	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	extracellular region
0	A2A863	ITB4_MOUSE	Mus musculus	Integrin beta-4	25.019509	S227	S773;S1071;S1121;S1451;S1454;S1470;T1483;S1490;T1526;S1787	34418053	MAGPCCSPWVKLLLLAAMLSASLPG DLANRCKKAQVKSCTECIRVDKSCA YCTDELFKERRCNTQAELLAAGCRG ESILVMESSLEITENTQIDTSLHRSQ VSPQGLQVRLRPGEERSFVFQVFEP LESPVDLYILMDFSNSMSDDLDNLK QMGQNLAKILRQLTSDYTIGFGKFV DKVSVPQTDMRPEKLKEPWPNSDP PFSFKNVISLTENVEEFWNKLQGER ISGNLDAPEGGFDAILQTAVCTRDIG WRADSTHLLVFSTESAFHYEADGAN VLAGIMNRNDEKCHLDASGAYTQYK TQDYPSVPTLVRLLAKHNIIPIFAVTN YSYSYYEKLHKYFPVSSLGVLQEDSS NIVELLEEAFYRIRSNLDIRALDSPR GLRTEVTSDTLQKTETGSFHIKRGEV GTYNVHLRAVEDIDGTHVCQLAKED QGGNIHLKPSFSDGLRMDASVICDV CPCELQKEVRSARCHFRGDFMCGH CVCNEGWSGKTCNCSTGSLSDTQP CLREGEDKPCSGHGECQCGRCVCY GEGRYEGHFCEYDNFQCPRTSGFLC NDRGRCSMGECVCEPGWTGRSCDC PLSNATCIDSNGGICNGRGYCECGR CHCNQQSLYTDTTCEINYSAIRLGLC EDLRSCVQCQAWGTGEKKGRACDD CPFKVKMVDELKKAEEVVEYCSFRD EDDDCTYSYNVEGDGSPGPNSTVLV HKKKDCPPGSFWWLIPLLIFLLLLLA LLLLLCWKYCACCKACLGLLPCCNR GHMVGFKEDHYMLRENLMASDHL DTPMLRSGNLKGRDTVRWKITNNV QRPGFATHAASTSPTELVPYGLSLRL GRLCTENLMKPGTRECDQLRQEVE ENLNEVYRQVSGAHKLQQTKFRQQ PNTGKKQDHTIVDTVLLAPRSAKQM LLKLTEKQVEQGSFHELKVAPGYYT VTAEQDARGMVEFQEGVELVDVRV PLFIRPEDDDEKQLLVEAIDVPVGTA TLGRRLVNITIIKEQASGVVSFEQPEY SVSRGDQVARIPVIRHILDNGKSQVS YSTQDNTAHGHRDYVPVEGELLFHP GETWKELQVKLLELQEVDSLLRGRQ VRRFQVQLSNPKFGARLGQPSTTTVI LGEHDETDRSLINQTLSSPPPPHGD LGAPQNPNAKAAGSRKIHFNWLPPP GKPMGYRVKYWIQGDSESEAHLLDS KVPSVELTNLYPYCDYEMKVCAYGA QGEGPYSSLVSCRTHQEVPSEPGRL AFNVVSSTVTQLSWAEPAETNGEIT AYEVCYGLVNEDNRPIGPMKKVLVD NPKNRMLLIENLRESQPYRYTVKAR NGAGWGPEREAIINLATQPKRPMSI PIIPDIPIVDAQGGEDYENFLMYSDD VLRSPASSQRPSVSDDTGCGWKFEP LLGEELDLRRVTWRLPPELIPRLSAS SGRSDEDGSVAGGVEGEGSGWIRGA TPRPPGEHLVNGRMDFAYPGSANSL HRMTAANVAYGTHLSPHLSHRVLST SSTLTRDYHSLTRTEHSHSGTLPRDY STLTSLSSQDSRGAVGVPDTPTRLVF SALGPTSLKVSWQEPQCDRMLLGYS VEYQLLNGGEMHRLNIPNPGQTSVV VEDLLPNHSYVFRVRAQSQEGWGR EREGVITIESQVHPQSPLCPLPGSAF TLSTPSAPGPLVFTALSPDSLQLSWE RPRRPNGDILGYLVTCEMAQGGAPA RTFRVDGDNPESRLTVPGLSENVPY KFKVQARTTEGFGPEREGIITIESQV GGPFPQLGSHSGLFQNPVQSEFSSV TSTHSTTTEPFLMDGLTLGTQRLEA GGSLTRHVTQEFVTRTLTASGSLST HMDQQFFQT	None	None	None	None	None	None	None	None	None