

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							
P00520	ABL1_MOUSE	Mus musculus	Tyrosine-protein kinase ABL1	25.875327	S187	S50;T70;T115;T128;T139;T172;T185;T215;T226;S229;T253;T257;T393;T413;S446;T547;S559;S569;S618;S619;S620;S658;S682;S717;T734;T750;T812;T821;T844;S909;S970	30059200	MLEICLKLVGCKSKKGLSSSSCYLE EALQRPVASFDFEPOGLSEARWNSK ENLLAGPSENDPNLFVALYDFVASG DNLTLSITKGEKLRVLGYNHNGEWCE AQTKNGQGWVPSNYITPVNSLEKHS WYHGPVSRNAAEYLLSSGINGSFLV RESESSPGQRSISLRYEGRVYHYRIN TASDGKLYVSSSESRFNTLAELVHHH STVADGLITTLHYAPKRNKPTIYGV SPNYDKWEMERTDITMKHKLGGGQ YGEVYEGVWKYSLTVAVKTLKEDT MEVEEFLKEAAVMKEIKHPNLVQLL GVCTREPPFYIITEFMTYGNLLDYLR ECNRQEVSAVLLYMATQISSAMEY LEKKNFIHRDLAARNCLVGENHLVK VADFGLSRLMTGDTYTAHAGAKFPI KWTAPELAYNKFSIKSDVWAFGVL LWEIATYGMSPYPGIDLSQVYELLEK DYRMERPEGCEKVVYELMRACQWQ NPSDRPSFAEIHQAFETMFQESSISD EVEKELGKRGRTRGAGSMLQAPELP TKTRTCRRAAEQKADPDTPELLHTK GLGESDALDSEPAVSPLLPRKERGPP DGSLNEDERLLPRDRKTNLFSALIK KKKKMAPTPPKRSSSFREMDGQPD RRGASEDDSRCLCNGPPALTSDAAE PTKSPKASNGAGVPNGAFREPGNSG FRSPHMKKSSSTLTGSRLAAEEES GMSSSKRFLRSCSASCMPHGARDT EWRSVTLPRDLPSAGKQFDSSTFGG HKSEKPALPRKRTSESRSEQVAKST AMPPPRLVKKNEAAEEGFKDTESS PGSSPPLTPKLLRRQVTASPSGSL HKEEATKGSASGMGTAPATAEPAPPS NKVGLSKASSEMRVRRHKHSSESP GRDKGRLAKLKPAPPPACTGKAG KPAQSPSQEAGEAGGPTTKCTSLA MDAVNTDPTKAGPPGEGLRKPVPPS VPKQSTAKPPGTPTSPVSTPSTAPA PSPLAGDQQPSSAAFPLISTRVSLRK TROPFERIASGTITKGVLDSTEALCL AISRNSEQMASHSAVLEAGKNLYTF CVSYVDSIQMRNKFAFREAINKLE SNLRELQICPATASSGPAATQDFSKL LSSVKEISDIVRR	None	None	None	None	None	None	None	None	None	None	None	None	None	None	None	None