Name	Gene Sequence	Translation
phiHau3 phage large terminase subunit gene	>NC_018836.1:2329-3995 Streptomyces phage phiHau3, complete genome GTGAGTCCCATCTCAACCCTGACCACTGAAGAGATCGAGGCCCTGGCGCCTACGTTCCTCGGGCCTACCT GGGCGAAGGATTCCCTGGGGCAGTGGAAGCTGCCGCAGCGCACGCTCGGCTGGCAGATCGCCGGCTGGTG CGCGGAGTACCTGCGCGCCGAGGACGGCGGCCCGTGGAAGTTCACGCGGGAGCAGCTCCGCTTCGTCCTG TGGTGGTATGCAGTCGATGAGAACGGGCGGTTCGTCTACCGCAAGGGCGTTCTTCAGCGGCTGAAGGGTT GGGGC_**TTA**_**CTCCGGT**_AAGGACCCCCTCCTTGCAGTGGTCTGCATGGTCGAGTTCGTGGGGCCGTCTCGGT TCTCGCACTTCGACGAGGCCGGCGATCCGGTCGGCATCCCTCACCCGCAGGCGTGGGTGCAGGTGGCCGC GGTGAGCCGTGACCAGACCCGTAACACCATGACCTTGTTCCCGTCGCTGATGAGTGACCGGCTCATCGAG ACGTACGGGATCAAGGCGGGAGCCGAGCTGATCCGCGGCGAACGGCGGACGTCAGCGCCTTGAGGCGGTGA CGAGTAGCTACCGGGCCCTTGAGGGGGCCCGGTCT_**TTA**_**ACGGTCC**_ACGTTCGTAGTGCTCAACGAAACCC ATCACTGGGTGACGGGTAACAACGGCGACAAGATGTACTCGACGATCGACGGTAACGCGACCAAGAAGGA CTCGCGGTACCTGGCGATCACCAACGCTTACCTGCCCGGCGAGGACAGCGTGGCCGAGCGGATGCGCGAG GCGTACGACAAGATCCGCGAGGGCAAGGCCGTCGACATCGGCTTCATGTACGACAGCATCGAGGCGCATC CTTCGACGCCGTTGACGGTCGAGGCGATCCGGATCGTGCTGCCGAAGATCCGCGGCGATGCCTCTTGGCT GAACGTCGAGACGATCATCCAGTCCATCATGGACGCGACGATCGCTCCGTCGCGCAGCCGGCGCATGTGG TTCAACCAGATCGTGGCCGAGGAAGACGCGCTGTACGGGCCTGAGCAGTGGGCGGACATCCTGCATGAGG GTGCGACGCTCCAGCCGGGCGACGAGATCGTCATGGGCTTCGATGGCGGTAAGAGTGACGATGCCACGGC CCTCGTTGCGATCCGCGTGCGGGACATGTGCGCGTTCGTGCTCGGCCTGTGGGAGAAGCCCGACGGCCCG AAGGGTGACGGCTGGTCCGTACCTCGGGCCGAGGTCGACTCGGCCGTGCATGACGCCTTCCGCGTGTACG ACGTGAAGGCGTTCTACGCCGACGTCGCCCTCTGGGAGAGCTACATCTCCGAGTGGGACGAGCTGTACGG CGAGGGCCTGTCGGTGAAGTCGCCGGTCGGCAAGGACCGGATCGGCTGGGACATGCGTTCCTCGCTGAAG CTGTCGACGATGGCGCACGAGCGCCTGATGCGGAGCATCTTCGACAAGAAGCTCCGGGTACGACGGTGACC TGACCTTGCGCCGGCACGCGCTGAACGCGCGTCGCCGGTCGAACAACTACGGCATCAGCTTCGGCAAGGA GTCGCGCGAGTCGCCCCGCAAGGTCGACGCGTACGCGGCCCTGATGCTGGCGCACGAGGCGCTGTACGAC CTGCGTGCGCGCGGGAAGAAGGTCCGGGCTCGCTCGGGCCGGGGTTACTTCATGTAG	>g6 VSPISTLTTEEIEALAPTFLGPTWAKDSLGQWKLPQRTLGWQIAGWCAEYLRAEDGGPWK FTREQLRFVLWWYAVDENGRFVYRKGVLQRLKGWG **TTA_CTCCGGT** >g7 KDPLLAVVCMVEFVGPSRFSHFDEAGDPVGIPHPQAWVQVAAVSRDQTRNTMTLFPSLMS DRLIETYGIKAGAELIRANGGRQRLEAVTSSYRALEGARS **TTA_ACGGTCC** >g8 TFVVLNETHHWVTGNNGDKMYSTIDGNATKKDSRYLAITNAYLPGEDSVAERMREAYDKI REGKAVDIGFMYDSIEAHPSTPLTVEAIRIVLPKIRGDASWLNVETIIQSIMDATIAPSR SRRMWFNQIVAEEDALYGPEQWADILHEGATLQPGDEIVMGFDGGKSDDATALVAIRVRD MCAFVLGLWEKPDGPKGDGWSVPRAEVDSAVHDAFRVYDVKAFYADVALWESYISEWDEL YGEGLSVKSPVGKDRIGWDMRSSLKLSTMAHERLMRSIFDKKLRYDGDLTLRRHALNARR RSNNYGISFGKESRESPRKVDAYAALMLAHEALYDLRARGKKVRARSGRGYFM
StrepC1 prophage large terminase subunit gene	>ACEW01000274.1:c42728-41083 Streptomyces sp. C cont1.274 GTGAGTCCTATTTCAGCCCTCACAGCAGAAGAGATCGACGCCTTGGAGCCGACGTTCCTCGGCCCGACAT GGCTGCGGAACCCTGACCGGTCCTGGAAGCTGCCCGAGCACACACTCGGCTGGCAGATCGCCGGTTGGGC CGCAGAGTTCCTCAAGGCGGAGGACGGCGGGCCCTGGCGCTTCACGCGCGAGCAGCTCCGCTTCGTCCTG TGGTGGTACGCGGTCGACGAGAACGGCCGCTTCGTCTACCGCAAGGGAGTTCTCCAGCGCTTGAAGGGCT GGGGC_**TTA**_**CCGGC**_AAGGACCCTCTCCTCGCGGTCGTGTCTCGCTCGTCGAGTTCGTAGGCCCGAGCCGCTTT TCCCACTGGCAGGACGGGCAGCCGGTAGGCGTCCCCCACCCCCAGGCGTGGGTACAGATCGCGGCCGTAT CGCGCGACCAGACCCGCAACACCATGACCCTGATGCCGTCCCTGATGAGCGACAAGCTGATCGAGACGTA CGGCATCAAGGCGGGCGCCGAGCTGATCCGTGCGAACGGTGGCCGGCAGAGACTTGAAGCGGTCACCAGC TCCTTCCGTGCCCTGGAGGGCGGCCGGGTCACCTTCACCGTGCTGAACGAAACGCACCACTGGGTGACCG GCAATAACGGCGATCGCATGTACGAGACGATCGACGGTAACGCCACCAAGAAGGACAGCCGTTACCTCGC GATCACGAACGCCTACCTCCCCGGCGAGGATTCAGTCGCCGAGCGGATGCGCGAAGCCTTCGAGAAGATC CGCGAAGGCCGGGCCTCGGACATCGGCTTCATGTACGACTCGATCGAGGCGCACCCGGCAACCCCACTGA CGCCCGAGGCGATCCGGATCGTCCTGCCGAAGATCAGGGGCGACGCCGTCTGGCTCCGGGTCGAAACGAT CCTTCAGTCCATCCTCGACACGACGATCGCGCCGAGCCGCTCGCGGCGTATGTGGCTGAACCAGATCGTT GCCTCCGAGGATGCCCTGTACGGCCCGGCCGAGTGGGATGTCCTGCGGCGCGATGAGCTGGAGCTGAAGC CCGGCGACGAGATCGTCATGGGCTTCGATGGCGGCCTGAGAGACGACAGCACAGCCTTGATCGGGCTGCG CATCTCGGACTCGTACGCCTTCGTGATCGGCCTGTGGGAGAAGCCGGACGGCCCGGCCGGTAAGGACTGG GAAGTCCCACGCTTGCAGGTCGACAGCGCCGTGCACGACGCCTTCAAGGTGTTCTCCGTGCAGGGCTTCT ACGCCGATGTTGCCTTGTGGGAGTCGTACATCTCCGAGTGGTCGGAGACGTACGGCGAGGGCCTGGCCGT GAAGGCGCCCGGCAAGGACGCGATCGGCTGGGACATGCGGTCCTCGCTGAAGGCCGCGACGATGGCGCAC GAGCGCCTGATGCGCACGGTCTTCGACAAGAAGCTCGTCCACGACGGCGACCTCAAGCTCCGCCGGCACG TGCTGAATGCAGTCCGGCGCACGAACAACTACGGCGTCTCCTTCGGCAAGGAAAGCCGGGAGTCGCCCCG CAAGGTCGACGCCTACGCCGCGCTCATGTTGGCGCACGAGGCCCTGTTCGACCTGCGCGCGCCCGAGGCAAG AAGGTCCGTCAACGGTCCGGCCGAGGGTTCTTCCTG	>g6 VSPISALTAEEIDALEPTFLGPTWLRNPDRSWKLPEHTLGWQIAGWAAAEFLKAEDGGPWR FTREQLRFVLWWYAVDENGRFVYRKGVLQRLKGWG **TTA_CCGGC** >g78 KDPLLAVVSLVEFVGPSRFSHWQDGQPVGVPHPQAWVQIAAVSRDQTRNTMTLMPSLMSD KLIETYGIKAGAELIRANGGRQRLEAVTSSFRALEGGRVTFTVLNETHHWVTGNNGDRMY ETIDGNATKKDSRYLAITNAYLPGEDSVAERMREAFEKIREGRASDIGFMYDSIEAHPAT PLTPEAIRIVLPKIRGDAVWLRVETILQSILDTTIAPSRSRRMWLNQIVASEDALYGPAE WDVLRRDELELKPGDEIVMGFDGGLRDDSTALIGLRISDSYAFVIGLWEKPDGPAGKDWE VPRLQVDSAVHDAFKVFSVQGFYADVALWESYISEWSETYGEGLAVKAPGKDAIGWDMRS SLKAATMAHERLMRTVFDKKLVHDGDLKLRRHVLNAVRRTNNYGVSFGKESRESPRKVDA YAALMLAHEALFDLRARGKKVRQRSGRGFFL