

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	ext ref
Q460N5	PAR14_HUMAN	Homo sapiens	Protein mono-ADP-ribosyltransferase PARP14	22.604328	S1104	S33;S1403;S1411	28411811;30379171;36240223	MAVPGSFPLLVEGSGWGPDPKLNLT KLQMYFQSPKRSGGGCEVRODPR SPSRFLVFFYPEDVVRQKVLERKNHE LVWQKGTFKLTVOLPATPDEIDHV FEEELLTKESKTKEDVKEPDVSEELD TKLPLDGGLDKMEDIPPEECENISLV AFENLKANVTDIMLILLVENISGLSN DDFQVEIIRDFDVAVVTFQKHIDTIR FVDDCTKHHSIKQLQSPRLEVTN TIRVENLPPGADDYSLKLFENPYNG GGRVANVEYFPEESSALIEFFDRKVL DTIMATKLDNFKNMPLSVFFPYASLG TALYGKEKPLIKLPAPFEESLDLPLW KFLOKKNHLIEEINDEMRRCHCELT WSQLSGKVTRPAATLVNEGRPRIKT WQADTSTLLSIRSIRSKYKVNPIKVDPT MWDTIKNDVKDDRILIEFDLTKEMV ILAGKSEDEVQSIIEVQVRELIESTTQKI KREEQSLKEKMIISPGRYFLCHSSL LDHLLTECPEIEICYDRVTQHLCLKG PSADVYKAKCEIQEKVYVYMAQKNIQ VSPFIFQFLQVNWKEFSKCLFIAQK ILALYELEGTTVLLTSCSSEALLEAEK QMLSALNYKRIEVENKEVLHGKKW KGLTHNLLKKQNSPNTVHINELTSE TTAEVIITGCVKEVNETYKLLNFVFE QNMKIERLVEVKPSLVIDYKTEKLL FWPKIKKVNQVSNPENKQKQKILL TGSKTEVLKAVDIVKQVWDSVCVKS VHTDKPGAKQFFQDKARFYQSEIKR LFGCYIELQENEVMEKGGSPAGQKC FSRTVLAPGVVLIQQGDLARLPVDV VVNASNEDLKHYGGLAAALSKAAGP ELQADCDQIVKREGRLLPGNATISKA GKLPYHHVIHAVGPRWVSGYEAPRCV YLLRRAVQLSLCLAEKYKRSIAIPAI SSGVFGFPLGRCVETIVSAIKENFQF KKDGHCLKEIYLVVSEKTVFAFAEA VKTVFKATLPDTAAPPGLPAAAGPG KTSWEKGSVSPGGLQMLLVKEGV QNAKTDVVVNSVPLDLVLSRGLSK SLEKAGPELQEEELDTVGQGVAVSM GTVLKTSSWNLDCRYVLHVVAPEW RNGSTSSLKIMEDIIRECMEITESLS LKSIAFPAIGTGNLGFPPKNIFAELIIE VFKFSSKNQLKTLQEVHLLHPSDH ENIQAFSDEFARRANGNLVSDKIPK AKDTQGFYGTVSSPDSGVYEMKIGSI IFQVASGDITKEEADVIVNSTSNFVN LKAGVSKAILECAGQVVERECSQQA QQRKNDYIITGGGFLRCKNIHVIGG NDVKSVS SVLQCEKKNYSSICLPA IGTGNAKQHPDKVAEAIIDAIEDFVQ KGSASVKKVVFVLPQVLDVIFYAN MKKREGTQLSSQSVMSKLASFLGF SKQSPQKKNHLVLEKKTESATFRVC GENVTVEYAIISWLQDLIEKQCPYT SEDECIKDFDEKEYQELNELQKKNLNI NISLDHKRPLIKVLGSRDVMQARDE IEAMIKRVRLAKEQESRADCISEFIE WQYNDNNTSHCFNKMTNLKLEDA RREKKKTVDVKINHRHYTVNLNTYT ATDTKGHSLSVQRLTKSKVDIPAHW SDMKQQNFCVVPELLPSDEYNTVAS KFNQTCSHFRIEKIERIQNPDLWNS YQAKKTMDAKNGQTMNEKQLFH GTDAGSVPHVNRNGFNRSYAGKNA VAYGGTYFAVNNANYANDTYSRPD ANGRKHVYVVRVLTGIYTHGNHSLIV PPSKNPQNPTDLYDTVDNVHHPSL FVAFYDYQAYPEYLITFRK	True	True	4.747	4.128	1.842	1.592	0.982	4.519	1.6