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*H I (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*J I (7): 934, 944, 2892, 4303, 4442, 4579, 4869
*Bse*A I (0):
Bsg I (2): 69, 523
Bsg I (3): 11, 3534, 3734
*Bsi*E I (6): 960, 1643, 1792, 2715, 3139, 4657
*Bsi*W I (0):
*Bsi*Y I (11): 264, 861, 1037, 2568, 2847, 3013, 3031, 3244, 4090, 4334, 4785
Bsl 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
*Eco*R V (1): 4116
Esp I (0):
*Esp*3 I (1): 4277
*Esp*3 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
*Hin*c II (4): 182, 949, 1620, 4172
*Hin*d II (4): 182, 949, 1620, 4172
*Hin*d III (0):
*Hin*f I (10): 952, 2165, 2682, 3078, 3153, 3296, 4092, 4347, 4538, 4876
*Hin*p 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
   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 GTTCCGCGTG GATCCCCGGA ATTCCCGGGT CGACTCGAGC
 961 GGCCGCATCG TGACTGACTG ACGATCTGCC TCGCGCGTTT CGGTGATGAC 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 GGCACTTTTC
1261 GGGGAAATGT GCGCGGAACC CCTATTTGTT TATTTTTCTA AATACATTCA AATATGTATC
1321 CGCTCATGAG ACAATAACCC TGATAAATGC TTCAATAATA TTGAAAAAGG AAGAGTATGA
1381 GTATTCAACA TTTCCGTGTC GCCCTTATTC CCTTTTTTGC GGCATTTTGC CTTCCTGTTT
1441 TTGCTCACCC AGAAACGCTG GTGAAAGTAA AAGATGCTGA AGATCAGTTG GGTGCACGAG
1501 TGGGTTACAT CGAACTGGAT CTCAACAGCG GTAAGATCCT TGAGAGTTTT CGCCCCGAAG
1561 AACGTTTTCC AATGATGAGC ACTTTTAAAG TTCTGCTATG TGGCGCGGTA TTATCCCGTG
1621 TTGACGCCGG GCAAGAGCAA CTCGGTCGCC GCATACACTA TTCTCAGAAT GACTTGGTTG
1681 AGTACTCACC AGTCACAGAA AAGCATCTTA CGGATGGCAT GACAGTAAGA GAATTATGCA
1741 GTGCTGCCAT AACCATGAGT GATAACACTG CGGCCAACTT ACTTCTGACA ACGATCGGAG
1801 GACCGAAGGA GCTAACCGCT TTTTTGCACA ACATGGGGGA TCATGTAACT CGCCTTGATC
1861 GTTGGGAACC GGAGCTGAAT GAAGCCATAC CAAACGACGA GCGTGACACC ACGATGCCTG
1921 CAGCAATGGC AACAACGTTG CGCAAACTAT TAACTGGCGA ACTACTTACT CTAGCTTCCC
1981 GGCAACAATT AATAGACTGG ATGGAGGCGG ATAAAGTTGC AGGACCACTT CTGCGCTCGG
2041 CCCTTCCGGC TGGCTGGTTT ATTGCTGATA AATCTGGAGC CGGTGAGCGT 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 CCCCGTAGAA 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 CATACCTCGC TCTGCTAATC CTGTTACCAG
2641 TGGCTGCTGC CAGTGGCGAT AAGTCGTGTC TTACCGGGTT GGACTCAAGA CGATAGTTAC
2701 CGGATAAGGC GCAGCGGTCG GGCTGAACGG GGGGTTCGTG CACACAGCCC AGCTTGGAGC
2761 GAACGACCTA CACCGAACTG AGATACCTAC AGCGTGAGCT ATGAGAAAGC GCCACGCTTC
2821 CCGAAGGGAG AAAGGCGGAC AGGTATCCGG TAAGCGGCAG GGTCGGAACA GGAGAGCGCA
2881 CGAGGGAGCT TCCAGGGGGA AACGCCTGGT ATCTTTATAG TCCTGTCGGG TTTCGCCACC
2941 TCTGACTTGA GCGTCGATTT TTGTGATGCT CGTCAGGGGG GCGGAGCCTA TGGAAAAACG
3001 CCAGCAACGC GGCCTTTTTA CGGTTCCTGG CCTTTTGCTG GCCTTTTGCT CACATGTTCT
3061 TTCCTGCGTT ATCCCCTGAT 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 TGTCGCAGAG TATGCCGGTG
3361 TCTCTTATCA GACCGTTTCC CGCGTGGTGA ACCAGGCCAG CCACGTTTCT GCGAAAACGC
```

```
3421 GGGAAAAAGT GGAAGCGGCG ATGGCGGAGC TGAATTACAT TCCCAACCGC GTGGCACAAC
3481 AACTGGCGGG CAAACAGTCG TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG
3541 CGCCGTCGCA AATTGTCGCG GCGATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG
3601 TGGTGTCGAT GGTAGAACGA AGCGGCGTCG AAGCCTGTAA AGCGGCGGTG CACAATCTTC
3661 TCGCGCAACG CGTCAGTGGG CTGATCATTA 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 GACTGGAAAG CGGGCAGTGA GCGCAACGCA ATTAATGTGA GTTAGCTCAC TCATTAGGCA
4441 CCCCAGGCTT TACACTTTAT GCTTCCGGCT CGTATGTTGT GTGGAATTGT GAGCGGATAA
4501 CAATTTCACA CAGGAAACAG CTATGACCAT GATTACGGAT TCACTGGCCG TCGTTTTACA
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 GTTTGTTCCC ACGGAGAATC CGACGGGTTG TTACTCGCTC ACATTTAATG TTGATGAAAG
4921 CTGGCTACAG GAAGGCCAGA CGCGAATTAT TTTTGATGGC GTTGGAATT
```