Table **S1** Information of EA patients

No.	Age(year)	Gender	Clinical symptoms	Other allergy	IgE(kU/I)
1	33	Male	AR	Animal allergy	12.8
2	51	Male	AR	Timothy allergy	15.8
3	49	Male	AR	Shrimp allergy	16.5
4	28	Male	AR	Timothy allergy	24.9
5	16	Male	AR	Peanut allergy	26.3
6	47	Female	AR	None	64.6

AR, allergic rhinitis

Table S2 Glycated peptides of OVA samples

Native peptide	Position	Δppm	sequence	Glycated peptide	DSP (%)	Glycated site
			OVA-All			
1105.5166^{+2}	1–20	-3.22	(-)MGSIGAASMEFCFDVFKELK(V)	1186.5938^{+2}	14.78±0.82	K17/K20
595.7994^{+2}	18–27	0.21	(K)ELKVHHANEN(I)	676.8630^{+2}	4.63±0.46	K20
381.7343^{+2}	55–60	-0.99	(I)NKVVRF(D)	462.7611^{+2}	63.26±1.55	K56
381.7343^{+2}	55–60	-0.99	(I)NKVVRF(D)	462.2443^{+2}	42.31±4.48	R59
589.2911^{+2}	61–71	1.17	(F)DKLPGFGDSIE(A)	670.3202^{+2}	64.11±11.50	K62
379.7113^{+2}	85–90	-0.27	(L) RDILNQ(I)	460.7093^{+2}	2.38±0.14	R85
465.2379^{+2}	89-96	-0.17	(L)NQITKPND(V)	546.2649^{+2}	24.17±2.01	K93
518.7693^{+2}	91–99	0.35	(Q)ITKPNDVYS(F)	599.7980^{+2}	71.81±3.18	K93
415.6877^{+2}	107–112	0.25	(L)YAEERY(P)	496.2110^{+2}	5.10±0.48	**R111**
548.2831^{+2}	120–128	-2.39	(L)QCVKELYRG(G)	629.8242^{+2}	0.71±0.22	K123/R127
404.2216^{+2}	124–130	-0.01	(K)ELYRGGL(E)	485.2030^{+2}	0.78±0.25	R127
401.7243^{+2}	142–148	-0.52	(Q)ARELINS(W)	482.7276^{+2}	1.89±0.06	R143
364.2448^{+2}	157–162	-0.22	(G)IIRNVL(Q)	445.7182^{+2}	67.04±9.64	R159
563.8332^{+2}	157–166	1.1	(G)IIRNVLQPSS(V)	644.8016^{+2}	11.69±0.85	R159
431.7631^{+2}	179–185	0.44	(A)IVFKGLW(E)	512.7898^{+2}	13.09±2.94	**K182**
477.2146^{+2}	188–195	0.89	(K)AFKDEDTQ(A)	558.2404^{+2}	1.15±0.12	K190
504.2541^{+2}	197–204	3.02	(A)MPFRVTEQ(E)	585.2795^{+2}	0.19±0.06	R200

438.7326^{+2}	198–204	0.60	(M)PFRVTEQ(E)	519.2724^{+2}	5.18±1.64	R200
473.7365^{+2}	204–211	-0.54	(E)QESKPVQM(M)	554.7639^{+2}	48.87±6.82	K207
409.7073^{+2}	205–211	-0.54	(Q)ESKPVQM(M)	490.7342^{2+}	55.15±4.64	K207
355.6862^{+2}	218–223	-0.39	(L)FRVASM(A)	436.2662^{2+}	7.34±2.16	**R219**
566.8132^{+2}	318–328	-1.51	(S)SAESLKISQAV(H)	647.8063^{2+}	2.94±1.30	**K323**
810.4254^{+2}	318–333	-3.9	(S)SAESLKISQAVHAAHA(E)	891.9540^{2+}	16.59±1.71	**K323**
787.3975^{+2}	326–340	3.02	(S)QAVHAAHAEINEAGR(E)	868.4183^{2+}	2.61±0.05	**R340**
500.7279^{+2}	357–364	0.23	(S)EEFRADHP(F)	581.7853^{2+}	47±1.12	**R360**
613.8680^{+2}	369–379	2.57	(C)IKHIATNAVLF(F)	694.8956^{2+}	1.13±0.38	**K370**
383.1894^{+2}	380–386	0.39	(F)FGRCVSP(-)	464.7294^{2+}	1.43±0.03	**R382**
			OVA-Gal			
474.2563^{+2}	18–25	-0.44	(K)ELKVHHAN(E)	555.7860^{+2}	28.29±1.12	K20
620.3224^{+2}	43–53	3.82	(V)YLGAKDSTRTQ(I)	782.8384^{+2}	29.68±0.44	K47, R51
589.2910^{+2}	61–71	1	(F)DKLPGFGDSIE(A)	670.3182^{+2}	52.01±6.47	K62
379.7115^{+2}	85–90	0.25	(L)RDILNQ(I)	460.7511^{+2}	1.63±0.62	R85
518.7695^{+2}	91–99	0.74	(Q)ITKPNDVYS(F)	599.7964^{+2}	56.26±2.97	K93
592.3040^{+2}	91–100	1.15	(Q)ITKPNDVYSF(S)	673.3317^{+2}	45.58±10.13	K93
460.2478^{+2}	109–115	1.43	(A)EERYPIL(P)	541.7914^{+2}	3.11±1.8	**R111**
562.7851^{+2}	117–125	-2.4	(P)EYLQCVKEL(Y)	643.3199^{+2}	3.40±1.36	K123
817.9497^{+2}	122–135	1.26	(C)VKELYRGGLEPINF(Q)	899.4775^{+2}	78.92±3.82	K123/R127
364.2447^{+2}	157–162	-0.49	(G)IIRNVL(Q)	445.7184^{+2}	10.02±5.56	R159
563.8329^{+2}	157–166	0.56	(G)IIRNVLQPSS(V)	644.8018^{+2}	11.12±0.61	R159

664.7935^{+2}	189–199	-2.26	(A)FKDEDTQAMPF(R)	745.8197^{+2}	35.96±5.36	K190
374.7031^{+2}	198–203	0.14	(M)PFRVTE(Q)	455.7233^{+2}	2.43±1.86	R200
438.7327^{+2}	198–204	0.83	(M)PFRVTEQ(E)	519.2717^{+2}	3.73±0.08	R200
473.7370^{+2}	204–211	0.51	(E)QESKPVQM(M)	554.7635^{+2}	69.68±13.48	K207
355.6861^{+2}	218–223	-0.68	(L)FRVASM(A)	436.2662^{+2}	1.48±0.73	**R219**
646.8487^{+2}	223–233	-3.97	(S)MASEKMKILEL(P)	727.3584^{+2}	71.45±11	**K227/K229**
440.7238^{+2}	261–267	-0.85	(I)NFEKLTE(W)	521.7288^{+2}	1.22±0.26	K264
453.7304^{+2}	263–269	0.19	(F)EKLTEWT(S)	534.2555^{+2}	2.32±1.33	K264
809.4227^{+2}	323–337	2.34	(L)KISQAVHAAHAEINE(A)	890.4494^{+2}	22.66±5.92	**K323**
787.3971^{+2}	339–355	3.36	(A)GREVVGSAEAGVDAASV(S)	$868.419^{+2}6$	2.97±0.07	**R340**
566.2833^{+2}	358–366	1.02	(E)EFRADHPFL(F)	647.8231^{+2}	1.81±1.03	**R360**
501.7629^{+2}	359–366	2.94	(E)FRADHPFL(F)	582.7881^{+2}	0.18±0.04	**R360**
383.1893^{+2}	380–386	0.13	(F)FGRCVSP(-)	464.7289^{+2}	7.38±0.62	**R382**
			OVA-Ido			
595.7988^{+2}	18–27	-0.79	(K)ELKVHHANEN(I)	676.3191^{+2}	6.03±2.06	K20
484.5999^{+3}	42–54	-0.09	(M)VYLGAKDSTRTQI(N)	538.6177^{+3}	82.656±0.21	K47
589.2906^{+2}	61–71	0.32	(F)DKLPGFGDSIE(A)	670.3173^{+2}	48.88±14.82	K62
379.7111^{+2}	85–90	-0.79	(L)RDILNQ(I)	460.7090^{+2}	1.84±0.58	R85
465.2377^{+2}	89–96	-0.60	(L)NQITKPND(V)	546.2651^{+2}	3.85±2.3	K93
415.6873^{+2}	107–112	-0.71	(L)YAEERY(P)	496.2111^{+2}	9.31±1.87	**R111**
404.2214^{+2}	124–130	-0.50	(K)ELYRGGL(E)	485.2032^{+2}	3.39±0.47	R127
401.7240^{+2}	142–148	-1.27	(Q)ARELINS(W)	482.7278^{+2}	21.40±5.31	R143

563.8335^{+2}	157–166	1.63	(G)IIRNVLQPSS(V)	644.8016^{+2}	8.81±1.35	R159
778.4267^{+2}	157–170	1.46	(G)IIRNVLQPSSVDSQ(T)	859.4024^{+2}	5.07±3.75	R159
431.7628^{+2}	179–185	-0.24	(A)IVFKGLW(E)	512.7894^{+2}	7.14±1.07	**K182**
477.2142^{+2}	189–196	0.06	(A)FKDEDTQA(M)	558.2410^{+2}	11.47±1.62	K190
374.7029^{+2}	198–203	-0.39	(M)PFRVTE(Q)	455.7235^{2+}	2.35±0.38	R200
438.7320^{+2}	198–204	-0.76	(A)PFRVTEQ(E)	519.2715^{+2}	4.96±0.32	R200
409.7071^{+2}	205–211	-0.91	(Q)ESKPVQM(M)	490.7337^{+2}	63.39±8.71	K207
355.6860^{+2}	218–223	-0.96	(L)FRVASM(A)	436.2292^{+2}	12.5±0.21	**R219**
440.7231^{+2}	261–267	-2.44	(I)NFEKLTE(W)	521.7293^{+2}	15.74±6.69	K264
378.2121^{+3}	323–333	-0.37	(L)KISQAVHAAHA(E)	432.2295^{3+}	6.61±1.07	**K323**
459.2195^{+2}	334–341	-0.62	(A)EINEAGRE(V)	540.7567^{+2}	0.52±0.16	**R340**
423.2271^{+2}	338–346	-0.75	(E)AGREVVGSA(E)	504.2661^{2+}	15.21±1.93	**R340**
428.2279^{+2}	360–366	1.59	(F)RADHPFL(F)	509.2493^{+2}	2.58±0.35	**R360**
			OVA-Man			
669.3479^{+2}	58–69	2.76	(V)VRFDKLPGFGDS(I)	750.8539^{+2}	9.42±1.05	R59/K62
567.2956^{+2}	62–72	0.18	(D)KLPGFGDSIEA(Q)	648.346^{+2}	10.43±1.46	K62
518.7693^{+2}	91–99	0.36	(Q)ITKPNDVYS(F)	599.7968^{+2}	77.83±0.51	K93
577.2997^{+2}	106–114	2.88	(R)LYAEERYPI(L)	658.8264^{+2}	1.59±0.17	**R111**
545.6351^{+3}	122–135	0.41	(C)VKELYRGGLEPINF(Q)	599.6541^{+3}	63.53±11.35	K123/R127
682.3330^{+2}	133–144	-0.98	(P)INFQTAADQARE(L)	763.3306^{+2}	9.55±0.22	R143
364.2446^{+2}	157–162	-0.77	(G)IIRNVL(Q)	445.7819^{+2}	2.21±0.46	R159
431.7629^{+2}	179–185	-0.02	(A)IVFKGLW(E)	512.7891^{+2}	44.86±3.27	**K182**

438.7323^{+2}	198–204	-0.08	(M)PFRVTEQ(E)	519.2715^{+2}	2.67±1.14	R200
473.7373^{+2}	204–211	0.56	(E)QESKPVQM(M)	554.7631^{+2}	1.35±0.14	K207
497.2661^{+2}	260–267	-0.21	(I)INFEKLTE(W)	578.2926^{+2}	65.91±1.91	K264
453.2292^{+2}	272–278	0.22	(S)NVMEERK(I)	534.2808^{+2}	1.64±0.47	**R277/K278**
509.7696^{+2}	272–279	-3.01	(S)NVMEERKI(-K)	671.3365^{+2}	36.04±3.64	**R277, K278**
809.4217^{+2}	323–337	1.1	(L)KISQAVHAAHAEINE(A)	890.9218^{+2}	8.09±0.35	**K323**
383.1892^{+2}	380–386	-0.13	(F)FGRCVSP(-)	464.7287^{+2}	2.72±0.01	**R382**
			OVA-Glu			
589.2913^{+2}	61–71	1.51	(F)DKLPGFGDSIE(A)	670.3203^{+2}	78.81±12.64	K62
379.7115^{+2}	85–90	0.26	(L)RDILNQ(I)	670.3175^{+2}	3.41±0.61	R85
518.7694^{+2}	91–99	0.55	(Q)ITKPNDVYS(F)	599.7969^{+2}	67.79±0.82	K93
592.3041^{+2}	91–100	1.32	(Q)ITKPNDVYSF(S)	599.2183^{+2}	64.50±4.97	K93
771.8785^{+2}	107–118	1.45	(L)YAEERYPILPEY(L)	852.4627^{+2}	81.44±7.75	**R111**
364.2448^{+2}	157–162	-0.22	(G)IIRNVL(Q)	445.7189^{+2}	2.01±1.47	R159
431.7639^{+2}	179–185	2.3	(A)IVFKGLW(E)	512.7910^{+2}	77.66±2.83	**K182**
504.2537^{+2}	197–204	2.23	(A)MPFRVTEQ(E)	585.2797^{+2}	2.88±0.12	R200
438.7327^{+2}	198–204	0.83	(M)PFRVTEQ(E)	519.2717^{+2}	2.12±0.49	R200
409.7075^{+2}	205–211	0.07	(Q)ESKPVQM(M)	490.7339^{+2}	4.76±0.41	K207
381.2330^{+2}	226 – 231	-0.33	(S)EKMKIL(E)	543.2864^{+2}	64.36±9.48	**K227, K229**
440.7241^{+2}	261–267	-0.17	(I)NFEKLTE(W)	521.764^{+2}	1.071±0.25	K264
402.7267^{+2}	320–326	-0.04	(A)ESLKISQ(A)	483.7532^{+2}	31.36±8.5	**K323**
566.2837^{+2}	360–366	1.73	(E) EFRADHPFL(F)	647.3198^{+2}	0.54±0.07	**R360**

The glycated sites locating at the mian strands of β-sheet were indicated in bold.

Table S3 Peptide mapping of N-Oval

No.	m/z	MH+ experimental	MH+ theoretical	Δppm	Start	End	Sequence
1	920.4112+2	1839.8151	1839.8114	2.01	1	17	(-)MGSIGAASMEFCFDVFK(E)
2	1108.5546^{+3}	3323.6492	3323.6414	2.36	12	40	(F)CFDVFKELKVHHANENIFYCPIAIMSALA(M)
3	750.4035	750.4035	750.4032	0.357	14	19	(F)DVFKEL(K)
4	442.2338	442.2338	442.2336	0.345	28	30	(N)IFY(C)
5	404.2191+3	1210.6427	1210.6426	0.0988	42	52	(M)VYLGAKDSTRT(Q)
6	522.6145+3	1565.8289	1565.8282	0.479	42	55	(M)VYLGAKDSTRTQIN(K)
7	520.3241	520.3241	520.3242	-0.18	57	60	(K)VVRF(D)
8	522.2919	522.2919	522.2922	-0.622	60	63	(R)FDKL(P)
9	629.2736+2	1257.5399	1257.5399	0.0384	61	71	(F)DKLPGFGDS(Phospho)IE(A)
10	664.7926+2	1328.5779	1328.577	0.703	61	72	(F)DKLPGFGDS(Phospho)IEA(Q)
11	1010.4077	1010.4077	1010.4095	-1.8	68	77	(G)DSIEAQCGTS(V)
12	444.2166^{+2}	887.4259	887.4217	4.72	75	83	(C)GTSVNVHSS(L)
13	516.3139	516.3139	516.314	-0.239	84	87	(S)LRDI(L)
14	592.6479+3	1775.9291	1775.9286	0.286	85	99	(L)RDILNQITKPNDVYS(F)
15	465.2376+2	929.4679	929.4687	-0.82	89	96	(L)NQITKPND(V)
16	639.8199+2	1278.6325	1278.6325	0.0522	89	99	(L)NQITKPNDVYS(F)

17	646.3885	646.3885	646.3883	0.386	101	106	(F)SLASRL(Y)
18	577.2983^{+2}	1153.5893	1153.5888	0.453	106	114	(R)LYAEERYPI(L)
19	682.3641^{+2}	1363.7209	1363.7256	-3.45	106	116	(R)LYAEERYPILP(E)
20	844.4818	844.4818	844.4815	0.376	113	119	(Y)PILPEYL(Q)
21	762.4038	762.4038	762.4032	0.745	115	120	(I)LPEYLQ(C)
22	562.7849^{+2}	1124.5625	1124.5656	-2.76	117	125	(P)EYLQCVKEL(Y)
23	639.8462^{+2}	1278.6851	1278.6841	0.802	125	135	(E)LYRGGLEPINF(Q)
24	568.7699^{+2}	1136.5325	1136.5331	-0.487	135	144	(N)FQTAADQARE(L)
25	495.2360^{+2}	989.4647	989.4647	0.061	136	144	(F)QTAADQARE(L)
26	929.9893^{+2}	1858.9713	1858.9658	3	144	159	(R)ELINSWVESQTNGIIR(N)
27	613.3667^{+2}	1225.7261	1225.7263	-0.142	157	167	(G)IIRNVLQPSSV(D)
28	681.8324^{+2}	1362.6575	1362.657	0.416	161	173	(N)VLQPSSVDSQTAM(V)
29	588.7995^{+2}	1176.5917	1176.5929	-1	167	177	(S)VDSQTAMVLVN(A)
30	492.6257^{+3}	1475.8625	1475.8654	-1.96	171	184	(Q)TAMVLVNAIVFKGL(W)
31	676.4377	676.4377	676.4392	-2.25	179	184	(A)IVFKGL(W)
32	428.7217+4	1711.865	1711.869	-2.35	180	193	(I)VFKGLWEKAFKDED(T)
33	477.2140+2	953.4207	953.4211	-0.36	188	195	(K)AFKDEDTQ(A)
34	542.7343^{+2}	1084.4613	1084.4616	-0.21	189	197	(A)FKDEDTQAM(P)
35	591.2610+2	1181.5147	1181.5143	0.345	189	198	(A)FKDEDTQAMP(F)
36	591.2610^{+2}	1181.5147	1181.5143	0.345	190	199	(F)KDEDTQAMPF(R)
37	789.9045^{+2}	1578.8017	1578.7945	4.6	199	211	(P)FRVTEQESKPVQM(M)
38	473.7367+2	946.4661	946.4662	-0.126	204	211	(E)QESKPVQM(M)

39	475.2275+2	949.4477	949.4482	-0.449	205	212	(Q)ESKPVQMM(Y)
40	740.3981	740.3981	740.3978	0.469	213	218	(M)YQIGLF(R)
41	710.366	710.366	710.3654	0.835	218	223	(L)FRVASM(A)
42	412.7039+2	824.4005	824.4005	0.0629	223	229	(S)MASEKMK(I)
43	588.3373+2	1175.6673	1175.6671	0.232	229	239	(M)KILELPFASGT(M)
44	696.8414^{+2}	1392.6755	1392.6749	0.437	237	249	(A)SGTMSMLVLLPDE(V)
45	716.3466	716.3466	716.3461	0.682	247	253	(L)PDEVSGL(E)
46	504.2665	504.2665	504.2664	0.19	249	253	(D)EVSGL(E)
47	518.2458	518.2458	518.2457	0.253	254	257	(L)EQLE(S)
48	722.3725	722.3725	722.3719	0.786	258	263	(E)SIINFE(K)
49	536.3079	536.3079	536.3079	0.0463	262	265	(N)FEKL(T)
50	619.3299	619.3299	619.3297	0.27	263	267	(F)EKLTE(W)
51	597.7855+2	1194.5637	1194.5637	0.0126	263	272	(F)EKLTEWTSSN(V)
52	509.7694+2	1018.5315	1018.535	-3.4	272	279	(S)NVMEERKI(K)
53	481.5758^{+3}	1442.7128	1442.713	-0.128	285	295	(P)RMKMEEKYNLT(S)
54	682.3043	682.3043	682.3042	0.0787	289	293	(M)EEKYN(L)
55	400.5327^{+3}	1199.5835	1199.5799	3.05	292	302	(K)YNLTSVLMAMG(I)
56	600.2954+2	1199.5835	1199.5799	3.03	292	302	(K)YNLTSVLMAMG(I)
57	865.4492	865.4492	865.4522	-3.44	294	301	(N)LTSVLMAM(G)
58	736.3696	736.3696	736.3732	-4.88	298	304	(V)LMAMGIT(D)
59	851.4005	851.4005	851.4001	0.426	298	305	(V)LMAMGITD(V)
60	734.3720^{+2}	1467.7367	1467.7326	2.83	302	316	(M)GITDVFSSSANLSGI(S)

61	850.4162	850.4162	850.4153	1.11	314	322	(L)SGISSAESL(K)
62	402.7266+2	804.4459	804.4462	-0.293	320	326	(A)ESLKISQ(A)
63	517.2979	517.2979	517.298	-0.268	324	328	(K)ISQAV(H)
64	581.2863^{+2}	1161.5653	1161.5647	0.527	327	337	(Q)AVHAAHAEINE(A)
65	487.7488^{+2}	974.4903	974.4901	0.178	337	346	(N)EAGREVVGSA(E)
66	698.8092^{+2}	1396.6111	1396.6104	0.508	338	351	(E)AGREVVGS(Phospho)AEAGVD(A)
67	839.3782	839.3782	839.3781	0.072	352	359	(D)AASVSEEF(R)
68	566.2827^{+2}	1131.5581	1131.5582	-0.0407	358	366	(E)EFRADHPFL(F)
69	721.9113^{+2}	1442.8153	1442.8188	-2.42	366	378	(F)LFCIKHIATNAVL(F)
70	426.2387	426.2387	426.2387	-0.0773	378	380	(V)LFF(G)
71	482.2188	482.2188	482.218	1.63	380	383	(F)FGRC(V)

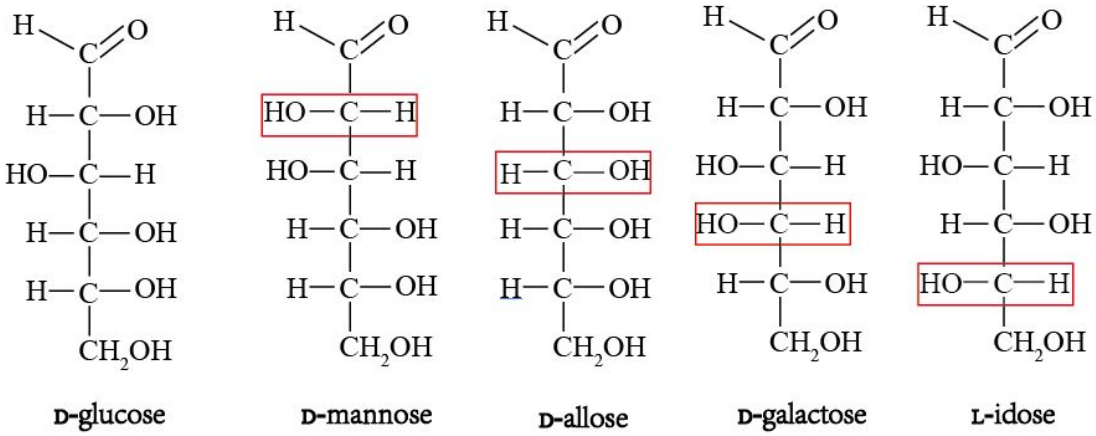

Figure S1. D-glucose and its epimers with respect to C-2, C-3,C-4 and C-5

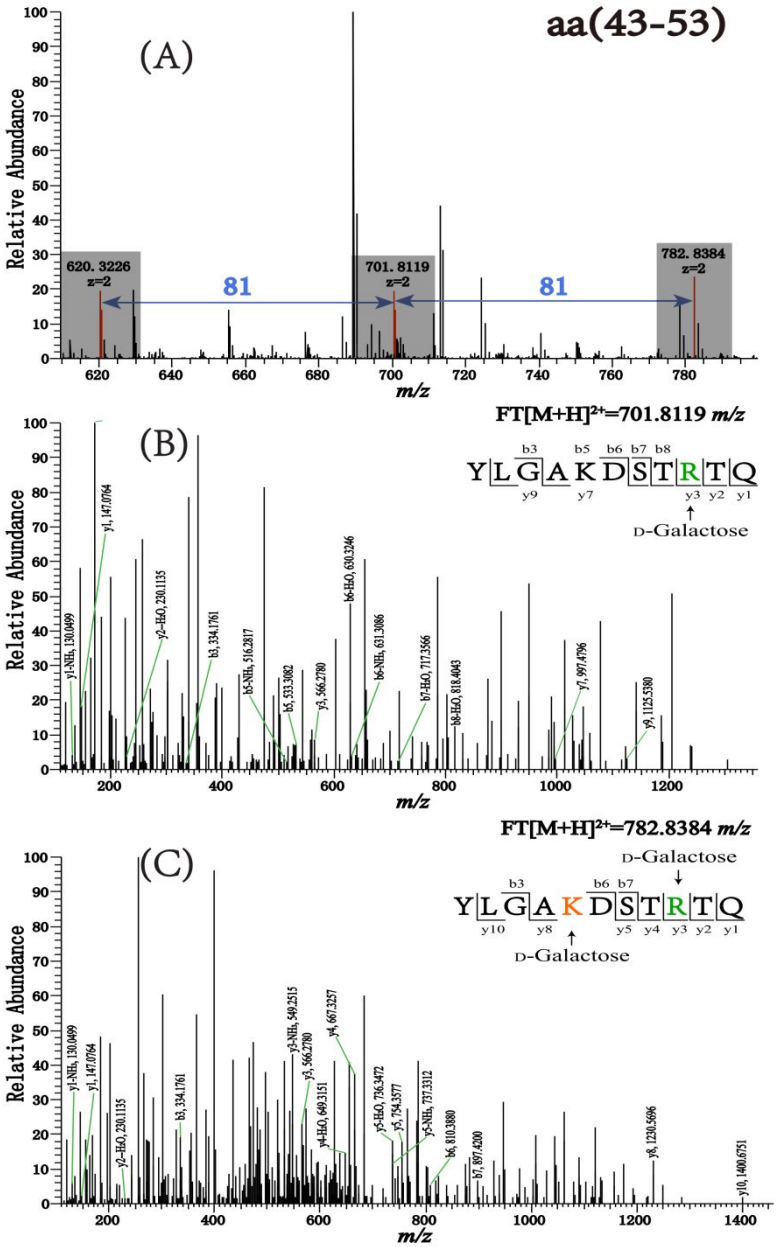

Figure S2. MS spectrum of peptide 43−53 (A) and HCD-MS/MS spectrum of mono-glycated peptide 43−53 at *m/z* 701.8119 (B) and dual-glycated peptide 43−53 at *m/z* 782.8384 from OVA-Gal. The *m/z* differences are indicated with numbers and arrows. The lysine- and arginine-related glycation sites (orange and green, respectively) is shown by arrows. The b, b-17 (NH_3), b-18 (H_2O), y, y-17, (NH_3) and y-18 (H_2O) ion fragment mass peaks are indicated in the mass spectrum.