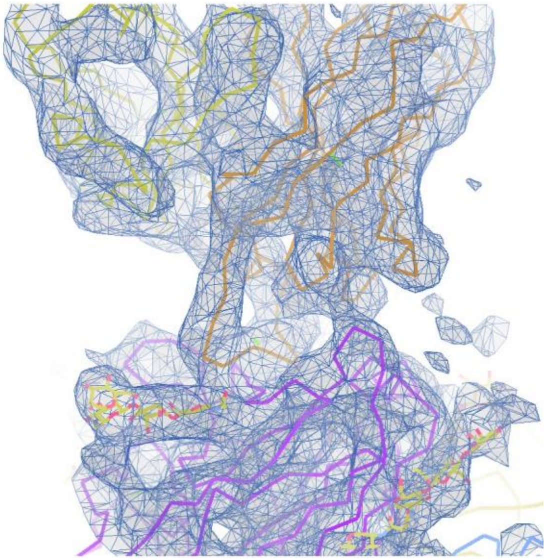
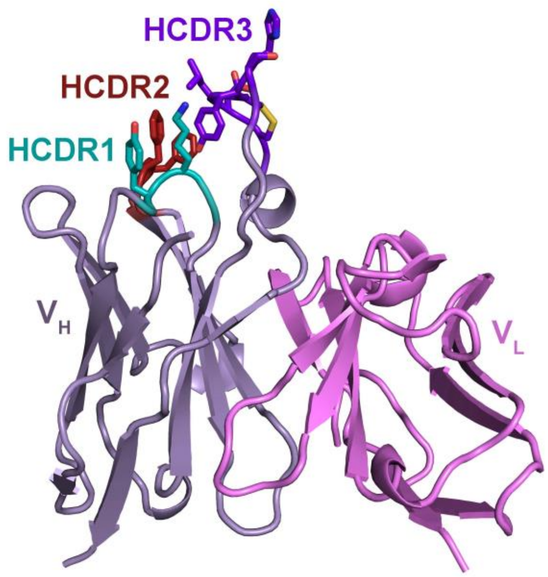
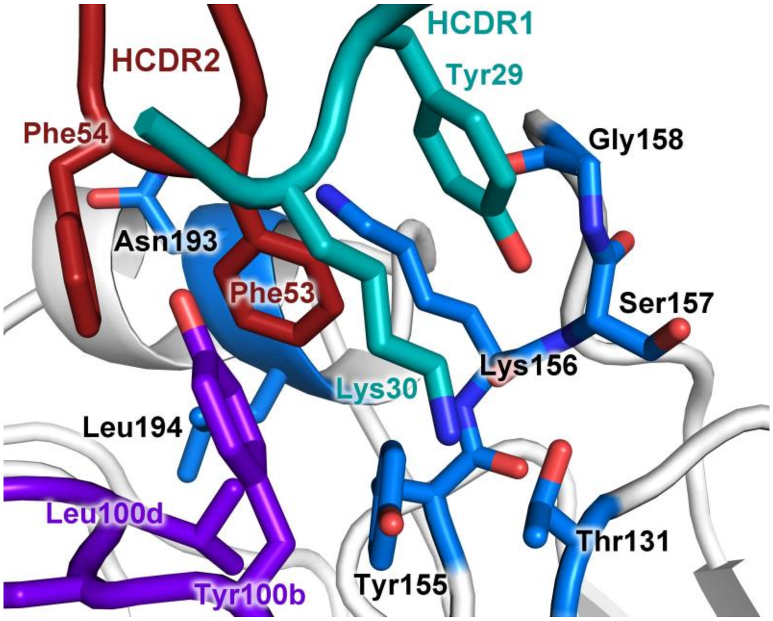


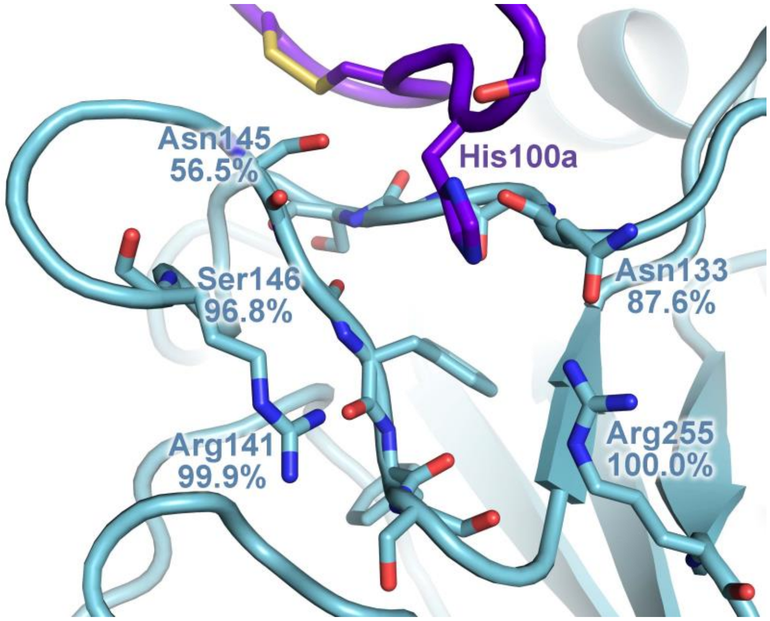
Supplementary Figure 1 | Representative electron density at the F045-092-Vic2011/H3 interface. The protein models are depicted as ribbons with the Fab in orange and yellow and the HA in purple. Glycans are represented as sticks. The $2F_o$–F_c electron density map (blue mesh) is contoured at 1σ.



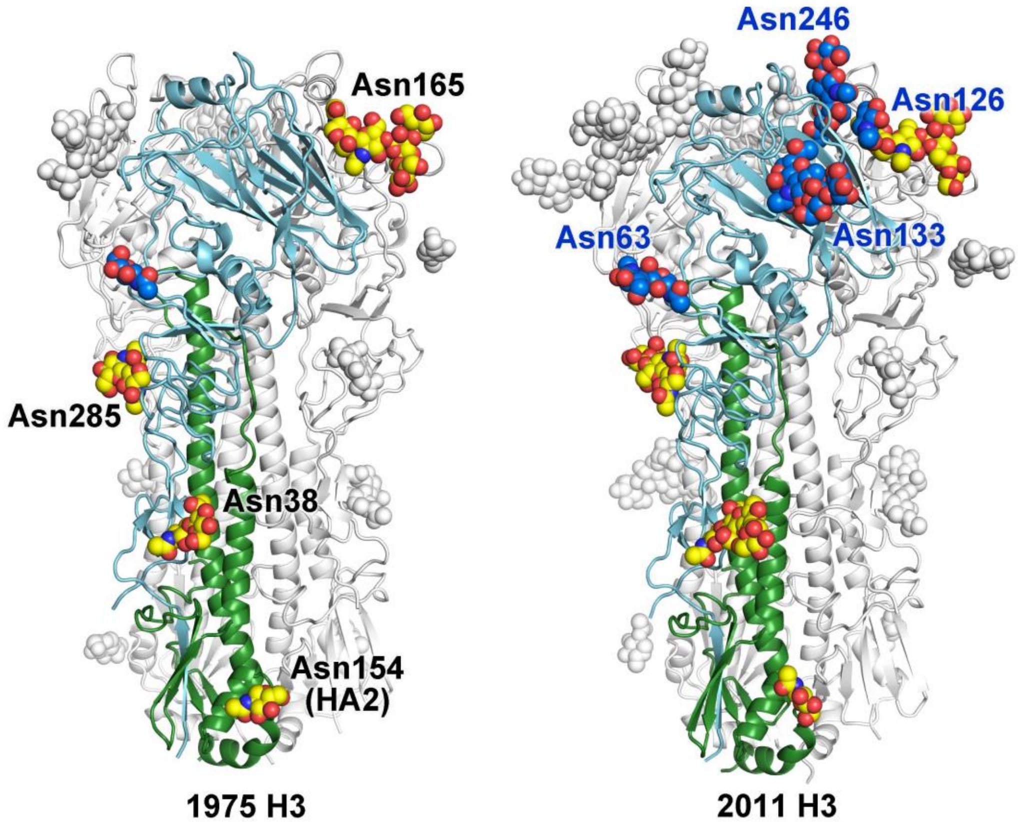
Supplementary Figure 2 | Fab F045-092 crystal structure depicting the protruding ridge formed by the heavy chain CDRs. Only the Fab variable domains are illustrated here as a cartoon and residues from the heavy chain CDRs that interact with the HA are labeled and shown as sticks.



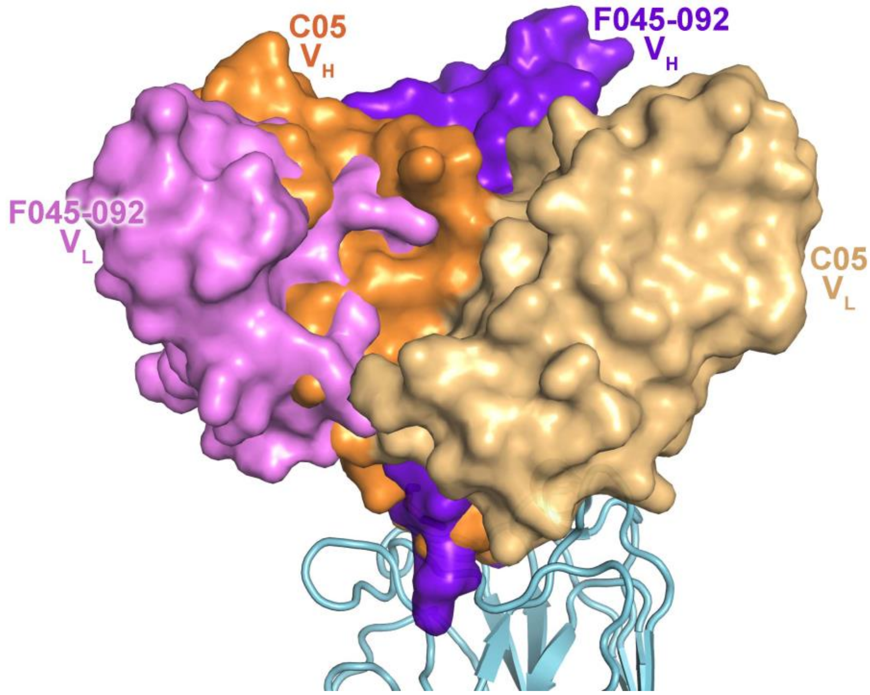
Supplementary Figure 3 | Interaction of Fab F045-092 with the Vic1975/H3 HA 150 loop and 190 helix. Contacting residues are colored and shown as sticks.



Supplementary Figure 4 | Conservation of the groove in the HA receptor-binding site formed near the HA 130 and 140 loops. The percent conservation for the most common H3 residue is labeled and is not always identical to the residue at that position in the Vic1975/H3 sequence. The F045-092 HCDR3 loop, which inserts into this site, is colored purple.

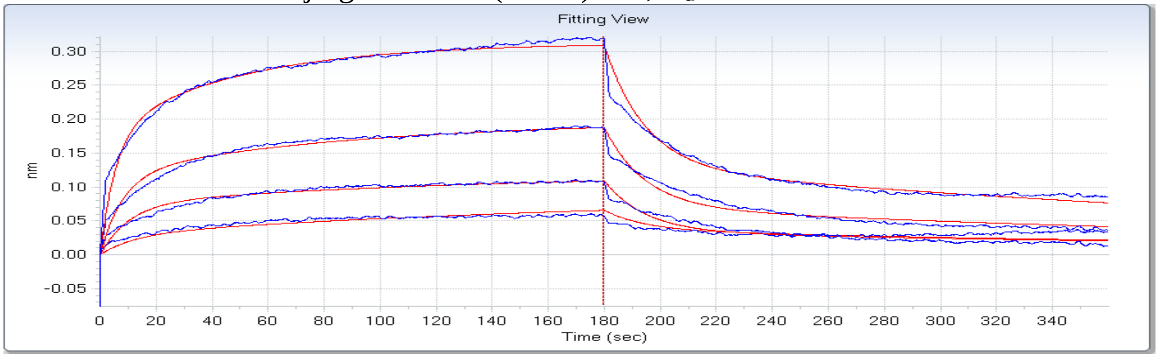


Supplementary Figure 5 | Additional glycosylation on the HAs of Vic1975/H3 and Vic2011/H3 from the Fab-HA complexes. Only one HA protomer for each structure is colored. Absolutely conserved PNGs on human H3 HAs are shown as yellow spheres on the Vic1975/H3 structure as well as an additional glycan at Asn63; the PNG at Asn22 was the only conserved glycan not modeled. Further additional PNGs that were accumulated in H3 HAs from 1968-2013 are shown as blue spheres on the Vic2011/H3 structure. The PNGs at Asn positions 45, 122, and 144 were not modeled. Glycans on the other protomers of the trimer are shown in white spheres.



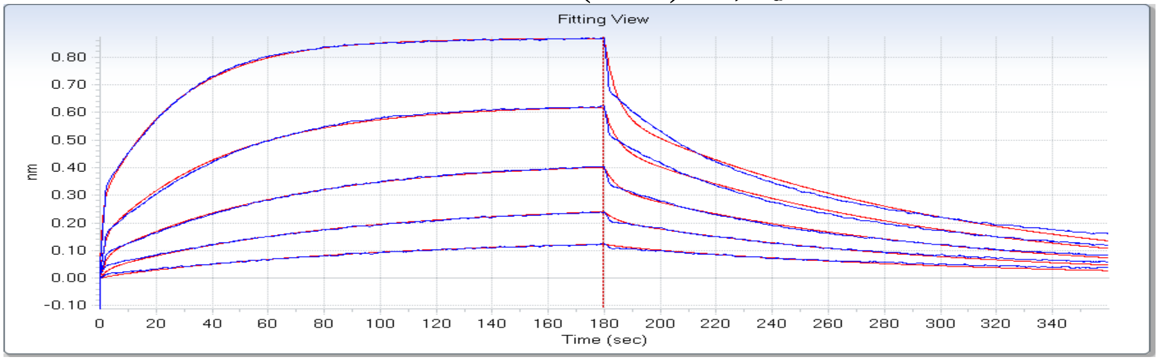
Supplementary Figure 6 | Comparison of the angle of approach of antibodies F045-092 and C05 on the HA receptor-binding site. The HAs from the C05-HA (PDB 4FP8) and F045-092-Vic1975/H3 complexes were aligned. Superimposition of the Fab variable domains, depicted as molecular surfaces, of F045-092 and C05 illustrate that the antibodies differ in their approach angle to the HA by ~113º. Only the Vic1975/H3 HA is shown (blue cartoon).

F045-092 Fab vs A/Beijing/262/1995 (H1N1) HA, K_d = 820 nM



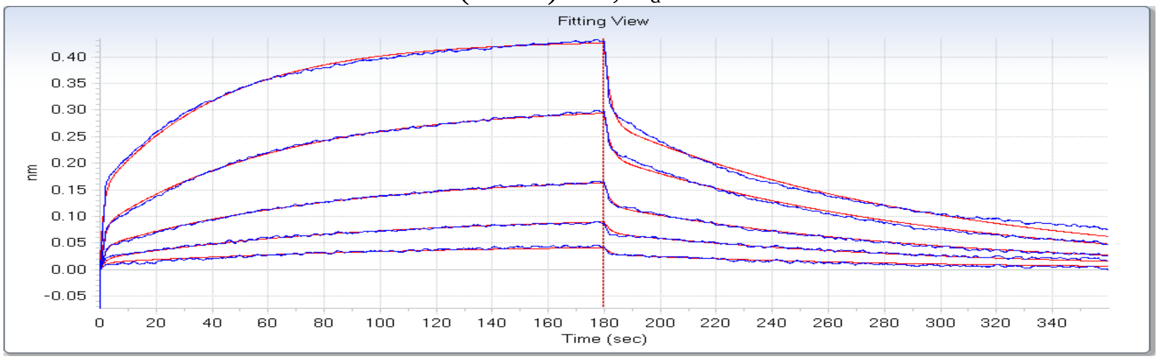
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 1300 nM and K_{d2} = 340 nM (although k_{on} and k_{off} differ for the two binding processes). As these two binding processes have similar affinities, we report the affinity as the average of K_{d1} and K_{d2}, ~820 nM.

F045-092 Fab vs A/New Caledonia/20/1999 (H1N1) HA, K_d = 540 nM



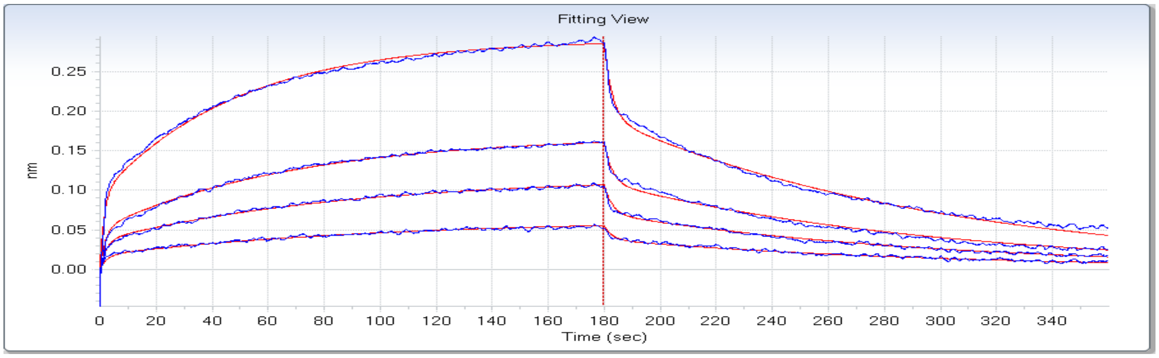
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 610 nM and K_{d2} = 460 nM (although k_{on} and k_{off} differ for the two binding processes). As these two binding processes have similar affinities, we report the affinity as the average of K_{d1} and K_{d2}, ~540 nM.

F045-092 Fab vs A/Adachi/2/1957 (H2N2) HA, K_d = 1700 nM



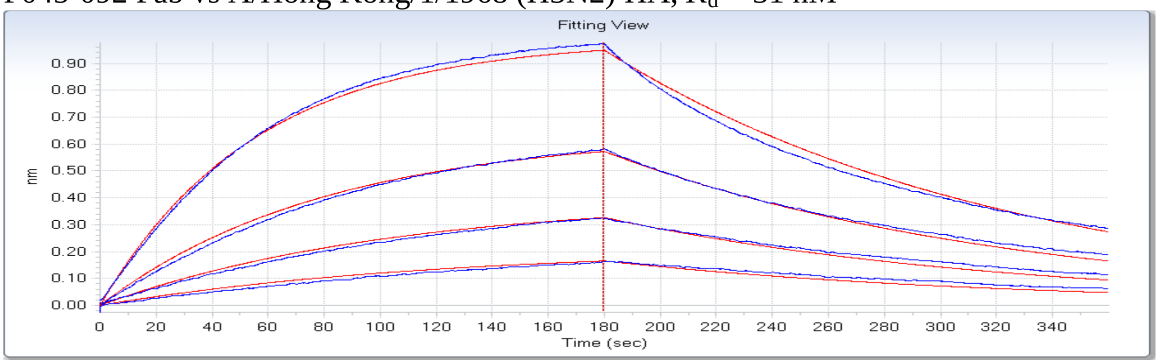
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 1200 nM and K_{d2} = 2200 nM (although k_{on} and k_{off} differ for the two binding processes). As these two binding processes have similar affinities, we report the affinity as the average of K_{d1} and K_{d2}, ~1700 nM.

F045-092 Fab vs A/duck/Ukraine/1/1963 (H3N8) HA, K_d = 1700 nM

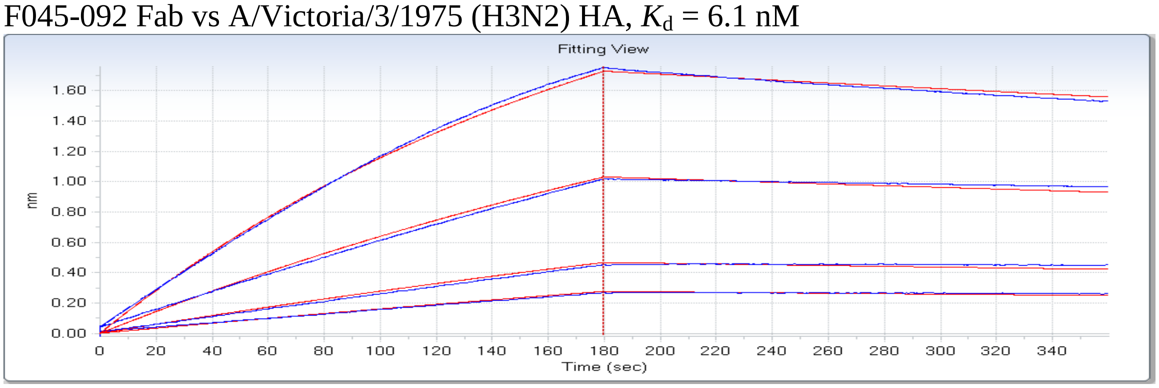


These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 1300 nM and K_{d2} = 2000 nM (although k_{on} and k_{off} differ for the two binding processes). As these two binding processes have similar affinities, we report the affinity as the average of K_{d1} and K_{d2}, ~1700 nM.

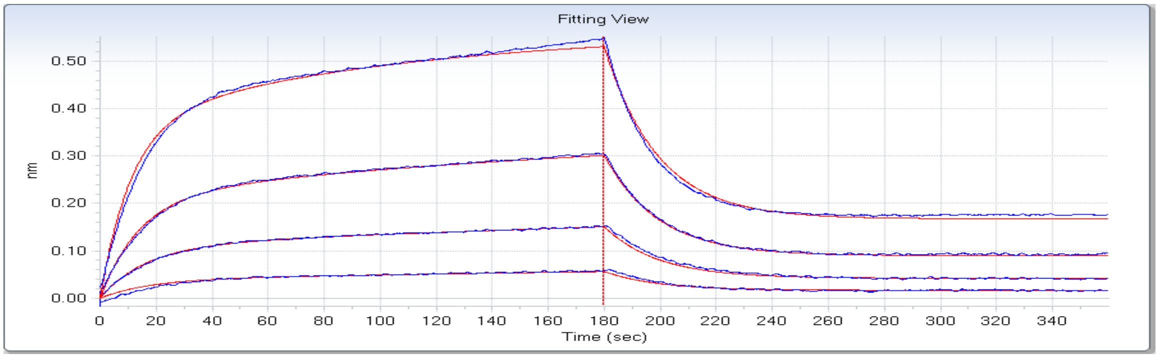
F045-092 Fab vs A/Hong Kong/1/1968 (H3N2) HA, K_d = 31 nM



F045-092 Fab vs A/Victoria/3/1975 (H3N2) HA, K_d = 6.1 nM

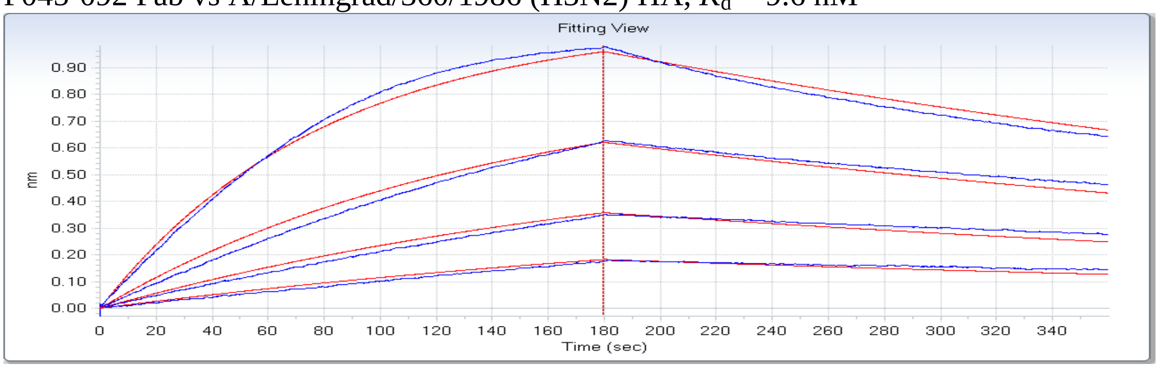


F045-092 Fab vs A/Bangkok/1/1979 (H3N2) HA, K_d = 140 nM

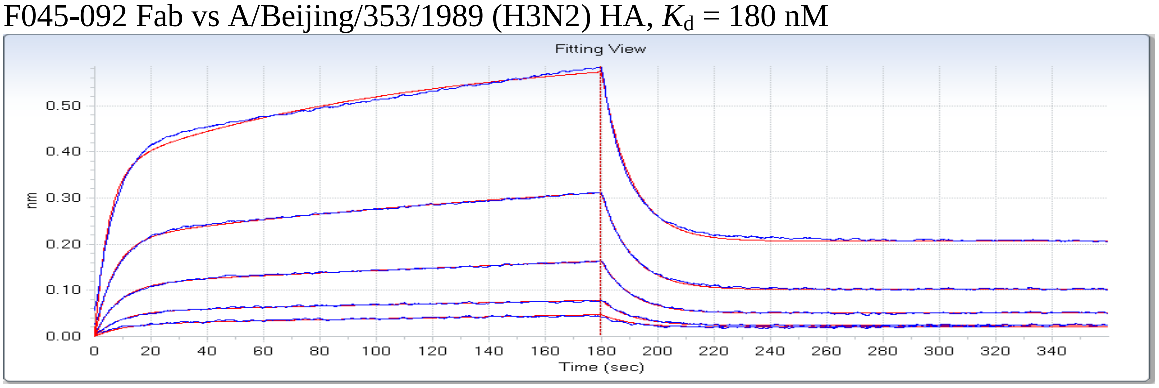


These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 140 nM and K_{d2} = 0.2 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 140 nM) whereas the higher affinity process may reflect a non-specific interaction. The maximum Fab concentration tested in this experiment was 200 nM. Therefore, we report the affinity for this interaction as 140 nM.

F045-092 Fab vs A/Leningrad/360/1986 (H3N2) HA, K_d = 9.6 nM

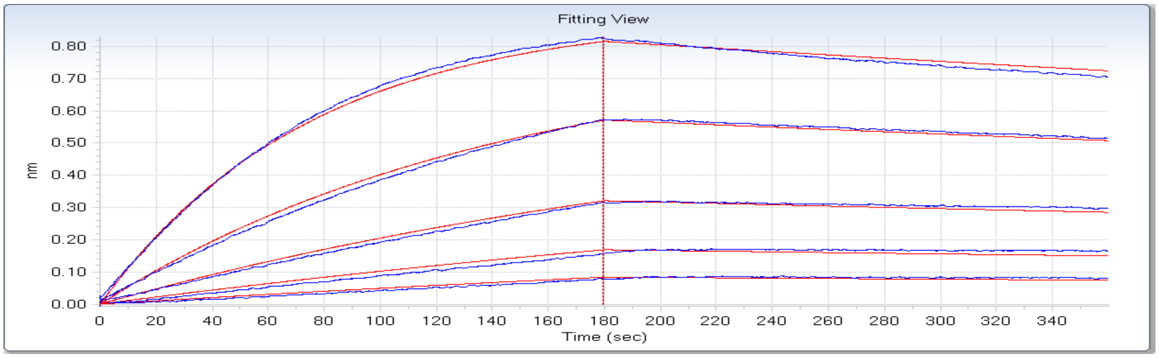


F045-092 Fab vs A/Beijing/353/1989 (H3N2) HA, K_d = 180 nM

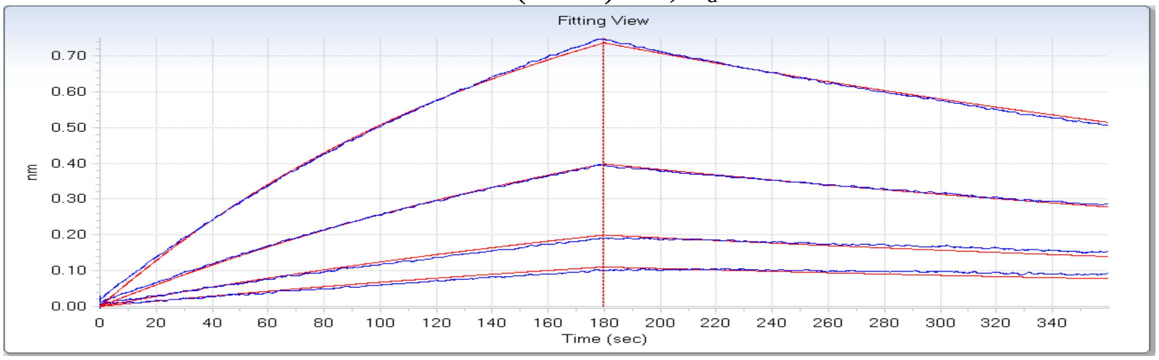


These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 180 nM, K_{d2} = 2 pM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 180 nM) whereas the higher affinity process may reflect a non-specific interaction. The maximum Fab concentration tested in this experiment was 200 nM. Therefore, we report the affinity for this interaction as 180 nM.

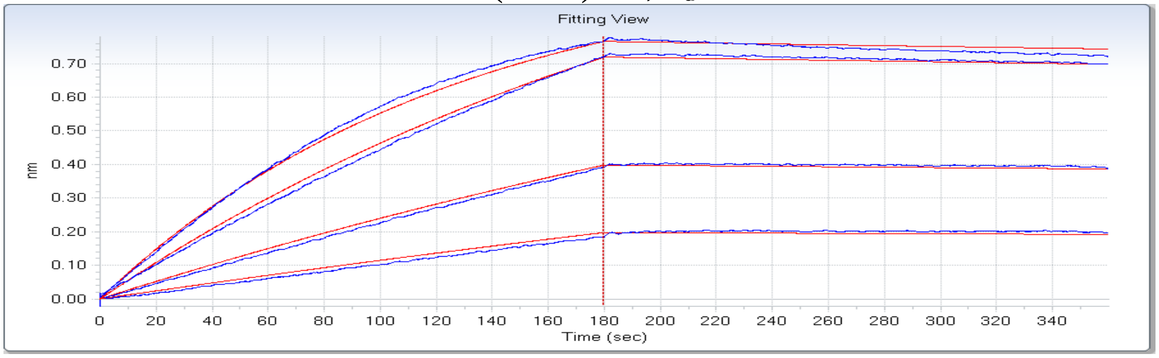
F045-092 Fab vs A/Shangdong/9/1993 (H3N2) HA, K_d = 2.6 nM



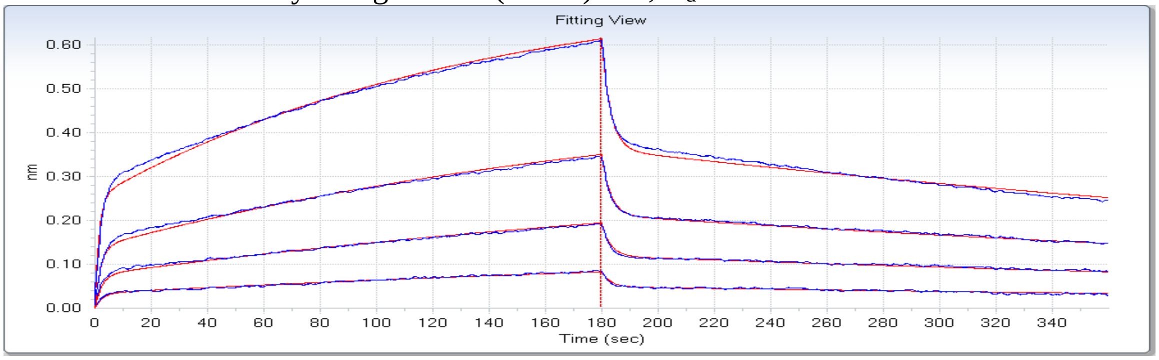
F045-092 Fab vs A/Panama/2007/1999 (H3N2) HA, K_d = 23 nM



F045-092 Fab vs A/Moscow/10/1999 (H3N2) HA, K_d = 1.1 nM

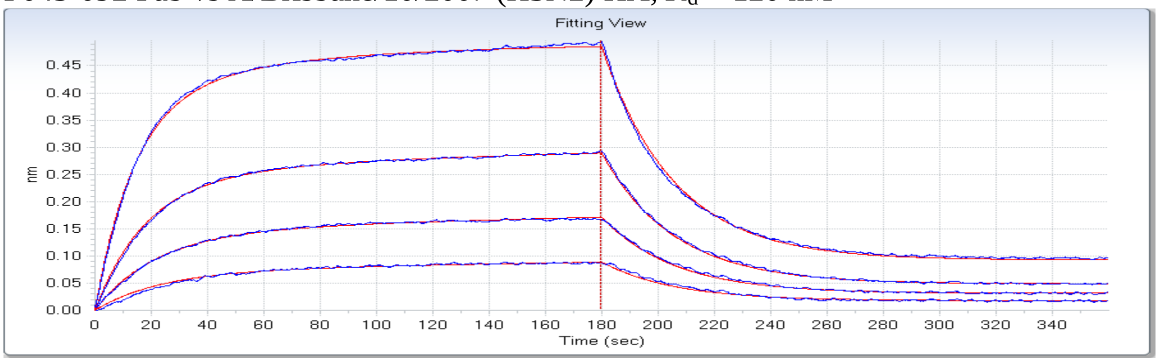


F045-092 Fab vs A/Wyoming/3/2003 (H3N2) HA, K_d = 630 nM



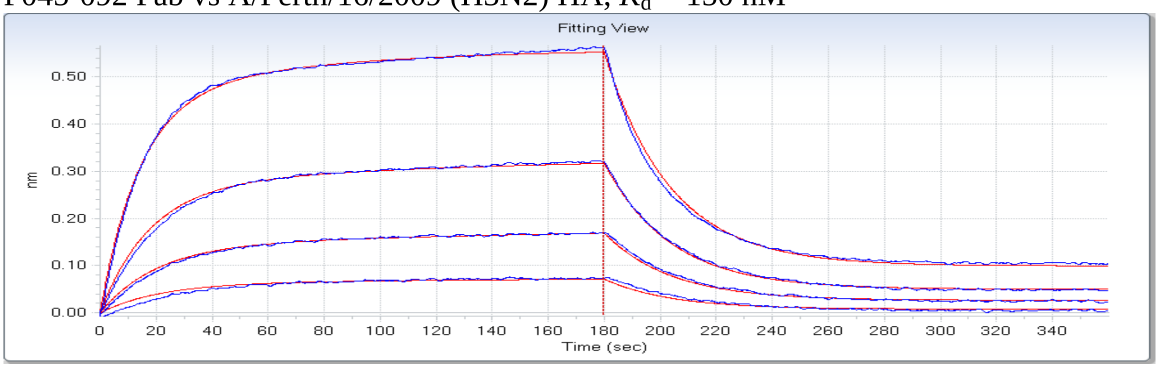
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 370 nM and K_{d2} = 890 nM (although k_{on} and k_{off} differ for the two binding processes). As these two binding processes have similar affinities, we report the affinity as the average of K_{d1} and K_{d2}, ~630 nM.

F045-092 Fab vs A/Brisbane/10/2007 (H3N2) HA, K_d = 120 nM



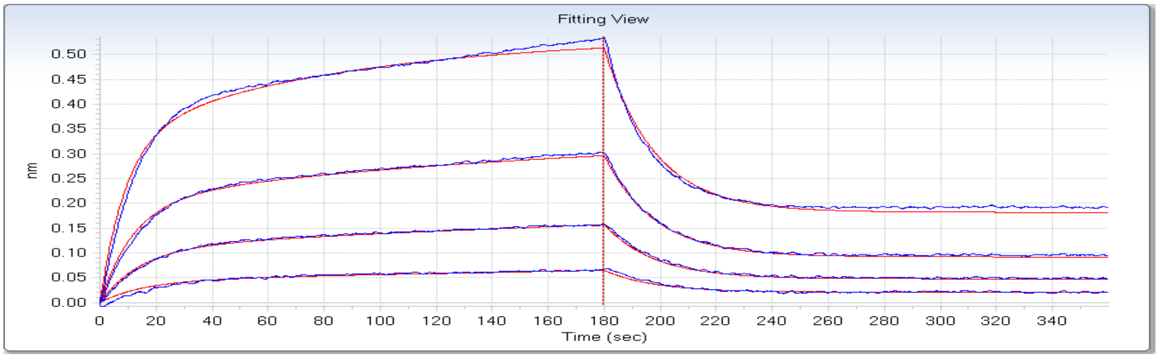
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 120 nM, K_{d2} = 40 pM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 120 nM) whereas the higher affinity process may reflect a non-specific interaction. The maximum Fab concentration tested in this experiment was 200 nM. Therefore, we report the affinity for this interaction as 120 nM.

F045-092 Fab vs A/Perth/16/2009 (H3N2) HA, K_d = 150 nM



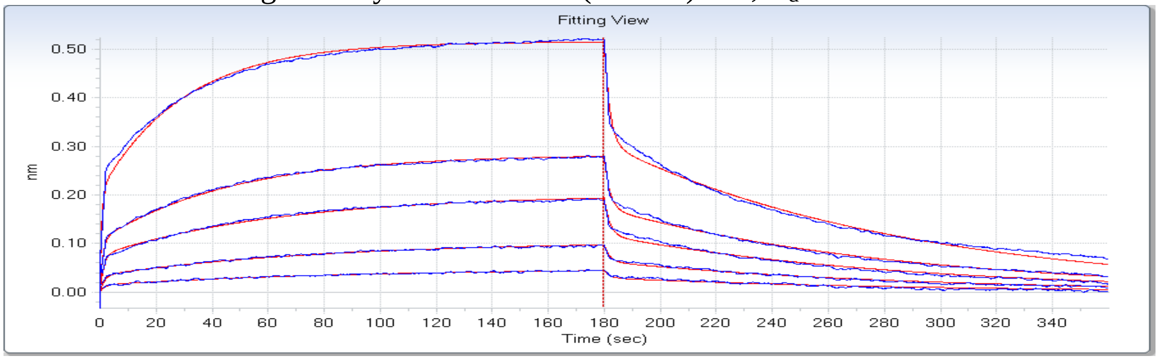
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 150 nM, K_{d2} = 90 pM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 150 nM) whereas the higher affinity process may reflect a non-specific interaction. The maximum Fab concentration tested in this experiment was 200 nM. Therefore, we report the affinity for this interaction as 150 nM.

F045-092 Fab vs A/Victoria/361/2011 (H3N2) HA, K_d = 110 nM



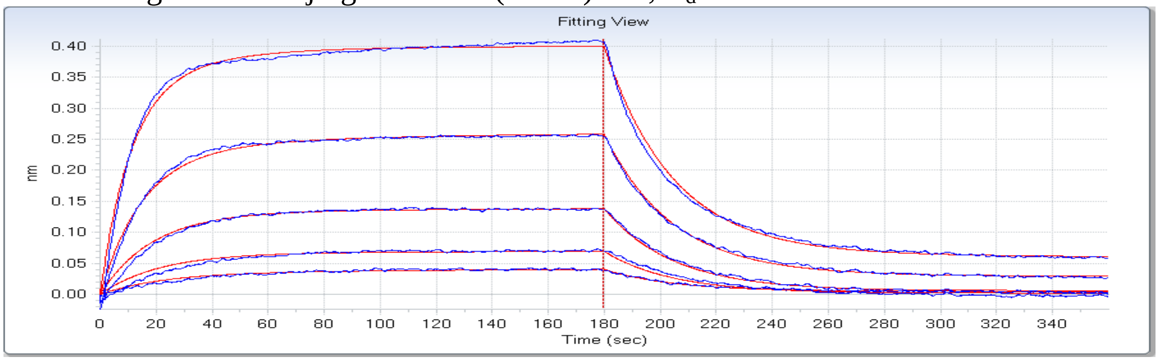
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 110 nM, K_{d2} = 0.4 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 110 nM) whereas the higher affinity process may reflect a non-specific interaction. The maximum Fab concentration tested in this experiment was 200 nM. Therefore, we report the affinity for this interaction as 110 nM.

F045-092 Fab vs A/gull/Maryland/704/1977 (H13N6) HA, K_d = 870 nM



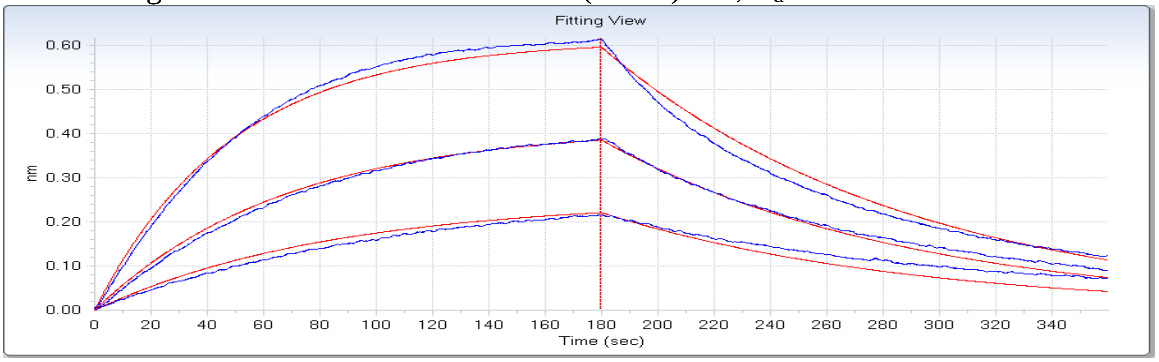
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 790 nM and K_{d2} = 940 nM (although k_{on} and k_{off} differ for the two binding processes). As these two binding processes have similar affinities, we report the affinity as the average of K_{d1} and K_{d2}, ~480 nM.

F045-092 IgG vs A/Beijing/262/1995 (H1N1) HA, K_d = 40 nM

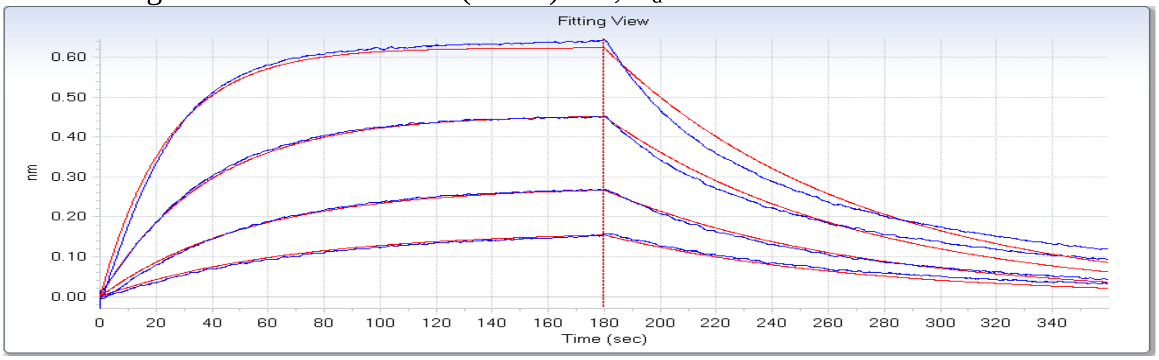


These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 40 nM, K_{d2} = 0.7 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 40 nM) whereas the higher affinity process may reflect a non-specific interaction. The maximum Fab concentration tested in this experiment was 50 nM. Therefore, we report the affinity for this interaction as 40 nM.

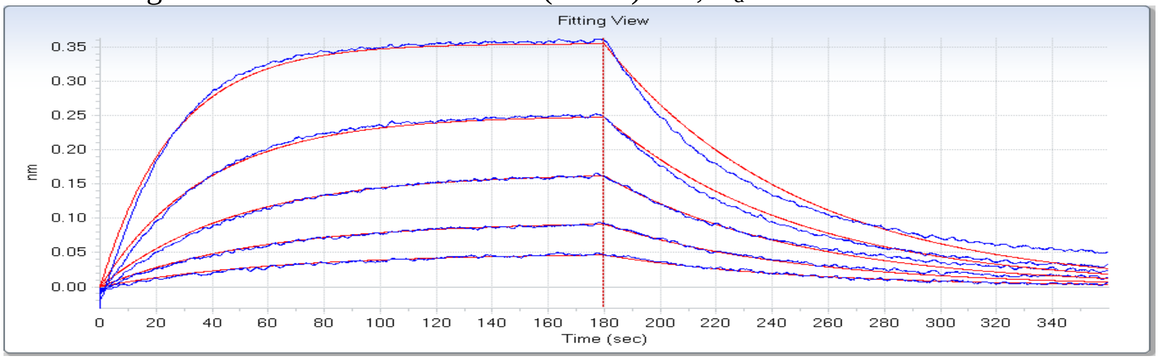
F045-092 IgG vs A/New Caledonia/20/1999 (H1N1) HA, K_d = 10 nM



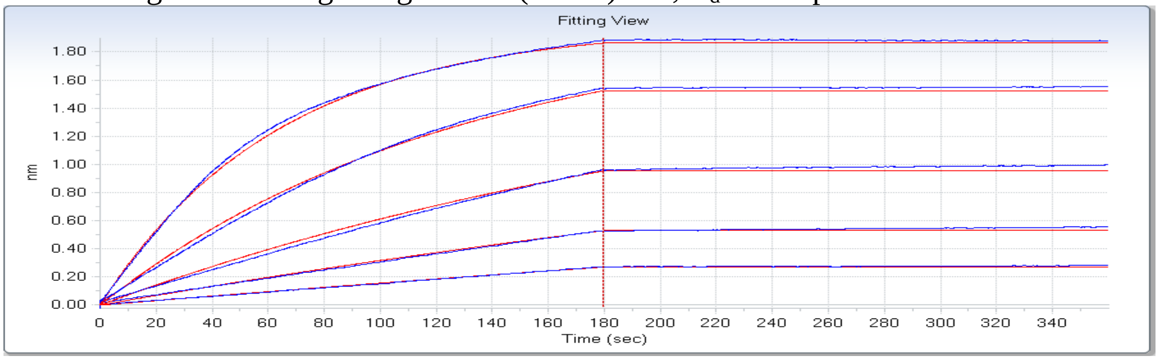
F045-092 IgG vs A/Adachi/2/1957 (H2N2) HA, K_d = 18 nM



F045-092 IgG vs A/duck/Ukraine/1/1963 (H3N8) HA, K_d = 31 nM

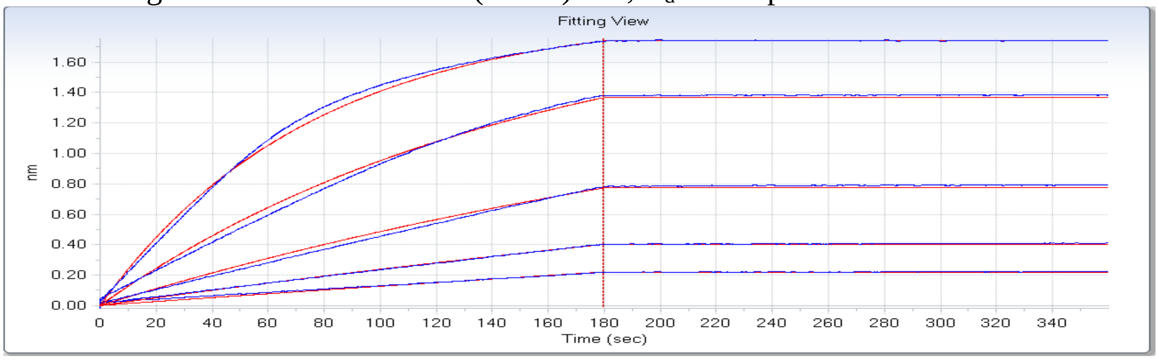


F045-092 IgG vs A/Hong Kong/1/1968 (H3N2) HA, K_d = <10 pM



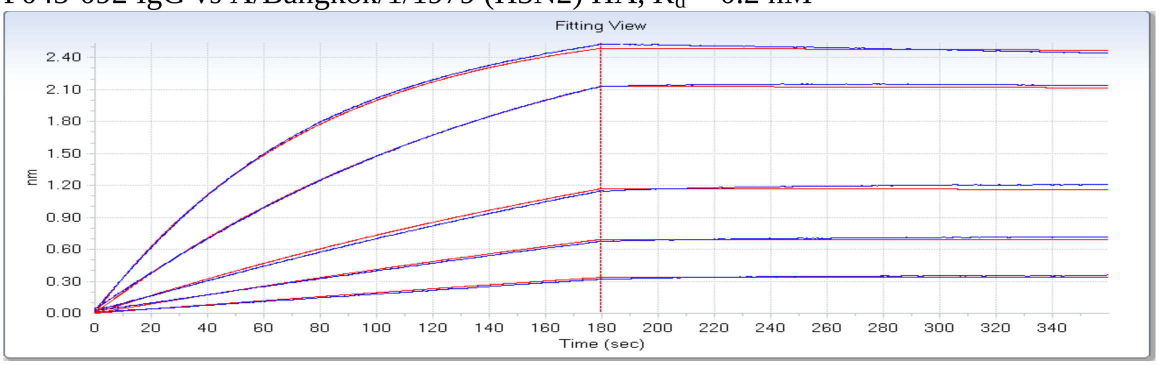
These data were fit with a 1:1 binding model, yielding apparent K_d = 2.2 fM, which is beyond the specified detection limit of 10 pM. Therefore, we report the affinity for this interaction is stronger than 10 pM.

F045-092 IgG vs A/Victoria/3/1975 (H3N2) HA, K_d = <10 pM

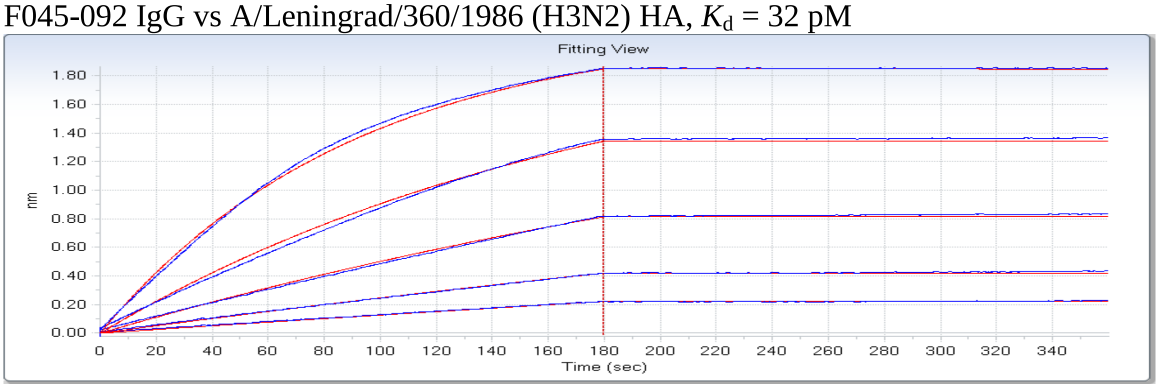


These data were fit with a 1:1 binding model, yielding apparent K_d = 2.6 fM, which is beyond the specified detection limit of 10 pM. Therefore, we report the affinity for this interaction is stronger than 10 pM.

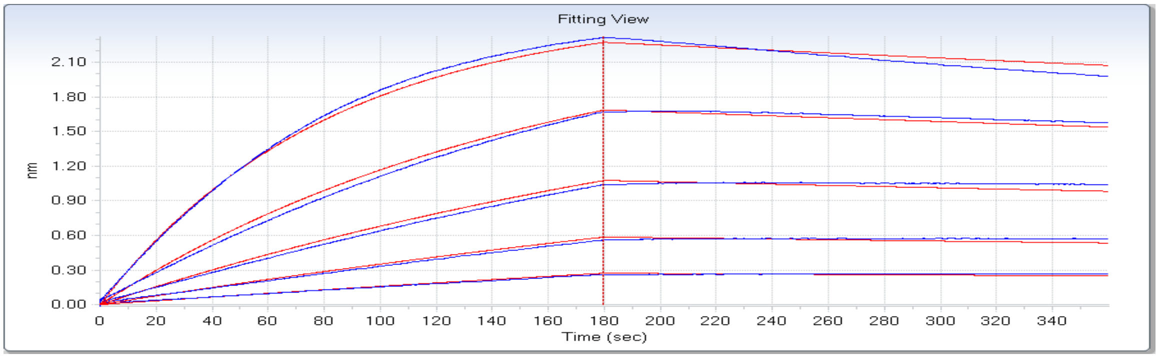
F045-092 IgG vs A/Bangkok/1/1979 (H3N2) HA, K_d = 0.2 nM



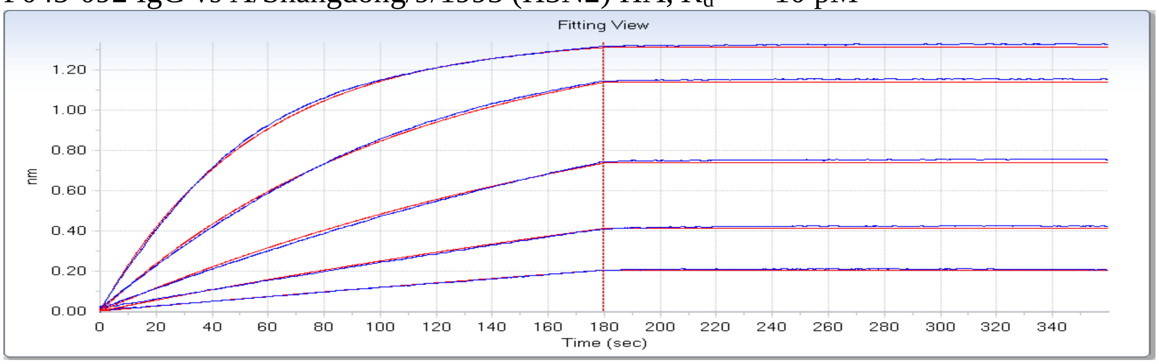
F045-092 IgG vs A/Leningrad/360/1986 (H3N2) HA, K_d = 32 pM



F045-092 IgG vs A/Beijing/353/1989 (H3N2) HA, K_d = 2.2 nM

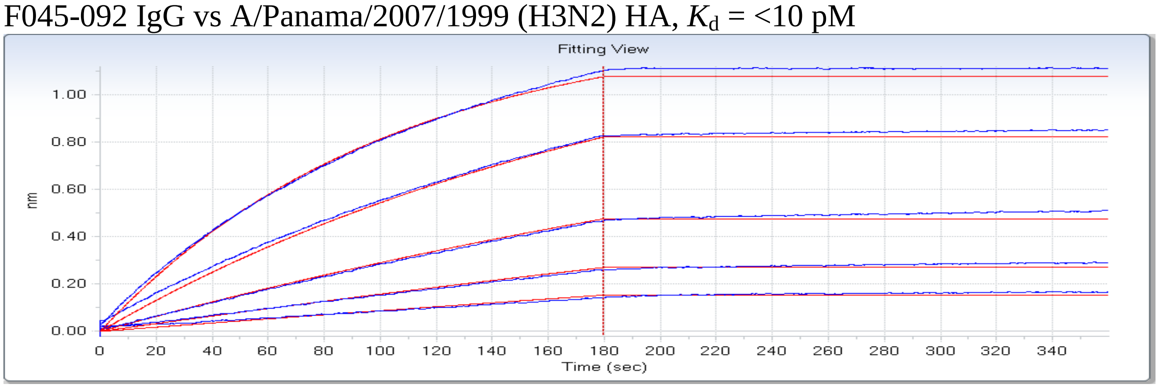


F045-092 IgG vs A/Shangdong/9/1993 (H3N2) HA, K_d = <10 pM



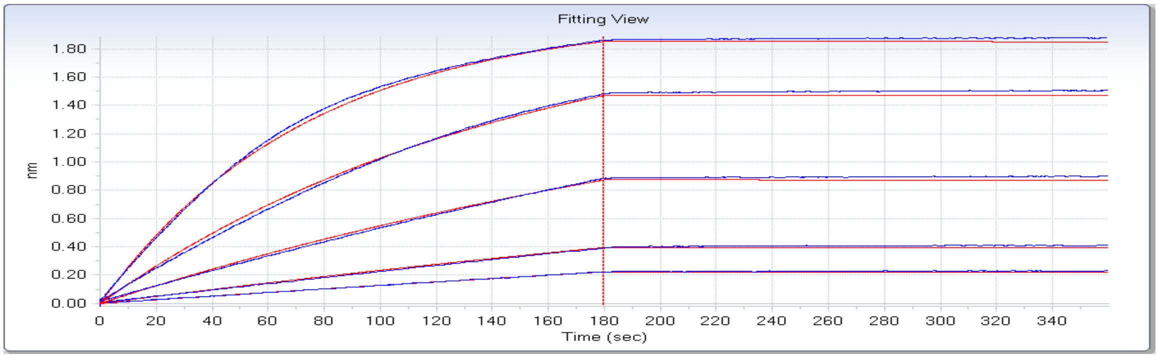
These data were fit with a 1:1 binding model, yielding apparent K_d = 1.9 fM, which is beyond the specified detection limit of 10 pM. Therefore, we report the affinity for this interaction is stronger than 10 pM.

F045-092 IgG vs A/Panama/2007/1999 (H3N2) HA, K_d = <10 pM

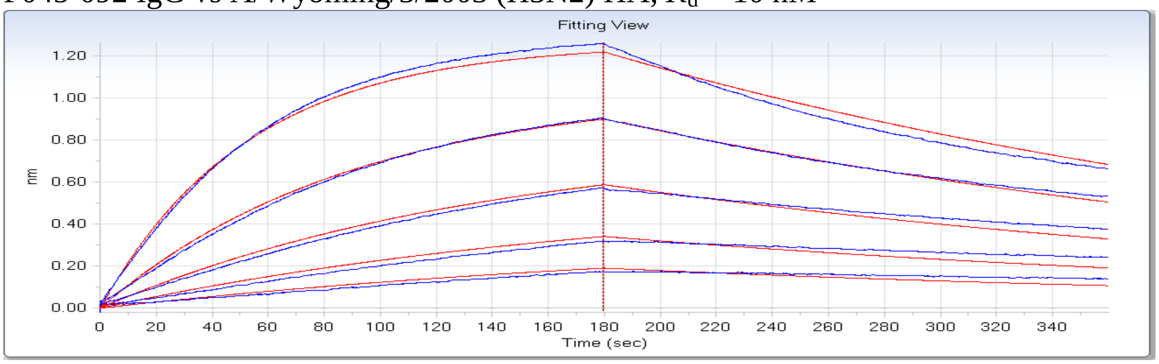


These data were fit with a 1:1 binding model, yielding apparent K_d = 14 fM, which is beyond the specified detection limit of 10 pM. Therefore, we report the affinity for this interaction is stronger than 10 pM.

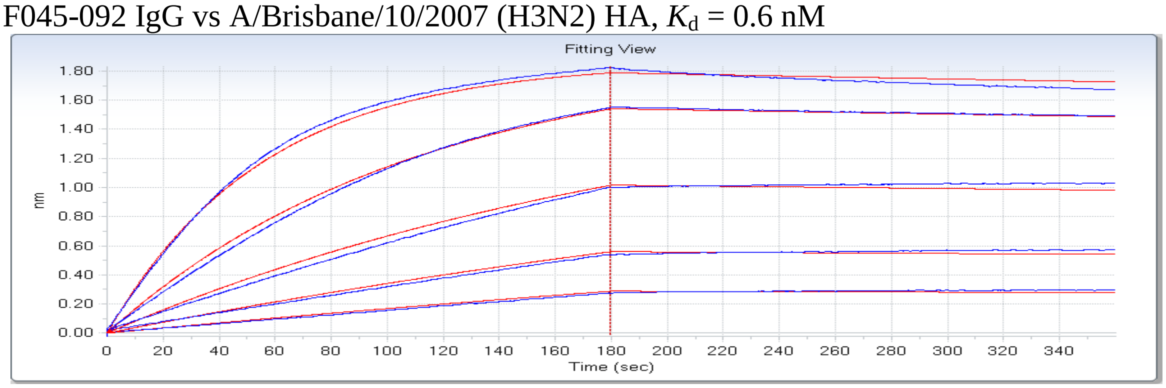
F045-092 IgG vs A/Moscow/10/1999 (H3N2) HA, K_d = 23 pM



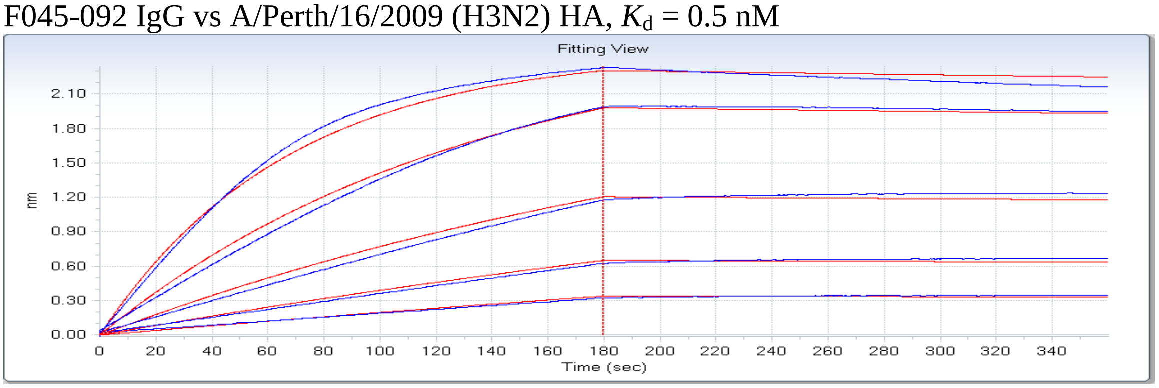
F045-092 IgG vs A/Wyoming/3/2003 (H3N2) HA, K_d = 10 nM



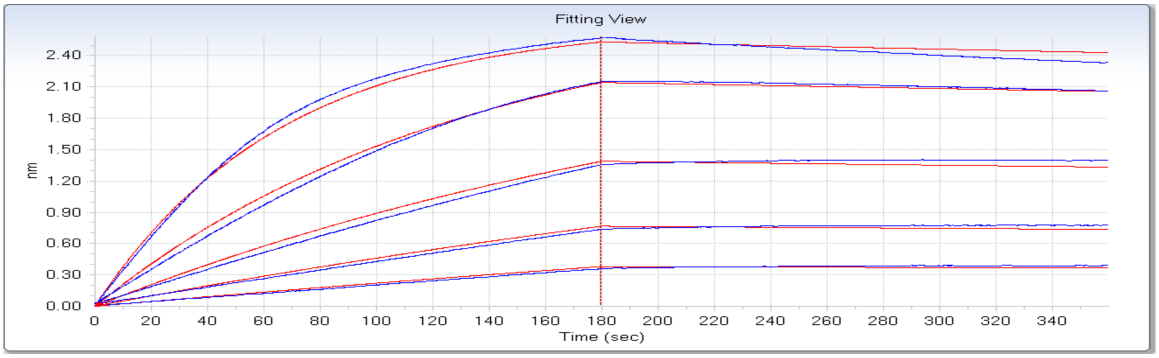
F045-092 IgG vs A/Brisbane/10/2007 (H3N2) HA, K_d = 0.6 nM



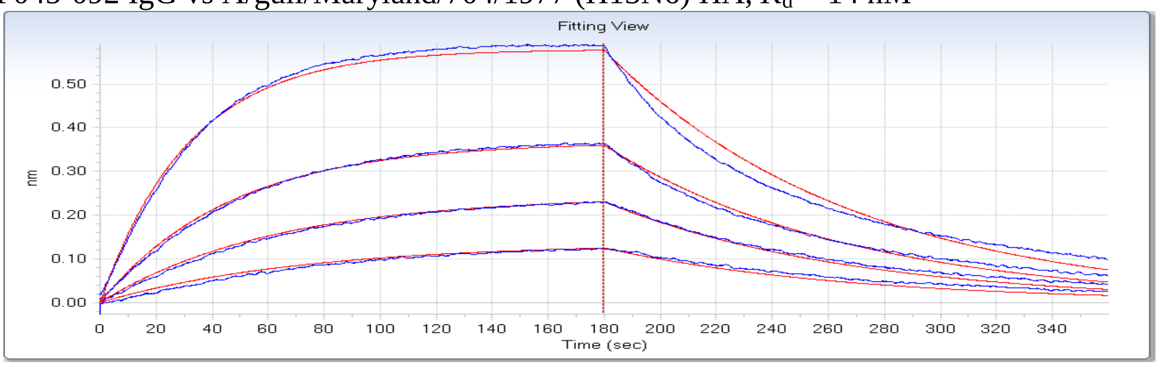
F045-092 IgG vs A/Perth/16/2009 (H3N2) HA, K_d = 0.5 nM



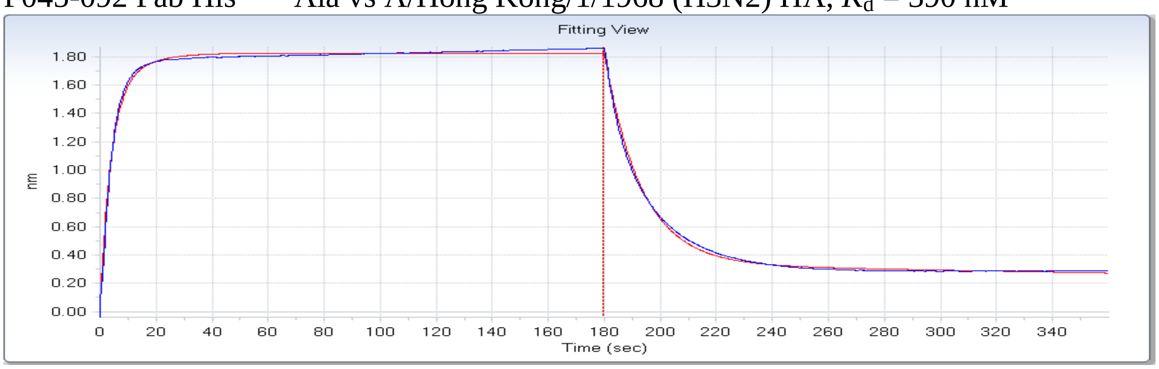
F045-092 IgG vs A/Victoria/361/2011 (H3N2) HA, K_d = 0.8 nM



F045-092 IgG vs A/gull/Maryland/704/1977 (H13N6) HA, K_d = 14 nM

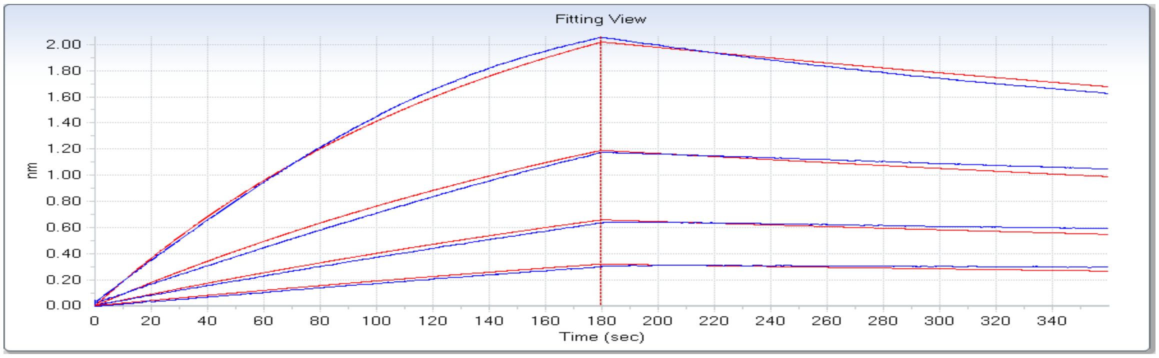


F045-092 Fab His[H100a]Ala vs A/Hong Kong/1/1968 (H3N2) HA, K_d = 390 nM

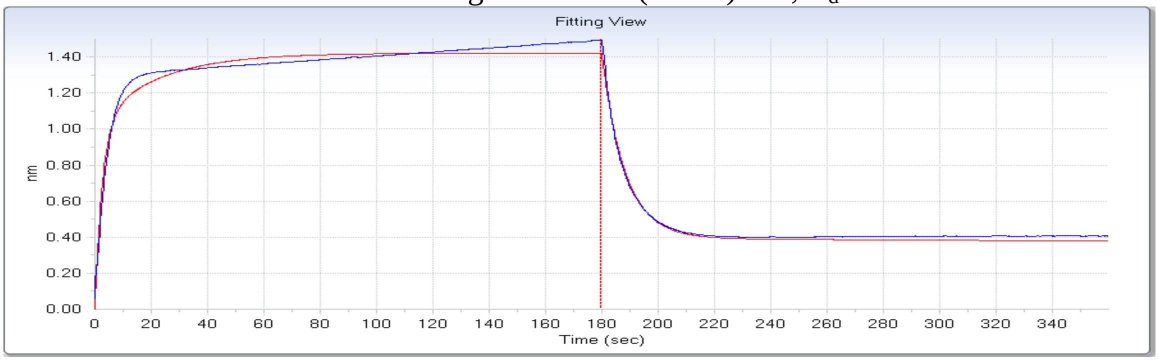


These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 390 nM, K_{d2} = 13 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 390 nM) whereas the higher affinity process may reflect a non-specific interaction. The Fab concentration tested in this experiment was 1000 nM. Therefore, we report the affinity for this interaction as ~390 nM.

F045-092 Fab His[H100a]Ala vs A/Victoria/3/1975 (H3N2) HA, K_d = 8.9 nM

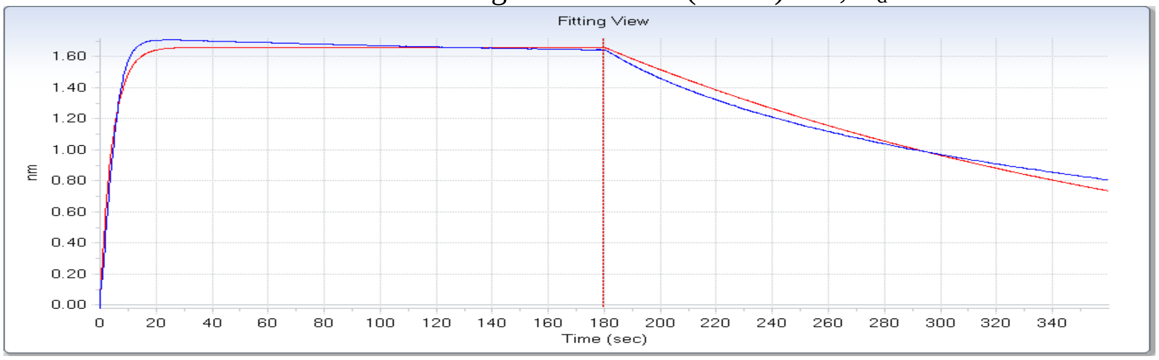


F045-092 Fab His^{H100a}Ala vs A/Bangkok/1/1979 (H3N2) HA, K_d = 480 nM

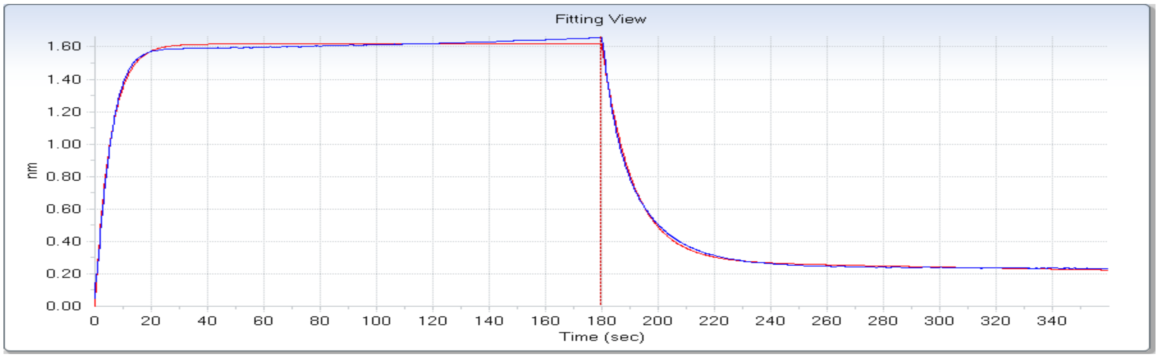


These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 480 nM, K_{d2} = 5.4 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 480 nM) whereas the higher affinity process may reflect a non-specific interaction. The Fab concentration tested in this experiment was 1000 nM. Therefore, we report the affinity for this interaction as ~480 nM.

F045-092 Fab His^{H100a}Ala vs A/Leningrad/360/1986 (H3N2) HA, K_d = 20 nM

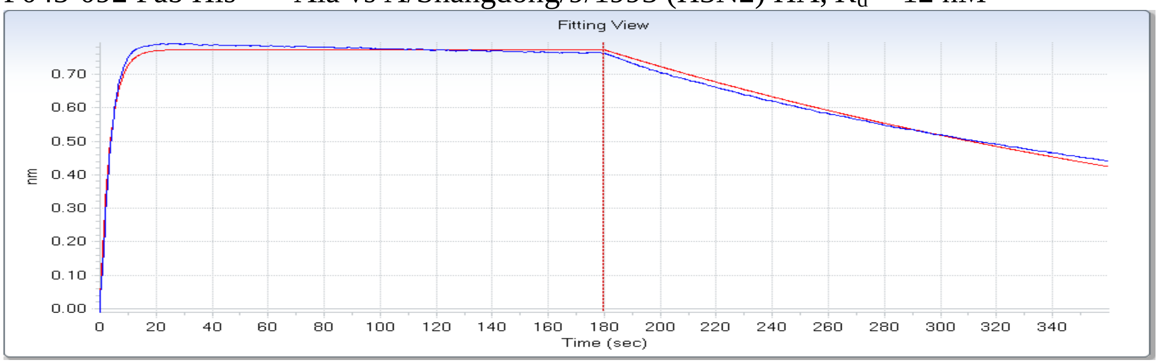


F045-092 Fab His^{H100a}Ala vs A/Beijing/353/1989 (H3N2) HA, K_d = 1000 nM

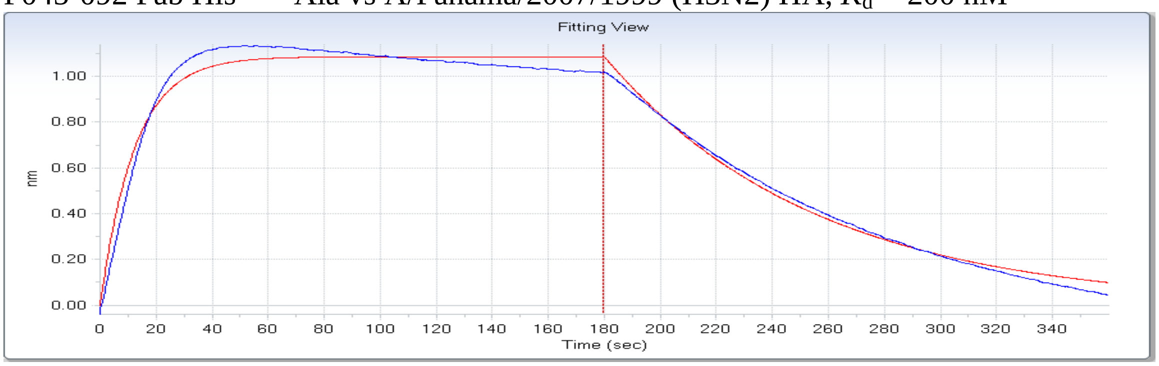


These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 1000 nM, K_{d2} = 7.5 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 1000 nM) whereas the higher affinity process may reflect a non-specific interaction. The Fab concentration tested in this experiment was 1000 nM. Therefore, we report the affinity for this interaction as ~1000 nM.

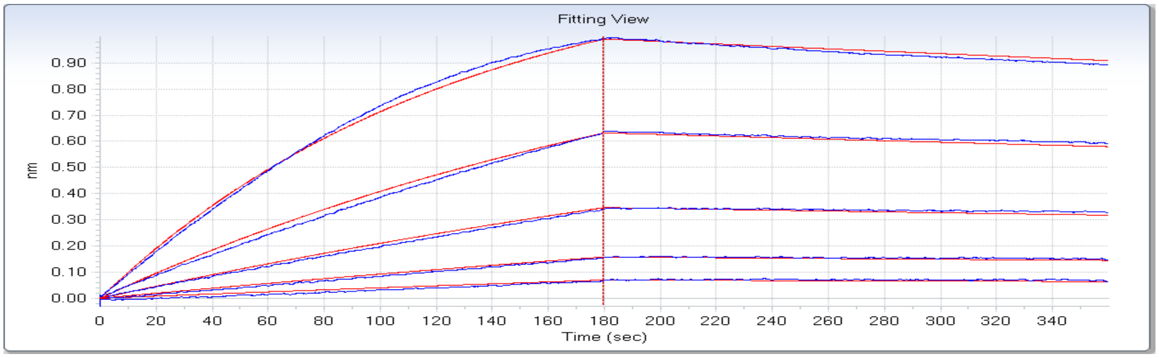
F045-092 Fab His^{H100a}Ala vs A/Shangdong/9/1993 (H3N2) HA, K_d = 12 nM



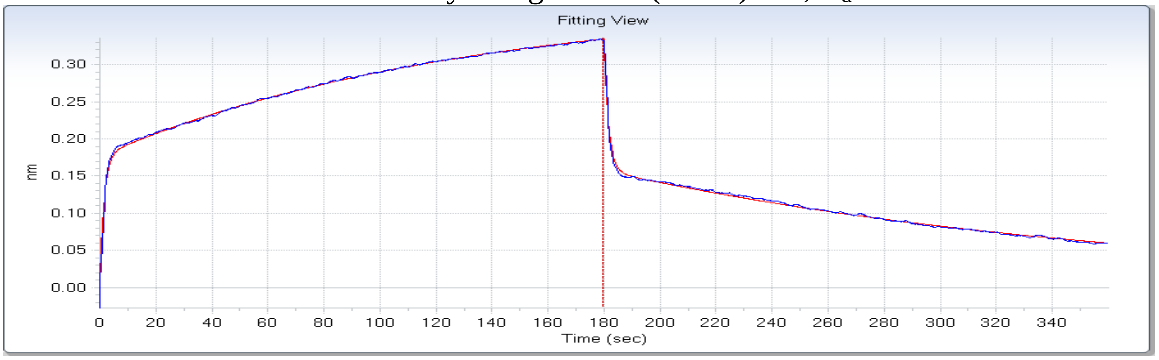
F045-092 Fab His^{H100a}Ala vs A/Panama/2007/1999 (H3N2) HA, K_d = 200 nM



F045-092 Fab His^{H100a}Ala vs A/Moscow/10/1999 (H3N2) HA, K_d = 3.3 nM

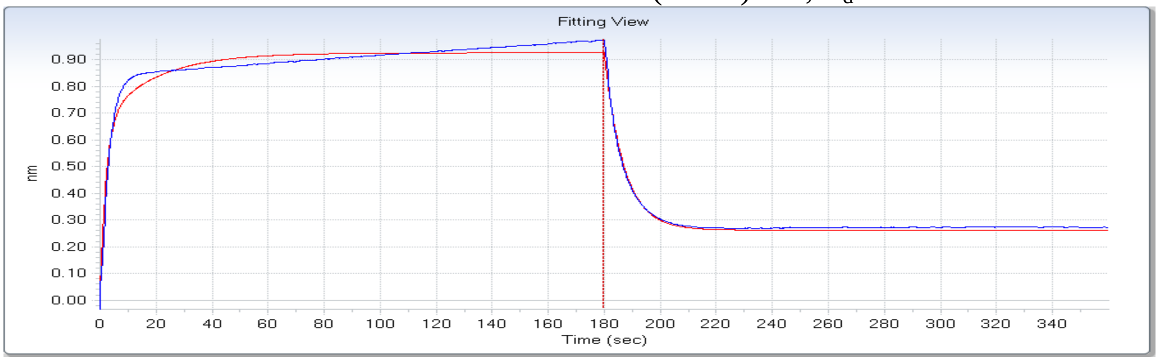


F045-092 Fab His^{H100a}Ala vs A/Wyoming/3/2003 (H3N2) HA, K_d = 6600 nM



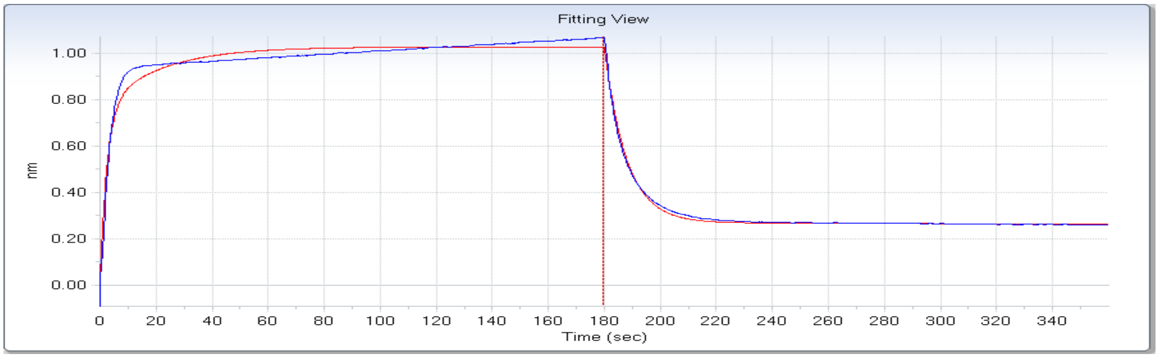
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 11000 nM and K_{d2} = 2200 nM (although k_{on} and k_{off} differ for the two binding processes). As these two binding processes have similar affinities, we report the affinity as the average of K_{d1} and K_{d2}, ~6600 nM.

F045-092 Fab His^{H100a}Ala vs A/Brisbane/10/2007 (H3N2) HA, K_d = 440 nM



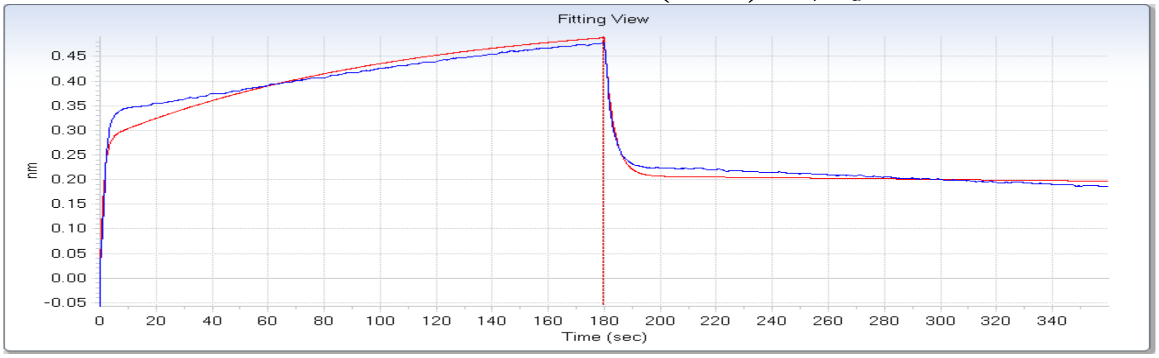
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 440 nM, K_{d2} = 1.2 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 440 nM) whereas the higher affinity process may reflect a non-specific interaction. The Fab concentration tested in this experiment was 1000 nM. Therefore, we report the affinity for this interaction as ~440 nM.

F045-092 Fab His^{H100a}Ala vs A/Perth/16/2009 (H3N2) HA, K_d = 450 nM



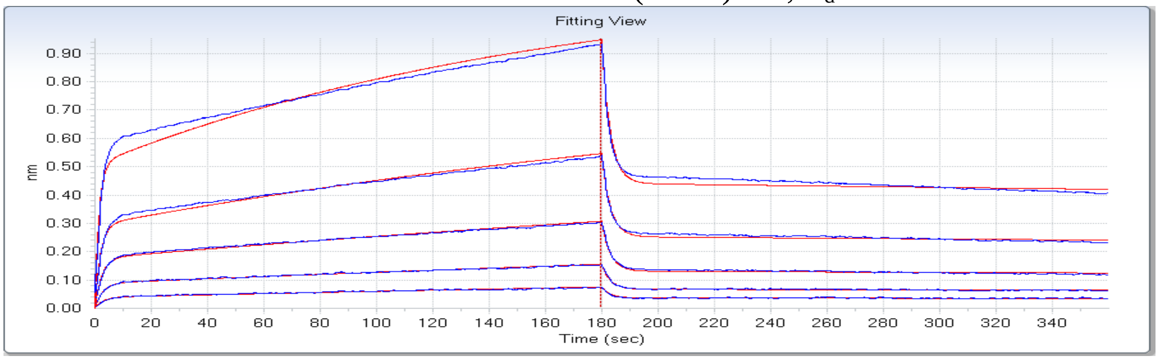
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 450 nM, K_{d2} = 2.8 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 450 nM) whereas the higher affinity process may reflect a non-specific interaction. The Fab concentration tested in this experiment was 1000 nM. Therefore, we report the affinity for this interaction as ~450 nM.

F045-092 Fab His^{H100a}Ala vs A/Victoria/361/2011 (H3N2) HA, K_d = 590 nM



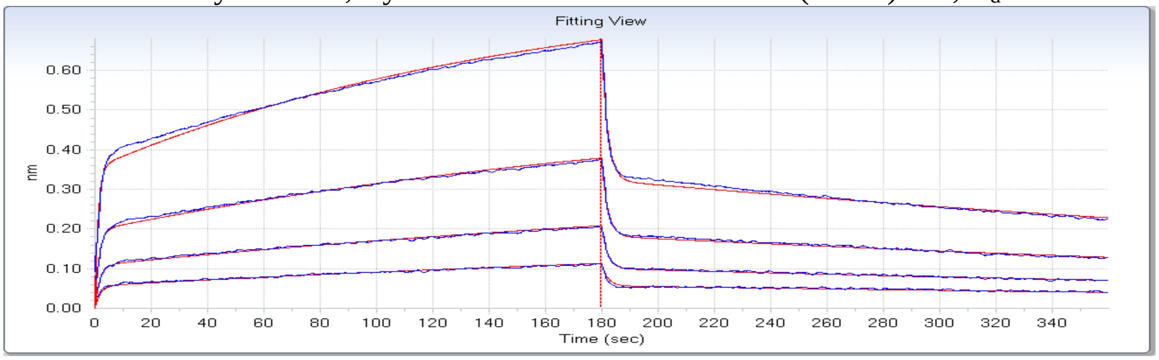
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 590 nM, K_{d2} = 32 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 590 nM) whereas the higher affinity process may reflect a non-specific interaction. The Fab concentration tested in this experiment was 1000 nM. Therefore, we report the affinity for this interaction as ~590 nM.

F045-092 Fab Leu^{H100d}Ala vs A/Victoria/3/1975 (H3N2) HA, K_d = 960 nM



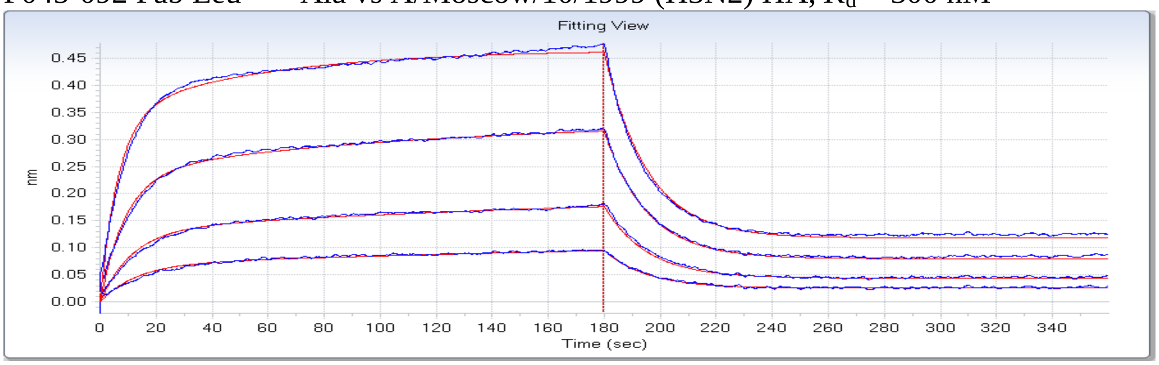
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 960 nM, K_{d2} = 47 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 960 nM) whereas the higher affinity process may reflect a non-specific interaction. The maximum Fab concentration tested in this experiment was 1000 nM. Therefore, we report the affinity for this interaction as 960 nM.

F045-092 Fab Cys^{H100c}Ala, Cys^{H100f}Ala vs A/Victoria/3/1975 (H3N2) HA, K_d = 810 nM



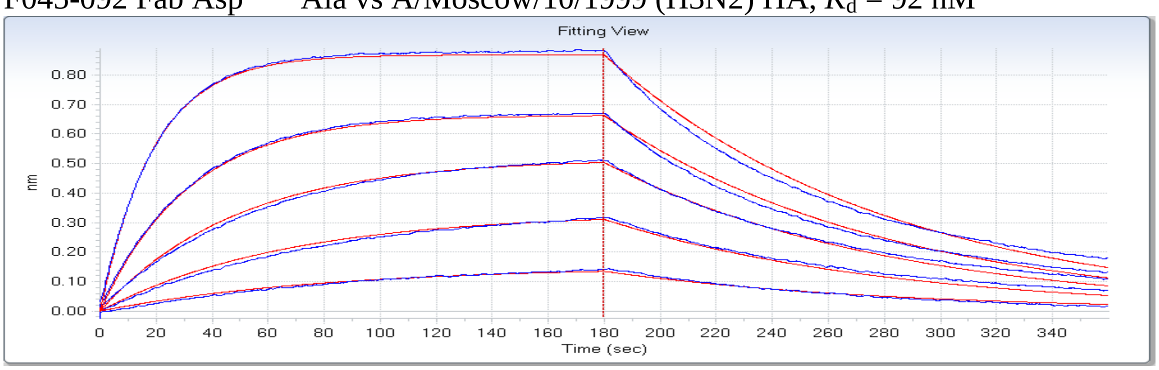
These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 420 nM and K_{d2} = 1200 nM (although k_{on} and k_{off} differ for the two binding processes). As these two binding processes have similar affinities, we report the affinity as the average of K_{d1} and K_{d2}, ~810 nM.

F045-092 Fab Leu^{H100d}Ala vs A/Moscow/10/1999 (H3N2) HA, K_d = 300 nM

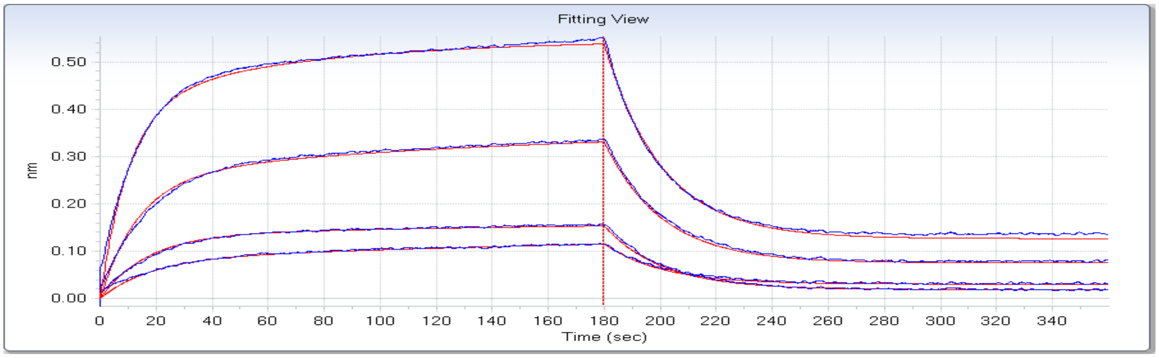


These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 300 nM, K_{d2} = 0.4 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 300 nM) whereas the higher affinity process may reflect a non-specific interaction. The maximum Fab concentration tested in this experiment was 800 nM. Therefore, we report the affinity for this interaction as 300 nM.

F045-092 Fab Asp^{H100e}Ala vs A/Moscow/10/1999 (H3N2) HA, K_d = 92 nM



F045-092 Fab Cys^{H100c}Ala, Cys^{H100f}Ala vs A/Moscow/10/1999 (H3N2) HA, K_d = 410 nM



These data were fit with a 2:1 binding model, yielding apparent K_{d1} = 410 nM, K_{d2} = 0.4 nM. The dominant binding process (accounting for the majority of the shift in observed wavelength) corresponds to the lower affinity process (K_{d1} = 410 nM) whereas the higher affinity process may reflect a non-specific interaction. The maximum Fab concentration tested in this experiment was 800 nM. Therefore, we report the affinity for this interaction as 410 nM.

Supplementary Figure 7 | Binding curves for reported K_d values for F045-092 Fab, IgG, and Fab mutants with various HA isolates. Blue curves are the experimental traces obtained from bio-layer interferometry experiments and the red curves are the best global fits to the data used to calculate the K_d values. Single point binding curves were measured using 1000 nM F045-092 Fab His^{100a}Ala unless otherwise shown.

Supplementary Table 1 | HA strains not bound by F045-092 Fab or IgG.

Subtype	Strain	Binding		Neutralization*
		F045-092 Fab	F045-092 IgG	F045-092 IgG
H1N1	A/South Carolina/1/1918	–	–	NT
H1N1	A/WSN/1933	–	–	NT
H1N1	A/Puerto Rico/8/1934	–	–	NT
H1N1	A/AA/Marton/1943	–	–	NT
H1N1	A/duck/Alberta/345/1976	–	–	NT
H1N1	A/USSR/90/1977	–	–	NT
H1N1	A/swine/Hokkaido/2/1981	NT	NT	–
H1N1	A/Singapore/6/1986	–	–	NT
H1N1	A/Texas/36/1991	–	–	NT
H1N1	A/Solomon Islands/3/2006	–	±	NT
H1N1	A/California/04/2009	–	–	NT
H1N1	A/Suita/1/2009 pdm	NT	NT	–
H2N2	A/Japan/305/1957	–	–	NT
H2N2	A/duck/Hong Kong/273/1978	NT	NT	±
H4N6	A/duck/Czechoslovakia/1956	–	–	NT
H5N1	A/duck/Mongolia/54/2001-A/duck/Mongolia/47/2001	NT	NT	±
H5N1	A/Indonesia/05/2005	–	±	NT
H6N2	A/turkey/Massachusetts/3740/1965	–	±	NT
H7N7	A/Netherlands/219/2003	–	–	NT
H9N2	A/turkey/Wisconsin/1/1966	–	–	NT
H10N7	A/chicken/Germany/N/1949	–	–	NT
H11N6	A/duck/England/1956	–	–	NT
H12N5	A/duck/Alberta/60/1976	–	–	NT
H14N5	A/mallard duck/Astrakhan/263/1982	–	–	NT
H15N8	A/shearwater/Western Australia/2576/1979	–	±	NT
H16N3	A/black-headed gull/Sweden/4/1999	–	±	NT

***Virus neutralizing activities adapted from Ohshima *et al*.[1]
NT, not tested
– no detectable binding or no neutralization activity
± $K_d \geq 5000$ nM or $IC_{50} > 200$ µg/mL

Supplementary Table 2 | Buried molecular surface area of Fab-HA complexes.

Antibody	PDB code	Epitope	Buried Surface Area (Å^2)	
			HA	Fab
F045-092	4O58	RBS	490	480
CR8043	4NM8	Stem	510	550
HC19	2VIR	RBS	520	480
F10	3FKU	Stem	570	530
C05	4FP8	RBS	570	540
CH67	4HKX	RBS	610	590
2G1	4HG4	RBS	610	580
BH151	1EO8	Head	630	590
FI6V3 (H3)	3ZTJ	Stem	630	590
CR8020	3SDY	Stem	640	640
CR6261 (H5)	3GBM	Stem	650	590
CH65	3SM5	RBS	650	610
5J8	4M5Z	RBS	660	640
CR6261 (H1)	3GBN	Stem	670	600
FI6V3 (H1)	3ZTN	Stem	670	650
CR9114	4FQI	Stem	670	640
HC63	1KEN	RBS	680	740
8F8	4HF5	RBS	720	690
HC45	1QFU	Head	730	710
S139/1	4GMS	RBS	730	720
C179	4HLZ	Stem	730	690
2D1	3LZF	Head	740	760
1F1	4GXU	RBS	770	760
8M2	4HFU	RBS	770	760
H5M9	4MHH	Head	820	800

RBS, receptor-binding site.

Molecular protein surface areas buried upon Fab binding were calculated using MS^2 and sorted by increasing HA buried surface area. For crystal structures containing multiple symmetry-related copies, the average buried surface area of each copy is listed.

Supplementary Table 3 | Sequence identity of residues in the F045-092 epitope of the Vic1975/H3 and Vic2011/H3 HAs.

HA residue	H3 consensus	Vic1975/H3 sequence	Vic2011/H3 sequence
131	T (76.2)	T (76.2)	T (76.2)
133	N* (87.6)	N (87.6)	N* (87.6)
134	G (100.0)	G (100.0)	G (100.0)
135	T (86.3)	G (7.7)	T (86.3)
136	S (100.0)	S (100.0)	S (100.0)
137	S (82.9)	S (82.9)	S (82.9)
145	N (56.5)	S (16.4)	N (56.5)
153	W (99.9)	W (99.9)	W (99.9)
155	T (71.5)	Y (4.2)	T (71.5)
156	H (69.4)	K (11.7)	H (69.4)
157	L (87.8)	S (12.1)	L (87.8)
158	K (46.2)	G (2.9)	N (37.5)
193	F (55.9)	N (4.7)	F (55.9)
194	L (98.3)	L (98.3)	L (98.3)
226	I (65.0)	L (10.9)	I (65.0)

Number in parentheses indicates sequence identity of that residue at that position for human H3 isolates. An asterisk (*) indicates a potential N-linked glycan at that position. Only the Vic1975/H3 contact residues are listed in the left column.

Supplementary Table 4 | Binding breadth of wild type and mutants of F045-092 Fab with avian and human H3 isolates (1963-2011).

Subtype	Strain	Wild type	$H^{100a}A$	$L^{100d}A$	$D^{100e}A$	$C^{100c}A$, $C^{100f}A$
H3N8	A/duck/Ukraine/1/1963	+	–	–	–	–
H3N2	A/Hong Kong/1/1968	+++	++	±	–	–
H3N2	A/Victoria/3/1975	+++	+++	+	–	+
H3N2	A/Bangkok/1/1979	++	++	–	–	–
H3N2	A/Leningrad/360/1986	+++	+++	±	–	–
H3N2	A/Beijing/353/1989	++	+	–	–	–
H3N2	A/Shangdong/9/1993	++++	+++	±	±	±
H3N2	A/Panama/2007/1999	+++	++	–	–	–
H3N2	A/Moscow/10/1999	++++	++++	++	++	++
H3N2	A/Wyoming/3/2003	+	±	–	–	–
H3N2	A/Brisbane/10/2007	++	++	–	–	–
H3N2	A/Perth/16/2009	++	++	–	–	–
H3N2	A/Victoria/361/2011	++	+	–	–	–

Dissociation constants:

– no detectable binding

± $K_d \geq 5,000$ nM

\+ $K_d = 500–5,000$ nM

++ $K_d = 50–500$ nM

+++ $K_d = 5–50$ nM

++++ $K_d \leq 5$ nM

Supplementary Methods

Sequences of HA proteins used in binding studies. The sequences listed below represent the full-length ORF as cloned in the baculovirus transfer vector. Most of the N-terminal signal peptide (MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFA) is presumably removed during secretion, leaving four non-native residues (ADPG) at the N-terminus of HA1. The C-terminal BirA biotinylation site, thrombin cleavage site, trimerization domain, and a His_6 tag are retained on all proteins.

>A/South Carolina/1/1918 (H1N1)
```
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDSHNGKLCKLKGIAPLQLGKCNIAGWLLGNPECDLLLTASSWSYIVETSNSENGTCYPGDFIDYEELREQLS
SVSSFEKFEIFPKTSSWPNHETTKGVTAACSYAGASSFYRNLLWLTKKGSSYPKLSKSYVNNKGKEVLVLWGVH
HPPTGTDQQSLYQNADAYVSVGSSKYNRRFTPEIAARPKVRDQAGRMNYYWTLLEPGDTITFEATGNLIAPWYA
FALNRGSGSGIITSDAPVHDCNTKCQTPHGAINSSLPFQNIHPVTIGECPKYVRSTKLRMATGLRNIPSIQSRG
LFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAIDGITNKVNSVIEKMNTQFTAVGKEFNNLER
RIENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVRNLYEKVKSQLKNNAKEIGNGCFEFYHKCDDACM
ESVRNGTYDYPKYSEESKLNREEIDGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDG
EWVLLSTFLGHHHHHH
```

>A/WSN/1933 (H1N1)
```
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTIFEKNVAVTHSVNL
LEDRHNGKLCKLKGIAPLQLGKCNITGWLLGNPECDSLLPARSWSYIVETPNSENGACYPGDFIDYEELREQLS
SVSSLERFEIFPKESSWPNHTFNGVTVSCSHRGKSSFYRNLLWLTKKGDSYPKLTNSYVNNKGKEVLVLWGVHH
PSSSDEQQSLYSNGNAYVSVASSNYNRRFTPEIAARPKVKDQHGRMNYYWTLLEPGDTIIFEATGNLIAPWYAF
ALSRGFESGIITSNASMHECNTKCQTPQGSINSNLPFQNIHPVTIGECPKYVRSTKLRMVTGLRNIPSIQYRGL
FGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSIIEKMNTQFTAVGKEFNNLEKR
MENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDLNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCDNECME
SVRNGTYDYPKYSEESKLNREKIDGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGE
WVLLSTFLGHHHHHH
```

>A/Puerto Rico/8/1934 (H1N1)
```
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDSHNGKLCRLKGIAPLQLGKCNIAGWLLGNPECDPLLPVRSWSYIVETPNSENGICYPGDFIDYEELREQLS
SVSSFERFEIFPKESSWPNHNTNGVTAACSHEGKSSFYRNLLWLTEKEGSYPKLKNSYVNKKGKEVLVLWGIHH
PPNSKEQQNLYQNENAYVSVVTSNYNRRFTPEIAERPKVRDQAGRMNYYWTLLKPGDTIIFEANGNLIAPMYAF
ALSRGFGSGIITSNASMHECNTKCQTPLGAINSSLPYQNIHPVTIGECPKYVRSAKLRMVTGLRNIPSIQSRGL
FGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNTVIEKMNIQFTAVGKEFNKLEKR
MENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCDNECME
SVRNGTYDYPKYSEESKLNREKVDGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGE
WVLLSTFLGHHHHHH
```

>A/AA/Marton/1943 (H1N1)
```
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDSHNGKLCRLKGIAPLQLGKCNIAGWILGNPECESLLSERSWSYIVETPNSENGTCYPGDFIDYEELREQLS
SVSSFERFEIFSKESSWPKHNTTRGVTAACSHAGKSSFYRNLLWLTEKDGSYPNLNNSYVNKKGKEVLVLWGVH
```

HPSNIKDQQTLYQKENAYVSVVSSNYNRRFTPEIAERPKVRGQAGRMNYYWTLLKPGDTIMFEANGNLIAPWYA
FALSRGFGSGIITSNASMHECDTKCQTPQGAINSSLPFQNIHPVTIGECPKYVRSTKLRMVTGLRNIPSIQSRG
LFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNNLEK
RMENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKNQLRNNAKEIGNGCFEFYHKCNNECM
ESVKNGTYDYPKYSEESKLNREKIDSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEW
VLLSTFLGHHHHHH

>A/duck/Alberta/345/1976 (H1N1)
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LEDSHNGKLCSLNGIAPLQLGKCNVAGWLLGNPECDLLLTANSWSYIIETSNSENGTCYPGEFIDYEELREQLS
SISSFEKFEIFPKASSWPNHETTKGVTAACSYSGASSFYRNLLWITKKGTSYPKLSKSYTNNKGKEVLVLWGVH
HPPSVSEQQSLYQNADAYVSVGSSKYNRRFAPEIAARPEVRGQAGRMNYYWTLLDQGDTITFEATGNLIAPWYA
FALNKGSDSGIITSDAPVHNCDTRCQTPHGALNSSLPFQNVHPITIGECPKYVKSTKLRMATGLRNVPSIQSRG
LFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAIDGITNKVNSVIEKMNTQFTAVGKEFNNLER
RIENLNKKVDDGFLDVWTYNAELLVLLENERTLDFHDSNVRNLYEKVKSQLRNNAKEIGNGCFEFYHKCDDECM
ESVKNGTYDYPKYSEESKLNREEIDSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEW
VLLSTFLGHHHHHH

>A/USSR/90/1977 (H1N1)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDSHNGKLCRLKGIAPLQLGKCNIAGWILGNPECESLFSKKSWSYIAETPNSENGTCYPGYFADYEELREQLS
SVSSFERFEIFPKERSWPKHNVTRGVTASCSHKGKSSFYRNLLWLTEKNGSYPNLSKSYVNNKEKEVLVLWGVH
HPSNIEDQKTIYRKENAYVSVVSSNYNRRFTPEIAERPKVRGQAGRINYYWTLLEPGDTIIFEANGNLIAPWHA
FALNRGFGSGIITSNASMDECDTKCQTPQGAINSSLPFQNIHPVTIGECPKYVRSTKLRMVTGLRNIPSIQSRG
LFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLEK
RMENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCNNECM
ESVKNGTYDYPKYSEESKLNREKIDSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEW
VLLSTFLGHHHHHH

>A/Singapore/6/1986 (H1N1)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDSHNGKLCRLKGIAPLQLGNCSIAGWILGNPECESLFSKKSWSYIAETPNSENGTCYPGYFADYEELREQLS
SVSSFERFEIFPKESSWPNHTVTKGVTASCSHKGRSSFYRNLLWLTKKNGSYPNLSKSYVNNKEKEVLVLWGVH
HPSNIGDQRAIYHTENAYVSVVSSHYNRRFTPEIAKRPKVRDQEGRINYYWTLLEPGDTIIFEANGNLIAPWYA
FALSRGFGSGIITSNASMDECDAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSTKLRMVTGLRNIPSIQSRG
LFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLER
RMENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCNNECM
ESVKNGTYDYPKYSEESKLNREKIDSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEW
VLLSTFLGHHHHHH

>A/Texas/36/1991 (H1N1)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDSHNGKLCRLKGIAPLQLGNCSVAGWILGNPKCESLFSKESWSYIAETPNPENGTCYPGYFADYEELREQLS
SVSSFERFEIFPKESSWPNHTVTKGVTTSCSHNGKSSFYRNLLWLTEKNGLYPNLSKSYVNNKEKEVLVLWGVH
HPSNIRDQRAIYHTENAYVSVVSSHYSRRFTPEIAKRPKVRGQEGRINYYWTLLEPGDTIIFEANGNLIAPWYA
FALSRGFGSGIITSNASMDECDAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSTKLRMVTGLRNIPSIQSRG
LFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLER
RMENLNKKVDDGFLDIWTYNAELLVLLENGRTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCNNECM
ESVKNGTYDYPKYSEESKLNRGKIDSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEW
VLLSTFLGHHHHHH

>A/Beijing/262/1995 (H1N1)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDSHNGKLCRLKGIAPLQLGNCSVAGWILGNPECESLISKESWSYIVETPNPENGTCYPGYFADYEELREQLS

SVSSFERFEIFPKESSWPNHTVTGVTASCSHNGKSSFYRNLLWLTEKNGLYPNLSNSYVNNKEKEVLVLWGVHH
PSNIGVQRAIYHTENAYVSVVSSHYSRRFTPEIAKRPKVRGQEGRINYYWTLLEPGDTIIFEANGNLIAPWYAF
ALSRGFGSGIITSNAPMNECDAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSTKLRMVTGLRNIPSIQSRGL
FGAIAGFIEGGWTGMMDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLERR
MENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCNNECME
SVKNGTYDYPKYSEESKLNREKIDSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWV
LLSTFLGHHHHHH

>A/New Caledonia/20/1999 (H1N1)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDSHNGKLCRLKGIAPLQLGNCSVAGWILGNPECELLISKESWSYIVETPNPENGTCYPGYFADYEELREQLS
SVSSFERFEIFPKESSWPNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYVNNKEKEVLVLWGVHH
PPNIGNQRALYHTENAYVSVVSSHYSRRFTPEIAKRPKVRDQEGRINYYWTLLEPGDTIIFEANGNLIAPWYAF
ALSRGFGSGIITSNAPMDECDAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSAKLRMVTGLRNIPSIQSRGL
FGAIAGFIEGGWTGMVDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLERR
MENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCNNECME
SVKNGTYDYPKYSEESKLNREKIDSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWV
LLSTFLGHHHHHH

>A/Solomon Islands/3/2006 (H1N1)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTICIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDSHNGKLCRLKGIAPLQLGNCSVAGWILGNPECELLISRESWSYIVEKPNPENGTCYPGHFADYEELREQLS
SVSSFERFEIFPKESSWPNHTTTGVSASCSHNGESSFYKNLLWLTGKNGLYPNLSKSYANNKEKEVLVLWGVHH
PPNIGDQRALYHKENAYVSVVSSHYSRKFTPEIAKRPKVRDQEGRINYYWTLLEPGDTIIFEANGNLIAPRYAF
ALSRGFGSGIINSNAPMDECDAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSAKLRMVTGLRNIPSIQSRGL
FGAIAGFIEGGWTGMVDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLERR
MENLNKKVDDGFIDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCNDECME
SVKNGTYDYPKYSEESKLNREKIDSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWV
LLSTFLGHHHHHH

>A/California/04/2009 HA2 E54G(H1N1)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDTLCIGYHANNSTDTVDTVLEKNVTVTHSVNL
LEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTASSWSYIVETPSSDNGTCYPGDFIDYEELREQLS
SVSSFERFEIFPKTSSWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIH
HPSTSADQQSLYQNADTYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYA
FAMERNAGSGIIISDTPVHDCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNIPSIQSRG
LFGAIAGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQNAIDGITNKVNSVIEKMNTQFTAVGKEFNHLEK
RIENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDNTCM
ESVKNGTYDYPKYSEEAKLNREEIDSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEW
VLLSTFLGHHHHHH

>A/Japan/305/1957 (H2N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDQICIGYHANNSTEKVDTILERNVTVTHAKDI
LEKTHNGKLCKLNGIPPLELGDCSIAGWLLGNPECDRLLSVPEWSYIMEKENPRDGLCYPGSFNDYEELKHLLS
SVKHFEKVKILPKDRWTQHTTTGGSRACAVSGNPSFFRNMVWLTEKGSNYPVAKGSYNNTSGEQMLIIWGVHHP
NDETEQRTLYQNVGTYVSVGTSTLNKRSTPEIATRPKVNGQGGRMEFSWTLLDMWDTINFESTGNLIAPEYGFK
ISKRGSSGIMKTEGTLENCETKCQTPLGAINTTLPFHNVHPLTIGECPKYVKSEKLVLATGLRNVPQIESRGLF
GAIAGFIEGGWQGMVDGWYGYHHSNDQGSGYAADKESTQKAFDGITNKVNSVIEKMNTQFEAVGKEFSNLERRL
ENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMNS
VKNGTYDYPKYEEESKLNRNEIKSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVL
LSTFLGHHHHHH

>A/Adachi/2/1957 (H2N2)

MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDQICIGYHANNSTEKVDTILERNVTVTHAKDI
LEKTHNGKLCKLNGIPPLELGDCSIAGWLLGNPECDRLLSVPEWSYIMEKENPRNGLCYPGSFNDYEELKHLLS
SVKHFEKVKILPKDRWTQHTTTGGSQACAVSGNPSFFRNMVWLTKKGSDYPVAKGSYNNTSGEQMLIIWGVHHP
IDETEQRTLYQNVGTYVSVGTSTLNKRSTPEIATRPKVNGLGSRMEFSWTLLDMWDTINFESTGNLIAPEYGFK
ISKRGSSGIMKTEGTLENCETKCQTPLGAINTTLPFHNVHPLTIGECPKYVKSEKLVLATGLRNVPQIESRGLF
GAIAGFIEGGWQGMVDGWYGYHHSNDQGSGYAADKESTQKAFDGITNKVNSVIEKMNTQFEAVGKEFGNLERRL
ENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMNS
VKNGTYDYPKYEEESKLNRNEIKSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVL
LSTFLGHHHHHH

>A/duck/Ukraine/1/1963 (H3N8)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTIVKTITDDQIEVTNATEL
VQSSSTGKICNNPHRILDGRACTLIDALLGDPHCDVFQNETWDLFVERSNAFSNCYPYDIPDYASLRSLVASSG
TLEFITEGFTWTGVTQNGGSSACKRGPANGFFSRLNWLTKSESAYPVLNVTMPNNDNFDKLYIWGVHHPSTNQE
QTDLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGQPGRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGK
SSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPGKQTRGLFGAIAGF
IENGWEGMIDGWYGFRHQNSEGTGQAADLKSTQAAIDQINRKLNRVIEKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLADSEMNKLFEKTRRQLRENAEDMGNGCFKIYHKCDNACIESIRNGTY
DHDIYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Hong Kong/1/1968 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTLVKTITDDQIEVTNATEL
VQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSG
TLEFITEGFTWTGVTQNGGSNACKRGPGSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYIWGVHHPSTNQE
QTSLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGK
SSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGAIAGF
IENGWEGMIDGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRVIEKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTGRQLRENAEDMGNGCFKIYHKCDNACIESIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Victoria/3/1975 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTLVKTITNDQIEVTNATEL
VQSSSTGKICNNPHRILDGINCTLIDALLGDPHCDGFQNEKWDLFVERSKAFSNCYPYDVPDYASLRSLVASSG
TLEFINEGFNWTGVTQNGGSSACKRGPDSGFFSRLNWLYKSGSTYPVQNVTMPNNDNSDKLYIWGVHHPSTDKE
QTNLYVQASGKVTVSTKRSQQTIIPNVGSRPWVRGLSSRISIYWTIVKPGDILVINSNGNLIAPRGYFKMRTGK
SSIMRSDAPIGTCSSECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMIDGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRVIEKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Bangkok/1/1979 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTLVKTITNDQIEVTNATEL
VQSSSTGRICDSPHRILDGKNCTLIDALLGDPHCDGFQNEKWDLFVERSKAFSNCYPYDVPDYASLRSLVASSG
TLEFINEGFNWTGVTQSGGSYACKRGSDNSFFSRLNWLYESESKYPVLNVTMPNNGNFDKLYIWGVHHPSTDKE
QTNLYVRASGRVTVSTKRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKPGDILLINSNGNLIAPRGYFKIRTGK
SSIMRSDAPIGTCSSECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRVIEKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRRQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Leningrad/360/1986 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTLVKTITNDQIEVTNATEL
VQSSSTGRICDSPHRILDGKNCTLIDALLGDPHCDGFQNEKWDLFIERSKAFSNCYPYDVPDYASLRSLVASSG
TLEFINEGFNWTGVTQSGGSYTCKRGSVNSFFSRLNWLYESEYKYPALNVTMPNNGKFDKLYIWGVHHPSTEKE
QTNLYVRASGRVTVSTKRSQQTVIPNIGSRPWVRGLSSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRTGK
SSIMRSDAPIGTCSSECITPNGSIPNDKPFQNVNKITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRLIEKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQYTIDLTDSEMNKLFEKTRKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Beijing/353/1989 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTLVKTITNDQIEVTNATEL
VQSSSTGRICDSPHRILDGKNCTLIDALLGDPHCDGFQNKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSG
TLEFINEDFNWTGVAQSGESYACKRGSVKSFFSRLNWLHESEYKYPALNVTMPNNGKFDKLYIWGVHHPSTDRE
QTNLYVRASGRVTVSTKRSQQTVIPNIGSRPWVRGLSSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRTGK
SSIMRSDAPIGTCSSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRLIEKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Shangdong/9/1993 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTLVKTITNDQIEVTNATEL
VQSSSTGRICGSPHRILDGKNCTLIDALLGDPHCDGFQNKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSG
TLEFINEDFNWTGVAQDGGSYACKRGSVNSFFSRLNWLHKLEYKYPALNVTMPNNGKFDKLYIWGVHHPSTDSD
QTSLYVRASGRVTVSTKRSQQTVTPNIGSRPWVRGQSSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRNGK
SSIMRSDAPIGNCSSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGTGQAADLKSTQAAIDQINGKLNRLIEKTNEKFQQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTRKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Panama/2007/1999 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVSNGTLVKTITNDQIEVTNATEL
VQSSSTGRICDSPHQILDGENCTLIDALLGDPHCDGFQNKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSG
TLEFNNESFNWTGVAQNGTSSACKRRSNKSFFSRLNWLHQLKYKYPALNVTMPNNEKFDKLYIWGVLHPSTDSD
QISLYAQASGRVTVSTKRSQQTVIPNIGSRPWVRGVSSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGK
SSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGTGQAADLKSTQAAINQINGKLNRLIEKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFERTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Moscow/10/1999 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTLVKTITNDQIEVTNATEL
VQSSSTGRICDSPHQILDGENCTLIDALLGDPHCDGFQNKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSG
TLEFNNESFNWTGVAQNGTSSACKRRSINSFFSRLNWLHQLKYRYPALNVTMPNNDKFDKLYIWGVHHPSTDSD
QTSLYTQASGRVTVSTKRSQQTVIPNIGSRPWVRGISSRISIYWTIVKPGDILLIKSTGNLIAPRGYFKIRSGK
SSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMMDGWYGFRHQNSEGTGQAADLKSTQAAINQINGKLNRLIEKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFERTRKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Wyoming/3/2003 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTIVKTITNDQIEVTNATEL
VQSSSTGGICDSPHQILDGENCTLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSG
TLEFNNESFNWAGVTQNGTSSACKRRSNKSFFSRLNWLTHLKYKYPALNVTMPNNEKFDKLYIWGVHHPVTDSD
QISLYAQASGRITVSTKRSQQTVIPNIGFRPRVRDISSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGK
SSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGTGQAADLKSTQAAINQINGKLNRLIGKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFERTKKQLRENAEDMGNGCFKIYHKCDNACIESIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Brisbane/10/2007 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTIVKTITNDQIEVTNATEL
VQSSSTGEICDSPHQILDGENCTLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSG
TLEFNNESFNWTGVTQNGTSSACIRRSNNSFFSRLNWLTHLKFKYPALNVTMPNNEKFDKLYIWGVHHPGTDND
QIFPYAQASGRITVSTKRSQQTVIPNIGSRPRVRNIPSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGK
SSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGIGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Perth/16/2009 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTIVKTITNDQIEVTNATEL
VQSSSTGEICDSPHQILDGKNCTLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSG
TLEFNNESFNWTGVTQNGTSSACIRRSKNSFFSRLNWLTHLNFKYPALNVTMPNNEQFDKLYIWGVHHPGTDKD
QIFLYAQASGRITVSTKRSQQTVSPNIGSRPRVRNIPSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGK
SSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/Victoria/361/2011 (H3N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGATLCLGHHAVPNGTIVKTITNDQIEVTNATEL
VQNSSIGEICDSPHQILDGENCTLIDALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSG
TLEFNNESFNWTGVTQNGTSSACIRRSNNSFFSRLNWLTHLNFKYPALNVTMPNNEQFDKLYIWGVHHPGTDKD
QIFLYAQSSGRITVSTKRSQQAVIPNIGSRPRIRNIPSRISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGK
SSIMRSDAPIGKCNSECITPNGSIPNDKPFQNVNRITYGACPRYVKQSTLKLATGMRNVPEKQTRGIFGAIAGF
IENGWEGMVDGWYGFRHQNSEGRGQAADLKSTQAAIDQINGKLNRLIGKTNEKFHQIEKEFSEVEGRIQDLEKY
VEDTKIDLWSYNAELLVALENQHTIDLTDSEMNKLFEKTKKQLRENAEDMGNGCFKIYHKCDNACIGSIRNGTY
DHDVYRDEALNNRFQIKGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLSTF
LGHHHHHH

>A/duck/Czechoslovakia/1956 (H4N6)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGPVICMGHHAVANGTMVKTLADDQVEVVTAQEL
VESQNLPELCPSPLRLVDGQTCDIINGALGSPGCDHLNGAEWDVFIERPNAVDTCYPFDVPEYQSLRSILANNG
KFEFIAEEFQWNTVKQNGKSGACKRANVNDFFNRLNWLVKSDGNAYPLQNLTKINNGDYARLYIWGVHHPSTDT
EQTNLYKNNPGRVTVSTKTSQTSVVPNIGSRPLVRGQSGRVSFYWTIVEPGDLIVFNTIGNLIAPRGHYKLNNQ
KKSTILNTAIPIGSCVSKCHTDKGSLSTTKPFQNISRIAVGDCPRYVKQGSLKLATGMRNIPEKASRGLFGAIA
GFIENGWQGLIDGWYGFRHQNAEGTGTAADLKSTQAAIDQINGKLNRLIEKTNDKYHQIEKEFEQVEGRIQDLE
KYVEDTKIDLWSYNAELLVALENQHTIDVTDSEMNKLFERVRRQLRENAEDKGNGCFEIFHKCDNNCIESIRNG

TYDHDIYRDEAINNRFQIQGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLS
TFLGHHHHHH

>A/Indonesia/05/2005 (H5N1)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDQICIGYHANNSTEQVDTIMEKNVTVTHAQDI
LEKTHNGKLCDLDGVKPLILRDCSVAGWLLGNPMCDEFINVPEWSYIVEKANPTNDLCYPGSFNDYEELKHLLS
RINHFEKIQIIPKSSWSDHEASSGVSSACPYLGSPSFFRNVVWLIKKNSTYPTIKKSYNNTNQEDLLVLWGIHH
PNDAAEQTRLYQNPTTYISIGTSTLNQRLVPKIATRSKVNGQSGRMEFFWTILKPNDAINFESNGNFIAPEYAY
KIVKKGDSAIMKSELEYGNCNTKCQTPMGAINSSMPFHNIHPLTIGECPKYVKSNRLVLATGLRNSPQRESRRK
KRGLFGAIAGFIEGGWQGMVDGWYGYHHSNEQGSGYAADKESTQKAIDGVTNKVNSIIDKMNTQFEAVGREFNN
LERRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDN
ECMESIRNGTYNYPQYSEEARLKREEISSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKD
GEWVLLSTFLGHHHHHH

>A/turkey/Massachusetts/3740/1965 (H6N2)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDKICIGYHANNSTTQVDTILEKNVTVTHSVEL
LESQKEERFCRVLNKTPLDLKGCTIEGWILGNPQCDILLGDQSWSYIVERPGAQNGICYPGVLNEVEELKAFIG
SGEKVQRFEMFPKSTWTGVDTNSGVTRACPYTTSGSSFYRNLLWIIKTRSAAYPVIKGTYNNTGSQPILYFWGV
HHPPNTDEQNTLYGSGDRYVRMGTESMNFAKSPEIAARPAVNGQRGRIDYYWSVLKPGETLNVESNGNLIAPWY
AYKFTSSNNKGAIFKSNLPIENCDAVCQTVAGALKTNKTFQNVSPLWIGECPKYVKSESLRLATGLRNVPQAET
RGLFGAIAGFIEGGWTGMIDGWYGYHHENSQGSGYAADKESTQKAIDGITNKVNSIIDKMNTQFEAVEHEFSNL
ERRIDNLNKRMEDGFLDVWTYNAELLVLLENERTLDLHDANVKNLYEKVKSQLRDNAKDLGNGCFEFWHKCDDE
CINSVKNGTYDYPKYQDESKLNRQEIDSVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRK
DGEWVLLSTFLGHHHHHH

>A/Netherlands/219/2003 (H7N7)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDKICLGHHAVSNGTKVNTLTERGVEVVNATET
VERTNVPRICSKGKRTVDLGQCGLLGTITGPPQCDQFLEFSADLIIERREGSDVCYPGKFVNEEALRQILRESG
GIDKETMGFTYSGIRTNGTTSACRRSGSSFYAEMKWLLSNTDNAAFPQMTKSYKNTRKDPALIIWGIHHSGSTT
EQTKLYGSGNKLITVGSSNYQQSFVPSPGARPQVNGQSGRIDFHWLILNPNDTVTFSFNGAFIALDRASFLRGK
SMGIQSEVQVDANCEGDCYHSGGTIISNLPFQNINSRAVGKCPRYVKQESLLLATGMKNVPEIPKRRRRGLFGA
IAGFIENGWEGLIDGWYGFRHQNAQGEGTAADYKSTQSAIDQITGKLNRLIEKTNQQFELIDNEFTEVERQIGN
VINWTRDSMTEVWSYNAELLVAMENQHTIDLADSEMNKLYERVKRQLRENAEEDGTGCFEIFHKCDDDCMASIR
NNTYDHSKYREEAIQNRIQIDPVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVL
LSTFLGHHHHHH

>A/chicken/Germany/N/1949 (H10N7)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDRICLGHHAVANGTIVKTLTNEQEEVTNATET
VESTNLNKLCMKGRSYKDLGNCHPVGMLIGTPVCDPHLTGTWDTLIERENAIAHCYPGATINEEALRQKIMESG
GISKMSTGFTYGSSINSAGTTKACMRNGGDSFYAELKWLVSKTKGQNFPQTTNTYRNTDTAEHLIIWGIHHPSS
TQEKNDLYGTQSLSISVESSTYQNNFVPVVGARPQVNGQSGRIDFHWTLVQPGDNITFSHNGGLIAPSRVSKLT
GRGLGIQSEALIDNSCESKCFWRGGSINTKLPFQNLSPRTVGQCPKYVNQRSLLLATGMRNVPEVVQGRGLFGA
IAGFIENGWEGMVDGWYGFRHQNAQGTGQAADYKSTQAAIDQITGKLNRLIEKTNTEFESIESEFSETEHQIGN
VINWTKDSITDIWTYQAELLVAMENQHTIDMADSEMLNLYERVRKQLRQNAEEDGKGCFEIYHTCDDSCMESIR
NNTYDHSQYREEALLNRLNINSVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVL
LSTFLGHHHHHH

>A/duck/Alberta/60/1976 (H12N5)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDKICIGYQTNNSTETVNTLSEQNVPVTQVEEL
VHGGIDPILCGTELGSPLVLDDCSLEGLILGNPKCDLYLNGREWSYIVERPKEMEGVCYPGSIENQEELRSLFS
SIKKYERVKMFDFTKWNVTYTGTSKACNNTSNQGSFYRSMRWLTLKSGQFPVQTDEYKNTRDSDIVFTWAIHHP
PTSDEQVKLYKNPDTLSSVTTDEINRSFKPNIGPRPLVRGQQGRMDYYWAVLKPGQTVKIQTNGNLIAPEYGHL
ITGKSHGRILKNNLPMGQCVTECQLNEGVMNTSKPFQNTSKHYIGKCPKYIPSGSLKLAIGLRNVPQVQDRGLF
GAIAGFIEGGWPGLVAGWYGFQHQNAEGTGIAADRDSTQRAIDNMQNKLNNVIDKMNKQFEVVNHEFSEVESRI

NMINSKIDDQITDIWAYNAELLVLLENQKTLDEHDANVRNLHDRVRRVLRENAIDTGDGCFEILHKCDNNCMDT
IRNGTYNHKEYEEESKIERQKVNGVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEW
VLLSTFLGHHHHHH

>A/gull/Maryland/704/1977 (H13N6)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDRICVGYLSTNSSERVDTLLENGVPVTSSIDL
IETNHTGTYCSLNGVSPVHLGDCSFEGWIVGNPACTSNFGIREWSYLIEDPAAPHGLCYPGELNNNGELRHLFS
GIRSFSRTELIPPTSWGEVLDGTTSACRDNTGTNSFYRNLVWFIKKNNRYPVISKTYNNTTGRDVLVLWGIHHP
VSVDETKTLYVNSDPYTLVSTKSWSEKYKLETGVRPGYNGQRSWMKIYWSLIHPGEMITFESNGGFLAPRYGYI
IEEYGKGRIFQSRIRMSRCNTKCQTSVGGINTNRTFQNIDKNALGDCPKYIKSGQLKLATGLRNVPAISNRGLF
GAIAGFIEGGWPGLINGWYGFQHQNEQGTGIAADKESTQKAIDQITTKINNIIDKMNGNYDSIRGEFNQVEKRI
NMLADRIDDAVTDIWSYNAKLLVLLENDKTLDMHDANVKNLHEQVRRELKDNAIDEGNGCFELLHKCNDSCMET
IRNGTYDHTEYAEESKLKRQEIDGISGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEW
VLLSTFLGHHHHHH

>A/mallard duck/Astrakhan/263/1982 (H14N5)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGPIICLGHHAVENGTSVKTLTDNHVEVVSAKEL
VETNHTDELCPSPLKLVDGQDCDLINGALGSPGCDRLQDTTWDVFIERPTAVDTCYPFDVPDYQSLRSILASSG
SLEFIAEQFTWNGVKVDGSSSACLRGGRNSFFSRLNWLTKATNGNYGPINVTKENTGSYVRLYLWGVHHPSSDN
EQTDLYKVATGRVTVSTRSDQISIVPNIGSRPRVRNQSGRISIYWTLVNPGDSIIFNSIGNLIAPRGHYKISKS
TKSTVLKSDKRIGSCTSPCLTDKGSIQSDKPFQNVSRIAIGNCPKYVKQGSLMLATGMRNIPGKQAKGLFGAIA
GFIENGWQGLIDGWYGFRHQNAEGTGTAADLKSTQAAIDQINGKLNRLIEKTNEKYHQIEKEFEQVEGRIQDLE
KYVEDTKIDLWSYNAELLVALENQHTIDVTDSEMNKLFERVRRQLRENAEDQGNGCFEIFHQCDNNCIESIRNG
TYDHNIYRDEAINNRIKINPVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVLLS
TFLGHHHHHH

>A/shearwater/West Australia/2576/1979 (H15N8)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDKICLGHHAVANGTKVNTLTERGVEVVNATET
VEITGIDKVCTKGKKAVDLGSCGILGTIIGPPQCDLHLEFKADLIIERRNSSDICYPGRFTNEEALRQIIRESG
GIDKESMGFRYSGIRTDGATSACKRTVSSFYSEMKWLSSSMNNQVFPQLNQTYRNTRKEPALIVWGVHHSSSLD
EQNKLYGTGNKLITVGSSKYQQSFSPSPGARPKVNGQAGRIDFHWMLLDPGDTVTFTFNGAFIAPDRATFLRSN
APSGIEYNGKSLGIQSDAQIDESCEGECFYSGGTINSPLPFQNIDSRAVGKCPRYVKQSSLPLALGMKNVPEKI
RTRGLFGAIAGFIENGWEGLIDGWYGFRHQNAQGQGTAADYKSTQAAIDQITGKLNRLIEKTNKQFELIDNEFT
EVEQQIGNVINWTRDSLTEIWSYNAELLVAMENQHTIDLADSEMNKLYERVRRQLRENAEEDGTGCFEIFHRCD
DQCMESIRNNTYNHTEYRQEALQNRIMINPVSGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYV
RKDGEWVLLSTFLGHHHHHH

>A/black-headed gull/Sweden/4/1999 (H16N3)
MVLVNQSHQGFNKEHTSKMVSAIVLYVLLAAAAHSAFAADPGDKICIGYLSNNSTDTVDTLTENGVPVTSSIDL
VETNHTGTYCSLNGVSPIHLGDCSFEGWIVGNPSCASNINIREWSYLIEDPNAPHKLCFPGEVDNNGELRHLFS
GVNSFSRTELIPPSKWGDILEGTTASCQNRGANSFYRNLIWLVNKLNKYPVVKGEYNNTTGRDVLVLWGIHHPD
TEATANKLYVNKNPYTLVSTKEWSRRYELEIGTRIGDGQRSWMKIYWHLMHPGERITFESSGGLLAPRYGYIIE
KYGTGRIFQSGVRLAKCNTKCQTSMGGINTNKTFQNIERNALGDCPKYIKSGQLKLATGLRNVPSIVERGLFGA
IAGFIEGGWPGLINGWYGFQHQNEQGTGIAADKTSTQKAINEITTKINNIIEKMNGNYDSIRGEFNQVEKRINM
IADRVDDAVTDIWSYNAKLLVLIENDRTLDLHDANVRNLHEQIKRALKDNAIDEGDGCFSILHKCNDSCMETIR
NGTYNHEDYKEESQLKRQEIEGISGGGGLNDIFEAQKIEWHERLVPRGSPGSGYIPEAPRDGQAYVRKDGEWVL
LSTFLGHHHHHH

Supplementary References

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