	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	ext reg
0	E9PYK3	PARP4_MOUSE	Mus musculus	Protein mono-ADP-ribosyltransferase PARP4	40.197708	S1239	S1229	40997131;40885482;30059200	MTLGIFANCIFCLKVKYLPRQQKKL QTDIKENGGKFSFLLNPQCTHVIVD SADVLSRCHLNSIQKNDVQIANPAFI QDSVRQRRLLDVRNYDPLSPAPAAP PAERSRSEVQSEYLPSDNTPEKENT EVTEVSAENVEIPPFLQDFEVVKYNI LEKVGGPETVVVELQSSQDPESCPF VITAHFLLADQKTRRESTGKQTSEGA IEYYESYVEDLKRQGFLLQEHFTAEA TQLASEKLQALLLEEVISSGALSQEV SDLLEVIWTEALGHLENTLLKPVNS MSLNDVSKAEGILLLVKTALKNGDS PGQLQKTMAEFYRLLPHRHPASEEV NLRLLAQKEDLCQLVRDMVNVCET NLSKPNPPSLAKYRALRCKIEHVDQ NTEEFSRVRKEVLQNNRSEQPVDIL QIFRVGRVNEATEFLSKLGNVRLLF HGSPVRNILGILSRGLLLPKVAEDRG VQRTDVGNLGSGIYFSDSLSTSIKYA HAGETDGSRLLVVCDVALGKCVNLF KKDFSLTEAPPGYDSVHGVSETTSVP TDFQDDEFVVYKTNQVKMKYIVKFC TPGDQIKEFHPHENTEVEEQRAEPS SVPEAGDFQLPDIKPFTNIKAGLQDA SANPVPLDSVHIKGRVIDFVAQVIVF QTYTNQSHVPIEAKYIFPLDDKAAVC GFEAFINGKHIVGEIKEKEEARQEYR EAVSQGHGAYLMDQDTPDVFTVSV GNLPPRAKVLIKITYITELSIQSPVAIF FIPGTVAPWQQDKALNENLQDTVET IRIKEIGAEQSFSLAMSIEMPYMIEFI SSDTHELRQKSTDCKAVVSTVEGSS LDSGGFSLHIGLRDAYLPRMWVEKH PEKESEACMLVFQPELADVLPDLRG KNEVIICLDCSSSMEGVTFTQAKQV ALYALSLLGEEQKVNIMQFGTGYKE LFSYPKCITDSKMATEFIMSAAPSMG NTDFWKVLRYLSLLYPSEGFRNILLI SDGHLQSESLTLQLVKRNIQHTRVF TCAVGSTANRHILRTLSQCGAGVFE YFNSKSKHSWKKQIEAQMTRIRSPS CHSVSVKWQQLSRDAPEPLQAPAW VPSLFHNDRLLVYGFIPHCTQATLQA FIQEKEFCTMVSTTELQKTTGTMIH KLAARALIRDYEDGILHDDETNHEM KKNIMKSLIIELSKENSLITQFTSFVA VEKRDVNEIPFANVPNISELVAKEDV DFLPYVSWQEKQPEASISQTEIDSSR LKHNKLSDGHGVLQPVSVSSEVNEK PSLLLAAKKRKIKTIKKCSLDISEDFE DRTAVAQSPATAQSLNFHLPLSVRP QLKAVEQQLHGNRLEPKQRGGFRK LLMAKKCRNVPDSLVSSAPAVTAEF SYLSACSSSSAFLSPLCDIPSSLPPHP LGGTHPPPPLPLPDGTHLPSPLFGST HPPPPLFGGTLIPPPSSLFGGTHLPP PPPLPGGTHIPPPPPIPGGTLIPPSSSL FGGTHLPPPPLLSAGTHIPPPPLLSA GTHLPPPPLLPAGTHIPPPPPITGSTH PPPPSSLFGGTHLPPPPPLPGGTHIP PPPPIPGGTLIPSPSSLFGGTHLPPPP LLPAGTHIPPPPPITGSTHPPPPSSLF GGTHLPPPPPAGTQFSLSPIGFIPPKL GPPKLSHSHKLVGDTNIHDSEPPLL GFKDLCSRDMGFSCGTAFSGSFASS KDFDPGKFSQGPNNISFSPKAPEMG VLHQSPFCSPPKPPSAPPLVTNVLCS EAPQSYFLNLQSAAVHQSPNNRVSE IIMESVESSLPSDYSSRDASSYLALE GAEDSLLGGSSFETDTDEAAAFIAN DLLTSIETSSDEECAFCDEDQESPVP WASLFALQTENGFWKLTPELGLILN LNVNALLTSLEEKGIRSLGTKGRERL LDLIATLLVLQFLYTKLEQEGMVAKS LIKMDDAFISRNIPWAFENIKKARE WARKTEGQYPSICQRLELGKDWESA TKQLLGIQPQANTSLHRILYYSQG	True	False	3.094	5.0	1.905	1.514	0.685	1.191	1.7