

**Table S1** Peptide profile of RSH identified by UPLC-qTOF-MS/MS

No	Charge	RT meas.[min]	m/z calc.	m/z meas.	Peptide sequence	Percentage of hydrophobic amino acids/%	Length	Peptide ranker score
1	1	7.6	245.1860	245.1859	I(L)L	100	2	0.39(0.62)
2	1	6.3	231.1703	231.1704	I(L)V	100	2	0.06(0.10)
3	1	6.0	848.3838	848.3848	FAGDDAPR	50	8	0.64
4	1	6.7	532.2588	532.2611	I(L)GVDE	40	5	0.07(0.07)
5	1	4.3	260.1969	260.1969	I(L)K	50	2	0.10(0.17)
6	1	8.1	503.2685	503.2708	I(L)EEI(L)	50	4	0.05(0.06)
7	1	4.4	219.1339	219.1342	TV	100	2	0.03
8	1	6.7	237.1234	237.1234	AF	100	2	0.97
9	1	5.0	318.1660	318.1657	I(L)AD	66.7	3	0.14(0.16)
10	1	6.7	457.2657	457.2654	VI(L)EP	50	4	0.10(0.11)
11	2	5.3	878.4134	440.2139	VAPEEHPT	37.5	8	0.14
12	1	7.8	475.2399	475.2396	I(L)VDE	50	4	0.04(0.04)
13	1	7.9	403.2551	403.2544	I(L)GI(L)T	50	4	0.21(0.31)
14	1	4.3	189.1234	189.1238	AV	100	2	0.06
15	1	9.0	441.3071	441.3067	I(L)I(L)VP	75	4	0.23(0.28)
16	1	5.7	304.1867	304.1865	I(L)TA	75	3	0.08(0.102)
17	1	2.8	269.1608	269.1607	I(L)H	50	2	0.21(0.34)
18	1	5.2	348.1765	348.1763	I(L)SE	33.3	3	0.06(0.06)
19	1	5.7	295.1288	295.1288	FE	50	2	0.59
20	1	5.2	253.1183	253.1184	AY	100	2	0.35
21	1	5.9	279.1339	279.134	PY	100	2	0.74
22	1	5.1	269.1132	269.1132	SY	50	2	0.26
23	1	2.9	246.1448	246.1449	VQ	50	2	0.04
24	1	1.6	161.0921	161.0926	AA	100	2	0.19
25	1	1.6	235.0925	235.0925	SE	50	2	0.04
26	1	6.1	261.1445	261.1445	EI(L)	50	2	0.05(0.07)
27	1	5.3	267.1339	267.1340	TF	50	2	0.83
28	1	4.8	311.1238	311.1238	YE	50	2	0.07
29	1	6.0	223.1077	223.1080	FG	50	2	0.99
30	1	2.1	277.1030	277.1028	EE	0	2	0.02
31	1	1.7	255.1452	255.1452	VH	50	2	0.07
32	1	6.8	572.2926	572.2923	VI(L)DPE	60	5	0.11(0.11)
33	1	6.3	715.3752	716.3809	TTPLTPS	42.9	7	0.11
34	2	9.5	812.4644	407.2394	DKILDPL	42.9	7	0.49
35	2	9	798.4487	400.2316	TLDALGPL	62.5	8	0.40
36	2	8.9	798.4487	400.2315	ATAILDVPV	75	8	0.18
37	2	5.6	640.3908	321.2026	IVAPGKG	57.1	7	0.25
No	Charge	RT meas.[min]	m/z calc.	m/z meas.	Peptide sequence	Percentage of hydrophobic amino acids/%	Length	Peptide ranker score
38	1	5.2	239.1026	239.1028	GY	50	2	0.74

39	1	7.5	332.2180	332.2174	I(L)SI(L)	66.7	3	0.17(0.29)
40	1	7.4	389.2395	389.2389	VAI(L)S	75	4	0.07(0.09)
41	2	7.5	938.4246	470.2196	GVDNPGHPF	44.4	9	0.72
42	2	4.6	700.3140	351.1642	AGDDAPR	42.9	7	0.54
43	1	9.4	451.2187	451.2187	GI(L)DF	50	4	0.83(0.86)
44	1	7.1	265.1547	265.1544	VF	100	2	0.82
45	1	6.4	348.1765	348.1764	SEI(L)	33.3	3	0.07(0.10)
46	1	3.6	348.1401	348.1399	AEE	33.3	3	0.03
47	1	9.9	707.4582	708.4641	VILPVPA	100	7	0.25
48	2	6.4	1042.4931	522.2543	DNIKDLDPN	33.3	9	0.20
49	1	5.3	376.1714	376.1714	I(L)DE	33.3	3	0.06(0.07)
50	1	5.1	294.1812	294.1800	KF	50	2	0.91
51	1	2.1	232.1292	232.1292	VN	50	2	0.05
52	1	6.5	658.3056	658.3038	EI(L)PDGQ	33.3	6	0.16(0.19)
53	1	2.1	274.1874	274.1872	VR	50	2	0.11
54	1	1.5	218.1135	218.1136	AE	50	2	0.05
55	1	6.6	318.2023	318.2021	VSI(L)	66.7	3	0.10(0.10)
56	1	1.5	207.0975	207.0977	ST	0	2	0.06
57	2	6.1	868.4654	435.2400	TEAPLNPK	50	8	0.22
58	1	5.5	288.1918	288.1917	I(L)R	50	2	0.33(0.57)
59	1	7.6	276.1343	276.1343	AW	100	2	0.97
60	1	6.8	380.1816	380.1813	VFD	66.7	3	0.41
61	1	7.8	546.2745	546.2770	I(L)EGDI(L)	40	5	0.13(0.24)
62	1	1.5	347.1925	347.1919	I(L)SQ	33.3	3	0.11(0.13)
63	1	6.2	508.2878	508.2876	AI(L)APH	80	5	0.35(0.36)
64	1	6.4	375.1874	375.1873	NEI(L)	33.3	3	0.05(0.07)
65	1	8.2	385.2445	385.2439	VGPL	75	4	0.58
66	1	7.6	306.1448	306.1446	TW	50	2	0.81
67	1	8.9	715.3575	716.3626	ADVMLPA	85.7	7	0.48
68	1	6.4	657.2970	658.3039	ELPDGGA	42.9	7	0.27
69	2	7.7	793.3793	397.6969	MFLAANQ	71.4	7	0.32
70	2	7.7	775.4228	388.7186	IEAPPHI	71.4	7	0.29
71	1	2.6	422.1882	422.1882	SGGTT	0	5	0.23
72	1	6.5	280.1292	280.1291	NF	50	2	0.94
73	1	8.5	332.2180	332.2175	SI(L)I(L)	66.7	3	0.20(0.45)
74	1	1.3	227.1139	227.1141	AH	50	2	0.21
75	1	4.8	368.1452	368.1453	YEG	33.3	3	0.15
76	1	8.7	374.2286	374.2284	NQI(L)	33.3	3	0.10(0.18)

No	Charge	RT meas.[min]	m/z calc.	m/z meas.	Peptide sequence	Percentage of hydrophobic amino acids/%	Length	Peptide ranker score
77	1	1.8	386.1670	386.1669	TEH	0	3	0.04
78	1	4.2	378.1507	378.1507	TEE	0	3	0.02
79	1	7.9	907.3923	908.3922	SYELPDGQ	37.5	8	0.27
80	1	9.1	894.5062	895.5070	IVPIVEPE	75	8	0.10
81	3	9.5	2427.3155	810.4459	AKTVPSTAGQRVLAQMLAEELKA	52.2	23	0.16
82	1	9.0	745.3680	746.3728	VSEMLPA	71.4	7	0.30
83	2	9.2	1014.5750	508.2951	LFDKPVSPL	66.7	9	0.52

84	1	1.6	246.1812	246.1813	VK	50	2	0.03
85	1	1.1	234.1448	234.1451	SK	0	2	0.07
86	1	2.2	187.1077	187.1081	PA	100	2	0.53
87	1	9.6	350.2074	350.2070	I(L)AF	100	3	0.82(0.87)
88	1	3.1	310.1761	310.1760	YK	50	2	0.15
89	1	7.4	292.1292	292.1288	SW	50	2	0.93
90	1	3.9	347.1561	347.1559	AGAE	50	4	0.13
91	1	8.6	537.2555	537.2578	I(L)EEF	50	4	0.20(0.21)
92	1	2.5	272.1717	272.1718	PR	50	2	0.79
93	1	6.3	635.2883	635.2876	SADI(L)TE	33.3	6	0.12(0.13)
94	1	2.4	414.1619	414.1618	EEH	0	3	0.04
95	1	7.3	737.4165	737.4164	TVPPAVPG	75	8	0.30
96	1	10.1	540.3756	540.3756	VI(L)I(L)PV	100	5	0.16(0.18)
97	3	9.8	2544.3408	849.4619	AQTVDVLRINRVLSDNIRSF	40.9	22	0.26
98	1	10.2	822.4851	823.4885	DVILPVPA	87.5	8	0.28
99	1	8.5	802.4072	803.4085	LESDLVQ	42.7	7	0.08
100	1	7.7	788.3916	789.3956	DEADVLR	57.1	7	0.13
101	2	8.0	993.4767	497.7458	ILPDGDHDL	44.4	9	0.28
102	2	4.7	660.3079	331.1635	ATANTSP	42.9	7	0.09
103	2	7.3	617.3384	310.1759	IGGSALT	42.9	7	0.23
104	1	9.5	586.3784	586.3808	I(L)VI(L)I(L)E	80	5	0.07(0.09)
105	1	9.2	401.2758	401.2756	I(L)GVI(L)	75	4	0.18(0.57)
106	1	3.1	364.1351	364.1352	TDE	0	3	0.03
107	1	9.3	676.3260	676.3292	AI(L)NDPF	66.7	6	0.79(0.79)
108	1	9.3	313.1547	313.1544	FF	100	2	1.00
109	1	9.8	358.2700	358.2699	I(L)I(L)I(L)	100	3	0.23(0.57)
110	1	3.7	457.2041	457.2038	ATHE	25	4	0.05
111	1	2.7	173.0921	173.0927	GP	50	2	0.91
112	1	2.6	377.1667	377.1666	TEQ	0	3	0.03
113	1	3.6	400.1463	400.1461	DHE	0	3	0.07
114	1	7.3	518.2821	518.2817	I(L)TGDI(L)	40	5	0.14(0.26)
115	1	8.7	346.2336	346.2334	I(L)TI(L)	66.7	3	0.10(0.19)

No	Charge	RT meas.[min]	m/z calc.	m/z meas.	Peptide sequence	Percentage of hydrophobic amino acids/%	Length	Peptide ranker score
116	1	2.9	375.2238	375.2236	VEK	33.3	3	0.02
117	1	2.7	319.1612	319.1611	VSN	33.3	3	0.06
118	1	2.6	404.1776	404.1776	QEK	0	3	0.04
119	1	1.7	535.1874	536.1950	GDGGGSS	0	7	0.21

Hydrophobic amino acids: Ala, Cys, Val, Met, Ile, Leu, Tyr, Phe and Pro

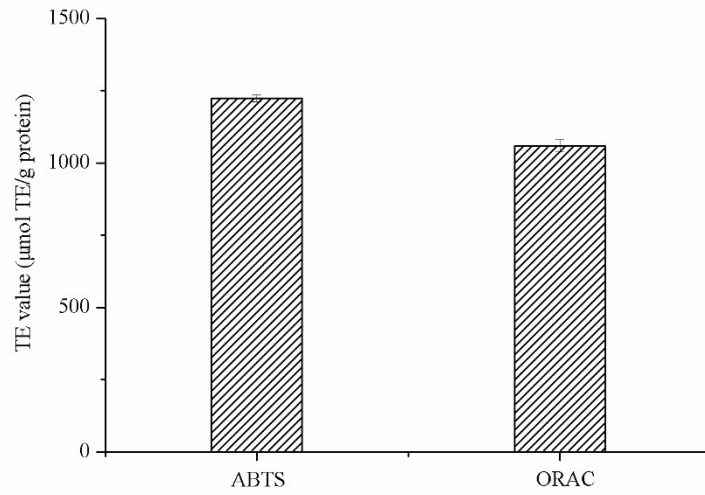


Fig S1 Free-radical scavenging activity of RSH determined in ABTS and ORAC assay. The data are represented as means  $\pm$  SD.