**Table S1 Free amino acid content of straw mushroom enzymatic digest**

|  |  |  |  |
| --- | --- | --- | --- |
| **Amino acids** | **Content（mg/ml）** | | |
| **Monoenzyme** | **Dual Enzyme** | **Trienzyme** |
| Asp | 0.0862±0.01b | 0.0856±0.02b | 0.1091±0.01a |
| Glu | 0.4301±0.02c | 0.4412±0.01b | 0.5425±0.03a |
| Ser | 0.0310±0.01b | 0.0290±0.02c | 0.0422±0.01a |
| His | 0.0467±0.01a | 0.0412±0.01a | 0.0550±0.01b |
| Gly | 0.0503±0.01c | 0.0547±0.01b | 0.0604±0.01a |
| Thr | 0.1695±0.01b | 0.1567±0.01b | 0.1871±0.01a |
| Arg | 0.2386±0.02b | 0.2113±0.01b | 0.2574±0.01a |
| Ala | 0.2208±0.01a | 0.2124±0.01a | 0.2590±0.01a |
| Tyr | 0.1561±0.01b | 0.1401±0.01c | 0.1580±0.01a |
| Cys | 0.0084±0.01a | 0.0020±0.01b | 0.0151±0.01a |
| Val | 0.1494±0.01a | 0.1373±0.01c | 0.1624±0.01b |
| Met | 0.0449±0.01a | 0.0177±0.02b | 0.0295±0.01b |
| Phe | 0.2013±0.01a | 0.1523±0.01b | 0.1777±0.01a |
| Ile | 0.1624±0.02a | 0.1410±0.01a | 0.1688±0.02a |
| Leu | 0.2887±0.03a | 0.1778±0.01b | 0.2106±0.01a |
| Lys | 0.2185±0.01b | 0.1992±0.01b | 0.2393±0.01a |
| Pro | 0.0498±0.01b | 0.0568±0.01b | 0.0635±0.01a |
| Total | 2.5526±0.02 b | 2.2563±0.06 c | 2.7377±0.05 a |

Note: Using a one-way ANOVA, the same letter of the marker indicates that there is no statistical difference between the amounts of free amino acids obtained using different enzymatic methods (p>0.05).

**Table S2 Results of the peptide molecular weight distribution**

|  |  |  |  |
| --- | --- | --- | --- |
| **Peptide molecular mass/Da** | **Mass fraction /%** | | |
| **Monoenzyme** | **Dual Enzyme** | **Trienzyme** |
| <500 | 85.70±0.02c | 86.33±0.03b | 87.01±0.02a |
| 500-1000 | 8.77±0.02a | 8.54±0.01b | 8.69±0.02c |
| 1000-3000 | 4.33±0.01c | 4.08±0.01b | 3.31±0.02a |
| >3000 | 1.19±0.01c | 1.06±0.01b | 0.99±0.02a |

Note: Using one-way ANOVA, the different letters of the markers indicate statistical differences in the content of peptides of different molecular weights obtained using different enzymatic digestion methods (p>0.05).

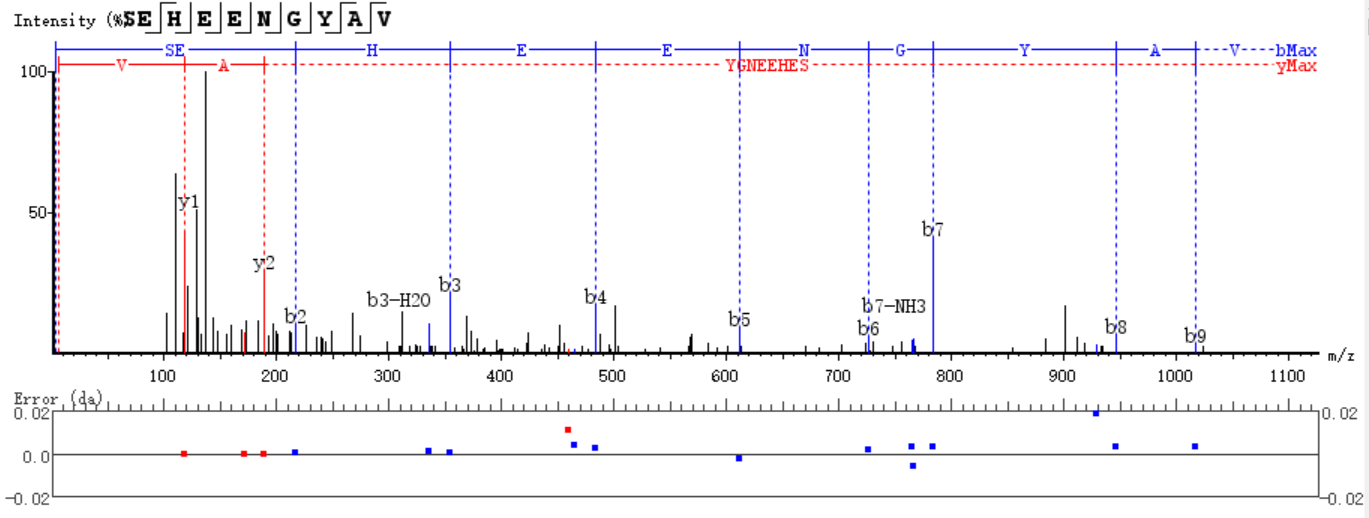
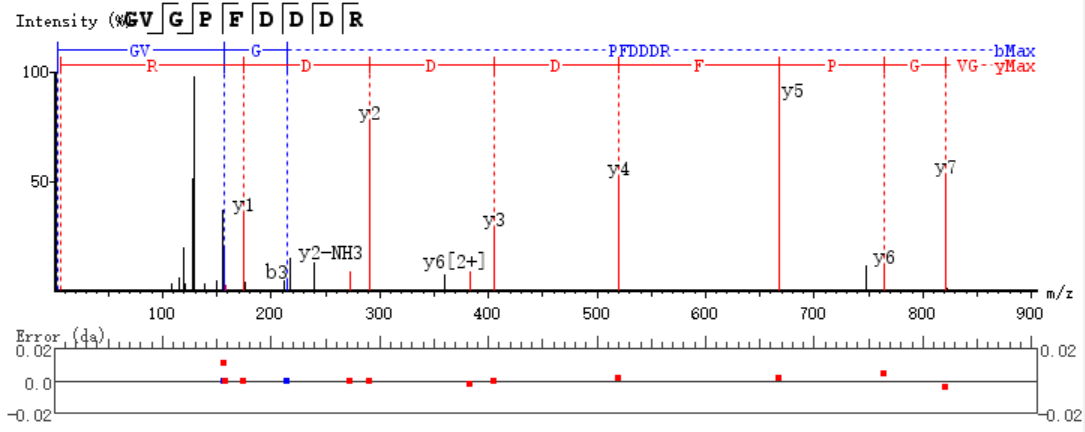
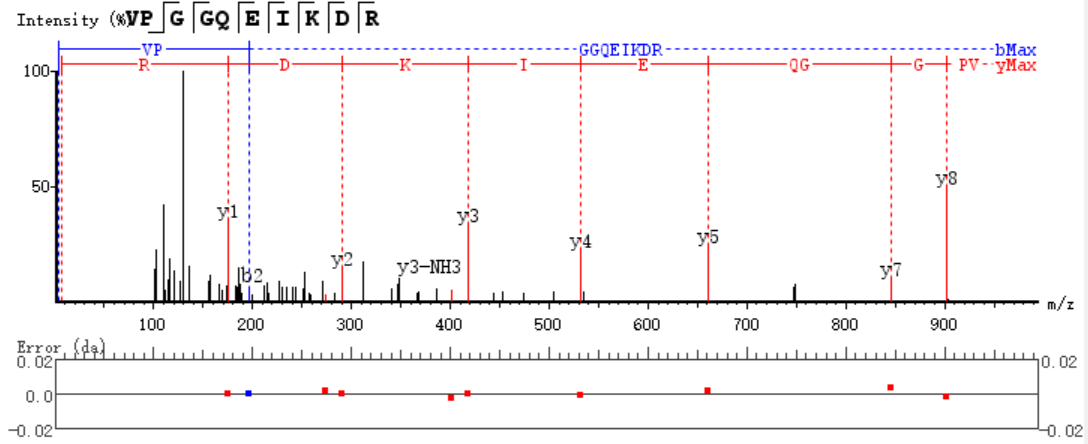
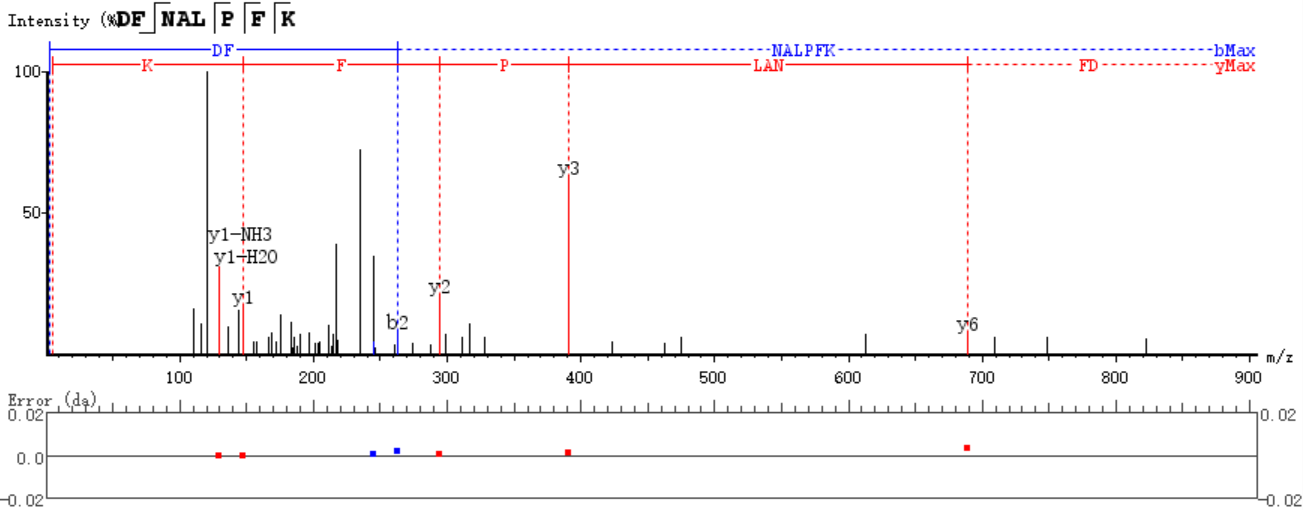
**Table S3 The parameters of the power functions and the relationship between the natural logarithmic salt concentration and the natural logarithmic intensity of saltiness.**

|  |  |  |  |
| --- | --- | --- | --- |
| Control | A1 | A2 | A3 |
| y=1.21483x+0.682 | y=1.0736x+1.06555 | y=0.9207x+1.47065 | y=1.04752x+1.15109 |
|
| （R²=0.95546） | （R²=0.97125） | （R²=0.98241） | （R²=0.97629） |

**Table S4 The dose-response relationship of three synthetic peptides on saltiness intensity of 0.5g/L NaCl solution**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| VP10+0.5g/L NaCl | | YN9+0.5g/L NaCl | | DF8+0.5g/L NaCl | |
| VP10  (mM) | saltiness intensity | YN9  (mM) | saltiness intensity | DF8  (mM) | saltiness intensity |
| 0 | 1 | 0 | 1 | 0 | 1 |
| 0.2 | 2.0±0.1b | 0.2 | 1.5±0.1a | 0.2 | 7.5±0.3b |
| 0.4 | 4.5±0.1b | 0.4 | 2.5±0.3a | 0.4 | 8.0±0.4c |
| 0.8 | 6.5±0.3b | 0.8 | 5.0±0.1a | 0.8 | 8.5±0.6c |
| 1.6 | 7.8±0.4c | 1.6 | 6.5±0.1a | 1.6 | 7.0±0.4b |
| 3.2 | 8.0±0.2c | 3.2 | 1.2±0.3a | 3.2 | 2.5±0.5b |

Note: Using one-way ANOVA, the different letters of the markers indicate statistical differences in the content of peptides of different molecular weights obtained using different enzymatic digestion methods (p>0.05).



**Figure S1.** MS/MS spectra of DFNALPFK (m/z 574.25, A), VPGGQEIKDR (m/z 366.87, B), GVGPFDDDR (m/z 489.22, C), SEHEENGYAV (m/z 567.75, D), YNEDNGIVK (m/z 526.26, E), IDNEPEFRWA (m/z 638.81, F), DKLHEGIK (m/z 313.85, G), and IGDEAAENRN (m/z 544.75, H). The y and b ions refer to fragment ions of each peptide.

