

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondri
Q9UKK3	PARP4_HUMAN	Homo sapiens	Protein mono-ADP-ribosyltransferase PARP4	22.355849	T1312;S1314;S1325;S1335;S1338	T101;T333;S1236;S1335;S1504	29351928;37217939;39531497;34725712;28657654;38665916;31492838;35132862;30059200;35254053	MVMGIFANCIFCLKVKYLPQQQKKK LQTDIKENGGKFSFSLNPQCTHILD NADVLSQYQLNSIQKNVHIANPDF IWKSIREKRLLDVKNYDPYKPLDITP PPDQKASSSEVKTEGLCPDSATEEE DTVELTEFGMQNVEIHPHPQDFEVA KYNTLEKVGMEGGQEAUVVELQCS RDSRDCPFLISSHFLLDDGMETRRQ FAIKKTSSEDASEYFENYIEELKKQGF LLREHFTPEATQLASEQLQALLLEEV MNSSTLSQEVSDLVEMIWAALGH LEHMLLKPVNRIISLNDVSKAEGILL VKAALKNGETAELQKMMTEFYRLI PHKGTMPKEVNLGLLAKKADLCQLI RDMVNVCEINLSKPNPPSLAKYRAL RCKIEHVEQNTTEFLRVRKEVLQNH HSKSPVDVLQIFRVGRVNETTEFLSK LGNVRPLLHGSPVQNVIGILCRGLL PKVVEDRGVQRTDVGNLGSGIYFSD SLSTSICYSHPGETDGTLLICDVAL GKCMDLHEKDFSLTEAPPGYDSVH GVSQTASVTDDFEDDEFVYKTNQV KMKYIIFSMGPDQIKDFHPSDHTE LEEYRPEFSNFSKVEDYQLPDAKTSS STKAGLQDASGNLPLEDVHIKGRHI DTVAQVIVFQTYTNKSHVPIEAKYIFP LDDKAAVCGFEAFINGKHIVGEIKEK EEAQQEYLEAVTQGHGAYLMSQDA PDVFTVSVGNLPPKAKVLIKITYITEL SILGTVGVFFMPATVAPWQDKALN ENLQDTVEKICIKEIGTKQSFSLTMSI EMPYVIEFIFSDTHELKQKRTDCKAV ISTMEGSSLDSSGFSLHIGLSAAYLP RMWVEKHPEKESEACMLVFPDLD VDLPDLASESEVIICLDCSSSMEGVT FLQAKQIALHALSLVGEKQKVNIIQF GTGYKELFSYPKHITSNTMAAEFIMS ATPTMGNTDFWKTLLRYSLLYPARG SRNILLVSDGHLQDESLTLQLVKRS RPHTRLFACGIGSTANRHVLRILSQC GAGVFEYFNASKKHSWRKQIEDQM TRLCSFSCSHSVSVKQQLNPDVPEA LQAPAVPVSFLNDRLLVYGFIHPCT QATLICALIQEKEFRMTVSTTELQKTT GTMHKLAAARALIRDYEDGILHENET SHEMCKQTLKSLIILSKENSLITQF TSFVAVEKRDENESPFDPKPVSELI AKEDVDLFPYMSWQGEPEAVRNQ SLLASSEWPELRLSKRKHKIPFSKR KMELSQPEVSEDFEEDGLGVLPAPT SNLERGGVEKLLDSWTESCKPTAT EPLFKKVPWETSTSSFFPILAPAVG SYLPPTARAHSPASLSFASYRQVASF GSAAPPRQFDASQFSQGPVPGTCAD WIPQASASCPTGPPQNPPSSPYCGIVF SGSSLSSAQSAPLQHPGGFTTRPSA GTFPELDSPLHFSPLTDPPIRGFG SYHPSASSPFHFQPSAASLTANLRLP MASALPEALCSQSRTTPVDLCLLEES VGSLEGSRCPVFAFQSSDTEDELS EVLQDSCFLQIKCDTKDDSLCFLEV KEEDEIVCIQHWQDAPVWTELLSLO TEDGFWKLTPELGLILNLTNGLHS FLKQKGIQSLGVKGRECLDLIATML VLQFIRTRLEKEGIVFKSLMKMDDA SISRNPWAFEAIKQASEWVRRTEGO YPSICPRELGNWDSATKQLLGLQ PISTVSPHLRVLHYSQG	True	False	4.503	5.0	1.916