

A

$\alpha$ -N-Zar1 (aa 33-49)

B

	10	20	30	40	50	60	70	80	90
Xt genomic	A	C	G	G	T	C	A	C	T
Xt EST	-	-	-	-	A	G	A	C	T
XI Zar1a	-	-	-	A	A	G	G	A	C
XI Zar1b	-	-	-	G	T	A	G	C	T

  

	100	110	120	130	140	150	160	170	180
Xt genomic	A	G	A	C	G	C	A	G	T
Xt EST	-	-	-	-	-	G	G	T	A
XI Zar1a	A	G	A	C	G	C	A	G	T
XI Zar1b	A	G	A	C	G	C	A	G	T

  

	190	200	210	220	230	240	250	260	270
Xt genomic	G	T	A	C	C	G	C	-	-
Xt EST	G	T	A	C	G	T	G	A	G
XI Zar1a	G	T	A	C	C	G	A	G	A
XI Zar1b	G	T	A	C	C	G	A	G	A

C

### conserved upstream in-frame stop sites

Sequence alignment of Xt Zar1, XI Zar1a, and XI Zar1b. The alignment shows the first 90 amino acids. Two potential starting methionines are indicated by inverted triangles below the sequence. The sequence starts at position 10 for Xt Zar1 and XI Zar1a, and at position 11 for XI Zar1b.

	10	20	30	40	50	60	70	80	90
Xt Zar1	P G S I A V	F F L E K L R L S S P *	G A G K S H	S H L D D	S D Q P L L K Q A A G S C C *	P D I M A S F S E E A M D	S Y M Y P A Y N P Y S Y R Y	L T P K N K G M S W R Q	- - - - -
XI Zar1a	- - - - -	K M D T L R L T P R G	G L K S H *	H L D Y * *	D Q P L L K Q A A G S C C *	P D I M A S F S E E A M D	S Y M Y P A Y N P Y S Y R Y	L T P R N K G M S W R Q K N Y	L A S Y
XI Zar1b	- - - - -	- - - - -	N H E G Q	H L D Y * *	D Q P L L K Q A A G S C C *	P D I M A S F S E E A M D	S Y M Y P A Y N P Y S Y R Y	M T P K N K G M S W R Q K N Y	L A S Y

Potential starting methionines