Supplementary material:

$P_{epitope}$ is calculated as:

$$P_{epitope} = \frac{\text{Number of amino acid differences in the epitope}}{\text{Total number of amino acids in the epitope}}$$

Table 1: Identity (Similarity) of amino acid composition in HA protein sequences of selected strains

	X-31*	UKR63	ALB70	PC73	PH82	SYD97	MOS99	WIS05	BR07
X-31*	100(100)								
UKR63	95.8 (97)	100(100)							
ALB70	98.6 (99)	95.8 (97)	100(100)						
PC73	96.3 (98)	94.3 (96)	97.2 (98)	100(100)					
PH82	89.6 (94)	88.3 (93)	89.8 (94)	91.7 (95)	100(100)				
SYD97	88.3 (94)	87.3 (93)	89.0 (94)	90.8 (95)	90.3 (94)	100(100)			
MOS99	89.0 (94)	88.0 (93)	89.4 (94)	91.0 (95)	90.3 (94)	98.0 (99)	100(100)		
WIS05	86.2 (94)	86.4 (92)	87.0 (93)	88.3 (93)	88.5 (93)	94.3 (97)	94.2 (97)	100(100)	
BR07	86.6 (92)	86.7 (92)	87.0 (92)	89.0 (93)	89.0 (92)	94.2 (96)	94.0 (96)	98.2 (99)	100(100)

* X-31corresponds to the 'Hongkong' pandemic influenza A/X-31/1968 (H3N2), the reference strain in this study.
N.B.: Numbers denote percentages.

Table 2: Number of mutations in the known epitopes of HA proteins of various strains with respect to X-31

Strain→ ↓Epitope	UKR63	X-31*	ALB70	PC73	PH82	MOS99	WIS05	BR07
A	3	0	0	2	9	11	12	13
B	2	0	0	5	8	10	13	14
C	0	0	0	1	6	8	8	8
D	5	0	1	3	7	8	10	10
E	3	0	2	2	4	9	10	11

Table 3: PROCHECK Analyses of the protein structures

Protein structures	Sequence identity with template (%)	Occupancy* in Ramachandran plot (%)	Minimized Energy (kJ/mol)
ALB70	98.53	98.4	-28835.67
PC73	98.36	98.1	-28797.88
PH82	91.29	97.9	-28579.02
MOS99	88.06	98.0	-29832.88
WIS05	84.50	98.2	-29397.53
BR07	86.60	98.2	-29148.36
X-31 (1EO8)	100	99.5	-28233.07

*N.B. Occupancy in Ramachandran Plot denotes the percentage of amino acids in the favourable and generously allowed regions

Table 4: List of contacts between antibody BH151 and the antigens

X-31				ALB70			
Ag HA1	Ab BH151	Interaction Type	Distance[Å]	Ag HA1	Ab BH151	Interaction Type	Distance[Å]
D76	Y32	H-Bond	2.97	N112	T31	H-Bond	0.5
D79	R94	H-Bond	2.74	K156	Y32	H-Bond	2.5
H91	W100	H-Bond	2.78	D93	R98	H-Bond	1.8
D287	T31	H-Bond	2.82	P90	R98	H-Bond	3.2
D79	R94	Salt Bridge	2.7	K156	G26	H-Bond	2.6
E98	R98	Salt Bridge	3.7				

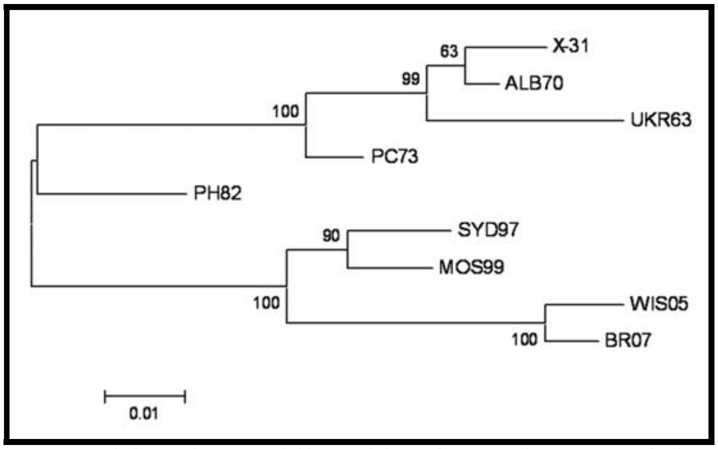
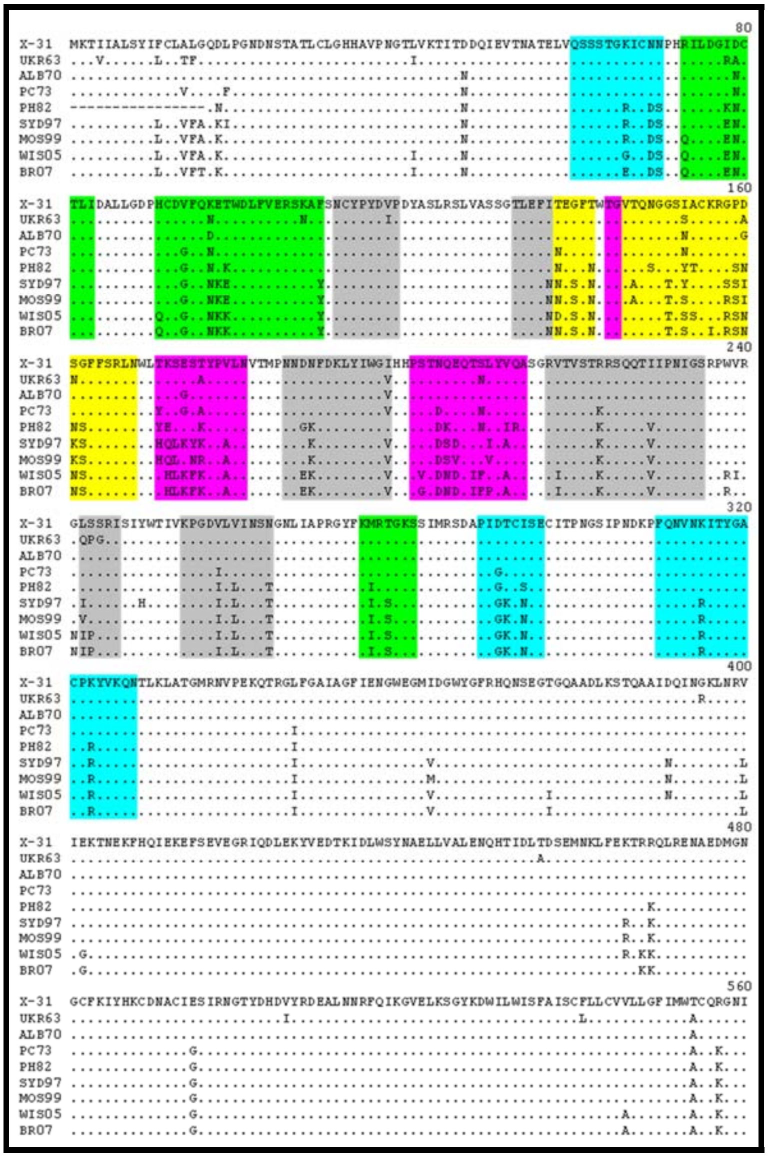


Figure S1: Phylogenetic tree (Neighbor –Joining) of HA protein sequences of selected H3N2 strains (with bootstrap analysis as test of phylogeny with 10000 replications) as obtained from MEGA 4.0.



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                                                                                      80
X-31   MKTIIALSYIFCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTITDDQIEVTNATELVQSSSTGKICNNPHRILDGIDC
UKR63  ...V......L..TF.........................I....................................RA.
ALB70  ..............................................N...............................N.
PC73   .............V....F...........................N...............................N.
PH82   ----------------.N............................N..................R..DS.......KN.
SYD97  ..........L..VFA.KI...........................N..................R..DS.......EN.
MOS99  ..........L..VFA.K............................N..................R..DS..Q....EN.
WIS05  ..........L..VFA.K......................I.....N..................G..DS..Q....EN.
BR07   ..........L..VFT.K......................I.....N..................E..DS..Q....EN.
                                                                                     160
X-31   TLIDALLGDPHCDVFQKETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFITEGFTWTGVTQNGGSIACKRGPD
UKR63  ................N..........N.........I..................................S......A
ALB70  ................D.......................................................N......G
PC73   .............G..N........................................N..............N.......
PH82   .............G..N.K......................................N...N......S...YT....SN
SYD97  .............G..NKE..........Y..........................NN.S.N....A...T.Y....SSI
MOS99  .............G..NKE..........Y..........................NN.S.N....A...T.S....RSI
WIS05  ..........Q..G..NKK..........Y..........................ND.S.N........T.SS...RSN
BR07   ..........Q..G..NKK..........Y..........................NN.S.N........T.S..I.RSN
                                                                                     240
X-31   SGFFSRLNWLTKSESTYPVLNVTMPNNDNFDKLYIWGIHHPSTNQEQTSLYVQASGRVTVSTRRSQQTIIPNIGSRPWVR
UKR63  N..............A.....................V..........N...............................
ALB70  .............G.......................V..........................................
PC73   ..........Y..G.A.....................V.....D....N.............K.................
PH82   NS........YE...K...........GK..............DK...N..IR.........K.....V...........
SYD97  KS........HQLKYK..A.........K........V.....DSD...I.A..........K.....V...........
MOS99  KS........HQL.NR..A.........K........V.....DSV...V............K.....V...........
WIS05  NS.........HLKFK..A........EK........V...V.DND.IF..A.....I....K.....V........RI.
BR07   NS.........HLKFK..A........EK........V...G.DND.IFP.A.....I....K.....V........R..
                                                                                     320
X-31   GLSSRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGA
UKR63  .QPG............................................................................
ALB70  ................................................................................
PC73   .................I................................G.............................
PH82   .................I.L...T...........I..............G..S..........................
SYD97  .I......H........I.L...T...........I.S............GK.N....................R.....
MOS99  .V...............I.L...T...........I.S............GK.N....................R.....
WIS05  NIP..............I.L...T...........I.S............GK.N....................R.....
BR07   NIP..............I.L...T...........I.S............GK.N....................R.....
                                                                                     400
X-31   CPKYVKQNTLKLATGMRNVPEKQTRGLFGAIAGFIENGWEGMIDGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRV
UKR63  ..........................................................................R.....
ALB70  ................................................................................
PC73   ..........................I.....................................................
PH82   ..R.......................I.....................................................
SYD97  ..R.......................I...............V...........................N........L
MOS99  ..R.......................I...............M...........................N........L
WIS05  ..R.......................I...............V.............I.............N........L
BR07   ..R.......................I...............V.............I......................L
                                                                                     480
X-31   IEKTNEKFHQIEKEFSEVEGRIQDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQLRENAEDMGN
UKR63  .......................................................A........................
ALB70  ................................................................................
PC73   ................................................................................
PH82   ....................................................................K...........
SYD97  .................................................................R..K...........
MOS99  .................................................................R..K...........
WIS05  .G...............................................................R.KK...........
BR07   .G.................................................................KK...........
                                                                                     560
X-31   GCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKGVELKSGYKDWILWISFAISCFLLCVVLLGFIMWTCQRGNI
UKR63  .........................I..................................L............A......
ALB70  .........................................................................A......
PC73   ..............G..........................................................A..K...
PH82   ..............G..........................................................A..K...
SYD97  ..............G..........................................................A..K...
MOS99  ..............G..........................................................A..K...
WIS05  ..............G..................................................A.......A..K...
BR07   ..............G..................................................A.......A..K...
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Figure S2: Multiple alignment of Hemagglutinin (HA) protein sequences from H3N2 strains. Epitopes A, B, C, D and E are highlighted in Yellow, Pink, Cyan, Grey and Green respectively. All references to amino acid numbering in the text are in accordance with sequence nomenclature followed in this alignment.