










A

PLIN1 HUMAN	181	IGSIEKVEYFLPADKESAPAFGHQQAQKS-----FKAKPSLISRVGALNNTLSRYTVTMMARATEQGHVFM-----WIPGVVHSSSLA	261
PLIN1 MOUSE	181	IGSIEKVEFLPDPKESAPSSG-RQRTQKA-----FKAKPSLVRVSTLANTLSRHTMATTAWADKQGHSLM-----WIPGVVHSSSLA	260
PLIN2 HUMAN	180	IKSELEVEQYHPLTEEELEKEDKKVEGFDL-----VQKPSYVRLGSLSTKLSHRAYQALSRVKEAKQKSQQTISCHSTVHLIEFA	263
PLIN2 MOUSE	178	IKSPMLVIQYHPLTQEELEMDKKVEGFDL-----VQKPSNMRLESLSLTKLCSRAMHQALS RVKEAKQKSQQTISCHSTVHLIEFA	261
PLIN3 HUMAN	193	ICKSEEWAINHPLITTEFLARITSLDGFIVASVQQCRQEQSYEVRLGSLSERLRQHAYEHSIGKIRATRQRQAELLQISQALSIMETV	282
PLIN3 MOUSE	197	IVKSDAWAINRPLITTEFLALITPPEDSDIASLQQCRQEQNYEVRLGSLSERLRNHAYEHSIGKIQNARQKQQTLCQHTSVGLMESV	286
PLIN4 HUMAN	1139	QNELEGLGIIIFEMNPEEQAQIPLASQPGPKLSA-----EQGSEYVRLGDTGPFSTRQRAEHAHSVHCHGGQFCARDTLAQIQDCFLTEKA	1224
PLIN5 HUMAN	155	EKSEPEVHIFEMVTEFLAALDAEAEGPEVGSVEDCRQQGYEVRLGSLSARLRHLYAHSVGVKIRQSKHRRQDTLAHQIQTETFLIDHM	244
2nd Struct	197		281
H Cleft	197		286
Sub-domains	197		286
PLIN1 HUMAN	262	QWASVAMCAISRRRSEVVRVWIHSLAAACEEDHEDCTDTEGEITEE---EETELETEENKFESEVALPGPRGILGGVAHILCKLQITIS	348
PLIN1 MOUSE	261	QWASAAACVYSRRCEVVRVWIHNLAASQDESHDDCTDTEGEFTDDEEEEESEAEENVLREVITALPNPRGILGGVVHIVCNLRNTIS	350
PLIN2 HUMAN	264	RKNVYSANCKIQDAQIKLYLSVVEWKRISICYDDTDES-----HCAEHIESRTIATARNITQCLCTCHILIS	330
PLIN2 MOUSE	262	RKNMHSANCKIQGACIKLYVSVVEWKRISICYDDTDES-----HCVEHIESRTIATARNITQCLCTCQITVIV	328
PLIN3 HUMAN	283	KQGV---DCKVEGCEKHQMNLSWNQKQIQGPEKEF-----FKPEQVESRAITFRIDIAQLQACTSIGE	346
PLIN3 MOUSE	287	KQGV---DCKVEGCEKHQMNLSWNQKTEQDAEKDE-----AKPEQVEARALSMFRITITQCLQSMCVVIGA	350
PLIN4 HUMAN	1225	QQAP---EGQPRLDGSG-----ASA-----EDA-----AVQEEFDAGVLSFVCGLLRGLHTAYSGLVS	1275
PLIN5 HUMAN	245	QQGV---TFTAPARPKVHELIGEWGQRP-----PES-----RRRSQAELETIVISRSITQCLCGVEMTES	303
2nd Struct	282		344
H Cleft	287		350
Sub-domains	287		350
PLIN1 HUMAN	349	ANTWAEAAVLMAGRVLHLTPAFA-----VSSTKGRAMSLSDALKGVTLNVVDTVVHYVPPLPRLSIMBESEFERDI	419
PLIN1 MOUSE	351	ANTWAEAAVLTGVRILHLTPAFA-----VSSTKGRAMSLSDALKGVTLNVVDTVVHYVPLPRLSIMBESEFERDI	421
PLIN2 HUMAN	331	NQGVVEQNIQDQAKHGMVAGDIYSVVERNAASEFKEVSDSLTSSGQLQKMKESLDVMDYLVNNTPIINLVG---PFYPCLTE	411
PLIN2 MOUSE	329	NQGVVEQNIQDQAKHGMVAGDIYSVVERNAASEFKEVSDGVLTSSTGQLQKMKESLDVMDYFVNNTPIINLVG---PFYPCLTE	409
PLIN3 HUMAN	347	SIQGLEITNKDQVQQARRQVEDIQATEFSSIHSEFQDSSSITAQSERVASAREALDHVVEYVAQNTPEVNLVG---PFAPGITE	427
PLIN3 MOUSE	351	SIQGLEISHVREQAQQARSQVNDIQATEFSGIHSEFQDSAGVLAQTRERARAREALNTVEYVAQNTPEVNLVG---PFAPGITE	431
PLIN4 HUMAN	1276	SIQGLEIAEIQQPVGRARHSLCEIYGVIVASAGSVEEFAERIVQSEGVHQAWQGEQLTEGLQHNEPISNLVG---PFAL----	1352
PLIN5 HUMAN	304	SIWGLEIAGAQEKVAEVRRSVDAIQTAFAADARCFRDIFAAAIAEGGRVAHAHACVLELELVVQAVELPVLVG---PFAPILVE	384
2nd Struct	345		408
H Cleft	351		431
Sub-domains	351		431

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PERI_Human-WT ³⁹⁷TVVHYVP L P R L S L MEPE S EF RDI ⁴¹⁹
 PERI_Human-p.Leu404fs ³⁹⁷TVVHYVPA V ADG ARE R I PGHRQP ⁴¹⁹
 PERI_Human-p.Val398fs ³⁹⁷TGALRAAP Q AVA D GARE R I PGHR ⁴¹⁹