	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	
0	Q8IWN7	RP1L1_HUMAN	Homo sapiens	Retinitis pigmentosa 1-like 1 protein	24.491385	S320;S1617	NaN	28411811;30379171;30620550;31492838	MNSTPRNAQAPSHRECFLPSVARTP SVTKVTPAKKITFLKRGDPRFAGVRL AVHQRAFKTFSALMDELSQRVPLSF GVRSVTTPRGLHSLSALEQLEDGGC YLCSDKKPPKTPSGPGRPQERNPTA QQLRDVEGQREAPGTSSSRKSLKTP RRILLIKNMDPRLQQTVVLSHRNTR NLAAFLGKASDLLRFPVKQLYTTSGK KVDSLQALLHSPSVLVCAGHEAFRT PAMKNARRSEAETLSGLTSRNKNGS WGPKTKPSVIHSRSPPGSTPRLPERP GPSNPPVGPAPGRHPQDTPAQSGPL VAGDDMKKKVRMNEDGSLSVEMK VRFHLVGEDTLLWSRRMGRASALTA ASGEDPVLGEVDPLCCVWEGYPWG FSEPGVWGPRPCRVGCREVFGRGG QPGPKYEIWTNPLHASQGERVAARK RWGLAQHVRCSGLWGHGTAGRERC SQDSASPASSTGLPEGSEPESSCCPR TPEDGVDSASPSAQIGAERKAGGSL GEDPGLCIDGAGLGGPEQGGRLTPR ARSEEGASSDSSASTGSHEGSSEWG GRPQGCPGKARAETSQQEASEGGDP ASPALSLSSLRSDDLQAETQGQGTE QATGAAVTREPLVLGLSCSWDSEGA SSTPSTCTSSQQGQRRHRSRASAMS SPSSPGLGRVAPRGHPRHSHYRKDT HSPLDSSVTKQVPRPPERRRACQDG SVPRYSGSSSSTRTQASGNLRPPSSG SLPSQDLLGTSSATVTPAVHSDFVSG VSPHNAPSAGWAGDAGSRTCSPAPI PPHTSDSCSKSGAASLGEEARDTPQ PSSPLVLQVGRPEQGAVGPHRSHCC SQPGTQPAQEAQRGPSPEASWLCGR YCPTPPRGRPCPQRRSSSCGSTGSS HQSTARGPGGSPQEGTRQPGPTPSP GPNSGASRRSSASQGAGSRGLSEEK TLRSGGGPQGQEEASGVSPSSLPRS SPEAVVREWLDNIPEEPILMTYELAD ETTGAAGGGLRGPEVDPGDDHSLEG LGEPAQAGQQSLEGDPGQDPEPEGA LLGSSDTGPQSGEGVPQGAAPEGVS EAPAEAGADREAPAGCRVSLRALPG RVSASTQIMRALMGSKQGRPSSVPE VSRPMARRLSCSAGALITCLASLQLF EEDLGSPASKVRFKDSPRYQELLSIS KDLWPGCDVGEDQLDSGLWELTWS QALPDLGSHAMTENFTPTSSSGVDI SSGSGGSGESSVPCAMDGTLVTQGT ELPLKTSNQRPDSRTYESPGDLENQ QQCCFPTFLNARACACATNEDEAER DSEEQRASSNLEQLAENTVQEEVQL EETKEGTEGEGLQEEAVQLEETKTE EGLQEEGVQLEETKETEGEGQQEEE AQLEEIEETGGEGLQEEGVQLEEVK EGPEGGLQGEALEEGLKEEGLPEEG SVHGQELSEASSPDGKGSQEDDPVQ EEEAGRASASAEPCPAEGTEEPTEPP SHLSETDPSASERQSGSQLEPGLEK PPGATMMGQEHTQAQPTQGAAERS SSVACSAALDCDPIWVSVLLKKTEKA FLAHLASAVAELRARWGLQDNDLLD QMAAELQQDVAQRLQDSTKRELQK LQGRAGRMVLEPPREALTGELLLQT QQRRHRLRGLRNLSAFSERTLGLGP LSFTLEDEPALSTALGSQLGEEAEGE EFCPCEACVRKKVSPMSPKATMGAT RGPIKEAFDLQQILQRKRGEHTDGE AAEVAPGKTHTDPTSTRTVQGAEGG LGPGLSQGPGVDEGEDGEGSQRLN RDKDPKLGEAEGDAMAQEREGKTH NSETSAGSELGEAEQEGEGISERGE TGGQGSGHEDNLQGEAAAGGDQDP GQSDGAEGIEAPEAEGEAQPESEGV EAPEAEGDAQEAEGEAQPESEDVEA PEAEGEAQPESEDVETPEAEWEVQP ESEGAEAPEAEKEAQPETESVEALET EGEDEPESEGAEAQEAEEAAQEAEG QTQPESEVIESQEAEEEAQPESEDVE ALEVEVETQEAEGEAQPESEDVEAP	None	None	None	None	None	None	None	None	

									EAEGEMQEAEEEAQPESDGVEAQP KSEGEEAQEVEGETQKTEGDAQPES DGVEAPEAEEEAQEAEGEVQEAEGE AHPESEDVDAQEAEGEAQPESEGVE APEAEGEAQKAEGIEAPETEGEAQP ESEGIEAPEAEGEAQPESEGVEAQD AEGEAQPESEGIEAQEAEEEAQPEL EGVEAPEAEGEAQPESEGIEAPEAEG EAQPELEGVEAPEAEEEAQPEPEGV ETPEAEGEAQPESEGETQGEKKGSP QVSLGDGQSEEASESSSPVPEDRPT PPPSPGGDTPHQRPGSQTGPSSSRA SSWGNCWQKDSENDHVLGDTRSP DAKSTGTPHAERKATRMYPESSTSE QEEAPLGSRTPEQGASEGYDLQEDQ ALGSLAPTEAVGRADGFGQDDLDF								