

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	extracellular region
Q6ZTR5	CFA47_HUMAN	Homo sapiens	Cilia- and flagella-associated protein 47	22.903221	S816;S1065;T1072	NaN	38253038	MNTQKGLTINVHRGSLAMSIQRGS LVPRDMDSSGRDMQLRVPAEVKFL DTMAGRVRYLPIVHNICRWQKIR FKEPVKQPKLMLTSLDKELASGLQ MTAMVEYHPDKDEDTDFRLLSIEI KTTEIPLIGLIPSCLEIEISVNFGLT VANSKVYSKEITITNHGKAPGIFKAE YHGQLPILIFPTSGIVDAKSSMVIKVD FCADQPRIVDEEAIVILQGOPEMLLS IKAHVVEQIHELLSMSSDRRLCEIHF GPVFFGSSKIKHARVYNNSPPEINW VAIIQDDAVGEEELGTDIQRTDIALN NLTYIRKIKNIDTTHIISCLPNEGTLQP YQKTVITFCFTPKLMAVGKKDIGPSY RDYALFLRFESVSGSKDGFLRDDDDY KTIKSERFQKVELALGTGLPVLLQF DPGPVLNFKPCFMGERSEIQCIKNQ CELLPVTYHFKKTANFEIDPEKGGIT GGGMVDVMCSFVPHQLGVFKVKQ MIEIHLVAEEDLQSLSVKSFHHVYL AFNSICKASTKKVVMKFPDGLPSIR NPTGKFVVKDLAKRKNYAPVAMLQS AMTRTHNHRSCPEPVKDMLLAFP DRAATIRSKDHHKHFRIPTKVPRFN YVNHDFAYTTFEKQKQLHENYYA MYLKYLRSVRLQKKQAERERMYSYD DTDIGLEPGSGLKSPSEAEIEEELS SAANSIRANRLLTTRGIASQEEESVR RKVLKGLKSEPSTPQEKHDCSLMLT PKQIHQVIVGPSVLNFGNICVNSPNT HLLHVINMLPMHVLLQLDLDLEELQ KTNQFSYVILPTSSTYISMVFDSPYIG KFWKSFTFTVNNVPSGHILVAVVQ PVTLELSSNELVLRPRGFFMKTCFR GTVRLYNRQNCQAQFQWQPVNTGR GIAFSICPAKGTVEAYSSLECEVTWQ QGFSSPEEGEFILHVFQGNALKLKC VAHLGRTKVLLQPRILFSNCPQGLT TWRKAILQNVGQNHAYFKVCSQSLL PIINIIPSQGVVFGGITVLNISKPTV AEKFDTRAKVSIRHANVIDLRIGGSA EADVEINPDVFNFSGAYIGGTQIIPF VIKNGGITRARVEFNLDKDFPDFSMD LKDKSEEFKDPVAVPYISLELEENTS LECSITFSPEKVTVEFIIQVQINFFE SSKLYTKYLSSSPSNPKTVPLIRPCYV QATALQSPNLSSTKFVFEIPLHEM NPNNKVTKQNLVLYNITKHHVTW TLDLNNTGKLFKDGTFKFSVLNGLIR PNEKYNVSI SFCPNRPGTYADIPML LNYIPVCYKILHLTGEVKSPELLFDPP FIFFTPVLDITTVMDINILPQNYFRN STLCVQIPTVRLLDGEEIHPHSVKFP KGRVIPGSHSGINNKLTCHLSFKSSK PVSFFTNLLFCDDRKNWFLPVTAT AENCILTYPYMAIHLDKQNIILKNDK DEYLKTRDGVLPYQDAKPPSPASI KTYTTSKFNDAEPAKGNLFIGVEVL PENLHLDSEETSEEDHGSLEKEKYE QFLSLEEGTKAHYFFEKVVNAAQTW FSLFGWPEGPHSFSIPETIRRDVYKM QFYSSTSPQKFSRQNDFSKYNKTIY DVLLHLSGKMPPGINSSQSLPVDNH EKRVQLHLQHSLLDFLNAQGGCI SHVLEPFLLPEDYKRWIEIMSSNT MPVSSCTPKKCSIVIEMSKFEAWS KRAWTDVFLQIYKVLVLSRVVYCSN NMPPICVQNTPKVNPCFASNNIYSD SERILLSWMNINYEENTRHVWKNCH KDVIPSERWIVNFDKDLSDGLVFAT QLGAYCPFLIESHFINMYTRPKSPEE YLHNCLHIVNTLYEIDFVIEIQATDIC DPNPILMLMLCVYMYERLPTYLPKK VVSFECTLHDTVLNKILLKNSSSRNL VYNARIVGRDAADFSLSQKGNVVTIS PRNEINVTLKFTSRFIRPAEASLLIS KPKNAVRGITMTFALKGKVLDFKAID IHKCESPCYQFQEVTVNVKNPFHTAG	None	None	None	None	None	None	None	None	

DFSVILVESSTFVSSPTKLTESRQYPK
HDDDMSSSGSDTDQCCSDSPNVLH
TSIKSTFIREFFCSMHTVHLGVKGT
SLELRFLPFNMHVRYCVIILSNKKIG
QLIYVAEGKGMTPLPSSCLPMNTSS
SPVYVSTTREETGPNKKYPVLYLKCKP
YQILYVDLKLPMTNEAKEKALAFAA
QQQMSSEIYERRLITGTLESSIRVAI
ALLGLTKIETLMLFRISKLRKPKTVSY
TTEVSLPKYFYIPEKISIPWIPEPQVIK
LSKAKASDGSVPLPLQFLPLQSGRYP
CKILLKSRVDVRAIYVEGIVNEEQPE
AKFEFETPAFEALTQNIPIKNQNTDK
WTFQVTIEGEWFGPVDLHVGPDEI
VEYPLTFKPIFEVITGKLLQNEVDG
REHIFDIKGVGKKPSALEHITVECQV
GNVTQKHITLPHFTNTALTFKVTADL
PIVWGNPQITVYPYKEILYLIHVRPW
KRGILKGTITFSTTRRCTTRKHDDY
EEDTDQDQALSCLDSITEQSSILDDA
DTYGNFNLRFWYNLEIHSTPGPPI
EIMEMTCIALDSTCIEIPLSNPKDRG
LHLEVQLTSAALNGDNEIILSPLQCT
KYIVWYSPATTGYSDESIIFQPEMAE
EFWYLLKLTIELPKPTTMPEIQCDLG
KHVTQIPLVNCETHETLKLQVTNSNP
ENFVLDINRKSQLIHSPHSTTELPVLF
YPSALGRADHQACINFYCTQFTEWK
FYLSGVGLFPQPLDTERITRIGLQST
IVPFKNPTMEDVLIDILTSVEHPRN
LVMDHCWDSFIYESSAFRFSSPSEIQ
GIALPPKGNIDISLLFIPQIMKLNKTM
VIEMTKANGKYWPIDNFDLIDIKFK
SIVGIDSEEIQAHWYPIVGLPQAPP
KSPVVIQCQSRKRAEEKVEIILNAG
FFGFSLTPDLTEVLVIPKRNSHNFC
DPNEIPKIHFEFEYEQFESEAMKSKL
ESCVALYMIKSYDIMAKRITFIFNLV
FTPCKPLRSHITLKECVTEGIWKFP
MLIATEPDTDAVIDIEGVGLFKESVF
ELRLKSQTRNPEPFTAHLPGSDLE
FFVKPQAGELLPFNTNGTLITVGFKP
KMYCRKYKATLVIQTEEMYWKYEIN
GLTPTTVPKNAKAKIDATHKTHDN
MPVRPHNFVRENTKLIRTVSSTIK
GAPLVKNO