

Structure-based discovery of potent and selective SARS-CoV-2 3-chymotrypsin-like cysteine protease inhibitors using a multiplex screening platform

Koen Vanduyck¹, Jerome Deval², Dorothée Bardiot⁵, Leonid Beigelman^{1,2}, Lawrence M. Blatt^{1,2}, Sandro Boland⁵, Patrick Chaltin^{3,5}, Kusum Gupta², Zachary A. Gurard-Levin⁶, Andreas Jekle², Dirk Jochmans⁴, Pieter Leyssen⁴, Cheng Liu², Arnaud Marchand⁵; *Pierre Raboisson¹, Suping Ren², Michael D. Scholle⁶, Vladimir Serebryany², Antitsa Stoycheva², Julian A. Symons², and Johan Neyts⁴

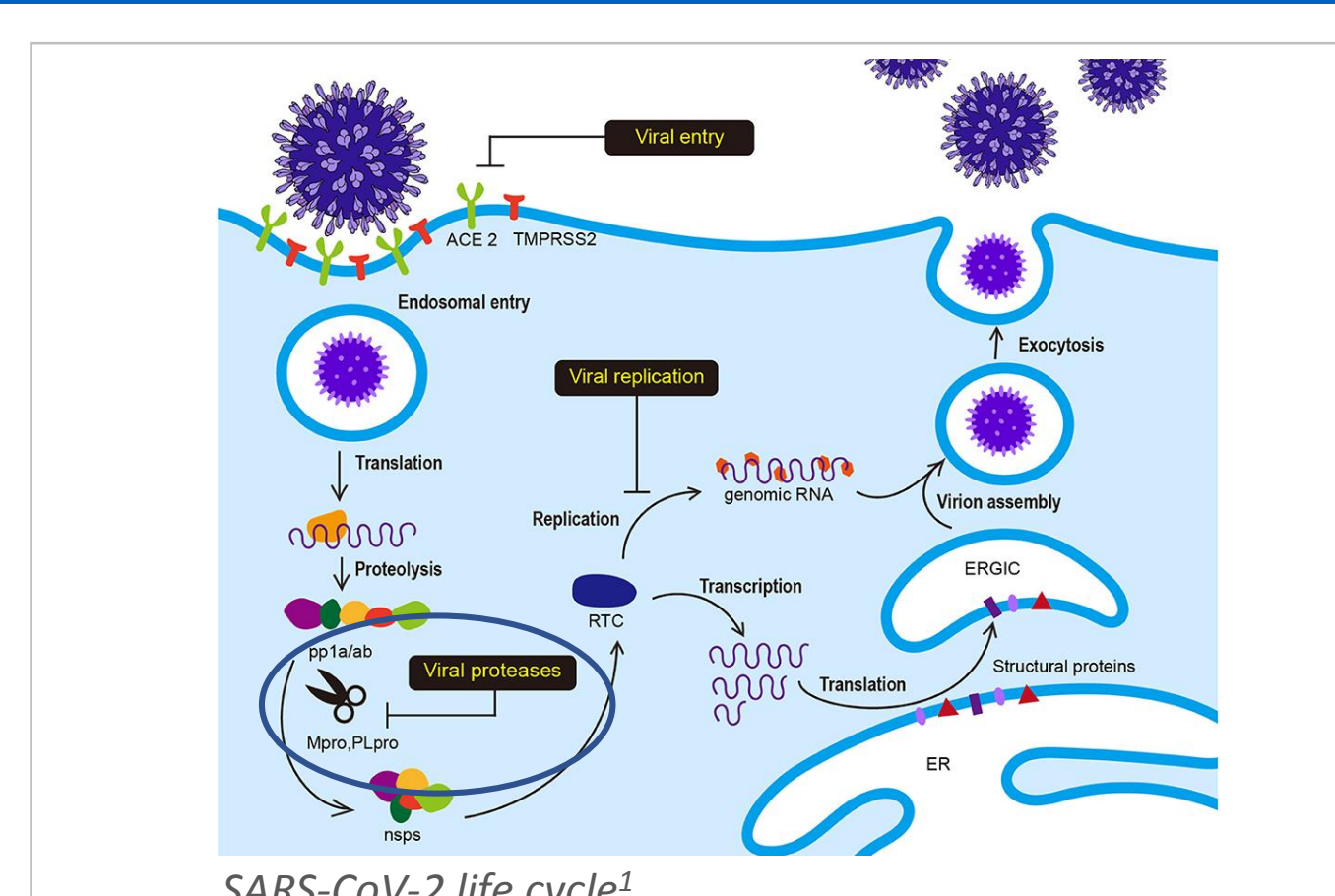
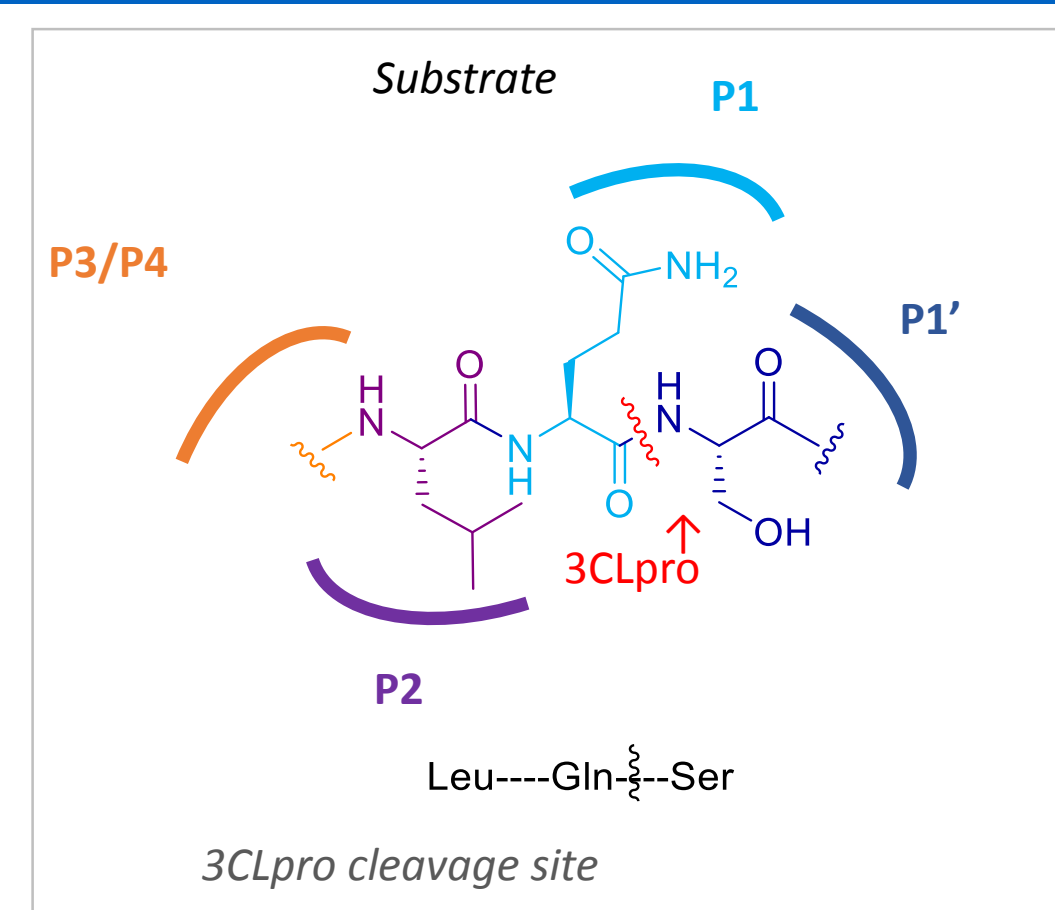
¹Aligos Belgium BV, Leuven, Belgium; ²Aligos Therapeutics, Inc., South San Francisco, CA; ³Centre for Drug Design and Discovery (CD3), KU Leuven, Leuven, Belgium; ⁴Rega Institute for Medical Research, KU Leuven, Leuven, Belgium; ⁵SCISTIM Leuven vzw, Leuven, Belgium; ⁶SAMD1 Tech, Inc., Chicago, USA. *Corresponding author



Background:

The 3-chymotrypsin-like cysteine protease (3CLpro) of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is considered a major target for the discovery of direct antiviral agents. Currently, at least two 3CLpro inhibitors are in (pre)clinical development for the treatment of COVID-19: GC-376 and PF-07304814 (a prodrug of PF-00835231). Both agents exhibit different degrees of cathepsin L inhibition. Cathepsin L has been shown to block SARS-CoV-2 infection of human and monkey cells by proteolytic cleavage of the SARS-CoV-2 spike protein. Therefore, it can be hypothesized that the cell-based activity of several 3CL protease inhibitors described in literature is at least partially mediated by inhibition of host cathepsin L.

SARS-CoV-2 3CLpro (Mpro) Represents an Attractive Target



- 3CLpro is conserved within the group of CoVs, and in a related form, by members of the Enterovirus genus (picornavirus)
- 3CLpro operates at multiple sites on the large polyprotein 1ab
- No human homologue of 3CLpro

SARS-CoV-2 3CLpro (Mpro) Inhibitors

- At least two 3CLpro inhibitors have been reported in early development for treating SARS-CoV-2 infection
- Both PF-00835231 (active of PF-07304814) and GC-376 are 'repurposed drugs' for SARS-CoV-2

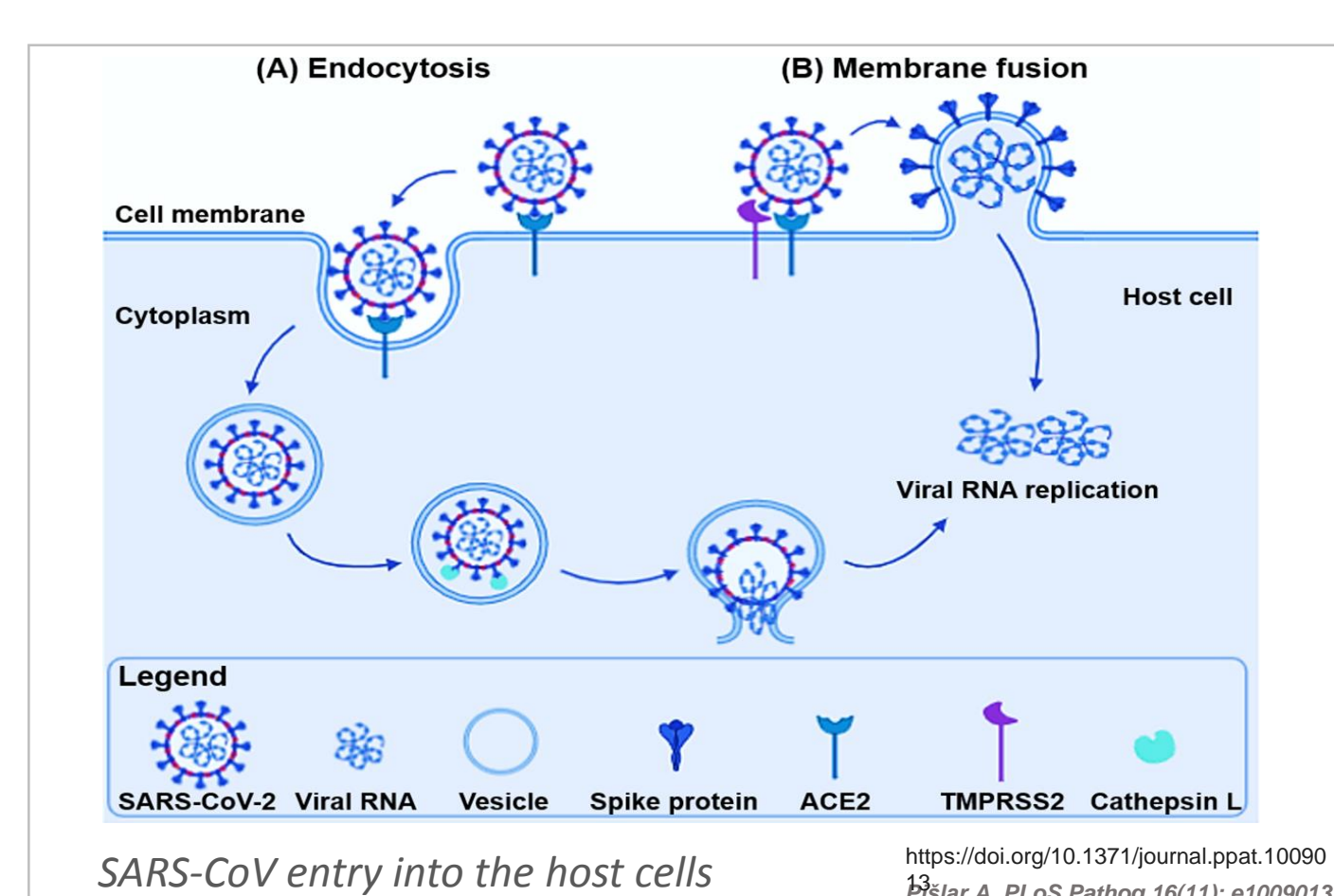
Structure	IV	F%	t _{1/2}
	PF-231 ²	<0.1-1.4% (monkey/rat)	1-1.6h (Rat/dog/Monkey)
	GC-376 ³	3% (rat)	1.3 h (rat)

R= -H; PF-00835231 : SARS-CoV-2 3CLp IC₅₀ (SAMD1) = 7 nM
R= -PO₃H₂; PF-07304814

GC-376 (Anivive): SARS-CoV-2 3CLp IC₅₀ (SAMD1) = 8 nM

- Both PF-07304814 and GC-376 are injectable drug candidates with limited oral bioavailability and short half-life

Cathepsin L Regulates SARS-CoV-2 Entry into Host Cells



Biochemical and cellular activity of K11777⁴

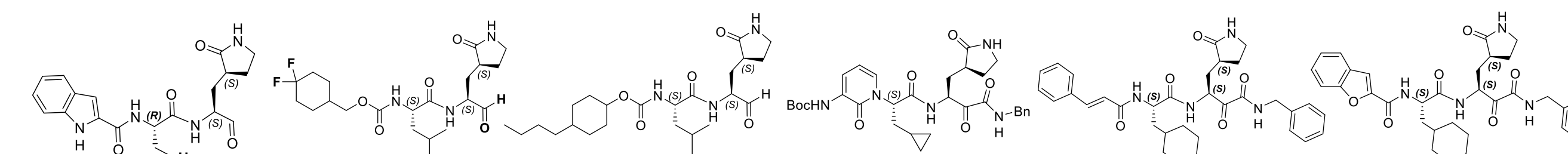
Protease activity	Ki (μM)
Cathepsin L	0.005
Cathepsin B/K/S	3.0/0.4/0.002
SARS-CoV-2 3CL Pro/PL	>100

SARS-CoV-2 activity	EC ₅₀ (μM)
VeroE6	0.07-0.62
A549/Hela-ACE2	<0.08/0.004
Calu-3	3.7

https://doi.org/10.1101/2020.10.23.347524

- Cathepsin L is involved in SARS-CoV-2 entry into host cells
- Cathepsin L inhibitors have demonstrated cellular potency versus SARS-CoV-2 in different cell lines
- Monitoring Cathepsin L inhibition of SARS-CoV-2 3CL_{pro} inhibitors, is considered essential to analyze their intrinsic cellular potency related to on target 3CL_{pro} inhibition

Reported SARS-CoV-2 3CLpro Inhibitors vs. Cathepsin L

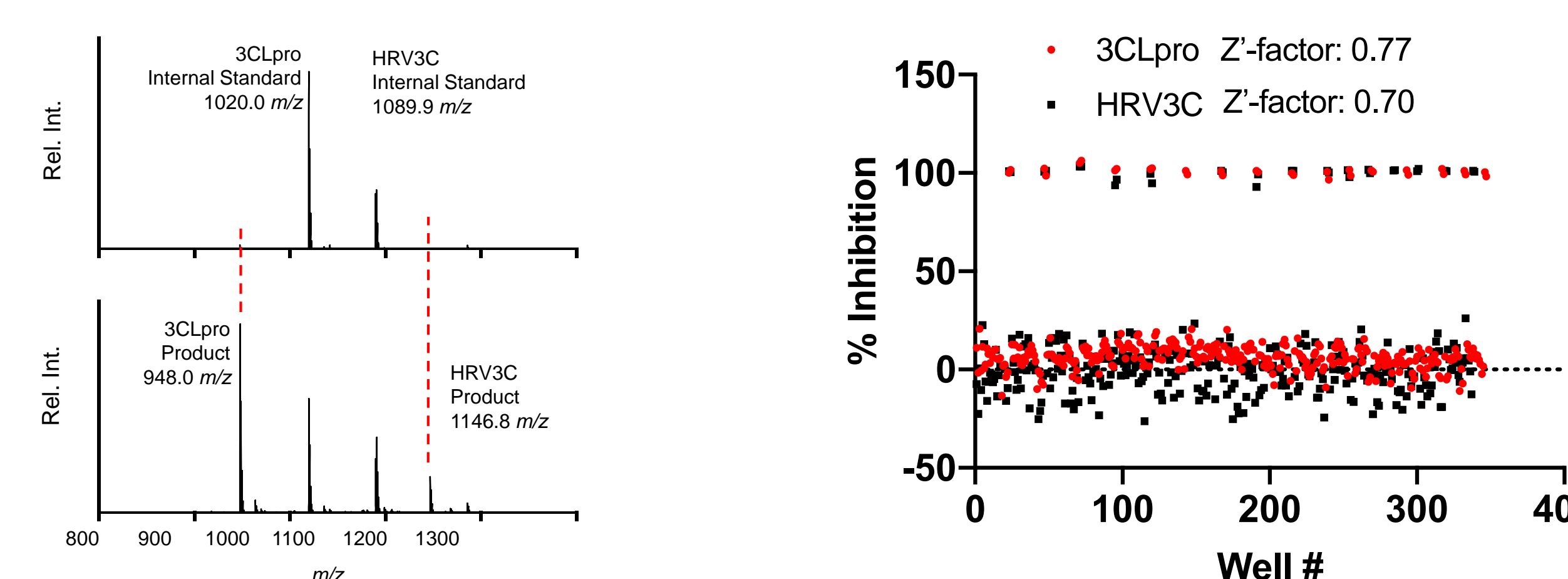


	Cpd 11a ⁵	6j ⁶	6e ⁶	Cpd 13b ⁷	Cpd 11r ⁸	A9 ⁹
	W Dai et al, Science (2020)	Rathnayake, A. et al Science Translational Medicine (2020)		L. Zhang et al., Science (2020)	L. Zhang et al J.Med Chem (2020)	WO2020030143
Cathepsin L IC ₅₀ (nM)	<0.5	<0.5	<0.5	214	<0.5	<0.5
SARS-CoV-2 IC ₅₀ (nM)	7	11	9	510	1290	7118
SARS-CoV-2 Huh-7 EC ₅₀ (nM)*	<50	<50	242	3676	2	<46

EC₅₀ E64D: 80 nM; Z-F-FMK <50 nM

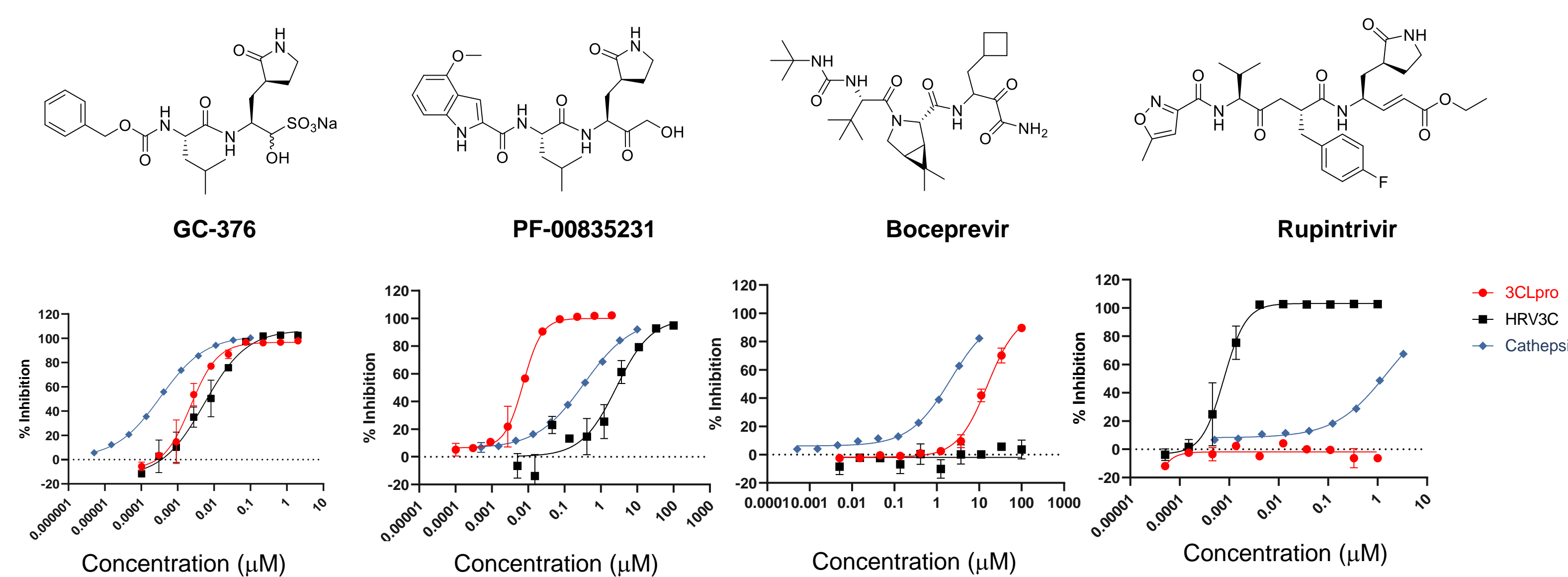
- The majority of reported SARS-CoV-2 Mpro inhibitors are also cathepsin L inhibitors

Development of a Multiplex 3CLpro/HRV3C Protease Assay



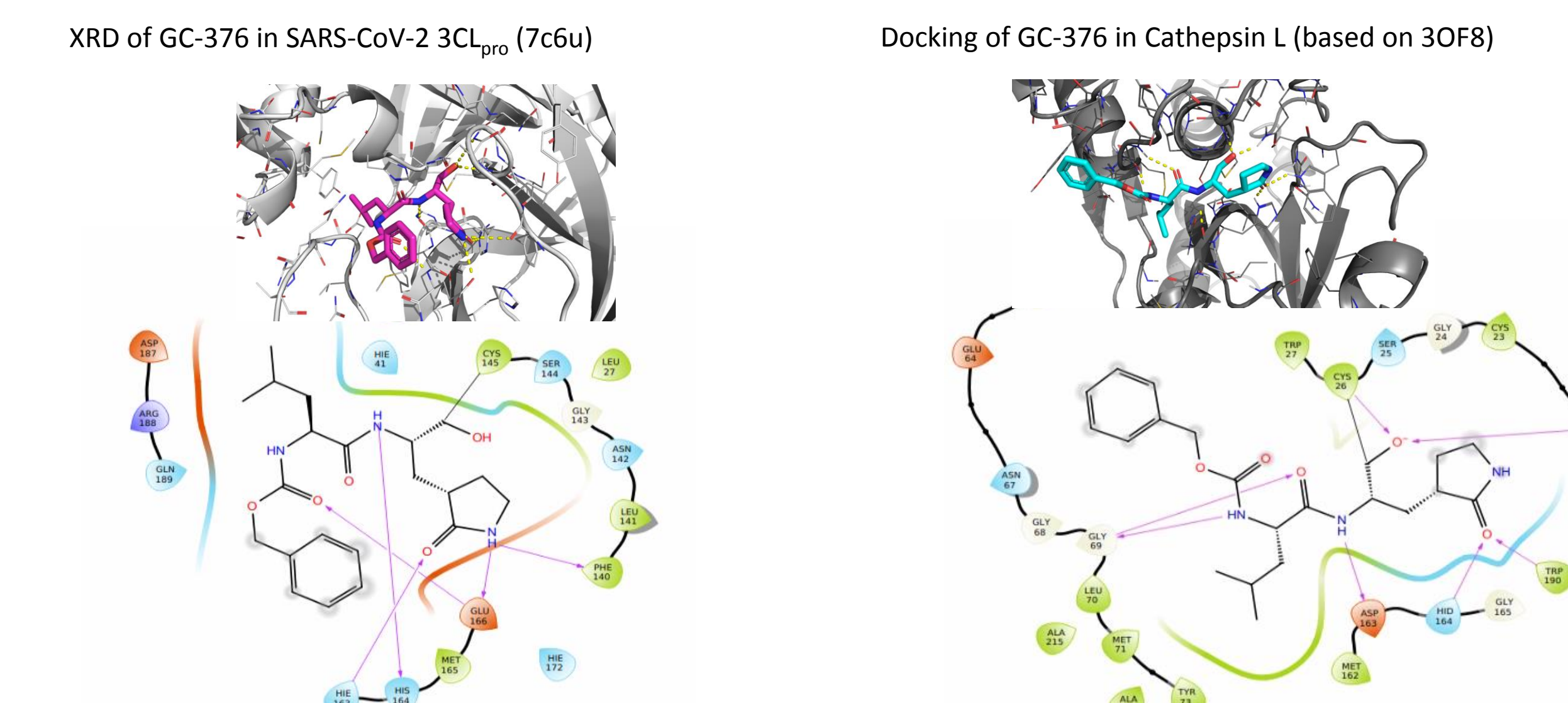
- The 3CLpro/HRV3C protease assay is based on mass spectrometry relies on high enzyme/substrate specificity
- Each compound was tested against 3CLpro/HRV3C and cathepsin L (FRET assay)

Activity of Selected Compounds vs. SARS-Cov-2 3CLpro, HRV3C and Cathepsin L



- GC-376 inhibits cathepsin L more potently than 3CLpro and HRV3C
- PF-00835231, boceprevir, and rupintrivir all show some degree of 3CLpro selectivity

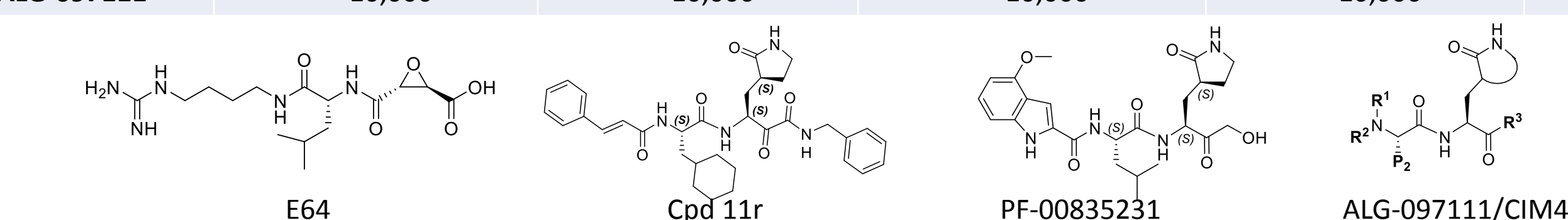
Structure Analysis of GC-376 Bound to SARS-CoV-2 3CLpro/Cathepsin L



- Despite very low identity overlap (<10%), GC-376 is active on both SARS-CoV-2 3CLpro and cathepsin L

SARS-CoV-2pro Inhibitors can Achieve a High Degree of Selectivity towards Cathepsin L

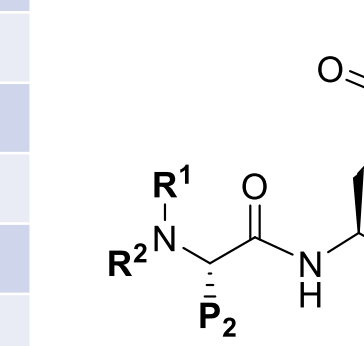
Compound ID	Cathepsin L 84 μM Substrate 10 uM IC ₅₀ (nM)	Cathepsin L 50 μM Substrate 20 uM IC ₅₀ (nM)	Cathepsin L 50 μM Substrate 20 uM IC ₅₀ (nM)	Cathepsin L 10 μM Substrate 2 uM IC ₅₀ (nM)	Cathepsin L 10 μM Substrate 2 uM IC ₅₀ (nM)
E64	1.9	4.4	4.1	4.9	5.6
Cpd 11r	<0.5	0.21	0.17	0.18	0.35
PF-00835231	2,250	1,308	1,085	456	427
ALG-097111	>>10,000	>>10,000	>>10,000	>>10,000	>>10,000



- Unlike all SARS-CoV-2_{pro} tested benchmarks, ALG-097111 did not inhibit Cathepsin L protease activity

Conclusions and Perspectives

	ALG-097111/CIM412	ALG-161/CIM780
SARS-CoV-2 3CLp IC ₅₀ (SAMD1)/Ki (FRET) (μM)	0.008/0.001	0.008/-
Cathepsin L IC ₅₀ (μM)	>10	>10
SARS-CoV2 Huh-7 EC ₅₀ /CC ₅₀ (μM)	1.3 (n=2)/ >100	ongoing
OC43(Hela) EC ₅₀ /CC ₅₀ (μM)	0.134 (n=3)/ >100	0.057 (n=2)/ >100
HLM t _{1/2} (min)	>60	49.5
Human Hepatocyte t _{1/2} (min)	>360	ongoing
Kin Sol (μM) PBS/Fassif/FeSSIF/pH2	>500	ongoing
CYP inhibition at 10 uM	All <50%	ongoing
Plasma stability (R/H) t _{1/2} (min)	>480 ea	ongoing
SIF + Pancreatin/SGF t _{1/2} (min)	>480 ea	ongoing



- SARS-CoV-2 3CLpro (Mpro) represents an attractive target
- Cellular potency of reported SARS-CoV-2 3CLpro is at least partially mediated by Cathepsin L protease activity
- We have developed a multiplex protease assay that was used to optimize our series of SARS-CoV-2 3CLpro inhibitors
- Our lead compound ALG-097111 is a potent SARS-CoV-2 3CLpro inhibitor, which did not inhibit Cathepsin L protease activity up to the highest concentration tested (IC₅₀>10μM)
- ALG-097111 exhibits promising drug-like properties

References

1. Therapeutic Strategies Against COVID-19 and Structural Characterization of SARS-CoV-2: A Review. Jeong GU et al. (2020) *Front. Microbiol.* 11:1723. doi: 10.3389/fmicb.2020.01723
2. a) Discovery of Ketone-Based Covalent Inhibitors of Coronavirus 3CL Proteases for the Potential Therapeutic Treatment of COVID-19 Hoffman, R. L et al. *J. Med. Chem.* 2020, DOI: 10.1021/acs.jmedchem.0c01063 *J. Med. Chem.* 2020, 63, 21, 12725–12747; b) Discovery of a Novel Inhibitor of Coronavirus 3CL Protease as a Clinical Candidate for the Potential Treatment of COVID-19 Boras, B.; et al. *bioRxiv* 2020, DOI: 10.1101/2020.09.12.293498
3. Broad-spectrum Antivirals Against 3c or 3c-like Proteases of Picornavirus-like Supercluster: Picornaviruses and Coronaviruses WO2013049382
4. A cysteine protease inhibitor blocks SARS-CoV-2 infection of human and monkey cells Mellott, D. et al, *bioRxiv* 2020 DOI:10.1101/ 2020.10.23.347534
5. Structure-based design of antiviral drug candidates targeting the SARS-CoV-2 main protease W. Dai et al., *Science* 10.1126/science.abb4489 (2020).
6. 3C-like protease inhibitors block coronavirus replication in vitro and improve survival in MERS-CoV-infected mice Rathnayake et al. *Science Translational Medicine* (2020), Vol. 12, Issue 557, eabc5332. DOI: 10.1126/scitranslmed.abc5332
7. Crystal structure of SARS-CoV-2 main protease provides a basis for design of improved α-ketoamide inhibitors L. Zhang et al., *Science* DOI: 10.1126/science.abb3405 (2020).
8. α-Ketoamides as Broad-Spectrum Inhibitors of Coronavirus and Enterovirus Replication: Structure-Based Design, Synthesis, and Activity Assessment. L. Zhang et al. *J. Med. Chem.* 2020, 63, 9, 4562–4578; DOI:10.1021/acs.jmedchem.9b01828
9. Ketoamide Compound and Preparation Method, Pharmaceutical Composition, and use thereof WO2020030143