

Table S1. The amino acid (AA) residues surrounding the ZIKV and DENV glycosylation site (defined by the outer docking contour) used for statistical analysis to highlight the differences in amino acid composition between both binding sites. The residues sequence number in the ZIKV and DENV envelope proteins was also reported. The residues were grouped according to their side chain type.

Side chain type	ZIKV			DENV	
	AA	AA Count	AA Sequence number	AA Count	AA Sequence number
Aliphatic	ALA	5	35, 165, 178, 319, 361	3	150, 313, 369
	GLY	9	5, 28, 29, 145, 150, 157, 181, 182, 184	9	5, 28, 146, 152, 156, 159, 177, 296, 318
	ILE	8	1, 4, 43, 139, 152, 317, 359, 365	15	4, 6, 23, 46, 139, 141, 162, 308, 312, 320, 322, 335, 352, 357, 367
	LEU	9	25, 45, 141, 180, 186, 298, 300, 376, 378	10	25, 41, 45, 175, 277, 278, 283, 287, 292, 294
	MET	5	34, 140, 151, 374, 375	3	1, 34, 289
	PRO	4	39, 318, 338, 363	4	39, 143, 356, 364
	VAL	13	6, 12, 31, 33, 41, 46, 143, 153, 167, 326, 328, 330, 364	11	12, 21, 24, 31, 140, 151, 309, 321, 324, 354, 365
Polar	CYS	2	3, 30	2	3, 30
	ASN	3	8, 154, 163	3	8, 153, 366
	GLN	2	147, 331	2	43
	SER	8	7, 142, 146, 149, 185, 285, 368, 372	3	7, 29, 145
	THR	15	32, 40, 47, 48, 156, 160, 179, 313, 315, 321, 325, 327, 360, 366, 369	11	32, 33, 40, 48, 138, 142, 155, 176, 315, 319, 353
Aromatic	PHE	3	11, 183, 314	2	11, 43
	TRP	0		1	391
	TYR	2	137, 332	2	137, 178
Negatively Charged	ASP	5	10, 42, 155, 161, 379	4	10, 22, 42, 154
	GLU	9	26, 44, 159, 162, 168, 177, 329, 367, 377	10	26, 44, 49, 136, 147, 148, 161, 311, 314, 368
Positively Charged	HIS	4	27, 144, 148, 158	5	27, 144, 149, 158, 317
	LYS	6	38, 166, 297, 301, 316, 373	9	38, 47, 157, 160, 163, 284, 295, 307, 310
	ARG	5	2, 9, 138, 164, 299	3	2, 9, 323

Table S2. The primary structural analysis carried out to study the occurrence of the amino acids in the top 0.1% ranked peptides. The chemical class aminoacid occurrence was reported and highlighted in different colors. The colorimetric scale was added to the table, to highlight differences in aminoacid occurrence. The aminoacids within the eight peptides selected for the experimental part were evaluated comparing the occurrence to the one of best statistical aminoacid in the corresponding position (best stat. AA).

ZIKV						DENV					
AA	1P	2P	3P	4P		1P	2P	3P	4P		
ALA	5	8	32	8		22	21	12	24		
CYS	4	12	3	7		4	10	13	7		
ASP	1	2	2	2		4	0	0	0		
GLU	0	1	4	0		2	0	1	0		
PHE	6	2	0	2		4	7	0	1		
GLY	0	10	63	11		42	28	58	22		
HIS	10	9	9	25		3	1	1	1		
ILE	4	4	0	8		2	1	2	7		
LYS	1	1	0	18		8	16	18	0		
LEU	27	1	0	4		2	2	7	11		
MET	0	16	1	0		0	5	6	1		
ASN	8	1	3	12		5	2	5	0		
PRO	6	23	12	19		5	33	17	34		
GLN	33	0	0	2		0	0	0	0		
ARG	7	9	0	0		17	10	1	13		
SER	10	29	13	25		10	5	7	10		
THR	10	7	15	7		17	5	3	18		
VAL	9	6	1	6		2	8	8	9		
TRP	12	18	0	0		1	0	0	0		
TYR	7	1	2	4		10	6	1	2		
	160	160	160	160	Av		160	160	160	160	Av
Aliphatic	32%	43%	68%	35%	44%	Aliphatic	47%	61%	69%	68%	61%
Polar	41%	31%	21%	33%	31%	Polar	23%	14%	18%	22%	19%
Aromatic	16%	13%	1%	4%	8%	Aromatic	9%	8%	1%	2%	5%
Negative	1%	2%	4%	1%	2%	Negative	4%	0%	1%	0%	1%
Positive	11%	12%	6%	27%	14%	Positive	18%	17%	13%	9%	14%
QMSK						QMSK					
		Q	M	S	K			Q	M	S	K
		21%	10%	8%	11%			0%	3%	4%	0%

Peptides selected for experimental	LWGH	L	W	G	H		LWGH	L	W	G	H
		17%	11%	39%	16%			1%	0%	36%	1%
	best stat AA	Q	S	G	H		best stat AA	G	P	G	P
		21%	18%	39%	16%			26%	21%	36%	21%

ZIKV						DENV				
AA	1P	2P	3P	4P	5P	1P	2P	3P	4P	5P
ALA	12	8	27	3	8	6	7	35	11	12
CYS	2	3	2	3	11	8	8	4	1	4
ASP	0	0	0	0	1	1	0	1	0	0
GLU	0	0	0	1	1	0	0	0	0	0
PHE	1	9	0	0	0	3	0	0	0	2
GLY	6	1	21	39	19	8	38	13	20	38
HIS	1	4	0	21	3	0	1	0	7	4
ILE	4	2	0	0	3	3	4	2	0	1
LYS	1	2	0	0	0	2	1	3	10	0
LEU	11	1	0	1	5	21	2	1	0	0
MET	0	14	0	0	2	0	0	1	0	0
ASN	6	2	5	2	5	7	1	1	0	8
PRO	2	0	31	1	9	8	16	10	8	9
GLN	13	1	0	0	2	1	1	0	0	0
ARG	3	6	2	3	0	2	0	0	0	0
SER	29	13	7	4	10	8	15	17	43	12
THR	0	7	5	22	8	8	2	7	0	4
VAL	7	4	0	0	13	12	2	5	0	5
TRP	1	18	0	0	0	1	1	0	0	0
TYR	1	5	0	0	0	1	1	0	0	1

	100	100	100	100	100	Av		100	100	100	100	100	Av
Aliphatic	42%	30%	79%	44%	59%	51%	Aliphatic	58%	69%	67%	39%	65%	60%
Polar	50%	26%	19%	31%	36%	32%	Polar	32%	27%	29%	44%	28%	32%
Aromatic	3%	32%	0%	0%	0%	7%	Aromatic	5%	2%	0%	0%	3%	2%
Negative	0%	0%	0%	1%	2%	1%	Negative	1%	0%	1%	0%	0%	0%
Positive	5%	12%	2%	24%	3%	9%	Positive	4%	2%	3%	17%	4%	6%
	SWPGQ	S	W	P	G	Q		SWPGQ	S	W	P	G	Q

Peptides selected for experimental	LRGHA	29%	18%	31%	39%	2%	LRGHA	8%	1%	10%	20%	0%
		L	R	G	H	A		L	R	G	H	A
		11%	6%	21%	21%	8%		21%	0%	13%	7%	12%
	best stat AA	S	W	P	G	G	best stat AA	L	G	A	S	G
		29%	18%	31%	39%	19%		21%	38%	35%	43%	38%

ZIKV								DENV							
AA	1P	2P	3P	4P	5P	6P		1P	2P	3P	4P	5P	6P		
ALA	14	8	7	68	4	7		11	15	20	41	22	21		
CYS	9	9	0	1	3	6		3	2	11	4	7	23		
ASP	1	0	3	4	1	2		0	0	0	0	1	1		
GLU	0	7	0	0	0	0		0	0	0	1	0	0		
PHE	15	1	0	0	0	2		2	5	0	0	0	10		
GLY	14	5	13	8	19	12		21	9	3	8	19	21		
HIS	7	2	0	2	4	7		2	2	0	0	2	0		
ILE	7	4	1	2	3	2		7	2	1	0	1	0		
LYS	12	1	9	0	0	0		2	0	1	0	11	0		
LEU	6	9	2	0	0	0		11	4	0	0	0	0		
MET	3	3	1	0	0	5		13	2	0	0	0	2		
ASN	1	7	38	5	3	10		6	1	2	2	1	4		
PRO	11	17	8	11	6	52		2	7	22	9	2	2		
GLN	0	5	1	0	1	0		4	1	0	2	0	0		
ARG	4	7	11	1	2	0		3	0	0	2	0	0		
SER	10	7	6	3	21	3		21	32	39	34	25	14		
THR	6	12	15	11	44	0		4	2	21	14	21	4		
VAL	0	11	4	1	3	6		8	5	0	2	8	9		
TRP	0	5	0	0	3	0		0	17	0	1	0	0		
TYR	0	0	1	3	3	6		0	14	0	0	0	9		
	120	120	120	120	120	120	Av	120	120	120	120	120	120	Av	
Aliphatic	46%	48%	30%	75%	29%	70%	50%	Aliphatic	61%	37%	38%	50%	43%	46%	46%
Polar	22%	33%	50%	17%	60%	16%	33%	Polar	32%	32%	61%	47%	45%	38%	42%
Aromatic	13%	5%	1%	3%	5%	7%	5%	Aromatic	2%	30%	0%	1%	0%	16%	8%
Negative	1%	6%	3%	3%	1%	2%	3%	Negative	0%	0%	0%	1%	1%	1%	0%
Positive	19%	8%	17%	3%	5%	6%	10%	Positive	6%	2%	1%	2%	11%	0%	3%
	KRNATP	K	R	N	A	T	P		KRNATP	K	R	N	A	T	P

Peptides selected for experimental	KTDAYS	10%	6%	32%	57%	37%	43%		KTDAYS	2%	0%	2%	34%	18%	2%		
		K	T	D	A	Y	S			K	T	D	A	Y	S		
		10%	10%	3%	57%	3%	3%			2%	2%	0%	34%	0%	12%		
best stat AA		F	P	N	A	T	P		best stat AA	G	S	S	A	S	C		
		13%	14%	32%	57%	37%	43%			18%	27%	33%	34%	21%	19%		
ZIKV								DENV									
AA	1P	2P	3P	4P	5P	6P	7P		1P	2P	3P	4P	5P	6P	7P		
ALA	21	8	2	19	93	2	19		19	12	24	12	26	9	7		
CYS	17	6	8	2	1	1	19		10	3	2	15	3	9	8		
ASP	1	0	0	0	1	4	0		0	0	0	0	4	0	3		
GLU	0	4	3	0	0	1	0		0	0	0	0	0	0	0		
PHE	2	27	0	1	0	0	0		1	0	0	0	1	0	12		
GLY	38	9	16	1	6	12	15		56	51	11	6	16	38	19		
HIS	3	18	1	0	1	10	4		3	1	0	0	0	3	5		
ILE	2	5	9	0	1	0	3		1	6	2	14	10	2	0		
LYS	4	0	8	8	1	0	2		3	1	0	1	0	0	1		
LEU	1	5	18	1	1	3	0		1	1	11	6	0	0	0		
MET	2	3	3	2	1	0	0		0	1	1	2	12	3	1		
ASN	1	17	12	50	10	9	7		7	28	18	15	8	2	4		
PRO	20	14	22	6	9	4	56		7	7	35	22	31	18	51		
GLN	0	7	8	0	0	1	0		0	3	0	0	0	2	0		
ARG	3	2	17	1	6	0	0		0	4	0	1	0	6	0		
SER	12	4	3	3	2	20	3		18	11	16	10	8	10	2		
THR	11	2	4	39	4	70	2		13	2	11	26	16	34	1		
VAL	2	4	4	3	3	1	9		1	9	9	10	3	2	2		
TRP	0	0	2	0	0	0	0		0	0	0	0	0	0	0		
TYR	0	5	0	4	0	2	1		0	0	0	0	2	2	24		
		140	140	140	140	140	140	Av		140	140	140	140	140	140	140	Av
Aliphatic	61%	34%	53%	23%	81%	16%	73%	49%	Aliphatic	61%	62%	66%	51%	70%	51%	57%	60%
Polar	29%	26%	25%	67%	12%	72%	22%	36%	Polar	34%	34%	34%	47%	25%	41%	11%	32%
Aromatic	1%	23%	1%	4%	0%	1%	1%	4%	Aromatic	1%	0%	0%	0%	2%	1%	26%	4%
Negative	1%	3%	2%	0%	1%	4%	0%	1%	Negative	0%	0%	0%	0%	3%	0%	2%	1%
Positive	7%	14%	19%	6%	6%	7%	4%	9%	Positive	4%	4%	0%	1%	0%	6%	4%	3%
GSKANNG		G	S	K	A	N	N	G	GSKANNG		G	S	K	A	N	N	G

Peptides selected for experimental	SHRNATA	27%	3%	6%	14%	7%	6%	11%	SHRNATA	40%	8%	0%	9%	6%	1%	14%
		S	H	R	N	A	T	A		S	H	R	N	A	T	A
		9%	13%	12%	36%	66%	50%	14%		13%	1%	0%	11%	19%	24%	5%
	best stat AA	G	F	P	N	A	T	P	best stat AA	G	G	P	T	P	G	P
		27%	19%	16%	36%	66%	50%	40%		40%	36%	25%	19%	22%	27%	36%