

Protein databases

Protein database:

The **Protein database** is a collection of sequences from several sources, including translations from annotated coding regions in GenBank, RefSeq and TPA, as well as records from SwissProt, PIR, PRF, and PDB.

Protein sequences are the fundamental determinants of biological structure and function.

▪ How to **retrieve protein sequence?**

The screenshot shows the NCBI Protein search results for 'TRF2'. The interface includes a search bar at the top with 'Protein' selected and 'TRF2' entered. A 'Species' filter is active on the left, showing a list of taxonomic groups. A 'Customize...' button is highlighted with a red box and the number 4. A 'Species' dialog box is open, showing a list of species with 'Homo sapiens' selected and highlighted with a red box and the number 7. The 'Add' button in this dialog is highlighted with a red box and the number 6. The main search results list shows 'telomeric repeat-binding factor 2 [Homo sapiens]' with a '542 aa protein' entry highlighted with a red box and the number 8. Other search results are visible but partially obscured.

■ Protein database interface

[telomeric repeat-binding factor 2 \[Homo sapiens\]](#)

2. **542 aa protein** a

Accession: NP_005643.2 GI: 429535832

[BioProject](#) [Nucleotide](#) [PubMed](#) [Taxonomy](#)

[GenPept](#) [Identical Proteins](#) [FASTA](#) [Graphics](#)

telomeric repeat-binding factor 2 [Homo sapiens]

NCBI Reference Sequence: NP_005643.2 a

[Identical Proteins](#) [FASTA](#) [Graphics](#)

Go to: ☺

LOCUS NP_005643 542 aa linear PRI 20-DEC-2020

DEFINITION telomeric repeat-binding factor 2 [Homo sapiens].

ACCESSION NP_005643

VERSION NP_005643.2

DBSOURCE REFSEQ: accession NM_005652.5

KEYWORDS RefSeq; MANE Select.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

FASTA ▾

telomeric repeat-binding factor 2 [Homo sapiens]

NCBI Reference Sequence: NP_005643.2

[GenPept](#) [Identical Proteins](#) [Graphics](#) b

>NP_005643.2 telomeric repeat-binding factor 2 [Homo sapiens]
 MAAGAGTAGPASGGVVRDPAASQPRKRPGREGGEGARRSDTMAGGGSSDGSRAAGRRASRSSGRARR
 GRHEPGLGGPAERGAEGEARLEEAVNRWLKIFYHEALRAFGRSRYGDFRQIRDIMQALLVRPLGKEHTVS
 RLLRVMQCLSRIEEGENDLCSFDMAEALTPLESAINVLEMIKTEFTLTEAVVSSRKLKVEAAVVICIKN
 KEFEKASKILKXHMMSKDPTTQKLRNDLLNIIREKNLAHPVIQNFYSYETFQKMLRFLESHLDDAEPYLLT
 MAKKALKSESAASSTGKEDKQAPAGPVEKPPREPARQLRNPPPTIGMNTLKAAFKTLGSAQDSEAFKAL
 DQKDLVLPQALPASPALKNRPRKDNESAPADGEGGSELQPKNKRMTISRVLVEEDSQSTEPSAGLN
 SSQEAASAPPSPKPTVNLNPLPGEKNPKVPKGMNNSNGVEEKETWVEEDELQVQAAPDEDSTNITKQK
 KWTVEESEWVKAGVQYGEENMAAISKNYFVNRATAVMIKDRWRTMKRLGMN

Summary: This gene encodes a telomere specific protein, TERF2, which is a component of the telomere nucleoprotein complex. This protein is present at telomeres in metaphase of the cell cycle, is a second negative regulator of telomere length and plays a key role in the protective activity of telomeres. While having similar telomere binding activity and domain organization, TERF2 differs from TERF1 in that its N terminus is basic rather than acidic. [provided by RefSeq, Jul 2008].

Region 87..286

[/region_name="TRFH"](#)

[/note="Telomeric Repeat binding Factor or TTAGGG Repeat binding Factor, central \(dimerization\) domain Homology; TRFH. Telomeres are protein/DNA complexes that make up the physical ends of eukaryotic linear chromosomes and are essential for chromosome stability; cd00200"](#)

[/db_xref="CDD:238174"](#)

Region 318..358

[/region_name="TERF2_RBM"](#)

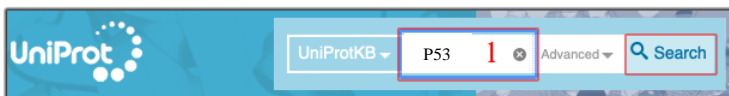
[/note="Telomeric repeat-binding factor 2 Rap1-binding motif; pfam16772"](#)

[/db_xref="CDD:293377"](#)

UniProt:

UniProt is the world's leading high-quality, comprehensive and freely accessible resource of protein sequence and functional information.

■ How to retrieve protein entry using UniProt?



<input type="checkbox"/> P04637	P53_HUMAN	Cellular tumor antigen p53[...]	TP53, P53	2	Homo sapiens (Human)	393 AA
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■ Protein **nomenclature** and **3D structure**

Function

Names & Taxonomy **a**

Subcellular Location

Names & Taxonomyⁱ

Protein namesⁱ **a**

Recommended name	Cellular tumor antigen p53
Alternative names	Antigen NY-CO-13 Phosphoprotein p53 Tumor suppressor p53

Gene namesⁱ

Name	TP53
Synonyms	P53

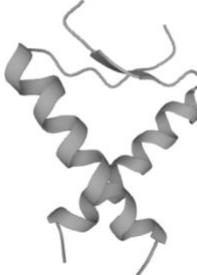
Expression

Interaction

Structure **b**

Structureⁱ

b



■ Protein **Function**

Function

Names & Taxonomy

Subcellular Location

Functionⁱ

Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type (PubMed:[11025664](#), PubMed:[12524540](#), PubMed:[12810724](#), PubMed:[15186775](#), PubMed:[15340061](#), PubMed:[17317671](#), PubMed:[17349958](#), PubMed:[19556538](#), PubMed:[20673990](#), PubMed:[20959462](#), PubMed:[22726440](#), PubMed:[24051492](#), PubMed:[9840937](#), PubMed:[24652652](#)).

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 (PubMed:[11025664](#), PubMed:[12524540](#), PubMed:[12810724](#), PubMed:[15186775](#), PubMed:[15340061](#), PubMed:[17317671](#), PubMed:[17349958](#), PubMed:[19556538](#), PubMed:[20673990](#), PubMed:[20959462](#), PubMed:[22726440](#), PubMed:[24051492](#), PubMed:[9840937](#), PubMed:[24652652](#)).

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. Its pro-apoptotic activity is activated via its interaction with PPP1R13B/ASPP1 or TP53BP2/ASPP2 (PubMed:[12524540](#)).

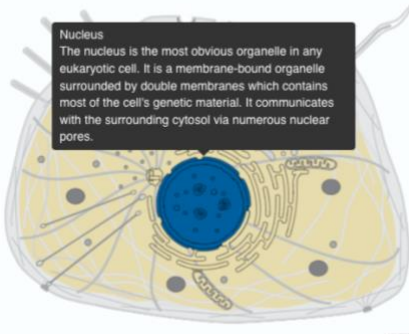
▪ Protein subcellular localization

Subcellular Location

Disease & Variants

PTM/Processing

UniProt Annotation GO Annotation



- Cytoplasm 5 Publications
- Nucleus 6 Publications**
- Nucleus, PML body 2 Publications
- Endoplasmic reticulum 1 Publication
- Mitochondrion matrix 3 Publications
- Cytoplasm, cytoskeleton, microtubule organizing center, centrosome 1 Publication

Note: Recruited into PML bodies together with CHEK2 (PubMed:12810724).
Translocates to mitochondria upon oxidative stress (PubMed:22726440).
Translocates to mitochondria in response to mitomycin C treatment (PubMed:27323408).

Isoform 1

- Nucleus 1 Publication
- Cytoplasm

▪ Protein quaternary structure

Expression

Interaction

Structure

Interactionⁱ

Subunitⁱ

Forms **homodimers and homotetramers** (PubMed:19011621).

▪ Protein Cofactor

Function

Names & Taxonomy

Subcellular Location

Cofactorⁱ

Protein has 1 cofactor binding site:

Zn²⁺ (UniProtKB | Rhea | CHEBI:29105) 7 Publications

Note: Binds 1 zinc ion per subunit. 7 Publications

▪ Different biological processes and pathway protein is involved in

Function 1

Names & Taxonomy

Subcellular Location

GO annotationsⁱ

Slimming set: 2

generic

a. Biological processes

ASPECT	TERM
Biological Process	autophagy Source:CAFA 1 Publication
Biological Process	B cell lineage commitment Source:Ensembl
Biological Process	bone marrow development Source:UniProtKB 1 Publication
Biological Process	cardiac muscle cell apoptotic process Source:Ensembl
Biological Process	cardiac septum morphogenesis Source:Ensembl

b. Biological pathways

Enzyme and pathway databases

PathwayCommons | [P04637](#)

Reactome

- [R-HSA-111448](#) Activation of NOXA and translocation to mitochondria
- [R-HSA-139915](#) Activation of PUMA and translocation to mitochondria
- [R-HSA-1912408](#) Pre-NOTCH Transcription and Translation
- [R-HSA-2559580](#) Oxidative Stress Induced Senescence
- [R-HSA-2559584](#) Formation of Senescence-Associated Heterochromatin Foci (SAHF)

- **Disease and variants** associated with a protein

Subcellular Location
Disease & Variants
PTM/Processing

a. Diseases associated

Disease & Variants¹

Involvement in disease¹

No disease ID

Note TP53 is found in increased amounts in a wide variety of transformed cells. TP53 is frequently mutated or inactivated in about 60% of cancers. TP53 defects are found in Barrett metaplasia a condition in which the normally stratified squamous epithelium of the lower esophagus is replaced by a metaplastic columnar epithelium. The condition develops as a complication in approximately 10% of patients with chronic gastroesophageal reflux disease and predisposes to the development of esophageal adenocarcinoma

Esophageal cancer (ESCR)

Note The disease is caused by variants affecting the gene represented in this entry

Description A malignancy of the esophagus. The most common types are esophageal squamous cell carcinoma and adenocarcinoma. Cancer of the esophagus remains a devastating disease because it is usually not detected until it has progressed to an advanced incurable stage.

See also MIM:133239 [↗](#)

a. Variants (*polymorphism/mutations*) associated

Features

Showing features for natural variant¹, mutagenesis¹.

TYPE	ID	POSITION(S)	DESCRIPTION
▶ Natural variant	VAR_044547	11	in sporadic cancers; somatic mutation; dbSNP: rs201382018 ↗
▶ Natural variant	VAR_044548	11	in sporadic cancers; somatic mutation; dbSNP: rs201382018 ↗
▶ Natural variant	VAR_044549	15	in a sporadic cancer; somatic mutation
▶ Mutagenesis		15	Loss of interaction with PPP2R5C, PPP2CAANDPPP2R1A. 1 Publication
▶ Natural variant	VAR_044550	16	in a sporadic cancer; somatic mutation
▶ Natural variant	VAR_044551	17	in a sporadic cancer; somatic mutation

▪ **Post-transnactional modification** associated with a protein

<p>Subcellular Location</p> <p>Disease & Variants</p> <p>IPTM/Processing</p> <p>Expression</p> <p>Interaction</p> <p>Structure</p>	<p>Post-translational modification¹</p> <p>Acetylation of Lys-382 by CREBBP enhances transcriptional activity PubMed:10656795, PubMed:15448695, PubMed:20228809, PubMed:23431171).</p> <p>Acetylation of Lys-382 by EP300 (PubMed:10656795, PubMed:15448695, PubMed:20228809, PubMed:23431171).</p> <p>Deacetylation of Lys-382 by SIRT1 impairs its ability to induce proapoptotic program and modulate cell senescence (PubMed:10656795, PubMed:15448695, PubMed:20228809, PubMed:23431171).</p> <p>Deacetylation by SIRT2 impairs its ability to induce transcription activation in a AKT-dependent manner (PubMed:10656795, PubMed:15448695, PubMed:20228809, PubMed:23431171, PubMed:29681526).</p> <p>Acetylation at Lys-381 increases stability (PubMed:29474172).</p> <p>Deacetylation at Lys-381 by SIRT6 decreases its stability, thereby regulating cell senescence (PubMed:29474172). 6 Publications</p>
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PTM databases

GlyCosmos | [P04637](#) 1 site, 1 glycan

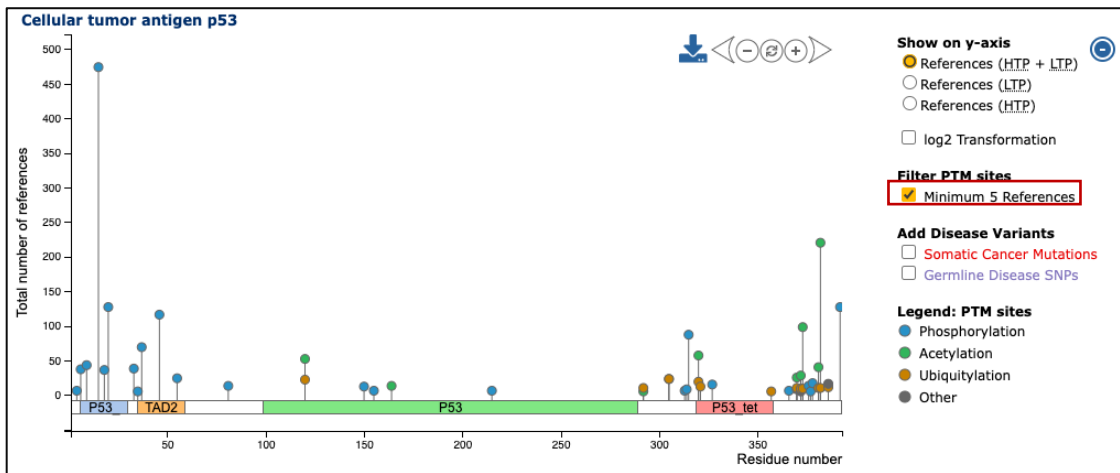
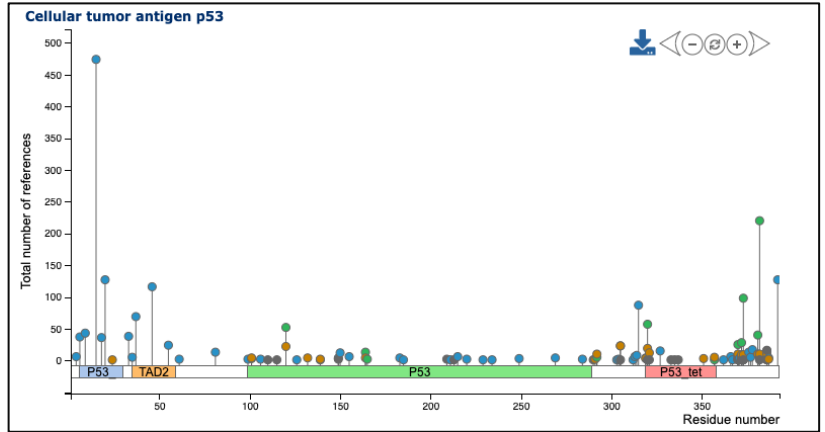
GlyGen | [P04637](#) 1 site, 1 O-linked glycan (1 site)

MetOSite | [P04637](#)

PhosphoSitePlus | [P04637](#)

SwissPalm | [P04637](#)

iPTMnet | [P04637](#)



Protein tissue specific expression

PTM/Processing
Expression
 Interaction

Expression¹

Tissue specificity¹

Ubiquitous. Isoforms are expressed in a wide range of normal tissues but in a tissue-dependent manner. Isoform 2 is expressed in most normal tissues but is not detected in brain, lung, prostate, muscle, fetal brain, spinal cord and fetal liver. Isoform 3 is expressed in most normal tissues but is not detected in lung, spleen, testis, fetal brain, spinal cord and fetal liver. Isoform 7 is expressed in most normal tissues but is not detected in prostate, uterus, skeletal muscle and breast. Isoform 8 is detected only in colon, bone marrow, testis, fetal brain and intestine. Isoform 9 is expressed in most normal tissues but is not detected in brain, heart, lung, fetal liver, salivary gland, breast or intestine. [1 Publication](#)

Induction¹

Up-regulated in response to DNA damage. Isoform 2 is not induced in tumor cells in response to stress. [2 Publications](#)

Gene expression databases

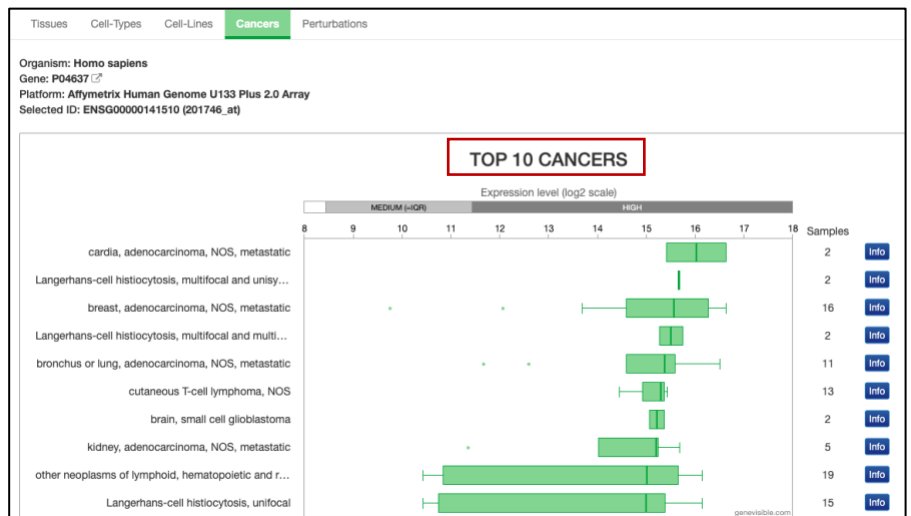
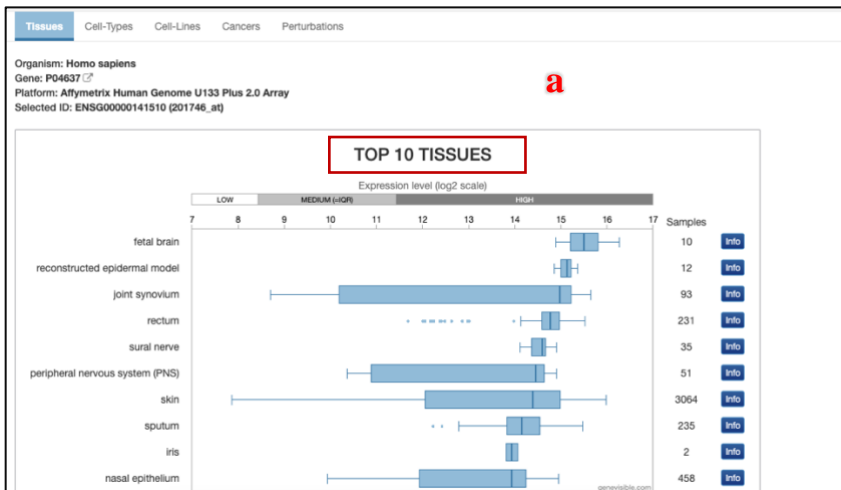
[Bgee](#) | [ENSG00000141510](#) Expressed in ventricular zone and 142 other tissues








[ExpressionAtlas](#) | [P04637](#) baseline and differential


[Genevisible](#) | [P04637](#) HS **a**

Organism-specific databases

[HPA](#) | [ENSG00000141510](#) Low tissue specificity **b**


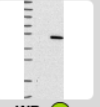







b TP53       

PROTEIN SUMMARY
SECTION OVERVIEW
GENE INFORMATION
RNA DATA
ANTIBODY DATA 

Antibody HPA051244

ANTIBODY INFORMATION

Provider	Atlas Antibodies Sigma-Aldrich
Product name	HPA051244
Host species	Rabbit
Clonality ¹	pAb
Concentration	0.1545 mg/ml
Purity	Affinity purified using the PrEST-antigen as affinity ligand
Released in version ¹	12.0
References ¹	
Proper citation	Atlas Antibodies Cat#HPA051244, RRID:AB_2681403
Validation summary ¹	   



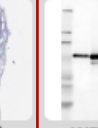

ICC  IHC  WB  PA 




Antibody CAB002973



Agilent (Formerly DakoCytomation)

M7001
Mouse
mAb
Not known
Not known
1.2

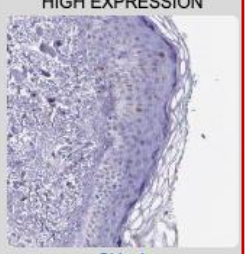
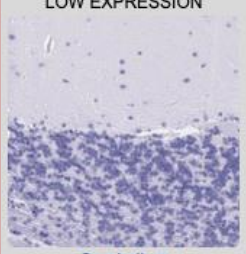
Agilent Cat#M7001, RRID:AB_2206626

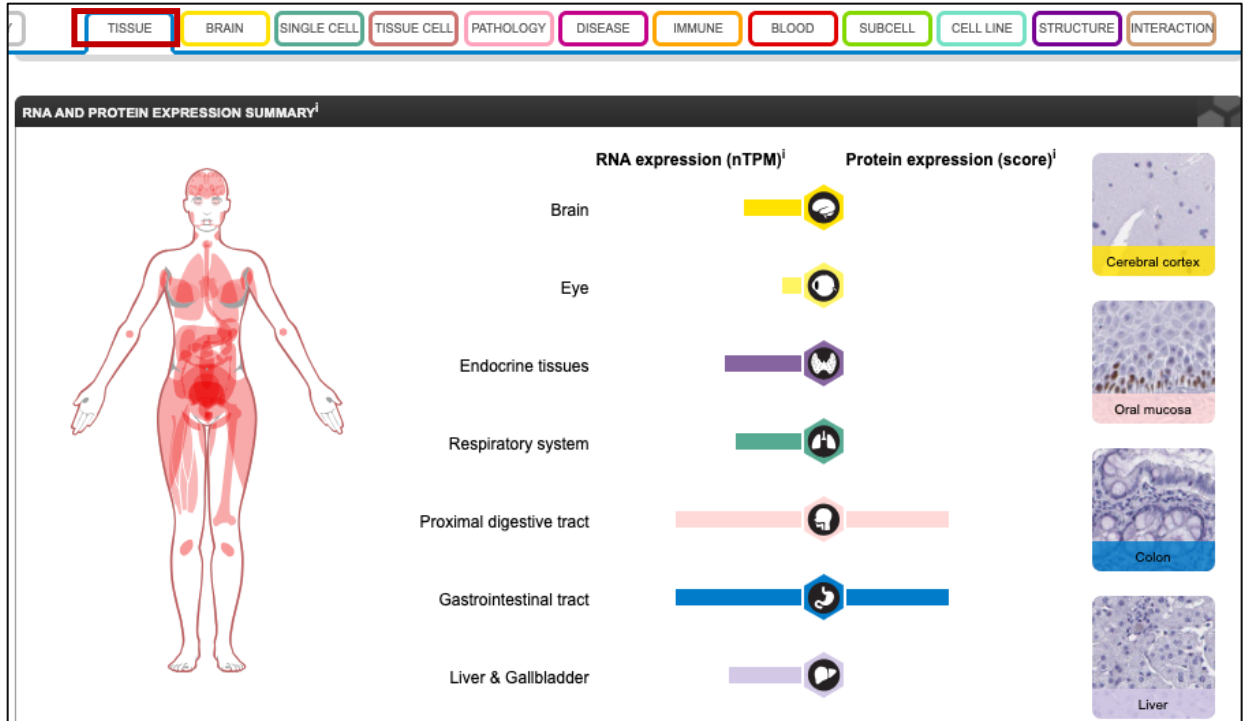
   

ICC  IHC  WB  PA 

 Enhanced - Orthogonal 

Antibody staining mainly consistent with RNA expression data across 45 tissues.

HIGH EXPRESSION	LOW EXPRESSION
	
Skin 1 RNA expression: 36.4 nTPM	Cerebellum RNA expression: 2.4 nTPM



■ Protein interactions

Expression

Interaction

Structure

Protein-protein interaction databases

a **BioGRID** | 113010 [↗](#) 2269 interactors

CORUM | P04637 [↗](#)

b **ComplexPortal** | **CPX-6093** [↗](#) p53-MDM2-MDM4 transcriptional regulation complex

CPX-663 [↗](#) p53-MDM4 transcriptional regulation complex

CPX-759 [↗](#) p53-MDM2 transcriptional regulation complex

Participants

Legend	Description	Stoichiometry
●	protein - TP53 (unspecified role) P04637 ↗ Cellular tumor antigen p53	
●	protein - MDM2 (enzyme) Q00987 ↗ E3 ubiquitin-protein ligase Mdm2	
●	protein - MDM4 (unspecified role) O15151 ↗ Protein Mdm4	

TP53

BCC7, LFS1, P53, TRP53
tumor protein p53

Glioblastoma Project

GO Process (61) | GO Function (25) | GO Component (14)

CRISPR Database [↗](#) | HGNC [↗](#) | Alliance of Genome Resources [↗](#) | OMIM [↗](#) | VEGA [↗](#)
 Entrez Gene [↗](#) | RefSeq [↗](#) | UniprotKB [↗](#) | Ensembl [↗](#) | HPRD [↗](#)

[Download Curated Data for this Protein](#)

Interactor Statistics

Proteins/Genes	Chemicals	Publications
2,274	2	1,626

- Interactors w/ Physical (HTP) Evidence (1,161)
- Interactors w/ Physical (LTP) Evidence (580)
- Interactors w/ Genetic (HTP) Evidence (149)
- Interactors w/ Genetic (LTP) Evidence (131)
- Interactors w/ More than One Evidence Type (253)
- Chemical Interactors (2)

■ Protein motifs and domains

Switch View: **Interactors 2,276** | Interactions 5,407 | Chemical Interactions 2 | Network | PTM Sites 223

Showing 1 to 300 of 2,276 unique interactors

Interactor	Organism / Chemical Type	Aliases	Description	Evidence
MDM2	H. sapiens	HDMX, hdm2, ACTFS	MDM2 proto-oncogene, E3 ubiquitin protein ligase	13 549 1 View
EP300	H. sapiens	p300, RSTS2, KAT3B, RP1-85F18.1	E1A binding protein p300	1 96 1 View
MDM4	H. sapiens	MDMX, MRP1, HDMX, RP11-430C7.1	MDM4, p53 regulator	8 68 View
USP7	H. sapiens	TEF1, HAUSP	ubiquitin specific peptidase 7 (herpes virus-associated)	6 39 View
TP53	H. sapiens	P53, LFS1, BCC7, TRP53	tumor protein p53	6 28 View
CREBBP	H. sapiens	CBP, RSTS, KAT3A	CREB binding protein	1 32 1 View

Structure

Family & Domains

Sequence & Isoforms

Family & Domains¹

Features
Showing features for region¹, motif¹, compositional bias¹.

TYPE	ID	POSITION(S)	DESCRIPTION	BLAST	Add
▶ Region		1-44	Transcription activation (acidic)	BLAST	🔖 Add
▶ Region		1-83	Interaction with HRMT1L2 1 Publication	BLAST	🔖 Add
▶ Region		1-320	Interaction with CCAR2 1 Publication	BLAST	🔖 Add
▶ Motif		17-25	TAD1	BLAST	🔖 Add

▪ **Protein isoforms**

Family & Domains

Sequence & Isoforms

Similar Proteins

Sequence & Isoforms¹

Align 9 isoforms

This entry describes **9 isoforms** produced by **Alternative promoter usage & Alternative splicing**.