

**Evolution of H5N1 Influenza Virus
through Proteotyping of Hemagglutinin
with High Resolution Mass Spectrometry**

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Table S1

Host-specific correlation table of all avian (1507) versus human (222) H5 hemagglutinin sequences from all regions 1997-2010 showing the frequency of occurrence (Po) of peptides in each host

Residues	Sequence #	<i>m/z</i> [M+H] ⁺ monoisotopic	Avian Po	Human Po	ΔPo
276-282	GDSTIMK	751.3654	0.61	0.56	0.05
517-523	EEISGVK	761.4039	0.96	0.98	-0.02
333-339	NSPQGER	787.3693	0.41	0.32	0.09
124-129	INHFEK	787.4097	0.87	1.00	-0.13
398-404	VNSIIDK	788.4512	0.96	0.98	-0.02
390-397	AIDGVTNK	817.4414	0.96	0.99	-0.02
327-334	LVLATGLR	842.5458	0.98	0.97	0.00
162-168	NVVWLIK	871.5400	0.89	0.80	0.09
415-421	EFNNLER	921.4424	0.93	0.95	-0.02
168-175	DNAYPTIK	921.4676	0.25	0.17	0.08
170-177	NSTYPTIK	923.4833	0.21	0.51	-0.30
405-414	MNTQFEAVGR	1152.5466	0.97	0.99	-0.02
453-462	TLDFHDSNVK	1175.5691	0.99	1	-0.01
490-499	CDNECMESVR	1185.4332	0.74	0.67	0.07
283-293	SELEYGNCNTK	1257.5416	0.76	0.78	-0.02
478-489	ELGNGCFEFYHK	1443.6361	0.53	0.69	-0.17
57-69	LCDLDGVKPLILR	1454.8400	0.85	0.76	0.10
39-51	NVTVTHAQDILEK	1467.7802	0.96	0.98	-0.02
500-513	NGTYDYPQYSEEAR	1692.7136	0.76	0.66	0.09
206-224	LYQNPTTYISVGTSTLNQR	2156.0981	0.74	0.66	0.08
134-154	SSWSDHEASSGVSSACPYQGR	2197.9204	0.24	0.09	0.14
83-102	ANPTNDLCYPGSFNDYEELK	2289.9968	0.01	0.23	-0.22
97-116	INPANDLCYPGNFNDYEELK	2329.0442	0.30	0.22	0.08
1-222	DQICIGYHANNSTEQVDTIMEK	2509.1333	0.93	0.96	-0.03
120-145	SSWSDHEASSGVSSACPYLGSPSFFR	2748.1995	0.03	0.23	-0.20
430-452	MEDGFLDVWTYNAELLVLMENER	2787.3003	0.99	0.99	-0.01
292-318	CQTPIGAINSSMPFHNIHPLTIGECPK	2905.4158	0.52	0.41	0.10
278-304	CQTPMGAINSSMPFHNIHPLTIGECPK	2923.3721	0.42	0.55	-0.13

Sequences used to establish residue positions were: A/HongKong/483/1997 (AAF74330),
 A/HongKong/213/1997 (ABP51975), A/CygnusOlor/742/2006 (ABD52284),
 A/Indonesia/CDC742/2006 (ABI49407)