

# Target interaction network

**Molecular Target Synopsis**

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**BRAF (P15056) - Overview - Molecular Target Synopsis**

**Protein**

BRAF, Serine/threonine-protein kinase Braf  
 Enzyme Classification 2.2.11.1  
 UniProt Q15508

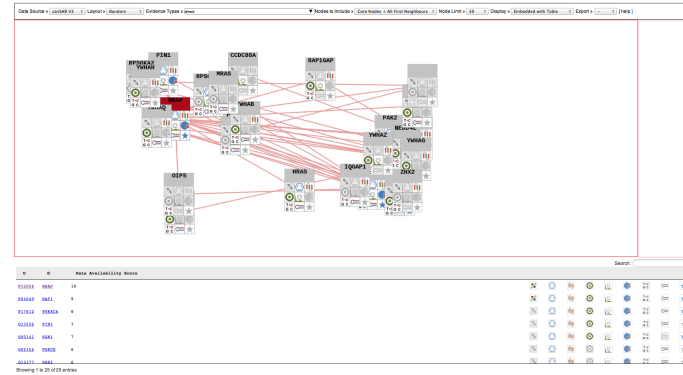
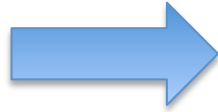
Also Known as BRAF\_HUMAN, BRAF, BRAF1, RAFB1

Protein kinase involved in the transduction of mitogenic signals from the cell membrane to the nucleus. May play a role in the postreceptor responses of heterocellular neuron. Phosphorylates MAP2K1, and thereby contributes to the MAP kinase signal transduction pathway. Monomer. Homodimer. Heterodimerizes with RAF1, and the heterodimer possesses a highly increased kinase activity compared to the respective homodimers or monomers. Heterodimerization is mitogen-regulated and enhanced by 14-3-3 proteins. MAPK1/ERK2 activation can induce a negative feedback that promotes the dissociation of the heterodimer by phosphorylating BRAF at Thr323. Found in a complex with at least BRAF, HRAS, MAP2K1, MAP3K and RGS14. Interacts with RIT1, interacts via its terminal with RGS14 (via RBD domain), the interaction mediates the formation of a ternary complex with RAF1, a ternary complex inhibited by GNAI1 (by similarly, interacts with GGN1, interacts with PRMT5, interacts with KSR2.

UniProt deposition date (2004-02-05)  
 THE COMPLEX OF WILD-TYPE BRAF AND BAX39008  
 RCSB PDB  
 InRBD Structure  
 See all 3D Structures for BRAF

**isoforms / Transcripts (Protein Coding)**

Protein Length	Ensembl Gene	Ensembl Transcript	Ensembl Protein	Uniprot Isoform
766	ENSG00000157764	ENST00000289602	ENSP00000289602	P15056-1
378	ENSG00000157764	ENST00000496384	ENSP00000496380	
194	ENSG00000157764	ENST00000497784	ENSP00000492119	
102	ENSG00000157764	ENST00000479637	ENSP00000418033	



Select 'Interaction Matrix' on the molecular target synopsis side menu.



This will display a network of interactions between the target protein (red) and other proteins. The canSAR human interactome is comprised of the following key data sources:

- 1) Non-predictive interactions from the IMEx consortium (Orchard et al., 2012)
- 2) Protein interactions from HPRD (Peri et al., 2003)
- 3) Phosphorylation reactions from Phosphosite (Hornbeck et al., 2015)
- 4) Crystallographically-resolved protein binding interfaces from PDBePISA (Krissinel and Henrick, 2007) with complexation significance score greater than zero or interface binding site area greater than 400 square angstrom
- 5) Functional interaction definitions from Reactome (Milacic et al 2012)
- 6) Transcriptional signalling events from TFactS (Essaghir et al., 2010)

Data Source » canSAR V3 | Layout » Random | Evidence Types » **direct**

- complex
- direct
- Reactome-FI
- phosphorylation
- transcriptional
- reaction

Nodes to Include » Core Nodes + All First Neighbours | Node Limit » 50 | Display » Embedded with Table | **Export** »

Use the drop down menus above the network to select the source of interactions displayed (canSAR V3 or STRING), to change the network layout, number and type of nodes displayed and more. The network view can be exported as an image (Export -> PNG) or as a network file for use in Cytoscape (Export -> JSON). Note: JSON files can only be imported into Cytoscape 3.1.0+.