

Additional file 2. Alignment of a selection of human FERM proteins from Lobe 2 through the 16 kDa fragment of 4.1R

FERM Lobe B

PTN3_HUMAN	QTRHLYFQLKMDCEGRITCPLNSAVVIASYAVQSHFCDYNSSIHPGILSDSHFIPDO-----NEDFLTKVESLHEQHS-GLKQSEAESCYINIARTLDFYGVELHSGRDLNLD
PTN4_HUMAN	YTRYQYFDQIKQDILTGRPPPSNTAAIASFAVQSELGDYDQSENLSGMLSDYSFIPNQ-----PQDFEKEIAKLHQHQHI-GLSPAEEAFNYNLNTARTLELYGVEFHARDQSNNE
41_HUMAN	ITRYYLCLQLRQDIVAGRPPCSFATLALLGSYTIQSELGDYDPLEHGVDMSDFKLAAPNQ-----TKEEEKVMELHKSYR-SMTPAQADLEFLENAKKLSMYGVDLHKAKDLEGVD
E4L1_HUMAN	ITRYYLCLQLRQDITGRPPCSFVTHALLGSYTQAEIGDYDAEEHVGNMVSCLRAPNQ-----TREERIMELHKTYRGMTPEGEAEIHFLENAKKLSMYGVDLHH-AKDSEGID
E4L2_HUMAN	ITRYFLCLQLRQDIAASERPPCSFVTHALLGSYTQAEIGDYDPEEEHGSIDLSEFOFAPTO-----TKEEEKVAELHKTHRGLSPAQADSQFLENAKRLLSMYGVDLHH-AKDSEGVD
E4L3_HUMAN	ITRYFLCLQLRQDITGRPPCSFVTHALLGSYTQAEIGDYDPEEEHGSIDLSEFOFAPTO-----TKEEEKVAELHKTHRGLSPAQADSQFLENAKRLLSMYGVDLHH-AKDSEGVD
E4LB_HUMAN	FTRYLFVQLRLHDILSCKLKCPYETAVELAALCLOAELGECELPFHTPELVSEFRFIPNQ-----TEAMEFDIQFWKECRGKSPAQAEQSYLNKAKWEMYGVDMVVGRDGCEY
Q9Y4F1	LTRYLFALQVKQDILAQGRUTNDTSALLISHIVQSEICDFDEALDR-EHLAKNKYIPOQ-----DALEDKIVEFHNNHI-GQTPAESDFQLLEIARRLEMYGIRLHPAKDREGTK
E41LA_HUMA	ITRYQFFLQVKQDVLOQRLPCPVNTAAQLGAYAIQSELGDYDPYKHTAGVSSEYRVPDQ-----KEELEEAIERIHKTLTM-QQIPSEAEQNLRTAKSLEMYGVDLHPVYGENKSE
Q86WP8	LTRYLLYQKIKRDIFHGRLLCSFSDAAYLGACIVQAEGLDYDPDEHPENVISFEIFPKQ-----SQKLERKIVEIHKNELRGQSPPVAEFNLLLKAHTLETYGVDPHPCKDSTGTT
EZRI_HUMAN	ITQKLLFLQVKEGIISDEIYCPPEAVVLLGSYAVQAKFGDYINKEVHKSGILSERLIPQRVMDQHKLTRDQWEDEIIVQVWHAEH-RGMLKDNAMEYLKIAQDLEMYGINYFEIKNKKGTD
TLN1_HUMAN	VQLNLLYVQARDIILSHPVSFDACEFAGFQCOIQFGPHNEQKHAGFLDLKDFLPKKEYVKQKGERKIFQAHKNCGQMSEIEAKVRYVKLARSLKTYGVSSFLVKEKMKGKKNLKVPR
JAK3_HUMAN	LEHLFAQHRSIDLVSGLRPVGLSLKEQGECLSLAVLDLARMAREQAQRPGEELLKTVSYKACLPPSLRDLIQGLSFVTRRIRRTVRRALRRVAAACQADRHSMAKYIMDLERLDPAGAAET
FAK2_HUMAN	TTRYLFFYQQIRNDYMQRYASKVSEGMALQLGCLELRRFKDMPHNALDKKSNFELLEKEVGLDLFFPKMQMENLKPQFRKMIQQTFFQQYASLRREEECVMKFNTLAGFANIDQETYRC
Consensus/51%	1TRYbbbLQ1+pDI1sGRLsCsbsTAAlltSasVQtELGDYDspcHhssY1s-b+FbPsQ.....scCEcKlbclHKpap.sbsssstbpbpbpst+pbpbbstspbH.s+Dppts-

FERM Lobe C

FERM domain ← → 16 kDa fragment

PTN3_HUMAN	IMIGIASACGAVVTKYICTSF--YPWNILKISFKRKKEFIHQFQKQAESREHIVAFNMLNY--RSCKNLWKSCVEHHHTFQAKKLLPQEKNVL-SQWTMGSR-----
PTN4_HUMAN	IMIGVMSGGILINKNRVRMNT-FPWLKIVKISFKCKQEFIQLRKELEHESRETLLGENMVNY--RACKNLWKACVEHHHTFRLRPLPPQKNFF-AHYFTLGSKFRYCGRTEVQSVQYG
41_HUMAN	IIIGCVCSSGLLVIKDKLRLINR-FPWPKVLKISYKRSSRFIKIIPGEQEYQESTIGEKLPSY--RAAKKLWKVCVEHHHTFRL-TSTDТИPK--SKFLALGSKFRYSGRTQAQTRQAS
E4L1_HUMAN	IMIGVCANGLLIVRDRRLRINR-FAWPKILKISYKRSNFYIKIIPGEYEQFESTIGEKLPNH--RSAKRLWKVCIEHHHTFRLVSP--EPPP--GFLVMGSKFRYSGRTQAQTRQAS
E4L2_HUMAN	IMIGVCASGLLIVRDRRLRINR-FAWPKVLKISYKRNNFYIKIIPGEFEQFESTIGEKLPNH--RAAKRLWKVCVEHHHTFRL--EAPPK--KFLTLGSKFRYSGRTQAQTRRAS
E4L3_HUMAN	SLGLPTGTILLIPEGANKIGLF-FWPKITKMDFKSKLTLVVVEDDQGR-EQEHTFVFLRDSARTCKHLWKCAVEHHHTFRLRTPGNSKSNR--SDFIRLGSRERFSGRTEYQATHGS
E4LB_HUMAN	INQAVANTGILVFQGFTKINA-FNWAKVRKLSFKRKRELKLRPDANSAYQDTLEGLMASR--DFCKSFWKICVEHHHTFRL--FEEFKPKPK--PVLFSRGSSERFSGRTQKVLDYV
Q9Y4F1	YFLGLLTPVGVVVVKNNKKQVVK--YFWPRITKVFHKETQE-BLRVLGKDCNETSFFEARSK--TACKHLWKCSVEHHHTFRLMPENESNSLSRKLSKFGSIRYKHYSGRTALQMSRDL
E41LA_HUMA	TFLGFTAAGFVVFRGNKRIHL--IKWPDVCKLKFEGKTEYV--IGTQKEKKAMLAFTSTPAACKHLWKCGVENQAEYKYA-KSSQIKTVSSSKIFFKGSRFRYSGCKVAKEVVEAS
Q86WP8	LWLGVDALGLNIEKDDKLTPKIGFPWSEIRNISFNDKKEV1K--PIDKKAPDFVYAPIVRLRINKRILQLCMGNHELY-MRRRKPDTEVQQMKAQAREEKHQKQLERQOLETEKKRR
EZRI_HUMAN	LGITKECVMRVDDEKTKEV1QEWNLNTNIKRWAAASKSFTLDFGYQDGYYSVQTTGEQIAQLIAGYIDIILKKKSKDHFGLEGDEESTMLEDVSPKSTVLQQQYNRVGVEHGSVAL
TLN1_HUMAN	FHVGLPGLGGHDGLGLLRVAGDGGIAWTQGEQEVLPQFCDFPEIVDISIKQAPRVGPAGEHRLVTVTRTDNQILEAEFPGLPEALSFVALVLDGYFRLITDSQHFFCKEVAPPRLLEVA
JAK3_HUMAN	LIOQWNITVDLIGPKGIRQLTSQDAKPTCLAEFKQIRSIRCLPLEEGQAVIQLGIEGAPQALSIKTSSLAAEENMADLIDGYCRLQGEHQGSЛИИHPRKDGEKRNSLPQIPMLNLEARR
FAK2_HUMAN	1bLG1stsG111Y+s+b+lsb...FsWs+1bK1sAkCppFaIclRssbb-pbEsslsFbb.sp...+tsKpLWKhssVEHHsFFRb.ps.spbssp..tcabsbGS+FraSGRTbbQsppst
Consensus/51%	

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PTN3_HUMAN	-NTKKSVNNQYCKKVIIGGMVNPNAMRRSLSVHELETKSLPSRS-PPITPNWRSPRLRHEIRKPRHSSADNLANEMTYITETEDVFYTYKGSL
PTN4_HUMAN	KEKAN-KDRVIFARSPSKPLARKLMDWEVSRNSISDDRLETQSLPSRS-PPGTPNHRNSTFTQEGTRLRPSSVGHLDHMVH-TSPSEVFVNQRSPS
41_HUMAN	ALID-RPAPFERTASKRASRSLDGAIAAVDSADRSRPTSAAPAITQG-QVAE--GGVLDASAKKTVVPKAQKETVKAEVKKEDEPPEQAEPEPTEAW
E4L1_HUMAN	ALID-RPAPFERTSSSKRYTMSRSRSLDGA--AEFSRPAVSENHADCPGDKRDEDGESGGQRSEAEEGEVRTPTKIKELKPEQETTPRHKQEFFLDK
E4L2_HUMAN	TLID-RPAPFERTSSSKRVSRSRSLDGA-PIGVMDQSLMKDFPGAAGEISAYGPLVSIAVVQDGDGRREVRSPTKAPHQLQIEGKKNSLRVEGDNIYV
E4L3_HUMAN	ALID-RPAPFERTSSSKRYTMSRSRSLDGEVGTGQYATTKGIISQTNLIITVTPPEKAAEEERDEEEDKRRKGEVTP--ISAIRHEGKSPGLGTSCPLS
E4LB_HUMAN	RL---RRTSTPERKPSKRYPSRRHSTFKASNPNVIAAQLCSKTNPEVHNYPQYHPSQPRWPHSPNVSYPLPSPVLSLSDRLPFGIEENGTP
Q9Y4F1	KE-GGHKKVPERKHSKIHISRLASQPTELNSEVLEQSQQSTSLSLTFG--EGAESPQQSCRRGKEPKVSAEPGSHSPAPRSPAGNKQADGAASA
E41LA_HUMA	S1QLPFDQNVTRSRSKTYPKRIAQTQPAESNTISRITANMENGENG-TIKIIAPSPVKSFKKAKNENSPDTQRSKSLMHSWEENGQPSGLYNSPS
Q86WP8	SKIQREPPE-VHRANITQSRS-HSLNKQLIINMEPLQPLLPSPSEQEEEPLGEGVPLPKEEENISAPILSSPVAAREYEDPPSEEEDKIKEEPL
EZRI_HUMAN	ETVEREKEQMMREKEELMLRLQDYEEKTKAERELSEQIQRALQLEERKRAQEEAERLEADRMAALRAKEELERQAVDQIKSQEQLAAELAEYTA
TLN1_HUMAN	PAIMRSAGSGPENFQVGSMPPAQQTTSQGMHRGHMPPLTSAAQALTGTINSQMAVQAAQATLDDFTLPPLGQDAASKAWRKNMDKESHEHSQ
JAK3_HUMAN	EQCHGPITLDHAINKLXGGSRPGSYVLRSPQDFDSFLLTVCVNQPLGPDYKGCLIRRSPGTGFLLVGLSRPHSSRLLELLATCWDGLHVGDGAVT
FAK2_HUMAN	SHLSESCSIESDIYAEIPDETLLRRPGGPQYGIAREDVVLNRILGEGFFGEVYEGVYTNHKGEKINAVAKTCKKDCTLDNKEKFMSEAVIMKNLDHPH
Consensus/51%	sblp.css.pF-RssSKpbpbshsspsbtspsssss.sps...sbp.sshpssppchspsssspbccppsssbpbpsps