
Genome Analysis Linking Recent European and African Influenza (H5N1) Viruses

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To better understand the ecology and epidemiology of the highly pathogenic avian influenza virus in its transcontinental spread, we sequenced and analyzed the complete genomes of 36 recent influenza A (H5N1) viruses collected from birds in Europe, northern Africa, and southeastern Asia. These sequences, among the first complete genomes of influenza (H5N1) viruses outside Asia, clearly depict the lineages now infecting wild and domestic birds in Europe and Africa and show the relationships among these isolates and other strains affecting both birds and humans. The isolates fall into 3 distinct lineages, 1 of which contains all known non-Asian isolates. This new Euro-African lineage, which was the cause of several recent (2006) fatal human infections in Egypt and Iraq, has been introduced at least 3 times into the European-African region and has split into 3 distinct, independently evolving sublineages. One isolate provides evidence that 2 of these sublineages have recently reassorted.

The first cases of human infection with highly pathogenic avian influenza (HPAI) strain H5N1 occurred in Hong Kong in 1997; it was brought under control by mas-

sive culling of the chicken population (1,2). An antigenically distinct strain emerged in 2002, in the same location, and has since spread to hundreds of millions of birds (3,4). More alarming has been the growing number of human influenza (H5N1) infections; by September 2006, 251 human cases had been reported, resulting in 148 deaths (2). From late 2005 to early 2006, HPAI (H5N1) was detected for the first time in birds in eastern Europe, the Middle East, and northern Africa, indications that the virus was spreading, possibly aided by wild bird migration. Human cases were reported beginning in January 2006 in Egypt, Iraq, Turkey, Djibouti, and Azerbaijan.

Methods

We sequenced and analyzed the genomes of 36 recent isolates of highly pathogenic influenza (H5N1) viruses collected from Europe, northern Africa, the Middle East, and Asia. We used high-throughput methods described previously (5).

Sample Collection

Samples primarily consisting of pooled trachea and lung tissue, pooled intestines, or tracheal and cloacal swabs collected from dead or moribund animals were processed for attempted virus isolation as described (6). Hemagglutinating isolates were typed either by reverse transcription-PCR (RT-PCR) or by serologic methods (7). RNA was extracted with the High Pure Extraction Kit (Roche, Indianapolis, IN, USA), according to manufacturer's instructions.

Primer Design

Sequences from recent human and avian influenza (H5N1) isolates were downloaded from GenBank and were aligned with MUSCLE (8). Degenerate primers were designed on the basis of consensus sequences generated with

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BioEdit (9). An M13 sequence tag was added to the 5' end of each primer to be used for sequencing. Four of the reactions were analyzed by electrophoresis on an agarose gel for quality control purposes. Primer design was optimized by analysis of the sequence success rate of each primer pair. Primers that did not perform well were redesigned and replaced in the primer set. Primers were designed to produce ≈ 500 -nt overlapping amplicons to provide $2\times$ coverage of each genomic segment. Additionally, a second set of primers was designed to produce 500-nt amplicons offset ≈ 250 nt from the original primer pair, which gave at least $4\times$ sequence coverage of each segment.

cDNA Synthesis

Amplicons tiling the genome of the influenza isolates were generated with a OneStep RT-PCR kit (QIAGEN, Valencia, CA, USA). They were treated with shrimp alkaline phosphatase-exonuclease I (U.S. Biologicals, Swampscott, MA, USA) before sequencing.

Sequencing and Assembly

Sequencing reactions were performed as described previously (5). After sequencing, each segment was downloaded, trimmed to remove amplicon primer-linker sequence as well as low-quality sequence, and assembled. A small genome assembler called Elvira, based on the open-source Minimus assembler (<http://cbcb.umd.edu/software>), has been developed to automate these tasks. The Elvira pipeline delivers exceptions, including failed reads, failed amplicons, insufficient coverage of a reference sequence (as obtained from GenBank), ambiguous consensus sequence calls, and low-coverage areas. Additional sequencing and targeted RT-PCR were conducted to close gaps and to increase coverage in low-coverage or ambiguous regions.

All sequence data used in this study are available from GenBank and also from <ftp.cbcb.umd.edu/pub/data/flu>. GenBank accession numbers are available in the supplementary data (online Technical Appendix 1, available from www.cdc.gov/EID/content/13/5/713-app1.txt).

Phylogenetic Analysis

Multiple sequence alignments of nucleotide data were performed by using MUSCLE (8) with default parameters. Most alignments of segments within a subtype lack internal gaps. Leading and trailing gaps were not considered in tree-length calculations, but all nucleotide positions were considered.

The phylogenetic trees for Figures 1, 2A, and online Appendix Figures 1–3 (available from www.cdc.gov/EID/content/13/5/713-appG1.htm, www.cdc.gov/EID/content/13/5/713-appG2.htm, and www.cdc.gov/EID/content/13/5/713-appG3.htm) were constructed by using the neighbor-joining method as implemented in PAUP* version

4.0b10 (10,11) using the F84 distance between nucleotide sequences and the default parameters. The phylogeny of 71 complete genomes (avian isolates) and 3 hemagglutinin (HA) sequences (human isolates) in Figure 2B comprises isolates chosen because they formed the European-Middle Eastern-African (EMA) clades and the Russian and Chinese sister clades in a larger analysis of 759 influenza (H5N1) isolates from the locales and host range of all H5N1 sequences published since 1996. The figure includes every member of the EMA clade for which the complete genome sequence is currently available, except chicken/Nigeria/1047–62/2006 and chicken/Kurgan/05/2005, which appear to be reassortants.

To find optimal phylogenetic trees for Figure 2B, we used a combination of tree search algorithms available in the “new technology” heuristic strategies in the TNT (12) software package (available from www.zmuc.dk/public/phylogeny/TNT). These strategies include a successive combination of hill-climbing techniques (branch swapping) followed by simulated annealing (ratcheting), divide-and-conquer (sectorial searches), and genetic algorithms (tree fusion). Figure 2B depicts a strict consensus based on 286 minimal-length trees resulting from a parsimony search of 1,000 replicates in TNT under the command “xmult = lev5.” Each component tree had a tree length of 1,613 steps. Gaps were treated as a fifth state, and all edit costs

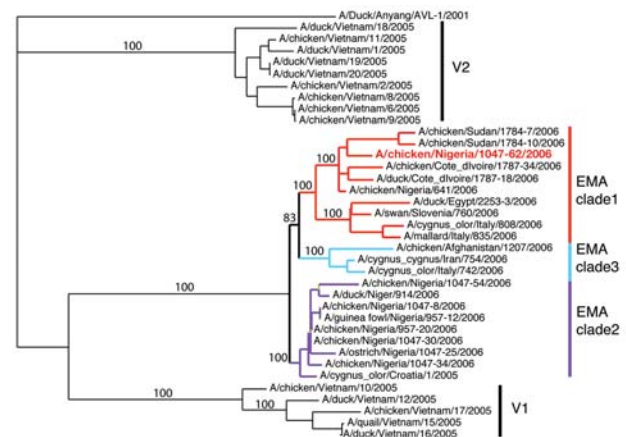


Figure 1. Phylogenetic tree of hemagglutinin (HA) segments from 36 avian influenza samples. A 2001 strain (A/duck/Anyang/AVL-1/2001) is used as an outgroup at top. Clade V1 comprises the 5 Vietnamese isolates at the bottom of the tree, and clade V2 comprises the 9 Vietnamese isolates near the top of the tree. The European-Middle Eastern-African (EMA) clade contains the remaining 22 isolates sequenced in this study; the 3 subclades are indicated by red, blue, and purple lines. The reassortant strain, A/chicken/Nigeria/1047–62/2006, is highlighted in red. Note that 4 segments including HA from this reassortant fall in EMA-1; the other 4 fall in EMA-2, as shown in online Appendix Figure 1. Bootstrap values supporting the 3 distinct EMA clades are taken from a consensus tree based on concatenated whole-genome sequences, excluding the reassortant strain. The consensus tree is provided as online Appendix Figure 2.

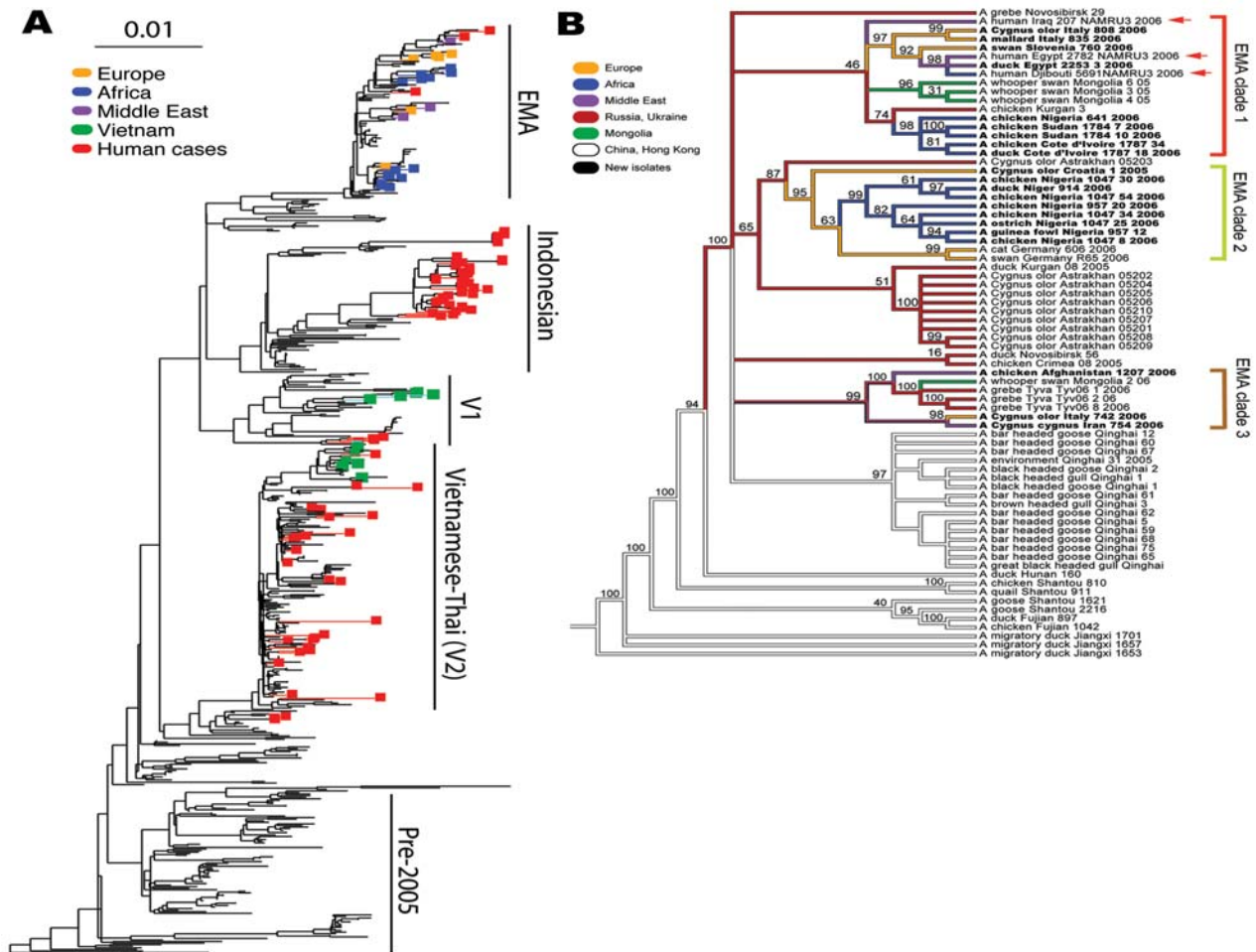


Figure 2. A) Phylogenetic tree relating the influenza A (H5N1) hemagglutinin (HA) segments of 589 avian, feline, and human viruses. The tree includes all HA segments isolated since 2000 from humans (82 isolates, minimum sequence length 1,000 nt), birds (503 isolates, minimum length 1500 nt), and cats (4 isolates). The 36 newly sequenced genomes are highlighted in color. Human cases, which occur in all 4 of the major influenza (H5N1) clades, are highlighted in red. The scale bar indicates an F84 distance of 0.01. A full-scale version of this tree is provided as online Appendix Figure 3. B) Phylogeny of 71 complete genomes (avian isolates, all 8 segments concatenated) and 3 HA sequences (human isolates, marked with red arrows) from Europe, the Middle East, Africa, Russia, and Asia. Bootstrap values represent the percentage of 1,000 bootstrap replicates for which the partition implied by the edge was observed; see Methods for further details. The 3 European-Middle Eastern-African (EMA) subclades from Figure 1 are indicated with the same color scheme. Isolates from human hosts are found only in EMA-1. Colors indicate locales. The names of the isolates newly sequenced in this study are shown in boldface text.

were given equal weights under the parsimony criterion. The heuristic tree strategy was run until a stable strict consensus was achieved. This strict consensus is a conservative estimate of the phylogenetic relationship between the isolates, where an edge is included only if it was observed in all 286 optimal trees. Separately, RAxML (13) was run over the same data for maximum likelihood analyses under the general time-reversible (GTR) mixed model of nucleotide substitution. This likelihood analysis produced a tree with the same clade contents as the parsimony tree, preserving the 3 EMA clades. Branches were traced with colors to represent the locale of isolation of the virus.

Results and Discussion

The 36 new isolates reported here greatly expand the amount of whole-genome sequence data available from recent avian influenza (H5N1) isolates. Before our project, GenBank contained only 5 other complete genomes from Europe for the 2004–2006 period, and it contained no whole genomes from the Middle East or northern Africa. Our analysis showed several new findings. First, all European, Middle Eastern, and African samples fall into a clade that is distinct from other contemporary Asian clades, all of which share common ancestry with the original 1997 Hong Kong strain. Phylogenetic trees built on each of the

8 segments show a consistent picture of 3 lineages, as illustrated by the HA tree shown in Figure 1. Two of the clades contain exclusively Vietnamese isolates; the smaller of these, with 5 isolates, we label V1; the larger clade, with 9 isolates, is V2. The remaining 22 isolates all fall into a third, clearly distinct clade, labeled EMA, which comprises samples from Europe, the Middle East, and Africa. Trees for the other 7 segments display a similar topology, with clades V1, V2, and EMA clearly separated in each case. Analyses of all available complete influenza (H5N1) genomes and of 589 HA sequences placed the EMA clade as distinct from the major clades circulating in People's Republic of China, Indonesia, and Southeast Asia.

The influenza (H5N1) viruses isolated in Europe, the Middle East, and Africa show a close relationship, despite the fact that they were collected from a widely dispersed geographic region, including Côte d'Ivoire, Nigeria, Niger, Sudan, Egypt, Afghanistan, Iran, Slovenia, Croatia, and Italy. The shared lineage of the viruses suggests a single genetic source for introduction of influenza (H5N1) into western Europe and northern and western Africa; our analysis places this source most recently in either Russia or Qinghai Province in China (Figure 2B; online Appendix Table [available from www.cdc.gov/EID/content/13/5/713-appT.htm]). The broad dispersal of these isolates throughout these countries during a relatively short period, coupled with weak biosecurity standards in place in most rural areas, implicates human-related movement of live poultry and poultry commodities as the source of introduction of influenza (H5N1) into some of these countries. The virus' presence in wild birds leaves open the alternative possibility that migratory birds may have been the primary source, with secondary spread possibly caused by human-related activities.

A phylogenetic tree containing 589 isolates from 2001 through 2006 (Figure 2A and online Appendix Figure 3) shows the relationship of the 36 recent isolates from this study to previous isolates and shows the 3 major lineages of influenza (H5N1) that are now circulating in Asia plus the fourth lineage, EMA, that has spread west into Europe and Africa. Figure 2B depicts a consensus view of the parsimony-based analysis of 74 isolates of complete genomes from the EMA lineage. The EMA clade contains all known European, Middle Eastern, and North African cases (which began appearing in late 2005), as well as cases from China, Russia, and Mongolia in 2005 and 2006. Some of the EMA clade isolates appear in clusters of influenza (H5N1) infection that were reported in geese in Qinghai Province, China (14), and in mute swans in Astrakhan (15), both of which are possible sources of spread through migration.

The evolutionary relationships shown in Figure 2B provide clear evidence that 3 distinct clades, labeled EMA 1–3, are circulating in the European and African region. These clades clearly share a common ancestor in Asia. The

3 clades may represent separate introductions or, alternatively, a single introduction from Asia into Russia, Europe, or another western site that has subsequently evolved into 3 lineages. More data will be required to pinpoint when and where the 3 clades split apart. All previously reported European and Middle Eastern isolates belong to EMA-1.

Our results show that EMA-2 has spread to Europe and that EMA-3 has spread to both Europe and the Middle East. These results agree in part with a recent study (16) that reported 3 distinct introductions of influenza (H5N1) into Nigeria. Our analysis, based on all available HA sequences (online Appendix Figure 3), indicates that the Nigerian isolates fall into just 2 clades, EMA 1–2, that likely resulted from at least 2 introductions of influenza (H5N1).

European countries have been affected by each of the 3 introductions of the EMA strains. For example, the Italian sequences can be segregated into 2 subgroups (Figure 2B). Two isolates in EMA-1 (Co/Italy/808/06 and Md/Italy/835/2006) are closely related in all segments and likely share a common ancestor with isolates found in Slovenia (Sw/Slovenia/760/2006), Bavaria, and the Czech Republic (Co/Czech Republic/5170/2006). The third Italian strain from our study (Co/Italy/742/2006) falls into EMA-3, along with our newly sequenced isolates from Iran (Co/Iran/754/2006) and Afghanistan (Ck/Afghanistan/1207/2006). EMA-2 contains 1 European isolate, from a swan in Croatia, and multiple isolates from domesticated birds in Nigeria and Niger. This group shares a common ancestor with a group of isolates from Astrakhan and Kuragan (Russia).

Of the 22 EMA isolates newly sequenced in this study, 20 have the amino acid lysine (K) at position 627 of the polymerase basic protein 2 (PB2), while only 2 have glutamic acid (E). (These last 2 are both from Italy and both in EMA-1.) The 627K mutation is associated with virulence in mice and adaptation to mammalian hosts (17) and with increased host range (18). Lysine at this position is common in human viruses: all 65 human influenza (H5N1) isolates from 2001 through 2006 for which the PB2 sequence is available have lysine at position 627. Before the analysis of our collection, the PB2 627K was a relatively rare finding in avian influenza (H5N1) viruses: it was present in only 42 of 385 isolates previously collected from 2001 through 2006. Our analysis shows that all 42 of these fall in the EMA clade (Figure 2 and supplementary data available in online Technical Appendix 2, available from www.cdc.gov/EID/content/13/5/713-app2.txt). Excluding our current European, Middle Eastern, and African isolates, this mutation appears primarily in isolates obtained from wild birds in Astrakhan (15) and at Qinghai Lake (14,17). This mutation also occurs in the recent isolate A/Guinea fowl/Shantou/1341/2006 and in a mouse-adapted 2001 Asian isolate, A/pheasant/Hong Kong/Fy155/01-MB. This find-

ing is in keeping with current knowledge of the acquisition of such mutations.

Our study increases current knowledge on strains circulating in Asia before the westward spread of influenza A (H5N1). The Vietnamese samples fall into 2 clusters, the larger of which (V2 in Figure 1) is the same strain responsible for multiple cases in Southeast Asia since 2004, particularly in Vietnam and Thailand. These isolates all seem to derive from earlier Hong Kong samples (including 2 cases of human infection) in 2002 and 2003. The second cluster, V1, which contains 5 samples, significantly expands our understanding of this distinct Vietnamese influenza (H5N1) lineage. The only other isolate from this cluster was recently reported in a Vietnamese duck (*A/duck/Vietnam/568/2005*) and labeled a “recent Vietnam introduction” (4). This sample groups with the V1 clade when shown in the context of a larger tree of HA sequences (online Appendix Figure 3). The 5 newly sequenced isolates in clade V1 show the same phylogenetic relationship for all segments except PB2 (online Appendix Figure 1). The isolates in clade V1 appear to have undergone the same reassortment as was suggested (4) for the 1 previous example of this Vietnamese clade, *A/duck/Vietnam/568/2005*; i.e., they have acquired a new PB2 segment. This PB2 is similar to older (1996–2002), *A/duck/Guangdong/1/96*-like viruses from China. V1 clade isolates are associated with a distinct set of human cases, from China’s Anhui and Guangxi Provinces in 2005, a finding that provides additional support to the hypothesis that this group of influenza (H5N1) viruses was introduced into Vietnam from China (4).

Although EMA has split into 3 independently evolving clades, 1 isolate, *A/chicken/Nigeria/1047–62/2006*, shows clear evidence of reassortment. In this genome, 4 segments—HA, (nucleocapsid protein, nonstructural protein, and PB1—belong to EMA-1, as seen in Figure 1 and online Appendix Figure 1. The other 4 segments—neuraminidase, matrix protein, PA, and PB2—belong to EMA-2 (online Appendix Figure 1). Individual segment trees based on all available sequences in GenBank corroborate this pattern and consistently split the 8 segments of this Nigerian isolate into 2 distinct clades. Reassortment events such as this can only be discovered by sequencing multiple virus segments.

The presence of all 3 EMA sublineages in the same geographic region creates ample opportunities for reassortment. Isolate *A/chicken/Nigeria/1047–62/2006* is the most recent of the Nigerian isolates, consistent with the hypothesis that this reassortant was generated in Africa. Additional surveillance will be necessary to determine if this reassortant strain spreads further in the avian population and to assess its ability to infect mammals.

As shown in Figure 2A, the EMA clade is a distinct lineage evolving independently of the 3 exclusively Asian

lineages. All 3 human influenza (H5N1) cases that have been sequenced outside east Asia—from Iraq (19), Djibouti, and Egypt—belong to the EMA lineage. The human sequences *A/Djibouti/5691/NAMRU3/06* and *A/Egypt/2782/NAMRU3/06* group closely together and consistently fall in EMA-1. The placement of *A/Iraq/207/NAMRU3/06* is slightly less certain; it also groups with EMA-1 (Figure 2B) but with lower bootstrap support. EMA viruses isolated from humans are thus quite distinct from the recent large clusters of human cases in Indonesia and China, which fall into separate clades containing none of our samples. The EMA isolates are also distinct from other human cases in Southeast Asia, which fall into the clades (V1 and V2) containing our Vietnamese samples.

The emergence of 3 (or more) substrains from the EMA clade represents multiple new opportunities for avian influenza (H5N1) to evolve into a human pandemic strain. In contrast to strains circulating in Southeast Asia, EMA viruses are derived from a progenitor that has the PB2 627K mutation. These viruses are expected to have enhanced replication characteristics in mammals, and indeed the spread of EMA has coincided with the rapid appearance of cases in mammals—including humans in Turkey, Egypt, Iraq, and Djibouti, and cats in Germany, Austria, and Iraq. Unfortunately, the EMA-type viruses appear to be as virulent as the exclusively Asian strains: of 34 human infections outside of Asia through mid-2006, 15 have been fatal (2).

Analyses of the complete HA tree (Figure 2A and online Appendix Figure 3) suggest that the earliest sequenced relatives of the EMA clade are from the Yunnan region of China (*A/duck/Yunnan/6255,6445/2003*), Hong Kong, (*A/chicken/Hong Kong/WF157/2003*), and South Korea (*A/chicken/Korea/ES/2003*, *A/duck/Korea/ESD1/2003*), which were part of a regional outbreak in 2003 (20). Experiments on the 2 Korean isolates showed them to be infectious but not fatal in mice (21).

These findings show how whole-genome analysis of influenza (H5N1) viruses is instrumental to the better understanding of the evolution and epidemiology of this infection, which is now present in the 3 continents that contain most of the world’s population. This and related analyses, facilitated by global initiatives on sharing influenza data (22,23), will help us understand the dynamics of infection between wild and domesticated bird populations, which in turn should promote the development of control and prevention strategies.

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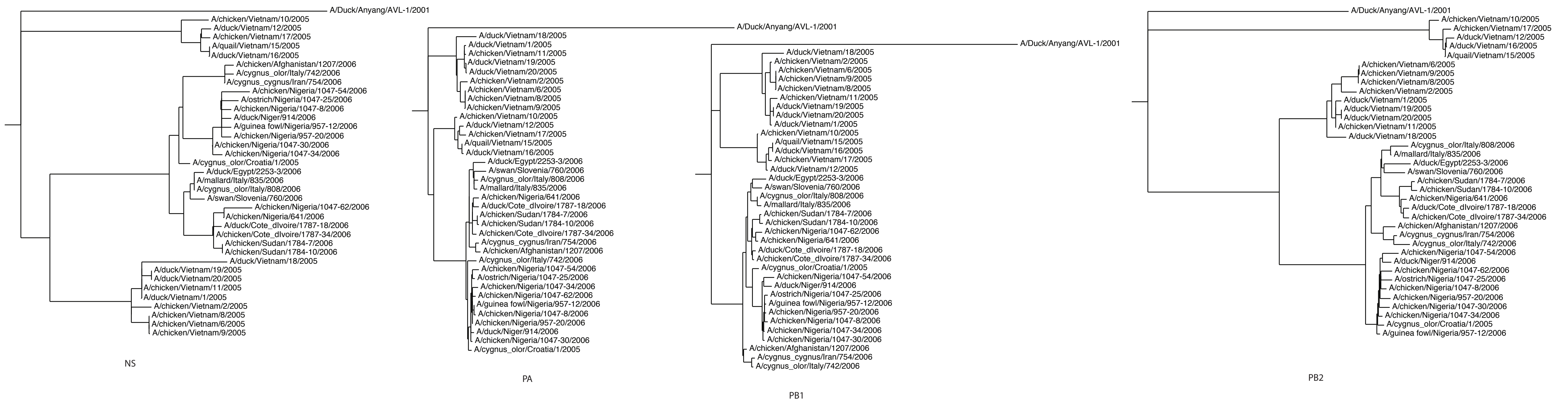
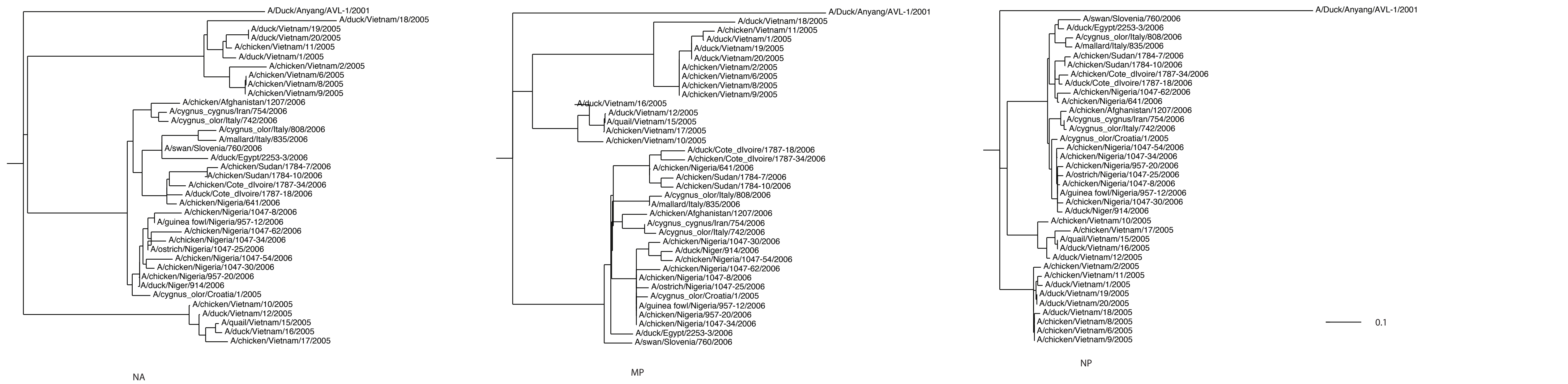
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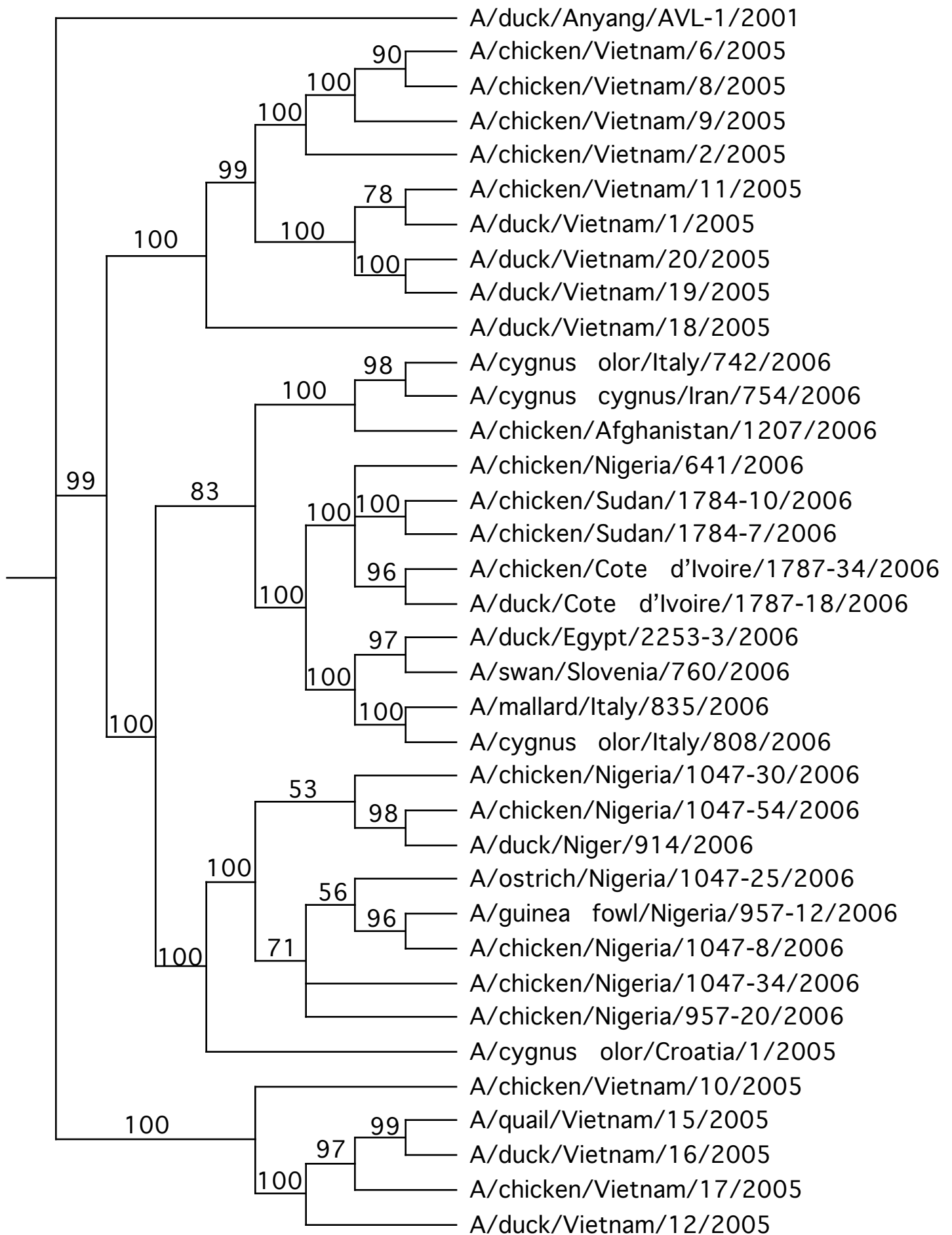
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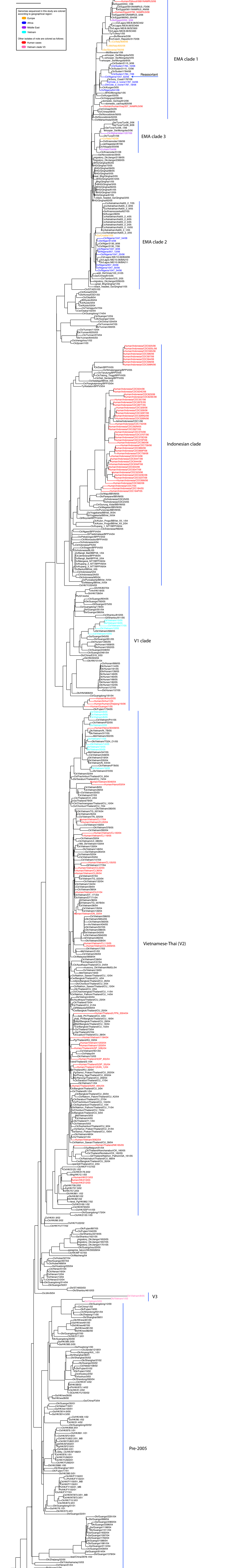


Genomes sequenced in this study are colored according to geographical region:

- Europe
- Africa
- Middle East
- Vietnam

Other isolates of note are colored as follows:

- Human cases
- Vietnam clade V3



EMA clade 1

EMA clade 3

EMA clade 2

Indonesian clade

V1 clade

Vietnamese-Thai (V2)

V3

Pre-2005

Appendix Table.

Isolate name	PB2	PB1	PA	HA	NP	NA	M	NS
A/bar-headed goose/Qinghai/12	DQ095761	DQ095741	DQ095721	DQ095621	DQ095681	DQ095661	DQ095641	DQ095701
A/bar-headed goose/Qinghai/5	DQ095757	DQ095737	DQ095717	DQ095617	DQ095677	DQ095657	DQ095637	DQ095697
A/bar-headed goose/Qinghai/59	DQ095752	DQ095732	DQ095712	DQ095612	DQ095672	DQ095652	DQ095632	DQ095692
A/bar-headed goose/Qinghai/60	DQ095755	DQ095695	DQ095715	DQ095615	DQ095675	DQ095615	DQ095635	DQ095695
A/bar-headed goose/Qinghai/61	DQ095758	DQ095738	DQ095718	DQ095618	DQ095678	DQ095658	DQ095638	DQ095698
A/bar-headed goose/Qinghai/62	DQ095760	DQ095740	DQ095720	DQ095620	DQ095640	DQ095660	DQ095640	DQ095700
A/bar-headed goose/Qinghai/65	DQ095762	DQ095742	DQ095722	DQ095622	DQ095682	DQ095662	DQ095642	DQ095702
A/bar-headed goose/Qinghai/67	DQ095763	DQ095743	DQ095723	DQ095623	DQ095683	DQ095663	DQ095643	DQ095703
A/bar-headed goose/Qinghai/68	DQ095753	DQ095733	DQ095713	DQ095613	DQ095673	DQ095653	DQ095633	DQ095693
A/bar-headed goose/Qinghai/75	DQ095759	DQ095739	DQ095719	DQ095619	DQ095679	DQ095659	DQ095639	DQ095699
A/black-headed goose/Qinghai/1	DQ100542	DQ100546	DQ100550	DQ100554	DQ100558	DQ100562	DQ100566	DQ100570
A/black-headed goose/Qinghai/2	DQ100543	DQ100547	DQ100551	DQ100555	DQ100559	DQ100563	DQ100567	DQ100571
A/black-headed gull/Qinghai/1	DQ100544	DQ100548	DQ100552	DQ100556	DQ100560	DQ100564	DQ100568	DQ100572
A/brown headed gull/Qinghai/3	DQ095756	DQ095736	DQ095716	DQ095616	DQ095676	DQ095656	DQ095636	DQ095696
A/cat Germany/606/2006	DQ643980	DQ643979	DQ643981	DQ643982	DQ643983	DQ643984	DQ643985	DQ643986
A/chicken/Afghanistan/1207/2006	CY016794	CY016793	CY016792	CY016787	CY016790	CY016789	CY016788	CY016791
A/chicken/Cote d'Ivoire/1787/34	CY016818	CY016817	CY016816	CY016811	CY016814	CY016813	CY016812	CY016815
A/chicken/Crimea/08/2005	DQ650670	DQ650669	DQ650668	DQ650663	DQ650666	DQ650665	DQ650664	DQ650667
A/chicken/Fujian/1042	DQ320810	DQ321271	DQ321205	DQ320876	DQ321073	DQ321008	DQ320942	DQ321139
A/chicken/Kurgan/3	DQ449639	DQ449638	DQ449637	DQ449632	DQ449635	DQ449634	DQ449633	DQ449636
A/chicken/Nigeria/1047/30/2006	CY016946	CY016945	CY016944	CY016939	CY016942	CY016941	CY016940	CY016943
A/chicken/Nigeria/1047/34/2006	CY016954	CY016953	CY016952	CY016947	CY016950	CY016949	CY016948	CY016951
A/chicken/Nigeria/1047/54/2006	CY016930	CY016929	CY016928	CY016923	CY016926	CY016925	CY016924	CY016927
A/chicken/Nigeria/1047/8/2006	CY016914	CY016913	CY016912	CY016907	CY016910	CY016909	CY016908	CY016911
A/chicken/Nigeria/641/2006	CY016283	CY016282	CY016281	CY016276	CY016279	CY016278	CY016277	CY016280

A/chicken/Nigeria/957/20/2006	CY016291	CY016290	CY016289	CY016284	CY016287	CY016286	CY016285	CY016288
A/chicken/Shantou/810	DQ095766	DQ095746	DQ095726	DQ095626	DQ095686	DQ095666	DQ095646	DQ095706
A/chicken/Sudan/1784/10/2006	CY016307	CY016306	CY016305	CY016300	CY016303	CY016302	CY016301	CY016304
A/chicken/Sudan/1784/7/2006	CY016299	CY016298	CY016297	CY016292	CY016295	CY016294	CY016293	CY016296
A/Cygnus cygnus/Iran/754/2006	CY016786	CY016785	CY016784	CY016779	CY016782	CY016781	CY016780	CY016783
A/Cygnus olor/Astrakhan/05201	DQ389161	DQ394578	DQ394579	DQ389158	DQ394577	DQ389159	DQ394576	DQ389160
A/Cygnus olor/Astrakhan/05202	DQ343506	DQ343505	DQ343504	DQ343502	DQ359694	DQ343503	DQ359692	DQ359693
A/Cygnus olor/Astrakhan/05203	DQ358750	DQ358749	DQ358748	DQ358746	DQ358751	DQ358747	DQ358739	DQ358752
A/Cygnus olor/Astrakhan/05204	DQ363916	DQ363915	DQ363917	DQ363918	DQ363929	DQ363919	DQ363925	DQ363926
A/Cygnus olor/Astrakhan/05205	DQ365011	DQ365008	DQ365007	DQ365004	DQ365006	DQ365005	DQ365009	DQ365010
A/Cygnus olor/Astrakhan/05206	DQ365001	DQ365000	DQ364999	DQ364996	DQ364998	DQ364997	DQ365002	DQ365003
A/Cygnus olor/Astrakhan/05207	DQ363921	DQ363920	DQ363922	DQ363923	DQ363930	DQ363924	DQ363928	DQ363927
A/Cygnus olor/Astrakhan/05208	DQ386305	DQ386304	DQ399537	DQ399540	DQ399539	DQ399541	DQ399542	DQ399538
A/Cygnus olor/Astrakhan/05209	DQ399543	DQ406738	DQ406737	DQ399547	DQ399545	DQ399546	DQ400912	DQ399544
A/Cygnus olor/Astrakhan/05210	DQ434890	DQ423612	DQ434891	DQ434889	DQ440579	DQ440579	DQ434888	DQ434887
A/Cygnus olor/Croatia/1/2005	CY016826	CY016825	CY016824	CY016819	CY016822	CY016821	CY016820	CY016823
A/Cygnus olor/Italy/742/2006	DQ533586	DQ533585	DQ533584	DQ412997	DQ533582	DQ533581	DQ533580	DQ533583
A/Cygnus olor/Italy/808/2006	tigr/ 1101672593770	tigr/ 1101672593770	tigr/ 1101672593770	tigr/ 1101672593770	tigr/ 1101672593770	tigr/ 1101672593770	tigr/ 1101672593770	tigr/ 1101672593770
A/Djibouti/5691NAMRU3/2006				DQ666146				
A/duck/Cote d'Ivoire/1787/18/2006	CY016810	CY016809	CY016808	CY016803	CY016806	CY016805	CY016804	CY016807
A/duck/Egypt/2253/3/2006	CY016906	CY016905	CY016904	DQ862002	CY016902	CY016901	CY016900	CY016903
A/duck/Fujian/897	DQ320809	DQ321270	DQ321204	DQ320875	DQ321072	DQ321007	DQ320941	DQ321138
A/duck/Hunan/160	DQ320841	DQ321302	DQ321236	DQ320907	DQ321104	DQ321039	DQ320973	DQ321170
A/duck/Kurgan/08/2005	DQ449647	DQ449646	DQ449645	DQ449640	DQ449643	DQ449642	DQ449641	DQ449644
A/duck/Niger/914/2006	CY017034	CY017033	CY017032	DQ659113	CY017030	CY017029	CY017028	CY017031
A/duck/Novosibirsk/56	DQ232608	DQ232606	DQ234076	DQ230522	DQ232610	DQ230524	DQ234078	DQ234074
A/Egypt/2782/NAMRU3/2006				DQ464377				

A/Environment/Qinghai/31/2005	DQ320856	DQ321317	DQ321251	DQ320922	DQ321119	DQ321054	DQ320988	DQ321185
A/goose/Shantou/1621	DQ095768	DQ095748	DQ095728	DQ095628	DQ095688	DQ095668	DQ095648	DQ095708
A/goose/Shantou/2216	DQ320849	DQ321310	DQ321244	DQ320915	DQ321112	DQ321047	DQ320981	DQ321178
A/great black-headed gull/Qinghai	DQ095754	DQ095734	DQ095714	DQ095614	DQ095674	DQ095654	DQ095634	DQ095694
A/grebe/Novosibirsk/29	DQ232607	DQ232605	DQ234075	DQ230521	DQ232609	DQ230523	DQ234077	DQ234073
A/grebe/Tyva/Tyv06/1/2006	DQ914807	DQ914810	DQ978999	DQ914808	DQ916293	DQ914809	DQ914805	DQ914806
A/grebe/Tyva/Tyv06/2/06	DQ852607	DQ852606	DQ852603	DQ852600	DQ852602	DQ852601	DQ852604	DQ852605
A/Grebe/Tyva/Tyv06/8/2006	DQ863510	DQ863509	DQ863508	DQ863503	DQ863506	DQ863507	DQ863504	DQ863505
A/guinea fowl/Nigeria/957/12	CY017186	CY017185	CY017184	CY017179	CY017182	CY017181	CY017180	CY017183
A/human/Iraq/207/NAMRU3/2006				DQ435202				
A/mallard/Italy/835/2006	CY016802	CY016801	CY016800	DQ449031	CY016798	CY016797	CY016796	CY016799
A/migratory duck/Jiangxi/1653	DQ320850	DQ321311	DQ321245	DQ320916	DQ321113	DQ321048	DQ320982	DQ321179
A/migratory duck/Jiangxi/1657	DQ320851	DQ321312	DQ321246	DQ320917	DQ321114	DQ321049	DQ320983	DQ321180
A/migratory duck/Jiangxi/1701	DQ320852	DQ321313	DQ321247	DQ320918	DQ321115	DQ321050	DQ320984	DQ321181
A/ostrich/Nigeria/1047/25/2006	CY016922	CY016921	CY016920	CY016915	CY016918	CY016917	CY016916	CY016919
A/quail/Shantou/911	DQ095767	DQ095747	DQ095727	DQ095627	DQ095687	DQ095667	DQ095647	DQ095707
A/swan/Germany/R65/2006	DQ464357	DQ464361	DQ464360	DQ464354	DQ464359	DQ464355	DQ464356	DQ464358
A/swan/Slovenia/760/2006	CY017050	CY017049	CY017048	CY017043	CY017046	CY017045	CY017044	CY017047
A/whooper swan/Mongolia/2/06	AB264769	AB264770	AB263751	AB263752	AB263753	AB265202	AB265203	AB265204
A/whooper swan/Mongolia/3/05	AB239307	AB239308	AB239309	AB233320	AB239310	AB239311	AB239312	AB239313
A/whooper swan/Mongolia/4/05	AB239314	AB239315	AB239316	AB233321	AB239317	AB239318	AB239319	AB239320
A/whooper swan/Mongolia/6/05	AB239321	AB239322	AB239323	AB233322	AB239324	AB239325	AB239326	AB239327

POSITION 627 IN PB2 PROTEIN FOR ALL 420 SEQUENCES AVAILABLE FROM 2001-2006 AS OF November 2006
Column 1: amino acid, either E (glutamic acid) or K (lysine). All 64 lysines appear at the bottom of the file. Column 2 is the isolate identifier, and the 36 new sequences added by this study have a label in column 3.

E A/bird/Thailand/3.1/2004(H5N1)
E A/chicken/Ayutthaya/Thailand/CU-23/04(H5N1)
E A/chicken/Bangli_Bali/BBPV6-1/2004(H5N1)
E A/chicken/Bangli_Bali/BPPV6-2/2004(H5N1)
E A/chicken/Dairi/BPPVI/2005(H5N1)
E A/chicken/Deli_Serdang/BPPVI/2005(H5N1)
E A/chicken/Fujian/10039/2005(H5N1)
E A/chicken/Fujian/1042/2005(H5N1)
E A/chicken/Fujian/10567/2005(H5N1)
E A/chicken/Fujian/11933/2005(H5N1)
E A/chicken/Fujian/12239/2005(H5N1)
E A/chicken/Fujian/584/2006(H5N1)
E A/chicken/Fujian/9821/2005(H5N1)
E A/chicken/Guangdong/174/04(H5N1)
E A/chicken/Guangdong/178/04(H5N1)
E A/chicken/Guangdong/191/04(H5N1)
E A/chicken/Guangxi/1212/2006(H5N1)
E A/chicken/Guangxi/12/2004(H5N1)
E A/chicken/Guangxi/1951/2006(H5N1)
E A/chicken/Guangxi/3154/2005(H5N1)
E A/chicken/Guangxi/3791/2005(H5N1)
E A/chicken/Guangxi/463/2006(H5N1)
E A/chicken/Guangxi/4989/2005(H5N1)
E A/chicken/Guangxi/604/2005(H5N1)
E A/chicken/Guangxi/683/2006(H5N1)
E A/chicken/Guiyang/1655/2006(H5N1)
E A/chicken/Guiyang/2147/2005(H5N1)
E A/chicken/Guiyang/2173/2005(H5N1)
E A/chicken/Guiyang/237/2006(H5N1)
E A/chicken/Guiyang/29/2006(H5N1)
E A/chicken/Guiyang/3055/2005(H5N1)
E A/chicken/Guiyang/3570/2005(H5N1)
E A/chicken/Guiyang/3721/2005(H5N1)
E A/chicken/Guiyang/3923/2005(H5N1)
E A/chicken/Guiyang/4059/2005(H5N1)
E A/chicken/Guiyang/441/2006(H5N1)
E A/chicken/Gunung_Kidal/BBVW/2005(H5N1)
E A/chicken/Hebei/108/02(H5N1)
E A/chicken/Hebei/326/2005(H5N1)
E A/chicken/Hebei/718/2001(H5N1)
E A/chicken/Henan/1/2004(H5N1)
E A/chicken/Henan/12/2004(H5N1)
E A/chicken/Henan/13/2004(H5N1)
E A/chicken/Henan/16/2004(H5N1)
E A/chicken/Henan/wu/2004(H5N1)
E A/chicken/Hong_Kong/282/2006(H5N1)
E A/chicken/Hong_Kong/947/2006(H5N1)
E A/Chicken/HongKong/FY150/01(H5N1)
E A/Chicken/HongKong/FY150/01-MB(H5N1)
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E A/Chicken/HongKong/YU822.2/01-MB(H5N1)
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E A/chicken/Hunan/999/2005(H5N1)
E A/chicken/Indonesia/CDC24/2005(H5N1)
E A/chicken/Indonesia/CDC25/2005(H5N1)
E A/chicken/Jiangsu/cz1/2002(H5N1)
E A/chicken/Jilin/9/2004(H5N1)
E A/chicken/Jilin/ha/2003(H5N1)
E A/chicken/Jilin/hd/2002(H5N1)
E A/chicken/Jilin/he/2002(H5N1)
E A/chicken/Jilin/hf/2002(H5N1)
E A/chicken/Jilin/hg/2002(H5N1)
E A/chicken/Jilin/hj/2003(H5N1)
E A/chicken/Jilin/hk/2004(H5N1)
E A/chicken/Jilin/hl/2004(H5N1)
E A/chicken/Jilin/hm/2003(H5N1)
E A/chicken/Jilin/xw/2003(H5N1)
E A/chicken/Korea/ES/03(H5N1)
E A/chicken/Kulon_Progo/BBVet-XII-1/2004(H5N1)

E A/chicken/Kulon_Progo/BBVet-XII-2/2004(H5N1)
E A/chicken/Kulon_Progo/BBVW/2005(H5N1)
E A/chicken/Kupang-2-NTT/BPPV6/2004(H5N1)
E A/chicken/Kupang-3-NTT/BPPV6/2004(H5N1)
E A/chicken/Kyoto/3/2004(H5N1)
E A/chicken/Magetan/BBVW/2005(H5N1)
E A/chicken/Malang/BBVet-IV/2004(H5N1)
E A/chicken/Mangarai-NTT/BPPV6/2004(H5N1)
E A/chicken/Nakorn-Patom/Thailand/CU-K2/2004(H5N1)
E A/chicken/Oita/8/2004(H5N1)
E A/chicken/Purwakarta/BBVet-IV/2004(H5N1)
E A/chicken/Purworejo/BBVW/2005(H5N1)
E A/chicken/Salatiga/BBVet-I/2005(H5N1)
E A/chicken/Shantou/1233/2006(H5N1)
E A/chicken/Shantou/3840/2006(H5N1)
E A/chicken/Shantou/3923/2006(H5N1)
E A/chicken/Shanxi/2/2006(H5N1)
E A/chicken/Simalanggang/BPPVI/2005(H5N1)
E A/chicken/Tarutung/BPPVI/2005(H5N1)
E A/chicken/Tebing_Tinggi/BPPVI/2005(H5N1)
E A/chicken/Thailand/Kanchanaburi/CK-160/2005(H5N1)
E A/chicken/Thailand/Nontaburi/CK-162/2005(H5N1)
E A/chicken/Thailand/NP-172/2006(H5N1)
E A/chicken/Thailand/PC-168/2006(H5N1)
E A/chicken/Thailand/PC-170/2006(H5N1)
E A/chicken/Tula/Russia/Oct-5/2005(H5N1)
E A/chicken/Viet_Nam/10/2005(H5N1)
E A/chicken/Viet_Nam/11/2005(H5N1)
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E A/chicken/Viet_Nam/DN-045/2004(H5N1)
E A/chicken/Viet_Nam/DT-015/2004(H5N1)
E A/chicken/Viet_Nam/DT-171/2004(H5N1)
E A/chicken/Viet_Nam/HCM-022/2004(H5N1)
E A/chicken/Viet_Nam/LA-024/2004(H5N1)
E A/chicken/Viet_Nam/LD-080/2004(H5N1)
E A/chicken/Viet_Nam/TG-023/2004(H5N1)
E A/chicken/Viet_Nam/TN-025/2004(H5N1)
E A/chicken/Viet_Nam/VL-008/2004(H5N1)
E A/chicken/Wajo/BBVM/2005(H5N1)
E A/chicken/Yamaguchi/7/2004(H5N1)
E A/chicken/Yogjakarta/BBVet-IX/2004(H5N1)
E A/Ck/Indonesia/BL/2003(H5N1)
E A/Ck/Indonesia/PA/2003(H5N1)
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E A/common_magpie/Hong_Kong/2125/2006(H5N1)
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E A/crested_myna/Hong_Kong/540/2006(H5N1)
E A/crow/Kyoto/53/2004(H5N1)
E A/crow/Osaka/102/2004(H5N1)
E A/Cygnus_olor/Astrakhan/Ast05-2-4/2005(H5N1)
E A/Dk/Indonesia/MS/2004(H5N1)
E A/Dk/Thailand/71.1/2004(H5N1)
E A/Dk/Viet_Nam/11/2004(H5N1)
E A/Duck/Anyang/AVL-1/2001(H5N1)
E A/duck/China/E319-2/03(H5N1)
E A/duck/Fujian/01/2002(H5N1)
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E A/duck/Fujian/11311/2005(H5N1)
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E A/duck/Guangxi/1681/2004 (H5N1)
E A/duck/Guangxi/1793/2004 (H5N1)
E A/duck/Guangxi/1830/2006 (H5N1)
E A/duck/Guangxi/2143/2006 (H5N1)
E A/duck/Guangxi/22/2001 (H5N1)
E A/duck/Guangxi/2291/2004 (H5N1)
E A/duck/Guangxi/2396/2004 (H5N1)
E A/duck/Guangxi/2775/2005 (H5N1)
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E A/duck/Guangxi/351/2004 (H5N1)
E A/duck/Guangxi/35/2001 (H5N1)
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E A/duck/Guangxi/3741/2005 (H5N1)
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E A/duck/Guangxi/392/2006 (H5N1)
E A/duck/Guangxi/4016/2005 (H5N1)
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E A/duck/Guangxi/4665/2005 (H5N1)
E A/duck/Guangxi/4830/2005 (H5N1)
E A/duck/Guangxi/50/2001 (H5N1)
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E A/duck/Guangxi/5165/2005 (H5N1)
E A/duck/Guangxi/5270/2005 (H5N1)
E A/duck/Guangxi/53/2002 (H5N1)
E A/duck/Guangxi/5457/2005 (H5N1)
E A/duck/Guangxi/619/2006 (H5N1)
E A/duck/Guangxi/668/2004 (H5N1)
E A/duck/Guangxi/744/2006 (H5N1)
E A/duck/Guangxi/793/2005 (H5N1)
E A/duck/Guangxi/804/2006 (H5N1)
E A/duck/Guangxi/89/2006 (H5N1)
E A/duck/Guangxi/951/2005 (H5N1)
E A/duck/Guangxi/xa/2001 (H5N1)
E A/duck/Guangzhou/20/2005 (H5N1)
E A/duck/Guiyang/1081/2006 (H5N1)
E A/duck/Guiyang/1588/2006 (H5N1)
E A/duck/Guiyang/1722/2006 (H5N1)
E A/duck/Guiyang/2231/2005 (H5N1)
E A/duck/Guiyang/293/2006 (H5N1)
E A/duck/Guiyang/3009/2005 (H5N1)
E A/duck/Guiyang/3242/2005 (H5N1)
E A/duck/Guiyang/3834/2005 (H5N1)
E A/duck/Guiyang/3996/2005 (H5N1)
E A/duck/Guiyang/497/2006 (H5N1)
E A/duck/Hokkaido/Vac-1/04 (H5N1)
E A/duck/Hong_Kong/821/02 (H5N1)
E A/duck/Hubei/wg/2002 (H5N1)
E A/duck/Hubei/wp/2003 (H5N1)
E A/duck/Hubei/wq/2003 (H5N1)
E A/duck/Hunan/1204/2006 (H5N1)
E A/duck/Hunan/1265/2005 (H5N1)
E A/duck/Hunan/1608/2005 (H5N1)
E A/duck/Hunan/1652/2005 (H5N1)
E A/duck/Hunan/324/2006 (H5N1)
E A/duck/Hunan/344/2006 (H5N1)
E A/duck/Hunan/5106/2005 (H5N1)
E A/duck/Hunan/5152/2005 (H5N1)
E A/duck/Hunan/5472/2005 (H5N1)

E A/duck/Hunan/856/2006(H5N1)
E A/duck/Hunan/988/2006(H5N1)
E A/duck/Korea/ESD1/03(H5N1)
E A/duck/Kurgan/08/2005(H5N1)
E A/duck/Novosibirsk/02/05(H5N1)
E A/duck/Parepare/BBVM/2005(H5N1)
E A/duck/Shandong/093/2004(H5N1)
E A/duck/Shanghai/08/2001(H5N1)
E A/duck/Shanghai/13/2001(H5N1)
E A/duck/Shanghai/35/2002(H5N1)
E A/duck/Shanghai/37/2002(H5N1)
E A/duck/Shanghai/38/2001(H5N1)
E A/duck/Shanghai/xj/2002(H5N1)
E A/duck/Shantou/13323/2005(H5N1)
E A/duck/Shantou/4610/2003(H5N1)
E A/duck/Vietnam/1/2005(H5N1)
E A/duck/Viet_Nam/1/2005(H5N1)
E A/duck/Viet_Nam/12/2005(H5N1)
E A/duck/Viet_Nam/18/2005(H5N1)
E A/duck/Viet_Nam/19/2005(H5N1)
E A/duck/Viet_Nam/20/2005(H5N1)
E A/duck/Vietnam/8/05(H5N1)
E A/duck/Viet_Nam/CM-V7/2004(H5N1)
E A/duck/Viet_Nam/TG-007A/2004(H5N1)
E A/duck/Viet_Nam/TV-V2/2004(H5N1)
E A/duck/Yokohama/aq10/2003(H5N1)
E A/duck/Yunnan/4400/2005(H5N1)
E A/duck/Yunnan/4589/2005(H5N1)
E A/duck/Yunnan/5133/2005(H5N1)
E A/duck/Yunnan/5236/2005(H5N1)
E A/duck/Yunnan/5251/2005(H5N1)
E A/duck/Yunnan/5820/2005(H5N1)
E A/duck/Yunnan/5877/2005(H5N1)
E A/duck/Yunnan/6332/2005(H5N1)
E A/duck/Yunnan/6607/2005(H5N1)
E A/duck/Zhejiang/bj/2002(H5N1)
E A/egret/Hong_Kong/757.2/03(H5N1)
E A/Gf/HK/38/2002(H5N1)
E A/goose/Fujian/bb/2003(H5N1)
E A/goose/Guangdong/xb/2001(H5N1)
E A/goose/Guangxi/1097/2004(H5N1)
E A/goose/Guangxi/1198/2004(H5N1)
E A/goose/Guangxi/1458/2006(H5N1)
E A/goose/Guangxi/1633/2006(H5N1)
E A/goose/Guangxi/1832/2004(H5N1)
E A/goose/Guangxi/1898/2006(H5N1)
E A/goose/Guangxi/2112/2004(H5N1)
E A/goose/Guangxi/224/2006(H5N1)
E A/goose/Guangxi/2383/2004(H5N1)
E A/goose/Guangxi/3017/2005(H5N1)
E A/goose/Guangxi/3316/2005(H5N1)
E A/goose/Guangxi/345/2005(H5N1)
E A/goose/Guangxi/4289/2005(H5N1)
E A/goose/Guangxi/4513/2005(H5N1)
E A/goose/Guangxi/532/2006(H5N1)
E A/goose/Guangxi/5414/2005(H5N1)
E A/goose/Guangxi/582/2006(H5N1)
E A/goose/Guangxi/914/2004(H5N1)
E A/goose/Guiyang/1461/2006(H5N1)
E A/goose/Guiyang/1636/2006(H5N1)
E A/goose/Guiyang/1794/2006(H5N1)
E A/goose/Guiyang/337/2006(H5N1)
E A/goose/Guiyang/3422/2005(H5N1)
E A/goose/Guiyang/4030/2005(H5N1)
E A/goose/Guiyang/4180/2005(H5N1)
E A/goose/Guiyang/538/2006(H5N1)
E A/goose/Guiyang/765/2006(H5N1)
E A/goose/Jilin/hb/2003(H5N1)
E A/goose/Shantou/18442/2005(H5N1)
E A/goose/Shantou/2086/2006(H5N1)
E A/goose/Shantou/2216/2005(H5N1)
E A/goose/Shantou/239/2006(H5N1)
E A/goose/Shantou/3265/2006(H5N1)
E A/goose/Shantou/3295/2006(H5N1)
E A/goose/Shantou/3624/2006(H5N1)
E A/goose/Vietnam/3/05(H5N1)
E A/goose/Yunnan/3315/2005(H5N1)
E A/goose/Yunnan/3644/2005(H5N1)
E A/goose/Yunnan/3720/2005(H5N1)
E A/goose/Yunnan/4129/2005(H5N1)
E A/goose/Yunnan/4494/2005(H5N1)

E A/goose/Yunnan/4804/2005 (H5N1)
E A/goose/Yunnan/5299/2005 (H5N1)
E A/goose/Yunnan/5539/2005 (H5N1)
E A/goose/Yunnan/6027/2005 (H5N1)
E A/goose/Yunnan/6368/2005 (H5N1)
E A/house_crow/Hong_Kong/2648/2006 (H5N1)
E A/Japanese_white-eye/Hong_Kong/1038/2006 (H5N1)
E A/large-billed_crow/Hong_Kong/2512/2006 (H5N1)
E A/little_egret/Hong_Kong/718/2006 (H5N1)
E A/mallard/Guangxi/wt/2004 (H5N1)
E A/mallard/Italy/835/2006 (H5N1)
E A/migratory_duck/Jiangxi/2300/2005 (H5N1)
E A/munia/Hong_Kong/2454/2006 (H5N1)
E A/peregrine_falcon/HK/D0028/2004 (H5N1)
E A/Pheasant/HongKong/FY155/01 (H5N1)
E A/pheasant/Shantou/2239/2006 (H5N1)
E A/pigeon/Thailand/KU-03/04 (H5N1)
E A/Qa/Thailand/57/2004 (H5N1)
E A/quail/Guangxi/575/2005 (H5N1)
E A/quail/Thailand/Nakhon_Pathom/QA-161/2005 (H5N1)
E A/quail/Viet_Nam/15/2005 (H5N1)
E A/quail/Vietnam/36/04 (H5N1)
E A/quail/Viet_Nam/TG-007B/2004 (H5N1)
E A/quail/Yogjakarta/BBVet-IX/2004 (H5N1)
E A/R(duck/Mongolia/54/01-duck/Mongolia/47/01) (H5N1)
E A/robin/Hong_Kong/366/2006 (H5N1)
E A/robin/Hong_Kong/75/2006 (H5N1)
E A/SCK/HK/YU100/2002 (H5N1)
E A/swan/Guangxi/307/2004 (H5N1)
E A/Tree_sparrow/Henan/1/2004 (H5N1)
E A/Tree_sparrow/Henan/2/2004 (H5N1)
E A/Tree_sparrow/Henan/3/2004 (H5N1)
E A/Tree_sparrow/Henan/4/2004 (H5N1)
E A/white-backed_munia/Hong_Kong/2469/2006 (H5N1)
E A/wild_duck/Guangdong/314/2004 (H5N1)
E A/wild_duck/Shantou/21498/2005 (H5N1)
(H5N1) E A/Ck/HK/31.4/02
(H5N1) E A/Ck/HK/YU777/02
K A/bar-headed_goose/Mongolia/1/05 (H5N1)
K A/bar-headed_goose/Qinghai/0510/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/12/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/5/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/59/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/60/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/61/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/62/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/65/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/67/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/68/05 (H5N1)
K A/Bar-headed_Goose/Qinghai/75/05 (H5N1)
K A/black-headed_goose/Qinghai/1/2005 (H5N1)
K A/black-headed_goose/Qinghai/2/2005 (H5N1)
K A/black-headed_gull/Qinghai/1/2005 (H5N1)
K A/Brown-headed_Gull/Qinghai/3/05 (H5N1)
K A/chicken/Afghanistan/1207/2006 (H5N1)
K A/chicken/Cote_d'Ivoire/1787-34/2006 (H5N1)
K A/chicken/Crimea/08/2005 (H5N1)
K A/chicken/Kurgan/05/2005 (H5N1)
K A/chicken/Kurgan/3/2005 (H5N1)
K A/chicken/Nigeria/1047-30/2006 (H5N1)
K A/chicken/Nigeria/1047-34/2006 (H5N1)
K A/chicken/Nigeria/1047-54/2006 (H5N1)
K A/chicken/Nigeria/1047-62/2006 (H5N1)
K A/chicken/Nigeria/1047-8/2006 (H5N1)
K A/chicken/Nigeria/641/2006 (H5N1)
K A/chicken/Nigeria/641/2006 (H5N1)
K A/chicken/Nigeria/957-20/2006 (H5N1)
K A/chicken/Sudan/1784-10/2006 (H5N1)
K A/chicken/Sudan/1784-7/2006 (H5N1)
K A/cygnus_cygnus/Iran/754/2006 (H5N1)
K A/Cygnus_olor/Astrakhan/Ast05-2-10/2005 (H5N1)
K A/Cygnus_olor/Astrakhan/Ast05-2-1/2005 (H5N1)
K A/Cygnus_olor/Astrakhan/Ast05-2-2/2005 (H5N1)
K A/Cygnus_olor/Astrakhan/Ast05-2-3/2005 (H5N1)
K A/Cygnus_olor/Astrakhan/Ast05-2-5/2005 (H5N1)
K A/Cygnus_olor/Astrakhan/Ast05-2-6/2005 (H5N1)
K A/Cygnus_olor/Astrakhan/Ast05-2-7/2005 (H5N1)
K A/Cygnus_olor/Astrakhan/Ast05-2-8/2005 (H5N1)
K A/Cygnus_olor/Astrakhan/Ast05-2-9/2005 (H5N1)
K A/cygnus_olor/Croatia/1/2005 (H5N1)
K A/cygnus_olor/Italy/742/2006 (H5N1)

K A/Cygnus_olor/Italy/742/2006(H5N1)
K A/duck/Cote_d'Ivoire/1787-18/2006(H5N1)
K A/duck/Egypt/2253-3/2006(H5N1)
K A/duck/Niger/914/2006(H5N1)
K A/duck/Novosibirsk/56/05(H5N1)
K A/great_black-headed_gull/Qinghai/1/2005(H5N1)
K A/Great_Black-headed_Gull/Qinghai/2/05(H5N1)
K A/grebe/Novosibirsk/29/05(H5N1)
K A/grebe/Tyva/Tyv06-1/06(H5N1)
K A/grebe/Tyva/Tyv06-2/06(H5N1)
K A/Grebe/Tyva/Tyv06-8/2006(H5N1)
K A/guinea_fowl/Nigeria/957-12/2006(H5N1)
K A/Guinea_fowl/Shantou/1341/2006(H5N1)
K A/ostrich/Nigeria/1047-25/2006(H5N1)
K A/Pheasant/HongKong/FY155/01-MB(H5N1)
K A/swan/Astrakhan/Russia/Nov-2/2005(H5N1)
K A/swan/Germany/R65/2006(H5N1)
K A/swan/Slovenia/760/2006(H5N1)
K A/whooper_swan/Mongolia/2/06(H5N1)
K A/whooper_swan/Mongolia/3/05(H5N1)

1: CY017194
Influenza A virus (A/duck/Viet Nam/19/2005(H5N1)) segment 1, complete sequence
gi|117571368|gb|CY017194.1|[117571368]

2: CY017193
Influenza A virus (A/duck/Viet Nam/19/2005(H5N1)) segment 2, complete sequence
gi|117571365|gb|CY017193.1|[117571365]

3: CY017192
Influenza A virus (A/duck/Viet Nam/19/2005(H5N1)) segment 3, complete sequence
gi|117571363|gb|CY017192.1|[117571363]

4: CY017191
Influenza A virus (A/duck/Viet Nam/19/2005(H5N1)) segment 8, complete sequence
gi|117571359|gb|CY017191.1|[117571359]

5: CY017190
Influenza A virus (A/duck/Viet Nam/19/2005(H5N1)) segment 5, complete sequence
gi|117571357|gb|CY017190.1|[117571357]

6: CY017189
Influenza A virus (A/duck/Viet Nam/19/2005(H5N1)) segment 6, complete sequence
gi|117571355|gb|CY017189.1|[117571355]

7: CY017188
Influenza A virus (A/duck/Viet Nam/19/2005(H5N1)) segment 7, complete sequence
gi|117571351|gb|CY017188.1|[117571351]

8: CY017187
Influenza A virus (A/duck/Viet Nam/19/2005(H5N1)) segment 4, complete sequence
gi|117571349|gb|CY017187.1|[117571349]

9: CY017186
Influenza A virus (A/guinea fowl/Nigeria/957-12/2006(H5N1)) segment 1, complete sequence
gi|117571327|gb|CY017186.1|[117571327]

10: CY017185
Influenza A virus (A/guinea fowl/Nigeria/957-12/2006(H5N1)) segment 2, complete sequence
gi|117571323|gb|CY017185.1|[117571323]

11: CY017184
Influenza A virus (A/guinea fowl/Nigeria/957-12/2006(H5N1)) segment 3, complete sequence
gi|117571321|gb|CY017184.1|[117571321]

12: CY017183
Influenza A virus (A/guinea fowl/Nigeria/957-12/2006(H5N1)) segment 8, complete sequence
gi|117571318|gb|CY017183.1|[117571318]

13: CY017182
Influenza A virus (A/guinea fowl/Nigeria/957-12/2006(H5N1)) segment 5, complete sequence
gi|117571315|gb|CY017182.1|[117571315]

14: CY017181
Influenza A virus (A/guinea fowl/Nigeria/957-12/2006(H5N1)) segment 6, complete sequence
gi|117571313|gb|CY017181.1|[117571313]

15: CY017180
Influenza A virus (A/guinea fowl/Nigeria/957-12/2006(H5N1)) segment 7, complete sequence
gi|117571309|gb|CY017180.1|[117571309]

16: CY017179
Influenza A virus (A/guinea fowl/Nigeria/957-12/2006(H5N1)) segment 4, complete sequence
gi|117571307|gb|CY017179.1|[117571307]

17: CY017058
Influenza A virus (A/quail/Viet Nam/15/2005(H5N1)) segment 1, complete sequence
gi|116070400|gb|CY017058.1|[116070400]

18: CY017057
Influenza A virus (A/quail/Viet Nam/15/2005(H5N1)) segment 2, complete sequence
gi|116070397|gb|CY017057.1|[116070397]

19: CY017056
Influenza A virus (A/quail/Viet Nam/15/2005(H5N1)) segment 3, complete sequence
gi|116070395|gb|CY017056.1|[116070395]

20: CY017055
Influenza A virus (A/quail/Viet Nam/15/2005(H5N1)) segment 8, complete sequence
gi|116070392|gb|CY017055.1|[116070392]

21: CY017054
Influenza A virus (A/quail/Viet Nam/15/2005(H5N1)) segment 5, complete sequence
gi|116070390|gb|CY017054.1|[116070390]

22: CY017053
Influenza A virus (A/quail/Viet Nam/15/2005(H5N1)) segment 6, complete sequence
gi|116070388|gb|CY017053.1|[116070388]

23: CY017052
Influenza A virus (A/quail/Viet Nam/15/2005(H5N1)) segment 7, complete sequence
gi|116070385|gb|CY017052.1|[116070385]

24: CY017051
Influenza A virus (A/quail/Viet Nam/15/2005(H5N1)) segment 4, complete sequence
gi|116070383|gb|CY017051.1|[116070383]

25: CY017066
Influenza A virus (A/chicken/Viet Nam/17/2005(H5N1)) segment 1, complete sequence
gi|116070381|gb|CY017066.1|[116070381]

26: CY017065
Influenza A virus (A/chicken/Viet Nam/17/2005(H5N1)) segment 2, complete sequence
gi|116070378|gb|CY017065.1|[116070378]

27: CY017064
Influenza A virus (A/chicken/Viet Nam/17/2005(H5N1)) segment 3, complete sequence
gi|116070376|gb|CY017064.1|[116070376]

28: CY017063
Influenza A virus (A/chicken/Viet Nam/17/2005(H5N1)) segment 8, complete sequence
gi|116070373|gb|CY017063.1|[116070373]

29: CY017062
Influenza A virus (A/chicken/Viet Nam/17/2005(H5N1)) segment 5, complete sequence
gi|116070371|gb|CY017062.1|[116070371]

30: CY017061
Influenza A virus (A/chicken/Viet Nam/17/2005(H5N1)) segment 6, complete sequence
gi|116070369|gb|CY017061.1|[116070369]

31: CY017060
Influenza A virus (A/chicken/Viet Nam/17/2005(H5N1)) segment 7, complete sequence
gi|116070366|gb|CY017060.1|[116070366]

32: CY017059
Influenza A virus (A/chicken/Viet Nam/17/2005(H5N1)) segment 4, complete sequence
gi|116070364|gb|CY017059.1|[116070364]

33: CY017035

Influenza A virus (A/cygnus olor/Italy/742/2006(H5N1)) segment 4, complete sequence
gi|116070055|gb|CY017035.1|[116070055]

34: CY017074
Influenza A virus (A/duck/Viet Nam/18/2005(H5N1)) segment 1, complete sequence
gi|116070110|gb|CY017074.1|[116070110]

35: CY017073
Influenza A virus (A/duck/Viet Nam/18/2005(H5N1)) segment 2, complete sequence
gi|116070107|gb|CY017073.1|[116070107]

36: CY017072
Influenza A virus (A/duck/Viet Nam/18/2005(H5N1)) segment 3, complete sequence
gi|116070105|gb|CY017072.1|[116070105]

37: CY017071
Influenza A virus (A/duck/Viet Nam/18/2005(H5N1)) segment 8, complete sequence
gi|116070102|gb|CY017071.1|[116070102]

38: CY017070
Influenza A virus (A/duck/Viet Nam/18/2005(H5N1)) segment 5, complete sequence
gi|116070100|gb|CY017070.1|[116070100]

39: CY017069
Influenza A virus (A/duck/Viet Nam/18/2005(H5N1)) segment 6, complete sequence
gi|116070098|gb|CY017069.1|[116070098]

40: CY017068
Influenza A virus (A/duck/Viet Nam/18/2005(H5N1)) segment 7, complete sequence
gi|116070095|gb|CY017068.1|[116070095]

41: CY017067
Influenza A virus (A/duck/Viet Nam/18/2005(H5N1)) segment 4, complete sequence
gi|116070093|gb|CY017067.1|[116070093]

42: CY017050
Influenza A virus (A/swan/Slovenia/760/2006(H5N1)) segment 1, complete sequence
gi|116070091|gb|CY017050.1|[116070091]

43: CY017049
Influenza A virus (A/swan/Slovenia/760/2006(H5N1)) segment 2, complete sequence
gi|116070088|gb|CY017049.1|[116070088]

44: CY017048
Influenza A virus (A/swan/Slovenia/760/2006(H5N1)) segment 3, complete sequence
gi|116070086|gb|CY017048.1|[116070086]

45: CY017047
Influenza A virus (A/swan/Slovenia/760/2006(H5N1)) segment 8, complete sequence
gi|116070083|gb|CY017047.1|[116070083]

46: CY017046
Influenza A virus (A/swan/Slovenia/760/2006(H5N1)) segment 5, complete sequence
gi|116070081|gb|CY017046.1|[116070081]

47: CY017045
Influenza A virus (A/swan/Slovenia/760/2006(H5N1)) segment 6, complete sequence
gi|116070079|gb|CY017045.1|[116070079]

48: CY017044
Influenza A virus (A/swan/Slovenia/760/2006(H5N1)) segment 7, complete sequence
gi|116070076|gb|CY017044.1|[116070076]

49: CY017043
Influenza A virus (A/swan/Slovenia/760/2006(H5N1)) segment 4, complete sequence

gi|116070074|gb|CY017043.1|[116070074]

50: CY017042

Influenza A virus (A/cygnus olor/Italy/742/2006(H5N1)) segment 1, complete sequence
gi|116070072|gb|CY017042.1|[116070072]

51: CY017041

Influenza A virus (A/cygnus olor/Italy/742/2006(H5N1)) segment 2, complete sequence
gi|116070069|gb|CY017041.1|[116070069]

52: CY017040

Influenza A virus (A/cygnus olor/Italy/742/2006(H5N1)) segment 3, complete sequence
gi|116070067|gb|CY017040.1|[116070067]

53: CY017039

Influenza A virus (A/cygnus olor/Italy/742/2006(H5N1)) segment 8, complete sequence
gi|116070064|gb|CY017039.1|[116070064]

54: CY017038

Influenza A virus (A/cygnus olor/Italy/742/2006(H5N1)) segment 5, complete sequence
gi|116070062|gb|CY017038.1|[116070062]

55: CY017037

Influenza A virus (A/cygnus olor/Italy/742/2006(H5N1)) segment 6, complete sequence
gi|116070060|gb|CY017037.1|[116070060]

56: CY017036

Influenza A virus (A/cygnus olor/Italy/742/2006(H5N1)) segment 7, complete sequence
gi|116070057|gb|CY017036.1|[116070057]

57: CY017034

Influenza A virus (A/duck/Niger/914/2006(H5N1)) segment 1, complete sequence
gi|116070053|gb|CY017034.1|[116070053]

58: CY017033

Influenza A virus (A/duck/Niger/914/2006(H5N1)) segment 2, complete sequence
gi|116070050|gb|CY017033.1|[116070050]

59: CY017032

Influenza A virus (A/duck/Niger/914/2006(H5N1)) segment 3, complete sequence
gi|116070048|gb|CY017032.1|[116070048]

60: CY017031

Influenza A virus (A/duck/Niger/914/2006(H5N1)) segment 8, complete sequence
gi|116070045|gb|CY017031.1|[116070045]

61: CY017030

Influenza A virus (A/duck/Niger/914/2006(H5N1)) segment 5, complete sequence
gi|116070043|gb|CY017030.1|[116070043]

62: CY017029

Influenza A virus (A/duck/Niger/914/2006(H5N1)) segment 6, complete sequence
gi|116070041|gb|CY017029.1|[116070041]

63: CY017028

Influenza A virus (A/duck/Niger/914/2006(H5N1)) segment 7, complete sequence
gi|116070038|gb|CY017028.1|[116070038]

64: CY017027

Influenza A virus (A/duck/Niger/914/2006(H5N1)) segment 4, complete sequence
gi|116070036|gb|CY017027.1|[116070036]

65: CY016874

Influenza A virus (A/chicken/Viet Nam/10/2005(H5N1)) segment 1, complete sequence
gi|115953527|gb|CY016874.1|[115953527]

66: CY016873
Influenza A virus (A/chicken/Viet Nam/10/2005(H5N1)) segment 2, complete sequence
gi|115953523|gb|CY016873.1|[115953523]

67: CY016872
Influenza A virus (A/chicken/Viet Nam/10/2005(H5N1)) segment 3, complete sequence
gi|115953520|gb|CY016872.1|[115953520]

68: CY016871
Influenza A virus (A/chicken/Viet Nam/10/2005(H5N1)) segment 8, complete sequence
gi|115953516|gb|CY016871.1|[115953516]

69: CY016870
Influenza A virus (A/chicken/Viet Nam/10/2005(H5N1)) segment 5, complete sequence
gi|115953513|gb|CY016870.1|[115953513]

70: CY016869
Influenza A virus (A/chicken/Viet Nam/10/2005(H5N1)) segment 6, complete sequence
gi|115953510|gb|CY016869.1|[115953510]

71: CY016868
Influenza A virus (A/chicken/Viet Nam/10/2005(H5N1)) segment 7, complete sequence
gi|115953506|gb|CY016868.1|[115953506]

72: CY016867
Influenza A virus (A/chicken/Viet Nam/10/2005(H5N1)) segment 4, complete sequence
gi|115953503|gb|CY016867.1|[115953503]

73: CY016842
Influenza A virus (A/chicken/Viet Nam/2/2005(H5N1)) segment 1, complete sequence
gi|115953095|gb|CY016842.1|[115953095]

74: CY016841
Influenza A virus (A/chicken/Viet Nam/2/2005(H5N1)) segment 2, complete sequence
gi|115953092|gb|CY016841.1|[115953092]

75: CY016840
Influenza A virus (A/chicken/Viet Nam/2/2005(H5N1)) segment 3, complete sequence
gi|115953090|gb|CY016840.1|[115953090]

76: CY016839
Influenza A virus (A/chicken/Viet Nam/2/2005(H5N1)) segment 8, complete sequence
gi|115953087|gb|CY016839.1|[115953087]

77: CY016838
Influenza A virus (A/chicken/Viet Nam/2/2005(H5N1)) segment 5, complete sequence
gi|115953085|gb|CY016838.1|[115953085]

78: CY016837
Influenza A virus (A/chicken/Viet Nam/2/2005(H5N1)) segment 6, complete sequence
gi|115953083|gb|CY016837.1|[115953083]

79: CY016836
Influenza A virus (A/chicken/Viet Nam/2/2005(H5N1)) segment 7, complete sequence
gi|115953080|gb|CY016836.1|[115953080]

80: CY016835
Influenza A virus (A/chicken/Viet Nam/2/2005(H5N1)) segment 4, complete sequence
gi|115953078|gb|CY016835.1|[115953078]

81: CY016850
Influenza A virus (A/chicken/Viet Nam/6/2005(H5N1)) segment 1, complete sequence
gi|115953015|gb|CY016850.1|[115953015]

82: CY016849
Influenza A virus (A/chicken/Viet Nam/6/2005(H5N1)) segment 2, complete sequence
gi|115953012|gb|CY016849.1|[115953012]

83: CY016848
Influenza A virus (A/chicken/Viet Nam/6/2005(H5N1)) segment 3, complete sequence
gi|115953010|gb|CY016848.1|[115953010]

84: CY016847
Influenza A virus (A/chicken/Viet Nam/6/2005(H5N1)) segment 8, complete sequence
gi|115953007|gb|CY016847.1|[115953007]

85: CY016846
Influenza A virus (A/chicken/Viet Nam/6/2005(H5N1)) segment 5, complete sequence
gi|115953005|gb|CY016846.1|[115953005]

86: CY016845
Influenza A virus (A/chicken/Viet Nam/6/2005(H5N1)) segment 6, complete sequence
gi|115953003|gb|CY016845.1|[115953003]

87: CY016844
Influenza A virus (A/chicken/Viet Nam/6/2005(H5N1)) segment 7, complete sequence
gi|115953000|gb|CY016844.1|[115953000]

88: CY016843
Influenza A virus (A/chicken/Viet Nam/6/2005(H5N1)) segment 4, complete sequence
gi|115952998|gb|CY016843.1|[115952998]

89: CY016858
Influenza A virus (A/chicken/Viet Nam/8/2005(H5N1)) segment 1, complete sequence
gi|115952912|gb|CY016858.1|[115952912]

90: CY016857
Influenza A virus (A/chicken/Viet Nam/8/2005(H5N1)) segment 2, complete sequence
gi|115952907|gb|CY016857.1|[115952907]

91: CY016856
Influenza A virus (A/chicken/Viet Nam/8/2005(H5N1)) segment 3, complete sequence
gi|115952904|gb|CY016856.1|[115952904]

92: CY016855
Influenza A virus (A/chicken/Viet Nam/8/2005(H5N1)) segment 8, complete sequence
gi|115952899|gb|CY016855.1|[115952899]

93: CY016854
Influenza A virus (A/chicken/Viet Nam/8/2005(H5N1)) segment 5, complete sequence
gi|115952895|gb|CY016854.1|[115952895]

94: CY016853
Influenza A virus (A/chicken/Viet Nam/8/2005(H5N1)) segment 6, complete sequence
gi|115952892|gb|CY016853.1|[115952892]

95: CY016852
Influenza A virus (A/chicken/Viet Nam/8/2005(H5N1)) segment 7, complete sequence
gi|115952888|gb|CY016852.1|[115952888]

96: CY016851
Influenza A virus (A/chicken/Viet Nam/8/2005(H5N1)) segment 4, complete sequence
gi|115952885|gb|CY016851.1|[115952885]

97: CY016866
Influenza A virus (A/chicken/Viet Nam/9/2005(H5N1)) segment 1, complete sequence
gi|115952810|gb|CY016866.1|[115952810]

98: CY016865
Influenza A virus (A/chicken/Viet Nam/9/2005(H5N1)) segment 2, complete sequence
gi|115952806|gb|CY016865.1|[115952806]

99: CY016864
Influenza A virus (A/chicken/Viet Nam/9/2005(H5N1)) segment 3, complete sequence
gi|115952801|gb|CY016864.1|[115952801]

100: CY016863
Influenza A virus (A/chicken/Viet Nam/9/2005(H5N1)) segment 8, complete sequence
gi|115952798|gb|CY016863.1|[115952798]

101: CY016862
Influenza A virus (A/chicken/Viet Nam/9/2005(H5N1)) segment 5, complete sequence
gi|115952795|gb|CY016862.1|[115952795]

102: CY016861
Influenza A virus (A/chicken/Viet Nam/9/2005(H5N1)) segment 6, complete sequence
gi|115952793|gb|CY016861.1|[115952793]

103: CY016860
Influenza A virus (A/chicken/Viet Nam/9/2005(H5N1)) segment 7, complete sequence
gi|115952789|gb|CY016860.1|[115952789]

104: CY016859
Influenza A virus (A/chicken/Viet Nam/9/2005(H5N1)) segment 4, complete sequence
gi|115952786|gb|CY016859.1|[115952786]

105: CY016882
Influenza A virus (A/chicken/Viet Nam/11/2005(H5N1)) segment 1, complete sequence
gi|115952239|gb|CY016882.1|[115952239]

106: CY016881
Influenza A virus (A/chicken/Viet Nam/11/2005(H5N1)) segment 2, complete sequence
gi|115952236|gb|CY016881.1|[115952236]

107: CY016880
Influenza A virus (A/chicken/Viet Nam/11/2005(H5N1)) segment 3, complete sequence
gi|115952233|gb|CY016880.1|[115952233]

108: CY016879
Influenza A virus (A/chicken/Viet Nam/11/2005(H5N1)) segment 8, complete sequence
gi|115952229|gb|CY016879.1|[115952229]

109: CY016878
Influenza A virus (A/chicken/Viet Nam/11/2005(H5N1)) segment 5, complete sequence
gi|115952226|gb|CY016878.1|[115952226]

110: CY016877
Influenza A virus (A/chicken/Viet Nam/11/2005(H5N1)) segment 6, complete sequence
gi|115952224|gb|CY016877.1|[115952224]

111: CY016876
Influenza A virus (A/chicken/Viet Nam/11/2005(H5N1)) segment 7, complete sequence
gi|115952220|gb|CY016876.1|[115952220]

112: CY016875
Influenza A virus (A/chicken/Viet Nam/11/2005(H5N1)) segment 4, complete sequence
gi|115952217|gb|CY016875.1|[115952217]

113: CY016890
Influenza A virus (A/duck/Viet Nam/12/2005(H5N1)) segment 1, complete sequence
gi|115951830|gb|CY016890.1|[115951830]

114: CY016889

Influenza A virus (A/duck/Viet Nam/12/2005(H5N1)) segment 2, complete sequence
gi|115951826|gb|CY016889.1|[115951826]

115: CY016888
Influenza A virus (A/duck/Viet Nam/12/2005(H5N1)) segment 3, complete sequence
gi|115951824|gb|CY016888.1|[115951824]

116: CY016887
Influenza A virus (A/duck/Viet Nam/12/2005(H5N1)) segment 8, complete sequence
gi|115951820|gb|CY016887.1|[115951820]

117: CY016886
Influenza A virus (A/duck/Viet Nam/12/2005(H5N1)) segment 5, complete sequence
gi|115951818|gb|CY016886.1|[115951818]

118: CY016885
Influenza A virus (A/duck/Viet Nam/12/2005(H5N1)) segment 6, complete sequence
gi|115951815|gb|CY016885.1|[115951815]

119: CY016884
Influenza A virus (A/duck/Viet Nam/12/2005(H5N1)) segment 7, complete sequence
gi|115951812|gb|CY016884.1|[115951812]

120: CY016883
Influenza A virus (A/duck/Viet Nam/12/2005(H5N1)) segment 4, complete sequence
gi|115951804|gb|CY016883.1|[115951804]

121: CY016818
Influenza A virus (A/chicken/Cote d'Ivoire/1787-34/2006(H5N1)) segment 1, complete sequence
gi|115609313|gb|CY016818.1|[115609313]

122: CY016817
Influenza A virus (A/chicken/Cote d'Ivoire/1787-34/2006(H5N1)) segment 2, complete sequence
gi|115609310|gb|CY016817.1|[115609310]

123: CY016816
Influenza A virus (A/chicken/Cote d'Ivoire/1787-34/2006(H5N1)) segment 3, complete sequence
gi|115609308|gb|CY016816.1|[115609308]

124: CY016815
Influenza A virus (A/chicken/Cote d'Ivoire/1787-34/2006(H5N1)) segment 8, complete sequence
gi|115609305|gb|CY016815.1|[115609305]

125: CY016814
Influenza A virus (A/chicken/Cote d'Ivoire/1787-34/2006(H5N1)) segment 5, complete sequence
gi|115609303|gb|CY016814.1|[115609303]

126: CY016813
Influenza A virus (A/chicken/Cote d'Ivoire/1787-34/2006(H5N1)) segment 6, complete sequence
gi|115609301|gb|CY016813.1|[115609301]

127: CY016812
Influenza A virus (A/chicken/Cote d'Ivoire/1787-34/2006(H5N1)) segment 7, complete sequence
gi|115609298|gb|CY016812.1|[115609298]

128: CY016811
Influenza A virus (A/chicken/Cote d'Ivoire/1787-34/2006(H5N1)) segment 4, complete sequence
gi|115609292|gb|CY016811.1|[115609292]

129: CY016898
Influenza A virus (A/duck/Viet Nam/20/2005(H5N1)) segment 1, complete sequence
gi|115609777|gb|CY016898.1|[115609777]

130: CY016897
Influenza A virus (A/duck/Viet Nam/20/2005(H5N1)) segment 2, complete sequence

gi|115609774|gb|CY016897.1|[115609774]

131: CY016896

Influenza A virus (A/duck/Viet Nam/20/2005(H5N1)) segment 3, complete sequence
gi|115609771|gb|CY016896.1|[115609771]

132: CY016895

Influenza A virus (A/duck/Viet Nam/20/2005(H5N1)) segment 8, complete sequence
gi|115609768|gb|CY016895.1|[115609768]

133: CY016894

Influenza A virus (A/duck/Viet Nam/20/2005(H5N1)) segment 5, complete sequence
gi|115609765|gb|CY016894.1|[115609765]

134: CY016893

Influenza A virus (A/duck/Viet Nam/20/2005(H5N1)) segment 6, complete sequence
gi|115609762|gb|CY016893.1|[115609762]

135: CY016892

Influenza A virus (A/duck/Viet Nam/20/2005(H5N1)) segment 7, complete sequence
gi|115609759|gb|CY016892.1|[115609759]

136: CY016891

Influenza A virus (A/duck/Viet Nam/20/2005(H5N1)) segment 4, complete sequence
gi|115609756|gb|CY016891.1|[115609756]

137: CY016834

Influenza A virus (A/duck/Viet Nam/1/2005(H5N1)) segment 1, complete sequence
gi|115609715|gb|CY016834.1|[115609715]

138: CY016833

Influenza A virus (A/duck/Viet Nam/1/2005(H5N1)) segment 2, complete sequence
gi|115609712|gb|CY016833.1|[115609712]

139: CY016832

Influenza A virus (A/duck/Viet Nam/1/2005(H5N1)) segment 3, complete sequence
gi|115609710|gb|CY016832.1|[115609710]

140: CY016831

Influenza A virus (A/duck/Viet Nam/1/2005(H5N1)) segment 8, complete sequence
gi|115609707|gb|CY016831.1|[115609707]

141: CY016830

Influenza A virus (A/duck/Viet Nam/1/2005(H5N1)) segment 5, complete sequence
gi|115609704|gb|CY016830.1|[115609704]

142: CY016829

Influenza A virus (A/duck/Viet Nam/1/2005(H5N1)) segment 6, complete sequence
gi|115609702|gb|CY016829.1|[115609702]

143: CY016828

Influenza A virus (A/duck/Viet Nam/1/2005(H5N1)) segment 7, complete sequence
gi|115609699|gb|CY016828.1|[115609699]

144: CY016827

Influenza A virus (A/duck/Viet Nam/1/2005(H5N1)) segment 4, complete sequence
gi|115609697|gb|CY016827.1|[115609697]

145: CY016810

Influenza A virus (A/duck/Cote d'Ivoire/1787-18/2006(H5N1)) segment 1, complete sequence
gi|115609556|gb|CY016810.1|[115609556]

146: CY016809

Influenza A virus (A/duck/Cote d'Ivoire/1787-18/2006(H5N1)) segment 2, complete sequence
gi|115609551|gb|CY016809.1|[115609551]

147: CY016808
Influenza A virus (A/duck/Cote d'Ivoire/1787-18/2006(H5N1)) segment 3, complete sequence
gi|115609549|gb|CY016808.1|[115609549]

148: CY016807
Influenza A virus (A/duck/Cote d'Ivoire/1787-18/2006(H5N1)) segment 8, complete sequence
gi|115609546|gb|CY016807.1|[115609546]

149: CY016806
Influenza A virus (A/duck/Cote d'Ivoire/1787-18/2006(H5N1)) segment 5, complete sequence
gi|115609544|gb|CY016806.1|[115609544]

150: CY016805
Influenza A virus (A/duck/Cote d'Ivoire/1787-18/2006(H5N1)) segment 6, complete sequence
gi|115609542|gb|CY016805.1|[115609542]

151: CY016804
Influenza A virus (A/duck/Cote d'Ivoire/1787-18/2006(H5N1)) segment 7, complete sequence
gi|115609538|gb|CY016804.1|[115609538]

152: CY016803
Influenza A virus (A/duck/Cote d'Ivoire/1787-18/2006(H5N1)) segment 4, complete sequence
gi|115609536|gb|CY016803.1|[115609536]

153: CY016954
Influenza A virus (A/chicken/Nigeria/1047-34/2006(H5N1)) segment 1, complete sequence
gi|115608218|gb|CY016954.1|[115608218]

154: CY016953
Influenza A virus (A/chicken/Nigeria/1047-34/2006(H5N1)) segment 2, complete sequence
gi|115608215|gb|CY016953.1|[115608215]

155: CY016952
Influenza A virus (A/chicken/Nigeria/1047-34/2006(H5N1)) segment 3, complete sequence
gi|115608213|gb|CY016952.1|[115608213]

156: CY016951
Influenza A virus (A/chicken/Nigeria/1047-34/2006(H5N1)) segment 8, complete sequence
gi|115608210|gb|CY016951.1|[115608210]

157: CY016950
Influenza A virus (A/chicken/Nigeria/1047-34/2006(H5N1)) segment 5, complete sequence
gi|115608208|gb|CY016950.1|[115608208]

158: CY016949
Influenza A virus (A/chicken/Nigeria/1047-34/2006(H5N1)) segment 6, complete sequence
gi|115608206|gb|CY016949.1|[115608206]

159: CY016948
Influenza A virus (A/chicken/Nigeria/1047-34/2006(H5N1)) segment 7, complete sequence
gi|115608203|gb|CY016948.1|[115608203]

160: CY016947
Influenza A virus (A/chicken/Nigeria/1047-34/2006(H5N1)) segment 4, complete sequence
gi|115608201|gb|CY016947.1|[115608201]

161: CY016946
Influenza A virus (A/chicken/Nigeria/1047-30/2006(H5N1)) segment 1, complete sequence
gi|115608199|gb|CY016946.1|[115608199]

162: CY016945
Influenza A virus (A/chicken/Nigeria/1047-30/2006(H5N1)) segment 2, complete sequence
gi|115608196|gb|CY016945.1|[115608196]

163: CY016944
Influenza A virus (A/chicken/Nigeria/1047-30/2006(H5N1)) segment 3, complete sequence
gi|115608194|gb|CY016944.1|[115608194]

164: CY016943
Influenza A virus (A/chicken/Nigeria/1047-30/2006(H5N1)) segment 8, complete sequence
gi|115608191|gb|CY016943.1|[115608191]

165: CY016942
Influenza A virus (A/chicken/Nigeria/1047-30/2006(H5N1)) segment 5, complete sequence
gi|115608189|gb|CY016942.1|[115608189]

166: CY016941
Influenza A virus (A/chicken/Nigeria/1047-30/2006(H5N1)) segment 6, complete sequence
gi|115608187|gb|CY016941.1|[115608187]

167: CY016940
Influenza A virus (A/chicken/Nigeria/1047-30/2006(H5N1)) segment 7, complete sequence
gi|115608184|gb|CY016940.1|[115608184]

168: CY016939
Influenza A virus (A/chicken/Nigeria/1047-30/2006(H5N1)) segment 4, complete sequence
gi|115608182|gb|CY016939.1|[115608182]

169: CY016938
Influenza A virus (A/chicken/Nigeria/1047-62/2006(H5N1)) segment 1, complete sequence
gi|115608180|gb|CY016938.1|[115608180]

170: CY016937
Influenza A virus (A/chicken/Nigeria/1047-62/2006(H5N1)) segment 2, complete sequence
gi|115608177|gb|CY016937.1|[115608177]

171: CY016936
Influenza A virus (A/chicken/Nigeria/1047-62/2006(H5N1)) segment 3, complete sequence
gi|115608175|gb|CY016936.1|[115608175]

172: CY016935
Influenza A virus (A/chicken/Nigeria/1047-62/2006(H5N1)) segment 8, complete sequence
gi|115608172|gb|CY016935.1|[115608172]

173: CY016934
Influenza A virus (A/chicken/Nigeria/1047-62/2006(H5N1)) segment 5, complete sequence
gi|115608170|gb|CY016934.1|[115608170]

174: CY016933
Influenza A virus (A/chicken/Nigeria/1047-62/2006(H5N1)) segment 6, complete sequence
gi|115608168|gb|CY016933.1|[115608168]

175: CY016932
Influenza A virus (A/chicken/Nigeria/1047-62/2006(H5N1)) segment 7, complete sequence
gi|115608165|gb|CY016932.1|[115608165]

176: CY016931
Influenza A virus (A/chicken/Nigeria/1047-62/2006(H5N1)) segment 4, complete sequence
gi|115608163|gb|CY016931.1|[115608163]

177: CY016930
Influenza A virus (A/chicken/Nigeria/1047-54/2006(H5N1)) segment 1, complete sequence
gi|115608161|gb|CY016930.1|[115608161]

178: CY016929
Influenza A virus (A/chicken/Nigeria/1047-54/2006(H5N1)) segment 2, complete sequence
gi|115608158|gb|CY016929.1|[115608158]

179: CY016928
Influenza A virus (A/chicken/Nigeria/1047-54/2006(H5N1)) segment 3, complete sequence
gi|115608156|gb|CY016928.1|[115608156]

180: CY016927
Influenza A virus (A/chicken/Nigeria/1047-54/2006(H5N1)) segment 8, complete sequence
gi|115608153|gb|CY016927.1|[115608153]

181: CY016926
Influenza A virus (A/chicken/Nigeria/1047-54/2006(H5N1)) segment 5, complete sequence
gi|115608151|gb|CY016926.1|[115608151]

182: CY016925
Influenza A virus (A/chicken/Nigeria/1047-54/2006(H5N1)) segment 6, complete sequence
gi|115608149|gb|CY016925.1|[115608149]

183: CY016924
Influenza A virus (A/chicken/Nigeria/1047-54/2006(H5N1)) segment 7, complete sequence
gi|115608146|gb|CY016924.1|[115608146]

184: CY016923
Influenza A virus (A/chicken/Nigeria/1047-54/2006(H5N1)) segment 4, complete sequence
gi|115608144|gb|CY016923.1|[115608144]

185: CY016922
Influenza A virus (A/ostrich/Nigeria/1047-25/2006(H5N1)) segment 1, complete sequence
gi|115608142|gb|CY016922.1|[115608142]

186: CY016921
Influenza A virus (A/ostrich/Nigeria/1047-25/2006(H5N1)) segment 2, complete sequence
gi|115608139|gb|CY016921.1|[115608139]

187: CY016920
Influenza A virus (A/ostrich/Nigeria/1047-25/2006(H5N1)) segment 3, complete sequence
gi|115608137|gb|CY016920.1|[115608137]

188: CY016919
Influenza A virus (A/ostrich/Nigeria/1047-25/2006(H5N1)) segment 8, complete sequence
gi|115608134|gb|CY016919.1|[115608134]

189: CY016918
Influenza A virus (A/ostrich/Nigeria/1047-25/2006(H5N1)) segment 5, complete sequence
gi|115608132|gb|CY016918.1|[115608132]

190: CY016917
Influenza A virus (A/ostrich/Nigeria/1047-25/2006(H5N1)) segment 6, complete sequence
gi|115608130|gb|CY016917.1|[115608130]

191: CY016916
Influenza A virus (A/ostrich/Nigeria/1047-25/2006(H5N1)) segment 7, complete sequence
gi|115608127|gb|CY016916.1|[115608127]

192: CY016915
Influenza A virus (A/ostrich/Nigeria/1047-25/2006(H5N1)) segment 4, complete sequence
gi|115608125|gb|CY016915.1|[115608125]

193: CY016914
Influenza A virus (A/chicken/Nigeria/1047-8/2006(H5N1)) segment 1, complete sequence
gi|115608123|gb|CY016914.1|[115608123]

194: CY016913
Influenza A virus (A/chicken/Nigeria/1047-8/2006(H5N1)) segment 2, complete sequence
gi|115608120|gb|CY016913.1|[115608120]

195: CY016912

Influenza A virus (A/chicken/Nigeria/1047-8/2006(H5N1)) segment 3, complete sequence
gi|115608118|gb|CY016912.1|[115608118]

196: CY016911
Influenza A virus (A/chicken/Nigeria/1047-8/2006(H5N1)) segment 8, complete sequence
gi|115608115|gb|CY016911.1|[115608115]

197: CY016910
Influenza A virus (A/chicken/Nigeria/1047-8/2006(H5N1)) segment 5, complete sequence
gi|115608113|gb|CY016910.1|[115608113]

198: CY016909
Influenza A virus (A/chicken/Nigeria/1047-8/2006(H5N1)) segment 6, complete sequence
gi|115608111|gb|CY016909.1|[115608111]

199: CY016908
Influenza A virus (A/chicken/Nigeria/1047-8/2006(H5N1)) segment 7, complete sequence
gi|115608108|gb|CY016908.1|[115608108]

200: CY016907
Influenza A virus (A/chicken/Nigeria/1047-8/2006(H5N1)) segment 4, complete sequence
gi|115608106|gb|CY016907.1|[115608106]

201: CY016906
Influenza A virus (A/duck/Egypt/2253-3/2006(H5N1)) segment 1, complete sequence
gi|115608104|gb|CY016906.1|[115608104]

202: CY016905
Influenza A virus (A/duck/Egypt/2253-3/2006(H5N1)) segment 2, complete sequence
gi|115608101|gb|CY016905.1|[115608101]

203: CY016904
Influenza A virus (A/duck/Egypt/2253-3/2006(H5N1)) segment 3, complete sequence
gi|115608099|gb|CY016904.1|[115608099]

204: CY016903
Influenza A virus (A/duck/Egypt/2253-3/2006(H5N1)) segment 8, complete sequence
gi|115608096|gb|CY016903.1|[115608096]

205: CY016902
Influenza A virus (A/duck/Egypt/2253-3/2006(H5N1)) segment 5, complete sequence
gi|115608094|gb|CY016902.1|[115608094]

206: CY016901
Influenza A virus (A/duck/Egypt/2253-3/2006(H5N1)) segment 6, complete sequence
gi|115608092|gb|CY016901.1|[115608092]

207: CY016900
Influenza A virus (A/duck/Egypt/2253-3/2006(H5N1)) segment 7, complete sequence
gi|115608089|gb|CY016900.1|[115608089]

208: CY016899
Influenza A virus (A/duck/Egypt/2253-3/2006(H5N1)) segment 4, complete sequence
gi|115608087|gb|CY016899.1|[115608087]

209: CY016826
Influenza A virus (A/cygnus olor/Croatia/1/2005(H5N1)) segment 1, complete sequence
gi|115608085|gb|CY016826.1|[115608085]

210: CY016825
Influenza A virus (A/cygnus olor/Croatia/1/2005(H5N1)) segment 2, complete sequence
gi|115608082|gb|CY016825.1|[115608082]

211: CY016824
Influenza A virus (A/cygnus olor/Croatia/1/2005(H5N1)) segment 3, complete sequence

gi|115608080|gb|CY016824.1|[115608080]

212: CY016823

Influenza A virus (A/cygnus olor/Croatia/1/2005(H5N1)) segment 8, complete sequence
gi|115608077|gb|CY016823.1|[115608077]

213: CY016822

Influenza A virus (A/cygnus olor/Croatia/1/2005(H5N1)) segment 5, complete sequence
gi|115608075|gb|CY016822.1|[115608075]

214: CY016821

Influenza A virus (A/cygnus olor/Croatia/1/2005(H5N1)) segment 6, complete sequence
gi|115608073|gb|CY016821.1|[115608073]

215: CY016820

Influenza A virus (A/cygnus olor/Croatia/1/2005(H5N1)) segment 7, complete sequence
gi|115608070|gb|CY016820.1|[115608070]

216: CY016819

Influenza A virus (A/cygnus olor/Croatia/1/2005(H5N1)) segment 4, complete sequence
gi|115608068|gb|CY016819.1|[115608068]

217: CY016802

Influenza A virus (A/mallard/Italy/835/2006(H5N1)) segment 1, complete sequence
gi|115608066|gb|CY016802.1|[115608066]

218: CY016801

Influenza A virus (A/mallard/Italy/835/2006(H5N1)) segment 2, complete sequence
gi|115608063|gb|CY016801.1|[115608063]

219: CY016800

Influenza A virus (A/mallard/Italy/835/2006(H5N1)) segment 3, complete sequence
gi|115608061|gb|CY016800.1|[115608061]

220: CY016799

Influenza A virus (A/mallard/Italy/835/2006(H5N1)) segment 8, complete sequence
gi|115608058|gb|CY016799.1|[115608058]

221: CY016798

Influenza A virus (A/mallard/Italy/835/2006(H5N1)) segment 5, complete sequence
gi|115608056|gb|CY016798.1|[115608056]

222: CY016797

Influenza A virus (A/mallard/Italy/835/2006(H5N1)) segment 6, complete sequence
gi|115608054|gb|CY016797.1|[115608054]

223: CY016796

Influenza A virus (A/mallard/Italy/835/2006(H5N1)) segment 7, complete sequence
gi|115608051|gb|CY016796.1|[115608051]

224: CY016795

Influenza A virus (A/mallard/Italy/835/2006(H5N1)) segment 4, complete sequence
gi|115608049|gb|CY016795.1|[115608049]

225: CY016794

Influenza A virus (A/chicken/Afghanistan/1207/2006(H5N1)) segment 1, complete sequence
gi|115608047|gb|CY016794.1|[115608047]

226: CY016793

Influenza A virus (A/chicken/Afghanistan/1207/2006(H5N1)) segment 2, complete sequence
gi|115608044|gb|CY016793.1|[115608044]

227: CY016792

Influenza A virus (A/chicken/Afghanistan/1207/2006(H5N1)) segment 3, complete sequence
gi|115608042|gb|CY016792.1|[115608042]

228: CY016791
Influenza A virus (A/chicken/Afghanistan/1207/2006(H5N1)) segment 8, complete sequence
gi|115608039|gb|CY016791.1|[115608039]

229: CY016790
Influenza A virus (A/chicken/Afghanistan/1207/2006(H5N1)) segment 5, complete sequence
gi|115608037|gb|CY016790.1|[115608037]

230: CY016789
Influenza A virus (A/chicken/Afghanistan/1207/2006(H5N1)) segment 6, complete sequence
gi|115608035|gb|CY016789.1|[115608035]

231: CY016788
Influenza A virus (A/chicken/Afghanistan/1207/2006(H5N1)) segment 7, complete sequence
gi|115608032|gb|CY016788.1|[115608032]

232: CY016787
Influenza A virus (A/chicken/Afghanistan/1207/2006(H5N1)) segment 4, complete sequence
gi|115608030|gb|CY016787.1|[115608030]

233: CY016786
Influenza A virus (A/cygnus cygnus/Iran/754/2006(H5N1)) segment 1, complete sequence
gi|115608028|gb|CY016786.1|[115608028]

234: CY016785
Influenza A virus (A/cygnus cygnus/Iran/754/2006(H5N1)) segment 2, complete sequence
gi|115608025|gb|CY016785.1|[115608025]

235: CY016784
Influenza A virus (A/cygnus cygnus/Iran/754/2006(H5N1)) segment 3, complete sequence
gi|115608023|gb|CY016784.1|[115608023]

236: CY016783
Influenza A virus (A/cygnus cygnus/Iran/754/2006(H5N1)) segment 8, complete sequence
gi|115608020|gb|CY016783.1|[115608020]

237: CY016782
Influenza A virus (A/cygnus cygnus/Iran/754/2006(H5N1)) segment 5, complete sequence
gi|115608018|gb|CY016782.1|[115608018]

238: CY016781
Influenza A virus (A/cygnus cygnus/Iran/754/2006(H5N1)) segment 6, complete sequence
gi|115608016|gb|CY016781.1|[115608016]

239: CY016780
Influenza A virus (A/cygnus cygnus/Iran/754/2006(H5N1)) segment 7, complete sequence
gi|115608013|gb|CY016780.1|[115608013]

240: CY016779
Influenza A virus (A/cygnus cygnus/Iran/754/2006(H5N1)) segment 4, complete sequence
gi|115608011|gb|CY016779.1|[115608011]

241: CY016307
Influenza A virus (A/chicken/Sudan/1784-10/2006(H5N1)) segment 1, complete sequence
gi|115344810|gb|CY016307.1|[115344810]

242: CY016306
Influenza A virus (A/chicken/Sudan/1784-10/2006(H5N1)) segment 2, complete sequence
gi|115344807|gb|CY016306.1|[115344807]

243: CY016305
Influenza A virus (A/chicken/Sudan/1784-10/2006(H5N1)) segment 3, complete sequence
gi|115344805|gb|CY016305.1|[115344805]

244: CY016304
Influenza A virus (A/chicken/Sudan/1784-10/2006(H5N1)) segment 8, complete sequence
gi|115344802|gb|CY016304.1|[115344802]

245: CY016303
Influenza A virus (A/chicken/Sudan/1784-10/2006(H5N1)) segment 5, complete sequence
gi|115344800|gb|CY016303.1|[115344800]

246: CY016302
Influenza A virus (A/chicken/Sudan/1784-10/2006(H5N1)) segment 6, complete sequence
gi|115344798|gb|CY016302.1|[115344798]

247: CY016301
Influenza A virus (A/chicken/Sudan/1784-10/2006(H5N1)) segment 7, complete sequence
gi|115344795|gb|CY016301.1|[115344795]

248: CY016300
Influenza A virus (A/chicken/Sudan/1784-10/2006(H5N1)) segment 4, complete sequence
gi|115344793|gb|CY016300.1|[115344793]

249: CY016299
Influenza A virus (A/chicken/Sudan/1784-7/2006(H5N1)) segment 1, complete sequence
gi|115344791|gb|CY016299.1|[115344791]

250: CY016298
Influenza A virus (A/chicken/Sudan/1784-7/2006(H5N1)) segment 2, complete sequence
gi|115344788|gb|CY016298.1|[115344788]

251: CY016297
Influenza A virus (A/chicken/Sudan/1784-7/2006(H5N1)) segment 3, complete sequence
gi|115344786|gb|CY016297.1|[115344786]

252: CY016296
Influenza A virus (A/chicken/Sudan/1784-7/2006(H5N1)) segment 8, complete sequence
gi|115344783|gb|CY016296.1|[115344783]

253: CY016295
Influenza A virus (A/chicken/Sudan/1784-7/2006(H5N1)) segment 5, complete sequence
gi|115344781|gb|CY016295.1|[115344781]

254: CY016294
Influenza A virus (A/chicken/Sudan/1784-7/2006(H5N1)) segment 6, complete sequence
gi|115344779|gb|CY016294.1|[115344779]

255: CY016293
Influenza A virus (A/chicken/Sudan/1784-7/2006(H5N1)) segment 7, complete sequence
gi|115344776|gb|CY016293.1|[115344776]

256: CY016292
Influenza A virus (A/chicken/Sudan/1784-7/2006(H5N1)) segment 4, complete sequence
gi|115344774|gb|CY016292.1|[115344774]

257: CY016291
Influenza A virus (A/chicken/Nigeria/957-20/2006(H5N1)) segment 1, complete sequence
gi|115344772|gb|CY016291.1|[115344772]

258: CY016290
Influenza A virus (A/chicken/Nigeria/957-20/2006(H5N1)) segment 2, complete sequence
gi|115344769|gb|CY016290.1|[115344769]

259: CY016289
Influenza A virus (A/chicken/Nigeria/957-20/2006(H5N1)) segment 3, complete sequence
gi|115344767|gb|CY016289.1|[115344767]

260: CY016288
Influenza A virus (A/chicken/Nigeria/957-20/2006(H5N1)) segment 8, complete sequence
gi|115344764|gb|CY016288.1|[115344764]

261: CY016287
Influenza A virus (A/chicken/Nigeria/957-20/2006(H5N1)) segment 5, complete sequence
gi|115344762|gb|CY016287.1|[115344762]

262: CY016286
Influenza A virus (A/chicken/Nigeria/957-20/2006(H5N1)) segment 6, complete sequence
gi|115344760|gb|CY016286.1|[115344760]

263: CY016285
Influenza A virus (A/chicken/Nigeria/957-20/2006(H5N1)) segment 7, complete sequence
gi|115344757|gb|CY016285.1|[115344757]

264: CY016284
Influenza A virus (A/chicken/Nigeria/957-20/2006(H5N1)) segment 4, complete sequence
gi|115344755|gb|CY016284.1|[115344755]

265: CY016283
Influenza A virus (A/chicken/Nigeria/641/2006(H5N1)) segment 1, complete sequence
gi|115344753|gb|CY016283.1|[115344753]

266: CY016282
Influenza A virus (A/chicken/Nigeria/641/2006(H5N1)) segment 2, complete sequence
gi|115344750|gb|CY016282.1|[115344750]

267: CY016281
Influenza A virus (A/chicken/Nigeria/641/2006(H5N1)) segment 3, complete sequence
gi|115344748|gb|CY016281.1|[115344748]

268: CY016280
Influenza A virus (A/chicken/Nigeria/641/2006(H5N1)) segment 8, complete sequence
gi|115344745|gb|CY016280.1|[115344745]

269: CY016279
Influenza A virus (A/chicken/Nigeria/641/2006(H5N1)) segment 5, complete sequence
gi|115344743|gb|CY016279.1|[115344743]

270: CY016278
Influenza A virus (A/chicken/Nigeria/641/2006(H5N1)) segment 6, complete sequence
gi|115344741|gb|CY016278.1|[115344741]

271: CY016277
Influenza A virus (A/chicken/Nigeria/641/2006(H5N1)) segment 7, complete sequence
gi|115344738|gb|CY016277.1|[115344738]

272: CY016276
Influenza A virus (A/chicken/Nigeria/641/2006(H5N1)) segment 4, complete sequence
gi|115344736|gb|CY016276.1|[115344736]