SUPPLEMENTARY MATERIAL

Table S1: Peptides predicted to be B-cell epitopes with the software BepiPred-2.0 for A0A251QUN8 (R-mandelonitrile-lyase). Sequences corresponding to epitopes confirmed experimentally are marked in red.

Peptide number	Sequence	Position	Length
1	FYSETGIEWDLDLVNK	148-163	16
2	VEDAIVVKPNNQSWQS	168-183	16
3	AGILPDNGFSLDH	192-204	13
4	SDGNS	266-270	5
5	GPESYLSSL	300-308	9
6	PPNPIEASVV	335-344	10
7	SDYYQVSLSSL	351-361	11
8	FPTTSYPLPN	371-380	10
9	SSDVRIAPN	404-412	9
10	YYSNST	417-422	6
11	ERSIRLEAIHNIH	544-556	13

Table S2: Peptides predicted to be B-cell epitopes with the software BepiPred-3.0 for A0A251QUN8. Sequences corresponding to epitopes confirmed experimentally are marked in red.

Peptide number	Sequence	Position	Lenght
1	LANTSAHDFSYLKFVYN	28-44	17
2	TDTSLEGS	46-53	8
3	TEYPN	88-92	5
4	LTADGFAYNLQQQDDGKTP	94-112	19
5	ERFVSEDGID	113-122	10
6	VKPNNQSWQS	174-183	10
7	LPDNGF	194-199	6
8	DNNGTRH	216-222	7
9	NKGDPNN	229-235	7
10	SNTSNLS	251-257	7
11	SDGNS	266-270	5
12	PNPIEASVVTVLGITSDY	336-353	18
13	SSLPFSTPPFS	359-369	11
14	PTTSYPLPNST	372-382	11
15	QERSIRLEAIHNIHESK	542-559	17

Table S3: Designed peptides covering the sequence of A0A251QUN8. The 37 positive peptides are marked in red.

Peptide number	Sequence	Position	O.D.
1	VHSLANTSAHDFSYL	25-39	0.166
2	TSAHDFSYLKFVYNA	31-45	0.608
3	SYLKFVYNATDTSLE	37-51	0.034
4	YNATDTSLEGSYDYI	43-57	0.057
5	SLEGSYDYIVIGGGT	49-63	0.050
6	DYIVIGGGTSGCPLA	55-69	0.007
7	GGTSGCPLAATLSEK	61-75	1.519
8	PLAATLSEKFKVLLL	67-81	0.067
9	SEKFKVLLLERGTIA	73-87	0.106
10	LLLERGTIATEYPNT	79-93	0.046
11	TIATEYPNTLTADGF	85-99	0.040
12	PNTLTADGFAYNLQQ	91-105	0.125
13	DGFAYNLQQQDDGKT	97-111	0.087
14	LQQQDDGKTPVERFV	103-117	0.047
15	GKTPVERFVSEDGID	109-123	0.076
16	RFVSEDGIDNVRARI	115-129	0.044
17	GIDNVRARILGGTTI	121-135	0.043
18	ARILGGTTIINAGVY	127-141	0.072
19	TTIINAGVYARANIS	133-147	0.154
20	GVYARANISFYSETG	139-153	0.042
21	NISFYSETGIEWDLD	145-159	0.035
22	ETGIEWDLDLVNKTY	151-165	0.098
23	DLDLVNKTYEWVEDA	157-171	0.066
24	KTYEWVEDAIVVKPN	163-177	0.209
25	EDAIVVKPNNQSWQS	169-183	0.149
26	KPNNQSWQSVIGEGF	175-189	0.328
27	WQSVIGEGFLEAGIL	181-195	0.070
28	EGFLEAGILPDNGFS	187-201	0.109
29	GILPDNGFSLDHEAG	193-207	0.057
30	GFSLDHEAGTRLTGS	199-213	0.122
31	EAGTRLTGSTFDNNG	205-219	0.063
32	TGSTFDNNGTRHAAD	211-225	0.006
33	NNGTRHAADELLNKG	217-231	0.281
34	AADELLNKGDPNNLL	223-237	0.104
35	NKGDPNNLLVAVQAS	229-243	0.121
36	QASVEKILFSSNTSN	241-255	0.155
37	ILFSSNTSNLSAIGV	247-261	0.040
44	GTPQLLLLSGVGPES	289-303	0.064
45	LLSGVGPESYLSSLN	295-309	0.052
46	SLNITVIQPNPYVGQ	307-321	0.035
47	IQPNPYVGQFVYDNP	313-327	0.030
48	VGQFVYDNPRNFINI	319-333	0.057
49	DNPRNFINILPPNPI	325-339	0.016
50	INILPPNPIEASVVT	331-345	0.082
51	NPIEASVVTVLGITS	337-351	0.084
52	VVTVLGITSDYYQVS	343-357	0.030
53	ITSDYYQVSLSSLPF	349-363	0.036
54	QVSLSSLPFSTPPFS	355-369	0.058
55	LPFSTPPFSLFPTTS	361-375	0.340
56	PFSLFPTTSYPLPNS	367-381	0.079
57	TTSYPLPNSTFAHIV	373-387	1.362
58	PNSTFAHIVSQVPGP	379-393	0.979
59	HIVSQVPGPLSHGSV	385-399	0.712
60	PGPLSHGSVTLNSSS	391-405	0.031
61	GSVTLNSSSDVRIAP	397-411	0.031
62	SSSDVRIAPNIKFNY	403-417	0.038
63	IAPNIKFNYYSNSTD	409-423	0.011
64	FNYYSNSTDLANCVS	415-429	3.438
65	STDLANCVSGTKKLG	421-435	3.002
66	CVSGTKKLGDLLRTK	427-441	0.628
67	KLGDLLRTKALEPYK	433-447	0.212
68	RTKALEPYKARDVPG	439-453	0.372
69	PYKARDVPGIDGFNY	445-459	0.238
70	VPGIDGFNYLGVPLP	451-465	0.151
71	FNYLGVPLPENQTDD	457-471	0.111
72	PLPENQTDDASFETF	463-477	0.040
73	TDDASFETFCLDNVA	469-483	3.451
74	ETFCLDNVASYWHYH	475-498	0.020
75	NVASYWHYHGGSLVG	481-495	0.016
76	HYHGGSLVGKVLDDS	487-501	0.315
77	LVGKVLDDSFRVMGI	493-507	0.043
78	DDSFRVMGIKALRVV	499-513	0.408
79	MGIKALRVVDASTFP	505-519	0.020
80	RVVDASTFPDEPNSH	511-525	0.806

Peptide number	Sequence	Position	O.D.
38	TSNLSAIGVIYTDSD	253-267	0.046
39	IGVIYTDSDGNSHQA	259-275	0.053
40	DSDGNSHQAFVRGYG	265-279	0.130
41	HQAFVRGYGEVIVSA	271-285	0.037
42	GYGEVIVSAGTIGTP	277-291	0.073
43	VSAGTIGTPQLLLLS	283-297	0.019

Peptide number	Sequence	Position	O.D.
81	TFPDEPNSHPQGFYL	517-531	1.338
82	NSHPQGFYLMLGRYV	523-537	2.482
83	FYLMLGRYVGLQILQ	529-543	0.030
84	RYVGLQILQERSIRL	535-549	0.164
85	ILQERSIRLEAIHNI	541-555	0.357
86	RSIRLEAIHNIHESK	545-559	0.945

doi: 10.18176/jiaci.1052

Table S4: Number of regions containing strong T-cell epitopes (rank<0.5) predicted for each MHC-II allele with NetMHCIIpan-4.1 in R-mandelonitrile-lyase.

		Core peptides: position/sequence				
MHC-II Allele	**Number of T-cell epitopes**	**1**	**2**	**3**	**4**	**5**
HLA-DPA1*01:03/DPB1*02:01	3	36-43/FSYLKFVYN	159-167/LVNKTYEWV	184-192/VIGEGFLEA	N/A	N/A
HLA-DPA1*01:03/DPB1*04:01	2	36-43/FSYLKFVYN	184-192/VIGEGFLEA	N/A	N/A	N/A
HLA-DPA1*02:01/DPB1*01:01	3	36-43/FSYLKFVYN	184-192/VIGEGFLEA	209-217/LTGSTFDNN	N/A	N/A
HLA-DPA1*02:01/DPB1*05:01	2	36-43/FSYLKFVYN	184-192/VIGEGFLEA	N/A	N/A	N/A
HLA-DPA1*02:01/DPB1*14:01	1	221-229/RHAADELLN	N/A	N/A	N/A	N/A
HLA-DPA1*03:01/DPB1*04:02	2	36-43/FSYLKFVYN	184-192/VIGEGFLEA	N/A	N/A	N/A
HLA-DQA1*01:01/DQB1*05:01	2	165-173/YEWVEDAIV	443-451/LEPYKARDV	N/A	N/A	N/A
HLA-DQA1*01:02/DQB1*06:02	4	124-132/NVRARILGG	235-243/NLLVAVQAS	395-403/SHGSVTLNS	402-410/NSSSDVRIA	N/A
HLA-DQA1*04:01/DQB1*04:02	2	178-186/NQSWQSVIG	443-451/LEPYKARDV	N/A	N/A	N/A
HLA-DQA1*05:01/DQB1*02:01	2	86-94/IATEYPNTL	91-99/PNTLTADGF	N/A	N/A	N/A
HLA-DRB1*01:01	2	331-339/INILPPNPI	529-537/FYLMLGRYV	N/A	N/A	N/A
HLA-DRB1*04:01	2	262-270/IYTDSDGNS	417-425/YYSNSTDLA	N/A	N/A	N/A
HLA-DRB1*04:05	5	43-51/YNATDTSLE	189-197/FLEAGILPD	512-520/VVDASTFPD	536-544/YVGLQILQE	549-557/LEAIHNIHE
HLA-DRB1*07:01	2	304-312/YLSSLNITV	370-378/LFPTTSYPL	N/A	N/A	N/A
HLA-DRB1*08:02	2	172-180/IVVKPNNQS	530-538/YLMLGRYVG	N/A	N/A	N/A
HLA-DRB1*09:01	0	N/A	N/A	N/A	N/A	N/A
HLA-DRB1*11:01	1	530-538/YLMLGRYVG	N/A	N/A	N/A	N/A
HLA-DRB1*12:01	5	310-318/ITVIQPNPY	331-339/INILPPNPI	407-415/VRIAPNIKF	510-518/LRVVDASTF	539-547/LQILQERSI

doi: 10.18176/jiaci.1052

		Core peptides: position/sequence				
MHC-II Allele	**Number of T-cell epitopes**	**1**	**2**	**3**	**4**	**5**
HLA-DRB1*13:02	2	172-180/IVVKPNNQS	409-417/IAPNIKFNY	N/A	N/A	N/A
HLA-DRB1*15:01	4	146-154/ISFYSETGI	172-180/IVVKPNNQS	407-415/VRIAPNIKF	443-451/LEPYKARDV	N/A
HLA-DRB3*01:01	2	194-202/ILPDNGFSL	322-330FVYDNPRNF	N/A	N/A	N/A
HLA-DRB3*02:02	4	41-49/FVYNATDTS	99-107/FAYNLQQQD	249-257/FSSNTSNLS	417-425/YYSNSTDLA	N/A

N/A: Not applicable. Sequences in red contain the core of higher binder peptides (rank<0.1).