

| 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 |
|--------------|------------|--------------|--------------------------|--------------|---------------|-----------------------|----------|--|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|----------------------|
| Q8BL66       | EEA1_MOUSE | Mus musculus | Early endosome antigen 1 | 25.629171    | NaN           | S52;S70               | 36288343 | MFRRLQRTPGRVGSQSDLDSSAT<br>PINTVDVNNESSEGFICPQCMKSL<br>GSADELFKHYQAVHDAGNDSGHGG<br>EAGLALTRDDITLLRQEVQDLQASLK<br>EEKWYSEELKKELEKYQGLQQEAK<br>SDGLVTDSSAELQALEQQLEEAQTE<br>NFNIKQMKDLFEQKAAQLATEIADIK<br>SKYDEEKSLRAAAEQKVTHLTEDLN<br>KQTTVIQDLKTELLQRPGIEDVAVLK<br>KELVQVQTLMDNMTLERERESEKL<br>KDECKKLQSEHAHLEATINQLRSEL<br>AKGPQEVAVYVQEIQKLGKGSINELTQ<br>KNQNLTEKQLQKDDLYTHLEEKHN<br>EESASRKTQASLHQRDLDCQQLOA<br>RLTASESSLQRAQGELEKAEAAQK<br>LREELREVESTROHLKVEVKLQQQ<br>REEKEQHGLQLQGEVSQLHCKLLET<br>ERQLGEAHGRLKEQRQLSSEKLME<br>KEQQVADLQLKLSRLEEQLKEKVTN<br>STELQHLEKSKQQHQEQQALQOS<br>ATAKLREAQNDLEQVLRQIGDKDQK<br>IQNLEALLQKGKESVSLLEKEREDLY<br>AKIQAGEGETAVLNQLQEKNHALQQ<br>QLTQLTEKLNQSESHKQAEENLH<br>DQVQEQKAHLRAAQRVLSLETSSVS<br>ELSSQLNESKEKVSQLDIQIKAKTEL<br>LLSAEAAKAAQRADLQNHLDTAQHA<br>LQDKQQELNKVSVQLDQLTAKFQEK<br>QEHCICLESHLKDHEKHLSEKQV<br>EDLEGHKKLEADALEVKASKEQAL<br>QSLQQQRQLSTDLELRNAELSRELO<br>EQEEVVSTKLDLQNKSEILENIKQT<br>LTKKEEENVVLKQEFELKSQDSKTQ<br>HKELGDRMQAAVTELTAVKAQKDA<br>LLAELSTTKEKLSKVSDSLKNSKSEF<br>EKENQKGAAVLDLEKACKELKHQL<br>QVQAESALKEQEDLKKSLKEKETS<br>QQLKIELNSVKGEVSAQNTLKOKE<br>KDEQQLOQTINQLKQSAEQKKKQIE<br>ALQGEVKNVAVSQTVLENKLQQSS<br>QAAQELAAEKGLSALQSNYEKCQA<br>DLKQLQSDLYGKESELLATRODLKS<br>VEEKLTLAQEDLISNRNQIGNQKSI<br>QELQAAKASLEQDSAKKEALLKEQS<br>KALEDAQREKSVKEKELVAEKSKLA<br>EMEEIKCRQEKETKLNELKSHKQ<br>ESIKEITNLKDAKQLLIQOKLELQGR<br>VDSLKAALQEKESSQLMREQVKKE<br>EKKRKEEFSEKEAKLHSEIKEKEAG<br>MKKHEENEAKLTMQVTTLNENLGT<br>VKKEWQSSQRRVSELEKQTDLLRG<br>EIAVLEATVQNNQDERRALLERCLK<br>GEGEIEKLQTKALELQKLDNTTAA<br>VQELGRENQSLQIKHTQALNRRKWA<br>EDNEVQNCMSCGKCFSVTVRRHHC<br>RQCGNIFCAECSTKNALTPSSKKPV<br>RVCDACFNDLQG | True          | False         | 4.736   | 3.817   | 2.185         | 2.567                 | 2.957           | 2.943           | 2.435                |