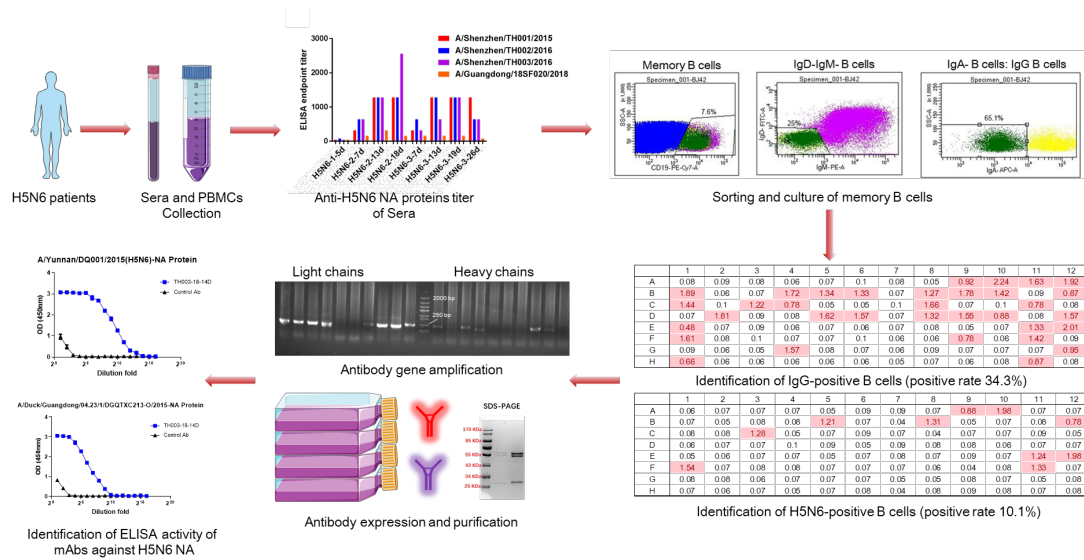


**A human monoclonal antibody targeting the monomeric N6 neuraminidase
confers protection against avian H5N6 influenza virus infection**

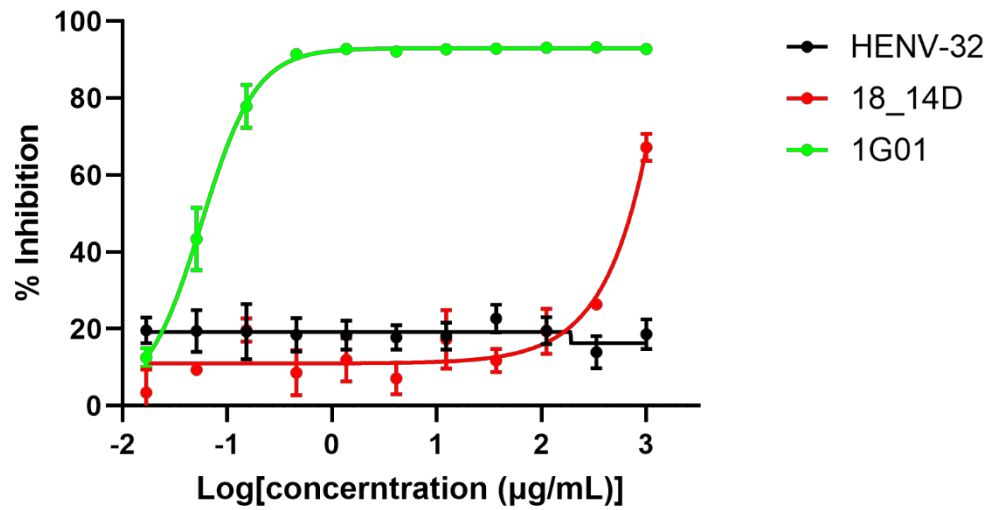
Min Wang, Yuan Gao, Chenguang Shen, Wei Yang, Qi Peng, Jinlong Cheng, Han-
Ming Shen, Yang Yang, George Fu Gao, Yi Shi

Supplementary Fig. 1-8

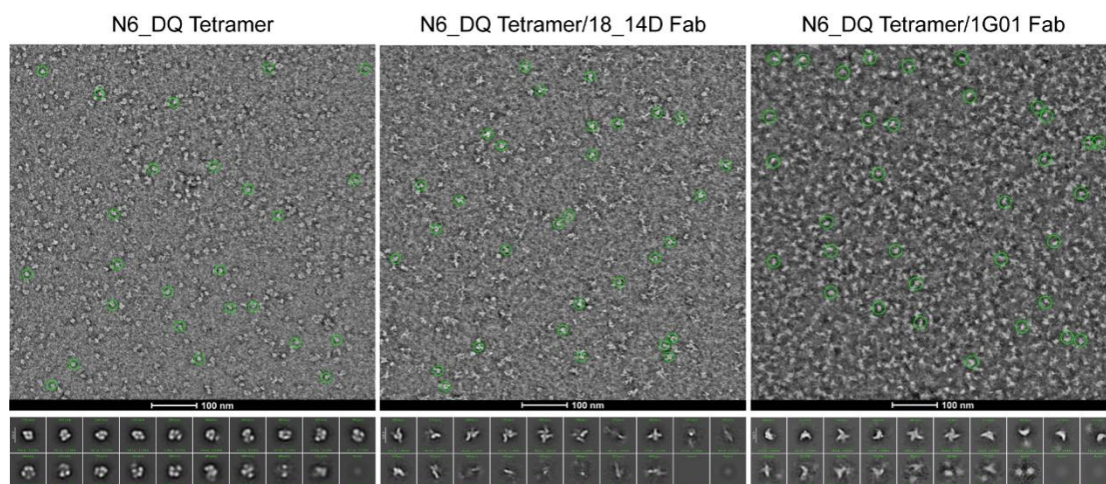
Supplementary Table. 1-5



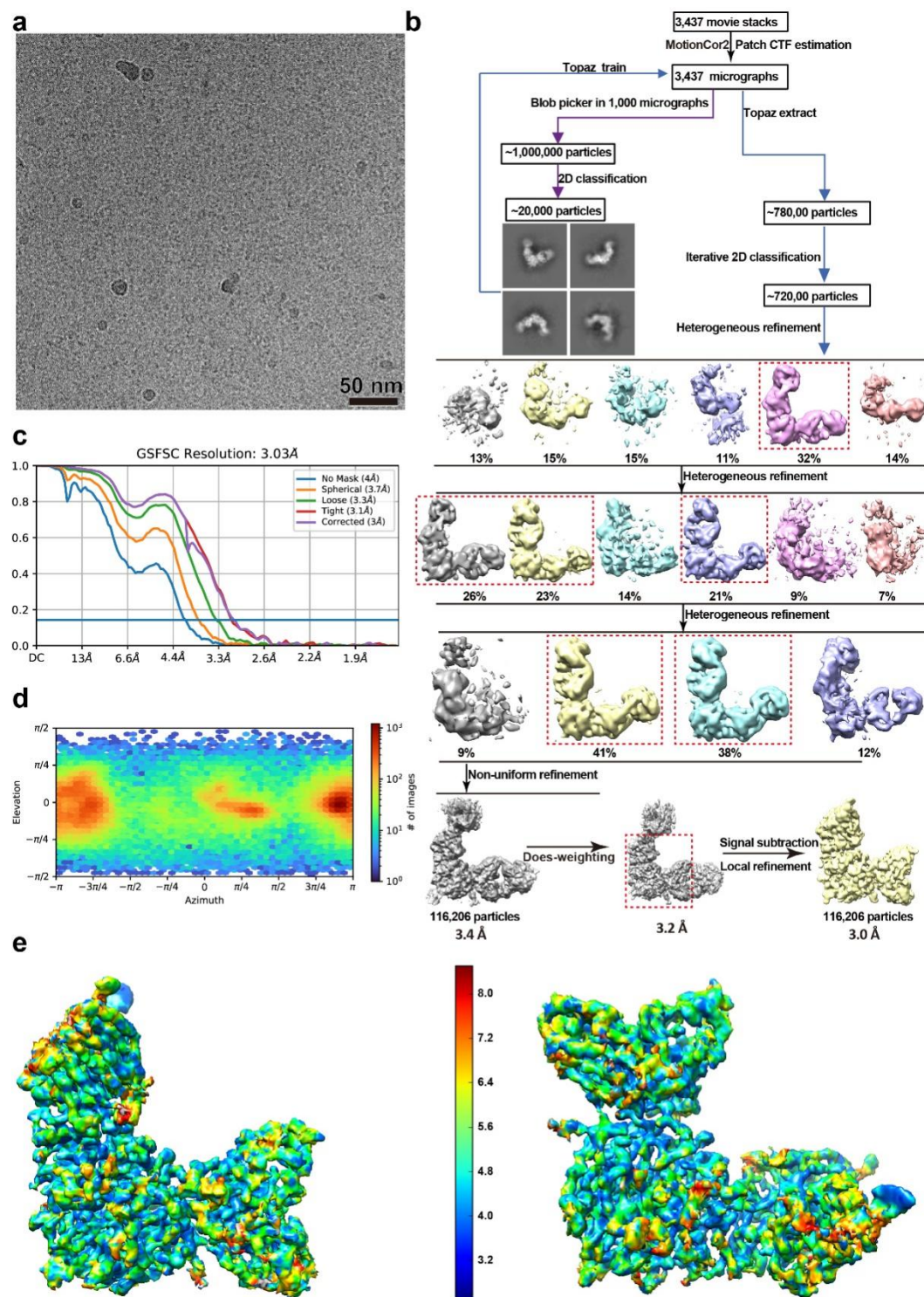
Supplementary Fig. 1 | Screening of H5N6 NA-specific human monoclonal antibody. PBMCs of H5N6 infected patient at 18 days post illness onset was collected, and CD19⁺IgM⁺IgA⁺IgD⁺ memory B cells were cultured in 96-well cell culture plates. The secretion of IgG and H5N6 HA or NA-specific antibodies in the supernatant of cultivated memory B cells were tested via ELISA method. The heavy chain and light chain coding genes of B cells in positive cell wells were amplified and cloned to the expression vector. After expression in 293T cells, the supernatants were used to measure the binding activity of antibodies to H5N6 HA and NA proteins.



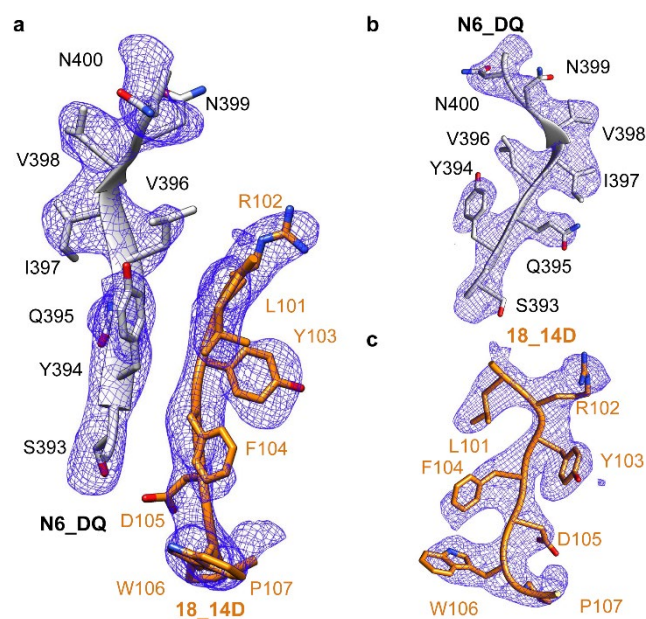
Supplementary Fig. 3 | Inhibition of the enzymatic activity of H5N6 virus by 18_14D measured in ELLA. Fetuin was used as substrate. Data represents one of three independent experiments, shown as mean $\pm$ SD of three technical replicates. 1G01¹ and HENV-32² were used as controls.



Supplementary Fig. 4 | Negative staining EM and 2D classifications of N6_DQ and N6-antibody complexes. Negative staining EM images and 2D classifications of N6_DQ Tetramer (left), N6_DQ Tetramer/18_14D Fab (middle) and N6_DQ Tetramer/1G01 Fab (right).



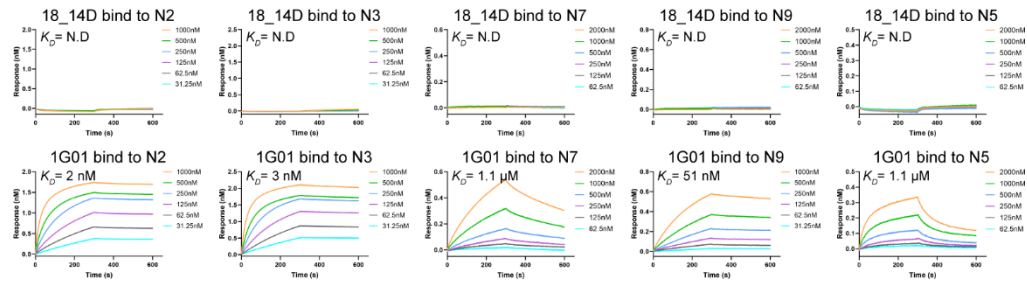
Supplementary Fig. 5 | Cryo-EM analysis of N6_DQ/18_14D/1G01. (a) A representative micrograph of N6_DQ/18_14D/1G01. (b) Image processing workflow of N6_DQ/18_14D/1G01. (c) FSC curves. (d) Euler angle distribution. (e) Local resolution distribution of N6_DQ/18_14D/1G01.



Supplementary Fig. 6 | Cryo-EM densities and atomic models. (a-c) Cryo-EM density map and atomic models of HCDR3 of 18_14D (colored in orange) and S393-N400 of N6_DQ (colored in light grey).

A/Yunnan/DQ001/2015 (H5N6)	1	MNPNQKI	T	CISATGV	TLSVSVLLIGIANLGLNIGLHYKV	S	D	S	T	T	T	N	I	P	N	M	N	S	T	N	P	T	T	...	
ken/Nanchang/7-010/2000 (H3N6)	1	MNPNQKI	T	CISATGM	TLSVSVLLIGIANLGLNIGLHYKV	G	D	T	P	D	V	N	I	P	N	M	N	D	T	N	S	T	T	I	
A/Yunnan/DQ001/2015 (H5N6)	58		T	N	I	T	N	I	I	V	N	K	N	E	R	T	F	L	N	L	T	K	F	L	C
ken/Nanchang/7-010/2000 (H3N6)	61	NNHTQNNF	T	N	I	T	N	I	I	V	N	K	N	E	K	G	T	F	L	N	L	T	K	F	L
A/Yunnan/DQ001/2015 (H5N6)	110	Y	L	S	C	D	P	Q	G	C	R	M	F	A	L	S	Q	G	T	T	L	R	G	R	H
ken/Nanchang/7-010/2000 (H3N6)	121	Y	L	S	C	D	P	Q	G	C	R	M	F	A	L	S	Q	G	T	T	L	R	G	R	H
A/Yunnan/DQ001/2015 (H5N6)	170	S	T	S	C	H	D	G	I	S	R	M	S	I	C	T	S	G	P	N	N	N	A	S	
ken/Nanchang/7-010/2000 (H3N6)	181	S	T	S	C	H	D	G	I	S	R	M	S	I	C	M	S	G	P	N	N	N	A	S	
A/Yunnan/DQ001/2015 (H5N6)	230	V	M	T	D	G	P	A	N	N	K	A	A	T	K	I	I	Y	F	K	E	G	K	I	
ken/Nanchang/7-010/2000 (H3N6)	241	V	M	T	D	G	P	A	N	N	R	A	A	T	K	I	I	Y	F	K	E	G	K	I	
A/Yunnan/DQ001/2015 (H5N6)	290	R	P	I	T	I	D	P	E	M	M	T	H	T	S	K	Y	L	C	S	K	I	L	T	
ken/Nanchang/7-010/2000 (H3N6)	301	R	P	V	I	T	I	D	P	E	M	M	T	H	T	S	K	Y	L	C	S	K	I	L	
A/Yunnan/DQ001/2015 (H5N6)	350	S	W	L	G	R	T	I	S	K	D	S	R	S	G	Y	E	M	L	K	V	P	N	A	
ken/Nanchang/7-010/2000 (H3N6)	361	S	W	L	G	R	T	I	S	K	D	S	R	S	G	Y	E	M	L	K	V	P	N	A	
A/Yunnan/DQ001/2015 (H5N6)	410	N	P	C	F	Y	V	E	L	I	R	G	R	P	K	E	I	D	V	L	W	A	S		
ken/Nanchang/7-010/2000 (H3N6)	421	N	P	C	F	Y	V	E	L	I	R	G	R	P	K	E	S	S	V	L	W	T	S		

Supplementary Fig. 7 | Sequence alignment of NA proteins from A/Yunan/DQ001/2016 (H5N6) and A/Chicken/Nanchang/7-010/2000 (H3N6). Residues of 392, 394 and 396 of N6 were labeled with blue circles.



Supplementary Fig. 8 | Binding affinities of 18_14D and 1G01 Fabs to different NAs. N.D. represents not detected.

Supplementary Table. 1 Summary of antibody genes in the ELISA positive cell well for N6.

Cell wells	Germline	Amino Acid Sequence	CDR Analysis
TH003-18-14D-H1	IGHV3-53*01	QVQLVQSGGGLIQPGGSLRLSCAASGFTVSSNYMS WVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCARDLEGYYD SSGPPGYYYYGMDVWGQGTITVTVSS	GFTVSSNY....__IYSGG ST...__ARDLEGYYDSS GPPGYYYYGMDV
TH003-18-14D-H2	IGHV1-69*01	QVQLVQSGAEVKKPGSSVKVSKASGGTFSSYAIS WVRQAPQGGLWMMGGIPIFGTANYAQKFQGRVTI TAEDESTSTAYMELSSLRSEDVAVYYCARGQLRYFD WPTIPSSYYGMDVWGQGTITVTVSS	GGTFSSYA....__IPIFG TA..__ARGQLRYFDWP TIPSSYYGMDV
TH003-18-14D-κ1	IGKV3-15*01	DIQLTQSPATLSVSPGERATLSCRASQSVSSNLAWY QQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEFT LTISLQSEDFAVYYCQQYRTFGQGTKVEIK QSVLTQPASVSGSPGQSITISCTGTSSDVGGYNYVS	QSVSSN.....__GAS..... __QQYRT
TH003-18-14D-λ1	IGLV2-14*04	WYQQHPGKAPKLMYDVSKRPSGVSNRFGSGSKSG NTASLTISGLQAEDEADYYCSSYTSSSTWVFGGGT KLTVL	SSDVGGYNY...__DVS..__SSYTSSSTWV
TH003-16-3D-H1	IGHV3-7*01	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYWM SWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGR FTISRDNANKNSLYLQMNSLRAEDTAVYYCAGGSS WWELLGNYYYYGMDVWGQGTITVTVSS	GFTFSSYW....__IKQDG SEK..__AGGSSWWELL LGNYYYYYGMDV
TH003-16-3D-κ1	IGKV1-9*01	DIQLTQSPSSLSASVGDRTITCRASQGISSYLAWY QQKAGKAPKLLIYAASLTQSGVPSRFSGSGSGTDFT LTISPPQPEDFATYYCQQLNSYPFTFGPGTKVDIK	QGISSY.....__AAS....._ __QQLNSYPFT
TH003-16-3D-κ2	IGKV3-20*01	DIQMTQSPGTLSLSPGERATLSCRASQSVSSSYLAW YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGADF TLTISRLEPEDFAVYYCQQYGSSPMYTFGQGTKLEI K PVCADAATLSVWDPRAEGHLLFWKQLQHRSNIV	QSVSSSY.....__GAS..... __QQYGSSPMYT
TH003-16-3D-λ1	IGLV1-44*01	NWYHQLPGTAPKLLIYSDSQRASGVDPDRFSASKSG TSASLAISGLQSKDESDYYCATWDSSLDGWVFGGG TKLTVV	QLQHRSLN....__SDS..... ..__ATWDSSLDGWV
TH003-11-15A-H1	IGHV3-48*02	EVDLVESGGGLVQPGGSLRLSCEASGFTLSRHSMN WVRQAPGKGLEWVSYISGSSSIMYHADPVKGRFTI SRDNANKNSLFLQMNSLRDEDTAVYYCARDTISIFG VISDAFDIWGQGTMTVTVSS	GFTLSRHS....__ISGSSS IM..__ARDTISIFGVISD AFDI
TH003-11-15A-H2	IGHV1-3*01	QVQLVQSGAGVKKPGASVKVSCMASGYNFKTYG MHWVRQAPQGGLWMMGWITAGNGNTKYSQKFQ	GYNFKTYG....__ITAG NGNT..__ARSGAAYS GSGSYYSYFFDY

GRVTISRATSANTAYLELRSLRSEDVAVYYCARSG
AAYSYGSGSYYSYFFDYWGQGILVTVSS

TH003-11- 15A-λ1	IGLV1- 44*01	SYELTQPPSASGTPGQGVITISCSGSSSNIGSNPVNW YQQLPGTAPTLIMYYNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYYCAAWDDSLDGVVFGGGT KLTVL	SSNIGSNP....__YNN..... .___AAWDDSLNGVV
TH003-4- 5D-H1	IGHV3- 23*04	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSHAMN WVRQAPGKGLEWVSSISGSGSTYYADSVDRFTI SRDNSKNTVYLQMNSLRAEDTAVYYCARDRVNY YGLEYYFDYWGQALVTVSS	GFTFSSHA....__ISGSG GST..__ARDRVNYGL EYYFDY
TH003-4- 5D-κ1	IGKV2D- 28*01	EIVLTQSPSLPVTGPASISCRSSQSLHNSGNFNLY DWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSG TDFTLKISRVEAEDVGYYCMQALQPLTFGGGKTK VEIK	QSLHNSGNFNLY.___LGS__MQALQPLT
TH003-4- 5D-κ2	IGKV1- 9*01	DIQLTQSPSSLSASVGDRVTITCRASQGISSYLAWY QQKAGKAPKLLIYAASLTQSGVPSRFSGSGSGTDFT LTISSLQPEDFATYYCQQYYRYPLTFGGGKTKVEIK	QGISSY.....__AAS....._ __QQYYRYPLT
TH003-14- H	IGHV3- 23*01	VPGSTGDQVQLVQSGGSLRLSCAASGFTFSSYAMS WVRQTPGKGLEWVSVISGSGSTYYADSVKGRITI SRDNSKNTLYLQMNSLRAEDTAVYYCAMEGSGSY FFDYWGQGTLLTVS	GFTFSSYA....__ISGSG GST..__AMEGSGSYFF DY
TH003-14- κ1	IGKV1D- 39*01	DIQMTQSPSSLSASVGDRVTITCRASQGISSYLNWY QQEPGKAPKLLVYGASNLQSGVPSRFSGSGSGTDFT TLTISSLQPEDFATYYCQQSYRTPIITFGQGTLL	QGISSY.....__GAS....._ __QQSYRTPIIT
TH003-1- 3A-H	IGHV157	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMS WVRQAPGKGLEWVSAISGSGSTYYADSVKGRFTI SRDNSKNTLYLQMNSLRAEDTAVYYCAKDPLWIA VA	GFTFSSYA....__ISGSG GST..__AKDPLWIAVA
TH003-1- 3A-λ1	IGLV1- 36*01	PSVSEAPRQRTISCSGSSSNIGNNAVNWYQQLPGK APKLLIYYDDLPSGVSDRFSGSKSGTSASLAISGLQ SEDEADYYCAARDDSLNGVLFGGGTKLTVL	SSNIGNNA....__YDD.... ...__AARDDSLNGVL
TH003-2- H	IGHV1- 2*02	QVQLVQSGAEVKKPGASVKVSCQASGYTFTGYFL HWVRQAPGQGLEWMGRINPNSGGTNYAQKFQGR VTMTRDTSISTVYMDLSRLRSDDTAVYYCARERY GWGVVAGPLGHYGMDEVWGQGTITVTVSS	GYTFTGYF....__INPNS GGT..__ARERYGWGV VAGPLGHYGMDEV
TH003-2- λ1	IGLV1- 40*01	QSVLTQPPSVSGAPQRVTISCTGSTSNIGTTFDVH WYQQLPGTAPKLLIYANNARPSGVPDRFSGSKSGT SASLAITGLQAEDEGDYFCQCYDSSLGGHYVFGSG TKVTVL	TSNIGTTFD...__ANN.... ...__QCYDSSLGGHYV

TH003-22- H	IGHV5- 51*01	QVQLVQSGAEVKKPGESLKISCKTSGYDFTNYWIG WVRQTPGKGLEWMGFIYPDDSDTRYNPSFRGQVTI SADRSIRIAYLQWSSLKASDTAMYYCVRDRGYTHP GRGHFDYWGQGTLSVSVSS	GYDFTNYW....__IYPD DSDT..__VRDRGYTHP GRGHFDY
TH003-22- κ1	IGKV3- 15*01	DIQMTQSPATLSVSPGERATLSCRASQSVSSNLAW YQQKPGQAPRLLIYGASTRATGIPARFSGSGSGTEF TLTISSLQSEDFAVYYCQQYRTFGQG	QSVSSN.....__GAS..... __QQYRT
TH003-34- H	IGHV3- 74*01	QVQLVQSGGGLVQPGGSLRLSCAASGLTFSDYWM HWVRQVPGKGLVWVSTINGDASATFYPSVKGRF TISRDNAKNTVYLQMNSLRAEDTAVYYCGTVFNN WGQGTSLTVTVSS	GLTFSDYW....__INGD ASAT..__GTVFNN
TH003-34- λ1	IGLV10- 54*01	QSVLTQPPSVSKGLGQTATFTCTGNNNNVGNQGAS WLQQHQGHPPKLLSYRNDNRPSGISERFSASRSGST ASLTITGLQPEDEADYYCSAWDTSLNAVLFGGGTK LTVL	NNNVGNQG....__RND..__SAWDTSLNAVL

Supplementary Table. 2 Binding of different paired antibodies to the HA and NA proteins.

ELISA Values (OD 450)				
Abs	Antigens			
	H5_DG (H5N6)	N6_DG (H5N6)	H5_TH002 (H5N6)	N6_DQ (H5N6)
TH003-18-14D-H2+ λ 1	0.182	3.215	0.089	3.095
TH003-18-14D-H2+ κ 1	0.168	0.189	0.124	0.088
TH003-18-14D-H2+ λ 1	0.105	0.122	0.105	0.114
TH003-18-14D-H2+ κ 1	0.107	0.089	0.121	0.092
TH003-16-3D-H1+ κ 1	0.089	0.105	0.099	0.12
TH003-16-3D-H1+ κ 2	0.089	0.121	0.114	0.147
TH003-16-3D-H1+ λ 1	0.121	0.103	0.091	0.104
TH003-11-15A-H1+ λ 1	0.086	0.124	0.078	0.081
TH003-11-15A-H2+ λ 1	0.132	0.114	0.079	0.104
TH003-4-5D-H1+ κ 1	0.114	0.107	0.147	0.112
TH003-4-5D-H1+ κ 2	0.089	0.075	0.112	0.079
TH003-1-3A-H+ λ 1	0.121	0.094	0.085	0.113
TH003-2-H+ λ 1	0.094	0.125	0.142	0.075
TH003-14-H+ κ 1	0.102	0.112	0.094	0.085
TH003-22-H+ κ 1	0.068	0.082	0.123	0.092
TH003-34-H+ λ 1	0.153	0.183	0.132	0.157
MEDI8852 (Anti-HA antibody) ⁹	1.342	0.089	1.201	0.072

Supplementary Table. 3 Cryo-EM data processing and refinement statistics for N6_DQ/18_14D/1G01 complex.

N6_DQ/18_14D/1G01	
Data collection and processing	
Microscope	Titan Krios
Detector	K2 subunit
Voltage (kV)	300
Electron exposure (e ⁻ /Å ²)	60
Defocus range (μm)	-1.5 to -3.0
Pixel size (Å)	0.82
Symmetry imposed	C1
Final particle images (no.)	116,206
Map resolution (Å)	3.0
FSC threshold	0.143
Refinement	
Initial model used (PDB code)	6Q23
Model resolution range (Å)	Up to 3.0
Map sharpening methods	DeepEMhancer (no B factor value)
Map correlation coefficient	
CC_Volume	0.75
CC_mask	0.74
Model composition	
Non-hydrogen atoms	6327
Protein residues	821
Ligands	CA:1
	NAG:2
R.m.s. deviations	
Bond lengths (Å)	0.005
Bond angles (°)	0.695
Validation	
MolProbity score	2.10
Clashscore	11.39
Poor rotamers (%)	1.31
Ramachandran plot	
Favored (%)	93.17
Allowed (%)	6.34
Disallowed (%)	0.50

Supplementary Table. 4 Interactions between 18-14D and N6_DQ

		18_14D	Contacts ^a	N6_DQ
Light	LCDR1	Y34	6	S457
Chain	LCDR2	S58	2	Q401
		G27	3,1	N330, K369
		T28	8,8	N330, K369
	HCDR1	S30	1,2	R365, I367
		S31	2,3,6	I367, E376, Y394
		Y32	5	N400
	HCDR2	I54	1,2,2	R365, L378, Y394
		F55	1,8,10,1,7	L378, P391, T392, S393, Y394
	FR3	G74	1	N330
Heavy		Q100	1,1,4,1	I367, Y394, L396, N400
Chain		L101	5,4	Y394, L396
		R102	6,4,8,10	Y394, Q395, L396, W460
		Y103	10,4,22,8	Y394, L455, G456, S457
	HCDR3	F104	2,6,14,1	T392, S393, Y394, L455
		D105	5,5,1	S393, R454, L455
		W106	2	T392
		P107	8	R454
		T108	4,1,1	L455, G456, W458

^a. Numbers represent the number of atom to atom contacts between 18_14D residues and N6_DQ residues, which were analyzed by the Contact program in CCP4 suite (the distance cutoff is 4.5 angstroms).

Supplementary Table. 5 Conservation analysis of 18_14D binding epitope residues.

18_14D binding epitope residues	H3N6 (332)	H4N6 (1810)	H5N6 (2275)	H5N6 2.3.4.4b (406)	other H5N6s (1869)	H6N6 (1024)	H7N6 (99)	H13N6 (252)	Other N6s (165)
N330	N:307,92.47% T:20,6.02% Others:5,1.51%	N:1680,92.82% Others:130,7.18%	N:2260,99.34% Others:15,0.66%			N:1021,99.71% Others:3,0.29%	N:70,70.71% L:25,25.25% Others:4,4.04%	N:234,92.86% S:17,6.75% L:1,0.40%	N:159,96.36% Others: 6,3.64%
R365	R:332,100%	R:1809,99.94% K:1,0.06%	R:2274,99.96% Others:1,0.04%			R:1021,99.71% Others:3,0.29%	R:99,100%	R:252,100%	R:165,100%
I367	I:328,98.80% V:4,1.20%	I:1777,98.18% Others:33,1.82%	I:2138,93.98% Others:37,1.63%			I:1020,99.61% Others:4,0.39%	I:99,100%	I:252,100%	I:162,98.18% T:3,1.82%
K369	K:330,99.40% R:2,0.60%	K:1807,99.89% Others:3,0.11%	K:2267,99.65% Others:8,0.35%			K:916,89.45% R:108,10.55%	K:99,100%	K:252,100%	K:165,100%
E376	E:357,100%	E:1810,100%	E:2275,100%			E:1023,99.90% V:1,0.10%	E:99,100%	E:252,100%	E:165,100%
L378	L:332,100%	L:1808,99.89% Others:2,0.11%	L:2272,99.87% Others:3,0.13%			L:1023,99.90% V:1,0.10%	L:99,100%	L:247,98.02% I:5,1.98%	L:165,100%
P391	P:331,99.7% A:1,0.3%	P:1801,99.50% Others:9,0.50%	P:2097,92.18% A:172,7.56% Others:6,0.26%			P:691,67.48% A:310,30.27% Others:23,2.25%	P:99,100%	P:252,100%	P:159,96.36% A:6,3.64%
T392	V:188,56.63% T:89,26.81% I:55,16.57%	V:1085,59.94% T:502,27.73% I:219,12.10% Others:4,0.22%	I:1357,59.65% T:870,38.24% Others:48,2.11%			I:730,71.29% T:267,26.07% Others:27,2.64%	V:53,53.54% T:36,36.36% I:10,10.10%	I:195,77.38% V:45,17.86% T:11,4.37% S:1,0.4%	T:77,46.67% V:59,35.76% I:29,17.58%
S393	A:210,63.25% S:120,36.14% E:2,0.60%	A:1122,61.99% S:678,37.46% Others:10,0.55%	S:2248,98.81% Others:27,1.19%			S:936,91.41% Others:88,8.59%	A:52,52.53% S:47,47.47%	A:232,92.06% S:15,5.95% T:5,1.98%	S:96,58.18% A:67,40.61% Others:2,1.21%
Y394	H:311,93.67% Y:20,6.02% N:1,0.30%	H:1800,99.45% Others:10,0.55%	Y:1915,84.18% H:341,14.99% Others:19,0.84%	H:319,78.57% Y:87,21.43%	Y:1828,97.81% H:22,1.18% Others:19,1.02%	Y:657,64.16% H:361,35.25% Others:6,0.59%	H:89,89.90% Y:10,10.10%	H:241,95.63% N:11,4.37%	H:111,67.27% Y:46,27.88% N:8,4.85%
Q395	Q:332,100%	Q:1810,100%	Q:2274,99.96% L:1,0.04%			Q:1021,99.71% Others:3,0.29%	Q:99,100%	Q:252,100%	Q:165,100%
L396	V:279,84.04% I:33,9.94% L:16,4.82% Others: 4,1.20%	V:1668,92.15% Others:142,7.85%	L:1910,83.96% I:302,13.27% Others:63,2.77%	I:296,72.91% L:91,22.41% V:10,2.46% Others:9,2.22%	L:1819,97.32% I:6,0.32% Others:44,2.35%	L:401,39.16% M:243,23.73% T:209,20.41% L:125,12.21% V:46,4.49%	V:91,91.92% L:5,5.05% I:3,3.03%	V:250,99.21% Others:2,0.79%	V:102,61.82% L:44,26.67% I:15,9.09% Others:4,2.42%
N400	N:332,100%	N:1805,99.72% Others:5,0.28%	N:2273,99.91% Others:2,0.09%			N:1020,99.61% Others:4,0.39%	N:99,100%	N:246,100%	N:153,92.73% I:12,7.27%
Q401	Q:331,99.70% L:1,0.3%	Q:1799,99.40% Others:11,0.60%	Q:2161,94.99% P:110,4.84% Others:4,0.18%			Q:984,96.09% L:36,3.52% Others:4,0.39%	Q:71,71.72% L:26,26.26% P:2,2.02%	Q:251,99.60% Others:1,0.4%	Q:164,99.39% Others:1,0.61%
R454	R:332,100%	R:1803,99.61% Q:7,0.39%	R:2198,96.62% Q:72,3.16% Others:5,0.22%			R:1023,99.90% Others:1,0.10%	R:99,100%	R:252,100%	R:165,100%
L455	L:332,100%	L:1810,100%	L:2274,99.96% Others:1,0.04%			L:1024,100%	L:99,100%	L:252,100%	L:165,100%
G456	G:332,100%	G:1810,100%	G:2274,99.96% Others:1,0.04%			G:1024,100%	G:99,100%	G:252,100%	G:165,100%
S457	S:332,100%	S:1810,100%	S:2274,99.96% Others:1,0.04%			S:1024,100%	S:99,100%	S:252,100%	S:165,100%
W458	W:332,100%	W:1810,100%	W:2273,99.91% Others:2,0.09%			W:1024,100%	W:99,100%	W:252,100%	W:165,100%
W460	W:332,100%	W:1800,99.45% Others:10,0.55%	W:2273,99.91% Others:2,0.09%			W:1023,99.90% Others:1,0.10%	W:99,100%	W:252,100%	W:165,100%

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