

| 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<br>P31260  | HXA10_HUMAN | Homo sapiens | Homeobox protein Hox-A10 | 23.519607    | NaN           | NaN                   | 32870666;37217939 | MSARKGYLLPSPNYPTTMSCESPA<br>ANSFLVDSLSSGRGEAGGGGGGAG<br>GGGGGGYYAHGGVYLPAAADLPYGL<br>QSCGLFPTLGGKRNEAASPGSGGGG<br>GGLGPGAHGYPSPIDLWLDAPRSC<br>RMEPPDGPPPPQPPPPPPPPQP<br>APQATSCSFAQNIKEESSYCLYDSAD<br>KCPKVSATAELAPFPRGPPDGAL<br>GTSSGVPVPGYFRLSQAYGTAKGYG<br>SGGGGAQLGAGPFPAPPPGRGFDL<br>PPALAGSADAARKERALDSPPPTL<br>ACSGGGSQGEAHASSSAEELS<br>PAPSESSKASPEKDSLGNKGENAA<br>NWLTAKSGRKKRCPYTKHQTFLELEK<br>EFLFNMYLTRRRLIERSVHLTDR<br>QVKIWFQNRMRMMLKMMNRENRIRE<br>LTANFNFS | True          | False         | 1.591   | 5.0     | 1.766        | 1.361                 | 0.984           | 1.934           | 2.042                |