

| UniprotKB ID | Entry name | organism | full name | oglnacscore | oglnac sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | p |
|--------------|-------------|--------------|--------------------------------|-------------|---------------------|-----------------------|---|---|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|---|
| 070546 | KDM6A_MOUSE | Mus musculus | Lysine-specific demethylase 6A | 47.760692 | S552;S554;T566;S580 | S769;T827;S829 | 22645316;40885482;36852467;34678516;30059200;40997131 | MKSCGVS LATAAAAAAAAAFGDEEK KMAAGKASGESEASPSLTAEEREA LGGLDSRLFGFVRFHEDGARMKALL GKAVRCYESLILKAEGKVESDFFCQL GHFNLLLEDYPKALSAYQRYYSLSQ DYWKNAAFLYGLGLVYFHYNFQW AIKAFQEVLYVDPSCFRAKEIHLRLG LMFKVNTDYESSLKHFLALVDCNP CTLSNAEIQFHIAHLYETQRKYHSAK EAYEQLLQTNLSAQVKATILQQLG WMHHTVDLLGDKATKESYAIQYLQK SLEADPNSSGQSWYFLGRCYSSIGKV QDAFISYRQSIDKSEASADTWCSIGV LYQQQNQPMDALQAYICAVQLDHG HAAAWMDLGTLYESCNPQDAIKC YLNATRSKNCSNTSGLAARIKYLQA QLCNLPQGS LQNKTKLLPSIEEAW LPIPAELTSRQGMNTAQNTSDN WSGGNAPPVVEQQTHTSWCLTPQKL QHLEQLRANRNNLNPAQKLMLEQL ESQFVLMQQHQMRQTGVAQVRPTG ILNGPTVDSSLPTNSVSGQQPOLPLT RMPSVSPQGVHTACPROTLANGPFS AGHVPCSTSRTLGSTDVTLIGNNHV TGSGSNGNVPYLQRNAPTLPHNRT NLTSSTEEPWKNQLSNSTQGLHKG PSSHLAGPNGERPLSSTGPSQHLQA AGSGIQNQNGHPTLPSNSVTQGAAL NHLSSHATSGGQOGITLTKESKPS GNLTVPETSRTGETPNSTASVEG LPNHVHQVMADAVCSPSHGDGSKSP GLLSSDNPQLSALLMGKANNVGP GTCDKVNNIHPTVHTKTDNSVASSP SSAISTATSPKSTEQTTTNSVTSLN SPHSGLHTINGEGMEESQSPIKTDL LLVSHRPSPOIIPMSVSIYPSAEVL KACRNLGKNGLSNSSILLDKPPPR PPSSPYPLPKDKLNPPTPSYLENK RDAFFPPLHQFCTNPNNPVTVIRGL AGALKLDLGLFSTKTLVEANNEHVM EVRTQLLQPADENWDPTGTKKIWH CESNRSHHTIAKYAQYQASSFOESLR EENEKRSHHKDHSDESTSSDMSG KRRKGPFKTKFGTNDLSDDKKWK LQLHELTKLPAFVVRVVSAGNLLSHV GHTILGMNTVQLYMKVPGSRTPGH QENNNFCSVNINIGPGDCEWVFPVE GYWGVLNDFCCKNNLNFLMGSWW PNLEDLYEANVPVYRFIQRPGDLVWI NAGTVHVVQAIGWCNNAIWNVGPL TACQYKLAVERYEWNKLQNVKSIVP MVHLSWNMARNIKVSDPKLFEMIK YCLRRLTKQCQTLREALIAAGKEIHW HGRTKEEPAHYCSICEVEVFDLLFVT NESNSRKYIVHCQDCARKTSGNLE NFWVLEQYKMEDLMQVYDQFTLAP PLPSASS | True | False | 2.665 | 5.0 | 2.069 | 1.449 | 0.886 | 1 |