Supplementary Table S3A: The polypeptide predictions for the *SLA-2* sequences.

region of interest	Domain name	refseq accession	original feature annotation in the refseq (nucl)		columns in largest_compact_alignment		num. codons
			begin	end	begin	end	
largest alignment		AJ251829.1			1	1056	352
exon 1	Peptide leader	AJ251829.1	144585	144648	1	31	10
exon 2 (PBR)	α1	AJ251829.1	144963	145232	32	304	91
exon 3 (PBR)	α2	AJ251829.1	145460	145735	305	580	92
exon 4	α3	AJ251829.1	146344	146619	581	856	92
exon 5	Transmembrane domain	AJ251829.1	146739	146849	857	967	37
exon 6	Cytoplasmic tail	AJ251829.1	147294	147326	968	1000	11
exon 7	Cytoplasmic tail	AJ251829.1	147454	147504	1001	1051	17
exon 8	3' UTR	AJ251829.1	147665	147669	1052	1056	2

Supplementary Table S3B: The SLA polypeptide predictions for the *DQB1* sequences.

Region of interest	Domain name	Refseq accession	Original feature annotation in the RefSeq (Nucl)		Region spanned by our data with reference to the RefSeq (Nucl)		columns in largest_compact_alignment		No of codons
			begin	end	begin	end	begin	end	
Largest alignment		NM_001113694.1			82	840	1	759	253
Exon 1	Peptide leader	NM_001113694.1	1	160	82	160	1	79	26
Exon 2 (PBR)	β1	NM_001113694.1	161	430	161	430	80	349	90
Exon 3	β2	NM_001113694.1	431	712	431	712	350	631	94
Exon 4	Transmembrane domain	NM_001113694.1	713	823	713	823	632	742	37
Exon 5	Cytoplasmic tail	NM_001113694.1	824	1194	824	840	743	759	5.67