

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q8WWI1	LMO7_HUMAN	Homo sapiens	LIM domain only protein 7	26.509012	S295;S318;T652;S805;T818;S822;S876;S895;S1185;T1406;S1500;S1563;S1565;S1570;S1573;T1576;S1577;T1578;T1579;T1583;T1584;S1586;T1588;S1593	T185;S246;S257;S276;S342;S704;S706;S709;S751;S805;S867;S873;S879;S895;T913;S919;S926;T932;T949;T956;S960;S988;S991;S994;S995;S1026;S1032;S1044;T1048;S1177;S1304;S1307;S1423;S1454;S1493;S1510;S1516;S1563;S1586;S1593;S1595;S1597;S1601;S342;S345	31637018;30379171;33214551;30059200;20068230;31492838;33465208;28657654;32574038;29351928;31373491;29237092;34019948;30620550;28510447	MKKIRICHIFTFFYSWMSYDVLFORTE LGALEIWRQLICAHVICVGLWLYLRD RVCSSKDIILRTEQNSGRITLIKAVTE KNFETKDFRASLENGVLLCDLINKL KPGVIKKINRLSTPIAGLDNINVFLKA CEQIGLKEAQLFHPGDLQDLSNRVT VKQEETDRRVKNVLTLYWLGKRAQ SNPYNPGPHLNLKAFENLLGQALTK ALEDSSFLKRSGRDSGYGDIWCPPER GEFLAPPRHHKREDSFESLDSLGSER SLTSCSSDITLRGGREGFESDTESEF TFKMQDYNKDDMSYRRISAVEPKTA LPFNRLFPNKSQPSYVPAPLRKPKK DKHEDNRRSWASPVYTEADGTFSS NORRIWGTNVENWPTVQGTSKSSC YLEEEKAKTRSIPNIVKDDLYVRKLS PVMNPNGNADFQFLPKCWTPEDVN WKRIKRETYKPYKEFQGFSSQFLLL QALQTYSDDLSSETHTKIDPTS GPR LITRRKNLSYAPGYRRDDLEMAALD PDLENDFFVRKTGVFHANPYVLRRA FEDFRKFSEQDSDVERDIILQCREGE LVLPDLEKDDMIVRRIPAQKKEVPLS GAPDRYHPVFPPEPWTLPPEIQAKFL CVFERTCPSKEKSNSCRILVPSYRQK KDDMLTRKIQSWKLGTTVPPISTPG PCSEADLKRWEAIREASRLRHKKRL MVERLFQKIYGENGSKSMSDVSAED VQNLRLRYEEMQKIKSQLKEQDQ KWQDDLAKWKDRRSYTSDLQKKK EEREIEKQALEKSKRSSKTFKEML QDRESQNKSTVPSRRRMYSFDDV LEEGRPPTMTVSEASYQSERVEEK GATYPSEIPKEDSTTFAKREDRVTEI QLPSQSPVEEQSPASLSSLRSRSTQ MESTRVSASLPRSYRKTDTVRLTSVV TPRPFQSQTRGISSLPRSYTMDDAW KYNQGDVEDIKRTPNNVVSTPAPSPD ASQLASSLSSQKEVAATEEDVTRLPS PTSPFSSLSQDQAATSKATLSSTSGL DLMSESGEGEISPQREVSRSDQFS DMRISINQTPGKSLDFGFTIKWDIPG IFVASVEAGSPAEFSQLQVDEI IAIN NTKFSYNDKKEWEEAMAKAQETGH LVMDVRRYKAGSPETKWI DATSGI YNSEKSSNLSVTDFSESLQSSNIES KEINGIHDESNAFESKASESISLKNL KRRSQFFEQGSDDSVV PDLPVPTISA PSRWVWDQEEERKRQERWQKEQD RLLQEKYQREQEKLREEWQRAKQE AERENSKYLDEELMVLSSNSMSLTT REPLATWEATWSEGSKSSDREGTR AGEEERRQPQEEVVEDHEDQGKKPQD QLVIERERKWEQQLQEEQEQRLQA EAEQKRPAAEQKRAEIERETSVRI YQYRRPVDSYDIPKTEEASSGFLPGD RNKSRSTTELDYSTNKNNGNKNYL DQIGNMTSSQRRSKKEQVPSGAELE RQQILQEMRKRTPLHNDNSWIRQR SASVNKEPVSLPGIMRRGESLDNLD SPRSNSWRQPWLNQPTGFYASSSV

