

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondr
Q8C196	CPSM_MOUSE	Mus musculus	Carbamoyl-phosphate synthase [ammonia], mitochondrial	31.625891	T109;T110;S537;S872;T1078;S1331;T1332	S148;S189;S537;S540;S569;S896;S898;S1036;S1079;S1090;S1093;S1203;S1419;S1431	37453647;35285892;36064721;29562282	MTRILTACKVVKTLKSGFGFANVTK ROWDFSRPGIRLLSVKAKTAHVLEED GTYPEALDDPAYKGOILTMANPIIGN GGAPDPTTARDELGLNKYMESDGIV AGLLVLNYSNDYNHHLATKSLGQW LQEEKVPAIYGVDTRMLTKIIRDKGT MLGKIEFEGQSVDFVDPNKQNLIAE VSTKDVKVFVGGKGNPTKVAVVDCGIK NNVIRLLVVRGAEVHLPVWNHDFI QMEYDGLLIAGGPGNPALAQPLIQN VKKILES DRKEPLFGISTGNIITGLAA GAKSYKMSMANRQGNQPVLNITNR QAFITAQNHGYALDNTLPAGWKPFL VNVNDQTNNEGIMHESKPPFAVOFH PEVSPGPTDTEYLFDSFFSLIKKGGK TTITSVLPKPALVASRVEVSKVLILGS GGLSIGQAGEFDYSSQAVKAMKEE NVKTVLMNPNIASVQTNVGLKQAD AVYFLPITPQFVTEVIKAEKRPDGLILG MGGQTALNCGVELFKRGVLEKEYGV KVLGTSVESIMATEDRQLFSDKLNEI NEKIAPSFAVESMEDALKAADTIGYP VMIRSAYALGGLGSGICPNKETLIDL GTKAFAMTNQILVERSVTGWKEIEY EVVRDADDNCVTVCNMENVVAMG VHTGDSVVVAPAQTL SNAEFQMLRR TSVNVVRHLGIVGECNIOFALHPTS MEYCIIEVNARLSRSSALASKATGYP LAFIAAKIALGIPLPEIKNVVSGKTS CFEPLSDYMTKIPRWLDRFHGTS SRIGSSMKSVGEVMAIGRTFEEFQ KALRMCHPSVDGFTPRLPMNKEWP ANLDLKKELSEPSSTRYIAIAKALEN NMSLDEIVRLTSIDKWFLYKMRDIL NMDKTLKGLNSDSVTEETLRKAKEI GFSKQISKCLGLTEAQTRELRK NIHPWVKQIDTLAAEYPSVTNYLYVT YNGQEHDIKFDEHGIMVLGCGPYHI GSSVEFDWCAVSSIRTLRQLGKKT VVNCNPETVSTDFDECDKLYFEELS LERILDYHQEACNGCIISVGGQIPN NLAVPLYKNGVKIMGTSPLOIDRAE DRSIFSAVLDELKVAQAPWKAVNTL NEALEFANSVGYPCLLRPSYVLSGSA MNVVFESEDEMKRFLEEATRVSQEH PVVLTKFVEGAREVEMDAVGEKGRV ISHAISEHVEDAGVHSGDATLMLPT QTISQGAIEKVKDATRKLAKAFAISGP FNVQFLVKGNDVLEICNLRASRSF PFVSKTLGVDFIDVATKVMIGESIDE KRLPTLEQPIPSDYVAIKAPMFSWP RLRDADPILRCCEMASTGEVACFGEI HTAFLKAMLSSTGFKIPQKGLIGIQQ SFRPRFLGVAEQLHNEGKLFATEA TSDWLNANNVPATPVAVPWSQEQGN PSLSSIRKLIRDGSDLVINLPNNNTK FVHDNYVIRRTAVDSGIALLTNFQVT KLF AEAVQKSRTVDSKSLFHYRQYS AGKAA	True	False	2.838	3.744	5.0