

SUPPLEMENTARY DATA

The TSG-6/HC2-mediated transfer is a dynamic process shuffling HCs between glycosaminoglycans

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Table S1.

Peptide mass fingerprinting analyses of HC•HA complexes (Fig. 4)

TSG-6/HC2 was allowed to transfer HCs from IαI to HA. The sample was subjected to reduced SDS-PAGE followed by Coomassie blue staining (Fig. 4). To identify the protein content in the expected HC•HA complexes (Fig. 4, band a-c), the bands of interest were excised from the gel, the proteins digested with trypsin, and finally identified by peptide mass fingerprinting analyses using a Micromass Q-TOF Ultima Global mass spectrometer (Waters). The table shows the significant hits as defined by Mascot probability analysis. The migration in the gel and the identifications shown below strongly suggest that “band a” contains HC1•HA•HC2 complexes, “band b” contains HC2•HA complexes, and “band c” contains HC1•HA complexes.

Proteins identified in band a:

Inter-alpha-trypsin inhibitor heavy chain H2 precursor (Human)

Accession number:	P19823
Protein score:	85
Number of mass values searched:	62
Number of mass values matched:	10
Sequence coverage (%):	14

Peptide	Mr (expt)	Mr (calc)	Δ Mr
VVNNSPQPQNVVFDVQIPK	2121,09	2121,12	-0,03
VQFELHYQEVK	1418,72	1418,72	0,00
IYLPGR	845,48	845,48	0,00
HLEVDVWVIEPQGLR	1788,95	1788,95	0,00
FLHVPDTFEGHFDGVPVISK	2240,10	2240,13	-0,03
AHVSFKPTVAQQR	1467,81	1467,79	0,02
AEDHFSVIDFNQIR	1803,88	1803,85	0,03
IQPSGGTNINEALLR	1581,84	1581,85	-0,01
LSNENHGIAQR	1237,62	1237,62	0,00
FYNQVSTPLLR	1336,71	1336,71	0,00

Inter-alpha-trypsin inhibitor heavy chain H1 precursor (Human)

Accession number: P19827

Protein score: 94

Number of mass values searched: 62

Number of mass values matched: 10

Sequence coverage (%): 16

Peptide	Mr (expt)	Mr (calc)	Δ Mr
QAVDTAVDGVFIR	1389,72	1389,73	-0,01
FAHYVVTSQVVNTANEAR	2004,94	2005,00	-0,06
EVAFDLEIPK	1159,59	1159,61	-0,02
TAFISDFAVTADGNAFIGDIK	2172,06	2172,07	-0,01
AAISGENAGLVR	1156,61	1156,62	-0,01
LDAQASFLPK	1088,56	1088,59	-0,03
GSLVQASEANLQAAQDFVR	2002,99	2003,01	-0,02
GFSLDEATNLNGLLR	1675,88	1675,85	0,03
QYYEGSEIVVAGR	1469,70	1469,71	-0,01
TFVSALQPSPHSSSNTQR	2157,06	2157,08	-0,02

Total score of P19823 and P19827 mixture: 179

Protein identified in band b:

Inter-alpha-trypsin inhibitor heavy chain H2 precursor (Human)

Accession number: P19823
Protein score: 90
Number of mass values searched: 25
Number of mass values matched: 8
Sequence coverage (%): 10

Peptide	Mr (expt)	Mr (calc)	Δ Mr
VQSTITSR	890,49	890,48	0,01
VVNNSPQPQNVVFDVQIPK	2121,12	2121,12	0,00
IYLQPGR	845,48	845,48	0,00
AHVSFKPTVAQQR	1467,83	1467,79	0,04
AEDHFSVIDFNQNIR	1803,87	1803,85	0,02
IQPSGGTNINEALLR	1581,84	1581,85	-0,01
LSNENHGIAQR	1237,62	1237,62	0,00
FYNQVSTPLLR	1336,71	1336,71	0,00

Protein identified in band c:

Inter-alpha-trypsin inhibitor heavy chain H1 precursor (Human)

Accession number: P19827
Protein score: 84
Number of mass values searched: 47
Number of mass values matched: 8
Sequence coverage (%): 14

Peptide	Mr (expt)	Mr (calc)	Δ Mr
QAVDTAVDGVFIR	1389,73	1389,73	0,00
TAFISDFAVTADGNAFIGDIK	2172,06	2172,07	-0,01
AAISGENAGLVR	1156,61	1156,62	-0,01

QLVHHFEIDVDIFEPQGISK	2350,19	2350,2	-0,01
GSLVQASEANLQAAQDFVR	2003,01	2003,01	0,00
GFSLDEATNLNGGLLR	1675,89	1675,85	0,04
QYYEGSEIVVAGR	1469,72	1469,71	0,01
TFVSALQPSPTHSSSNTQR	2157,06	2157,08	-0,02