

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	pl m
O60437	PEPL_HUMAN	Homo sapiens	Periplakin	14.945781	T553	S14;S465;S887;S949;S1584;S1657	35138101;36240223;37217939;38665916	MNSLFRKRNRKGYSPVQTRISINKELSLLEQLQKNADQVEKNIVDTFEAKMQSDLARLQEGRQPEHRDVTLQKVLDSEKLLYVLEADAAIAKHMKHPQGDMIAEDIRQLKERVNTNLRGKHKQIYRLAVKEVDPQVNWAALVEEKLDKLNQSFQGTDLPLVDHQQVEEHNIFHNEVKAIGPHLAKDGDKEQNSLRRAKYQKLLAASQARQQHLSLQDYMQRCTNELYWLQQAQKGRMQDWSDRNLDYPSRRRQYENFINRNLEAKEERI NKLHSEGDQLLAAEHPGRNSIEAHMEAVHADWKEYLNLICEESHLYMEDIYHGFHEDVKDAQELLRKVDSDLNQKYGPDFKDRYQIEILLRELDQEKVLDKYEDVVQGLQKRGQVPLKYRRETPLKPIPVEALCDFEAGEGLISRGYSYTLQKNNGESWELMDSAGNKLIAPAVCFVIPPDPPEALALADSLGSQYRSVVRQKAAGSKRTLQQRYEVLKTE NPGDASDLQGRQLLAGLDKVASDLDROEKAITGILRPPLEQGRAVQDSAERAKDLKNITNELLRIEPEKTRSTAEGEAFIQALPGSGTTPLLRTRVEDTNRKYEHLLQLDLAQEKVDVANRLEKSLQ QSWELLATHENHLNQDDTVPESSRVLDKSGQELAAMACELQAQKSLLGEVEQNLQAAKQCSSTLASRFQEHCPDLERQEAHVHKLGRFNNLRQOVERRAQSLQSAKAAYEHFHRGHDHVLQFLVSIPSYEPQETDLSLQMETKLNQKNLLDEIASREQEVQKICANSQQYQAVKDYELEAEKLRSLDLENGRRSHVSKRARLQSPATKVKEEAAALAAKFTEVYAINRQRLQNLFEALNLRQQPEVEVTHETLQRNRPDSGVVEAWKIRKELDEETERRRQLENEVKSTQEEI WTLRNQGPQESVVRKEVLKVPDPVLEESFQQLQRTLAEEQHKNOLLQEELEALQLQRLALEQETRDGGQEVVVK EVLRIEPRADRAQAEVQLREELEALRROKGAAREVLLQQRVAALAEKESRAQEKVTEKEVVKLQNDPQLEAEYQQLQEDHQRQDQLREKQEEELSFLQDKLKRLEKERAMAEKGITVKEVLKVEKDAATEREVSDLTRQYEDEAAKARASQREKTELLRKKIWALEENAKVVVQEKVREIVRPPDKAASEVANLRLELVEQERKYRGAEELRSYQSELEALRRRGPQVEVKEVTEKVIKYKTDPEMEKELQRLREEIVDKTRLIERCDLEIYQLKKEIQALKDTPQVQTKEVVQEIQLQFQEDPQTKEEVASLRAKLSSEEQKKQVDLERERASQEEQIARKEEELSRVKERVVQQEVVRYEEEPGLRAEASAFESIDVELRQIDKLRAELRRLQRRRTELERQLEELERERQARREAREVQRLQQLLAALQEEEAAREKVTHTKVVLQQDPQQAREHALLRQLQEEEQHRRQLLEGELETLLRRKLALEKAEVKEKVVLS ESVQVEKGDTEQEIQLKSSLEESRSKRELDVEVSRLEARLSELEFHNSKSSKELDFLREHNHKLQLERQNLQLETRRLQSEINMAATETRDLRNMTVADSGTNHDSRLWSLERELDDLKRLSKDKDLEIDELQKRLGSAVKREQRENHLRRSIVVIHPDTGRELSPEEAHRAGLIDWNMFVKLRSQECDWEEISVKGPNGESSVIHDRKSGKKSIEEALQSGRLTPAQYDRYVNDMSIQELAVLVSGQK	True	True	4.557	3.158	1.606	1.477	0.841	4.