

# P38398 · BRCA1\_HUMAN

**Protein<sup>i</sup>****Breast cancer type 1 susceptibility protein****Amino acids**1863 ([go to sequence](#))**Gene<sup>i</sup>****BRCA1****Protein existence<sup>i</sup>**

Evidence at protein level

**Status<sup>i</sup>**

UniProtKB reviewed (Swiss-Prot)

**Annotation score<sup>i</sup>**

5/5

**Organism<sup>i</sup>****Homo sapiens (Human)**[Entry](#)[Variant viewer](#) 9,944[Feature viewer](#)[Genomic coordinates](#)[Publications](#)[Tools](#) ▾ [Download](#) [Add](#) [Community curated \(1\)](#) [Add a publication](#) [Entry feedback](#)

## Function<sup>i</sup>

E3 ubiquitin-protein ligase that specifically mediates the formation of 'Lys-6'-linked polyubiquitin chains and plays a central role in DNA repair by facilitating cellular responses to DNA damage

(PubMed:[10500182](#), PubMed:[12887909](#), PubMed:[12890688](#), PubMed:[14976165](#), PubMed:[16818604](#), PubMed:[17525340](#), PubMed:[19261748](#)).

It is unclear whether it also mediates the formation of other types of polyubiquitin chains (PubMed:[12890688](#)).

The BRCA1-BARD1 heterodimer coordinates a diverse range of cellular pathways such as DNA damage repair, ubiquitination and transcriptional regulation to maintain genomic stability

(PubMed:[12890688](#), PubMed:[14976165](#), PubMed:[20351172](#)).

Regulates centrosomal microtubule nucleation (PubMed:[18056443](#)).

Required for appropriate cell cycle arrests after ionizing irradiation in both the S-phase and the G2 phase of the cell cycle (PubMed:[10724175](#), PubMed:[11836499](#), PubMed:[12183412](#), PubMed:[19261748](#)).

Required for FANCD2 targeting to sites of DNA damage (PubMed:[12887909](#)).

Inhibits lipid synthesis by binding to inactive phosphorylated ACACA and preventing its dephosphorylation (PubMed:[16326698](#)).

Contributes to homologous recombination repair (HRR) via its direct interaction with PALB2, fine-tunes recombinational repair partly through its modulatory role in the PALB2-dependent loading of BRCA2-RAD51 repair machinery at DNA breaks (PubMed:[19369211](#)).

Component of the BRCA1-RBBP8 complex which regulates CHEK1 activation and controls cell cycle G2/M checkpoints on DNA damage via BRCA1-mediated ubiquitination of RBBP8 (PubMed:[16818604](#)).

Acts as a transcriptional activator (PubMed:[20160719](#)).  15 Publications

## ⚠ Caution

An article that concluded that AURKA-mediated phosphorylation of BRCA1 Ser-308 plays a role in the normal cell cycle G2/M transition was withdrawn due to data manipulation of flow cytometry data.

2 Publications

## Catalytic activity<sup>i</sup>

S-ubiquitinyl-[E2 ubiquitin-conjugating enzyme]-L-cysteine + [acceptor protein]-L-lysine = [E2 ubiquitin-conjugating enzyme]-L-cysteine + N<sub>6</sub>-ubiquitinyl-[acceptor protein]-L-lysine.

6 Publications

EC:2.3.2.27 ([UniProtKB](#) | [ENZYME](#) | [Rhea](#))

## Activity regulation<sup>i</sup>

The E3 ubiquitin-protein ligase activity is inhibited by phosphorylation by AURKA. Activity is increased by phosphatase treatment.

1 Publication

## Pathway<sup>i</sup>

Protein modification; protein ubiquitination.

## Gene Ontology<sup>i</sup>

[GO annotations](#)

[GO-CAM models](#) New

Gene Ontology (GO) annotations organized by slimming set.

| ASPECT             | TERM  | Source  |
|--------------------|---|---|
| Molecular Function | <a href="#">damaged DNA binding</a>                       | <small>Source:Ensembl</small>                   |
| Molecular Function | <a href="#">DNA binding</a>                               | <small>Source:Proteinc</small> 1 Publication    |
| Molecular Function | <a href="#">enzyme binding</a>                            | <small>Source:UniProtKB</small> 1 Publication   |
| Molecular Function | <a href="#">histone H2AK127 ubiquitin ligase activity</a> | <small>Source:ARUK-UCL</small><br>1 Publication |
| Molecular Function | <a href="#">histone H2AK129 ubiquitin ligase activity</a> | <small>Source:ARUK-UCL</small><br>1 Publication |
| Molecular Function | <a href="#">identical protein binding</a>                 | <small>Source:IntAct</small> 3 Publications     |
| Molecular          |   |   |

Expand table

[Access the complete set of GO annotations on QuickGO](#)

## PAN-GO

[P38398 ↗](#) 11 GO annotations based on evolutionary models

## Keywords<sup>i</sup>

### Molecular function

[#Activator](#)

[#DNA-binding](#)

[#Transferase](#)

### Biological process

[#Cell cycle](#)

[#DNA damage](#)

[#DNA recombination](#)

[#DNA repair](#)

[#Fatty acid biosynthesis](#)

[More keywords](#)

### Ligand

[#Metal-binding](#)

[#Zinc](#)

## Enzyme and pathway databases

### BRENDA

[2.3.2.27 ↗](#) 2681

### PathwayCommons

[P38398 ↗](#)

### Reactome

[R-HSA-1221632 ↗](#) Meiotic synapsis

[R-HSA-3108214 ↗](#) SUMOylation of DNA damage response and repair proteins

[R-HSA-5685938 ↗](#) HDR through Single Strand Annealing (SSA)

[R-HSA-5685942 ↗](#) HDR through Homologous Recombination (HRR)

[R-HSA-5689901 ↗](#) Metalloprotease DUBs

[More Reactome links](#)

### SIGNOR

[P38398 ↗](#)

### SignaLink

[P38398 ↗](#)

### UniPathway

[UPA00143](#)

### ENZYME

[Search... ↗](#)

## Protein family/group databases

### MoonProt

[P38398 ↗](#)

## Names & Taxonomy<sup>i</sup>

## Protein names<sup>i</sup>

### Recommended name

Breast cancer type 1 susceptibility protein

### EC number

EC:2.3.2.27 ([UniProtKB](#) | [ENZYME](#) | [Rhea](#))  6 Publications

### Alternative names

RING finger protein 53

RING-type E3 ubiquitin transferase BRCA1  Curated

## Gene names<sup>i</sup>

### Name

BRCA1

### Synonyms

RNF53

## Organism names

### Taxonomic identifier<sup>i</sup>

9606 ([NCBI](#))

### Organism<sup>i</sup>

**Homo sapiens (Human)**

### Taxonomic lineage<sup>i</sup>

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

## Accessions<sup>i</sup>

### Primary accession

P38398

### Secondary accessions

E9PFZ0

O15129

Q1RMC1

Q3LRJ0

Q3LRJ6

[More accessions](#)

## Proteomes<sup>i</sup>

### Identifier

[UP000005640](#)

### Component<sup>i</sup>

Chromosome 17

## Organism-specific databases

AGR

HGNC:1100 ↗

HGNC

HGNC:1100 ↗ BRCA1

MIM

113705 ↗ gene

114480 ↗ phenotype

167000 ↗ phenotype

604370 ↗ phenotype

614320 ↗ phenotype

617883 ↗ phenotype

VEuPathDB

HostDB:ENSG00000012048 ↗

neXtProt

NX\_P38398 ↗

## Subcellular Location<sup>i</sup>

UniProt Annotation

GO Annotation

Nucleus  6 Publications

Chromosome  3 Publications

Cytoplasm  1 Publication

Note: Localizes at sites of DNA damage at double-strand breaks (DSBs); recruitment to DNA damage sites is mediated by ABRAXAS1 and the BRCA1-A complex (PubMed:26778126).

Translocated to the cytoplasm during UV-induced apoptosis (PubMed:20160719).  2 Publications

## Isoform 3

Cytoplasm

## Isoform 5

Cytoplasm  1 Publication

## Keywords<sup>i</sup>

Cellular component

#Chromosome

#Cytoplasm

#Nucleus

## Disease & Variants<sup>i</sup>

### Involvement in disease<sup>i</sup>

Breast cancer (BC)

 22 Publications

## Note

Disease susceptibility is associated with variants affecting the gene represented in this entry. Mutations in BRCA1 are thought to be responsible for 45% of inherited breast cancer. Moreover, BRCA1 carriers have a 4-fold increased risk of colon cancer, whereas male carriers face a 3-fold increased risk of prostate cancer. Cells lacking BRCA1 show defects in DNA repair by homologous recombination

## Description

A common malignancy originating from breast epithelial tissue. Breast neoplasms can be distinguished by their histologic pattern. Invasive ductal carcinoma is by far the most common type. Breast cancer is etiologically and genetically heterogeneous. Important genetic factors have been indicated by familial occurrence and bilateral involvement. Mutations at more than one locus can be involved in different families or even in the same case.

## See also

MIM:[114480](#)

## Natural variants in BC

| VARIANT ID                 | POSITION(S) | CHANGE | DESCRIPTION  |
|----------------------------|-------------|--------|--|
| <a href="#">VAR_070458</a> | 4           | S>F    | in BC; uncertain significance;<br>dbSNP: <a href="#">rs786203152</a>                     |
| <a href="#">VAR_020679</a> | 10          | E>K    | in BC and BROVCA1  |
| <a href="#">VAR_063899</a> | 18          | M>T    | in BC; pathogenic; dbSNP: <a href="#">rs80356929</a>                                     |
| <a href="#">VAR_007756</a> | 22          | L>S    | in BC; dbSNP: <a href="#">rs80357438</a>   |
| <a href="#">VAR_020680</a> | 23          | E>K    | in BC and BROVCA1  |
| <a href="#">VAR_070459</a> | 45          | K>Q    | in BC; benign; functionally neutral in vitro;<br>dbSNP: <a href="#">rs769650474</a>      |
| <a href="#">VAR_007757</a> | 61          | C>G    | in BC and OC; pathogenic; no interaction with<br>BAP1; dbSNP: <a href="#">rs28897672</a> |
| <a href="#">VAR_007758</a> | 64          | C>G    | in BC; no interaction with BAP1;   |

[Expand table](#)

## Breast-ovarian cancer, familial, 1 (BROVCA1)

[6 Publications](#)

## Note

Disease susceptibility is associated with variants affecting the gene represented in this entry. Mutations in BRCA1 are thought to be responsible for more than 80% of inherited breast-ovarian cancer

## Description

A condition associated with familial predisposition to cancer of the breast and ovaries. Characteristic features in affected families are an early age of onset of breast cancer (often before age 50), increased chance of bilateral cancers (cancer that develop in both breasts, or both ovaries,

independently), frequent occurrence of breast cancer among men, increased incidence of tumors of other specific organs, such as the prostate.

## See also

MIM:[604370](#)

### Natural variants in BROVCA1

| VARIANT ID                 | POSITION(S) | CHANGE | DESCRIPTION   |
|----------------------------|-------------|--------|---|
| <a href="#">VAR_020679</a> | 10          | E>K    | in BC and BROVCA1 <span>1 Publication</span>  |
| <a href="#">VAR_020680</a> | 23          | E>K    | in BC and BROVCA1 <span>1 Publication</span>  |
| <a href="#">VAR_020684</a> | 835         | H>Y    | in BROVCA1; uncertain significance; dbSNP: <a href="#">rs751656678</a> <span>1 Publication</span> |
| <a href="#">VAR_007773</a> | 841         | R>W    | in BROVCA1; benign; dbSNP: <a href="#">rs1800709</a> <span>2 Publications</span>                  |
| <a href="#">VAR_020690</a> | 1187        | S>I    | in BC and BROVCA1 <span>1 Publication</span>  |
| <a href="#">VAR_020691</a> | 1200        | Q>H    | in BC and BROVCA1; benign; dbSNP: <a href="#">rs56214134</a> <span>1 Publication</span>           |
| <a href="#">VAR_020695</a> | 1217        | S>Y    | in BC and BROVCA1 <span>1 Publication</span>  |
| <a href="#">VAR_020696</a> | 1226        | F>L    | in BROVCA1 <span>1 Publication</span>   |
| <a href="#">VAR_020697</a> | 1243        | R>G    | in BROVCA1 <span>1 Publication</span>   |

[Expand table](#)

## Ovarian cancer (OC)

4 Publications

### Note

Disease susceptibility is associated with variants affecting the gene represented in this entry

### Description

The term ovarian cancer defines malignancies originating from ovarian tissue. Although many histologic types of ovarian tumors have been described, epithelial ovarian carcinoma is the most common form. Ovarian cancers are often asymptomatic and the recognized signs and symptoms, even of late-stage disease, are vague. Consequently, most patients are diagnosed with advanced disease.

## See also

MIM:[167000](#)

### Natural variants in OC

| VARIANT ID                 | POSITION(S) | CHANGE | DESCRIPTION  |
|----------------------------|-------------|--------|--|
| <a href="#">VAR_007757</a> | 61          | C>G    | in BC and OC; pathogenic; no interaction with BAP1; dbSNP: <a href="#">rs28897672</a> <span>7 Publications</span>                      |
| <a href="#">VAR_020699</a> | 1411        | M>T    | in BC and OC; uncertain significance; decreased interaction with PALB2; dbSNP: <a href="#">rs273900729</a> <span>3 Publications</span> |

| VARIANT ID | POSITION(S) | CHANGE | DESCRIPTION  |
|------------|-------------|--------|--|
| VAR_020702 | 1697        | C>R    | in OC; pathogenic; dbSNP: <a href="#">rs80356993</a> ↗<br>1 Publication  |
| VAR_075666 | 1699        | R>W    | in BC, OC and FANCS; impairs protein stability;<br>functionally impaired in vitro; dbSNP: <a href="#">rs55770810</a><br>↗ 5 Publications |
| VAR_079607 | 1780        | L>P    | in BC, BROVCA1 and OC; uncertain significance;<br>dbSNP: <a href="#">rs80357474</a> ↗<br>1 Publication                                   |

## Pancreatic cancer 4 (PNCA4)

1 Publication

### Note

Disease susceptibility is associated with variants affecting the gene represented in this entry

### Description

A malignant neoplasm of the pancreas. Tumors can arise from both the exocrine and endocrine portions of the pancreas, but 95% of them develop from the exocrine portion, including the ductal epithelium, acinar cells, connective tissue, and lymphatic tissue.

### See also

MIM:[614320](#) ↗

## Fanconi anemia, complementation group S (FANCS)

3 Publications

### Note

Disease susceptibility is associated with variants affecting the gene represented in this entry

### Description

A form of Fanconi anemia, a disorder affecting all bone marrow elements and resulting in anemia, leukopenia and thrombopenia. It is associated with cardiac, renal and limb malformations, dermal pigmentary changes, and a predisposition to the development of malignancies. At the cellular level it is associated with hypersensitivity to DNA-damaging agents, chromosomal instability (increased chromosome breakage) and defective DNA repair.

### See also

MIM:[617883](#) ↗

## Natural variants in FANCS

| VARIANT ID | POSITION(S) | CHANGE  | DESCRIPTION  |
|------------|-------------|---------|--|
| VAR_080693 | 903-1863    | missing | in FANCS<br>1 Publication  |
| VAR_075666 | 1699        | R>W     | in BC, OC and FANCS; impairs protein stability;<br>functionally impaired in vitro; dbSNP: <a href="#">rs55770810</a><br>↗ 5 Publications |
| VAR_070506 | 1736        | V>A     | in BC and FANCS; pathogenic; decreased<br>localization to DNA damage sites and reduced   |

## VARIANT ID POSITION(S) CHANGE DESCRIPTION

interaction with UIMC1/RAP80;

dbSNP:[rs45553935](#)

 2 Publications

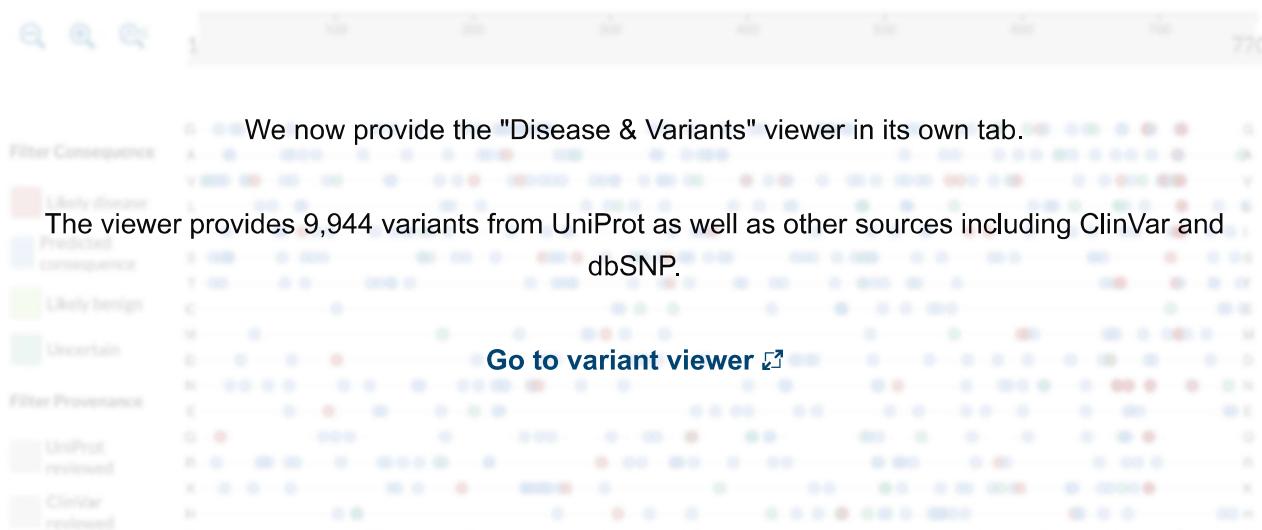
## Features

Showing features for natural variant<sup>i</sup>, mutagenesis<sup>i</sup>.

| TYPE |                 | ID                         | POSITION(S) | DESCRIPTION   |
|------|-----------------|----------------------------|-------------|---|
| ±    | All             |                            |             |   |
| +    | Natural variant | <a href="#">VAR_070458</a> | 4           | in BC; uncertain significance;<br>dbSNP: <a href="#">rs786203152</a>                                  |
| +    | Natural variant | <a href="#">VAR_020679</a> | 10          | in BC and BROVCA1   |
|      |                 |                            |             |  1 Publication       |
| +    | Natural variant | <a href="#">VAR_007754</a> | 11          | found in breast-ovarian cancer patients; uncertain significance;<br>dbSNP: <a href="#">rs80357017</a> |
|      |                 |                            |             |                    |

[Expand table](#)

## Variants



## Keywords<sup>i</sup>

Disease

#Disease variant

#Fanconi anemia

#Tumor suppressor

## Organism-specific databases

[DisGeNET](#)

672 ↗

[GeneReviews](#)

BRCA1 ↗

[MIM](#)

113705 ↗ gene

114480 ↗ phenotype

167000 ↗ phenotype

604370 ↗ phenotype

614320 ↗ phenotype

617883 ↗ phenotype

[MalaCards](#)

BRCA1 ↗

[OpenTargets](#)

ENSG0000012048 ↗

[Orphanet](#)

70567 ↗ Cholangiocarcinoma

1333 ↗ Familial pancreatic carcinoma

1331 ↗ Familial prostate cancer

84 ↗ Fanconi anemia

145 ↗ Hereditary breast and/or ovarian cancer syndrome

[More Orphanet links](#)

[PharmGKB](#)

PA25411 ↗

## Miscellaneous

[Pharos](#)

P38398 ↗ Tchem

## Chemistry

[ChEMBL](#)

CHEMBL5990 ↗

## Genetic variation databases

[BioMuta](#)

BRCA1 ↗

[ClinGen](#)

HGNC:1100 ↗

[DMDM](#)

728984 ↗

[GenCC](#)

HGNC:1100 ↗

## PTM/Processing<sup>i</sup>

### Features

Showing features for modified residue<sup>i</sup>, chain<sup>i</sup>, modified residue (large scale data)<sup>i</sup>, cross-link<sup>i</sup>.

| TYPE               | ID | POSITION(S) | SOURCE  |
|--------------------|----|-------------|---------|
| + ▾ All            |    |             | All     |
| + Modified residue | 1  |             | UniProt |

| TYPE    | ID             | SOURCE      |         |
|---------|----------------|-------------|---------|
|         |                | POSITION(S) |         |
| + Chain | PRO_0000055830 | 1-1863      | UniProt |

[Expand table](#)

## Post-translational modification<sup>i</sup>

Phosphorylated in response to IR, UV, and various stimuli that cause checkpoint activation, probably by ATM or ATR (PubMed:[11114888](#), PubMed:[12183412](#), PubMed:[21144835](#)).

Phosphorylation at Ser-988 by CHEK2 regulates mitotic spindle assembly (PubMed:[10724175](#),  
 ▲ PubMed:[20364141](#)).

Phosphorylation by AURKA regulates centrosomal microtubule nucleation (PubMed:[18056443](#)).

 6 Publications

Autoubiquitinated, undergoes 'Lys-6'-linked polyubiquitination. 'Lys-6'-linked polyubiquitination does not promote degradation.  2 Publications

## Keywords<sup>i</sup>

PTM

#Acetylation

#Isopeptide bond

#Phosphoprotein

#Ubl conjugation

## Proteomic databases

CPTAC

CPTAC-2610 ↗

CPTAC-2611 ↗

CPTAC-3218 ↗

CPTAC-3219 ↗

CPTAC-916 ↗

MassIVE

P38398 ↗

PaxDb

9606-ENSP00000418960 ↗

PeptideAtlas

P38398 ↗

ProteomicsDB

20208 ↗

55287 ↗ [P38398-1]

55288 ↗ [P38398-2]

55289 ↗ [P38398-3]

55290 ↗ [P38398-4]

[More ProteomicsDB links](#)

Pumba

P38398 ↗

jPOST

P38398 ↗

## PTM databases

## GlyConnect

2024 ↗ 1 N-Linked glycan (1 site)

## GlyCosmos

P38398 ↗ 1 site, 2 glycans

## GlyGen

P38398 ↗ 3 sites, 3 N-linked glycans (2 sites), 1 O-linked glycan (1 site)

## PhosphoSitePlus

P38398 ↗

## iPTMnet

P38398 ↗

# Expression<sup>i</sup>

## Tissue specificity<sup>i</sup>

Isoform **1** and isoform **3** are widely expressed. Isoform **3** is reduced or absent in several breast and ovarian cancer cell lines.

## Gene expression databases

### Bgee

ENSG00000012048 ↗ Expressed in ventricular zone and 135 other cell types or tissues

### ExpressionAtlas

P38398 ↗ baseline and differential

## Organism-specific databases

### HPA

ENSG00000012048 ↗ Low tissue specificity

# Interaction<sup>i</sup>

## Subunit<sup>i</sup>

Heterodimer with BARD1 (PubMed:[11573085](#), PubMed:[12890688](#), PubMed:[14976165](#)).

Part of the BRCA1-associated genome surveillance complex (BASC), which contains BRCA1, MSH2, MSH6, MLH1, ATM, BLM, PMS2 and the MRE11-RAD50-NBN protein (MRN) complex (PubMed:[10783165](#)).

This association could be a dynamic process changing throughout the cell cycle and within subnuclear domains (PubMed:[10783165](#)).

Component of the BRCA1-A complex, at least composed of BRCA1, BARD1, UIMC1/RAP80, ABRAKAS1, BRCC3/BRCC36, BABAM2 and BABAM1/NBA1 (PubMed:[19261746](#), PubMed:[19261748](#), PubMed:[19261749](#), PubMed:[20351172](#)).

Interacts (via the BRCT domains) with ABRAKAS1 (phosphorylated form); this is important for recruitment to sites of DNA damage (PubMed:[17525340](#), PubMed:[17643121](#), PubMed:[17643122](#), PubMed:[23269703](#), PubMed:[24316840](#), PubMed:[26778126](#)).

Can form a heterotetramer with two molecules of ABRAKAS1 (phosphorylated form) (PubMed:[26778126](#)).

Component of the BRCA1-RBBP8 complex (PubMed:[16101277](#)).

Interacts (via the BRCT domains) with RBBP8 ('Ser-327' phosphorylated form); the interaction

ubiquitinates RBBP8, regulates CHEK1 activation, and involves RBBP8 in BRCA1-dependent G2/M checkpoint control on DNA damage (PubMed:[16818604](#), PubMed:[9811458](#)).

Associates with RNA polymerase II holoenzyme (PubMed:[9662397](#)).

Interacts with SMC1A, NELFB, DCLRE1C, CLSPN (PubMed:[11739404](#), PubMed:[11877377](#), PubMed:[15096610](#), PubMed:[15456891](#)).

Interacts with CHEK1, CHEK2, BAP1, BRCC3, UBXN1 and PCLAF (PubMed:[10724175](#), PubMed:[11836499](#), PubMed:[14636569](#), PubMed:[20351172](#), PubMed:[21673012](#)).

Interacts (via BRCT domains) with BRIP1 (phosphorylated form) (PubMed:[11301010](#), PubMed:[15133502](#), PubMed:[21473589](#)).

Interacts with FANCD2 (ubiquitinated form) (PubMed:[11239454](#)).

Interacts with H2AX (phosphorylated on 'Ser-140') (PubMed:[12419185](#)).

Interacts (via the BRCT domains) with ACACA (phosphorylated form); the interaction prevents dephosphorylation of ACACA (PubMed:[12360400](#), PubMed:[16326698](#), PubMed:[16698035](#), PubMed:[18452305](#)).

Part of a BRCA complex containing BRCA1, BRCA2 and PALB2 (PubMed:[19369211](#)).

Interacts directly with PALB2; the interaction is essential for its function in HRR (PubMed:[19369211](#), PubMed:[28319063](#)).

Interacts directly with BRCA2; the interaction occurs only in the presence of PALB2 which serves as the bridging protein (PubMed:[19369211](#)).

Interacts (via the BRCT domains) with LMO4; the interaction represses the transcriptional activity of BRCA1 (PubMed:[11751867](#)).

Interacts (via the BRCT domains) with CCAR2 (via N-terminus); the interaction represses the transcriptional activator activity of BRCA1 (PubMed:[20160719](#)).

Interacts with EXD2 (PubMed:[26807646](#)).

Interacts (via C-terminus) with DHX9; this interaction is direct and links BRCA1 to the RNA polymerase II holoenzyme (PubMed:[9662397](#)).

Interacts with DNA helicase ZGRF1; the interaction is increased following DNA damage induction (PubMed:[34552057](#)).  43 Publications

## Binary interactions<sup>i</sup>



| TYPE   | ENTRY 1                | ENTRY 2                          | NUMBER OF EXPERIMENTS | INTACT  |
|--------|------------------------|----------------------------------|-----------------------|---|
| BINARY | <a href="#">P38398</a> | <b>ABRAXAS1</b><br><b>Q6UWZ7</b> | 16                    | <a href="#">EBI-349905</a> ,<br><a href="#">EBI-1263451</a> ↗ |
| BINARY | <a href="#">P38398</a> | <b>ACACA</b><br><b>Q13085</b>    | 2                     | <a href="#">EBI-349905</a> ,<br><a href="#">EBI-717681</a> ↗  |
| BINARY | <a href="#">P38398</a> | <b>BAP1</b> <b>Q92560</b>        | 3                     | <a href="#">EBI-349905</a> ,<br><a href="#">EBI-1791447</a> ↗ |
| BINARY | <a href="#">P38398</a> | <b>BARD1</b><br><b>Q99728</b>    | 19                    | <a href="#">EBI-349905</a> ,<br><a href="#">EBI-473181</a> ↗  |

| TYPE         | ENTRY 1 | ENTRY 2 | NUMBER OF EXPERIMENTS | INTACT |
|--------------|---------|---------|-----------------------|--------|
| Expand table |         |         |                       |        |

## Complex viewer<sup>i</sup>

Select complex

CPX-715 BRCA1-BARD1 complex



[View interactors in UniProtKB](#)

[View CPX-715 in Complex Portal](#)

## Protein-protein interaction databases

### BioGRID

[107140](#) 1284 interactors

### CORUM

[P38398](#)

### ComplexPortal

[CPX-715](#) BRCA1-BARD1 complex

[CPX-845](#) BRCA1-PALB2-BRCA2 homologous recombination DNA repair complex

[CPX-955](#) BRCC E3 ubiquitin ligase complex

### DIP

[DIP-5971N](#)

### FunCoup

[P38398](#) 1566 interactors

### IntAct

[P38398](#) 258 interactors

### MINT

[P38398](#)

### STRING

[9606.ENSP00000418960](#)

## Chemistry

### BindingDB

[P38398](#)

## Miscellaneous

### RNAAct

[P38398](#) protein

## Structure<sup>i</sup>



## 3D structure databases

[AlphaFoldDB](#)

[P38398 ↗](#)

[BMRB](#)

[P38398 ↗](#)

[EMDB](#)

[EMD-23591 ↗](#)

[EMD-34212 ↗](#)

[EMD-4344 ↗](#)

[EMD-6340 ↗](#)

[EMD-6400 ↗](#)

[SMR](#)

[P38398 ↗](#)

[ModBase](#)

[Search... ↗](#)

[PDBe-KB](#)

[Search... ↗](#)

## Miscellaneous

[EvolutionaryTrace](#)

[P38398 ↗](#)

## Family & Domains<sup>i</sup>

### Features

Showing features for zinc finger<sup>i</sup>, region<sup>i</sup>, compositional bias<sup>i</sup>, domain<sup>i</sup>.

| Type                 | ID      | Position(s)  | Description                         | Tools                  | Add                |
|----------------------|---------|--|-------------------------------------|------------------------|--------------------|
| + Zinc finger        | 24-65   | RING-type<br><small>PROSITE-ProRule Annotation</small>           | <small>Automatic Annotation</small> | <small>Tools</small> ↗ | <small>Add</small> |
| + Region             | 230-270 | Disordered   | <small>Automatic Annotation</small> | <small>Tools</small> ↗ | <small>Add</small> |
| + Compositional bias | 248-260 | Basic and acidic residues<br><small>Automatic Annotation</small> | <small>Automatic Annotation</small> | <small>Tools</small> ↗ | <small>Add</small> |
| + Region             | 306-338 | Disordered<br><small>Automatic Annotation</small>                | <small>Automatic Annotation</small> | <small>Tools</small> ↗ | <small>Add</small> |
|                      |         | Basic and acidic residues  |                                     | <small>Tools</small> ↗ |                    |

## Domain<sup>i</sup>

The BRCT domains recognize and bind phosphorylated pSXXF motif on proteins. The interaction with the phosphorylated pSXXF motif of ABRAKAS1, recruits BRCA1 at DNA damage sites.  1 Publication

The RING-type zinc finger domain interacts with BAP1.  1 Publication

## Keywords<sup>i</sup>

**Domain**

**#Repeat**

**#Zinc-finger**

## Phylogenomic databases

**GeneTree**

[ENSGT00440000034289](#) ↗

**HOGENOM**

[CLU\\_002290\\_0\\_0\\_1](#) ↗

**InParanoid**

[P38398](#) ↗

**OMA**

[ATCQQSP](#) ↗

**OrthoDB**

[6105938at2759](#) ↗

**PAN-GO**

[P38398](#) ↗ 11 GO annotations based on evolutionary models

**PhylomeDB**

[P38398](#) ↗

**eggNOG**

[KOG4362](#) ↗ Eukaryota

## Family and domain databases

 View all family and domain features for this entry's canonical sequence in the [UniParc Feature Viewer](#).

**CDD**

[cd17735](#) ↗ BRCT\_BRCA1\_rpt1 1 hit

[cd17721](#) ↗ BRCT\_BRCA1\_rpt2 1 hit

[cd16498](#) ↗ RING-HC\_BRCA1 1 hit

**IDEAL**

[IID00042](#) ↗

**InterPro**

[View protein in InterPro](#) ↗

[IPR011364](#) ↗ BRCA1

[IPR031099](#) ↗ BRCA1-associated

[IPR025994](#) ↗ BRCA1\_serine\_dom

[IPR001357](#) ↗ BRCT\_dom

[More InterPro links](#)

**PANTHER**

[PTHR13763:SF0](#) ↗ BREAST CANCER TYPE 1

SUSCEPTIBILITY PROTEIN 1 hit

[PTHR13763](#) ↗ BREAST CANCER TYPE 1

SUSCEPTIBILITY PROTEIN BRCA1 1 hit

**Gene3D**

[3.40.50.10190](#) ↗ BRCT domain 2 hits

[3.30.40.10](#) ↗ Zinc/RING finger domain, C3HC4 (zinc finger) 1 hit

**PIRSF**

**PIRSF001734** ↗ BRCA1 1 hit

**PRINTS**

**PR00493** ↗ BRSTCANCERI

**PROSITE**

**View protein in PROSITE** ↗

**PS50172** ↗ BRCT 2 hits

**PS00518** ↗ ZF\_RING\_1 1 hit

**PS50089** ↗ ZF\_RING\_2 1 hit

**Pfam**

**View protein in Pfam** ↗

**PF00533** ↗ BRCT 2 hits

**PF12820** ↗ BRCT\_assoc 1 hit

**PF00097** ↗ zf-C3HC4 1 hit

**SMART**

**View protein in SMART** ↗

**SM00292** ↗ BRCT 2 hits

**SM00184** ↗ RING 1 hit

**SUPFAM**

**SSF52113** ↗ BRCT domain 2 hits

**SSF57850** ↗ RING/U-box 1 hit

**MobiDB**

**Search...** ↗

# Sequence & Isoforms<sup>i</sup>

[Align isoforms \(8\)](#) [Add isoforms](#)

**Sequence status<sup>i</sup>**

Complete

This entry describes **8** isoforms<sup>i</sup> produced by **Alternative splicing & Alternative initiation**.

## P38398-1

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.

**Name**

1

**See also**

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

**Length**

1,863

**Mass (Da)**

207,721

**Last updated**

1995-02-01 v2

**MD5 Checksum<sup>i</sup>**

E40F752DEDF675E2F7C99142EBB2607A

MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITK  
RSLQESTRFSQLVEELLKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQ  
SEPNENPSLQETSLSVQLSNLGTVRTLRTKQRQPQKTSVYIELGSDSSEDTVNKATYCSVGDQELLQIT

PQGTRDEISLDSAKKAACEFSETDVTNTTEHHQPSNNDLNTTEKRAAERHPEKYQGSSVSNLHVEPCG  
TNTHASSLQHENSSLTLKDRMNVEKAECFCNKSQPGGLARSQHNRWAGSKETCNDRRTPSTEKKVD  
LNADPLCERKEWNKQKLPSENPRDTEDVPWITLNSSIQKVNEWFSRSDELLGSDDSHGESESNA  
KVADVLDVLNEVDEYSGSSEKIDLLASDPHEALICKSERVHSKSVESNIEDKIFGKTYRKASLPNLSHV  
TENLIIGAFVTEPQIIQERPLTNKLKRKRRPTSGLHPEDFIKKADLAVQKTPEMINQGTNQTEQNGQVM  
NITNSGHENKTGDSIQNEKNPNPIESLEKESAFTKAEPISSSISNMELELNIHNSKAPKKNRLRRKSS  
TRHIHALEVSVRNLSPPNCTELQIDSCSSSEEIKKKYNQMPVRHSRNLQLMEGKEPATGAKKSNP  
NEQTSKRHDSDTFPELKLTNAPGSFTKCSNTSELKEFVNPSLPRREEKEEKLETVKVSNNAEDPKDML  
SGERVLQTERSVESSISLVPGTDYGTQESISLEVSTLGAKTEPNKCVSQCAAFENPKGLIHGCSKD  
NRNDTEGFKYPLGHEVNHSRETSIEMEESELEDAQYLQNTFKVSKRQSAPFSNPGNAEEECATFSAH  
SGSLKKQSPKVTFCEQKEENQGKNESNIKPVQTVNITAGFPVGQDKPVDNAKCSIKGGSRFCLS  
SQFRGNETGLTPNKHGLLQNPyRIPPLFPIKSFVTKCKNLLEENFEEHSMSPEREMGNENIPSTVS  
TISRNNIRENVFKEASSSNINEVGSSSTNEVGSSINEIGSSDENIQAEGRNRGPKLNAMLR LGVLQPEV  
YKQSLPGSNCKHPEIKKQEYEEVVQTVNTDFSPYLISDNLEQPMGSSHASQVCSETPDDLDDGEIKE  
DTSFAENDIKESSAVFSKSVQKGELSRSRSPFTHTHLAQGYRRGAKKLESSEENLSSEDEELPCFQHL  
LFGKVNNIPSQSTRHSTVATECLSKNTEENLLSLKNSLDCSNQVILAKASQEHHLSEETKCSASFSS  
QCSELEDLTANTNTQDPFLIGSSKQMRHQSESQGVGLSDKELVSDDEERGTGLEENNQEEQSMDSN  
LGEAASGCESETS VSEDCSGLSSQSDILTQQRTDMQHNLIK LQQMAELEAVLEQHGSQPSNSYPSI  
ISDSSALEDLRNPEQSTSEKAVL TSQKSSE YPISQNPEGLSADKFEVSADSSTS KNKEPGVERSSPSK  
CP SLDDR WYM HSCSGSLQRNYP SQEELIK VVDVEEQQLE ESGPHDLTETSYLPRQDLEGTPYLES  
GISLF SDDPES D PSED RAP ESAR VGNIPS STSALK VPQL KVAESA QSPAAH TT TAGY NAME EES VSR  
EKPELTASTERVNKRMSMVSGLTPEEFMLVYKFARKHHITLTNLITEETTHVVMKTDAE FVCERTLKY  
FLGIAGGKWVVSYFWVTQSIKERKMLNEHDFEVRGDVNGRNHQGPKRARES QDRKIFR GLEICCY  
GPFTNMPTDQLEWMVQLCGASVVKELSSFTLGTGVHPIVVVQPDAWTEDNGFHAIGQMCEAPVVTR  
EWVLD SVALYQCQELDTY LIPQIPHSHY

## P38398-2

**Name**

2

**Note**

May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay.

Curated

**See also**

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

**Differences from canonical**

[64-1863](#): Missing 1 Publication

## P38398-3

**Name**

3

**Synonyms**

Delta11b

**See also**

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

**Differences from canonical**

[264-1366](#): Missing 2 Publications

[1453-1453](#): Missing 2 Publications

## P38398-4

**Name**

4

**Synonyms**

DeltaBRCA1(17aa)

**Note**

Produced by alternative initiation at Met-18 of isoform 1.

Curated

**See also**

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

**Differences from canonical**

**1-17:** Missing 

## P38398-5

**Name**

5

**Synonyms**

Delta11, Delta772-3095

**See also**

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

**Differences from canonical**

**224-1365:** Missing 

## P38398-6

**Name**

6

**See also**

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

**Differences from canonical**

**264-1366:** Missing 

**1453-1453:** Missing 

**1778-1863:**

DQLEWMVQLCGASVVKELSSFTLGTGVHPIVVVQPDAW  
TEDNGFHAIGQMCEAPVVTREWVLDSVALYQCQELDTY  
LIPQIPHSHY →  
GCPPNCGCAARCLDRGQWLPCNWADV 

## P38398-7

**Name**

7

**See also**

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

**Differences from canonical**

**1453-1453:** A → DSHIHGQRNNNSMFSKRPREHIS

 1 Publication

## P38398-8

**Name**

8

**Note**

The N-terminus is confirmed by several cDNAs.



**See also**

sequence in [UniParc](#) or sequence clusters in [UniRef](#)

**Differences from canonical**

**1-47:** Missing

## Computationally mapped potential isoform sequences<sup>i</sup>

There are 20 potential isoforms mapped to this entry

[Align](#)  [Add](#) [View all](#)

| <input type="checkbox"/> Entry                  | Entry name   | Gene name | Length |
|---|--|-----------|--------|
| <input type="checkbox"/> <a href="#">C9IZW4</a> |  C9IZW4_HUMAN | BRCA1     | 1567   |
| <input type="checkbox"/> <a href="#">G1UI37</a> |  G1UI37_HUMAN | BRCA1     | 23     |

| Entry   | Entry name       | Gene name | Length |
|---|------------------|-----------|--------|
| <input type="checkbox"/> <a href="#">A0A2R8Y7V5</a> | A0A2R8Y7V5_HUMAN | BRCA1     | 1885   |
| <input type="checkbox"/> <a href="#">A0A2R8Y6Y9</a> | A0A2R8Y6Y9_HUMAN | BRCA1     | 81     |
| <input type="checkbox"/> <a href="#">A0A0U1RRA9</a> | A0A0U1RRA9_HUMAN | BRCA1     | 1822   |
| <input type="checkbox"/> <a href="#">E7EWN5</a>     | E7EWN5_HUMAN     | BRCA1     | 649    |
| <input type="checkbox"/> <a href="#">E7EUM2</a>     | E7EUM2_HUMAN     | BRCA1     | 759    |
| <input type="checkbox"/> <a href="#">E7EQW4</a>     | E7EQW4_HUMAN     | BRCA1     | 1861   |
| <input type="checkbox"/> <a href="#">E9PC22</a>     | E9PC22_HUMAN     | BRCA1     | 59     |
| <input type="checkbox"/> <a href="#">Q3B891</a>     | Q3B891_HUMAN     | BRCA1     | 473    |
| <input type="checkbox"/> <a href="#">H0Y8D8</a>     | H0Y8D8_HUMAN     | BRCA1     | 1821   |
| <input type="checkbox"/> <a href="#">H0Y8B8</a>     | H0Y8B8_HUMAN     | BRCA1     | 717    |
| <input type="checkbox"/> <a href="#">H0Y850</a>     | H0Y850_HUMAN     | BRCA1     | 1862   |
| <input type="checkbox"/> <a href="#">A0A9Y1QPT7</a> | A0A9Y1QPT7_HUMAN | BRCA1     | 713    |
| <input type="checkbox"/> <a href="#">A0A8V8TPY7</a> | A0A8V8TPY7_HUMAN | BRCA1     | 544    |
| <input type="checkbox"/> <a href="#">C6YB45</a>     | C6YB45_HUMAN     | BRCA1     | 173    |
| <input type="checkbox"/> <a href="#">A0A494C182</a> | A0A494C182_HUMAN | BRCA1     | 601    |
| <input type="checkbox"/> <a href="#">K7EJW3</a>     | K7EJW3_HUMAN     | BRCA1     | 96     |
| <input type="checkbox"/> <a href="#">E7ENB7</a>     | E7ENB7_HUMAN     | BRCA1     | 1837   |
| <input type="checkbox"/> <a href="#">K7EPC7</a>     | K7EPC7_HUMAN     | BRCA1     | 354    |

## Sequence caution<sup>i</sup>

The sequence [AAB61673.1](#) differs from that shown. Reason: Erroneous translation Wrong choice of CDS. Curated

The sequence [AAI15038.1](#) differs from that shown. Reason: Erroneous initiation Truncated N-terminus. Curated

The sequence [AAI15038.1](#) differs from that shown. Reason: Erroneous termination Truncated C-terminus. Curated

## Features

Showing features for alternative sequence<sup>i</sup>, sequence conflict<sup>i</sup>, compositional bias<sup>i</sup>.

| Type                   | ID         | Position(s) | Description                    |  |
|------------------------|------------|-------------|--------------------------------|--|
| All                    |            |             |                                |  |
| + Alternative sequence | VSP_035396 | 1-17        | in isoform 4<br>Curated        | <a href="#">Tools</a><br><a href="#">Add</a> |
| + Alternative sequence | VSP_057569 | 1-47        | in isoform 8                   | <a href="#">Tools</a><br><a href="#">Add</a> |
| + Alternative sequence | VSP_047891 | 64-1863     | in isoform 2<br>1 Publication  | <a href="#">Tools</a><br><a href="#">Add</a> |
| + Sequence conflict    |            | 89          | in Ref. 4; AAB61673<br>Curated |  |
| + Sequence conflict    |            | 148         | in Ref. 4; AAB61673            |  |

[Expand table](#)

## Polymorphism<sup>i</sup>

There is evidence that the presence of the rare form of Gln-356-Arg and Leu-871-Pro polymorphisms may be associated with an increased risk for developing ovarian cancer.

## Keywords<sup>i</sup>

**Coding sequence diversity**

**#Alternative initiation**

**#Alternative splicing**

**Technical term**

**#3D-structure**

**#Direct protein sequencing**

**#Proteomics identification**

**#Reference proteome**

## Sequence databases

### CCDS

**CCDS11453.1** ↗ [P38398-1]

**CCDS11454.2** ↗ [P38398-3]

**CCDS11455.2** ↗ [P38398-6]

**CCDS11456.2** ↗ [P38398-7]

**CCDS11459.2** ↗ [P38398-8]

### PIR

**A58881** ↗ A58881

## RefSeq

NP\_001394512.1 ↗ NM\_001407583.1 ↗

[P38398-7]

NP\_001394514.1 ↗ NM\_001407585.1 ↗

[P38398-7]

NP\_001394522.1 ↗ NM\_001407593.1 ↗

[P38398-1]

NP\_001394523.1 ↗ NM\_001407594.1 ↗

[P38398-1]

NP\_001394525.1 ↗ NM\_001407596.1 ↗

[P38398-1]

[More RefSeq links](#)

| NUCLEOTIDE<br>SEQUENCE                      | PROTEIN SEQUENCE                              | MOLECULE<br>TYPE | STATUS                |
|---|---|------------------|-----------------------|
| U14680<br><br>EMBL ↗ · GenBank ↗ · DDBJ ↗   | AAA73985.1<br><br>EMBL ↗ · GenBank ↗ · DDBJ ↗ | mRNA             |                       |
| L78833<br><br>EMBL ↗ · GenBank ↗ · DDBJ ↗   | AAC37594.1<br><br>EMBL ↗ · GenBank ↗ · DDBJ ↗ | Genomic DNA      |                       |
| U64805<br><br>EMBL ↗ · GenBank ↗ · DDBJ ↗   | AAC00049.1<br><br>EMBL ↗ · GenBank ↗ · DDBJ ↗ | mRNA             |                       |
| AF005068<br><br>EMBL ↗ · GenBank ↗ · DDBJ ↗ | AAB61673.1<br><br>EMBL ↗ · GenBank ↗ · DDBJ ↗ | mRNA             | Sequence<br>problems. |

[Expand table](#)

## Genome annotation databases

### Ensembl

ENST00000352993.7 ↗ ENSP00000312236.5

↗ ENSG00000012048.26 ↗ [P38398-5]

ENST00000357654.9 ↗ ENSP00000350283.3

↗ ENSG00000012048.26 ↗ [P38398-1]

ENST00000461221.5 ↗ ENSP00000418548.1

↗ ENSG00000012048.26 ↗ [P38398-2]

ENST00000461798.5 ↗ ENSP00000417988.1

↗ ENSG00000012048.26 ↗ [P38398-2]

ENST00000468300.5 ↗ ENSP00000417148.1

↗ ENSG00000012048.26 ↗ [P38398-6]

[More Ensembl links](#)

### GeneID

672 ↗

### KEGG

hsa:672 ↗

### MANE-Select

ENST00000357654.9 ↗ ENSP00000350283.3

↗ NM\_007294.4 ↗ NP\_009225.1 ↗

### UCSC

uc002icq.4 ↗ human [P38398-1]

uc010cyx.4 ↗ human

# Similar Proteins<sup>i</sup>

## UniRef clusters<sup>i</sup>



## Orthologs & paralogs<sup>i</sup>



## Disclaimer

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| Species (Proteomes)        | Taxonomy                   | Align               | About & Help              |
| Protein clusters (UniRef)  | Keywords                   | Retrieve/ID mapping | UniProtKB manual          |
| Sequence archive (UniParc) | Subcellular locations      | Peptide search      | Technical corner          |
|                            | Cross-referenced databases | Tool results        | Expert biocuration        |
|                            | Diseases                   |                     | Statistics                |

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