Electronic Supplementary Information

Analyst

Top-Down Mass Spectrometry of Hybrid Materials with Hydrophobic Peptide and Hydrophilic or Hydrophobic Polymer Blocks

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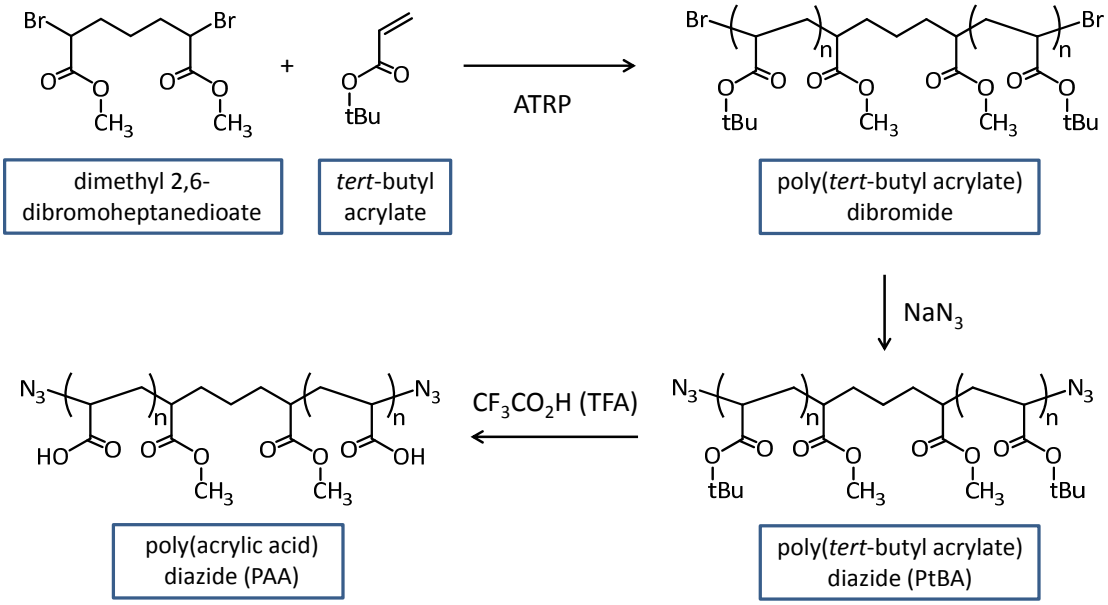

Scheme S1. Synthesis of azide-functionalized, telechelic poly(acrylic acid) (PAA).

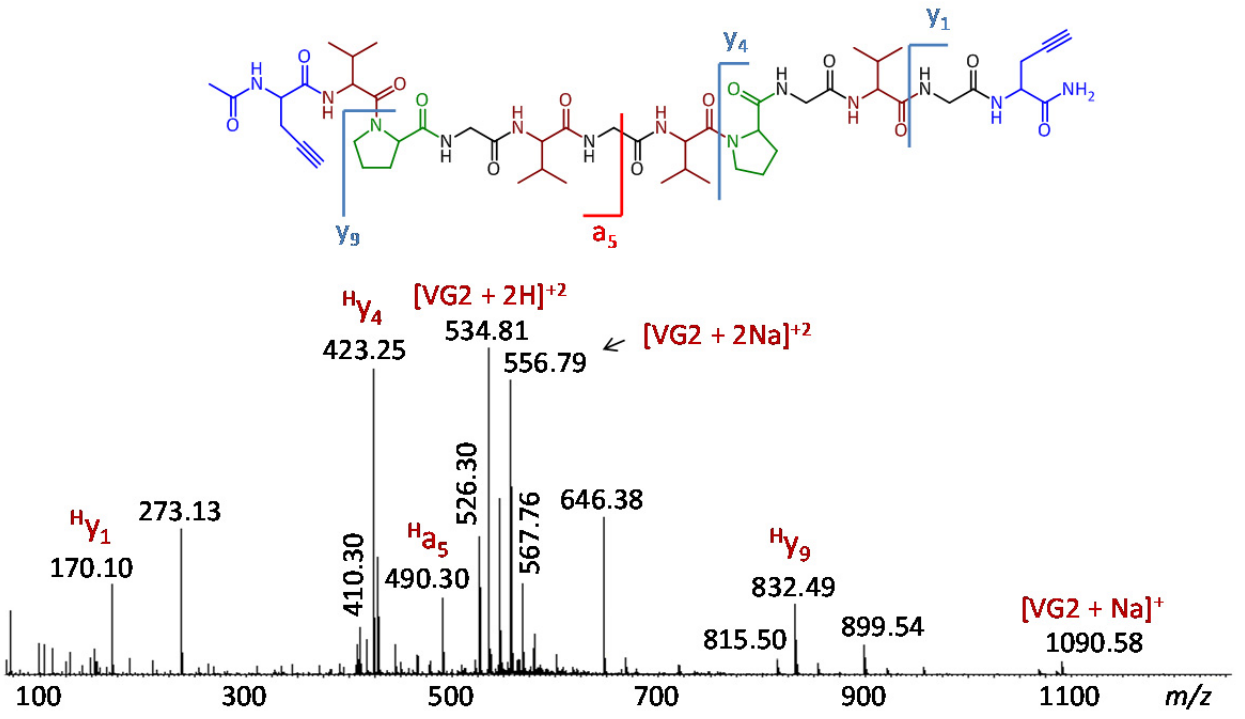

Fig. S1. ESI mass spectrum of VG2 peptide dissolved in aqueous ammonium acetate buffer (pH = 6.64). The structure of the peptide is depicted on top of the spectrum. Fragments from the protonated precursor are also observed; these are labeled by a superscripted H to indicate that they do not contain Na.

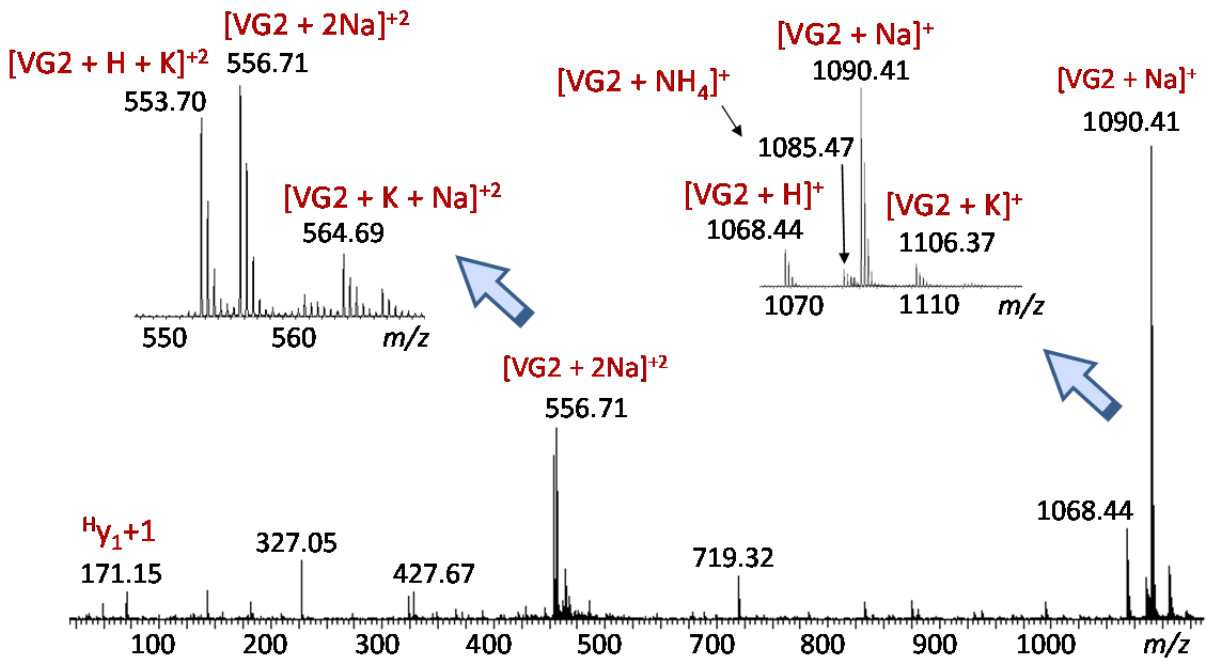

Fig. S2. ESI mass spectrum of VG2 peptide dissolved in aqueous n-dodecyl-α-D-maltoside. The insets show expanded views of the *m/z* regions of doubly and singly charged VG2.

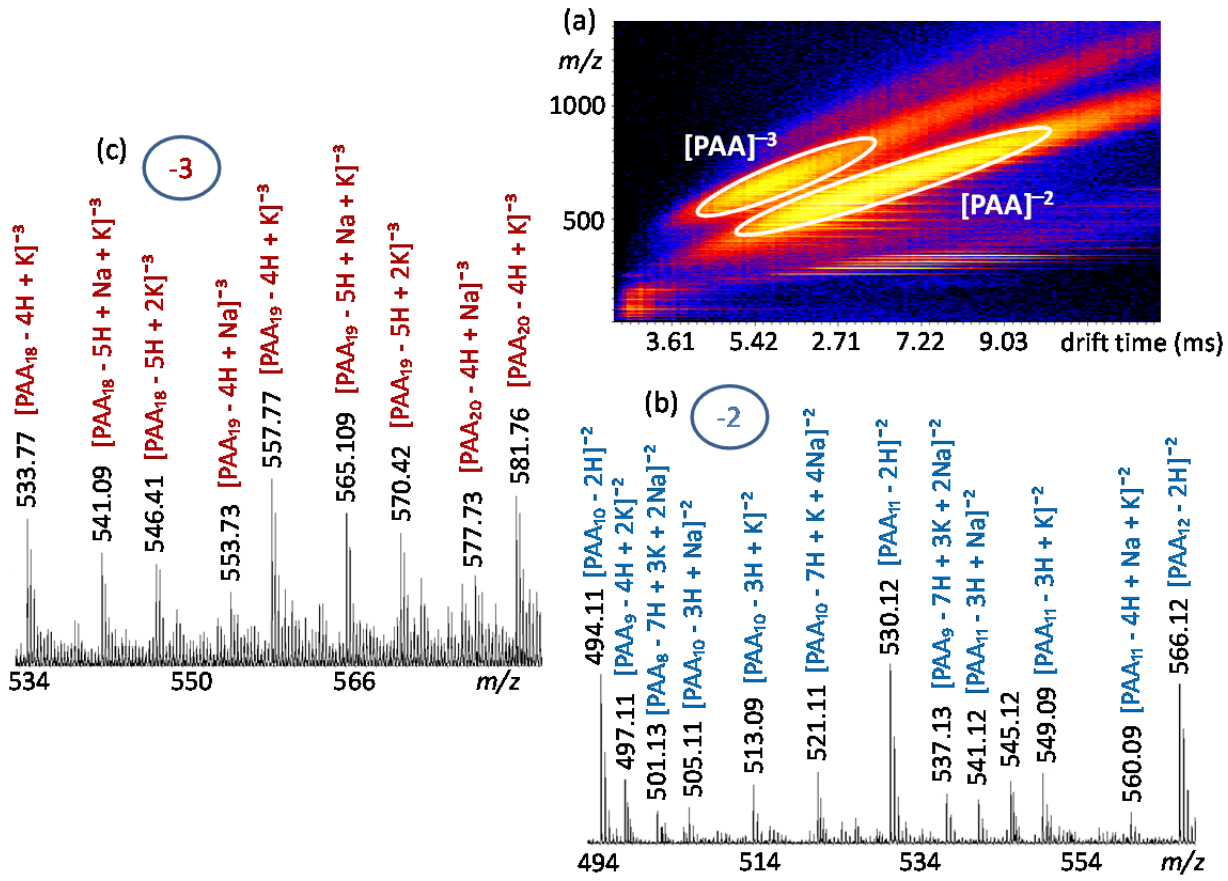

Fig. S3. (a) 2-D IM-MS plot (*m/z* vs. drift time) of diazide-terminated poly(acrylic acid), PAA, acquired in negative ion mode. The mobility regions of doubly and triply charged PAA anions are enclosed in ovals. (b,c) Mass spectra extracted from the mobility regions of (b) -2 and (c) -3 ions, in which $[PAA - 2H]^{-2}$ and $[PAA - 4H + K]^{-3}$ anions, respectively, dominate.

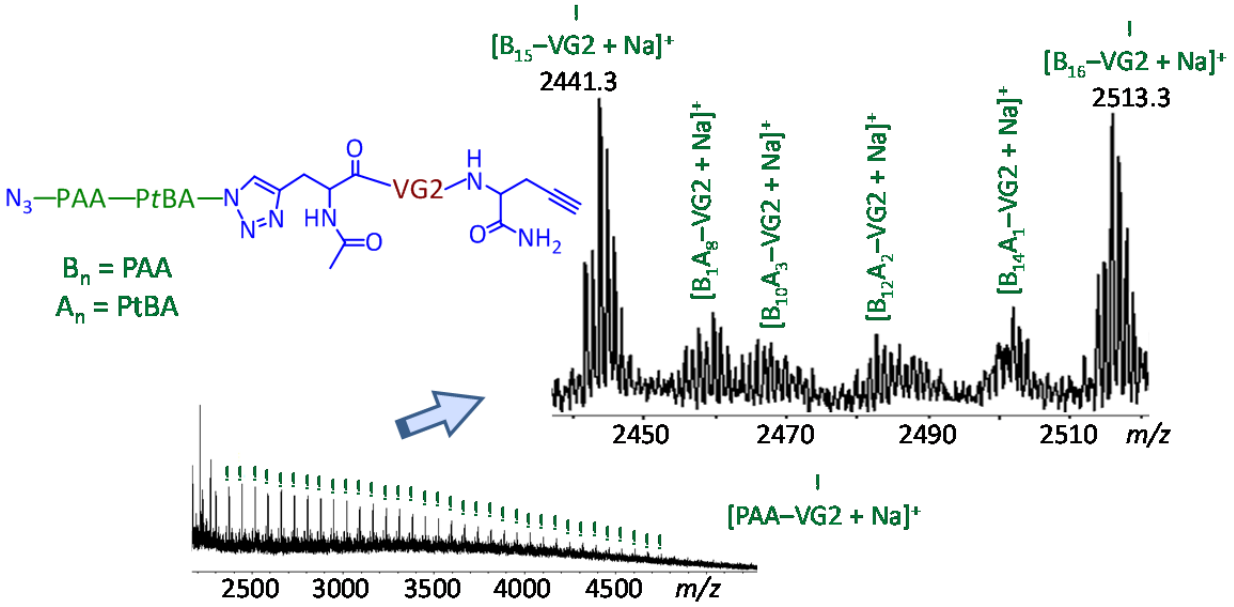

Fig. S4. MALDI mass spectrum of the PAA-VG2 hybrid material in positive ion mode; B_n and A_n designate the number of PAA and remaining (unhydrolyzed) PtBA repeat units, respectively. The main distribution (marked by !) arises from the completely hydrolyzed product.

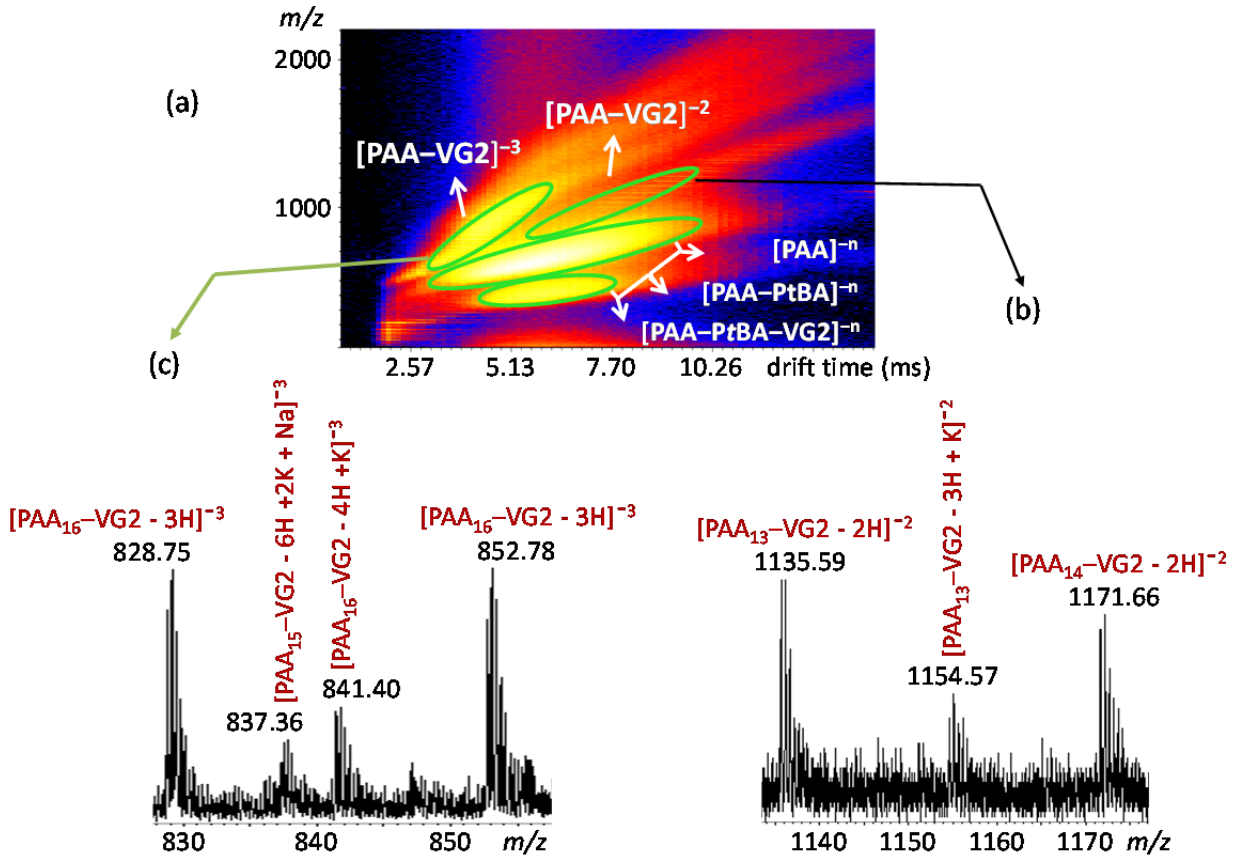

Fig. S5. (a) 2-D IM-MS plot of the PAA-VG2 hybrid material in negative ion mode; the mobility regions of doubly and triply charged PAA-VG2 anions and of incompletely hydrolyzed hybrid as well as unreacted polymer are enclosed in ovals. (b,c) Mass spectra extracted from the mobility regions of (b) -2 and (c) -3 ions of PAA-VG2, in which doubly and triply deprotonated oligomers, respectively, dominate.

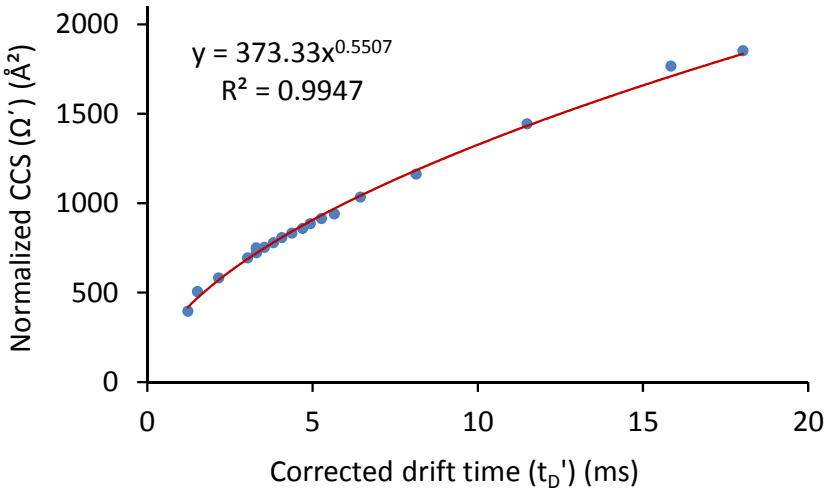

Fig. S6. Drift time calibration curve, obtained by plotting the corrected drift times of singly and doubly protonated polyalanine oligomers vs. the corresponding normalized collision cross-sections.[1-3] The data used to construct this curve are listed in Table S1.

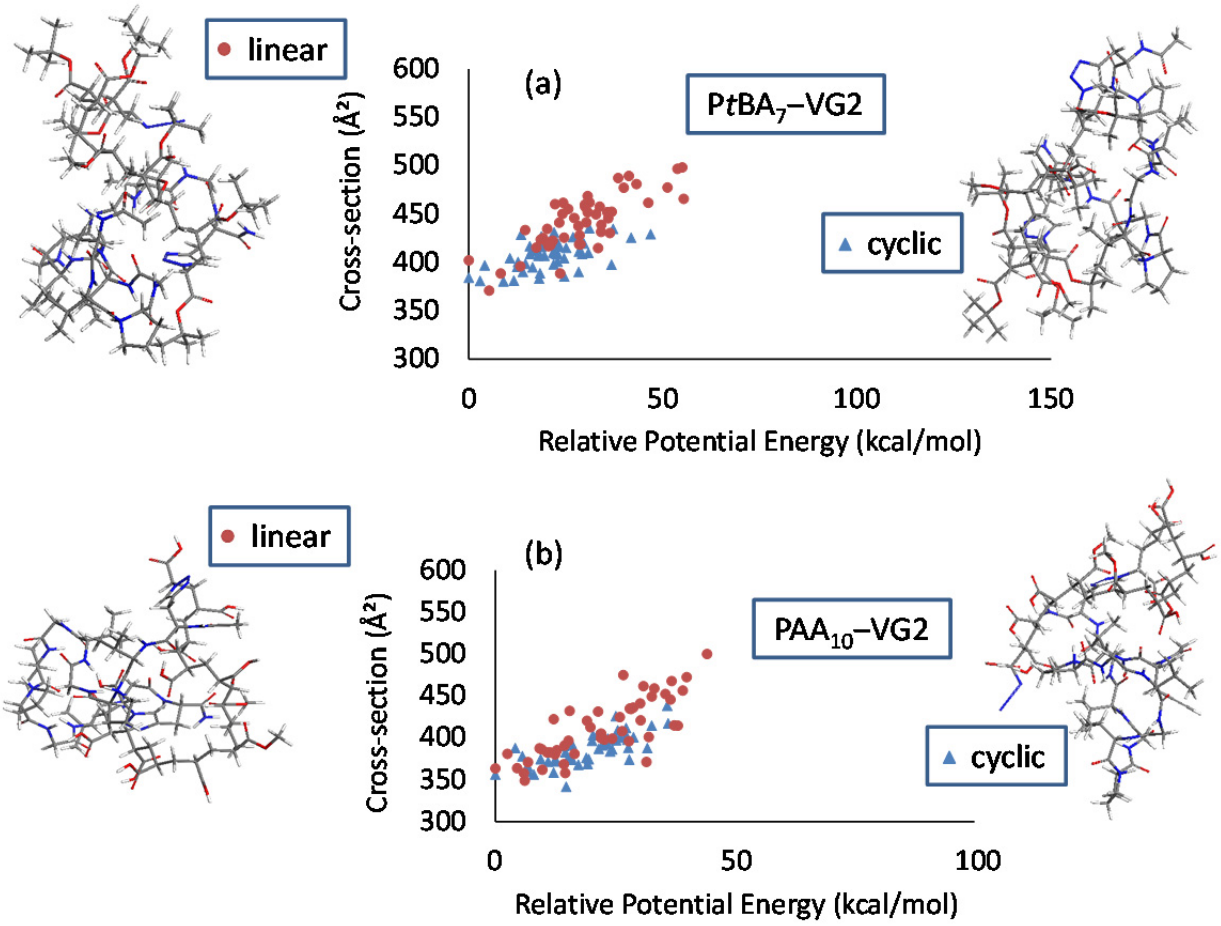

Fig. S7. Calculated collision cross-section (Ω_{cald} in $Å^2$) vs. relative energy for 50 energy-minimized structures of (a) $[PtBA_7\text{-VG2} + 2H]^{+2}$ (*m/z* 1118) and (b) $[PAA_{10}\text{-VG2} + 2H]^{+2}$ (*m/z* 1029) with linear (orange circle) or cyclic (blue triangle) architecture. On average, the cyclic architectures are more stable by (a) 2.9 kcal/mol and (b) 4.0 kcal/mol. Representative linear and cyclic structures are shown on the left and right sides of the plots, respectively.

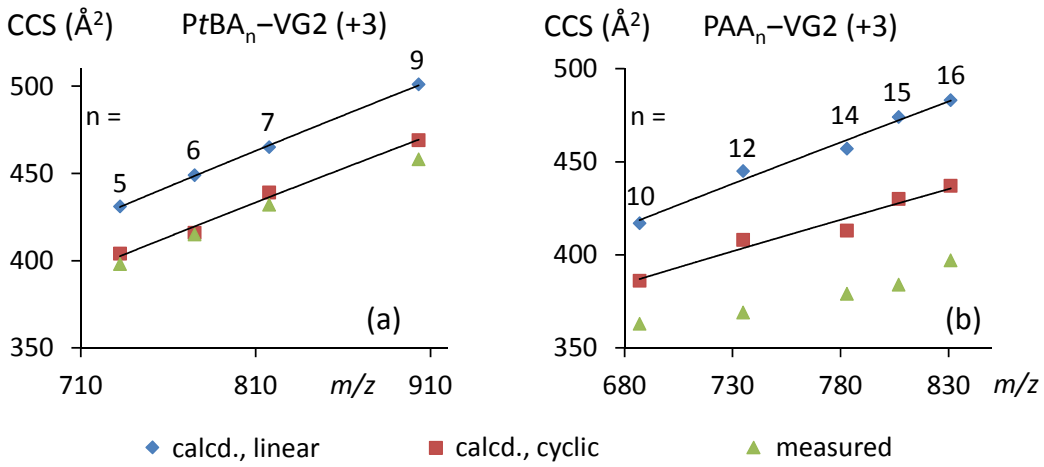

Fig. S8. Calculated collision cross-section (PA method) for triply protonated oligomers of (a) P*t*BA-VG2 and (b) PAA-VG2 with linear or cyclic architecture, and experimental collision cross-section of the same ions vs. *m/z* ratio. The triply protonated P*t*BA-VG2 oligomers also contain 3 hydrolyzed PAA repeat units in addition to the listed P*t*BA repeat units.

Table S1 Drift time and collision cross-section data of singly and doubly protonated polyalanine oligomers, H–(Ala)$_n$–OH, which served as calibrant ions for the determination of unknown collision cross-sections

z	n	*m/z*	t_D (ms)[a]	t_D' (ms)[b]	Ω (Å^2)[c]	Ω' (Å^2)[d]	Ω (Å^2)[e]	Ω' (Å^2)[d,e]
1	2	161.09	1.25	1.232			81	395.5
1	3	232.16	1.54	1.519	89	444.9	101	504.8
1	4	303.12	2.19	2.166	100	506.3	115	582.2
1	6	445.16	3.33	3.300	128	657.0	146	749.4
1	10	729.25	6.49	6.452	181	940.0	199	1033.5
1	12	871.30	8.18	8.138	206	1073.1	223	1161.7
1	16	1155.70	11.54	11.492			276	1443.3
1	20	1439.92	15.90	15.847			337	1766.4
1	22	1581.99	18.08	18.024			353	1851.9
2	17	613.72	3.07	3.035	265	693.4		
2	18	649.22	3.34	3.304	276	722.6		
2	19	684.74	3.58	3.543	287	751.8		
2	20	720.39	3.86	3.822	297	778.4		
2	21	755.77	4.11	4.071	308	807.6		
2	22	791.28	4.42	4.380	317	831.5		
2	23	826.78	4.75	4.705	327	858.1		
2	24	862.30	4.98	4.934	337	884.6		
2	25	897.82	5.32	5.276	348	913.8		
2	26	933.33	5.71	5.662	358	940.3		

[a] Measured drift time. [b] Corrected drift time, $t_D' = t_D - [C(m/z)^{0.5}/1000]$ (C = 1.41). [c] CCS (Ω_{He}) from ref. 4. [d] $\Omega' = \Omega(\mu^{0.5}/z)$, where z is the ion charge and μ is the reduced mass of the ion and drift gas (N_2). [e] Calculated in this study (Ω_{He}), using the projection approximation, from energy-minimized structures (50 per oligomer) obtained by molecular mechanics/dynamics simulations.

Cross-sectional data of calibrant ions

Calibration in traveling-wave IM-MS studies involves the derivation of a correlation between measured drift times and collision cross-sections.[1-3] Since the CCS variable used in this procedure is the mass- and charge-normalized quantity Ω', calibrant ions in different charge states can be combined which is often necessary in order to obtain a calibration curve that covers the cross-sectional range of interest. With the drift times measured in this study, the reported collision cross-sections for singly protonated polyalanine[4] (Ω'_{He}) did not fit onto the same calibration curve as the reported collision cross-sections (Ω'_{He}) for doubly protonated polyalanine.[4] An acceptable fit of both charge states onto the same regression line (Fig. S6) could be obtained by using calculated CCSs for the singly charged ions (cf. Table S1), which are 8-12% higher than the literature values.[5] The calibration curve constructed from the combined experimental/calculated data was validated by using it to determine known CCSs, including those of triply protonated polyalanine oligomers and several charge states of small proteins, cf. Table S2. The values obtained this way compare favorably with the previously reported CCSs of these ions (within 3% for polyalanine[4] and 8% for the proteins[6-8]). In contrast, the values deduced using the old CCSs of singly protonated polyalanine showed substantially higher discrepancies (10% and 20%, respectively).

Table S2 Comparison of published collision cross-sections with collision cross-sections determined in this study using the calibration plot in Fig. S6

sample	z^a	*m/z*	t_D (ms)	t_D' (ms)^b	Ω' (Å^2)^c	Ω (Å^2)^d	Ω_{publ} (Å^2)^e
H–$(Ala)_{27}$–OH	+3	646.22	3.52	3.484	742.4	424	438
H–$(Ala)_{29}$–OH	+3	693.58	3.97	3.933	793.6	453	465
H–$(Ala)_{30}$–OH	+3	717.33	4.24	4.202	823.1	470	479
H–$(Ala)_{31}$–OH	+3	740.93	4.51	4.472	851.7	486	490
H–$(Ala)_{32}$–OH	+3	764.59	4.60	4.561	861.1	491	502
H–$(Ala)_{33}$–OH	+3	788.28	4.87	4.830	888.7	507	516
ubiquitin	+9	952.13	5.00	4.956	901.4	1535	1649
ubiquitin	+11	779.21	3.98	3.941	794.5	1654	1802
cytochrome C	+13	951.35	5.00	4.957	901.4	2217	2391
cytochrome C	+14	883.47	4.62	4.578	862.8	2285	2473
cytochrome C	+17	727.78	3.85	3.812	780.1	2509	2723
cytochrome C	+18	687.45	3.59	3.553	750.4	2555	2766
cytochrome C	+19	651.35	3.33	3.294	719.8	2587	2800

[a] $[M + zH]^{+z}$ ions. [b] $t_D' = t_D - [C(m/z)^{0.5}/1000]$ (C = 1.41). [c] Normalized CCS (Ω'), obtained from the calibration plot in Fig. S6. [d] CCS measured in this study, calculated from Ω' via the equation $\Omega = \Omega'(z/\mu^{0.5})$ where z is the ion charge and μ is the reduced mass of the ion and drift gas (N_2). [e] CCS (Ω_{He}) from ref. 4 (triply protonated polyalanine) or refs. 6-8 (ubiquitin and cytochrome C ions).

References

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