

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
P40547	VID28_YEAST	Saccharomyces cerevisiae	Vacuolar import and degradation protein 28	24.475439	NaN	S226	33229814	MTVAYSLENLKKISNSLVGDQLAKV DYFLAPKCQIFQCLLSIEQSDGVELK NAKLDLLYTLHLLEPQQRDIVGTYYF DIVSAIYKSM SLASSFTKNNSSTNYK YIKLLNLCAGVYPNCGFPDLQYLQN GFIQLVNHKFLRSCKIDEVVTHELL KLFLLVDEKNCSDFNKSKFMEERE VTETSHYQDFKMAESLEHIIIVKISSK YLDQISLKYIVRLKVS RPASPSSVKN DPFDNKGVDCTRAIPKINISNMYD SSLLSALLLYLRHYMIPGDRKLRN DATFKMFVLGLLKSNVNRVVALK FLLQPYFTEDKKWEDTRTLEKILPYL VKSFNYPDLPWWFDPFDMLDSLIVL YNEITPMNPNVLTTLAHTNVIFCILS RFAOQLSLPQHNEATLKTITTKFIKIC ASFAASDEKYRLLLLNDTLLLNHLEY GLESHTLIQDFISLKDEIKETTTESH SMCLPPIYDHD FVAAWLLLLKFSR SVSALRRTLKRNKIAQLLLQILSKTYT LTKECYFAGQDFMKPEIMIMGITLG SICNFVVEFSNLQSFMLRNGHDIIEK MLTDPLFNSKKA WDDNEDERRIAL QGIPVHEVKANSLWVLRHLMYNCQ NEEKFQLLAKIPMNLILDFINDPCW AVQAQCFQLLRNLTCNSRKIVNILLE KFKDVEYKIDPQTGNKISIGSTYLFEF LAKKMRLLNPLDTQKKAMEGILYII VNLAAVNENKKQLVIEQDEILNIMS EILVETTTDSSSNGNDSNLKLA CLW VLNNLLWNSSVSHYQYAIENGLEP GHSPDSEN PQSTVTIGYNESVAGG YSRGKYDEPDGDDSSSNANDED DDNDEGDDEGDEFVRTPAAKGSTS NVQVTRATVERCRKLVVEGLYDLVR KNITDESLSVREKARTLLYHMDLLL KVK	None	None	None	None	None	None	None		

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