Table S1: MHC class I T cell epitopes (nine-mer)

Protein	**Intermediate affinity binding**		**High affinity binding**	
	Sequence	**Position**	**Sequence**	**Position**
MAP1297	SETEYGSAL	25-33		
	ALYAGRFTL	226-234		
MAP1653	NPINTVGEL	9-17	AATRNTQVL	44-52
MAP3393c	GMVASATPL	77-85	TEAPRVAVI	4-12
	RIVEFQTQL	144-152		
	VSAHRTPGV	41-49		
	VPLGRLDGL	92-100		
	FQTQLADSV	148-156		
	AEFDVPAEV	30-38		
MAP2872c	WAPLLWTSL	116-124	GSIVNTASI	135-143
	LTLERFGSV	75-83	MYNATKAAL	154-162
	YNATKAALI	155-163	HEDPLSSSI	199-207
	LERFGSVDI	77-85		
	IEQDHARFA	100-108		
	DPLSSSIAL	201-209		
	TGASRGIGL	14-22		
MAP1589c	PAYELTALI	11-19	LPFPMLSDI	106-114
	VVFFWPKDF	49-57		
	RELSLATGV	116-124		
MAP4340	FQVVSIPTL	76-84		

	CGPCKMVAP	38-46		
	VSIPTLILF	79-87		
MAP2698c	HAIALRNYL	110-118	IALRNYLVV	112-120
	IMLLLKDNL	71-79	RPVANALTL	4-12
	NYLVVTREV	116-124	LEEPILSGL	173-181
	TYSQVETLV	145-153	EEPILSGLV	174-182
	NEEARVQYV	129-137	HELFFSNLV	192-200
	VPYDRGENF	38-46	LEYTRDETI	204-212
	EEARVQYVM	130-138	TENDLRQVI	246-254
	EELWFAHDY	29-37	DEPALKPFV	265-273
	LEDYWGRWL	92-100	HRELVEHFI	83-91
MAP1168c	AGPRTIEEF	184-192	PYLAGPRTI	181-189
	AAPSFPVRV	143-151	VPINPRHPL	66-74
	QQLSFYETI	232-240		
	IEEFIVPRI	189-197		
	PEESVLRQV	263-271		
	SELSAAPSF	139-147		
	RIIAAVPVL	210-218		
MAP3567	VIRAAWPHF	130-138	VGLINSLAL	172-180
	IAPIAATRM	192-200	RAVANYDSV	65-73
	TEDILPKEV	201-209	KYNIHANAI	184-192
	AEPAGAENI	74-82	NPNSASVFV	230-238

	EENPNSASV	228-236		
	VTYDKPPTV	255-263		
	DEFGAVHGV	88-96		
MAP1017c	VNRAFETTL	217-225	AEAERSGLV	174-182
	CELAMMCDV	116-124	FETTLAEGL	221-229
	VEREERVGI	14-22		
	GKAKAMDLI	157-165		
MAP2487c	SSFEGPLPM	16-24		
	YASSFEGPL	14-22		
	QRLLGTREI	75-83		
	KPPWAAEAF	112-120		
	PPWAAEAFA	113-121		
	MPPSKHVAV	24-32		
MAP3268	IEASYRDGV	102-110	IEASYRDGV	102-110
MAP1698c	MNMLRFDPF	1-9	LPESLDVNV	56-64
	GVFSRQVYL	92-100		
	AEAAKPRKI	125-133		
	VEFDLPGVL	48-56		
MAP3651c	ISNARRSGL	177-185	VSMPCYVRV	83-91
	VAGQGFSQM	249-257	CYVRVTEQL	87-95
	SVGNYLADM	302-310	SNARRSGLI	178-186
	TEDQKRAYL	121-129	MEAGMAKLF	336-344
	RESVRWAQV	16-24	IEQMKRIGI	61-69

	EEDMLVATV	27-35	SPVSMPCYV	81-89
	LVATVRAFI	31-39		
	QEYDVERYF	367-375		
	TEQLARGWM	92-100		
	LPRMASGEI	129-137		
MAP3523c	ESPQWSAGV	313-321	NATTNCFPM	115-123
	GGPSLIDCE	556-564	AYAQADNEI	247-255
	SGPGFLNAL	102-110	SEFDSNQQI	331-339
	SAGVKFVQV	318-326		
	HPMRFYNAL	393-401		
	ASGIRYLGF	67-75		
	ADNEIRRFV	251-259		
	VESTGIPFL	259-267		
	CDALAARPI	355-363		
	YRLPVTVVI	488-496		
	RPGGVYLDI	182-190		
	LPMSMAKGL	267-275		
	HPHGRSRHM	7-15		
MAP0187c	WAVLGYDTV	125-133	LEPHISGQ	16-24
	WNVVNWADV	182-190	NEDHAAIFL	53-61
	AFYLQYKNV	165-173	VPLGIIPLL	149-157
	AIFLNEKNL	58-66		
	DYAALEPHI	12-20		

	GYDTVGSRL	129-137		
	HHATYVKGV	32-40		
	NEKNLAFHL	62-70		
MAP3974c	WGPVTGGTA	90-98	VEVVTLQVI	57-65
	IGARLAELI	151-159		
MAP2312c	AYYDAAAKM	306-314	NEEQKRKWL	108-116
	YGFMNEYPV	349-357	KEAAIAKMI	322-330
	VAITLEAGV	88-96	NEYPVARHY	353-361
	EYQDLRDTV	13-21	SYQAISFKI	285-293
	GYANFLSIL	239-247	YGFMNEYPV	349-357
	KYAKERQSF	271-279		
	DYFALSLAL	70-78		
	EEHSFPYEV	38-46		
	QPIGSYQAI	281-289		
	APVSAKHDE	30-38		
	FPYEVVAKM	42-50		

The predicted epitope result is based on the scores of antigenic peptide processing (proteasomal cleavage and TAP transport) and MHC binding affinity. Score is categorized as intermediate binding affinity ($IC_{50} < 500$ nM) and high binding affinity ($IC_{50} < 50$ nM).

Table S2: MHC class II T cell epitopes (fifteen-mers)

Protein	Sequence	Position	Sequence	Position
MAP1297	LYAGRFTLPQALAAV	227-241	YAGRFTLPQALAAVA	228-242
	ALYAGRFTLPQALAA	226-240	AGRFTLPQALAAVAE	229-243
MAP1653	RTFNERAAGAGATVL	65-79	FNERAAGAGATVLNV	67-81
	TFNERAAGAGATVLN	66-80	NERAAGAGATVLNVS	68-82
	ERAAGAGATVLNVSK	69-83	VGELPSVGSKAPAFS	14-28
	TVGELPSVGSKAPAF	13-27	AGLLARAIVVVGADG	125-139
	PMAGLLARAIVVVGA	123-137	MAGLLARAIVVVGAD	124-138
	GLLARAIVVVGADGN	126-140	LLARAIVVVGADGNV	127-141
MAP3393c	LPGMVASATPLPVIG	75-89	HLPGMVASATPLPVI	74-88
	AHLPGMVASATPLPV	73-87	PGMVASATPLPVIGV	76-90
	GMVASATPLPVIGVP	77-91	SIVQMPAGVPVATVS	105-119
	LSIVQMPAGVPVATV	104-118	LLSIVQMPAGVPVAT	103-117
	IVQMPAGVPVATVSI	106-120	SLLSIVQMPAGVPVA	102-116
MAP2872c	LAIAQQLAAAGANVV	22-36	IAQQLAAAGANVVLT	24-38
	AQQLAAAGANVVLTA	25-39	QQLAAAGANVVLTAR	26-40
	VDILVNNAGTNPAYG	83-97	SVDILVNNAGTNPAY	82-96
	ILVNNAGTNPAYGPL	85-99	DILVNNAGTNPAYGP	84-98
	VLGAAQGFRPAPTPS	245-259	ADEAAAQVGPQALGV	45-59
	DEAAAQVGPQALGVG	46-60	EAAAQVGPQALGVGA	47-61
	GSVDILVNNAGTNPA	81-95		
MAP2698c	LGGRDWDPSSATLPR	49-63	FLGGRDWDPSSATLP	48-62

	GGRDWDPSSATLPRP	50-64	GRDWDPSSATLPRPL	51-65
	RDWDPSSATLPRPLT	52-66		
MAP1168c	VYVAAMGPKALQVTG	159-173	YVAAMGPKALQVTGE	160-174
	VAAMGPKALQVTGEL	161-175	GTPIPVYVAAMGPKA	154-168
	HGSELSAAPSFPVRV	137-151	GSELSAAPSFPVRVP	138-152
	SELSAAPSFPVRVPG	139-153	PLIVASLAQTAQAAA	73-87
	HPLIVASLAQTAQAA	72-86	DDVEGARAAAAQQLS	221-235
	SDDVEGARAAAAQQL	220-234	AVDFHGSELSAAPSF	133-147
	VDFHGSELSAAPSFP	134-148	LLSDDVEGARAAAAQ	218-232
	LSDDVEGARAAAAQQ	219-233	FHGSELSAAPSFPVR	136-150
	GIILMAHPDAANLVD	4-18	AGIILMAHPDAANLV	3-17
	DFHGSELSAAPSFPV	135-149	GAVDFHGSELSAAPS	132-146
	IPVYVAAMGPKALQV*	157-171	PVYVAAMGPKALQVT*	158-172
	TPIPVYVAAMGPKAL*	155-169	PIPVYVAAMGPKALQ*	156-170
MAP3567	NIHANAIAPIAATRM	186-200	AKYNIHANAIAPIAA	183-197
	KYNIHANAIAPIAAT	184-198	YNIHANAIAPIAATR	185-199
	IHANAIAPIAATRMT	187-201		
MAP2487c	GYASSFEGPLPMPPS	13-27	YASSFEGPLPMPPSK	14-28
	AGYASSFEGPLPMPP	12-26	SSFEGPLPMPPSKHV	16-30
	ASSFEGPLPMPPSKH	15-29	HNAGYASSFEGPLPM	10-24
	QEETGIKPPWAAEAF	106-120	NAGYASSFEGPLPMP	11-25
	EETGIKPPWAAEAFA	107-121		
MAP1698c	WGAVPWGTAAQPALV	21-35		

MAP3651c	ELSFGNFRAPATAVL	232-246	LSFGNFRAPATAVLG	233-247
	CELSFGNFRAPATAV	231-245	SCELSFGNFRAPATA	230-244
	SFGNFRAPATAVLGG	234-248	LAVPEEYGGSPVSMP	72-86
	AVPEEYGGSPVSMPC	73-87	FGNFRAPATAVLGGV	235-249
	DQKRAYLPRMASGEI	123-137	EDQKRAYLPRMASGE	122-136
MAP3523c	GPGFLNALPALANAT	103-117	PGFLNALPALANATT	104-118
	GFLNALPALANATTN	105-119	FLNALPALANATTNC	106-120
	NRNPASAASPAAVSA	578-592	ANRNPASAASPAAVS	577-591
	LANRNPASAASPAAV	576-590	RNPASAASPAAVSAG	579-593
	LNALPALANATTNCF	107-121	NPASAASPAAVSAGA	580-594
	HLANRNPASAASPAA	575-589	SGPGFLNALPALANA	102-116
	MSATSASAGPAPESA	15-29	TSGPGFLNALPALAN	101-115
	SATSASAGPAPESAR	16-30	ATSASAGPAPESARL	17-31
	GHLANRNPASAASPA	574-588	TSASAGPAPESARLI	18-32
	GFRQEASAGNAAAAA	74-88	HMSATSASAGPAPES	14-28
	FRQEASAGNAAAAAG	75-89	SASAGPAPESARLID	19-33
	SGHLANRNPASAASP	573-587	LGFRQEASAGNAAAA	73-87
	VDPAPRQLPAPEAVD	212-226	PAPRQLPAPEAVDRA	214-228
	VVDPAPRQLPAPEAV	211-225	DPAPRQLPAPEAVDR	213-227
	RHMSATSASAGPAPE	13-27	FGGKGYHVSTAAELR	532-546
	AFGGKGYHVSTAAEL	531-545	GGKGYHVSTAAELRA	533-547
	TTSGPGFLNALPALA	100-114	APRQLPAPEAVDRAL	215-229
	RQEASAGNAAAAAGF	76-90	QEASAGNAAAAAGFL	77-91

	ESGHLANRNPASAAS	572-586	PMRFYNALGAIRAVL	394-408
	HPMRFYNALGAIRAV	393-407	PHPMRFYNALGAIRA	392-406
	YLGFRQEASAGNAAA	72-86		
MAP0187c	VQKRYAAATSKAQGL	190-204	ADVQKRYAAATSKAQ	188-202
	DVQKRYAAATSKAQG	189-203	QKRYAAATSKAQGLI	191-205
	KRYAAATSKAQGLIF	192-206	DLDWDYAALEPHISG	8-22
	LDWDYAALEPHISGQ	9-23	PDLDWDYAALEPHIS	7-21
	WDYAALEPHISGQIN	11-25	DWDYAALEPHISGQI	10-24
	FDKFRAQFSAAANGL	106-120	GSFDKFRAQFSAAAN	104-118
	DKFRAQFSAAANGLQ	107-121	SFDKFRAQFSAAANG	105-119
	RYAAATSKAQGLIFG	193-207	KFRAQFSAAANGLQG	108-122
	FGSFDKFRAQFSAAA	103-117	WADVQKRYAAATSKA	187-201
MAP2312c	KIARMEARAHVARTA	292-306		

The predicted epitope is the result of consensus prediction between ARB and SMM_align algorithm methods. Except for the protein encoded by MAP1168c all the proteins were predicted only with intermediate binding affinity ($IC_{50} < 500$ nM). Protein encoded by MAP1168c was also predicted with high binding affinity* ($IC_{50} < 50$ nM) epitopes in addition to intermediate binding affinity epitopes.

Table S3: The 3D structure template and description used for epitope prediction

Protein	PDB ID	Description of 3D structure template molecule
MAP1297	2VEP	Crystal structure of the bifunctional protein pria (Wright et al 2008)
MAP1653	1Y25	Structure of *Mycobacterial* thiol peroxidase *Tpx* (Stehr et al 2006)
MAP3393c	1O4V	Crystal structure of phosphoribosylaminoimidazole mutase *PurE* (Tm0446) from *Thermotoga maritima* A (Schwarzenbacher et al 2004)
MAP2872c	2ZAT	Crystal structure of a mammalian reductase (Tanaka et al 2008)
MAP1589c	2BMX	*Mycobacterium tuberculosis AhpC* (Guimaraes et al 2005)
MAP4340	1NW2*	The crystal structure of the mutant R82e of thioredoxin from *Alicylobacillus acidocaldarius* (Pedone et al 1999)
	2ILU	Crystal structure of lactaldehyde dehydrogenase from *E. coli*: the binary complex with NADPH aldehyde dehydrogenase A
MAP2698c	1ZAO	X-ray structure of putative Acyl-Acp desaturase *DesA2* from *Mycobacterium tuberculosis* H37rv (Dyer et al 2005)
MAP1168c	1EZW	Structure of co-enzyme F420 dependent tetrahydromethanopterin reductase from *Methanopyrus kandleri* (Shima et al 200)
MAP3567	1ZBQ	Crystal structure of human 17-beta-hydroxysteroid dehydrogenase type 4 in complex with NAD (Lukacik et al 2006**)**
MAP1017c	3H81	Crystal structure of enoyl-CoA hydratase from *Mycobacterium tuberculosis* (Edwards et al unpublished)
MAP2487c	1YLK	Crystal structure of Rv1284 from *Mycobacterium tuberculosis* in complex with thiocyanate (Covarrubias et al 2005)

MAP3268	1SHS	Small heat shock protein from *Methanococcus jannaschii* (Kim et al 1998)
MAP1698c	1SHS	Small heat shock protein from *Methanococcus jannaschii* (Kim et al 1998)
MAP3651c	2PGO*	Crystal structure of Acyl-CoA dehydrogenase from *Geobacillus kaustophilus* (Chen et al unpublished)
	2CX9	Crystal structure of acyl-CoA dehydrogenase
MAP3523c	2Q27*	Crystal structure of oxalyl-CoA decarboxylase from *E. coli* (Werther et al 2006)
	2Q29	Crystal structure of oxalyl-coA decarboxylase from *Escherichia coli* in complex with acetyl coenzyme A oxalyl-CoA decarboxylase (Werther et al 2006)
MAP0187c	1GN3	H145q mutant of *Mycobacterium tuberculosis* iron-superoxide dismutase (Bunting et al unpublished)
MAP2312c	1JQI	Crystal structure of rat short chain Acyl-CoA dehydrogenase complexed with acetoacetyl-CoA (Battaile et al 2002)

3D structure templates were modelled by both Ellipro and SWISS-MODEL Workspace.

* 3D structure template modelled only by Ellipro but not by SWISS-MODEL Workspace.

Table S4: Conformational B cell epitope at minimum cut-off score of 0.8

Protein-PDB ID	Residue	No.	Score
MAP1297-2VEP			
Epitope 1	D84, D85, D86	3	0.853
Epitope 2	A113, R114, Q160	3	0.849
Epitope 3	M1, S203, D205, R208, A239, A240, A242, E243	8	0.843
MAP1653-1Y25			
Epitope 1	G8, N9, P10	3	0.976
Epitope 2	G94, A95, E96, G97, I98, E99	6	0.822
MAP3393c-1O4V			
Epitope 1	L166, H167, G168, K169, V170, T171, G172, Q173	8	0.931
Epitope 2	E161, A162, Q164, R165	4	0.887
Epitope 3	M1, S2, V3, T4, E5	5	0.858
MAP2872c-2ZAT			
Epitope 1	M1, T2, S3, Q4	4	0.921
Epitope 2	A50, G53, P54, Q55, A56, L57	6	0.849
Epitope 3	P94, A95, Y96, G97, P98, L99, I100, E101, Q102, D103, H104, A105, R106, F107, A151	15	0.845
Epitope 4	K41, Q42, E43, D46	4	0.840
Epitope 5	L195, W196, K197, D198, H199, E200, D201, P202, S204, S205, S206, A208, L209, G210, R211, G243, T244, A255, P256, T257, P258, S259	22	0.816
MAP1589c-2BMX			

Epitope 1	E189, L190, L191, K192, A193, S194, A195	7	0.978
Epitope 2	K180, G181, D182, P183, T184, L185, N186, A187, T188	9	0.933
Epitope 3	D22, L23, S24, K25, V26, D27, A28, K29, Q30, P31, G32, D33	12	0.859
MAP4340-1NW2			
Epitope 1	M1, T2, D3, A4, E5, K6, A7, S8	8	0.855
Epitope 2	H58, S110, V113, P114, N115, L116, G117	7	0.808
MAP2698c-1ZA0A			
Epitope 1	V38, P39, Y40, D41, R42, G43, E44, N45, F46, A47, F48	11	0.921
Epitope 2	R259, A260, W261	3	0.914
Epitope 3	G262, V263, A264, D265, E266, P267, A268, L269, K270	9	0.891
Epitope 4	Y206, T207, R208, D209	4	0.885
MAP1168c-1EZWA			
Epitope 1	R244, A248, G251, L252, S253, N254, A255, V256, E257, L258, A259, A260, I261, G262**,** P263, E264, E265, S266, R269	19	0.918
Epitope 2	H130, S131, G132, A133, V134, D135, F136, H137, G138, S139, E140, L141, S142, A143, A144, P145, S146, F147, P148, V149, R150, V151, P152, G153	24	0.850
Epitope 3	K199, A202, E203, A204, G205, R206, P207	7	0.849

Epitope 4	D222, V223, E224, G225, A226, R227, V293	7	0.842
MAP3567-1ZBQE			
Epitope 1	Q251, N252, A253, G254, V255, T256, Y257, D258, K259, P260, P261, T262, V263, Q264, D265, V266, A267, A268, R269, W270, D271, E272, I273, T274, D275, L276, S277, A278, A279	29	0.918
Epitope 2	F108, M111, L112, F113	4	0.887
Epitope 3	K285, L286, G287	3	0.848
Epitope 4	L205, P206, K207, E208, V209, A211, K212, L213	8	0.835
Epitope 5	D105, G106, T107, H109, K110, N158, F159, G160	8	0.814
MAP1017c-3H81C			
Epitope 1	A77, E78, L79, T80, F81, A82, D83, A84, Y85, G86, D88	11	0.895
Epitope 2	E222, T223, T224, L225, A226, E227, L229, L230, R233, R234, H237, S238, F240, A241, T242, A243, Q245, T246, E247, G248, M249, A250, A251, F252, V253, E254, K255, R256, A257, P258, N259, F260	32	0.876
Epitope 3	M1, T2, D3, S4, T5, D6, T8, F9	8	0.804
Epitope 4	G157, K158, A159	3	0.801
MAP2487c-1YLKA			
Epitope 1	A2, D5, L8, A9, A12, G13, A15, S16, S17, F18, E19, G20, P21, L22	14	0.879
Epitope 2	K102, R103, G104, I105, Q106, E107, E108, T109,	14	0.879

	G110, I111, K112, P113, P114, W115		
MAP3268-1SHSD			
Epitope 1	T138, E139, T140, A141, R142, E143, V144, V145, N146, A147	10	0.874
Epitope 2	A79, T80, E81, R82, P83, R84, G85, V86, F87, S88, R89, E90	12	0.860
Epitope 3	D72, P73, S74, R75, E76	5	0.838
Epitope 4	L113, H114, I115, P116, V117	5	0.823
MAP1698c-1SHSD			
Epitope 1	H140, Q141, R142, A143, I144, N145, A146	7	0.962
Epitope 2	I133, E134, V135, A136, A137, G138, K139	7	0.889
Epitope 3	N83, G84, V85, V86, S87, E88, R89	7	0.827
Epitope 4	D79, E80, D81, R82	4	0.803
MAP3651c-2PGO			
Epitope 1	R16, E17, S18, V19, R20	5	0.966
Epitope 2	A396, L399, V400, T401, R402, G403, G404, I405	8	0.936
Epitope 3	Y286, A287, Q288, Q289, R290, E291, S292, F293, G294, Q295, P296, I297, W298, Q299, H300, Q301, S302, V303, G304, N305, Y306	21	0.916
Epitope 4	L160, P161, D162, P163, D164, S165, D166, G167	8	0.886
Epitope 5	T192, D193, P194, K195, A196, T197, P198	7	0.860
Epitope 6	G361, G362, Y363, Y365, S366, Q367, E368, Y369	8	0.843
Epitope 7	V7, A9, Q10, Q11, V12, D13, V14, W21, A22, Q23	10	0.831

Epitope 8	G213, G236, N237	3	0.818
Epitope 9	M1, G2, A3, N4, S5	5	0.812
Epitope 10	N25, D26, E27	3	0.807
MAP3523c-2Q27			
Epitope 1	M1, A2, G3, Q4	4	0.995
Epitope 2	Y5, P6, H7, P8, H9, G10, R11	7	0.986
Epitope 3	S12, R13, H14, M15, S16, A17, T18, S19, A20, S21, A22, G23, P24, A25, P26, E27, S28, A29, R30	19	0.939
Epitope 4	A582, S583, A584, A585, S586, P587, A588, A589, V590, S591, A592, G593, A594	13	0.920
Epitope 5	P220, A221, P222, E223, A224, V225, D226, R227, A228, L229, D230, V231, L232, A233, D234, A235, R236, R237, P238, S261, T262, G263, I264, A295, D296, D356, A357, L358, A359, A360, R361, P362, I363, T364, V365, P366, A367, E371	38	0.852
Epitope 6	R504, G505, D506, E507, A508, P509, H510, G511, D512, D513, P514, A515, P516, T517, V518, P567	16	0.841
Epitope 7	S130, D131, A133, L134, V135, D136, L137, R138, R139, G140, D141, Y142, D144, L145	14	0.832
Epitope 8	L519, S520, A521, R522, A523, R524, L527, E530, A531, F532, H538	11	0.816
Epitope 9	S318, A319, G320, V321, K322	5	0.809
MAP0187c-1GN3			

Epitope 1	S199, K200, A201, Q202, G203, L204, I205, F206, G207	9	0.900
Epitope 2	A45, K46, L47, E48, E49, A50, R51, A52, N53, E54, D55, H56, A57, A58, I59, F60, L61	17	0.895
MAP2312c-1JQI			
Epitope 1	A382, R383, S384, L385, G386, L387, S388	7	0.938
Epitope 2	Y272, A273, K274, E275, R276, Q277, S278, F279, G280, Q281, P282, I283, G284, S285, Y286, Q287, A288, I289, S290, F291	20	0.936
Epitope 3	G347, G348, Y349, F351, M352, N353, E354, Y355	8	0.870
Epitope 4	A7, G8, T9, L10, P11, K12, Q15, D16	8	0.863
Epitope 5	R147, L148, E149, D150, G151, E152, V154, N156, T198, P199, G200, S223, D224, R226, E229	15	0.859
Epitope 6	G180, T181, V182, G183, A184, D185, K187, G237	8	0.850
Epitope 7	M1, T2, T3	3	0.808
Epitope 8	A316, G317, K318, P319	4	0.807