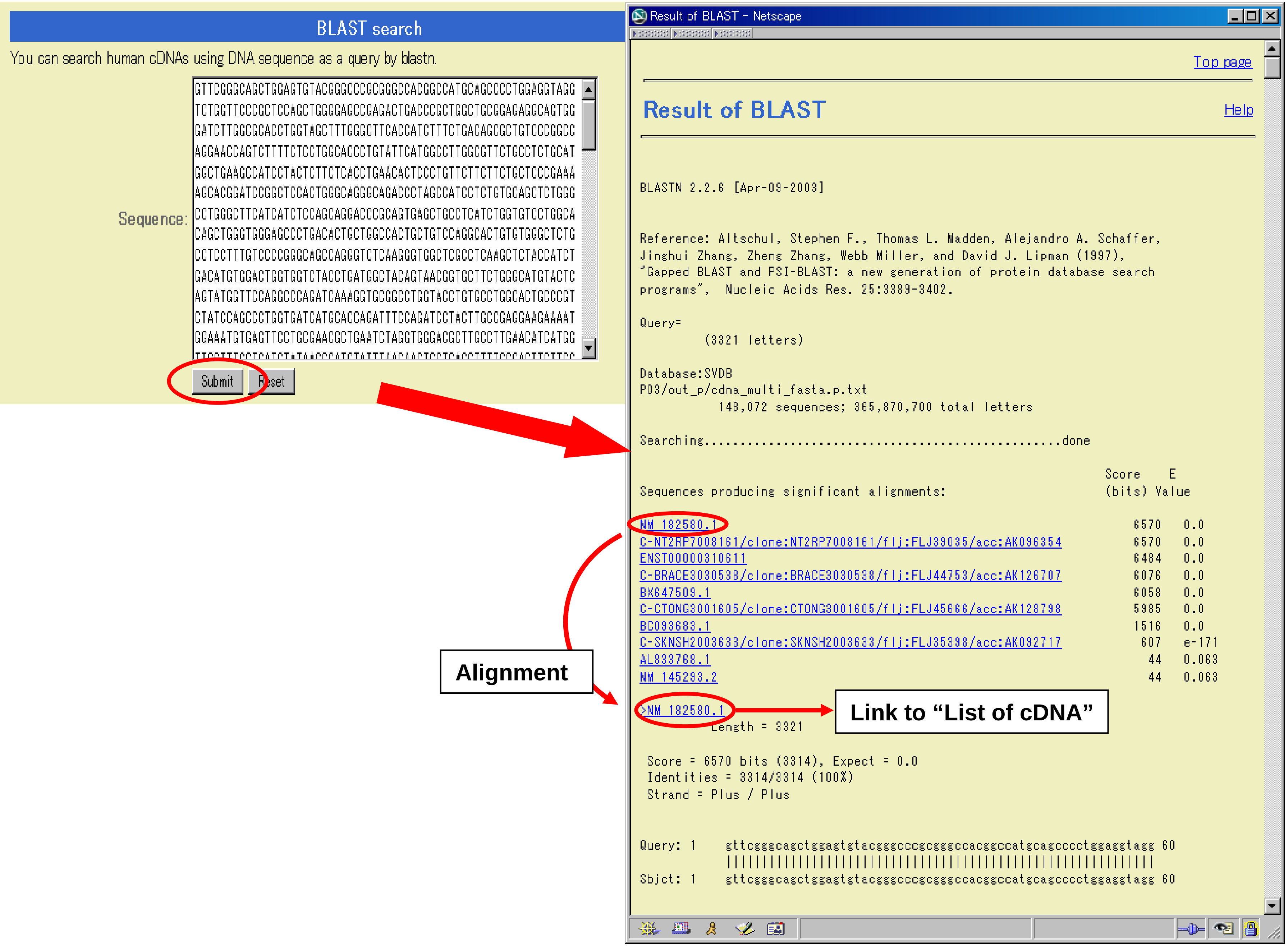
Fig2-06 BLAST search



You can search human cDNAs using DNA sequence as a query by blastn.

Sequence:

```
GTTCGGGCAGCTGGAGTGTACGGGCCCGCGGGCCACGGCCATGCAGCCCCTGGAGGTAGG
TCTGGTTCCCGCTCCAGCTGGGGAGCCGAGACTGACCCGCTGGCTGCGGAGAGGCAGTGG
GATCTTGGCGCACCTGGTAGCTTTGGGCTTCACCATCTTTCTGACAGCGCTGTCCCGGCC
AGGAACCAGTCTTTTCTCCTGGCACCCTGTATTCATGGCCTTGGCGTTCTGCCTCTGCAT
GGCTGAAGCCATCCTACTCTTCTCACCTGAACACTCCCTGTTCTTCTTCTGCTCCCGAAA
AGCACGGATCCGGCTCCACTGGGCAGGGCAGACCCTAGCCATCCTCTGTGCAGCTCTGGG
CCTGGGCTTCATCATCTCCAGCAGGACCCGCAGTGAGCTGCCTCATCTGGTGTCCTGGCA
CAGCTGGGTGGGAGCCCTGACACTGCTGGCCACTGCTGTCCAGGCACTGTGTGGGCTCTG
CCTCCTTTGTCCCCGGGCAGCCAGGGTCTCAAGGGTGGCTCGCCTCAAGCTCTACCATCT
GACATGTGGACTGGTGGTCTACCTGATGGCTACAGTAACGGTGCTTCTGGGCATGTACTC
AGTATGGTTCCAGGCCCAGATCAAAGGTGCGGCCTGGTACCTGTGCCTGGCACTGCCCGT
CTATCCAGCCCTGGTGATCATGCACCAGATTTCCAGATCCTACTTGCCGAGGAAGAAAAT
GGAAATGTGAGTTCCTGCGAACGCTGAATCTAGGTGGGACGCTTGCCTTGAACATCATGG
```

Result of BLAST

```
BLASTN 2.2.6 [Apr-09-2003]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query=
         (3321 letters)

Database:SYDB
P03/out_p/cdna_multi_fasta.p.txt
           148,072 sequences; 365,870,700 total letters

Searching..................................................done


                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

NM_182580.1                                                          6570   0.0
C-NT2RP7008161/clone:NT2RP7008161/flj:FLJ39035/acc:AK096354          6570   0.0
ENST00000310611                                                      6484   0.0
C-BRACE3030538/clone:BRACE3030538/flj:FLJ44753/acc:AK126707          6076   0.0
BX647509.1                                                           6058   0.0
C-CTONG3001605/clone:CTONG3001605/flj:FLJ45666/acc:AK128798          5985   0.0
BC093683.1                                                           1516   0.0
C-SKNSH2003633/clone:SKNSH2003633/flj:FLJ35398/acc:AK092717           607   e-171
AL833768.1                                                             44   0.063
NM_145293.2                                                            44   0.063

>NM_182580.1
          Length = 3321

 Score = 6570 bits (3314), Expect = 0.0
 Identities = 3314/3314 (100%)
 Strand = Plus / Plus


Query: 1    gttcgggcagctggagtgtacgggcccgcgggccacggccatgcagcccctggaggtagg 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    gttcgggcagctggagtgtacgggcccgcgggccacggccatgcagcccctggaggtagg 60
```

Alignment

Link to "List of cDNA"