

Table S1: Identification of disulfide bond connected HCV E2e peptides resulting from tryptic digest

Peptide Π	Amino acid sequence	predicted mass *	determined mass ‡
JFH-1			
J1	FDSSGC ₄₅₂ PGR	925,9911	n.f.
J2	LSAC ₄₅₉ R	549,6654	n.f.
J3	IGWGT _{LQYEDDVTNPEDMRPYC₄₈₆WHYPPKPC₄₉₄GVVPAR}	4192,7303	n.f.
J4	SVC ₅₀₃ GPVYC ₅₀₈ FTPSPVVGGTTDRR	2341,7051	2341,37
J5	ADFDASTDLLC ₅₈₁ PTDC ₅₈₅ FR	1891,0769	n.f.
J6	C ₆₀₇ LVHYPYR	1051,2508	1050,63
J7	LTAAC ₆₄₄ NFTR	998,1414	998,05
	J1 + J2	1472,6515	1471,71
	J3	4190,7569	n.f.
	J4	2339,7141	2339,3
	J5	1889,0822	n.f.
	J6 + J7	2046,3921	2045,37
UKN2b_2.8			
U1	TALNC ₄₂₉ DDSLQTGFLASLFYVK	2307,6228	2308,00
U2	IGWGT _{LLEYETDATNDEDMRPYC₄₈₆WHYPPRPC₄₉₄GIVSAR}	4201,6514	n.f.
U3	TVC ₅₀₃ GPVYC ₅₀₈ FTPSPVVGGTTDR	2199,5445	2195,75
U4	QGVP _{TYSWGEDETDVFLLDSTRPPQGAWFGC₅₅₂TWMDGT} GFTK	4586,0192	n.f.
U5	DHDSTLDLLC ₅₈₁ PTDC ₅₈₅ FR	1852,0432	1851,50
U6	C ₆₀₇ LVDYPYR	1029,1983	1028,80
U7	LNAAC ₆₄₄ DFTR	1011,1401	1010,87
	U1 + U4	6890,6802	n.f.
	U2	4199,6775	n.f.
	U3	2197,5525	2194,94
	U5	1850,0483	1849,64
	U6 + U7	2037,338	2037,59
H77			
H1	FDSSGC ₄₅₂ PER	998,0547	n.f.
H2	LASC ₄₅₉ R	549,6654	n.f.
H3	LTDF _{AQGWPISYADGSGGLDERPYC₄₈₆WHYPPRPC₄₉₄GIVP} AK	4322,8613	n.f.
H4	VC ₅₆₄ GAPPC ₅₆₉ VIGGVDNTLLC ₅₈₁ PTDC ₅₈₅ FR	2508,9457	2508,81
H5	C ₆₀₇ MVDYPYR	1047,2315	n.f.
H6	LEAAC ₆₄₄ DWTR	1065,1884	1065,98
H7	C ₆₅₂ DLEDRDR	750,8011	n.f.
H8	SELSPLLLSTTQWQVLPC ₆₇₇ SF....SSIASWAIK	6100,0588	n.f.
	H1 + H2	1544,715	1544,29
	H3	4320,8851	4321,98
	H4	2504,9486	2504,50
	H5 + H6	2109,4239	2110,35
	H7 + H8	6847,8954	6849,91

Π Peptides were named after the isolate and numbered sequentially according to their appearance in the E2 amino acid sequence.

* Molecular mass predictions were performed using MS-BRIDGE [12] for disulfide-connected peptides and using PeptideMass for reduced peptides [13].

‡ n.f. - peptide was not found in mass spectrometry