

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extrace region
Q12271	INP53_YEAST	Saccharomyces cerevisiae	Polyphosphatidylinositol phosphatase INP53	24.475439	NaN	S497;S986;S1035;T1105	33229814	MIIFVSEEPERRLAIVSNLYALVLKPV GKKPSDKPLCAIELLQKNDLKKYGF KRLTSEHIFGVIGLIEVNGLLFVGAIT GKSKVAQPCPGETVNKIFAVDFCL NDNSWDFIEIDSSGYPVLPETASTEY QDALPKHPCYELKKLLSNGSFYYSS DFDLTSTLQHRGYGQHSLSLDTYEE EYMWNSFLMQEMITYRDHLDTNLK QILDDEGFLTIVIRGFAETVFSYVKK LKVALTHSKQSWKRAGRFNRARGVD DEANVANFVETEFIMYSSQCYAFT QIRGSIPVFEWQGTSLINPRVQITRS FEATQPVFDKHKMSVEKYGPVHV NLLSTKSSEIELSKRYKEHLTHSKKL NFNKDIFLTFDFHFKETSQEGFSGV RKLIPILDSLLSSGYYSYDVREKKN SEQHGIFRTNCLDCLDRNLAAQIIS LAAFRTFLEDFRLISSNSFIDDDDFV SKHNTLWADHGDQISQIYGTNALK SSFSRKGKMSLAGALSDATKSVSRIY INNFMDKEKQONIDTLGRLPYQKA VQYDPVNEYVSTKLQSMSDKFTST SNINLLIGSFNVNGATKKVDLSKWL FPIGKFKPDIVVLGLQEVIELSAGSI LNADYSKSSFVENLVGDCLNQYDD KYLRLRVEQMTSLLLFFVKADKAKY VKQVEGATKKTGFRGMAGNKGAVSI RFEYGATSFVFNHLAGATNVEE RRSDYESIVRGITFTRTKMIPHHSIF WLGDMNYRINLPNEDVRRELLNQE EGYDKLLHFDQLTLGINSVFEFEGF KEPTLKFRPTYKYDPGTGYDSSEKE RTPSWTDRIIYKGENLLPLSYSDAPI MISDHRPVYAYRAKITFVDDKERLS LKKRLFTYKQEHPEEPGSLISDLS LDLDNKSTDGFKSSSESLLDIDPIM AQPTASSVASSPVSASASLQPVRT QNSSQSRTPIKKPVLRPPPPAHKSV SAPAPSTSKEKSPPTQTSTASLSSVT KNIQENKPLAQNRRIPPPFGSQNILT PKSTSNLSPMSSKVDLYNSASEST RSAQDARQOTPTAFAASRDVNGQPE ALLGDENPIEPEEKAKLNHMTLDSW QPLTPK	None	None	None	None	None	None	None		

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