

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence	intracellular	extracellular	cytosol	nucleus	mitochondrion	endoplasmic reticulum	golgi apparatus	plasma membrane	extracellular region
A0A096P6L8	A0A096P6L8_RAT	Rattus norvegicus	Fibronectin	25.563465	NaN	NaN	34502162	MLRGPFGPGRLLLLLAVLCLGTSVRCETGKSKRQAQQIVQPPSPVAVSQSKPGCFDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCEKPEPEETCFDKYTGNTRYKVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIGDKWRRPHETGGYMLECLCLGNGKGEWTCPIAEKCFDHAAGTSYVVVGETWEKPYQGWMMVDCCLGEGNGRICTSRNRCDQDTRTSYRIGDTWSKDNDRGNLLQCVCTGNRGEWKCHERHVLQASASAGSGSFTDVRTAIYQPQTHPQPAPYGHCVTDSGVVYVSGMQWLKSSQGDQKMLCTCLGNGVSCQETAVTQTYGGNSNGEPCVLPFTYNGRTFYSCITEGRQDGHLCWSTTSNYEQDQKYSFCTDHAVLVQTRGGNSNGALCHFPFLYNNRNYTDCTSEGRRDNMKWCGETTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQWDKQHDLGHMMRCTCVGNRGEWACIPYSQLRDQCIVDDITYNVNDTFHKRHEEGHMLNCTCFGQGRGRWKCDPIDQCQDSETRTFYQIGDSWEKFGVHGVRYQCYCYGRGIGEWHCQPLQTYPGTTGPVQVIITETPSQPNSHPIQWNAPEPSHITKYLLRWRPKTSTGRWKEATIPGHLNSYTIKGLTPGVYEGQLISIQYGHQEVTRFDFTTSASTPVTSTNTVTGETAPFSPVVATSESVTEITASSFVSVWSASDTVSGFRVEYELSEEGDEPOYLDLPS TATSVNIPDLLPGRKYIVNVYQISEEGKQSLILSTSQTAPDAPPDPTVDQVDDTSSIVVRWSRPAQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYNITTYAVEENQESTPVFIQOETTGVPRSDDDVPAPKDLQFVEVTDVKVTIMWTPPNSAVTGYRVDVLPVNLPEHGQRLPVNRNTFAEVTGLSPGVTYLTKVFAVHQGRESKPLTAQQTTKLDAPTNLQFVNETDRITVLTWTPPRARIAGYRLTVGLTRGGQPKQYNVGPMAKYPLRNLQPGSEYVTLMAVKGNQQSPKATGVFTTLQPLRSIPPYNTEVTETTIVITWTPAPRIGFKLGVRPSQGGAPREVTSDSGSIVVSGLTPGVEYTYTIQVLRDGQERDAPIVNRVVTPLSPPTNLHLEANPDGTGLTVSWERSTTPTDITGYRITTTPTNGQQGTALEEVVHADQSSCTFENLNPGLYVNSVYTVKDDKESAPISDTVIPEVPQLTDLDFVDITDSSIGLRWTPLNSSSTIIGYRITVVAAGEGIPFEDFVDSVGYTVTGLEPGIDYDISVITLINGGESAPTTLQQTAVPPPTDLRF TNIGPDTMRVWAPPSPSIELNLLVRYSPVKNEDVAELSISPSDNVAVLTNLLPGTEYLVSVSSVYEQHESIPLRGRQKTGLDSPTGFDSSDVTANSFTVHWVAPRAPITGYIIRHHAHESAGRPRQDRVPPSRNSITLNLNPGTEYIVTIAVNGREESPLIGQQSTVSDVPRDLEVIASTPTSLLSWEPPAVSVRYRITYGETGGNSPVQEFVPGSKSTATINNIKPGADYTITLYAVTGRGDSPASSKPVSI NYQTEIDKPSQMQVTDVQDNSISVRLWPSTSPVTGYRVTTAPKNGLGPTKSQTVPDQTEMTEIQLQPTVEYVSVYAQNRRNGESQPLVQAVTNIDRPKGLAFTDQVDSIKIAWESPGQVSRYRVTYSSPEDGIHELFPAPDGEDTAELHGLRPGSEYTVSVVALHGGMESQPLIGVQSTAIPAPTNLKFTQVSPPTLTAQWTAPSVKLTGYRVRVTPKEKTGPMKEINLSPDSTSVVSGMLVATKYEVSVYALKDILTSTRPAQGVVTTLENVSPRRARVTDATETTTISWRKTETITGFQVDAIPANGQTPVQRTISPDVRSYTTITG	False	True	2.084	2.711	2.278	2.165	1.675	4.554	5.0

								LQPGTDYKIHLYTLNDNARSSPVVID ASTAIDAPSNLRFLTTTPNSLLVSWQ APRARITGYIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYIYVIALKN NQKSEPLIGRKKTDDELQVLVTLPHF NLHGPEILDVPSTVQKTPFVTNPGYD TENGIQLPGTSHQQPSVGGQMIFFEE HGFRRTTPPTAATPVRLRPRPYLPNV DEEVQIGHVPRGDVDYHLYPHVPGGL NPNASTGQEALSQTTISWTPFQESS EYIISCQPVGTDEEPLQFQVPGTSTS ATLTGLTRGVTYNIIVEALHNQRRHK VREEVTVGNTVNEGLNQPTDDSCF DPYTVSHYAVGEEWERLSDSGFKLT COCLGFGSGHFRCDSSKWCHDNGV NYKIGEKWDRQGENGQRMSCTCLG NGKGEFKCDPHEATCYDDGKTYHV GEOQWKEYLGAICSCTCFGGQRGW RCDNCRPGAAEPSDGTGHTYN QYTRQHRTNTNVNCPICFMPLD VQADRDSRE							
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