

1

LT2	1	-.-.FF-----T-----R-A---L---QQ-AYE---PI---	38
LT1	1	-----FRS-----	39
LT1_1A	1	-G-R-----R-----HN-----	40
CT	1	NDDKLYRADSRPPDEIKQSGGLMPRGQSEYFDRGTQMNIN	40
		---E-----V--NT--N-----TVT--Q---I--N--GS-	78
		-----Y-----	79
		-----Y-----L-----A--S---Y	80
		LYDHARGTQTGFVRHDDGYVST <u>S</u> ISLRS <u>A</u> HLVGQTILSGH	80
		NE-----V-P---L-D--G---R---Y-S-N-FA-----	118
		-LTIYI---...-----IS-----	116
		-----V---Y-----	120
		STYYIYVIATAPNMFNVNDVLGAYSPHPDEQEVSALGGIP	120
		L---I-----SF-A-EGGMQ---D--GDLF-G-TV--N--	158
		-----	156
		-----N---I--R-----E-----R--N---E-	160
		YSQIYGWYRVHFGVLDEQLHRNRYRDRYYSNLDIAPAAD	160
		---Q-----SNFP---M--STF--EQ-VPNNKEFK-GV-I	198
		-----	196
		---R-----D-Q-----Q---DSS-TITGD--N	200
		GYGLAGFPPEHRAWREEPWIIHAPPGCGNAPRSSMSNTCD	200
		SA-NV--KYD-MNFKKLL--RLALTFFM--D-F-GVHGE----	241
		-----	236
		-E--N-STIY-R-----D-.-EV-.IY---.R---	240
		EKTQSLGVKFLDEYQSKVKRQIFSGY.QSDID.THNRI.KDEL	240

Figure 1

LT	AATGGCGACAGATTATACCGTGCTGACTCTAGACCCCCAGATGAAATAAAACGTTTCCGG	
	N G D R L Y R A D S R P P D E I K R F R	20

	N D D K L Y R A D S R P P D E I K Q S G	20
CT	AATGATGATAAGTTATATCGGGCAGATTCTAGACCTCCTGATGAAATAAAGCAGTCAGGT	
LT	AGTCTTATGCCCAGAGGT...AATGAGTACTTCGATAGAGGAACTCAAATGAATATTAAT	
	S L M P R G Q N E Y F D R G T Q M N I N	39

	G L M P R G Q S E Y F D R G T Q M N I N	40
CT	GGTCTTATGCCAAGAGGACAGAGTGAGTACTTTGACCGAGGTACTCAAATGAATATCAAC	
LT	CTTTATGATCAGCGAGAGGAACACAAACCGGCTTTGTCAGATATGATGACGGATATGTT	
	L Y D H A R G T Q T G F V R Y D D G Y V	59

	L Y D H A R G T Q T G F V R H D D G Y V	60
CT	CTTTATGATCATGCAAGAGGAACTCAGACGGGATTTGTTAGGCACGATGATGGATATGTT	
LT	TCCACTTCTCTTAGTTTGAGAAGTGCTCACTTAGCAGGACAGTATATATTATCAGGATAT	
	S T S L S L R S A H L A G Q Y I L S G Y	79

	S T S I S L R S A H L V G Q T I L S G H	80
CT	TCCACCTCAATTAGTTTGAGAAGTGCCCCACTTAGTGGGTCAAACCTATATTGTCTGGTCAT	
LT	TCCTTACTATATATATATCGTTATAGCA.....AATATGTTTAATGTTAATGATGTA	
	S L T I Y I V I A N M F N V N D V	96

	S T Y Y I Y V I A T A P N M F N V N D V	100
CT	TCTACTTATTATATATATGTTATAGCCACTGCACCCAACATGTTTAACGTTAATGATGTA	
LT	ATTAGCGTATACAGCCCTCACCCATATGAACAGGAGGTTTCTGCGTTAGGTGGAATACCA	
	I S V Y S P H P Y E Q E V S A L G G I P	116

	L G A Y S P H P D E Q E V S A L G G I P	120
CT	TTAGGGGCATACAGTCCTCATCCAGATGAACAAGAAGTTTCTGCTTTAGGTGGGATTCCA	

Figure 2a

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LT  TATTCTCAGATATATGGATGGTATCGTGTTAATTTTGGTGTGATTGATGAACGATTACAT
    Y S Q I Y G W Y R V N F G V I D E R L H 136
-----
    Y S Q I Y G W Y R V H F G V L D E Q L H 140
CT  TACTCCCAAATATATGGATGGTATCGAGTTCATTTTGGGGTGCTTGATGAACAATTACAT
-----
LT  CGTAACAGGGAATATAGAGACCGGTATTACAGAAATCTGAATATAGCTCCGGCAGAGGAT
    R N R E Y R D R Y Y R N L N I A P A E D 156
-----
    R N R G Y R D R Y Y S N L D I A P A A D 160
CT  CGTAATAGGGGCTACAGAGATAGATATTACAGTAACTTAGATATTGCTCCAGCAGCAGAT
-----
LT  GGTACAGATTAGCAGGTTTCCACCGGATCACCAAGCTTGGAGAGAAGAACCCTGGATT
    G Y R L A G F P P D H Q A W R E E P W I 176
-----
    G Y G L A G F P P E H R A W R E E P W I 180
CT  GGTATGGATTGGCAGGTTTCCCTCCGGAGCATAGAGCTTGGAGGGAAGACCCGTGGATT
-----
LT  CATCATGCACCACAAGTTGTGGAGATTCATCAAGAACAATCACAGGTGATACTTGTAAT
    H H A P Q G C G D S S R T I T G D T C N 196
-----
    H H A P P G C G N A P R S S I S N T C D 200
CT  CATCATGCACCGCCGGTTGTGGGAATGCTCCAAGATCATCGATCAGTAATACTTCCGAT
-----
LT  GAGGAGACCCAGAATCTGAGCACAATATATCTCAGGGAATATCAATCAAAAGTTAAGAGG
    E E T Q N L S T I Y L R E Y Q S K V K R 216
-----
    E K T Q S L G V K F L D E Y Q S K V K R 220
CT  GAAAAAACCCAAAGTCTAGGTGTAAAATTCCTTGACGAATACCAATCTAAAGTTAAAAGA
-----
LT  CAGATATTTTCAGACTATCAGTCAGAGGTTGACATATATAACAGAATTCGGGATGAATTATGA
    Q I F S D Y Q S E V D I Y N R I R D E L *
-----
    Q I F S G Y Q S D I D T H N R I K D E L *
CT  CAAATATTTTCAGGCTATCAATCTGATATTGATACACATAATAGAATTAAGGATGAATTATGA

```

Figure 2b

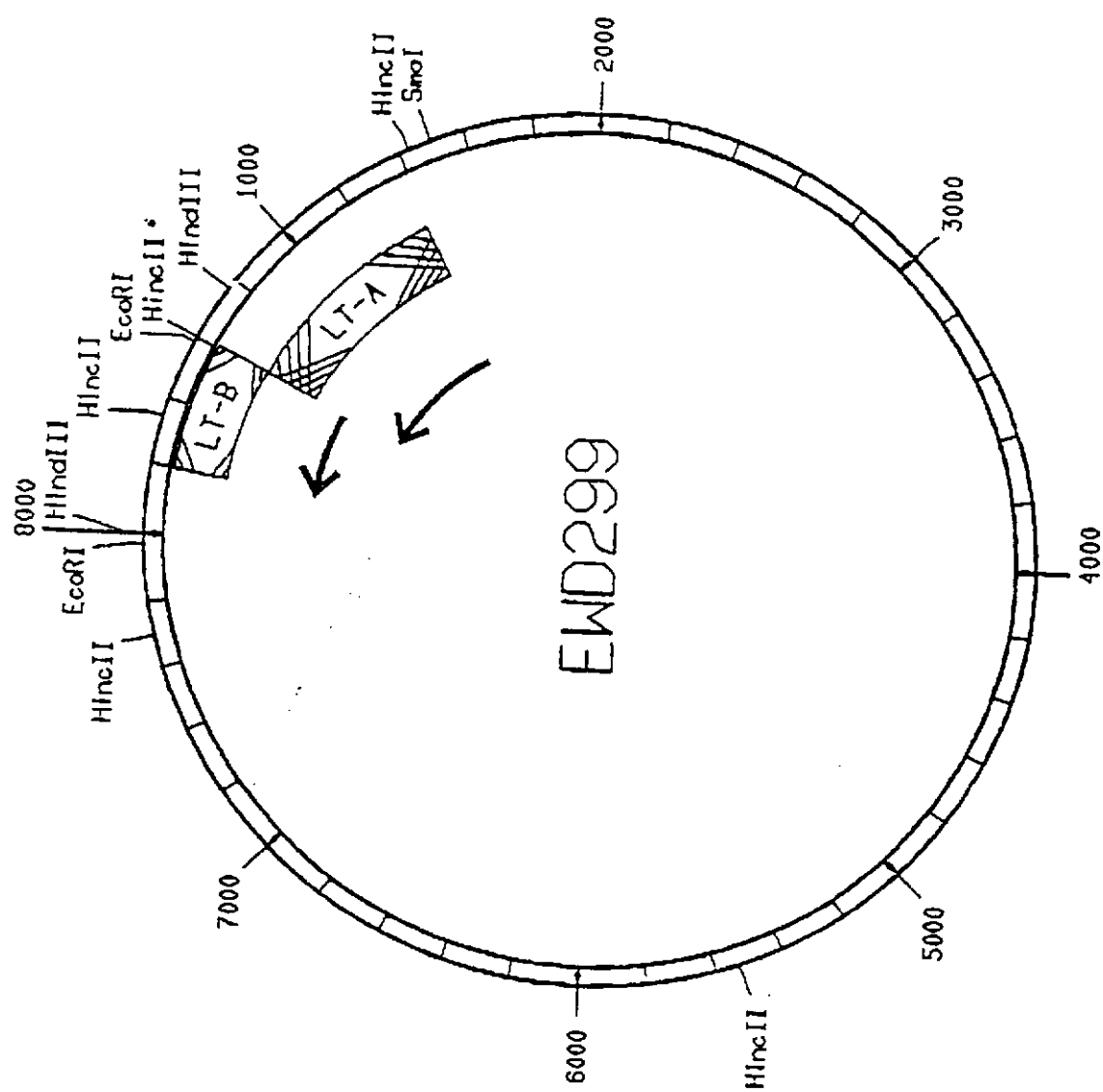


FIGURE 3