

Restriction sites for pGEX-4T-2

The following restriction site table was compiled using DNASIS software for sequence analysis. The enzymes chosen are those which we believe to have been commercially available in June 1992.

The vector pGEX-4T-2 was not tested with each enzyme and therefore the accuracy of the table cannot be guaranteed. Please contact your local Pharmacia subsidiary if a discrepancy is identified.

Please note that enzymes with non-palindromic recognition sequences are listed twice. You must combine both entries to obtain the total number of sites for these enzymes.

Locations represent the 5' end of the recognition sequence for each restriction enzyme.

Enzyme (# sites): Locations

Aat II (1): 1242
Acc I (1): 950
Acc65 I (0):
Aci I (20): 924, 964, 1321, 1650, 1817, 2461, 2605, 3101, 3122, 3129, 3228, 3381, 3468, 3697, 4168, 4224, 4325, 4335, 4652, 4857
Aci I (39): 225, 549, 960, 1066, 1105, 1115, 1157, 1274, 1420, 1529, 1606, 1771, 2008, 2099, 2470, 2715, 2836, 2855, 2982, 3010, 3172, 3189, 3215, 3269, 3420, 3436, 3445, 3487, 3559, 3623, 3643, 3646, 3874, 3958, 4114, 4252, 4391, 4494, 4728
Afl II (0):
Afl III (3): 496, 3053, 3669
Age I (0):
Aha II (5): 34, 1242, 1624, 3625, 4308
Alu I (25): 54, 178, 482, 631, 809, 1034, 1053, 1811, 1874, 1974, 2495, 2752, 2798, 2888, 3114, 3449, 3729, 4153, 4268, 4361, 4425, 4520, 4629, 4740, 4920
Alw I (7): 914, 930, 1518, 1839, 2303, 2401, 2487
Alw I (4): 926, 1531, 2311, 2408
AlwN I (1): 2639
Apa I (1): 3876
Apal I (4): 18, 1493, 2739, 3649
Apo I (3): 940, 3234, 3944
Asc I (0):
Ase I (4): 189, 1989, 4353, 4412
Asu I (13): 290, 752, 1185, 1801, 2023, 2040, 2119, 3531, 3876, 3877, 4221, 4245, 4649
Asu II (1): 654
Ava I (2): 945, 955
Ava II (4): 752, 1801, 2023, 4221

Ava III (0):
Avr II (0):
Bal I (1): 463
Bam HI (1): 930
Ban I (6): 2212, 3589, 4308, 4438, 4718, 4730
Ban II (1): 3876
Bbr P I (0):
Bbs I (3): 1175, 3808, 4147
Bbs I (0):
Bbv I (11): 42, 1032, 1129, 1921, 2110, 2712, 3131, 3149, 4359, 4608, 4681
Bbv I (7): 1732, 2426, 2632, 2635, 3718, 4089, 4218
Bcg I (1): 3972
Bcg I (2): 299, 1638
Bcl I (2): 692, 3683
Bfa I (4): 270, 1972, 2307, 2560
Bfr I (0):
Bgl I (2): 2041, 4684
Bgl II (0):
Bpm I (3): 2075, 3975, 4746
Bpm I (1): 3522
Bpu 102 I (0):
Bsa I (1): 2093
Bsa I (0):
BsaA I (1): 1145
BsaB I (0):
BsaH I (5): 34, 1242, 1624, 3625, 4308
BsaI (7): 935, 945, 2893, 4304, 4443, 4580, 4870
BseA I (0):
Bsg I (2): 69, 523
Bsg I (3): 11, 3535, 3735
Bsf E I (6): 961, 1644, 1793, 2716, 3140, 4658
Bsi W I (0):
BsiY I (11): 264, 861, 1038, 2569, 2848, 3014, 3032, 3245, 4091, 4335, 4786
Bsl I (11): 264, 861, 1038, 2569, 2848, 3014, 3032, 3245, 4091, 4335, 4786
Bsm I (0):
Bsm I (0):
BsmA I (5): 2094, 3361, 3766, 3892, 4279
BsmA I (2): 1037, 1324
Bsp 1286 I (6): 18, 1493, 1578, 2739, 3649, 3876
BspD I (0):
BspE I (0):
BspH I (3): 1220, 1325, 2333
BspM I (0):
BspM I (1): 63
BspM II (0):
BspW I (26): 102, 866, 1921, 2041, 2429, 3001, 3115, 3180, 3346, 3436, 3532, 3634, 3721, 3858, 3865, 4066, 4073, 4075, 4217, 4311, 4395, 4439, 4654, 4684, 4693, 4719
Bsr I (14): 1515, 1954, 1997, 2115, 2521, 3483, 3585, 3822, 3974, 4284, 4383, 4544, 4570, 4792
Bsr I (6): 1139, 1689, 2637, 2650, 3324, 3523
BsrF I (2): 2080, 3355
BssH II (1): 4080
Bst 1107 I (0):
BstB I (1): 654
BstE II (1): 3850
BstN I (12): 764, 936, 2893, 2906, 3027, 3393, 3708, 4248, 4305, 4444, 4581, 4708
BstU I (27): 360, 925, 993, 995, 1098, 1273, 1605, 2098, 2428, 3009, 3268, 3382, 3419, 3469, 3540, 3558, 3574, 3663, 3670, 3818, 3864, 3899, 4081, 4105, 4336, 4338, 4942
BstX I (3): 3464, 3593, 3716
BstY I (8): 914, 930, 1518, 1535, 2303, 2315, 2401, 2412
Bsu 36 I (1): 4761
Cfr 10 I (2): 2080, 3355
Cla I (0):
Dde I (8): 624, 1238, 1664, 2204, 2370, 2779, 4241, 4762
Dpn I (23): 660, 693, 915, 931, 984, 1483, 1519, 1536, 1794, 1840, 1858, 2199, 2304, 2316, 2394, 2402, 2413, 2488, 3580, 3684, 4057, 4659, 4755
Dpn II (23): 660, 693, 915, 931, 984, 1483, 1519, 1536, 1794, 1840, 1858, 2199, 2304, 2316, 2394, 2402, 2413, 2488, 3580, 3684, 4057, 4659, 4755
Dra I (5): 683, 792, 1585, 2277, 2296
Dra II (2): 289, 1184
Dra III (0):
Drd I (2): 1082, 2945
Dsa I (1): 4870
Dsa V (21): 764, 936, 945, 946, 1038, 1073, 1628, 1979, 2675, 2893, 2906, 3027, 3288, 3393, 3708, 4097, 4248, 4305, 4444, 4581, 4708
Eae I (5): 463, 961, 1772, 4343, 4546
Eag I (1): 961
Eam 1105 I (1): 2160
Ear I (0):
Ear I (5): 338, 1367, 3171, 3288, 4640
Ecl 136 II (0):
Eco 47 III (0):
Eco 57 I (1): 1478
Eco 57 I (1): 2526
EcoN I (1): 264
EcoO 109 I (2): 289, 1184
EcoR I (1): 940
EcoR II (12): 764, 936, 2893, 2906, 3027, 3393, 3708, 4248, 4305,

4444, 4581, 4708
EcoR V (1): 4117
Esp I (0):
Esp3 I (1): 4278
Esp3 I (1): 1037
*Fnu*4HI (30): 42, 960, 963, 1032,
 1129, 1420, 1649, 1744, 1771,
 1921, 2110, 2438, 2644, 2647,
 2712, 2855, 3010, 3128, 3131,
 3149, 3436, 3559, 3623, 3643,
 3730, 4101, 4230, 4359, 4608,
 4681
Fok I (7): 767, 1068, 1713, 2000,
 2181, 3702, 3711
Fok I (3): 692, 887, 4601
Fsp I (2): 1940, 4678
Hae II (6): 2809, 3179, 3284, 4065,
 4308, 4699
Hae III (21): 291, 464, 859, 962,
 1186, 1773, 2040, 2120, 2578,
 3012, 3030, 3041, 3396, 3531,
 3877, 4246, 4344, 4547, 4649,
 4766, 4935
Hga I (3): 726, 1624, 4940
Hga I (8): 25, 1089, 2364, 2942,
 3616, 3661, 3890, 3896
*Hgi*A I (5): 18, 1493, 1578, 2739,
 3649
Hha I (34): 109, 138, 359, 994, 1097,
 1127, 1272, 1604, 1941, 2034,
 2427, 2536, 2710, 2810, 2877,
 3147, 3180, 3285, 3541, 3575,
 3664, 3865, 3898, 4066, 4073,
 4080, 4082, 4104, 4309, 4337,
 4402, 4679, 4700, 4815
Hinc II (4): 182, 950, 1621, 4173
Hind II (4): 182, 950, 1621, 4173
Hind III (0):
Hinf I (10): 953, 2166, 2683, 3079,
 3154, 3297, 4093, 4348, 4539,
 4877
Hinp I (34): 109, 138, 359, 994,
 1097, 1127, 1272, 1604, 1941,
 2034, 2427, 2536, 2710, 2810,
 2877, 3147, 3180, 3285, 3541,
 3575, 3664, 3865, 3898, 4066,
 4073, 4080, 4082, 4104, 4309,
 4337, 4402, 4679, 4700, 4815
Hpa I (1): 4173
Hpa II (20): 946, 1039, 1073, 1628,
 1870, 1980, 2047, 2081, 2485,
 2675, 2701, 2848, 3289, 3356,
 3748, 3989, 4097, 4466, 4716,
 4734
Hph I (12): 369, 438, 690, 1003,
 1012, 1461, 2083, 2310, 3312,
 3387, 4254, 4287
Hph I (3): 1439, 1680, 3845
Kas I (1): 4308
Kpn I (0):
Ksp632 I (0):
Ksp632 I (5): 338, 1367, 3171, 3288,
 4640
Mae I (4): 270, 1972, 2307, 2560
Mae II (13): 1, 473, 800, 882, 1146,
 1243, 1563, 1936, 2352, 3331,
 3404, 4562, 4831
Mae III (19): 699, 971, 1048, 1143,
 1505, 1693, 1846, 1904, 2235,
 2518, 2634, 2697, 3328, 3851,
 4567, 4587, 4807, 4833, 4891
Mam I (0):
Mbo I (23): 660, 693, 915, 931, 984,
 1483, 1519, 1536, 1794, 1840,
 1858, 2199, 2304, 2316, 2394,
 2402, 2413, 2488, 3580, 3684,
 4057, 4659, 4755
Mbo II (4): 412, 2397, 3650, 4750
Mbo II (13): 330, 342, 657, 1175,
 1371, 1480, 1558, 2313, 3175,
 3292, 3808, 4147, 4644
Mlu I (1): 3669
Mnl I (7): 1792, 1998, 2876, 3159,
 4014, 4640, 4757
Mnl I (11): 903, 990, 1020, 1188,
 2135, 2216, 2616, 2940, 3521,
 4328, 4786
Msc I (1): 463
Mse I (23): 190, 286, 445, 450, 684,
 793, 1214, 1586, 1951, 1990,
 2225, 2278, 2292, 2297, 2349,
 3566, 3689, 3883, 4174, 4354,
 4413, 4597, 4906
Msp I (20): 946, 1039, 1073, 1628,
 1870, 1980, 2047, 2081, 2485,
 2675, 2701, 2848, 3289, 3356,
 3748, 3989, 4097, 4466, 4716,
 4734
Mun I (0):
Nae I (0):
Nar I (1): 4308
Nci I (9): 945, 946, 1038, 1073,
 1628, 1979, 2675, 3288, 4097
Nco I (0):
Nde I (0):
*Ngo*M I (0):
Nhe I (0):
Nla III (22): 257, 497, 696, 716, 749,
 856, 1029, 1134, 1221, 1326,
 1719, 1755, 1833, 1843, 2334,
 3054, 3278, 3805, 3984, 4005,
 4157, 4529
Nla IV (16): 752, 920, 930, 1276,
 1866, 2077, 2118, 2212, 2984,
 3023, 3589, 3876, 4308, 4438,
 4718, 4730
Not I (1): 960
Nru I (0):
Nsi I (0):
Nsp I (3): 496, 1028, 3053
*Nsp*B II (8): 1103, 1527, 2468, 2713,
 3697, 4267, 4360, 4628
Pac I (0):
*Pae*R7 I (1): 955
*Pfl*M I (1): 3245
Ple I (2): 948, 2678
Ple I (4): 2166, 3154, 3297, 4093
Pme I (0):
Pml I (0):
*Ppu*M I (0):

Pst I (1): 1919
Pvu I (2): 1793, 4658
Pvu II (3): 4267, 4360, 4628
Rsa I (3): 830, 1683, 3815
Rsr II (0):
Sac I (0):
Sac II (0):
Sal I (1): 950
Sau I (1): 4761
*Sau*3A I (23): 660, 693, 915, 931,
 984, 1483, 1519, 1536, 1794,
 1840, 1858, 2199, 2304, 2316,
 2394, 2402, 2413, 2488, 3580,
 3684, 4057, 4659, 4755
*Sau*96 I (13): 290, 752, 1185, 1801,
 2023, 2040, 2119, 3531, 3876,
 3877, 4221, 4245, 4649
Sca I (2): 829, 1682
Sce I (0):
Sce I (0):
*Scr*F I (21): 764, 936, 945, 946, 1038,
 1073, 1628, 1979, 2675, 2893,
 2906, 3027, 3288, 3393, 3708,
 4097, 4248, 4305, 4444, 4581,
 4708
Sdu I (6): 18, 1493, 1578, 2739,
 3649, 3876
Sec I (7): 935, 945, 2893, 4304, 4443,
 4580, 4870
*Sfa*N I (5): 966, 1704, 3207, 3834,
 4025
*Sfa*N I (10): 759, 1060, 1465, 1905,
 2957, 3177, 3703, 4032, 4790,
 4803
Sfc I (4): 1919, 2597, 2788, 4926
Sfi I (0):
*Sgr*A I (0):
Sin I (4): 752, 1801, 2023, 4221
Sma I (1): 945
*Sna*B I (0):
Spe I (0):
Sph I (0):
Spl I (0):
Spo I (0):
Srf I (0):
*Sse*8387 I (0):
Ssp I (2): 164, 1358
Stu I (0):
Sty I (0):
Swa I (1): 682
Taq I (11): 7, 308, 576, 655, 951,
 956, 1511, 2955, 3248, 3607, 3629
Tfi I (4): 3079, 4348, 4539, 4877
*Tth*111 I (1): 1137
Xba I (0):
Xcm I (3): 3518, 4034, 4052
Xho I (1): 955
Xho II (8): 914, 930, 1518, 1535,
 2303, 2315, 2401, 2412
Xma I (1): 945
Xmn I (2): 647, 1561

LOCUS pGEX-4T-2 4970 bp

BASE COUNT 1226 A 1202 C 1292 G 1250 T

ORIGIN

```
1 ACGTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
61 GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCCT
121 TCTGGATAAT GTTTTTTTGCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC
181 TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAATTTCA
241 CACAGGAAAC AGTATTCATG TCCCCTATAC TAGGTTATTG GAAAATTAAG GGCCTTGTGC
301 AACCCACTCG ACTTCTTTTG GAATATCTTG AAGAAAAATA TGAAGAGCAT TTGTATGAGC
361 GCGATGAAGG TGATAAATGG CGAAACAAAA AGTTTGAATT GGGTTTGGAG TTTCCCAATC
421 TTCCTTATTA TATTGATGGT GATGTTAAAT TAACACAGTC TATGGCCATC ATACGTTATA
481 TAGCTGACAA GCACAACATG TTGGGTGGTT GTCCAAAAGA GCGTGCAGAG ATTTCAATGC
541 TTGAAGGAGC GGTTTTGGAT ATTAGATACG GTGTTTCGAG AATTGCATAT AGTAAAGACT
601 TTGAAACTCT CAAAGTTGAT TTTCTTAGCA AGCTACCTGA AATGCTGAAA ATGTTCGAAG
661 ATCGTTTATG TCATAAAACA TATTTAAATG GTGATCATGT AACCCATCCT GACTTCATGT
721 TGTATGACGC TCTTGATGTT GTTTTATACA TGGACCCAAT GTGCCTGGAT GCGTTCCCAA
781 AATTAGTTTG TTTTAAAAAA CGTATTGAAG CTATCCACA AATTGATAAG TACTTGAAAT
841 CCAGCAAGTA TATAGCATGG CCTTTCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
901 ATCCTCCAAA ATCGGATCTG GTTCCGCGTG GATCCCCAGG AATTCCCAGG TCGACTCGAG
961 CGGCCGCATC GTGACTGACT GACGATCTGC CTCGCGCGTT TCGGTGATGA CCGTGAAAAC
1021 CTCTGACACA TGCAGCTCCC GGAGACGGTC ACAGCTTGTC TGTAAGCGGA TGCCGGGAGC
1081 AGACAAGCCC GTCAGGGCGC GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC AGCCATGACC
1141 CAGTCACGTA GCGATAGCGG AGTGTATAAT TCTTGAAGAC GAAAGGGCCT CGTGATACGC
1201 CTATTTTTTAT AGGTTAATGT CATGATAATA ATGGTTTCTT AGACGTCAGG TGGCACTTTT
1261 CGGGGAAATG TGCGCGGAAC CCCTATTTGT TTATTTTTTCT AAATACATTC AAATATGTAT
1321 CCGCTCATGA GACAATAACC CTGATAAATG CTTCAATAAT ATTGAAAAAG GAAGAGTATG
1381 AGTATTCAAC ATTTCCGTGT CGCCCTTATT CCCTTTTTTTG CGGCATTTTG CCTTCTGTT
1441 TTTGCTCACC CAGAAACGCT GGTGAAAGTA AAAGATGCTG AAGATCAGTT GGGTGCACGA
1501 GTGGGTTACA TCGAACTGGA TCTCAACAGC GGTAAGATCC TTGAGAGTTT TCGCCCCGAA
1561 GAACGTTTTTC CAATGATGAG CACTTTTTAAA GTTCTGCTAT GTGGCGCGGT ATTATCCCCT
1621 GTTGACGCCG GGCAAGAGCA ACTCGGTCGC CGCATACTACT ATTCTCAGAA TGACTTGGTT
1681 GAGTACTCAC CAGTCACAGA AAAGCATCTT ACGGATGGCA TGACAGTAAG AGAATTATGC
1741 AGTGCTGCCA TAACCATGAG TGATAACACT GCGGCCAACT TACTTCTGAC AACGATCGGA
1801 GGACCGAAGG AGCTAACCGC TTTTTTGCAC AACATGGGGG ATCATGTAAC TCGCCTTGAT
1861 CGTTGGGAAC CGGAGCTGAA TGAAGCCATA CCAAACGACG AGCGTGACAC CACGATGCCT
1921 GCAGCAATGG CAACAACGTT GCGCAAATA TTAAGTGGCG AACTACTTAC TCTAGCTTCC
1981 CGGCAACAAT TAATAGACTG GATGGAGGCG GATAAAGTTG CAGGACCACT TCTGCGCTCG
2041 GCCCTTCCGG CTGGCTGGTT TATTGCTGAT AAATCTGGAG CCGGTGAGCG TGGGTCTCGC
2101 GGTATCATTG CAGCACTGGG GCCAGATGGT AAGCCCTCCC GTATCGTAGT TATCTACACG
2161 ACGGGGAGTC AGGCAACTAT GGATGAAACGA AATAGACAGA TCGCTGAGAT AGGTGCCTCA
2221 CTGATTAAGC ATTGGTAACT GTCAGACCAA GTTTACTCAT ATATACTTTA GATTGATTTA
2281 AAACCTCATT TTTAATTTAA AAGGATCTAG GTGAAGATCC TTTTGGATAA TCTCATGACC
2341 AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA AAAGATCAAA
2401 GGATCTTCTT GAGATCCTTT TTTTCTGCGC GTAATCTGCT GCTTGCAAAC AAAAAACCA
2461 CCGCTACCAG CGGTGGTTTTG TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA
2521 ACTGGCTTCA GCAGAGCGCA GATACCAAAT ACTGTCCTTC TAGTGTAGCC GTAGTTAGGC
2581 CACCCTTCA AGAACTCTGT AGCACCCTT ACATACCTCG CTCTGCTAAT CCTGTTACCA
2641 GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT CTTACCGGGT TGGACTCAAG ACGATAGTTA
2701 CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCTG GCACACAGCC CAGCTTGGAG
2761 CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC TATGAGAAAG CGCCACGCTT
2821 CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC
2881 ACGAGGGAGC TTCCAGGGGG AAACGCTGG TATCTTTATA GTCCTGTCGG GTTTCGCCAC
2941 CTCTGACTTG AGCGTCGATT TTTGTGATGC TCGTCAGGGG GCGGAGCCT ATGGAAAAAC
3001 GCCAGCAACG CGGCCTTTTT ACGGTTCTCTG GCCTTTTGCT GGCCTTTTGC TCACATGTTT
3061 TTTCTGCGT TATCCCCTGA TTCTGTGGAT AACCGTATTA CCGCCTTTGA GTGAGCTGAT
3121 ACCGCTCGCC GCAGCCGAAC GACCGAGCGC AGCGAGTCAG TGAGCGAGGA AGCGGAAGAG
3181 CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTACACCCG CATAAATTCC
3241 GACACCATCG AATGGTGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC GGAAGAGAGT
3301 CAATTCAGGG TGGTGAATGT GAAACCAGTA ACGTTATACG ATGTGCGAGA GTATGCCGGT
3361 GTCTCTTATC AGACCGTTTC CCGGTGGTG AACCAAGCCA GCCACGTTTC TGCGAAAACG
```

3421 CGGGAAAAAG TGGAAGCGGC GATGGCGGAG CTGAATTACA TTCCCAACCG CGTGGCACAA
3481 CAACTGGCGG GCAAACAGTC GTTGCTGATT GCGTTGCCA CCTCCAGTCT GGCCCTGCAC
3541 GCGCCGTCGC AAATTGTCGC GGCGATTAAA TCTCGCGCCG ATCAACTGGG TGCCAGCGTG
3601 GTGGTGTCTGA TGGTAGAACG AAGCGGCGTC GAAGCCTGTA AAGCGGCGGT GCACAATCTT
3661 CTCGCGCAAC GCGTCAGTGG GCTGATCATT AACTATCCGC TGGATGACCA GGATGCCATT
3721 GCTGTGGAAG CTGCCTGCAC TAATGTTCCG GCGTTATTTT TTTGATGTCTC TGACCAGACA
3781 CCCATCAACA GTATTATTTT CTCCCATGAA GACGGTACGC GACTGGGCGT GGAGCATCTG
3841 GTCGCATTGG GTCACCAGCA AATCGCGCTG TTAGCGGGCC CATTAAAGTTC TGTCTCGGCG
3901 CGTCTGCGTC TGGCTGGCTG GCATAAATAT CTCACTCGCA ATCAAATTCA GCCGATAGCG
3961 GAACGGGAAG GCGACTGGAG TGCCATGTCC GGTTTTCAAC AAACCATGCA AATGCTGAAT
4021 GAGGGCATCG TTCCCACTGC GATGCTGGTT GCCAACGATC AGATGGCGCT GGGCGCAATG
4081 CGCGCCATTA CCGAGTCCGG GCTGCGCGTT GGTGCGGATA TCTCGGTAGT GGGATACGAC
4141 GATACCGAAG ACAGCTCATG TTATATCCCG CCGTTAACCA CCATCAAACA GGATTTTCGC
4201 CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT CTCAGGGCCA GCGGTTGAAG
4261 GGCAATCAGC TGTTGCCCGT CTCACTGGTG AAAAGAAAAA CCACCCTGGC GCCCAATACG
4321 CAAACCGCCT CTCCCCGCGC GTTGGCCGAT TCATTAATGC AGCTGGCACG ACAGGTTTCC
4381 CGACTGGAAA GCGGGCAGTG AGCGCAACGC AATTAATGTG AGTTAGCTCA CTCATTAGGC
4441 ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATGTTG TGTGGAATTG TGAGCGGATA
4501 ACAATTTTAC ACAGGAAAACA GCTATGACCA TGATTACGGA TTCACTGGCC GTCGTTTTAC
4561 AACGTCGTGA CTGGGAAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC
4621 CTTTTCGCCAG CTGGCGTAAT AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC
4681 GCAGCCTGAA TGGCGAATGG CGCTTTGCCCT GGTTTCCGGC ACCAGAAGCG GTGCCGGAAA
4741 GCTGGCTGGA GTGCGATCTT CCTGAGGCCG ATACTGTCTG CGTCCCCTCA AACTGGCAGA
4801 TGCACGGTTA CGATGCGCCC ATCTACACCA ACGTAACCTA TCCCATTACG GTCAATCCGC
4861 CGTTTGTTC CACGGAGAAT CCGACGGGTT GTTACTCGCT CACATTTAAT GTTGATGAAA
4921 GCTGGCTACA GGAAGGCCAG ACGCGAATTA TTTTGTGATGG CGTTGGAATT