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 ACGTACGGGATCAAGGCGGGAGCCGAGCTGATCCGCGCGAACGGCGGACGTCAGCGCCTTGAGGCGGTGA CGAGTAGCTACCGGGCCCTTGAGGGGGCCCGGTCT_**TTA**_**ACGGTCC**_ACGTTCGTAGTGCTCAACGAAACCC ATCACTGGGTGACGGGTAACAACGGCGACAAGATGTACTCGACGATCGACGGTAACGCGACCAAGAAGGA CTCGCGGTACCTGGCGATCACCAACGCTTACCTGCCCGGCGAGGACAGCGTGGCCGAGCGGATGCGCGAG GCGTACGACAAGATCCGCGAGGGCAAGGCCGTCGACATCGGCTTCATGTACGACAGCATCGAGGCGCATC CTTCGACGCCGTTGACGGTCGAGGCGATCCGGATCGTGCTGCCGAAGATCCGCGGCGATGCCTCTTGGCT GAACGTCGAGACGATCATCCAGTCCATCATGGACGCGACGATCGCTCCGTCGCGCAGCCGGCGCATGTGG TTCAACCAGATCGTGGCCGAGGAAGACGCGCTGTACGGGCCTGAGCAGTGGGCGGACATCCTGCATGAGG GTGCGACGCTCCAGCCGGGCGACGAGATCGTCATGGGCTTCGATGGCGGTAAGAGTGACGATGCCACGGC CCTCGTTGCGATCCGCGTGCGGGACATGTGCGCGTTCGTGCTCGGCCTGTGGGAGAAGCCCGACGGCCCG AAGGGTGACGGCTGGTCCGTACCTCGGGCCGAGGTCGACTCGGCCGTGCATGACGCCTTCCGCGTGTACG ACGTGAAGGCGTTCTACGCCGACGTCGCCCTCTGGGAGAGCTACATCTCCGAGTGGGACGAGCTGTACGG CGAGGGCCTGTCGGTGAAGTCGCCGGTCGGCAAGGACCGGATCGGCTGGGACATGCGTTCCTCGCTGAAG CTGTCGACGATGGCGCACGAGCGCCTGATGCGGAGCATCTTCGACAAGAAGCTCCGGTACGACGGTGACC TGACCTTGCGCCGGCACGCGCTGAACGCGCGTCGCCGGTCGAACAACTACGGCATCAGCTTCGGCAAGGA GTCGCGCGAGTCGCCCCGCAAGGTCGACGCGTACGCGGCCCTGATGCTGGCGCACGAGGCGCTGTACGAC CTGCGTGCGCGCGGGAAGAAGGTCCGGGCTCGCTCGGGCCGGGGTTACTTCATGTAG	>g6 VSPISTLTTEEIEALAPTFLGPTWAKDSLGQWKLPQRTLGWQIAGWCAEYLRAEDGGPWK FTREQLRFVLWWYAVDENGRFVYRKGVLQRLKGWG **TTA_CTCCGGT** >g7 KDPLLAVVCMVEFVGPSRFSHFDEAGDPVGIPHPQAWVQVAAVSRDQTRNTMTLFPSLMS DRLIETYGIKAGAELIRANGGRQRLEAVTSSYRALEGARS **TTA_ACGGTCC** >g8 TFVVLNETHHWVTGNNGDKMYSTIDGNATKKDSRYLAITNAYLPGEDSVAERMREAYDKI REGKAVDIGFMYDSIEAHPSTPLTVEAIRIVLPKIRGDASWLNVETIIQSIMDATIAPSR SRRMWFNQIVAEEDALYGPEQWADILHEGATLQPGDEIVMGFDGGKSDDATALVAIRVRD MCAFVLGLWEKPDGPKGDGWSVPRAEVDSAVHDAFRVYDVKAFYADVALWESYISEWDEL YGEGLSVKSPVGKDRIGWDMRSSLKLSTMAHERLMRSIFDKKLRYDGDLTLRRHALNARR RSNNYGISFGKESRESPRKVDAYAALMLAHEALYDLRARGKKVRARSGRGYFM
Streptomyces sp. C prophage large terminase subunit gene	>ACEW01000274.1:c42728-41083 Streptomyces sp. C cont1.274 GTGAGTCCTATTTCAGCCCTCACAGCAGAAGAGATCGACGCCTTGGAGCCGACGTTCCTCGGCCCGACAT GGCTGCGGAACCCTGACCGGTCCTGGAAGCTGCCCGAGCACACACTCGGCTGGCAGATCGCCGGTTGGGC CGCAGAGTTCCTCAAGGCGGAGGACGGCGGGCCCTGGCGCTTCACGCGCGAGCAGCTCCGCTTCGTCCTG TGGTGGTACGCGGTCGACGAGAACGGCCGCTTCGTCTACCGCAAGGGAGTTCTCCAGCGCTTGAAGGGCT GGGGC_**TTA**_**CCGGC**_AAGGACCCTCTCCTCGCGGTCGTCTCGCTCGTCGAGTTCGTAGGCCCGAGCCGCTTT TCCCACTGGCAGGACGGGCAGCCGGTAGGCGTCCCCCACCCCCAGGCGTGGGTACAGATCGCGGCCGTAT CGCGCGACCAGACCCGCAACACCATGACCCTGATGCCGTCCCTGATGAGCGACAAGCTGATCGAGACGTA CGGCATCAAGGCGGGCGCCGAGCTGATCCGTGCGAACGGTGGCCGGCAGAGACTTGAAGCGGTCACCAGC TCCTTCCGTGCCCTGGAGGGCGGCCGGGTCACCTTCACCGTGCTGAACGAAACGCACCACTGGGTGACCG GCAATAACGGCGATCGCATGTACGAGACGATCGACGGTAACGCCACCAAGAAGGACAGCCGTTACCTCGC GATCACGAACGCCTACCTCCCCGGCGAGGATTCAGTCGCCGAGCGGATGCGCGAAGCCTTCGAGAAGATC CGCGAAGGCCGGGCCTCGGACATCGGCTTCATGTACGACTCGATCGAGGCGCACCCGGCAACCCCACTGA CGCCCGAGGCGATCCGGATCGTCCTGCCGAAGATCAGGGGCGACGCCGTCTGGCTCCGGGTCGAAACGAT CCTTCAGTCCATCCTCGACACGACGATCGCGCCGAGCCGCTCGCGGCGTATGTGGCTGAACCAGATCGTT GCCTCCGAGGATGCCCTGTACGGCCCGGCCGAGTGGGATGTCCTGCGGCGCGATGAGCTGGAGCTGAAGC CCGGCGACGAGATCGTCATGGGCTTCGATGGCGGCCTGAGAGACGACAGCACAGCCTTGATCGGGCTGCG CATCTCGGACTCGTACGCCTTCGTGATCGGCCTGTGGGAGAAGCCGGACGGCCCGGCCGGTAAGGACTGG GAAGTCCCACGCTTGCAGGTCGACAGCGCCGTGCACGACGCCTTCAAGGTGTTCTCCGTGCAGGGCTTCT ACGCCGATGTTGCCTTGTGGGAGTCGTACATCTCCGAGTGGTCGGAGACGTACGGCGAGGGCCTGGCCGT GAAGGCGCCCGGCAAGGACGCGATCGGCTGGGACATGCGGTCCTCGCTGAAGGCCGCGACGATGGCGCAC GAGCGCCTGATGCGCACGGTCTTCGACAAGAAGCTCGTCCACGACGGCGACCTCAAGCTCCGCCGGCACG TGCTGAATGCAGTCCGGCGCACGAACAACTACGGCGTCTCCTTCGGCAAGGAAAGCCGGGAGTCGCCCCG CAAGGTCGACGCCTACGCCGCGCTCATGTTGGCGCACGAGGCCCTGTTCGACCTGCGCGCCCGAGGCAAG AAGGTCCGTCAACGGTCCGGCCGAGGGTTCTTCCTG	>g6 VSPISALTAEEIDALEPTFLGPTWLRNPDRSWKLPEHTLGWQIAGWAAEFLKAEDGGPWR FTREQLRFVLWWYAVDENGRFVYRKGVLQRLKGWG **TTA_CCGGC** >g78 KDPLLAVVSLVEFVGPSRFSHWQDGQPVGVPHPQAWVQIAAVSRDQTRNTMTLMPSLMSD KLIETYGIKAGAELIRANGGRQRLEAVTSSFRALEGGRVTFTVLNETHHWVTGNNGDRMY ETIDGNATKKDSRYLAITNAYLPGEDSVAERMREAFEKIREGRASDIGFMYDSIEAHPAT PLTPEAIRIVLPKIRGDAVWLRVETILQSILDTTIAPSRSRRMWLNQIVASEDALYGPAE WDVLRRDELELKPGDEIVMGFDGGLRDDSTALIGLRISDSYAFVIGLWEKPDGPAGKDWE VPRLQVDSAVHDAFKVFSVQGFYADVALWESYISEWSETYGEGLAVKAPGKDAIGWDMRS SLKAATMAHERLMRTVFDKKLVHDGDLKLRRHVLNAVRRTNNYGVSFGKESRESPRKVDA YAALMLAHEALFDLRARGKKVRQRSGRGFFL