



**Comments for pRc/CMV:  
5542 nucleotides**

CMV promoter: bases 209-864  
 T7 promoter: bases 865-883  
 Polylinker: bases 890-995  
 Sp6 promoter: bases 1008-1017  
 BGH poly A signal: bases 1019-1250  
 f1 origin: bases 1306-1828  
 SV40 Promoter: bases 1890-2215  
 SV40 origin of replication: bases 2084-2169  
 Neo ORF: bases 2251-3045  
 SV40 poly A: bases 3219-3348  
 ColE1 origin: bases 3728-4400  
 Ampicillin resistance gene: bases 5406-4546  
 (complementary strand)

\* There is an ATG upstream of the Xba I site.

**pRc/CMV**  
hCMV immediate early promoter  
Polylinker  
Primer binding sites  
Bovine Growth Hormone polyA



↓ 5' end of hCMV promoter/enhancer  
224 ATATACGCGT TGACATTGAT TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT  
284 AGTTCATAGC CCATATATGG AGTTCGCGCT TACATAACTT ACGGTAAATG GCCCGCCTGG  
344 CTGACCGCCC AACGACCCCC GCCCATTGAC GTCAATAATG ACGTATGTTC CCATAGTAAC  
404 GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGACTAT TTACGGTAAA CTGCCCACTT  
464 GGCAGTACAT CAAGTGTATC ATATGCCAAG TACGCCCCCT ATTGACGTCA ATGACGGTAA  
524 ATGGCCCGCC TGGCATTATG CCCAGTACAT GACCTTATGG GACTTTCCTA CTTGGCAGTA  
584 CATCTACGTA TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG  
644 GCGTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATTTG ACGTCAATGG  
704 GAGTTTGT TGGCACCAAA ATCAACGGGA CTTTCCAAAA TGTCGTAACA ACTCCGCCCC  
764 ATTGACGCAA ATGGGCGGTA GGC GTGTACG GTGGGAGGTC TATATAAGCA GAGCTCTCTG  
824 GCTAACTAGA GAACCCACTG CTTAACTGGC TTATCGAAAT TAATACGACT CACTATAGGG  
884 AGACCCAAGC TTGGTACCGA GCTCGGATCC ACTAGTAACG GCCGCCAGTG TGCTGGAATT  
944 CTGCAGATAT CCATCACACT GCGCGCCGCT CGAGCATGCA TCTAGAGGGC CCTATTCTAT  
1004 AGTGTCACCT AAATGCTAGA GCTCGCTGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC  
1064 CATCTGTTGT TTGCCCTCC CCCGTGCCTT CCTTGACCCT GGAAGGTGCC ACTCCCCTG  
1124 TCCTTTCCTA ATAAAATGAG GAAATTGCAT

API  
enhancer region (3' end)  
CAAT  
TATA  
3' end of hCMV  
putative transcriptional start  
T7 promoter  
Hind III  
Bst XI  
Bst XI  
Not I  
Xba I  
Apa I  
Sp6 promoter  
BGH polyA

**NOTE: There is an ATG upstream of the Xba I and Apa I sites**



General Description

DNA pRc/CMV

Entire molecule length: 5542 bp

Restriction Map

Enzyme	# of cuts	Positions
AatI	1	2169
AatII	5	376 429 512 698 5542
Acc65I	2	897 1829
AccI	3	34 3358 5542
Acil	69	62 309 337 349 363 530 621(c) 654(c) 758 779(c) 926 966(c) 970 1253(c) 1277(c) 1326(c) 1340(c) 1343(c) 1371 1398 2018 2030 2039 2051 2061 2072 2118 2289 2352 2446(c) 2510(c) 2611(c) 2614(c) 2854 2894(c) 2899 2949(c) 2965 2991 3047(c) 3116 3119 3185(c) 3417 3520 3576(c) 3586(c) 3610 3653(c) 3660(c) 3681(c) 3772 3800 3927 3946 4067 4177(c) 4312 4321(c) 4683 4774 4965(c) 5011 5132(c) 5176 5253 5362 5461(c) 5508
Acsl	6	128 940 1727 1738 1841 3270
Acyl	9	373 426 509 695 2380 3082 3161 5157 5539
AflIII	2	229 3727
AluI	26	136 817 893 905 1025 1290 1457 1714 1837 2134 2188 2198 2486 2944 3235 3370 3392 3487 3551 3669 3895 4031 4288 4809 4909 4972
Alw44I	2	4041 5287
AlwI	23	13 16(c) 904(c) 917 1301(c) 1314 2224 2248 2559 2624(c)

		2805 3168(c) 3197 3345(c) 3358 4288(c) 4374(c) 4376 4472(c) 4473 4936(c) 5253 5257(c)
AlwNI	2	81 4143
Aosl	2	2482 4842
Apal	1	995
ApaLI	2	4041 5287
Apol	6	128 940 1727 1738 1841 3270
Asel	5	258 864 3498 3557 4792
Asnl	5	258 864 3498 3557 4792
Asp700	1	5219
Asp718	2	897 1829
AspEI	1	4620
AspHI	9	819 907 1027 1839 2493 2683 4045 5206 5291
Aspl	1	2498
Asull	1	3062
Aval	4	973 1297 2191 3363
Avall	3	2896 4758 4980
Avill	2	2482 4842
Avrll	1	2170
BamHI	3	909 1306 3350
BanI	9	716 897 1109 1503 1829 2379 2414 3471 4568
BanII	8	819 907 995 1027 1262 1298 1839 2745
BbsI	1	1233
BbvI	18	188(c) 1374 2327(c) 2453 2495 2511(c) 2604(c) 3016 3244 3538(c) 3619(c) 3637(c) 4056(c) 4146 4149 4355 4658(c) 5049
Bcgl	1	5159
BcII	2	1031 2221
Bfal	12	251 830 916 986 1020 1053 1391 2171 3305 4222 4475 4810
BgII	5	341 463 534 2123 4740
BgIII	1	13
BlnI	1	2170
BmyI	15	819 907 995 1027 1262 1298 1839

		2326 2419 2493 2683 2745 4045 5206 5291
Bpml	3	3163(c) 3220 4690(c)
BpuAI	1	1233
BsaAI	3	591 1544 2684
BsaBI	2	954 2239
BsaHI	9	373 426 509 695 2380 3082 3161 5157 5539
Bsal	2	878(c) 4681(c)
BsaJI	15	611 1101 1821 1881 1890 1954 2077 2112 2121 2170 2191 2543 2812 3466 3887
BsaWI	4	2411 3933 4080 4911
BsiEI	7	926 970 2289 3643 4067 4990 5139
BsiHKAI	9	819 907 1027 1839 2493 2683 4045 5206 5291
BsiYI	15	300 894 1325 1651 1798 1895 2078 2361 2905 3186 3575 3749 3767 3933 4212
BsII	15	300 894 1325 1651 1798 1895 2078 2361 2905 3186 3575 3749 3767 3933 4212
BsmAI	5	685 878(c) 2222(c) 4681(c) 5457
BsmFI	9	426 577 745 1863(c) 1936(c) 2000(c) 2531 3063 3172
BsmI	1	3300(c)
Bsp120I	1	991
Bsp1286I	15	819 907 995 1027 1262 1298 1839 2326 2419 2493 2683 2745 4045 5206 5291
BspHI	2	4447 5455
BspMI	3	2267(c) 2648 3098
BspWI	38	198 341 463 495 534 627 651 850 975 1250 1274 1335 1337 1379 1406 1436 1892 1915 1987 2038 2117 2123 2371 2455

		2478 2617 2623 2740 2776 2823 3090 3471 3515 3599 3666 3780 4352 4740
BsrBI	7	972(c) 1400(c) 2993(c) 3047 3419(c) 3660 5461
BsrDI	3	2613 4681 4855(c)
BsrFI	5	1439 2699 2880 3163 4700
BsrI	18	75(c) 546(c) 854 929(c) 967 1633 2055(c) 2324 2525 3527(c) 4135 4148 4260(c) 4666(c) 4784(c) 4827(c) 5096 5266(c)
BssHII	1	2777
BstBI	1	3062
BstNI	12	341 534 1103 1883 1892 1939 1956 2767 3467 3755 3876 3889
BstUI	19	121 209 231 311 1316 1340 1360 1736 2446 2747 2779 3185 3574 3576 3774 4355 4685 5178 5510
BstXI	2	936 962
BstYI	14	13 909 1306 2216 2551 2797 3189 3350 4368 4379 4465 4477 5245 5262
CfoI	30	121 201 1318 1331 1340 1362 1388 1396 2374 2382 2446 2483 2749 2779 2781 3009 3185 3511 3576 3604 3637 3907 3974 4074 4248 4357 4750 4843 5180 5512
Cfr10I	5	1439 2699 2880 3163 4700
Csp45I	1	3062
Csp6I	12	44 214 469 494 549 582 633 790 898 1830 2685 5099
Ddel	11	40 110 181 1163 1272 2130 3043 4002 4411 4577

		5117
Dpnl	30	7 15 23 911 1033 1308 2218 2223 2242 2553 2631 2712 2721 2799 3175 3191 3352 4295 4370 4381 4389 4467 4479 4584 4925 4943 4989 5247 5264 5300
DpnII	30	5 13 21 909 1031 1306 2216 2221 2240 2551 2629 2710 2719 2797 3173 3189 3350 4293 4368 4379 4387 4465 4477 4582 4923 4941 4987 5245 5262 5298
DraI	4	1769 4486 4505 5197
DraII	2	991 992
DraIII	1	1547
DrdI	3	1591 2407 3835
DsaI	3	611 2077 2812
DsaV	21	339 532 1101 1820 1881 1890 1937 1954 2190 2191 2382 2542 2765 3155 3465 3753 3874 3887 4105 4801 5152
EaeI	8	923 967 2286 2460 2851 2878 3566 5008
EagI	3	923 967 2286
Eam1105I	1	4620
EarI	4	2724(c) 2934(c) 3611 5415
Ecl136II	4	817 905 1025 1837
EclXI	3	923 967 2286
Eco57I	4	2526 2958 4275 5287(c)
EcoO109I	2	991 992
EcoRI	2	940 1841
EcoRII	12	339 532 1101 1881 1890 1937 1954 2765 3465 3753 3874 3887
EcoRV	2	952 2205
Fnu4HI	40	62 202 926 967 970 1327 1341 1363

		2118 2289 2341 2352 2442 2447 2484 2525 2612 2615 2618 2854 2950 2991 3005 3119 3233 3552 3633 3651 3654 3772 3927 4070 4135 4138 4344 4672 5011 5038 5133 5362
FnuDII	19	121 209 231 311 1316 1340 1360 1736 2446 2747 2779 3185 3574 3576 3774 4355 4685 5178 5510
FokI	10	1262 1457(c) 2021(c) 2247 2704 2729 3183 4586(c) 4767(c) 5054(c)
Fspl	2	2482 4842
HaeII	5	1389 1397 2383 3605 3975
HaeIII	24	220 335 528 925 969 993 1552 1694 2111 2117 2126 2169 2288 2462 2853 2880 3568 3742 3753 3771 4205 4663 4743 5010
Hgal	6	777 3090 3169 3838 4416 5146(c)
HgiAI	9	819 907 1027 1839 2493 2683 4045 5206 5291
HhaI	30	121 201 1318 1331 1340 1362 1388 1396 2374 2382 2446 2483 2749 2779 2781 3009 3185 3511 3576 3604 3637 3907 3974 4074 4248 4357 4750 4843 5180 5512
HinP1I	30	119 199 1316 1329 1338 1360 1386 1394 2372 2380 2444 2481 2747 2777 2779 3007 3183 3509 3574 3602 3635 3905 3972 4072 4246 4355 4748 4841



		5178 5510
HincII	4	1 35 235 3359
HindII	4	1 35 235 3359
HindIII	1	891
Hinfl	16	36 174 661 871 1592 1614 2865 2999 3051 3109 3146 3562 3627 3702 4098 4615
HpaII	23	1440 1821 2192 2285 2362 2384 2412 2543 2633 2700 2881 3156 3164 3445 3934 4081 4107 4297 4701 4735 4802 4912 5154
HphI	9	627 1001(c) 1544 2558(c) 4463(c) 4690(c) 5106 5312(c) 5347
ItaI	40	62 202 926 967 970 1327 1341 1363 2118 2289 2341 2352 2442 2447 2484 2525 2612 2615 2618 2854 2950 2991 3005 3119 3233 3552 3633 3651 3654 3772 3927 4070 4135 4138 4344 4672 5011 5038 5133 5362
KasI	1	2379
KpnI	2	901 1833
Ksp632I	4	2724(c) 2934(c) 3611 5415
MaeI	12	251 830 916 986 1020 1053 1391 2171 3305 4222 4475 4810
MaeII	17	373 385 426 509 590 695 1433 1543 1586 1598 1757 2496 2683 4430 4846 5219 5539
MaeIII	18	312 399 748 918 1007 1354 1366 2500 2806 3244 4083 4146 4262 4545 4876 4934 5087 5275
MamI	2	954 2239
MboI	30	5 13 21 909 1031

		1306 2216 2221 2240 2551 2629 2710 2719 2797 3173 3189 3350 4293 4368 4379 4387 4465 4477 4582 4923 4941 4987 5245 5262 5298
Mboll	14	183 1238 1405(c) 1780(c) 2741 2951 3031(c) 3198(c) 3598(c) 4389 4460(c) 5215(c) 5293(c) 5402(c)
Mcrl	7	926 970 2289 3643 4067 4990 5139
Mfel	1	162
Mlul	1	229
MluNI	1	2462
Mnll	33	96(c) 792(c) 982(c) 1048 1090 1135(c) 1210(c) 1267(c) 1293(c) 1517 2101(c) 2107(c) 2131 2137 2144(c) 2147(c) 2159(c) 2231(c) 2295(c) 2431(c) 2788(c) 2981 3187 3372 3576(c) 3626 3835(c) 3909 4159(c) 4559(c) 4640(c) 4787 4993
Mslcl	1	2462
Msel	23	70 132 258 846 864 1334 1605 1703 1720 1731 1743 1754 1768 3498 3557 4433 4485 4490 4504 4557 4792 4831 5196
Msll	6	616 1014 2817 4872 5031 5390
MspA1l	6	1290 2486 3551 4069 4314 5255
Mspl	23	1440 1821 2192 2285 2362 2384 2412 2543 2633 2700 2881 3156 3164 3445 3934 4081 4107 4297 4701 4735 4802 4912 5154
Munl	1	162
Mval	12	341 534 1103 1883

		1892 1939 1956 2767 3467 3755 3876 3889
Mvnl	19	121 209 231 311 1316 1340 1360 1736 2446 2747 2779 3185 3574 3576 3774 4355 4685 5178 5510
Mwol	38	198 341 463 495 534 627 651 850 975 1250 1274 1335 1337 1379 1406 1436 1892 1915 1987 2038 2117 2123 2371 2455 2478 2617 2623 2740 2776 2823 3090 3471 3515 3599 3666 3780 4352 4740
Nael	3	1441 2882 3165
Narl	1	2380
Ncil	9	1822 2192 2193 2384 2544 3157 4107 4803 5154
Ncol	3	611 2077 2812
Ndel	1	485
Ndell	30	5 13 21 909 1031 1306 2216 2221 2240 2551 2629 2710 2719 2797 3173 3189 3350 4293 4368 4379 4387 4465 4477 4582 4923 4941 4987 5245 5262 5298
NgoMI	3	1439 2880 3163
NlaIII	23	171 555 615 982 1244 1918 1990 2081 2254 2599 2785 2816 2842 3198 3346 3385 3731 4451 4942 4952 5030 5066 5459
NlaIV	22	718 899 911 993 1111 1308 1484 1505 1831 1887 1960 2381 2416 3352 3473 3759 3798 4570 4664 4705 4916 5506
NotI	1	967

Nrul	1	209
Nsil	3	984 1920 1992
Nspl	6	982 1244 1918 1990 2785 3731
NspV	1	3062
PaeR7I	3	973 1297 3363
PleI	9	30(c) 655(c) 865(c) 1600 1608(c) 3045(c) 3621(c) 4106 4609(c)
Ppu10I	3	980 1916 1988
Psp1406I	3	1757 4846 5219
PstI	2	949 2433
Pvul	1	4990
Pvull	3	1290 2486 3551
Rcal	2	4447 5455
Rsal	12	45 215 470 495 550 583 634 791 899 1831 2686 5100
RsrII	1	2896
Sacl	4	819 907 1027 1839
Sall	3	33 3357 5541
Sapl	3	2724(c) 2934(c) 3611
Sau3AI	30	5 13 21 909 1031 1306 2216 2221 2240 2551 2629 2710 2719 2797 3173 3189 3350 4293 4368 4379 4387 4465 4477 4582 4923 4941 4987 5245 5262 5298
Sau96I	11	218 334 527 991 992 1550 2896 4662 4741 4758 4980
Scal	1	5100
ScrFI	21	341 534 1103 1822 1883 1892 1939 1956 2192 2193 2384 2544 2767 3157 3467 3755 3876 3889 4107 4803 5154
SexAI	1	1937
SfaNI	19	48(c) 608(c) 991 1160 1240(c) 1479 1927 1999 2338(c) 2593(c) 2679 2743 2809(c) 3018 3272 3824 4876 5067(c) 5316
Sfcl	8	877 945 1001 1321 2429 3992 4183 4861

Sfil	1	2123
Sful	1	3062
Smal	1	2193
SnaBI	1	591
Snol	2	4041 5287
Spel	2	250 915
SphI	5	982 1244 1918 1990 2785
Sspl	3	1752 1773 5424
Stul	1	2169
Styl	4	611 2077 2170 2812
Swal	1	1769
TaqI	19	34 858 974 1040 1298 1509 1839 2493 2649 2673 2709 2871 3062 3107 3358 3364 3827 5271 5542
Tfil	7	174 2865 2999 3109 3146 3562 3702
Thal	19	121 209 231 311 1316 1340 1360 1736 2446 2747 2779 3185 3574 3576 3774 4355 4685 5178 5510
Tru9I	23	70 132 258 846 864 1334 1605 1703 1720 1731 1743 1754 1768 3498 3557 4433 4485 4490 4504 4557 4792 4831 5196
Tsp509I	20	128 162 269 861 940 1146 1727 1738 1764 1841 1924 1996 2088 3270 3407 3424 3499 4487 4793 5048
Tth111I	1	2498
Xbal	1	985
Xcml	1	846
XhoI	3	973 1297 3363
XhoII	14	13 909 1306 2216 2551 2797 3189 3350 4368 4379 4465 4477 5245 5262
Xmal	1	2191
XmaIII	3	923 967 2286
Xmnl	1	5219

No cuts: AccIII, AflIII, AgeI, AscI, BbrPI, BfrI, Bpu1102I, BseAI, BsgI, BsiWI, BspDI, BspEI, BsrGI, Bst1107I, BstEII, Bsu36I, CelII, ClaI, Eco47III, EcoNI, Esp3I, EspI, HpaI, KspI, MroI, NheI, PacI, PflMI, PinAI, PmaCI, PmeI, PmlI, PpuMI, SacII, SgrAI, SspBI, Van91I

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      10          20          30          40          50          60
GACGGATCGG GAGATCTCCC GATCCCCTAT GGTCGACTCT CAGTACAATC TGCTCTGATG

      70          80          90         100         110         120
CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT GGAGGTCGCT GAGTAGTGCG

     130         140         150         160         170         180
CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC

     190         200         210         220         230         240
TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC CAGATATACG CGTTGACATT

     250         260         270         280         290         300
GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA

     310         320         330         340         350         360
TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC

     370         380         390         400         410         420
CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC

     430         440         450         460         470         480
ATTGACGTCA ATGGGTGGAC TATTTACGGT AACTGCCCA CTTGGCAGTA CATCAAGTGT

     490         500         510         520         530         540
ATCATATGCC AAGTACGCC CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT

     550         560         570         580         590         600
ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA

     610         620         630         640         650         660
TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA TAGCGGTTTG

     670         680         690         700         710         720
ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC

     730         740         750         760         770         780
AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG

     790         800         810         820         830         840
GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA
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850	860	870	880	890	900
CTGCTTAACT	GGCTTATCGA	AATTAATACG	ACTCACTATA	GGGAGACCCA	AGCTTGGTAC
910	920	930	940	950	960
CGAGCTCGGA	TCCACTAGTA	ACGGCCGCCA	GTGTGCTGGA	ATTCTGCAGA	TATCCATCAC
970	980	990	1000	1010	1020
ACTGGCGGCC	GCTCGAGCAT	GCATCTAGAG	GGCCCTATTC	TATAGTGTCA	CCTAAATGCT
1030	1040	1050	1060	1070	1080
AGAGCTCGCT	GATCAGCCTC	GACTGTGCCT	TCTAGTTGCC	AGCCATCTGT	TGTTTGCCCC
1090	1100	1110	1120	1130	1140
TCCCCCGTGC	CTTCCTTGAC	CCTGGAAGGT	GCCACTCCCA	CTGTCCTTTC	CTAATAAAAT
1150	1160	1170	1180	1190	1200
GAGGAAATTG	CATCGCATTG	TCTGAGTAGG	TGTCATTCTA	TTCTGGGGGG	TGGGGTGGGG
1210	1220	1230	1240	1250	1260
CAGGACAGCA	AGGGGGAGGA	TTGGGAAGAC	AATAGCAGGC	ATGCTGGGGA	TGCGGTGGGC
1270	1280	1290	1300	1310	1320
TCTATGGCTT	CTGAGGCGGA	AAGAACCAGC	TGGGGCTCGA	GGGGGGATCC	CCACGCGCCC
1330	1340	1350	1360	1370	1380
TGTAGCGGCG	CATTAAGCGC	GGCGGGTGTG	GTGGTTACGC	GCAGCGTGAC	CGCTACACTT
1390	1400	1410	1420	1430	1440
GCCAGCGCCC	TAGCGCCCGC	TCCTTTCGCT	TTCTTCCCTT	CCTTTCTCGC	CACGTTTCGCC
1450	1460	1470	1480	1490	1500
GGCTTTCCCC	GTCAAGCTCT	AAATCGGGGC	ATCCCTTTAG	GGTTCCGATT	TAGTGCTTTA
1510	1520	1530	1540	1550	1560
CGGCACCTCG	ACCCCAAAAA	ACTTGATTAG	GGTGATGGTT	CACGTAGTGG	GCCATCGCCC
1570	1580	1590	1600	1610	1620
TGATAGACGG	TTTTTCGCCC	TTTGACGTTG	GAGTCCACGT	TCTTTAATAG	TGGACTCTTG
1630	1640	1650	1660	1670	1680
TTCCAAACTG	GAACAACACT	CAACCCTATC	TCGGTCTATT	CTTTTGATTT	ATAAGGGATT
1690	1700	1710	1720	1730	1740



TTGGGGATTT	CGGCCTATTG	GTTAAAAAAT	GAGCTGATTT	AACAAAAAATT	TAACGCGAAT
1750	1760	1770	1780	1790	1800
TTTAACAAAA	TATTAACGTT	TACAATTTAA	ATATTTGCTT	ATACAATCTT	CCTGTTTTTTG
1810	1820	1830	1840	1850	1860
GGGCTTTTCT	GATTATCAAC	CGGGGTGGGT	ACCGAGCTCG	AATTCTGTGG	AATGTGTGTC
1870	1880	1890	1900	1910	1920
AGTTAGGGTG	TGGAAAGTCC	CCAGGCTCCC	CAGGCAGGCA	GAAGTATGCA	AAGCATGCAT
1930	1940	1950	1960	1970	1980
CTCAATTAGT	CAGCAACCAG	GTGTGGAAAG	TCCCCAGGCT	CCCCAGCAGG	CAGAAGTATG
1990	2000	2010	2020	2030	2040
CAAAGCATGC	ATCTCAATTA	GTCAGCAACC	ATAGTCCCGC	CCCTAACTCC	GCCCATCCCG
2050	2060	2070	2080	2090	2100
CCCCTAACTC	CGCCAGTTC	CGCCATTCT	CCGCCCATG	GCTGACTAAT	TTTTTTTATT
2110	2120	2130	2140	2150	2160
TATGCAGAGG	CCGAGGCCGC	CTCGGCCTCT	GAGCTATTCC	AGAAGTAGTG	AGGAGGCTTT
2170	2180	2190	2200	2210	2220
TTTGGAGGCC	TAGGCTTTTTG	CAAAAAGCTC	CCGGGAGCTT	GGATATCCAT	TTTCGGATCT
2230	2240	2250	2260	2270	2280
GATCAAGAGA	CAGGATGAGG	ATCGTTTCGC	ATGATTGAAC	AAGATGGATT	GCACGCAGGT
2290	2300	2310	2320	2330	2340
TCTCCGGCCG	CTTGGGTGGA	GAGGCTATTC	GGCTATGACT	GGGCACAACA	GACAATCGGC
2350	2360	2370	2380	2390	2400
TGCTCTGATG	CCGCCGTGTT	CCGGCTGTCA	GCGCAGGGGC	GCCCGGTTCT	TTTTGTCAAG
2410	2420	2430	2440	2450	2460
ACCGACCTGT	CCGGTGCCCT	GAATGAACTG	CAGGACGAGG	CAGCGCGGCT	ATCGTGGCTG
2470	2480	2490	2500	2510	2520
GCCACGACGG	GCGTTCCTTG	CGCAGCTGTG	CTCGACGTTG	TCACTGAAGC	GGGAAGGGAC
2530	2540	2550	2560	2570	2580
TGGCTGCTAT	TGGGCGAAGT	GCCGGGGCAG	GATCTCCTGT	CATCTCACCT	TGCTCCTGCC

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2590      2600      2610      2620      2630      2640
GAGAAAGTAT CCATCATGGC TGATGCAATG CGGCGGCTGC ATACGCTTGA TCCGGCTACC

2650      2660      2670      2680      2690      2700
TGCCCATTCG ACCACCAAGC GAAACATCGC ATCGAGCGAG CACGTACTCG GATGGAAGCC

2710      2720      2730      2740      2750      2760
GGTCTTGTCG ATCAGGATGA TCTGGACGAA GAGCATCAGG GGCTCGCGCC AGCCGAACTG

2770      2780      2790      2800      2810      2820
TTCGCCAGGC TCAAGGCGCG CATGCCCGAC GGCGAGGATC TCGTCGTGAC CCATGGCGAT

2830      2840      2850      2860      2870      2880
GCCTGCTTGC CGAATATCAT GGTGGAAAAT GGCCGCTTTT CTGGATTTCAT CGACTGTGGC

2890      2900      2910      2920      2930      2940
CGGCTGGGTG TGGCGGACCG CTATCAGGAC ATAGCGTTGG CTACCCGTGA TATTGCTGAA

2950      2960      2970      2980      2990      3000
GAGCTTGGCG GCGAATGGGC TGACCGCTTC CTCGTGCTTT ACGGTATCGC CGCTCCCGAT

3010      3020      3030      3040      3050      3060
TCGCAGCGCA TCGCCTTCTA TCGCCTTCTT GACGAGTTCT TCTGAGCGGG ACTCTGGGGT

3070      3080      3090      3100      3110      3120
TCGAAATGAC CGACCAAGCG ACGCCCAACC TGCCATCACG AGATTTTCGAT TCCACCGCCG

3130      3140      3150      3160      3170      3180
CCTTCTATGA AAGGTTGGGC TTCGGAATCG TTTTCCGGGA CGCCGGCTGG ATGATCCTCC

3190      3200      3210      3220      3230      3240
AGCGCGGGGA TCTCATGCTG GAGTTCTTCG CCCACCCCAA CTTGTTTATT GCAGCTTATA

3250      3260      3270      3280      3290      3300
ATGGTTACAA ATAAAGCAAT AGCATCACAA ATTTCACAAA TAAAGCATT TTTTCACTGC

3310      3320      3330      3340      3350      3360
ATTCTAGTTG TGGTTTGTCC AACTCATCA ATGTATCTTA TCATGTCTGG ATCCCGTCGA

3370      3380      3390      3400      3410      3420
CCTCGAGAGC TTGGCGTAAT CATGGTCATA GCTGTTTCCT GTGTGAAATT GTTATCCGCT
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3430	3440	3450	3460	3470	3480
CACAATCCA	CACAACATAC	GAGCCGGAAG	CATAAAGTGT	AAAGCCTGGG	GTGCCTAATG
3490	3500	3510	3520	3530	3540
AGTGAGCTAA	CTCACATTAA	TTGCGTTGCG	CTCACTGCC	GCTTTCCAGT	CGGGAAACCT
3550	3560	3570	3580	3590	3600
GTCGTGCCAG	CTGCATTAAT	GAATCGGCCA	ACGCGCGGGG	AGAGGCGGTT	TGCGTATTGG
3610	3620	3630	3640	3650	3660
GCGCTCTTCC	GCTTCCTCGC	TCACTGACTC	GCTGCGCTCG	GTCGTTCCGGC	TGCGGCGAGC
3670	3680	3690	3700	3710	3720
GGTATCAGCT	CACTCAAAGG	CGGTAATACG	GTTATCCACA	GAATCAGGGG	ATAACGCAGG
3730	3740	3750	3760	3770	3780
AAAGAACATG	TGAGCAAAAG	GCCAGCAAAA	GGCCAGGAAC	CGTAAAAAGG	CCGCGTTGCT
3790	3800	3810	3820	3830	3840
GGCGTTTTTC	CATAGGCTCC	GCCCCCTGA	CGAGCATCAC	AAAAATCGAC	GCTCAAGTCA
3850	3860	3870	3880	3890	3900
GAGGTGGCGA	AACCCGACAG	GACTATAAAG	ATACCAGGCG	TTTCCCCCTG	GAAGCTCCCT
3910	3920	3930	3940	3950	3960
CGTGCGCTCT	CCTGTTCCGA	CCCTGCCGCT	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC
3970	3980	3990	4000	4010	4020
GGGAAGCGTG	GCGCTTTCTC	AATGCTCACG	CTGTAGGTAT	CTCAGTTCGG	TGTAGGTCGT
4030	4040	4050	4060	4070	4080
TCGCTCCAAG	CTGGGCTGTG	TGCACGAACC	CCCCGTTTCCAG	CCCGACCGCT	GCGCCTTATC
4090	4100	4110	4120	4130	4140
CGGTAACTAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	TTATCGCCAC	TGGCAGCAGC
4150	4160	4170	4180	4190	4200
CACTGGTAAC	AGGATTAGCA	GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG
4210	4220	4230	4240	4250	4260
GTGGCCTAAC	TACGGCTACA	CTAGAAGGAC	AGTATTTGGT	ATCTGCGCTC	TGCTGAAGCC
4270	4280	4290	4300	4310	4320

AGTTACCTTC	GGAAAAAGAG	TTGGTAGCTC	TTGATCCGGC	AAACAAACCA	CCGCTGGTAG
4330	4340	4350	4360	4370	4380
CGGTGGTTTT	TTTGTTTGCA	AGCAGCAGAT	TACGCGCAGA	AAAAAAGGAT	CTCAAGAAGA
4390	4400	4410	4420	4430	4440
TCCTTTGATC	TTTTCTACGG	GGTCTGACGC	TCAGTGGAAC	GAAAACCTCAC	GTTAAGGGAT
4450	4460	4470	4480	4490	4500
TTTGGTCATG	AGATTATCAA	AAAGGATCTT	CACCTAGATC	CTTTTAAATT	AAAAATGAAG
4510	4520	4530	4540	4550	4560
TTTTAAATCA	ATCTAAAGTA	TATATGAGTA	AACTTGGTCT	GACAGTTACC	AATGCTTAAT
4570	4580	4590	4600	4610	4620
CAGTGAGGCA	CCTATCTCAG	CGATCTGTCT	ATTTTCGTTCA	TCCATAGTTG	CCTGACTCCC
4630	4640	4650	4660	4670	4680
CGTCGTGTAG	ATAACTACGA	TACGGGAGGG	CTTACCATCT	GGCCCCAGTG	CTGCAATGAT
4690	4700	4710	4720	4730	4740
ACCGCGAGAC	CCACGCTCAC	CGGCTCCAGA	TTTATCAGCA	ATAAACCCAGC	CAGCCGGAAG
4750	4760	4770	4780	4790	4800
GGCCGAGCGC	AGAAGTGGTC	CTGCAACTTT	ATCCGCCTCC	ATCCAGTCTA	TTAATTGTTG
4810	4820	4830	4840	4850	4860
CCGGGAAGCT	AGAGTAAGTA	GTTTCGCCAGT	TAATAGTTTG	CGCAACGTTG	TTGCCATTGC
4870	4880	4890	4900	4910	4920
TACAGGCATC	GTGGTGTAC	GCTCGTCGTT	TGGTATGGCT	TCATTCAGCT	CCGGTTCCCA
4930	4940	4950	4960	4970	4980
ACGATCAAGG	CGAGTTACAT	GATCCCCCAT	GTTGTGCAAA	AAAGCGGTTA	GCTCCTTCGG
4990	5000	5010	5020	5030	5040
TCCTCCGATC	GTTGTCAGAA	GTAAGTTGGC	CGCAGTGTTA	TCACTCATGG	TTATGGCAGC
5050	5060	5070	5080	5090	5100
ACTGCATAAT	TCTCTTACTG	TCATGCCATC	CGTAAGATGC	TTTTCTGTGA	CTGGTGAGTA
5110	5120	5130	5140	5150	5160
CTCAACCAAG	TCATTCTGAG	AATAGTGTAT	GCGGCGACCG	AGTTGCTCTT	GCCCGGCGTC

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5170      5180      5190      5200      5210      5220
AATACGGGAT AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAACG

5230      5240      5250      5260      5270      5280
TTCTTCGGGG CGAAAACTCT CAAGGATCTT ACCGCTGTTG AGATCCAGTT CGATGTAACC

5290      5300      5310      5320      5330      5340
CACTCGTGCA CCCAACTGAT CTTCAGCATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC

5350      5360      5370      5380      5390      5400
AAAAACAGGA AGGCAAAATG CCGCAAAAAA GGGAATAAGG GCGACACGGA AATGTTGAAT

5410      5420      5430      5440      5450      5460
ACTCATACTC TTCCTTTTTTC AATATTATTG AAGCATTTAT CAGGGTTATT GTCTCATGAG

5470      5480      5490      5500      5510      5520
CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC GCACATTTCC

5530      5540      5550      5560      5570      5580
CCGAAAAGTG CCACCTGACG TC..... .....
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