
Bioinformatics

Biological databases

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Bioinformatics

- It was born in the late '70s in conjunction with the development of **nucleic acid sequencing techniques**.

Sequencing refers to any method or technology that is used to determine the exact order of the four bases (ACGT) in a strand of DNA.

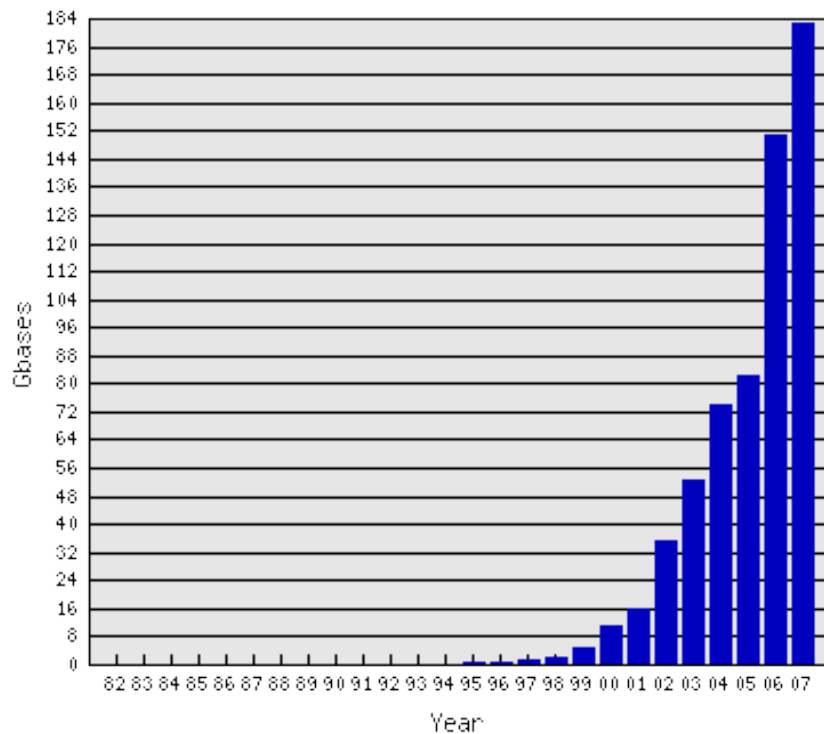


- Since the invention of sequencing technology, the amount of biological data has increased exponentially.

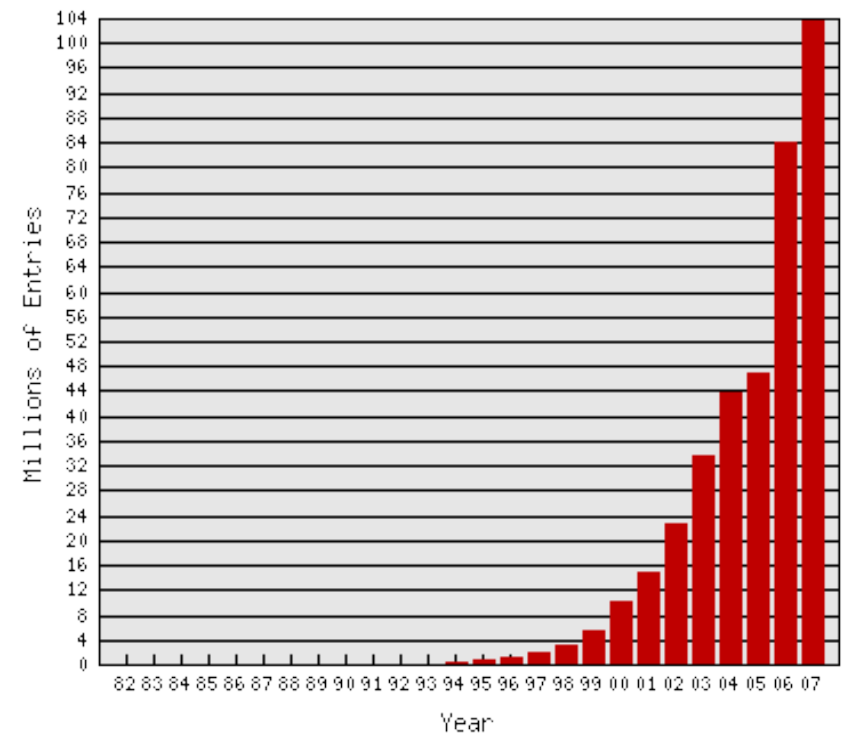


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Total Nucleotides



Number of entries

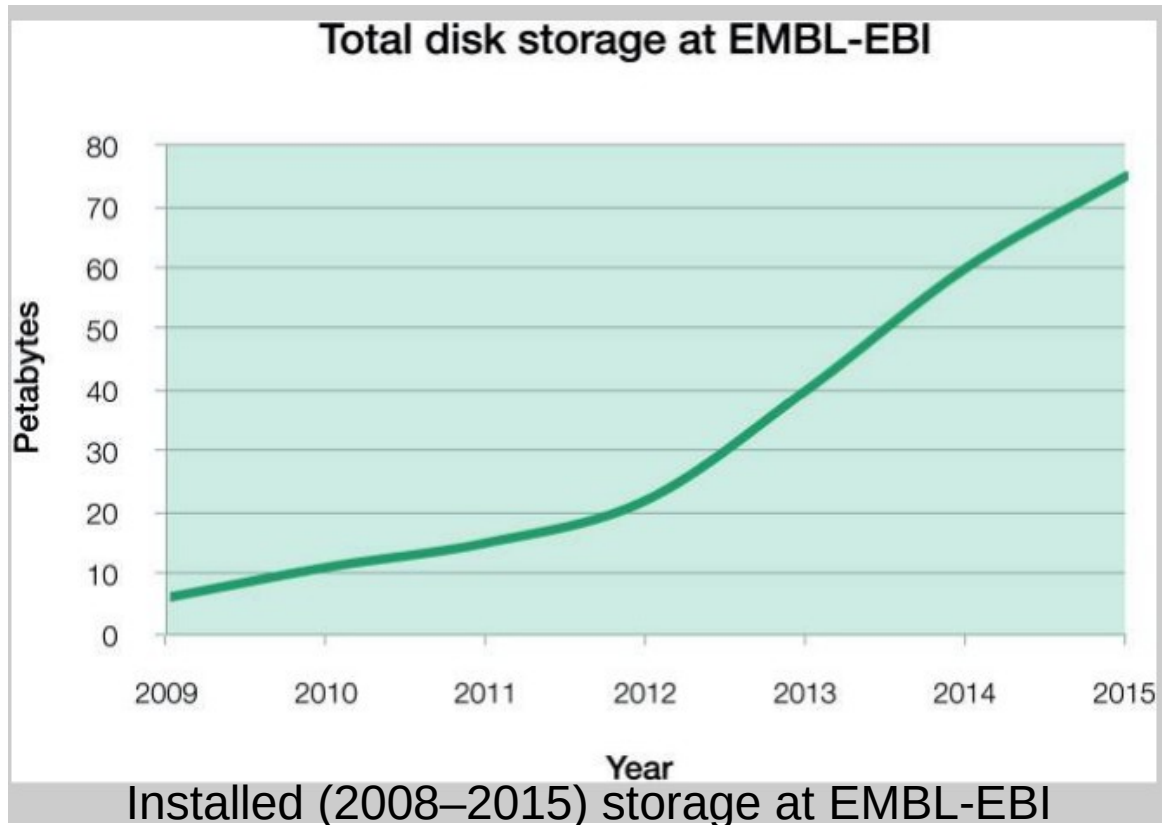


Growth of data in EMBL database

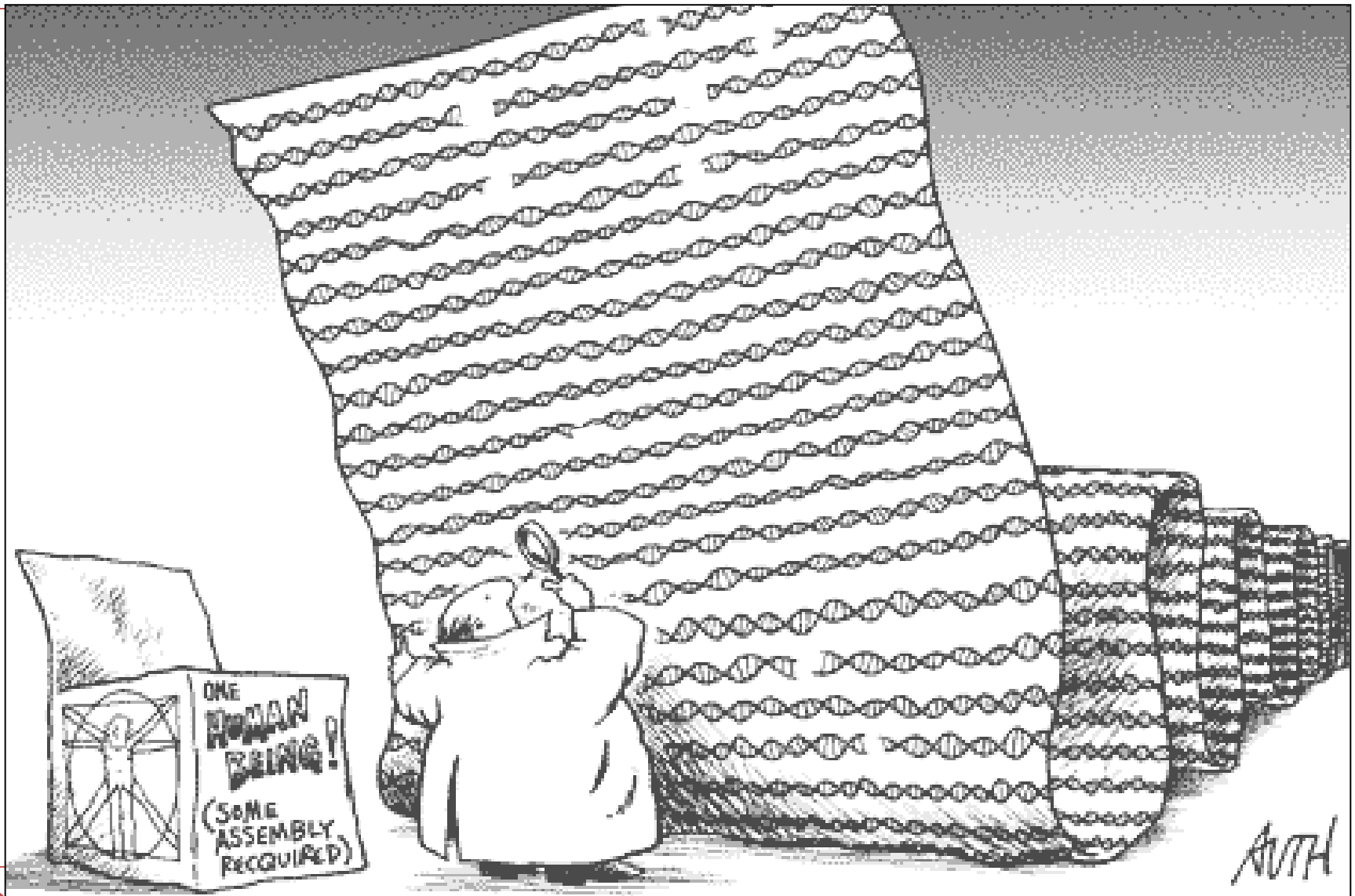


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Growth of data in EMBL database

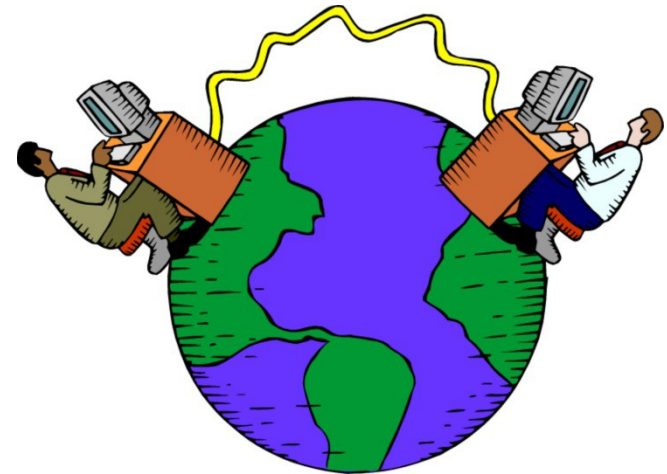


- All this data cannot be stored on paper!



Bioinformatics

- ▣ Advances in sequencing technologies led to the ever-increasing availability of genomic data
- ▣ This surge in data led computers to become indispensable for the data management, data storage and data organization
- ▣ Moreover, the advent of the internet allowed for an immediate way to exchange data



Bioinformatics

- ▢ Bioinformatics became essential to handle the large quantities of biological data:

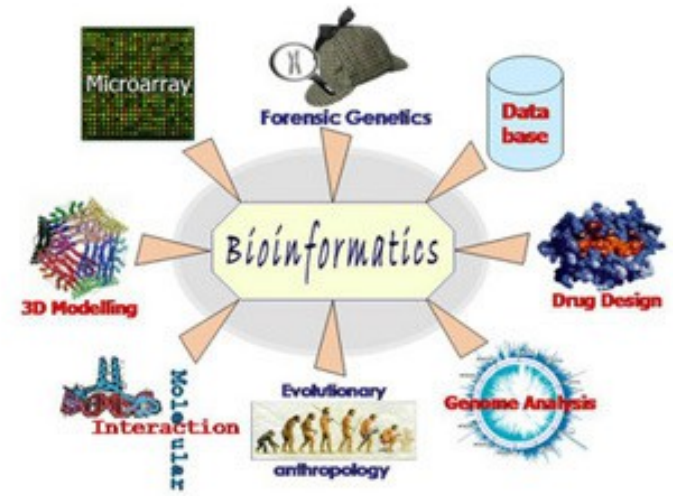
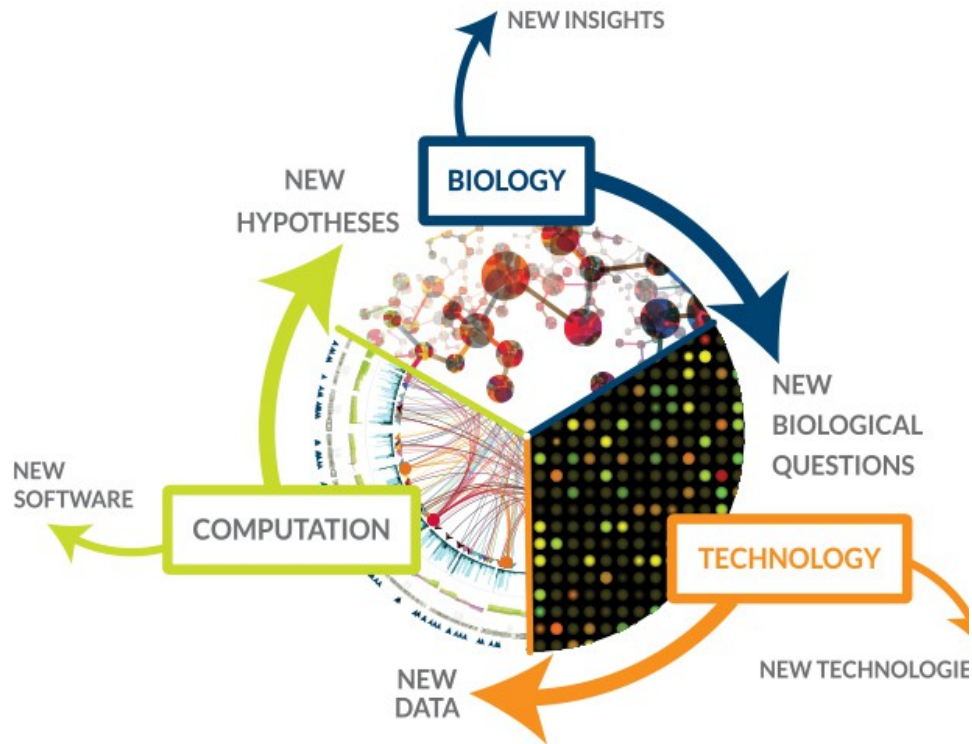
- ▢ data management
- ▢ data storage
- ▢ data characterization



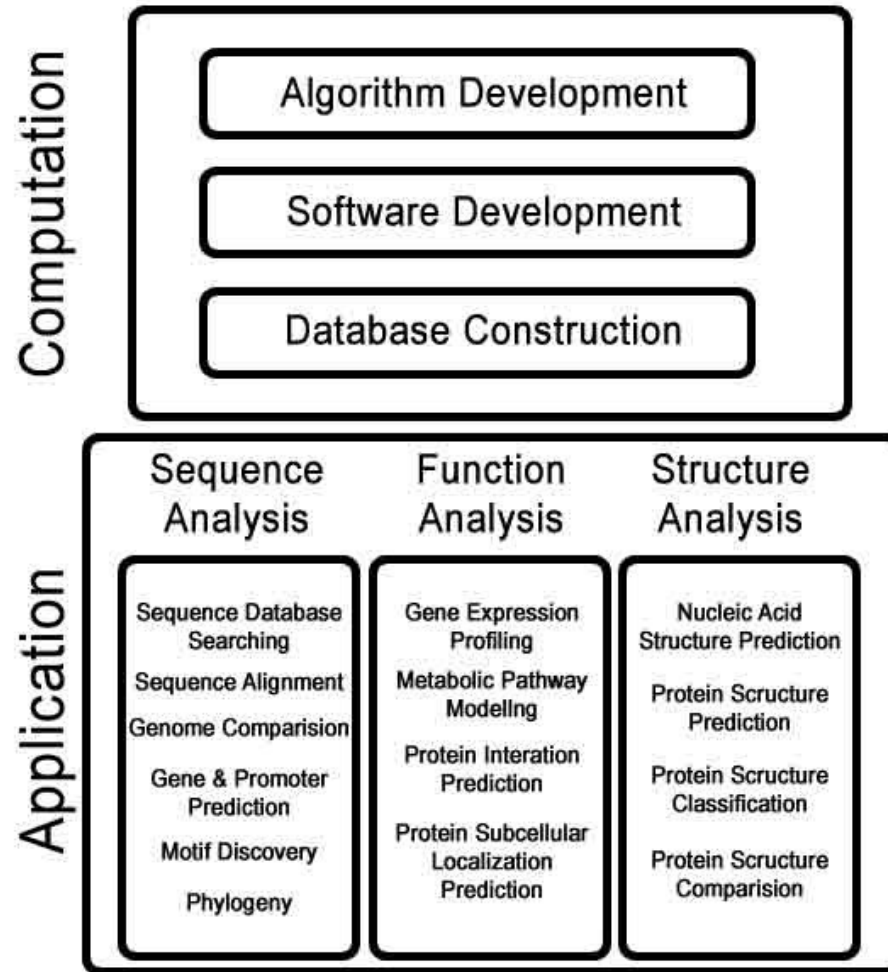
- ▢ The evolution of bioinformatics had a huge advancement with the **human genome project**, started in 1990 (first release in 2001) by the effort of an international public consortium
 - ▢ **AIM:** to map and sequence all the human genome in order to identify genes and understand the associations between genes and genetic diseases



Bioinformatics



Bioinformatics



Database

- ▮ In Computer Science, the term **database** refers to a collection of data, which are:
 - ▮ **Elementary** and **homogeneous** (regarding the same subject, or more topics related to each other)
 - ▮ **Ordered** (structured) and **usable** to allow their use by software applications
- ▮ In addition to the primary data (e.g. sequence), a database also includes additional information (**annotation**) (e.g. organism, cell type, conservation...).

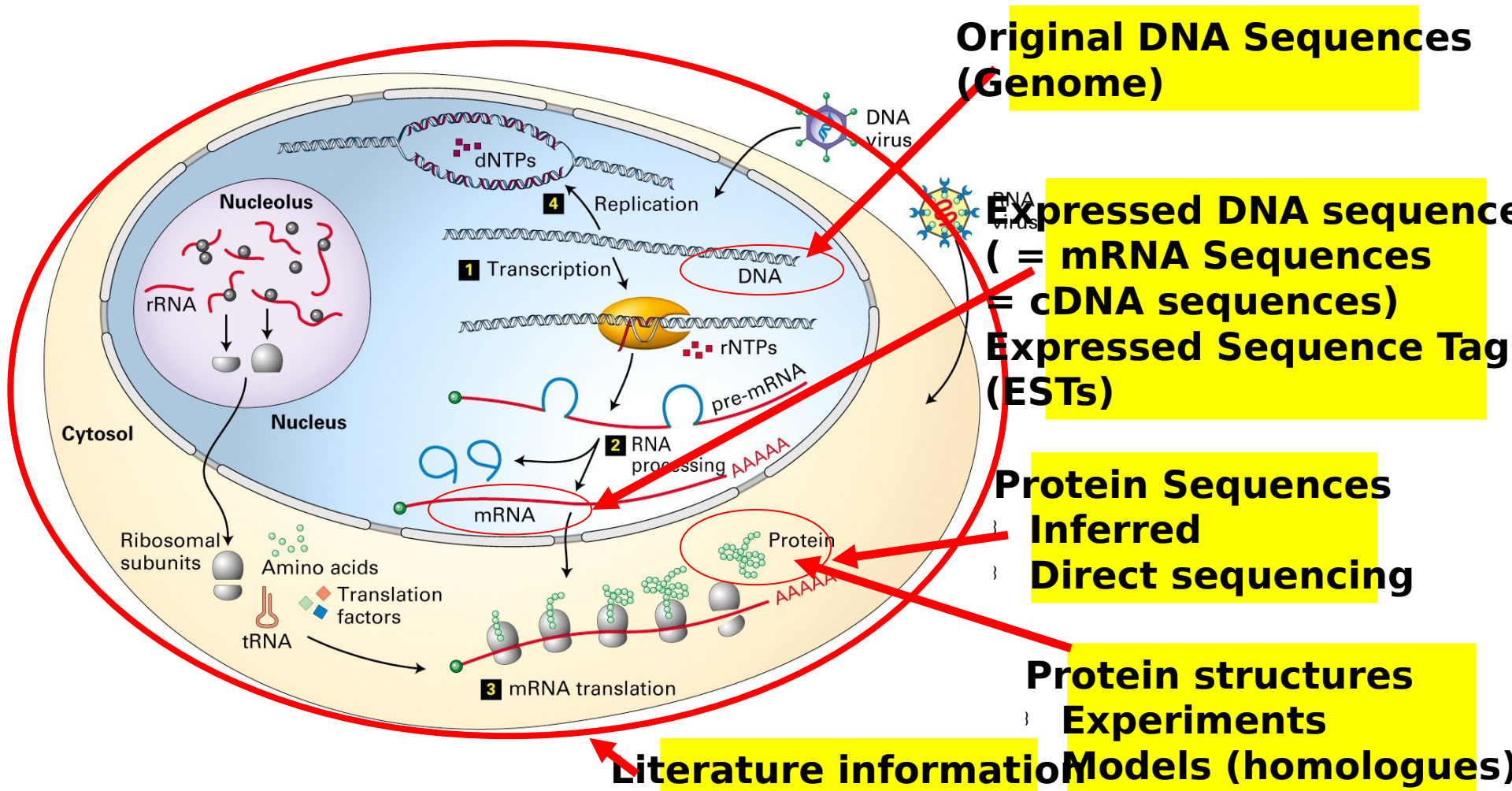


What is a biological DB

- ▣ **Biological databases** are indispensable tools for an efficient and rational storage, accession, and dissemination of the huge amount of biological data
- ▣ Biological databases collect information and data coming from:
 - ▣ Literature
 - ▣ Experimental analysis (*in vitro and in vivo*)
 - ▣ Bioinformatics analysis (*in silico*)



Biological data



Databases classification

- ▮ Biological databases can be divided into *primary*, *secondary* or *specialized*:
- ▮ **Primary** databases are populated with experimentally-derived data ("raw" data such as nucleotide sequence, protein sequence or macromolecular structure) produced by experimental laboratories. Experimental results are submitted directly into the database by researchers.



Databases classification

- ▮ Biological databases can be divided into *primary*, *secondary* or *specialized*:
- ▮ *Secondary* databases comprise data derived from the results of analyzing information found in primary databases. They are often referred to **as curated databases** but this is a bit of a misnomer because primary databases are also curated to ensure that the data in them is consistent and accurate. They are **highly curated**, often using a complex combination of computational algorithms and manual analysis and interpretation to derive new knowledge. They also draw upon information from numerous sources (other DBs, controlled vocabularies, literature)



Databases classification

- ▮ Biological databases can be divided into *primary*, *secondary* or *specialized*:
 - ▮
 - ▮ *Specialized* databases collect only the information relating to a specific field, collected according to specific sorting criteria (particular organism, domains and protein motifs, protein structures, genes, transcriptome, expression profiles, metabolic pathways, etc.)



Essential aspects of primary and secondary DB

	Primary database	Secondary database
Synonyms	Archival database	Curated database; knowledgebase
Source of data	Direct submission of experimentally-derived data from researchers	Results of analysis, literature research and interpretation, often of data in primary databases
Examples	• ENA, GenBank and DDBJ (nucleotide sequence) • ArrayExpress Archive and GEO (functional genomics data) • Protein Data Bank (PDB; coordinates of three-dimensional macromolecular structures)	• InterPro (protein families, motifs and domains) • UniProt Knowledgebase (sequence and functional information on proteins) • Ensembl (variation, function, regulation and more layered onto whole genome sequences)



Primary Databases

Biological DB of amino acid sequences and protein structures:

- ▮ **Atlas of Protein Sequence and Structure** (65 amino acid sequences - the first effort to systematically collect the sequence information derived from the parallel development of the experimental sequencing techniques - 1968) later merged with **PIR** (Protein Information Resource)

- ▮ **Protein Information Resource** (PIR, NBRF – National Biomedical Research Foundation – 1984)

- ▮ **SWISS-PROT** (nowadays, UniProt joint project with TrEMBL and PIR– 1985)

- ▶ ▮ **Protein Data Bank** (BNL – Brookhaven National Laboratory – 1971)

Primary Databases

- ▣ Biological DB of nucleic acid sequences (DNA, RNA):
 - ▣ **EMBL datalibrary** (EMBL – European Molecular Biology Laboratory – Heidelberg 1982). Nowadays, it is curated and maintained by the EBI (European Bioinformatics Institute)
 - ▣ **GenBank** (realized and realised by NCBI – National Center for Biotechnology Information – Los Alamos National Laboratory 1983)
 - ▣ **DDBJ** (DNA Database of Japan – 1984)
- ▣ There is an international agreement - *International Nucleotide Sequence Database Collaboration* (INSDC) – among the three data banks such that data entry added in one, involves the automatic insertion in the other ones
- ▣ In 2005 the INSDC collected over 100 Giga bases (10⁹) extracted from more than 200,000 organisms



Biological Databases structure



Entry

- ▮ Each biological database is characterized by a **biological central element** (in the case of DNA and RNA databases, the central element is the nucleotide sequence, for the protein data banks the central element is the protein sequence, etc.).
- ▮ The central biological element is characterized by a set of information defined as **attributes** or rather the annotation data of the sequence (name of the species, functions, the bibliographic references, etc ...)
- ▮ The biological central element together with its annotations are the "**entry**" of the database



Cross-referencing

- ▮ Several centers have been encouraged to integrate and share their data through the use of **cross-references**
 - ▮ the exponential growth in the number of database
 - ▮ the consequent possibility of having a comprehensive data visualization
 - ▮ the need to decrease redundancy and available information overload
 - ▮ the need to have immediately access to distribute information among different databases
- ▮ Cross-referencing searches for a connection among data through the "relationship" existing between the data recorded in a specific database with data in other databases



Cross-referencing

- ▮ On internet this mechanism is implemented with the hyperlink
- ▮ Essential prerequisite such that data in a database can be effectively shared through the cross references is the use of *unique and stable identifiers* (USI) or accession numbers
- ▮ In order to be consistent, it is necessary that this identifier remains constant over time
- ▮ The use of a protein name, often subject to revision or changes, as a stable identifier of a sequence is not a good choice.





NCBI



NCBI ± <http://www.ncbi.nlm.nih.gov/>

- **NCBI** - National Center for Biotechnology Information.

It manages a large number of databases (DB) including:

- **Gene**

integrated collection of genes from a wide range of species. A record may include nomenclature, Reference Sequences (RefSeqs), maps, pathways, variations, phenotypes, and links to genome-, phenotype-, and locus-specific resources worldwide, and the related scientific literature.

- **Nucleotide:**

Integrated collection of nucleotide sequences (both protein coding or non-coding) from all the characterized species from several sources.

- **Protein:**

It has the same structure of *Nucleotide* DB but is related to the amino acid sequences.

- **Pubmed:**

collection of scientific publications of biological and biomedical topics. For each article, the abstract is available. PubMed Central contains articles freely downloadable.

- **Taxonomy:**

A curated classification and nomenclature for all of the organisms in the public sequence databases

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July 6th NCBI Minute: Quickly Find Coding Sequences Using ORFfinder
27 Jun 2016

In one week, we'll show you how to use the redesigned Open Reading Frame

Human genome Annotation Release 108 incorporates new RefSeq sequences, predicts new variants
24 Jun 2016

The Eukarvotic Genome Annotation

GenBank release 214.0 is now available via FTP
23 Jun 2016

GenBank release 214.0 (06/14/2016) has 194.463.572 traditional records

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NCBI National Center for Biotechnology Information

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All Databases

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- Conserved Domains
- dbGaP
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- EST
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Gene

Gene integrates information from a wide range of species. A record may include nomenclature, Reference Sequences (RefSeqs), maps, pathways, variations, phenotypes, and links to genome-, phenotype-, and locus-specific resources worldwide.

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CCDS

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Status

Current

Chromosome locations

more...

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Send to:

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Filters: [Manage Filters](#)

Results by taxon

Top Organisms [\[Tree\]](#)

Homo sapiens (1176)

Mus musculus (48)

Rattus norvegicus (37)

Jaculus jaculus (22)

Cricetulus griseus (19)

All other taxa (1921)

More...

Find related data

Database:

Find items

Search details

TP53[All Fields] AND alive[prop]

Search See more...

Recent activity

Turn Off Clear

TP53 AND (alive[prop]) (3223)

Gene

See more...

Did you mean TP53 as a gene symbol?

Search Gene for [TP53](#) as a symbol.

Search results

Items: 1 to 20 of 3223

See also 47 discontinued or replaced items.

Name/Gene ID	Description	Location	Aliases	MIM
☒ TP53 ID: 7157	tumor protein p53 [<i>Homo sapiens</i> (human)]	Chromosome 17, NC_000017.11 (7668402..7687550, complement)	BCC7, LFS1, P53, TRP53	191170
☐ Tp53 ID: 24842	tumor protein p53 [<i>Rattus norvegicus</i> (Norway rat)]	Chromosome 10, NC_005109.4 (56187013..56198449)	Trp53, p53	
☐ tp53 ID: 30590	tumor protein p53 [<i>Danio rerio</i> (zebrafish)]	Chromosome 5, NC_007116.6 (23582427..23594005)	brp53, drp53, etID22686.5, fb40d06, p53, wu:fb40d06, zgc:111919	
☐ TP53 ID: 403869	tumor protein p53 [<i>Canis lupus familiaris</i> (dog)]	Chromosome 5, NC_006587.3 (32561406..32565149, complement)	P53	
☐ TP53 ID: 397276	tumor protein p53 [<i>Sus scrofa</i> (pig)]	Chromosome 12, NC_010454.3 (55220545..55234668)	P53	
☐ TP53 ID: 281542	tumor protein p53 [<i>Bos taurus</i> (cattle)]	Chromosome 19, AC_000176.1 (27985492..27997883, complement)		

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Gene Advanced Help

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TP53 tumor protein p53 [*Homo sapiens* (human)]

Gene ID: 7157, updated on 16-Jun-2016

Summary

Official Symbol TP53 provided by HGNC

Official Full Name tumor protein p53 provided by HGNC

Primary source [HGNC:HGNC:11988](#)

See related [Ensembl:ENSG00000141510](#) [HPRD:01859](#) [MIM:191170](#) [Vega:OTTHUMG00000192125](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Homo sapiens](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo

Also known as P53; BCC7; LFS1; TRP53

Summary This gene encodes a tumor suppressor protein containing transcriptional activation, DNA binding, and oligomerization domains. The encoded protein responds to diverse cellular stresses to regulate expression of target genes, thereby inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism. Mutations in this gene are associated with a variety of human cancers, including hereditary cancers such as Li-Fraumeni syndrome. Alternative splicing of this gene and the use of alternate promoters result in multiple transcript variants and isoforms. Additional isoforms have also been shown to result from the use of alternate translation initiation codons (PMIDs: 12032546, 20693727). [provided by RefSeq, Feb 2013]

Orthologs [mouse](#) [all](#)

Genomic context

Location: 17p13.1 [See TP53 in Genome Data Viewer Epigenomics Map Viewer](#)

Exon count: 12

Annotation release	Status	Assembly	Chr	Location
108	current	GRCh38.p7 (GCF_000001405.33)	17	NC_000017.11 (7668402..7687550, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	17	NC_000017.10 (7571720..7590898, complement)

Chromosome 17 - NC_000017.11

Genomic regions, transcripts, and products

Genomic Sequence: [NC_000017.11](#) [Chromosome 17 Reference GRCh38.p7 Primary Assembly](#)

Go to reference sequence details

Go to nucleotide: [Graphics](#) [FASTA](#) [GenBank](#)

NC_000017.11: 7,774,774 (25Kbp) C + Find:

Genes, NCBI Homo sapiens Annotation Release 108, 2016-06-07

TP53

TP53 transcripts and isoforms are shown as green bars with arrows indicating the direction of transcription. The diagram includes various isoforms such as TP53-1, TP53-2, TP53-3, TP53-4, TP53-5, TP53-6, TP53-7, TP53-8, TP53-9, TP53-10, TP53-11, TP53-12, TP53-13, TP53-14, TP53-15, TP53-16, TP53-17, TP53-18, TP53-19, TP53-20, TP53-21, TP53-22, TP53-23, TP53-24, TP53-25, TP53-26, TP53-27, TP53-28, TP53-29, TP53-30, TP53-31, TP53-32, TP53-33, TP53-34, TP53-35, TP53-36, TP53-37, TP53-38, TP53-39, TP53-40, TP53-41, TP53-42, TP53-43, TP53-44, TP53-45, TP53-46, TP53-47, TP53-48, TP53-49, TP53-50, TP53-51, TP53-52, TP53-53, TP53-54, TP53-55, TP53-56, TP53-57, TP53-58, TP53-59, TP53-60, TP53-61, TP53-62, TP53-63, TP53-64, TP53-65, TP53-66, TP53-67, TP53-68, TP53-69, TP53-70, TP53-71, TP53-72, TP53-73, TP53-74, TP53-75, TP53-76, TP53-77, TP53-78, TP53-79, TP53-80, TP53-81, TP53-82, TP53-83, TP53-84, TP53-85, TP53-86, TP53-87, TP53-88, TP53-89, TP53-90, TP53-91, TP53-92, TP53-93, TP53-94, TP53-95, TP53-96, TP53-97, TP53-98, TP53-99, TP53-100, TP53-101, TP53-102, TP53-103, TP53-104, TP53-105, TP53-106, 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TP53-307, TP53-308, TP53-309, TP53-310, TP53-311, TP53-312, TP53-313, TP53-314, TP53-315, TP53-316, TP53-317, TP53-318, TP53-319, TP53-320, TP53-321, TP53-322, TP53-323, TP53-324, TP53-325, TP53-326, TP53-327, TP53-328, TP53-329, TP53-330, TP53-331, TP53-332, TP53-333, TP53-334, TP53-335, TP53-336, TP53-337, TP53-338, TP53-339, TP53-340, TP53-341, TP53-342, TP53-343, TP53-344, TP53-345, TP53-346, TP53-347, TP53-348, TP53-349, TP53-350, TP53-351, TP53-352, TP53-353, TP53-354, TP53-355, TP53-356, TP53-357, TP53-358, TP53-359, TP53-360, TP53-361, TP53-362, TP53-363, TP53-364, TP53-365, TP53-366, TP53-367, TP53-368, TP53-369, TP53-370, TP53-371, TP53-372, TP53-373, TP53-374, TP53-375, TP53-376, TP53-377, TP53-378, TP53-379, TP53-380, TP53-381, TP53-382, TP53-383, TP53-384, TP53-385, TP53-386, TP53-387, TP53-388, TP53-389, TP53-390, TP53-391, TP53-392, TP53-393, TP53-394, TP53-395, TP53-396, TP53-397, TP53-398, TP53-399, TP53-400, TP53-401, TP53-402, TP53-403, TP53-404, TP53-405, TP53-406, TP53-407, TP53-408, TP53-409, TP53-410, TP53-411, TP53-412, TP53-413, TP53-414, TP53-415, TP53-416, TP53-417, TP53-418, TP53-419, TP53-420, TP53-421, TP53-422, TP53-423, TP53-424, TP53-425, TP53-426, TP53-427, TP53-428, TP53-429, TP53-430, TP53-431, TP53-432, TP53-433, TP53-434, TP53-435, TP53-436, TP53-437, TP53-438, TP53-439, TP53-440, TP53-441, TP53-442, TP53-443, TP53-444, TP53-445, TP53-446, TP53-447, TP53-448, TP53-449, TP53-450, TP53-451, TP53-452, TP53-453, TP53-454, TP53-455, TP53-456, TP53-457, TP53-458, TP53-459, TP53-460, TP53-461, TP53-462, TP53-463, TP53-464, TP53-465, TP53-466, TP53-467, TP53-468, TP53-469, TP53-470, TP53-471, TP53-472, TP53-473, TP53-474, TP53-475, TP53-476, TP53-477, TP53-478, TP53-479, TP53-480, TP53-481, TP53-482, TP53-483, TP53-484, TP53-485, TP53-486, TP53-487, TP53-488, TP53-489, TP53-490, TP53-491, TP53-492, TP53-493, TP53-494, TP53-495, TP53-496, TP53-497, TP53-498, TP53-499, TP53-500, TP53-501, TP53-502, TP53-503, TP53-504, TP53-505, TP53-506, 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TP53-607, TP53-608, TP53-609, TP53-610, TP53-611, TP53-612, TP53-613, TP53-614, TP53-615, TP53-616, TP53-617, TP53-618, TP53-619, TP53-620, TP53-621, TP53-622, TP53-623, TP53-624, TP53-625, TP53-626, TP53-627, TP53-628, TP53-629, TP53-630, TP53-631, TP53-632, TP53-633, TP53-634, TP53-635, TP53-636, TP53-637, TP53-638, TP53-639, TP53-640, TP53-641, TP53-642, TP53-643, TP53-644, TP53-645, TP53-646, TP53-647, TP53-648, TP53-649, TP53-650, TP53-651, TP53-652, TP53-653, TP53-654, TP53-655, TP53-656, TP53-657, TP53-658, TP53-659, TP53-660, TP53-661, TP53-662, TP53-663, TP53-664, TP53-665, TP53-666, TP53-667, TP53-668, TP53-669, TP53-670, TP53-671, TP53-672, TP53-673, TP53-674, TP53-675, TP53-676, TP53-677, TP53-678, TP53-679, TP53-680, TP53-681, TP53-682, TP53-683, TP53-684, TP53-685, TP53-686, TP53-687, TP53-688, TP53-689, TP53-690, TP53-691, TP53-692, TP53-693, TP53-694, TP53-695, TP53-696, TP53-697, TP53-698, TP53-699, TP53-700, TP53-701, TP53-702, TP53-703, TP53-704, TP53-705, TP53-706, TP53-707, TP53-708, TP53-709, TP53-710, TP53-711, TP53-712, TP53-713, TP53-714, TP53-715, TP53-716, TP53-717, TP53-718, TP53-719, TP53-720, TP53-721, TP53-722, TP53-723, TP53-724, TP53-725, TP53-726, TP53-727, TP53-728, TP53-729, TP53-730, TP53-731, TP53-732, TP53-733, TP53-734, TP53-735, TP53-736, TP53-737, TP53-738, TP53-739, TP53-740, TP53-741, TP53-742, TP53-743, TP53-744, TP53-745, TP53-746, TP53-747, TP53-748, TP53-749, TP53-750, TP53-751, TP53-752, TP53-753, TP53-754, TP53-755, TP53-756, TP53-757, TP53-758, TP53-759, TP53-760, TP53-761, TP53-762, TP53-763, TP53-764, TP53-765, TP53-766, TP53-767, TP53-768, TP53-769, TP53-770, TP53-771, TP53-772, TP53-773, TP53-774, TP53-775, TP53-776, TP53-777, TP53-778, TP53-779, TP53-780, TP53-781, TP53-782, TP53-783, TP53-784, TP53-785, TP53-786, TP53-787, TP53-788, TP53-789, TP53-790, TP53-791, TP53-792, TP53-793, TP53-794, TP53-795, TP53-796, TP53-797, TP53-798, TP53-799, TP53-800, TP53-801, TP53-802, TP53-803, TP53-804, TP53-805, TP53-806, 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TP53-907, TP53-908, TP53-909, TP53-910, TP53-911, TP53-912, TP53-913, TP53-914, TP53-915, TP53-916, TP53-917, TP53-918, TP53-919, TP53-920, TP53-921, TP53-922, TP53-923, TP53-924, TP53-925, TP53-926, TP53-927, TP53-928, TP53-929, TP53-930, TP53-931, TP53-932, TP53-933, TP53-934, TP53-935, TP53-936, TP53-937, TP53-938, TP53-939, TP53-940, TP53-941, TP53-942, TP53-943, TP53-944, TP53-945, TP53-946, TP53-947, TP53-948, TP53-949, TP53-950, TP53-951, TP53-952, TP53-953, TP53-954, TP53-955, TP53-956, TP53-957, TP53-958, TP53-959, TP53-960, TP53-961, TP53-962, TP53-963, TP53-964, TP53-965, TP53-966, TP53-967, TP53-968, TP53-969, TP53-970, TP53-971, TP53-972, TP53-973, TP53-974, TP53-975, TP53-976, TP53-977, TP53-978, TP53-979, TP53-980, TP53-981, TP53-982, TP53-983, TP53-984, TP53-985, TP53-986, TP53-987, TP53-988, TP53-989, TP53-990, TP53-991, TP53-992, TP53-993, TP53-994, TP53-995, TP53-996, TP53-997, TP53-998, TP53-999, TP53-1000, TP53-1001, TP53-1002, TP53-1003, TP53-1004, TP53-1005, TP53-1006, TP53-1007, TP53-1008, TP53-1009, TP53-1010, TP53-1011, TP53-1012, TP53-1013, TP53-1014, TP53-1015, TP53-1016, TP53-1017, TP53-1018, TP53-1019, TP53-1020, TP53-1021, TP53-1022, TP53-1023, TP53-1024, TP53-1025, TP53-1026, TP53-1027, TP53-1028, TP53-1029, TP53-1030, TP53-1031, TP53-1032, TP53-1033, TP53-1034, TP53-1035, TP53-1036, TP53-1037, TP53-1038, TP53-1039, TP53-1040, TP53-1041, TP53-1042, TP53-1043, TP53-1044, TP53-1045, TP53-1046, TP53-1047, TP53-1048, TP53-1049, TP53-1050, TP53-1051, TP53-1052, TP53-1053, TP53-1054, TP53-1055, TP53-1056, TP53-1057, TP53-1058, TP53-1059, TP53-1060, TP53-1061, TP53-1062, TP53-1063, TP53-1064, TP53-1065, TP53-1066, TP53-1067, TP53-1068, TP53-1069, TP53-1070, TP53-1071, TP53-1072, TP53-1073, TP53-1074, TP53-1075, TP53-1076, TP53-1077, TP53-1078, TP53-1079, TP53-1080, TP53-1081, TP53-1082, TP53-1083, TP53-1084, TP53-1085, TP53-1086, TP53-1087, TP53-1088, TP53-1089, TP53-1090, TP53-1091, TP53-1092, TP53-1093, TP53-1094, TP53-1095, TP53-1096, TP53-1097, TP53-1098, TP53-1099, TP53-1100, TP53-1101, TP53-1102, TP53-1103, TP53-1104, TP53-1105, TP53-1106, TP53-1107, TP53-1108, TP53-1109, TP53-1110, TP53-1111, TP53-1112, TP53-1113, TP53-1114, TP53-1115, TP53-1116, TP53-1117, TP53-1118, TP53-1119, TP53-1120, TP53-1121, TP53-1122, TP53-1123, TP53-1124, TP53-1125, TP53-1126, TP53-1127, TP53-1128, TP53-1129, TP53-1130, TP53-1131, TP53-1132, TP53-1133, TP53-1134, TP53-1135, TP53-1136, TP53-1137, TP53-1138, TP53-1139, TP53-1140, TP53-1141, TP53-1142, TP53-1143, TP53-1144, TP53-1145, TP53-1146, TP53-1147, TP53-1148, TP53-1149, TP53-1150, TP53-1151, TP53-1152, TP53-1153, TP53-1154, TP53-1155, TP53-1156, TP53-1157, TP53-1158, TP53-1159, TP53-1160, TP53-1161, TP53-1162, TP53-1163, TP53-1164, TP53-1165, TP53-1166, TP53-1167, TP53-1168, TP53-1169, TP53-1170, TP53-1171, TP53-1172, TP53-1173, TP53-1174, TP53-1175, TP53-1176, TP53-1177, TP53-1178, TP53-1179, TP53-1180, TP53-1181, TP53-1182, TP53-1183, TP53-1184, TP53-1185, TP53-1186, TP53-1187, TP53-1188, TP53-1189, TP53-1190, TP53-1191, TP53-1192, TP53-1193, TP53-1194, TP53-1195, TP53-1196, TP53-1197, TP53-1198, TP53-1199, TP53-1200, TP53-1201, TP53-1202, TP53-1203, TP53-1204, TP53-1205, TP53-1206, TP53-1207, TP53-1208, TP53-1209, TP53-1210, TP53-1211, TP53-1212, TP53-1213, TP53-1214, TP53-1215, TP53-1216, TP53-1217, TP53-1218, TP53-1219, TP53-1220, TP53-1221, TP53-1222, TP53-1223, TP53-1224, TP53-1225, TP53-1226, TP53-1227, TP53-1228, TP53-1229, TP53-1230, TP53-1231, TP53-1232, TP53-1233, TP53-1234, TP53-1235, TP53-1236, TP53-1237, TP53-1238, TP53-1239, TP53-1240, TP53-1241, TP53-1242, TP53-1243, TP53-1244, TP53-1245, TP53-1246, TP53-1247, TP53-1248, TP53-1249, TP53-1250, TP53-1251, TP53-1252, TP53-1253, TP53-1254, TP53-1255, TP53-1256, TP53-1257, TP53-1258, TP53-1259, TP53-1260, TP53-1261, TP53-1262, TP53-1263, TP53-1264, TP53-1265, TP53-1266, TP53-1267, TP53-1268, TP53-1269, TP53-1270, TP53-1271, TP53-1272, TP53-1273, TP53-1274, TP53-1275, TP53-1276, TP53-1277, TP53-1278, 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TP53 tumor protein p53 [*Homo sapiens* (human)]

Gene ID: 7157, updated on 16-Jun-2016

Summary

Official Symbol: TP53 provided by HGNC
Official Full Name: tumor protein p53 provided by HGNC
Primary source: HGNC:HGNC:11968
See related: Ensembl:ENSG00000141510 HPRO:01859 MIM:191170 Vega:OTTHUMS00000162126
Gene type: protein coding
RefSeq status: REVIEWED
Organism: [Homo sapiens](#)
Lineage: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo
Also known as: P53; BCC1; LFS1; TRP53
Summary: This gene encodes a tumor suppressor protein containing transcriptional activation, DNA binding, and oligomerization domains. The encoded protein responds to diverse cellular stresses to regulate expression of target genes, thereby inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism. Mutations in this gene are associated with a variety of human cancers, including hereditary cancers such as Li-Fraumeni syndrome. Alternative splicing of this gene and the use of alternate promoters result in multiple transcript variants and isoforms. Additional isoforms have also been shown to result from the use of alternate translation initiation codons (PMIDs: 12032546, 20937277). [provided by RefSeq, Feb 2013]
Orthologs: [mouse](#) [all](#)

Genomic context

Location: 17p13.1 See TP53 in [Genome Data Viewer](#) [Epigenomics](#) [Map Viewer](#)
Exon count: 12

Annotation release	Status	Assembly	Chr	Location
108	current	GRCh38.p7 (GCF_000001405.33)	17	NC_000017.11 (7688402..7687550, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	17	NC_000017.10 (7571720..7560898, complement)

Chromosome 17 - NC_000017.11

Genomic regions, transcripts, and products

Genomic Sequence: NC_000017.11 Chromosome 17 Reference GRCh38.p7 Primary Assembly

Exons ☐ dark rectangles (coding)

Introns ☐ thin lines

pale rectangles (non-coding, 3'UTR)

TP53

PubChem Substance
PubMed
PubMed (GeneRIF)
PubMed (OMIM)
PubMed (nucleotide/PMC)
RefSeq Proteins
RefSeq RNAs
RefSeqGene
SNP
SNP (GeneView)

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TP53 tumor protein p53 [*Homo sapiens* (human)]

Gene ID: 7157, updated on 16-Jun-2016

Summary

Official Symbol **TP53** provided by HGNC
Official Full Name **tumor protein p53** provided by HGNC
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See related **Ensembl:ENSG00000141510 HPRD:01859 MIM:191170 Vega:OTTHUM300000162126**
Gene type **protein coding**
RefSeq status **REVIEWED**
Organism ***Homo sapiens***
Lineage **Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo**
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Summary **This gene encodes a tumor suppressor protein containing transcriptional activation, DNA binding, and oligomerization domains. The encoded protein responds to diverse cellular stresses to regulate expression of target genes, thereby inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism. Mutations in this gene are associated with a variety of human cancers, including hereditary cancers such as Li-Fraumeni syndrome. Alternative splicing of this gene and the use of alternate promoters result in multiple transcript variants and isoforms. Additional isoforms have also been shown to result from the use of alternate translation initiation codons (PMIDs: 12032548, 20937277). [provided by RefSeq, Feb 2013]**
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Chromosome 17 - NC_000017.11

Genomic regions, transcripts, and products

Genomic Sequence: [NC_000017.11](#) [Chromosome 17 Reference GRCh38.p7 Primary Assembly](#) [Go to reference sequence details](#)

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NC_000017.11: 7,74M..7,74M (25Kbp) C + Find:

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Cell cycle and p53 gate the direct conversion of human fibroblasts to dopaminergic neurons.

Jiang H^{1,2}, Xu Z^{2,3}, Zhong P^{1,2}, Ren Y², Liang G⁴, Schilling HA², Hu Z⁵, Zhang Y⁴, Wang X⁶, Chen S³, Yan Z^{1,2}, Feng J^{1,2,6}.

Author information

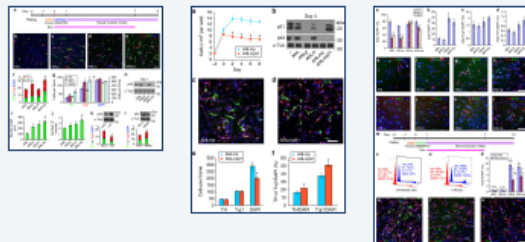
Abstract

The direct conversion of fibroblasts to induced dopaminergic (iDA) neurons and other cell types demonstrates the plasticity of cell fate. The low efficiency of these relatively fast conversions suggests that kinetic barriers exist to safeguard cell-type identity. Here we show that suppression of p53, in conjunction with cell cycle arrest at G1 and appropriate extracellular environment, markedly increase the efficiency in the transdifferentiation of human fibroblasts to iDA neurons by Ascl1, Nurr1, Lmx1a and miR124. The conversion is dependent on Tet1, as G1 arrest, p53 knockdown or expression of the reprogramming factors induces Tet1 synergistically. Tet1 knockdown abolishes the transdifferentiation while its overexpression enhances the conversion. The iDA neurons express markers for midbrain DA neurons and have active dopaminergic transmission. Our results suggest that overcoming these kinetic barriers may enable highly efficient epigenetic reprogramming in general and will generate patient-specific midbrain DA neurons for Parkinson's disease research and therapy.

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Published online 2015 Dec 7. doi: [10.1038/ncomms10100](https://doi.org/10.1038/ncomms10100)

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Cell cycle and p53 gate the direct conversion of human fibroblasts to dopaminergic neurons

[Houbo Jiang](#),^{1,2} [Zhimin Xu](#),^{2,3} [Ping Zhong](#),^{1,2} [Yong Ren](#),² [Gaoyang Liang](#),⁴ [Haley A. Schilling](#),² [Zihua Hu](#),⁵ [Yi Zhang](#),⁴ [Xiaomin Wang](#),⁶ [Shengdi Chen](#),³ [Zhen Yan](#),^{1,2} and [Jian Feng](#)^{a,1,2,6}

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The direct conversion of fibroblasts to induced dopaminergic (iDA) neurons and other cell types demonstrates the plasticity of cell fate. The low efficiency of these relatively fast conversions suggests that kinetic barriers exist to safeguard cell-type identity. Here we show that suppression of p53, in conjunction with cell cycle arrest at G1 and appropriate extracellular environment, markedly increase the efficiency in the transdifferentiation of human fibroblasts to iDA neurons by Ascl1, Nurr1, Lmx1a and miR124. The conversion is dependent on Tet1, as G1 arrest, p53 knockdown or expression of the reprogramming factors induces Tet1 synergistically. Tet1 knockdown abolishes the transdifferentiation while its overexpression enhances the conversion. The iDA neurons express markers for midbrain DA neurons and have active dopaminergic transmission. Our results suggest that overcoming these kinetic barriers may enable highly efficient epigenetic reprogramming in general and will generate patient-specific midbrain DA neurons for Parkinson's disease research and therapy.

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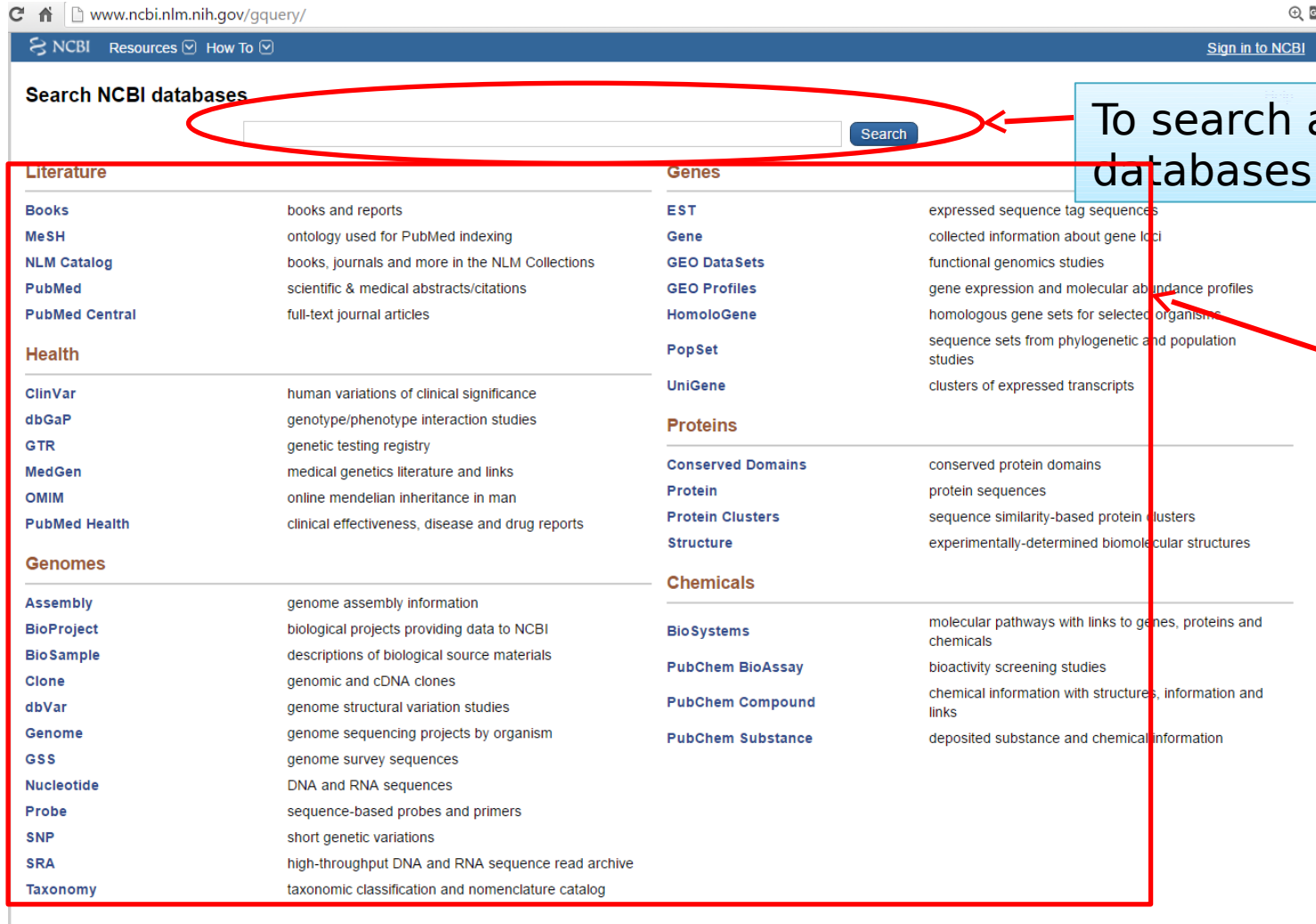
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- SNP** short genetic variations
- SRA** high-throughput DNA and RNA sequence read archive
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- EST** expressed sequence tag sequences
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- GEO DataSets** functional genomics studies
- GEO Profiles** gene expression and molecular abundance profiles
- HomoloGene** homologous gene sets for selected organisms
- PopSet** sequence sets from phylogenetic and population studies
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- Structure** experimentally-determined biomolecular structures

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PubMed Central	22,001	full-text journal articles

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GTR	325	genetic testing registry
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OMIM	323	online mendelian inheritance in man
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Assembly	0	genome assembly information
BioProject	301	biological projects providing data to NCBI
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Clone	532	genomic and cDNA clones
dbVar	2,134	genome structural variation studies
Genome	8	genome sequencing projects by organism
GSS	6	genome survey sequences
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Probe	1,532	sequence-based probes and primers
SNP	4,484	short genetic variations
SRA	1,512	high-throughput DNA and RNA sequence read archive

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PubChem Substance	616	deposited substance and chemical information





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Gene sources

Genomic

Categories

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Name/Gene ID	Description	Location	Aliases	MIM
☐ TP53 ID: 7157	tumor protein p53 [<i>Homo sapiens</i> (human)]	Chromosome 17, NC_000017.11 (7668402..7687550, complement)	BCC7, LFS1, P53, TRP53	191170
☐ Tp53 ID: 24842	tumor protein p53 [<i>Rattus norvegicus</i> (Norway rat)]	Chromosome 10, NC_005109.4 (56187013..56198449)	Trp53, p53	
☐ tp53 ID: 30590	tumor protein p53 [<i>Danio rerio</i> (zebrafish)]	Chromosome 5, NC_007116.6 (23582427..23594005)	brp53, drp53, etlD22686.5, fb40d06, p53, wu:fb40d06, zgc:111919	
☐ TP53 ID: 403869	tumor protein p53 [<i>Canis lupus familiaris</i> (dog)]	Chromosome 5, NC_006587.3 (32561406..32565149, complement)	P53	
☐ TP53 ID: 397276	tumor protein p53 [<i>Sus scrofa</i> (pig)]	Chromosome 12, NC_010454.3 (55220545..55234668)	P53	
☐ TP53 ID: 281542	tumor protein p53 [<i>Bos taurus</i> (cattle)]	Chromosome 19, AC_000176.1 (27985492..27997883, complement)		
☐ TP53 ID: 396200	tumor protein p53 [<i>Gallus gallus</i> (chicken)]			

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Results by taxon

Top Organisms [\[Tree\]](#)
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Create alert Advanced Help

Gene sources
Genomic

Categories
Alternatively spliced
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☐ Tp53 ID: 24842	tumor protein p53 [<i>Rattus norvegicus</i> (Norway rat)]	Chromosome 10, NC_005066.4 (56187013..56198449)		
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NCBI

Resources

How To

Sign in to NCBI

Gene

Gene

TP53

Search

Create alert

Advanced

Help

Gene sources

Genomic

Categories

Alternatively spliced

Annotated genes

Non-coding

Protein-coding

Pseudogene

Sequence content

CCDS

Ensembl

RefSeq

RefSeqGene

Status

Current

Chromosome locations

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Clear all

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20 per page

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Nucleotide

p53 protein [Homo sapiens]

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Gene sources

Genomic

Categories

Alternatively spliced

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locations

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<< First < Prev Page 1 of 59 Next > Last >>

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Name/Gene ID	Description	Location	Aliases	MIM
☐ TP53 ID: 7157	tumor protein p53 [<i>Homo sapiens</i> (human)]	Chromosome 17, NC_000017.11 (7668402..7687550, complement)	BCC7, LFS1, P53, TRP53	191170
☐ TP53BP1 ID: 7158	tumor protein p53 binding protein 1 [<i>Homo sapiens</i> (human)]	Chromosome 15, NC_000015.10 (43403064..43510509, complement)	53BP1, TDRD30, TP53, p202, p53BP1	605230
☐ RRM2B ID: 50484	ribonucleotide reductase regulatory TP53 inducible subunit M2B [<i>Homo</i> <i>sapiens</i> (human)]	Chromosome 8, NC_000008.11 (102204501..102239118, complement)	MTDPS8A, MTDPS8B, P53R2	604712
☐ WRAP53 ID: 55135	WD repeat containing antisense to TP53 [<i>Homo sapiens</i> (human)]	Chromosome 17, NC_000017.11 (7686071..7703502)	DKCB3, TCAB1, WDR79	612661
☐ TIGAR ID: 57103	TP53 induced glycolysis regulatory phosphatase [<i>Homo</i> <i>sapiens</i> (human)]	Chromosome 12, NC_000012.12 (4321193..4360028)	C12orf5, FR2BP	610775
☐ EGFR ID: 1956	epidermal growth factor receptor [<i>Homo</i> <i>sapiens</i> (human)]	Chromosome 7, NC_000007.14 (55019032..55207338)	ERBB, ERBB1, HER1, NISBD2, PIG61, mENA	131550

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Genomic

Categories

Alternatively spliced

Annotated genes

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Items: 1 to 20 of 1176

<< First < Prev Page 1 of 59 Next > Last >>

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☐ TP53 ID: 7157	tumor protein p53 [Homo sapiens (human)]	Chromosome 17, NC_000017.11	BCC7, LFS1, P53, TRP53	191170
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☐ EGFR ID: 1956	epidermal growth factor receptor [Homo sapiens (human)]	Chromosome 7, NC_000007.14 (55019032..55207338)	ERBB, ERBB1, HER1, NISBD2, PIG61, mENA	131550

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TP53 tumor protein p53 [*Homo sapiens* (human)]

Gene ID: 7157, updated on 16-Jun-2016

Summary

Official Symbol TP53 provided by [HGNC](#)
Official Full Name tumor protein p53 provided by [HGNC](#)
Primary source [HGNC:HGNC:11998](#)
See related [Ensembl:ENSG00000141510](#) [HPRD:01859](#) [MIM:191170](#) [Vega:OTTHUMG00000162125](#)
Gene type protein coding
RefSeq status REVIEWED
Organism [Homo sapiens](#)
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as P53; BCC7; LFS1; TRP53
Summary This gene encodes a tumor suppressor protein containing transcriptional activation, DNA binding, and oligomerization domains. The encoded protein responds to diverse cellular stresses to regulate expression of target genes, thereby inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism. Mutations in this gene are associated with a variety of human cancers, including hereditary cancers such as Li-Fraumeni syndrome. Alternative splicing of this gene and the use of alternate promoters result in multiple transcript variants and isoforms. Additional isoforms have also been shown to result from the use of alternate translation initiation codons (PMIDs: 12032546, 20937277). [provided by RefSeq, Feb 2013]
Orthologs [mouse](#) [all](#)

Genomic context

Location: 17p13.1**Exon count:** 12

Annotation release	Status	
108	current	
105	previous assembly	GRCh37.p13 (GCF_000001405.25) 17 NC_000017.10 (7571720..7590868, complement)

Table of contents

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The GeneID, the current official symbol or database identifier if no official symbol is available, the full name, the gene type, the RefSeq status of the name, the organism, a comma-separated set of aliases, brief summary



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TP53 tumor protein p53 [*Homo sapiens* (human)]

Gene ID: 7157, updated on 16-Jun-2016

Summary

Official Symbol TP53 provided by [HGNC](#)

Official Full Name tumor protein p53 provided by [HGNC](#)

Primary source [HGNC:HGNC:11998](#)

See related [Ensembl:ENSG00000141510](#) [HPRD:01859](#) [MIM:191170](#) [Vega:OTTHUMG00000162125](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Homo sapiens](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

Also known as P53; BCO7; LFS1; TRP53

Summary This gene encodes a tumor suppressor protein containing transcriptional activation, DNA binding, and oligomerization domains. The encoded protein responds to diverse cellular stresses to regulate expression of target genes, thereby inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism. Mutations in this gene are associated with a variety of human cancers, including hereditary cancers such as Li-Fraumeni syndrome. Alternative splicing of this gene and the use of alternate promoters result in multiple transcript variants and isoforms. Additional isoforms have also been shown to result from the use of alternate translation initiation codons (PMIDs: 12032546, 20937277). [provided by RefSeq, Feb 2013]

Orthologs [mouse](#) [all](#)

Taxonomy Browser: Organism classification

Genomic context

Location: 17p13.1**Exon count:** 12See TP53 in [Genome Data Viewer](#) [Epigenomics Map Viewer](#)

Annotation release	Status	Assembly	Chr	Location
108	current	GRCh38.p7 (GCF_000001405.33)	17	NC_000017.11 (7668402..7687550, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	17	NC_000017.10 (7571720..7590868, complement)

Table of contents

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Lineage (full): [root](#); [cellular organisms](#); [Eukaryota](#); [Opisthokonta](#); [Metazoa](#); [Eumetazoa](#); [Bilateria](#); [Deuterostomia](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Gnathostomata](#); [Teleostomi](#); [Euteleostomi](#); [Sarcopterygii](#); [Dipnotetrapodomorpha](#); [Tetrapoda](#); [Amniota](#); [Mammalia](#); [Theria](#); [Eutheria](#); [Boreoeutheria](#); [Euarchontoglires](#); [Primates](#); [Haplorrhini](#); [Simiiformes](#); [Catarrhini](#); [Hominoidea](#); [Hominidae](#); [Homininae](#); [Homo](#)

- [Homo sapiens](#) (human) *Click on organism name to get more information.*
 - [Homo sapiens neanderthalensis](#) (Neandertal)
 - [Homo sapiens ssp. Denisova](#) (Denisova hominin)

Organism classification

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TP53 tumor protein p53 [*Homo sapiens* (human)]

Gene ID: 7157, updated on 16-Jun-2016

Summary

Official Symbol TP53 provided by [HGNC](#)**Official Full Name** tumor protein p53 provided by [HGNC](#)**Primary source** [HGNC:HGNC:11998](#)**See related** [Ensembl:ENSG00000141510](#) [HPRD:01859](#) [MIM:191170](#) [Vega:OTTHUMG00000162125](#)**Gene type** protein coding**RefSeq status** REVIEWED**Organism** [Homo sapiens](#)**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo**Also known as** P53; BCC7; LFS1; TRP53**Summary** This gene encodes a tumor suppressor protein containing transcriptional activation, DNA binding, and oligomerization domains. The encoded protein responds to diverse cellular stresses to regulate expression of target genes, thereby inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism. Mutations in this gene are associated with a variety of human cancers, including hereditary cancers such as Li-Fraumeni syndrome. Alternative splicing of this gene and the use of alternate promoters result in multiple transcript variants and isoforms. Additional isoforms have also been shown to result from the use of alternate translation initiation codons (PMIDs: 12032546, 20937277). [provided by RefSeq, Feb 2013]**Orthologs** [mouse](#) [all](#)

Database with Sequence information: here
HGNC

Genomic context

Location: 17p13.1**Exon count:** 12See TP53 in [Genome Data Viewer](#) [Epigenomics Map Viewer](#)

Annotation release	Status	Assembly	Chr	Location
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APPROVED NAME
HGNC ID
PREVIOUS SYMBOLS & NAMES
SYNONYMS
LOCUS TYPE
CHROMOSOMAL LOCATION
HCOP

TP53
tumor protein p53
HGNC:11998
-
LFS1, "Li-Fraumeni syndrome", p53
gene with protein product
17p13.1
[Orthology Predictions for TP53](#)

Gene name and official gene symbol

External links

HOMOLOGS

	Symbol	Database
Mus musculus	Trp53	MGI:98834 C
Rattus norvegicus	Tp53	RGD:3889 D

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Entrez Gene: [7157](#) C
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Symbol Report: TP53

APPROVED SYMBOL	TP53
APPROVED NAME	tumor protein p53
HGNC ID	HGNC:11998
PREVIOUS SYMBOLS & NAMES	-
SYNONYMS	LFS1, "Li-Fraumeni syndrome", p53
LOCUS TYPE	gene with protein product
CHROMOSOMAL LOCATION	17p13.1
HCOP	Orthology Predictions for TP53

Unique ID provided by HGNC:
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External links

HOMOLOGS

	Symbol	Database
Mus musculus	Trp53	MGI:98834
Rattus norvegicus	Tp53	RGD:3889

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APPROVED SYMBOL	TP53
APPROVED NAME	tumor protein p53
HGNC ID	HGNC:11998
PREVIOUS SYMBOLS & NAMES	-
SYNONYMS	LFS1, "Li-Fraumeni syndrome", p53
LOCUS TYPE	gene with protein product
CHROMOSOMAL LOCATION	17p13.1
HCOP	Orthology Predictions for TP53

Alias

External links

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	Symbol	Database
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Rattus norvegicus	Tp53	RGD:3889

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Symbol Report: TP53

APPROVED SYMBOL

TP53

APPROVED NAME

tumor protein p53

HGNC ID

HGNC:11998

PREVIOUS SYMBOLS & NAMES

-

SYNONYMS

LFS1, "Li-Fraumeni syndrome", p53

LOCUS TYPE

gene with protein product

CHROMOSOMAL LOCATION

17p13.1

HCOP

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Gene position or chromosomal region

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HOMOLOGS

	Symbol	Database
Mus musculus	Trp53	MGI:98834
Rattus norvegicus	Tp53	RGD:3889

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APPROVED NAME

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HGNC ID

HGNC:11998

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SYNONYMS

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17p13.1

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	Symbol	Database
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Link to related gene in other organisms (Mouse and Rattus)





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Symbol Report: TP53

APPROVED SYMBOL TP53

APPROVED NAME tumor protein p53

HGNC ID HGNC:11998

PREVIOUS SYMBOLS & NAMES -

SYNONYMS LFS1, "Li-Fraumeni syndrome", p53

LOCUS TYPE gene with protein product

CHROMOSOMAL LOCATION 17p13.1

HCOP Orthology Predictions for TP53

External links

HOMOLOGS

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Rattus norvegicus	Tp53	RGD:3889 D

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APPROVED NAME

tumor protein p53

HGNC ID

HGNC:11998

PREVIOUS SYMBOLS & NAMES

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SYNONYMS

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Homo sapiens p53 protein mRNA, complete cds

GenBank: AF307851.1

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LOCUS AF307851 2521 bp mRNA linear PRI 29-JAN-2001
DEFINITION Homo sapiens p53 protein mRNA, complete cds.
ACCESSION AF307851
VERSION AF307851.1 GI:11066969
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2521)
AUTHORS Chang,N.-S., Pratt,N., Heath,J., Schultz,L., Sleeve,D., Carey,G.B.
and Zevotek,N.
TITLE Hyaluronidase induction of a WW domain-containing oxidoreductase
that enhances tumor necrosis factor cytotoxicity
J. Biol. Chem. 276 (5), 3361-3370 (2001)
PUBMED [11058590](#)
REFERENCE 2 (bases 1 to 2521)
AUTHORS Chang,N.-S., Pratt,N. and Heath,J.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-2000) Laboratory of Molecular Immunology, Guthrie
Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA

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FEATURES

source

Location/Qualifiers

1..2521

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/db_xref="taxon:9606"

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Sequence Features:
introns, exons,
promoters, enhancers, ...

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sequence

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1847162"

136..1317

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/db_xref="GI:11066970"

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CDS

Link to the Protein Coding Sequence: pointed out its starting (136) and end points (1317)

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Articles about the TP53 gene

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Pathways for the TP53 gene

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/protein_id="AAG28785.1"
/db_xref="GI:11066970"
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AIYKQSQHMT
PYEPPEVGS
CPGRDRRTE
RERFEMFRE
D"

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Nucleotide number 136
representing the starting point
of the protein coding
sequence

ORIGIN

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241  ccgtcccaag caatggatga ttgatgctg tccccggagc atattgaaca atggttcact
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841  tacatgtgta acagtctctg catggggggc atgaaccgga ggcccatcct caccatcacc
901  acactggaag actccagtgg taatctactg ggacgggaaca gctttgaggt gcgtgtttgt
961  gcctgtcctg ggagagaccg gcgcacagag gaagagaatc tccgcaagaa agggggagct
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2521  a

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Nucleotide 1317
representing the
end point of the
protein coding
sequence

Reference sequence information

RefSeq alternative splicing
See 15 reference mRNA sequence splice
variants for the TP53 gene.

More about the TP53 gene

This gene encodes a tumor suppressor protein
containing transcriptional activation, DNA
binding, and oligomerization domains. The
encoded pr...

Also Known As: BCC7, LFS1, P53, TRP53

Homologs of the TP53 gene

The TP53 gene is conserved in chimpanzee,
Rhesus monkey, dog, cow, mouse, rat,
zebrafish, and frog.

Related information

BioSystems

Full text in PMC

Gene

Map Viewer

OMIM

Probe

Protein

PubMed

PubMed (Weighted)

Taxonomy

UniGene

GO Profiles

LinkOut to external resources

Antibodies

[ExactAntigen/Labome]

Antibody reviews

[ExactAntigen/Labome]

Full-length cDNA clone

[GeneCopoeia Inc.]

Full-length cDNA clone

[Plasmid Repository at Harvard...]

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Nucleotide

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Homo sapiens p53 protein mRNA, complete cds

GenBank: AF307851.1

[FASTA](#) [Graphics](#)

Go to:

Research Institute, 100 Main St, Suite 100, Boston, MA 02110, USA

FEATURES

Location/Qualifiers

source

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[CDS](#)

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Link to the
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Articles about the TP53 gene

[RELATIONSHIP BETWEEN p53/p21/Rb AND MAPK SIGNALING PATHWAYS [Tsitolgia. 2015]

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The expression and significance of p53 protein and Ki-67 protein in ptery [Vojnosanit Pregl. 2016]

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Pathways for the TP53 gene

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p53 protein [Homo sapiens]

GenBank: AAG28785.1

[Identical Proteins](#) [FASTA](#) [Graphics](#)[Go to:](#) ▾

LOCUS AF307851.1 393 aa linear PRI 29-JAN-2001
DEFINITION p53 protein [Homo sapiens].
ACCESSION AAG28785
VERSION AAG28785.1 GI:11066970
DBSOURCE accession [AF307851.1](#)
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 393)
AUTHORS Chang,N.S., Pratt,N., Heath,J., Schultz,L., Sleva,D., Carey,G.B.
and Zevotek,N.
TITLE Hyaluronidase induction of a WW domain-containing oxidoreductase
that enhances tumor necrosis factor cytotoxicity
J. Biol. Chem. 276 (5), 3361-3370 (2001)
PUBMED [11058590](#)
REFERENCE 2 (residues 1 to 393)
AUTHORS Chang,N.-S., Pratt,N. and Heath,J
TITLE Direct Submission
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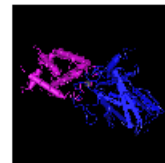
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Protein
sequence

Analyze this sequence

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Protein 3D Structure



Solution Structure Of The
Complex Between Bcl-xl
And The P53 Core Domain
PDB: 2MEJ
Source: Homo sapiens
Method: Solution Nmr

[See all 130 structures..](#)

Articles about the TP53 gene

The Significance of Combined Measurement of
p53 Antibody and [Hepatogastroenterology. 2015]

Evaluation of p53 Polymorphism in Patients with
Pannus-Derived Prostheses [J Heart Valve Dis. 2015]

"p53 mutation spectrum and its role in prognosis

Homo sapiens p53 protein mRNA, complete cds

GenBank: AF307851.1

[FASTA](#) [Graphics](#)

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ORIGIN

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```

mRNA
sequence
related to the
gene

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Articles about the TP53 gene

[RELATIONSHIP BETWEEN p53/p21/Rb AND MAPK SIGNALING PATHWAYS [Tsitologia. 2015]

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Pathways for the TP53 gene

Regulation of TP53 Activity through Acetylation

Regulation of TP53 Activity through Methylation

Regulation of TP53 Activity through Association with Co-factors

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Format

- ☐ Summary
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- ☐ GenBank (full)
- ☐ FASTA
- ☐ FASTA (text)
- ☐ Graphics
- ☐ ASN.1
- ☐ Revision History
- ☐ Accession List
- ☐ GI List

s p53 protein mRNA, complete cds

Visualization mode

1
2521 bp mRNA linear PRI 29-JAN-2001
Homo sapiens p53 protein mRNA, complete cds.
1
1.1 GI:11066969

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2521)

AUTHORS Chang,N.S., Pratt,N., Heath,J., Schultz,L., Sleve,D., Carey,G.B.
and Zevotek,N.TITLE Hyaluronidase induction of a WW domain-containing oxidoreductase
that enhances tumor necrosis factor cytotoxicity

J. Biol. Chem. 276 (5), 3361-3370 (2001)

PUBMED [11058590](#)

REFERENCE 2 (bases 1 to 2521)

AUTHORS Chang,N.-S., Pratt,N. and Heath,J.

TITLE Direct Submission

JOURNAL Submitted (21-SEP-2000) Laboratory of Molecular Immunology, Guthrie
Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA

FEATURES Location/Qualifiers

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CDS
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Nucleotide

Nucleotide

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Format

- ☐ Summary
- ☒ GenBank
- ☐ GenBank (full)
- ☐ FASTA
- ☐ FASTA (text)
- ☐ Graphics
- ☐ ASN.1
- ☐ Revision History
- ☐ Accession List
- ☐ GI List

p53 protein mRNA, complete cds

1
2521 bp mRNA linear PRI 29-JAN-2001
Homo sapiens p53 protein mRNA, complete cds.
1
1.1 GI:11066969

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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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and Zevotek,N.
TITLE Hyaluronidase induction of a WW domain-containing oxidoreductase
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Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA
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Location/Qualifiers
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MAPK SIGNALING PATHWAY! [Tsitolgia. 2015]

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Pathways for the TP53 gene

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Reference sequence information

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Nucleotide

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Homo sapiens p53 protein mRNA, complete cds

GenBank: AF307851.1

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```

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Homo sapiens p53 protein mRNA, complete cds

GenBank: AF307851.1

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Go to:

LOCUS AF307851 2521 bp mRNA linear PRI 29-JAN-2001
DEFINITION Homo sapiens p53 protein mRNA, complete cds.
ACCESSION AF307851
VERSION AF307851.1 GI:11066969
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA
FEATURES Location/Qualifiers

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- ☐ Coding Sequences

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- ☐ Clipboard
- ☐ Collections
- ☐ Analysis Tool

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Articles about the TP53 gene

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[See all...](#)

Pathways for the TP53 gene

Regulation of TP53 Activity through Acetylation

Regulation of TP53 Activity through Methylation

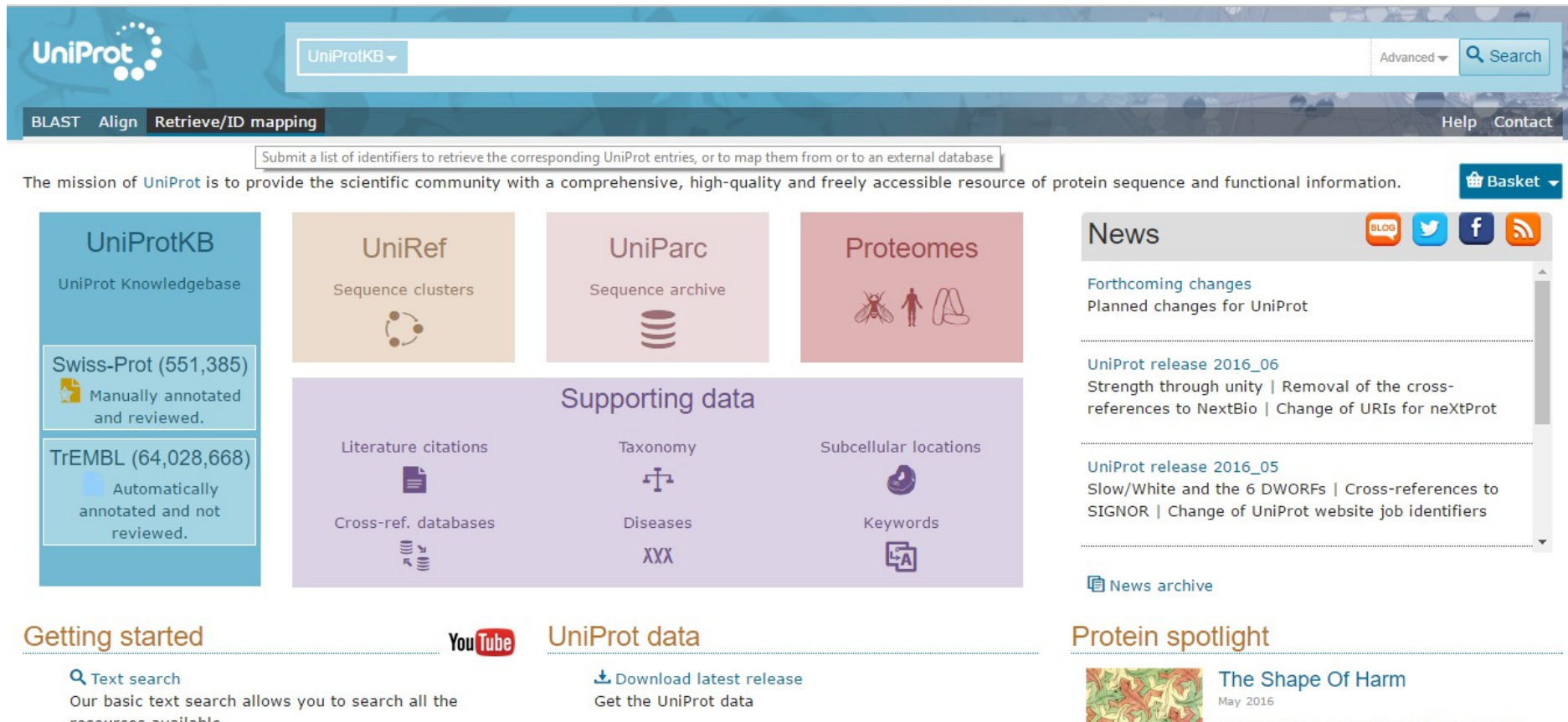
Other Database

- **SWISSPROT/UNIPROT ():** original DB developed in Switzerland.
 - It is a central access point for extensive curated protein information, including function, classification, and cross-reference.
 - It is manually annotated and is reviewed.
 - It provides entry flat-file differing from EMBL mainly about the features that describe the presence of aa modified, peptide regions corresponding to isoforms, structural domains and sites of polymorphisms.
 - Together with TrEMBL, it is part of the UNIPROT database. TrEMBL contains the translation of all the coding sequence contained in the EMBL database not yet integrated in Swiss-Prot. TrEMBL entries are automatically annotated by computer softwares.

UNIPROT - <http://www.uniprot.org>



UNIPROT - <http://www.uniprot.org>



The screenshot shows the UniProt website homepage. At the top is the UniProt logo and a search bar with a dropdown menu set to 'UniProtKB'. Below the search bar is a navigation bar with links for 'BLAST', 'Align', 'Retrieve/ID mapping', 'Help', and 'Contact'. A mission statement is displayed: 'The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.' The main content area is divided into several sections: 'UniProtKB' (UniProt Knowledgebase) with links to 'Swiss-Prot (551,385)' and 'TrEMBL (64,028,668)'; 'UniRef' (Sequence clusters); 'UniParc' (Sequence archive); 'Proteomes'; and 'Supporting data' which includes 'Literature citations', 'Taxonomy', 'Subcellular locations', 'Cross-ref. databases', 'Diseases', and 'Keywords'. On the right side, there is a 'News' section with links to 'Forthcoming changes', 'UniProt release 2016_06', and 'UniProt release 2016_05'. At the bottom, there are three sections: 'Getting started' with a 'Text search' link, 'UniProt data' with a 'Download latest release' link, and 'Protein spotlight' featuring 'The Shape Of Harm'.

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BLAST Align Retrieve/ID mapping Help Contact

Submit a list of identifiers to retrieve the corresponding UniProt entries, or to map them from or to an external database

The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information. [Basket](#)

UniProtKB
UniProt Knowledgebase

Swiss-Prot (551,385)
Manually annotated and reviewed.

TrEMBL (64,028,668)
Automatically annotated and not reviewed.

UniRef
Sequence clusters

UniParc
Sequence archive

Proteomes

Supporting data

Literature citations
Cross-ref. databases

Taxonomy
Diseases
XXX

Subcellular locations
Keywords

News

[Forthcoming changes](#)
Planned changes for UniProt

[UniProt release 2016_06](#)
Strength through unity | Removal of the cross-references to NextBio | Change of URIs for nextProt

[UniProt release 2016_05](#)
Slow/White and the 6 DWORFs | Cross-references to SIGNOR | Change of UniProt website job identifiers

[News archive](#)

Getting started

[Text search](#)
Our basic text search allows you to search all the resources available

UniProt data

[Download latest release](#)
Get the UniProt data

Protein spotlight

[The Shape Of Harm](#)
May 2016

UNIPROT - <http://www.uniprot.org>



UniProtKB ▾ P53

x Advanced ▾

 Search

BLAST Align Retrieve/ID mapping

Help Contact

Retrieve/ID mapping

How to use this tool

Enter or upload a list of identifiers to do one of the following:

Retrieve the corresponding UniProt entries to download them or work with them on this website.

Convert identifiers which are of a different type to UniProt identifiers or vice versa and download the identifier lists.

1. Enter identifiers, separated by a space or a new line, into the form field, for example:

P31946 P62258

ALBU_HUMAN

EFTU_ECOLI

2. If you need to convert to another identifier type, select the source and target type from the dropdown menus.

3. Click the Go button.

 Help

 Help video

 Other tutorials and videos

 Downloads

1. Provide your identifiers

e.g. P31946 P62258 ALBU_HUMAN EFTU_ECOLI

OR upload your own file: Nessun file selezionato

UNIPROT - <http://www.uniprot.org>

UniProt

UniProtKB p53

Advanced Search

BLAST Align Retrieve/ID mapping Help Contact

UniProtKB results

About UniProtKB Basket

Filter by

Reviewed (2,092) Swiss-Prot

Unreviewed (23,712) TrEMBL

Popular organisms

Human (1,144)

Mouse (709)

Rat (367)

Zebrafish (317)

Bovine (307)

Other organisms

Go

Search terms

Filter "p53" as:

1 to 25 of 25,804 Show 25

BLAST Align Download Add to basket Columns

Entry	Entry name	Protein names	Gene names	Organism	Length
P04637	P53_HUMAN	Cellular tumor antigen p53	TP53 P53	Homo sapiens (Human)	393
P02340	P53_MOUSE	Cellular tumor antigen p53	Tp53 P53,Trp53	Mus musculus (Mouse)	387
Q00987	MDM2_HUMAN	E3 ubiquitin-protein ligase Mdm2	MDM2	Homo sapiens (Human)	491
Q9N6D8	Q9N6D8_DROME	GH11591p	p53 prac,CG33336,Dmel_CG33336	Drosophila melanogaster (Fruit fly)	385
P10361	P53_RAT	Cellular tumor antigen p53	Tp53 P53	Rattus norvegicus (Rat)	391
Q9TUB2	P53_PIG	Cellular tumor antigen p53	TP53 P53	Sus scrofa (Pig)	386
Q8IMZ4	Q8IMZ4_DROME	P53 protein long form variant 1	p53 CG33336,Dmel_CG33336	Drosophila melanogaster (Fruit fly)	495
P56424	P53_MACMU	Cellular tumor antigen p53	TP53 P53	Macaca mulatta (Rhesus macaque)	393
O15350	P73_HUMAN	Tumor protein p73	TP73 P73	Homo sapiens (Human)	636

UNIPROT - <http://www.uniprot.org>

UniProtKB - P04637 (P53_HUMAN)

Display

Entry

Feature viewer

Feature table

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequences (9)

Gene references

BLAST Align Format Add to basket History

Protein Cellular tumor antigen p53

Gene TP53

Organism *Homo sapiens (Human)* ← The Organism

Status Reviewed - Annotation score: Experimental evidence at protein levelⁱ

Functionⁱ

Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression. In cooperation with mitochondrial PPIF is involved in activating oxidative stress-induced necrosis; the function is largely independent of transcription. Induces the transcription of long intergenic non-coding RNA p21 (lincRNA-p21) and lincRNA-Mkn1. LincRNA-p21 participates in TP53-dependent transcriptional repression leading to apoptosis and seem to have to effect on cell-cycle regulation. Implicated in Notch signaling cross-over. Prevents CDK7 kinase activity when associated to CAK complex in response to DNA damage, thus stopping cell cycle progression. Isoform 2 enhances the transactivation activity of isoform 1 from some but not all TP53-inducible promoters. Isoform 4 suppresses transactivation activity and impairs growth suppression mediated by isoform 1. Isoform 7 inhibits isoform 1-mediated apoptosis. Regulates the circadian clock by repressing CLOCK-ARNTL/BMAL1-mediated transcriptional activation of PER2 (PubMed:24051492).

12 Publications

Cofactorⁱ

Zn²⁺

Note: Binds 1 zinc ion per subunit.

UNIPROT - <http://www.uniprot.org>

Display

[Entry](#)[Feature viewer](#)[Feature table](#)

None

- ☒ Function
- ☒ Names & Taxonomy
- ☒ Subcellular location
- ☒ Pathology & Biotech
- ☒ PTM / Processing
- ☒ Expression
- ☒ Interaction
- ☒ Structure
- ☒ Family & Domains
- ☒ Sequences (9)
- ☒ Cross-references
- ☒ Publications
- ☒ Entry information
- ☒ Miscellaneous
- ☒ Similar proteins

[Top](#)

Sequences (9)ⁱ

Sequence statusⁱ: Complete.This entry describes 9 isoformsⁱ produced by **alternative promoter usage** and **alternative splicing**.[Align](#)[Add to basket](#)**Isoform 1** (identifier: **P04637-1**) [UniParc][FASTA](#)[Add to basket](#)*Also known as:* p53, p53alpha*This isoform has been chosen as the 'canonical' sequence. All positional information in this entry refers to it. This is also the sequence that appears in the downloadable versions of the entry.*[« Hide](#)**Length:** 393**Mass (Da):** 43,653**Last modified:** November 24, 2009 - v4**Checksum:**ⁱ AD5C149FD8106131

BLAST

[GO](#)

10	20	30	40	50
MEEPQSDPSV	EPPLSQETFS	DLWKLLPENN	VLSPLPSQAM	DDLMLSPDDI
60	70	80	90	100
EQWFTEDPGP	DEAPRMPEAA	PPVAPAPAAP	TPAAPAPAPS	WPLSSSVPSQ
110	120	130	140	150
KTYQGSYGFR	LGFLHSGTAK	SVTCTYSPAL	NKMFCQLAKT	CPVQLWVDST
160	170	180	190	200
PPPGTRVRAM	AIYKQSQHMT	EVVRRCPHHE	RCSDSDGLAP	PQHILIRVEGN
210	220	230	240	250
LRVEYLDDRN	TFRHSVVVPY	EPPEVGSDCT	TIHYNMCNS	SCMGGMNRRP
260	270	280	290	300
ILTIITLED	SGNLLGRNSF	EVRVCACPGR	DRRTEENLR	KKGEPHHELP
310	320	330	340	350
PGSTKRALPN	NTSSSPQPKK	KPLDGEYFTL	QIRGRERFEM	FRELNEALEL
360	370	380	390	
KDAQAGKEPG	GSRAHSSHLK	SKKGQSTSRH	KKLMFKTEGP	DSD

UNIPROT - <http://www.uniprot.org>

The screenshot shows the UniProt website interface. At the top, there is a search bar with the UniProt logo and a dropdown menu for UniProtKB. Below the search bar, there are links for BLAST, Align, and Retrieve/ID mapping. The main header displays the entry name "UniProtKB - P04637 (P53_HUMAN)" and a "Basket" button. On the left side, there is a "Display" section with a list of features to be displayed, including Function, Names & Taxonomy, Subcellular location, Pathology & Biotech, PTM / Processing, Expression, Interaction, Structure, Family & Domains, Sequences (9), and Cross-references. The main content area shows the protein details for P53_HUMAN, including a "View format" dropdown menu with options like Text, FASTA (canonical), FASTA (canonical & isoform), XML, RDF/XML, and GFF. The "Function" section describes the protein's role as a tumor suppressor, involved in cell cycle regulation and apoptosis. The "Cofactor" section lists Zn²⁺ as a cofactor, and the "Sites" section is partially visible.

UniProt

UniProtKB

BLAST Align Retrieve/ID mapping

UniProtKB - P04637 (P53_HUMAN)

Display

Entry

Feature viewer

Feature table

Function

Names & Taxonomy

Subcellular location

Pathology & Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequences (9)

Cross-references

BLAST Align Format Add to basket History

View format

Text

FASTA (canonical)

FASTA (canonical & isoform)

XML

RDF/XML

GFF

Protein | Cellul

Gene | TP53

Organism | Homo

Status | Re

immental evidence at protein levelⁱ

Functionⁱ

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12 Publications

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Sites

UNIPROT - <http://www.uniprot.org>

```
>sp|P04637|P53_HUMAN Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4
MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDPGP
DEAPRMPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLLGFLHSGTAK
SVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHE
RCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNMCNS
SCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEENLRKKGEPHHELP
PGSTKRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG
GSRAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD
```

UNIPROT - <http://www.uniprot.org>

Display

Entry

Feature viewer

Feature table

None

- ☒ Function
- ☒ Names & Taxonomy
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- ☒ Structure
- ☒ Family & Domains
- ☒ Sequences (9)
- ☒ Cross-references
- ☒ Publications
- ☒ Entry information

▪ zinc ion binding  Source: UniProtKB

GO - Biological processⁱ

- base-excision repair  Source: UniProtKB
- cell aging  Source: UniProtKB
- cell cycle arrest  Source: UniProtKB
- cell differentiation  Source: UniProtKB
- cell proliferation  Source: UniProtKB
- cellular protein localization  Source: UniProtKB
- cellular response to DNA damage stimulus  Source: UniProtKB
- cellular response to drug  Source: UniProtKB
- cellular response to glucose starvation  Source: UniProtKB
- cellular response to hypoxia  Source: UniProtKB
- cellular response to ionizing radiation  Source: BHF-UCL
- cellular response to UV  Source: GO_Central
- chromatin assembly  Source: UniProtKB
- circadian behavior  Source: UniProtKB
- determination of adult lifespan  Source: BHF-UCL
- DNA damage response, signal transduction by p53 class mediator  Source: BHF-UCL
- DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest  Source: Reactome
- DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator  Source: BHF-UCL
- DNA strand renaturation  Source: UniProtKB
- entrainment of circadian clock by photoperiod  Source: UniProtKB

Ensembl Genome Browser



Genome Browsers

- It is an interactive website offering access to genome sequence data from a variety of vertebrate and invertebrate species and major model organisms, integrated with a large collection of aligned annotations. Two major genome browser exist; both resources use the same assembly but each annotates it using their own pipeline with different gene definitions.
- Ensembl: <http://www.ensembl.org/index.html>
- UCSC: <https://genome.ucsc.edu/>



Ensembl



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Search all species...



Search: for

e.g. **BRCA2** or **rat 5:62797383-63627669** or **rs699** or **coronary heart disease**

Browse a Genome

Ensembl is a genome browser for vertebrate genomes that supports research in comparative genomics, evolution, sequence variation and transcriptional regulation. Ensembl annotate genes, computes multiple alignments, predicts regulatory function and collects disease data. Ensembl tools include BLAST, BLAT, BioMart and the Variant Effect Predictor (VEP) for all supported species.

Favourite genomes



Human
GRCh38.p7



Human
GRCh37



Mouse
GRCm38.p5



Zebrafish
GRCz10

[Edit favourites](#)

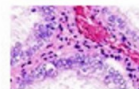
Still using Human GRCh37?



Variant Effect Predictor



Gene expression in different tissues



Find SNPs and other variants for my gene

GTTTATACATT
CTTAAAGTCTT
CTTCTAATT
GTAACATTTCC

Retrieve gene sequence

GCGTGACTTCGGGTTG
GGGCTTGTGGCGGAGC
GGGCTCTGCTGGGCT
AGGGGACAGATTGTG
CACCTCTGAGCGGT
CCCACTCCAGCGTGGC

Compare genes across species



What's New in Ensembl Release 87 (December 2016)

- **Chicken:** Gene set update
- **Mouse:** update to Ensembl-Havana GENCODE gene set
- **New dbSNP data for Sheep**
- **Zebrafish:** update to Ensembl-Havana merged gene set
- **New table on Regulation Summary page**

[Full details](#) | [All web updates, by release](#) | [More news on our blog](#)

- 24 Mar 2017: [Contacting the Ensembl Helpdesk? Let us know how to reach you.](#)
- 17 Feb 2017: [Free online course – mark II](#)
- 03 Feb 2017: [What's coming in Ensembl release 88](#)

[Go to Ensembl blog](#)

Tweets by @ensembl

catalogue of AS events in my, worm using #modENCODE data IDs corresponding

<https://www.youtube.com/watch?v=ZpnQOOxXufM>

Biomart

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 Search all species... 

[New](#) [Count](#) [Results](#)

[★ URL](#) [↔ XML](#) [📄 Perl](#) [? Help](#)

Dataset
[None selected]

- CHOOSE DATABASE - ▾

<https://www.youtube.com/watch?v=QvGT2G0-hYA>

