

## SAV1 (Salvador homolog 1 (Drosophila))

### Identity

|             |   |
|-------------|---|
| Other names | <b>Salvador</b><br><b>WW45</b><br><b>WWP4</b> |
| Hugo        | <b>SAV1</b>                                   |
| Location    | 14q13-q23                                     |
| Local_order | telomeric to SPG3A and centromeric to ZF405P  |

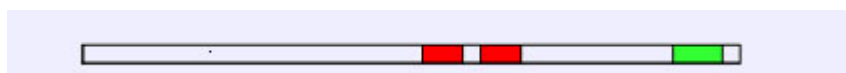
### DNA/RNA



SAV1 is encoded by five exons represented by the boxes. The blue shaded region indicates the Sav1 coding region while the untranslated regions (UTR) are shown in white.

|               |   |
|---------------|---|
| Description   | The Sav1 gene spans 34.7 kb.  |
| Transcription | The longest SAV1 mRNA transcript of 3.0 kb encodes an open reading frame (ORF) of 1152 bases and untranslated regions of 338 and 1541 bases at the 5' and 3' ends, respectively. No splice variants have been reported for SAV1. Smaller transcripts of 1.8 kb and 2.1 kb, encoding the identical ORF, have been isolated which may be the result of alternative sites of poly-adenylation. |

### Protein



SAV1 contains two central proline-binding WW domains (red) and a C-terminal SARAH (for Salvador/Rassf/Hippo) domain (green).

|              |   |
|--------------|---|
| Description  | Sav1 is 383 amino acids in length with an expected weight of 44,606 Da. WW1: residues 199-232; WW2: 234-267; SARAH domain: residues 321-368. The SARAH domain partially overlaps with a predicted coiled-coil domain: 344-373.  |
| Expression   | SAV1 mRNA is ubiquitously expressed in adult tissues with highest expression in the placenta, pancreas, heart, kidney, lung and aorta and lowest expression in skeletal muscle. Expression was higher in fetal heart compared with adult heart.   |
| Localisation | SAV1 is localized to the centrosome during interphase and metaphase and localizes with the contractile ring during cytokinesis. SAV1 co-localizes with MST2, <a href="#">RASSF1A</a> and LATS1 during anaphase, interphase, metaphase and cytokinesis.  |
| Function     | Sav1 is a scaffold protein and able to homodimerize independently of its SARAH domain. Sav1 binds to <a href="#">MST1/2</a> kinases and RASSF1A in an interaction that requires their homologous SARAH domains. The binding of MST stabilizes SAV1 abundance and enhances the association of SAV1 with RASSF1A. SAV1 is phosphorylated by MST1/2 but the consequence of this is not known. The MST2/SAV1/RASSF1A complex can recruit LATS1 kinase resulting in the activation of LATS1 by MST2. The MST2/SAV1/RASSF1A/LATS1 complex may function in regulating cell-cycle exit. In Drosophila, dSav mutant tissue is more resistant to apoptosis and grows more quickly compared with wild type tissue suggesting dSav is a dual regulator of cell proliferation and apoptosis. |
| Homology     | mSav1 is 94% identical to hSav1. hSav1 is 31% identical and 44% similar to dSav from Drosophila melanogaster, however, the similarity increases to 59% if only the  |

sequences comprising the WW and SARAH domains are compared. There is no recognizable orthologue of hSav1 in *S.cerevisiae*.

### Mutations

|          |  |
|----------|--|
| Note     | The cDNA sequence for SAV1 is conflicted at codons 5 (K/Q), 18 (Q/R), 292 (L/F) and 373 (Q/stop).  |
| Germinal | No germline mutations for SAV1 have been reported.   |
| Somatic  | In one study of 52 cancer cell lines, SAV1 was deleted in two renal cancer cell lines (ACHN and 786-O) and a C to A mutation at nucleotide 554 (Ala185Asp) was detected in a colon cancer cell line (HCT15). A second study from the Korean population failed to detect the C554A polymorphism or any additional mutations of SAV1 in 324 cancer cell lines. A third study failed to detect hypermethylation the SAV1 promoter in 44 <a href="#">soft tissue sarcomas</a> and 6 sarcoma cell lines. These results suggest that (1) the C554A mutation found in the colon cancer cell line might be a true mutation and (2) that SAV1 is not frequently mutated in human cancers. |

### Implicated in

**Entity** To date SAV1 is not implicated in any diseases.

### External links

[Hugo](#)  
[GDB](#)  
[Entrez\\_Gene](#)

[Atlas](#)  
[GeneCards](#)  
[Ensembl](#)  
[Genatlas](#)  
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### Nomenclature

[SAV1](#)  
[SAV1](#)  
[SAV1\\_60485](#) salvador homolog 1 (Drosophila)

### Cards

[SAV1ID42206ch14q13](#)  
[SAV1](#)  
[SAV1](#) [Search\_View] [ENSG00000151748](#) [Gene\_View]  
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[SAV1](#)  
[SAV1](#)  
[60485](#)

### Genomic and cartography

[SAV1](#) - [chr14:50170110-50204773 - 14q13-q23](#) (hg18-Mar\_2006)  
[SAV1 - 14q13-q23 \[CytoView\]](#)  
[Mapview](#)  
[Disease map \[OMIM\]](#)  
[SAV1](#)

### Gene and transcription

[AF088000](#) [ ENTREZ ]  
[AJ292969](#) [ ENTREZ ]  
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[AK023071](#) [ ENTREZ ]  
[AK095903](#) [ ENTREZ ]  
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[SAV1](#) AceView - NCBI

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[Hs.642842](#) [ SRS ] [Hs.642842](#) [ NCBI ]

[HS642842](#) [ spliceNest ]

[208](#) (alternative variants)

**Protein : pattern, domain, 3D structure**

[17088](#)

**Protein Interaction databases**

**Polymorphism : SNP, mutations, diseases**

[607203](#) [ map ]

[607203](#)

[SAV1](#) [dbSNP-NCBI]

[NM\\_021818](#) [SNP-NCI]

[SAV1](#) [GeneSNPs - Utah] [SAV1](#) [HGBASE - SRS]

[SAV1](#) [HAPMAP]

[SAV1](#) [Somatic mutation (COSMIC-CGP-Sanger)]

[SAV1](#)

**General knowledge**

[SAV1](#) [UCSC Family Browser]

[NM\\_021818](#)

[Hs.642842](#)

[Hs.642842](#)

[signal transduction](#) [Amigo] [signal transduction](#)

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[SAV1](#)

**Other databases**

**Probes**

[SAV1 Related clones \(RZPD - Berlin\)](#)

**PubMed**

[11 Pubmed reference\(s\) in LocusLink](#)

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Medline [17538946](#)

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**Contributor(s)**

**Written** 06-2007 Bernard A Callus  
Biochemistry Department, La Trobe University, Bundoora VIC 3086,  
Australia

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