



Article

Tristetraprolin/ZFP36 Regulates the Turnover of Autoimmune-Associated HLA-DQ mRNAs

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Figure S1. Sfold Structure Comparison of 3'UTR of DQA1* and DQB1*. Each of the riboprobe sequences was analysed with Sfold to predict statistical ensembles of structures. The ensembles permit many different conformations of the structures and clustering indicating the most likely conformations adopted by each sequence. The minimum-free energy (MFE) structure is also predicted and its parent cluster identified. **A.** 3DQA101, **B.** 3DQA105, **C.** 3DQB105 and **D.** 3DQB102 show the ensemble structures to contain fewer conserved base pairings (grey boxes) than the MFE structure indicating the structure is more dynamic/flexible outside of these regions. This is particularly evident in **D.** 3DQB102 where there is little conservation of base pairings in the large stem as seen in the other structures.

Δ								
А.	3DQA101	UGAA	UCCCAUCCUGG	AA <mark>G</mark> GGAA-GUG	CAUCGCCAUCUA		AGAGUGGACUUG	
	3DQA105	UGAA	UCCCAUCCUGG	AAUGGAA-GUG	CAUCGCCAUCUA	CAGGAGCAGA	AGAGUGGACUUG	
	H2-Aa-204	G	UCACACCCUGG	 AAAGGAAGGCG		 JCAGGGAAGAA	GUGGUGUGCUGG	
	3DQA101	CU-A	CAUGACCUAGC	ACUAUUCUCUG	GCCCGAUUUAUC	AUAUCCCUUU	UCUCCUCCAAAU	
	3DQA105	CU-A	CAUGACCUAGC	AUUAUUUUUUU	GCCCC <u>AUUUA</u> UC	AUAUCCCUUU	UCUCCUCCAAAU	
	H2-Aa-204	 GUGA	 CCUGGCACAGU	G–UGUU <mark>U</mark> UCUG	 GACCAAUUCAUG	GUGUUCUUUC	 UCUUCUUCAAGU	
	3DQA101	AUUU	CUCCUCUCACC	UUUUCUGUGGG	ACUUAAGCUGCU	JAUAUCCCCUC	AGAGCUCACAAA	
	3DQA105		CUCCUCUCACC	u <mark>c</mark> nncneneee	ACUUAAAUUGCU	JAUAUCUGCUC	AGAGCUCACAAA	
	H2-Aa-204	GACC	 CCCAACUUGCU	 UUUCUCUUGAC	CCUGAG <mark>GC</mark> UGU-	cc <mark>c</mark> ucuc	 ACAGCUCACACA	
	3DQA101	UGUC	טטט					
	3DQA105	UG <mark>C</mark> C	UUU					
	H2-Aa-204	C– <mark>C</mark> C	 UUG					
В.			3DQA101	3DQA105	H2-Aa-204	GC		
	3DQ	A101		94.1	57.8	0.46		
	3DQ	A105	174/185		57.8	0.44		
	H2-A	\a-204	108/187	108/187		0.52		
C.								
	3DQB102	UGAC	UCCUGAGACUA	UUUUA-ACU <mark>GO</mark>	GAUUGGUUA	UCACUUUUCU	GUAACGCCU	
	3DQB105	UGAC	 UCCUGAGACU <mark>G</mark>	 UUUUA-ACUAA	GACUGGUUA	UCACUCUUCU	GUGAUGCCU	
	H2-Ab1-201	UGAC	UGACUCAGUUGACUGUCUCAGACUGUAAGACCUGAAUGUCUCUGCUCCGAAUUCCU					
	3DQB102	GCUU	GUCCCUGCC	CA	GAAUUCCCAG	cugucugugu	CAGCCUG	
	3DQB105	GCUU	GUCCCUGCC	 CP	GAAUUCCCAG	CUGCCUGUGU	CAGCUUG	
	H2-Ab1-201	 L GCCA	 GUCCACCUGCC	 ACUCCGACUCA	GAGUCUAGCAUG	GUA <mark>C</mark> UAUUGU	AUCCACCAC <mark>C</mark> UC	
	3DQB102	UCCC	CCUGAGAUC-A	GAGUCCUACAG	UGGCUGUC	ACGCAGCCAC	CAGGU	
	3DQB105	UCCC	 CCUGAGAUC-A	AAGUCCUACAG	UGGCUGUC	ACGCAACCAC	 CAGGU	
	H2-Ab1-201	L AGCU	 CUUGUGAUCUG	GAGUCCCCCAG	UCUCUGUCUGU#	GCUCU <mark>G</mark> CUCC	 UUGGUGAUUCCA	
	3DQB102		CAUCUCCU	UUCAUCCCCAC	CUUGAGGCGGAU	IGGCUGUGACC	C	
	3DQB105		CAUCUCCU	UCAUCCCCACC <mark>CC</mark> AAGGCG- <mark>C</mark> U		 GGCUGUGACUC		
	H2-Ab1-201	GAGA	CUCCAUCUGUG	 UACAGCCGCAC	IACAGCCGCACC <mark>C</mark> AGGCUUU <mark>C</mark> UC		UGUAGUAAACCA	
	3DQB102		-UACUU	CCUGCACU-	6	GACCCACAGCC		
	3DQB105UGCUU-							
	3DQB105		-0GCUU	CCUGCACU-		ACCCAGAGCC		
	3DQB105 H2-Ab1-201	AUGU	-UGCUU AUGCUUAUCCC	CCUGCACU- CACCUAGAUUA	CAAAUAAACGAG	ACUCAGAGCC		
П	3DQB105 H2-Ab1-201	AUGU		CACCUAGAUUA		ACUCAGAGECC		
D.	3DQB105 H2-Ab1-201	AUGU	-UGCUU AUGCUUAUCCO 3DQA102	CCUGCACU- CACCUAGAUUA 3DQA105	CAAAUAAACGAG H2-Ab1-201	GC		
D.	3DQB105 H2-Ab1-201 3DQ 3DQ	AUGU	-UGCUU AUGCUUAUCCO 3DQA102 193/209	CCUGCACU- CACCUAGAUUA 3DQA105 92.3	САААUAAACGAG H2-Ab1-201 43.4 45.8	GC 0.55 0.55		

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Figure S2. Sequence Alignment for human and mouse homologs for DQA1* and DQB1* alleles. The sequence alignments for the human DQA1* and DQB1* 3'UTR sequences in Figure 1A and B have been extended to include the mouse homologs H2-Aa and H2-Ab1. **A**. The DQA1* alignment for the human alleles and mouse homolog show high sequence identity between the human alleles at 94.1% but a much lower identity between the human and mouse sequences (<60%) as summarised in **B. C**. The DQB1* alignment for the human alleles and mouse homolog show a low sequence identity of <45% between species but >90% for the human sequences as summarised in **D**. The low level of conservation between human and mouse (<60% for DQA and <45%DQB) will result in different locations of AU rich motifs and affect their presentation in single stranded RNA structure regions.