

An Example

Steps to Identify a Gene

- **Gene-Search (Find ORF)**
- **Translate to Protein**
- **Annotation**

Open Reading Frame Search & Annotation

	...AGATGCGAAAAA	TCTACGGCAA	TTACATTACG	CAGAAGCGTC	TCGGTTCAGG
	AAGTTTTCGGA	GAGGTTTGGG	AAGCTGTCAG	TCATTTCGACC	GGACAAAAGG
101	TTGCTCTCAA	ATTAGAGCCC	CGAAACTCTA	GTGTTCCACA	ATTATTTTTTC
	GAAGCCAAGC	TATACTCAAT	GTTTCAGGCT	TCAAAATCCA	CAAATAATAG
201	TGTAGAACCA	TGCAACAACA	TTCCAGTTGT	TTATGCGACT	GGTCAAACAG
	AGACAACATA	CTACATGGCC	ATGGAATTAC	TTGGCAAGTC	TCTGGAAGAT
301	TTAGTTTCAT	CGGTCCCTAG	ATTTTCCCAA	AAGACAATAT	TAATGCTTGC
	CGGACAAATG	ATTTCCCTGTG	TTGAATTTCGT	TCACAAACAT	AATTTTATTC
401	ACCGCGACAT	CAAGCCAGAT	AATTTTGCAG	TGGGAGTCAG	TGAGAACTCA
	AACAAAATTT	ATATTATCGA	TTTTGGACTT	TCCAAGAAGT	ACATTGACCA
501	AAATAATCGT	CATATTAGAA	ATTGCACAGG	AAAATCACTT	ACCGGAACCG
	CAAGATATTC	ATCAATTAAT	GCGCTCGAAG	GAAAGGAACA	GTCTATAAGA
601	GATGACATGG	AATCTTTGGT	ATATGTCTGG	GTTTATTTAC	TTCATGGACG
	TCTTCCTTGG	ATGAGCTTAC	CTACAACAGG	CCGCAAGAAG	TATGAGGCCA
701	TTTTAATGAA	GAAGAGATCA	ACGAAACCCG	AAGAATTATG	TTTAGGACTT
	AATAGTTTCT	TTGTAAACTA	CTTAATAGCA	GTTTCGTCAT	TGAAATTTGA
801	AGAAGAACCA	AATTACGCGA	TGTACAGGAA	AATGATATAC	GACGCAATGA
	TTGCTGATCA	AATTCCTTTT	GATTATCGCT	ATGATTGGGT	CAAACGAGA
901	ATTGTTTCGCC	CACAACGTGA	AAACCAATCA	CAGTTGTCCG	AACGTCAAGA
	AGGAAAATGT	CCAAACTCAG	CTGAGTTTGA	TGGTTTCTCC	TCCATCAAAG
1001	GATATTCTTC	GCACAGACAA	GTACAAAGCC	CCGTTTCATC	TAGAGATGTC
	ATTAAGAACA	GTAGTTCAAG	TCCATCAAAG	GATATTTTGC	AATCATCAAC
1101	CCTTGATGAA	TCATCTCAAG	ATAAAAAGCC	AATCAAAGCT	GTCGAATCGA
	ATCAGAAACC	ATATACACCG	CCACGTACAA	TTAATACTAC	CGAAACAAGA
1201	ATGAGATCAA	AGACTACAAT	CAATACTGCA	AGAACAACAG	CAAAGAACTC
	TTCGGCAGTT	AAGAAAGAAT	CGTCAGCAAC	AAGGACTGTT	AAGAAAGAAA
1301	CACATCCTGC	AACTACAAAA	ACAACAAAAA	CTGTAAATAG	ACAATTGAAC
	TCTTCTACAA	CGAAACCGGC	AACTACGAGC	TCTCACAAAG	ACTCAGAACC
1401	GGCTTCATCA	AGACGTACAT	CAACTCTACG	TTCAAGTCGC	CGCCAAAATG
	ACGGAATTTCG	CCCTGCAAAG	GAAAGAACTG	CGCTTTTCAC	AGCTACAGCC
1501	AGTAAGCCTC	CGGTATCTTA	CCGTACTGGA	ATGCTTCCGA	AATGGATGAT
	GGCTCCTCTC	ACATCTCGTC	GCTGAAA TAT	ATTTTTTATA	TTATTTATTT
	TTTTCTTTTT	CTATCTGTAT	ATTAAATGTA	TTTCTATATT	ATTAAAAAAA

Sequence Comparison

01B1
04E12
14G2
PFCK
Yeast
Human
Mouse
TcCK1.1
TcCK1.2



01B1
04E12
14G2
PFCK
Yeast
Human
Mouse
TcCK1.1
TcCK1.2

01B1
04E12
14G2
PFCK
Yeast
Human
Mouse
TcCK1.1
TcCK1.2

01B1
04E12
14G2



Comparing Sequences and Multiple Sequence Alignment

Multiple sequence file (msf)

Pairwise Comparision

```
137 AGACCAACCTGGCCAACATGGTGAAATCCCATCTCTAC.AAAAATACAAA 185
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1   AGACCAGCCTGGCCAACATGGTGAAACTCCATCTCTACTGAAAATACAAA 50
```

Multiple Sequence Alignment

```

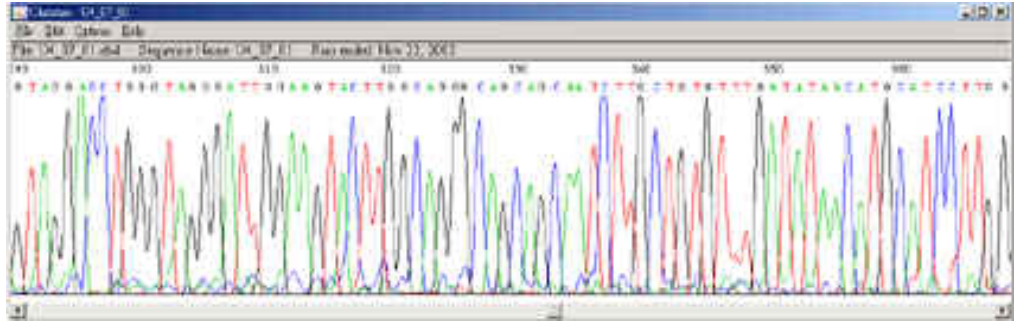
1                                                                 50
S11448 ~~~~~~ MTFD GAIGIDLGTT YSCVGVWQNE
S06443 ~~~~~~ MTFD GAIGIDLGTT YSCVGVWQNE
A25398 ~~~~~~ MTYE GAIGIDLGTT YSCVGVWQNE
S06158 ~~~~~~ MTYE GAIGIDLGTT YSCVGVWQNE
S42164 ~~~~~~ MS  KAVGIDLGTT YSCVAHFAND
S20139 ~~~~~~ MS  KAVGIDLGTT YSCVAHFSND
B36590 ~~~~~~ MS  KAVGIDLGTT YSCVAHFAND
A25089 ~~~~~~ MAKSEG PAIGIDLGTT YSCVGLWQHD
S03250 ~~~~~~ MAGKGE PAIGIDLGTT YSCVGVWQHD
A27077 ~~~~~~ MSKG  PAVGIDLGTT YSCVGVFQHG
S07197 ~~~~~~ MSKG  PAVGIDLGTT YSCVGVFQHG
```

```

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TGATGCCGTACAAATGCGGGGAGAAATGCTCTCCTCGACTGCTCCCGGAGTCCGACCGGAGGATCCCA
GTGATCAAGTGGGAAGAAGATGGCATTCATCTGGCCTGGGAATGGATGGAATGGAATGGAATGGAATGGA
ATGGGCTCTCGCTGATACAAAACATACTTCATTCAGACACAACAAGCAAGATGAGGCTCTTACATATGG
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AGTTCCCTTTTACAGACAGAATCTGTCACAGCCTTCATGGGAGACACAGTCTCAATGGAAGTCAAGTCA
TTGGGGAGCCCATGCCAACAAATCCACTGGCAGAAGAACAACAAGACCTGACTCCAATCCCAGGTGACTC
CCGAGTGGTGGTCTTGCCCTCTGGAGCATTCGAGATCAGCGACTCCAACCGGGGGACATTTGAAATTTAC
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CAGGATCGATAGACAGCTGTATTTCTGCAAGAGCAATCCAATGTAGTAGCATTGAAAGGAAAGATGCG
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TTATTACCGGTATAAAAATTCGACACAGAAAAGCAGACCCGAGGGTGAGATGGAACAACCTGGAGCCAAA
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AAAAGGAGTGGGGCACTCTCTGATCCATCCTCTCAGGACTGAAAGTGGAAACACCTTGACAAAATG
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CCCTAAATGAGCCGCAATTTGGACAAATGGACCCACCCCCGACTGGCAGTGTCACTCTCAGAAGAACAGCAA
CCTGCTTGTGATCAATGTGGTCAACCTTGGTGTATCACAGTGTGGTGTGATGATGATGATGATGATGAT
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AGCACACCTGTGTCAAGAACTCTAACAGGTGACAGGTCAACCATCAGGACCACTCAGTTAAGGAAGAT
CCTGAAGCAGTTCAGAAGGAATAAGCATTCCTTCTTACAGGCATCAGGAATTTGCAAAATGATGATTA
GAGTTCCTTAAACAAAAGCAAGATGCATTTTCACTGCAATGTCAAAGTTTAGTCTC

```

Sequence Formats



- GenBank ●●
- EMBL ●●
- FASTA ●
- GCG ●
- NGS ●

Today's Softwares

 **Sequence Manipulation Suite (V2)**

<http://www.bioinformatics.org/sms2/index.html>

 **The European Molecular Biology Open Software Suite**

<http://bioinfo.nhri.org.tw/gui/>

 **NCBI ORF Finder**

<https://www.ncbi.nlm.nih.gov/orffinder/>

 **BioEdit**

<http://www.mbio.ncsu.edu/BioEdit/bioedit.html>

Today's Sequences

- (1) Homo sapiens tumor protein p53 (TP53), transcript variant 4, mRNA
- (2) All p53 reference transcripts (15 transcripts)

<http://www.ncbi.nlm.nih.gov/omim>

NCBI Online Mendelian Inheritance in Man Johns Hopkins University

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OMIM[®] - Online Mendelian Inheritance in Man[®]

Welcome to OMIM[®], Online Mendelian Inheritance in Man[®]. OMIM is a comprehensive, authoritative, and timely compendium of human genes and genetic phenotypes. The full-text, referenced overviews in OMIM contain information on all known mendelian disorders and over 12,000 genes. OMIM focuses on the relationship between phenotype and genotype. It is updated daily, and the entries contain copious links to other genetics resources.

This database was initiated in the early 1960s by Dr. Victor A. McKusick as a catalog of mendelian traits and disorders, entitled Mendelian Inheritance in Man (MIM). Twelve book editions of MIM were published between 1966 and 1998. The online version, OMIM, was created in 1985 by a collaboration between the National Library of Medicine and the William H. Welch Medical Library at Johns Hopkins. It was made generally available on the internet starting in 1987. In 1995, OMIM was developed for the World Wide Web by NCBI, the National Center for Biotechnology Information.

OMIM is authored and edited at the McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, under the direction of Dr. Ada Hamosh.

NLM's Profiles in Science -- The McKusick Papers [More...](#)

NOTE: OMIM is intended for use primarily by physicians and other professionals concerned with genetic disorders, by genetics researchers, and by advanced students in science and medicine. While the OMIM database is open to the public, users seeking information about a personal medical or genetic condition are urged to consult with a qualified physician for diagnosis and for answers to personal questions.

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All (584)

[OMIM UniSTS \(67\)](#)[OMIM dbSNP \(135\)](#)[Manage Filters](#) [*191170 - TUMOR PROTEIN p53; TP53](#)

1. Cytogenetic locations: 17p13.1

OMIM: 191170

[Gene summaries](#) [Genetic tests](#) [Medical literature](#) [*605426 - TUMOR PROTEIN p53-REGULATED APOPTOSIS-INDUCING PROTEIN 1; TP53AIP1](#)

2. Cytogenetic locations: 11q24.3

OMIM: 605426

[Gene summaries](#) [Genetic tests](#) [Medical literature](#) [*614502 - CHROMOSOME 9 OPEN READING FRAME 116; C9ORF116](#)

3. Cytogenetic locations: 9q34.3

OMIM: 614502

[Gene summaries](#) [Genetic tests](#) [Medical literature](#) [*605157 - p53-RESPONSIVE GENE 1](#)

4. Cytogenetic locations: 19q13.31

OMIM: 605157

[Gene summaries](#) [Genetic tests](#) [Medical literature](#) [*605159 - APOPTOSIS-INDUCING FACTOR, MITOCHONDRION-ASSOCIATED, 2; AIFM2](#)

5. OMIM: 605159

[Gene summaries](#) [Genetic tests](#) [Medical literature](#) [*606185 - TUMOR PROTEIN p53-INDUCIBLE NUCLEAR PROTEIN 1; TP53INP1](#)

6. Cytogenetic locations: 8q22.1

OMIM: 606185

[Gene summaries](#) [Genetic tests](#) [Medical literature](#) [*605160 - p53-RESPONSIVE GENE 4](#)

7. OMIM: 605160

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🔍 p53 (584)

OMIM

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*191170

[Table of Contents](#)[Title](#)[Gene-Phenotype Relationships](#)[Text](#)[Description](#)[Cloning and Expression](#)[Gene Structure](#)[Mapping](#)[Gene Function](#)[Biochemical Features](#)[Molecular Genetics](#)[Other Features](#)[Animal Model](#)[Allelic Variants](#)[Table View](#)[See Also](#)[References](#)[Contributors](#)[Creation Date](#)[Edit History](#)

* 191170

TUMOR PROTEIN p53; TP53

Alternative titles; symbols

P53

TRANSFORMATION-RELATED PROTEIN 53; TRP53

HGNC Approved Gene Symbol: TP53

Cytogenetic location: 17p13.1 Genomic coordinates (GRCh38): 17:7,668,401-7,687,549 (from NCBI)

Gene-Phenotype Relationships

Location	Phenotype	Phenotype MIM number	Inheritance	Phenotype mapping key
17p13.1	Adrenal cortical carcinoma	202300	AR	3
	Breast cancer	114480	AD	3
	Choroid plexus papilloma	260500	AD	3
	Colorectal cancer	114500	AD	3
	Hepatocellular carcinoma	114550	SMu	3
	Li-Fraumeni syndrome	151623	AD	3
	Nasopharyngeal carcinoma	607107		3
	Osteosarcoma	259500	AR	3
	Pancreatic cancer	260350	Mu , AD , SMu	3
	{Basal cell carcinoma 7}	614740		3
	{Glioma susceptibility 1}	137800	AD , SMu	3

External Links

[Genome](#)[DNA](#)[Ensembl](#)[NCBI RefSeq](#)[UCSC Genome Browser](#)[Protein](#)[Gene Info](#)[Clinical Resources](#)[Variation](#)[Animal Models](#)[Cellular Pathways](#)

Download Homo sapiens tumor protein p53 (TP53), transcript variant 4, mRNA in **FASTA** format

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Species Summary 20 per page Sort by Default order Send to Filter your results:

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Source databases RefSeq (15) Customize ...

Sequence length Custom range...

Release date Custom range...

Revision date Custom range...

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Items: 15
Selected: 1 **Select the first sequence**

[Homo sapiens tumor protein p53 \(TP53\), transcript variant 4](#)
1. 2,651 bp linear mRNA
Accession: NM_001126113.2 GI: 371502116
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Homo sapiens tumor protein p53 \(TP53\), transcript variant 5](#)
2. 2,724 bp linear mRNA
Accession: NM_001126114.2 GI: 371502117
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Homo sapiens tumor protein p53 \(TP53\), transcript variant 6](#)
3. 2,404 bp linear mRNA
Accession: NM_001276698.1 GI: 454545206
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

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Source

databases

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Sequence

length

Custom range...

Release date

Custom range...

Revision date

Custom range...

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Summary 20 per page Sort by Default order

Items: 15 Do not select any sequence

[Homo sapiens tumor protein p53 \(TP53\), transcript varian](#)

1. 2,651 bp linear mRNA
 Accession: NM_001126113.2 GI: 371502116
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Homo sapiens tumor protein p53 \(TP53\), transcript varian](#)

2. 2,724 bp linear mRNA
 Accession: NM_001126114.2 GI: 371502117
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

[Homo sapiens tumor protein p53 \(TP53\), transcript varian](#)

3. 2,404 bp linear mRNA
 Accession: NM_001276698.1 GI: 454545206
[Protein](#) [PubMed](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

Send to: Filter your results:

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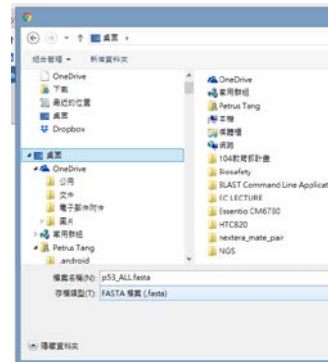
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Save as p53_ALL.fasta to your desktop

Database: Select

Find items

Open Reading Frame Finder

ORF finder searches for open reading frames (ORFs) in the DNA sequence you enter. The program returns the range of each ORF, along with its protein translation. Use ORF finder to search newly sequenced DNA for potential protein encoding segments, verify predicted protein using newly developed SMART BLAST or regular BLASTP.

This web version of the ORF finder is limited to the subrange of the query sequence up to 50 kb long. Stand-alone version, which doesn't have query sequence length limitation, is available for [Linux x64](#).

Examples (click to set values, then click Submit button) :

- NC_011604 Salmonella enterica plasmid pWES-1; genetic code: 11; 'ATG' and alternative initiation codons; minimal ORF length: 300 nt
- NM_000059; genetic code: 1; start codon: 'ATG only'; minimal ORF length: 150 nt



Enter Query Sequence

Enter accession number, gi, or nucleotide sequence in FASTA format:

```
TTCCCTCTCCCTGTTGGTCGGTGGGTTGGTAGTTTCTACAGTTGGGCAGCTGGTTAGGTAGAGGGAGTTG
TCAAGTCTCTGCTGGCCAGCCAAACCCTGTCTGACAACTCTTGGTGAACCTTAGTACCTAAAAGGAAA
TCTCACCCATCCACACCCTGGAGGATTCATCTCTTGTATATGATGATCTGGATCCACCAAGACTTGT
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TTTTATATCGATCTCTTATTTACAATAAAACTTTGCTGCCACCTGTGTGTCTGAGGGGT
```



Copy & paste p53_V4.fasta

From: To:

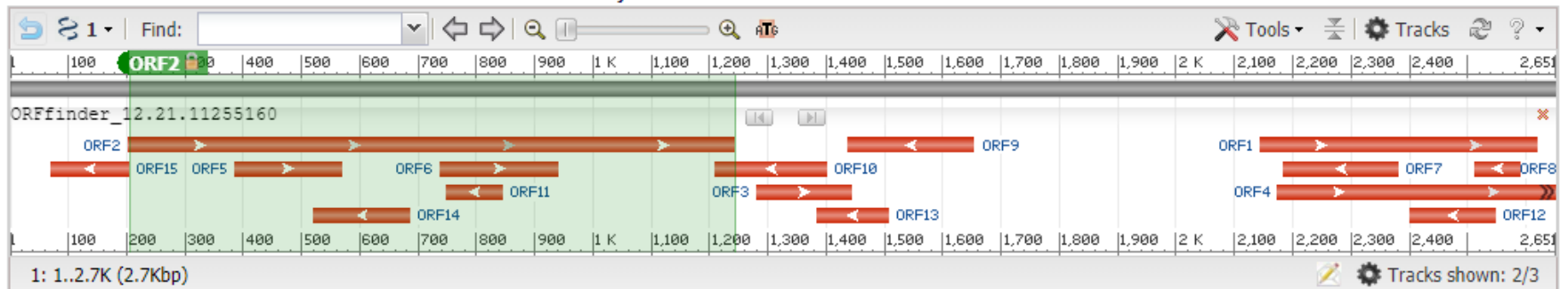
Choose Search Parameters

- Minimal ORF length (nt):
- Genetic code:
- ORF start codon to use:
 - "ATG" only
 - "ATG" and alternative initiation codons
 - Any sense codon
- Ignore nested ORFs:

Open Reading Frame Viewer

Sequence

ORFs found: 15 Genetic code: 1 Start codon: 'ATG' only



Six-frame translation...

ORF2 (346 aa) Display ORF as... Mark

Mark subset... Marked: 0 Download marked set as Protein FASTA

```
>|c1|ORF2
MEEPQSDPSVEPPLSQETFSDLWKLLENMVLSPPLSQAMDDLMLSPDDI
EQMFTEDPGDEAPRMPEAAPVAPAPAAPTPAAPAPAPSWPLSSVPSQ
KTYQGSYGRFLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDST
PPPGRVRAMAIYKQSQHMTVVRRCPHERCSDSDGLAPPQHLIRVEGN
LRVEYLDDRNTFRHSVVVPEPEVGSCTTIHYNMCMNSSCMGGMRRP
ILTIIILEDSSGNLLGRNSFEVRCACPGRRRTEENLRKKGEPHHEL
PGSTKRALPNNTSSSPQPKKKPLDGEYFTLQMLDLRWCYFLINSS
```

Copy the amino acid sequence

Label	Strand	Frame	Start	Stop	Length (nt aa)
ORF7	-	1	2381	2184	198 65
ORF10	-	2	1402	1208	195 64
ORF5	+	3	384	569	186 61
ORF14	-	3	687	520	168 55
ORF3	+	2	1280	1444	165 54
ORF12	-	3	2547	2401	147 48
ORF15	-	3	204	70	135 44
ORF13	-	3	1506	1384	123 40
ORF11	-	2	844	749	96 31
ORF8	-	2	2590	2513	78 25

ORF2

Marked set (0)

SmartBLAST

SmartBLAST best hit titles...

BLAST

BLAST

BLAST Database:

UniProtKB/Swiss-Prot (swissprot)



Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

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NEWS

IgBLAST 1.8.0 released

A new version of IgBLAST is now available.
Wed, 15 Nov 2017 16:00:00 EST

[More BLAST news...](#)

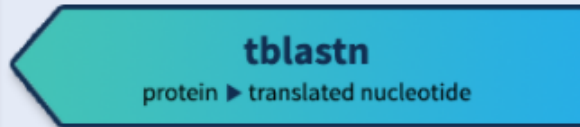
Web BLAST




Nucleotide BLAST
nucleotide ► nucleotide



blastx
translated nucleotide ► protein



tblastn
protein ► translated nucleotide



Protein BLAST
protein ► protein

Standard Protein BLAST

blastn **blastp** blastx tblastn tblastx

BLASTP programs search protein databases using a protein query. [more...](#)

[Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

[Clear](#)

Query subrange

```
KTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDST
PPPGTRVRAMAIYKQSQHMTQVRRCPHHERCSDSDGLAPPQHLIRVEGN
LRVEYLDDRNTRFHSVWVPEPEVGSDCCTIIHYNMCMSSCMGGMMRRP
ILTIITLEDSSGNLLGRNSFEVRVCACPGDRRTEENLRKKGEPHHELP
PGSTKRALPNNTSSSPQPKKPLDGEYFTLQMLLDLRWCYFLINSS
```

From

To

Or, upload file

選擇檔案

未選擇任何檔案

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database

Non-redundant protein sequences (nr)

Organism
Optional

Enter organism name or id—completions will be suggested

Exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude
Optional

Models (XM/XP) Uncultured/environmental sample sequences

Entrez Query
Optional

[YouTube](#) [Create custom database](#)

Enter an Entrez query to limit search

Program Selection

Algorithm

Quick BLASTP (Accelerated protein-protein BLAST) **New**

blastp (protein-protein BLAST)

PSI-BLAST (Position-Specific Iterated BLAST)

PHI-BLAST (Pattern Hit Initiated BLAST)

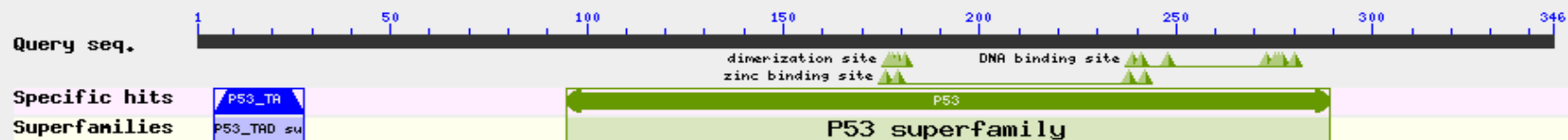
DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

BLAST

Search database Non-redundant protein sequences (nr) using Blastp (protein-protein BLAST)

Putative conserved domains have been detected, click on the image below for detailed results.



Download [GenPept](#) [Graphics](#)

Next Previous Descriptions

cellular tumor antigen p53 isoform c [Homo sapiens]

Sequence ID: [NP_001119585.1](#) Length: 346 Number of Matches: 1

[See 1 more title\(s\)](#)

Range 1: 1 to 346 [GenPept](#) [Graphics](#)

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
716 bits(1847)	0.0	Compositional matrix adjust.	346/346(100%)	346/346(100%)	0/346(0%)

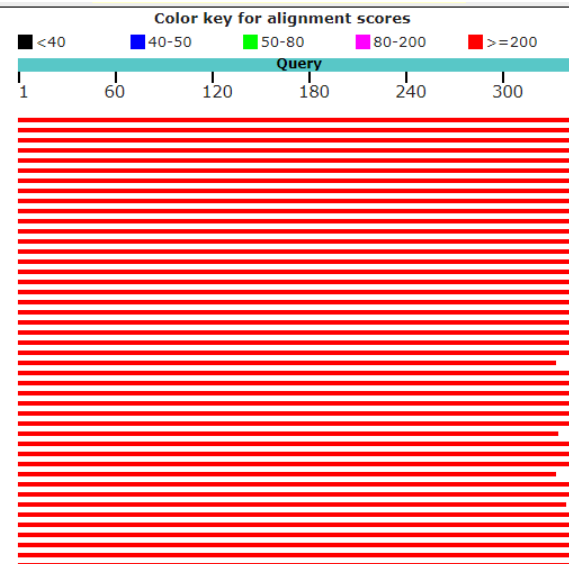
Query	1	MEEPQSDPVSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDPGP	60
Sbjct	1	MEEPQSDPVSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDPGP	60
Query	61	DEAPRMPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAK	120
Sbjct	61	DEAPRMPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAK	120
Query	121	SVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGRVVRAMAIYKQSQHMEVVRRCPHHE	180
Sbjct	121	SVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGRVVRAMAIYKQSQHMEVVRRCPHHE	180
Query	181	RCSDSDGLAPPQHLIRVEGNLRVEYLLDRNTFRHSVVVPYEPPEVGSDCITIIHNYMCNS	240
Sbjct	181	RCSDSDGLAPPQHLIRVEGNLRVEYLLDRNTFRHSVVVPYEPPEVGSDCITIIHNYMCNS	240
Query	241	SCMGGMNRRLPILTIITLEDSSGNLLGRNSFEVRVCACPGRRRTEENLRKKGEPHHELP	300
Sbjct	241	SCMGGMNRRLPILTIITLEDSSGNLLGRNSFEVRVCACPGRRRTEENLRKKGEPHHELP	300
Query	301	PGSTKRALPNNTSSSPQPKKKPLDGEYFTLQMLLDLRWCYFLINSS	346
Sbjct	301	PGSTKRALPNNTSSSPQPKKKPLDGEYFTLQMLLDLRWCYFLINSS	346

Related Information

[Gene](#) - associated gene details

[Map Viewer](#) - aligned genomic context

[Identical Proteins](#) - Identical proteins to NP_001119585.1



SMS

Sequence Manipulation Suite:

ORF Finder

ORF Finder searches for open reading frames (ORFs) in the DNA sequence you enter. The program returns the range of each ORF, along with its protein translation. Use ORF Finder to search newly sequenced DNA for potential protein encoding segments. ORF Finder supports the entire IUPAC alphabet and several genetic codes.

Paste the text into the text area below. Input limit is 100000 characters.

```
AGGGTCAACATC
TTTTACATTCTGCAAGCACATCTGCATTTTCACCCACCTTCCCCTCCTTCTCCCTT
TTTATATCCCAT
TTTTATATCGATCTCTTATTTTACAATAAAACTTTGCTGCCACCTGTGTGTCTGAGGG
GTG
```

Please check the [browser compatibility page](#) before using this program.

- ORFs can begin with: .
- Search for ORFs in reading frame on the strand.
- Only return ORFs that are at least codons long.
- Use the genetic code.

*This page requires JavaScript. See [browser compatibility](#).

*You can [mirror this page](#) or use it off-line.

[new window](#) | [home](#) | [citation](#)

2.4.4-Tue Feb 12 18:40:19 2008



- Format Conversion
 - Combine FASTA
 - EMBL to FASTA
 - EMBL Feature Extractor
 - EMBL Trans Extractor
 - Filter DNA
 - Filter Protein
 - GenBank to FASTA
 - GenBank Feature Extractor
 - GenBank Trans Extractor
 - One to Three
 - Range Extractor DNA
 - Range Extractor Protein
 - Reverse Complement
 - Split Codons
 - Split FASTA
 - Three to One

- Sequence Analysis
 - Codon Plot
 - Codon Usage
 - CpG Islands
 - DNA Pattern Find
 - DNA Stats
 - Fuzzy Search DNA
 - Fuzzy Search Protein
 - Ident and Sim
 - Multi Rev Trans
 - Mutate for Digest
 - ORF Finder
 - Pairwise Align Codons
 - Pairwise Align DNA
 - Pairwise Align Protein
 - PCR Primer Stats
 - PCR Products

>ORF number 1 in reading frame 2 on the direct strand extends from base 203 to base 1243.

```
ATGGAGGAGCCGCGAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA
GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG
GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCCTGAAGACCCAGGTCCA
GATGAAGCTCCCGAATGCCAGAGGCTGCTCCCCCGTGGCCCCTGCACCAGCAGCTCCT
ACACCGGCGGCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG
AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG
TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC
TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG
GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCACCATGAG
CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT
TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT
GAGCCGCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACACTACATGTGTAACAGT
TCCTGCATGGGCGGCATGAACCGGAGGCCATCCTCACCATCATCACACTGGAAGACTCC
AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA
GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC
CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCAGCCAAAGAAG
AAACCACTGGATGGAGAATATTTACCCTTCAGATGCTACTTGACTTACGATGGTGTAC
TTCCTGATAAACTCGTCGTAA
```

>Translation of ORF number 1 in reading frame 2 on the direct strand.

```
MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDEPGP
DEAPRMPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAK
SVTCTYSPALNKMFCQLAKTQPVQLWVDSTPPPGRVVRAMAIYKQSQHMTEVVRRCPHHE
RCSDSGLAPPQHLIRVEGNLRVEYLDNRNFRHSVVVPEPPEVGSDDCTTIHNYMCNS
SCMGMNRRPILTIITLEDSSGNLLGRNSFEVVRVCAACPRDRRTEENLRKKGEPHHELP
PGSTKRALPNNTSSSPQPKKPLDGEYFTLQMLLDLRWCYFLINSS*
```

Format Conversion

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- Range Extractor Protein
- Reverse Complement
- Split Codons
- Split FASTA
- Three to One

Sequence Analysis

- Codon Plot
- Codon Usage
- CpG Islands
- DNA Pattern Find

- The Sequence Manipulation Suite is a collection of JavaScript programs for generating, formatting, and analyzing short DNA and protein sequences. It is commonly used by molecular biologists, for teaching, and for program and algorithm testing.
- See the [about the Sequence Manipulation Suite](#) page for more information about individual Sequence Manipulation Suite programs.
- You can easily [mirror the Sequence Manipulation Suite](#) on your own web site, or you can use it [off-line](#).
- This version of the Sequence Manipulation Suite represents a complete re-write of the previous version. The new version is much faster and has many new features. The [previous version](#) of the Sequence Manipulation Suite can still be accessed.
- Send questions and comments to stothard@ualberta.ca.

[new window](#) | [home](#) | [citation](#)

2.4.4-Tue Feb 12 18:40:19 2008



Download

- **The Sequence Manipulation Suite. Copyright (C) 2000, 2004 Paul Stothard.** This program is free software; you can redistribute it and/or modify it under the terms of the [GNU General Public License](#) as published by the Free Software Foundation; either version 2 of the License, or (at your option) any later version. This program is distributed in the hope that it will be useful, but WITHOUT ANY WARRANTY; without even the implied warranty of MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE. See the GNU General Public License for more details. You should have received a copy of the GNU General Public License along with this program; if not, write to the Free Software Foundation, Inc., 59 Temple Place - Suite 330, Boston, MA 02111-1307, USA.
- Download the Sequence Manipulation Suite ([sms2.zip](#) or [sms2.tar.gz](#))
- **To mirror the Sequence Manipulation Suite:** Extract [sms2.zip](#) or [sms2.tar.gz](#) and place the resulting sms2 directory into a directory from which your server will serve HTML files.
- **To run the Sequence Manipulation Suite locally** [Extract sms2.zip](#) or [sms2.tar.gz](#) and load [index.html](#) from the resulting sms2 directory into your web browser.

BioEdit In-House BLAST



Copyright ©1997-2005
Tom Hall
Ibis Therapeutics
Carlsbad, CA 92008

BioEdit is a biological sequence alignment editor written for Windows 95/98/NT/2000/XP. An intuitive multiple document interface with convenient features makes alignment and manipulation of sequences relatively easy on your desktop computer. Several sequence manipulation and analysis options and links to external analysis programs facilitate a working environment which allows you to view and manipulate sequences with simple point-and-click operations.

BioEdit.zip
(full installation 12.6 Mb)

Bug fixes / changes

BioEdit
General information

BioDoc.pdf
(pdf format help doc)

View Screenshots

BioEdit's features include:

New version is WinXP compatible

- Several modes of hand alignment
- Automated ClustalW alignment
- Automated Blast searches (local and WWW)
- Plasmid drawing and annotation
- Accessory application configuration
- Restriction mapping
- RNA comparative analysis tools
- Graphical matrix data viewing tools
- Shaded alignment figures
- Translation-based nucleic acid alignment
- ABI trace viewing, editing and printing
- Customizable ... [other features](#)

Note: Although BioEdit was recently updated, it is no longer being reliably maintained, and the documentation is out of date and no longer maintained. It is being updated slowly, but there is no guaranteed finish date. Until documentation is complete, play with the menus and see what happens, or email with a question.

BioEdit Sequence Alignment Editor

File Accessory Application RNA World Wide Web Options Window Help

Add / Remove / Modify an Accessory Application

- BLAST
 - Local BLAST
 - NCBI BLAST over the Internet
 - Create a local protein database file
 - Create a local nucleotide database file
- CAP contig assembly program
- DNADist ---> Neighbor phylogenetic tree
- DNADist DNA distance matrix
- DNAmI DNA Maximum Likelihood program
- DNAmIc DNA Maximum Likelihood program with molecular clock
- DNAPars DNA parsimony method
- FastDNAmI DNA maximum likelihood
- Fitch -- Fitch-Margoliash and Least-Squares Distance Methods
- Kitsch -- Fitch-Margoliash and Least Squares Methods with Evolutionary Clock
- NEIGHBOR -- Neighbor-Joining and UPGMA methods
- ProML Protein Maximum Likelihood program
- ProtDist ---> Fitch phylogenetic tree
- ProtDist ---> Neighbor phylogenetic tree
- ProtDist protein distance matrix
- Protpars protein parsimony method

Open file to create database from ...

搜尋位置(I): 桌面

最近的位置

- 桌面
- 媒體櫃
- 本機
- 網路

	nrc1454.pdf	Adobe Acrobat 文件	279 KB
	NVF.seq.txt	Text Document	459 個位元組
	NVF[2006].pdf	Adobe Acrobat 文件	8.03 MB
	p53_ALL.fasta	FASTA 檔案	38.6 KB
	p53_V4.fasta	FASTA 檔案	2.70 KB

檔案名稱(N): p53_ALL.fasta 開啟(O)

檔案類型(T): All Files (*.*) 取消



File Accessory Application RNA World Wide Web Options Window Help



Add / Remove / Modify an Accessory Application

BLAST

- CAP contig assembly program
- DNADist ---> Neighbor phylogenetic tree
- DNADist DNA distance matrix
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Local BLAST

- NCBI BLAST over the Internet
- Create a local protein database file
- Create a local nucleotide database file



BLAST is government software obtained from the NCBI. For reference see:

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.

Program: Nucleotide Database:
Protein Database:

Query:

Paste From Clipboard

Load From File

Output file name: Specify (default = file opened but not saved)

- Open output
- Filter sequences for low-complexity regions
- Do Gapped BLAST (not available for tblastx)
- Show GI's in defines
- Tabular output

Expectation Value (E):

Matrix:

Max number of hits to report: Effective database size: (0 = real size)
Max number of alignments to show:
Threshold for extending hit:

Additional parameters:

Warning! The complete combined command line (including file paths and auto-set paramters) cannot exceed 128 characters Under DOS. I have not yet found a way around this. If the program doesn't run, try saving the query file to C:\Temp first.

Usage

```
blastall arguments:  
  
-p Program Name [String] (set internally with BioEdit)  
-d Database [String] (set internally with BioEdit)  
-i Query File [File In] (set internally with BioEdit)
```

Do Search

Dismiss

BLAST release notes

NCBI BLAST help

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= NM_001126113.2 Homo sapiens tumor protein p53 (TP53),
transcript variant 4, mRNA
(2651 letters)

Database: C:\BioEdit\database\p53_ALL.fasta
15 sequences; 37,828 total letters

	Score	E
Sequences producing significant alignments:	(bits)	Value
NM_001276695.1 Homo sapiens tumor protein p53 (TP53), transcript...	5255	0.0
NM_001126113.2 Homo sapiens tumor protein p53 (TP53), transcript...	5255	0.0
NM_001276699.1 Homo sapiens tumor protein p53 (TP53), transcript...	4113	0.0
NM_001126117.1 Homo sapiens tumor protein p53 (TP53), transcript...	4113	0.0
NM_001276696.1 Homo sapiens tumor protein p53 (TP53), transcript...	2892	0.0
NM_001126116.1 Homo sapiens tumor protein p53 (TP53), transcript...	2892	0.0
NM_001276698.1 Homo sapiens tumor protein p53 (TP53), transcript...	2892	0.0
NM_001126114.2 Homo sapiens tumor protein p53 (TP53), transcript...	2892	0.0
NM_001276760.1 Homo sapiens tumor protein p53 (TP53), transcript...	2767	0.0
NM_001126115.1 Homo sapiens tumor protein p53 (TP53), transcript...	2767	0.0
NM_001276697.1 Homo sapiens tumor protein p53 (TP53), transcript...	2767	0.0
NM_001126112.2 Homo sapiens tumor protein p53 (TP53), transcript...	2767	0.0
NM_000546.5 Homo sapiens tumor protein p53 (TP53), transcript va...	2767	0.0
NM_001276761.1 Homo sapiens tumor protein p53 (TP53), transcript...	2767	0.0
NM_001126118.1 Homo sapiens tumor protein p53 (TP53), transcript...	2767	0.0