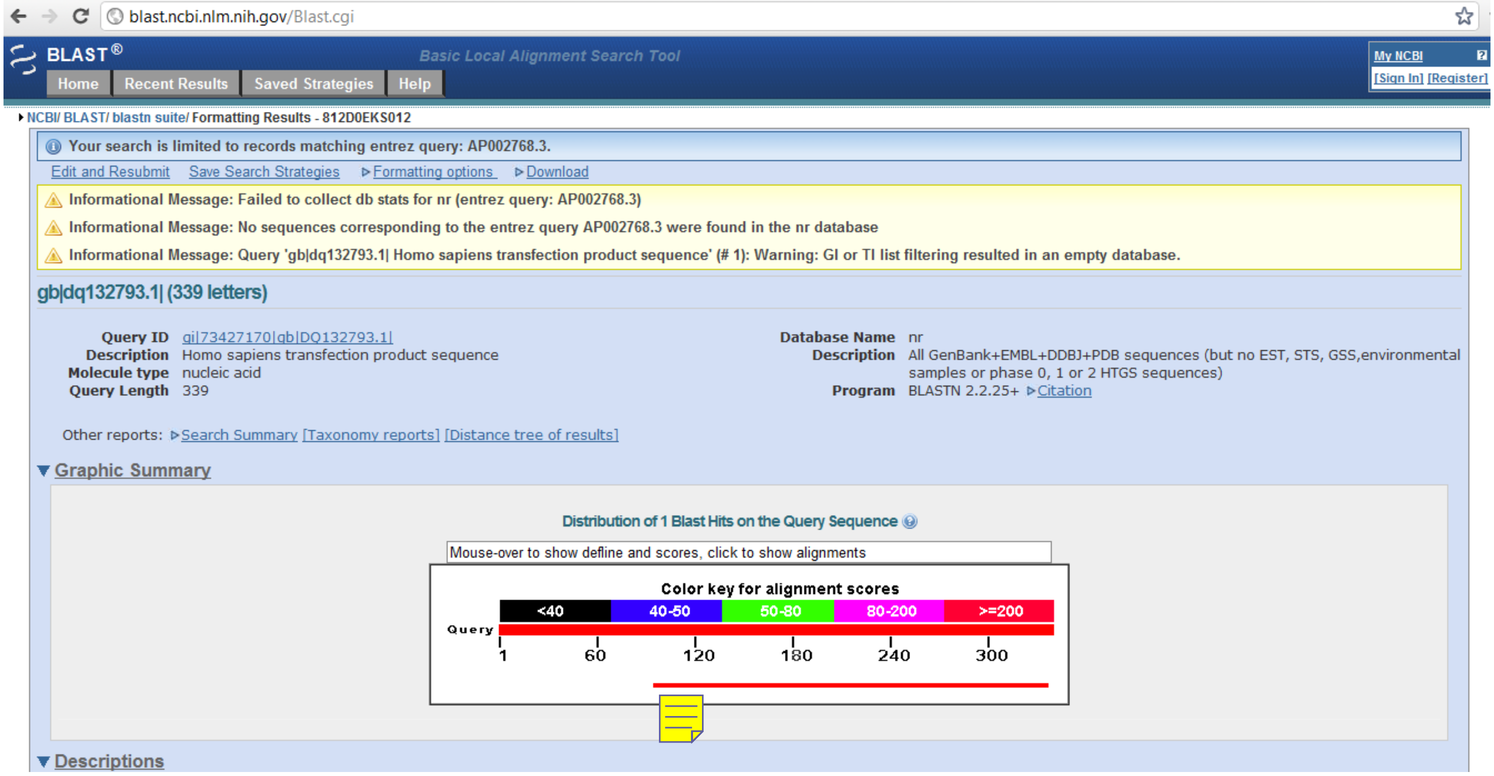


Your search is limited to records matching entrez query: AP002768.3.

Informational Message: Failed to collect db stats for nr (entrez query: AP002768.3)

Informational Message: No sequences corresponding to the entrez query AP002768.3 were found in the nr database

Informational Message: Query 'gb|dq132793.1| Homo sapiens transfection product sequence' (# 1): Warning: GI or TI list filtering resulted in an empty database.

gb|dq132793.1| (339 letters)

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, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
Molecule type	nucleic acid	**Program**	BLASTN 2.2.25+ Citation
Query Length	339		

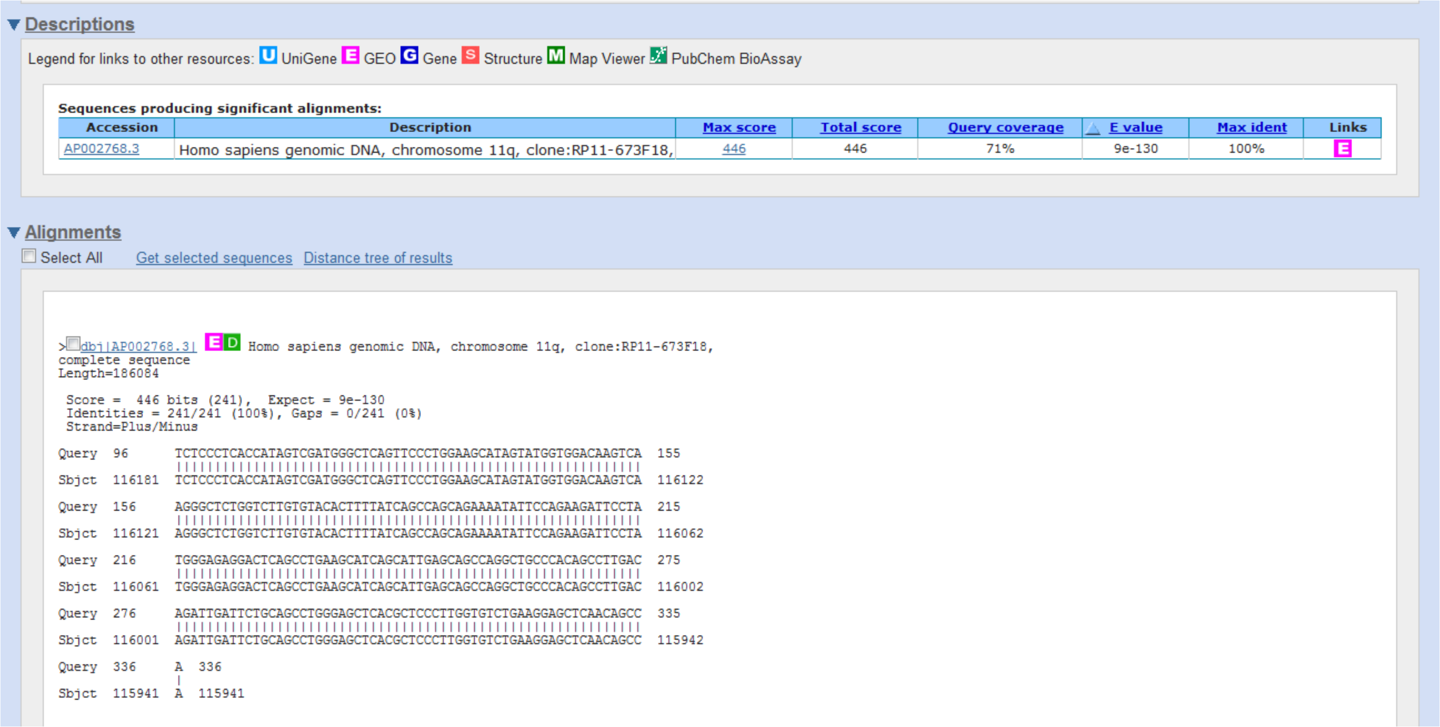
Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments

Descriptions



Descriptions

Legend for links to other resources: U UniGene E GEO G Gene S Structure M Map Viewer PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
AP002768.3	Homo sapiens genomic DNA, chromosome 11q, clone:RP11-673F18,	446	446	71%	9e-130	100%	E

Alignments

☐ Select All   Get selected sequences   Distance tree of results

```
>☐dbj|AP002768.3| E D Homo sapiens genomic DNA, chromosome 11q, clone:RP11-673F18,
complete sequence
Length=186084

 Score =  446 bits (241),  Expect = 9e-130
 Identities = 241/241 (100%), Gaps = 0/241 (0%)
 Strand=Plus/Minus

Query  96      TCTCCCTCACCATAGTCGATGGGCTCAGTTCCCTGGAAGCATAGTATGGTGGACAAGTCA  155
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116181  TCTCCCTCACCATAGTCGATGGGCTCAGTTCCCTGGAAGCATAGTATGGTGGACAAGTCA  116122

Query  156     AGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATATTCCAGAAGATTCCTA  215
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116121  AGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATATTCCAGAAGATTCCTA  116062

Query  216     TGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGGCTGCCCACAGCCTTGAC  275
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116061  TGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGGCTGCCCACAGCCTTGAC  116002

Query  276     AGATTGATTCTGCAGCCTGGGAGCTCACGCTCCCTTGGTGTCTGAAGGAGCTCAACAGCC  335
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  116001  AGATTGATTCTGCAGCCTGGGAGCTCACGCTCCCTTGGTGTCTGAAGGAGCTCAACAGCC  115942

Query  336     A  336
               |
Sbjct  115941  A  115941
```