATGATAGCATCC			2693
Query 601	ATCACAGTTAGGGGAATTTGTAATGGCTGTTTTCCAGAGTTTGCACACTTCAACAGTT			660
Sbjct 2692	ATCACAGTTAGGGGAATTTGTAATGGCTGTTTTCCAGAGTTTGCACACTTCAACAGTT			2633
Query 661	ACATAAACCTTTTGTGACCGGAATGCAGTATGCTGACATCAACTGAGGGCTTCAATA			720
Sbjct 2632	ACATAAACCTTTTGTGACCGGAATGCAGTATGCTGACATCAACTGAGGGCTTCAATA			2573
Query 721	TATGTAGTTAATCGGCTTGAATATCTTGTGCTACTGACTTACTGTTTTCCAGCTACC			780
Sbjct 2572	TATGTAGTTAATCGGCTTGAATATCTTGTGCTACTGACTTACTGTTTTCCAGCTACC			2513
Query 781	TGAACCTTACCTATGTAAGGATAAAAAATAGTCCGTGAGAAATACCCAGTTACCCGTA			840
Sbjct 2512	TGAACCTTACCTATGTAAGGATAAAAAATAGTCCGTGAGAAATACCCAGTTACCCGTA			2453
Query 841	TCACCTGCACTACGATATTGACCAAGGAGTGTGTAATCCGGATGATCCCATACCGTA			900
Sbjct 2452	TCACCTGCACTACGATATTGACCAAGGAGTGTGTAATCCGGATGATCCCATACCGTA			2393
Query 901	ACCATGAGCACATCAACCACACCAATGCGATACTCATAAATTTTAAATAGTTATCCAAC			960
Sbjct 2392	ACCATGAGCACATCAACCACACCAATGCGATACTCATAAATTTTAAATAGTTATCCAAC			2333
Query 961	TGAGGATTGAGCGTGTATAAACCAGTTCCGGACGGAGTTGATCTATTAGACCTGGCGTC			1020
Sbjct 2332	TGAGGATTGAGCGTGTATAAACCAGTTCCGGACGGAGTTGATCTATTAGACCTGGCGTC			2273
Query 1021	ATAGGATAAACATTCAACAGCTTATCCAAATCGTAGTCGCTATCCGGGAGTTTACACAG			1080
Sbjct 2272	ATAGGATAAACATTCAACAGCTTATCCAAATCGTAGTCGCTATCCGGGAGTTTACACAG			2213
Query 1081	TTTTTACGACACTGTTCAATCCCTGACCAAGGATGATGTACAACCTGATAAAAAACCA			1140
Sbjct 2212	TTTTTACGACACTGTTCAATCCCTGACCAAGGATGATGTACAACCTGATAAAAAACCA			2153
Query 1141	ATTGCCAATGCTAATGCGGAAAACTAAACAAGTTTTTCTTCATAATGTACATCATCAG			1200
Sbjct 2152	ATTGCCAATGCTAATGCGGAAAACTAAACAAGTTTTTCTTCATAATGTACATCATCAG			2093
Query 1201	TAAATCAAAAATTTGCCAATTCCTGAGCAGCTGTACACGCCGTTGCTTCCCTGCCGGCTTG			1260
Sbjct 2092	TAAATCAAAAATTTGCCAATTCCTGAGCAGCTGTACACGCCGTTGCTTCCCTGCCGGCTTG			2033
Query 1261	TGGAGAGATAAAAAGCTGACTGCGTCTGACGCGCTACCACTCTCTCTCTAATTTTCAAG			1320
Sbjct 2032	TGGAGAGATAAAAAGCTGACTGCGTCTGACGCGCTACCACTCTCTCTCTAATTTTCAAG			1973
Query 1321	CATTGAGCTTATAAATCAAAAGGATTTCTATCCCTGCACTGGCCCCAACGCTCATCGCT			1380
Sbjct 1972	CATTGAGCTTATAAATCAAAAGGATTTCTATCCCTGCACTGGCCCCAACGCTCATCGCT			1913
Query 1381	GTCGCTGTTGTTCCGCTGGTGTAC 1405			
Sbjct 1912	GTCGCTGTTGTTCCGCTGGTGTAC 1888			

FIG. S1 BLAST results for comparison of *wza* in TOPO® construct and *E. coli* WT *wza* sequence. The BLAST shows a 100% identity. The reference sequence is the *E. coli* K30 capsule biosynthesis cluster, partial sequence, (accession no. AF104912.3).

TABLE S1 Available qPCR primer sequences and melting temperature

Primer	Primer sequence (5' to 3')	Melting temperature (°C)
Forward	AGA ACT CCC GGA TAG CGA CT	57.6
Reverse	CCA ACT GAG GAT TCG AGC GT	57.2