Supplementary Data

Comparison of taste mechanism of umami and bitter peptide from fermented mandarin fish (*Chouguiyu*) based on molecular docking and electronic tongue technology

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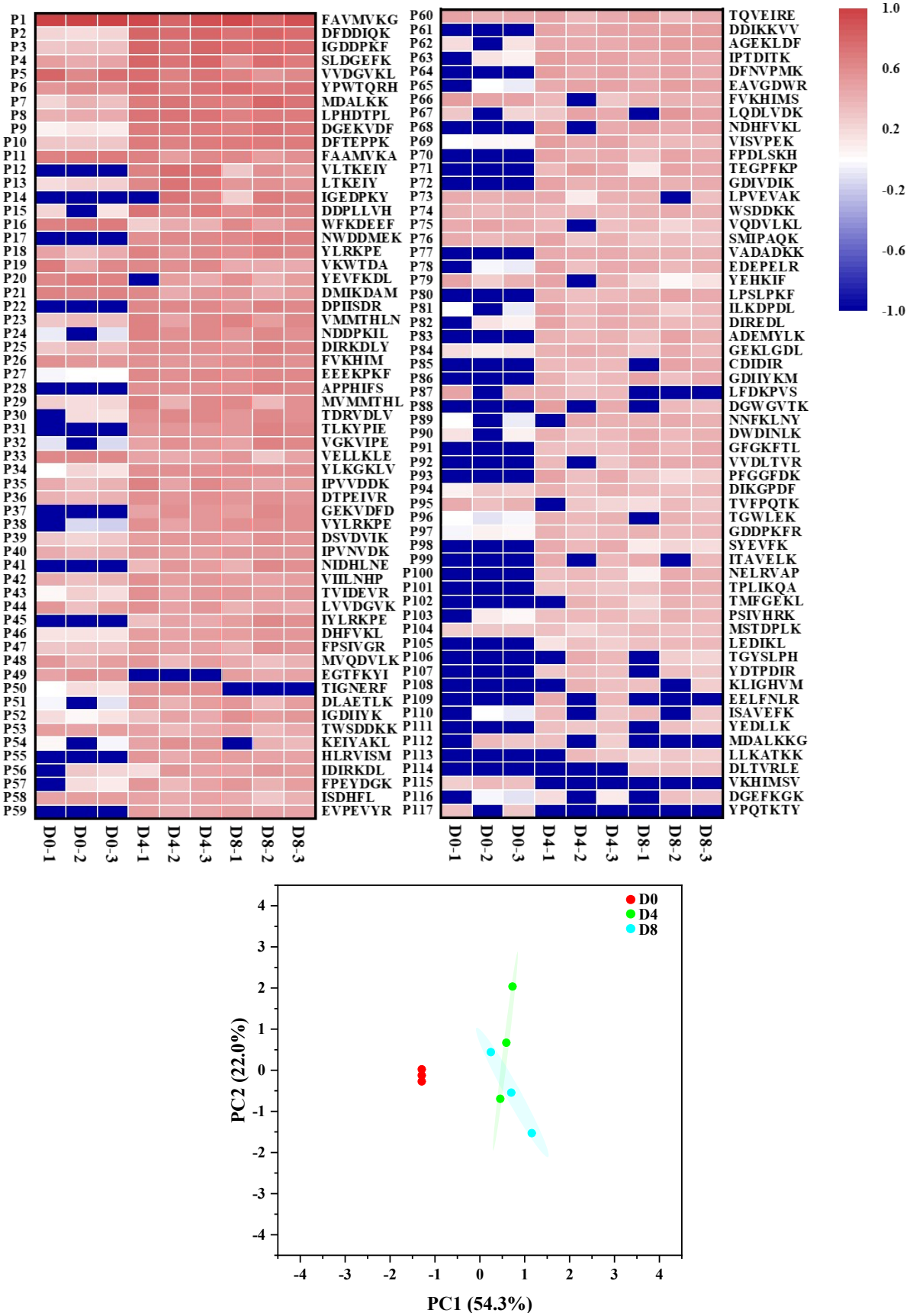


Fig. S1. Abundance heatmap and principal component analysis of 117 oligopeptides at different fermentation time in *Chouguiyu.*

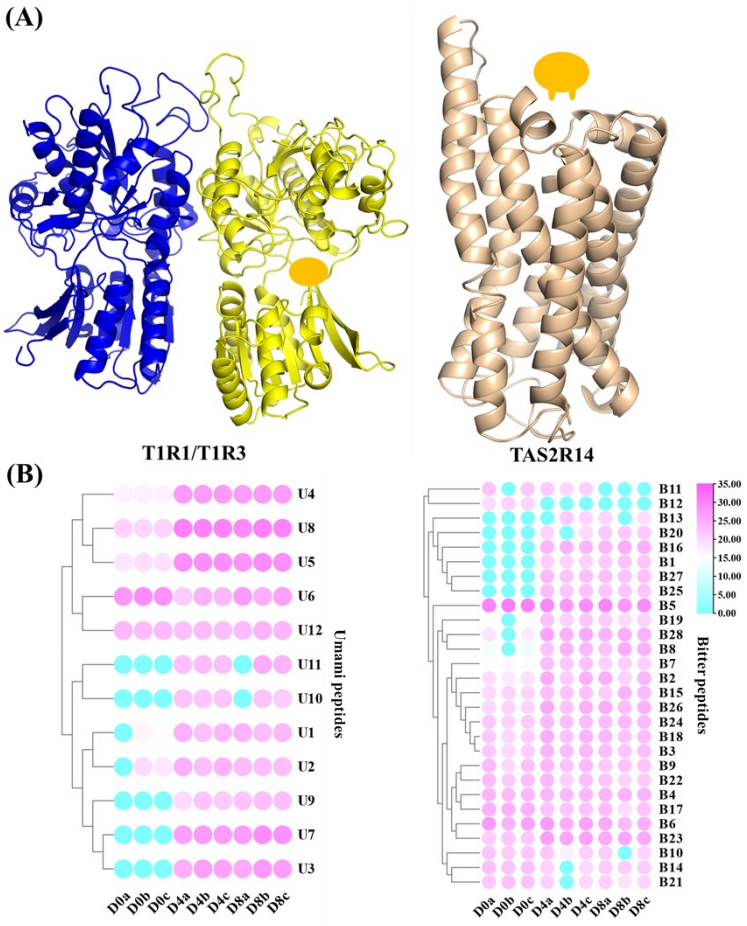


Fig. S2. Identification of different taste peptides from *Chouguiyu*. (A) Three-dimensional structure of umami (T1R1/T1R3) and bitter (TAS2R14) taste receptors constructed by homologous simulation and their tentative binding sites. (B) Abundance heatmaps of umami and bitter peptides at different fermentation time.

Table S1 Sequence and taste classification of 117 peptides from *Chouguiyu*

Peptide number	Peptide sequence	Amino acids	Bitter AAs (%)	Umami AAs (%)	Label
P1	FAVMVKG	7	57.14	0	B5
P2	DFDDIQK	7	28.57	42.86	U8
P3	IGDDPKF	7	42.86	28.57	-
P4	SLDGEFK	7	28.57	28.57	-
P5	VVDGVKL	7	57.14	14.29	B6
P6	YPWTQRH	7	28.57	0	-
P7	MDALKK	6	33.33	16.67	-
P8	LPHDTPL	7	57.14	14.29	B23
P9	DGEKVDF	7	28.57	42.86	U5
P10	DFTEPPK	7	42.86	28.57	-
P11	FAAMVKA	7	42.86	0	-
P12	VLTKEIY	7	42.86	14.29	-
P13	LTKEIY	6	33.33	16.67	-
P14	IGEDPKY	7	28.57	28.57	-
P15	DDPLLVH	7	57.14	28.57	B28
P16	WFKDEEF	7	42.86	42.86	U6
P17	NWDDMEK	7	28.57	42.86	U7
P18	YLRKPE	6	33.33	16.67	-
P19	VKWTDA	6	33.33	16.67	-
P20	YEVFKDL	7	42.86	28.57	-
P21	DMIKDAM	7	42.86	28.57	-
P22	DPIISDR	7	42.86	28.57	-
P23	VMMTHLN	7	57.14	0	B26
P24	NDDPKIL	7	42.86	28.57	-
P25	DIRKDLY	7	28.57	28.57	-
P26	FVKHIM	6	66.67	0	B4
P27	EEEKPKF	7	28.57	42.86	U4
P28	APPHIFS	7	57.14	0	B16
P29	MVMMTHL	7	71.43	0	B2
P30	TDRVDLV	7	42.86	28.57	-
P31	TLKYPIE	7	42.86	14.29	-
P32	VGKVIPE	7	57.14	14.29	B8
P33	VELLKLE	7	57.14	28.57	B17
P34	YLKGKLV	7	42.86	0	-
P35	IPVVDDK	7	57.14	28.57	B18
P36	DTPEIVR	7	42.86	28.57	-
P37	GEKVDFD	7	28.57	42.86	U3
P38	VYLRKPE	7	42.86	14.29	-
P39	DSVDVIK	7	42.86	28.57	-
P40	IPVNVDK	7	57.14	14.29	B24
P41	NIDHLNE	7	28.57	28.57	-
P42	VIILNHP	7	71.43	0	B3
P43	TVIDEVR	7	42.86	28.57	-
P44	LVVDGVK	7	57.14	14.29	B9
P45	IYLRKPE	7	42.86	14.29	-
P46	DHFVKL	6	50	16.67	-
P47	FPSIVGR	7	57.14	0	B15
P48	MVQDVLK	7	57.14	14.29	B22
P49	EGTFKYI	7	28.57	14.29	-
P50	TIGNERF	7	28.57	14.29	-
P51	DLAETLK	7	28.57	28.57	-
P52	IGDIIYK	7	42.86	14.29	-
P53	TWSDDKK	7	14.29	28.57	-
P54	KEIYAKL	7	28.57	14.29	-

P55	HLRVISM	7	57.14	0	B27
P56	IDIRKDL	7	42.86	28.57	-
P57	FPEYDGK	7	28.57	28.57	-
P58	ISDHFL	6	50	16.67	-
P59	EVPEVYR	7	42.86	28.57	-
P60	TQVEIRE	7	28.57	28.57	-
P61	DDIKKVV	7	42.86	28.57	-
P62	AGEKLDF	7	28.57	28.57	-
P63	IPTDITK	7	42.86	14.29	-
P64	DFNVPMK	7	57.14	14.29	B25
P65	EAVGDWR	7	28.57	28.57	-
P66	FVKHIMS	7	57.14	0	B14
P67	LQDLVDK	7	42.86	28.57	-
P68	NDHFVKL	7	42.86	14.29	-
P69	VISVPEK	7	57.14	14.29	B7
P70	FPDLSKH	7	42.86	14.29	-
P71	TEGPFKP	7	42.86	14.29	-
P72	GDIVDIK	7	42.86	28.57	-
P73	LPVEVAK	7	57.14	14.29	B10
P74	WSDDKK	6	16.67	33.33	U12
P75	VQDVLKL	7	57.14	14.29	B21
P76	SMIPAQK	7	42.86	0	-
P77	VADADKK	7	14.29	28.57	-
P78	EDEPELR	7	28.57	57.14	U1
P79	YEHKIF	6	33.33	16.67	-
P80	LPSLPKF	7	71.43	0	B1
P81	ILKDPDL	7	57.14	28.57	B19
P82	DIREDL	6	33.33	50	U2
P83	ADEMYLK	7	28.57	28.57	-
P84	GEKLGDL	7	28.57	28.57	-
P85	CDIDIR	6	33.33	33.33	U11
P86	GDIIYKM	7	42.86	14.29	-
P87	LFDKPVS	7	57.14	14.29	B11
P88	DGWGVTK	7	28.57	14.29	-
P89	NNFKLNY	7	28.57	0	-
P90	DWDINLK	7	42.86	28.57	-
P91	GFGKFTL	7	42.86	0	-
P92	VVDLTVR	7	57.14	14.29	B20
P93	PFGGFDK	7	42.86	14.29	-
P94	DIKGPDF	7	42.86	28.57	-
P95	TVFPQTK	7	42.86	0	-
P96	TGWLEK	6	33.33	16.67	-
P97	GDDPKFR	7	28.57	28.57	-
P98	SYEVFK	6	33.33	16.67	-
P99	ITAVELK	7	42.86	14.29	-
P100	NELRVAP	7	42.86	14.29	-
P101	TPLIKQA	7	42.86	0	-
P102	TMFGEKL	7	42.86	14.29	-
P103	PSIVHRK	7	42.86	0	-
P104	MSTDPLK	7	42.86	14.29	-
P105	LEDIKL	6	50	33.33	U9
P106	TGYSLPH	7	28.57	0	-
P107	YDTPDIR	7	28.57	28.57	-
P108	KLIGHVM	7	57.14	0	B13
P109	EELFNLR	7	42.86	28.57	-
P110	ISAVEFK	7	42.86	14.29	-
P111	YEDLLK	6	33.33	33.33	U10
P112	MDALKKG	7	28.57	14.29	-
P113	LLKATKK	7	28.57	0	-

P114	DLTVRLE	7	42.86	28.57	-
P115	VKHIMSV	7	57.14	0	B12
P116	DGEFKGK	7	14.29	28.57	-
P117	YPQTKTY	7	14.29	0	-

Note: Threshold of umami and bitter was >30% and >50%, respectively. Umami peptides and bitter peptides were marked as U and B, respectively

Table S2 Characteristics of peptides with different taste from *Chouguiyu*

Number	Isoelectric point	Molecular weight (Da)	Charge	Toxin	Hydrophobicity(kcal/mol)	Hydropathicity	Hydrophilicity
U1	4.00	887.00	-3.00	Non	23.13	-2.33	1.89
U2	4.03	759.89	-2.00	Non	18.25	-1.12	1.4
U3	4.03	808.93	-2.00	Non	20.59	-1.11	1.14
U4	4.79	906.09	-1.00	Non	22.82	-2.44	1.79
U5	4.03	808.93	-2.00	Non	20.59	-1.11	1.14
U6	4.14	1000.16	-2.00	Non	16.09	-1.39	0.51
U7	4.03	937.08	-2.00	Non	19.70	-2.41	1.07
U8	3.93	880.01	-2.00	Non	19.56	-1.51	1.13
U9	4.37	729.96	-1.00	Non	14.35	0.2	0.6
U10	4.37	779.97	-1.00	Non	14.76	-0.77	0.52
U11	4.21	733.91	-1.00	Non	14.73	0	0.73
U12	5.96	777.90	0.00	Non	19.15	-2.75	1.48
B1	8.75	801.09	1.00	Non	7.23	0.36	-0.4
B2	6.49	862.24	0.50	Non	6.76	1.4	-1.16
B3	6.71	805.10	0.50	Non	7.27	1.24	-1.03
B4	8.76	774.08	1.50	Non	9.07	1.05	-0.77
B5	8.75	751.05	1.00	Non	9.05	1.51	-0.61
B6	5.81	728.99	0.00	Non	12.86	1.23	-0.04
B7	5.97	771.02	0.00	Non	12.89	0.44	0.21
B8	5.97	741.00	0.00	Non	13.58	0.5	0.17
B9	5.84	728.99	0.00	Non	12.86	1.23	-0.04
B10	6.00	755.02	0.00	Non	12.80	0.71	0.1
B11	5.84	805.03	0.00	Non	11.52	0.14	0.07
B12	8.73	813.13	1.50	Non	10.78	0.99	-0.47
B13	8.76	797.14	1.50	Non	10.68	0.99	-0.56
B14	8.76	861.17	1.50	Non	9.53	0.79	-0.61
B15	9.75	775.01	1.00	Non	8.17	0.6	-0.36
B16	6.79	767.97	0.50	Non	8.64	0.27	-0.71
B17	4.53	843.14	-1.00	Non	13.75	0.67	0.3
B18	4.21	785.00	-1.00	Non	16.08	0.06	0.6
B19	4.21	813.06	-1.00	Non	14.50	-0.06	0.51
B20	5.81	801.05	0.00	Non	10.97	1.1	-0.1
B21	5.81	814.10	0.00	Non	11.69	0.73	-0.06
B22	5.59	832.13	0.00	Non	12.27	0.46	0.01
B23	5.08	792.00	-0.50	Non	11.90	-0.43	-0.21
B24	5.84	784.02	0.00	Non	13.29	0.06	0.2
B25	5.84	850.09	0.00	Non	12.49	-0.51	0.13
B26	6.71	845.15	0.50	Non	8.28	0.63	-0.94
B27	9.76	855.17	1.50	Non	9.00	0.84	-0.51
B28	4.20	808.00	-1.50	Non	14.69	0	0.06

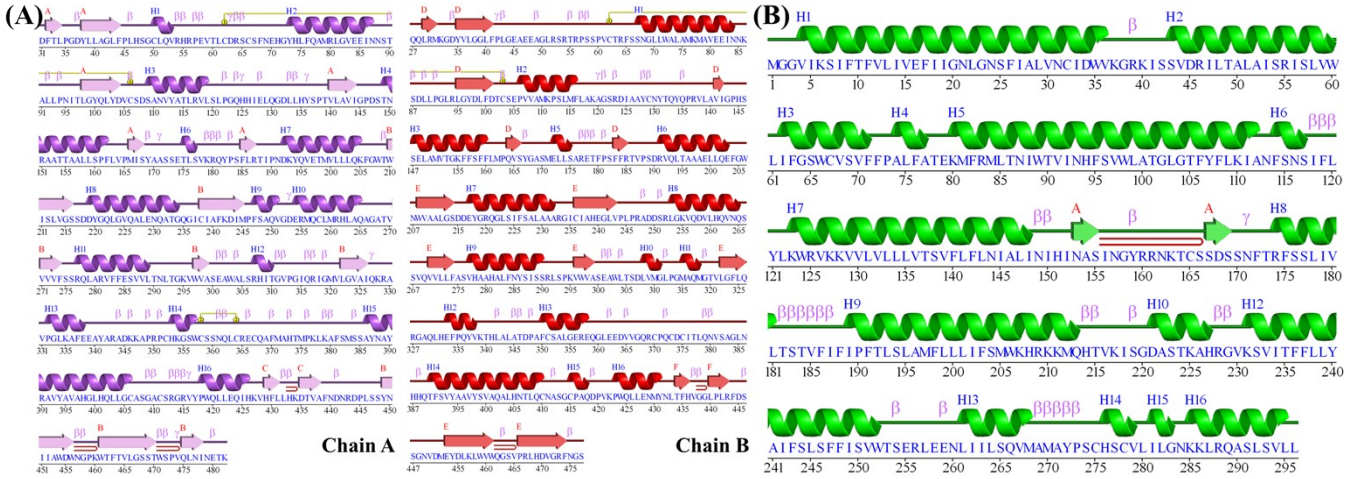


Fig. S3. Secondary structure of umami and bitter taste receptors after simulation.

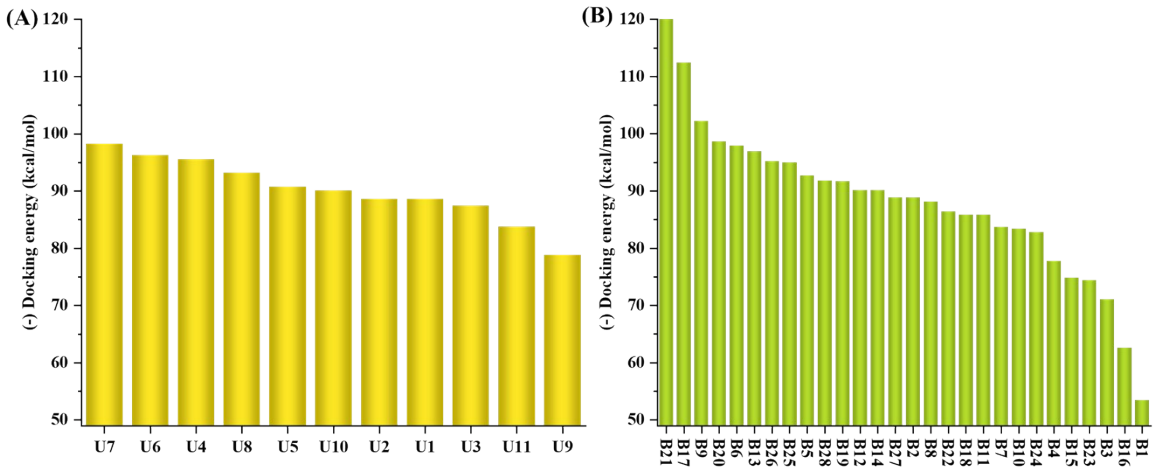


Fig. S4. Docking energy of umami (A) and bitter (B) peptides with the corresponding taste receptors using molecular docking.

Table S3 Molecule docking energy between umami taste receptor and umami peptides.

Name	Sequence	$\Delta E_{docking}$ (kcal/mol)	$\Delta E_{interaction}$ (kcal/mol)	$\Delta E_{binding}$ (kcal/mol)	ΔE_{vdw} (kcal/mol)	ΔE_{ele} (kcal/mol)
U1	EDEPELR	-88.59	-72.71	-153.66	-27.13	-182.33
U2	DIREDL	-88.65	-47.41	-169.23	-27.41	-171.03
U3	GEKVDFD	-87.52	-67.37	-130.91	-24.13	-140.06
U4	EEEKPKF	-95.58	-74.15	-187.27	-27.23	-200.26
U5	DGEKVDF	-90.79	-61.74	-207.63	-23.00	-211.51
U6	WFKDEEF	-96.30	-62.26	-159.04	-25.14	-170.39
U7	NWDDMEK	-98.25	-64.22	-195.29	-23.31	-213.18
U8	DFDDIQK	-93.21	-55.24	-224.22	-23.52	-227.05
U9	LEDIKL	-78.85	-55.66	-179.60	-26.09	-178.89
U10	YEDLLK	-90.06	-62.01	-211.53	-24.85	-217.03
U11	CDIDIR	-83.81	-59.62	-195.76	-19.36	-198.18
U12	WSDDKK	-79.24	-54.08	-123.69	-17.41	-129.27
Glu	E	-14.31	-11.25	-21.41	-3.24204	-23.2728

Table S4 Molecule docking energy between bitter taste receptor and bitter peptides.

Name	Sequence	$\Delta E_{docking}$ (kcal/mol)	$\Delta E_{interaction}$ (kcal/mol)	$\Delta E_{binding}$ (kcal/mol)	ΔE_{vdw} (kcal/mol)	ΔE_{ele} (kcal/mol)
B1	LPSLPKF	-53.47	-65.28	-137.71	-25.25	-160.01
B2	MVMMTHL	-88.86	-65.39	-210.26	-29.46	-212.16
B3	VIILNHP	-71.11	-64.16	-214.50	-31.50	-226.64
B4	FVKHIM	-77.80	-55.84	-176.77	-27.95	-169.68
B5	FAVMVKG	-92.73	-71.17	-193.80	-23.21	-192.57
B6	VVDGVKL	-97.90	-70.75	-213.60	-23.65	-212.23
B7	VISVPEK	-83.76	-77.40	-140.09	-24.09	-157.10
B8	VGKVIPE	-88.11	-92.18	-121.04	-25.93	-135.76
B9	LVVDGVK	-102.24	-70.47	-217.19	-22.78	-217.97
B10	LPVEVAK	-83.41	-76.86	-183.10	-26.21	-190.41
B11	LFDKPVS	-85.85	-73.83	-183.88	-21.45	-200.02
B12	VKHIMSV	-90.15	-68.73	-199.56	-27.21	-201.54
B13	KLIGHVM	-96.90	-74.51	-210.00	-29.93	-205.49
B14	FVKHIMS	-90.13	-59.99	-211.20	-28.67	-209.42
B15	FPSIVGR	-74.81	-68.49	-155.81	-19.81	-169.73
B16	APPHIFS	-62.58	-62.62	-162.59	-22.95	-185.55
B17	VELLKLE	-112.45	-92.72	-183.79	-29.51	-184.12
B18	IPVVDDK	-85.89	-77.15	-108.91	-27.84	-128.32
B19	ILKDPDL	-91.75	-89.16	-150.29	-29.92	-162.64
B20	VVDLTVR	-98.63	-70.14	-222.17	-24.15	-229.04
B21	VQDVLKL	-120.19	-90.39	-239.41	-30.52	-236.53
B22	MVQDVLK	-86.45	-61.72	-251.00	-27.90	-252.96
B23	LPHDTPL	-74.42	-81.50	-157.23	-26.91	-183.11
B24	IPVNVDK	-82.82	-67.32	-178.55	-29.80	-189.57
B25	DFNVPMK	-94.99	-84.18	-237.90	-25.03	-252.34
B26	VMMTHLN	-95.27	-66.04	-236.36	-28.64	-242.94
B27	HLRVISM	-88.91	-58.75	-209.80	-27.44	-213.37
B28	DDPLLVH	-91.81	-85.42	-191.32	-30.95	-197.71
Pro	P	-17.64	-34.31	24.99	-2.13	7.45

Table S5 Detailed information of interactions between umami taste receptor and umami peptides as well as positive control

Name	Interaction position	Distance	Category	Type	From	From chemistry	To	To chemistry
U7	B:Arg52:NE - U7:O117	4.41329	Electrostatic	Attractive charge	B:Arg52:NE	Positive	U7:O117	Negative
	B:Arg247:NE - U7:O93	5.21391	Electrostatic	Attractive charge	B:Arg247:NE	Positive	U7:O93	Negative
	B:Arg247:NE - U7:O117	3.03238	Electrostatic	Attractive charge	B:Arg247:NE	Positive	U7:O117	Negative
	B:Arg52:HH12 - U7:O92	2.66042	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH12	H-donor	U7:O92	H-Acceptor
	B:Arg52:HH12 - U7:O117	2.67952	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH12	H-donor	U7:O117	H-Acceptor
	B:Arg247:HH11 - U7:O116	1.98656	Hydrogen bond	Conventional hydrogen bond	B:Arg247:HH11	H-donor	U7:O116	H-Acceptor
	B:Ala248:HN - U7:O93	2.37699	Hydrogen bond	Conventional hydrogen bond	B:Ala248:HN	H-donor	U7:O93	H-Acceptor
	B:Val277:HN - U7:O48	2.08417	Hydrogen bond	Conventional hydrogen bond	B:Val277:HN	H-donor	U7:O48	H-Acceptor
	B:Arg247:HA - U7:O93	2.44776	Hydrogen bond	Carbon hydrogen bond	B:Arg247:HA	H-donor	U7:O93	H-Acceptor
	B:Ser276:HB2 - U7:O48	2.56105	Hydrogen bond	Carbon hydrogen bond	B:Ser276:HB2	H-donor	U7:O48	H-Acceptor
	U7:H29 - B:Ser306:OG	2.86841	Hydrogen bond	Carbon hydrogen bond	U7:H29	H-donor	B:Ser306:OG	H-Acceptor
	U7:H55 - B:His278:NE2	2.4734	Hydrogen bond	Carbon hydrogen bond	U7:H55	H-donor	B:His278:NE2	H-Acceptor
	U7:O93 - B:His278	4.43356	Electrostatic	Pi-anion	U7:O93	Negative	B:His278	Pi-Orbitals
U6	B:Arg52:NE - U6:O91	5.00861	Electrostatic	Attractive charge	B:Arg52:NE	Positive	U6:O91	Negative
	B:Arg52:NE - U6:O129	3.12163	Electrostatic	Attractive charge	B:Arg52:NE	Positive	U6:O129	Negative
	B:Arg247:NE - U6:O91	4.18429	Electrostatic	Attractive charge	B:Arg247:NE	Positive	U6:O91	Negative
	B:Arg52:HH11 - U6:O129	1.89158	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH11	H-donor	U6:O129	H-Acceptor
	B:Arg52:HH12 - U6:O90	2.27344	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH12	H-donor	U6:O90	H-Acceptor
	B:Arg247:HE - U6:O90	2.28914	Hydrogen bond	Conventional	B:Arg247:HE	H-donor	U6:O90	H-Acceptor

	U6:H63 - B:Gly50:O	2.62954	Hydrogen bond	Conventional hydrogen bond	U6:H63	H-donor	B:Gly50:O	H-Acceptor
	U6:H64 - B:Gly50:O	2.53872	Hydrogen bond	Conventional hydrogen bond	U6:H64	H-donor	B:Gly50:O	H-Acceptor
	U6:H95 - B:His278:NE2	2.63104	Hydrogen bond	Conventional hydrogen bond	U6:H95	H-donor	B:His278:NE2	H-Acceptor
U4	B:Arg52:HE - U4:O44	2.04749	Hydrogen bond;electrostatic	Salt bridge;attractive charge	B:Arg52:HE	H-donor;positive	U4:O44	H-Acceptor;Negative
	B:Arg247:NE - U4:O29	4.73363	Electrostatic	Attractive charge	B:Arg247:NE	Positive	U4:O29	Negative
	B:Arg52:HH11 - U4:O43	2.48258	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH11	H-donor	U4:O43	H-Acceptor
	B:Arg52:HH12 - U4:O16	2.4497	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH12	H-donor	U4:O16	H-Acceptor
	B:Arg52:HH12 - U4:O28	2.80824	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH12	H-donor	U4:O28	H-Acceptor
	B:Arg247:HE - U4:O16	2.89981	Hydrogen bond	Conventional hydrogen bond	B:Arg247:HE	H-donor	U4:O16	H-Acceptor
	B:Arg247:HE - U4:O28	1.99366	Hydrogen bond	Conventional hydrogen bond	B:Arg247:HE	H-donor	U4:O28	H-Acceptor
	B:Arg247:HH11 - U4:O28	2.36076	Hydrogen bond	Conventional hydrogen bond	B:Arg247:HH11	H-donor	U4:O28	H-Acceptor
	B:Thr305:HN - U4:O122	2.46618	Hydrogen bond	Conventional hydrogen bond	B:Thr305:HN	H-donor	U4:O122	H-Acceptor
	B:Thr305:HG1 - U4:O122	2.05793	Hydrogen bond	Conventional hydrogen bond	B:Thr305:HG1	H-donor	U4:O122	H-Acceptor
	B:His278:HE1 - U4:O13	2.42398	Hydrogen bond	Carbon hydrogen bond	B:His278:HE1	H-donor	U4:O13	H-Acceptor
	B:Ser306:HA - U4:O123	2.67901	Hydrogen bond	Carbon hydrogen bond	B:Ser306:HA	H-donor	U4:O123	H-Acceptor
	B:Ser306:HB1 - U4:O123	2.70211	Hydrogen bond	Carbon hydrogen	B:Ser306:HB1	H-donor	U4:O123	H-Acceptor

				bond				
	U4:H97 - B:His278:NE2	2.44975	Hydrogen bond	Carbon hydrogen bond	U4:H97	H-donor	B:His278:NE2	H-Acceptor
	B:His388 - U4	4.13556	Hydrophobic	Pi-pi stacked	B:His388	Pi-orbitals	U4	Pi-Orbitals
	U4 - B:Leu304	5.19339	Hydrophobic	Pi-alkyl	U4	Pi-orbitals	B:Leu304	Alkyl
	U4 - B:Leu325	5.29918	Hydrophobic	Pi-alkyl	U4	Pi-orbitals	B:Leu325	Alkyl
U8	B:Arg247:HE - U8:O11	2.01261	Hydrogen bond;electrostatic	Salt bridge;attractive charge	B:Arg247:HE	H-donor;positive	U8:O11	H-Acceptor;Negative
	B:Arg52:NE - U8:O11	5.27346	Electrostatic	Attractive charge	B:Arg52:NE	Positive	U8:O11	Negative
	B:Arg52:HH11 - U8:O10	2.12983	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH11	H-donor	U8:O10	H-Acceptor
	B:Arg52:HH12 - U8:O11	2.58165	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH12	H-donor	U8:O11	H-Acceptor
	B:Arg247:HH11 - U8:O11	2.96663	Hydrogen bond	Conventional hydrogen bond	B:Arg247:HH11	H-donor	U8:O11	H-Acceptor
	B:Val277:HN - U8:O115	1.97402	Hydrogen bond	Conventional hydrogen bond	B:Val277:HN	H-donor	U8:O115	H-Acceptor
	U8:H111 - B:Ala302:O	2.94446	Hydrogen bond	Conventional hydrogen bond	U8:H111	H-donor	B:Ala302:O	H-Acceptor
	U8:H111 - B:Trp303:O	2.31327	Hydrogen bond	Conventional hydrogen bond	U8:H111	H-donor	B:Trp303:O	H-Acceptor
	B:Ser276:HB2 - U8:O115	2.41109	Hydrogen bond	Carbon hydrogen bond	B:Ser276:HB2	H-donor	U8:O115	H-Acceptor
	U8:H109 - B:Ala302:O	2.47366	Hydrogen bond	Carbon hydrogen bond	U8:H109	H-donor	B:Ala302:O	H-Acceptor
	U8:C64 - B:Val277	4.72817	Hydrophobic	Alkyl	U8:C64	Alkyl	B:Val277	Alkyl
	U8:C64 - B:Leu308	4.23868	Hydrophobic	Alkyl	U8:C64	Alkyl	B:Leu308	Alkyl
U5	B:Arg52:HE - U5:O33	2.21916	Hydrogen bond;electrostatic	Salt bridge;attractive charge	B:Arg52:HE	H-donor;positive	U5:O33	H-Acceptor;Negative
	B:Arg247:HE - U5:O11	2.01275	Hydrogen	Salt bridge;attractive	B:Arg247:HE	H-	U5:O11	H-

			bond;electrostatic	charge		donor;positive		Acceptor;Negative
	B:Arg52:NE - U5:O11	5.52869	Electrostatic	Attractive charge	B:Arg52:NE	Positive	U5:O11	Negative
	B:Arg52:HH11 - U5:O33	2.0208	Hydrogen bond	Conventional hydrogen bond	B:Arg52:HH11	H-donor	U5:O33	H-Acceptor
	U5:H53 - B:Ser306:OG	2.01803	Hydrogen bond	Conventional hydrogen bond	U5:H53	H-donor	B:Ser306:OG	H-Acceptor
	B:His387:HE1 - U5:O105	2.57013	Hydrogen bond	Carbon hydrogen bond	B:His387:HE1	H-donor	U5:O105	H-Acceptor
	B:His388:HD2 - U5:O104	2.52737	Hydrogen bond	Carbon hydrogen bond	B:His388:HD2	H-donor	U5:O104	H-Acceptor
Glu	Glu:H2 - B:His278:NE2	2.94788	Hydrogen bond	Conventional hydrogen bond	Glu:H2	H-donor	B:His278:NE2	H-Acceptor
	Glu:H15 - B:Ser306:OG	2.06167	Hydrogen bond	Conventional hydrogen bond	Glu:H15	H-donor	B:Ser306:OG	H-Acceptor
	Glu:H5 - B:His278:NE2	2.62862	Hydrogen bond	Carbon hydrogen bond	Glu:H5	H-donor	B:His278:NE2	H-Acceptor

Table S6 Detailed information of interactions between bitter taste receptor and bitter peptides as well as positive control

Name	Interaction position	Distance	Category	Type	From	From chemistry	To	To chemistry
B21	A:Arg228:NE - B21:O122	4.36718	Electrostatic	Attractive charge	A:Arg228:NE	Positive	B21:O122	Negative
	A:Arg288:NE - B21:O122	4.57836	Electrostatic	Attractive charge	A:Arg288:NE	Positive	B21:O122	Negative
	A:Arg209:HH21 - B21:O29	1.9756	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH21	H-donor	B21:O29	H-Acceptor
	A:Arg209:HH21 - B21:O102	2.29919	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH21	H-donor	B21:O102	H-Acceptor
	A:Arg209:HH12 - B21:O46	1.83044	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH12	H-donor	B21:O46	H-Acceptor
	A:Arg209:HH12 - B21:O81	2.4878	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH12	H-donor	B21:O81	H-Acceptor
	A:Arg209:HH22 - B21:O81	1.95419	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH22	H-donor	B21:O81	H-Acceptor
	A:Arg288:HH22 - B21:O122	1.85769	Hydrogen bond	Conventional hydrogen bond	A:Arg288:HH22	H-donor	B21:O122	H-Acceptor
	B21:H3 - A:Gly283:O	2.90655	Hydrogen bond	Conventional hydrogen bond	B21:H3	H-donor	A:Gly283:O	H-Acceptor
	B21:H99 - A:Ser219:O	1.87465	Hydrogen bond	Conventional hydrogen bond	B21:H99	H-donor	A:Ser219:O	H-Acceptor
	A:Arg228:HD2 - B21:O29	3.05616	Hydrogen bond	Carbon hydrogen bond	A:Arg228:HD2	H-donor	B21:O29	H-Acceptor
	A:Lys285:HE1 - B21:O122	2.49518	Hydrogen bond	Carbon hydrogen bond	A:Lys285:HE1	H-donor	B21:O122	H-Acceptor
	A:Lys285:HE2 - B21:O17	2.48393	Hydrogen bond	Carbon hydrogen bond	A:Lys285:HE2	H-donor	B21:O17	H-Acceptor
B17	A:Arg228:NE - B17:O123	4.19869	Electrostatic	Attractive charge	A:Arg228:NE	Positive	B17:O123	Negative
	A:Arg228:NE - B17:O126	5.49477	Electrostatic	Attractive charge	A:Arg228:NE	Positive	B17:O126	Negative
	A:Arg288:NE - B17:O126	5.09704	Electrostatic	Attractive charge	A:Arg288:NE	Positive	B17:O126	Negative
	A:Arg209:HH21 - B17:O110	2.52549	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH21	H-donor	B17:O110	H-Acceptor

	A:Arg209:HH12 - B17:O32	2.92412	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH12	H-donor	B17:O32	H-Acceptor
	A:Arg209:HH12 - B17:O51	2.33624	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH12	H-donor	B17:O51	H-Acceptor
	A:Arg209:HH22 - B17:O91	2.1909	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH22	H-donor	B17:O91	H-Acceptor
	A:Lys285:HZ2 - B17:O17	2.04619	Hydrogen bond	Conventional hydrogen bond	A:Lys285:HZ2	H-donor	B17:O17	H-Acceptor
	A:Arg288:HH12 - B17:O126	1.80997	Hydrogen bond	Conventional hydrogen bond	A:Arg288:HH12	H-donor	B17:O126	H-Acceptor
	A:Arg288:HH22 - B17:O125	1.83282	Hydrogen bond	Conventional hydrogen bond	A:Arg288:HH22	H-donor	B17:O125	H-Acceptor
	B17:H19 - A:His208:NE2	2.34852	Hydrogen bond	Conventional hydrogen bond	B17:H19	H-donor	A:His208:NE2	H-Acceptor
	A:His208:HE1 - B17:O29	2.72747	Hydrogen bond	Carbon hydrogen bond	A:His208:HE1	H-donor	B17:O29	H-Acceptor
	A:Arg228:HD1 - B17:O123	2.54277	Hydrogen bond	Carbon hydrogen bond	A:Arg228:HD1	H-donor	B17:O123	H-Acceptor
	B17:H21 - A:His208:NE2	2.62736	Hydrogen bond	Carbon hydrogen bond	B17:H21	H-donor	A:His208:NE2	H-Acceptor
	A:Met212:SD - B17:O32	3.29282	Other	Sulfur-x	A:Met212:SD	Sulfur	B17:O32	O,N,S
	B17:C12 - A:Ile111	5.21283	Hydrophobic	Alkyl	B17:C12	Alkyl	A:Ile111	Alkyl
	B17:C65 - A:Ile218	5.01215	Hydrophobic	Alkyl	B17:C65	Alkyl	A:Ile218	Alkyl
	B17:C101 - A:Ile218	4.74972	Hydrophobic	Alkyl	B17:C101	Alkyl	A:Ile218	Alkyl
	B17:C105 - A:Ile218	4.65997	Hydrophobic	Alkyl	B17:C105	Alkyl	A:Ile218	Alkyl
	A:His208 - B17:C12	4.19001	Hydrophobic	Pi-alkyl	A:His208	Pi-orbitals	B17:C12	Alkyl
	A:Arg228:NE - B9:O109	3.59851	Electrostatic	Attractive charge	A:Arg228:NE	Positive	B9:O109	Negative
	A:Arg288:NE - B9:O109	4.97101	Electrostatic	Attractive charge	A:Arg288:NE	Positive	B9:O109	Negative
B9	A:Arg209:HH12 - B9:O64	3.03845	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH12	H-donor	B9:O64	H-Acceptor
	A:Arg209:HH22 - B9:O52	1.8857	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH22	H-donor	B9:O52	H-Acceptor

	A:Thr224:HG1 - B9:O87	2.83104	Hydrogen bond	Conventional hydrogen bond	A:Thr224:HG1	H-donor	B9:O87	H-Acceptor
	A:Arg228:HH21 - B9:O36	1.696	Hydrogen bond	Conventional hydrogen bond	A:Arg228:HH21	H-donor	B9:O36	H-Acceptor
	A:Lys285:HN - B9:O20	2.2226	Hydrogen bond	Conventional hydrogen bond	A:Lys285:HN	H-donor	B9:O20	H-Acceptor
	A:Arg288:HH12 - B9:O109	2.54416	Hydrogen bond	Conventional hydrogen bond	A:Arg288:HH12	H-donor	B9:O109	H-Acceptor
	A:Arg288:HH22 - B9:O109	2.31114	Hydrogen bond	Conventional hydrogen bond	A:Arg288:HH22	H-donor	B9:O109	H-Acceptor
	A:Asp221:HA - B9:O71	2.58923	Hydrogen bond	Carbon hydrogen bond	A:Asp221:HA	H-donor	B9:O71	H-Acceptor
	A:Thr224:HB - B9:O71	2.81504	Hydrogen bond	Carbon hydrogen bond	A:Thr224:HB	H-donor	B9:O71	H-Acceptor
	B9:H24 - A:Gly283:O	2.86709	Hydrogen bond	Carbon hydrogen bond	B9:H24	H-donor	A:Gly283:O	H-Acceptor
	B9:C27 - A:Lys110	4.36326	Hydrophobic	Alkyl	B9:C27	Alkyl	A:Lys110	Alkyl
	B9:C27 - A:Ile111	5.05985	Hydrophobic	Alkyl	B9:C27	Alkyl	A:Ile111	Alkyl
	B9:C31 - A:Lys110	5.07568	Hydrophobic	Alkyl	B9:C31	Alkyl	A:Lys110	Alkyl
	B9:C43 - A:Met205	4.62003	Hydrophobic	Alkyl	B9:C43	Alkyl	A:Met205	Alkyl
	B9:C47 - A:Ile111	4.48061	Hydrophobic	Alkyl	B9:C47	Alkyl	A:Ile111	Alkyl
B20	A:Arg228:HE - B20:O43	1.95976	Hydrogen bond; electrostatic	Salt bridge; attractive charge	A:Arg228:HE	H-donor; positive	B20:O43	H-Acceptor; Negative
	A:Arg209:NE - B20:O43	5.42828	Electrostatic	Attractive charge	A:Arg209:NE	Positive	B20:O43	Negative
	A:Arg209:HE - B20:O42	2.84036	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HE	H-donor	B20:O42	H-Acceptor
	A:Arg209:HH21 - B20:O42	1.98749	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH21	H-donor	B20:O42	H-Acceptor
	A:Arg209:HH22 - B20:O71	1.82615	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH22	H-donor	B20:O71	H-Acceptor
	A:Lys285:HZ1 - B20:O78	2.45152	Hydrogen bond	Conventional hydrogen bond	A:Lys285:HZ1	H-donor	B20:O78	H-Acceptor

	A:Lys285:HZ2 - B20:O17	2.91364	Hydrogen bond	Conventional hydrogen bond	A:Lys285:HZ2	H-donor	B20:O17	H-Acceptor
	A:Arg288:HH22 - B20:O45	2.07079	Hydrogen bond	Conventional hydrogen bond	A:Arg288:HH22	H-donor	B20:O45	H-Acceptor
	B20:H116 - A:Ser219:O	1.81706	Hydrogen bond	Conventional hydrogen bond	B20:H116	H-donor	A:Ser219:O	H-Acceptor
	B20:H117 - A:Gly220:O	3.02711	Hydrogen bond	Conventional hydrogen bond	B20:H117	H-donor	A:Gly220:O	H-Acceptor
	B20:H117 - A:Thr224:OG1	2.1367	Hydrogen bond	Conventional hydrogen bond	B20:H117	H-donor	A:Thr224:OG1	H-Acceptor
	B20:H119 - A:Ser219:O	2.11729	Hydrogen bond	Conventional hydrogen bond	B20:H119	H-donor	A:Ser219:O	H-Acceptor
	B20:C8 - A:Met212	4.65896	Hydrophobic	Alkyl	B20:C8	Alkyl	A:Met212	Alkyl
	B20:C24 - A:Lys285	4.17145	Hydrophobic	Alkyl	B20:C24	Alkyl	A:Lys285	Alkyl
	A:Arg228:NE - B6:O43	5.18709	Electrostatic	Attractive charge	A:Arg228:NE	Positive	B6:O43	Negative
	A:Arg288:NE - B6:O43	5.16893	Electrostatic	Attractive charge	A:Arg288:NE	Positive	B6:O43	Negative
	A:Arg209:HH12 - B6:O68	1.76689	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH12	H-donor	B6:O68	H-Acceptor
	A:Arg209:HH22 - B6:O45	2.33138	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH22	H-donor	B6:O45	H-Acceptor
	A:Arg209:HH22 - B6:O68	1.91586	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH22	H-donor	B6:O68	H-Acceptor
B6	A:Thr224:HG1 - B6:O17	2.16854	Hydrogen bond	Conventional hydrogen bond	A:Thr224:HG1	H-donor	B6:O17	H-Acceptor
	A:Lys285:HZ1 - B6:O52	1.97992	Hydrogen bond	Conventional hydrogen bond	A:Lys285:HZ1	H-donor	B6:O52	H-Acceptor
	A:Arg288:HH12 - B6:O43	1.94025	Hydrogen bond	Conventional hydrogen bond	A:Arg288:HH12	H-donor	B6:O43	H-Acceptor
	A:Arg288:HH22 - B6:O42	1.85353	Hydrogen bond	Conventional hydrogen bond	A:Arg288:HH22	H-donor	B6:O42	H-Acceptor
	B6:H2 - A:Gly220:O	2.21359	Hydrogen bond	Conventional hydrogen bond	B6:H2	H-donor	A:Gly220:O	H-Acceptor

	B6:H2 - A:Thr224:OG1	1.99273	Hydrogen bond	Conventional hydrogen bond	B6:H2	H-donor	A:Thr224:OG1	H-Acceptor
	B6:H3 - A:Ser219:O	2.67101	Hydrogen bond	Conventional hydrogen bond	B6:H3	H-donor	A:Ser219:O	H-Acceptor
	A:Gly220:HA2 - B6:N1	2.66913	Hydrogen bond	Carbon hydrogen bond	A:Gly220:HA2	H-donor	B6:N1	H-Acceptor
	A:Lys285:HE1 - B6:O42	2.62772	Hydrogen bond	Carbon hydrogen bond	A:Lys285:HE1	H-donor	B6:O42	H-Acceptor
	A:Lys285:HE2 - B6:O42	3.07887	Hydrogen bond	Carbon hydrogen bond	A:Lys285:HE2	H-donor	B6:O42	H-Acceptor
	B6:C103 - A:Lys110	4.61836	Hydrophobic	Alkyl	B6:C103	Alkyl	A:Lys110	Alkyl
	B6:C103 - A:Ile111	5.07022	Hydrophobic	Alkyl	B6:C103	Alkyl	A:Ile111	Alkyl
	A:Phe114 - B6:C99	4.802	Hydrophobic	Pi-alkyl	A:Phe114	Pi-orbitals	B6:C99	Alkyl
	A:Phe114 - B6:C103	5.22656	Hydrophobic	Pi-alkyl	A:Phe114	Pi-orbitals	B6:C103	Alkyl
Pro	A:Arg228:NE - Pro:O15	3.87449	Electrostatic	Attractive charge	A:Arg228:NE	Positive	Pro:O15	Negative
	A:Arg288:NE - Pro:O15	4.78158	Electrostatic	Attractive charge	A:Arg288:NE	Positive	Pro:O15	Negative
	A:Arg209:HH22 - Pro:N1	2.1217	Hydrogen bond	Conventional hydrogen bond	A:Arg209:HH22	H-donor	Pro:N1	H-Acceptor
	A:Arg288:HH12 - Pro:O15	2.15693	Hydrogen bond	Conventional hydrogen bond	A:Arg288:HH12	H-donor	Pro:O15	H-Acceptor
	A:Lys285:HE1 - Pro:O14	3.04799	Hydrogen bond	Carbon hydrogen bond	A:Lys285:HE1	H-donor	Pro:O14	H-Acceptor
	A:Lys285:HE2 - Pro:O14	2.95925	Hydrogen bond	Carbon hydrogen bond	A:Lys285:HE2	H-donor	Pro:O14	H-Acceptor

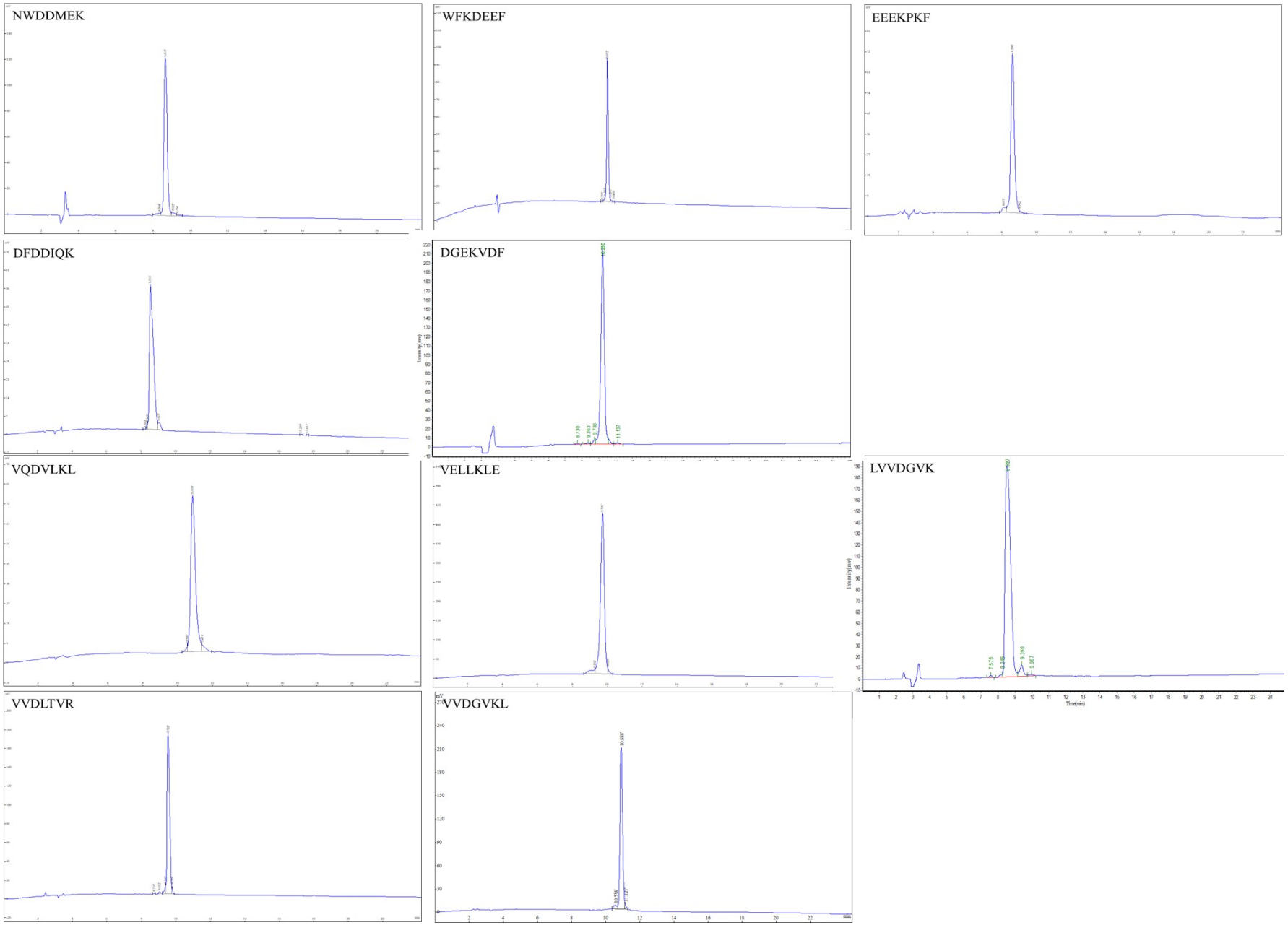
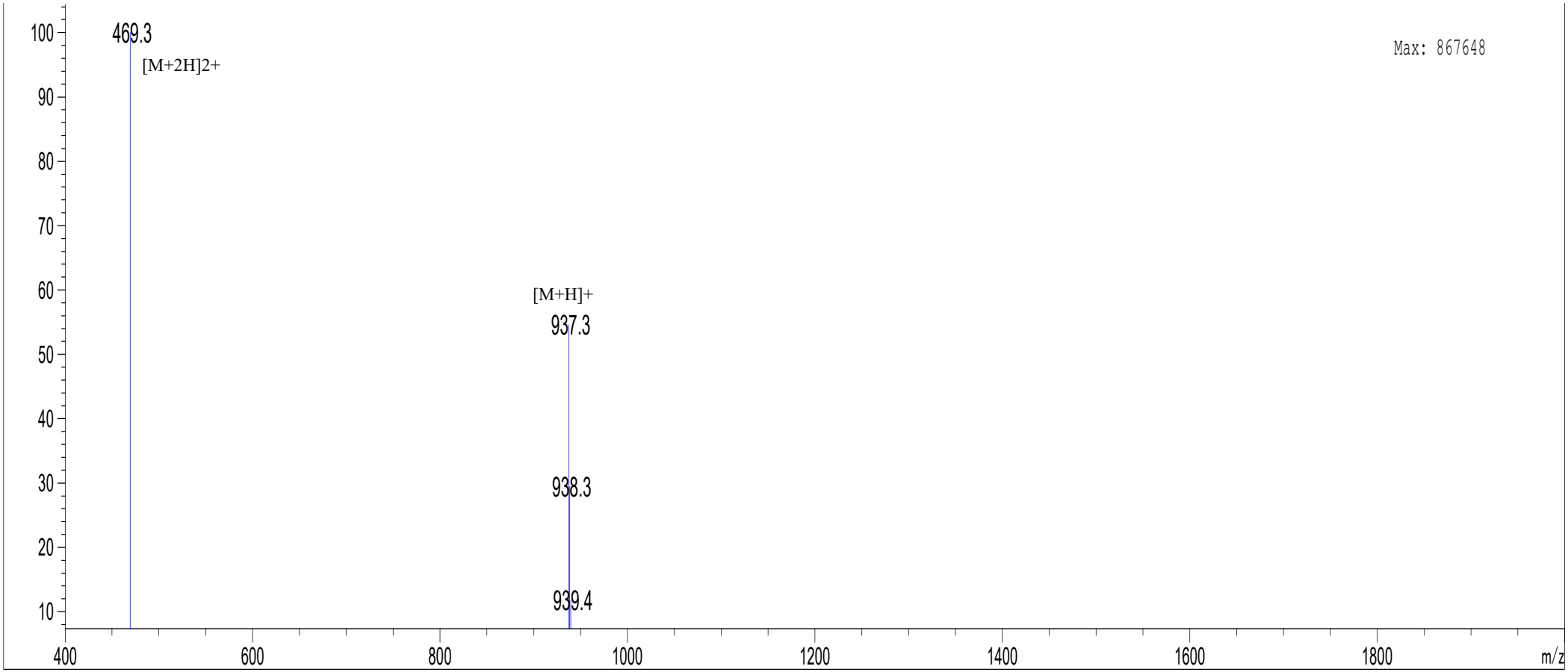
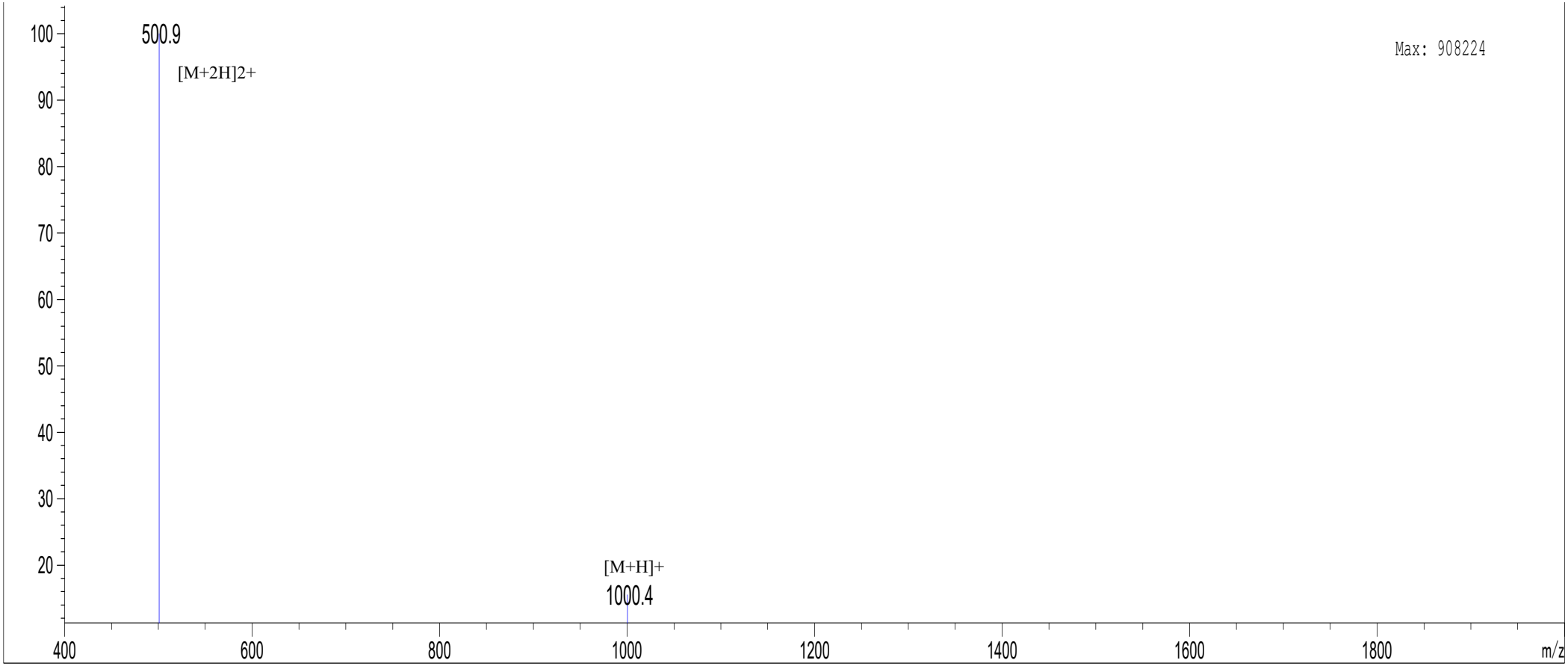


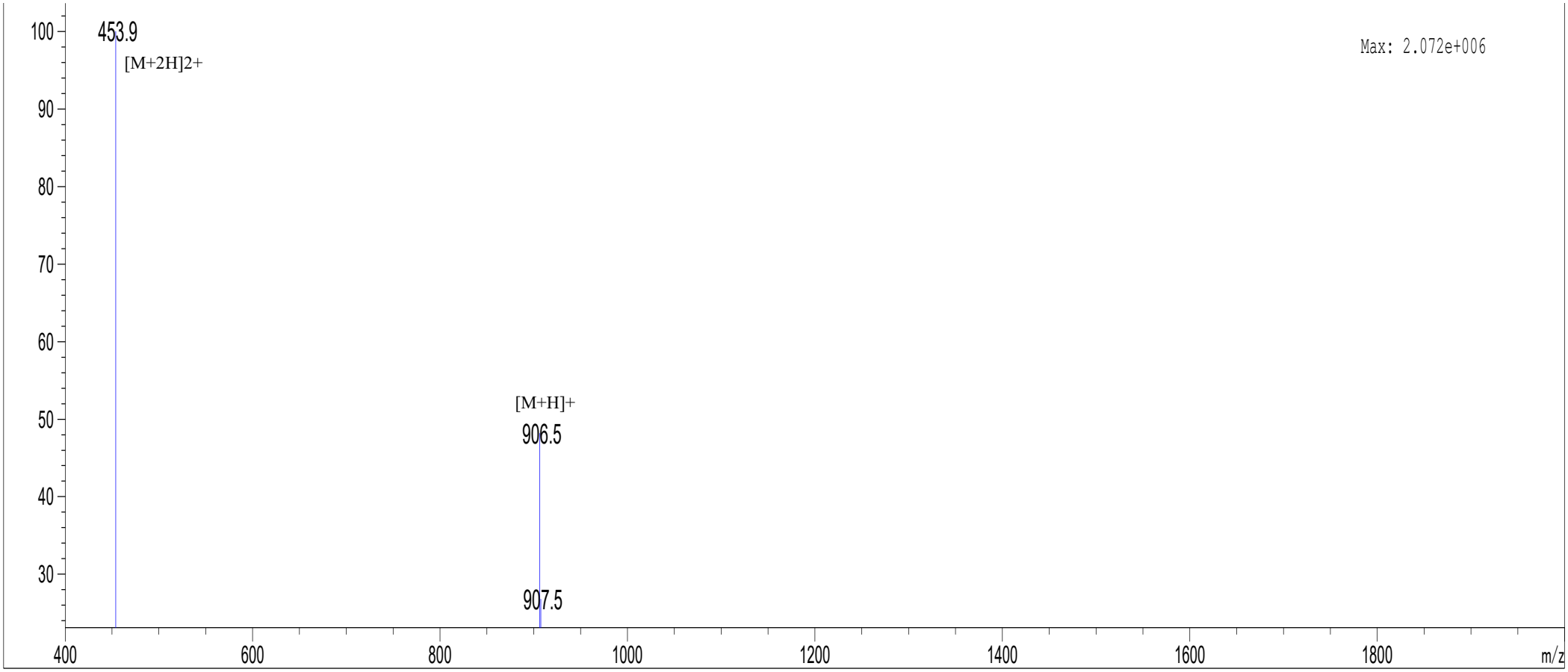
Fig. S5. Purity of the synthetic peptide analyzed by HPLC



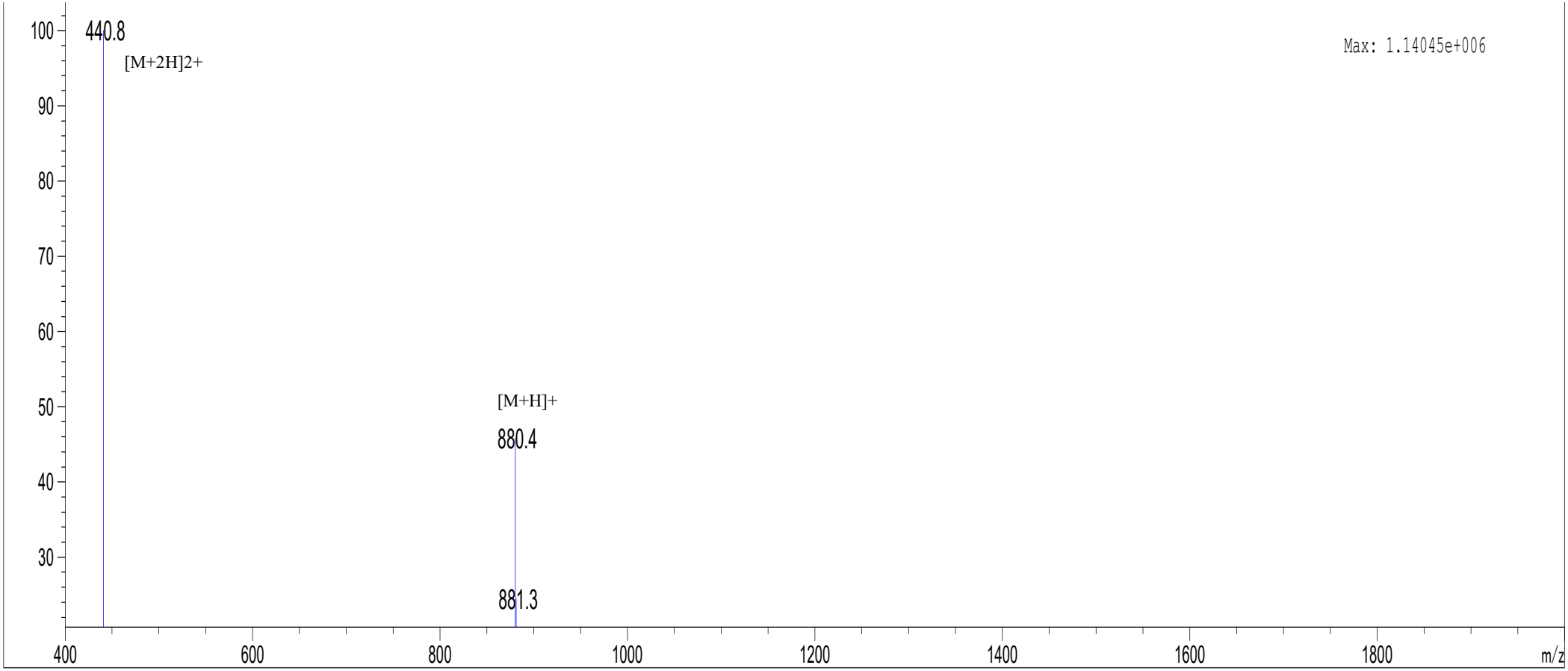
Sample Description		Instrument	Agilent-6125B		
Analyzed date:	2022-11-16	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	NWDDMEK	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	936.98	CDL Temp.:	250 °C	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-810805	Block Temp.:	200 °C		



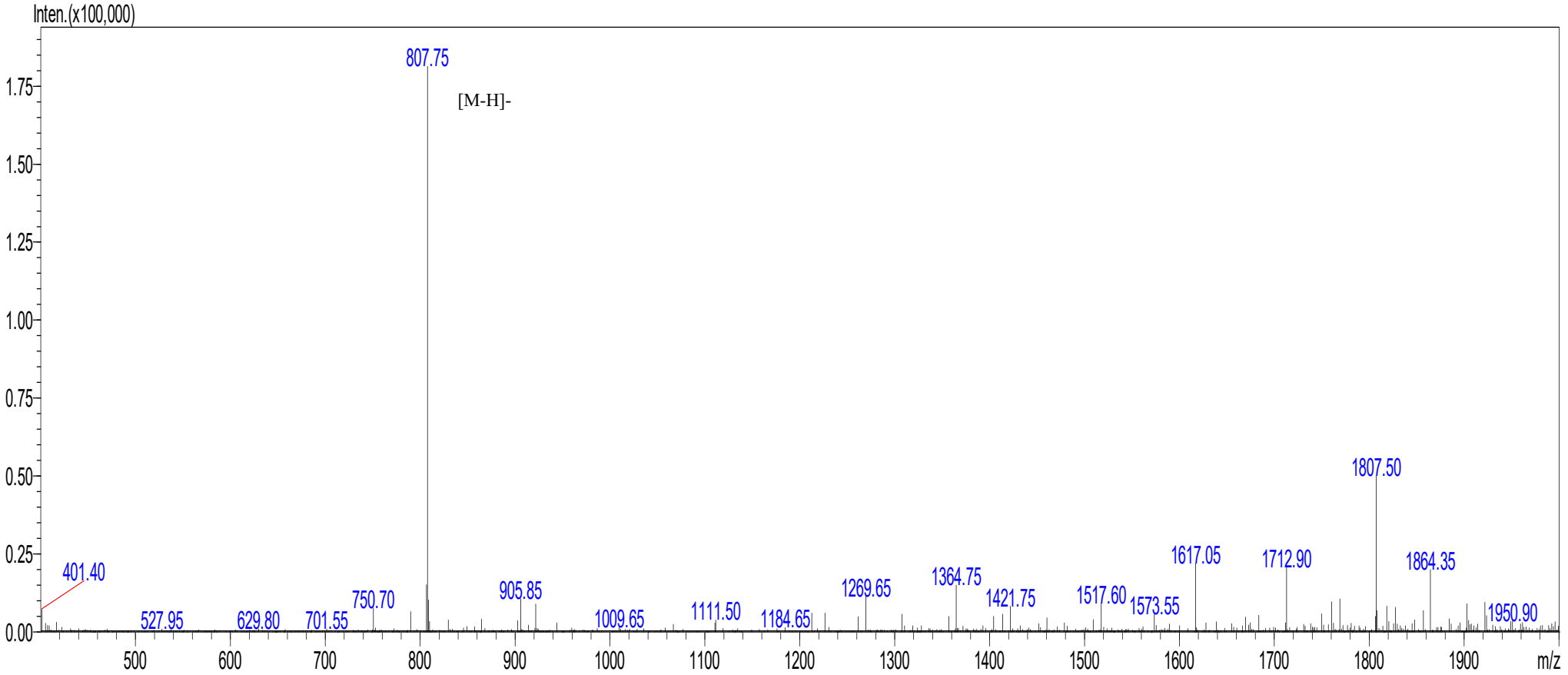
Sample Description		Instrument	Agilent-6125B		
Analyzed date:	2022-11-15	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	WFKDEEF	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	1000.06	CDL Temp.:	250 ℃	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-1027858	Block Temp.:	200 ℃		



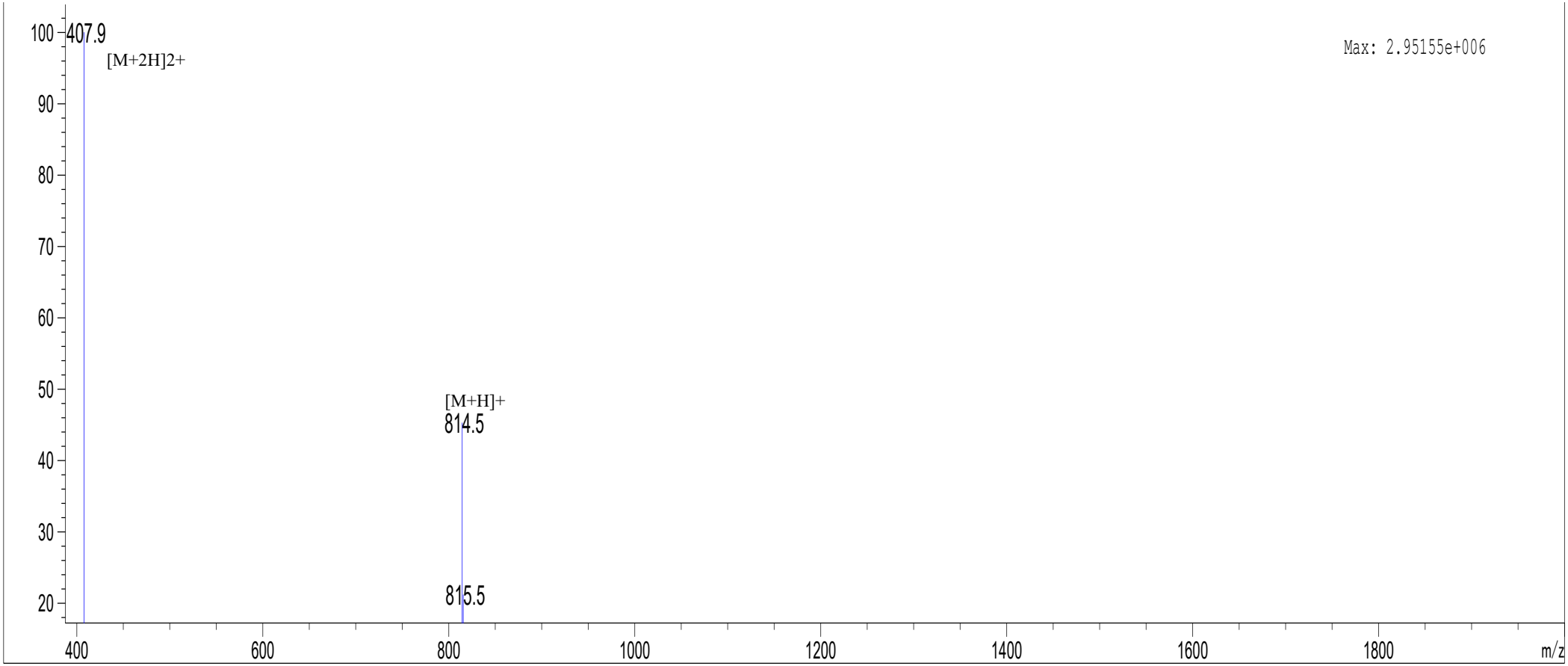
Sample Description		Instrument	Agilent-6125B		
Analyzed date:	2022-11-16	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	EEEKPKF	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	905.99	CDL Temp.:	250 ºC	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-1027859	Block Temp.:	200 ºC		



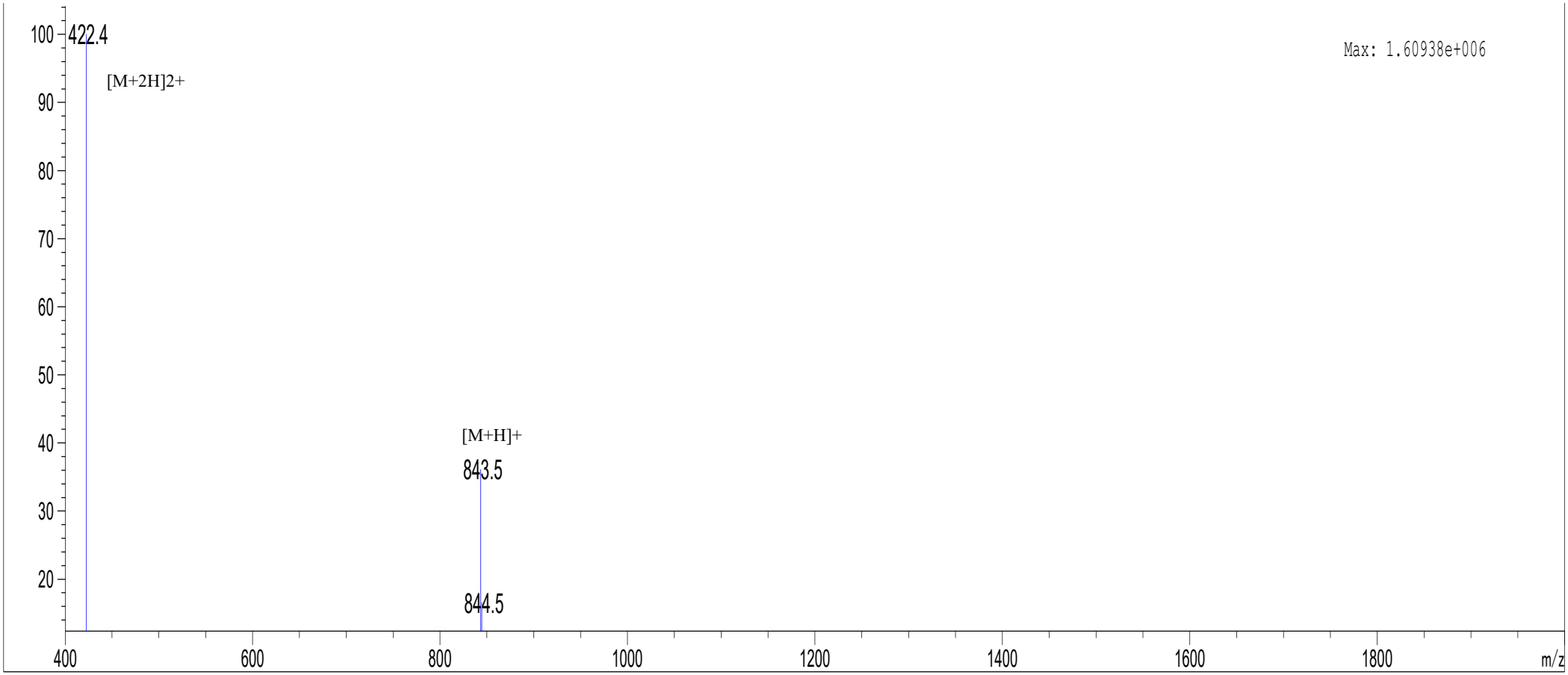
Sample Description		Instrument	Agilent-6125B		
Analyzed date:	2022-11-16	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	DFDDIQK	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	879.9	CDL Temp.:	250 °C	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-982727	Block Temp.:	200 °C		



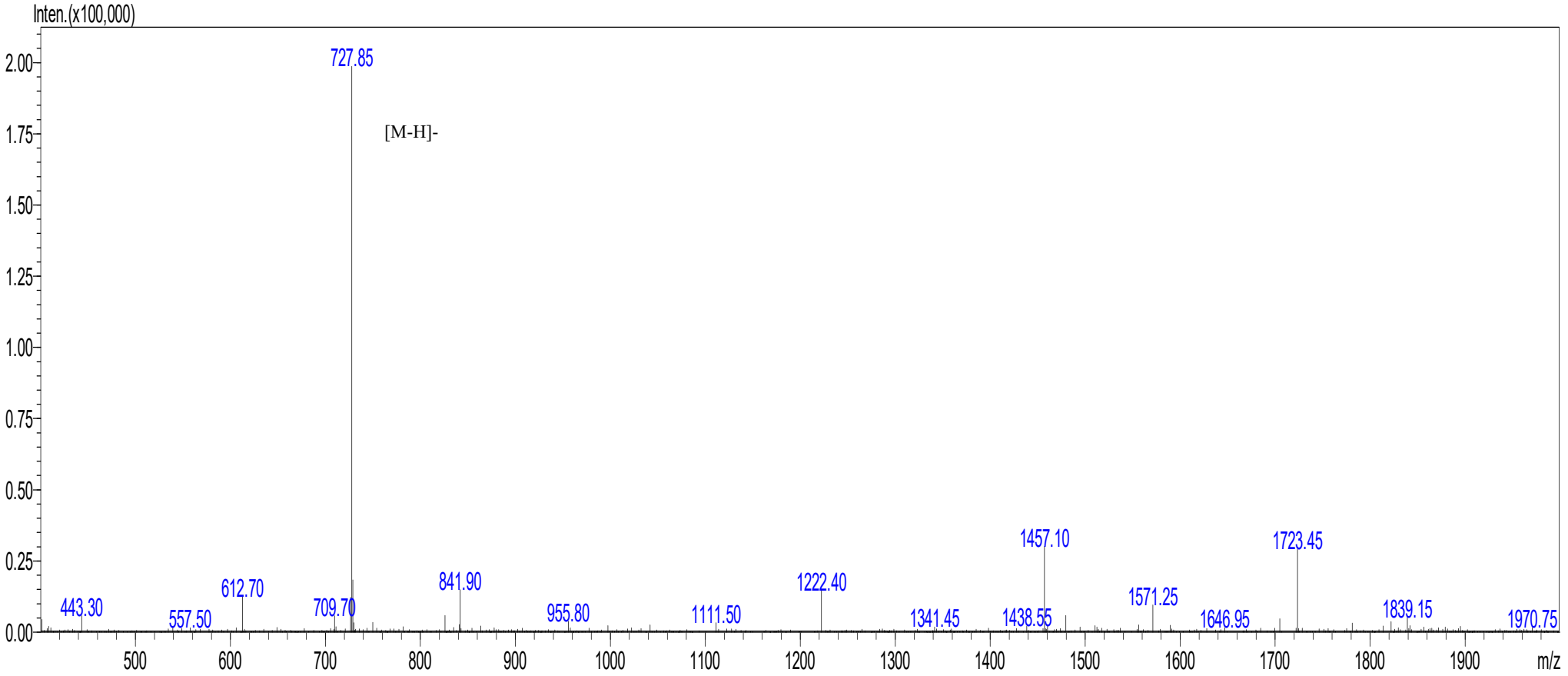
Sample Description		Instrument	SHIMADZU LCMS-2020		
Analyzed date:	2022-11-15	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	DGEKVDF	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	808.83	CDL Temp.:	250℃	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-1027860	Block Temp.:	200℃		



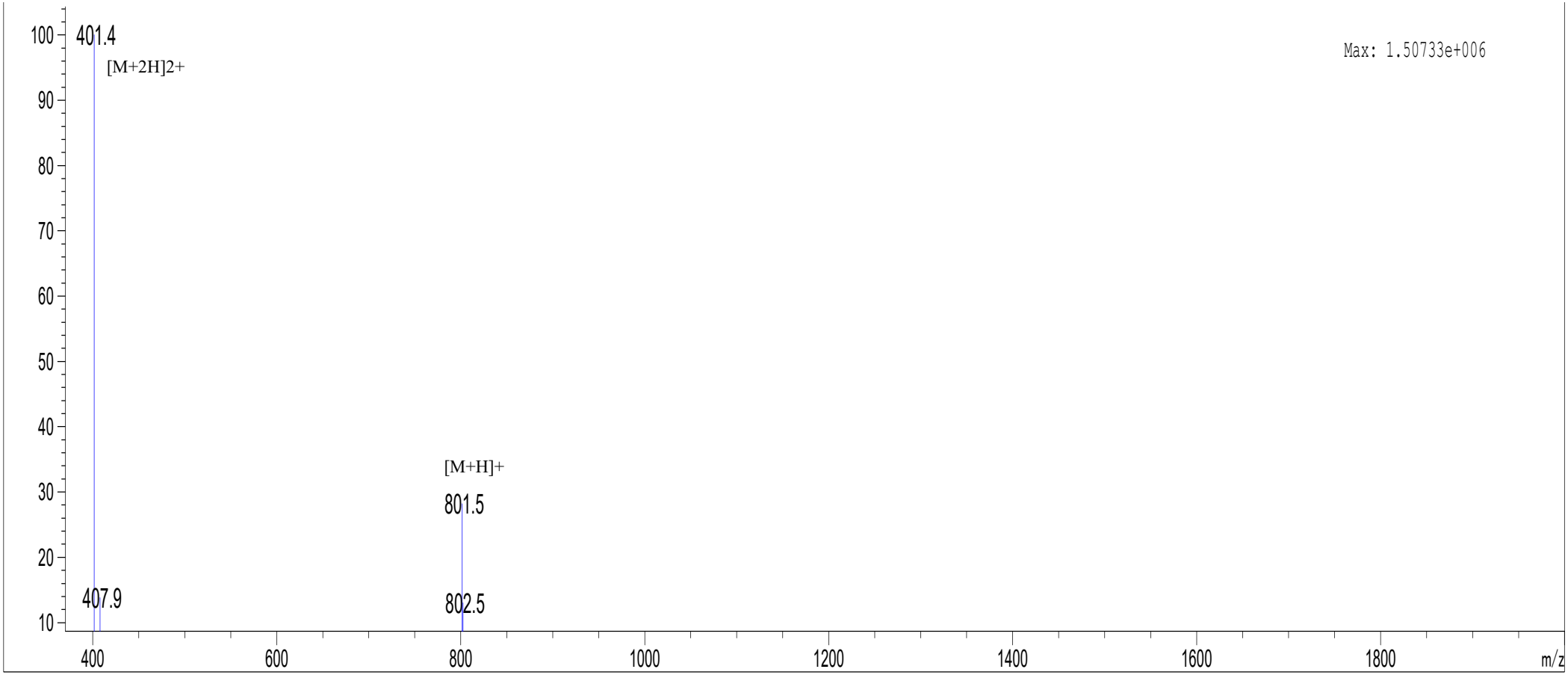
Sample Description		Instrument	Agilent-6125B		
Analyzed date:	2022-11-16	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	VQDVLKL	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	813.98	CDL Temp.:	250 ºC	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-1027848	Block Temp.:	200 ºC		



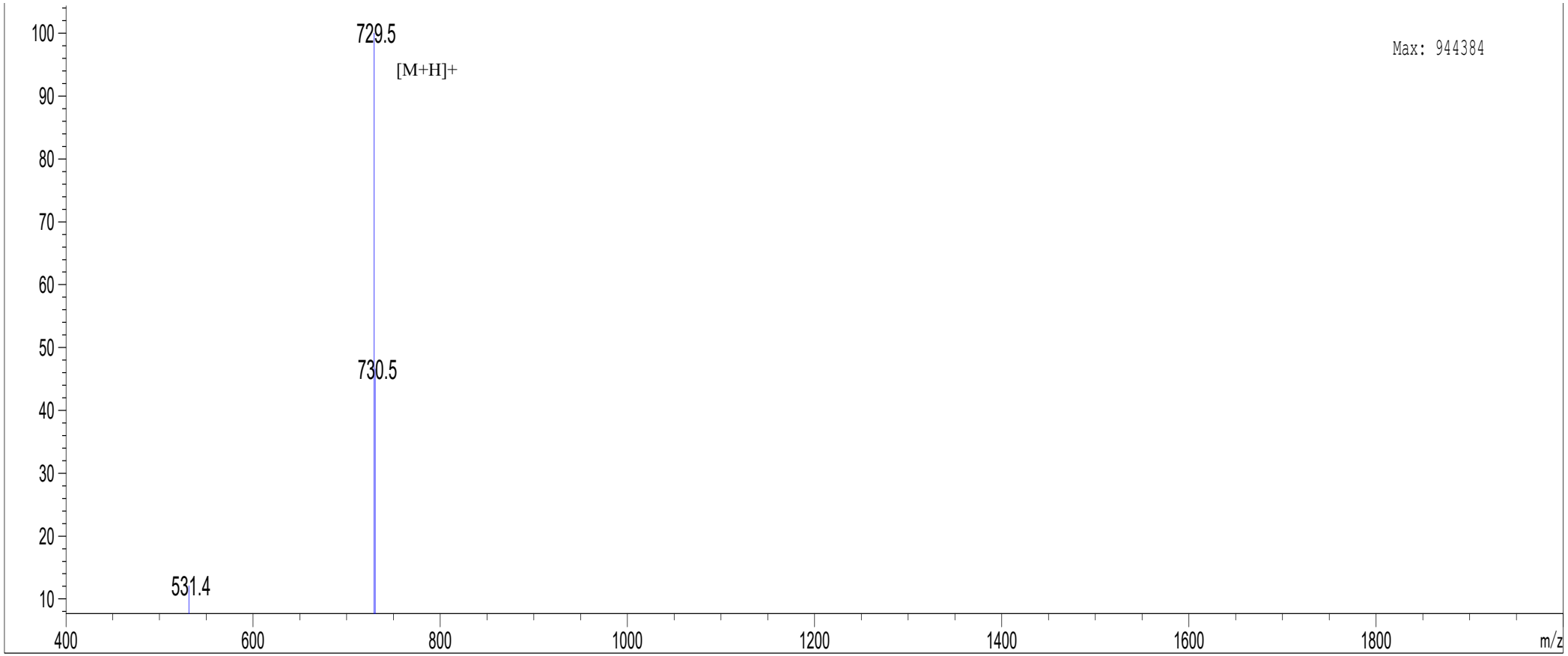
Sample Description		Instrument	Agilent-6125B		
Analyzed date:	2022-11-16	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	VELLKLE	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	843.01	CDL Temp.:	250 °C	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-1027849	Block Temp.:	200 °C		



Sample Description		Instrument	SHIMADZU LCMS-2020		
Analyzed date:	2022-11-15	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	LVVDGVK	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	728.87	CDL Temp.:	250 °C	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-1027850	Block Temp.:	200 °C		



Sample Description		Instrument	Agilent-6125B		
Analyzed date:	2022-11-16	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	VVDLTVR	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	800.94	CDL Temp.:	250 ℃	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-1027851	Block Temp.:	200 ℃		



Sample Description		Instrument	Agilent-6125B		
Analyzed date:	2022-11-16	Probe:	ESI	Probe Bias:	＋4.5kv
Analyst:	YDQ	Nebulizer Gas Flow:	1.5L/min	Detector:	1.5kv
Sample:	VVDGVKL	CDL:	-20.0v	T. Flow:	0.2ml/min
M.W.:	728.87	CDL Temp.:	250 ℃	B. Conc.:	50%H2O/50%ACN
Lot. No.:	Yuanpeptide-1027852	Block Temp.:	200 ℃		

Fig. S6. Secondary MS map of synthetic peptides

Table S7 Detailed information of electronic tongue sensor response

Group	CA0	CT0	AAE	C00	AE1	cpa(AAE)	cpa(CT0)	cpa(CA0)	cpa(C00)	cpa(AE1)
U6-1	1.02	0.4	0.2	0	-0.26	0.63	-0.24	1.02	1.05	-4.24
U6-2	0.77	0.4	0.22	-0.01	-0.26	0.71	-0.18	1.03	1.65	-3.77
U6-3	0.74	0.4	0.24	-0.01	-0.27	0.74	-0.13	1.03	1.72	-3.82
U6-4	0.73	0.4	0.25	-0.02	-0.29	0.74	-0.11	1.02	1.71	-3.75
B20-1	1.85	-0.02	0.11	0.12	-0.75	0.55	-0.73	1.01	2.4	-2.22
B20-2	0.96	-0.01	0.13	0.12	-0.72	0.62	-0.63	1.03	2.92	-2.11
B20-3	0.87	0	0.14	0.09	-0.71	0.64	-0.56	1.03	2.9	-2.32
B20-4	0.81	0	0.15	0.07	-0.72	0.65	-0.53	1.03	2.87	-2.36
B6-1	1.86	0.01	0.12	0.15	-0.71	0.55	-0.65	1.01	4.41	-2.07
B6-2	0.96	0.02	0.14	0.13	-0.67	0.62	-0.59	1.03	4.65	-2.03
B6-3	0.88	0.04	0.15	0.11	-0.68	0.65	-0.47	1.04	4.94	-2.21
B6-4	0.81	0.03	0.17	0.09	-0.69	0.66	-0.49	1.04	4.2	-2.44
B21-1	1.12	-1.15	0.07	0.23	-1.64	0.61	-1.93	0.95	2.35	-2.72
B21-2	0.59	-1.12	0.09	0.24	-1.61	0.66	-1.79	0.97	2.19	-2.71
B21-3	0.51	-1.12	0.1	0.2	-1.61	0.67	-1.66	0.97	2.15	-2.9
B21-4	0.45	-1.1	0.12	0.16	-1.62	0.68	-1.55	0.97	2.07	-3.09
B17-1	2.56	0.29	0.12	0.09	-0.53	0.61	-0.61	1	2.1	-2.1
B17-2	1.34	0.3	0.14	0.09	-0.5	0.67	-0.52	1.02	2.25	-2.04
B17-3	1.26	0.31	0.15	0.07	-0.48	0.69	-0.46	1.01	2.75	-2.21
B17-4	1.19	0.31	0.16	0.05	-0.49	0.7	-0.42	1.02	2.37	-2.33
U7-1	1.11	0.32	0.14	-0.04	-0.43	0.62	-0.49	1.03	1.52	-4.83
U7-2	0.84	0.32	0.16	-0.05	-0.44	0.72	-0.42	1.05	2.08	-4.24
U7-3	0.82	0.32	0.18	-0.06	-0.45	0.73	-0.37	1.04	2.17	-4.35
U7-4	0.83	0.33	0.19	-0.06	-0.47	0.74	-0.33	1.03	2.04	-4.31
B9-1	1.92	0.09	0.13	0.14	-0.64	0.56	-0.58	1.01	3.36	-2.04
B9-2	0.99	0.1	0.15	0.14	-0.6	0.63	-0.5	1.02	3.24	-1.94
B9-3	0.92	0.12	0.16	0.11	-0.59	0.65	-0.43	1.03	3.25	-2.14
B9-4	0.86	0.12	0.17	0.09	-0.6	0.65	-0.41	1.03	3.21	-2.32
U4-1	0.91	-0.06	0.14	0	-0.75	0.61	-0.86	1.01	1.33	-5.62
U4-2	0.68	-0.05	0.16	-0.02	-0.77	0.71	-0.73	1.03	1.93	-4.8
U4-3	0.65	-0.04	0.17	-0.03	-0.78	0.72	-0.68	1.02	1.97	-4.95
U4-4	0.63	-0.04	0.19	-0.04	-0.8	0.73	-0.63	1.01	1.83	-4.85
U5-1	0.99	0.21	0.11	-0.06	-0.49	0.58	-0.52	1.02	1.29	-4.9
U5-2	0.74	0.22	0.13	-0.08	-0.5	0.68	-0.44	1.03	2.03	-4.29
U5-3	0.71	0.22	0.14	-0.08	-0.51	0.7	-0.39	1.03	2.02	-4.32
U5-4	0.71	0.23	0.16	-0.09	-0.53	0.71	-0.36	1.02	1.86	-4.31
U8-1	0.95	0.27	0.12	-0.06	-0.43	0.59	-0.46	1.04	1.6	-4.79
U8-2	0.72	0.27	0.14	-0.07	-0.44	0.68	-0.37	1.05	2.45	-4.23
U8-3	0.7	0.27	0.16	-0.08	-0.45	0.71	-0.31	1.05	2.63	-4.21
U8-4	0.69	0.28	0.17	-0.08	-0.47	0.71	-0.29	1.04	2.61	-4.22