

e Figure 1: Protein alignment of DRB1*04:01, DRB1*04:02 and DRB1*07:01.

AA Pos.	10	20	30	40	50	60	70	80	90	100
DRB1*01:01:01:01	GDTRPRFLWQ	LKFECHFFNG	TERVRLLERC	IYNQEESVRF	DSDVGEYRAV	TELGRPD AEY	WNSQKDLLEQ	RRAAVDTYCR	HN YGVGESFT	VQRRVEPKVT
DRB1*04:01:01:01	-----E-	V-H-----	----F-D-Y	F-H---Y---	-----	-----	-----	K-----	-----	----Y-E--
DRB1*04:02:01	-----E-	V-H-----	----F-D-Y	F-H---Y---	-----	-----	-----I--D	E-----	----V----	----Y-E--
DRB1*07:01:01:01	---Q-----	G-YK-----	---QF---L	F-----F---	-----	-----V--S	-----I--D	--GQ---V--	-----	----H-E--
AA Pos.	110	120	130	140	150	160	170	180	190	200
DRB1*01:01:01:01	VYPSKTQPLQ	HHNLLVCSVS	GFYPGSIEVR	WFRNGQEEKA	GVVSTGLIQN	GDWTFQTLVM	LETVPRSGEV	YTCQVEHPSV	TSPLTVEWRA	RSESAQSKML
DRB1*04:01:01:01	---A-----	-----N	-----	-----T	-----	-----	-----	-----L	-----	-----
DRB1*04:02:01	---A-----	-----N	-----	-----T	-----	-----	-----	-----L	-----	-----
DRB1*07:01:01:01	---A-----	-----	-----	-----	-----	-----	-----	-----M-----	-----	-----
AA Pos.	210	220	230							
DRB1*01:01:01:01	SGVGGFVLGL	LFLGAGLFIY	FRNQKGHSGL	QPTGFLS						
DRB1*04:01:01:01	-----	-----	-----	-----						
DRB1*04:02:01	-----	-----	-----	-----						
DRB1*07:01:01:01	-----	-----	-----	-----						

eTable 1: HLA association effects with risk in all DRB1*07:01 heterozygous anti-LGI1 cases and controls, analyzed using a generalized linear equation modeling after control for 3 Principal

Allele	OR	P-value				
		Intercept	Allele *	PC1	PC2	PC3
DRB1*09:01	9.74	3.41E-07	1.26E-03	3.64E-01	9.05E-01	5.61E-01
DRB1*01:01	2.81	5.44E-07	3.17E-03	7.67E-03	6.54E-01	7.94E-01
DRB1*04:02	4.58	3.84E-06	2.26E-02	1.43E-02	3.67E-01	7.72E-01
DRB1*15:01	0.38	4.66E-03	2.30E-02	2.89E-02	4.69E-01	9.09E-01

* P-value FDR corrected

al Components.

eTable 2: HLA association effects in all anti-LGI1 cases versus controls, analyzed using a Generalized Linear Equation modeling after control of three Principal Components.

Iteration	Allele	OR	P-value										
			Intercept	Allele *	PC1	PC2	PC3	DRB1*07:01	DPB1*03:01	DRB1*04:02	DRB1*01:01	DRB1*09:01	DRB4*01:01
1	DRB1*07:01	27.85	3.70E-76	1.72E-52	4.44E-02	4.24E-01	3.95E-01	N/A	N/A	N/A	N/A	N/A	N/A
2	DPB1*03:01	0.19	8.15E-73	3.32E-04	1.22E-01	4.44E-01	2.48E-01	2.23E-54	N/A	N/A	N/A	N/A	N/A
3	DRB1*04:02	5.16	3.89E-70	3.18E-03	6.64E-02	7.45E-01	9.84E-01	3.37E-52	3.73E-05	N/A	N/A	N/A	N/A
4	DRB1*01:01	2.51	4.54E-69	1.82E-03	2.98E-02	6.40E-01	9.79E-01	7.34E-53	1.60E-05	8.17E-05	N/A	N/A	N/A
5	DRB1*09:01	4.61	1.19E-69	9.09E-04	4.32E-01	4.48E-01	9.35E-01	2.36E-52	1.78E-05	4.57E-05	3.97E-05	N/A	N/A
6	DRB4*01:01	1.77	3.30E-72	5.66E-03	2.43E-01	2.60E-01	6.49E-01	1.01E-39	1.69E-05	2.75E-05	6.05E-05	2.88E-05	N/A
7	DRB4*01:03	1.67	4.63E-60	2.80E-02	2.31E-01	2.39E-01	5.72E-01	4.58E-29	1.47E-05	1.52E-04	1.76E-05	2.78E-04	1.52E-04

*: P-value corrected for multiple comparisons; N/A: Not applicable

eTable 3: HLA association effects with age in all LGI1 cases, analyzed using a generalized linear equation modeling after control for three Principal Components.

Iteration	Allele	Allele	P-value							
		Coefficient	Intercept	Allele *	PC1	PC2	PC3	DRB1*07:01	DRB1*04:02	DPB1*11:01
1	DRB1*07:01	9.39	1.44E-76	3.23E-05	3.74E-02	1.55E-01	1.53E-01	N/A	N/A	N/A
2	DRB1*04:02	-6.68	1.57E-77	9.78E-03	2.59E-02	2.52E-01	5.27E-02	5.99E-05	N/A	N/A
3	DPB1*11:01	-4.31	1.79E-81	2.13E-02	1.40E-02	1.88E-01	7.78E-02	1.48E-05	1.14E-02	N/A
4	DQA1*01:02	-4.76	1.00E-78	2.49E-02	9.75E-03	2.03E-01	9.03E-02	2.33E-04	5.09E-03	1.69E-02

* P values not corrected due to low sample size

eTable 4: FBDS presence and mRS of DRB1*07:01 and DRB1*04:02 LGI1 patients.

Allele 1	Allele 2	LGI1% (n=267)	FBDS		Onset mRS		Max mRS		Mast mRS	
			%	P-value	Mean ± Std.	P-value	Mean ± Std.	P-value	Mean ± Std.	P-value
DRB1*07:01 neg	DRB1*04:02 pos	0.015 (4)	100	0.157	2.75 ± 0.50	0.102	2.75 ± 0.50	0.161	1.0 ± 0.82	0.374
DRB1*07:01 pos	DRB1*04:02 pos	0.056 (15)	46	0.600	2.73 ± 0.96	0.049	3.21 ± 1.05	0.991	2.00 ± 1.30	0.133
DRB1*07:01 neg	DRB1*04:02 neg	0.094 (25)	39	0.084	2.14 ± 2.22	0.891	3.39 ± 1.08	0.450	1.96 ± 1.76	0.164
DRB1*07:01 pos	DRB1*07:01 pos	0.112 (30)	52	0.171	2.22 ± 1.15	0.863	3.21 ± 0.99	0.986	1.39 ± 1.45	0.900
DRB1*07:01 pos	DRB1*04:02 neg	0.725 (193)	60	Ref	2.18 ± 1.12	Ref	3.21 ± 0.97	Ref	1.43 ± 1.22	Ref

* All patients included. Clinical data was not available for 2 patients. Abbreviations; FBDS: Faciobrachial Dystonic Seizures, mRS: Modified Ranking Score

Table 5: HLA association effects with risk patients with non-thymoma tumors, and no tumors.

Allele	Non-Thymoma (n=29)	Controls (n=247)	OR	P-value*	No tumor (n=224)	Controls (n=1228)	OR	P-value*
DRB1*07:01	0.86 (25)	0.27 (66)	17.14	1.98E-08	0.92 (205)	0.25 (311)	31.81	2.25E-80
DRB1*04:02	0.00 (0)	0.02 (4)	Inf.	NA	0.08 (19)	0.02 (22)	5.08	1.76E-05

*FDR corrected.
No significant difference in DRB1*07:01 carrier frequency was found between non-thymoma tumorous patients and non-tumorous patients.
10 cases were removed due to missing clinical information regarding tumour status. 3 cases were excluded from the analysis due to low imputation probability.

Table 6: LG11 peptides predicted as medium or strong binders for DRB1*07:01 (% rank <3), and their % rank predicted for other DRB1.

Position	Peptide	Core †	PTM: ‡	DRB1													
				07:01	01:01	03:01	04:01	04:02	04:04	04:05	04:07	08:01	09:01	11:02	11:04	13:01	13:02
81	EEGGFTTPRLGL	FLTPPLQL	pT900(P4),p502(P6)	0.81	19.92	14.41	20.96	64.46	62.78	20.31	27.08	24.87	3.14	31.4	46.44	13.4	27.08
82	EEGGFTTPRLGL	FLTPPLQL	pT900(P4),p502(P6)	0.36	6.74	18.87	13.03	53.57	18.07	11.51	13.58	20.98	1.4	35.44	47.53	35.44	13.03
83	EEGGFTTPRLGL	FLTPPLQL	pT900(P4),p502(P6)	0.83	5.63	18.12	13.45	56.76	38.4	12.04	13.69	22.46	1.7	35.79	47.31	35.79	13.27
84	EGGFTTPRLGLL	FLTPPLQL	pT900(P4),p502(P6)	0.59	6.00	40.09	17.74	60.79	39.47	14.06	15.58	26.09	2.33	36.16	50.98	34.8	15.58
85	GGFTTPRLGLLTP	FLTPPLQL	pT900(P4),p502(P6)	1.89	16.07	57.53	35.97	79.08	66.1	28.53	33.2	47.05	7.21	60.38	74.74	60.38	33.28
114	LHLLELLENNKK	VLFEENNK		1.35	7.36	29.8	1.15	14.27	7.81	7.29	2.06	12.6	3.04	29.41	31.42	29.41	8.01
115	PHLELENNKKK	VLFEENNK		0.8	1.09	11.7	1.43	7.41	4.33	1.47	1.09	7.43	0.79	16.12	21.41	16.12	4.33
116	LHLLELLENNKK	VLFEENNK		0.97	1.12	8.81	1.07	6.25	4.44	1.75	0.97	7.92	2.26	13.29	20.52	13.27	6.51
313	SIANRFKIDDEL	PKIDDEL	wK320(P3)	3.00	5.47	35.81	7.00	22.52	12.61	3.54	1.68	20.77	7.32	34.08	48.27	34.08	20.3
314	FANRFKIDDEL	PKIDDEL	wK320(P3)	1.43	1.76	15.09	4.86	5.96	4.7	2.69	1.98	11.51	3.4	13.22	15.04	15.23	4.86
315	ANRFKIDDELK	PKIDDEL	wK320(P3)	1.64	1.89	12.65	2.83	5.77	4.76	1.96	2.3	13.86	3.67	14.05	20.03	14.05	5.43
341	INNNVYVVAADSK	PVVAADSK	pS351(P6),pS352(P7),mK353(P8)	1.82	0.8	12.78	0.19	5.77	2.46	1.72	0.38	5.03	0.10	24.93	13.79	24.93	11.46
342	INNNVYVVAADSK	PVVAADSK	pS351(P6),pS352(P7),mK353(P8)	2.12	0.67	4.39	0.13	4.86	1.87	1.06	0.33	4.58	0.26	23.2	13.22	23.2	0.13
343	INNNVYVVAADSK	PVVAADSK	pS351(P6),pS352(P7),mK353(P8)	2.14	0.52	2.52	0.12	3.83	1.49	2.00	0.3	7.03	0.4	19.99	10.93	19.99	0.38
363	NGNGPFSHLSHAK	FFSHLSHA		2.54	4.18	31.06	2.94	2.63	7.63	5.01	3.74	6.84	4.92	13.96	13.74	13.96	6.72
364	ONGPFSHLSHAK	FFSHLSHA		1.89	10.89	25.77	1.44	1.49	5.7	8.28	4.82	3.73	9.34	30.00	9.28	2.47	10.28
372	SLHAWRDTDEYLE	YRDTDEYL	pT380(P4),pT381(P8)	2.46	27.74	3.63	6.89	49.59	29.76	8.63	7.57	30.00	3.63	35.46	50.57	35.46	10.12
373	SLHAWRDTDEYLE	YRDTDEYL	pT380(P4),pT381(P8)	1.94	23.05	3.76	7.05	56.14	29.9	8.52	7.2	42.12	2.78	42.31	66.99	42.31	18.74
374	SLHAWRDTDEYLE	YRDTDEYL	pT380(P4),pT381(P8)	1.89	21.6	1.45	20.76	64.74	36.98	11.03	9.18	44.66	2.45	52.47	75.64	52.47	24.06
406	DRPVYQWKAQLG	YQWKAQLG		1.05	2.95	15.89	15.00	2.24	9.71	20.8	20.37	6.28	2.12	0.75	1.40	0.71	1.08
407	RPVYQWKAQLG	YQWKAQLG		1.25	1.71	14.22	15.17	3.89	16.93	21.00	18.68	5.7	1.43	0.6	1.24	0.6	0.56
408	PVYQWKAQLGTH	YQWKAQLG		0.29	1.19	19.79	13.95	11.83	28.16	29.2	16.13	10.06	1.02	7.28	4.04	7.28	0.06
409	YVQWKAQLGTHG	YQWKAQLG		2.74	3.57	39.02	27.48	42.53	59.78	87.33	30.72	21.11	2.81	12.88	20.93	12.88	4.49
493	GSYPTDYVYWDGK	YPTDYVWD	pS497(P2)	2.76	12.17	65.84	7.28	18.4	10.84	5.61	7.43	22.55	3.52	45.9	42.58	45.9	20.52
494	GSYPTDYVYWDGK	YPTDYVWDGK		2.79	1.79	19.2	3.49	5.29	4.75	2.98	1.59	12.63	4.93	19.9	21.8	19.9	12.96
495	DTPTDYVYWDGKA	YTDYVWDGA		2.89	3.23	56.17	2.00	3.41	3.16	2.52	2.8	9.9	4.34	27.45	19.54	27.45	10.95
501	VYWDGKAFAFVYQ	WDAFAFVY	mK508(P5),wK510(P7)	2.86	0.31	30.32	15.75	44.52	44.53	29.39	21.41	28.27	1.89	28.16	42.63	28.16	15.52
507	KAATPKAFAFVYQ	FAFVYQ	wK513(P3)	2.21	4.74	29.55	0.47	1.96	10.25	3.74	9.08	5.43	4.44	6.08	12.06	6.08	4.84
508	KAATPKAFAFVYQ	FAFVYQ	wK513(P3)	1.46	3.22	20.66	5.21	2.83	5.31	4.47	4.57	8.41	2.81	5.39	7.65	5.39	2.78
530	INNNLFASSPKGN	FLFASSPK	pS540(P6)	1.02	0.79	41.74	0.47	3.1	3.2	2.42	1.6	4.58	0.53	20.72	8.47	20.72	12.71
531	INNNLFASSPKGN	FLFASSPK	pS540(P6)	0.7	0.26	34.31	0.21	1.79	2.00	1.76	0.36	0.7	0.11	1.32	13.1	0.65	12.48
532	INNNLFASSPKGN	FLFASSPK	pS540(P6)	0.53	0.24	29.09	0.13	1.2	1.94	1.4	0.57	1.88	0.21	9.32	3.77	9.32	0.32
533	INNNLFASSPKGN	FLFASSPK	pS540(P6)	2.32	1.14	45.82	1.33	4.16	4.22	4.2	3.03	6.86	1.2	24.76	10.96	24.76	18.68

LRR domain is colored in orange and EAR/EPTP domain in green

Peptides predicted as strong binders for DRB1*07:01 and also for other DRB1 are colored in yellow

†Core peptides predicted for DRB1*07:01

‡Post-translational modifications (PTMs): m, methylation; p, phosphorylation; u, ubiquitylation. Predicted PTMs and their pocket position (P1-P9) are shown only for the core peptides of DRB1*07:01. Note that new binders may be created by PTMs in cores that are not predicted without the modification, these are not listed here; and that PTMs may modify the affinity of the core peptides shown in the table

Table 7: LGII peptides predicted as medium or strong binders for DRB1*04:02 (% rank ≤3), and their % rank predicted for other DRB1

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LRR domain is colored in orange and EAR/ETP domain in green

Peptides predicted as strong binders for ORG10450 and also for other ORG1 are colored in yellow

Core peptides predicted for ORB1*04.02

eTable 8: HLA association effects with risk in all DRB1*07:01 negative

LGI1 cases and controls, analyzed using a generalized linear equation modeling after control for 3 Principal Components.

Allele	OR	P-value				
		Intercept	Allele *	PC1	PC2	PC3
DRB1*04:02	7.72	2.97E-68	1.37E-03	7.98E-01	5.01E-02	5.75E-01
DRB1*08:01	4.36	4.83E-64	5.10E-03	8.52E-01	1.25E-02	1.05E-01
DPB1*12:01	5.01	2.00E-67	5.28E-03	6.23E-01	2.29E-02	1.54E-01
DRB1*13:03	3.95	4.38E-70	3.98E-02	7.53E-01	5.60E-02	1.65E-01

* P-value not corrected due to low sample size