Supporting information for: Selective inhibitors of Human Neuraminidase-3

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Protein expression

Optimized Neu3 and Neu4 genes were synthesized and subcloned into vector pMAL-c2x in DNA2.0. The plasmids of MBP-Neu3 and MBP-Neu4 were transformed into expression cells, *E. coli* TB1. Protein was isolated by culturing *E. coli* TB1 cells containing plasmid pMBP-*Neu3* or *Neu4* in LB medium containing 0.2% glucose and ampicillin (100 μ g/mL). The culture was grown at 30 °C with shaking until the OD₆₀₀ reached 0.3. The temperature was decreased to 20 °C, and fusion protein was induced by adding IPTG to a final concentration of 0.3 mM when OD₆₀₀ reached 0.5-0.6. Cells were harvested by centrifugation after 20 h of induction. The pellet was resuspended (50 mL per liter of medium) in resuspension buffer (20 mM MOPS, pH 7.2, 300 mM NaCl, 1mM EDTA, 10% glycerol and 0.05% triton X-100) and supplemented with a protease inhibitor tablet (Roche). The lysate was passed through a cell disruptor once at 20,000 psi and then immediately pelleted by centrifugation at 105,000 x g for 60 min at 4 °C. The supernatant was loaded onto an amylose column (New England Biolabs) equilibrated with 20 mM MOPS (10% glycerol and 300 mM NaCl, pH 7.2). MBP-fusion protein was eluted with running buffer containing 10% glycerol (v/v) and 10 mM maltose.

Table S.1: HPLC Gradient elution used to check purity of inhibitors

Purity of compounds for enzymatic assay was tested by HPLC using a C18 reverse phase column (XTerra RP C18, analytical, particle size: 3.5 μ m, column dimensions: 4.8 × 150 mm). The gradient elution program was summarized below where solvent A was 0.1% trifluoroacetic acid in milliQ water and solvent B was 0.1% trifluoroacetic acid in acetonitrile. See Figure S.4 for HPLC traces.

Time	Flow rate (mL/min)	A%	B%
0	1	100	0
3	1	100	0
13	1	0	100
18	1	0	100

Compound	HPLC Trace		HRMS	
	Retention Time min	Area %	Calculated m/z	Found m/z
1(DANA)	1.657	98.70	290.0876	290.0879
2(C9-BA-DANA)	1.861	99.97%	373.1616	373.1614
6(Zanamivir)	1.939	99.78	333.1405	333.1400
7a	11.085	97.69	460.1832	460.1834
7b	12.302	99.92	474.1625	474.1636
7c	4.433	97.35	432.1529	432.1513
7d	13.240	98.94	431.1567	431.1568
7e	12.674	98.74	447.1516	447.1527
7f	12.834	96.36	435.1316	435.1324
7g	13.886	99.11	485.1284	485.1282
7h	12.200	99.05	461.1309	461.1316
7i	14.041	99.97	493.1723	493.1729
7j	14.027	98.49	509.1672	509.1674
8 a	12.307	97.04	502.1686	502.1683
8b	1.561	97.84	534.2101	534.2105
13	12.978	99.27	486.1373	486.1378
15	11.983	95.11	460.1468	460.1482
18	12.209	97.58	575.1738	575.1738
25a	3.100	99.05	345.1298	345.1302
25b	10.823	98.98	373.1611	373.1612
25c	1.805	98.52	357.1298	357.1305
25d	16.854	97.44	371.1454	371.1458

 Table S.2: Summary of HPLC and HRMS data for tested compounds

Figure S.1: Inhibition of human neuraminidase isoforms by tested compounds IC₅₀ curves using 4Mu-NANA as substrate

1(DANA)



2(C9-BA-DANA)



6(Zanamivir)



































Ŧ Ŧ

100-

Activity %











IC₅₀ curves using GM3 as substrate DANA with NEU3



DANA with NEU4





7i with NEU4















Figure S.3: NMR (¹H and ¹³C) spectra 1(DANA)

499.808 MHz H1 1D in CD3OD



1-OMe (DANA-OMe)

499.808 MHz H1 1D in D2O



34

2(C9-BA-DANA)

499.808 MHz H1 1D in CD3OD



2-OMe (C9-BA-DANA-OMe)

499.808 MHz H1 1D in CD3OD



36
6(Zanamivir)

499.808 MHz H1 1D in D2O



499.808 MHz H1 1D in CD₃OD -8.11 7.65 7.65 7.65 7.65 6.82











7b

7c

499.808 MHz H1 1D in CD3OD





499.808 MHz H1 1D in CD3OD 625---824 -2.34 <7.68 77.67 <7.23 соон нó 1.08 1.02 2.08-2.11-3.03ŝ .5 9.0 8.5 8.0 7.5 7.0 6.5 . 6.0 5.5 5.0 f1 (ppm) 4.5 4.0 3.5 . 3.0 2.5 2.0 1.5 1.0 0.



7e

499.808 MHz H1 1D in CD₃OD





7f







Ċ



125.691 MHz C13[H1] 1D in CD3OD



7g



499.808 MHz H1 1D in CD₃OD

20 210 200

(



125.691 MHz C13[H1] 1D in CD₃OD



499.808 MHz H1 1D in CD₃OD

7i-OMe



7i-OEt





7i-OPr





7i-OBu

699.765 MHz H1 1D in DMSO





125.691 MHz C13[H1] 1D in CD₃OD



499.808 MHz H1 1D in CD₃OD



8a



125.691 MHz C13[H1] 1D in CD₃OD



-1.98

499.808 MHz H1 1D in CD3OD

8b





499.808 MHz H1 1D in CD₃OD



499.808 MHz H1 1D in CD3OD







125.691 MHz C13[H1] DEPTq in CD₃OD









25b

499.808 MHz H1 1D in CD3OD







25c





499.808 MHz H1 1D in CD₃OD

Figure S.4: HPLC traces and LC-MS of esters 1(DANA)



	Retention Time	Area	% Area
1	0.992	106518	1.30
2	1.657	8078848	98.70

2(C9-BA-DANA)



	Retention Time	Area	% Area
1	1.864	25156549	99.97
2	11.514	7667	0.03





	Retention Time	Area	% Area
1	1.939	10488850	99.78
2	2.302	23638	0.22



	Retention Time	Area	% Area
1	11.085	1402254	97.69
2	13.703	7549	0.53
3	14.199	25646	1.79



1	11.515	17119	0.08
2	12.302	21018453	99.92



	Retention Time	Area	% Area
1	4.433	47355681	97.35
2	11.204	59740	0.12
3	11.591	798423	1.64
4	12.180	91828	0.19
5	12.554	43814	0.09
6	13.030	296047	0.61

7b







	Retention Time	Area	% Area
1	12.083	336719	1.26
2	12.674	26376013	98.74

7d



23226938

96.36



12.834

	Retention Time	Area	% Area
1	13.262	14442	0.07
2	13.459	30148	0.14
3	13.707	118468	0.55
4	13.886	21464337	99.11
5	14.257	29477	0.14



	Retention Time	Area	% Area
1	12.200	23946655	99.05
2	12.650	21704	0.09
3	13.335	59482	0.25
4	14.020	147588	0.61





	Retention Time	Area	% Area
1	13.366	6371	0.03
2	14.041	23867337	99.97

7h



2	13.888	32337	0.19
3	14.027	16503460	98.49

a



	Retention Time	Area	% Area
1	1.996	20928	2.96
2	12.307	686710	97.04



	Retention Time	Area	% Area
1	1.561	45407337	97.84
2	19.467	1016824	2.16



	Retention Time	Area	% Area
1	12.669	126606	0.73
2	12.978	17163838	99.27

8b



	Retention Time	Area	% Area
1	11.983	18920046	95.11
2	12.582	971880	4.89



	Retention Time	Area	% Area
1	1.535	34220	0.13
2	12.209	24814748	97.58
3	12.487	232178	0.91
4	12.698	298943	1.18
5	13.701	49206	0.19



	Retention Time	Area	% Area
1	2.716	257020	0.38
2	3.100	66909481	99.05
3	8.259	384493	0.57

25b



	Retention Time	Area	% Area
1	10.823	38232298	98.98
2	13.760	394274	1.02

25a



	Retention Time	Area	% Area
1	0.633	110356	0.34
2	0.819	372916	1.14
3	1.805	32192143	98.52

25d



	Retention Time	Area	% Area
1	9.799	737757	1.11
2	16.854	64505616	97.44
3	21.073	841157	1.27
4	27.164	118339	0.18

25c

LC-MS analysis of esters.

8.00

9.0

95.0

2.00

LC-MS Methods: Solvent A: 0.1%FA in H₂O Solvent B: 0.1%FA in ACN Flow=0.5mL/min First 0.3 mins: LC to waste Kinetex Luna Evo C18 Polar with guard, 2.1x50mm, 1.6um, 100Å, temperature 40°C Fragmentor: 150V DAD: 254nm Gradient: $\overline{\text{Time \%B}}$ 0.00 2.00 0.50 2.00 5.00 95.0
LC-MS results of DANA-OMe



Integration Peak List

Peak	Start	RT	End	Height	Area	Area %
1	0.79	0.86	1.04	1217.08	4634.97	100
2	1.61	1.67	1.76	0.85	3.74	0.08
3	1.88	1.97	2.17	1.41	6.5	0.14
4	2.28	2.4	2.59	2.28	11.28	0.24
5	3 50	3 73	3.81	1.27	5.76	0.13







Peak	Start	RT	End	Height	Area	Area %
1	0.75	0.86	1.33	19651359	190908482	100
2	1.55	1.68	1.84	365139	2259383	1.18
3	1.9	1.97	2.12	159857	885389	0.46
4	2.31	2.41	2.58	981508	5647166	2.96
5	2.71	2.75	2.8	398485	1459311	0.76
6	2.82	2.83	2.91	177032	516037	0.27
7	2.93	3.02	3.1	161134	710349	0.37
.8	3.13	3.18	3.29	50052	200265	0.1
9	3.67	3.73	3.84	256557	899922	0.47
10	6.57	6.65	6.78	549939	2092443	1.1

LC-MS results of DANA-OMe (continued)

Compound Table



210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 Counts vs. Mass-to-Charge (m/z)

LC-MS results of 2-OMe



LC-MS results of **5-OMe**





User Chromatogram Peak ListRTHeightHeight %2.0515.02100 RT Area Area % Area Sum % Width 100 50.61 100 100 0.05 **Ionization Mode** ESI Fragmentor Voltage 150 **Collision Energy** 0 x10 6 +ESI TIC Scan Frag=150.0V 16101405.d 5-. 2 06 4.5-4 3.5 3 2.5 2 1.5 1 0.5 0.6 0.8 1 12 1.4 1.6 1.8 2 22 2.4 2.6 2.8 3 3.2 3.4 3.6 3.8 4 4.2 4.4 4.6 4.8 5 5.2 5.4 5.6 5.8 6 6.2 6.4 6.6 6.8 7 7.2 7.4 7.6 7.8

Counts vs. Acquis

on Time (min)

User Chromatogram Peak List Area % Area Sum % Width DT

Ľ		rieigite	incigine /o		ra ca re		
ſ	2.06	3446556	100	15969380	100	100	0.3
2							

Compound Table							
Compound Label	RT	Mass	Abund	Formu	la	Tgt Mass	Diff (ppm)
Cpd 1: C15 H22 N4 O8	2.06	386.1432	21869	C15 H22 N4 O8		386.1438	-1.51
Compound Label	m/z	RT	Algorith	m	Mass		
Cpd 1: C15 H22 N4 O8	409.1333	2.06	Find By F	ormula	386.1432	2	



Counts vs. Acquis ion Time (min)

MS Spectrum



LC-MS results of 7i-OMe





Solvent blank for 7i-OEt, 7i-OPr, 7i-OBu

LC-MS results of 7i-OEt



User Chromatogram Peak List RT Height Height % 3.34 0 Area Area % Area Sum % Width 0.41 1.51 1.49 0.07 0 3.43 100 27.37 100 98.51 0.17 8.98 Collision Energy Fragmentor Voltage 0 Ionization Mode ESI 0 x10 6 +ESI TIC Scan 17041810.d 6.5 6-5.5-4.5-4-3.5-* 3.49 100.00 3-2.5-2-1.5-1 0.5 0-0.8 1 1.2 1.4 1.6 1.8 2 2.2 2.4 2.6 2.8 3 3.2 3.4 3.6 3.8 4 4.2 4.4 4.6 4.8 5 5.2 5.4 5.6 5.8 6 6.2 6.4 6.6 6.8 7 7.2 7.4

		Counts vs. Ac	quisition Time (min)	
User Chromatogram Peak List				
	1.0		TAXABLE TAXABLE	

RT	Height	Height %	Area	Area %	Area Sum %	Width
3 40	1891988	100	6750054	100	100	0.14

Compound	Table

Compound Label	RT	Mass	Abund	Formula	Tgt Mass	(ppm)
Cpd 3: C26 H28 N4 O7	3.38	508.1959	3737	C26 H28 N4 O7	508.1958	0.22
Cpd 2: C27 H30 N4 O7	3.51	522.21	309038	C27 H30 N4 O7	522.2114	-2.79

Compound Label	m/z	RT	Algorithm	Mass	
Cpd 3: C26 H28 N4 O7	509.2032	3.38	Find By Formula	508.1959	







LC-MS results of 7i-OPr



compound rubic	_						
Compound Label	RT	Mass	Abund	Formula		Tgt Mass	(ppm)
Cpd 3: C26 H28 N4 O7	3.35	508.1964	9659	C26 H28 N4 O7		508.1958	1.16
Cpd 2: C27 H30 N4 O7	3.48	522.2111	234	C27 H30 N4 O7		522.2114	-0.63
Cpd 1: C28 H32 N4 O7	3.62	536.2256	403346	C28 H32 N4 O7		536.2271	-2.86
Compound Label	m/z	RT	Algoriti	m	Mass		

Compound Label	m/z	RT	Algorithm	Mass	
Cpd 3: C26 H28 N4 O7	509.2038	3.35	Find By Formula	508.1964	

LC-MS results of 7i-OPr (continued)





LC-MS results of 7i-OBu



User Chromatogram Peak List

RT	Height	Height %	Area	Area %	Area Sum %	Width
3.27	0.84	1.32	4.67	2.41	2.34	0.15
3.59	0.19	0.3	1.16	0.6	0.58	0.14
3.69	63.87	100	193.51	100	97.08	0.2



User Chromatogram Peak List

RT	Height	Height %	Area	Area %	Area Sum %	Width
3.35	107239	2.01	307419	1.25	1.24	0.09
3.76	5327845	100	24545715	100	98.76	0.19

LC-MS results of 7i-OBu (continued)











LC-MS results of 8b-OMe (continued)

Compound Table Dif **Compound Label** RT Mass Abund Formula Tgt Mass (ppm) 549.2336 549.2324 386524 C27 H31 N7 O6 -2.14 Cpd 1: C27 H31 N7 O6 6.02 **Compound Label** m/z RT Algorithm Mass 549.2324 Find By Formula Cpd 1: C27 H31 N7 O6 275.6236 6.02 x10 6 Cpd 1: C27 H31 N7 O6: +ESI EIC(275.6241, 276.1255, 550.2409, 551.2438) Scan Frag=150.0V 16100714.... 5 6.02 4 3 2 1 5.55 7.79 0 4.5 5 5.5 Counts vs. Acquisition Time (min) 2.5 3 3.5 4 6 6.5 ż 7.5 MS Spectrum x10 5 Cpd 1: C27 H31 N7 O6: +ESI Scan (rt: 5.93-5.98, 6.07-6.17 min, 11 scans) Frag=150.0V 16100714.d Subtr... 550.2395 ([C27H31N7O6]+H)+ 5 275.6236 ([C27H31N7O6]+2H)+2 4 3 2 1 0

125 150 175 200 225 250 275 300 325 350 375 400 425 450 475 500 525 550 575 600 625 650 675 Counts vs. Mass-to-Charge (m/z)



Figure S.5: Starting structures for MD simulations of 8b with a) NEU2, b) NEU3, and c) NEU4. The inhibitors are shown with cyan carbons, and key active site residues are labeled.

	Neu2		Neu3		Neu4	
Cmpd	H-bond	Fraction Occupied	H-bond	Fraction Occupied	H-bond	Fraction Occupied
	$O7 \cdots H_2O^a$	56 %	$O7 - H_2O^a$	59 %	$O7 \cdots H_2O^a$	58 %
	$N11 \cdots H_2O^{a,c}$	35 %	$N11 \cdots H_2O^{a,c}$	29 %	$N11 \cdots H_2O^{a,c}$	19 %
	O7H O(N5Ac) ^b	40 %	O7H ··· E113	53 %	O7H … E111	70 %
8b	O8H ··· E218	53 %	O8H ··· E113	43 %	O8H E222	82 %
	O7	none	O7	none	O7 ··· Y179	< 1 %
	O8 ··· Y179	20 %	O8 ··· Y181	8 %	O8 ··· Y177	< 1 %
	N11 ··· R237 ^c	6 %	N10 ··· R245 ^c	5 %	N10 ··· G221 ^{c,d}	5 %

Table S.3: Most populated H-bonds to glycerol side chain during MD simulations.

^{*a*} H-bonds to solvent are indicated in italics.

^{*b*} Those in bold indicate intramolecular H-bonds.

^c Note that O9H and O9 have been replaced with a triazole. The atom listed indicates the most populated H-bond to a triazole nitrogen. See **Error! Reference source not found.** for atom numbers.

^{*d*} H-bond is to the backbone NH.

Table S.4: Key H-bonds to C4 substituent during MD simulations.

Neu2		Neu3		Neu4		
Cmpd	H-bond	Fraction Occupied	H-bond	Fraction Occupied	H-bond	Fraction Occupied
8b	$\begin{array}{l} Guanidine & H_2O^a \\ Guanidine & E39 \\ Guanidine & D46 \\ Guanidine & N86 \end{array}$	46 % 47 % 3 % 33 %	$\begin{array}{l} Guanidine & H_2O^a \\ Guanidine & E43 \\ Guanidine & D50 \\ Guanidine & N88 \end{array}$	41 % 92 % 27 % 50 %	$\begin{array}{l} Guanidine & H_2O^a\\ Guanidine & E41\\ Guanidine & D48\\ Guanidine & N86 \end{array}$	32 % 52 % 2 % 13 %

^{*a*} H-bonds to solvent are indicated in italics.

Table S.5: Most popula	ited water bridge	s between the	e inhibitor 8b	and enzyme	during MD
simulations.					

	Neu2	Neu3		Neu4		
Cmpd	Neu2 residues	Fraction Occupied	Neu3 residues	Fraction Occupied	Neu4 residues	Fraction Occupied
8b	E111 (glycerol) R237 (glycerol) R41 (C4) Q270 (triazole)	65 % 34 % 23 % 10 %	D50 (<i>C4</i>) R245 (glycerol) E113 (glycerol) H277 (triazole)	88 % 47 % 42 % 17 %	D48 (C4) E111 (glycerol) D48 & R83 (C4/N5Ac) R242 (glycerol)	64 % 55 % 32 % 27 %

^{*a*} The closest region of the inhibitor is indicated in parenthesis.

Test of the fluorescent properties of compounds screened. A solution of each compound (2.5 μ L; 4 mM), or of the sample combined with 4MU-NANA (2.5 μ L; 125 μ M), was diluted with water (15 μ L) and glycine buffer (100 μ L 0.2 M, pH 10.2) and transferred on 386-well plate. Fluorescence ($\lambda_{ex} = 365$ nm; $\lambda_{em} = 445$ nm) was detected by a plate reader (Molecular Devices, Sunnyvale CA). Compounds alone were not fluorescent, and no significant effects on the fluorescence of 4MU-NANA were observed.



Test of the NEU activity of HEK293E cells. The same amounts of Hek293E cells and a Lentivirus expressing Cathepsin A and Human neuraminidase 1(Cath-Neu1) with an N-terminal His6-tag transduced Hek293E cells were seeded in 10 cm² plates individually. After the cells reached confluence, they were washed 3 times with 1 mL of PBS and harvested in 300 μ L of PBS for each plate at the same density. The total harvested mixture was sonicated (10 seconds, 5 times at 60 Watt) on ice. Then lysis buffer (1 mM EDTA; 0.2 M NaCl; 20 mM MOPS; 0.1% Triton X-100. pH 7.2) was added, and left agitating for 1 hour on ice at 4°C. The neuraminidase activity of the crude cell lysate was determined with 50 μ M 4MU-NANA.