#### SUPPLEMENTARY INFORMATION

### Determinants of laminin polymerization revealed

### by the structure of the $\alpha$ 5 chain amino-terminal region

Sadaf-Ahmahni Hussain<sup>1</sup>, Federico Carafoli<sup>1</sup> & Erhard Hohenester<sup>1</sup>

<sup>1</sup>Department of Life Sciences, Imperial College London, London SW7 2AZ, UK

Supplementary Fig S1. Comparison of  $\alpha$ 5LN to galactose binding domains. (A) Superposition of laminin  $\alpha$ 5LN (pale blue) and the GBD of *Clostridium perfringens* NanJ (PDB entry 2v72, magenta). The r.m.s. deviation of 130 matched C $\alpha$  atoms is 2.2 Å. A calcium ion in NanJ is shown as a sphere. The chain break in the  $\alpha$ 5LN structure is labelled. (B) Structure of the calcium binding site in NanJ. Calcium ligands are shown in atomic detail and calcium-ligand bonds are indicated by black lines. (C) Region of  $\alpha$ 5LN corresponding to the NanJ calcium site. Selected residues are shown in atomic detail and hydrogen bonds are indicated by dashed lines. (D) Intrinsic fluorescence spectra of  $\alpha$ 5LN-LEa1-2 in the presence and absence of calcium. The solutions contained 4  $\mu$ M protein in 20 mM Na-HEPES pH 7.5, 150 mM NaCl, and either 2 mM CaCl<sub>2</sub> (black line) or 5 mM EDTA (red line). The spectra were recorded using a Jobin Yvon Horiba FluoroMax-3 fluorimeter at an excitation wavelength of 290 nm.

Supplementary Fig S2. Laminin  $\alpha$ 5LN-LEa1 interface. (A) Details of the  $\alpha$ 5LN-LEa1 interface in a view direction similar to Fig 1B. The LN, LEa1 and LEa2 domains are in pale blue, green and pink, respectively. Disulphide bridges and *N*-linked glycans are in yellow and magenta, respectively. Selected residues are shown in atomic detail. The side chain of Pro52 in the N-terminal segment is in orange. Three phosphate ions are shown with phosphorus atoms in green. Selected hydrogen bonds are indicated by dashed lines. (B) Another view of the  $\alpha$ 5LN-LEa1 interface rotated by ~180° relative to the view in A showing the interactions made by the N-terminal segment. The LN domain is shown as a pale blue surface, and the LEa1 domain as a semi-transparent pale green surface. The N-terminal segment is shown in atomic detail, with Pro52 highlighted in orange.

**Supplementary Fig S3.** Sequence alignment of selected laminin  $\alpha$  chain LN domains: mouse and zebrafish  $\alpha$ 1 and  $\alpha$ 5; mouse  $\alpha$ 2 and  $\alpha$ 3B; *Drosophila melanogaster*  $\alpha$ 1/2 (wing blister) and  $\alpha$ 3/5 (LamA); *Caenorhabditis elegans*  $\alpha$ 1/2 (lam-3) and  $\alpha$ 3/5 (epi-1). Identical residues are shaded yellow. Asparagine residues that are predicted to be modified by *N*-linked glycosylation are in magenta. The sequence numbering of the mouse laminin  $\alpha$ 5 chain is shown above the alignment.

Construct	UniProt	Residues <sup>a</sup>	Expression <sup>b</sup>	Monodisperse
	reference			protein <sup>c</sup>
α1LN-LEa1-2	P19137	25-403	Yes	Yes
α1LN-LEa1-4	P19137	25-509	Yes	Yes
α2LN-LEa1-2	Q60675	29-409	Yes	Yes
α2LN-LEa1-4	Q60675	29-513	Yes	Yes
α5LN-LEa1-2	Q61001	44-433	Yes	Yes
α5LN-LEa1-4	Q61001	44-546	Yes	Yes
β1LN-LEa1-2	P02469	22-397	No	
β1LN-LEa1-4	P02469	22-509	Yes	No
γ1LN-LEa1-2	P02468	34-395	Yes	Yes
γ1LN-LEa1-4	P02468	34-492	Yes	Yes

Supplementary Table S1. Summary of laminin short arm constructs.

<sup>a</sup>All mature proteins contain a vector-derived APLA sequence at the N-terminus and a AAAHHHHHH tag at the C-terminus.

<sup>b</sup>The criterion used is a yield of > 0.5 mg from 1 litre of conditioned cell culture medium. <sup>c</sup>The criterion used is > 90% of protein eluting as a single symmetric peak from a S200 size exclusion chromatography column run in 20 mM Na-HEPES pH 7.5, 150 mM NaCl, 2 mM CaCl<sub>2</sub>.

# Supplementary Figure S1 Hussain et al.



Supplementary Figure S2 Hussain et al.



В



## Supplementary Figure S3 Hussain et al.

LAMA5\_MOUSE LAMA5\_DANRE EPI1\_CAEEL LAMA DROME LAMA1\_MOUSE LAMA2\_MOUSE LAMA1\_DANRE LAMA3\_CAEEL WB\_DROME

LAMA5\_MOUSE LAMA5\_DANRE EPI1\_CAEEL LAMA\_DROME LAMAI\_MOUSE LAMA1\_DANRE LAMA1\_DANRE LAMA3\_CAEEL WB\_DROME

LAMA5\_MOUSE LAMA5\_DANRE EPI1\_CAEEL LAMA\_DROME LAMA1\_MOUSE LAMA1\_MOUSE LAMA1\_DANRE LAMA1\_CAEEL WB\_DROME

LAMA5\_MOUSE LAMA5\_DANRE EPI1\_CAEEL LAMA\_DROME LAMA1\_MOUSE LAMA1\_MOUSE LAMA1\_DANRE LAMA3\_CAEEL WB\_DROME

50	60	70	80	90	100	110
FSLHPPYFNL	AEGARTTASA	TCGEEAPTR	SVSRPTEDL	YCKLVGGP	VAGGDPNOT	
RSLHPPYFNL	AOAARIWATA	TCGERDPE-	-VSRPRPEL	FCKLVGGP	AAOGS-GHT	LOGOFCDYC
FS <mark>LHP</mark> PYFNL	AEGTK <mark>I</mark> TATA	TCGVDENE-	QPIQDL	YCKLVGGP	VSG-DPSQT:	IQGQYCDIC
QV <mark>L</mark> T <mark>P</mark> SQITI:	SHRKP <mark>I</mark> TATS	TCGEIQGQ-	PVTEI	YCSLTGST	QYTPLNSYS	YQDDE[17]GCGHC
AE <mark>LTP</mark> PYFNL	ATGRK <mark>I</mark> YATA	TCGQDTDG-	PEL	Y <mark>C</mark> KLVGAN	TEHDHIDYS	VIQGQVCDYC
RG <mark>LFP</mark> AILNL	ATNAH <mark>I</mark> SANA	TCGEKGPE-	M	F <mark>C</mark> KLVEHV	PGRPVRI	HAQCRVC
RGLFPAVLNL	ASNALITTNA	TCGEKGPE-	M	YCKLVEHV	PGQPVRI	NPQCRIC
RGLFPAILNL	ASNAEISTNA	TCGDPDPE-	M	FCKLVEHV	PGRRIRI	PQCRIC
CCLVPPL FNU	UPPAOTSUNA	TCGONGAE-	E	ICKLVERV.	DLKKIINIQ	
GGLIFFLIN	VFRAQISVINA	ICGONGAL-	E	IC NOV GAN		
	120	130	140	150	160	170
		1	1		1	
TAANSNKA	HPVSNAIDGT	ERWWQSPPL:	SRGLEYNEV	NVTLDLGQ	VFHVAYVLI	KFANSPRPDLWVLE
NSEDSRKA	HPASHAIDGS	ER <mark>WW</mark> Q <mark>SP</mark> PL:	ssgtqynq <mark>v</mark>	NLTLDLGQ	LFHVAYILI	KFA <mark>NSPRP</mark> DL <mark>WILE</mark>
SSQDTNRA	HPISNAIDGT	ERWWQSPPL:	SRSAKHNQ <mark>V</mark>	NVTLDLGQ	LFHVAYVLII	KFANSPRPDLWVLE
NAGNENSI	HPAANMVDGN	NSWWMSPPL:	SRGLQHNEV	NITIDLEQ	EFHVAYVWI	QMANSPRPGSWVLE
DPTVPERNI	HPPENAIDGT	EAWWQSPPL	SRGMEFNEV	NLTINFEQ	EFHVAILFI	KMGNSPRPGLWTLE
NONSENDYOR	HPISHAIDGT	NTWWOSPSI	UNGREIHWU	TVTLDLRQ	VFQVAILLI	CAANAPRPGNWILE
DANSONPKEOI	HPITNAIDGR	NLWWOSPST	KNGROFHWV	TVTLDLQQ	VFOVAYTTT	KAANSPREGNWILE
DANNVHKRI	HPIEYAIDGT	RRWWOSPSL	ANGLRFEKV	NITIDLRO	EYOVAYIIL	MGNSPRPGTWVLE
NAHS[14]SG	SGSGSGSGFE	EGWWQSPTL	QGGRQFEYV	TILLDLKQ	TFQIFSVWL	KSANSPRPASWILE
180	190	200	210	22	0 23	30 240
RSTDFGHTYQ	PWQFFASSKR	DCLERFGPR	TLERIT	QDDDVICT	TEYSRIVPL	ENGEIVVSLVNGRP
RSVDFGSTIS	PWQIFAHSKK	DEVEQFGQE	ANMALT	QDDQMLCV	TEISKIVPLI	INGEIVVSLINGRP
RSTDHCKTYO	PWFNFAFNAA	ECMEREGUE	SLSPIS	EDDSVTCR	TDMASLOPL	NAEMVIRILEHRP
KSTDYGKTWT	PWOHFSDTPA	DCETYFGKD	TYKPIT	RDDDVICT	TEYSKIVPL	ENGEIPVMLLNERP
RSVDG-VKFK	PWOYYAVSDT	ECLTRYKIT	PRRGPPTYR	ADNEVICT	SYYSKLVPL	HGEIHTSLINGRP
R <mark>SLDD-VEYK</mark>	DHOVUAUMD					
DOT DO IDIDO	PWQINAVIDI	ECLTLYNIY.	PRTGPPSYA	KDDEVI <mark>C</mark> T	SFYSKIH <mark>PL</mark>	ENGEIHISLINGRP
RSLDG-VNFQ	PWQIHAVIDI PWQFYAISDT	ECLTLYNIY. ECLTRYNIT:	PRTGPPSYA PRIGPPTYK	KDDEVI <mark>C</mark> T RDDEVI <mark>C</mark> T	SFYSKIH <mark>PL</mark> SYYSRLV <mark>PL</mark>	NGEIHISLING <mark>RP</mark> HGEIHTSLING <mark>RP</mark>
KSLDG-VNFQ KSLDG-EYYE	PWQIHAVIDI PWQFYAISDI PWQYYAMQDA	ECLTLYNIY. ECLTRYNIT: ECMRQFGIP.	PRTGPPSYA PRIGPPTYK ATTGVPRFQ	KDDEVI <mark>C</mark> T RDDEVICT KEDEVH <mark>C</mark> T	SFYSKIH <mark>PL</mark> SYYSRLV <mark>PL</mark> SEYSKIT <mark>PL</mark>	NGEIHISLING <mark>RP</mark> HGEIHTSLING <mark>RP</mark> NGEIHTSLVNG <mark>RP</mark>
KSLDG-VNFQ KSLDG-EYYE KSLDG-INFE	PWQIHAVIDI PWQFYAISDT PWQYYAMQDA PWQYFGLSDA	ECLTLYNIY ECLTRYNIT ECMRQFGIP D <mark>C</mark> QRRWNLS	PRTGPPSYA PRIGPPTYK ATTGVPRFQ GQNGKYVFQ	KDDEVI <mark>C</mark> T RDDEVICT KEDEVHCT NDTEIICS	SFYSKIH <mark>PLI</mark> SYYSRLVPLI SEYSKITPLI TQFSKPG <mark>PLI</mark>	NGEIHISLING <mark>RP</mark> HGEIHTSLING <mark>RP</mark> NGEIHTSLVNG <mark>RP</mark> NGVLHASLLKN <mark>RP</mark>
KSLDG-EYYE KSLDG-EYYE KSLDG-INFE	PWQFYAISDT PWQFYAISDT PWQYYAMQDA PWQYFGLSDA	ECLTLYNIY ECLTRYNIT ECMRQFGIP DCQRRWNLS	PRTGPPSYA PRIGPPTYK ATTGVPRFQ GQNGKYVFQ	KDDEVI <mark>C</mark> T RDDEVICT KEDEVHCT NDTEII <mark>C</mark> S	SFYSKIHPLI SYYSRLVPLI SEYSKITPLI TQFSKPGPLI	ENGEIHISLINGRP EHGEIHTSLINGRP ENGEIHTSLVNGRP ENGVLHASLLKNRP
KSLDG-VNFQ KSLDG-EYYE KSLDG-INFE	PWQTHAVIDI PWQFYAISDT PWQYYAMQDA PWQYFGLSDA 260	ECLTLYNIY ECLTRYNIT ECMRQFGIP DCQRRWNLS 270	PRTGPPSYA PRIGPPTYK ATTGVPRFQ GQNGKYVFQ 280	KDDEVI <mark>C</mark> T RDDEVICT KEDEVHCT NDTEII <mark>C</mark> S	SFYSKIHPLI SYYSRLVPLI SEYSKITPLI TQFSKPGPLI 290	ENGEIHISLINGRP EHGEIHTSLINGRP INGEIHTSLVNGRP ENGVLHASLLKNRP 300
KSLDG-VNFQ KSLDG-EYYE KSLDG-INFE 250	PWQIHAVIDI PWQFYAISDT PWQYYAMQDA PWQYFGLSDA 260	ECLTLYNIY ECLTRYNIT ECMRQFGIP DCQRRWNLS 270	PRTGPPSYA PRIGPPTYK ATTGVPRFQ GQNGKYVFQ 280   LLGHLMGKA	KDDEVICT RDDEVICT KEDEVHCT NDTEIICS	SFYSKIHPLI SYYSRLVPLI SEYSKITPLI TQFSKPGPLI 290   PTVTRRYYY	NGEIHISLINGRP HGEIHTSLINGRP NGEIHTSLVNGRP NGVLHASLLKNRP 300   SIKDISIGGR
RSLDG-VNFQ KSLDG-EYYE KSLDG-INFE 250   GALNFSYSPL GAKKFAFSDT	PWQIHAVIDI PWQYYAISDT PWQYYAMQDA PWQYFGLSDA 260   LRDFTKATNI LREFTKATNI	ECLTLYNIY ECLTRYNIT ECMRQFGIP DCQRRWNLS 270   RLRFLRTNT RLRFLRTNT	PRTGPPSYA PRIGPPTYK ATTGVPRFQ GQNGKYVFQ 280   LLGHLMGKA LLGHLISKA	KDDEVICT RDDEVICT KEDEVHCT NDTEIICS	SFYSKIH <mark>PLI</mark> SYYSRLVPLI SEYSKITPLI TQFSKPG <mark>PLI 290  </mark> PTVTRRYY <mark>Y</mark>	ENGEIHISLINGRP ENGEIHTSLINGRP ENGEIHTSLVNGRP ENGVLHASLLKNRP 300   SIKDISIGGR SIKDISIGGR
KSLDG-VNFQ KSLDG-EYYE KSLDG-INFE 250   GALNFSYSPL GAKKFAFSDT GAMNFSYSPV	PWQFHAVIDI PWQFYAISDT PWQYFGLSDA 260 LRDFTKATNI LREFTKATNI LREFTKATNI	ECLTLYNIY ECLTRYNIT: ECMRQFGIP DCQRRWNLS 270   RLRFLRTNT: RLRFLRTNT: RLRFLRTNT:	PRTGPPSYA PRIGPPTYK ATTGVPRFQ GQNGKYVFQ 280   LLGHLMGKA LLGHLISKA LLGHLISKA	KDDEVICT RDDEVICT KEDEVHCT NDTEIICS LRD LRD	SFYSKIHPLI SYYSRLVPLI SEYSKITPLI TQFSKPGPLI 290   PTVTRRYYY PTVTRRYYY PTVTRRYYY	SNGEIHISLINGRP SHGEIHTSLINGRP SNGEIHTSLVNGRP SNGVLHASLLKNRP SIGVLHASLLKNRP SIKDISIGGR SIKDISIGGR SIKDISVGGR SIKDISVGGR
KSLDG-VNFQ KSLDG-EYYE KSLDG-INFE 250   GALNFSYSPL GAKKFAFSDT GAMNFSYSPV SSRQFATSEA	PWQFHAVIDI PWQYYANQDA PWQYFGLSDA   LRDFTKATNI LREFTKATNI LREFTKATNI LQNFTRATNV	ECLTLYNIY ECLTRYNIT: ECMRQFGIP. DCQRRWNLS 270   RLRFLRTNT: RLRFLRTNT: RLRFLRTNT: RLRFLRTNT:	PRTGPPSYA PRIGPPTYK ATTGVPRFQ GQNGKYVFQ 280   LLGHLMGKA LLGHLMGKT LQGHLMDMN	KDDEVICT RDDEVICT KEDEVHCT NDTEIICS LRD LRD EWRD	SFYSKIHPLJ SYYSRLVPLJ SEYSKITPLJ TQFSKPGPLJ 290   PTVTRRYY PTVTRRYY PTVTRRYY PTVTRKYY PTVTRKYY	NGEIHISLINGRP BHGEIHTSLUNGRP SNGEIHTSLVNGRP SNGVLHASLLKNRP J SIKDISIGGR SIKDISIGGR SIKDISVGGR SIKDISIGGR AIKEIMIGGR
KSLDG-VNFQ KSLDG-EYYE Z50 GALNFSYSPL GAKKFAFSDT GAMNFSYSPV SSROFATSEA SSTNYFNSTV	PWQYHAYIDI PWQYYAMQDA PWQYFGLSDA 260   LRDFTKATNI LREFTKATNI LQNFTRATNV LQNFTRATNV	ECLTLYNIY ECLTRYNIT ECMRQFGIP DCQRRWNLS 270   RLRFLRTNT RLRFLRTNT RLRFLRTNT RLRFLRTNT RLRLLGTRT	PRTGPPSYA PRIGPPTYK ATTGVPRFQ GQNGKYVFQ 280   LLGHLMGKA LLGHLMGKT LQGHLMGKT LLGHLMSVA	KDDEVICT RDDEVICT KEDEVHCT NDTEIICS LRD LRD LRD RQD	SFYSKIHPLI SYYSRLVPLI SEYSKITPLI 290 PTVTRRYYY PTVTRRYYY PTVTRRYYY PTVTRRYFY PTVTRRYFY	NGEIHISLINGRP HGEIHISLINGRP SNGEIHISLVNGRP SNGEIHISLVNGRP SNGULHASLLKNRP SIKDISIGGR SIKDISUGGR SIKDISIGGR AIKEIMIGGR
KSLDG-EYYE KSLDG-EYYE Z50 GALWFSYSPL GAKKFAFSDT GAMNFSYSPV SSROFATSEA SSTNYFNSTV SADDPSPQ	PWQYYAMQDA PWQYYAMQDA PWQYFGLSDA 260   LRDFTKATNI LREFTKATNI LREFTKATNI LQNFTRATNV LQEWTRATNV LLEFTSARYI	ECLTRYNIT ECMRQFGIP. DCQRRWNLS 270   RLRFLRTNT RLRFLRTNT RLRFLRTNT RIRLLGTRT RIRLLGTRT RIRLLRTKN	PRTGPPSYA PRIGPPTYK ATTGVPRFQ GQNGKYVFQ   LLGHLMGKA LLGHLISKA LLGHLMGKA LLGHLMDMN LLGHLMSVA LNADLMTLS	KDDEVICT RDDEVICT KEDEVHCT NDTEIICS LRD ERD LRD EWRD HRDLRDLD	SFYSKIHPLI SYYSRLVPLI SEYSKITPLI QFSKPGPLI 290 PTVTRRYYY PTVTRRYYY PTVTRRYYY PTVTRRYFY PTVTRRYFY PTVTRRYFY PIVTRRYYY	NGETHISLINGRP HGEIHISLINGR NGEIHISLVNGRP NGEIHISLVNGRP SIKDISIGGR SIKDISIGGR AIKEIKNIGGR SIKDISIGGR SIKDISIGGR SIKDISIGGM
KSLDG-VNFQ KSLDG-EYYE Z50 GALNFSYSPI GAKNFAFSYSPI GAMNFSYSPY SSRQFATSEA SSTNYFNSTV SADDPSPQ SADDPSPE	PWQFYALSDT PWQYYAMQDA PWQYFGLSDA 260   LRDFTKATNI LREFTKATNI LCOFTRATNV LQEWTRATNV LLEFTSARYI LLEFTSARYI	ECLTRYNIT ECURRQFGIP, DCQRRWNLS 270   RLRFLRTNT; RLRFLRTNT; RLRFLRTNT; RLRLLGTRT; RIRLLGTRT; RLRLQRIRT; RLRLQRIRT;	PRTGPPSYA PRTGPPTYK ATTCVPRFQ GQNGKYVFQ LLGHLMGKT LLGHLMSKA LLGHLMSKA LLGHLMSKA LLGHLMSKA LNADLMMTS LNADLMMTA	KDDEVICT RDDEVICT KEDEVHCT NDTEIICS LRD ERD EWRD RQD HKDLRDLD HKDPREID	SFYSKIHPLI SYYSKITPLI SEYSKITPLI TQFSKPGPLI PTVTRKYYY PTVTRKYYY PTVTRKYYY PTVTRKYYY PTVTRKYYY PIVTRRYFY PIVTRRYYY PIVTRRYYY	NGETHISLINGRP BIGEIHISLINGR NGEIHISLVNGRP NGUHASLLVNRP 300 JINDISIGGR SIKDISVGGR SIKDISVGGR SIKDISIGGR SIKDISVGGM SIKDISVGGM
KSLDG-VNFQ KSLDG-EYYE KSLDG-INFE 250   GALNFSYSPL GAKFAFSDT GAMNFSYSPV SSROFATSEA SSTNYFNSTV SADDPSPE SADDLTPE SADDLTPE	PWQYAMQDA PWQYYAMQDA PWQYYGLSDA 260 LRDFTKATNI LREFTKATNI LREFTKATNI LQUWTTRATNV LQEWTRATNV LLEFTSARYI LLEFTSARYI	ECLTRYNIT ECTRRYNIT ECRRQFGIP DCQRRWNLS 270   RLRFLRTNT RLRFLRTNT RLRFLRTNT RLRLLGTRT RIRLLGTRT RLRLLQRIRT RLRCQRIRT RLRCQRIRT	PRTGPPSYA PRIGPPTYK ATTCVPRFQ GQNGKYVFQ LLGHLMGKA LLGHLMGKA LLGHLMGKT LQGHLMDMN LLGHLMSYA LNADLMTLS LNADLMTLS	KDDEVICT RDDEVICT KEDEVHCT NDTEIICS LRD EWRD EWRD RQD HRDLRDLD HKDPREID YRDPKDVD	SFYSKIHPLI SYYSRLVPLI SEYSKITPLI 290 PTVTRRYYY PTVTRRYYY PTVTRRYYY PTVTRRYFY PTVTRRYFY PIVTRRYFY PIVTRRYYY PIVTRRYYY	NGETHISLINGRP SHGEIHISLINGRP SHGEIHISLVNGRP SHGULHASLLKNRP SIKDISIGGR SIKDISIGGR SIKDISIGGR SIKDISIGGR SIKDISUGGR SIKDISUGGM SIKDISVGGM SIKDISVGGM
KSLDG-VNFQ KSLDG-EYYE KSLDG-INFE 250 GALWFSYSPL GAKKFAFSDT SSTNYFNSTV SSTOPATSEA SSTNYFNSTV SADDPSPQ SADDPSPQ GAENTSLE GAENTSLE	WQYHAVIDT PWQYYALDD PWQYFGLSDA PWQYFGLSDA LRFTKATNI LRFTKATNI LRFTKATNI CQWTRATNV LLFTSARYI LLFTSARYI LLFTSARYI LLFTSARYI LUFTSARYI	ECLTRYNIT ECTRRYNIT ECTRRYNIT ECRRQFGIP, DCQRRWNLS   RLRFLRTNT; RLRFLRTNT; RLRFLRTNT; RLRLLGTRT; RLRLQRIRT; RLRLQRIRT; RLRLQRIRT; RLRLQRIRT; RLRLQRIRT;	PRTGPPSYA PRIGPPTYK ATTCVPRFQ GQNGKYVFQ   LLGHLMGKA LLGHLMGKA LLGHLMGKA LLGHLMDMN LLGHLMSVA LNADLMTLS LNADLMTLS LNADLMIIN NADNSY	KDDEVICT RDDEVICT KEDEVHCT NDTEIICS LRD LRD LRD RQD HRDLRDLD YRDPKDVD KKS-DSLD	SFYSKIHPLI SYYSKIHPLI SYYSKLVFLI TQFSKPGPLJ 290   PTVTRRYYY PTVTRRYYY PTVTRRYYY PIVTRRYFY PIVTRRYFY PIVTRRYYY SSYMRYFY	NGETHISLINGRP HGEIHISLINGR NGEIHISLVNGRP SNGULHASLLKNRP SIKDISIGGR SIKDISUGGR SIKDISUGGR SIKDISUGGR SIKDISUGGM SUKDISUGGM SUKDISUGGM SIKDISUGGM SIKDISUGGM SISDISUGGA

110