

Restriction sites for pGEX-4T-3

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-3 was not tested with each enzyme and therefore the accuracy of the table cannot be guaranteed. Please contact your local Amersham Biosciences 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): 1240

Acc I (1): 948

*Acc*65 I (0):

Aci I (20): 924, 962, 1319, 1648, 1815, 2459, 2603, 3099, 3120, 3127, 3226, 3379, 3466, 3695, 4166, 4222, 4323, 4333, 4650, 4855

Aci I (39): 225, 549, 958, 1064, 1103, 1113, 1155, 1272, 1418, 1527, 1604, 1769, 2006, 2097, 2468, 2713, 2834, 2853, 2980, 3008, 3170, 3187, 3213, 3267, 3418, 3434, 3443, 3485, 3557, 3621, 3641, 3644, 3872, 3956, 4112, 4250, 4389, 4492, 4726

Afl II (0):

Afl III (3): 496, 3051, 3667

Age I (0):

Aha II (5): 34, 1240, 1622, 3623, 4306

Alu I (25): 54, 178, 482, 631, 809, 1032, 1051, 1809, 1872, 1972, 2493, 2750, 2796, 2886, 3112, 3447, 3727, 4151, 4266, 4359, 4423, 4518, 4627, 4738, 4918

Alw I (7): 914, 930, 1516, 1837, 2301, 2399, 2485

Alw I (4): 926, 1529, 2309, 2406

*Alw*N I (1): 2637

Apa I (1): 3874

*Apa*L I (4): 18, 1491, 2737, 3647

Apo I (3): 938, 3232, 3942

Asc I (0):

Ase I (4): 189, 1987, 4351, 4410

Asu I (13): 290, 752, 1183, 1799, 2021, 2038, 2117, 3529, 3874, 3875, 4219, 4243, 4647

Asu II (1): 654

Ava I (2): 943, 953

Ava II (4): 752, 1799, 2021, 4219

Ava III (0):

Avr II (0):

Bal I (1): 463

*Bam*H I (1): 930

Ban I (6): 2210, 3587, 4306, 4436, 4716, 4728

Ban II (1): 3874

*Bbr*P I (0):

Bbs I (3): 1173, 3806, 4145

Bbs I (0):

Bbv I (11): 42, 1030, 1127, 1919, 4606, 4679

Bbv I (7): 1730, 2424, 2630, 2633, 3716, 4087, 4216

Bcg I (1): 3970

Bcg I (2): 299, 1636

Bcl I (2): 692, 3681

Bfa I (4): 270, 1970, 2305, 2558

Bfr I (0):

Bgl I (2): 2039, 4682

Bgl II (0):

Bpm I (3): 2073, 3973, 4744

Bpm I (1): 3520

*Bpu*1102 I (0):

Bsa I (1): 2091

Bsa I (0):

*Bsa*A I (1): 1143

*Bsa*B I (0):

*Bsa*H I (5): 34, 1240, 1622, 3623, 4306

*Bsa*J I (6): 943, 2891, 4302, 4441, 4578, 4868

*Bse*A I (0):

Bsg I (2): 69, 523

Bsg I (3): 11, 3533, 3733

*Bsi*E I (6): 959, 1642, 1791, 2714, 3138, 4656

*Bsi*W I (0):

*Bsi*Y I (11): 264, 861, 1036, 2567, 2846, 3012, 3030, 3243, 4089, 4333, 4784

Bsl I (11): 264, 861, 1036, 2567, 2846, 3012, 3030, 3243, 4089, 4333, 4784

Bsm I (0):

Bsm I (0):

*Bsm*A I (5): 2092, 3359, 3764, 3890, 4277

*Bsm*A I (2): 1035, 1322

*Bsp*1286 I (6): 18, 1491, 1576, 2737, 3647, 3874

*Bsp*D I (0):

*Bsp*E I (0):

*Bsp*H I (3): 1218, 1323, 2331

*Bsp*M I (0):

*Bsp*M I (1): 63

*Bsp*M II (0):

*Bsp*W I (26): 102, 866, 1919, 2039, 2427, 2999, 3113, 3178, 3344, 3434, 3530, 3632, 3719, 3856, 3863, 4064, 4071, 4073, 4215, 4309, 4393, 4437, 4652, 4682, 4691, 4717

Bsr I (14): 1513, 1952, 1995, 2113,

2519, 3481, 3583, 3820, 3972, 4282, 4381, 4542, 4568, 4790

Bsr I (6): 1137, 1687, 2635, 2648, 3322, 3521

*Bsr*F I (2): 2078, 3353

*Bss*H II (1): 4078

*Bst*1107 I (0):

*Bst*B I (1): 654

*Bst*E II (1): 3848

*Bst*N I (11): 764, 2891, 2904, 3025, 3391, 3706, 4246, 4303, 4442, 4579, 4706

*Bst*U I (27): 360, 925, 991, 993, 1096, 1271, 1603, 2096, 2426, 3007, 3266, 3380, 3417, 3467, 3538, 3556, 3572, 3661, 3668, 3816, 3862, 3897, 4079, 4103, 4334, 4336, 4940

*Bst*X I (3): 3462, 3591, 3714

*Bst*Y I (8): 914, 930, 1516, 1533, 2301, 2313, 2399, 2410

*Bsu*36 I (1): 4759

*Cfr*10 I (2): 2078, 3353

Cla I (0):

Dde I (8): 624, 1236, 1662, 2202, 2368, 2777, 4239, 4760

Dpn I (23): 660, 693, 915, 931, 982, 1481, 1517, 1534, 1792, 1838, 1856, 2197, 2302, 2314, 2392, 2400, 2411, 2486, 3578, 3682, 4055, 4657, 4753

Dpn II (23): 660, 693, 915, 931, 982, 1481, 1517, 1534, 1792, 1838, 1856, 2197, 2302, 2314, 2392, 2400, 2411, 2486, 3578, 3682, 4055, 4657, 4753

Dra I (5): 683, 792, 1583, 2275, 2294

Dra II (2): 289, 1182

Dra III (0):

Drd I (2): 1080, 2943

Dsa I (1): 4868

Dsa V (20): 764, 943, 944, 1036, 1071, 1626, 1977, 2673, 2891, 2904, 3025, 3286, 3391, 3706, 4095, 4246, 4303, 4442, 4579, 4706

Eae I (5): 463, 959, 1770, 4341, 4544

Eag I (1): 959

*Eam*1105 I (1): 2158

Ear I (0):

Ear I (5): 338, 1365, 3169, 3286, 4638

*Ecl*136 II (0):

*Eco*47 III (0):

*Eco*57 I (1): 1476

*Eco*57 I (1): 2524

*Eco*N I (1): 264

*Eco*O109 I (2): 289, 1182

*Eco*R I (1): 938

*Eco*R II (11): 764, 2891, 2904, 3025, 3391, 3706, 4246, 4303, 4442,

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4579, 4706
EcoR V (1): 4115
Esp I (0):
Esp3 I (1): 4276
Esp3 I (1): 1035
Fnu4H I (30): 42, 958, 961, 1030, 1127, 1418, 1647, 1742, 1769, 1919, 2108, 2436, 2642, 2645, 2710, 2853, 3008, 3126, 3129, 3147, 3434, 3557, 3621, 3641, 3728, 4099, 4228, 4357, 4606, 4679
Fok I (7): 767, 1066, 1711, 1998, 2179, 3700, 3709
Fok I (3): 692, 887, 4599
Fsp I (2): 1938, 4676
Hae II (6): 2807, 3177, 3282, 4063, 4306, 4697
Hae III (21): 291, 464, 859, 960, 1184, 1771, 2038, 2118, 2576, 3010, 3028, 3039, 3394, 3529, 3875, 4244, 4342, 4545, 4647, 4764, 4933
Hga I (3): 726, 1622, 4938
Hga I (8): 25, 1087, 2362, 2940, 3614, 3659, 3888, 3894
HgiA I (5): 18, 1491, 1576, 2737, 3647
Hha I (34): 109, 138, 359, 992, 1095, 1125, 1270, 1602, 1939, 2032, 2425, 2534, 2708, 2808, 2875, 3145, 3178, 3283, 3539, 3573, 3662, 3863, 3896, 4064, 4071, 4078, 4080, 4102, 4307, 4335, 4400, 4677, 4698, 4813
Hinc II (4): 182, 948, 1619, 4171
Hind II (4): 182, 948, 1619, 4171
Hind III (0):
Hinf I (10): 951, 2164, 2681, 3077, 3152, 3295, 4091, 4346, 4537, 4875
Hinp I (34): 109, 138, 359, 992, 1095, 1125, 1270, 1602, 1939, 2032, 2425, 2534, 2708, 2808, 2875, 3145, 3178, 3283, 3539, 3573, 3662, 3863, 3896, 4064, 4071, 4078, 4080, 4102, 4307, 4335, 4400, 4677, 4698, 4813
Hpa I (1): 4171
Hpa II (20): 944, 1037, 1071, 1626, 1868, 1978, 2045, 2079, 2483, 2673, 2699, 2846, 3287, 3354, 3746, 3987, 4095, 4464, 4714, 4732
Hph I (12): 369, 438, 690, 1001, 1010, 1459, 2081, 2308, 3310, 3385, 4252, 4285
Hph I (3): 1437, 1678, 3843
Kas I (1): 4306
Kpn I (0):
Ksp632 I (0):
Ksp632 I (5): 338, 1365, 3169, 3286, 4638
Mae I (4): 270, 1970, 2305, 2558
Mae II (13): 1, 473, 800, 882, 1144, 1241, 1561, 1934, 2350, 3329, 3402, 4560, 4829
Mae III (19): 699, 969, 1046, 1141, 1503, 1691, 1844, 1902, 2233, 2516, 2632, 2695, 3326, 3849, 4565, 4585, 4805, 4831, 4889
Mam I (0):
Mbo I (23): 660, 693, 915, 931, 982, 1481, 1517, 1534, 1792, 1838, 1856, 2197, 2302, 2314, 2392, 2400, 2411, 2486, 3578, 3682, 4055, 4657, 4753
Mbo II (4): 412, 2395, 3648, 4748
Mbo II (13): 330, 342, 657, 1173, 1369, 1478, 1556, 2311, 3173, 3290, 3806, 4145, 4642
Mlu I (1): 3667
Mnl I (7): 1790, 1996, 2874, 3157, 4012, 4638, 4755
Mnl I (11): 903, 988, 1018, 1186, 2133, 2214, 2614, 2938, 3519, 4326, 4784
Msc I (1): 463
Mse I (23): 190, 286, 445, 450, 684, 793, 1212, 1584, 1949, 1988, 2223, 2276, 2290, 2295, 2347, 3564, 3687, 3881, 4172, 4352, 4411, 4595, 4904
Msp I (20): 944, 1037, 1071, 1626, 1868, 1978, 2045, 2079, 2483, 2673, 2699, 2846, 3287, 3354, 3746, 3987, 4095, 4464, 4714, 4732
Mun I (0):
Nae I (0):
Nar I (1): 4306
Nci I (9): 943, 944, 1036, 1071, 1626, 1977, 2673, 3286, 4095
Nco I (0):
Nde I (0):
NgoM I (0):
Nhe I (0):
Nla III (22): 257, 497, 696, 716, 749, 856, 1027, 1132, 1219, 1324, 1717, 1753, 1831, 1841, 2332, 3052, 3276, 3803, 3982, 4003, 4155, 4527
Nla IV (16): 752, 920, 930, 1274, 1864, 2075, 2116, 2210, 2982, 3021, 3587, 3874, 4306, 4436, 4716, 4728
Not I (1): 958
Nru I (0):
Nsi I (0):
Nsp I (3): 496, 1026, 3051
NspB II (8): 1101, 1525, 2466, 2711, 3695, 4265, 4358, 4626
Pac I (0):
PaeR7 I (1): 953
PflM I (1): 3243
Ple I (2): 946, 2676
Ple I (4): 2164, 3152, 3295, 4091
Pme I (0):
Pml I (0):
PpuM I (0):
Pst I (1): 1917
Pvu I (2): 1791, 4656
Pvu II (3): 4265, 4358, 4626
Rsa I (3): 830, 1681, 3813
Rsr II (0):
Sac I (0):
Sac II (0):
Sal I (1): 948
Sau I (1): 4759
Sau3A I (23): 660, 693, 915, 931, 982, 1481, 1517, 1534, 1792, 1838, 1856, 2197, 2302, 2314, 2392, 2400, 2411, 2486, 3578, 3682, 4055, 4657, 4753
Sau96 I (13): 290, 752, 1183, 1799, 2021, 2038, 2117, 3529, 3874, 3875, 4219, 4243, 4647
Sca I (2): 829, 1680
Sce I (0):
Sce I (0):
ScrF I (20): 764, 943, 944, 1036, 1071, 1626, 1977, 2673, 2891, 2904, 3025, 3286, 3391, 3706, 4095, 4246, 4303, 4442, 4579, 4706
Sdu I (6): 18, 1491, 1576, 2737, 3647, 3874
Sec I (6): 943, 2891, 4302, 4441, 4578, 4868
SfaN I (5): 964, 1702, 3205, 3832, 4023
SfaN I (10): 759, 1058, 1463, 1903, 2955, 3175, 3701, 4030, 4788, 4801
Sfc I (4): 1917, 2595, 2786, 4924
Sfi I (0):
SgrA I (0):
Sin I (4): 752, 1799, 2021, 4219
Sma I (1): 943
SnaB I (0):
Spe I (0):
Sph I (0):
Spl I (0):
Spo I (0):
Srf I (0):
Sse8387 I (0):
Ssp I (2): 164, 1356
Stu I (0):
Sty I (0):
Swa I (1): 682
Taq I (11): 7, 308, 576, 655, 949, 954, 1509, 2953, 3246, 3605, 3627
Tfi I (4): 3077, 4346, 4537, 4875
Tth111 I (1): 1135
Xba I (0):
Xcm I (3): 3516, 4032, 4050
Xho I (1): 953
Xho II (8): 914, 930, 1516, 1533, 2301, 2313, 2399, 2410
Xma I (1): 943
Xmn I (2): 647, 1559

LOCUS pGEX-4T-3 4968 bp

BASE COUNT 1225 A 1202 C 1291 G 1250 T

ORIGIN

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1 ACGTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
61 GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
121 TCTGGATAAT GTTTTTTTCG CCGACATCAT AACGGTTCTG GCAAATATTC TGAAATGAGC
181 TGTTGACAAT TAATCATCGG CTCGTATAAT GTGTGGAATT GTGAGCGGAT AACAAATTTCA
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 ATGTTTGAAG
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 GATCCCCGAA TTCCCGGGTC GACTCGAGCG
961 GCCGCATCGT GACTGACTGA CGATCTGCCT CGCGCGTTTC GGTGATGACG GTGAAAACCT
1021 CTGACACATG CAGCTCCCGG AGACGGTCAC AGCTTGTCTG TAAGCGGATG CCGGGAGCAG
1081 ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT CGGGGCGCAG CCATGACCCA
1141 GTCACGTAGC GATAGCGGAG TGTATAATTC TTGAAGACGA AAGGGCCTCG TGATACGCCT
1201 ATTTTTATAG GTTAATGTCA TGATAATAAT GGTTCCTTAG ACGTCAGGTG GCACTTTTCG
1261 GGGAAATGTG CGCGGAACCC CTATTTGTTT ATTTTCTAA ATACATTCAA ATATGTATCC
1321 GCTCATGAGA CAATAACCTT GATAAATGCT TCAATAATAT TGAAAAAGGA AGAGTATGAG
1381 TATTCAACAT TTCCGTGTCG CCCTTATTCC CTTTTTTCG GCATTTTGCC TTCCTGTTTT
1441 TGCTACCCA GAAACGCTGG TGAAAGTAAA AGATGCTGAA GATCAGTTGG GTGCACGAGT
1501 GGGTTACATC GAACTGGATC TCAACAGCGG TAAGATCCTT GAGAGTTTTT GCCCGAAGA
1561 ACGTTTTTCCA ATGATGAGCA CTTTTAAAGT TCTGCTATGT GCGCGGTAT TATCCCGTGT
1621 TGACGCCGGG CAAGAGCAAC TCGGTCGCCG CATACACTAT TCTCAGAATG ACTTGTTTGA
1681 GTACTACCA GTCACAGAAA AGCATCTTAC GGATGGCATG ACAGTAAGAG AATTATGCAG
1741 TGCTGCCATA ACCATGAGTG ATAACACTGC GGCCAACTTA CTTCTGACAA CGATCGGAGG
1801 ACCGAAGGAG CTAACCGCTT TTTTGCACAA CATGGGGGAT CATGTAAGTC GCCTTGATCG
1861 TTGGGAACCG GAGCTGAATG AAGCCATACC AAACGACGAG CGTGACACCA CGATGCCTGC
1921 AGCAATGGCA ACAACGTTGC GCAAATATT AACTGGCGAA CTACTTACTC TAGCTTCCCG
1981 GCAACAATTA ATAGACTGGA TGGAGGCGGA TAAAGTTGCA GGACCACTTC TCGCTCGGC
2041 CTTCCGGCT GGCTGGTTTA TTGCTGATAA ATCTGGAGCC GGTGAGCGTG GGTCTCGCGG
2101 TATCATTGCA GCACTGGGGC CAGATGGTAA GCCCTCCCGT ATCGTAGTTA TCTACACGAC
2161 GGGGAGTCAG GCAACTATGG ATGAACGAAA TAGACAGATC GCTGAGATAG GTGCCTCACT
2221 GATTAAGCAT TGGTAACTGT CAGACCAAGT TTAATCATAT ATACTTTAGA TTGATTTAAA
2281 ACTTCATTTT TAATTTAAAA GGATCTAGGT GAAGATCCTT TTTGATAATC TCATGACCAA
2341 AATCCCTTAA CGTGAGTTTT CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG
2401 ATCTTCTTGA GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC
2461 GCTACCAGCG GTGGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC
2521 TGGCTTCAGC AGAGCGCAGA TACCAAATAC TGTCTTCTA GTGTAGCCGT AGTTAGGCCA
2581 CCACTTCAAG AACTCTGTAG CACCGCTAC ATACCTCGCT CTGCTAATCC TGTTACCAGT
2641 GGCTGCTGCC AGTGGCGATA AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC
2701 GGATAAGGCG CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG
2761 AACGACCTAC ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC
2821 CGAAGGGAGA AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC
2881 GAGGGAGCTT CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCGGGT TTCGCCACCT
2941 CTGACTTGAG CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAACAAACG
3001 CAGCAACGCG GCCTTTTTTAC GGTTCCTGGC CTTTTGCTGG CTTTTGCTC ACATGTTCTT
3061 TCCTGCGTTA TCCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC
3121 CGCTCGCCGC AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG CGGAAGAGCG
3181 CCTGATGCGG TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TAAATTCGA
3241 CACCATCGAA TGGTGCAAAA CTTTTGCGG TATGGCATGA TAGCGCCCGG AAGAGAGTCA
3301 ATTCAGGGTG GTGAATGTGA AACCAGTAAC GTTATACGAT GTCGCAGAGT ATGCCGGTGT
3361 CTCTTATCAG ACCGTTTCCC GCGTGGTGAA CCAGGCCAGC CACGTTTCTG CGAAAACGCG
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3421 GGAAAAAGTG GAAGCGGCGA TGGCGGAGCT GAATTACATT CCCAACCGCG TGGCACAACA
3481 ACTGGCGGGC AAACAGTCGT TGCTGATTGG CGTTGCCACC TCCAGTCTGG CCCTGCACGC
3541 GCCGTCGCAA ATTGTGCGGG CGATTAAATC TCGCGCCGAT CAACTGGGTG CCAGCGTGGT
3601 GGTGTCGATG GTAGAACGAA GCGGCGTCGA AGCCTGTAAA GCGGCGGTGC ACAATCTTCT
3661 CGCGCAACGC GTCAGTGGGC TGATCATTA CTATCCGCTG GATGACCAGG ATGCCATTGC
3721 TGTGGAAGCT GCCTGCACTA ATGTTCCGGC GTTATTTCTT GATGTCTCTG ACCAGACACC
3781 CATCAACAGT ATTATTTTCT CCCATGAAGA CGGTACGCGA CTGGGCGTGG AGCATCTGGT
3841 CGCATTGGGT CACCAGCAAA TCGCGCTGTT AGCGGGCCCA TTAAGTTCTG TCTCGGCGCG
3901 TCTGCGTCTG GCTGGCTGGC ATAAATATCT CACTCGCAAT CAAATTCAGC CGATAGCGGA
3961 ACGGGAAGGC GACTGGAGTG CCATGTCCGG TTTTCAACAA ACCATGCAAA TGCTGAATGA
4021 GGGCATCGTT CCCACTGCGA TGCTGGTTGC CAACGATCAG ATGGCGCTGG GCGCAATGCG
4081 CGCCATTACC GAGTCCGGGC TCGCGCTTGG TCGGATATC TCGGTAGTGG GATACGACGA
4141 TACCGAAGAC AGCTCATGTT ATATCCCGCC GTTAACCACC ATCAAACAGG ATTTTCGCCT
4201 GCTGGGGCAA ACCAGCGTGG ACCGCTTGCT GCAACTCTCT CAGGGCCAGG CGGTGAAGGG
4261 CAATCAGCTG TTGCCCGTCT CACTGGTGAA AAGAAAAACC ACCCTGGCGC CCAATACGCA
4321 AACCGCCTCT CCCC GC GCGT TGGCCGATTC ATTAATGCAG CTGGCACGAC AGGTTTCCCG
4381 ACTGGAAAGC GGGCAGTGAG CGCAACGCAA TTAATGTGAG TTAGCTCACT CATTAGGCAC
4441 CCCAGGCTTT ACACTTTATG CTTCCGGCTC GTATGTTGTG TGGAATTGTG AGCGGATAAC
4501 AATTTACAC AGGAAACAGC TATGACCATG ATTACGGATT CACTGGCCGT CGTTTTACAA
4561 CGTCGTGACT GGGAAAACCC TGGCGTTACC CAACTTAATC GCCTTGCAGC ACATCCCCCT
4621 TTCGCCAGCT GGC GTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCA ACAGTTGCGC
4681 AGCCTGAATG GCGAATGGCG CTTTGCCTGG TTTCCGGCAC CAGAAGCGGT GCCGAAAGC
4741 TGGCTGGAGT GCGATCTTCC TGAGGCCGAT ACTGTCGTCG TCCCCTCAA CTGGCAGATG
4801 CACGGTTACG ATGCGCCCAT CTACACCAAC GTAACCTATC CCATTACGGT CAATCCGCCG
4861 TTTGTTCCA CGGAGAATCC GACGGGTTGT TACTCGCTCA CATTTAATGT TGATGAAAGC
4921 TGGCTACAGG AAGGCCAGAC GCGAATTATT TTTGATGGCG TTGGAATT