

Summarized results of predicted amplicon BLAST search against the RefSeq Genomes database (limited to Bacteria, taxid:2).

Summarized alignments of web-based BLAST search with the predicted PCR product of the primer pairs as query. The first line in the alignment represent the forward primer sequence (left) and the reverse-complement sequence of the reverse primer (right). The second line represents the predicted PCR product. Only one sequence per BLAST hit for a certain species is shown if the sequences were identical, the number of these redundant hits is given in the last row of the results table.

Ec_faeca_acuI_1_P0

Ecfaeca_acuI_P0	1	TCATTTCAAGCATTTCAGTTAAGAGA-----TCAACTAGAAACC
query_acuI_1	1	TCATTTCAAGCATTTCAGTTAAGAGACAAGNTACATCTGTTATTGGTCAACTAGAAACC
BLASTHIT_1	1	TCATTTCAAGCATTTCAGTTAAGAGACAAGATACATCTGTTATTGGTCAACTAGAAACC
BLASTHIT_2	1	TCATTTCAAGCATTTCAGTTAAGAGACAAGATACATCTGTTATTGGTCAACTAGAAACC
BLASTHIT_3	1	TCATTTCAAGCATTTCAGTTAAGAGACAAGGTACATCTGTTATTGGTCAACTAGAAACC
BLASTHIT_4	1	TCATTTCAAGCATTTCAGTTAAGAGACAAGATACATCTGTTATTGGTCAACTAGAAACC
BLASTHIT_5	1	TCATTTCAAGCATTTCAGTTAAGAGACAAGACACATCTGTTATTGGTCAACTAGAAACC
BLASTHIT_6	1	TCATTTCAAGCATTTCAGTTAAGAGACA-----TATTGGTCAAGTGTAGACC
BLASTHIT_7	1	-----GAAGAAGATTCACCTGTTATTGGTCAAGTGTAGACGCC
BLASTHIT_8	1	-----GAAGAAGATTCACCTGTTATTGGTCAAGTGTAGACGCC
BLASTHIT_9	1	-----TGGTCAAGCAGAAACC
BLASTHIT_10	1	-----TACATCTGTTATTGGTCAAGCAGAAACC
BLASTHIT_11	1	-----TGGTCAAGTGTAGACGAGT
BLASTHIT_12	1	-----ACAAGGAACATCTGTTATTGGTCAAGTGTAGACGAGT
BLASTHIT_13	1	-----AAAAGAACAGTTACTTTTGTATTGGTCAAGTGTAGACGAGT
BLASTHIT_14	1	-----ATTCCAAGCATTTCAGTTAAGAGACAAGGTAC-----TTCTTGATCAACTGTAGACC
BLASTHIT_15	1	-----CATCTGTTATTGGTCAACTGTAGACC
BLASTHIT_16	1	-----CAAGCATTTCAGTTAAGAGA-----TCAACTGTAGAAACC
BLASTHIT_17	1	-----TACGTTAAGAGACAAGATACA-----TCAACTGTAGAAACC
BLASTHIT_18	1	-----TACGTTAAGAGACAAGATACA-----TCAACTGTAGAAACC
BLASTHIT_19	1	-----TACGTTAAGAGACAAGATACA-----TCAACTGTAGAAACC
BLASTHIT_20	1	-----TACGTTAAGAGACAAGATACA-----TCAACTGTAGAAACC
...	1	-----TACGTTAAGAGACAAGATACA-----TCAACTGTAGAAACC
...	1	-----TACGTTAAGAGACAAGATACA-----TCAACTGTAGAAACC
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query_acuI_1	61	ATTACTTTAGACG
BLASTHIT_1	61	ATTACTTTAGACG
BLASTHIT_2	61	ATTACTTTAGACG
BLASTHIT_3	61	ATTACTTTAGACG
BLASTHIT_4	61	ATTACTTTAGACG
BLASTHIT_5	61	ATTACTTTAGACG
BLASTHIT_6	---	---
BLASTHIT_7	20	ATTACTTTAGACG
BLASTHIT_8	37	ATTACTTTAGACG
BLASTHIT_9	37	ATTACTTTAGACG
BLASTHIT_10	17	ATTACTTTAGACG
BLASTHIT_11	---	---
BLASTHIT_12	18	ATTACTTTAGACG
BLASTHIT_13	---	---
BLASTHIT_14	41	ATTACTTTAGACG
BLASTHIT_15	---	---
BLASTHIT_16	21	ATTACTTTAGACG
BLASTHIT_17	---	---
BLASTHIT_18	---	---
BLASTHIT_19	14	ATTACTTTAGACG
BLASTHIT_20	---	---
...	---	---
...	---	---
N=96	---	---

BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Enterococcus faecalis	100	99	NC_004668.1	690 x
2	Enterococcus sp.	100	99	NZ_JWBQ01000067.1	3 x
3	Enterococcus faecalis	100	99	NZ_JUXC01000095.1	-
4	Enterococcus faecalis	100	97	NZ_PHLF01000001.1	-
5	Enterococcus faecalis	100	97	NZ_KZ845811.1	-
6	Staphylococcus aureus	40	100	NZ_LJOC01000115.1	1 x
7	Anaerorhabdus furcosa	41	90	NZ_FUWY01000002.1	-
8	Oceanihabibans sediminis	53	82	NZ_QPIG01000005.1	1 x
9	Flavobacteriaceae bacterium	53	82	NZ_MPGM01000017.1	-
10	Nitrosotalea sp.	33	96	NZ_FRFC01000001.1	-
11	Collimonas fungivorans	36	92	NZ_CP013232.1	-
12	Nostoc piscinale	38	89	NZ_CP012036.1	-
13	Ewingella americana	34	92	NZ_JMPJ01000065.1	-
14	Neisseriaceae bacterium	55	80	NZ_CP024847.1	-
15	Clostridium kluyveri	46	80	NZ_CP018335.1	-
16	Planktothrix agardhii	41	87	NZ_CM002803.1	-
17	Hungateiclostridium cellulolyticum	27	100	NZ_JH556653.1	-
18	Pseudoalteromonas atlantica	27	100	NC_008228.1	-
19	Bacillus simplex	34	92	NZ_NQLS01000166.1	2 x
20	Olleya namhaensis	30	95	NZ_FORM01000001.1	-

* anomalous sequences excluded from alignment
gi|1423449487|ref|NZ_UEMU01000447.1|Escherichia coli strain KCRI-77E isolate RDK43_77E
gi|1005608163|ref|NZ_FFHQ01000001.1|Listeria monocytogenes strain 2842STDY5753961
gi|522836524|ref|NZ_KE352150.1|Enterococcus faecalis strain SB2C-2 Scaffold11
gi|1120478950|ref|NZ_FQTZ01000002.1|Enterococcus faecium isolate Hp_76-17_S13_

Ec_faeca_g3060_1_P0

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query_g3060_1 1 CCCTCTTTAACATTAAATGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_1 1 CCCTCTTTAACATTAAATGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_2 1 CCCTCTTTAACATTAAATGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_3 1 CCCTCTTTAACATTAAATGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_4 1 ---TCCTTAACATTAAATGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_5 1 -----GCAAGTATTT-TTAGTAAAG-CCAAGCCTAT
BLASTHIT_6 1 -----AATTATTTATTAGAAAAAG-CAAGCCTAT
BLASTHIT_7 1 -----AGTAAAGCCAAGCCCTT
BLASTHIT_8 1 -----CTTTAACATTAAATGGACTTCTTCAGCAA
BLASTHIT_9 1 -----CTTTAACATTAACTGGACTTCTTCAGCAA
BLASTHIT_10 1 -----CTTTAACATTAAATGGACTTCTTCAGCAA
BLASTHIT_11 1 -----TTGTTTATTAGTAAAGCTAAAGGCCTAT
BLASTHIT_12 1 -----AGCGATTATTTTATTAGTAAAGCCAAGCC--
BLASTHIT_13 1 -----TATTAGAAAAAGCCAAGCCTAT
BLASTHIT_14 1 -----TTACTTATTATTAGTAAAGCBAAGCTGT
BLASTHIT_15 1 -----ATTAGTAAAGCCATGGCCTAT
BLASTHIT_16 1 -----TTGTTTATTAGTAAAGCTAAAGGCCTAT
BLASTHIT_17 1 -----AATGATTTATTAGTAAAGCCAAAGCC--
BLASTHIT_18 1 -----ATTAGTAAAGCCAAGCCTAT
BLASTHIT_19 1 -----GGACTTG-GCAGCAATTATTTATTCTTCAAAGC--AGACTAT
BLASTHIT_20 1 -----ATTATTTATTAGTAAAGCCA-
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N=206 1 -----
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query_g3060_1 61 AAATTAAGAAATCA
BLASTHIT_1 61 AAATTAAGAAATCA
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BLASTHIT_4 58 AAATTAAGAAATCA
BLASTHIT_5 30 AAATTA-
BLASTHIT_6 29 AA-
BLASTHIT_7 19 AAATTAAGACATCA
BLASTHIT_8 -----
BLASTHIT_9 -----
BLASTHIT_10 -----
BLASTHIT_11 28 GAACFAAGAAAT-
BLASTHIT_12 -----
BLASTHIT_13 23 AATFAAGA-----
BLASTHIT_14 28 AATAAT-----
BLASTHIT_15 22 AA-----
BLASTHIT_16 28 GAACFAAGAAAT-
BLASTHIT_17 -----
BLASTHIT_18 22 -----
BLASTHIT_19 40 AA-----
BLASTHIT_20 -----
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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Enterococcus faecalis	100	99	NC_004668.1	687 x
2	Enterococcus sp.	100	99	NZ_JWBQ01000066.1	2 x
3	Enterococcus faecalis	100	99	NZ_GL454749.1	-
4	Enterococcus faecalis	96	99	NZ_PTYL01000009.1	-
5	Flavobacterium sp.	48	87	NZ_CP031557.1	-
6	Buchnera aphidicola	42	90	NC_004061.1	1 x
7	Acinetobacter johnsonii	43	88	NZ_FUUY01000018.1	-
8	Pasteurella multocida subsp. septica	39	90	NZ_UGSW01000001.1	1 x
9	Pasteurella multocida	39	90	NZ_PSQH01000001.1	4 x
10	Pasteurella multocida	39	90	NZ_CP023972.1	-
11	Enterococcus thailandicus	53	82	NZ_LWMN01000016.1	2 x
12	Algoriphagus halophilus	39	90	NZ_FSRC01000001.1	-
13	Candidatus Borrelia	41	89	NZ_CP025785.1	-
14	Elizabethkingia ursingii	43	89	NZ_MBDS01000002.1	-
15	Clostridiales bacterium	32	96	NZ_JQKL01000001.1	-
16	Enterococcus sp.	53	82	NZ_NGMR01000001.1	-
17	Flavobacterium beibuense	35	92	NZ_JRLV01000001.1	-
18	Aliterella atlantica	28	100	NZ_JYON01000010.1	-
19	Herpetosiphon geysericola	56	79	NZ_LGKP01000017.1	-
20	Corynebacterium kutscheri	28	100	NZ_CP011312.1	-

* anomalous sequences excluded from alignment
gi|1005608163|ref|NZ_FFHQ01000001.1|Listeria monocytogenes strain 2842STDY5753961
gi|522836690|ref|NZ_KE352316.1|Enterococcus faecalis strain SB2C-2 Scaffold89
gi|1120479204|ref|NZ_FQ TZ01000012.1|Enterococcus faecium isolate Hp_76-17_S13
gi|1129541613|ref|NZ_CWML01000029.1|Listeria monocytogenes isolate LM52

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query_cysS_3 1 GCAGCCACCAATTTACAACGANTGAAGAATACGTTTGACAATTTGAAATTCGCCCAAGAA
BLASTHIT_1 1 GCAGCCACCAATTTACAACGA CTGAAGAATACGTTTGACAATTTGAAATTCGCCCAAGAA
BLASTHIT_2 1 GCAGCCACCAATTTACAACGA CTGAAGAATACGTTTGACAATTTGAAATTCGCCCAAGAA
BLASTHIT_3 1 GCAGCCACCAATTTACAACGA CTGAAGAATACGTTTGACAATTTGAAATTCGCCCAAGAA
BLASTHIT_4 1 GCAGCCACCAATTTACAACGA TTGAAGAATACGTTTGACAATTTGAAATTCGCCCAAGAA
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BLASTHIT_6 1 GCAGCCACCAATTTACAACGA CTGAAGAATACGTTTGACAATTTGAAATTCGCCCAAGAA
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BLASTHIT_9 1 GCAGCCACCAATTTACAACGA CTGAAGAATACGTTTGACAATTTGAAATTCGCCCAAGAA
BLASTHIT_10 1 GCAGCCACCAATTTACAACGA TTGAAAAATACGTTTGATAATCTAAACTTCGG-----
BLASTHIT_11 1 GCAGCCACCAATTTACAACGCTTGAAAAATACGTTTGATAATCTAAACTTCGG-----
BLASTHIT_12 1 GCAGCCACCAATTTACAACGCTTGAAAAATACGTTTGATAATCTAAACTTCGG-----
BLASTHIT_13 1 GCAGCCACCAATTTACAACGCTTGAAAAATACGTTTGATAATCTAAACTTCGG-----
BLASTHIT_14 1 GCAGCCACCAATTTACAACGCTTGAAAAATACGTTTGATAATCTAAACTTCGG-----
BLASTHIT_15 1 GCAGCCACCAATTTACAACGCTTGAAAAATACGTTTGATAATCTAAACTTCGG-----
BLASTHIT_16 1 GCAGCCACCAATTTACAACGCTTGAAAAATACGTTTGATAATCTAAACTTCGG-----
BLASTHIT_17 1 -----CCAATTTCAACGATTGAAGAATACG-----AAGAA
BLASTHIT_18 1 -----TGAAGAATACGTTTGACAATGTTCAAATTC-----A
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query_cysS_3 61 ACTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_1 61 ACTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_2 61 ACTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_3 61 ACTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_4 61 ACTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_5 61 ACTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_6 61 ACTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_7 61 ACTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_8 61 ATTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_9 61 ACTGCCTCAGAGAATTGGCAGATGA
BLASTHIT_10 -----
BLASTHIT_11 -----
BLASTHIT_12 -----
BLASTHIT_13 -----
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BLASTHIT_15 -----
BLASTHIT_16 -----
BLASTHIT_17 -----
BLASTHIT_18 6 ACTGCCTCAGAGCAATTTGG-----
BLASTHIT_19 -----
BLASTHIT_20 2 ACTGCCTCAGAGAATTGGC-----
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... -----
N=44 -----

BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Enterococcus faecium	100	98	NC_017960.1	1051 x
2	Enterococcus sp.	100	98	NZ_AJRB03000003.1	37 x
3	Enterococcus faecium	100	98	NZ_PTV01000111.1	-
4	Enterococcus faecium	100	98	NZ_KB029683.1	-
5	Enterococcus sp.	100	97	NZ_KV829502.1	-
6	Enterococcus faecium	100	97	NZ_PUAH01000015.1	-
7	Enterococcus faecium	100	97	NZ_PUBG01000061.1	-
8	Enterococcus faecium	100	97	NZ_PTTS01000223.1	-
9	Enterococcus faecium	100	97	NZ_MJDZ01000007.1	-
10	Enterococcus mundtii	62	83	NZ_PTUS01000014.1	17 x
11	Enterococcus mundtii	62	83	NZ_PYGS01000082.1	-
12	Enterococcus mundtii	62	81	NC_022878.1	-
13	Enterococcus mundtii	62	81	NZ_AFWZ01000346.1	-
14	Enterococcus pernyi	62	81	NZ_KV388085.1	-
15	Enterococcus ratti	62	79	NZ_JXLB01000002.1	-
16	Enterococcus villorum	62	77	NZ_MJEB01000016.1	1 x
17	Bacillus okhensis	30	92	NZ_JRJU01000050.1	-
18	Anaplasma phagocytophilum	28	96	NZ_LANV01000001.1	17 x
19	Chitinophaga terrae	34	89	NZ_FNRL01000002.1	-
20	Amycolatopsis sacchari	24	100	NZ_FORP01000012.1	-

Ec_faeci_purD_2_P0

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query_purD_2 1 GGAATGAAAGAACTAGGACGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
BLASTHIT_1 1 GGAATGAAAGAACTAGGACGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
BLASTHIT_2 1 GGAATGAAAGAACTAGGACGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
BLASTHIT_3 1 GGAATGAAAGAACTAGGACGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
BLASTHIT_4 1 GGAATGAAAGAACTAGGACGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
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BLASTHIT_6 1 -----GGGCGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
BLASTHIT_7 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_8 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_9 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_10 1 -----GGGCGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
BLASTHIT_11 1 -----GGGCGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
BLASTHIT_12 1 -----GGGCGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
BLASTHIT_13 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_14 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_15 1 -----AGGTCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_16 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_17 1 -----ATGGAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_18 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_19 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_20 1 -----AATGGAAGAACTAGGACGCTTTTCACGGGTGTTTTATGCGGGTTTNAATTGCTACG
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N=67 1 -----

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query_purD_2 61 AAGGAAGGACC-
BLASTHIT_1 61 AAGGAAGGACC-
BLASTHIT_2 61 AAGGAAGGACC-
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BLASTHIT_6 46 AATGAAGGACC-
BLASTHIT_7 61 GCAGGAAGGACC-
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BLASTHIT_9 61 GCAGGAAGGACC-
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BLASTHIT_11 46 AATGAAGGACC-
BLASTHIT_12 46 AA-----
BLASTHIT_13 61 GCAGGAAGGACC-
BLASTHIT_14 47 AA-----
BLASTHIT_15 60 AGTTGAAGGACC-
BLASTHIT_16 57 GAAAGGAAGGACC-
BLASTHIT_17 57 GAAAGGAAGGACC-
BLASTHIT_18 57 GAAAGGAAGGACC-
BLASTHIT_19 57 GAAAGGAAGGACC-
BLASTHIT_20 59 AAGGAAGGACC-
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N=67 59 AAGGAAGGACC-

BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Enterococcus faecium	100	99	NC_017960.1	1080 x
2	Enterococcus sp.	100	99	NZ_AJRB03000044.1	37 x
3	Enterococcus sp.	100	99	NZ_NGMF01000001.1	-
4	Enterococcus faecium	100	99	NZ_JH804745.1	-
5	Enterococcus faecium	100	97	NZ_JWEB01000121.1	-
6	Bacillus cihuenis	75	87	NZ_AYSD01000010.1	-
7	Enterococcus mundtii	100	79	NZ_PYGS01000033.1	5 x
8	Enterococcus mundtii	100	79	NZ_FOUC01000005.1	-
9	Enterococcus mundtii	100	79	NZ_NGMS01000001.1	-
10	Paenibacillus sp.	76	83	NZ_LMBV01000002.1	-
11	Bacillus sp.	76	83	NZ_LMXG01000002.1	-
12	Bacillus loiseleuriae	66	85	NZ_LFW01000001.1	-
13	Enterococcus pernyi	83	80	NZ_KV388085.1	-
14	Enterococcus mundtii	100	76	NZ_PTUS01000023.1	-
15	Enterococcus faecalis	68	83	NZ_KE351686.1	-
16	Enterococcus gallinarum	99	76	NZ_BCQE01000018.1	9 x
17	Ureibacillus thermosphaericus	95	76	NZ_AJIK01000018.1	1 x
18	Enterococcus mundtii	83	78	NZ_AFWZ01000136.1	-
19	Enterococcus mundtii	83	78	NZ_PYGU01000006.1	-
20	Lysinibacillus sp.	97	75	NZ_LT985980.1	-

* anomalous sequences excluded from alignment
gi|1129541523|ref|NZ_CWML01000013.1|Listeria monocytogenes isolate LM52

Pd_acidi_asnS_2_P0

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BLASTHIT_1 1 GCCATCCACGAATTCCTCCA---AAAGAACAACTTTGCTACGTAAACACTCCGTTGATTACT
BLASTHIT_2 1 GCCATCCACGAATTCCTCCA---AAAGAATAAATTTGCTACGTAAACACTCCGTTGATTACT
BLASTHIT_3 1 GCCATCCACGAATTCCTCCA---AAAGAATAAATTTGCTACGTAAACACTCCGTTGATCAGT
BLASTHIT_4 1 -----CACGAATTCCTCAACACAATGACTTTGTTTACGTTAACACCCCAATCATCAC
BLASTHIT_5 1 -----AATTCCTCAAAAGCAACAACTTTGTTCAGTTAACACACCGATCATCAC
BLASTHIT_6 1 -----AATTCCTCAAAAGCAACAACTTTGTTCAGTTAACACACCGATTATCAC
BLASTHIT_7 1 -----AATTCCTCAAAAGCAACAACTTTGTTCAGTTAACACACCAATCATCACT
BLASTHIT_8 1 -----AATTCCTCAAAAGTAACAACTTTGTTCAGTTAACACACCAATCATCACT
BLASTHIT_9 1 -----CACGAATTCCTCAACACAATGACTTTGTTTACGTTAACACCCCAATCATCAC
BLASTHIT_10 1 -----CACGAATTCCTCAACACAATGACTTCGTTTACGTTAACACCCCAATCATCAC
BLASTHIT_11 1 -----CATGAATTCCTCAACACAATGACTTTGTTTACGTTAACACCCCAATCATCAC
BLASTHIT_12 1 -----CACGAATTCCTCAACACAATGACTTCGTTTACGTTAACACACCAATCATCAC
BLASTHIT_13 1 GCAAAATCAGCAATTCCTCAAGAGAGAAACTTTGCTATGTGCATACCTCCCTTGATCAC
BLASTHIT_14 1 GCAAAATCAGCAATTCCTCAAAAGAATGATTTCGCTCATGTTCATACCAATCATCACT
BLASTHIT_15 1 GCAAAATCACAAATTTTTCAGGAAAAGAACTTTGCTACGTTCAAACCTCCAATTTATCT
BLASTHIT_16 1 -----CATGAATTCCTCAACACAACGACTTCGTTTACGTTAACACCCCAATCATCAC
BLASTHIT_17 1 GCAAAATCACAAATTCCTTCAGGAGAGAAACTTTGCTATGTGCATACCTCCCTTGATCAC
BLASTHIT_18 1 GCCATCCACGAATTCCTTCAGGAGAGACGGCTTTGCTACGCCCACTCTCCGCTGATCAC
BLASTHIT_19 1 -----CATGAATTCCTCAACACAACGATTTCGTATACGTTAACACACCAATTTATCACT
BLASTHIT_20 1 GGTATCCACAAATTCCTTCAGGAGAGACGGCTTTGCTACGCTCACTCTCCGCTGATCAC
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...
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Pdacidi_asnS_P0 24 TCTAGTGATACGGAAGGTGC
query_asnS_2 61 TCTAGTGATACGGAAGGTGC
BLASTHIT_1 61 TCTAGTGATACGGAAGGTGC
BLASTHIT_2 61 TCTAGTGATACGGAAGGTGC
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BLASTHIT_5 51 AGCAGTGATACGAAGGTGC
BLASTHIT_6 51 AGCAGTGATACGAAGGTGC
BLASTHIT_7 51 AGCAGTGATACGAAGGTGC
BLASTHIT_8 51 AGCAGTGATACGAAGGTGC
BLASTHIT_9 55 AGTACTGATACGAAGGTGC
BLASTHIT_10 55 AGTACTGATACGAAGGTGC
BLASTHIT_11 55 AGTACTGATACGAAGGTGC
BLASTHIT_12 55 AGTACTGATACGAAGGTGC
BLASTHIT_13 61 GGAAGTGATACGAAGGTGC
BLASTHIT_14 61 AGTACTGATACGAAGGTGC
BLASTHIT_15 61 GGAAGTGATACGAAGGTGC
BLASTHIT_16 55 AGTACTGATACGAAGGTGC
BLASTHIT_17 61 GGAAGTGATACGAAGGTGC
BLASTHIT_18
BLASTHIT_19 55 AGCAGTGATACGAAGGTGC
BLASTHIT_20
...
...
N=128 -----

BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Pediococcus acidilactici	100.0	98.0	NZ_CP015206.1	16 x
2	Pediococcus acidilactici	100.0	98.0	NZ_QYRQ01000020.1	-
3	Pediococcus acidilactici	100.0	98.0	NZ_JQCC01000002.1	-
4	Lactobacillus kunkeei	92.0	78.0	NZ_CP012920.1	11 x
5	Pediococcus pentosaceus	88.0	79.0	NC_008525.1	11 x
6	Pediococcus pentosaceus	88.0	79.0	NZ_JDVW01000006.1	-
7	Pediococcus pentosaceus	88.0	79.0	NZ_JQBF01000008.1	-
8	Pediococcus pentosaceus	88.0	79.0	NC_022780.1	-
9	Lactobacillus kunkeei	92.0	77.0	NZ_JXCZ01000012.1	-
10	Lactobacillus kunkeei	92.0	77.0	NZ_JXDA01000004.1	-
11	Lactobacillus kunkeei	92.0	77.0	NZ_BDDX01000015.1	-
12	Lactobacillus kunkeei	92.0	77.0	NZ_JXDD01000007.1	-
13	Ruminiclostridium cellobioparum subsp. termitidis	100.0	74.0	NZ_AORV01000003.1	-
14	Lactobacillus sp.	100.0	74.0	NZ_CP031933.1	-
15	Leptotrichia sp.	100.0	74.0	NZ_CP016753.1	-
16	Lactobacillus kunkeei	92.0	74.0	NZ_JXDC01000005.1	-
17	Ruminiclostridium cellobioparum	100.0	72.0	NZ_JHYD01000026.1	-
18	Faecalibacterium prausnitzii	74.0	76.0	NZ_QVFB01000007.1	9 x
19	Lactobacillus sp.	92.0	73.0	NZ_CP032626.1	-
20	Faecalibacterium prausnitzii	74.0	76.0	NZ_NMTZ01000018.1	-

Pd_acidi_g1164_1_P0

Pdacidi_g1164_P 1 TTTAGGAGCAATCATCGCAATG-----GGTAG
query_g1164_1 1 TTTAGGAGCAATCATCGCAATGATTTTCGGCATTATCTGGGTCACGNNTGGCTTTGGTAG
BLASTHIT_1 1 TTTAGGAGCAATCATCGCAATGATTTTCGGCATTATCTGGGTCACGATTGGCTTTGGTAG
BLASTHIT_2 1 -----CAATCATCGCAATGATTTTGGGTTTTATCTG-----
BLASTHIT_3 1 TTTAGGAGCAATCATCGCAATCTTTTCGGCATT-----
BLASTHIT_4 1 -----GCAATGATTTTCGGCATTCTGGGGCAC-----
BLASTHIT_5 1 -----CAATCATCGCACTGATTATCGGGATTATC-----
BLASTHIT_6 1 -----CAATCATCGCACTGATTATCGGGATTATC-----
BLASTHIT_7 1 TTTAGGAGCAATCATCGCAATGAT-----
BLASTHIT_8 1 -----ATCATCGCAATATTTTCTGTATTTCTGGGTCACG-----
BLASTHIT_9 1 -----CGCAATATCTTTCGGCATTATCTGGGGCACG-----
BLASTHIT_10 1 TTTAGGAGCAATCATCGCAATGATTT-----
BLASTHIT_11 1 TTTAGGAGCAATCATCGCACTGATTT-----
BLASTHIT_12 1 TTTAGGAGCAATCATCGCAATGATTT-----
BLASTHIT_13 1 TTTAGGAGCAATCATCGCAATGATATT-----
BLASTHIT_14 1 TTTAGGAGCAATCATCGCAATGATATT-----
BLASTHIT_15 1 -----ATCATCGCAATATTTTAGTCATTATCTGGG-----
BLASTHIT_16 1 TTTAGGAGCAATCATCGCACTGATTT-----
BLASTHIT_17 1 -----ATCGCAATGATTTTCGGCATT-----
BLASTHIT_18 1 -----GCAATCATCGCAATGATTTTC-----
BLASTHIT_19 1 -----TTTTCGGCATTATCTGGGTCAC-----
BLASTHIT_20 1 -----CATCGAATGATTTTCGGCATTATCT-----
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... 1 -----
N=207 1 -----

Pdacidi_g1164_P 28 CGCGGTATTAGTTGG
query_g1164_1 61 CGCGGTATTAGTTGG
BLASTHIT_1 61 CGCGGTATTAGTTGG
BLASTHIT_2 -----
BLASTHIT_3 -----
BLASTHIT_4 -----
BLASTHIT_5 -----
BLASTHIT_6 -----
BLASTHIT_7 -----
BLASTHIT_8 -----
BLASTHIT_9 -----
BLASTHIT_10 -----
BLASTHIT_11 -----
BLASTHIT_12 -----
BLASTHIT_13 -----
BLASTHIT_14 -----
BLASTHIT_15 -----
BLASTHIT_16 -----
BLASTHIT_17 -----
BLASTHIT_18 -----
BLASTHIT_19 -----
BLASTHIT_20 -----
... -----
... -----
N=207 -----

BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Pediococcus acidilactici	100.0	97.0	NZ_CP015206.1	22 x
2	Helicobacter sp.	41.0	90.0	NZ_MLAM01000013.1	-
3	Gallibacterium genomosp.	47.0	86.0	NZ_JTJS01000032.1	-
4	Erwinia iniecta	39.0	90.0	NZ_JRXE01000016.1	1 x
5	Yersinia kristensenii	39.0	90.0	NZ_CWJK01000005.1	4 x
6	Yersinia frederiksenii	39.0	90.0	NZ_CP009364.1	1 x
7	Bacillus vietnamensis	32.0	96.0	NZ_LIXZ01000003.1	-
8	Catelicoccus marimammalium	48.0	83.0	NZ_AMYT01000022.1	-
9	Erwinia persicina	41.0	87.0	NZ_BCTN01000009.1	1 x
10	Megamonas rupellensis	35.0	92.0	NZ_KB899597.1	3 x
11	Acinetobacter kyonggiensis	35.0	92.0	NZ_FNPK01000003.1	-
12	Megamonas sp.	35.0	92.0	NZ_FOCY01000013.1	-
13	Macrocococcus epidermidis	36.0	92.0	NZ_PZJH01000003.1	-
14	Macrocococcus goetzii	36.0	92.0	NZ_MJBI02000002.1	-
15	Sphingobacterium faecium	41.0	87.0	NZ_QBKH01000003.1	-
16	Acinetobacter sp.	35.0	92.0	NZ_NEGM01000001.1	1 x
17	Bacillus sp.	28.0	100.0	NZ_LMTJ01000002.1	9 x
18	Pseudomonas batumici	28.0	100.0	NZ_JXDG01000015.1	-
19	Rhodovulum sp.	28.0	100.0	NZ_QPLK01000071.1	-
20	Roseovarius sp.	35.0	92.0	NZ_OUMZ01000007.1	-

* anomalous sequences excluded from alignment
gi|522836680|ref|NZ_KE352306.1|Enterococcus faecalis strain SB2C-2 Scaffold825

Pd_pento_nagK_1_P0

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Fdpento_nagK_P0      1 GGGTGTCTACTAACGGAGCAA-----
query_nagK_1         1 GGGTGTCTACTAACGGAGCAACNATCGCCCTTGATGATGGTGTAAGTTCTGGCTTAGTTTT
BLASTHIT_1           1 GGGTGTCTACTAACGGAGCAACCATCGCCCTTGATGATGGTGTAAGTTCTGGCTTAGTTTT
BLASTHIT_2           1 -----GGCGTAAGTTCAGGAATTGTTTT
BLASTHIT_3           1 -----TCTCGCTTAGTTTT
BLASTHIT_4           1 -----AAGTTATGGCTTAGTTTT
BLASTHIT_5           1 -----
BLASTHIT_6           1 -----TTCTTGTTTACTTTT
BLASTHIT_7           1 -----TTATTTTT
BLASTHIT_8           1 -----TTCTTGTTTACTTTT
BLASTHIT_9           1 -----ATCTCCCTCGATGATGGTGTAAGTTTGGGCTT-----
BLASTHIT_10          1 -----ATCGCCCTTGATTATGATTTAAGTTATGG--AGTTTT
BLASTHIT_11          1 -----TTCTGGCTTAGTTTT
BLASTHIT_12          1 -----ATCGCCCTTGATTATGATTTAAGTTATGG--AGTTTT
BLASTHIT_13          1 -----CTGGCTTACTTTT
BLASTHIT_14          1 -----CTGGCTTACTTTT
BLASTHIT_15          1 -----
BLASTHIT_16          1 -----CTGGTTTAGTTAT
BLASTHIT_17          1 -----TGATGATGGTGTAATTTCTGGATT-GTCTT
BLASTHIT_18          1 -----TTAGTTTT
BLASTHIT_19          1 -----TTAT
BLASTHIT_20          1 -----TGATGATGTTGTAGGTTCTGGCTTAG-----
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N=114
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Fdpento_nagK_P0      21 -----CTTACAAGCGGGCGGAATTG
query_nagK_1         61 AAATCACCAGATTTTTCTGGTTCCCACTTACAAGCGGGCGGAATTG
BLASTHIT_1           61 AAATCACCAGATTTTTCTGGTTCCCACTTACAAGCGGGCGGAATTG
BLASTHIT_2           24 AAACAACAAATCTTATCAGGCTCTCACTTACAAGCGGGCGGAATTG
BLASTHIT_3           15 AAATAGCCCGATTTTTTCT-----
BLASTHIT_4           19 AAATAA--AGATTTTT-----
BLASTHIT_5           1 -----CAGATTTTTTGGTTCCCACTTGCA-----
BLASTHIT_6           16 AAATCACCAGATTATT-----
BLASTHIT_7           9 AAATCATCAGATTTTTCT-----
BLASTHIT_8           16 AAATCACCAGATTATT-----
BLASTHIT_9           36 AA-----
BLASTHIT_10          16 CAATAACTTCCAGATTTTT-----
BLASTHIT_11          36 AA-----
BLASTHIT_12          14 AAATCACCAGA-----
BLASTHIT_13          14 AAATCACCAGA-----
BLASTHIT_14          1 -----TTTTTCTGGTTCCCACTTATTAAAG-----
BLASTHIT_15          14 TAACAACAAATTTTTTCTGGTT-----
BLASTHIT_16          30 AAA-----
BLASTHIT_17          9 ATTAATTACCAGATTTTTCTGACTTCGACTT-----
BLASTHIT_18          5 AAATCACCAGATCTTTCTGTTGCCA-----
BLASTHIT_19          5 AAATCACCAGATCTTTCTGTTGCCA-----
...
...
N=114
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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Pediococcus pentosaceus	100.0	99.0	NC_008525.1	14 x
2	Pediococcus stilesii	65.0	74.0	NZ_JQBX01000011.1	-
3	Zhouia amylytica	31.0	88.0	NZ_FPAG01000004.1	-
4	Clostridium perfringens	30.0	86.0	NZ_CYYX01000001.1	4 x
5	Flavobacterium haorarii	25.0	93.0	NZ_FQZH01000005.1	-
6	Acinetobacter bereziniae	30.0	88.0	NZ_QWV01000007.1	3 x
7	Mycoplasma auris	25.0	93.0	NZ_QKUB01000015.1	-
8	Acinetobacter sp.	30.0	88.0	NZ_AMFQ01000033.1	4 x
9	Thiomonas intermedia	30.0	88.0	NC_014153.1	-
10	Leptospira meyeri	34.0	80.0	NZ_AKXE01000002.1	1 x
11	Chryseobacterium scophthalmum	30.0	83.0	NZ_FSRQ01000001.1	-
12	Leptospira sp.	34.0	80.0	NZ_NPEB01000007.1	2 x
13	Acinetobacter brisouii	22.0	96.0	NZ_JZRE01000019.1	-
14	Acinetobacter sp.	22.0	96.0	NZ_KB851219.1	-
15	Clostridium pasteurianum	24.0	92.0	NC_021182.1	-
16	Mycoplasma pullorum	34.0	83.0	NZ_CP017813.1	1 x
17	Lutibacter profundus	30.0	87.0	NZ_CP013355.1	-
18	'Nostoc azollae'	35.0	80.0	NC_014248.1	-
19	Elizabethkingia meningoseptica	29.0	87.0	NZ_BARD01000013.1	19 x
20	Sporomusa silvacetica	24.0	92.0	NZ_LSLK01000054.1	-

Pd_pento_g4364_1_P0

Fdpento_g4364_P	1	TGCTTACCACCAACCTGCTT-----ACGG
query_g4364_1	1	TGCTTACCACCAACCTGCTTATAACCAAGCTNGTCAAAAGATAACGGTTAAATTTAACGG
BLASTHIT_1	1	TGCTTACCACCAACCTGCTTATAACCAAGCTAGTCAAAAGATAACGGTTAAATTTAACGG
BLASTHIT_2	1	TGCTTACCACCAACCTGCTTATAACCAAGCTGGTCAAAAGATAACGGTTAAATTTAACGG
BLASTHIT_3	1	-----AAAAGATAACGGTTAATGTTTAAAC
BLASTHIT_4	1	-----CAGCAACCTGCTCATAACCAAGCT-----
BLASTHIT_5	1	TGCTTGTACCAACCTGCTTATAACCAAG-----
BLASTHIT_6	1	-----CAACCTGCTCATAACCAAGCTCGTCA-----
BLASTHIT_7	1	-----GTCTGAAAAGAACGGTTAAATTTAACGG
BLASTHIT_8	1	-----GTTAAATCTAACGG
BLASTHIT_9	1	-----AAGATGGTCAAAAGATAACGGTTAA-----
BLASTHIT_10	1	-----AACGGTTAAATTTAACAG
BLASTHIT_11	1	-----AAAAGATAACGGTTCAATTTAACGG
BLASTHIT_12	1	TGCTTACCACCAACGTCCTTATCAGCAA-----
BLASTHIT_13	1	-----TAACGGTTAATTTTAACGG
BLASTHIT_14	1	-----AAAAATAACGGATAAATTTAACGA
BLASTHIT_15	1	-----GTCAAAAGATTACGGTTAAA-TTGACGG
BLASTHIT_16	1	-----ACCAACCTGCTTCTAACCAAGCT-----
BLASTHIT_17	1	-----GGTTAAATTTAACCG
BLASTHIT_18	1	-----CTTAACATCAAGCTATTTAAAGAAAAGCGGTTAAATTTTCATG
BLASTHIT_19	1	-----GTCAAAAGATTACGGTTAAA-TTGACGG
BLASTHIT_20	1	-----TAACGGTTAATTTTAACGG
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...	1	-----
N=37	1	-----

Fdpento_g4364_P	25	AAACCTAGAACGTCCA
query_g4364_1	61	AAACCTAGAACGTCCA
BLASTHIT_1	61	AAACCTAGAACGTCCA
BLASTHIT_2	61	AAACCTAGAACGTCCA
BLASTHIT_3	26	GGAAAC-----
BLASTHIT_4		-----
BLASTHIT_5		-----
BLASTHIT_6		-----
BLASTHIT_7	27	AA-----
BLASTHIT_8	15	AAACCTAGA-----
BLASTHIT_9		-----
BLASTHIT_10	19	AACTACCGAGAACG--
BLASTHIT_11	26	AAA-----
BLASTHIT_12		-----
BLASTHIT_13	20	AAAC-----
BLASTHIT_14	25	AAAGCCAGAG-----
BLASTHIT_15	28	AA-----
BLASTHIT_16		-----
BLASTHIT_17	16	AAACCTAG-----
BLASTHIT_18	44	GAAA-----
BLASTHIT_19	28	AA-----
BLASTHIT_20	20	AAAC-----
...		-----
...		-----
N=37		-----

BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Pediococcus pentosaceus	100.0	99.0	NC_008525.1	13 x
2	Pediococcus pentosaceus	100.0	99.0	NZ_JDVW01000004.1	-
3	Firmicutes bacterium	39.0	88.0	NZ_QUDS01000002.1	-
4	Pseudovibrio hongkongensis	32.0	96.0	NZ_LLWC01000022.1	-
5	Luteibacter rhizovicinus	38.0	90.0	NZ_JPLB01000036.1	1 x
6	Burkholderia multivorans	34.0	92.0	NZ_PVG01000058.1	-
7	Streptococcus gallolyticus	37.0	88.0	NZ_FNFJ01000002.1	1 x
8	Unicellular cyanobacterium	30.0	96.0	NZ_NETF01000197.1	-
9	Staphylococcus gallinarum	33.0	92.0	NZ_JXCF01000010.1	1 x
10	Pyrinomonas methylaliphatogenes	40.0	86.0	NZ_CBXV010000006.1	-
11	Maribacter sedimenticola	37.0	89.0	NZ_FZNV01000002.1	-
12	Mannheimia haemolytica	37.0	89.0	NC_021082.1	66 x
13	Hungateiclostridium thermocellum	30.0	96.0	NC_009012.1	6 x
14	Virgibacillus siamensis	43.0	85.0	NZ_FUIH01000007.1	-
15	Streptococcus sanguinis	38.0	89.0	NZ_GL890988.1	-
16	Bacillus sp.	30.0	96.0	NZ_QPJG01000005.1	-
17	Bacillus taeanensis	30.0	96.0	NZ_QOCW01000025.1	-
18	Actinobacillus minor	61.0	78.0	NZ_ACQL01000172.1	-
19	Streptococcus sp.	38.0	89.0	NZ_LSN01000035.1	-
20	Ruminiclostridium thermocellum	30.0	96.0	NZ_CP016502.1	1 x