

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
Q9D952	EVPL_MOUSE	Mus musculus	Envoplakin	25.810548	NaN	S1576;S1800;S2026	29187734	MFKGLSKGSQKGGSPKGPAGKSPK GSPNKHNRATQELALLISRMQANA DQVERDILETKKLLQDQRNGEQN QALQHQQETGRNLKEAEVLLKDLFL DVDKARRLKHQPAAEIEKDIKQLHE RVTQECSEYRALYKMLVPPDVGPR VDWARVLEQKQNLVREGHYGPGMA ELEQQVAEHNILQREIEAYGQQLRTL VGPDANTIRNQYRELLKAASWRRQS LGSlyTHLQGCTKQLSALADQGRl LQODWSDLMPDPAGVRRREYEHFKQ HELLAQERSINQLEDDADRMVELG HPAIGPIQVHQEALKMEWQNFNL CICQESQLQRVEDYRRFQEEADSVS QTLAKLSSNLDTKYGFGTGDSGSGP TELLQLAEAEKQLAIAERAVGDLQO RSQEVAPLPORRNPSKQPLHVDSIC DWDSGEVQLLRGERYTLKDNADPYT WLVQGGGETKSAPAACLIPADP EAVAKASRLATELQTLKQKLSTEKN RLKAAAVEHLQPGQAPAGSAPADP QGQTLLSQMTQDGDLDGQIERQVLS WARSPLSQSSSLKDLGRIHSCEGT AORLQSLGAEKAAQCEAFSTK PTGSAALQLPVVLSNVKNRYNDVQS LCHLYGKAKAALGLEKQIQEADRVl QGFEAALALEGPVPEGSALQERVS ELQRQRKELLQQQACVLLHRLKA TEHACSALQNNFQEFQDLPQQQR QVRALTDRYHAVGDQLDLREKIVQD ASLTYQQLRNSRDNLSSWLEQLPH HRVQPSDGPQISYKLAQAKRLIQEI LGREQDQATVSRRLTRDLOEALQDYE LQADTYRCSLEPALAVSAPKRLRVIS LQESIQAQEKNLAKAYTEVAAAEQQ QLRQLEFAKMLRKKELDEDIQAIH SARQGSQSPAHARTAESVLTQLE EERKRVAEVQRDLEEQRQLLQLR QQPVARLEEKEVVEFYRDPQLESNL SQAASRVEEEGKRRARLQAELEAVA QKVVHLEGKRKTMQPHLLTKEVTOI ERDPGLDSQVTQLHSEMORLRGEN GVLTAARLEELKDELLALEQKEMNVK EKVVVKEVVKVEKDLKEMVAAQT LQIEEDAARRKGAKETVAKIQARIK LEQAISSEPKVIVKEVKKVEQDPGL LKEASRLRSLLEEKNNVALAREL QELQEKYRVVEKQKPKVQLQERVSE IFQVLPETEQEIRRLRAQLQETGSKK SGVEQEVEKLLPELEVLRAQKPVVEY KEVTQEVVRHEKNPEVLREIDRLKA QLNELVNTNGRSQEQILRLQGERDE WKREERSKVETKMVSKEVVRHEKDP VLEKEAERLRQEVREAVORRRATED AVYELQNKLLLLERRRPEEQIVVQEV VVTQKDPKLRREHSRLSRSLDEEVG RRRQLELEVRQLGARVEEEEARLSF EEDRSKLLAAERELRQLTLKIQELEK RPPALQEKIIMEEVVLEKDPDLERS TEALRRELDQEKNRVTEHLHRECOGL QVQVDLLQKTKSQEKTIYKEVIRVEK DPVLEGERARVWEILNRERAARKGR EEDVRSLOERIDRAEALRRSWSREE AELQRARDQASQDCGRLQRLRELE QKQKARQLOEGRLLSQKTESER QKAAQRSQAVTQLEAAILQEKDKIYE KERTLRDLHTKVSREELNQETQTRE TNLSTKICILEPETGNDMSPYEAYKR GVIDRGQYLQLELECDWEEVITSS PCGEESVLLDRKSGKQYSIEAALRCR RISKEEYHRYKDGRLPISEFALLVAG ETKPSSSLSIGSIISKSPVCSPPQST GFFSPGLSFGLTEDSFPIAGYDITTD NKCSIKAAVAKNMLDPITGQKLEA QAATGGIVDLSRERYSVHKAVERG LIENTSTQRLLNAQKFTGIEDPVTR	False	True	3.559	3.403	1.483	1.212	1.194	5.0	1.851

