



Discovery of Antivirals Targeting Sars-CoV2 Viral Helicase

Viral helicase as a novel antiviral target

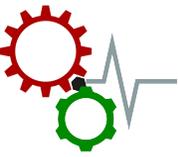
nsp8-a

nsp8-b

Antiviral Drug Discovery (AViDD) Open Science Forum
7/17/2024

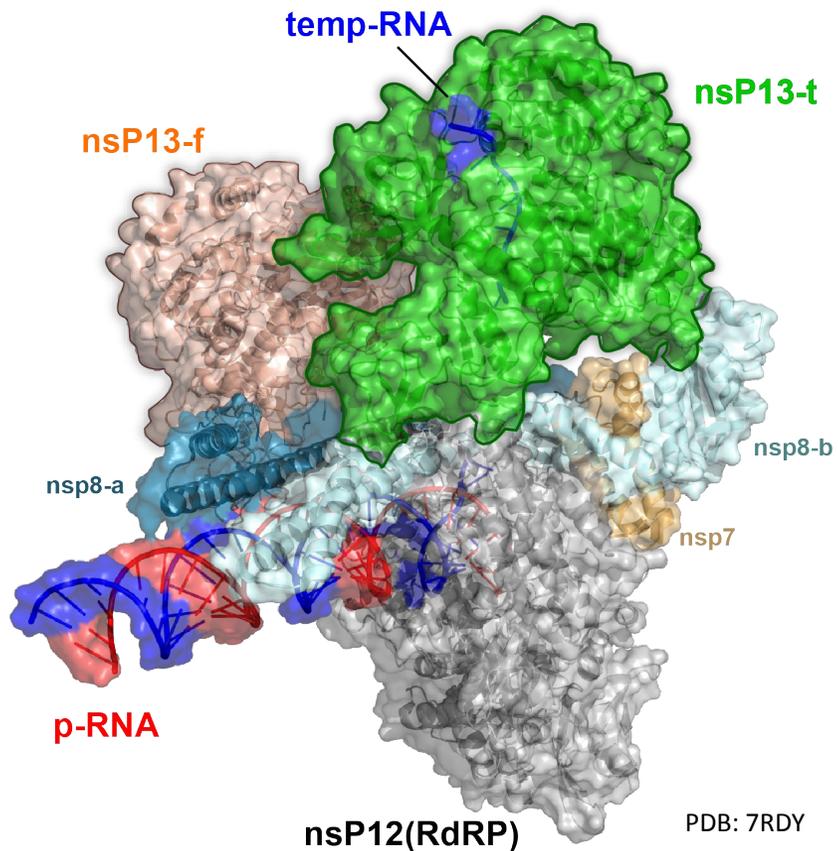
nsp7

Donghoon Chung
University of Louisville



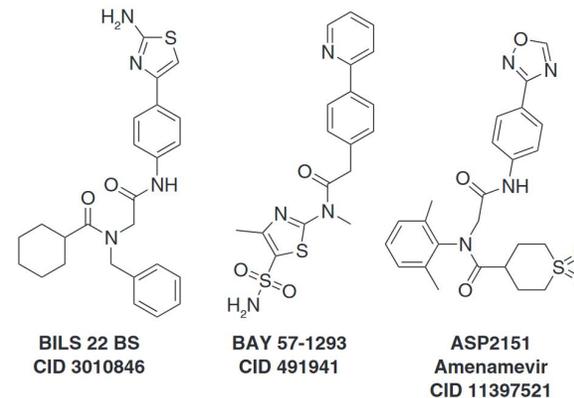
Viral helicases:

Novel, understudied antiviral target class.



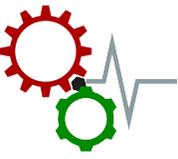
- Part of the viral replicase complex
 - unwinding of dsRNA
- Limited antiviral examples of targeting viral helicases

Anti-HSV compounds targeting the viral helicase/primase (UL5/UL52)

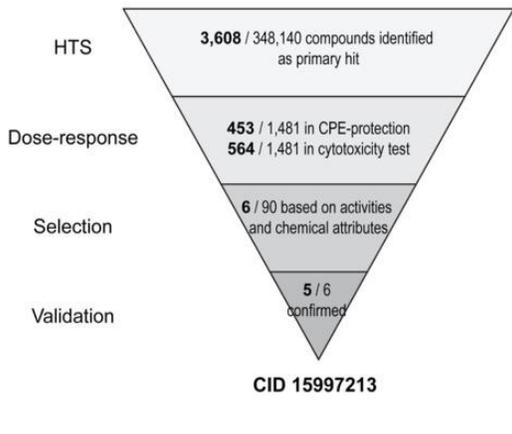


William R. Shadrack et al. DOI: 10.1177/10870571113482586

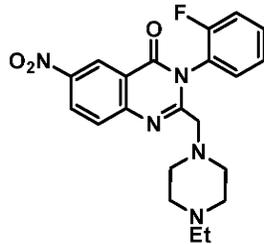
Alphavirus nsP2 and SARS-CoV2 nsP13 are functional and structural homologs : Superfamily I helicase



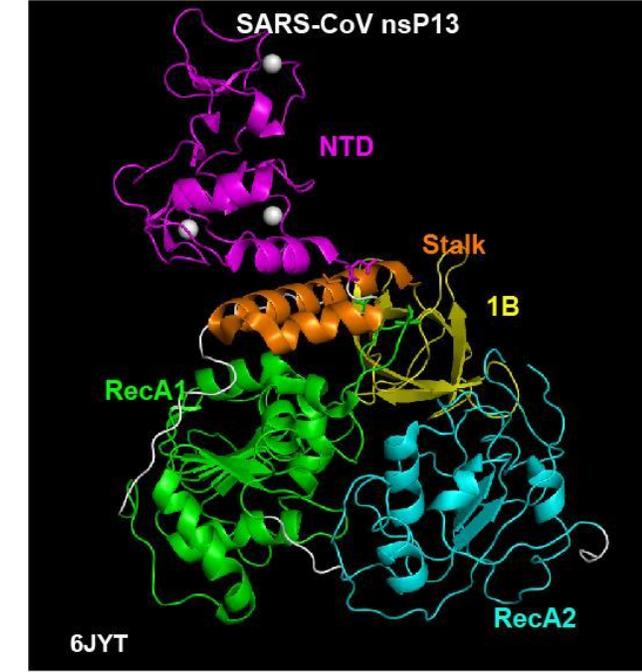
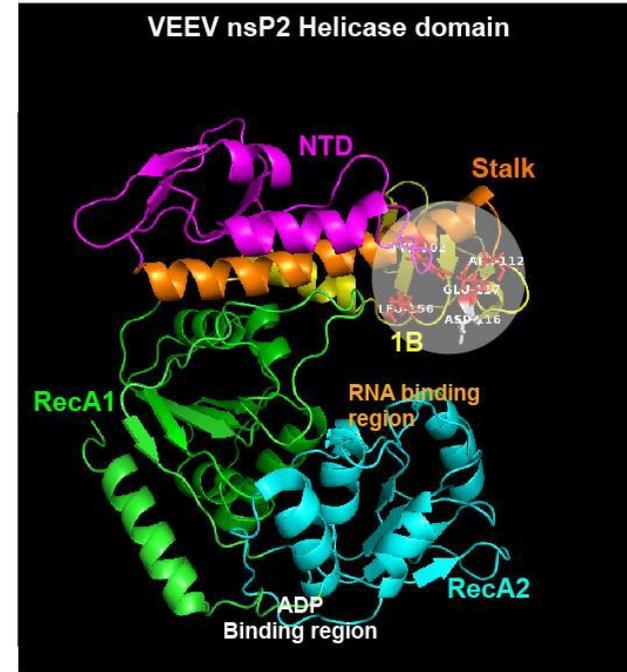
HTS of 348K MLSMR library for VEEV, alphavirus



quinazolinone hit
CID 15997213



VEEV $EC_{50} = 840 \text{ nM}$
VERO76 $CC_{50} > 50 \text{ }\mu\text{M}$



ML33

$EC_{50} = 30-40 \text{ nM}$



BDGR-4

$EC_{50} = 30-40 \text{ nM}$, improved virus yield reduction



BDGR-4
9

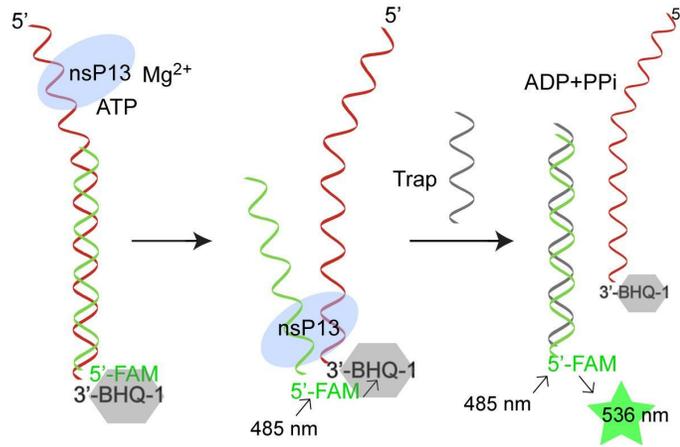
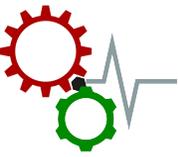
$EC_{50} = 1-10 \text{ nM}$, 100% protection with a 2 days delay of treatment in vivo

Table 1. Comparison of viral helicases proposed in this proposal

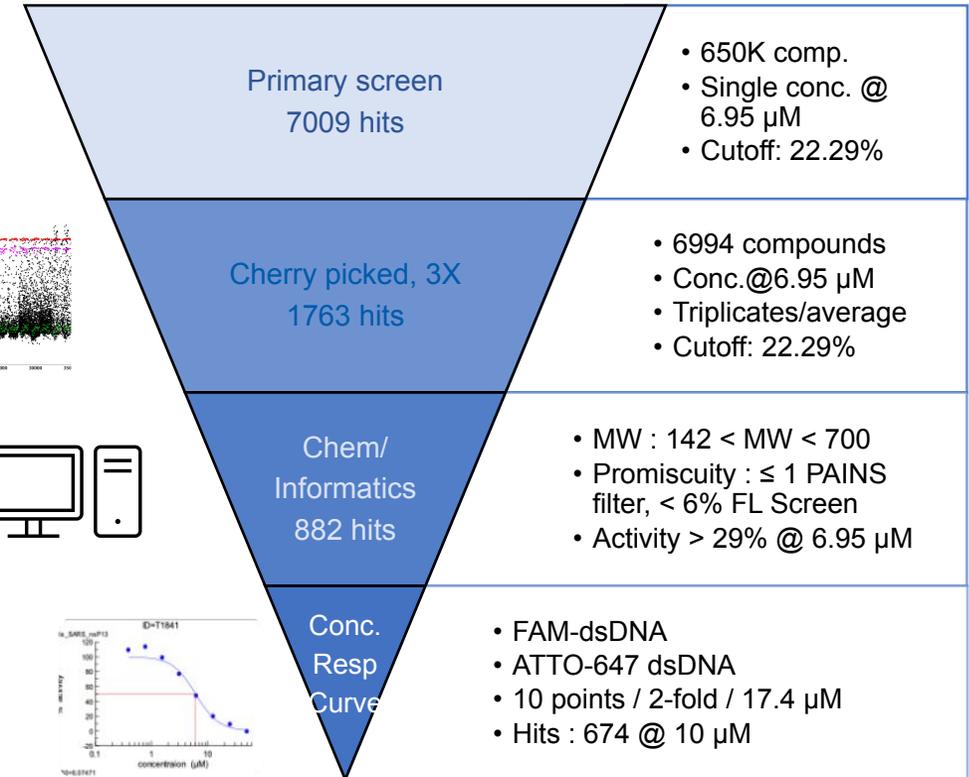
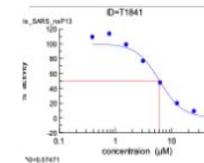
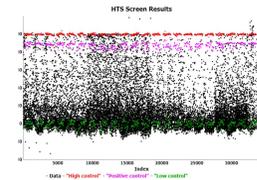
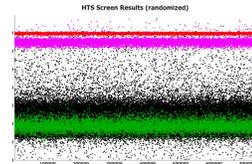
	Sars-CoV2	Alphavirus	Flavivirus	Human orthologs
Gene	nsP13	nsP2	nsP3	RecQ4L
Helicase superfamily	SF1	SF1	SF2	SF2
Substrate	DNA or RNA	RNA	DNA or RNA	DNA
Translocation direction	5'→3'	5'→3'	3'→5'	3'→5'

HTS-SCV2 helicase uHTS

Midwest AViDD Core B / UF-Scripps

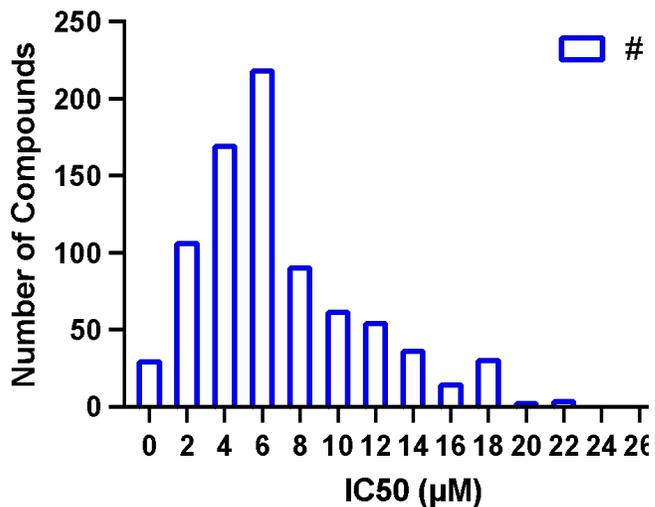


1536-well plate format



Screen	No. of plates	Ave Z'	Ave Z	Ave S:B	Hit cutoff	Hit rate
Primary (n=650K)	522	0.86 ± 0.05	0.61 ± 0.72	5.14 ± 0.55	22.29%	1.1%
Confirmatory (n=6994)	24	0.86 ± 0.03	0.24 ± 0.21	4.45 ± 0.11	22.29%	25.2%
CRC (n=881)	24	0.79 ± 0.05	-0.02 ± 0.10	4.19 ± 0.17		

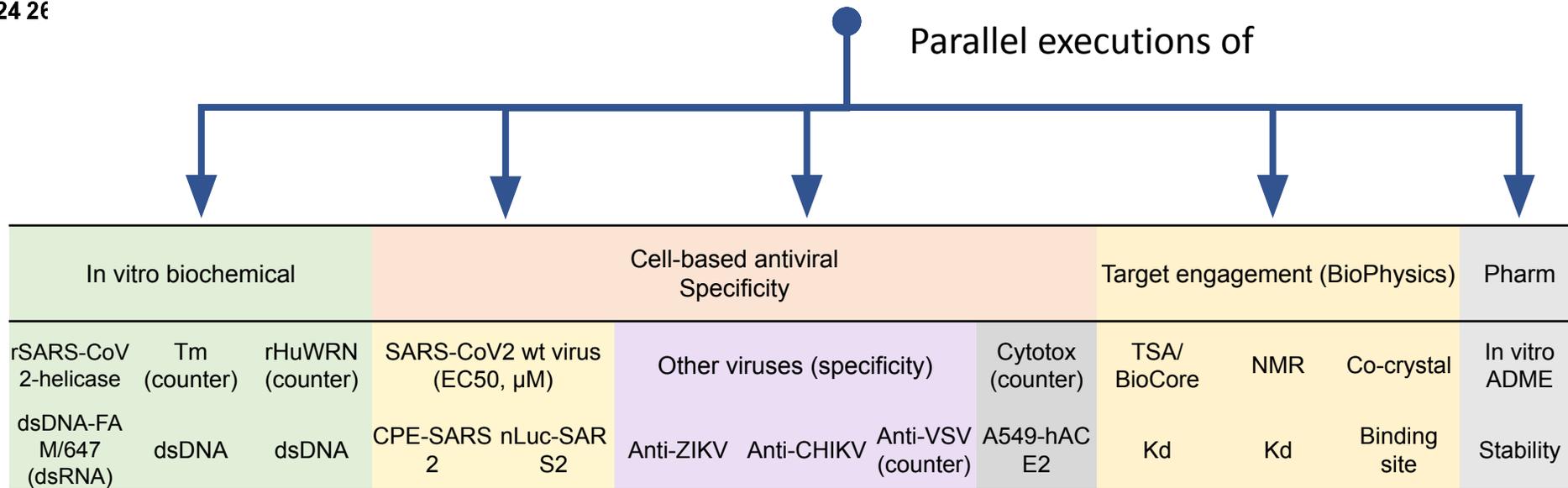
HTS Hit identification

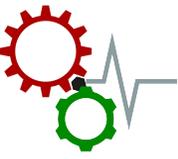


- A total of 217, active, curated compounds
/Anti-viral helicase library/



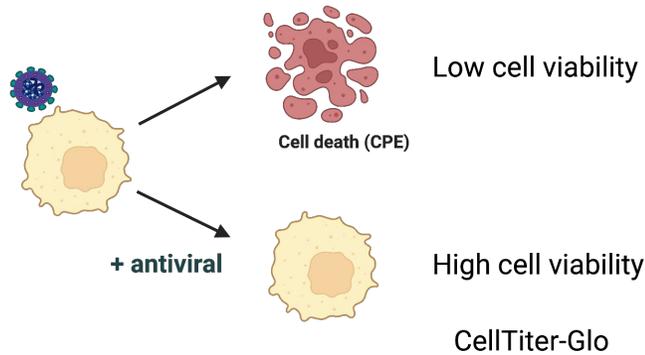
Criteria	No. of selected
Total	881
Non-PAINS	746
Max>50%/DR	677
IC50 < 10 µM	565
IC50 < 5 µM	266
IC50 < 1 µM	29



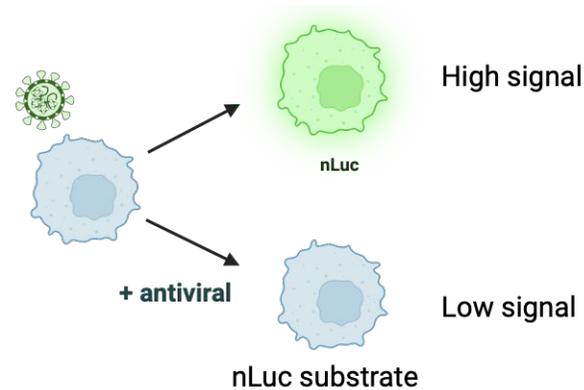


Frontline assays: anti-viral activity

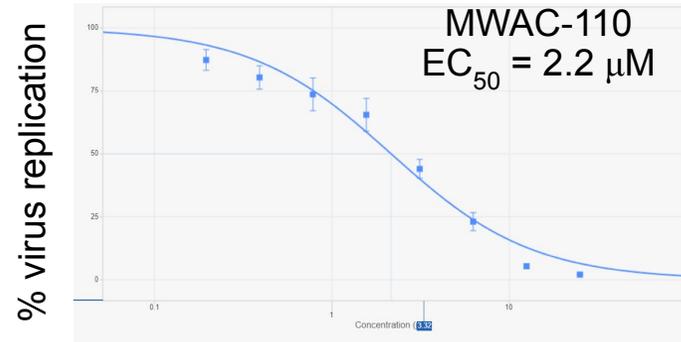
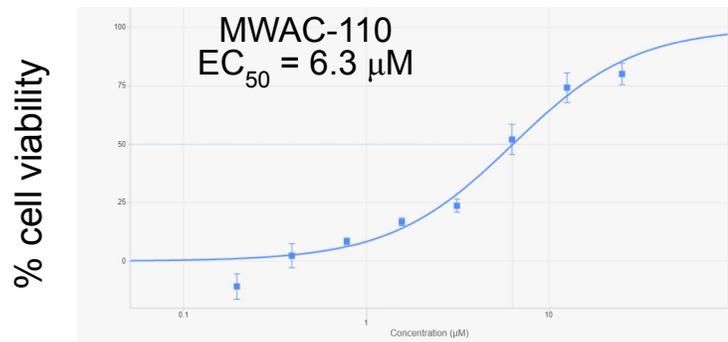
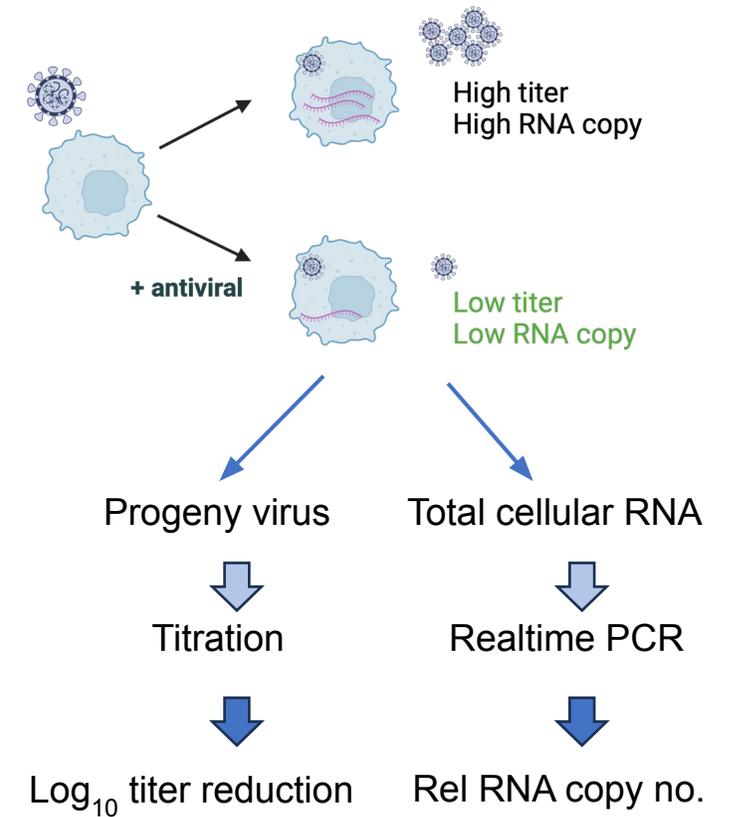
SARS-CoV-2 CPE
/A549-hACE2



SARS-CoV-2 nLuc
/A549-hACE2

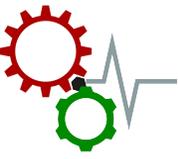


Virus yield reduction



concentration (μM)

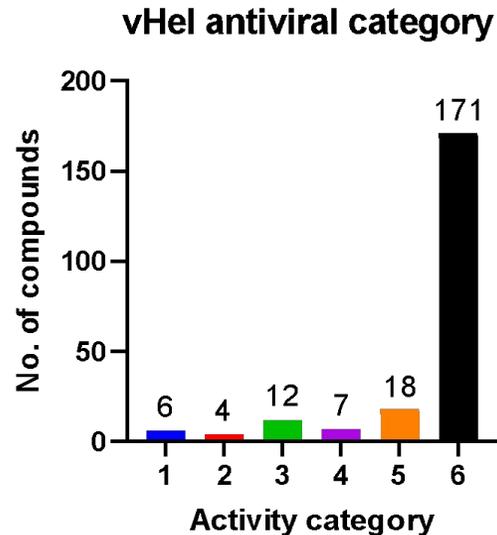
SARS-CoV-2 WT-1/A549-hACE2



Antiviral activities of uHTS-hit scaffold compounds

vHel library (~ 220
compounds)

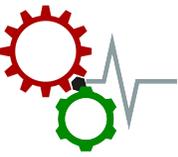
Cell-based antiviral assays
Anti-SARS-CoV2, CHIKV,
Cytotoxicity



- #1 : SARS-CoV2 specific
- #2 ; SARS-CoV2 specific with a low SI
- #3 : Anti-nLuc only-unknown mechanism
- #4 : Low SI50 - antiviral due to cytotoxicity
- #5 : Cytotoxic
- #6 : No antiviral activity

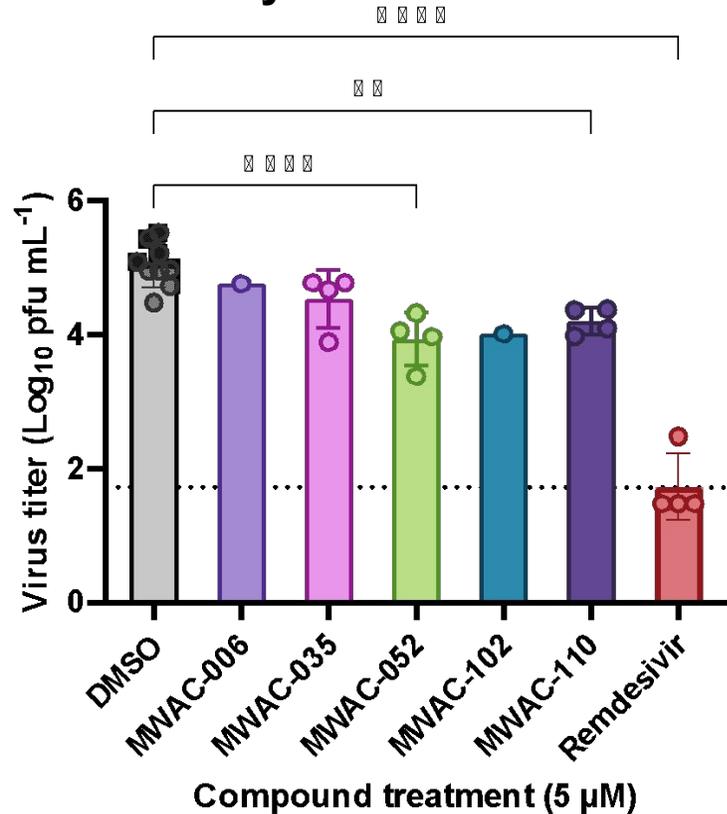
	EC ₅₀ -nLuc (SARS-CoV2-nLuc)	EC ₅₀ -CPE (SARS-CoV2 WT)	CC50 (A549-ACE2)	SI50
MWAC-002	8.5	3.83	22.4	2.6
MWAC-032	14.72	27.3	>50	>3.4
MWAC-046	16.11	30.6	>50	>3.1
MWAC-052	4.15	1.9	>50	>12.1
MWAC-102	2.8	6.02	>50	>17.9
MWAC-110	3.31	8.06	>50	>15.1
MWAC-140	3.83	4.49	17	4.4
MWAC-142	2.5	2	16	6.4

Units
(μ M)

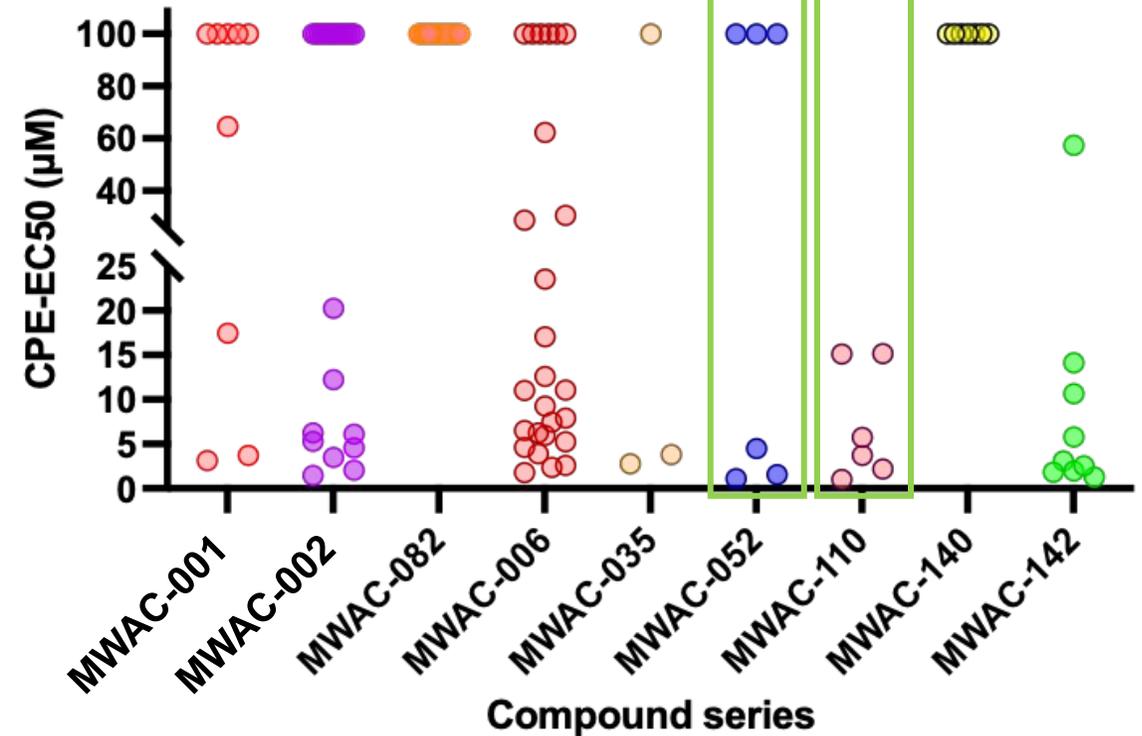


HTS Hit selection based on viral assays

Virus titer reduction activity



Performance of structural analogs



Virus : SARS-CoV2/2009/WT-1
Cells : A549-hACE2

Remdesivir
at 1 µM

Medicinal chemistry of the two leading series



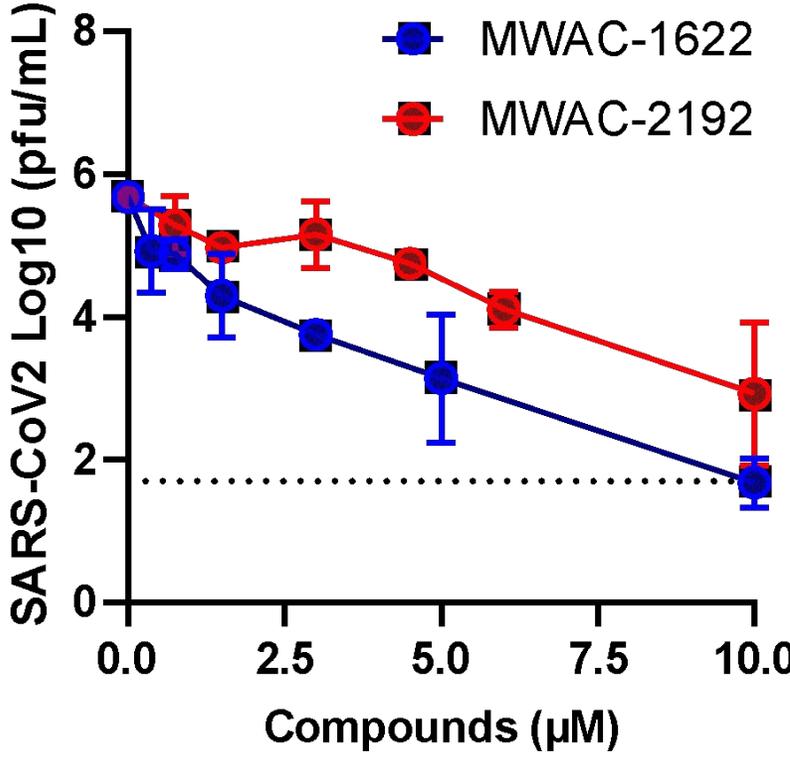
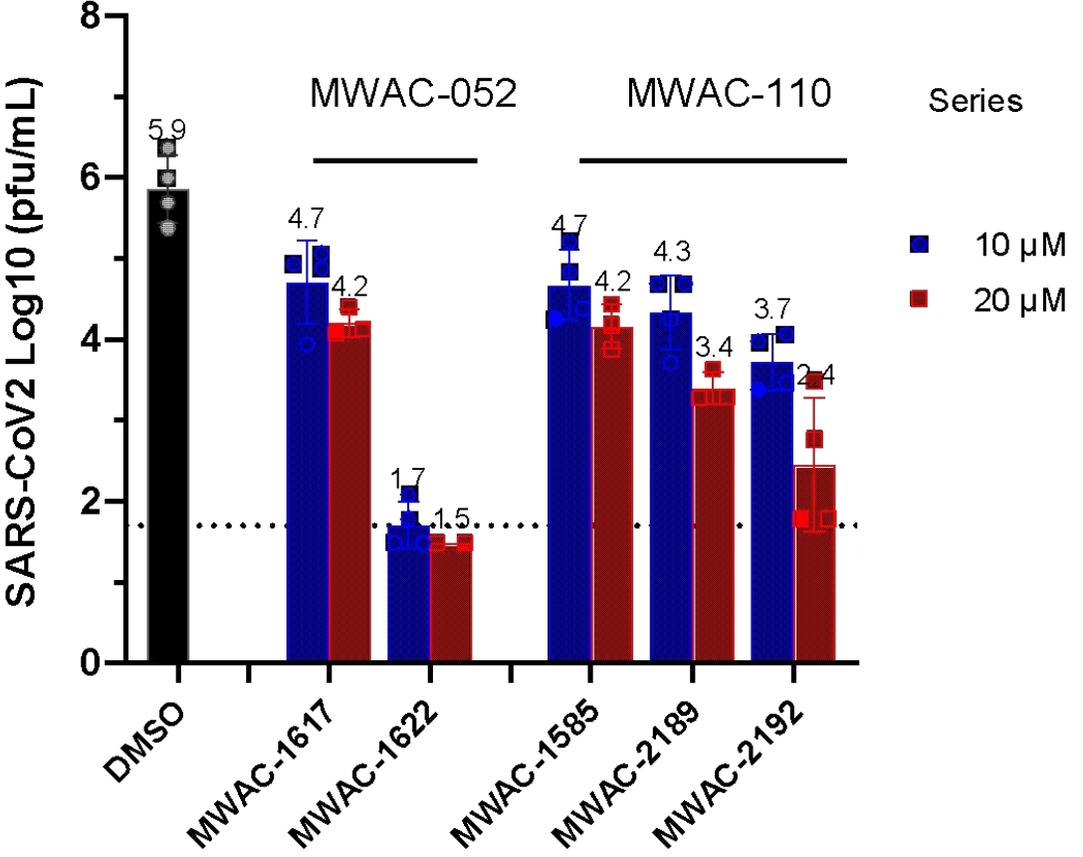
	MWAC-052 series					MWAC-110 series				
	MWAC-05 2	MWAC-16 18	MWAC-16 22	MWAC-28 43	MWAC-27 74	MWAC-01 10	MWAC-15 85	MWAC-15 86	MWAC-15 87	MWAC-21 92
SARS-CoV2 EC ₅₀ -CPE	1.9	4.5	0.32	0.11	1.0	5.3	2.2	3.7	1.0	1.1
SARS-CoV2 EC ₅₀ -nLuc	4.2	8.1	0.50	0.39	0.45	2.8	1.1	2.0	0.59	0.66
ZIKV EC ₅₀ -CPE	> 50	> 50	> 50	>50	> 25	> 50	> 50	> 50	> 50	> 50
CC ₅₀	>50	>50	> 50	51	32	>25	> 25	22	9.5	> 50
SI	>12	>6.2	> 100	131	32	>9	> 22	11	16	> 75

>35 analogs tested to date

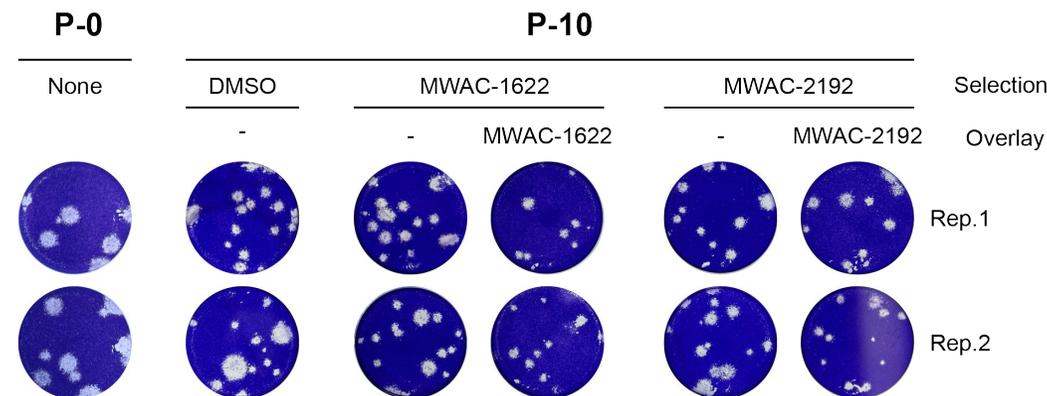
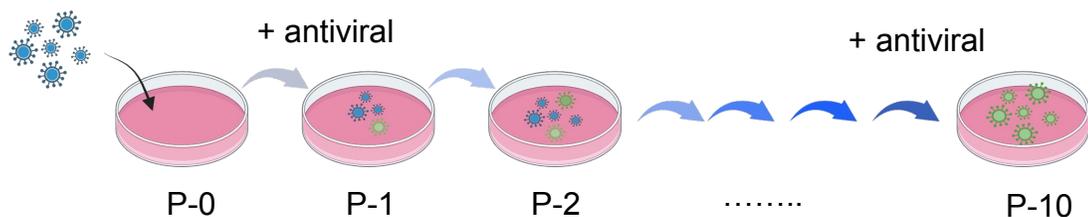
EC₅₀ and CC₅₀ (μM), Virus: SARS-CoV-2 WT-WA1 ;
CC₅₀: in A549-hACE2 cells

*Dr. Bannister
group*

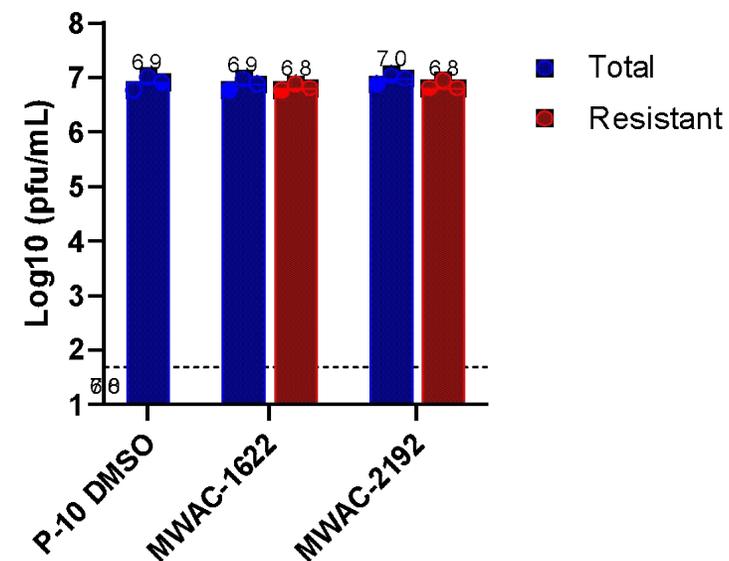
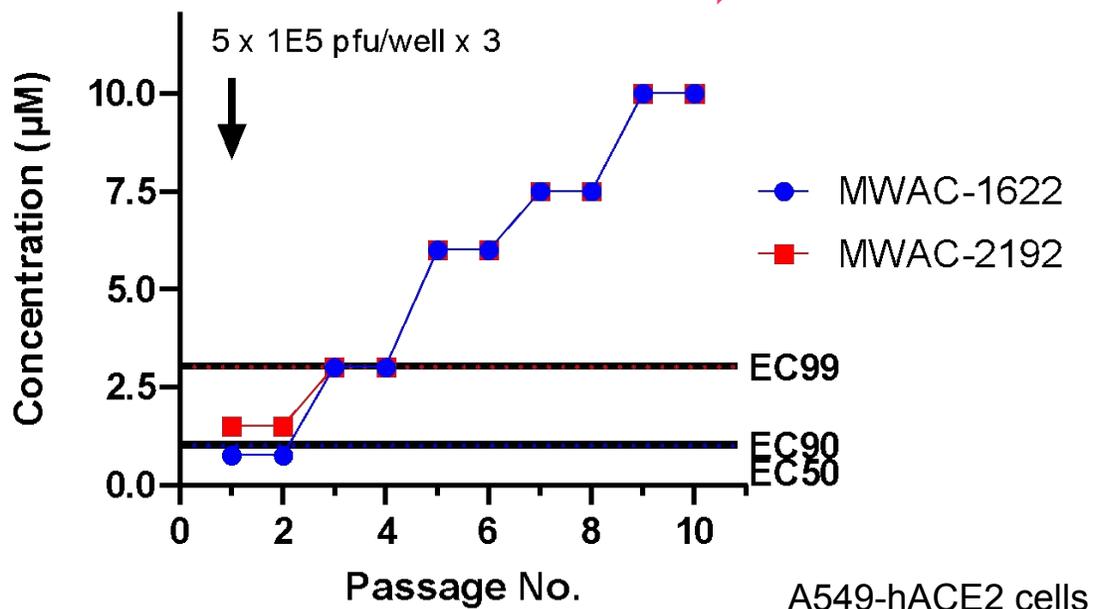
The two series showed anti-'VIRAL' activity



Genetic approach: Isolation of resistant virus



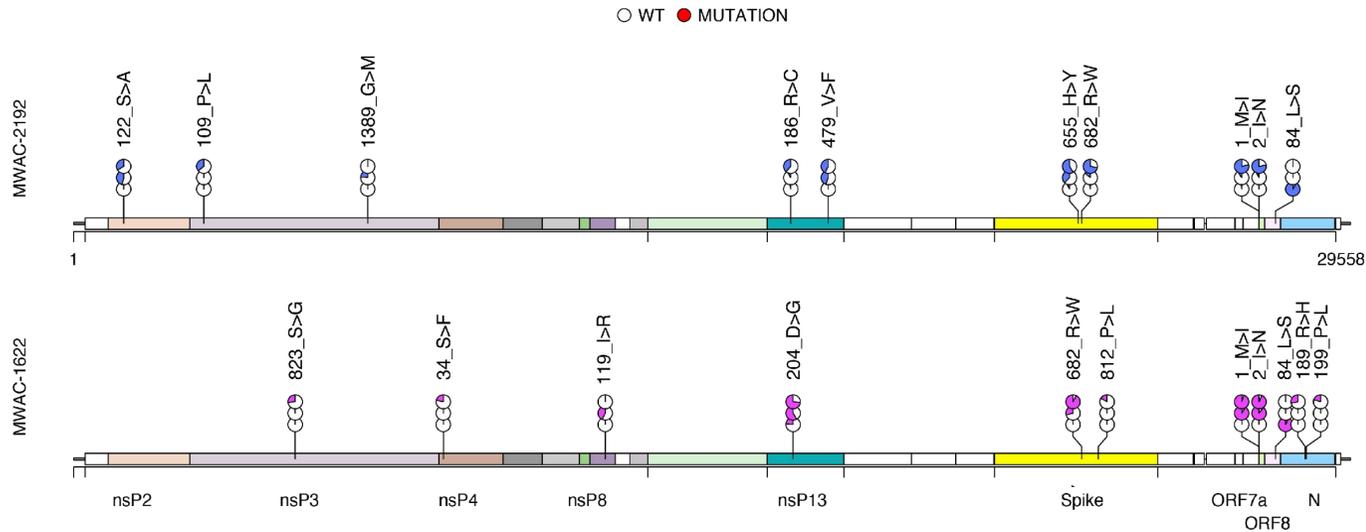
Clear CPE was noticeable.



Mutations identified in serially-passaged, resistant populations

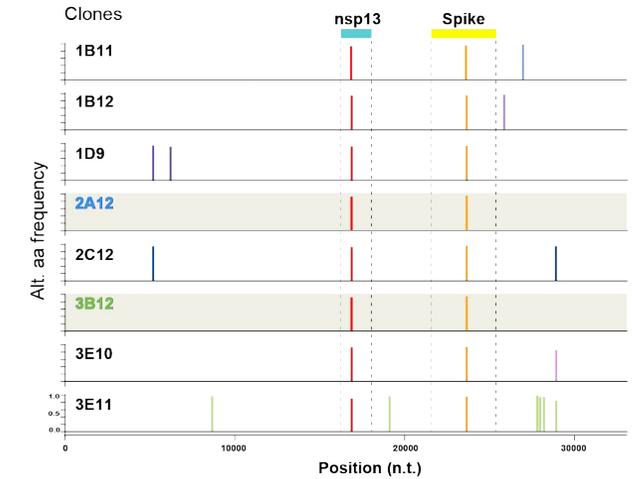


Total population sequencing

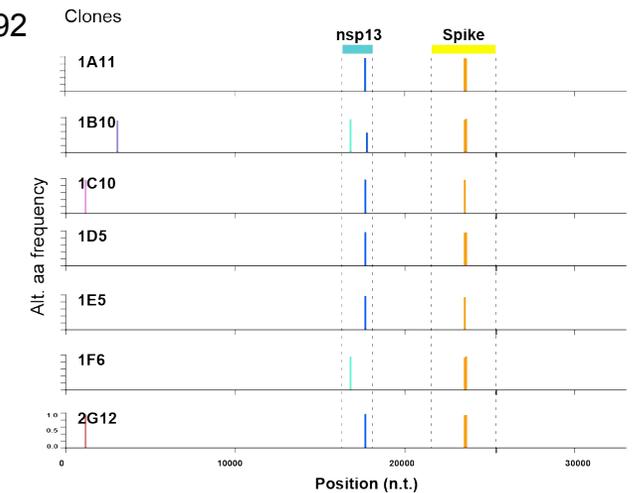


Individual isolates

MWAC-1622

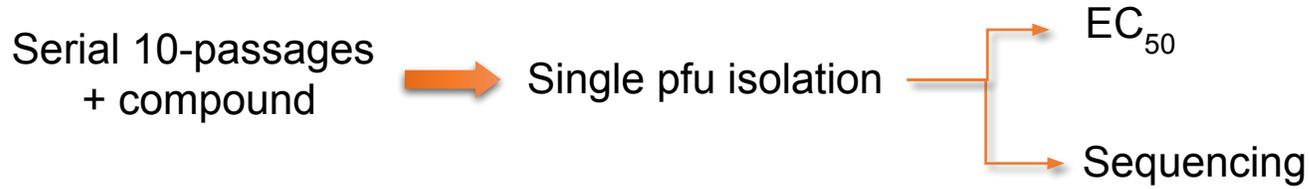


MWAC-2192

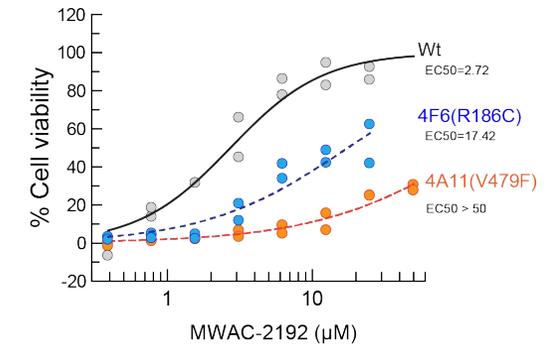
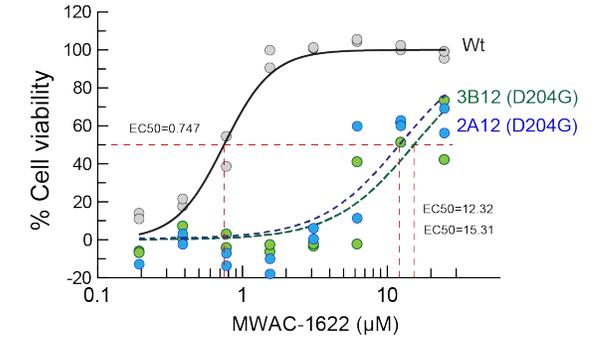


P-10	nsP2	nsP3	nsP4	nsP13		S		ORF7b		Np				
Mutations	122_S>V	109_P>L	823_S>G	34_S>F	186_R>C	204_D>G	479_V>F	655_H>Y	682_R>W	812_P>L	1_M>Y	2_I>N	189_R>H	199_P>L
MWAC-1622			0.26	0.21	0.74			0.93	0.16	0.96	0.94	0.28	0.20	
MWAC-2192	0.34	0.36			0.39	0.43		0.59	0.72		0.79	0.78		

Phenotypic resistance of MWAC-1622 and 2192 resistant clones



Selection compound	Genotype	Remdesivir		MWAC-1622		MWAC-2192	
		EC50 (μ M)	Fold-increase	EC50 (μ M)	Fold-increase	EC50 (μ M)	Fold-increase
	Wt	0.10	-	0.75	-	2.72	-
MWAC-1622	nsP13 D204G*	0.2 \pm 0.1	x 2	13.8	x 18.4	8.5	x 3
MWAC-2192	nsP13 R186C**	0.04	x 0.4	1.29	1.7	17.4	6.4
	nsP13 V479F**	0.10 \pm 0.07	x 1	3.55 \pm 1.9	4.7	> 50	> 18

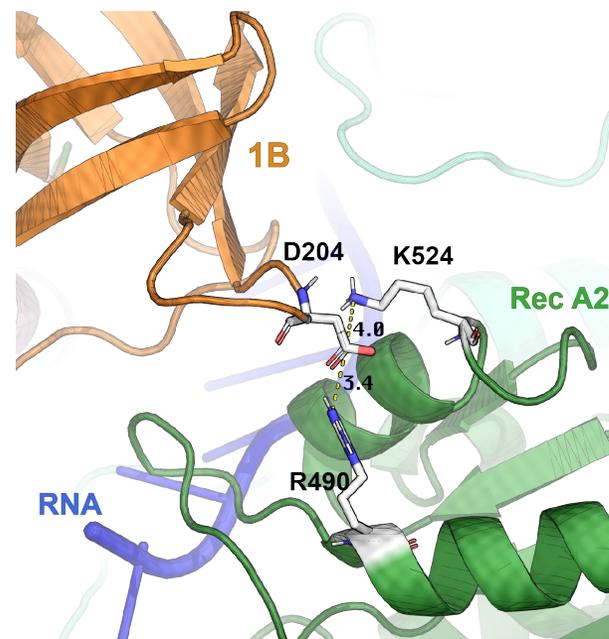
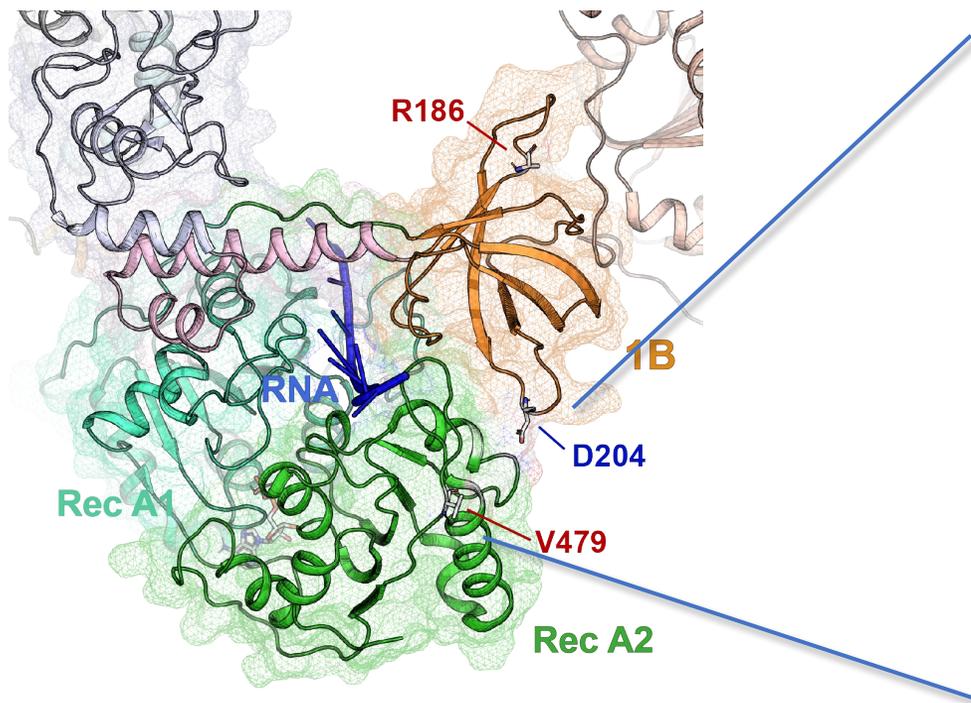


* Spike R682W; ** Spike H655Y/R682W were also found.

Confirmed nsP13 as the target.



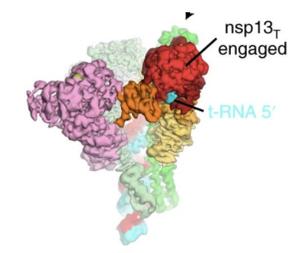
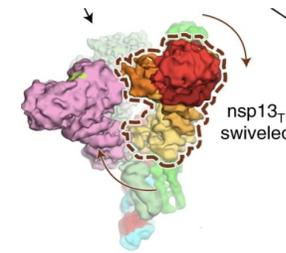
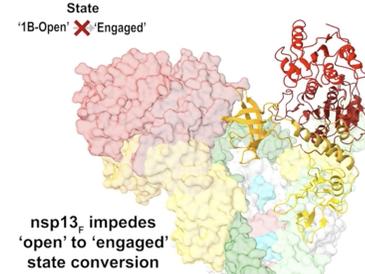
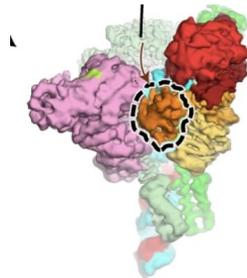
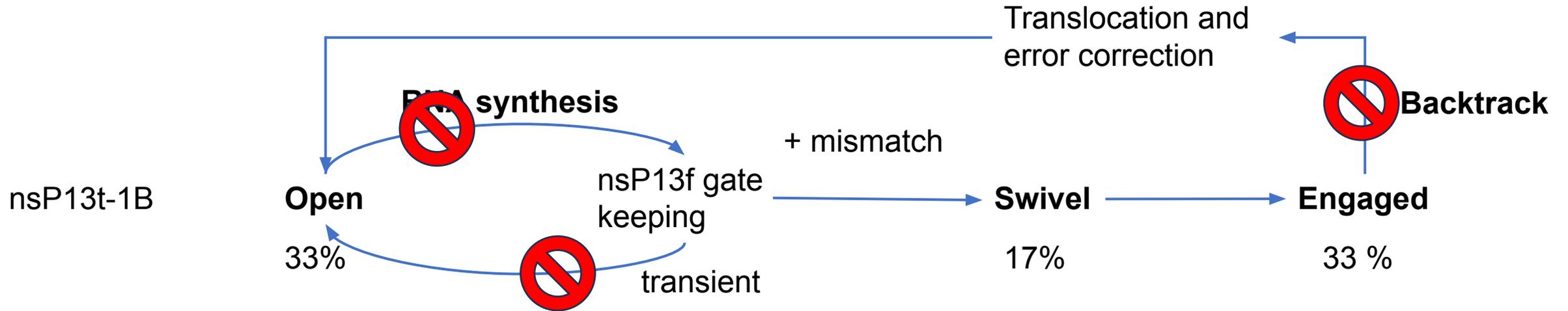
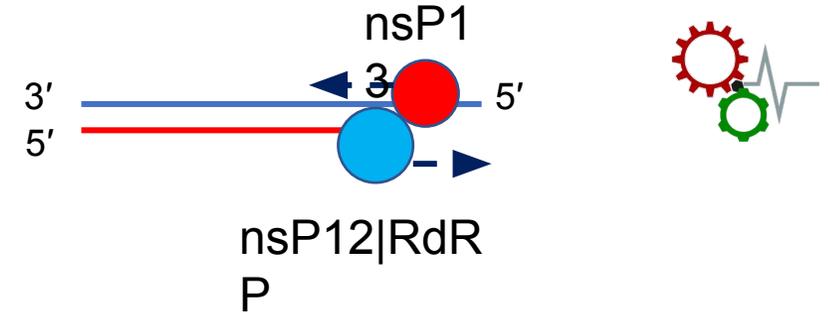
Molecular insights into the mechanism



Interaction between 1B domain and Rec A2 by a salt bridge via D204

Selection	Genotype	Location
MWAC-162 2	nsP13 D204G*	1B
MWAC-219 2	nsP13 R186C**	1B
	nsP13 V479F**	RecA2

nsP13 conundrum : a tug war



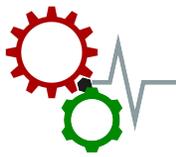
Interaction of
1B domain

?

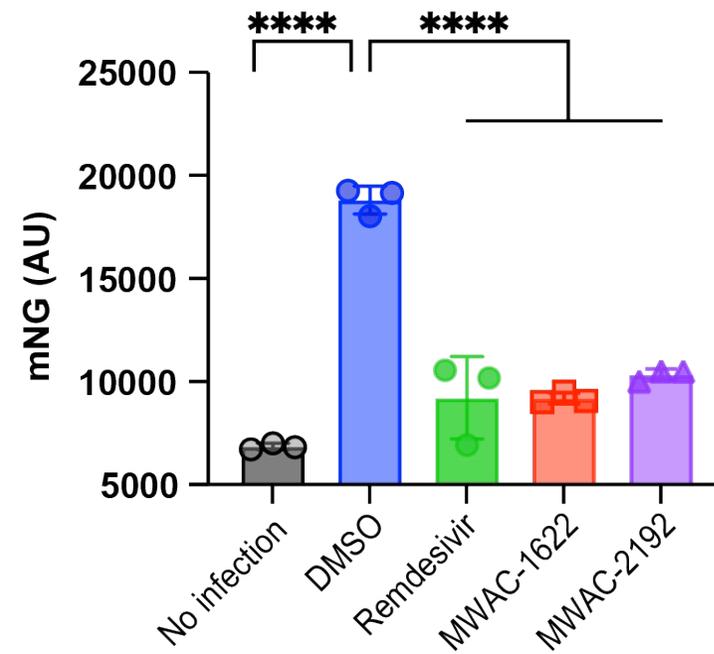
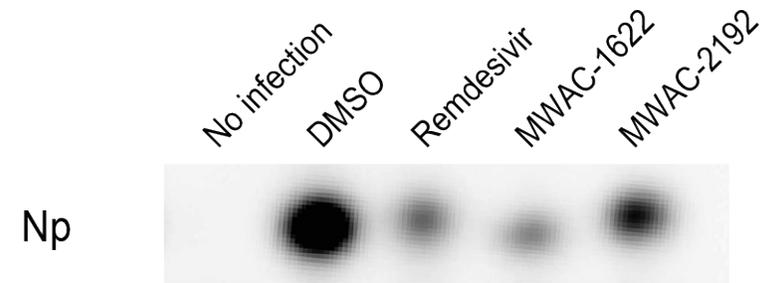
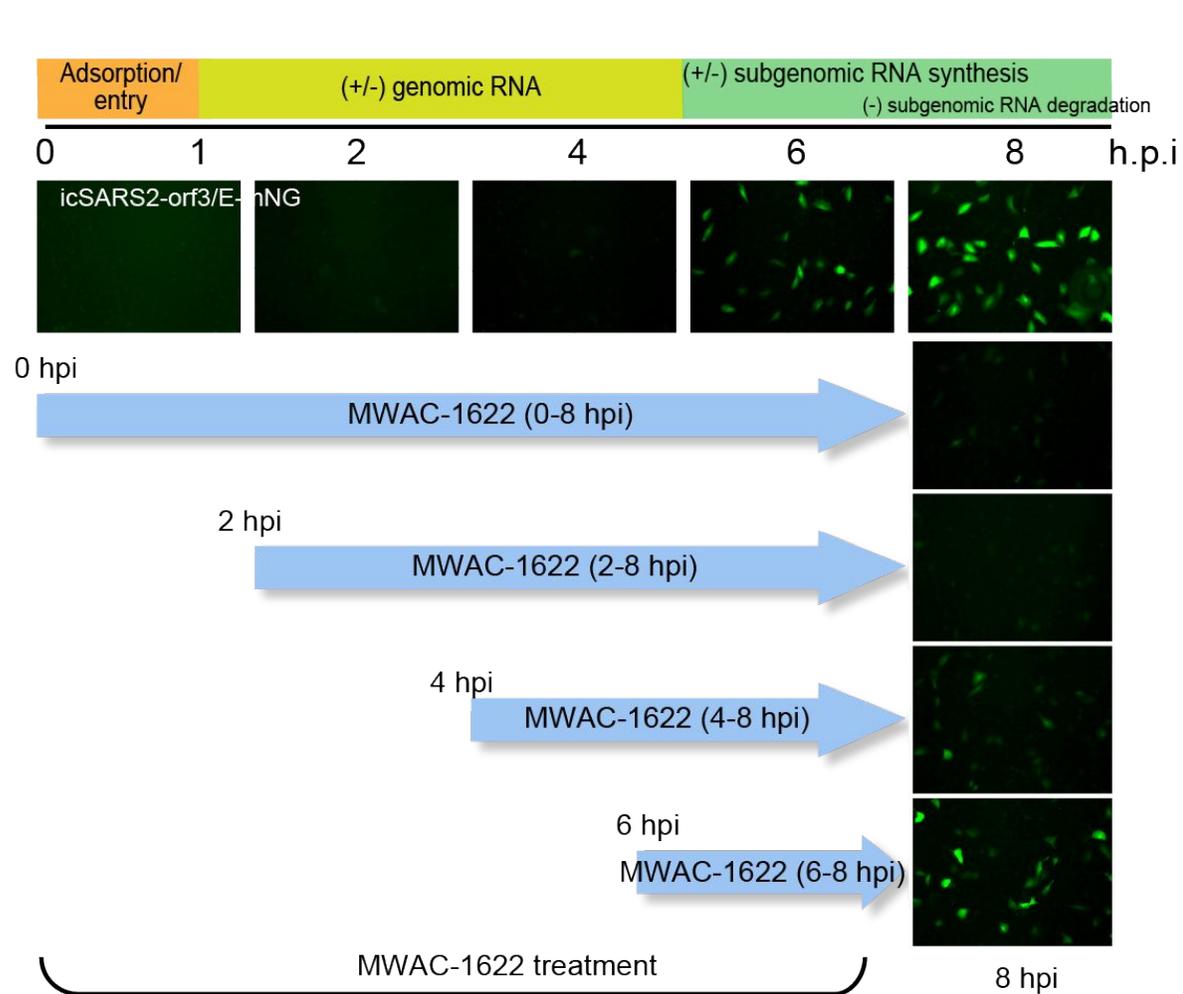
nsP13f

None?

nsP13t-RecA2

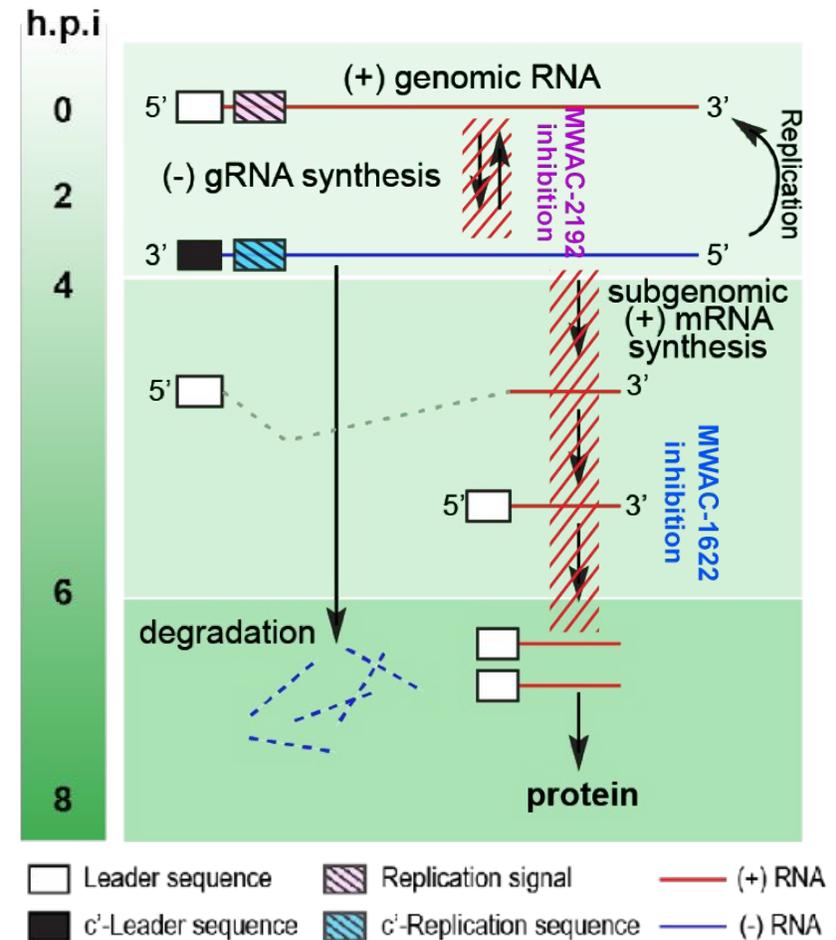
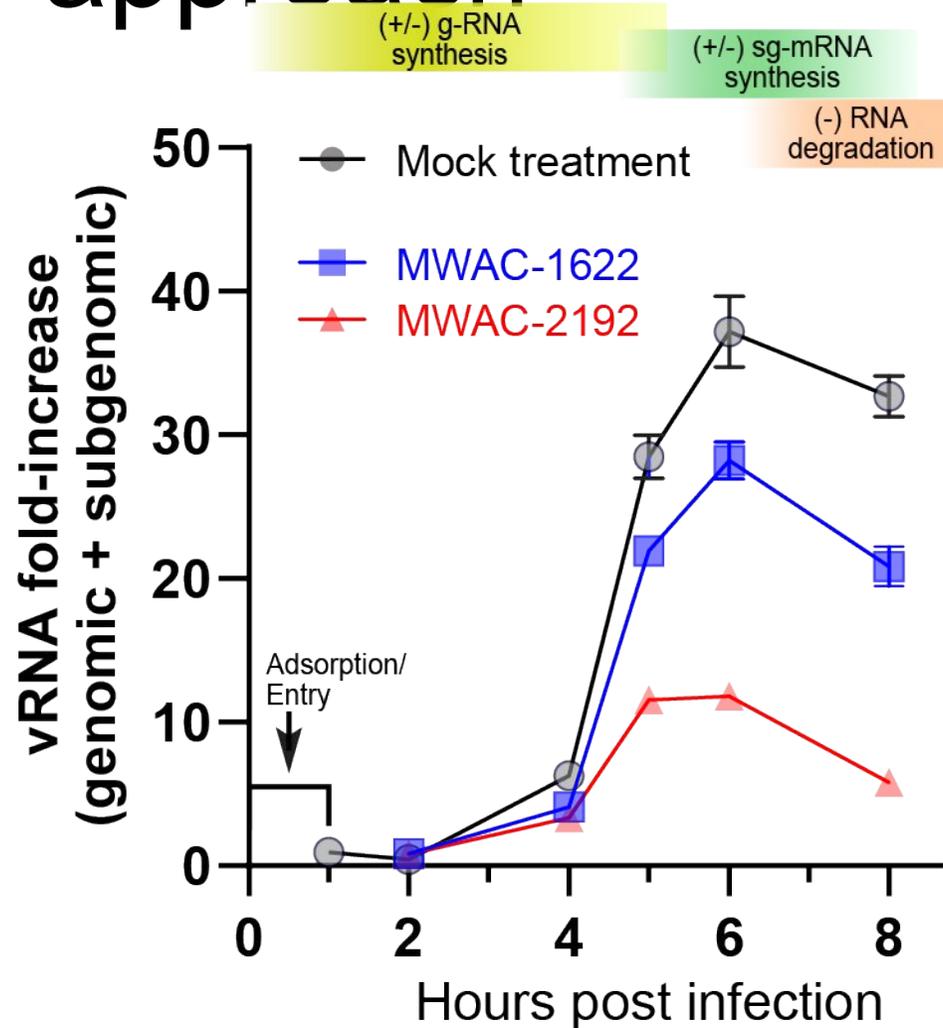


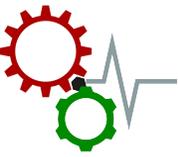
Hit characterization : Virological approaches



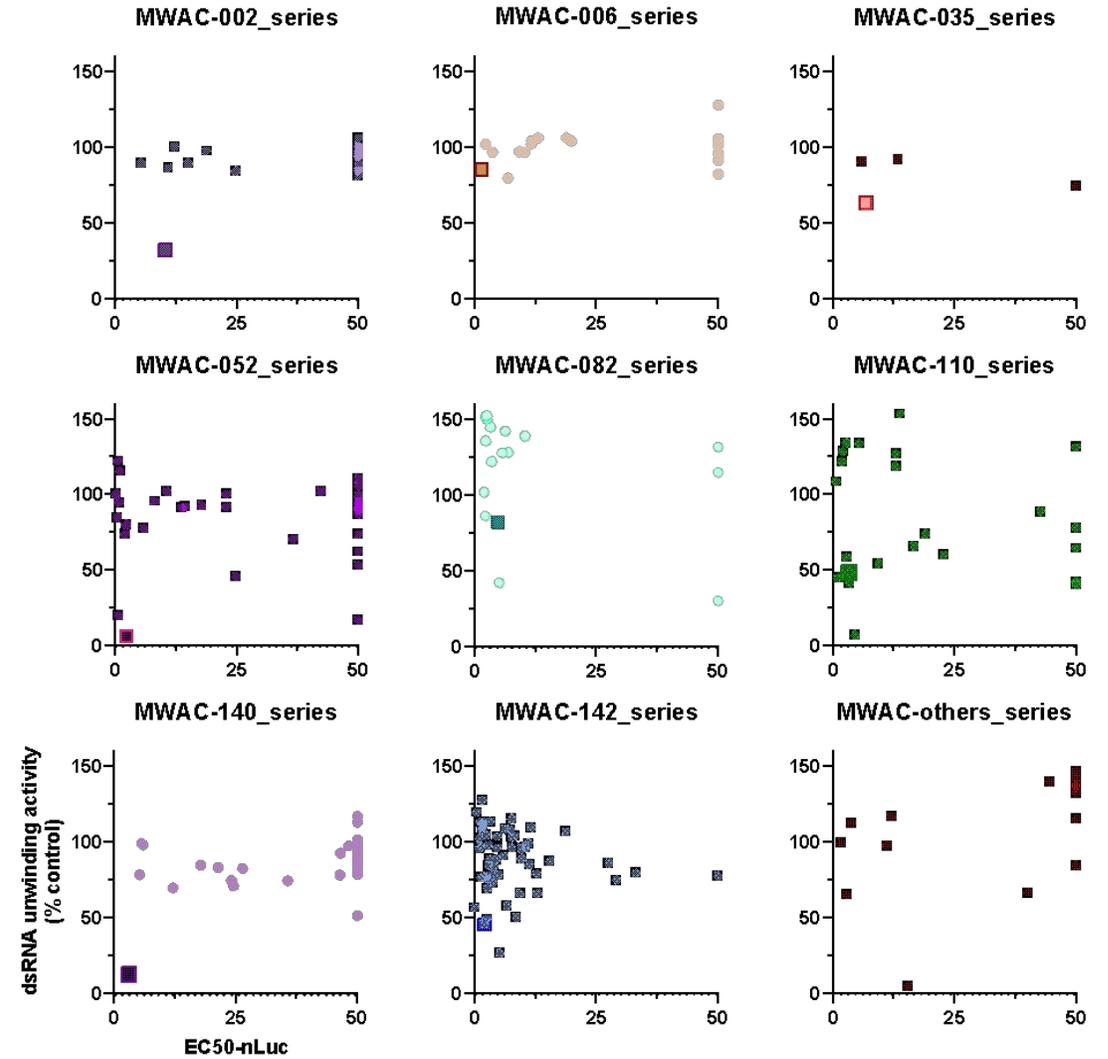
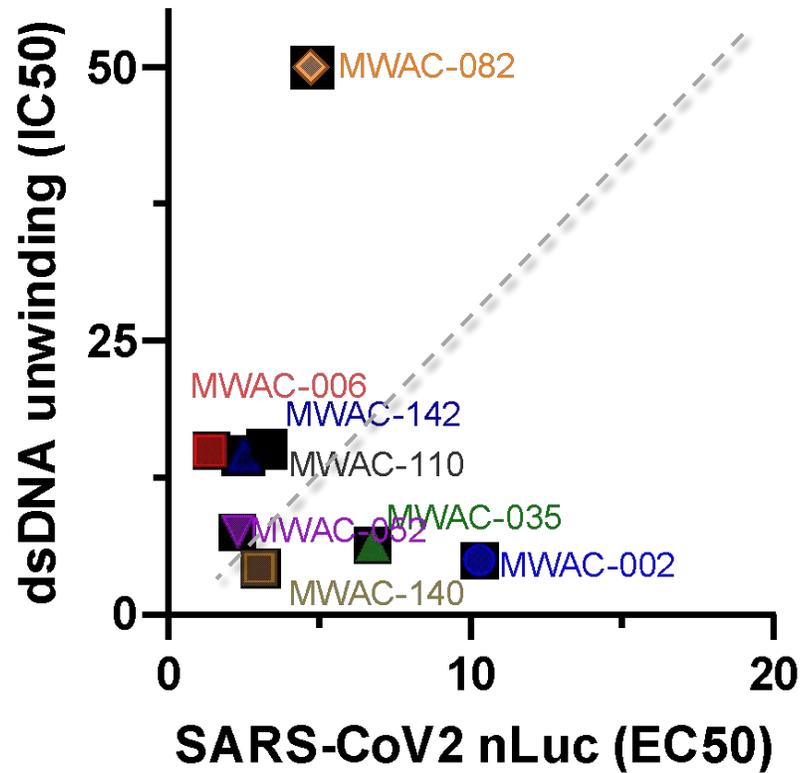


Mechanism of action : Virological approach





Anti-helicase vs. Anti-viral

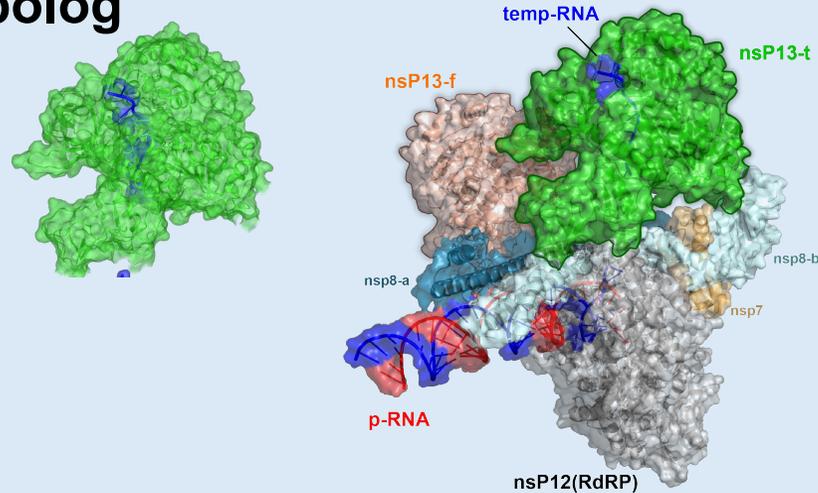




Nothing exists alone: nsP13 vs virus

Topology

y



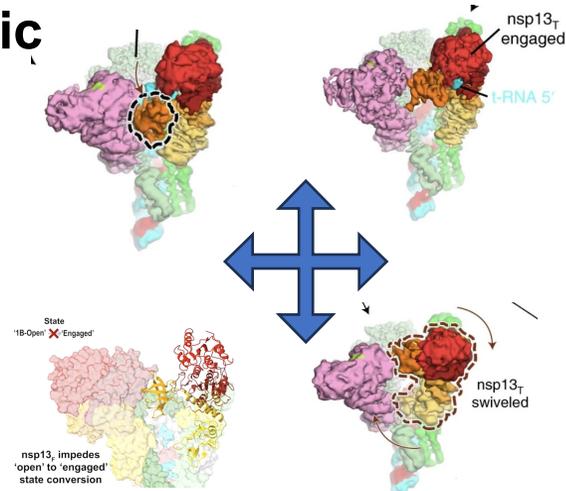
Biochemistry

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- Translocation/ATPase - 700 – 800 nt(ATP) /s
 - Mg^{2+} vs Fe-S cluster
 - *Nunziata Maio et al. PNAS, 2023*
- dsDNA > dsRNA

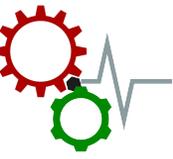
Dynamic

s



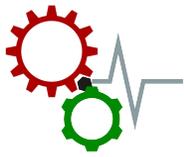
Virological issues

- Location of the replication complex (e.g., DMV)
- How much is enough to show phenotypic changes (e.g., viral titer difference)
- Etc.



Summary

- uHTS identified ~300 compounds with a good anti-nsP13 activity.
- 7 compound series were confirmed with SARS-CoV2-specific antiviral activity.
- Two leading series are being advanced with medicinal chemistry.
- The resistant mutation studies have identified mutations conferring resistance within the nsP13.
- NsP13 may be more than a “dsRNA unwinding engine”.



Acknowledgements

Project 5

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Dr. John Marecki

NTU

Dr. Dahai Luo
lab

Core B

UF-Scripps

HTS team:
Dr. Louis Scampavia
Dr. Tim Spicer
& HTS lab

Baylor College of Med

DEC-Tec team:
Dr. Damien Young lab
Dr. Srinivas Chamakuri

Core C

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Chemistry:
Dr. Thomas Bannister lab
Dr. Chao Wang
Dr. Sultan Ullah
Dr. Bilel Bderi

DMPK:

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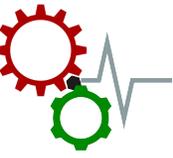
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HTL Committee



Questions?