

Restriction sites for pGEX-4T-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-4T-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): 1241

Acc I (1): 949

*Acc*65 I (0):

Aci I (20): 924, 963, 1320, 1649, 1816, 2460, 2604, 3100, 3121, 3128, 3227, 3380, 3467, 3696, 4167, 4223, 4324, 4334, 4651, 4856

Aci I (39): 225, 549, 959, 1065, 1104, 1114, 1156, 1273, 1419, 1528, 1605, 1770, 2007, 2098, 2469, 2714, 2835, 2854, 2981, 3009, 3171, 3188, 3214, 3268, 3419, 3435, 3444, 3486, 3558, 3622, 3642, 3645, 3873, 3957, 4113, 4251, 4390, 4493, 4727

Afl II (0):

Afl III (3): 496, 3052, 3668

Age I (0):

Aha II (5): 34, 1241, 1623, 3624, 4307

Alu I (25): 54, 178, 482, 631, 809, 1033, 1052, 1810, 1873, 1973, 2494, 2751, 2797, 2887, 3113, 3448, 3728, 4152, 4267, 4360, 4424, 4519, 4628, 4739, 4919

Alw I (7): 914, 930, 1517, 1838, 2302, 2400, 2486

Alw I (4): 926, 1530, 2310, 2407

*Alw*N I (1): 2638

Apa I (1): 3875

*Apa*L I (4): 18, 1492, 2738, 3648

Apo I (3): 939, 3233, 3943

Asc I (0):

Ase I (4): 189, 1988, 4352, 4411

Asu I (13): 290, 752, 1184, 1800, 2022, 2039, 2118, 3530, 3875, 3876, 4220, 4244, 4648

Asu II (1): 654

Ava I (2): 944, 954

Ava II (4): 752, 1800, 2022, 4220

Ava III (0):

Avr II (0):

*Bal*I (1): 463

*Bam*HI (1): 930

Ban I (6): 2211, 3588, 4307, 4437, 4717, 4729

Ban II (1): 3875

*Bbr*P I (0):

Bbs I (3): 1174, 3807, 4146

Bbs I (0):

Bbv I (11): 42, 1031, 1128, 1920, 2109, 2711, 3130, 3148, 4358, 4607, 4680

Bbv I (7): 1731, 2425, 2631, 2634, 3717, 4088, 4217

Bcg I (1): 3971

Bcg I (2): 299, 1637

Bcl I (2): 692, 3682

Bfa I (4): 270, 1971, 2306, 2559

Bfr I (0):

*Bgl*I (2): 2040, 4683

*Bgl*II (0):

Bpm I (3): 2074, 3974, 4745

Bpm I (1): 3521

*Bpu*1102 I (0):

Bsa I (1): 2092

Bsa I (0):

*Bsa*A I (1): 1144

*Bsa*B I (0):

*Bsa*H I (5): 34, 1241, 1623, 3624, 4307

*Bsa*L I (7): 934, 944, 2892, 4303, 4442, 4579, 4869

*Bse*A I (0):

Bsg I (2): 69, 523

Bsg I (3): 11, 3534, 3734

*Bst*E I (6): 960, 1643, 1792, 2715, 3139, 4657

*Bst*W I (0):

*Bst*Y I (11): 264, 861, 1037, 2568, 2847, 3013, 3031, 3244, 4090, 4334, 4785

*Bst*I (11): 264, 861, 1037, 2568, 2847, 3013, 3031, 3244, 4090, 4334, 4785

Bsm I (0):

Bsm I (0):

*Bsm*A I (5): 2093, 3360, 3765, 3891, 4278

*Bsm*A I (2): 1036, 1323

*Bsp*1286 I (6): 18, 1492, 1577, 2738, 3648, 3875

*Bsp*D I (0):

*Bsp*E I (0):

*Bsp*H I (3): 1219, 1324, 2332

*Bsp*M I (0):

*Bsp*M I (1): 63

*Bsp*M II (0):

*Bsp*W I (26): 102, 866, 1920, 2040, 2428, 3000, 3114, 3179, 3345, 3435, 3531, 3633, 3720, 3857, 3864, 4065, 4072, 4074, 4216, 4310, 4394, 4438, 4653, 4683, 4692, 4718

Bsr I (14): 1514, 1953, 1996, 2114,

2520, 3482, 3584, 3821, 3973, 4283, 4382, 4543, 4569, 4791

Bsr I (6): 1138, 1688, 2636, 2649, 3323, 3522

*Bsr*F I (2): 2079, 3354

*Bss*H II (1): 4079

*Bst*1107 I (0):

*Bst*B I (1): 654

*Bst*E II (1): 3849

*Bst*N I (11): 764, 2892, 2905, 3026, 3392, 3707, 4247, 4304, 4443, 4580, 4707

*Bst*U I (27): 360, 925, 992, 994, 1097, 1272, 1604, 2097, 2427, 3008, 3267, 3381, 3418, 3468, 3539, 3557, 3573, 3662, 3669, 3817, 3863, 3898, 4080, 4104, 4335, 4337, 4941

*Bst*X I (3): 3463, 3592, 3715

*Bst*Y I (8): 914, 930, 1517, 1534, 2302, 2314, 2400, 2411

*Bsu*36 I (1): 4760

*Cfr*10 I (2): 2079, 3354

Cla I (0):

Dde I (8): 624, 1237, 1663, 2203, 2369, 2778, 4240, 4761

Dpn I (23): 660, 693, 915, 931, 983, 1482, 1518, 1535, 1793, 1839, 1857, 2198, 2303, 2315, 2393, 2401, 2412, 2487, 3579, 3683, 4056, 4658, 4754

Dpn II (23): 660, 693, 915, 931, 983, 1482, 1518, 1535, 1793, 1839, 1857, 2198, 2303, 2315, 2393, 2401, 2412, 2487, 3579, 3683, 4056, 4658, 4754

Dra I (5): 683, 792, 1584, 2276, 2295

Dra II (2): 289, 1183

Dra III (0):

Drd I (2): 1081, 2944

Dsa I (1): 4869

Dsa V (21): 764, 935, 944, 945, 1037, 1072, 1627, 1978, 2674, 2892, 2905, 3026, 3287, 3392, 3707, 4096, 4247, 4304, 4443, 4580, 4707

Eae I (5): 463, 960, 1771, 4342, 4545

Eag I (1): 960

*Eam*1105 I (1): 2159

Ear I (0):

Ear I (5): 338, 1366, 3170, 3287, 4639

*Ecl*136 II (0):

*Eco*47 III (0):

*Eco*57 I (1): 1477

*Eco*57 I (1): 2525

*Eco*N I (1): 264

*Eco*O109 I (2): 289, 1183

*Eco*R I (1): 939

*Eco*R II (11): 764, 2892, 2905, 3026, 3392, 3707, 4247, 4304, 4443,

4580, 4707
EcoR V (1): 4116
Esp I (0):
Esp3 I (1): 4277
Esp3 I (1): 1036
*Fnu*4H I (30): 42, 959, 962, 1031, 1128, 1419, 1648, 1743, 1770, 1920, 2109, 2437, 2643, 2646, 2711, 2854, 3009, 3127, 3130, 3148, 3435, 3558, 3622, 3642, 3729, 4100, 4229, 4358, 4607, 4680
Fok I (7): 767, 1067, 1712, 1999, 2180, 3701, 3710
Fok I (3): 692, 887, 4600
Fsp I (2): 1939, 4677
Hae II (6): 2808, 3178, 3283, 4064, 4307, 4698
Hae III (21): 291, 464, 859, 961, 1185, 1772, 2039, 2119, 2577, 3011, 3029, 3040, 3395, 3530, 3876, 4245, 4343, 4546, 4648, 4765, 4934
Hga I (3): 726, 1623, 4939
Hga I (8): 25, 1088, 2363, 2941, 3615, 3660, 3889, 3895
*Hgi*A I (5): 18, 1492, 1577, 2738, 3648
Hha I (34): 109, 138, 359, 993, 1096, 1126, 1271, 1603, 1940, 2033, 2426, 2535, 2709, 2809, 2876, 3146, 3179, 3284, 3540, 3574, 3663, 3864, 3897, 4065, 4072, 4079, 4081, 4103, 4308, 4336, 4401, 4678, 4699, 4814
Hinc II (4): 182, 949, 1620, 4172
Hind II (4): 182, 949, 1620, 4172
Hind III (0):
Hinf I (10): 952, 2165, 2682, 3078, 3153, 3296, 4092, 4347, 4538, 4876
Hinp I (34): 109, 138, 359, 993, 1096, 1126, 1271, 1603, 1940, 2033, 2426, 2535, 2709, 2809, 2876, 3146, 3179, 3284, 3540, 3574, 3663, 3864, 3897, 4065, 4072, 4079, 4081, 4103, 4308, 4336, 4401, 4678, 4699, 4814
Hpa I (1): 4172
Hpa II (21): 936, 945, 1038, 1072, 1627, 1869, 1979, 2046, 2080, 2484, 2674, 2700, 2847, 3288, 3355, 3747, 3988, 4096, 4465, 4715, 4733
Hph I (12): 369, 438, 690, 1002, 1011, 1460, 2082, 2309, 3311, 3386, 4253, 4286
Hph I (3): 1438, 1679, 3844
Kas I (1): 4307
Kpn I (0):
*Ksp*632 I (0):
*Ksp*632 I (5): 338, 1366, 3170, 3287, 4639
Mae I (4): 270, 1971, 2306, 2559
Mae II (13): 1, 473, 800, 882, 1145, 1242, 1562, 1935, 2351, 3330, 3403, 4561, 4830
Mae III (19): 699, 970, 1047, 1142, 1504, 1692, 1845, 1903, 2234, 2517, 2633, 2696, 3327, 3850, 4566, 4586, 4806, 4832, 4890
Mam I (0):
Mbo I (23): 660, 693, 915, 931, 983, 1482, 1518, 1535, 1793, 1839, 1857, 2198, 2303, 2315, 2393, 2401, 2412, 2487, 3579, 3683, 4056, 4658, 4754
Mbo II (4): 412, 2396, 3649, 4749
Mbo II (13): 330, 342, 657, 1174, 1370, 1479, 1557, 2312, 3174, 3291, 3807, 4146, 4643
Mlu I (1): 3668
Mnl I (7): 1791, 1997, 2875, 3158, 4013, 4639, 4756
Mnl I (11): 903, 989, 1019, 1187, 2134, 2215, 2615, 2939, 3520, 4327, 4785
Msc I (1): 463
Mse I (23): 190, 286, 445, 450, 684, 793, 1213, 1585, 1950, 1989, 2224, 2277, 2291, 2296, 2348, 3565, 3688, 3882, 4173, 4353, 4412, 4596, 4905
Msp I (21): 936, 945, 1038, 1072, 1627, 1869, 1979, 2046, 2080, 2484, 2674, 2700, 2847, 3288, 3355, 3747, 3988, 4096, 4465, 4715, 4733
Mun I (0):
Nae I (0):
Nar I (1): 4307
Nci I (10): 935, 944, 945, 1037, 1072, 1627, 1978, 2674, 3287, 4096
Nco I (0):
Nde I (0):
*Ngo*M I (0):
Nhe I (0):
Nla III (22): 257, 497, 696, 716, 749, 856, 1028, 1133, 1220, 1325, 1718, 1754, 1832, 1842, 2333, 3053, 3277, 3804, 3983, 4004, 4156, 4528
Nla IV (16): 752, 920, 930, 1275, 1865, 2076, 2117, 2211, 2983, 3022, 3588, 3875, 4307, 4437, 4717, 4729
Not I (1): 959
Nru I (0):
Nsi I (0):
Nsp I (3): 496, 1027, 3052
*Nsp*B II (8): 1102, 1526, 2467, 2712, 3696, 4266, 4359, 4627
Pac I (0):
*Pae*R7 I (1): 954
*Pfl*M I (1): 3244
Ple I (2): 947, 2677
Ple I (4): 2165, 3153, 3296, 4092
Pme I (0):
Pml I (0):
*Ppu*M I (0):
Pst I (1): 1918
Pvu I (2): 1792, 4657
Pvu II (3): 4266, 4359, 4627
Rsa I (3): 830, 1682, 3814
Rsr II (0):
Sac I (0):
Sac II (0):
Sal I (1): 949
Sau I (1): 4760
*Sau*3A I (23): 660, 693, 915, 931, 983, 1482, 1518, 1535, 1793, 1839, 1857, 2198, 2303, 2315, 2393, 2401, 2412, 2487, 3579, 3683, 4056, 4658, 4754
*Sau*96 I (13): 290, 752, 1184, 1800, 2022, 2039, 2118, 3530, 3875, 3876, 4220, 4244, 4648
Sca I (2): 829, 1681
Sce I (0):
Sce I (0):
*Scr*F I (21): 764, 935, 944, 945, 1037, 1072, 1627, 1978, 2674, 2892, 2905, 3026, 3287, 3392, 3707, 4096, 4247, 4304, 4443, 4580, 4707
Sdu I (6): 18, 1492, 1577, 2738, 3648, 3875
Sec I (7): 934, 944, 2892, 4303, 4442, 4579, 4869
*Sfa*N I (5): 965, 1703, 3206, 3833, 4024
*Sfa*N I (10): 759, 1059, 1464, 1904, 2956, 3176, 3702, 4031, 4789, 4802
Sfc I (4): 1918, 2596, 2787, 4925
Sfi I (0):
*Sgr*A I (0):
Sin I (4): 752, 1800, 2022, 4220
Sma I (1): 944
*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, 1357
Stu I (0):
Sty I (0):
Swa I (1): 682
Taq I (11): 7, 308, 576, 655, 950, 955, 1510, 2954, 3247, 3606, 3628
Tfi I (4): 3078, 4347, 4538, 4876
*Tth*111 I (1): 1136
Xba I (0):
Xcm I (3): 3517, 4033, 4051
Xho I (1): 954
Xho II (8): 914, 930, 1517, 1534, 2302, 2314, 2400, 2411
Xma I (1): 944
Xmn I (2): 647, 1560

LOCUS pGEX-4T-1 4969 bp

BASE COUNT 1225 A 1202 C 1292 G 1250 T

ORIGIN

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1 ACGTTATCGA CTGCACGGTG CACCAATGCT TCTGGCGTCA GGCAGCCATC GGAAGCTGTG
61 GTATGGCTGT GCAGGTCGTA AATCACTGCA TAATTCGTGT CGCTCAAGGC GCACTCCCGT
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 CTATCCCACA AATTGATAAG TACTTGAAAT
841 CCAGCAAGTA TATAGCATGG CCTTTGCAGG GCTGGCAAGC CACGTTTGGT GGTGGCGACC
901 ATCCTCCAAA ATCGGATCTG GTTCCGCGTG GATCCCCGGA ATTCCCGGGT CGACTCGAGC
961 GGCCGCATCG TGA CTGACTG ACGATCTGCC TCGCGCGTTT CCGTGATGAC GGTGAAAACC
1021 TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA
1081 GACAAGCCCG TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCGCA GCCATGACCC
1141 AGTCACGTAG CGATAGCGGA GTGTATAATT CTTGAAGACG AAAGGGCCTC GTGATACGCC
1201 TATTTTTATA GGTTAATGTC ATGATAATAA TGGTTTCTTA GACGTCAGGT GGCACTTTTT
1261 GGGGAAATGT GCGCGGAACC CCTATTTGTT TATTTTTCTA AATACATTCA AATATGTATC
1321 CGCTCATGAG ACAATAACCC TGATAAATGC TTCAATAATA TTGAAAAAGG AAGAGTATGA
1381 GTATTCAACA TTTCCGTGTC GCCCTTATTC CCTTTTTTGC GGCATTTTGC CTTCTGTTT
1441 TTGCTCACCC AGAAACGCTG GTGAAAGTAA AAGATGCTGA AGATCAGTTG GGTGCACGAG
1501 TGGGTTACAT CGAACTGGAT CTCAACAGCG GTAAGATCCT TGAGAGTTTT CGCCCCGAAG
1561 AACGTTTTTC AATGATGAGC ACTTTTAAAG TTCTGCTATG TGGCGCGGTA TTATCCCGTG
1621 TTGACGCCGG GCAAGAGCAA CTCGGTCGCC GCATACACTA TTCTCAGAAAT GACTTGGTTG
1681 AGTACTCACC AGTCACAGAA AAGCATCTTA CGGATGGCAT GACAGTAAGA GAATTATGCA
1741 GTGCTGCCAT AACCATGAGT GATAACACTG CGGCCAACTT ACTTCTGACA ACGATCGGAG
1801 GACCGAAGGA GCTAACCGCT TTTTTCACAC ACATGGGGGA TCATGTAACCT CGCCTTGATC
1861 GTTGGGAACC GGAGCTGAAT GAAGCCATAC CAAACGACGA GCGTGACACC ACGATGCCTG
1921 CAGCAATGGC AACAACGTTG CGCAAATAT TAACTGGCGA ACTACTTACT CTAGCTTCCC
1981 GGCAACAATT AATAGACTGG ATGGAGGCGG ATAAAGTTGC AGGACCACTT CTGCGCTCGG
2041 CCCTTCCGGC TGGCTGGTTT ATTGCTGATA AATCTGGAGC CCGTGAGCGT GGGTCTCGCG
2101 GTATCATTGC AGCACTGGGG CCAGATGGTA AGCCCTCCCG TATCGTAGTT ATCTACACGA
2161 CGGGGAGTCA GGCAACTATG GATGAACGAA ATAGACAGAT CGCTGAGATA GGTGCCTCAC
2221 TGATTAAGCA TTGGTAACTG TCAGACCAAG TTTACTCATA TATACTTTAG ATTGATTTAA
2281 AACTTCATTT TTAATTTAAA AGGATCTAGG TGAAGATCCT TTTTGATAAT CTCATGACCA
2341 AAATCCCTTA ACGTGAGTTT TCGTTCCACT GAGCGTCAGA CCCCCTAGAA AAGATCAAAG
2401 GATCTTCTTG AGATCCTTTT TTTCTGCGCG TAATCTGCTG CTTGCAAACA AAAAAACCAC
2461 CGCTACCAGC GGTGGTTTGT TTGCCGGATC AAGAGCTACC AACTCTTTTT CCGAAGGTAA
2521 CTGGCTTCAG CAGAGCGCAG ATACCAAATA CTGTCCTTCT AGTGTAGCCG TAGTTAGGCC
2581 ACCACTTCAA GAACTCTGTA GCACCGCCTA CATACTCGC TCTGCTAATC CTGTTACCAG
2641 TGGCTGCTGC CAGTGGCGAT AAGTCGTGTC TTACCGGGTT GGA CTCAAGA CGATAGTTAC
2701 CGGATAAGGC GCAGCGGTCG GGCTGAACGG GGGGTTCTGT CACACAGCCC AGCTTGGAGC
2761 GAACGACCTA CACCGAACTG AGATACCTAC AGCGTGAGCT ATGAGAAAGC GCCACGCTTC
2821 CCGAAGGGAG AAAGGCGGAC AGGTATCCGG TAAGCGGCAG GGTGGAACA GGAGAGCGCA
2881 CGAGGGAGCT TCCAGGGGGA AACGCCTGGT ATCTTTATAG TCCTGTCGGG TTTGCCACC
2941 TCTGACTTGA GCGTCGATTT TTGTGATGCT CGTCAGGGGG GCGGAGCCTA TGGAAAAACG
3001 CCAGCAACGC GGCCTTTTTT CGGTTCTTGG CCTTTTGCTG GCCTTTTGCT CACATGTTCT
3061 TTCCTGCGTT ATCCCTTGAT TCTGTGGATA ACCGTATTAC CGCCTTTGAG TGAGCTGATA
3121 CCGCTCGCCG CAGCCGAACG ACCGAGCGCA GCGAGTCAGT GAGCGAGGAA GCGGAAGAGC
3181 GCCTGATGCG GTATTTTCTC CTTACGCATC TGTGCGGTAT TTCACACCGC ATAAATTCCG
3241 ACACCATCGA ATGGTGCAAA ACCTTTCGCG GTATGGCATG ATAGCGCCCG GAAGAGAGTC
3301 AATTCAGGGT GGTGAATGTG AAACCAGTAA CGTTATACGA TGTCGAGAG TATGCCGGTG
3361 TCTCTTATCA GACCGTTTCC CGCGTGGTGA ACCAGGCCAG CCACGTTTCT GCGAAAACGC
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3421	GGGAAAAAGT	GGAAGCGGCG	ATGGCGGAGC	TGAATTACAT	TCCCAACCGC	GTGGCACAAC
3481	AACTGGCGGG	CAAACAGTCG	TTGCTGATTG	GCGTTGCCAC	CTCCAGTCTG	GCCCTGCACG
3541	CGCCGTCGCA	AATTGTCGCG	GCGATTAAAT	CTCGCGCCGA	TCAACTGGGT	GCCAGCGTGG
3601	TGGTGTTCGAT	GGTAGAACGA	AGCGGCGTCG	AAGCCTGTAA	AGCGGCGGTG	CACAATCTTC
3661	TCGCGCAACG	CGTCAGTGGG	CTGATCATTG	ACTATCCGCT	GGATGACCAG	GATGCCATTG
3721	CTGTGGAAGC	TGCCTGCACT	AATGTTCCGG	CGTTATTTCT	TGATGTCTCT	GACCAGACAC
3781	CCATCAACAG	TATTATTTTC	TCCCATGAAG	ACGGTACGCG	ACTGGGCGTG	GAGCATCTGG
3841	TCGCATTGGG	TCACCAGCAA	ATCGCGCTGT	TAGCGGGCCC	ATTAAGTTCT	GTCTCGGCGC
3901	GTCTGCGTCT	GGCTGGCTGG	CATAAATATC	TCACTCGCAA	TCAAATTCAG	CCGATAGCGG
3961	AACGGGAAGG	CGACTGGAGT	GCCATGTCCG	GTTTTCAACA	AACCATGCAA	ATGCTGAATG
4021	AGGGCATCGT	TCCCACTGCG	ATGCTGGTTG	CCAACGATCA	GATGGCGCTG	GGCGCAATGC
4081	GCGCCATTAC	CGAGTCCGGG	CTGCGCGTTG	GTGCGGATAT	CTCGGTAGTG	GGATACGACG
4141	ATACCGAAGA	CAGCTCATGT	TATATCCCGC	CGTTAACCAC	CATCAAACAG	GATTTTCGCC
4201	TGCTGGGGCA	AACCAGCGTG	GACCGCTTGC	TGCAACTCTC	TCAGGGCCAG	GCGGTGAAGG
4261	GCAATCAGCT	GTTGCCCGTC	TCACTGGTGA	AAAGAAAAAC	CACCCTGGCG	CCCAATACGC
4321	AAACCGCCTC	TCCCCGCGCG	TTGGCCGATT	CATTAATGCA	GCTGGCACGA	CAGGTTTCCC
4381	GA CTGGAAAG	CGGGCAGTGA	GCGCAACGCA	ATTAATGTGA	GTTAGCTCAC	TCATTAGGCA
4441	CCCCAGGCTT	TACACTTTAT	GCTTCCGGCT	CGTATGTTGT	GTGGAATTGT	GAGCGGATAA
4501	CAATTTTACA	CAGGAAACAG	CTATGACCAT	GATTACGGAT	TCACTGGCCG	TCGTTTTTACA
4561	ACGTCGTGAC	TGGGAAAACC	CTGGCGTTAC	CCAACTTAAT	CGCCTTGCAG	CACATCCCCC
4621	TTTCGCCAGC	TGGCGTAATA	GCGAAGAGGC	CCGCACCGAT	CGCCCTTCCC	AACAGTTGCG
4681	CAGCCTGAAT	GGCGAATGGC	GCTTTGCCTG	GTTTCCGGCA	CCAGAAGCGG	TGCCGGAAAG
4741	CTGGCTGGAG	TGCGATCTTC	CTGAGGCCGA	TACTGTCGTC	GTCCCCTCAA	ACTGGCAGAT
4801	GCACGGTTAC	GATGCGCCCA	TCTACACCAA	CGTAACCTAT	CCCATTACGG	TCAATCCGCC
4861	GTTTGTTCCT	ACGGAGAATC	CGACGGGTTG	TTACTCGCTC	ACATTTAATG	TTGATGAAAG
4921	CTGGCTACAG	GAAGGCCAGA	CGCGAATTAT	TTTTGATGGC	GTTGGAATT	