

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
095477	ABCA1_HUMAN	Homo sapiens	Phospholipid-transporting ATPase ABCA1	26.21016	S350	S1042;S1296;S2054	29351928	MACWPQLRLLWKNLTFRRRTQQLLELVEAWPLFIFLILISVRLSYPPYEQHECHFPNKAMPAGTLPWWQGIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSADARLLLSYQKDTSMKDMRKVLRTLQQIKKSSNLKQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLDGQEVSELCGLPREKLAAAE RVLRSNMDILKPIRLTNSTSPFPSKELAEATKLLHSLGTLAQELFSMRSWSDMRQEVMLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNGTEEDAETFYDNSTTPYCNLDMKNLESSPLSRJIWKALP LLVGKILYTPDTPATROVMAEVNKTQELAVFHDLEGMWEELSPKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTQAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRTISRMECVNLNKLEPIATEVWLINKSMELDERKFWAGIVFTGITPGSIELPHHV KYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQAHRVLTGTEKKTGVYMQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIKGVYEKEARKETMRIMGLD NSILWFSWFISSLIPLLVSAGLLVILKLGNNLLPYSDPSVVFVFLSVFAVVTI LQCFLLISTLFSRANLAAACGGIYFTL YLPYVLCVAWQDYVGFLLKIFALLS PVAFGFGCEYFALFEEQIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTF LYGVMTWYIEAVFPGQYGIPRPWYF PCTKSYWFGEESDEKSHPGSNQKRI SEICMEEEPHTHLKLGVSQNLVKVYR DGMKVAVDGLALNFYEGQITSFLGH NGACKTTTMSILTGLFPPTSGTAYIL GKDIRSEMSTIRQNLGVCQPHNVLF DMLTVEEHIWFYARLKLSEKHVKA EMEQMALDVGLPSSKLKSKTSQLSG GMQRKLSVALAFVGGSKVILDEPT AGVDPYSRRGIWELLKYRQGRTHILSTHHMDEADVLDRIAISHGKLC VGSLLFLKNQLGTGYLLTLVKKDVES SLSSCRNSSSTVSYLKKEDSVSQSSS DAGLGS DHESDTLTDVSAISNLIRK HVSEARLVEDIGHELTYVLPYEAAKE GAFVELFHEIDDRLSDLGISSYGISET TLEEIFLKVAEESGVDAETSDGTLPARRNRRAFGDKQSCLRPFTEDDAADP NDSIDPESRETDLLSGMDGKGSYQ VKGWKLTQQQFVALLWKRLLIARRS RKGFFAQIVLPAVFVCIALVFLVPP FGKYPSELEQPWMYNEQYTFVSNDAPEDTGTLELLNALKDPGFGTRCMEGNPIPDTPCQAGEEWTAPVPQTI MDLFFQNGNWTMQNPSPACQCSSD KIKKMLPVCPPGAGGLPPPQRKQNT ADILQDLTGRNISDYLVKTYVQIIAKS LKNKIWVNEFRYGGFSLGVSNTQAL PPSQEVNDAIKQMKKHLKAKDSSA DRFLNSLGRFMTGLDTKNNVKVWF NNGGWHAISSFLNVINNALRANLQ KGENPSHYGITAFNHPLNLTKQQLS EVALMTTSVDVLSICVIFAMSFVPA SFVVFLIQERVSKAKHLQFISGVKPI YWLSNFVWDMCNYPVATLVIIIFIC FQKSYVSSNTLPLVALLLLLYGWSI TPLMYPASFVFKIPSTAYVVLTSVNL FIGINGSVATFVLELFTDNKLNININD ILKSVFLIFPHFCLGRGLIDMVKNQA MADALERFGENRFVPLSWDLVGR NLFAMAVEGVVFLITVLIQYRFFIRP RPVNAKLSPLNDEDEDVRRERQRIL DGGQNDILEIKELTKIYRRKRPAV DRICVGIPEGCFLLGVNGAGKSSST	False	True	2.699	3.669	2.72	4.541	3.302	5.0	3.416

