

1 LOCUS SYNBR322 4361 bp DNA circular SYN 18-SEP-1997
2 DEFINITION Cloning vector pBR322, complete genome.
3 ACCESSION J01749 K00005 L08654 M10282 M10283 M10286 M10356 M10784 M10785
4 M10786 M33694 V01119
5 NID g208958
6 VERSION J01749.1 GI:208958
7 KEYWORDS ampicillin resistance; beta-lactamase; cloning vector; drug
8 resistance protein; origin of replication; plasmid; tetracycline
9 resistance.
10 SOURCE Cloning vector pBR322 (tissue library: ATCC 31344, ATCC 37017) DNA;
11 Plasmid pSC101 DNA; Unclassified DNA; and Transposon Tn3 DNA.
12 ORGANISM Cloning vector pBR322
13 artificial sequence; cloning vectors.
14 REFERENCE 1 (bases 1 to 3; 3259 to 4361)
15 AUTHORS Sutcliffe,J.G.
16 TITLE Nucleotide sequence of the ampicillin resistance gene of
17 Escherichia coli plasmid pBR322
18 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 75 (8), 3737-3741 (1978)
19 MEDLINE 79012484
20 REFERENCE 2 (bases 1 to 4361)
21 AUTHORS Sutcliffe,J.G.
22 TITLE Complete nucleotide sequence of the Escherichia coli plasmid pBR322
23 JOURNAL Cold Spring Harb. Symp. Quant. Biol. 43 Pt 1, 77-90 (1979)
24 MEDLINE 80002802
25 REFERENCE 3 (bases 1500 to 2300)
26 AUTHORS Reed,R.R., Young,R.A., Steitz,J.A., Grindley,N.D. and Guyer,M.S.
27 TITLE Transposition of the Escherichia coli insertion element gamma
28 generates a five-base-pair repeat
29 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 76 (10), 4882-4886 (1979)
30 MEDLINE 80056597
31 REFERENCE 4 (bases 2207 to 2265)
32 AUTHORS Covarrubias,L., Cervantes,L., Covarrubias,A., Soberon,X.,
33 Vichido,I., Blanco,A., Kupersztoch-Portnoy,Y.M. and Bolivar,F.
34 TITLE Construction and characterization of new cloning vehicles. V.
35 Mobilization and coding properties of pBR322 and several deletion
36 derivatives including pBR327 and pBR328
37 JOURNAL Gene 13 (1), 25-35 (1981)
38 MEDLINE 81213464
39 REFERENCE 5 (bases 2000 to 2500)
40 AUTHORS Mariani,K.J., Soeller,W. and Zipursky,S.L.
41 TITLE Maximal limits of the Escherichia coli replication factor Y
42 effector site sequences in pBR322 DNA
43 JOURNAL J. Biol. Chem. 257 (10), 5656-5662 (1982)
44 MEDLINE 82167416
45 REFERENCE 6 (bases 1 to 80; 4151 to 4229; 4349 to 4361)
46 AUTHORS Brosius,J., Cate,R.L. and Perlmutter,A.P.
47 TITLE Precise location of two promoters for the beta-lactamase gene of
48 pBR322. S1 mapping of ribonucleic acid isolated from Escherichia
49 coli or synthesized in vitro
50 JOURNAL J. Biol. Chem. 257 (15), 9205-9210 (1982)
51 MEDLINE 82239419
52 REFERENCE 7 (bases 4241 to 4343)
53 AUTHORS Van Dyke,M.W., Hertzberg,R.P. and Dervan,P.B.
54 TITLE Map of distamycin, netropsin, and actinomycin binding sites on
55 heterogeneous DNA: DNA cleavage-inhibition patterns with
56 methidiumpropyl-EDTA.Fe(II)
57 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 79 (18), 5470-5474 (1982)
58 MEDLINE 83039392
59 REFERENCE 8 (bases 584 to 709)
60 AUTHORS Peden,K.W. and Nathans,D.
61 TITLE Local mutagenesis within deletion loops of DNA heteroduplexes
62 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 79 (23), 7214-7217 (1982)
63 MEDLINE 83117649
64 REFERENCE 9 (bases 373 to 649)
65 AUTHORS Peden,K.W.

66 TITLE Revised sequence of the tetracycline-resistance gene of pBR322
67 JOURNAL Gene 22 (2-3), 277-280 (1983)
68 MEDLINE 83263146
69 REFERENCE 10 (bases 132 to 181)
70 AUTHORS Watabe,H., Iino,T., Kaneko,T., Shibata,T. and Ando,T.
71 TITLE A new class of site-specific endodeoxyribonucleases. Endo.Sce I
72 isolated from a eukaryote, Saccharomyces cerevisiae
73 JOURNAL J. Biol. Chem. 258 (8), 4663-4665 (1983)
74 MEDLINE 83161053
75 REFERENCE 11 (bases 368 to 581)
76 AUTHORS Livneh,Z.
77 TITLE Directed mutagenesis method for analysis of mutagen specificity:
78 application to ultraviolet-induced mutagenesis
79 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (1), 237-241 (1983)
80 MEDLINE 83117828
81 REFERENCE 12 (bases 2627 to 2682; 2781 to 2828)
82 AUTHORS Mascharak,P.K., Sugiura,Y., Kuwahara,J., Suzuki,T. and Lippard,S.J.
83 TITLE Alteration and activation of sequence-specific cleavage of DNA by
84 bleomycin in the presence of the antitumor drug
85 cis-diamminedichloroplatinum(II)
86 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (22), 6795-6798 (1983)
87 MEDLINE 84070716
88 REFERENCE 13 (bases 4276 to 4336)
89 AUTHORS Schultz,P.G. and Dervan,P.B.
90 TITLE Sequence-specific double-strand cleavage of DNA by
91 penta-N-methylpyrrolocarboxamide-EDTA X Fe(II)
92 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (22), 6834-6837 (1983)
93 MEDLINE 84070724
94 REFERENCE 14 (bases 518 to 528)
95 AUTHORS Sutcliffe,J.G.
96 JOURNAL Unpublished (1984)
97 REFERENCE 15 (bases 2395 to 2495)
98 AUTHORS Fuller,R.S., Funnell,B.E. and Kornberg,A.
99 TITLE The dnaA protein complex with the E. coli chromosomal replication
100 origin (oriC) and other DNA sites
101 JOURNAL Cell 38 (3), 889-900 (1984)
102 MEDLINE 85024881
103 REFERENCE 16 (bases 2729 to 2731)
104 AUTHORS Lathe,R., Kieny,M.P., Skory,S. and Lecocq,J.P.
105 TITLE Linker tailing: unphosphorylated linker oligonucleotides for
106 joining DNA termini
107 JOURNAL DNA 3 (2), 173-182 (1984)
108 MEDLINE 84207440
109 REFERENCE 17 (bases)
110 AUTHORS Heusterspreute,M. and Davison,J.
111 TITLE Restriction site bank vectors. II. DNA sequence analysis of plasmid
112 pJRD158
113 JOURNAL DNA 3 (3), 259-268 (1984)
114 MEDLINE 84260952
115 REFERENCE 18 (bases 2113 to 2186; 2348 to 2415)
116 AUTHORS Abarzua,P., Soeller,W. and Marians,K.J.
117 TITLE Mutational analysis of primosome assembly sites. I. Distinct
118 classes of mutants in the pBR322 Escherichia coli factor Y DNA
119 effector sequences
120 JOURNAL J. Biol. Chem. 259 (22), 14286-14292 (1984)
121 MEDLINE 85054885
122 REFERENCE 19 (bases 2348 to 2415)
123 AUTHORS Soeller,W., Abarzua,P. and Marians,K.J.
124 TITLE Mutational analysis of primosome assembly sites. II. Role of
125 secondary structure in the formation of active sites
126 JOURNAL J. Biol. Chem. 259 (22), 14293-14300 (1984)
127 MEDLINE 85054886
128 REFERENCE 20 (bases 1 to 4361)
129 AUTHORS Van Dyke,M.M. and Dervan,P.B.
130 TITLE Echinomycin binding sites on DNA
131 JOURNAL Science 225 (4667) 1122-1127 (1984)

132 MEDLINE 84300294
133 REFERENCE 21 (sites)
134 AUTHORS Pouwels,P.H., Enger-Valk,B.E. and Brammar,W.J.
135 TITLE Vector I-A-iv-1
136 JOURNAL (in) Brammar,W.J. (Ed.);
137 CLONING VECTORS;
138 Elsevier Scientific Publishing, Amsterdam (1985)
139 REFERENCE 22 (bases 1 to 4361)
140 AUTHORS Watson,N.
141 TITLE A new revision of the sequence of plasmid pBR322
142 JOURNAL Gene 70 (2), 399-403 (1988)
143 MEDLINE 89108024
144 REFERENCE 23 (sites)
145 AUTHORS Gilbert,W.
146 TITLE Obtained from VecBase 3.0
147 JOURNAL Unpublished (1991)
148 COMMENT The circular sequence is numbered such that 0 is the middle of the
149 unique EcoRI site and the count increases first through the tet
150 genes, the pMB1 material, and finally through the Tn3 region.
151 Plasmid pBR322 contains ampicillin and tetracycline resistance
152 genes. The ampicillin resistance gene (amp-r) is a penicillin
153 beta-lactamase. Promoters P1 and P3 are for the beta-lactamase
154 gene. P3 is the natural promoter, and P1 is artificially created by
155 the ligation of two different DNA fragments to create pBR322. P2 is
156 in the same region as P1, but it is on the opposite strand and
157 initiates transcription in the direction of the tetracycline
158 resistance gene.
159 Mutational studies in the primosome assembly sites indicate four
160 types of mutations: Class I having no effect on the activities
161 elicited by the DNA site and the bases involved are probably
162 spacers; Class II requiring higher Mg-2+ concentrations than the
163 wild-type to be fully activated as factor Y ATPase effectors; Class
164 III co-inactivating both the ATPase effector and DNA replication
165 template activity of the site, indicating that they probably
166 represent essential contact points between factor Y and the DNA;
167 Class IV having a replication template activity intermediate that
168 of class III and class II mutant DNAs.
169 Specific sites within or near the origins of replication are
170 recognized by dnaA protein. Without dnaA binding to the origin of
171 replication chromosomal replication is not possible [15]. pBR322
172 DNA contains two separate regions on opposite strands and close to
173 the origin of replication which, when in single-stranded form, can
174 act as effectors for the ATPase activity of E.coli replication
175 factor Y [5]. Small fragments of DNA containing these sites when
176 cloned in an f1 phage vector act as origins of DNA replication
177 allowing the formation of complementary double-stranded DNA in
178 rifampicin-resistant, dna[B,G,C]-dependent fashion in vitro [5].
179 The biological activity of echinomycin is thought to be related to
180 the formation of complexes by intercalating with cellular DNA [20].
181 Complete source information:
182 Plasmid pBR322 from E.coli [2],[1],[3],[6],[11],[8],[5],[7],[12],
183 [13],[10],[9],[14],[18],[19],[15],[20],[16]; pBR322 DNA in pXf3
184 [4].
185 The following data and their annotation were supplied by Will
186 Gilbert under the auspices of the Curator Program.
187 CROSSREFERENCE
188 #parent
189 GenBank(50):pSC101C, GenBank(50):Trn3
190 #offspring
191 VecBase(3):pBR325, VecBase(3):pBR327,
192 VecBase(3):pBR328,
193 VecBase(3):pAT153, VecBase(3):pUC7,
194 VecBase(3):pJRD158,
195 VecBase(3):PiVX, VecBase(3):PiAN7,
196 VecBase(3):pSP64,
197 VecBase(3):nSP65 VecBase(3):nGFM1

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198     VecBase(3):pGEM2,
199         VecBase(3):pGEM3, VecBase(3):pGEM4,
200     VecBase(3):pKK223,
201         VecBase(3):pLBU3, VecBase(3):pTrS3,
202     VecBase(3):pRSVNeo,
203         VecBase(3):pSV2Cat, VecBase(3):M13mp9,
204     VecBase(3):pHC79,
205         VecBase(3):pV34, VecBase(3):pKTH601,
206     VecBase(3):pKTH604,
207         VecBase(3):pKTH605, VecBase(3):pKTH606,
208     VecBase(3):YEp24,
209         VecBase(3):YIp5, VecBase(3):YRp17,
210     VecBase(3):pSP18,
211         VecBase(3):pSP19,
212         VecBase(3):pSP6T3, VecBase(3):pSP6T719,
213     VecBase(3):pT712,
214         VecBase(3):pT713, VecBase(3):pT7T318,
215     VecBase(3):pT7T319,
216         VecBase(3):pT7T3A18, VecBase(3):pT7T3A19,
217     VecBase(3):pEX1,
218         VecBase(3):pEX2, VecBase(3):pEX3,
219     VecBase(3):pCKSP6,
220         VecBase(3):pACYC177, VecBase(3):pK01,
221     VecBase(3):pK02,
222         VecBase(3):pKM1,
223         VecBase(3):pKM2, VecBase(3):pMBL1,
224     VecBase(3):pMBL604,
225         VecBase(3):pMC1511, VecBase(3):pMC1871,
226     VecBase(3):pAA37X,
227         VecBase(3):pUR278, VecBase(3):pUR288,
228     VecBase(3):pUR289,
229         VecBase(3):pUR290, VecBase(3):pUR291,
230     VecBase(3):pUR292,
231         VecBase(3):pUR222.
232 FEATURES      Location/Qualifiers
233     source      1..4361
234                 /organism="Cloning vector pBR322"
235                 /db_xref="taxon:47470"
236                 /tissue_lib="ATCC 31344, ATCC 37017"
237     source      1..1762
238                 /organism="Plasmid pSC101"
239                 /plasmid="Plasmid pSC101"
240     misc_binding 24..27
241                 /bound_moiety="echinomycin"
242     promoter     complement(27..33)
243                 /note="promoter P1 [6]"
244     misc_binding 39..42
245                 /bound_moiety="echinomycin"
246     promoter     43..49
247                 /note="promoter P2 [6]"
248     misc_binding 53..56
249                 /bound_moiety="echinomycin"
250     misc_binding 67..70
251                 /bound_moiety="echinomycin"
252     misc_binding 80..83
253                 /bound_moiety="echinomycin"
254     gene         86..1276
255                 /gene="tet"
256     CDS          86..1276
257                 /gene="tet"
258                 /codon_start=1
259                 /transl_table=11
260                 /product="tetracycline resistance protein"
261                 /protein_id="AAB59735.1"
262                 /db_xref="PID:g208959"
263                 /dh_xref="GT:208959"

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263 /db_xref="GI:208959"
 264 /translation="MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIVHSDSIASH
 265 YGVLLALYALMQFLCAPVLGALSDRFGRRPVLLASLLGATIDYAIMATTPVLWILYAG
 266 RIVAGITGATGAVAGAYIADITDGEDRARHFGLMSACFGVGMVAGPVAGLLGAILSH
 267 APFLAAAVLNGLNLLLGCFLMQESHKGERRPMLRAFNPVSSFRWARGMTIVAALMTV
 268 FFIMQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGE
 269 KQAIAGMAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
 270 QLQGSALAALTSITSITGPLIVTAIYAASASTWNGLAWIVGAALYLVLCLPALRRGAWSR
 271 ATST"
 272 misc_feature complement(141..142)
 273 /gene="tet"
 274 /note="Endo.Sce I cleavage site coordinated with site at
 275 base 146 [10]"
 276 misc_feature 146..147
 277 /gene="tet"
 278 /note="Endo.Sce I cleavage site coordinated with site at
 279 base 142 [10]"
 280 misc_binding 411..414
 281 /gene="tet"
 282 /bound_moiety="echinomycin"
 283 conflict 426
 284 /gene="tet"
 285 /citation=[11]
 286 /replace=""
 287 misc_binding 469..472
 288 /gene="tet"
 289 /bound_moiety="echinomycin"
 290 old_sequence 526..528
 291 /gene="tet"
 292 /citation=[17]
 293 repeat_unit complement(1515..1519)
 294 /note="gamma-delta insertion target sequence"
 295 /rpt_type=direct
 296 misc_feature 1636..1762
 297 /note="from pSC101 (bp 1860-1986)"
 298 source 1763..3147
 299 /organism="Unclassified."
 300 repeat_unit complement(1788..1792)
 301 /note="gamma-delta insertion target sequence"
 302 /rpt_type=direct
 303 conflict 1891..1892
 304 /citation=[23]
 305 /replace="att"
 306 old_sequence 1892..1893
 307 /citation=[2]
 308 /citation=[22]
 309 RBS 1905..1910
 310 RBS 1905..1909
 311 /note="Shine-Dalgarno sequence"
 312 conflict 1913..1914
 313 /citation=[23]
 314 /replace="caa"
 315 old_sequence 1914..1915
 316 /citation=[17]
 317 CDS 1915..2106
 318 /codon_start=1
 319 /transl_except=(pos:1915..1917,aa:Met)
 320 /transl_table=11
 321 /product="ROP protein"
 322 /protein_id="AAB59736.1"
 323 /db_xref="PID:g456436"
 324 /db_xref="GI:456436"
 325 /translation="MTKQEKTALNMARFIRSQTLTLLLEKLNELDADEQADICESLHHDH
 326 ADELYRSCLARFGDDGENL"
 327 misc_feature 2011..2167
 328 /note="H-strand Y effector site"

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329      /citation=[5]
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331      /note="gamma-delta insertion target sequence"
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334      /note="L-strand Y effector site"
335      /citation=[5]
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337      /bound_moiety="dnaA"
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339      old_sequence      2729..2730
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341      /citation=[2]
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344      old_sequence      2729
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347      /note="revision according to [16]"
348      /citation=[2]
349      /citation=[16]
350      /replace="t"
351      old_sequence      2730
352      /citation=[17]
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354      /organism="Transposon Tn3"
355      /transposon="Transposon Tn3"
356      repeat_region     3148..3185
357      /note="corresponds to one of the 38bp repeats found in Tn3
358      (bp 1-38 and complement (4920-4957))"
359      /rpt_type=inverted
360      gene              complement(3293..4153)
361      /gene="bla"
362      CDS               complement(3293..4153)
363      /gene="bla"
364      /note="E-286"
365      /codon_start=1
366      /transl_table=11
367      /product="beta-lactamase"
368      /protein_id="AAB59737.1"
369      /db_xref="PID:g455370"
370      /db_xref="GI:455370"
371      /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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373      YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGPKELTAFLHNMGDHVTRL
374      DRWEPELNEAIPNDERDTTTPAAMATTLRKLTTGELLTLASRQQLIDWMEADKVAGPL
375      LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
376      EIGASLIKHW"
377      mat_peptide        complement(3296..4084)
378      /gene="bla"
379      /product="beta-lactamase"
380      sig_peptide        complement(4085..4153)
381      /gene="bla"
382      RBS               complement(4161..4165)
383      /note="Shine-Dalgarno sequence"
384      promoter          complement(4188..4194)
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386      misc_binding      complement(4268..4271)
387      /bound_moiety="echinomycin"
388      misc_binding      complement(4280..4283)
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390      misc_binding      complement(4285..4288)
391      /bound_moiety="echinomycin"
392      misc_binding      complement(4296..4299)
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394      misc_binding      complement(4311..4314)

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398 misc_binding complement(4331..4334)
399 /bound_moiety="echinomycin"
400 BASE COUNT 983 a 1210 c 1134 g 1034 t
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402 1 ttctcatggt tgacagctta tcatcgataa gctttaatgc ggtagtttat cacagttaaa
403 61 ttgctaacgc agtcaggcac cgtgtatgaa atctaacaat gcgctcatcg tcatcctcgg
404 121 caccgtcacc ctggatgctg taggcatagg cttggttatg ccggtactgc cgggcctcct
405 181 gcgggatatc gtccattccg acagcatcgc cagtcactat ggcgtgctgc tagcgctata
406 241 tgcgttgatg caatctctat gcgcacccgt tctcggagca ctgtccgacc gctttggccg
407 301 ccgccagtc ctgctcgctt cgctacttgg agccactatc gactacgcga tcatggcgac
408 361 cacaccgcgc ctgtggatcc tctacgccgg acgcatcgtg gccggcatca ccggcgccac
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411 541 actgttgggc gccatctcct tgcattgcacc attccttgcg gcggcggtgc tcaacggcct
412 601 caacctacta ctgggctgct tcctaattgca ggagtcgcat aaggagagac gtcgaccgat
413 661 gcccttgaga gccttcaacc cagtcagctc cttccgggtg gcgcggggca tgactatcgt
414 721 cgccgcactt atgactgtct tctttatcat gcaactcgtg ggacaggtgc cggcagcgtc
415 781 ctgggtcatt ttcggcgagg accgcttctg ctggagcgcg acgatgatcg ccctgctcgt
416 841 tgcggtattc ggaatcttgc acgccctcgc tcaagccttc gtcactggtc ccgccaccaa
417 901 acgtttcggc gagaagcagg ccattatcgc cggcatggcg gccgacgcgc tgggctacgt
418 961 cttgctggcg ttcgcgacgc gaggctggat ggcttcccc attatgattc ttctcgttc
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420 1081 tcagggacag cttcaaggat cgctcgcggc tcttaccagc ctaacttcga tcactggacc
421 1141 gctgatcgtc acggcgattt atgccgcctc ggcgagcaca tggaacgggt tggcatggat
422 1201 tgtaggcgcc gccctatacc ttgtctgcct ccccgcgttg cgtcgcggtg catggagccg
423 1261 ggccacctcg acctgaatgg aagccggcgg cacctcgtca acggattcac cactccaaga
424 1321 attggagcca atcaattctt gcggagaact gtgaatgcgc aaaccaacc ttggcagaac
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426 1441 tcttgccacc ggggtgcgat gatcgtgctc ctgtcgttga ggaccggct aggctggcg
427 1501 ggttgccctta ctggttagca gaatgaatca ccgatacgcg agcgaacgtg aagcagctgc
428 1561 tgctgcaaaa cgtctcgcac ctgagcaaca acatgaatgg tcttcggttt ccgtgtttcg
429 1621 taaagtctgg aaacgcggaa gtcagcgccc tgcaccatta tgttccggat ctgcatcgca
430 1681 ggatgctgct ggctaccctg tggaacacct acatctgtat taacgaagcg ctggcattga
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432 1801 cgttccagta accgggcatg ttcattcatca gtaaccgta tcgtgagcat cctctctcgt
433 1861 ttcattcggta tcattacccc catgaacaga aatccccctt acacggaggc atcagtgacc
434 1921 aaacaggaaa aaaccgccct taacatggcc cgctttatca gaagccagac attaacgctt
435 1981 ctggagaaac tcaacgagct ggacgcggat gaacaggcag acatctgtga atcgcttcac
436 2041 gaccacgctg atgagcttta ccgcagctgc ctcgcgcgtt tcggtgatga cggtgaaaac
437 2101 ctctgacaca tgcagctccc ggagacggtc acagcttgc tgaagcggg tgccgggagc
438 2161 agacaagccc gtcaggcgcc gtcagcgggt gttggcgggt gtcgggccc agccatgacc
439 2221 cagtcacgta gcgatagcgg agtgataact ggcttaacta tgcggcatca gacgagattg
440 2281 tactgagagt gcaccatatt cgggtgtgaaa taccgcacag atgcgtaagg agaaaatacc
441 2341 gcatcaggcg ctcttcgct tctcgcctca ctgactcgtc gcgctcggtc gttcggctgc
442 2401 ggcgagcgg atcagctcac tcaaggcgg taatacgggt atccacagaa tcaggggata
443 2461 acgaggaaa gaacatgtga gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg
444 2521 cgttgctggc gtttttccat aggctccgcc cccctgacga gcatacaaaa aatcgacgct
445 2581 caagtcagag gtggcgaaac ccgacaggac tataaagata ccaggcgttt ccccctggaa
446 2641 gtcacctcgt gcgctctcct gttccgacct tgccgcttac cggataacctg tccgccttc
447 2701 tcccttcggg aagcgtggcg ctttctcata gctcacgctg taggtatctc agttcgggtg
448 2761 aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc cgttcagccc gaccgctgcg
449 2821 cttatcccg taactatcgt cttgagctca acccgtaag acacgactta tcgccactgg
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459 3421 caatgatacc gcgagacca cgctcaccgg ctccagattt atcagcaata aaccagccag
460 3481 ccccccccc ccccccccc aatattctta cactttatc cactctcatc caatctatna

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461 3541 attgttgccg ggaagctaga gtaagtagtt cgccagttaa tagtttgccg aacgttggtg
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