



How Peptides Dissociate in Plasmonic Hot Spots

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How peptides dissociate in plasmonic hot spots

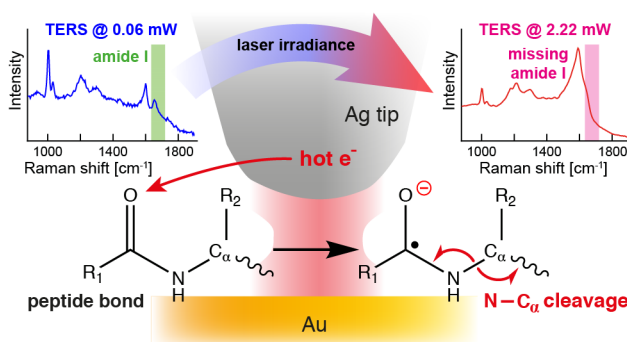
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Abstract

Plasmon-induced hot carriers enable dissociation of strong chemical bonds by visible light. This unusual chemistry has been demonstrated for several diatomic and small organic molecules. Here we extend the scope of plasmon-driven photochemistry to biomolecules and describe the reactivity of proteins and peptides in plasmonic hot spots. We use tip-enhanced Raman spectroscopy (TERS) to both drive the reactions and to monitor their products. Peptide backbone bonds are found to dissociate in the hot spot, which is reflected in the disappearance of the amide I band in the TERS spectra. The observed fragmentation pathway involves non-thermal activation, presumably by dissociative capture of a plasmon-induced hot electron. This fragmentation pathway is known from electron transfer dissociation (ETD) of peptides in gas-phase mass spectrometry (MS), which suggests a general similarity between plasmon-induced photochemistry and nonergodic reactions triggered by electron capture. This analogy may serve as a design principle for plasmon-induced reactions of biomolecules.

Keywords: hot electrons, plasmon-driven photocatalysis, tip-enhanced Raman spectroscopy, electron transfer dissociation, peptides, amide I band



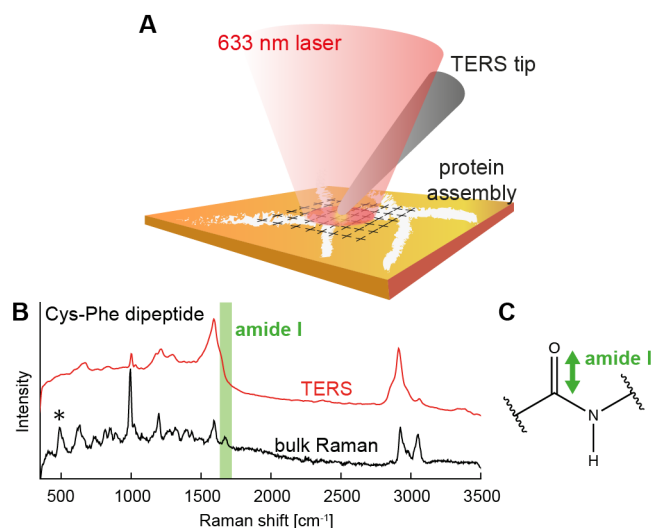
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22 **Introduction**

23 Plasmon-induced hot carriers have attracted the attention of catalysis research, because
24 they can be utilized to accelerate reactions with visible light^[1-3]. They also enable the
25 formation of unusual reaction products via non-thermal activation of the reactants^[4,5].
26 Since the field is new, the scope of chemistry that can be driven by hot carriers has not yet
27 been fully explored and so far includes mostly small molecules (like H₂, O₂ and NH₃)^[2,3,6]
28 and model organic molecules (mostly thiols, biphenyls and bipyridines)^[4,7-10]. Recently it
29 was proposed^[5,11] that plasmon-induced reactions rely on the same mechanism as
30 desorption induced by electronic transitions (DIET)^[11-14] – a process well known from
31 surface science studies of small molecules adsorbed on planar metal surfaces (electron
32 stimulated desorption^[15], surface femtochemistry^[16,17], x-ray photochemistry^[18] *etc.*).
33 DIET relies on the transfer of a hot electron from the metal to an adsorbed molecule,
34 which triggers nonergodic bond dissociation, *i. e.* occurring faster than a molecular
35 vibration (below 10⁻¹⁴ s)^[13]. The chemical transformation takes place before the molecule
36 reaches thermal equilibrium via exchange of energy between its internal degrees of
37 freedom. Hence, the reactivity of the radical formed upon electron capture may be very
38 different from that of the neutral precursor. Consequently, DIET results in non-thermal
39 fragmentation pathways that may not involve the weakest bond of the neutral adsorbate,
40 but the one that is destabilized through the attachment of a low-energy electron. The
41 similarity between plasmon-assisted photochemistry and DIET is helpful in
42 understanding and developing novel plasmon-assisted reactions, however it has been
43 restricted to small molecules investigated by surface science in high vacuum conditions.

44 Over the last decade several groups have demonstrated that plasmon-induced reactions
45 can occur during measurements with surface- and tip-enhanced Raman spectroscopy

46 (SERS and TERS)^[4,5,9,19]. These reactions are perceived detrimental for plasmon-
47 enhanced spectroscopies, because they change the investigated sample during the
48 measurement^[5,19]. This has become a pressing issue in the last decade, when TERS was
49 applied for nanoscale spectroscopic imaging of native protein assemblies^{[20],[21]} (Fig. 1A).
50 The photochemical degradation of the analyte leads to missing spectral features, large
51 fluctuations in the spectra^[5,22-24] and lack of resemblance to the bulk Raman spectra of
52 the same molecules^[25-33]. In particular, the amide I band (which is the clearest Raman
53 marker of peptide bonds) is frequently missing in the SER/TER spectra of proteins and
54 peptides^[34,35] (Fig. 1B, see detailed discussion in Section S1 of the Supporting
55 Information). This has been a long-lasting controversy in the SERS/TERS community,
56 with dedicated studies published on the topic by Blum *et al.*^[34] and Kurouski *et al.*^[35] The
57 proposed explanations of the absence of the amide I band included (among others)
58 shielding of the amide bond by bulky amino acid residues, chemical interaction between
59 Au and the peptide backbone, as well as differences in the selection rules between tip-
60 enhanced and normal Raman spectroscopy^[34-36].



61

62 **Figure 1.** (A) TERS imaging of a protein assembly: the TERS tip is raster-scanned over a sample deposited
 63 on a flat surface, and a TER spectrum is acquired at every pixel of the raster, yielding a nanoscale chemical
 64 image of the sample. In the case of protein imaging, the local conformation of the protein residing under the
 65 tip can, in principle, be mapped based on the positions of the amide bands in the TER spectrum. (B) Bulk
 66 Raman and TERS spectra of a dipeptide Cys-Phe. The amide I band (1630–1680 cm⁻¹) is a Raman marker of
 67 peptide bonds, which, however, is frequently missing in published SER/TER spectra of peptides and
 68 proteins. The $\nu(\text{S-S})$ vibration of Cys-Phe at 500 cm⁻¹ (marked with an asterisk *) in the bulk Raman
 69 spectrum is also absent in the TER spectrum, but for a different reason – cleavage of the disulfide bonds
 70 upon binding of the peptide to the Au surface through formation of Au-S bonds. (C) The amide I vibrational
 71 mode consists mostly of the C=O stretching vibration in the peptide bond, with contributions from the C-N
 72 stretch and the C-C-N deformation.

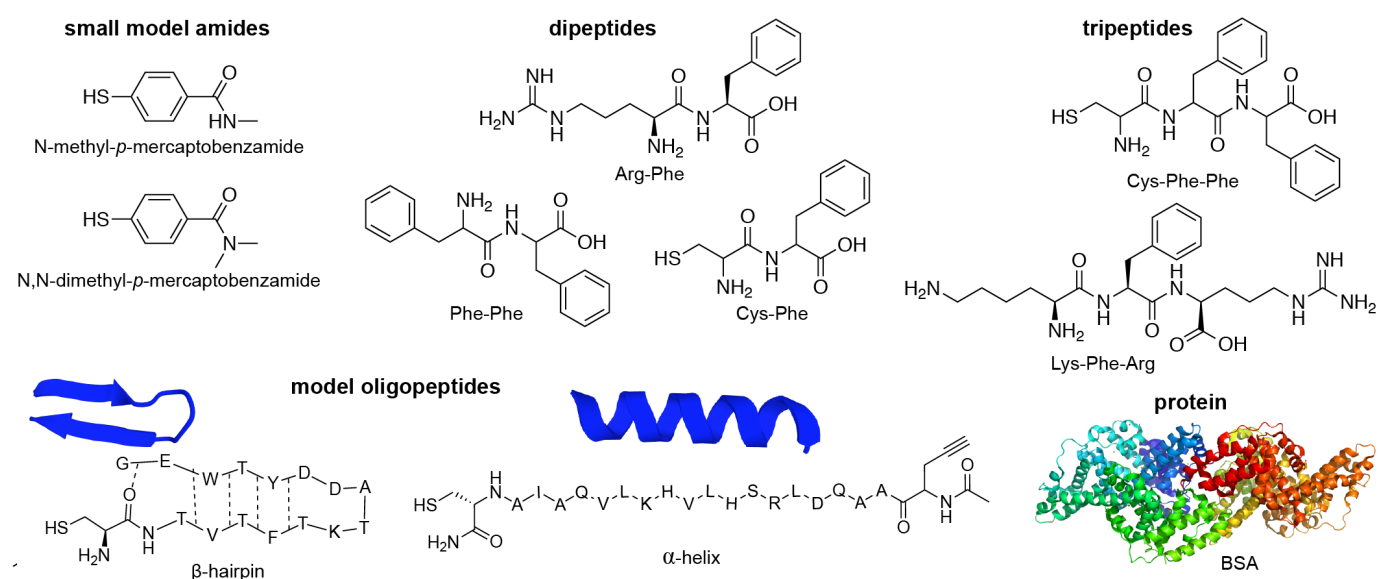
73 The discrepancy between bulk Raman and TERS spectra of peptides is problematic and
 74 raises questions regarding the reliability of peak assignments in TERS. In order to address
 75 these issues, SERS researchers have developed means to improve the reproducibility of
 76 the spectra of proteins, including pre-cleaning the surface of the SERS substrates^[37,38],
 77 reducing the interaction time between the protein and the nanostructure^[39], and coating
 78 the Ag nanoparticles with protective chemical layers^[40–42]. These approaches result in

79 clean spectra of proteins, including data where the amide I band is visible, but similarly
80 clean data sets have not been reported in the TERS literature.

81 Here, we employ TERS to study the reactivity of peptides and proteins in plasmonic hot
82 spots. Contrary to DIET experiments, TERS can be performed in ambient conditions, and
83 thus can accommodate a much broader scope of reactants, including biomolecules.
84 Comparison of TERS with MS/MS fragmentation techniques reveals nonergodic
85 dissociation of proteins and peptides in plasmonic hot spots, which allows us to propose
86 a general description of the underlying plasmon-driven chemistry. Furthermore, we
87 explain the impact of the plasmon-induced reactions on the TER spectra of biomolecules
88 and provide experimental guidelines to avoid sample degradation and maintain
89 consistency with bulk Raman spectra.

90 **Results**

91 In order to understand the reactivity of peptides in plasmonic hot spots, we performed
92 TERS measurements on 10 model compounds containing amide bonds (Fig. 2): two small
93 synthetic amides (<0.2 kDa), five di- and tri-peptides (0.25–0.50 kDa), two oligopeptides
94 composed of 16–20 amino acids (~2 kDa), and a protein with a molecular weight of 66
95 kDa. Thin molecular layers of the samples were prepared on a flat Au surface via self-
96 assembly, spin coating or dried droplet deposition (see Methods). TER spectra were
97 acquired at points on a grid cast over a square region on the sample, like in TERS imaging
98 (Fig. 1A). The large number of systems investigated in this study and the wide range of
99 their sizes enable general conclusions to be drawn on plasmon-induced photochemistry
100 of peptides and proteins. Below, we first describe the disappearance of the amide I band
101 from the TER spectra of peptides, and then we explain the underlying chemistry.

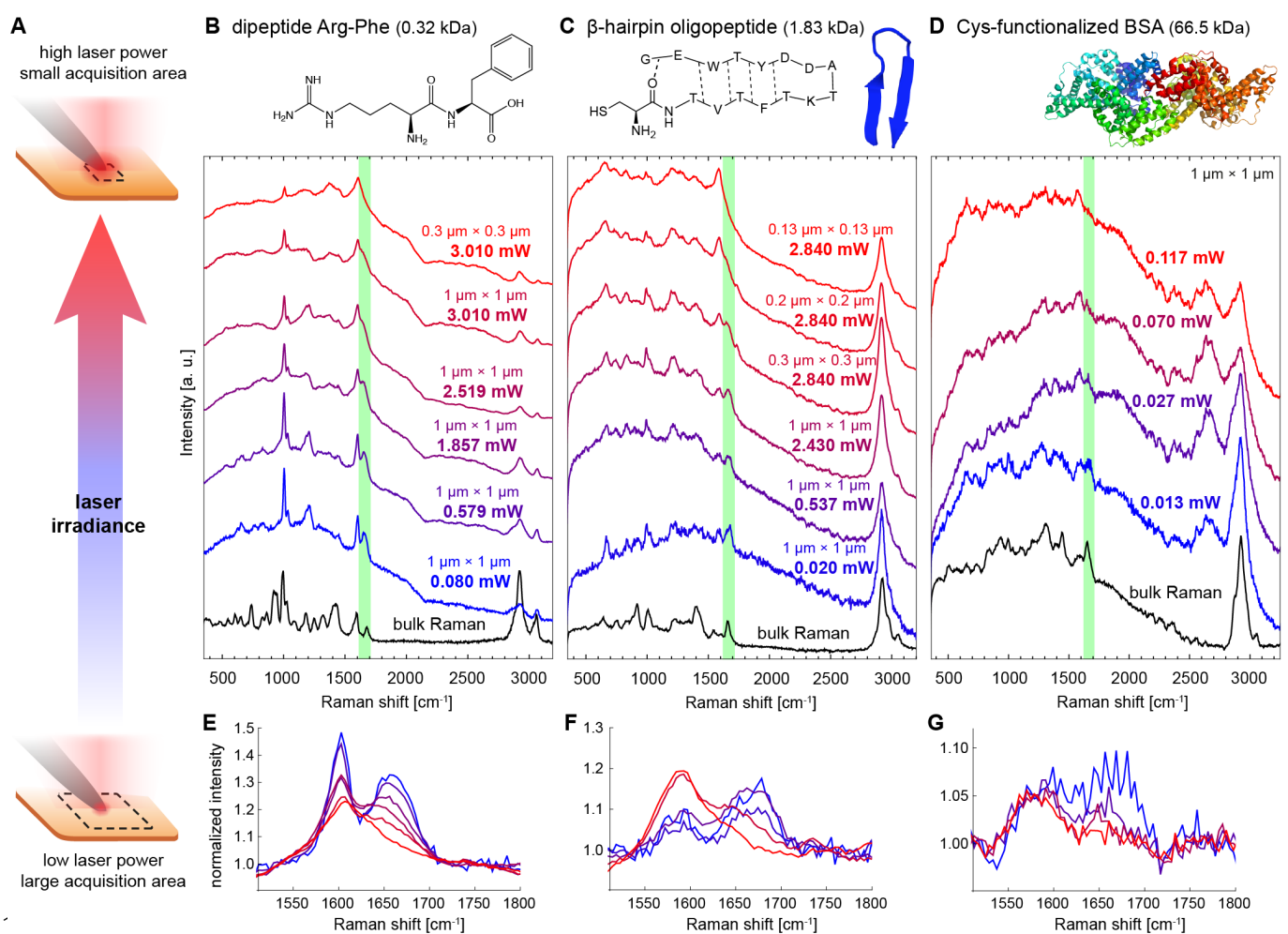


103 **Figure 2.** Amide-containing model compounds used in this study.

104 **Is the amide I band visible in TERS?** Photochemical transformations in plasmonic hot
 105 spots rely primarily on dissociative attachment of plasmon-induced hot electrons to the
 106 molecules under the tip^[5,11]. These charge-driven reactions act in synergy with thermal
 107 excitation^[3,5,11], because electronic transitions are easier to initiate from a vibrationally
 108 excited state. Therefore, we performed TERS measurements tuning both the laser power
 109 (0.007 – 2.840 mW) and the temperature in the hot spot. The temperature under the TERS
 110 tip depends not only on the laser power applied, but also on the size of the TERS image:
 111 the smaller the scan area, the more heat accumulates under the tip, resulting in higher
 112 temperature (for further discussion see Section S2). Hence, the temperature in the hot
 113 spot was controlled partially independent of the laser irradiance, by varying the size of
 114 the scan size (0.13 × 0.13 – 1 × 1 μm^2 squares, see Fig. 3A).

115 Fig. 3 illustrates the disappearance of the amide I band for three peptides of different
 116 sizes: a dipeptide Arg-Phe (Fig. 3B), a β -hairpin oligopeptide with 16 amino acids (Fig.
 117 3C), and the protein bovine serum albumin (BSA, Fig. 3D). Both β -hairpin and BSA were
 118 terminated with Cys residues to facilitate the formation of a monolayer on the Au surface.

119 The spectra depicted in blue in Fig. 3B,C,D were acquired at low laser exposure and
 120 resemble the bulk Raman spectra (black traces) of the same peptides, including the
 121 presence of the amide I band (highlighted in green). Small discrepancies are likely due to
 122 the binding of the peptide to Au through nitrogen, sulfur (see Fig. 1B), or π - π adsorption
 123 of the phenyl ring. Upon increasing the laser exposure (higher power, smaller scan size),
 124 the amide I band gradually disappears, and other symptoms of sample degradation arise
 125 as well.



127 **Figure 3.** Plasmon-induced backbone cleavage in peptides of various sizes. (A) TER spectra were acquired
 128 in imaging mode, similar to Fig. 1A. The laser power and scan size affect the rate of photoinduced sample
 129 degradation in (B) a dipeptide Arg-Phe, (C) a β -hairpin oligopeptide, (D) a Cys-terminated BSA. The amide
 130 I mode (highlighted in green) is visible in the TER spectra acquired at low laser exposure (blue traces).

131 These TER spectra are in reasonable agreement with the bulk Raman spectra of the same molecules (black
132 traces). The amide I band disappears upon increasing the laser irradiance, due to plasmon-induced
133 dissociation of the peptide backbone. The spectra are scaled to fit together in one graph, but not
134 background-corrected. (E, F, G) Zoom into the amide I region of the TER spectra. The background was
135 corrected by dividing of the spectra by the linear baseline fit.

136 Figures S2–S5 show a similar behavior for three other di- and tripeptides and an α -helical
137 oligopeptide with 20 amino acids. In all cases, the amide I band is clearly visible in the
138 spectra acquired at low laser exposure, regardless of the size and the amino acid
139 composition of the peptide. Consequently, the disappearance of the amide I band from the
140 TER spectra of peptides is an artifact, caused by inadequate measurement conditions.
141 More specifically, acquisition of TER spectra results in degradation of the analyte at high
142 laser irradiance and prolonged residence of the tip on a small region of the sample. As
143 shown in our recent work for model thiols^[5], the tip-induced sample degradation is
144 primarily a function of the incident laser irradiance, whereas the irradiation time is of
145 secondary importance.

146 Our findings contradict the hypothesis of steric shielding of the amide bond by bulky
147 amino acid residues proposed by Chumanov *et al.*^[36] and Kurouski *et al.*^[35]. Yet, similar to
148 these authors, we always observe the bands corresponding to the amino acid residues,
149 even if the amide I band is absent (*cf.* hexa-Tyr peptide in ref. ^[35]). We explain this
150 observation by preferential dissociation of the peptide backbone upon attachment of a
151 hot electron, resulting in disappearance of amide I, but not affecting the signal from the
152 side chains. For some amino acids the dissociative electron capture proceeds further and
153 affects the residues at higher laser irradiance – for example, guanidine can be released
154 from the Arg residues in argininamide (Fig. S5) and Lys-Phe-Arg (see below). However,
155 for most amino acids, the dissociation of the residue requires higher energy of the hot

156 electron than the backbone cleavage, so the disappearance of the amide I band is observed
157 first.

158 Surprisingly, the exact position of the amide I band in the TER spectra does not always
159 match the position of its bulk Raman counterpart. This is discussed in detail in the
160 Supporting Information (Section S3).

161 **How does the peptide backbone cleave?** As outlined in the introduction, plasmon-
162 driven reactions are analogous to DIET, a class of electron attachment reactions known
163 from surface science^[5,11]. We hypothesize that photochemical transformations in
164 plasmonic hot spots are also analogous to gas-phase reactions, where a 1–2 eV electron
165 attaches to the molecule and triggers its dissociation. Below we demonstrate that
166 dissociation of peptides under the TERS tip leads to products similar to those observed in
167 electron capture dissociation and ETD of peptides in the gas phase.

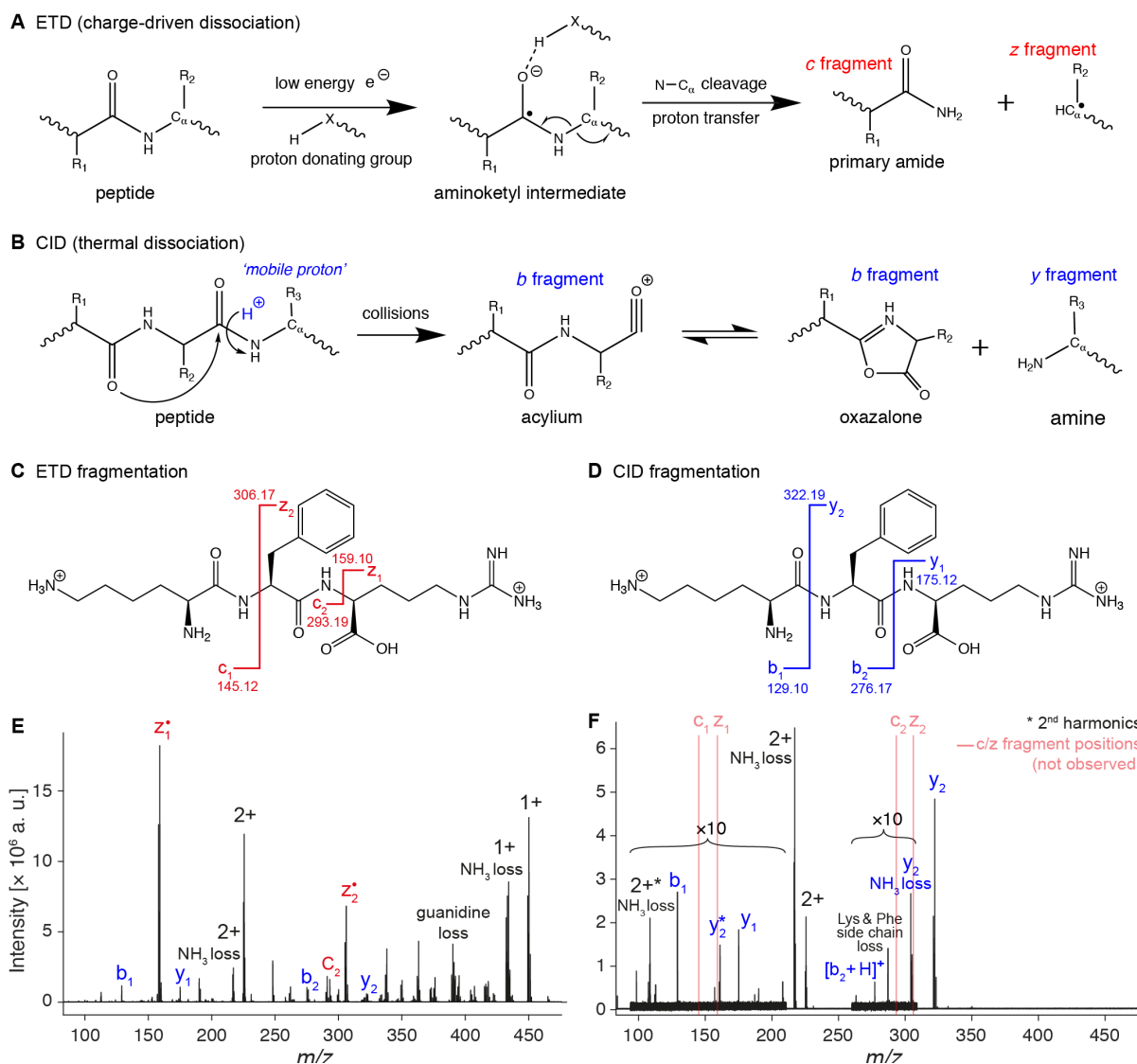
168 In ETD MS, a peptide M under study is gently ionized by electrospray ionization to obtain
169 intact, protonated peptide ions with various charge states $[M + nH]^{n+}$. The desired charge
170 state is mass-selected by removal of all other ions, including fragments formed during
171 ionization and desolvation. The isolated peptide ions are stored in an ion trap and
172 undergo collisions with a negatively charged electron transfer reagent, which donates a
173 low energy (1–2 eV) electron to the peptide. Upon attachment of the electron, the
174 $[M + nH]^{n+}$ cation is reduced to a reactive $[M + nH]^{(n-1)+\bullet}$ radical, which is prone to
175 dissociation via cleavage of the peptide backbone, or of the amino acid residues.
176 Importantly, the capture of a single electron results in a cascade of radical reactions,
177 leading to several backbone cleavages and side chain losses within the same peptide^[43].
178 ETD is frequently employed in MS/MS analysis of proteins, because it allows

179 fragmentation of macromolecules into smaller peptides, which enables sequencing and
180 analysis of post-translational modifications^[44].

181 Similar to DIET reactions^[13], ETD is a nonergodic process resulting in non-thermal
182 fragmentation pathways^[45]. The fragmentation rules are very characteristic to ETD and
183 different from fragmentation techniques that rely on thermal activation of the ion, for
184 example collision-induced dissociation (CID). Typical fragmentation pathways of the
185 peptide backbone in ETD and CID are shown in Fig. 4 A and B, respectively. In ETD of
186 peptides, the low energy electron attaches to the amide π^* system, forming an enol-
187 imidate radical anion^[46]. The radical cleaves the N-C $_{\alpha}$ bond, and the anion is neutralized
188 by proton transfer from a charged or neutral site in the vicinity (typically the residue of a
189 neighbor Arg or Lys). The dissociation leads to the formation of a *c* type fragment, which
190 is a primary amide or the enolimine tautomer (less favored), and of a *z* type fragment,
191 which consists of the C-terminal end of the peptide chain without the N-terminus.

192 In contrast, CID (Fig. 4B) occurs by gradual excitation of the molecule through collisions
193 with a neutral gas. The increasing energy enables conformational and structural
194 rearrangements of the molecule, resulting in higher energy intermediates. The
195 dissociation is initiated by intramolecular proton transfer to the amide oxygen or
196 nitrogen, which destabilizes the amide system. Subsequent cleavage of the weakest bond
197 in the system, namely the amide bond (C-N), leads to the formation of *b* and *y* type
198 fragments, which are a protonated acylium/oxazolone ion and a truncated peptide,
199 respectively. Fig. 4B represents the direct cleavage of the peptide bond, which is typical
200 for high-energy CID^[47]. For lower collision energies (as in the case of this study), *b/y* type
201 fragmentation occurs typically through additional rearrangement reactions. Discussion of

202 the possible rearrangement pathways lies beyond the scope of this paper. The reader is
 203 referred to an excellent review by Paizs *et al.*^[48]



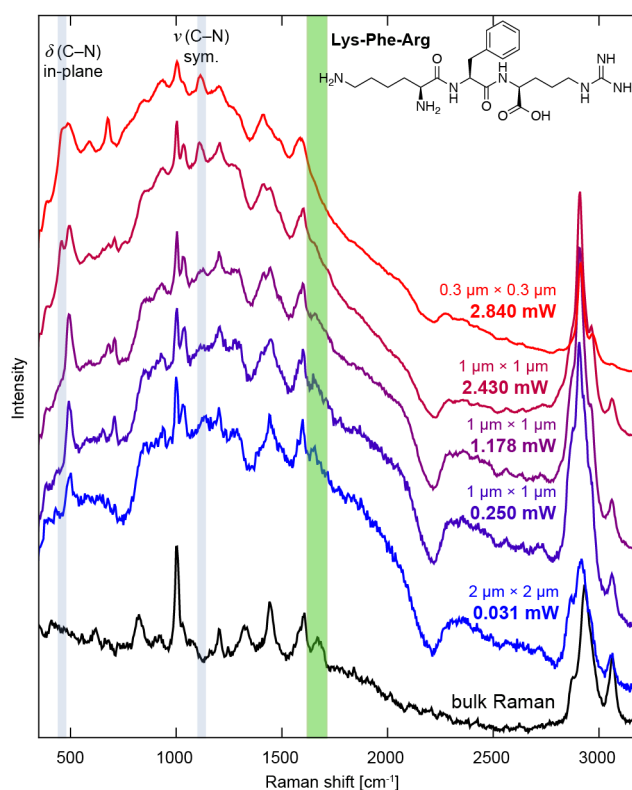
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205 **Figure 4.** ETD vs. CID dissociation of peptides. (A) ETD triggers *c/z* type fragmentation, resulting in
 206 formation of a primary amide (*c* fragment). (B) CID induces *b/y* type fragmentation, which leads to
 207 formation of an acylium ion (*b* ion) that can rearrange to an oxazolone. (C) ETD and (D) CID fragmentation
 208 expected for the model tripeptide Lys–Phe–Arg. (E) The ETD spectrum of Lys–Phe–Arg shows intense *c/z*
 209 peaks and residual *b/y* signals (present because of the long residence time of the ions in the reaction cell).
 210 (F) The CID spectrum of Lys–Phe–Arg shows major *b/y* peaks and no *c/z* fragments. Complete assignment
 211 of the mass spectra is presented in Supporting Tables S2 and S3.

212 In order to directly compare the fragmentation pathways in ETD and TERS, we performed
213 measurements on the same tripeptide Lys–Phe–Arg with both techniques. The sequence
214 was chosen such that: (i) there is a basic residue, Arg and Lys, at either end of the peptide
215 to facilitate the formation of a 2+ charge state, (ii) the middle amino acid is Phe, which
216 increases the Raman cross section of the molecule. The expected ETD and CID
217 fragmentation pathways of Lys–Phe–Arg are presented in Fig. 4 C and D, respectively. Fig.
218 4 E and F show the ETD and CID mass spectra of the peptide, acquired in the same
219 experimental setup. In line with the expected fragmentation pathway (Fig. 4C), the ETD
220 spectrum shows strong *c/z* peaks and very weak *b/y* peaks. The residual *b/y* species are
221 most likely formed by collisions within the reaction cell, due to the elevated pressure
222 during electron transfer. Besides *c/z* type fragmentation, we observed significant loss of
223 NH₃ and guanidine from the residues of Arg and Lys, which is also typical for ETD^[49]. The
224 CID spectrum of Lys–Phe–Arg (Fig. 4F) shows strong *b/y* peaks and no *c/z* peaks,
225 consistent with the pathway shown in Fig. 4D.

226 The TER spectra of Lys–Phe–Arg (Fig. 5) indicate the presence of reactions similar to
227 fragmentation in ETD: (i) the amide I band is clearly visible at low laser irradiance and
228 disappears gradually upon increase of the laser exposure. This is likely due to *c/z* type
229 fragmentation of the peptide backbone, leading to formation of enolamines
230 (thermodynamically disfavored) or primary amides, which are extremely susceptible to
231 photodamage and decay in TERS even at very low laser irradiance (see examples in Fig. S6
232 and S7), (ii) no $\nu(\text{C=O})$ vibrations are observed at 1700 cm⁻¹, which indicates that *b*
233 fragments are not formed – neither acylium, nor oxazolone species (see Fig. 4B), (iii) new
234 bands appear at 455 and 1110 cm⁻¹, indicating loss of guanidine from the Arg residue.
235 These bands arise also in the TER spectra of argininamide (Fig. S6). We attribute them to

236 the in-plane C-N scissoring (455 cm^{-1}) and symmetric C-N stretching (1110 cm^{-1})
237 vibrations of guanidine.



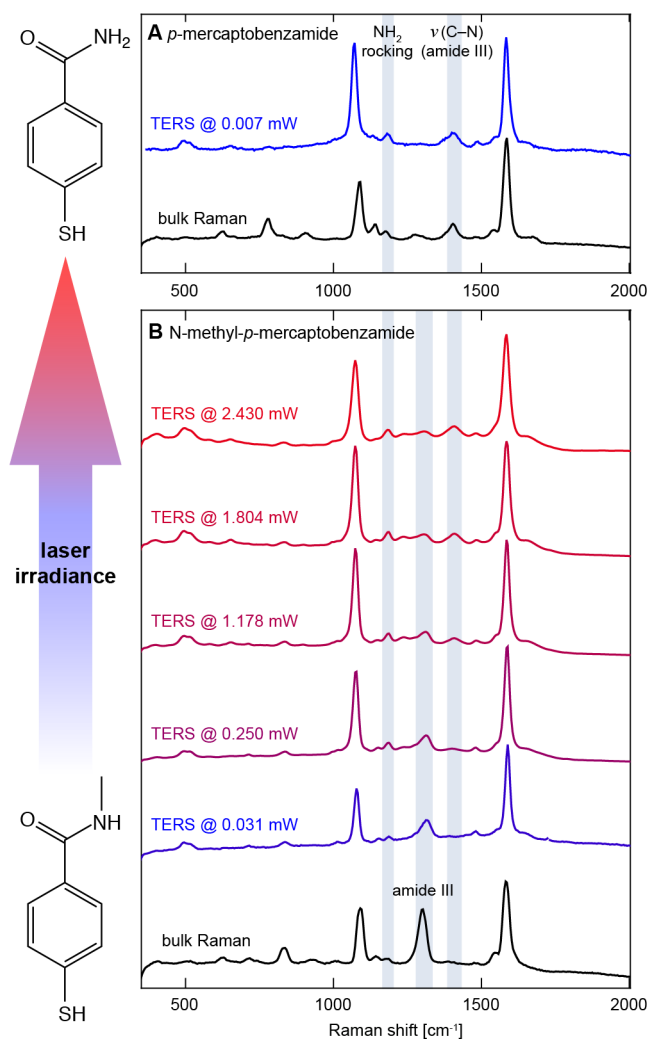
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239 **Figure 5.** Plasmon-induced dissociation of Lys-Phe-Arg. Similar to the peptides shown in Fig. 3, the TER
240 spectrum acquired at low laser irradiance (blue trace) closely resembles the bulk Raman spectrum of the
241 same compound. Upon increasing the laser irradiance, the amide I band gradually disappears, due to *c/z*
242 type dissociation of the peptide backbone. We do not observe any peak at 1700 cm^{-1} , which would indicate
243 the formation of *b* fragments. The new peaks at 455 and 1110 cm^{-1} likely correspond to loss of guanidine,
244 in line with the ETD spectrum shown in Fig. 4E.

245 The $\nu(\text{C=O})$ vibrations of *b* fragments (oxazolone or acylium-derived carbonyl species)
246 are absent not only in the spectra of Lys-Phe-Arg, but also in the spectra of almost all
247 peptides and proteins under study. The single exception is the TER spectrum of the β -
248 hairpin oligopeptide acquired at 2.840 mW (Fig. 3C). It shows a small side band at
249 1705 cm^{-1} for maximum laser irradiance and very high temperature under the tip, due to
250 accumulation of heat on a very small acquisition area ($0.2\text{--}0.3\ \mu\text{m}$). Hence, in this case,

251 thermally driven *b/y* type fragmentation may also occur. Carbonyl vibrations at 1720 cm⁻¹
252 appear also for the tripeptide Cys-Phe-Phe (Fig. S4). In that case, the 1720 cm⁻¹ peak
253 corresponds to the C=O vibration of the carboxyl group on the C-terminus of the peptide,
254 and is observed in both confocal Raman and TER spectra.

255 In order to directly observe the N-C_α dissociation of the amide system, we investigated a
256 small model amide N-methyl-*p*-mercaptobenzamide, whose TER spectrum is simple
257 enough to unambiguously identify the reaction products. Fig. 6B shows a gradual
258 transformation of N-methyl-*p*-mercaptobenzamide into *p*-mercaptobenzamide (Fig. 6A)
259 via plasmon-induced cleavage of the N-C_α bond. Similar to the peptides in Fig. 3 and 5, the
260 TER spectrum acquired at low laser irradiance (blue trace in Fig. 6B) resembles the bulk
261 Raman spectrum of N-methyl-*p*-mercaptobenzamide. The amide I band is very weak in
262 both bulk Raman and TER spectra of this molecule, probably due to the conjugation of the
263 amide system with the benzene ring. Upon increasing the laser power, the amide III band
264 at 1320 cm⁻¹ decreases gradually, and arises at 1410 cm⁻¹ – the amide III band has a
265 different position for primary and secondary amides. At the same time, a new peak arises
266 at 1195 cm⁻¹, indicating the NH₂ rocking vibration of the primary amide. The resulting
267 spectrum looks exactly the same as the TER spectrum of *p*-mercaptobenzamide (blue
268 trace in Fig. 6A), which unambiguously proves *c/z* type fragmentation. A similar
269 experiment was performed for another small amide, N,N-dimethyl-*p*-
270 mercaptobenzamide, and also resulted in preferential scission of the N-C_α bonds (see Fig.
271 S8).



272

273 **Figure 6.** Plasmon-induced N-C α dissociation of the amide system in N-methyl-*p*-mercaptobenzamide.
 274 Upon increasing the laser irradiance, the secondary amide shown in (B) gradually transforms into a primary
 275 amide (A) via *c/z* type fragmentation of the amide bond.

276 For both small amides, the observed reaction is clearly driven by electron capture, not by
 277 thermal excitation. Similar to peptides, thermal activation would lead to dissociation of
 278 the C-N bond (*b/y* type fragmentation), which is the weakest bond in the molecule. This
 279 is illustrated in the CID mass spectra of N-methyl-*p*-mercaptobenzamide and N,N-
 280 dimethyl-*p*-mercaptobenzamide (Fig. S9), where the dominant fragment is the *b* ion at
 281 $m/z = 137$.

282 **Discussion**

283 The similarity between the fragments forming in TERS and ETD supports the idea of an
284 electron-capture-induced and radical-mediated process, brought forward in our recent
285 work^[5]. Furthermore, it might also indicate a similarity of the reaction pathways in ETD
286 and TERS, although we do note that the molecules in ETD are charged, which may affect
287 the energetics of the electron capture and fragmentation process. However, considering
288 the proposed pathway in ETD (Figure 4A), the electron could analogously reside in the π^*
289 orbital of the C=O group, while the protonation might be an intra- or intermolecular
290 process involving acidic functional groups, instead of the protonated base.

291 The N-C $_{\alpha}$ dissociation of the peptide backbone is not the only reaction observed in the
292 reported TERS experiments, likely for two reasons. Firstly, the homolytic *c/z*
293 fragmentation results in the formation of radical *z'* species, which may undergo further
294 charge-driven reactions^[43]. Secondly, similar to ETD, the hot carriers may trigger the loss
295 of amino acid side chains and reactions therein^[49,50]. For example, the capture of a hot
296 electron by the benzyl group leads to a benzyl-centered radical that binds to the aromatic
297 systems of neighboring molecules. This reaction, previously reported for benzyl
298 mercaptan^[5], leads to a decrease in the intensity of the ring breathing modes at 1000 cm⁻¹
299 and to a broadening of the ring stretching bands at 1600 cm⁻¹, as observed in Figures 1B,
300 3B&C and 5.

301 At the same time, the presented data does not allow the estimation of the reaction yield.
302 In particular, the backbone fragmentation may involve less than 100% of the peptide
303 bonds present in the sample, leading to a residual intensity of the amide I band in the TER
304 spectra, or to the presence of a side shoulder (see Figures S2-S5). Accordingly, we do not

305 claim that the amide I band disappears completely from the spectra of all the peptides
306 measured. Instead, we notice that the TER spectra acquired at non-destructive, mild
307 conditions (blue traces in Figs. 3, 5, S2–S5) include a well-resolved amide I peak, similar
308 to the bulk Raman spectra of the same peptides (black traces), and contrary to the spectra
309 acquired at high laser irradiance (red traces). The lack of a well-resolved amide I band in
310 the TER spectra of proteins and peptides is a landmark of photoinduced sample
311 degradation. Such spectra may no longer reflect the native structure of the protein and
312 should not be interpreted, nevertheless they are frequently presented in the TERS
313 literature (see Table S1).

314 The spectral changes described in this paper are clearly a result of charge-driven
315 reactions and cannot be explained by a thermal mechanism. In particular, thermal
316 broadening of the TER spectral lines, which could possibly lead to merging of neighboring
317 peaks, is very small ($3\text{--}5\text{ cm}^{-1}$) for the temperature range investigated in this study. See
318 Section S6 for a detailed discussion.

319 The presented analogy between gas-phase reactions and ambient TERS has its
320 limitations. ETD and CID MS are carried out in vacuum, whereas TERS is typically
321 conducted in ambient conditions, with high availability of water and oxygen at the
322 reaction site. Hence, the reactive species forming upon the dissociation may lead to
323 different final products in MS and TERS experiments. For example, the acylium *b* ion
324 formed in CID of peptides, tautomerizes to an oxazolone structure in the gas phase (Fig.
325 4B)^[51,52], whereas at ambient conditions a truncated amino acid could be formed by the
326 addition of water. Oxygen and traces of water are generally present in ambient conditions
327 and may thus play a role in TERS. An extreme example is the disappearance of the amide
328 I band in the SER spectra of BSA upon treatment with H₂O₂, observed by Xu *et al.* ^[40]. In

329 that case, the HO• radical likely abstracts hydrogen from the α-carbon site, which
330 eventually results in the formation of either an α-ketoamide or imide^[53] by subsequent
331 reactions with oxygen and water. Despite the fact that oxygen and hydroxyl radicals may
332 be formed during the TERS process, we did not observe any of evidence for the expected
333 products in the present study. This renders a HO•-mediated degradation pathway
334 unlikely to be the dominant reason for the disappearance of the amide I band in ambient
335 TERS.

336 **Conclusions**

337 We demonstrated that plasmon-induced hot electrons can dissociate peptides, and
338 postulate that the underlying chemistry is analogous to the one known from the gas-
339 phase studies of low energy electron attachment. Our findings are consistent for a
340 comprehensive selection of model systems (10 molecules of various sizes). The identity
341 of fragments produced in ETD and plasmon-driven photocatalysis suggests that
342 intuitions from the gas-phase electron capture can be transferred at least partially to
343 plasmon-assisted catalysis on noble metal nanoparticles. Literature on dissociative
344 electron capture in the gas phase covers a broad scope of reactants, including
345 biomolecules – beyond small molecules and model thiols used in plasmon-assisted
346 catalysis. We postulate that the nonergodic chemical transformations known from the
347 electron attachment literature may be triggered by plasmonic nanostructures. These
348 pathways can be activated only by hot carriers (not by phonons), hence they are
349 considered ‘impossible’ within the framework of conventional (thermally activated)
350 catalysis. Performing these reactions at ambient pressure and room temperature would
351 be a valuable addition to the toolbox of chemical synthesis.

352 At the same time, these results resolve a long-lasting controversy in plasmonically
353 enhanced Raman experiments of peptides and proteins. We show that the disappearance
354 of the amide I band is caused by excessive energy deposition on the sample and is a sign
355 of peptide backbone degradation. Mild excitation (low laser power and short irradiation)
356 permits the acquisition of reliable TER spectra containing the amide I band.

357 To conclude, we postulate that TER spectra that include unexpected peaks and have little
358 in common with the corresponding Raman spectra should be critically appraised. Such
359 spectral changes are probably caused by some interesting chemistry occurring under the
360 TERS tip, which can now be predicted using the theoretical framework of DIET and ETD.
361 At the same time, we demonstrate that the reproducibility of TER spectra can be
362 dramatically improved by using mild measurement conditions (see Fig. S10), making
363 TERS a more reliable and reproducible analytical technique.

364 **Methods**

365 **TERS measurements.** TERS measurements were conducted similar to the previous work
366 by our group^[5,54,55]. Briefly, we performed top-illumination TERS with Ag tips and Au
367 substrates (gap mode). We used a scanning tunneling microscope (STM; Ntegra Spectra
368 Upright, NT-MDT), equipped with a 0.7 NA 100× objective (Mitutoyo), coupled to a
369 Raman spectrometer (Solar T-II, NT-MDT) with a CCD (Newton 971 UVB, Andor)
370 thermoelectrically cooled to -85 °C.

371 The STM was operated in constant current mode. In principle, the tunneling electrons
372 could induce similar reactions as the plasmon-induced hot carriers, similar as in inelastic
373 electron tunneling spectroscopy^[10,56]. However, such reactions can occur only if the
374 energy of the tunneling electron (*i. e.* the bias voltage) matches the energy of the

375 unoccupied orbitals of the molecular adsorbates. For organic molecules, this energy
376 typically exceeds 0.5 V. Therefore, we used a low bias voltage (0.1 V applied to the sample)
377 to avoid injection of tunneling electrons into the investigated molecules.

378 TERS tips were obtained by electrochemical etching, according to the procedure
379 described in ref. [57]. TER spectra were acquired on square grids with 100–400 pixels
380 (from 10×10 to 20×20 pixels), with laser illumination at 632.8 nm (HeNe laser) and
381 laser power between 0.007 and 2.880 mW. The integration time was 1–3 s. The TER
382 spectra presented in Fig. 1, 3, 5, 6, S2–S8 and S10–S11 are average spectra accumulated
383 over grids of pixels.

384 **Confocal Raman measurements.** Confocal Raman spectra of bulk samples were
385 obtained using the same instrument as TER spectra. The laser power was 2.88 mW and
386 the integration time was 60 s.

387 **Substrates.** Template–stripped Au substrates were prepared according to the protocol in
388 ref. [58,59]. Briefly, a Si wafer (SSP, Siegert Wafer) was pre-cleaned by soaking in a piranha
389 solution ($\text{H}_2\text{SO}_4 : \text{H}_2\text{O}_2$ 30%, 7 : 3 v/v) for 30 minutes, rinsed with Milli–Q water and dried
390 under a N_2 stream. Next, 150 nm of Au (99.99%, Acros) were thermally evaporated
391 (BAL–TEC MCS 010) on the clean Si wafer at a deposition rate of 0.05–0.10 nm/s, under
392 a pressure of 1×10^{-6} mbar. Glass substrates (25 mm x 7 mm x 1 mm) were attached onto
393 the Au layer using the Norland Optical Adhesive No. 61. The glue was cured by 20 minutes
394 of UV irradiation and overnight heating to 50 °C. The glass substrates were stripped off
395 the Si wafer directly before the sample preparation, revealing a flat and clean Au surface
396 on the glass support.

397 **Samples.** Thin layers of peptides were formed on the Au surface using three methods:

- 398 • self-assembly for all molecules including -SH groups (overnight incubation of the
399 substrate in a solution of the amide/peptide/protein; 1 mM ethanolic solution for
400 N-methyl-*p*-mercaptobenzamide, N,N-dimethyl-*p*-mercaptobenzamide and *p*-
401 mercaptobenzamide, Cys-Phe, Cys-Phe-Phe; 100 µg/mL aqueous solution for
402 the α -helical and β -hairpin peptides, and for the Cys-terminated BSA),
- 403 • dried-droplet deposition for molecules without -SH groups (40 µL of 1 mM
404 solution in water, dried in a desiccator at 15 mbar for Arg-Phe and Phe-Phe) -
405 the TERS measurements were conducted in the center of the dried-droplet ring,
406 where the sample was evenly distributed at a low coverage,
- 407 • spin coating for Lys-Phe-Arg, because it formed large crystals upon dried droplet
408 deposition (40 µL of 1 mM of solution was casted on the substrate spinning at 750
409 rpm for 1 min).

410 N-methyl-*p*-mercaptobenzamide, N,N-dimethyl-*p*-mercaptobenzamide and *p*-
411 mercaptobenzamide were purchased from Chemspace (Riga, Latvia; synthesis by FCH
412 Group, Kiev, Ukraine). Arg-Phe (> 99%) was obtained from Bachem. Phe-Phe (\geq 98%)
413 and L-argininamide dihydrochloride (\geq 98%) were purchased from Aldrich. Cys-Phe (\geq
414 98%) and Cys-Phe-Phe (\geq 98%) were acquired from CanPeptide (Montréal, Canada). 3-
415 phenylpropionamide (97%) was obtained from ABCR. Lys-Phe-Arg (97.6%), α -helical
416 (94.5%) and β -hairpin (92.6%) peptides were purchased from GenScript (Piscataway,
417 NJ). Cys-modified BSA (> 98%) was obtained from ProteinMods (Madison, WI).

418 **ETD and CID measurements.** ETD and CID experiments were performed on a Bruker
419 solariX (Bruker Daltonics GmbH, Bremen, Germany) Fourier-transform ion cyclotron
420 resonance mass spectrometer. Molecular ions of the tripeptide Lys-Phe-Arg were
421 generated by electrospray ionization, and the doubly protonated species ($m/z=225.64$)

422 was isolated. ETD experiments were carried out using methane radical anions as transfer
423 reagent and reaction times of 400 ms. Radical anions were generated by chemical
424 ionization within the instrument. Additionally, CID experiments were conducted on the
425 doubly charged peptide ion for comparison. Collision energies of 3.0 eV were employed.

426 Complete peak assignments of the ETD and CID spectra of Lys–Phe–Arg are presented in
427 Tables S2 and S3. We note that the sample obtained was contaminated with a C-
428 terminally amidated derivative of the tripeptide (Lys–Phe–Arg–NH₂). Thanks to the
429 excellent mass resolution of the FTICR analyser, we could discriminate between the amide
430 (M₂) and the free acid (M₁) and assign the peaks for both forms. The fragment ions *c* and
431 *y* always lose an additional hydrogen atom during fragmentation (see mechanism above),
432 which is included in the peak assignment without further comment.

433 **3D peptide structures.** The 3D structures of the α -helical and β -hairpin peptides shown
434 in Fig. 2 were obtained using PEP-FOLD3 software^[60], freely accessible online at
435 <http://bioserv.rpbs.univ-paris-diderot.fr/services/PEP-FOLD3/>.

436 **Supporting Information**

437 Supporting information available: summary of the presence/absence of the amide I band
438 in the TERS literature, effect of the size of the TERS image on the hot spot temperature,
439 comparison of the position of the amide I band in bulk Raman and TER spectra, TERS
440 measurements of Phe–Phe, Cys–Phe, Cys–Phe–Phe, the α -helical peptide, N,N-dimethyl-
441 *p*-mercaptobenzamide, argininamide and 3-phenylpropionamide, CID MS of N-methyl-
442 *p*-mercaptobenzamide and N,N-dimethyl-*p*-mercaptobenzamide, peak assignment of
443 the ETD and CID spectra of Lys–Phe–Arg, TER spectra of Arg–Phe acquired with five
444 different tips, quantification of thermal broadening of TER spectral lines.

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451 **Author Contributions**

452 J. S. conceived the project, performed the TERS experiments and wrote the first
453 manuscript. J. B. M. designed the MS experiments and interpreted their results. All authors
454 interpreted the TERS results, selected the model compounds and corrected the manuscript.

455 **Data Availability**

456 The data used in this publication are freely accessible from a curated data archive at ETH
457 Zurich (<https://www.research-collection.ethz.ch>) under the DOI ...

458 **Note**

459 The authors declare no competing financial interest.

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