	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
0	Q6NS46	RRP5_MOUSE	Mus musculus	Protein RRP5 homolog	29.185005	NaN	S7;S438;S1468;S1490	22645316	MANLEESFPRGGTRKLHKSEKSSQ QVVEQDNLFDVSTEEGPIKRKKSQK GPAKTKKLKIEKRKSIKSIKEKFEILS LESLCEGMRILGCVKEVSELELVVSL PNGLQGFVQVTEVCDAYTQKLNEQV AQEEPLEDLLRLPELFSPGMLVRCV VSSLDVTESGKKSVKLSVNPKRVNK VLSADALRPGMLLTGTVSSLEDHGY LVDIGVGGTRAFLSLKKAQEYIRQKN KGAKFKVGQYLTCVVEEVKSNGGVV SLSVEHSEVSSAFATEEQSWNLNNL LPGLLVKAQVQKVTQFGLQLNFLTF FKGLVDFMHLEPKKMGSYSSNQTV KACILCVHPRTRVVRLSLRPIFLHPG RPLTRISYQQLGAVLDDVPVQGFFK NAGAIFRLKDGVLAYARVSHLSDSK KAFNAEAFKPGSTHKCRIIDYSQMD ELALLSLRKSIIAAPFLRYHDIKIGTV VKGTVLAIKPFGILVKVGEQIKGLVPS MHLADIMMKNPEKKYSPGDEVKCR VLLCDPEAKKLIMTLKKTLVTSKLSLI TCYEGAKPGLQTHGVIIRVKDYGCIV KFYNDVQGLVPKHELSTQHIPDPET VFYTGQVVKVAVLSCEPSKERMLLS FRLLSDSRPKDPGVESSQKKTGAVRI GQLVDVKVLEKTKTGLEVAILPHNTP AFLPTPHLSDHAANGPLLHHWLQT GDTLHRVLCLSQSERHILLCRKPALV STVEGGQDPKSLSEIQPGMLLIGFVK CIKEYGVFVQFPSGLSGLSPKTIMSD KFVTTPSEHFVEGQTVVAKVTNVDE SKQRMLLSLRLSDCSLGDSASTSFL LLCQCLEELQGIRSLMSNQDSVLIQT LADMTPGMVLDAVVHEVLEDGSVV FSSDPVPDLVLRASRYHRAGQEVEP GQKKKVVVLHVDMLKLEVHVSLHQ DLVNRKTRKLRKSSRHQGIVQHLEE SFAVASLVETGHLVAFSLISHLNDTF HFDSEKLRVGQGVCLTLKTTEPGVT GLILAVEGPASKRTRMPVQRDSETV DDKGEEKEEEEEEEEKEEENLTVKS KKRHSLAIGDKVTGTIKAVKATHVVV TLADGFVGCIHASRILDDVPVGTSPT TTLKAGKKVTARVIGGRDVKTSKFLP ISHPRFVLTILELSVRPSELKGSYSAL NTHSESPVEKIRQYQAGQTVTCFFK KYNVMKKWLEVDIGPDIRGRIPLLLT SLSFKVLKHPDKKFQVGQAIEATVV DPDVPRAFLCLSLIGPYRLEEGEVAM GRVMKVVPNRGLTVSFPFGKIGKVS MFHLSDSYSEAPLEDFCPQKIVRCYI LSTAHRVLALSLRSSRTNRETKNRIE DPEINSIEDVKEGQLLRGYVKCVLPS SVIIGLGPSVLGLAKYSHVSECVPPE KELYNGCLPEGKLVTAKVLRVNPMK NLIELSLLPSDTGRPDVFSPAPEPKQ EERSGGAEEGQKRKEKNQKRREEK EEPQKSQRGGRGKRERQESESEQEL VNKRPKKSGAAEEDDSGVEVYYREG EDEVGEPKLPPRGKQTKSTEVPRLH LSSGFLWDVGLDSLTPALPLREESS DSEDEQPHQAKKKKGKKERELEKQ KAEKELSRIEEALMDPGRQPESADD FDRLVLSSPNSSILWLQYMAFHLQA TEIEKARAVAERALKTISFREEQEKL NVWVALLNLENMYGSQESLTKVFE RAVQYNEPLKVFLHLADIYTKSEKYK EAGELYNRMLKRFRQEKAVWIKYGA FVLGRSQAGASHRVLQRALECLPAK EHVDVIVKFAQLEFQLGDVERAKAIF ENTLSTYPKRTDVWSVYIDMTIKHG SQTAVRDIFERVIHLSLAPKRMKFFF KRYLDYEKQHGTEKDVQAVKAKALE YVEAKSSALED	True	False	5.0	4.298	0.943	0.659	0.621	0.899	0.717