Restriction sites for pGEX-6P-1

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-6P-1 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): 1256
Acc I (1): 964
*Acc*65 I (0)
Aci I (19): 978, 1335, 1664, 1831, 2475, 2619, 3115, 3136, 3143, 3242, 3395, 3482, 3711, 4182, 4238, 4339, 4349, 4666, 4871
Aci I (39): 225, 549, 974, 1080, 1119, 1129, 1171, 1288, 1434, 1543, 1620, 1785, 2022, 2113, 2484, 2729, 2850, 2869, 2996, 3024, 3186, 3203, 3229, 3283, 3434, 3450, 3459, 3501, 3573, 3637, 3657, 3660, 3888, 3972, 4128, 4266, 4405, 4508, 4742
Afl II (0)
Afl III (3): 496, 3067, 3683
Age I (0)
Aha II (5): 34, 1256, 1638, 3639, 4322
Alu I (25): 54, 178, 482, 631, 809, 1048, 1067, 1825, 1888, 1988, 2509, 2766, 2812, 2902, 3128, 3463, 3743, 4167, 4282, 4375, 4439, 4534, 4643, 4754, 4934
Alw I (7): 914, 945, 1532, 1853, 2317, 2415, 2501
Alw I (4): 941, 1545, 2325, 2422
*Alw*N I (1): 2653
Apa I (2): 936, 3890
*Apa*L I (4): 18, 1507, 2753, 3663
Apo I (3): 954, 3248, 3958
Asc I (0)
Ase I (4): 189, 2003, 4367, 4426
Asu I (15): 290, 752, 936, 937, 1199, 1815, 2037, 2054, 2133, 3545, 3890, 3891, 4235, 4259, 4663
Asu II (1): 654
Ava I (2): 959, 969
Ava II (4): 752, 1815, 2037, 4235
Ava III (0)
Avr II (0)
Bal I (1): 463
*Bam*H I (1): 945
Ban I (6): 2226, 3603, 4322, 4452, 4732, 4744
Ban II (2): 936, 3890
*Bbr*P I (0)
Bbs I (3): 1189, 3822, 4161
Bbs I (0)
Bbv I (11): 42, 1046, 1143, 1935, 2124, 2726, 3145, 3163, 4373, 4622, 4695
Bbv I (7): 1746, 2440, 2646, 2649, 3732, 4103, 4232
Bcg I (1): 3986
Bcg I (2): 299, 1652
Bcl I (2): 692, 3697
Bfa I (4): 270, 1986, 2321, 2574
Bfr I (0)
Bgl I (2): 2055, 4698
Bgl II (0)
Bpm I (3): 2089, 3989, 4760
Bpm I (1): 3536
*Bpu*1102 I (0)
Bsa I (1): 2107
Bsa I (0)
*Bsa*A I (1): 1159
*Bsa*B I (0)
*Bsa*H I (5): 34, 1256, 1638, 3639, 4322
*Bsa*J I (10): 932, 940, 941, 949, 959, 2907, 4318, 4457, 4594, 4884
*Bse*A I (0)
Bsg I (2): 69, 523
Bsg I (3): 11, 3549, 3749
*Bsi*E I (6): 975, 1658, 1807, 2730, 3154, 4672
*Bsi*W I (0)
*Bsi*Y I (11): 264, 861, 1052, 2583, 2862, 3028, 3046, 3259, 4105, 4349, 4800
Bsl I (11): 264, 861, 1052, 2583, 2862, 3028, 3046, 3259, 4105, 4349, 4800
Bsm I (0)
Bsm I (0)
*Bsm*A I (5): 2108, 3375, 3780, 3906, 4293
*Bsm*A I (2): 1051, 1338
*Bsp*1286 I (7): 18, 936, 1507, 1592, 2753, 3663, 3890
*Bsp*D I (0)
*Bsp*E I (0)
*Bsp*H I (3): 1234, 1339, 2347
*Bsp*M I (0)
*Bsp*M I (1): 63
*Bsp*M II (0)
*Bsp*W I (26): 102, 866, 1935, 2055, 2443, 3015, 3129, 3194, 3360, 3450, 3546, 3648, 3735, 3872, 3879, 4080, 4087, 4089, 4231, 4325, 4409, 4453, 4668, 4698, 4707, 4733
Bsr I (14): 1529, 1968, 2011, 2129, 2535, 3497, 3599, 3836, 3988, 4298, 4397, 4558, 4584, 4806
Bsr I (6): 1153, 1703, 2651, 2664, 3338, 3537
*Bsr*F I (2): 2094, 3369
*Bss*H II (1): 4094
*Bst*1107 I (0)
*Bst*B I (1): 654
*Bst*E II (1): 3864
*Bst*N I (13): 764, 932, 941, 2907, 2920, 3041, 3407, 3722, 4262, 4319, 4458, 4595,4722
*Bst*U I (26): 360, 1007, 1009, 1112, 1287, 1619, 2112, 2442, 3023, 3282, 3396, 3433, 3483, 3554, 3572, 3588, 3677, 3684, 3832, 3878, 3913, 4095, 4119, 4350, 4352, 4956
*Bst*X I (3): 3478, 3607, 3730
*Bst*Y I (8): 914, 945, 1532, 1549, 2317, 2329, 2415, 2426
*Bsu*36 I (1): 4775
*Cfr*10 I (2): 2094, 3369
Cla I (0)
Dde I (8): 624, 1252, 1678, 2218, 2384, 2793, 4255, 4776
Dpn I (23): 660, 693, 915, 946, 998, 1497, 1533, 1550, 1808, 1854, 1872, 2213, 2318, 2330, 2408, 2416, 2427, 2502, 3594, 3698, 4071, 4673, 4769
Dpn II (23): 660, 693, 915, 946, 998, 1497, 1533, 1550, 1808, 1854, 1872, 2213, 2318, 2330, 2408, 2416, 2427, 2502, 3594, 3698, 4071, 4673, 4769
Dra I (5): 683, 792, 1599, 2291, 2310
Dra II (4): 289, 935, 936, 1198
Dra III (0)
Drd I (2): 1096, 2959
Dsa I (1): 4884
Dsa V (23): 764, 932, 941, 950, 959, 960, 1052, 1087, 1642, 1993, 2689, 2907, 2920, 3041, 3302, 3407, 3722, 4111, 4262, 4319, 4458, 4595, 4722
Eae I (5): 463, 975, 1786, 4357, 4560
Eag I (1): 975
*Eam*1105 I (1): 2174
Ear I (0)
Ear I (5): 338, 1381, 3185, 3302, 4654
*Ecl*136 II (0)
*Eco*47 III (0)
*Eco*57 I (1): 1492
*Eco*57 I (1): 2540
*Eco*N I (1): 264
*Eco*O109 I (4): 289, 935, 936, 1198
*Eco*R I (1): 954
*Eco*R II (13): 764, 932, 941, 2907, 2920, 3041, 3407, 3722, 4262, 4319, 4458, 4595,4722
*Eco*R V (1): 4131

(continued on back)

Esp I (0)
*Esp*3 I (1): 4292
*Esp*3 I (1): 1051
*Fnu*4H I (30): 42, 974, 977, 1046, 1143, 1434, 1663, 1758, 1785, 1935, 2124, 2452, 2658, 2661, 2726, 2869, 3024, 3142, 3145, 3163, 3450, 3573, 3637, 3657, 3744, 4115, 4244, 4373, 4622, 4695
Fok I (7): 767, 1082, 1727, 2014, 2195, 3716,3725
Fok I (3): 692, 887, 4615
Fsp I (2): 1954, 4692
Hae II (6): 2823, 3193, 3298, 4079, 4322, 4713
Hae III (22): 291, 464, 859, 937, 976, 1200, 1787, 2054, 2134, 2592, 3026, 3044, 3055, 3410, 3545, 3891, 4260, 4358, 4561, 4663, 4780, 4949
Hga I (3): 726, 1638, 4954
Hga I (8): 25, 1103, 2378, 2956, 3630, 3675, 3904, 3910
*Hgi*A I (5): 18, 1507, 1592, 2753, 3663
Hha I (34): 109, 138, 359, 1008, 1111, 1141, 1286, 1618, 1955, 2048, 2441, 2550, 2724, 2824, 2891, 3161, 3194, 3299, 3555, 3589, 3678, 3879, 3912, 4080, 4087, 4094, 4096, 4118, 4323, 4351, 4416, 4693, 4714, 4829
*Hin*c II (4): 182, 964, 1635, 4187
*Hin*d II (4): 182, 964, 1635, 4187
*Hin*d III (0)
*Hin*f I (10): 967, 2180, 2697, 3093, 3168, 3311, 4107, 4362, 4553, 4891
*Hin*p I (34): 109, 138, 359, 1008, 1111, 1141, 1286, 1618, 1955, 2048, 2441, 2550, 2724, 2824, 2891, 3161, 3194, 3299, 3555, 3589, 3678, 3879, 3912, 4080, 4087, 4094, 4096, 4118, 4323, 4351, 4416, 4693, 4714, 4829
Hpa I (0)
Hpa II (21): 951, 960, 1053, 1087, 1642, 1884, 1994, 2061, 2095, 2499, 2689, 2715, 2862, 3303, 3370, 3762, 4003, 4111, 4480, 4730, 4748
Hph I (12): 369, 438, 690, 1017, 1026, 1475, 2097, 2324, 3326, 3401, 4268, 4301
Hph I (3): 1453, 1694, 3859
Kas I (1): 4322
Kpn I (0)
*Ksp*632 I (0)
*Ksp*632 I (5): 338, 1381, 3185, 3302, 4654
Mae I (4): 270, 1986, 2321, 2574
Mae II (13): 1, 473, 800, 882, 1160, 1257, 1577, 1950, 2366, 3345, 3418, 4576,4845
Mae III (19): 699, 985, 1062, 1157, 1519, 1707, 1860, 1918, 2249, 2532, 2648, 2711, 3342, 3865, 4581, 4601, 4821, 4847,4905
Mam I (0)
Mbo I (23): 660, 693, 915, 946, 998, 1497, 1533, 1550, 1808, 1854, 1872, 2213, 2318, 2330, 2408, 2416, 2427, 2502, 3594, 3698, 4071, 4673, 4769
Mbo II (4): 412, 2411, 3664, 4764
Mbo II (13): 330, 342, 657, 1189, 1385, 1494, 1572, 2327, 3189, 3306, 3822, 4161,4658
Mlu I (1): 3683
Mnl I (7): 1806, 2012, 2890, 3173, 4028, 4654,4771
Mnl I (11): 903, 1004, 1034, 1202, 2149, 2230, 2630, 2954, 3535, 4342, 4800
Msc I (1): 463
Mse I (22): 190, 286, 445, 450, 684, 793, 1228, 1600, 1965, 2004, 2239, 2292, 2306, 2311, 2363, 3580, 3703, 3897, 4368, 4427, 4611, 4920
Msp I (21): 951, 960, 1053, 1087, 1642, 1884, 1994, 2061, 2095, 2499, 2689, 2715, 2862, 3303, 3370, 3762, 4003, 4111, 4480, 4730, 4748
Mun I (0)
Nae I (0)
Nar I (1): 4322
Nci I (10): 950, 959, 960, 1052, 1087, 1642, 1993, 2689, 3302, 4111
Nco I (0)
Nde I (0)
*Ngo*M I (0)
Nhe I (0)
Nla III (22): 257, 497, 696, 716, 749, 856, 1043, 1148, 1235, 1340, 1733, 1769, 1847, 1857, 2348, 3068, 3292, 3819, 3998, 4019, 4171, 4543
Nla IV (18): 752, 935, 936, 937, 945, 1290, 1880, 2091, 2132, 2226, 2998, 3037, 3603, 3890, 4322, 4452, 4732, 4744
Not I (1): 974
Nru I (0)
Nsi I (0)
Nsp I (3): 496, 1042, 3067
*Nsp*B II (8): 1117, 1541, 2482, 2727, 3711, 4281, 4374, 4642
Pac I (0)
*Pae*R7 I (1): 969
*Pfl*M I (1): 3259
Ple I (2): 962, 2692
Ple I (4): 2180, 3168, 3311, 4107
Pme I (0)
Pml I (0)
*Ppu*M I (0)
*Psp*1406 I (3): 1576, 1949, 3344
Pst I (1): 1933
Pvu I (2): 1807, 4672
Pvu II (3): 4281, 4374, 4642
Rsa I (3): 830, 1697, 3829
Rsr II (0)
Sac I (0)
Sac II (0)
Sal I (1): 964
Sau I (1): 4775
*Sau*3A I (23): 660, 693, 915, 946, 998, 1497, 1533, 1550, 1808, 1854, 1872, 2213, 2318, 2330, 2408, 2416, 2427, 2502, 3594, 3698, 4071, 4673, 4769
*Sau*96 I (15): 290, 752, 936, 937, 1199, 1815, 2037, 2054, 2133, 3545, 3890, 3891, 4235, 4259, 4663
Sca I (2): 829, 1696
Sce I (0)
Sce I (0)
*Scr*F I (23): 764, 932, 941, 950, 959, 960, 1052, 1087, 1642, 1993, 2689, 2907, 2920, 3041, 3302, 3407, 3722, 4111, 4262, 4319, 4458, 4595, 4722
Sdu I (7): 18, 936, 1507, 1592, 2753, 3663,3890
Sec I (10): 932, 940, 941, 949, 959, 2907, 4318, 4457, 4594, 4884
*Sfa*N I (5): 980, 1718, 3221, 3848, 4039
*Sfa*N I (10): 759, 1074, 1479, 1919, 2971, 3191, 3717, 4046, 4804, 4817
Sfc I (4): 1933, 2611, 2802, 4940
Sfi I (0)
*Sgr*A I (0)
Sin I (4): 752, 1815, 2037, 4235
Sma I (1): 959
*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, 1372
Stu I (0)
Sty I (0)
Swa I (1): 682
Taq I (11): 7, 308, 576, 655, 965, 970, 1525, 2969, 3262, 3621, 3643
Tfi I (4): 3093, 4362, 4553, 4891
*Tth*111 I (1): 1151
Xba I (0)
Xcm I (3): 3532, 4048, 4066
Xho I (1): 969
Xho II (8): 914, 945, 1532, 1549, 2317, 2329, 2415, 2426
Xma I (1): 959
Xmn I (2): 647, 1575

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LOCUS       pGEX-6P-1      4984 bp
BASE COUNT      1228 A   1207 C   1297 G   1252 T
ORIGIN
        1 ACGTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
       61 GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
      121 TCTGGATAAT GTTTTTTGCG 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 CTATCCCACA AATTGATAAG TACTTGAAAT
      841 CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
      901 ATCCTCCAAA ATCGGATCTG GAAGTTCTGT TCCAGGGGCC CCTGGGATCC CCGGAATTCC
      961 CGGGTCGACT CGAGCGGCCG CATCGTGACT GACTGACGAT CTGCCTCGCG CGTTTCGGTG
     1021 ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC GGTCACAGCT TGTCTGTAAG
     1081 CGGATGCCGG GAGCAGACAA GCCCGTCAGG GCGCGTCAGC GGGTGTTGGC GGGTGTCGGG
     1141 GCGCAGCCAT GACCCAGTCA CGTAGCGATA GCGGAGTGTA TAATTCTTGA AGACGAAAGG
     1201 GCCTCGTGAT ACGCCTATTT TTATAGGTTA ATGTCATGAT AATAATGGTT TCTTAGACGT
     1261 CAGGTGGCAC TTTTCGGGGA AATGTGCGCG GAACCCCTAT TTGTTTATTT TTCTAAATAC
     1321 ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCCTGATA AATGCTTCAA TAATATTGAA
     1381 AAAGGAAGAG TATGAGTATT CAACATTTCC GTGTCGCCCT TATTCCCTTT TTTGCGGCAT
     1441 TTTGCCTTCC TGTTTTTGCT CACCCAGAAA CGCTGGTGAA AGTAAAAGAT GCTGAAGATC
     1501 AGTTGGGTGC ACGAGTGGGT TACATCGAAC TGGATCTCAA CAGCGGTAAG ATCCTTGAGA
     1561 GTTTTCGCCC CGAAGAACGT TTTCCAATGA TGAGCACTTT TAAAGTTCTG CTATGTGGCG
     1621 CGGTATTATC CCGTGTTGAC GCCGGGCAAG AGCAACTCGG TCGCCGCATA CACTATTCTC
     1681 AGAATGACTT GGTTGAGTAC TCACCAGTCA CAGAAAAGCA TCTTACGGAT GGCATGACAG
     1741 TAAGAGAATT ATGCAGTGCT GCCATAACCA TGAGTGATAA CACTGCGGCC AACTTACTTC
     1801 TGACAACGAT CGGAGGACCG AAGGAGCTAA CCGCTTTTTT GCACAACATG GGGGATCATG
     1861 TAACTCGCCT TGATCGTTGG GAACCGGAGC TGAATGAAGC CATACCAAAC GACGAGCGTG
     1921 ACACCACGAT GCCTGCAGCA ATGGCAACAA CGTTGCGCAA ACTATTAACT GGCGAACTAC
     1981 TTACTCTAGC TTCCCGGCAA CAATTAATAG ACTGGATGGA GGCGGATAAA GTTGCAGGAC
     2041 CACTTCTGCG CTCGGCCCTT CCGGCTGGCT GGTTTATTGC TGATAAATCT GGAGCCGGTG
     2101 AGCGTGGGTC TCGCGGTATC ATTGCAGCAC TGGGGCCAGA TGGTAAGCCC TCCCGTATCG
     2161 TAGTTATCTA CACGACGGGG AGTCAGGCAA CTATGGATGA ACGAAATAGA CAGATCGCTG
     2221 AGATAGGTGC CTCACTGATT AAGCATTGGT AACTGTCAGA CCAAGTTTAC TCATATATAC
     2281 TTTAGATTGA TTTAAAACTT CATTTTTAAT TTAAAAGGAT CTAGGTGAAG ATCCTTTTTG
     2341 ATAATCTCAT GACCAAAATC CCTTAACGTG AGTTTTCGTT CCACTGAGCG TCAGACCCCG
     2401 TAGAAAAGAT CAAAGGATCT TCTTGAGATC CTTTTTTTCT GCGCGTAATC TGCTGCTTGC
     2461 AAACAAAAAA ACCACCGCTA CCAGCGGTGG TTTGTTTGCC GGATCAAGAG CTACCAACTC
     2521 TTTTTCCGAA GGTAACTGGC TTCAGCAGAG CGCAGATACC AAATACTGTC CTTCTAGTGT
     2581 AGCCGTAGTT AGGCCACCAC TTCAAGAACT CTGTAGCACC GCCTACATAC CTCGCTCTGC
     2641 TAATCCTGTT ACCAGTGGCT GCTGCCAGTG GCGATAAGTC GTGTCTTACC GGGTTGGACT
     2701 CAAGACGATA GTTACCGGAT AAGGCGCAGC GGTCGGGCTG AACGGGGGGT TCGTGCACAC
     2761 AGCCCAGCTT GGAGCGAACG ACCTACACCG AACTGAGATA CCTACAGCGT GAGCTATGAG
     2821 AAAGCGCCAC GCTTCCCGAA GGGAGAAAGG CGGACAGGTA TCCGGTAAGC GGCAGGGTCG
     2881 GAACAGGAGA GCGCACGAGG GAGCTTCCAG GGGGAAACGC CTGGTATCTT TATAGTCCTG
     2941 TCGGGTTTCG CCACCTCTGA CTTGAGCGTC GATTTTTGTG ATGCTCGTCA GGGGGGCGGA
     3001 GCCTATGGAA AAACGCCAGC AACGCGGCCT TTTTACGGTT CCTGGCCTTT TGCTGGCCTT
     3061 TTGCTCACAT GTTCTTTCCT GCGTTATCCC CTGATTCTGT GGATAACCGT ATTACCGCCT
     3121 TTGAGTGAGC TGATACCGCT CGCCGCAGCC GAACGACCGA GCGCAGCGAG TCAGTGAGCG
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3181 AGGAAGCGGA AGAGCGCCTG ATGCGGTATT TTCTCCTTAC GCATCTGTGC GGTATTTCAC
3241 ACCGCATAAA TTCCGACACC ATCGAATGGT GCAAAACCTT TCGCGGTATG GCATGATAGC
3301 GCCCGGAAGA GAGTCAATTC AGGGTGGTGA ATGTGAAACC AGTAACGTTA TACGATGTCG
3361 CAGAGTATGC CGGTGTCTCT TATCAGACCG TTTCCCGCGT GGTGAACCAG GCCAGCCACG
3421 TTTCTGCGAA AACGCGGGAA AAAGTGGAAG CGGCGATGGC GGAGCTGAAT TACATTCCCA
3481 ACCGCGTGGC ACAACAACTG GCGGGCAAAC AGTCGTTGCT GATTGGCGTT GCCACCTCCA
3541 GTCTGGCCCT GCACGCGCCG TCGCAAATTG TCGCGGCGAT TAAATCTCGC GCCGATCAAC
3601 TGGGTGCCAG CGTGGTGGTG TCGATGGTAG AACGAAGCGG CGTCGAAGCC TGTAAAGCGG
3661 CGGTGCACAA TCTTCTCGCG CAACGCGTCA GTGGGCTGAT CATTAACTAT CCGCTGGATG
3721 ACCAGGATGC CATTGCTGTG GAAGCTGCCT GCACTAATGT TCCGGCGTTA TTTCTTGATG
3781 TCTCTGACCA GACACCCATC AACAGTATTA TTTTCTCCCA TGAAGACGGT ACGCGACTGG
3841 GCGTGGAGCA TCTGGTCGCA TTGGGTCACC AGCAAATCGC GCTGTTAGCG GGCCCATTAA
3901 GTTCTGTCTC GGCGCGTCTG CGTCTGGCTG GCTGGCATAA ATATCTCACT CGCAATCAAA
3961 TTCAGCCGAT AGCGGAACGG GAAGGCGACT GGAGTGCCAT GTCCGGTTTT CAACAAACCA
4021 TGCAAATGCT GAATGAGGGC ATCGTTCCCA CTGCGATGCT GGTTGCCAAC GATCAGATGG
4081 CGCTGGGCGC AATGCGCGCC ATTACCGAGT CCGGGCTGCG CGTTGGTGCG GATATCTCGG
4141 TAGTGGGATA CGACGATACC GAAGACAGCT CATGTTATAT CCCGCCGTCA ACCACCATCA
4201 AACAGGATTT TCGCCTGCTG GGGCAAACCA GCGTGGACCG CTTGCTGCAA CTCTCTCAGG
4261 GCCAGGCGGT GAAGGGCAAT CAGCTGTTGC CCGTCTCACT GGTGAAAAGA AAAACCACCC
4321 TGGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC CGATTCATTA ATGCAGCTGG
4381 CACGACAGGT TTCCCGACTG GAAAGCGGGC AGTGAGCGCA ACGCAATTAA TGTGAGTTAG
4441 CTCACTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC CGGCTCGTAT GTTGTGTGGA
4501 ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG ACCATGATTA CGGATTCACT
4561 GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC TTAATCGCCT
4621 TGCAGCACAT CCCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATCGCCC
4681 TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGCGCTTT GCCTGGTTTC CGGCACCAGA
4741 AGCGGTGCCG GAAAGCTGGC TGGAGTGCGA TCTTCCTGAG GCCGATACTG TCGTCGTCCC
4801 CTCAAACTGG CAGATGCACG GTTACGATGC GCCCATCTAC ACCAACGTAA CCTATCCCAT
4861 TACGGTCAAT CCGCCGTTTG TTCCCACGGA GAATCCGACG GGTTGTTACT CGCTCACATT
4921 TAATGTTGAT GAAAGCTGGC TACAGGAAGG CCAGACGCGA ATTATTTTTG ATGGCGTTGG
4981 AATT