Supplementary Information

Identification of influenza polymerase inhibitors targeting C-terminal domain of

PA through surface plasmon resonance screening

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Supplementary Figure



Figure S1. MST study of compound 387 with PAC.



Figure S2. MST study of compound 392 with PAC.



Figure S3. MST study of compound S2a with PAC.



Figure S4. MST study of compound S2b with PAC.



Figure S5. MST study of compound S2d with PAC.



Figure S6. MST study of compound S2e with PAC.

H5N1 H1N1 H2N2 H3N2	257	IEPFLKTTPRPLRLPDGPPCSQRSKFLLMDALKLSIEDPSHEGE IEPFLKSTPRPLRLPDGPPCSQRSKFLLMDALKLSIEDPSHEGE IEPFLKTTPRPIRLPDGPPCSQRSKFLLMDALKLSIEDPSHEGE IEPFLKTTPRPIRLPDGPPCFQRSKFLLMDALKLSIEDPSHEGE *****:****
H5N1 H1N1 H2N2 H3N2	301	GIPLYDAIKCM&TFFGWEPNIKPHEKGINPNYLLWWKQVLAELQDIENEKKIPWTKNM GIPLYDAIKCMRTFFGWKEPNVVKPHEKGINPNYLLSWKQVLAELQDIENEEKIPRTKNM GIPLYDAIKCMRTFFGWKEPYVVKPHEKGINPNYLLSWKQVLAELQDIENEEKIPRTKNM SIPLYDAIKCMRTFFGWKEPYIVKPHEKGINPNYLLSWKQVLAELQDIENEEKIPRTKNM ************************************
H5N1 H1N1 H2N2 H3N2	361	KKTSQLWALGENMAPEKVDF DCKDIDDLKQY SDEPELRSLASWIQNEFNKACELTDS KKTSQLKWALGENMAPEKVDFDCCKDVGDLKQYDSDEPELRSLASWIQNEFNKACELTDS KKTSQLKWALGENMAPEKVDFDCCRDTSDLKQYDSDEPELRSLSSWIQNEFNKACELTDS KKTSQLKWALGENMAPEKVDFDNCRDVSDLKQYDSDEPELRSLSSWIQNEFNKACELTDS ****** ******************************
H5N1 H1N1 H2N2 H3N2	421	SWIELDEIGEDVAPIEHIASMRRNYFTAEVSHCRATEYIMKGVYINTALLNASCAAMDDF SWIELDEIGEDAAPIEHIASMRRNYFTAEVSHCRATEYIMKGVYINTALLNASCAAMDDF IWIELDEIGEDVAPIEHIASMRRNYFTAEVSHCRATEYIMKGVYINTALLNASCAAMDDF TWIELDEIGEDVAPIEYIASMRRNYFTAEVSHCRATEYIMKGVYINTALLNASCAAMDDF ***********************************
H5N1 H1N1 H2N2 H3N2	481	QLIPMISKCRTKEGRRETNLYGFIEKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWEKY QLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWEKY QLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRLEPHKWEKY ************************************
H5N1 H1N1 H2N2 H3N2	541	CVLEIG MLLR AIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAES CVLEVGDMLLRSAIGHVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAES CVLEIGDMLLRSAIGQVSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAES CVLEIGDMLLRSAIGQMSRPMFLYVRTNGTSKIKMKWGMEMRRCLLQSLQQIESMIEAES ****:*
H5N1 H1N1 H2N2 H3N2	601	SEKEKDMTKEFFENESETWPIGESPKGVEEGSIGKVCRTLLAKSVFNSLYESPQLEGFSA SVKEKDMTKEFFENKSETWPVGESPKGVEEGSIGKVCRTLLAKSVFNSLYASPQLEGFSA SVKEKDMTKEFFENKSETWPIGESPKGVEGSIGKVCRTLLAKSVFNSLYASPQLEGFSA SVKEKDMTKEFFENKSETWPIGESPKGVEDGSIGKVCRTLLAKSVFNSLYASPQLEGFSA *:************
H5N1 H1N1 H2N2 H3N2	661	ESRKLLLIVQALRDNLEPGTFDLEGLYAIEECLINDPWVLLNASWFNSFLTHALR ESRKLLLIVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHALR ESRKLLLVVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLTHALR ESRKLLLVVQALRDNLEPGTFDLEGLYEAIEECLINDPWVLLNASWFNSFLTHALR

Figure S7. Sequence alignment of A/WSN/33 (H1N1), A/Japan/305/1957 (H2N2), A/HK/1/68 (H3N2) and A/HK/156/97 (H5N1) PAC. Distinct residues of H5N1 PAC are highlighted in red.

Compound ID.	Chemical Structure	Compound ID.	Chemical Structure
57		265	
95		270	
123		271	

Supplementary Table 1. Chemical structure of hit compounds from SPR screening.







Supplementary Table2. Cytotoxicity of compounds							
		CC ₅₀ ^a (µM)					
	Compound	293Ta	MDCK				
	57	>50	N.D.				
	95	>25	N.D.				
	123	>50	N.D.				
	131	>50	N.D.				
	190	>100	N.D.				
	198	>5	N.D.				
	203	>100	N.D.				
Hit compounds	221	>100	>100				
from SPR	263	>100	N.D.				
screening	265	>100	N.D.				
	270	82.0 ± 2.5	N.D.				
	271	>100	N.D.				
	272	>100	N.D.				
	273	>100	N.D.				
	280	>100	N.D.				
	283	>10	>10				
	345	>100	N.D.				
	S1a	>100	N.D.				
	S1b	>100	>100				
A	S1c	>100	N.D.				
Analogues	S1d	>100	N.D.				
through	S2a	84.6 ± 17.30	>100				
chemical	S2b	>100	42.8 ± 9.0				
modification	S2c	97.1 ± 16.10	N.D.				
	S2d	66.6 ± 6.09	35.6 ± 9.24				
	S2e	>100	53.1 ± 9.25				
	S2f	>100	>100				
	310	>100	>100				
	312	>100	>100				
	384	>100	>100				
	385	>100	N.D.				
	387	>100	>100				
Commercially	389	>100	>100				
available	390	>100	N.D.				
analogs	391	>100	N.D.				
	392	62.66 ± 18.7	87.03 ± 7.22				
	394	>100	N.D.				
	395	>100	N.D.				
	396	>100	N.D.				
	397	>100	N.D.				

^a293T or MDCK cells were incubated with test compounds for 24 hrs; CC50 is the concentration of test compounds which produces 50% cytotoxicity as determined by MTT assays; N.D., not determined; reported values represent means \pm standard deviation of data from three independent experiments.