

>(1)C Schwarzengrund_CP074340

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AGAATCCGGT GGAGCGG 257

>(2)C Thompson_NoNCBI match

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AACGCCGTAG CGCCGATGGT AGTGTGGGGT CTCCCATGC GAGAGTAGGG AACTGCCAGG 300

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AAGAATTCGG TGGAGCGG 498

>(7)C Infantis_NoNCBI match

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>(12)C Oranienburg_NoNCBI match

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361

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>(17)C Choleraesuis_NoNCBI match

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361

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TC 1202

>(51)C Genovar_12350N_noNCBI match

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>(148)C Unique_NoNCBI match

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TGCGCAGCAG CAAGGCGGCA AGCGAAGGAA AGGAAGGAGC ATACAGAAGT ATGTGACTGA 120

GTTTACGAGC GCAGGCAACG CCGCTGATGC GATAAAGAAT TGCGTACAGA GCACAAAGAA 180

TTTGCCTGGC GGCAGTAGCG CGGTGGTCCC ACCTGACCCC ATGCCGAACT CAGAAGTGAA 240

ACGCCGTAGC GCCGATGGTA GTGTGGGGTC TCCCATGCG AGAGTAGGGA ACTGCCAGGC 300

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G 361

>(149)C Unique_NoNCBI match

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AATTTGCGCA GCAGCAAGGC GGCAAGCGAA GGAAAGGAAG GAGCATACAG AAGTATGTGA 120

CTGACTTTAC GAGCGCAGGC AACGCCGCTG ATGCGATAAA GAATTGCGTA CTGAGCATAA 180

AAGAATTTGC TTGGCGGCAC TAGCGCGGTG GTCCACCTG ACCCATGCC GAACTCAGAA 240

GTGAAACGCC GTAGCGCCGA TGGTAGTGTG GGGTCTCCCC ATGCGAGAGT AGGGAAGTGC 300

CAGGCATCAA ATTAAGCAGT AAGCCGGTCA TAAACCGGTG GTTGTAAGAA AATCCGGTGG 360

AGCGG 365

>(150)C Unique_NoNCBI match

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CGGGTCTGAT AAAACAGAAT TTGCCTGGCG GCCTTAGCGC GGTGGTCCCA CCTGACCCCA 120

TGCCGAACTC AGAAGTGAAA CGCCGTAGCG CCGATGGTAG TGTGGGGTCT CCCCATGCGA 180

GAGTAGGGAA CTGCCAGGCA TCAAATTACG AAGAATGGCA CTGATCTTTG AGGCAGTTCA 240

CTACTCGATA AGAGAGTAGG ACAAAGCGA AAGCTTTTGA ACGTTGCGAA GCAACGGCCC 300

GAAGGGTGAA TCACGAAGTG ATTCATAAAC TGCCAGGCAT CAAATTAAGC AGTAAGCCGG 360

TCATAAAACC GGTGGTTGTA AAAGAATTCG GTGGAGCGG 399

>(151)C Brandenburg_NoNCBImatch

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ATAAGAGATT CGTTTCCGGC AACAGAATTT GCCTGGCGGC ACTAGCGCGG TGGTCCCACC 120

TGACCCCATG CCGAACTCAG AAGTGAAACG CCGTAGCGCC GATGGTAGTG TGGGGTCTCC 180

CCATGCGAGA GTAGGGAACT GCCAGGCATC AAATTAGAAG TATGGCATTACTTTTCGGGG 240

CAGTTCACTA CTCGACAGAG AGTAGGACAA AAGCGAAAGC TTTTGAACGT TGCGAAGCAA 300

CGGCCCCAAG GGTGAATCAC GAAGTGATTG ATAACTGCC AGGCATCAAA TTAAGCAGTA 360

AGCCGGTCAT AAAGTGGTGG TTGTAAAAAA ATTCGGTGGA GCGG 404

>(152)C Unique_NoNCBImatch

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>(153)C Unique_NoNCBI match

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TACGCTGAGA CAAGGCGGCA AACGCAGCGA CGGAAGGAGC ATACAGAAGT ATGTGACTGA 120

CGCCCGCAAG AGCAGCCAAC GCGGTATCAG TGTAAGAGAC ACAGGACAGA GCACAAAGAA 180

TTTGCCTGGC GCGACTAGCG CGGTGGTCCC ACCTGACCCC ATGCCGAAGT CAGAAGTGAA 240

ACGCCGTAGC GCCGATGGTA GTGTGGGGTC TCCCATGCG AGAGTAGGGA ACTGCCAGGC 300

ATCAAATTAG AAGTATGGCA TTAAC TTTCG GGGCAGTTCA C TACTCGACA GAGAGTAGGA 360

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AAGAATTCGG TGGAGCGG 498

>(154)C Unique_NoNCBI match

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GAGTGGCTTT ACGAGCGCAG GCAACCCCGT TGATGTGATA AAGAATTGGG TGGTGAGCAT 180

AAAAGAATTT CCCGGGGGGC GCTAGCCCGG GGGTCCCCC GGCCCCATC CGGAATTCAG 240

AAGGAAACC CGGTAGCCCC GAGGGTAGGG GGGGTTTTCC CCATGGGAGA GTAGGGA ACT 300

CCCAGCCATC AAATTCAGCA GTAAGCCGGT CATATACCGG TGGTTG TAAA AGAATTCGGT 360

GGAGCGG 367

>(155)C Unique_NoNCBI match

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TTGCGCAGCA GCAAGGCGGC AAGCGAAGGA AAGGAAGGAG CATAACAGAAG TATGTGACTG 120

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>(156)C Unique_NoNCBI match

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CGCCCGCAAG AGCAGCCAAC GCCGTATCAG TGTAAGGAC ACAGGACAGA GCACAAAGAA 180

TTTGCTGGC GGCAGTAGCG CGGTGGTCCC ACCTGACCCC ATGCCGAACT CAGAAGTGAA 240

ACGCCGTAGC GCCGATGGTA GTGTGGGGTC TCCCCATGCG AGAGTAGGGA ACTGCCAGGC 300

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TTCATAAACT GCCAGGCATC AAATTGCAGT AAACCGGGAT GAAAATCCGG GTTGTGACAA 480

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498

>(158)C Enteritidis_CP075019

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CTCGACAGAG AGTAGGACAA AAGCGAAAGC TTTTGAACAT TGCGAAGCAA CGGCCCGAAG 300

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TTCATAAACT GCCAGGCATC AAATTAAGCA GTAACTGAT GTAAAAATCA GTGGTTGTAA 480

AAGAATTCGG TGGAGCGG

498

>(161)C Enteritidis_CP009091

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AACGCCGTAG CGCCGATGGT AGTGTGGGGT CTCCCCATGC GAGAGTAGGG AACTGCCAGG 300

CATCAAATTA GAAGTATGGC ATTAAC TTTC GGGGCAGTTC ACTACTCGAC AGAGAGTAGG 360

ACAAAAGCGA AAGCTTTTGA ACGTTGCGAA GCAACGGCCC GAAGGGTGAA TCACGAAGTG 420

ATTCATAAAC TGCCAGGCAT CAAATTGCAG TAAACCGGGA TGAAAATCCG GGTTGTGACA 480

AAGAAATTCG GTGGAGCGG 499

>(162)C Infantis_NoNCBImatch

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>(163)C Stanley_CP036167

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GCAAGAGCAG CCAACGCCGT ATCAGTGTA AAGACACAGG ACAGAGCACA AAGAATTTGC 180

CTGGCGGCAC TAGCGCGGTG GTCCACCTG ACCCATGCC GAACTCAGAA GTGAAACGCC 240

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ATTAGAAGTA TGGCATTAA TTTGCGGGCA GTTCACTACT CGACAGAGAG TAGGACAAAA 360

GCGAAAGCTT TTGAACGTTG CGAAGCAACG GCCCGAAGGG TGAATCACGA AGTGATTCAT 420

AAACTGCCAG GCATCAATTT AAGCAGTAAA CTGATGTAAA AATCAGTGAT TGTA AAAAGAA 480

TTCGGTGGAG CGG

493

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CTTTACGAGC GCAGGCAACG CCGCTGATGC GATAAAGAAT TCGGTACAGA GCACAAAGAA 180

TTTGCTGGC GGCCTAGCG CGGTGGTCCC ACCTGACCCC ATGCCGAAGT CAGAAGTGAA 240

ACGCCGTAGC GCCGATGGTA GTGTGGGGTC TCCCCATGCG AGAGTAGGGA ACTGCCAGGC 300

ATCAAATTAA GCAGTAAGCC GGTCATAAAC CGGTGGTTGT AAAAGAATCC GGTGGAGCGG 360

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TTTGCCTGGC GGCCTAGCG CGGTGGTCCC ACCTGACCCC ATGCCGA ACT CAGAAGTGAA 240

ACGCCGTAGC GCCGATGGTA GTGTGGGGTC TCCCATGCG AGAGTAGGGA ACTGCCAGGC 300

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G 361

>(166)C Ouakam_NoNCBI match

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GACTTTACGA GCGCAGGCAA CGCCGCTGAT GCGATAAAGA ATTGCGTACT GAGCACAAAG 180

AATTTGCCTG GCGGCCGTAG CGCGGTGGTC CCACCTGACC CCATGCCGAA CTCAGAAGTG 240

AAACGCCGTA GCGCCGATGG TAGTGTGGGG TCTCCCATG CGAGAGTAGG GAACTGCCAG 300

GCATCAAATT GCAGTAAACC GGGATGAAAA TCCGGGTGGT GACAAAGAAA TTCGGTGGAG 360

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363

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GTTTACGAGC GCAGGCAACG CCGCTGATGC GATAAAGAAT TCGTACAGA GCACAAAGAA 180

TTGCCTGGC GGCCTAGCG CGGTGGTCCC ACCTGACCCC ATGCCGAAGT CAGAAGTGAA 240

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ATCAAATTAG AAGTATGGCA TTAACITTCG GGGCAGTTCA CTAICTGACA GAGAGTAGGA 360

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AAGAATTCGG TGGAGCGG

498

>(168)C Reading_CP093132

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CACCTGACCC CATGCCGAAC TCAGAAGTGA AACGCCGTAG CGCCGATGGT AGTGTGGGGT 180

CTCCCCATGC GAGAGTAGGG AACTGCCAGG CATCAAATTA GAAGTATGGC ATTAAC TTTC 240

GGGGCAGTTC ACTACTCGAC AGAGAGTAGG ACAAAGCGA AAGCTTTTGA ACGTTGCGAA 300

GCAACGGCCC GAAGGGTGAA TCACGAAGTG ATTGATAAAC TGCCAGGCAT CAAATTAAGC 360

AGTAAGCCGG TCATAAACTG GTGGTTGTAA AAAAATTCGG TGGAGCGG 408

>(169)X Ganimara_CP030288

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ATGTCGATCT GACGCTGATC ACTGGCCTCT CCGGTGATGC CGGT 1184

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498

>(171)C Unique_NoNCBI match

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GTTCGCAAGA GCAGCCAACG CCGTATCAGC GTAAAAGACA CAGGACAGAG CACAAAGAAT 180

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CGGGATGAAA ATCCGGGTTG TGACAAAGAA ATTCGGTGGA GCGG 404

>(173)C Dublin_CP032449

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AAGAATTTGC CTGGCGGCAC TAGCGCGGTG GTCCACCTG ACCCATGCC GAACTCAGAA 420

GTGAAACGCC GTAGCGCCGA TGGTAGTGTG GGGTCTCCCC ATGCGAGAGT AGGGAAGTGC 480

CAGGCATCAA ATTAGAAGTA TGGCATTAAAC TTTCGGGGCA GTTCACTACT CGACAGAGAG 540

TAGGACAAAA GCGAAAGCTT TTGAACGTTG CGAAGCAACG GCCCGAAGGG TGAATCACGA 600

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CGCGTAATGA GCTGAATATC ACCACCAAGA TCTGGATTGA AAACCTTAGC AAAGACAAGC 1140

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1244

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396

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