

gi 393068133 gb AKOR01000006.1 :34315-34513	gi 446797338 ref WP_000874594.1		
gi 446797338 ref WP_000874594.1 2399	258 323	3.26e-31	
QTSFNQGTYNFSNSATLSFNNSNFNQGTYHFNSAQSTFENSNFNQGTYNFNDNTSFNNDTFNQGAY			
QTSFNQGTYNFSNSATLSFNNSNFNQGTYHFNSAQSTFENSNFNQGTYNFNDNTSFNNDTFNQGTY	1	198	307
Helicobacter pylori	toxin-like outer membrane protein [Helicobacter pylori]		
gi 393068133 gb AKOR01000006.1 :34315-34513	gi 446797381 ref WP_000874637.1		
gi 446797381 ref WP_000874637.1 2529	258 323	1.63e-30	
QTSFNQGTYNFSNSATLSFNNSNFNQGTYHFNSAQSTFENSNFNQGTYNFNDNTSFNNDTFNQGAY			
QTSFNQGTYNFSNSATLSFNNSNFNQGTYHFNSTQSTFENSNFNQGTYNFNDNTSFNNDTFNQGTY	1	198	302
Helicobacter pylori	toxin outer membrane protein [Helicobacter pylori]		
gi 393068133 gb AKOR01000006.1 :34315-34513	gi 446797342 ref WP_000874598.1		
gi 446797342 ref WP_000874598.1 2399	258 323	2.63e-30	
QTSFNQGTYNFSNSATLSFNNSNFNQGTYHFNSAQSTFENSNFNQGTYNFNDNTSFNNDTFNQGAY			
QTSFNQGTYDFNSNSATLSFNNSNFNQGTYHFNSAQSTFENSNFNQGAYNFNDNTSFNNDTFNQGTY	1	198	301
Helicobacter pylori	toxin outer membrane protein [Helicobacter pylori]		
gi 393068133 gb AKOR01000006.1 :34315-34513	gi 1159760846 ref WP_079307344.1		
gi 1159760846 ref WP_079307344.1	2397 259 324	3.32e-30	
QTSFNQGTYNFSNSATLSFNNSNFNQGTYHFNSAQSTFENSNFNQGTYNFNDNTSFNNDTFNQGAY			
QTSFNQGTYNFSNSATLSFGNSNFNQGTYHFNSAQSTFENSNFNQGTYNFNDNVSFNNDTFNQGTY	1	198	300
Helicobacter pylori	toxin [Helicobacter pylori]		


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gi|451810799|gb|ANAE01000140.1|:57689-58634      gi|485835026|ref|WP_001446733.1|
gi|485835026|ref|WP_001446733.1|;gi|218706248|ref|YP_002413767.1| 172      2      167      1.36e-11
RCSAGARAGP--SPRARGSRHPHGHLHLHRSIPACAGLTHILALVGTSPVHPRVRGAHAHLGVGGDFATGSPRARGSP-----
TSWRWWGLRHRSSIPACAGLT--HILALVGTSPVHPRVRGAHPHLGVGGDFATGSPRARGSPTSWRWWGLRHRSSIPACAGLTHILA
KWSSTATVGPGLSPLARGTRWWRGQTEQSRRFIPAGAGNTLTYNTENHTLTVYPRWRGEHGHSPKQTQEVNGLSPLARGTPGFHLSKCMW-----
RFIPAGAGNTTPDIFATVVT--PVYPRWRGEHRNQTQRANGVAGLSPLARGTLALFLSGESRHRFIPAGAGNTYFLS      223      714      174
Escherichia coli;Escherichia coli UMN026 hypothetical protein [Escherichia coli]
gi|451810799|gb|ANAE01000140.1|:57689-58634      gi|485835026|ref|WP_001446733.1|
gi|485835026|ref|WP_001446733.1|;gi|218706248|ref|YP_002413767.1| 172      12      167      2.32e-10
GSPRARGSRAGHRWRVAGRSIPACAGLTRALALVGTSPVHPRVRGAHPHLGVGGDFATGSPRARGSRHRTVLSGCASRSIPACAGLTSSTWPPP
TPTPVHPRVRGAHPHLGVGGDFATGSPRARGSRRTSWRWWGLRHRSSIPACAGLTHILA
GLSPLARGTRWWRGQTEQSRRFIPAGAGNTLTYNTENHTLTVYPRWRGEHGHSPKQTQEVNGLSPLARGTPGFHLSKCMWRFIPAGAGNTTPDIFAT
VVTVPYPRWRGEHRNQTQRANGVAGLSPLARGTLALFLSGESRHRFIPAGAGNTYFLS      3      470      165      Escherichia
coli;Escherichia coli UMN026 hypothetical protein [Escherichia coli]
gi|451810799|gb|ANAE01000140.1|:57689-58634      gi|485835026|ref|WP_001446733.1|
gi|485835026|ref|WP_001446733.1|;gi|218706248|ref|YP_002413767.1| 172      12      167      1.15e-09
GSPRARGSPTSWRWW---GLRHRSSIPACAGLTHILALVGTSPVHPRVRGAHPHLGVGGDFATGSPRARGSP-----
TSWRWWGLRHRSSIPACAGLT--HILALVGTSPVHPRVRGAHPHLGVGGDFATGSPRARGSPTSWRWWGLRHRSSIPACAGLTHILA      GLSPLARGT----
RWWRGQTEQSRRFIPAGAGNTLTYNTENHTLTVYPRWRGEHGHSPKQTQEVNGLSPLARGTPGFHLSKCMW-----RFIPAGAGNTTPDIFATVVT--
PVYPRWRGEHRNQTQRANGVAGLSPLARGTLALFLSGESRHRFIPAGAGNTYFLS      430      897      160      Escherichia
coli;Escherichia coli UMN026 hypothetical protein [Escherichia coli]
gi|451810799|gb|ANAE01000140.1|:57689-58634      gi|485835026|ref|WP_001446733.1|
gi|485835026|ref|WP_001446733.1|;gi|218706248|ref|YP_002413767.1| 172      12      167      1.82e-08
GSPRARGSLVPWRWW---GLRHRSSIPACAGLTHILALVGTSPVHPRVRGAHVIGRCSAGARAGSPRARGSRHPHGHLHLHRSIPACAGLT--
HILALVGTSPVHPRVRGAHAHLGVGGDFATGSPRARGSPTSWRWWGLRHRSSIPACAGLTHILA      GLSPLARGT----
RWWRGQTEQSRRFIPAGAGNTLTYNTENHTLTVYPRWRGEHGHSPKQTQEVNGLSPLARGTPGFHLSKCMWRFIPAGAGNTTPDIFATVVT--
PVYPRWRGEHRNQTQRANGVAGLSPLARGTLALFLSGESRHRFIPAGAGNTYFLS      64      531      151      Escherichia
coli;Escherichia coli UMN026 hypothetical protein [Escherichia coli]
gi|451810799|gb|ANAE01000140.1|:57689-58634      gi|485835026|ref|WP_001446733.1|
gi|485835026|ref|WP_001446733.1|;gi|218706248|ref|YP_002413767.1| 172      12      163      3.34e-08
GSPRARGSPTSWRWW---GLRHRSSIPACAGLTHILALVGTSPVHPRVRGAHPHLGVGGDFATGSPRARGSP-----
TSWRWWGLRHRSSIPACAGLT--HILALVGTSPVHPRVRGAHPHLGVGGDFATGSPRARGSPTSWRWWGLRHRSSIPACAGLT      GLSPLARGT----
RWWRGQTEQSRRFIPAGAGNTLTYNTENHTLTVYPRWRGEHGHSPKQTQEVNGLSPLARGTPGFHLSKCMW-----RFIPAGAGNTTPDIFATVVT--
PVYPRWRGEHRNQTQRANGVAGLSPLARGTLALFLSGESRHRFIPAGAGNT      491      946      149      Escherichia
coli;Escherichia coli UMN026 hypothetical protein [Escherichia coli]
gi|451810799|gb|ANAE01000140.1|:57689-58634      gi|485668974|ref|WP_001310069.1|
gi|485668974|ref|WP_001310069.1|;gi|218706249|ref|YP_002413768.1| 126      12      122      6.39e-06
GSPRARGSRAGHRWRVAGRSIPACAGLTRALALVGTSPVHPRVRGAHPHLGVGGDFATGSPRARGSRHRTVLSGCASRSIPACAGLTSSTWPPP
TPTPVHPRVRGAH
GLSPLARGTRIFYRRMSRGNRFIPAGAGNTSAAPANVSAVTYPRWRGEHPRPSIISCASFLSPLARGTHQEADESARHARFIPAGAGNTQFHMSRR
AGSSVYPRWRGEH      3      335      130      Escherichia coli;Escherichia coli UMN026 hypothetical protein
[Escherichia coli]
# BLAST processed 1 queries

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Predicted CRISPR-Array: 4

ContigID: KQ087587.1 (Enterobacter_aerogenes_UCI97_GCA_001030185.1)

Start: 84822

Stop: 86069

<https://www.ncbi.nlm.nih.gov/projects/sviewer/?id=KQ087587.1&v=84822..86069>

PilerCR predicted Array

>gi|844486473|gb|KQ087587.1|:84822-86069 Enterobacter aerogenes strain UCI97 genomic scaffold aeuqd-supercont1.1, whole genome shotgun sequence

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GCGCCTTATCCGGGCTACGGTTCGGTATTTGGTTGGTAGCCCCGGTAAGCGTAAGCGCCACCGGGGAGG
ATTCCCGGATAGCGGCGGTAGCGCCTTATCCGGGCTACGGTTCGGTATGCGGTTGGTAGCCCCGGTAAG
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TCGGTTGGTAGCCCCGGTAAGCGTAAGCGCCACCGGGGAGGGTTCCTCGGATGGCGGCGCATGGCGCCTTA
TCCGGGCTACGGTTCGGTATTCGGTTCGGTAGCCCCGGTAAGCGTAAGCGCCACCGGGGAGGATTCCTCGGA
TAGCGGCGCATCGCGCCTTATCCGGGCTACGATTTCGGTATTCGGTTGGTAGCTCCGGTAAGCGTAAGCGC
CACCGGGGAGGGTTCCTCGGATGGCGGCGCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTAAACTGCGC
GCGTGGGTCGCCAGCTTCGGCCTGCTGTTGGTATTGGCTGCCCGGATCCGCAGCGTCTGCGGCGAAGCTT
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ATCCGGGCTACGGTTCGGTATTTGGTTGGTAGCCCCGGTAAGCGTAAGCGCCACCGGGGAGGATTCCTCG
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GCCACCGGGGAGGGTTCCTCGGATGGCGGCGCATAGCGCCTTATCCGGGCTACGGTTCGGTAGTCGGTTG
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TACGGTTCGGTATTCGGTTCGGTAGCCCCGGTAAGCGTAAGCGCCACCGGGGAGGATTCCTCGGATAGCGG
GCATCGCGCCTTATCCGGGCTACGATTTCGGTATTCGGTTGGTAGCTCCGGTAAGCGTAAGCGCCACCGG
GAGGGTTCCTCGGATGGCGGCGCATAGCGCCTTATCCGGGCTACGGTTCGGTAGTCGGT
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Top 10 BLASTX results in RefSeq:

Fields: query id, subject id, subject ids, subject length, s. start, s. end, evalue, query seq, subject seq, q. start, q. end, score, subject sci names, subject title
99 hits found

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gi|844486473|gb|KQ087587.1|:84822-86069 gi|1172898100|ref|WP_080967648.1|
gi|1172898100|ref|WP_080967648.1| 135 11 135 2.47e-77
RLPNRSPDKALCAAIREPSVALTLTGATNRIIPNRSPDKARCAAIRESSVALTLTGATDRIPNRSPDKAPCAAIREPSVALTLTGATNRLPNRSPD
KALCAAIREPSGGAYAYRGYPHTEP
RLPNRSPDKALCAAIREPSVALTLTGATNRIIPNRSPDKARCAAIRESSVALTLTGATDRIPNRSPDKAPCAAIREPSVALTLTGATNRLPNRSPD
KALCAAIREPSGGAYAYRGYPHTEP 1246 872 623 Enterobacter aerogenes hypothetical protein
[Klebsiella aerogenes]
gi|844486473|gb|KQ087587.1|:84822-86069 gi|1172898100|ref|WP_080967648.1|
gi|1172898100|ref|WP_080967648.1| 135 23 135 2.63e-68
AAIREPSVALTLTGATNRIIPNRSPDKARCAAIRESSVALTLTGATDRIPNRSPDKAPCAAIREPSVALTLTGATNRLPNRSPDKALCAAIREPS
GGAYAYRGYPHTEP
AAIREPSVALTLTGATNRIIPNRSPDKARCAAIRESSVALTLTGATDRIPNRSPDKAPCAAIREPSVALTLTGATNRLPNRSPDKALCAAIREPS
GGAYAYRGYPHTEP 447 109 563 Enterobacter aerogenes hypothetical protein [Klebsiella
aerogenes]
gi|844486473|gb|KQ087587.1|:84822-86069 gi|1172898100|ref|WP_080967648.1|
gi|1172898100|ref|WP_080967648.1| 135 11 135 1.27e-18
RLPELPTFYRIVARIRRDAPLSGNPPRWRLRPLPTEYRTVARIRRHAPPSGNPPRWRLRPLPTEYRTVARIRRYAPPSGNPPPVALTLTGATNR
IPNRSPDKALRAAIRESSPGGAYAYRGYPNTEP
RLPNRSPDKALCAAIREPSVALTLTGATNRIIPNRSPDKARCAAIRESSVALTLTGATDRIPNRSPDKAPCAAIRE-----
PSPVALTLTGATNRLPNRSPDKALCAAIREPSGGAYAYRGYPHTEP 413 18 225 Enterobacter aerogenes
hypothetical protein [Klebsiella aerogenes]
gi|844486473|gb|KQ087587.1|:84822-86069 gi|1172898100|ref|WP_080967648.1|
gi|1172898100|ref|WP_080967648.1| 135 11 135 1.60e-18
RLPELPTFYRIVARIRRDAPLSGNPPRWRLRPLPTEYRTVARIRRHAPPSGNPPRWRLRPLPTEYRTVARIRRYAPPSGNPPPVALTLTGATNR
IPNRSPDKALRAAIRESSPGGAYAYRGYPNTEP
RLPNRSPDKALCAAIREPSVALTLTGATNRIIPNRSPDKARCAAIRESSVALTLTGATDRIPNRSPDKAPCAAIRE-----
PSPVALTLTGATNRLPNRSPDKALCAAIREPSGGAYAYRGYPHTEP 1176 781 224 Enterobacter aerogenes
hypothetical protein [Klebsiella aerogenes]
gi|844486473|gb|KQ087587.1|:84822-86069 gi|1172898100|ref|WP_080967648.1|
gi|1172898100|ref|WP_080967648.1| 135 27 61 1.06e-13
```

NPPPVALTLTGATNQIPNRSPDKALCAAIRVFTPL	EPSPVALTLTGATNRIPNRSPDKARCAAIRESSPV	836	732
130	Enterobacter aerogenes hypothetical protein [Klebsiella aerogenes]		
gi 844486473 gb KQ087587.1 :84822-86069	gi 1172898100 ref WP_080967648.1		
gi 1172898100 ref WP_080967648.1	135 1 30 1.06e-13		
VALTLTGATNRIPNRSPDKALRAAIRESSP	MALTLTGATNRLPNRSPDKALCAAIREPSP	915	826 121
130	Enterobacter aerogenes hypothetical protein [Klebsiella aerogenes]		
gi 844486473 gb KQ087587.1 :84822-86069	gi 1172898100 ref WP_080967648.1		
gi 1172898100 ref WP_080967648.1	135 1 30 2.18e-10		
VALTLTGATNRIPNRSPDKALRAAIRESSP	MALTLTGATNRLPNRSPDKALCAAIREPSP	152	63 121
130	Enterobacter aerogenes hypothetical protein [Klebsiella aerogenes]		
gi 844486473 gb KQ087587.1 :84822-86069	gi 1172898100 ref WP_080967648.1		
gi 1172898100 ref WP_080967648.1	135 27 50 2.18e-10		
EPSPVALTLTGATNRIPNRSPDKA 73	2 101	Enterobacter aerogenes hypothetical protein	
[Klebsiella aerogenes]			
gi 844486473 gb KQ087587.1 :84822-86069	gi 1172898100 ref WP_080967648.1		
gi 1172898100 ref WP_080967648.1	135 87 120 1.13e-05		
NPPPVALTLTGATNQIPNRSPDKALCAAIRVFTPL	EPSPVALTLTGATNRLPNRSPDKALCAAIREPSP	836	735
130	Enterobacter aerogenes hypothetical protein [Klebsiella aerogenes]		
gi 844486473 gb KQ087587.1 :84822-86069	gi 1172898104 ref WP_080967652.1		
gi 1172898104 ref WP_080967652.1	105 1 105 9.68e-63		
VALTLTGATNRIPNRSPDKARCAAIRESSPV	ALTLTGATDRIPNRSPDKAPCAAIREPSP	VALTLTGATNRLPNRSPDKALCAAIREPSP	GGAYAYRG
YQPHTEP			
MALTLTGATNRIPNRSPDKARCAAIRESSPV	ALTLTGATDRIPNRSPDKAPCAAIREPSP	VALTLTGATNRLPNRSPDKALCAAIREPSP	GGAYAYRG
YQPHTEP 423	109 523	Enterobacter aerogenes hypothetical protein [Klebsiella aerogenes]	