

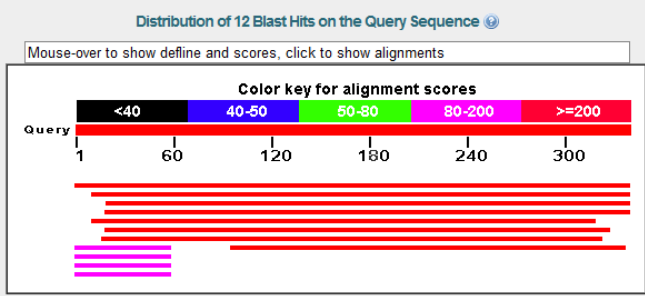
NCBI/BLAST/blastn suite/Formatting Results - 7TMVYGC016  
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**DQ132793:Homo sapiens transfection product...**

**Query ID** [gi|73427170|gb|DQ132793.1](#) **Database Name** nr  
**Description** Homo sapiens transfection product sequence **Description** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
**Molecule type** nucleic acid **Program** BLASTN 2.2.25+ [Citation](#)  
**Query Length** 339

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

**Graphic Summary**



**Descriptions**

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer [B](#) PubChem BioAssay

**Sequences producing significant alignments:**

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Link
<a href="#">DQ132793.1</a>	Homo sapiens transfection product sequence	623	623	100%	2e-175	100%	
<a href="#">DQ188102.1</a>	Homo sapiens transfection product sequence	604	604	97%	9e-170	99%	
<a href="#">DQ188104.1</a>	Homo sapiens transfection product sequence	588	588	94%	9e-165	99%	
<a href="#">DQ188100.1</a>	Homo sapiens transfection product sequence	586	586	94%	3e-164	99%	
<a href="#">DQ188105.1</a>	Homo sapiens transfection product sequence	566	566	90%	4e-158	99%	
<a href="#">DQ188103.1</a>	Homo sapiens transfection product sequence	562	562	91%	5e-157	99%	
<a href="#">DQ188101.1</a>	Homo sapiens transfection product sequence	556	556	90%	2e-155	99%	
<a href="#">AP002768.3</a>	Homo sapiens genomic DNA, chromosome 11q, clone:RP11-	446	446	71%	6e-122	100%	<a href="#">E</a>
<a href="#">AC145547.3</a>	Homo sapiens BAC clone RP11-143706 from UL, complete s	82.4	82.4	17%	2e-12	91%	
<a href="#">AC144916.3</a>	Homo sapiens BAC clone RP11-15L7 from UL, complete sequ	82.4	82.4	17%	2e-12	91%	
<a href="#">CR381572.5</a>	Human DNA sequence from clone bP-2168N6 on chromosom	82.4	82.4	17%	2e-12	91%	
<a href="#">BX546448.4</a>	Human DNA sequence from clone RP11-509J10 on chromos	82.4	82.4	17%	2e-12	91%	

**Alignments**

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```
>gb|DQ132793.1 Homo sapiens transfection product sequence
Length=339
Score = 623 bits (337), Expect = 2e-175
Identities = 339/339 (100%), Gaps = 0/339 (0%)
Strand=Plus/Plus

Query 1   CTCAACAGCCAGCATGTAAGATGCTGCTTCTCCTTCTGCCATGATTGGGAGTTTCT 60
Sbjct 1   CTCAACAGCCAGCATGTAAGATGCTGCTTCTCCTTCTGCCATGATTGGGAGTTTCT 60

Query 61  GGTAAAGATTAAAGGCTTTCACCGCAITCCCGCTCCCTCACCATAGTCGATGGGCT 120
Sbjct 61  GGTAAAGATTAAAGGCTTTCACCGCAITCCCGCTCCCTCACCATAGTCGATGGGCT 120

Query 121 CAGTTCCTGGAAGCATAGTATGTTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTT 180
Sbjct 121 CAGTTCCTGGAAGCATAGTATGTTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTT 180

Query 181 TATCAGCCAGCAGAAAATATCCAGAAGATTCCTATGGGAGAGGACTCAGCCTGAAGCAT 240
Sbjct 181 TATCAGCCAGCAGAAAATATCCAGAAGATTCCTATGGGAGAGGACTCAGCCTGAAGCAT 240

Query 241 CAGCAITGAGCAGCCAGGCTGCGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCT 300
Sbjct 241 CAGCAITGAGCAGCCAGGCTGCGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCT 300

Query 301  CACGCTCCCTTGGTGTCTGAAGGAGCTCAACAGCCAGCA 339
Sbjct 301  CACGCTCCCTTGGTGTCTGAAGGAGCTCAACAGCCAGCA 339

>gb|DQ188102.1 Homo sapiens transfection product sequence
Length=331
Score = 604 bits (327), Expect = 9e-170
Identities = 328/329 (99%), Gaps = 0/329 (0%)
Strand=Plus/Plus

Query 11  AGCATGTAAGATGCTGCTTCTCCTTCTGCCATGATTGGGAGTTTCTGGTAAAGATT 70
Sbjct 11  AGCATGTAAGATGCTGCTTCTCCTTCTGCCATGATTGGGAGTTTCTGGTAAAGATT 70
```

Query 71 AGGGCTNITTCACCGCAITCCCGTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTG 130  
Sbjct 61 AGGGCTGTTTCCACCGCAITCCCGTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTG 120

Query 131 GAAGCATAGTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAG 190  
Sbjct 121 GAAGCATAGTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAG 180

Query 191 CAGAAAATATCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCAATTGAG 250  
Sbjct 181 CAGAAAATATCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCAATTGAG 240

Query 251 CAGCCAGGCTGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCT 310  
Sbjct 241 CAGCCAGGCTGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCT 300

Query 311 TGGTGTCTGAAGGAGCTCAACAGCCAGCA 339  
Sbjct 301 TGGTGTCTGAAGGAGCTCAACAGCCAGCA 329

>[gb|DQ188104.1](#) Homo sapiens transfection product sequence  
Length=320

Score = 588 bits (318), Expect = 9e-165  
Identities = 319/320 (99%), Gaps = 0/320 (0%)  
Strand=Plus/Plus

Query 20 GATGTGCTTGCCTTCTCCTCTCCTCATGATTGGGAGTTTCTGGTAAGATTAAGGGCTNIT 79  
Sbjct 1 GATGTGCTTGCCTTCTCCTCTCCTCATGATTGGGAGTTTCTGGTAAGATTAAGGGCTGTT 60

Query 80 TCACCGCAITCCCGCTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGAAGCATAG 130  
Sbjct 61 TCACCGCAITCCCGCTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGAAGCATAG 120

Query 140 TATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATA 199  
Sbjct 121 TATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATA 180

Query 200 TTCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGGC 259  
Sbjct 181 TTCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGGC 240

Query 260 TCCCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCTTGGTGTCTG 319  
Sbjct 241 TCCCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCTTGGTGTCTG 300

Query 320 AAGGAGCTCAACAGCCAGCA 339  
Sbjct 301 AAGGAGCTCAACAGCCAGCA 320

>[gb|DQ188100.1](#) Homo sapiens transfection product sequence  
Length=321

Score = 586 bits (317), Expect = 3e-164  
Identities = 319/321 (99%), Gaps = 0/321 (0%)  
Strand=Plus/Plus

Query 19 AGATGTGCTTGCCTTCTCCTCTCCTCATGATTGGGAGTTTCTGGTAAGATTAAGGGCTNIT 78  
Sbjct 1 AGATGTGCTTGCCTTCTCCTCTCCTCATGATTGGGAGTTTCTGGTAAGATTAAGGGCTGT 60

Query 79 TTCACCGCAITCCCGCTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGAAGCAITA 138  
Sbjct 61 TTCACCGCAITCCCGCTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGAAGCAITA 120

Query 139 GTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATA 198  
Sbjct 121 GTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATA 180

Query 199 ATTCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGG 258  
Sbjct 181 ATTCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGG 240

Query 259 CTGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCTTGGTGTCT 318  
Sbjct 241 CTGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCTTGGTGTCT 300

Query 319 GAAGGAGCTCAACAGCCAGCA 339  
Sbjct 301 GAAGGAGCTCAACAGCCAGCA 321

>[gb|DQ188105.1](#) Homo sapiens transfection product sequence  
Length=308

Score = 566 bits (306), Expect = 4e-158  
Identities = 307/308 (99%), Gaps = 0/308 (0%)  
Strand=Plus/Plus

Query 11 AGCATGTAAGATGTGCTTCTCCTCTCCTCATGATTGGGAGTTTCTGGTAAGATTA 70  
Sbjct 1 AGCATGTAAGATGTGCTTCTCCTCTCCTCATGATTGGGAGTTTCTGGTAAGATTA 60

Query 71 AGGGCTNITTCACCGCAITCCCGTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTG 130  
Sbjct 61 AGGGCTGTTTCCACCGCAITCCCGTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTG 120

Query 131 GAAGCATAGTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAG 190  
Sbjct 121 GAAGCATAGTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAG 180

Query 191 CAGAAAATATCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCAATTGAG 250  
Sbjct 181 CAGAAAATATCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCAATTGAG 240

Query 251 CAGCCAGGCTGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCT 310  
Sbjct 241 CAGCCAGGCTGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCT 300

Query 311 TGGTGTCT 318  
Sbjct 301 TGGTGTCT 308

>[gb|DQ188103.1](#) Homo sapiens transfection product sequence  
Length=309

Score = 562 bits (304), Expect = 5e-157  
Identities = 307/309 (99%), Gaps = 0/309 (0%)  
Strand=Plus/Plus

Query 19 AGATGTGCTTGCCTTCTCCTCTCCTCATGATTGGGAGTTTCTGGTAAGATTAAGGGCTNIT 78  
Sbjct 1 AGATGTGCTTGCCTTCTCCTCTCCTCATGATTGGGAGTTTCTGGTAAGATTAAGGGCTGT 60

Query 79 TTCACCGCAITCCCGCTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGAAGCAITA 138  
Sbjct 61 TTCACCGCAITCCCGCTCTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGAAGCAITA 120

Query 139 GTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATA 198  
Sbjct 121 GTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATA 180

Query 199 ATTCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGG 258  
Sbjct 181 ATTCCAGAAGATTCTTATGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGG 240

Query 259 CTGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCTTGGTGTCT 318  
Sbjct 241 CTGCCACAGCCTTGACAGATTGATTCTGCAGCCTGGGAGCTCAGCTCCCTTGGTGTCT 300

Sbjct 241 CTGCCACAGCCTTGACAGATTGATTCTGCAGCTGGGAGCTCACGCTCCCTTGGTGTCT 300  
Query 319 GAAGGAGCT 327  
Sbjct 301 GAAGGAGCT 309

>[gb|DQ188101.1](#) Homo sapiens transfection product sequence  
Length=306

Score = 556 bits (301), Expect = 2e-155  
Identities = 304/306 (99%), Gaps = 0/306 (0%)  
Strand=Plus/Plus

Query 17 TAAGATGTGCTTGGCTTTCCTTCTGCCATGATTGGGAGTTTCTGGTAAGATTAAAGGCT 76  
Sbjct 11 TAAGATGTGCTTGGCTTTCCTTCTGCCATGATTGGGAGTTTCTGGTAAGATTAAAGGCT 60

Query 77 NITTCACCCGATTCCCGCTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGGAAGCA 136  
Sbjct 61 GITTCCACCATTCCTCCGCTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGGAAGCA 120

Query 137 TAGTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAA 196  
Sbjct 121 TAGTATGGTGGACAAGTCAAGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAA 180

Query 197 ATATTCAGAAAGATTCTATGGGAGAGACTCAGCTGAAGCATCAGCAITGAGCAGCCA 256  
Sbjct 181 ATATTCAGAAAGATTCTATGGGAGAGACTCAGCTGAAGCATCAGCAITGAGCAGCCA 240

Query 257 GGCTGCCACAGCCTTGACAGATTGATTCTGCAGCTGGGAGCTCACGCTCCCTTGGTGT 316  
Sbjct 241 GGCTGCCACAGCCTTGACAGATTGATTCTGCAGCTGGGAGCTCACGCTCCCTTGGTGT 300

Query 317 CTGAAG 322  
Sbjct 301 CTGAAG 306

>[dbj|AP002768.3](#) **E D** Homo sapiens genomic DNA, chromosome 11q, clone:RP11-673F18, complete sequence  
Length=186084

Score = 446 bits (241), Expect = 6e-122  
Identities = 241/241 (100%), Gaps = 0/241 (0%)  
Strand=Plus/Minus

Query 96 ICTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGGAAGCATAGTATGGTGGACAAGTCA 155  
Sbjct 116181 ICTCCCTCACCATAGTCGATGGGCTCAGTTCCTGGGAAGCATAGTATGGTGGACAAGTCA 116122

Query 156 AGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATATTCAGAAAGATTCTTA 215  
Sbjct 116121 AGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATATTCAGAAAGATTCTTA 116062

Query 216 TGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGGCTGCCACAGCCTTGAC 275  
Sbjct 116061 TGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGGCTGCCACAGCCTTGAC 116002

Query 276 AGATTGATTCTGCAGCCTGGGAGCTCACGCTCCCTTGGTGTCTGAAGGAGCTCAACAGCC 335  
Sbjct 116001 AGATTGATTCTGCAGCCTGGGAGCTCACGCTCCCTTGGTGTCTGAAGGAGCTCAACAGCC 115942

Query 336 A 336  
Sbjct 115941 A 115941

>[gb|AC145547.3](#) **D** Homo sapiens BAC clone RP11-143706 from UL, complete sequence  
Length=185637

Score = 82.4 bits (44), Expect = 2e-12  
Identities = 54/59 (92%), Gaps = 0/59 (0%)  
Strand=Plus/Minus

Query 1 CTCAACAGCCAGCATGTAAGATGTGCTTGTCTTCTCCTTCTGCCATGATTGGGAGTTTC 59  
Sbjct 64100 CTCACCTGCCACCATGTAAGATGTGCTTGTCTTCTCCTTCTGCCATGATTGTAAGTTTC 64042

>[gb|AC144916.3](#) **D** Homo sapiens BAC clone RP11-15L7 from UL, complete sequence  
Length=158759

Score = 82.4 bits (44), Expect = 2e-12  
Identities = 54/59 (92%), Gaps = 0/59 (0%)  
Strand=Plus/Minus

Query 1 CTCAACAGCCAGCATGTAAGATGTGCTTGTCTTCTCCTTCTGCCATGATTGGGAGTTTC 59  
Sbjct 98856 CTCACCTGCCACCATGTAAGATGTGCTTGTCTTCTCCTTCTGCCATGATTGTAAGTTTC 98798

>[emb|CR381572.5](#) **D** Human DNA sequence from clone bP-2168N6 on chromosome 21, complete sequence  
Length=184355

Score = 82.4 bits (44), Expect = 2e-12  
Identities = 54/59 (92%), Gaps = 0/59 (0%)  
Strand=Plus/Minus

Query 1 CTCAACAGCCAGCATGTAAGATGTGCTTGTCTTCTCCTTCTGCCATGATTGGGAGTTTC 59  
Sbjct 97917 CTCACCTGCCACCATGTAAGATGTGCTTGTCTTCTCCTTCTGCCATGATTGTAAGTTTC 97859

>[emb|BX546448.4](#) **D** Human DNA sequence from clone RP11-509J10 on chromosome 22, complete sequence  
Length=172149

Score = 82.4 bits (44), Expect = 2e-12  
Identities = 54/59 (92%), Gaps = 0/59 (0%)  
Strand=Plus/Plus

Query 1 CTCAACAGCCAGCATGTAAGATGTGCTTGTCTTCTCCTTCTGCCATGATTGGGAGTTTC 59  
Sbjct 84877 CTCACCTGCCACCATGTAAGATGTGCTTGTCTTCTCCTTCTGCCATGATTGTAAGTTTC 84935

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