

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
E9PYK3	PARP4_MOUSE	Mus musculus	Protein mono-ADP-ribosyltransferase PARP4	25.875327	S1239	S1229	30059200	MTLGIFANCIFCLKVLYLPRQKKKL QTDIKENGGKFSFLLNPQCTHVI SADVLSRCHLNSIQKNDVQIANPA QDSVRQRRLLDVRNYPDPLSPAPA PAERSRSEVQSEYLPDNTPEKENT EVTEVSAENVEIPPFLQDFEVVYNI LEKVGGPETVVVELQSSQDPESCP VITAHFLLADQKTRRESTGKQTS IEYYESYVEDLKRQGFLLQEHFTA TQLASEKLQALLLEVISSGALSQEV SDLLEVIWTEALGHLENTLLKPVNS MSLNDVSKAEGILLVKTALKNGDS PGQLQKTMAEFYRLPHRHPASEEV NLRLLAQKEDLCQLVRDMVNCET NLSKPNPPLAKYRALRCKIEHVDQ NTEEFSTRVKEVLQNNRSEQPVDIL QIFRVGRVNEATEFSLKLGVRLLF HGSPVRNIGILSRGLLLPKVAEDRG VQRTDVGNLGSGYFSDSLSTSIKYA HAGETDGSRLLVVCDVALGKCVNLF KKDFSLTEAPPGYDSVHGVSETTSVP TDFQDDEFVYKTNQVKMKYIVKFC TPGDQIKEFHPHENTEVEEQRAPES SVPEAGDFQLPDIKPFNIKAGLQDA SANPVLDVSHIKGRVIDFVAQVIVF QTYTNQSHVPIEAKYIFPLDDKA GFEAFINGKHIVGEIKEKEEARQEYR EAVSQGHGAYLMDQDTPDVFVSV GNLPPRAKVLIKITYTELSIQSPVAIF FIPGTVAPWQDKALNENLQDVTET IRIKEIGAEQSFSLAMSIEMPYMEFI SSDTHLRQKSTDCAVVSTVEGSS LDSGGFSLHIGLRDAYLPRMWVEKH PEKESEACMLVFQPELADVLPDLRG KNEVIICLDCSSMEGVTFTQAKQV ALYALSLGEEQKVNIMQFGTYKE LFSYPKCITDSKMATEFIMSAAPSMG NTDFWKVLRYSLLYPSSEGFNILLI SDGHLQSESLTLQLVKRNQHTRVF TCAVGSTANRHILRTLQSCGAGVFE YFNSKSKHSWKKQIEAQMTRIRSPS CHSVSVKQQLSRDAPEPLQAPAW VPSLFHNDRLLYVGFIPHCTQATLQA FIQEKEFCTMVSTTELQKTTGTMIH KLAARALIRDYEDGILHDDETNHEM KKNIMKSLIHLSKENSITQFTSFVA VEKRDVNEIPFANVNPISSELVAKEDV DFLPYVSWQEKQPEASISQTEIDSSR LKHNKLSDGHGVLQPVSVSSEVNEK PSLLAAKRRKIKTIKCKSLDISDFE DRTAVAQSPATAQSLNFHLPVSVRP QLKAVEQQLHGNRLEPKQGGFRK LLMAKKCRNVPSLVSSAPAVTAEF SYLSACSSSAFLSPLCDIPSSLPHP LGGTHPPPLPLPDGTHLPSPLFGST HPPPPFLGGTLIPPPSFLGGTHLPP PPPLPGGTHIPPPPIPGGTLIPSSSL FGGTHLPPPLLSAGTHIPPPPLLSA GTHLPPPLLPAGTHIPPPPIGTH PPPPSFLGGTHLPPPLPGGTHIP PPPIPGGTLIPSSSFLGGTHLPPPP LLPAGTHIPPPPIGTHIPPPSFL GGTHLPPPPAGTQFSLSPIGFIPPKL GPPKLSHSHKLVGDTNIHDSEPPLL GFKDLCSDMGFSCGTAFSGSFSS KDFDPGKFSQGNNISFSKAPEMG VLHQSPFCSPKPPSAPPLVTVLCS EAPQSYFLNLQSAAVHQSPNNRVSE IIMESVSSLPSDYSSRDASSYLALE GAEDSLLGSSFETDTDEAAAFIAN DLTSETSSDEECFCDEDEQSPVP WASLFALQTEGFWKLTPELGLILN LNVNALLTSLEEKGIRSLGKGRERL LDLIATLLVQLFLYTKLEQEGMVAKS LIKMDDAFISRNIPWAFENIKKARE WARKTEGQYPSICRLELGDWESA TKQLLGIQPQANTSLHRILYYSQG	True	False	3.093	5.0	1.905	1.514	0.684	1.191	1.773