

| UniprotKB ID | Entry name | organism | full name | oglcnaScore | oglcna sites | phosphorylation sites | PMIDS | sequence | intracellular | extracellular | cytosol | nucleus | mitochondrion | endoplasmic reticulum | golgi apparatus | plasma membrane | extracellular region |
|--------------|-------------|--------------|--|-------------|--------------|--|----------|--|---------------|---------------|---------|---------|---------------|-----------------------|-----------------|-----------------|----------------------|
| Q04692 | SMRCD_MOUSE | Mus musculus | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 | 25.685855 | NaN | T54;S57;S79;S124;S127;S132;S144;S145;S151;S210;S213;S235;S238;S298 | 39627609 | MNLFNLDLDRFRFEKRSKIEEAPPEAAP QPSQARPSPILSAEENAEAGEGSR ANTPDSVTEKTEDSSVPEPPDNER KASLSCFQNRRAIQEYIDLSSDTEDEV SPNCSSTVQEKKFSKDTVIIVSEPE DEESHDLPSVTRRNDSSSELEDLSEL EDLKDALKQLKELFPQRSDDLLK LIESTSTMDGAIAAALLMFGDAGGG PRKRKLSSEEDDVNDQSVKQPR GDRGEESNESAEASNWEKQESIVL KLQKEFPNFDKQELREVLKEHEWM YTEALESLKVFAEDQDVQCASQSEV TNGKEVARNQYNSKNATKIKMKOKI SVKPQNGFNKKRKNVFNPKKAVE DSEYDSGSDAGSSLDEYSSCEEV EDGYKGLHFLQVSSIAELTLIPKCS QKKAQKITELRPFNNWEALFTKMSK INGLSEDLIWNCKTVIQRDVVIRLM NKCEDISNKLTKQVTMLTGNGGGW NREQPSLLNQSLSLKPYQKVLNWL ALVHKHGLNGILADEMGLGKTIQAI AFLAYLFQEGNKGPHLIVVPASTIDN WLREVNLCPSLNVLCYYSQEEER KQIRFNIHNKYEDYNVIVTTYNCAIS SSDDRSLFRRLKLNIAIFDEGHMLK NMGSIYQHLMTINARNLLLLTGTP VQNNLLELMSLLNFVMPHMFSSST SEIRRMFSSKTKPADEQSIYKERIA HAKQIIKPFILRRVKEEVLKLLPPKID RIELCAMSEKQEQLYSGLFNRLKCSI NNLEKNTMCMNVMMQLRKMANNHP LLHRQYYTPELKEMSQLMLKEPTH CEANPDLIFEDEMEVMTDFELHVLCK QYQHINSYQLDMDLILDSGKFRALG CILSELKQKGDVVVLFQFTMMLDI LEVLLKHHQHRVLRDLGKTIQISERI HLIDEFNTDMDIFVLLSTKAGGLGI NLTSANVILHDIDCNFYNDKQAEED RCHRVGOTKEVLVLIKLSQGTIEESM LKINQQKLEQDMMTVDEADEGS MPADIATLLKTSMGL | True | False | 2.033 | 5.0 | 0.842 | False | False | 0.598 | 0.814 |