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Gene Information eXtension (GIX): effortless retrieval of gene product information on any website

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Abstract

Retrieving information about genes is a continuous and time-consuming aspect of systems biology. While there are resources that can fulfill this need, they require navigation to different and often complex websites, execution of a search (or searches) and selection of a result before the user can view pertinent information. To streamline this process, we developed a browser extension called GIX (Gene Information eXtension; https://gene-info.org) to allow users to retrieve gene information directly from a website without navigating to another page.

GIX is a browser extension for Google Chrome and Mozilla Firefox that allows users to retrieve customizable gene-product information—especially as it relates to proteins and their expression and functions—directly from a website. Simply double- clicking on (or, alternatively, mouse-dragging) a gene name or supported accession number (Ensembl, Entrez, neXtProt, RefSeq or UniProt) will open an information panel on the current page (Fig. 1). This panel will include gene synonyms, the full gene name, alternative names, the size and molecular weight of its canonical protein product, the UniProt description, protein domains and regions, Gene Ontology terms, protein localization, RNA tissue expression, associated diseases or phenotypes, pathways, protein interactors (from BioGRID and IntAct) and links to external resources (Ensembl, NCBI and UniProt for all species, and organism-specific databases including dictyBase, FlyBase, MGI, neXtProt, PomBase, SGD, TAIR, WormBase, Xenbase and ZFIN). GIX also offers an alternative tooltip mode that simply provides links to these external resources. The extension is fully customizable, allowing users to control the information they see, and it supports queries for *Homo sapiens* and ten model organisms: *Arabidopsis thaliana, Caenorhabditis elegans, Danio rerio, Dictyostelium*

CODE AVAILABILITY

COMPETING FINANCIAL INTERESTS

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J.D.R.K., P.S.T. and A.-C.G. conceived of the extension. J.D.R.K. wrote the code. M.T. provided input on the extension. J.D.R.K. and A.-C.G. wrote the manuscript with input from P.S.T. and M.T.

GIX is available for free without restriction at the Chrome Web Store and the Firefox Add-ons site. Download links, documentation, a tutorial video and source code can be found at https://gene-info.org.

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discoideum, Drosophila melanogaster, Gallus gallus, Mus musculus, Saccharomyces cerevisiae, Schizosaccharomyces pombe and *Xenopus laevis.* The extension provides a search bar for entering queries manually and an online "workspace" in which the user can paste gene lists from desktop applications for quick queries with GIX. Although double-clicking to retrieve results is not possible on websites with embedded content such as Google Docs or PDFs, querying with the search bar does work on such webpages. GIX collates data from BioGRID¹, Compartments², Gene Ontology³, HUGO Gene Nomenclature Committee⁴, the Human Protein Atlas⁵, IntAct⁶, OMIM⁷, Pfam⁸, Reactome⁹ and UniProt¹⁰. The GIX database is updated monthly to incorporate changes from these resources.

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Gene: UBAP2L				Activation method:	Information options:	to NCBI
Synonyms: KIAA0144, NICE-4, NICE4			Advanced	Double click	Basic	Help
Name: Ubiquitin-associate Alternative Names: • Protein NICE-4 Length: 1087aa		ated protein 2-like MW: 114.54kDa	eel.2017.12.020. Epub 2018 Jan 25.	Disable CTRL/% required Display options:	Description C RNA expression Domains	
Ensembl: ENSG00000143569 NCBI: 9898 UniProt: Q14157 neXtProt: NX_Q14157 Description: Plays an important role in the activity of long-term repopulating hematopoietic stem cells (LT-HSCs). EXPRESSION (RNA): Protein Atlas RNA expression values are reported as transcripts per million (TPM) and binned into expression level categories: no			Reveals the Subcellular Organization	Detailed report Tooltip report Theme:		
			imately degradation involve a series of dedicated prote ch as stress granules (SGs) and processing bodies (F analysis of 119 human proteins associated with differe ons with 1,792 proteins. Classical bait-prey analysis re d processes or complexes, including the splicing and 1 and the CCR4-NOT deadenylase complex (CEP85, R nous preys uncovers the spatial organization of RNA r f SGs and PBs. We report preexisting contacts betwee	Light Species:	Pathology Pathways	
				Homo sapiens	Interactors	ess of octa. 2009
					\$	or mRNA Res. 2015
				Search:		of RNA Sci. 2008
expression (none), low, medium or high. See HPA RNA-seq data for more.			nonstrate that several core SG proteins (UBAP2L, CS 3 SGs.		Q	es and mol. 2007
Tissue HEK 293	ТРМ 180.5	Level high		Documentation	Workspace Report issue Rate	Tudor-SN S J. 2015
HeLa Hep G2 U-2 OS	125 112.2 130.7	high high high	L; mass spectrometry; membraneless organelle; processing b	oody; proximity-based		See reviews See all
DOMAINS & REC	BIONS: Pfam		Sociology of Droplet Compartments. [Mol Cell. 2018]		Cited by 27 PubMed Cent articles	tral 🕒
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15-29	low_complexity				Chronic optogenetic inductio	

Figure 1.

Screenshot of GIX in the Chrome browser. Double-clicking on a gene name/symbol (in this case *UBAP2L*) opens an information panel (left side) displaying information about the queried gene. The extension has a number of settings that the user can customize by clicking on its icon in the browser toolbar (right side). The screenshot of PubMed is used courtesy of the National Library of Medicine (NLM), and the abstract is reproduced from *Mol. Cell*, Vol. 69, Youn, J.-Y. et al., High-density proximity mapping reveals the subcellular organization of mRNA-associated granules and bodies, 517–532.e11, 2018, with permission from Elsevier.