

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnacsites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
P98163	YL_DROME	Drosophila melanogaster	Putative vitellogenin receptor	25.496522	NaN	S1926	33925313	MCQAEHQVHPSEQIRVESPKMTA SRRGFNLTSTQTRAHPSSGGSTSSRY GNCQRTHLIINGRHVAISLLLLVGLC GGTAAGTPGSADTRCDAGQFQCRD GGCILQAKMCDGRGDCDSSDELD CDYRLCRPPHWFPCAQPHGACLAAE LMCNGIDNCPGGEDELNCPVRPGF RFGDTAHRMRSCKYEFMCQODRT CIPIDFMCDGRPDCTDKSDEVAGCK QAEITCPGEGHLCANGRCLRRKQW VCDGVDDCGDGSDERGCLNLCPEQ KGFFLCRNRETCLTLSEVCDGHSDC SDGSDETDLCHSKPDCDAKKCALGA KCHMMPASGAECFCPKGFRLAKFE DKCEDVDECKEQDDLCSQGCENTS GGYRCVCDAGYLLDKDNRTCRAVVY GSKEQQPLLLYTTQMTIMGMHLRE DNVRNHVYQVAGNLSKVIGVAYDGS HIYWTNIQNEAESIVKANGDGSNAEI LLTSGLDAPEDLAVDWLTQNIYFSD NIMRHIAVCSNDGLNCAVLVTQDVH QPRSLAVWPQKGLMFWTDWGEKP MIGRASMDGSRSPIVSDNIEWPNG IALDMHQQRIVWVDAKLGVSQTVRP DGTGRRTVLDGMLKHPYGLAIFEDQ LYWSDWATKSVHACHKFSGKDHRI LAKDRTIYAVHIYHPAKOPNSPHGCE NATCSHLCLLAEPEIGGHSCACPDG MRLAPDHRRCMLMEKRQRLFIGLG QVLLIEHTAFGRHQVSKSYTLPCLI NEMVYNRINGSLIADNDQRLILEFQ PESHESNVLVRSNLGNVSALAFDHL SRNLYWADTERAVIEVLSLQTRHRA LIRFFPGQEVPIGLTVMPAEGYLVV LKAKRHSHIDKIPLSGKGEQVHVFE DDLGDDEIKLVTDYETQTIFWSDSD LGRISYSNYRVPHSQIFRGKLRPPYS LAMVHHDLFWNELGTPRIYWHKS NMGPRKVIDIMEKDDPAAIMPYVPV ATPNGIPLAASSVPGQESHPCQQQN GGCSHICVGEQPYHSICLCPAGFVYR DAGNRTCVEALDCEFRCHSGECLT MNHRCNGRRDCVDNSDEMNCDEE HRRKPKVLCSPNQFACHSGEQCVD KERRCDNRKDCHDHSDEQHCEKFD KSKKCHVHQHGCDNGKCVDSSSLVC DGTNDCGDNSDELLCEATSRCEPG MFQCGSGSCIAGSWECDGRIDCS GSDEHDKCVHRSCPPDMQRCLLGO CLDRSLVCDGHNDGDKSDELNCG TDSSTMNISCAEDQYQCTSNLKICLP STVRCNGTTECPRGEDEADCGDVCS IYEFKCRSGRECIREFRCDGQKDC GDGSDLSCELEKGHNSQIQPW STSSRSCRPHLFDQDGECDVLSRV CNNFPDCTNGHDEGPKCATACRSA SGRQVCQHKCRATPAGAVCSFDGY RLDADQKSCLDIDECQEQPCAQLC ENTLGGYQCQCHADFMLRQDRVSC KSLQSGATLLFSSFNEVRNLSEQPV MLNVAVSANDSRITGFDLAMHRQ MGYFSAEDEGIVYQIDLQTKVIVRAL GLPAPTKLSVDWVTGNVYVLSGAQE IQACSFVGRMCGRIVHVKSPRHVKH LAVDGYHARIFYIVIRTEGYGQTSSEI HMARLDGSRRDMLLQRSEFMTAL TTDPHQQLLYFVDQHMRTLERSYR LKTGPMRRPEIMLQKSNALMHPSG LSVYENNAFIVNLGSVEAVQCALYG SRICHKISINVLNAQDIVVAGRSRQP QKASHPCAHAHCHGLCLQADYGYE CMCGNRLVAEGERCPHGSGNEVAV LGAVNSLELEHEHEQNGHFHWLM ALFVLAAGSLIAGLGYMYQYRQRG HTDLNINMHFQNPLATLGGTKAFLE	None	None	None	None	None	None	None		

