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European Bioinformatics Institute is an Outstation of the European Molecular Biology Laboratory.



Yasmin Alam-Faruque (PhD)¹, The IntAct Team¹, and UniProt Consortium^{1,2,3}

¹European Bioinformatics Institute, Wellcome Trust Genome Campus, Cambridge, UK ²Swiss Institute of Bioinformatics, Geneva, Switzerland

³Protein Information Resource, Georgetown University, Washington DC, USA

Features within a UniProtKB/SwissProt entry leading to connection with the IntAct database:

UniProtKB, IntAct and their relationship.

UniProt (Universal Protein Resource) provides a central resource on protein sequences and functional annotation [1].

UniProt Knowledgebase (UniProtKB) contains reviewed, high quality manually annotated, non-redundant protein sequence records in the UniProtKB/Swiss-Prot section, and the unreviewed, automatically annotated protein sequence records in the UniProtKB/TrEMBL section.

Within a UniProtKB/SwissProt entry, information from literature is added by the curator (via the CRISP editor) to a referenced general annotation section (providing information such as function, tissue specificity, developmental-specific expression, subunit structure, subcellular location, disease, isoforms, binary interactions), a feature table (FT) (showing domains/sites of interest with illustrations) and extensive cross-linking to other databases (e.g. IntAct, GO, EMBL, Ensembl, HGNC, OMIM, PDB, InterPro, ArrayExpress, PRIDE, KEGG, GeneID).

★ Reviewed, UniProtK Last modified March 3, 2009. Ver	KB/Swiss-Prot P11532 (DMD_HUMAN) Send fee Send fee P Send fee P Read columnation	AC DT DT DT DT DE edback mments (0) or add your own	PI1532; QU2295; Q14169; Q14170; Q5JYU0; Q7KZ48; O1-OCT-1989, integrated into UniProtKB/Swiss-Prot. 27-SEP-2005, sequence version 2. O3-MAR-2009, entry version 124. RecName: Full=Dystrophin; Name=DMD; Homo sapiens (Human).
🚡 📲 Clusters with 100%, 90%, 5	50% identity 🕒 Documents (6) 🎯 Third-party data 🐻 Customize display	ML RDF/XML GFF FASTA RP	[12] INTERACTION WITH SNTB1.
Names and origin · Protein attribu Entry information · Relevant docur	utes · General annotation (Comments) · Ontologies · Binary interactions · Alternative products · Sequence annotation (Features) · Sequences · References · Web re ments	esources · Cross-references · RA RT RL	MEDLINE=95146543; PubMed=7844150; DOI=10.1083/jcb.128.3.363; Ahn A.H., Kunkel L.M.; "Syntrophin binds to an alternatively spliced exon of dystrophin."; J. Cell Biol. 128:363-371(1995).
Names and origin		Hide Top RN	[13] INTERACTION WITH SNTAL AND SNTB2.
Protein names	Recommended name: Dystrophin	RX RA RT	MEDLINE=96162017; PubMed=8576247; DOI=10.1074/jbc.271.5.2724; Ahn A.H., Feener C.A., Gussoni E., Yoshida M., Ozawa E., Kunkel L.M.; "The three human syntrophin genes are expressed in diverse tissues,
Gene names	Name: DMD	RT	its relatives.";
Organism	Homo sapiens (Human)	RL	J. Biol. Chem. 271:2724–2730(1996). [14]
Taxonomic identifier	9606 [NCBI]	RP	INTERACTION WITH SNTG1 AND SNTG2. MEDITNE=20283612: PubMed=10747910: DOT=10.1074/ibc.M000439200:
Taxonomic lineage	Eukaryota > Metazoa > Chordata > Craniata > Vertebrata > Euteleostomi > Mammalia > Eutheria > Euarchontoglires > Primates > H Hominidae > Homo	laplorrhini > Catarrhini > RA RA RT RT	Piluso G., Mirabella M., Ricci E., Belsito A., Abbondanza C., Servidei S., Puca A.A., Tonali P., Puca G.A., Nigro V.; "Gamma1- and gamma2-syntrophins, two novel dystrophin-binding proteins localized in neuronal cells.";
Protein attributes		Hide Top RL	J. BIOI. Chem. 275:15851-15860(2000). [15]

Sequence length	3685 AA.
Sequence status	Complete.
Sequence processing	The displayed sequence is not processed.
Protein existence	Evidence at protein level.

			<u> </u>	piasma i
General annotation (Comments)	Hid	ellop	CC	-!- SUBUNIT
			CC III	and SNT
Function	May play a role in anchoring the cytoskeleton to the plasma membrane.	K	<u></u>	similar
		[CC .	-!- INTERAC
Subunit structure	Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTG1 and SNTG2. Interacts with KRT19. Interacts with SYNM (By similarity).		CC	070585:
Quile a livia a la cation	Colles and the second sec	r	CC .	P08727:
Subcellular location	Cell membrane > sarcolemma; Peripheral membrane protein; Cytopiasmic side. Cytopiasm > cytoskeleton.		CC .	Q13884:
Tissue specificity	Expressed in muscle fibers accumulating in the costameres of myonlasm at the sarcolemma. Isoform 5 is expressed in brain, liver, testis and	K	CC	Q13425:
rissue specificity	bapatama calla (Ref. 15)	C	CC	-!- SUBCELL
	nepatoma cells.	C	CC	membran
Involvement in disease	Defects in DMD are the cause of Duchenne muscular dystronby (DMD) [MIM:310200]. DMD is the most common form of muscular dystronby: a		<u> </u>	
involventent in disease	- Derects in DMD are the cause of Duchenne muscular dystrophy (DMD) [MMM.510200]. DMD is the most common of muscular dystrophy, a		DR	IntAct; P11
	sex-linked recessive disorder. It typically presents in boys aged 3 to 7 year as proximal muscle weakness causing waddling gait, toe-walking, lord		11	
	frequent fails, and difficulty in standing up and climbing up stairs. The pelvic girdle is affected first, then the shoulder girdle. Progression is steady a	and 🧗	FΤ	REGION
	most patients are confined to a wheelchair by age of 10 or 12. Flexion contractures and scoliosis ultimately occur. About 50% of patients have a lo	ower 🧗	FT	REGION
	IQ than their genetic expectations would suggest. There is no treatment. Ref.23 Ref.24 Ref.26 Ref.28		FΤ	REGION
	5 1 35		77	

Binary ii	hary interactions							
With	Entry	#Exp.	IntAct	Notes				
Dtnb	070585	1	EBI-295827,EBI-349714	From a different organism.				
KRT19	P08727	1	EBI-295827,EBI-742756					
SNTB1	Q13884	3	EBI-295827,EBI-295843					
SNTB2	Q13425	1	EBI-295827,EBI-80411					

In addition to a 'Subunit structure' annotation comment within a UniProtKB/SwissProt entry, there may be an 'Interaction' / 'Binary interactions' section which contains a link to IntAct that provides detailed information for the experimental support.

A graphical representation of the interactions can also be viewed:



Hide To	PP RT RL RN RP RX	localized in neuronal cells."; J. Biol. Chem. 275:15851-15860(2000). [15] INTERACTION WITH KRT19, AND TISSUE SPECIFICITY. PubMed=16000376; DOI=10.1091/mbc.E05-02-0112;		
	RA RT RT RL	Stone M.R., O'Neill A., Catino D., Bloch R.J.; "Specific interaction of the actin-binding domai intermediate filaments containing keratin 19."; Mol. Biol. Cell 16:4280-4293(2005).	n of dystroph	in with
Hide To		 -!- FUNCTION: May play a role in anchoring the oplasma membrane. -!- SUBUNIT: Interacts with the syntrophins SNTA and SNTG2. Interacts with KRT19. Interacts with similarity). -!- INTERACTION: 070585:Dtnb (xeno); NbExp=1; IntAct=EBI-295827. EBI-295827. 	:ytoskeleton to 1, SNTB1, SNTB vith SYNM (By 327, EBI-349714 31-742756:	o the B2, SNTG1 4;
d	UUUUU	Q13884:SNTB1; NbExp=3; IntAct=EBI-295827, EE Q13425:SNTB2; NbExp=1; IntAct=EBI-295827, EE -!- SUBCELLULAR LOCATION: Cell membrane, sarcole membrane protein; Cytoplasmic side. Cytoplas	8I-295843; 8I-80411; mma; Peripher; m, cytoskelet(al on.
7, a lordosis ady and a lower		IntAct; P11532; 8. REGION 1415 1913 Interaction with SY REGION 3058 3408 Interaction with SY REGION 3466 3518 Binds to SNTB1.	ΏΜ (By simila ΏΜ (By simila	rity). rity).
rch				
-295827,EBI-7 criteria mat	7 42756], tches are <mark>high</mark>	ighted)		R
me to view	more detail.		-12	
<u>erPro</u> <u>Sei</u>	lect all <u>Clea</u>		1	7 X
ne	Ac	Description	Experiment	Proteins
9-dmd-1	EBI-870934	spr Interaction between krt19 and actin-binding domain (ABD) of dmd	stone-2005-1	2
D C				
erPro Sei	lect all <u>Clea</u>			
earch				/
='EBL870934'	3			
arch criteria	matches are h	ghlighted)		

Reviewed;

DMD_HUMAN

Graph Path	InterPro Select all	<u>Clear all</u>									
Experiment 4	Name	AC	Interaction detection	Participant identification	Host						
PSI-MI 1.0 PSI-MI	stone-2005-1	EBI-870918	<u>spr</u>	predetermined	<u>in vitro</u>						
Description	Specific interaction	on of the actin-b	inding domain of dystrophi	n with intermediate filaments containing	; keratin 19.						
Annotation	author-list	Stone MR., 0	Stone MR., O'Neill A., Catino D., Bloch RJ.								
	contact-email	rbloch@uma	rbloch@umaryland.edu								
	figure legend	6B	6B								
	publication year	2005	2005								
	journal	Mol. Biol. Ce	II (1059-1524)								
Xref	pubmed	<u>16000376</u>	-	Type: primary-reference							

Interaction information from the literature is added to the SUBUNIT comment, the Reference citation/ Reference position (RP) of the relevant publication and within the FT sections within the UniProtKB entry. There may also be a single INTERACTION comment present within an entry which conveys information relevant to binary proteinprotein interactions. This is automatically derived from the IntAct database, along with the database cross-reference DR line and is updated on a tri-weekly basis.

Statistics: Release 57.0 (of 24-Mar-09) of UniProtKB/Swiss-Prot contains 428650 sequence entries.

IntAct provides a freely available, open source database system and analysis tools for protein-protein interaction data [2].

All interactions are derived from literature curation or direct submissions and all experimental information relating to binary protein-protein interactions is entered into the IntAct database by curators, via a webbased editor for Experiment, Interaction, Biosource, Protein, Small molecule, Nucleic acid and controlled vocabularies.

Interactions can be derived by any appropriate experimental method as described by the HUPO PSI-MI controlled vocabularies, in order to be successfully exported to the UniProtKB database.

<u>Annotation</u>	<u>comment</u>	<u>comment</u> The actin-binding domain (ABD) of DMD preferentially interacts with KRT19 in-vitro, which was confirmed with dot blot assays and by in-vivo transfection of COS7 cells with DS-Red-Dys-ABD together with K19.									
Interacting molecules	<u>Name</u>	Ac	Interactor type	Stoichiometry	Interactor description	Expression system	Identifier	Gene name	Role		
	dmd_human	EBI-295827	protein	-	Dystrophin	ecoli	<u>P11532</u>	-	prey		
	k1c19_human	EBI-742756	protein	-	Keratin, type I cytoskeletal 19	cerae-cos_7	<u>P08727</u>	-	<u>bait</u>		
Sequence features	Experimental modification: Histag n-terminus of dmd_human [n-n].										
	Binding site region	Binding site region of dmd_human [1-246] deletion analysis.									
					/~				7		

EBI-870934 physical interaction

'Specific interaction of the actin-binding domain of dystrophin with intermediate filaments containing keratin 19.' Stone M.R., O'Neill A., Catino D., Bloch R.J.

There is also a 'Protein-protein interaction database' / 'DR' cross-reference section within the entry which directs the user to additional interaction data for that molecule within IntAct.

Mol. Biol. Cell 1 Cited for: INTERA	6:4280-4293(2 CTION WITH KR1	1005) [Pub 119, TISSUE	Med: 16000376 SPECIFICITY.	i] [Abstrac	t]									
rotein-protein interactio	n databases													
ıtAct	(P11532.1	3 interactions.											
arch IntAct 📀	EBI > Databases : Results Query: P11532 Lucene Query:	> Proteomic D	↓ atabases 1 1532 pubid:p11532 p	pubauth:p115	32 spe <u>(s</u> e	ee entire que	<u>ery)</u>	This	search has identified 0	experiments	s, which contain a m	atch to your query ir	n the title or des	cription, and
Act Home dvanced Search bols ata Submission	Export Options Accession number molecule	Accession number molecule	3 7 Alternative id molecule A	Alternative id molecule	Names molecule A	Names molecule B	Species molecule A	Species molecule B	First Author	PubMed identifier	Interaction type	Interaction detection method	Source database(s)	Interaction details
cumentation FAQ	A 1 <u>P49407</u> , EBI-743313	B P11532, EBI-295827	ARR1	В	ARRB1	DMD	<u>9606(</u> human)	<u>9606(</u> human)	Xiao et al. (2007)	<u>17620599</u>	physical interaction	anti tag coip	<u>intact</u>	EBI-1642362
User manual Annotation manual Publications Statistics weloper Resources	2 <u>P02768</u> , <u>EBI-714423</u>	P11532, EBI-295827	PR00903, PR01708, PR02044, PR02619, PR02675, UNQ696/PR01341, GIG20		ALB	DMD	<u>9606(</u> human)	<u>9606(</u> human)	Zhou et al. (2004d)	<u>15174051</u>	physical interaction	<u>anti bait coip</u>	intact	EBI-1222961
evelopment Site ntact IntAct	3 <u>P11532</u> , <u>EBI-295827</u>	<u>P08727</u> , <u>EBI-742756</u>			DMD	KRT19	<u>9606(</u> human)	<u>9606(</u> human)	Stone et al. (2005) Stone et al. (2005)	<u>16000376</u> <u>16000376</u>	physical interaction physical interaction	<u>spr</u> <u>far western blotting</u>	<u>intact</u> intact	EBI-870934 EBI-875667
ter Friendly View	4 <u>P11532</u> . <u>EBI-295827</u>	<u>P05787</u> , <u>EBI-297852</u>		СҮК8	DMD	KRT8	<u>9606(</u> human)	<u>9606(</u> human)	Stone et al. (2005)	<u>16000376</u>	physical interaction	far western blotting	<u>intact</u>	EBI-875667
RSS	5 <u>P11532</u> , <u>EBI-295827</u>	Q9NRI5, EBI-529989		KIAA0457	DMD	DISC1	9606(human)	9606(human)	Camargo et al. (2007)	17043677	physical interaction	2 hybrid	intact	EBI-1105652
12, 2008 MI XML 1.0	6 <u>Q13884</u> , <u>EBI-295843</u>	<u>P11532</u> , <u>EBI-295827</u>	SNT2B1		SNTB1	DMD	<u>9606(</u> human)	<u>9606(</u> human)	Ann et al. (1995) Ahn et al. (1995) Ahn et al. (1996)	7844150 7844150 8576247	physical interaction physical interaction physical interaction	anti bait coip anti tag coip coip	intact intact intact	EBI-295853 EBI-295885 EBI-368367
ontinuation se note that IntAct is	7 <u>Q13425,</u> EBI-80411	P11532, EBI-295827	SNT2B2, D16S2531E, SNTL		SNTB2	DMD	<u>9606(</u> human)	<u>9606(</u> human)	Ahn et al. (1996)	8576247	physical interaction	coip	<u>intact</u>	EBI-368283
MIXML 1.0 as part of eekly release as of	8 <u>P11532,</u> <u>EBI-295827</u>	070585, EBI-349714			DMD	Dtnb	<u>9606(</u> human)	<u>10090(</u> mouse)	Macioce et al. (2003)	<u>14600269</u>	physical interaction	pull down	intact	EBI-374734

UniProtKB export is based on the method used to detect interaction. Methods deemed to demonstrate high quality binary interactions are exported to the general annotation section. Complementation assays require validation by a second method before export. For **INTERACTION** comment and **DR** line export, all proteins with interactions obeying the above criteria are exported. In addition, interactions judged by the curators to be high confidence are also exported.

You can perform a search within the IntAct database using: Gene name: DMD; UniProtKB AC: P11532; UniProtKB ID: DMD_HUMAN or PubMed ID: 16000376. There are links from the IntAct database to several other databases including UniProtKB, GO and InterPro.

Statistics: The IntAct Database (March-09) contains: 189082 binary interactions, comprising 56985 proteins and 10192 experiments.

References:

[1] The Universal Protein Resource (UniProt) 2009 The UniProt Consortium Nucleic Acids Res. Jan 2009 37: D169-74 PMID: 18836194.



[2] IntAct – Open Source Resource for Molecular Interaction Data S Kerrien, Y Alam-Faruque et al. Nucleic Acids Res. Jan 2007 35: D561-565 PMID:17145710.

Acknowledgements

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European Bioinformatics Institute (EMBL-EBI) Swiss Institute of Bioinformatics (SIB) Protein Information Resource (PIR) **PB**

Email: help@uniprot.org

URL: www.uniprot.org www.ebi.ac.uk/intact