gn 8615 4f

FBrf0132132

From [redacted] **Mon Nov 20 22:47:56 2000**
From: Robert Levis [redacted]
To: Gillian Millburn (Genetics) [redacted]
Subject: Re: Unannotated gap in genomic sequence and error in cn gene
Date: Mon, 20 Nov 2000 17:48:20 -0500

Gillian,

Here is a revised version of my message regarding the gap in cn[1].

In the course of mapping the flanking sequence of a P insertion line on the genomic sequence, I found evidence for a 1.8 kb deletion disrupting the cinnabar (cn) gene in the BDGP/Celera sequence, relative to a previously published sequence of the same region (GenBank accession U56245). When I asked Dr. Susan Celniker of the BDGP about this discrepancy, she replied that she is confident that the BDGP/Celera sequence in this region is correct. She noted that the genomic DNA sequenced by BDGP/Celera was from a strain with a mutant cn allele (genotype y; cn bw sp). One may therefore infer that this deletion is responsible for the mutant cn phenotype.

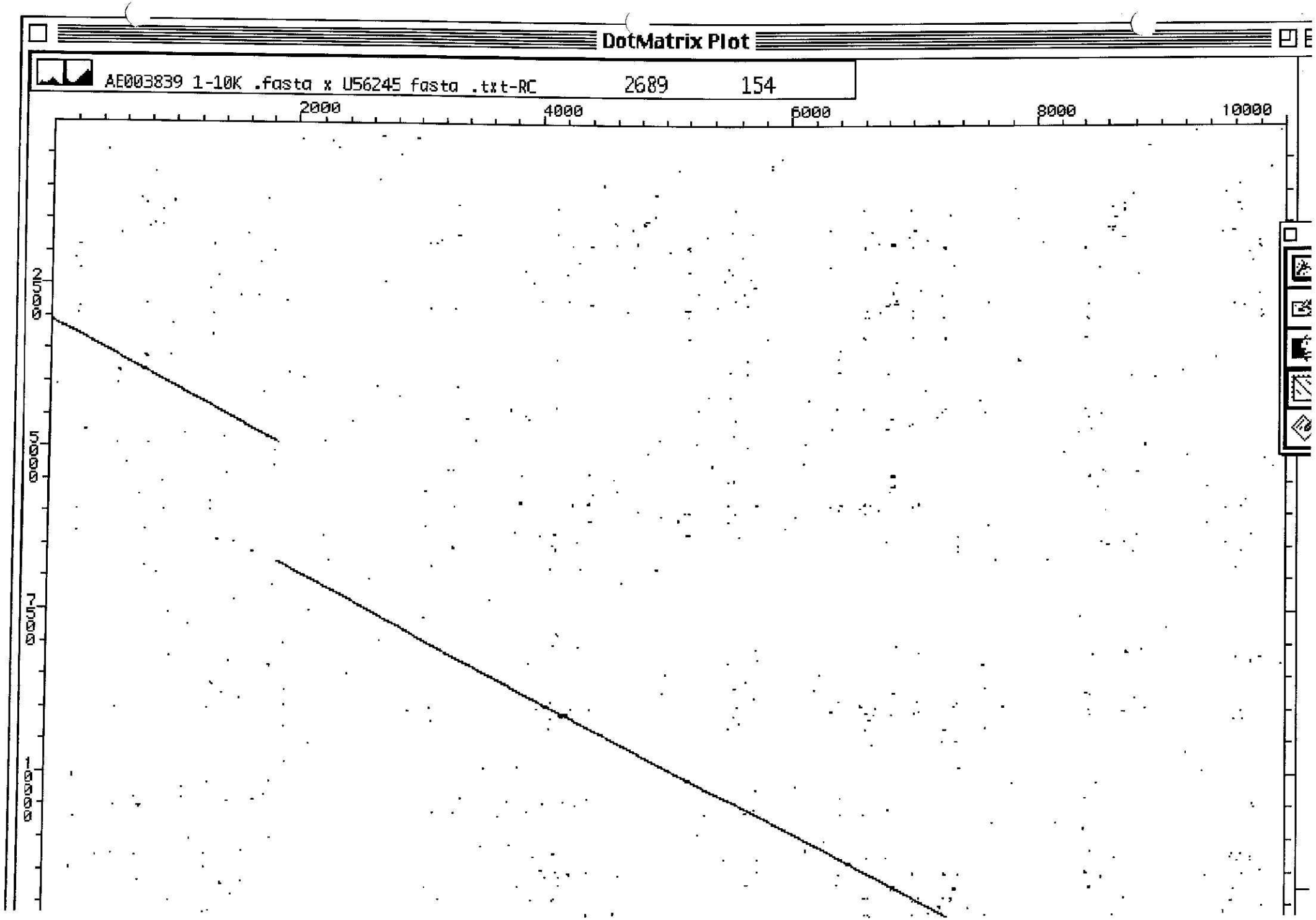
Here are the details of the putative cn[1] lesion. U56245 is a 12.3 kb genomic sequence that includes the cn gene from a strain with a wildtype cn allele. The U56245 sequence partially overlaps the BDGP/Celera scaffold segment AE003839. A dot plot of U56245 (reverse complement) (Y axis) vs AE003839 nts 1-10000 (X-axis) (see attached Picture File of the output window) shows a deletion of ~1.8 kb in AE003839 between nucleotides 1863 and 1864. I also did a BLAST of the entire AE003839 vs U56245 (see attached html file of the output). The deletion occurs at position 457 of the cn gene predicted amino acid sequence. The deletion fuses the truncated cn ORF to an unrelated ORF. The cn protein predicted by the wild-type U56245 sequence (GenPept locus AAC47351) is 524 aa, while that predicted by the cn[1] allele of the AE003839 sequence (GenPept locus AAF59196) is 504 aa. These two predicted proteins are nearly identical from 1-457 but then have no significant similarity beyond this point.

Bob Levis
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phone: [redacted]
fax:
email:

Re: Unannotated gap in genomic sequence and error in cn gene


DotMatrix Plot
AE003839 1-10K .fasta x U56245 fasta .txt-RC
2689
154
2000
4000
6000
8000
10000

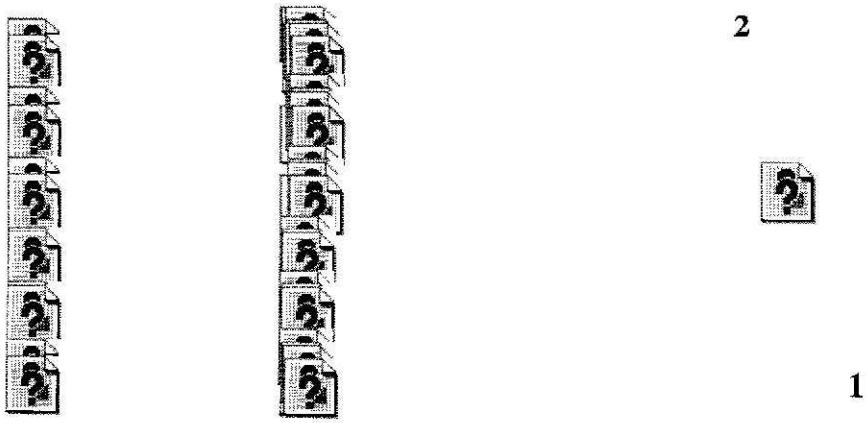
Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.1.2 [Oct-19-2000]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 50 expect: 10.000000 wordsize: 11 Filter Align

Sequence 1 gi 10727744	Drosophila melanogaster genomic scaffold 142000013386047 section 4 of 52	**Length** 262228	(1 .. 262228)
Sequence 2 gi 1336009	Drosophila melanogaster chromosome 2 cinnabar gene region, calcineurin B (dCNB2) and kynurenine 3-monooxygenase (cn) genes, complete cds.	**Length** 12340	(1 .. 12340)



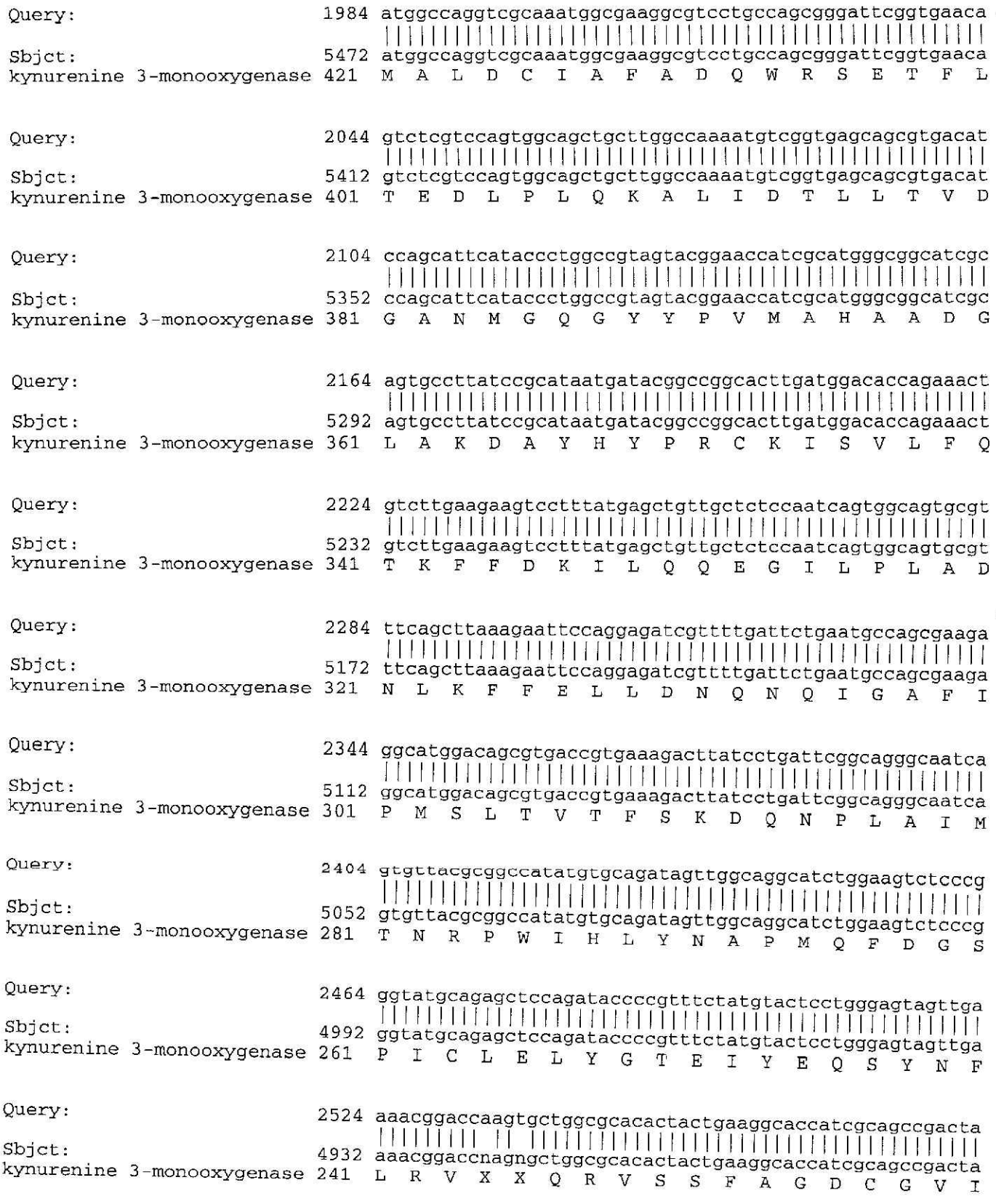
NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

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Identities = 4555/4572 (99%)
 Strand = Plus / Minus
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kynurenine 3-monooxygenase      446   L  R  F  T  W  R  K  T  L  D  R  M ~~~~~~~~~~~~~~~~

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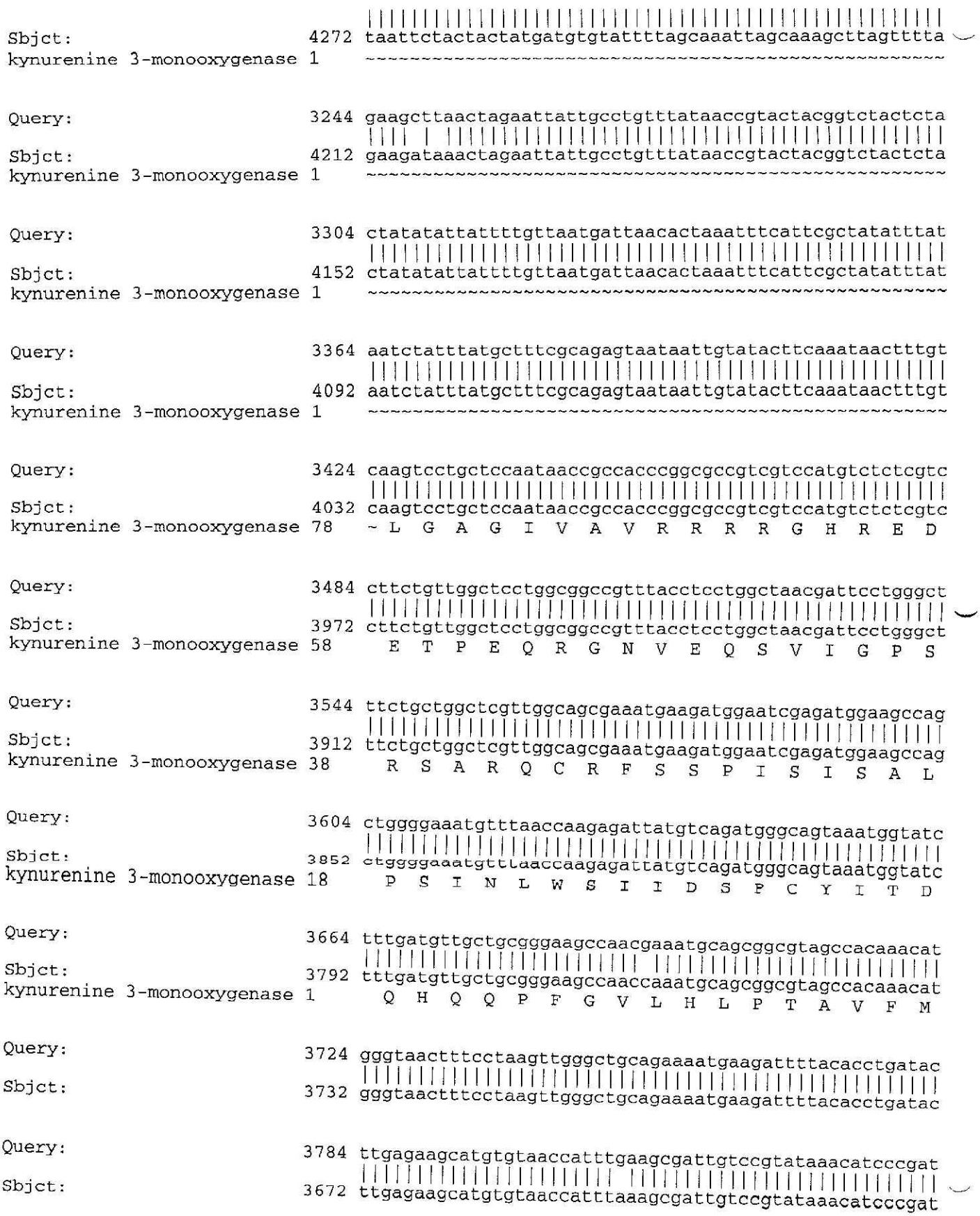
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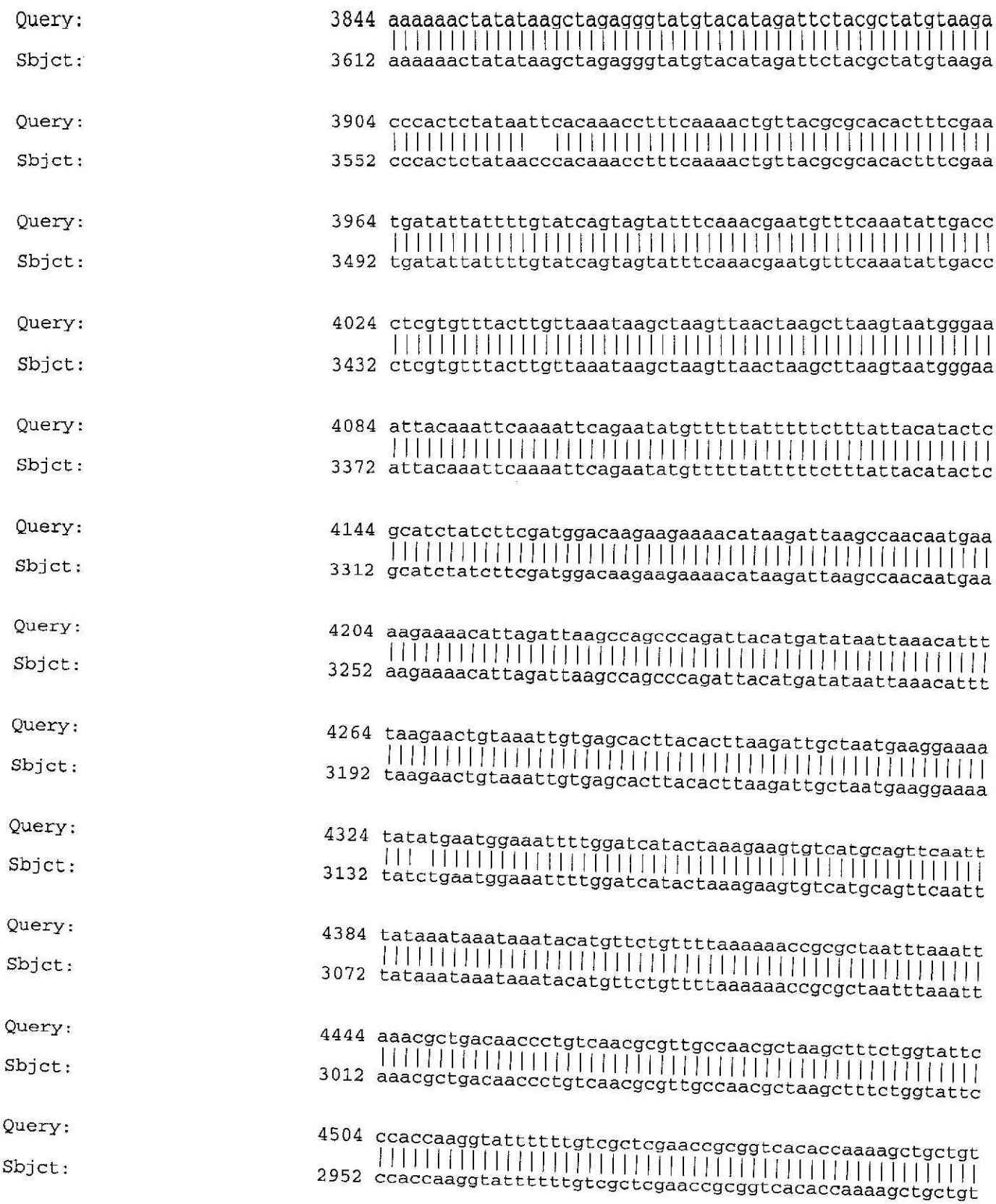
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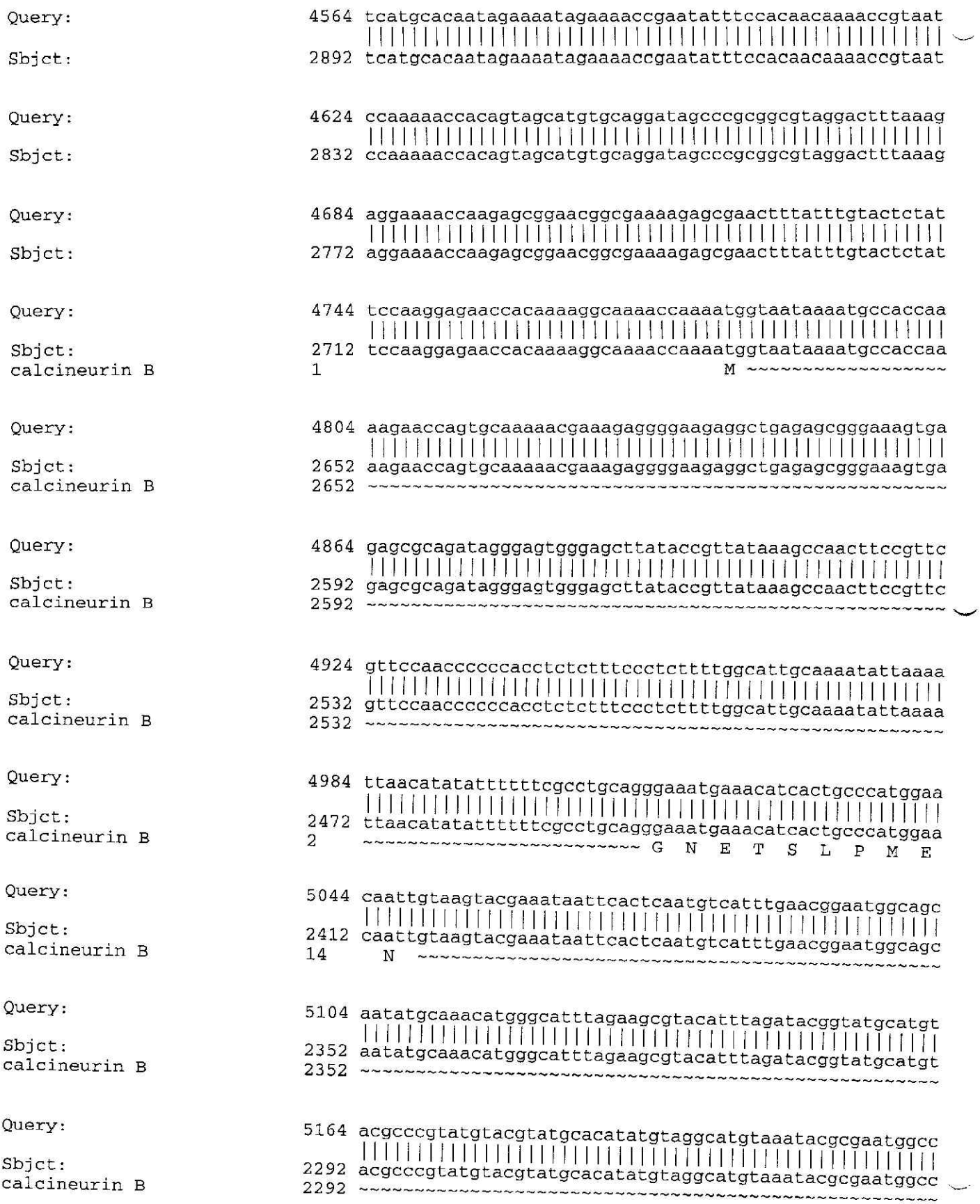
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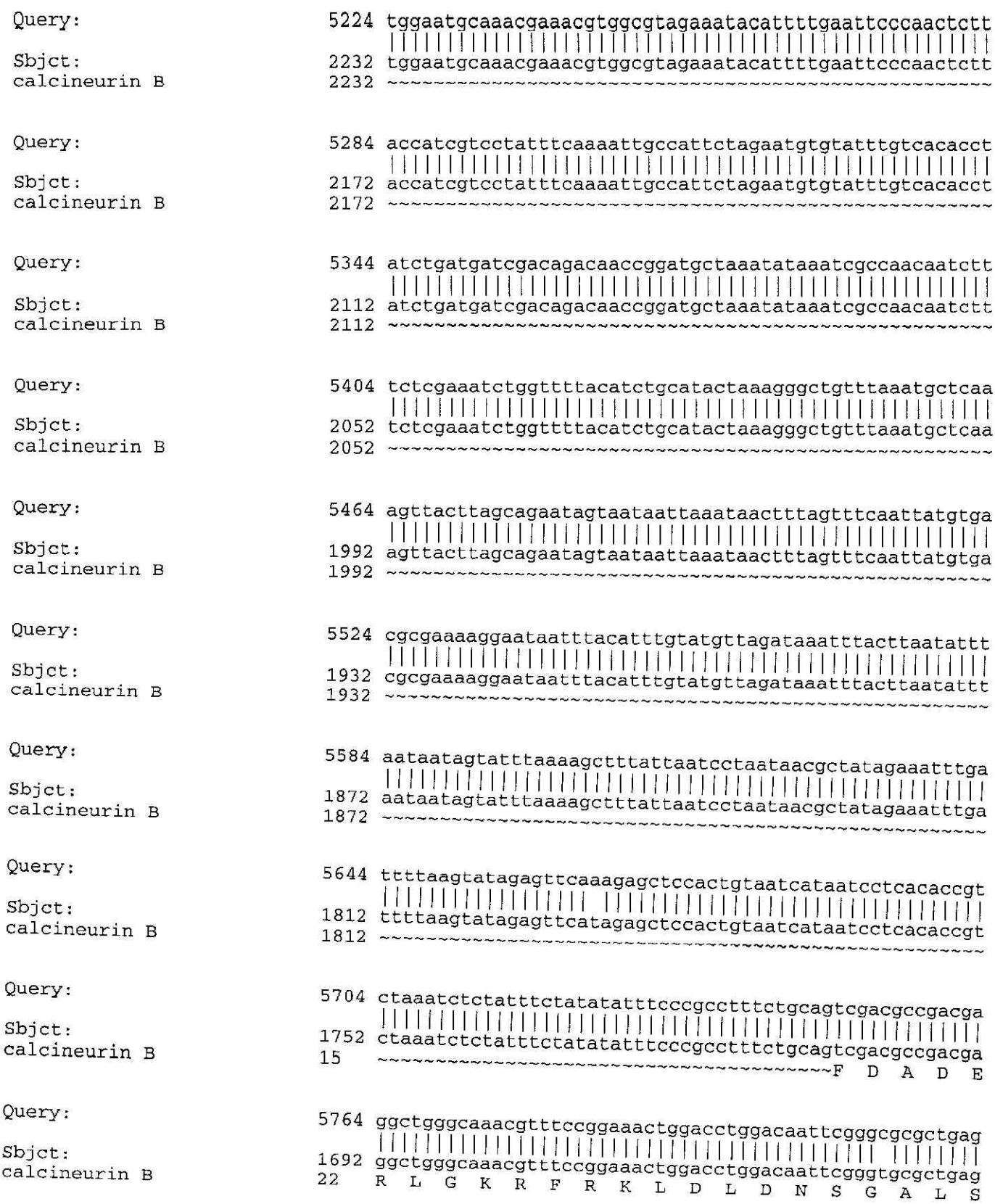
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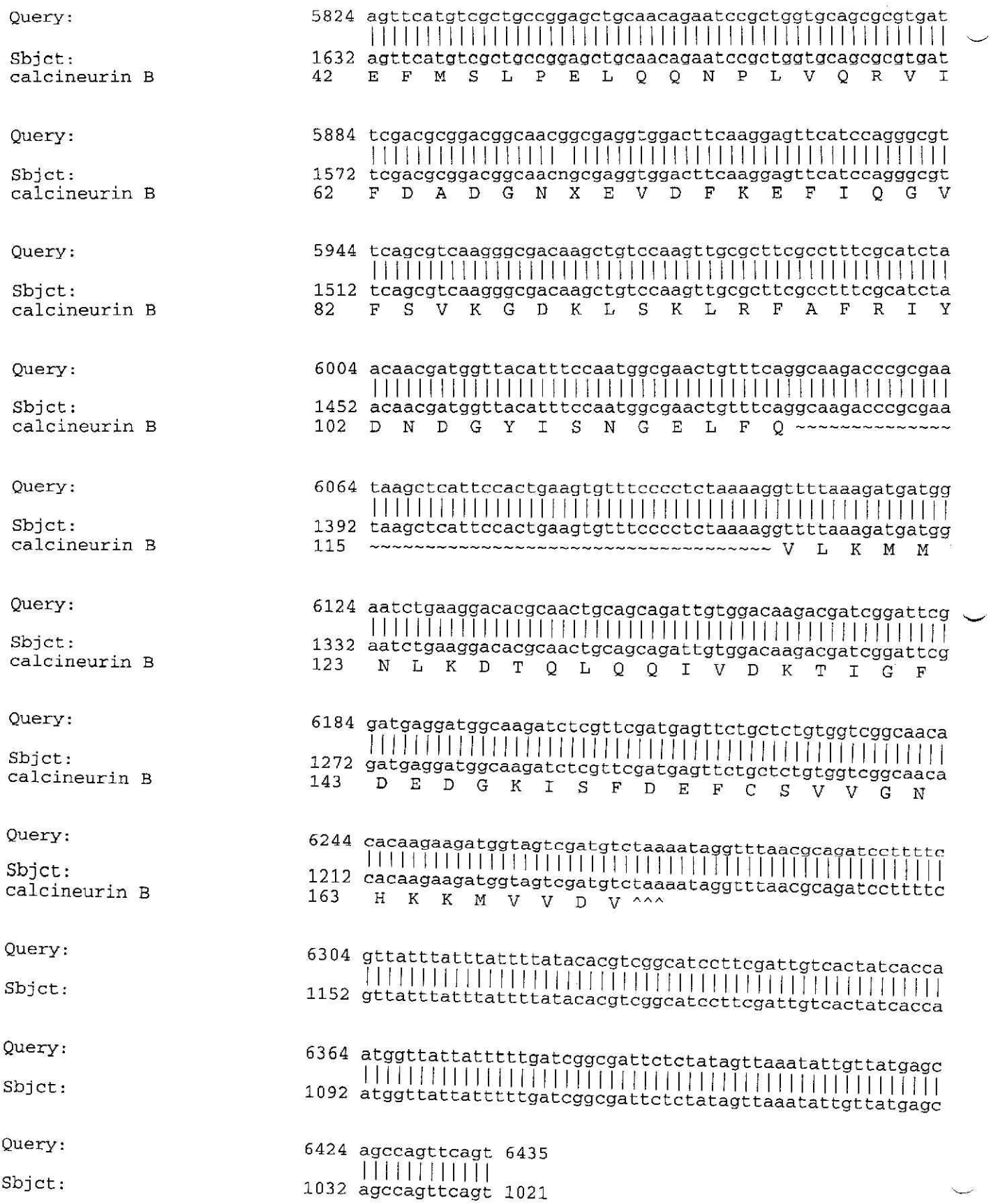
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Sbjct: 1512 tcagcgtcaagggcgacaagctgtccaagttgcgcttcgcctttcgcatcta
calcineurin B 82 F S V K G D K L S K L R F A F R I Y
Query: 6004 acaacgatggttacatttccaatggcgaactgtttcaggcaagacccgcgaa
Sbjct: 1452 acaacgatggttacatttccaatggcgaactgtttcaggcaagacccgcgaa
calcineurin B 102 D N D G Y I S N G E L F Q ~~~~~~~~~~~~~~~
Query: 6064 taagctcattccactgaagtgtttcccctctaaaaggttttaaagatgatgg
Sbjct: 1392 taagctcattccactgaagtgtttcccctctaaaaggttttaaagatgatgg
calcineurin B 115 ~~~~~~ V L K M M
Query: 6124 aatctgaaggacacgcaactgcagcagattgtggacaagacgatcggattcg
Sbjct: 1332 aatctgaaggacacgcaactgcagcagattgtggacaagacgatcggattcg
calcineurin B 123 N L K D T Q L Q Q I V D K T I G F
Query: 6184 gatgaggatggcaagatctcgttcgatgagttctgctctgtggtcggcaaca
Sbjct: 1272 gatgaggatggcaagatctcgttcgatgagttctgctctgtggtcggcaaca
calcineurin B 143 D E D G K I S F D E F C S V V G N
Query: 6244 cacaagaagatggtagtcgatgtctaaaataggtttaacgcagatccttttc
Sbjct: 1212 cacaagaagatggtagtcgatgtctaaaataggtttaacgcagatccttttc
calcineurin B 163 H K K M V V D V ^^^
Query: 6304 gttatttatttattttatacacgtcggcatccttcgattgtcactatcacca
Sbjct: 1152 gttatttatttattttatacacgtcggcatccttcgattgtcactatcacca
Query: 6364 atggttattatttttgatcggcgattctctatagttaaatattgttatgagc
Sbjct: 1092 atggttattatttttgatcggcgattctctatagttaaatattgttatgagc
Query: 6424 agccagttcagt 6435
Sbjct: 1032 agccagttcagt 1021

Score = 1994 bits (1037), Expect = 0.0
Identities = 1057/1067 (99%)
Strand = Plus / Minus



```
Query: 797  cacttttcgctcgcctgttgccgtatttgcttcgttgctttcggaccacgcgtttcgat 856
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct: 8493 cacttttcgctcgcctcttgccgtatttgcttcgttgctttcggaccacgcgtttcgat 8434

Query: 857  cgtttcgttttgcggaagcttgcccaaaagcttcgagaatgtggtttttcgatttaacag 916
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8433 cgtttcgttttgcggaagcttgcccaaaagcttcgagaatgtggtttttcgatttaacag 8374

Query: 917  caaaaagggctgaacaaagttgcacttgcacctgcctaaaaagagcgatattccggttgg 976
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct: 8373 caaaaagggctgaacaaagttgcacttgcacctggctaaaaagagcgatattccggttgg 8314

Query: 977  attatgggaatttttagtttgtgcaagtttaactgaactcctggtgagttgctaaagtca 1036
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8313 attatgggaatttttagtttgtgcaagtttaactgaactcctggtgagttgctaaagtca 8254

Query: 1037 atattctgtctaacggctgctctgcgttcgatcggatctcggtgggcactgtacagctcc 1096
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8253 atattctgtctaacggctgctctgcgttcgatcggatctcggtgggcactgtacagctcc 8194

Query: 1097 ctgtgtttggtctacttgagtgtcgaacatgtgacgagcaactgatggcgctggcctgct 1156
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8193 ctgtgtttggtctacttgagtgtcgaacatgtgacgagcaactgatggcgctggcctgct 8134

Query: 1157 ccattggtccgccggccaggcgaagacgcgcgacggcggcagcggtacagtgggtacagt 1216
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8133 ccactggtccgccggccaggcgaagacgcgcgacggcggcagcggtacagtgggtacagt 8074

Query: 1217 aaggcctgcctaaaagtactttcacttagaaagggcactcattgaaatcactggccattt 1276
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8073 aaggcctgcctaaaagtactttcacttagaaagggcactcattgaaatcactggccattt 8014

Query: 1277 gttttaaataaaaagtggctaaaacacatacatatgtatattttatttcacagctattg 1336
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8013 gttttaaataaaaagtggctaaaacacatacatatgtatattttatttcacagctattg 7954

Query: 1337 ggttcagaaaaataagagttattattcgattccattaataggttaattttcaacgttctt 1396
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7953 ggttcagaaaaataagagttattattcgattccattaataggttaattttcaacgttctt 7894

Query: 1397 aaagtctaatctctattaacgttcgatacattttacgctagttgaatacaaaaccataaa 1456
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7893 aaagtcttatctctattaacgttcgatacattttacgctagttgaatacaaaaccataaa 7834
```

```
Query: 1457 caagacattcggcaccgttcattgtataattaacattagtaaataatggtttgtcactat 1516
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7833 caagacattcggtaccgttcattgtataattaacattagtaaataatggtttgtcactat 7774

Query: 1517 ctggaagtttctagagtttaaatacgttttcataccttaagttttatgtacacgccattt 1576
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct: 7773 ctggaagtttctagagtttaaatacgttttcataccttaagttttatgtacacgccgttt 7714

Query: 1577 tgtaagaggattatgtacgtgattaactgcatatcatataaatcttattctcgtcgacgt 1636
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7713 tgtaagaggattatgtacgtgattaactgcatatcatataaatcttattctcgtcgacgt 7654

Query: 1637 tccactgtagtgagtgtgggcaaagcggaggcgccgacaattctagagagtgccatcgaa 1696
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7653 tccactgtagtgagtgtgggcaaagcggaggcgccgacaattctagagagtgccatcgaa 7594

Query: 1697 aagttcgcgaaacggaattagcaacaacaattaagtcggaaatgagcagctcgctgtctc 1756
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7593 aagttcgcgaaacggaattagcaacaacaattaagtcggaaatgagcagctcgctgtctc 7534

Query: 1757 tctcgctctctgaccatactaagctccccctctttaaatactcgaaaccatccatgtctt 1816
            |||||||||||||||||||||||| |||||||||| | |||||||||||| |||||||
Sbjct: 7533 tctcgctctctgaccatactaagctctccctctttaaacattcgaaaccatcgatgtctt 7474

Query: 1817 tctaccttcggcgaagaaaagcttttagagcttttgagtagtaggtc 1863
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7473 tctaccttcggcgaagaaaagcttttagagcttttgagtagtaggtc 7427

Score = 1396 bits (726), Expect = 0.0
Identities = 732/736 (99%)
 Strand = Plus / Minus
```





```
Query: 1    gaagatggagggaaaggtgtatgctgtggtgtgtgcctagattgttatccgcatttctgg 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9289 gaagatggagggaaaggtgtatgctgtggtgtgtgcctagattgttatccgcatttctgg 9230

Query: 61   tttgcttttcattataggcagaacagaatacaacaccatgcggcacgatgcgatctgcga 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9229 tttgcttttcattataggcagaacagaatacaacaccatgcggcacgatgcgatctgcga 9170

Query: 121  ataccccggaccctgagaatcggcgctgcagtcacgtagacccactaattgagcgagatc 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9169 ataccccggaccctgagaatcggcgctgcagtcacgtagacccactaattgagcgagatc 9110

Query: 181  aataacggtgattgtgtgtgcacctatatgcatatatatgtacgaatgtatttacctgaa 240
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct: 9109 aataacggtgattgtgtgtgcacctatatgcatacatatgtacgaatgtatttacctgaa 9050
```

```
Query: 241  caattcggacagctcgtgcctagtcgcgcattatccaaaattacgcagaacggcttcggg 300
            ||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||||
Sbjct: 9049 caattcggacagcncgtgcctagtcgcgcattatccaaaattacgcagaaccgcttcggg 8990

Query: 301  ttccgccgccgggtgctccttcttcgtagggttaaaaccgaacagaatcctagctaaagt 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8989 ttccgccgccgggtgctccttcttcgtagggttaaaaccgaacagaatcctagctaaagt 8930

Query: 361  ggggcacggattgctgaatttccaaagtatcgctatcggcggtggtctatcggtatcggt 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8929 ggggcacggattgctgaatttccaaagtatcgctatcggcggtggtctatcggtatcggt 8870

Query: 421  atgctaacgacgacgggcagcagggtgtgggggggagtttaccgttccggcgaaccgctgg 480
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct: 8869 atgctaacgacgacgggcagcagngtgtgggggggagtttaccgttccggcgaaccgctgg 8810

Query: 481  cagagcgccttaaactaaagtcgaagggcgggccaggatggcgatcggtgaatccggtat 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8809 cagagcgccttaaactaaagtcgaagggcgggccaggatggcgatcggtgaatccggtat 8750

Query: 541  tcggttttgattttggattactacggcaaggtaacaagccaaaactttcggttttctctg 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8749 tcggttttgattttggattactacggcaaggtaacaagccaaaactttcggttttctctg 8690

Query: 601  cgcacagattctgacagcttacaccccaattgctcggttaccgttacttttcgtcttacg 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8689 cgcacagattctgacagcttacaccccaattgctcggttaccgttacttttcgtcttacg 8630

Query: 661  ataccgttgcactgcacacactgagggacacttacgcacaaacacaaacacacgcgttcg 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8629 ataccgttgcactgcacacactgagggacacttacgcacaaacacaaacacacgcgttcg 8570

Query: 721  ctcactcaacttccaa 736
            ||||||||||||||||
Sbjct: 8569 ctcactcaacttccaa 8554

Score = 1133 bits (589), Expect = 0.0
Identities = 605/618 (97%)
 Strand = Plus / Minus
```





```
Query: 6832 caacaaaaccaatcgaaatgcaacaaatcgaaatatgaagtgcttatgatgagaaaggac 6891
            |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct: 618  caacaaaaccaatcgaaatgcaacaaatcgaaatatgaagtgtttatgatgagaaaggac 559

Query: 6892 agatgcgcggggcagctaagcaacctgcccgaaggaggtctcctctattgacttagtctt 6951
            |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 558  agatgcgcnggggcagctaagcaacctgcccgaaggaggtctcctctattgacttagtcta 499
```

```
Query: 6952 atttacacgttgtgtacttttttatatatttatacatacctacttgtactaatcgaatgtt 7011
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 498  atttacacgttgtgtacttttttatatatttatacatacctacttgtactaatcgaatgtt 439

Query: 7012 ataacctacgtaacgtatttttatatatcttgactaacttgataacaccagaggaaggcg 7071
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 438  ataacctacgtaacgtatttttatatatcttgactaacttgataacaccagaggaaggcg 379

Query: 7072 acgtttgccaagtttcttaagtctatcttaaccaatttctaacgccacttaactcaaatt 7131
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 378  acgtttgccaagtttcttaagtctatcttaaccaatttctaacgccacttaactcaaatt 319

Query: 7132 aatcaacgattctcacgcagaacgtagaacgcctcgaacgttttctaaaatacgctacat 7191
             ||||||||||||||||||||||||||||||  ||||||||||| ||||||||||||||
Sbjct: 318  aatcaacgattctcacgcagaacgtagaacgnntcgaacgttttcgaaaatacgctacat 259

Query: 7192 tttgcagtttataacgcgagttaactgaaaatcgaatagttattatacatcaaaacatac 7251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 258  tttgcagtttataacgcgagttaactgaaaatcgaatagttattatacatcaaaacatac 199

Query: 7252 atatgaagcaatgccgtgcggtgatattgcagtaacannnnnnnatacctaattatacta 7311
             ||||||||||||||||||||||||||||||||||||       ||||||||||||||||
Sbjct: 198  atatgaagcaatgccgtgcggtgatattgcagtaacatttttttatacctaattatacta 139

Query: 7312 gttaaagatgcaagaaaaccaaatagtaaaacgcatgttacaaattttacaattaacaaa 7371
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 138  gttaaagatgcaagaaaaccaaatagtaaaacgcatgttacaaattttacaattaacaaa 79

Query: 7372 tttttgcacactcgccactctcaattcgttagctaatcaattaaattccattgcattatt 7431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 78   tttttgcacactcgccactctcaattcgttagctaatcaattaaattccattgcattatt 19

Query: 7432 caaagtaatcgactcgag 7449
             |||||||||||||||||
Sbjct: 18   caaagtaatcgactcgag 1

Score =  344 bits (179), Expect = 1e-89
Identities = 179/179 (100%)
 Strand = Plus / Minus
```





```
Query: 6623 caaatatacatttaaagaattcaaaaaccccagaagcaaaactaaacttaactaaggcgg 6682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 829  caaatatacatttaaagaattcaaaaaccccagaagcaaaactaaacttaactaaggcgg 770

Query: 6683 aatccaagttcgtgcaagcaaaggcaaataaagcaacccaagttgaacgaatgctctatc 6742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 769  aatccaagttcgtgcaagcaaaggcaaataaagcaacccaagttgaacgaatgctctatc 710
```

```
Query: 6743 gaatgcactttcgctctatcatattgatgttatatttctaattctcctgtgattttgcc 6801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 709  gaatgcactttcgctctatcatattgatgttatatttctaattctcctgtgattttgcc 651

Score =  169 bits (88), Expect = 5e-37
Identities = 88/88 (100%)
 Strand = Plus / Minus
```




```
Query: 6476 acagcgatcgaaggcttagggagaaatcgcgaatgcaatgttgttatcctaagttgaaaa 6535
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 976  acagcgatcgaaggcttagggagaaatcgcgaatgcaatgttgttatcctaagttgaaaa 917


Query: 6536 gtggaataatgcgcctcctacttacttc 6563
           ||||||||||||||||||||||||||||
Sbjct: 916  gtggaataatgcgcctcctacttacttc 889

CPU time:     3.94 user secs.       0.14 sys. secs          4.08 total secs.

Gapped
Lambda      K       H
    1.33     0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 2337
Number of Sequences: 0
Number of extensions: 2337
Number of successful extensions: 323
Number of sequences better than 10.0: 1
length of query: 262228
length of database: 2,436,278,593
effective HSP length: 29
effective length of query: 262199
effective length of database: 2,436,278,564
effective search space: 638789803202236
effective search space used: 638789803202236
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 24 (46.8 bits)
```