Analyst

Ionization characteristics of amino acids in direct analysis in real time mass spectrometry

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Electronic Supplementary Material



Figure S1. (a) Positive- and (b) negative-ion DART mass spectra of glycine (Gly; Mr 75). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S2. (a) Positive- and (b) negative-ion DART mass spectra of L-alanine (Ala; Mr 89). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S3. (a) Positive- and (b) negative-ion DART mass spectra of L-valine (Val; Mr 117). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S4. (a) Positive- and (b) negative-ion DART mass spectra of L-leucine (Leu; Mr 131). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S5. (a) Positive- and (b) negative-ion DART mass spectra of L-isoleucine (Ile; Mr 131). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S6. (a) Positive- and (b) negative-ion DART mass spectra of L-serine (Ser; Mr 105). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S7. (a) Positive- and (b) negative-ion DART mass spectra of L-threonine (Thr; Mr 119). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S8. (a) Positive- and (b) negative-ion DART mass spectra of L-glutamine (Gln; Mr 146). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S9. (a) Positive- and (b) negative-ion DART mass spectra of L-lysine (Lys; Mr 146). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S10. (a) Positive- and (b) negative-ion DART mass spectra of L-aspartic acid (Asp; Mr 133). $A_{\rm BP}$ represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S11. (a) Positive- and (b) negative-ion DART mass spectra of L-methionine (Met; Mr 149). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S12. (a) Positive- and (b) negative-ion DART mass spectra of L-cysteine (Cys; Mr 121). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S13. (a) Positive- and (b) negative-ion DART mass spectra of L-phenylalanine (Phe; Mr 165). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S14. (a) Positive- and (b) negative-ion DART mass spectra of L-proline (Pro; Mr 115). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S15. (a) Positive- and (b) negative-ion DART mass spectra of L-tryptophane (Trp; Mr 204). $A_{\rm BP}$ represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.



Figure S16. (a) Positive- and (b) negative-ion DART mass spectra of L-histidine (His; Mr 155). A_{BP} represents the absolute abundance (arbitrary units) of the base peak in each mass spectrum.

Table S1. Absolute abundances of deprotonated analytes $[M - H]^-$ (M: Gly, Val, Asp and Phe) obtained under ambient air condition and N_2 atmosphere condition in the closed analyte ionization area.

Absolute abundan	ces of [M - H] ⁻ [arb.]	
Ambient air condition	N ₂ atmosphere condition	
1.54×10^{4}	1.61×10^{3}	
1.99 × 10 ⁵	4.43×10^{4}	
2.12×10^{4}	$2.05 imes 10^4$	
1.31 × 10 ⁵	2.98×10^{4}	
	Absolute abundanAmbient air condition 1.54×10^4 1.99×10^5 2.12×10^4 1.31×10^5	