	UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochndrion	endoplas reticulu
	Q63HN8	RN213_HUMAN	Homo sapiens	E3 ubiquitin-protein ligase RNF213	32.296876	S82;S88;T830;S1838;S3009;S4209;S4212;T4835	S208;S217;S1258;S2273	29351928;27655845;30379171;40914422;39302247;38253038	MECPSCQHVSKEETPKFCSQCGERL PPAAPIADSENNNSTMASASEGEME CGQELKEEGGPCLFPGSDSWQENP EEPCSKASWTVQESKKKKRKKKKKG NKSASSELASLPLSPASPCHLTLLSN PWPQDTALPHSQAQQSGPTGQPSQP PGTATTPLEGDGLSAPTEVGDSPLQA QALGEAGVATGSEAQSSPQFQDHTE GEDQDASIPSGGRGLSQEGTGPPTS AGEGHSRTEDAAQELLLPESKGGSS EPGTELQTTEQQAGASASMAVDAVA EPANAVKGAGKEMKEKTQRMKQPP ATTPPFKTHCQEAETKTKDEMAAAE EKVGKNEQGEPEDLKKPEGKNRSA AAVKNEKEQKNQEADVQEVKASTLS PGGGVTVFFHAIISLHFPFNPDLHKV FIRGGEEFGESKWDSNICELHYTRD LGHDRVLVEGIVCISKKHLDKYIPYK YVIYNGESFEYEFIYKHQQKKGEYVN RCLFIKSSLLGSGDWHQYYDIVYMK PHGRLQKVMNHITDGPRKDLVKGK QIAAALMLDSTFSILQTWDTINLNSF FTQFEQFCFVLQQPMIYEGQAQLWT DLQYREKEVKRYLWQHLKKHVVPLP DGKSTDFLPVDCPVRSKLKTGLIVLF VVEKIELLLEGSLDWLCHLLTSDASS PDEFHRDLSHILGIPQSWRLYLVNL CQRCMDTRTYTWLGALPVLHCCME LAPRHKDAWRQPEDTWAALEGLSF SPFREQMLDTSSLLQFMREKQHLLS IDEPLFRSWFSLLPLSHLVMYMENF IEHLGRFPAHILDCLSGIYYRLPGLE QVLNTQDVQDVQNVQNILEMLLRL LDTYRDKIPEEALSPSYLTVCLKLHE AICSSTKLLKFYELPALSAEIVCRMIR LLSLVDSAGQRDETGNNSVQTVFQG TLAATKRWLREVFTKNMLTSSGASF TYVKEIEVWRRLVEIQFPAEHGWKE SLLGDMEWRLTKEEPLSQITAYCNS CWDTKGLEDSVAKTFEKCIIEAVSSA CQSQTSILQGFSYSDLRKFGIVLSAVI TKSWPRTADNFNDILKHLLTLADVK HVFRLCGTDEKILANVTEDAKRLIAV ADSVLTKVVGDLLSGTILVGQLELIIK HKNQFLDIWQLREKSLSPQDEQCAV EEALDWRREELLLLKKEKRCVDSLL KMCGNVKHLIQVDFGVLAVRHSQD LSSKRLNDTVTVRLSTSSNSQRATH YHLSSQVQEMAGKIDLLRDSHIFQL FWREAAEPLSEPKEDQEAAELLSEP EEESERHILELEEVYDYLYQPSYRKFI KLHQDLKSGEVTLAEIDVIFKDFVNK YTDLDSELKIMCTVDHQDQRDWIKD RVEQIKEYHHLHQAVHAAKVILQVK ESLGLNGDFSVLNTLLNFTDNFDDF RRETLDQINQELIQAKKLLQDISEAR CKGLQALSLRKEFICWVREALGGIN ELKVFVDLASISAGENDIDVDRVACF HDAVQGYASLLFKLDPSVDFSAFMK HLKKLWKALDKDQYLPRKLCDSAR NLEWLKTVNESHGSVERSSLTLATA INQRGIYVIQAPKGGQKISPDTVLHLI LPESPGSHEESREYSLEEVKELLNKL MLMSGKKDRNNTEVERFSEVFCSV QRLSQAFIDLHSAGNMLFRTWIAMA YCSPKQGVSLQMDFGLDLVTELKEG GDVTELLAALCRQMEHFLDSWKRF VTQKRMEHFYLNFYTAEQLVYLSTE LRKQPPSDAALTMLSFIKSNCTLRDV LRASVGCGSEAARYRMRRVMEELPL MLLSEFSLVDKLRIIMEQSMRCLPA FLPDCLDLETLGHCLAHLAGMGGSP VERCLPRGLQVGQPNLVVCGHSEVL PAALAVYMQTPSQPLPTYDEVLLCTP ATTFEEVALLLRRCLTLGSLGHKVYS LLFADQLSYEVARQAEELFHNLCTQ QHREDYQLVMVCDGDWEHCYLPSA FSQHKVFVTPQAPLEAIQAYLAGHYR VPKQTLSAAAVFNDRLCVGIVASERA GVGKSLYVKRLHDKMKMQLNVKNV	True	False	4.675	4.557	1.739	1.485

									DVVDKTPVIRSVILKLLLKYSFHDVK DYIQEYLTLLKKKAFITEDKTELYML FINCLEDSILEKTSAYSRNDELNHLE EEGRFLKAYSPASRGREPANEASVE YLQEVARIRLCLDRAADFLSEPEGGP EMAKEKQCYLQQVKQFCIRVENDW HRVYLVRKLSSQRGMEFVQGLSKPG RPHQWVFPKDVVKQQGLRQDHPGQ MDRYLVYGDEYKALRDAVAKAVLEC KPLGIKTALKACKTPQSQQSAYFLLT LFREVAILYRSHNASLHPTPEQCEAV SKFIGECKILSPPDISRFATSLVDNSV PLLRAGPSDSNLDGTVTEMAIHAAA VLLCGQNELLEPLKNLAFSPATMAH AFLPTMPEDLLAQARRWKGLERVH WYTCPNGHPCSVGECGRPMEQSICI DCHAPIGGIDHKPRDGFHLVKDKAD RTQTGHVLGNPQRRDVVTCDRGLPP VVFLLIRLLTHLALLLGASQSSQALIN IIKPPVRDPKGFLQQHILKDLEQLAK MLGHSADETIGVVHLVLRRLLQEQH QLSSRRLLNFDTELSTKEMRNNWE KEIAAVISPELEHLDKTLPTMNNLIS QDKRISSNPVAKIIYGDPVTFLPHLPR KSVVHCSKIWSCRKRITVEYLQHIVE QKNGKERVPILWHFLQKEAELRLVK FLPEILALQRDLVKQFQNVQQVEYS SIRGFLSKHSSDGLRQLLHNRITVFL STWNKLRRSLETNGEINLPKDYCST DLDLDTEFEILLPRRRGLGLCATALV SYLIRLHNEIVYAVEKLSKENNSYSV DAAEVTELHVISYEVERDLTPLILSN CQYQVEEGRETVQEFDLEKIQRQIVS RFLQGKPRLSLKGIPTLVYRHDWNY EHLFMDIKNKMAQDSLPSSVISAISG QLQSYSDACEVLSVVEVTLGFLSTAG GDPNMQLNVYTQDILQMGDQTIHV LKALNRCQLKHTIALWQFLSAHKSE QLLRLHKEPFGEISSRYKADLSPENA KLLSTFLNQTGLDAFLLELHEMIILK LKNPQTQTEERFRPQWSLRDTLVSY MQTKESEILPEMASQFPEEILLASCV SVWKTAAVLKWNREMR						