

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q2M2H8	MGAL_HUMAN	Homo sapiens	Probable maltase-glucoamylase 2	22.903221	T772	NaN	38253038	MARKLSVLEVLLIIFCLIVVTIDILLLL LVEETSDDTSFTPECEPEIQSERIDCT PDQEVTEIDICRWQYKCCWSPVADA NVPRCFFPWNWGYEASNGHTNTST GFTAQLKRLPSPSLFGNDVATTLFTA EYQTSNRFHFKITDFNNIRYEV SHE NINLVDGIADASNLSYYVEVTDKPPS IKIMRTSNRRVLLDTSIGLPQFAQQY LQLSFRLPSANVYGLGEHVHQYRHR NMTWKTWPIFTRDATPTEGMINLYG AHTFFLCLEDARGSSFGVFLMNSNA MEVTLQPAPAITYRTIGGILDFYVFLG NTPQVQVQYELVGRPPFPYWSL GFQLSRRDYGINKLKEVVSRLA EIPYDVQYSDIDYMDGKKDFTVDEV AYSGLPDFVKELHDNGQKYLIMNP GISKNSNYEPYNNGLSKRWWILGSN GFAVGEYGPPTVFPDYTNPVCTEW WTDQVAKFHDHLEFDGVIEMNEV SLLQASNNQCESNNLNFPPFLPRV LDHLLFARTLCMDTEFHHGLHYDIH SLYGHSMARTTNLALETIFMNNRSF ILSRSTFAGSGKFAAHWLGDNAAW DDLRWSIPTILEFNLFGIPMVGANIC GYNNNVTEELCRRWMQLGAFYPLP RNHNGPFRDQDPAAFVDSLLLK SSRHYLNIRYTLPLYLTLFYHAHTR GETVARPLVHEFYQDSATWDVHEQ FLWGPGLLITPVLYEGVDEVKAYIPD ATWYDYETGVAISWRKQLVNMLLPG DKIGLHLRGGYIFPTQKPNTTTEASR RNSLGLIALDYKREAKGELYWDDG VSKDAVTEKKYLYDFSVTSNHLQAK IINNVMYMDTNDLMFTDITILGMDKQ PANFIVLLNNVATSSPSVYNASTKV VTTIDLQGLVLGGQEFSTRWNLPVSDL EKFNCPDDPTASEESCRQRGCLWE DTSTPGVPTCYDTPINYVASDIQYL NTSITADLSLPMAPESAAAAASDLSL AKISFLHLKVYHTATMLQVKYDPT NKRYEVPVLPNTPPQPVGDENRLY DVRIQNNPFGIQQRKNSSTVIWDSQ LPGFIFNDMFLSISTRLLPSQYIYGFGE TEHTTFRNMNWNWTWGMFAHDEP PAYKKNYSYGVHPYMALEEDGSAHG VLLLSNAMDVTLQPTALTYRTTG GILDFYVILGPTPELVTTQYTELIGRP AMIPYWALGFHLSRYGYQNDAEISS LYDAMVAAQIPYDVQHVVDIDYMNRR LDFTLSANFQNLSELLIEQMKNNGMR FILILDPAISGNETOYLPFIRGQENNV FIKWPDNDIVWGKVPDLPNVIVD GSLDHETQVKLYRAYVAFDPDFRNS TAAWVKKEIEELYANPREPEKSLKF DGLWIDMNEPSNFVDSVRCGSNE MLNNPPYMPYLESRDKGLSSKTLCLC MESQQILPDSSPVEHYNVHNLVYGW SQTRPTYEAVQEVTGQRGVITRSTF PSSGRWGGHRLGNNTAAWDQLGKS IIGMMEFSLFGIPYTGADICGFFGDA EYEMCVRWMQLGAFYPPSRNHNNI GTRRQDPVAVNSTFEMLSRKVLET RYTLPLYLTLMHKAHVEGSTVVRP LLHEFTDDRTTWDIDRQFMLGPAILI SPVLETSTFEISAYFPRARWYDYSTG TSSTSTGQRKILKAPLDHINLHVRGG YILPWQEPAMNTHSSRQNFMLGLIVA LDDNGTAEGQVFWDDGQSIDTYEN GNYFLANFIAAQNILQIQITHNKYLS DSNPLKVGYIRIWGVNTYVTQVSFTY DNRQFMETNFKSEPYNQILTIQLTD KTINLEKLTEVTWIDGGPVLPTPKT STIPMSSHPSPTTNATSSSETITSSAS ANTTTGTDTVPITTTSPSTTSVTITN TTVPDTTSPFPTSTTNASTNATVPITT TPPTSTIGVTTNATVPNTTAPFPTN	False	False	1.33	1.323	1.195	1.456	1.296	1.898	1.943

ASTASTNATVPITTTCFATSTIGVTTN  
ATVPDTTAPFPNTTTASTNATIPITT  
TPFATSTISVITSTIVPDTTAPFPST  
TSASTNATVPITTTLFATSTIGVTTG  
TIVPDTTAPFPSTTSTSTSATVPITT  
TPSPNTADANTSNTVPNTTSPST  
SSTTVSTIATVPISVTPSLTSTADATIS  
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TPVQNTTINASTSTNVANITATSHTS  
TDDTVPNNTVPVTAIPSLANTGVDTT  
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MSAGNITSNSISITTSFGNSVFPVT  
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FTTDKITNFPTPTNANTHFNLDTKS  
TMVIDATVTTTSTKDNTMSPDTTIVT  
SIDKFTTHITQFATPHSATTTTLALSH  
TSLAPTNLSNLGTMDDADNSSSV  
TGNTHISVSNLTTASVTITATGLDS  
QTPHMINSVATYLPITATSATDITT  
NITKYALNTTTPDSTVHTSATAPTYIA  
NAINATQVP