EXTENDED DATA TABLES

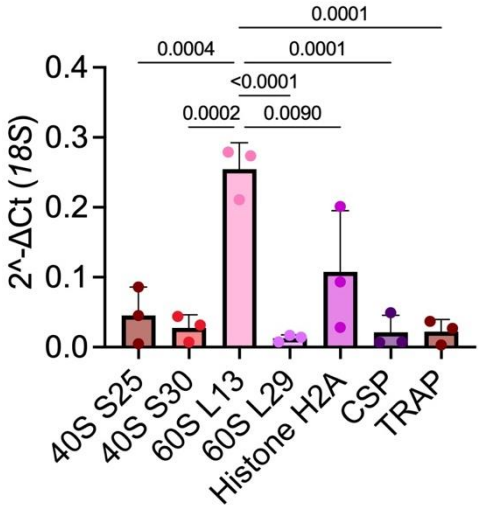
Extended data table 1 | *Plasmodium falciparum* homology

Protein name	Number of patients	*P. falciparum* homology (%)
60S L4/L1	7	83
ETRAMP A5KBH5	7	63
40S S2	6	97
Don Juan	6	53
ETRAMP A5K676	6	43
40S S11	5	99
Histone H2A A5K214	5	98
EF 1-alpha	5	98
40S S23	5	98
60S L32	5	94
60S L29	5	91
40S S8	5	89
40S S6	5	89
40S S30	5	89
40S S25	5	86
60S L13	5	80
Histone H2A A5K7L8	4	97
60S L37	4	97
60S L30	4	92
Alba domain	4	91
Ubiq/Rib	4	91
60S L36	4	90
60S L35	4	81
60S L23a	4	64
Unch. A5K8G9	4	33
Histone H3	3	100
60S L37a	3	100
50S S28e	3	97
60S L44	3	97
60S L10	3	96
60S L8	3	95
60S L9	3	94
60S L33-B	3	92
60S L18a	3	92
60S L13a	3	91
60S L34-A	3	91
60S L31	3	90
60S L17	3	89
60S L7a	3	84
PPR_long domain	3	59
Unch. A5K9Y3	3	43
PI3K/PI4K	3	36
Unch. A5K4L2	3	32
Unch. A5K8G8	3	0
Unch. A5KC18	3	23

Extended data table 2 | Primers used for *Plasmodium falciparum* liver stage expression

Primer	Sequence
NF135 40S S25-1F	5'-TCTCCCAGAGCTGTTTACCC-3'
NF135 40S S25-1R	5'-TCATCTTCCAAGTTGTCACACA-3'
NF135 40S S30-1F	5'-ATGGGAAAGGTACATGGATCATTAG-3'
NF135 40S S30-1R	5'-ACTTTGGGACTTTAGGAGTCTGG-3'
NF135 60S L13-1F	5'-AAGAGTTAAAGGGAGCCGGA-3'
NF135 60S L13-1R	5'-ACCTCCAATACCTTTCTTTGCT-3'
NF135 60S L29-1F	5'-ACCGTAAAGCCCATAAGAATGGA-3'
NF135 60S L29-1R	5'-GGATCCAACCCTTTACGCGA-3'
NF135 H2A-1F	5'-TAGGTTCCACAGCAGCAGTT-3'
NF135 H2A-1R	5'-AACACCACCACCAGCAATTG-3'
NF135 CSP-1F	5'-GCCAAATGACCCAAACCGAA-3'
NF135 CSP-1R	5'-GGTTTATTAGCAGAGCCAGGC-3'
NF135 TRAP-1F	5'-AGAGAAACACGTCCACATGG-3'
NF135 TRAP-1R	5'-TCCAGCTATTCCACCTGCAA-3'
18S rRNA (3D7) -1R	5'-GGGTTCTGGGGCGAGTATT-3'
18S rRNA (3D7) -1R	5'-GCCATGCATCACCATCCAAG-3'

EXTENDED DATA FIGURE



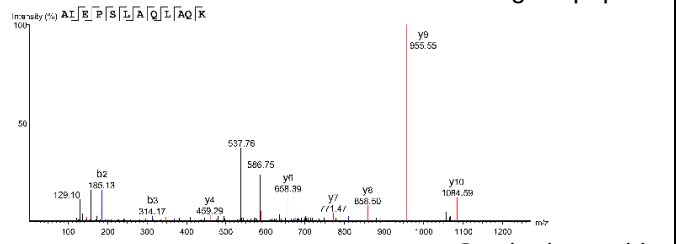
Extended data figure 1 | Antigen gene expression in humanized mouse livers infected with *Plasmodium falciparum* (*Pf*). The expression of genes related to antigens found in *P. vivax* immunopeptidomics was analysed in the liver stage of *Pf* infection. Pf 18S rRNA was used as endogenous gene. CSP and TRAP genes were used as positive control. Statistical analyse was performed by one-way ANOVA, with Turkey's multiple comparison test. Actual P values are shown.

Extended data figure 2 | Spectral match validation

Peptide			Biological peptide				Synthetic peptide				Validation
Sequence	ID	n	[m/z]	z	RT	Peaks Score	[m/z]	z	RT	Peaks Score	(y/n)
AIEPSLAQLAQK	Ubqt/ribos- 1	12	635.3643	2	41.42	37.49	634.8646	2	41.64	48.35	Y
AKAVKKQKKTLKPV	60S L31	14	523.0190	3	21.67	45.30	NA	NA	NA	NA	NA
ANKALLPTAGDD	60S L4/L1- 1	12	593.3108	2	34.53	50.03	593.3093	2	34.31	52.84	Y
APISAGIKKPHR	Hist. H3	12	425.5951	3	25.01	40.59	425.5946	3	23.20	23.34	Y
AQKIKKKKKLTPA	Don Juan	13	494.6678	3	24.09	36.08	494.6680	3	20.52	41.55	Y
ASGGVLPNIHNV	Hist. H2A- 2	12	589.3206	2	39.78	25.89	589.3203	2	39.89	37.05	Y
AVKKVGKIVK	60S L32-2	10	357.2537	3	22.97	22.03	357.2534	3	20.62	27.81	Y
DNNEHVVQEKTV	Unch A5JZN7.2	12	706.3463	2	27.81	53.74	706.3451	2	26.94	49.45	Y
DNNEHVVQEKTVSF	Unch A5JZN7.1	14	549.2657	3	35.20	61.62	549.2657	3	34.69	47.01	Y
EDYSPRKV	Unch A5K8G9	8	497.2546	2	26.23	39.03	497.2538	2	24.87	29.67	Y
GAFGKPNGV	60S L10	9	423.7279	2	30.37	19.14	423.7272	2	29.41	29.60	Y
GKGKNKEKL	40S S25- 1	9	501.3087	2	20.20	33.76	501.3089	2	19.19	25.14	Y
GKGKNKEKLNHAVF	40S S25- 2	14	523.9681	3	25.17	48.81	523.9667	3	24.09	25.39	Y
GLNQKQPTKGSNIQ	ETRAMP- 2	14	757.4133	2	24.53	37.29	756.9106	2	23.51	45.90	Y
GPKRATKIRK	40S S6- 3	10	385.5873	3	20.09	38.30	385.5876	3	18.95	33.14	Y
GRIGRYLKKGKYA	Hist. H2A- 4	13	378.2308	4	32.42	33.32	378.2307	4	26.84	33.94	Y
GRIGRYLKKGKYAK	Hist. H2A- 1	14	410.2536	4	30.86	33.56	410.2541	4	25.27	17.95	Y
GSKQVHVV	40S S8- 2	8	427.2482	2	24.78	41.76	427.2479	2	23.31	37.69	Y
GTGRKKGPNSKL	40S S30- 2	12	414.9137	3	20.78	46.04	414.9140	3	19.77	36.32	Y
GTPIEKLHPI	60S L13- 2	10	552.8251	2	34.59	27.43	552.8255	2	34.19	35.45	Y
GVKKDVAK	40S S6- 2	8	422.7661	2	19.95	34.31	422.7660	2	18.91	26.58	Y
KKVAAGYKKLTD	ETRAMP- 1	12	441.2663	3	24.33	41.58	441.2662	3	22.62	39.46	Y
KKYKNKKFKPY	60S L35	11	491.2969	3	27.30	25.41	491.6320	3	23.68	19.14	Y
KNIKSKNGIGGIPAD	60S L13- 3	15	504.6231	3	27.71	31.77	504.6229	3	26.84	16.62	Y
KSAGADSKSLKKLD	ETRAMP- 5	14	483.6093	3	23.95	34.26	483.2758	3	22.52	44.23	Y
KVPVPPTQAKKPKKN	Hist. H2A- 5	15	415.7615	4	23.19	35.10	415.7620	4	21.87	40.76	Y
LETYQNMKIQKQTP	40S S2	14	861.4510	2	32.68	40.56	861.9502	2	31.64	48.98	Y
LGGLNQKQPT	ETRAMP- 4	10	528.2960	2	28.65	37.38	528.2964	2	27.59	39.32	Y
LILRAAIKTK	Unch A5K8J8	10	1126.7635	1	54.45	17.89	376.2605	3	29.11	20.42	N
LNQKQPTKGSNIQ	ETRAMP- 3	13	728.4005	2	23.52	25.98	728.4000	2	22.49	41.12	Y
MYKKVYVID	60S 13a	9	579.8156	2	32.90	39.80	579.8154	2	31.92	31.61	Y
NKALLPTAGDD	60S L4/L1- 2	11	557.7906	2	34.65	43.43	557.7903	2	35.38	50.46	Y
NQLRPKKKLK	Ubqt/ribos- 2	10	418.2789	3	21.63	26.12	418.2785	3	19.94	19.81	Y
PKFFKNQRY	60S L29	9	409.8929	3	28.72	38.08	409.8927	3	27.66	31.37	Y
RLTGGKKKIHKKK	40S S8- 1	13	381.5072	4	20.20	43.53	NA	NA	NA	NA	NA
SDGTGRKKGPNSKL	40S S30- 1	14	482.2673	3	21.44	48.01	482.2670	3	20.18	37.03	Y
SFFNSKKIKKGSKS	40S S11	14	529.3069	3	25.90	41.15	397.2319	4	23.01	37.69	Y
SGGVLPNIHNV	Hist. H2A- 3	11	553.8022	2	39.63	29.28	533.8016	2	39.69	34.16	Y
SKNGKNRFIKPKIQ	40S S6- 1	14	415.2520	4	26.02	36.88	415.2518	4	24.19	30.73	Y
SSHAKGIVVEKV	40S S23	12	418.5784	3	27.41	44.55	418.5784	3	25.94	43.89	Y
TGRKKGPNSKL	40S S30- 3	11	395.9069	3	20.74	37.56	297.1819	4	19.67	25.63	N
TPIITNKPFG	ETRAMP- 6	10	544.3114	2	38.69	36.66	544.3113	2	38.87	46.35	Y
VITDVGDSDIIKTNE	60S L30	15	809.9135	2	41.55	55.90	809.9135	2	41.11	55.13	Y
VSEVTTVEKDE	60S L9	11	618.3045	2	30.31	35.50	618.3038	2	29.67	41.63	Y
YESIEVSKID	60S L13- 1	10	591.7995	2	38.03	40.35	591.7988	2	37.62	41.05	Y
YGRIFKKKITKK	60S L4/L1- 3	12	378.4963	4	28.58	35.21	378.2462	4	23.62	15.05	N

n amino acid length
[m/z] Mass over Charge
z charge state
RT Retention Time
NA Not Available

Biological peptide



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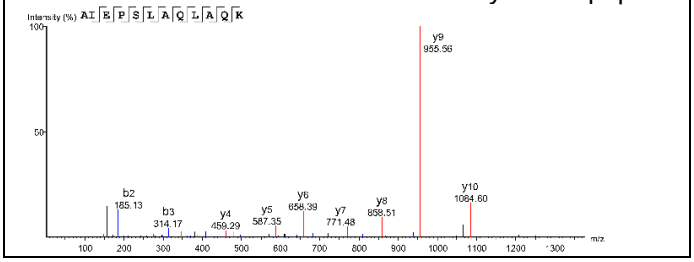

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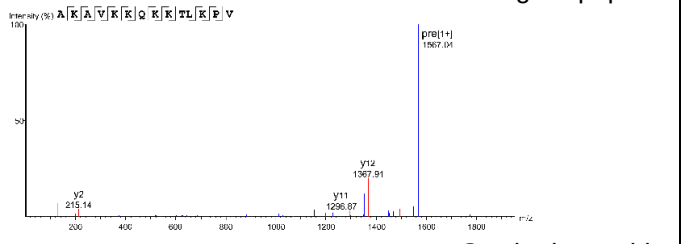
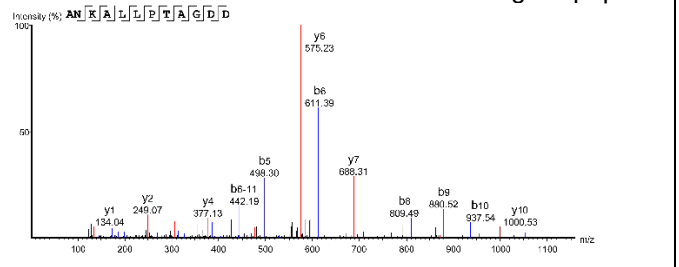


Synthetic peptide

NA

Biological peptide



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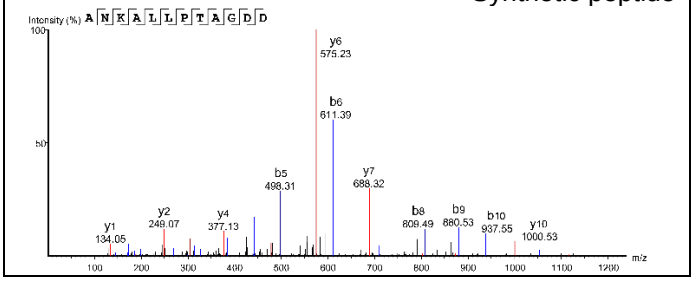
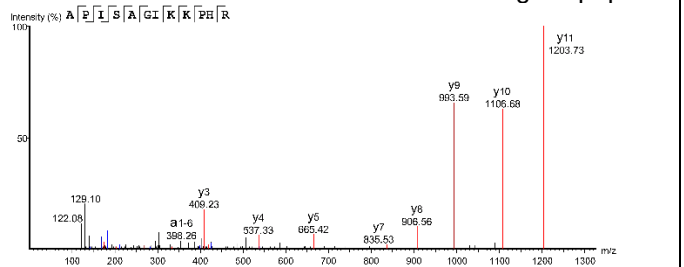


Biological peptide



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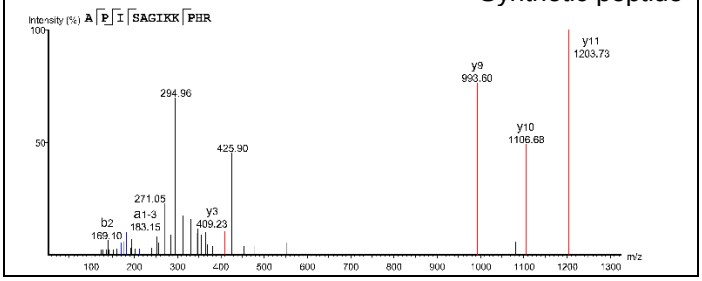
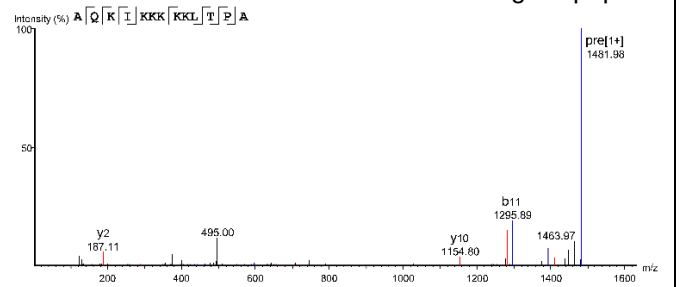


Biological peptide



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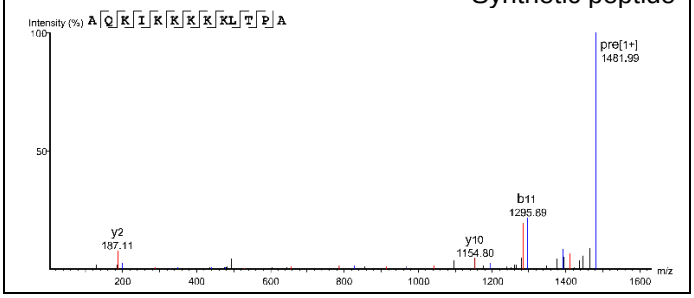

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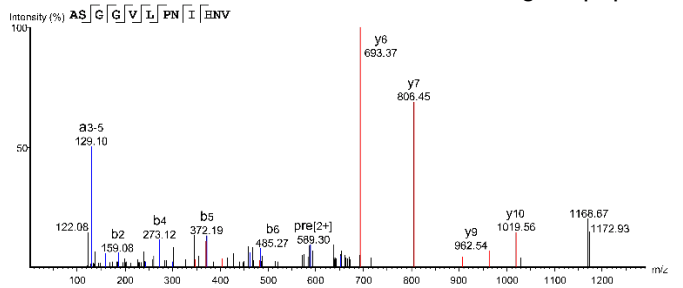

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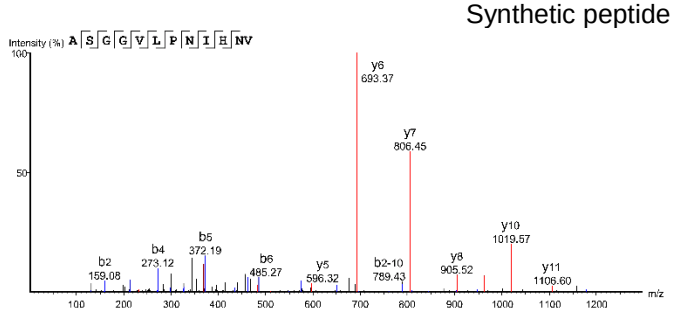

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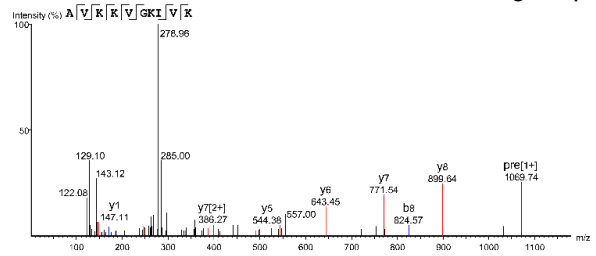

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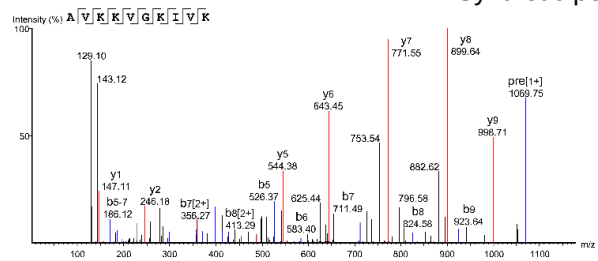
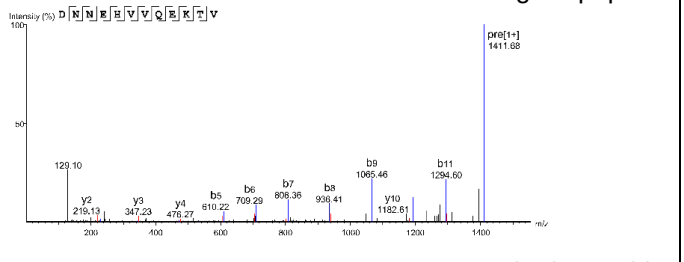


Biological peptide



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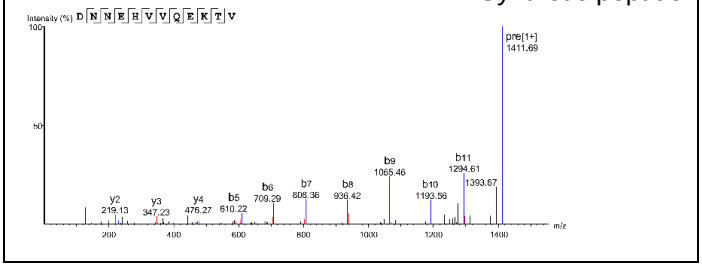
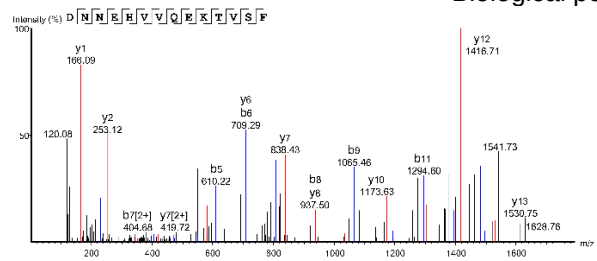


Biological peptide



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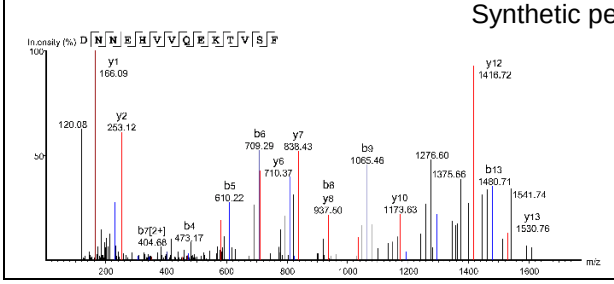

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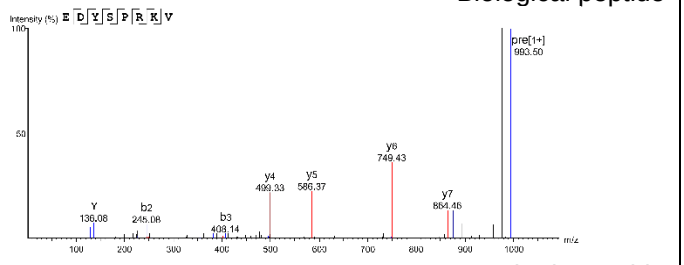

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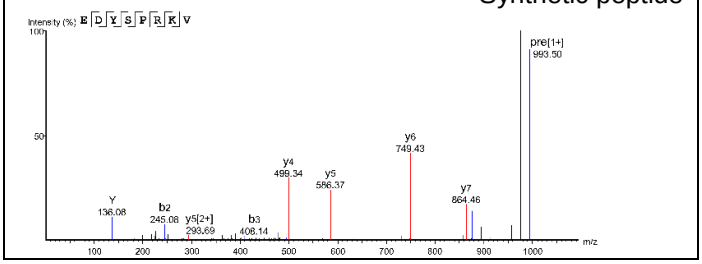

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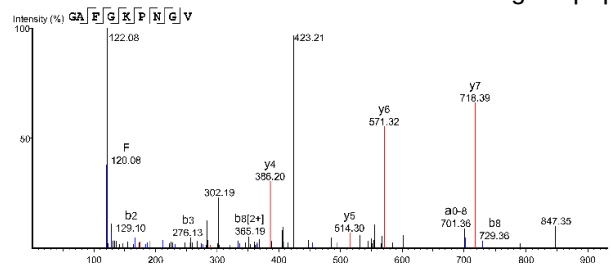

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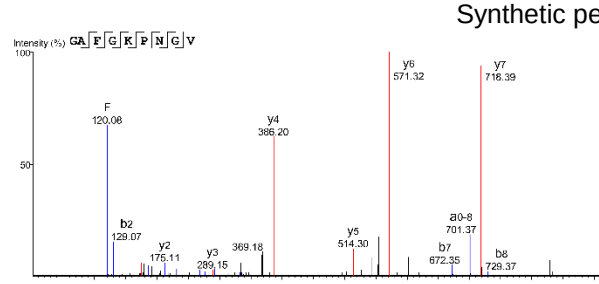
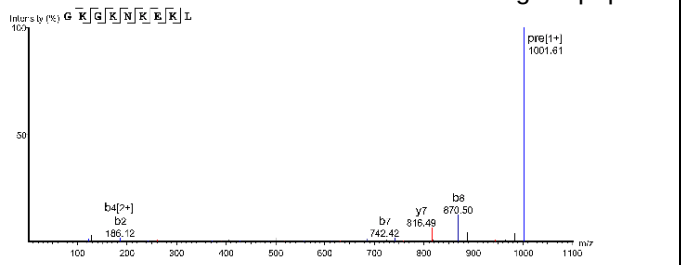


Biological peptide



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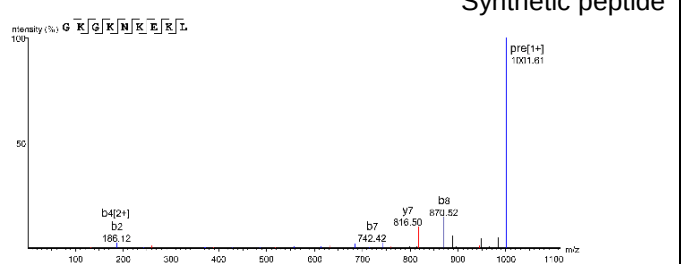

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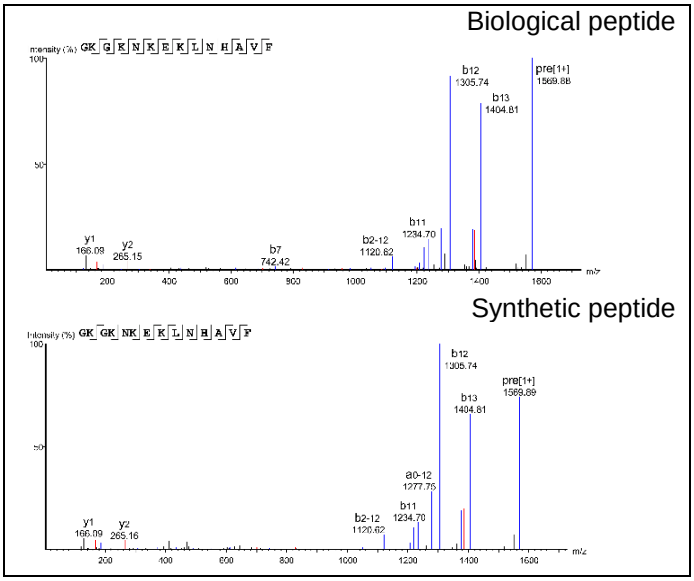
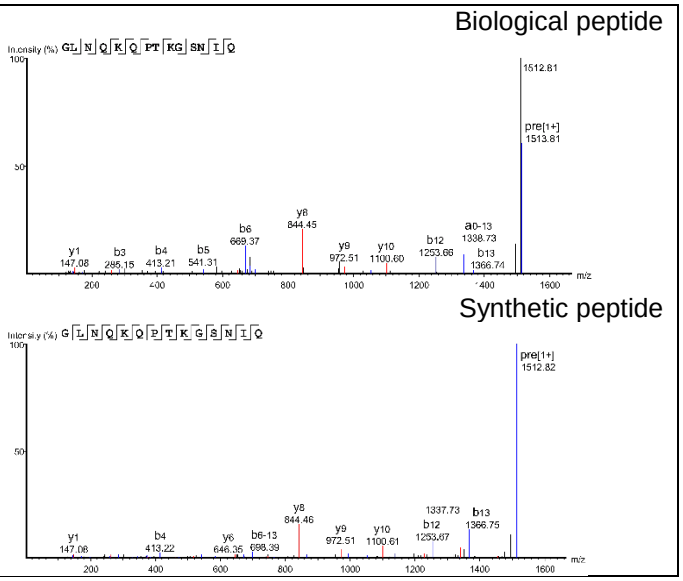


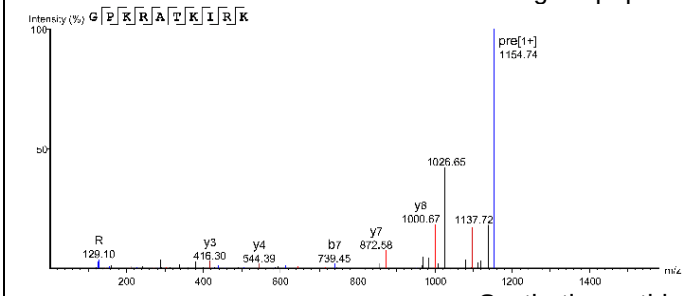
Synthetic peptide

Biological peptide

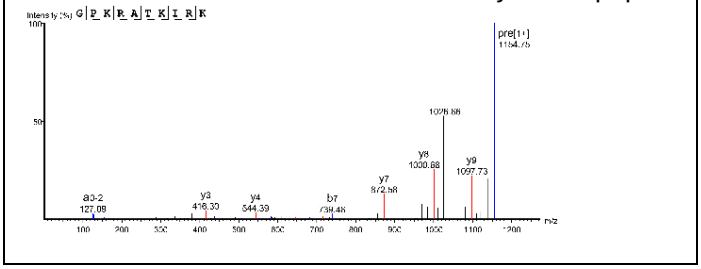


Synthetic peptide

Biological peptide



Synthetic peptide



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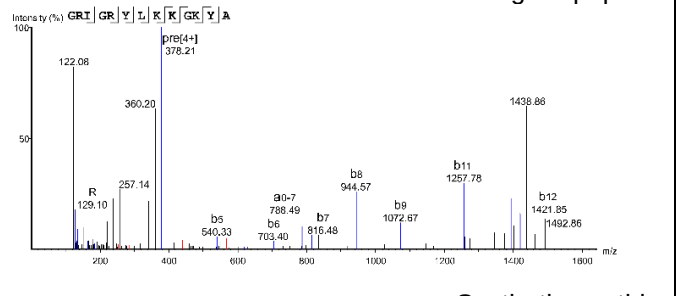

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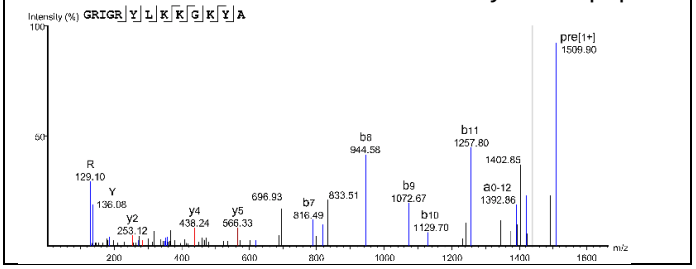
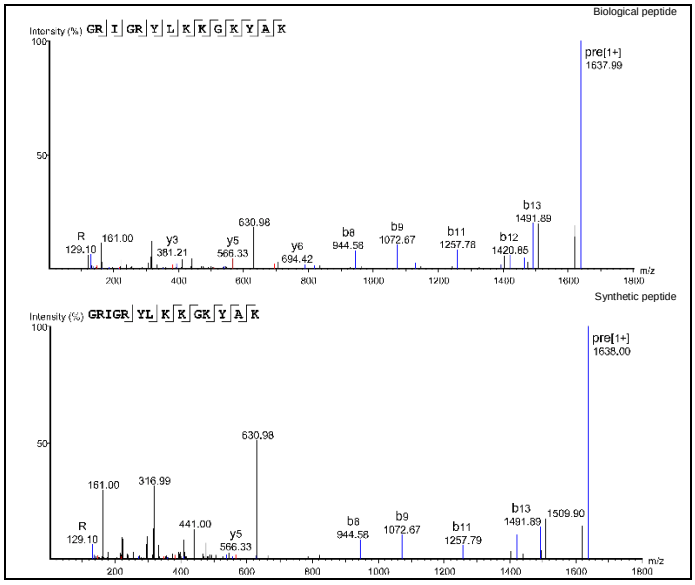
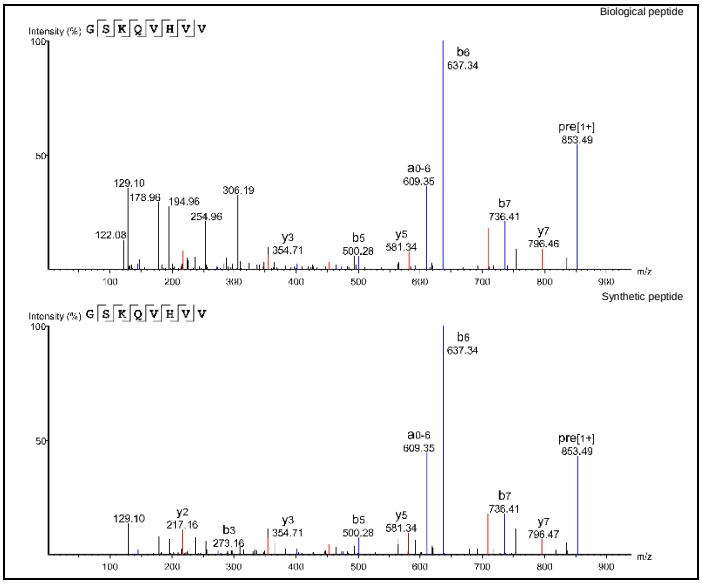
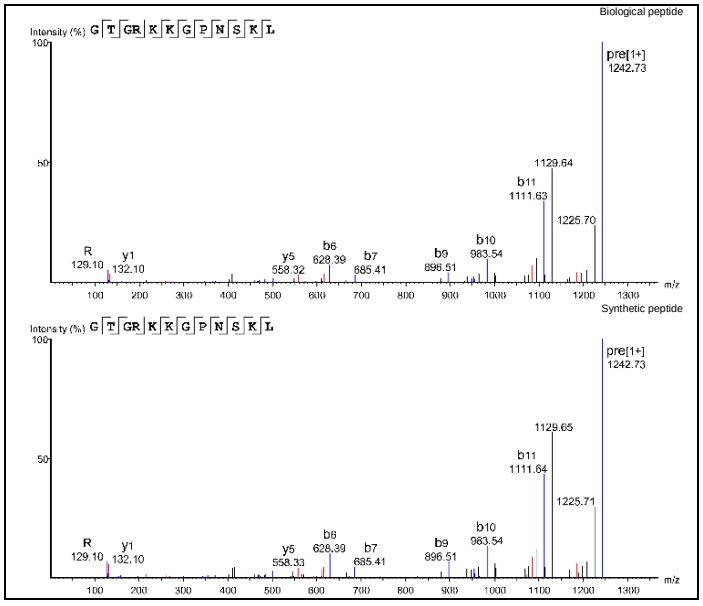
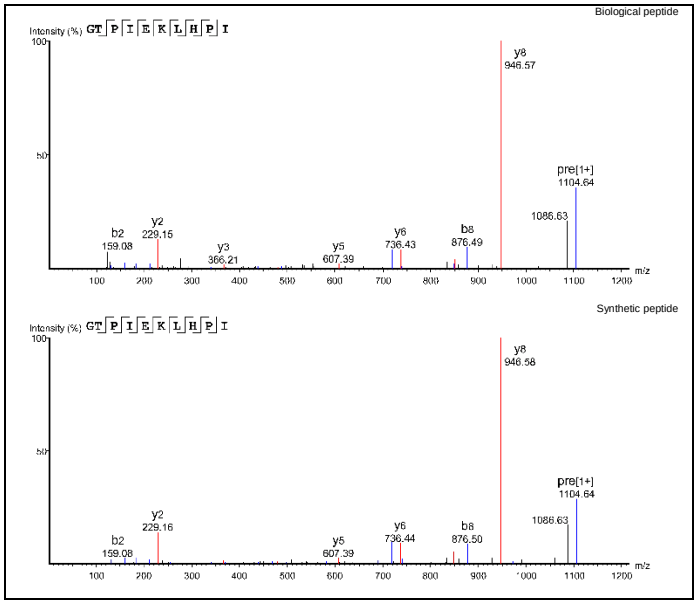
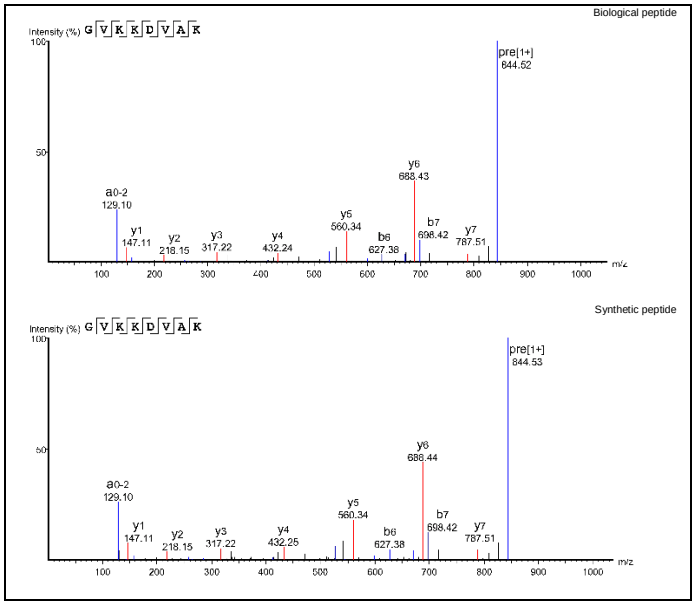


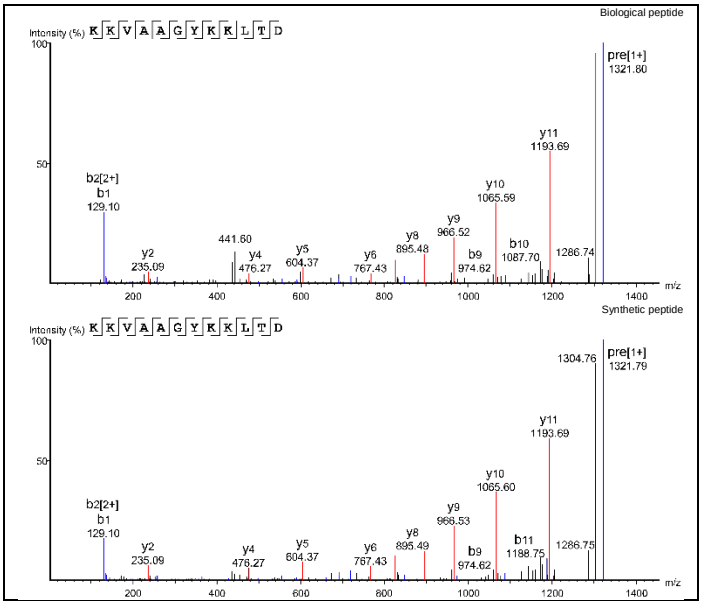

Biological peptide
Intensity (%) GR I GR Y L K K G K Y A K
pre[1+]
1637.99
630.98
b13
1491.89
y3
381.21
y5
566.33
y6
694.42
b8
944.58
b9
1072.67
b11
1257.78
b12
1420.85
R
129.10
161.00
Synthetic peptide
Intensity (%) GRIGR YL K K GK Y A K
pre[1+]
1638.00
630.98
161.00
316.99
441.00
y5
566.33
b8
944.58
b9
1072.67
b11
1257.79
b13
1491.89
1509.90
R
129.10
m/z

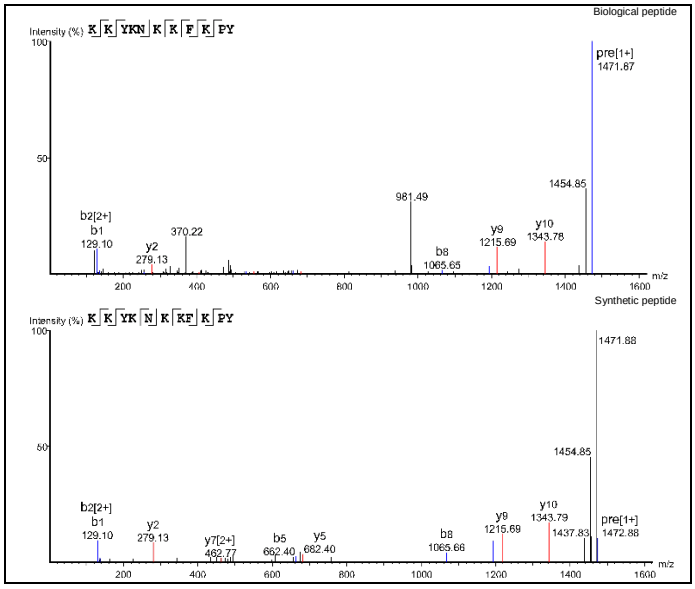

Biological peptide
Intensity (%) G S K Q V H V V
b6
637.34
pre[1+]
853.49
a0-6
609.35
b7
736.41
y7
796.46
129.10
178.96
194.96
254.96
306.19
122.08
y3
354.71
b5
500.28
y5
581.34
Synthetic peptide
Intensity (%) G S K Q V H V V
b6
637.34
a0-6
609.35
pre[1+]
853.49
b7
736.41
y7
796.47
129.10
y2
217.16
b3
273.16
y3
354.71
b5
500.28
y5
581.34
m/z

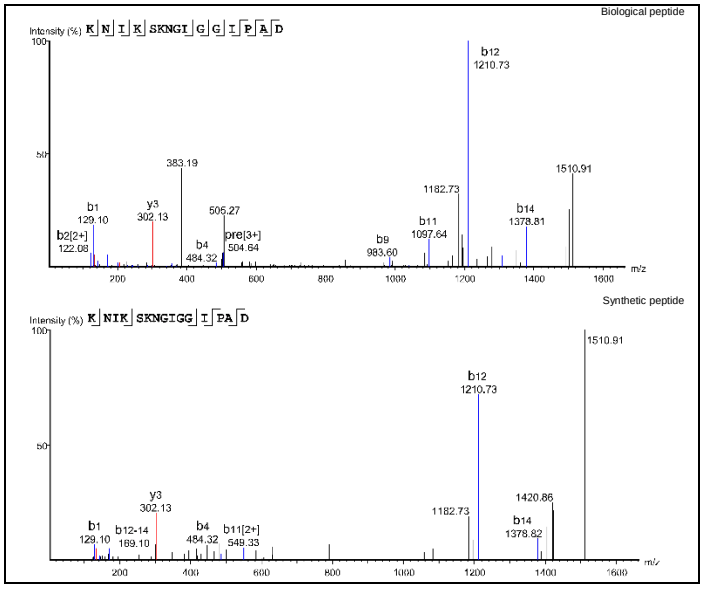

Biological peptide
Intensity (%) G T GR K K G P N S K L
pre[1+]
1242.73
1129.64
b11
1111.63
1225.70
b10
983.54
b6
628.39
b7
685.41
b9
896.51
y5
558.32
R
129.10
y1
132.10
Synthetic peptide
Intensity (%) G T GR K K G P N S K L
pre[1+]
1242.73
1129.65
b11
1111.64
1225.71
b10
983.54
b6
628.39
b7
685.41
b9
896.51
y5
558.33
R
129.10
y1
132.10
m/z

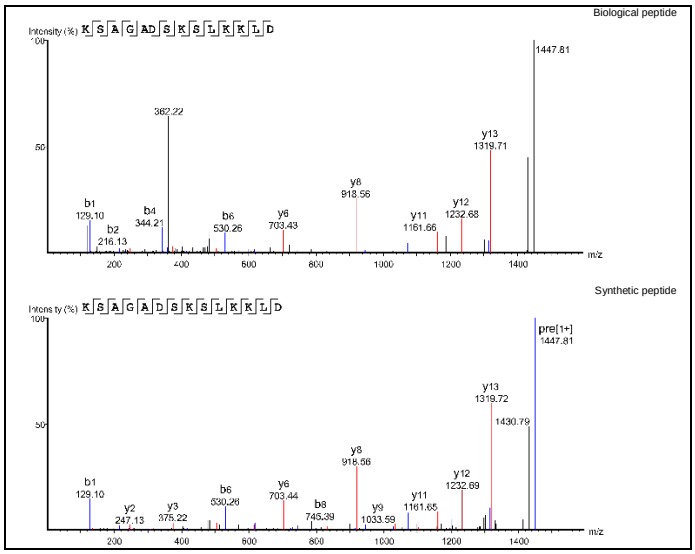

Biological peptide
Intensity (%) GT P I E K L H P I
y8
946.57
pre[1+]
1104.64
1086.63
y2
229.15
b2
159.08
y3
366.21
y5
607.39
y6
736.43
b8
876.49
Synthetic peptide
Intensity (%) GT P I E K L H P I
y8
946.58
pre[1+]
1104.64
1086.63
y2
229.16
b2
159.08
y5
607.39
y6
736.44
b8
876.50
m/z

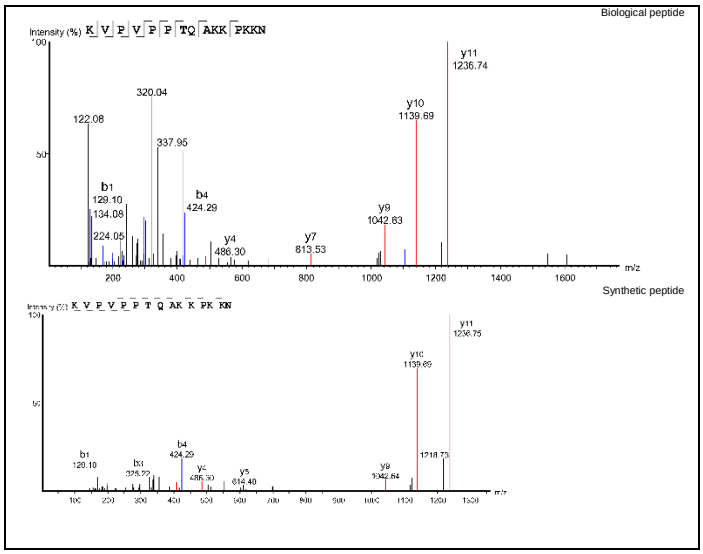

Biological peptide
Intensity (%) G V K K D V A K
pre[1+]
844.52
y6
688.43
a0-2
129.10
y5
560.34
b7
698.42
y7
787.51
b6
627.38
y1
147.11
y2
218.15
y3
317.22
y4
432.24
Synthetic peptide
Intensity (%) G V K K D V A K
pre[1+]
844.53
y6
688.44
a0-2
129.10
y5
560.34
b7
698.42
y7
787.51
b6
627.38
y1
147.11
y2
218.15
y3
317.22
y4
432.25
m/z

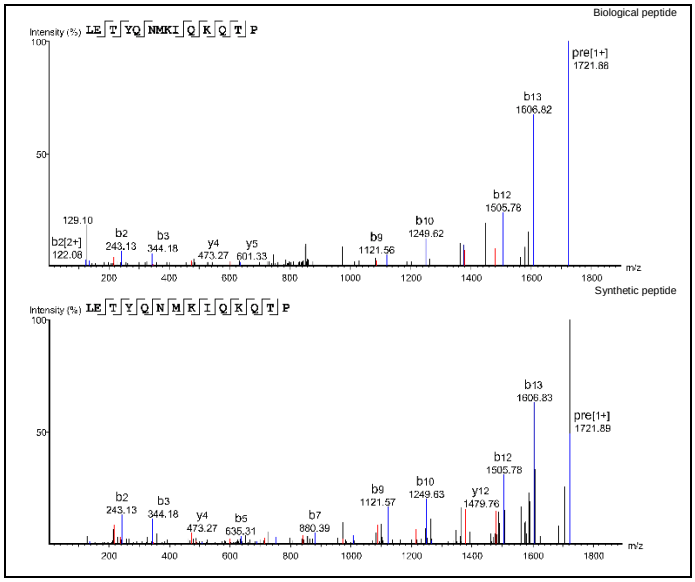

Biological peptide
Intensity (%) K K V A A G Y K K L T D
pre[1+]
1321.80
y11
1193.69
b2[2+]
b1
129.10
y10
1065.59
y9
966.52
y8
895.48
b10
1087.70
1286.74
441.60
y2
235.09
y4
476.27
y5
604.37
y6
767.43
b9
974.62
Synthetic peptide
Intensity (%) K K V A A G Y K K L T D
pre[1+]
1321.79
1304.76
y11
1193.69
y10
1065.60
b2[2+]
b1
129.10
y9
966.53
y8
895.49
b11
1188.75
1286.75
y2
235.09
y4
476.27
y5
604.37
y6
767.43
b9
974.62
m/z

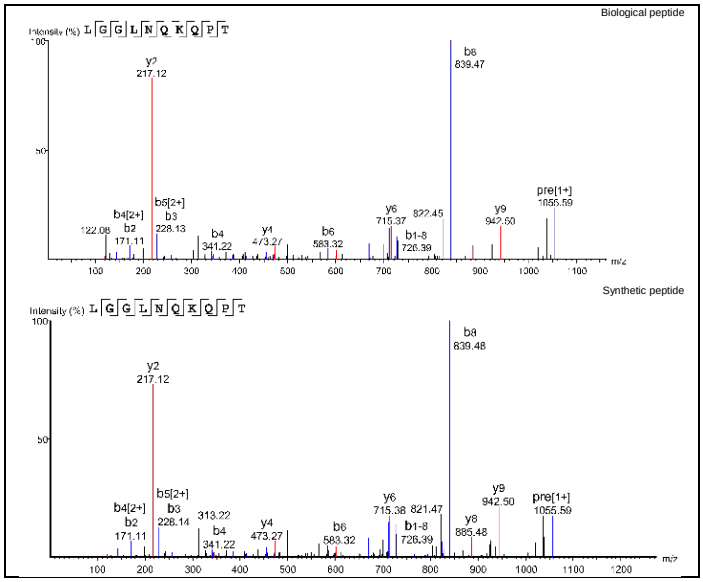

Biological peptide
Intensity (%) K K YKN K K F K PY
pre[1+]
1471.87
1454.85
981.49
b2[2+]
b1
129.10
370.22
y2
279.13
y9
1215.69
y10
1343.78
b8
1065.65
m/z
Synthetic peptide
Intensity (%) K K YK N K KF K PY
1471.88
1454.85
b2[2+]
b1
129.10
y2
279.13
y7[2+]
462.77
b5
662.40
y5
682.40
b8
1065.66
y9
1215.69
y10
1343.79
1437.83
pre[1+]
1472.88
m/z


Biological peptide
Intensity (%) K N I K SKNGI G G I P A D
b12
1210.73
383.19
1510.91
1182.73
b1
129.10
y3
302.13
506.27
b14
1378.81
b11
1097.64
b2[2+]
122.08
pre[3+]
504.64
b4
484.32
b9
983.60
m/z
Synthetic peptide
Intensity (%) K NIK SKNGIGG I PA D
1510.91
b12
1210.73
y3
302.13
1420.86
1182.73
b1
129.10
b12-14
189.10
b4
484.32
b11[2+]
549.33
b14
1378.82
m/z

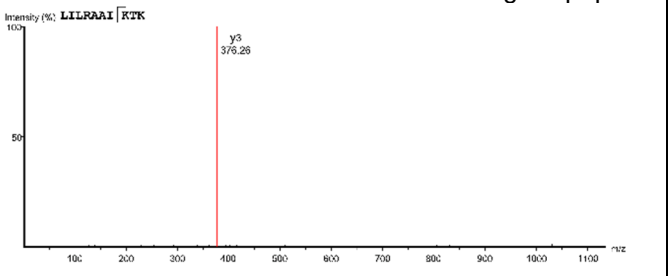

Biological peptide
Intensity (%) K S A G AD S K S L K K L D
1447.81
382.22
y13
1319.71
y8
918.56
b1
129.10
b4
344.21
b6
530.26
y6
703.43
y11
1161.66
y12
1232.68
b2
216.13
m/z
Synthetic peptide
Intens ty (%) K S A G A D S K S L K K L D
pre[1+]
1447.81
y13
1319.72
1430.79
y8
918.56
b1
129.10
b6
530.26
y6
703.44
y12
1232.69
y2
247.13
y3
375.22
b8
745.39
y9
1033.59
y11
1161.65
m/z


Biological peptide
Intensity (%) K V P V P P TQ AKK PKKN
y11
1236.74
320.04
y10
1139.69
122.08
337.95
b1
129.10
b4
424.29
134.08
y9
1042.63
224.05
y4
486.30
y7
813.53
m/z
Synthetic peptide
y11
1236.75
y10
1139.69
b4
424.29
b1
129.10
y5
814.40
1218.73
y9
1042.64
m/z

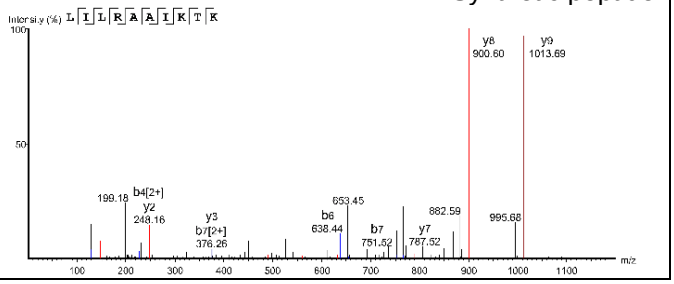

Biological peptide
Intensity (%) LE T YQ NMKI Q K Q T P
pre[1+]
1721.88
b13
1606.82
b12
1505.78
129.10
b10
1249.62
b2[2+]
122.08
b2
243.13
b3
344.18
y4
473.27
y5
601.33
b9
1121.56
m/z
Synthetic peptide
Intensity (%) LE T Y Q N M K I Q K Q T P
b13
1606.83
pre[1+]
1721.89
b12
1505.78
b9
1121.57
b10
1249.63
y12
1479.76
b2
243.13
b3
344.18
y4
473.27
b5
635.31
b7
880.39
m/z


Biological peptide
Intensity (%) L G G L N Q K Q P T
y2
217.12
b8
839.47
b5[2+]
b4[2+]
171.11
b3
228.13
122.08
b2
y4
473.27
y6
715.37
822.45
b6
583.32
b1-8
726.39
y9
942.50
pre[1+]
1055.59
m/z
Synthetic peptide
Intensity (%) L G G L N Q K Q P T
b8
839.48
y2
217.12
b5[2+]
b4[2+]
171.11
b3
228.14
313.22
b2
y4
473.27
341.22
b4
y6
715.38
821.47
b6
583.32
b1-8
726.39
y8
885.48
y9
942.50
pre[1+]
1055.59
m/z

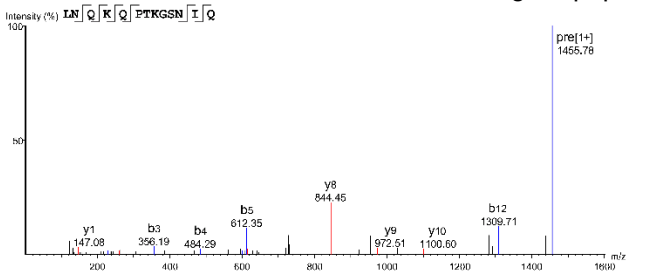
Biological peptide



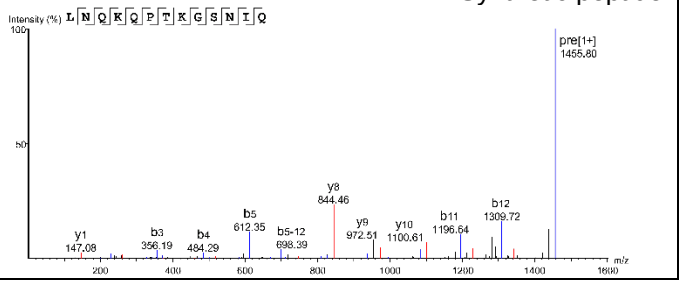
Synthetic peptide



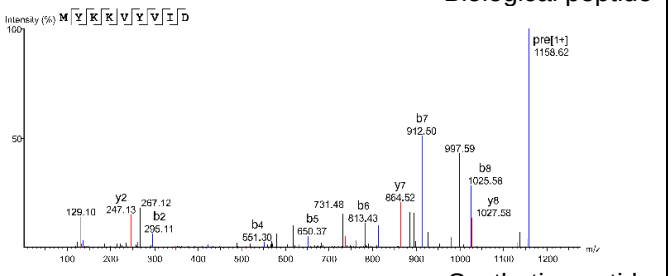
Biological peptide



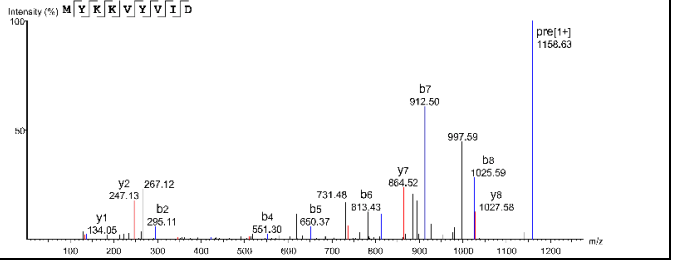
Synthetic peptide



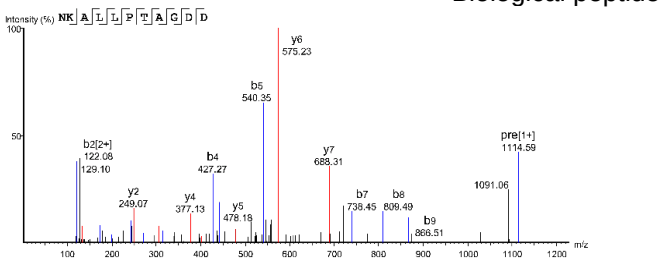
Biological peptide



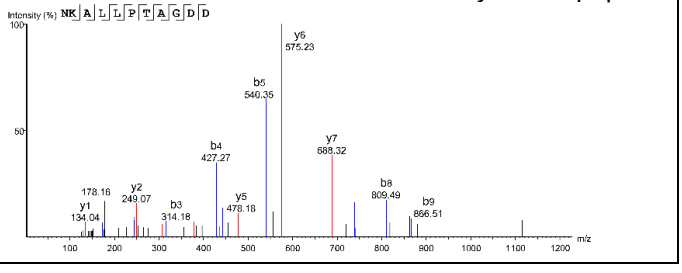
Synthetic peptide



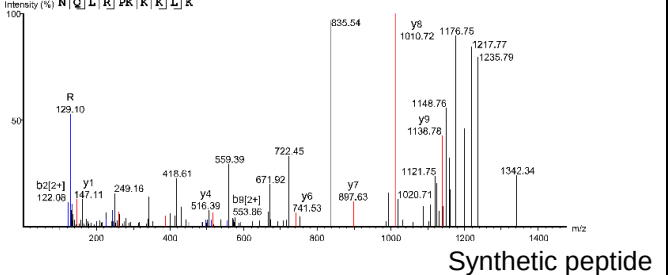
Biological peptide



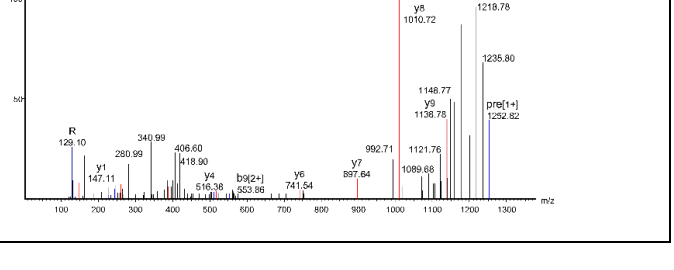
Synthetic peptide



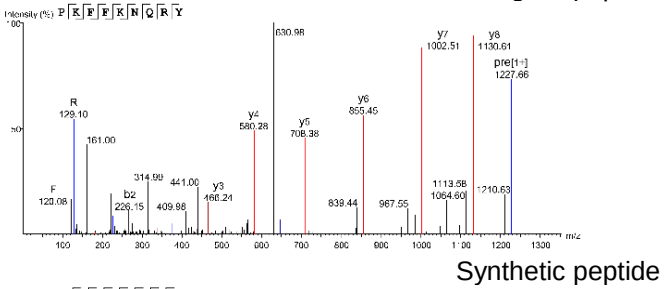
Biological peptide



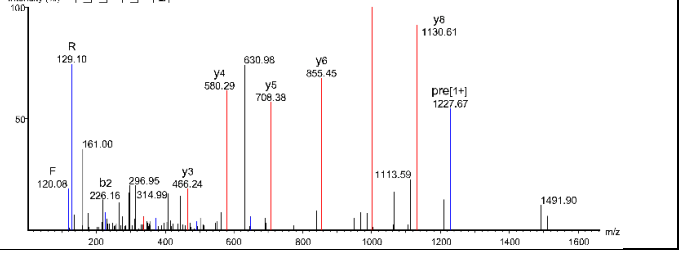
Synthetic peptide



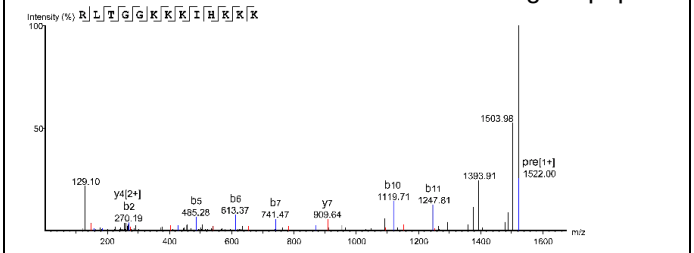
Biological peptide



Synthetic peptide



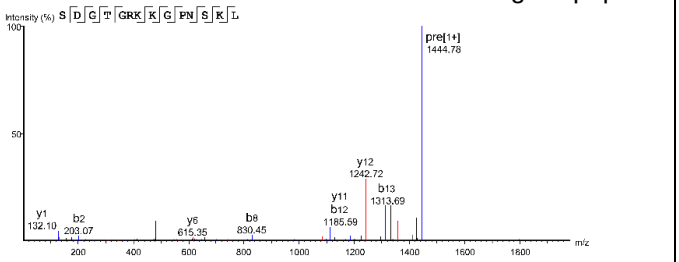
Biological peptide



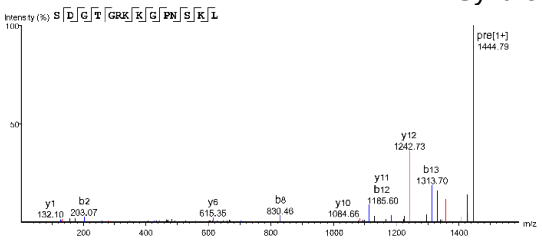
Synthetic peptide

NA

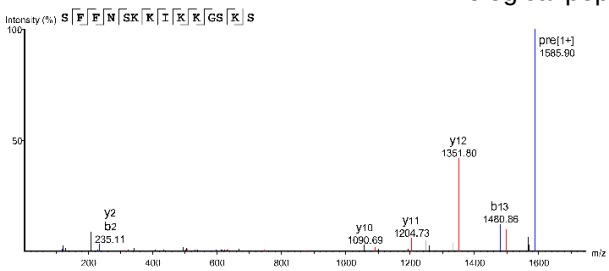
Biological peptide



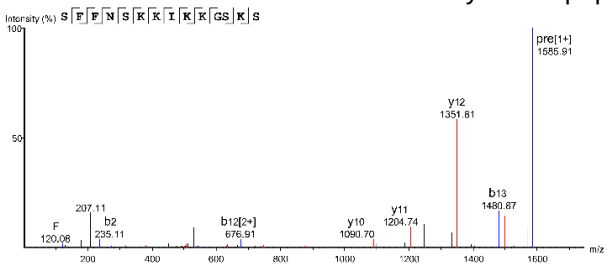
Synthetic peptide



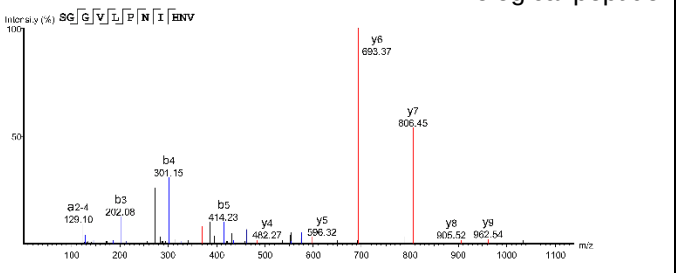
Biological peptide



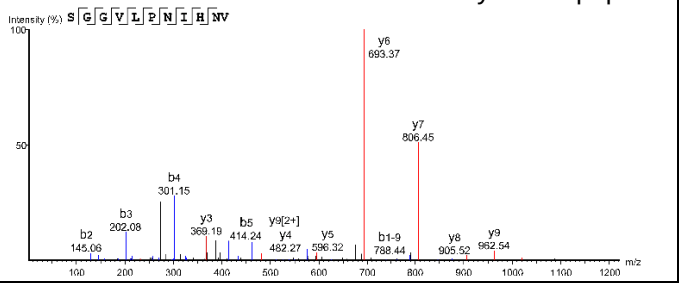
Synthetic peptide



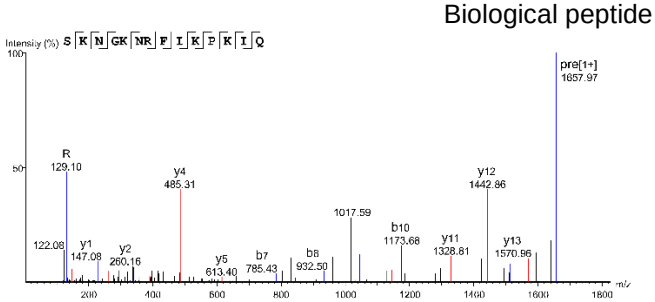
Biological peptide



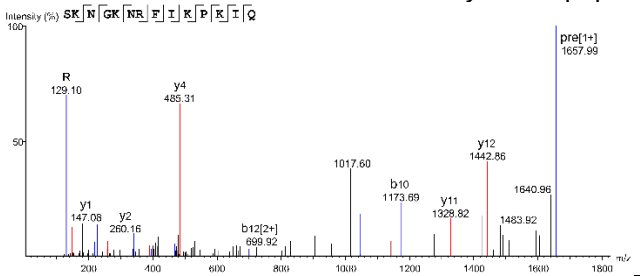
Synthetic peptide



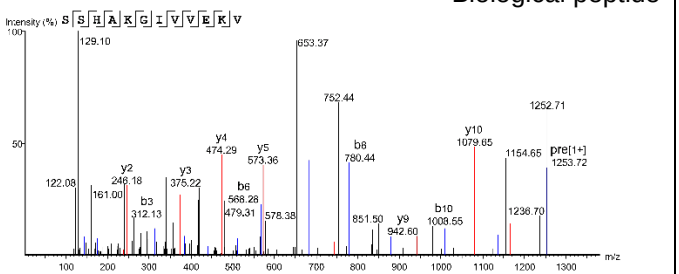
Biological peptide



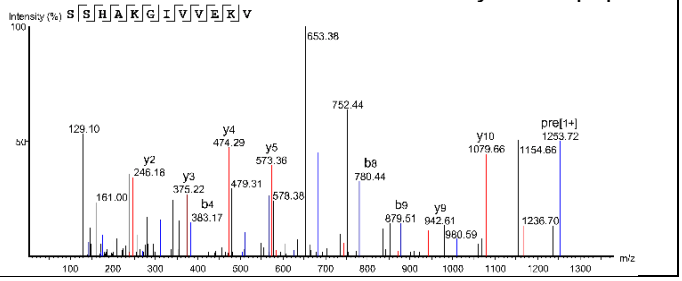
Synthetic peptide

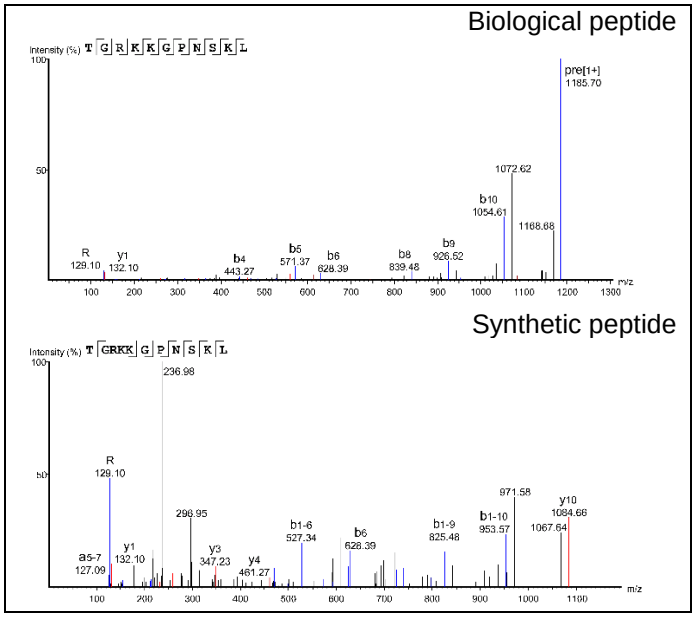


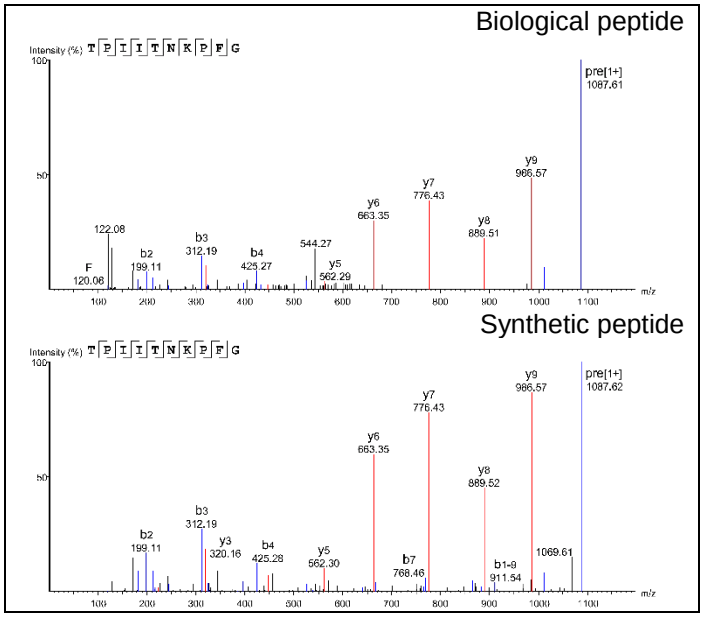
Biological peptide

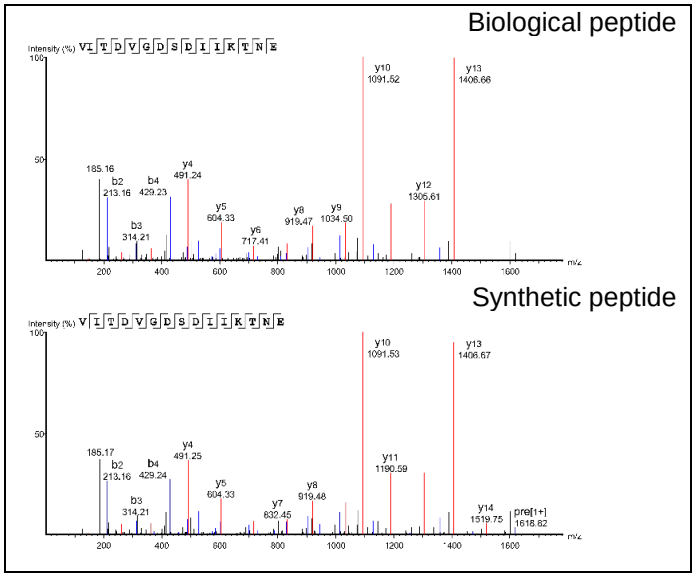


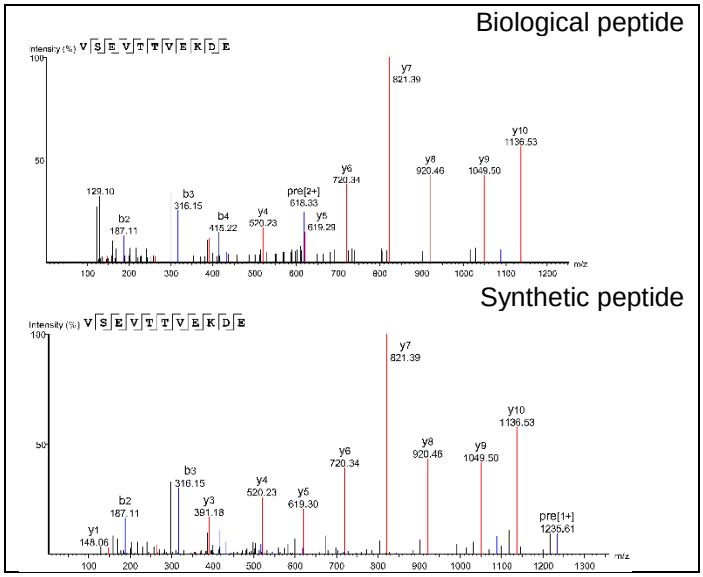
Synthetic peptide

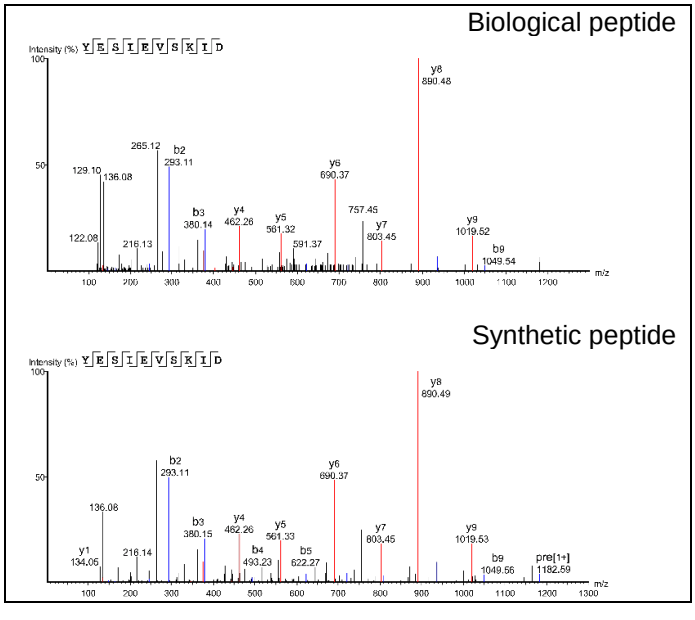


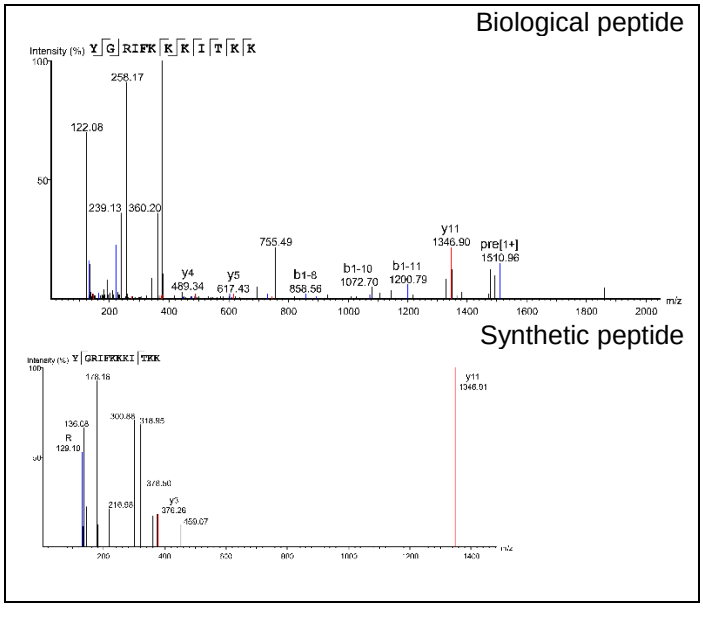

Biological peptide
Intensity (%) T G R K K G P N S K L
pre[1+]
1185.70
1072.62
b10
1054.61
1168.68
R
129.10
y1
132.10
b4
443.27
b5
571.37
b6
628.39
b8
839.48
b9
926.62
m/z
Synthetic peptide
Intensity (%) T GRKK G P N S K L
236.98
R
129.10
971.58
y10
1084.66
1067.64
298.95
b1-6
527.34
b6
628.39
b1-9
825.48
b1-10
953.57
as-7
127.09
y1
132.10
y3
347.23
y4
461.27
m/z

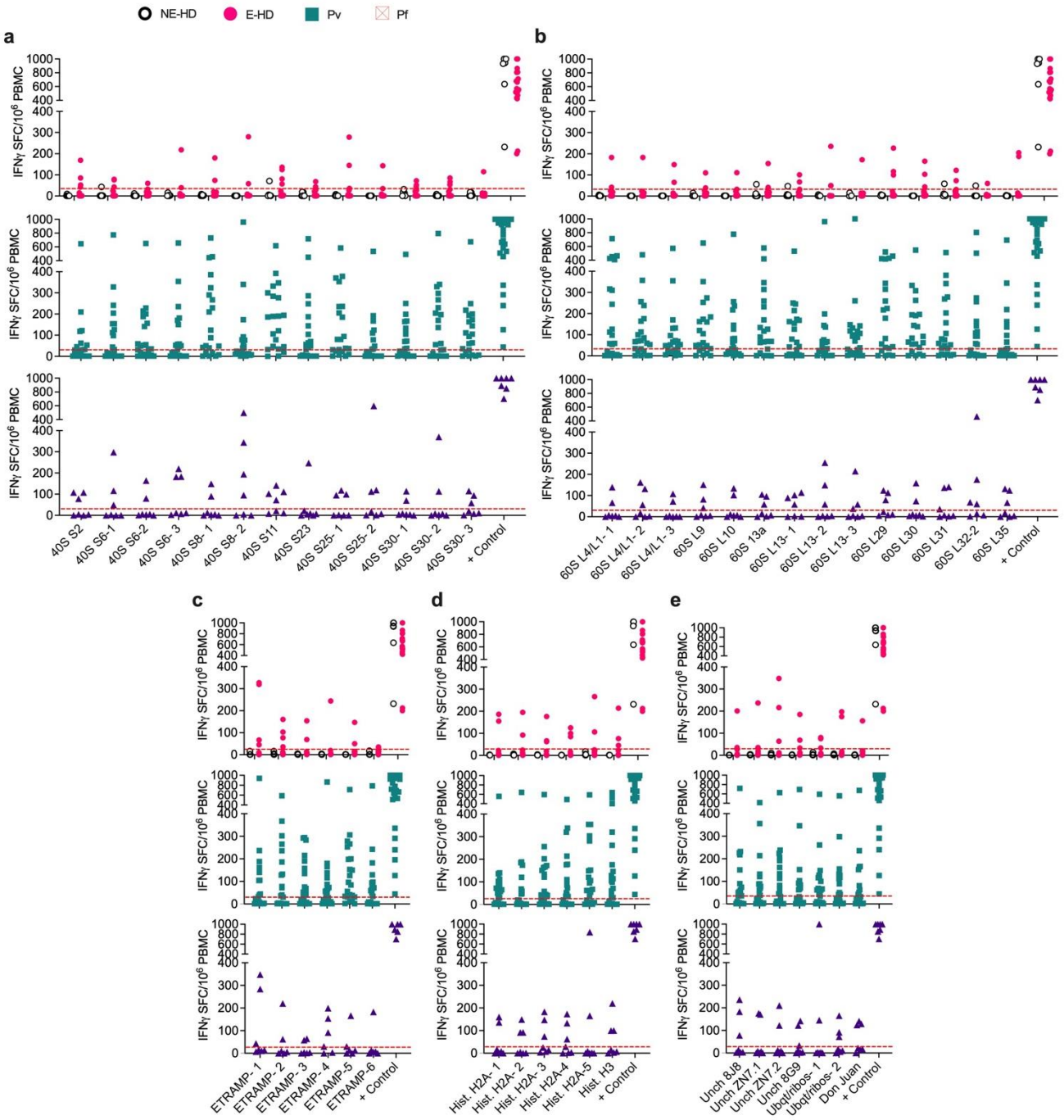

Biological peptide
Intensity (%) T P I I T N K P F G
pre[1+]
1087.61
y9
986.57
y7
776.43
y6
663.35
y8
889.51
122.08
b3
312.19
b4
544.27
b2
199.11
425.27
y5
562.29
F
120.06
m/z
Synthetic peptide
Intensity (%) T P I I T N K P F G
pre[1+]
1087.62
y9
986.57
y7
776.43
y6
663.35
y8
889.52
b3
312.19
b2
199.11
y3
320.16
b4
425.28
y5
562.30
b7
768.46
b1-9
911.54
1069.61
m/z


Biological peptide
Intensity (%) V L T D V G D S D I I K T N E
y10
1091.52
y13
1406.66
185.16
b2
213.16
b4
429.23
y4
491.24
y12
1305.61
y5
604.33
y8
919.47
y9
1034.50
b3
314.21
y6
717.41
m/z
Synthetic peptide
Intensity (%) V L T D V G D S D I I K T N E
y10
1091.53
y13
1406.67
185.17
b2
213.16
b4
429.24
y4
491.25
y11
1190.59
y5
604.33
y8
919.48
b3
314.21
y7
832.45
y14
1519.75
pre[1+]
1618.82
m/z

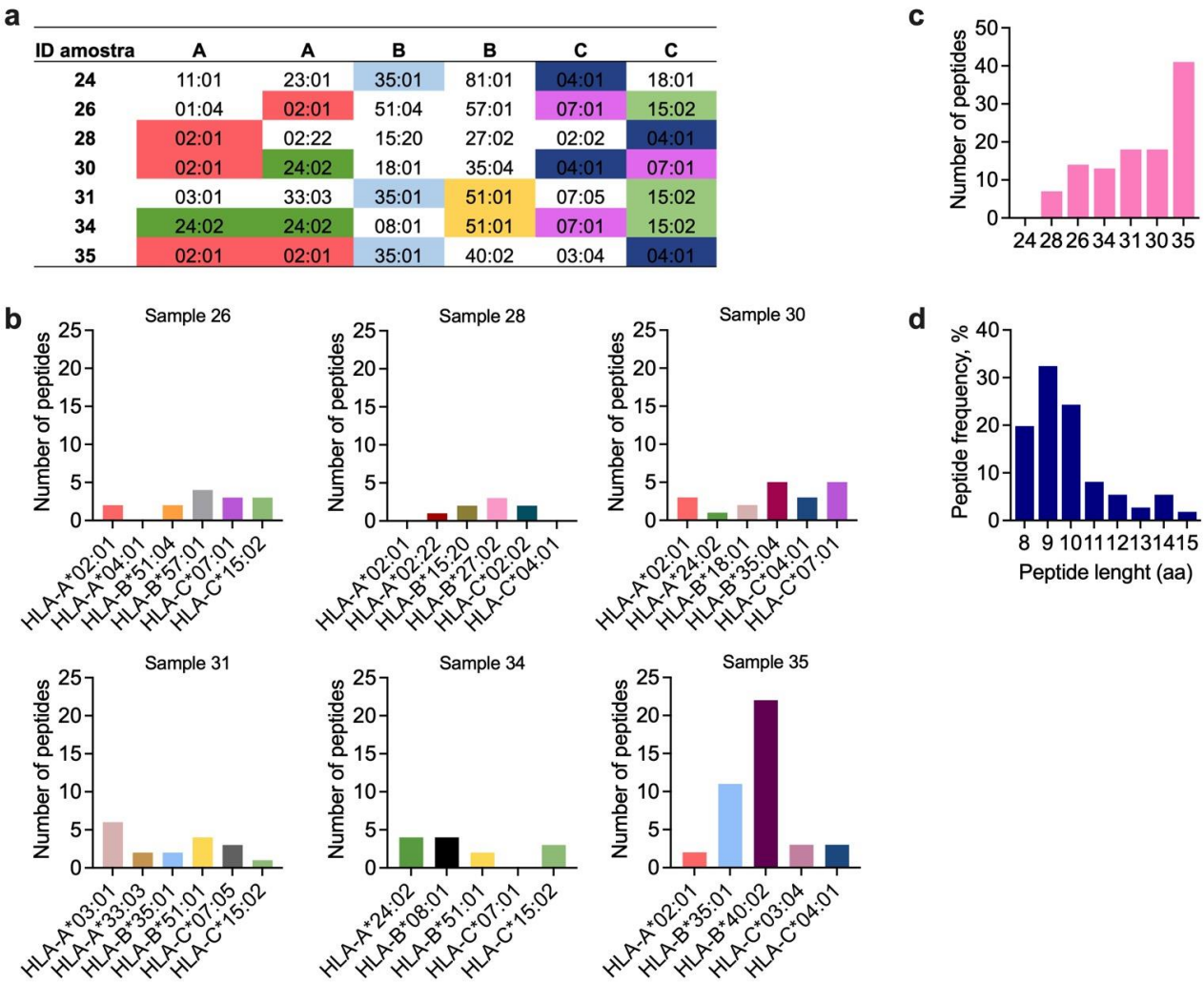

Biological peptide
Intensity (%) V S E V T T V E K D E
y7
821.39
y10
1136.53
y8
920.46
y9
1049.50
y6
720.34
129.10
b3
316.15
pre[2+]
618.33
b2
187.11
b4
415.22
y4
520.23
y5
619.29
m/z
Synthetic peptide
Intensity (%) V S E V T T V E K D E
y7
821.39
y10
1136.53
y8
920.46
y9
1049.50
y6
720.34
b3
316.15
y4
520.23
y5
619.30
b2
187.11
y3
391.18
y1
148.06
pre[1+]
1235.61
m/z


Biological peptide
Intensity (%) Y E S I E V S K I D
y8
890.48
265.12
b2
293.11
129.10
136.08
y6
690.37
757.45
b3
380.14
y4
462.26
y5
561.32
y7
803.45
y9
1019.52
122.08
216.13
591.37
b9
1049.54
m/z
Synthetic peptide
Intensity (%) Y E S I E V S K I D
y8
890.49
b2
293.11
y6
690.37
136.08
b3
380.15
y4
462.26
y5
561.33
y7
803.45
y9
1019.53
y1
134.06
216.14
b4
493.23
b5
622.27
b9
1049.56
pre[1+]
1182.59
m/z

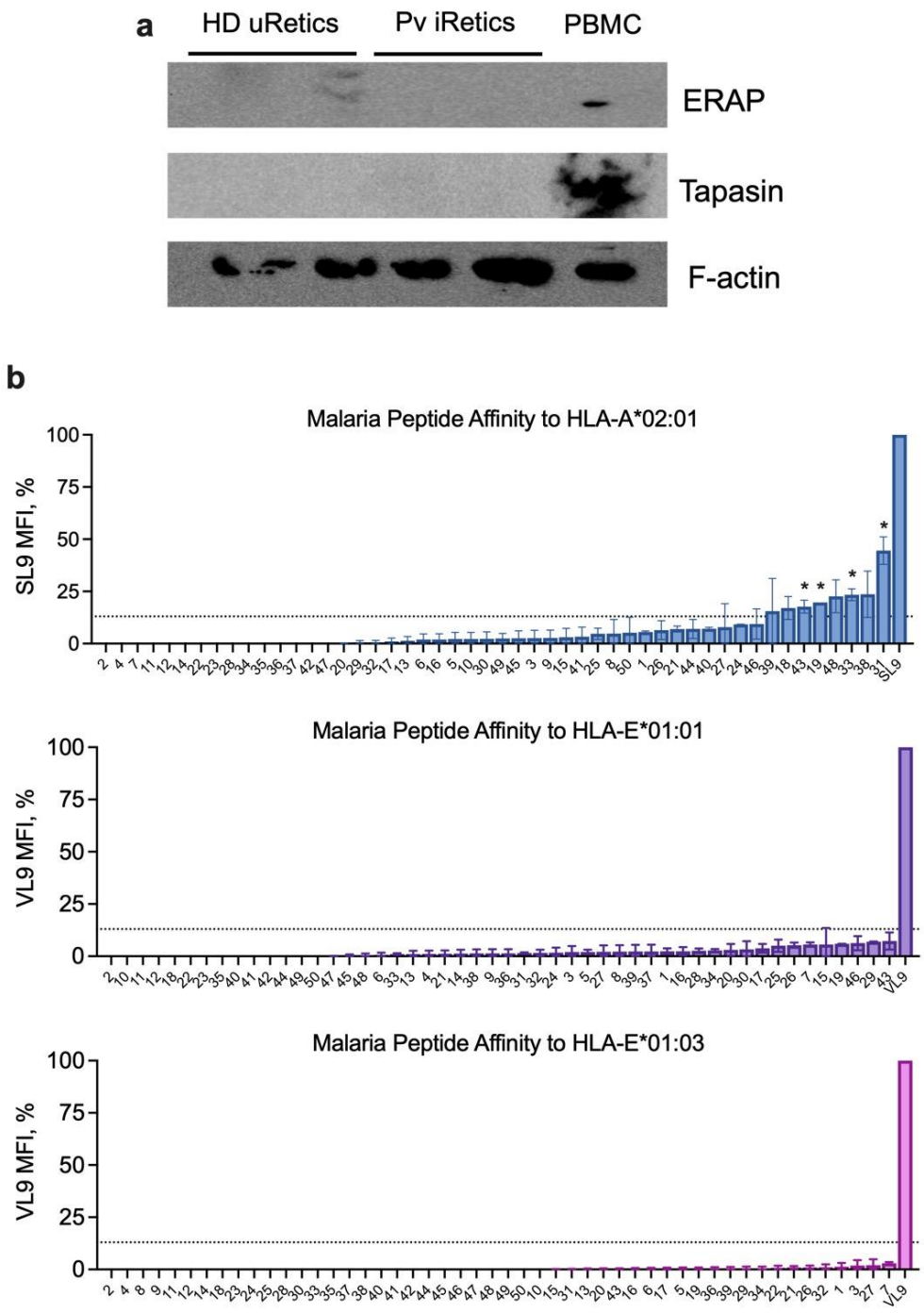

Biological peptide
Intensity (%) Y G R I F K K I T K K
258.17
122.08
239.13
360.20
755.49
y11
1346.90
pre[1+]
1510.96
y4
489.34
y5
617.43
b1-8
858.56
b1-10
1072.70
b1-11
1200.79
m/z
Synthetic peptide
Intensity (%) Y GRIFKKI TKK
y11
1346.91
136.08
R
129.10
300.88
318.85
216.88
y5
376.26
459.07
m/z



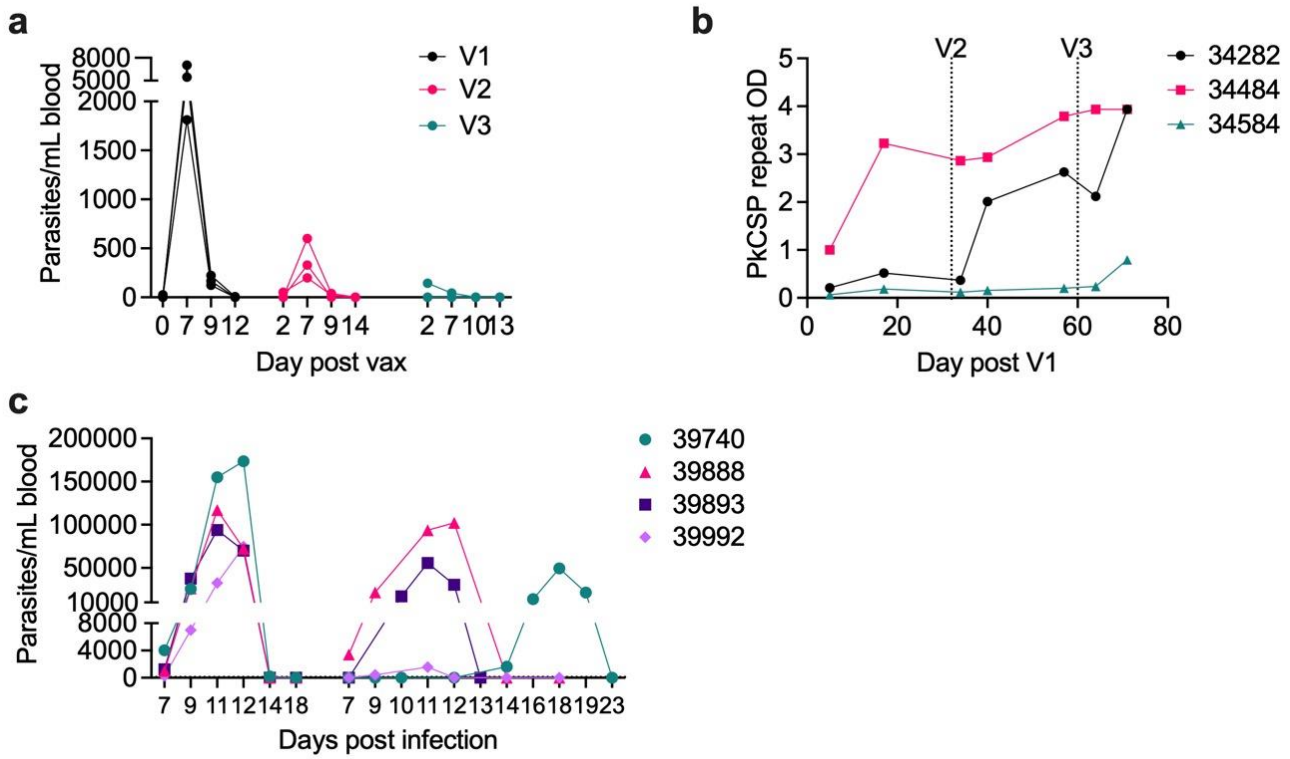
Extended data figure 3 | Peptide validation by ex *vivo* ELISpot assay. Selected peptides were tested using PBMC isolated from patients infected with *Plasmodium vivax* (*Pv*) (n = 24), *P. falciparum* (*Pf*) (n=7) and healthy donors from endemic (n = 15) and non-endemic (n = 6) regions for malaria. Cells were stimulated with **a,** 40S ribosomal protein peptides, **b,** 60S ribosomal protein peptides, **c,** ETRAMP peptides, **d,** Histone peptides, and **e,** other peptides. Each symbol represents one individual. Green squares are *Pv* patients, purple triangles are *Pf* patients, pink circles are endemic healthy donors, and white circles are non-endemic healthy donor. IFNγ production was measured by spot counting and the results are expressed as spot-forming cells (SFC) by $1x10^6$ PBMC. Positive peptides were considered as responses that induced ≥30 spots in each patient- above the red dashed line.



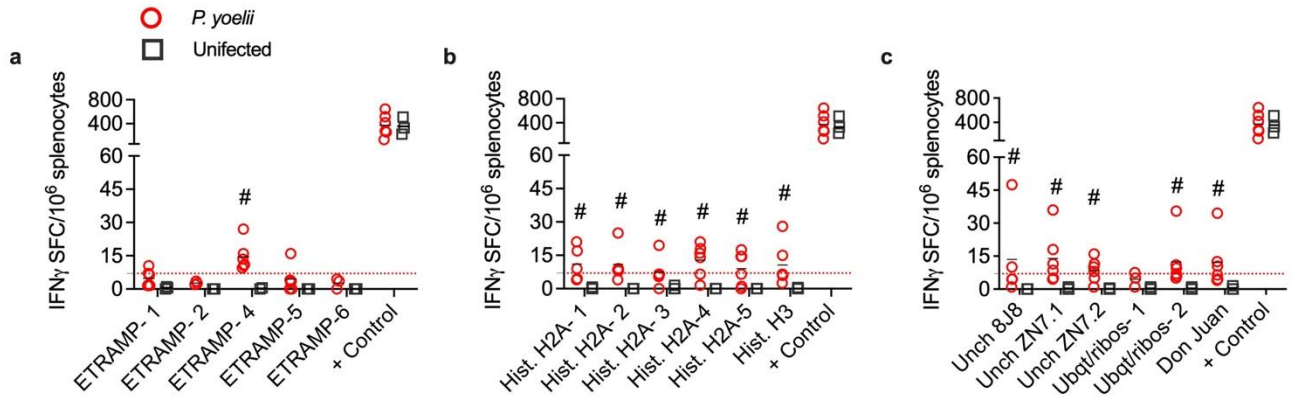
Extended data figure 4 | *Plasmodium vivax* peptides are presented by different HLAs. a, HLA-ABC genotyping typing of the 7 patients used in the immunopeptidome analysis. **b-d,** NetMHC bind analysis of peptides identified in each sample to their donor HLA type. **b,** Number of peptides identified as HLA-ABC binders for each sample. HLA-ABC genotyping of the donor of samples used in the immunopeptidomics assays. Alleles represented with same color mean that they were shared across different samples.



Extended data figure 5 | Tapasin and ERAP1 expression on reticulocytes. Western blot of cell lysates from two healthy donors (HD): uninfected Retics (uRetics) and PBMC; and three *Plasmodium vivax*-infected reticulocytes (Pv iRetics) from three patients were probed for the antigen processing protein Tapasin and Endoplasmic reticulum aminopeptidase 1 (ERAP1). PBMC was used as positive control. F-actin was loaded as endogen protein expression control. *In vitro* binding assay of all selected peptides pulsed in an HLA-A*02:01, HLA-E*01:01, and HLA-E*01:03 cell line, including control peptides. Those peptides marked with asterisk were considered HLA-A: 0201 binders by *in silico* affinity predictions.



Extended data figure 6 | Parasitemia during *Plasmodium knowlesi* (*Pk*) and *P. cynomolgi* (*Pcy*) infection of non-human primates. a, Parasitemia of *Pk* as measured by qRT-PCR following each immunization. **b,** Antibodies to *Pk* CSP repeat region throughout immunization as measured by single dilution ELISA OD value. **c,** Parasitemia of *Pcy* as measured by Giemsa-stained thin smears.



Extended data figure 7 | Peptide validation by *ex vivo* IFNγ ELISpot in mouse model. Immunogenicity in *Plasmodium yoelii* (*Py*) infected mice. Mice were intraperitoneally injected with 10^5 *Py* iRBC. At 12 days post-infection (dpi), mouse splenocytes were isolated and incubated with selected peptides. Cells were stimulated with **a**, ETRAMP peptides, **b**, Histone peptides and **c**, Miscellaneous peptides. Each symbol represents one individual. Red circles are *Py* infected mice (n=6), and black ones are non-infected mice (n=3). IFNγ production was measured by spot counting, and the results are expressed as SFC by $1x10^6$ splenocytes. Positive peptides (#) were considered as responses that induced ≥10 spots in each mouse – above the red dashed line – and P ≥0.05 by multiple unpaired student *t* tests.

MAIN FIGURES

Figure 1 | Peptide identification and immunogenicity validation.
Figure 2 | Classical and non-classical HLA peptide binders
Figure 3 | Novel *Plasmodium* antigens are recognized by T cells elicited during *P. knowlesi* and *P. cynomolgi* infection of non-human primates.
Figure 4 | Antigen validation in the *P. yoelii* malaria experimental model.

EXTENDED DATA TABLES

Extended data table 1 | *Plasmodium falciparum* homology
Extended data table 2 | Primers used for *Plasmodium falciparum* liver stage expression

EXTENDED DATA FIGURES

Extended data figure 1 | Antigen gene expression in humanized mouse livers infected with *P. falciparum*.
Extended data figure 2 | Spectral match validation
Extended data figure 3 | Peptide validation by e*x vivo* ELISpot assay.
Extended data figure 4 | *Pv* peptides are presented by different HLAs
Extended data figure 5 | Tapasin and ERAP1 expression on reticulocytes
Extended data figure 6 | Parasitemia during *P. knowlesi* and *P. cynomolgi* infection of non-human primates.
Extended data figure 7 | Peptide validation by *ex vivo* IFNγ ELISpot in mouse model.

SUPPLEMENTARY INFORMATION (SI)

Supplementary information 1 | Clinical information
Supplementary information 2 | Identified peptides
Supplementary information 3 | *Plasmodium vivax* orthologous gene expression in parasite life cycle.
Supplementary information 4 | Selected peptides used for in vitro stimulation
Supplementary information 5 | HLA binding