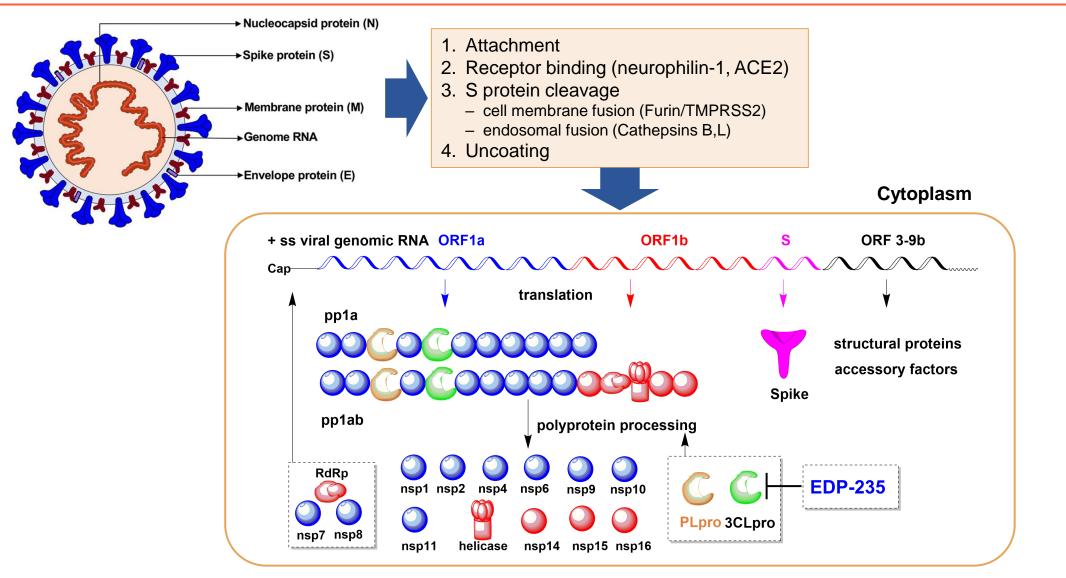


Molecular Basis for the Antiviral Action of EDP-235: A Potent and Selective SARS-CoV-2 3CLpro Inhibitor

Anand Balakrishnan

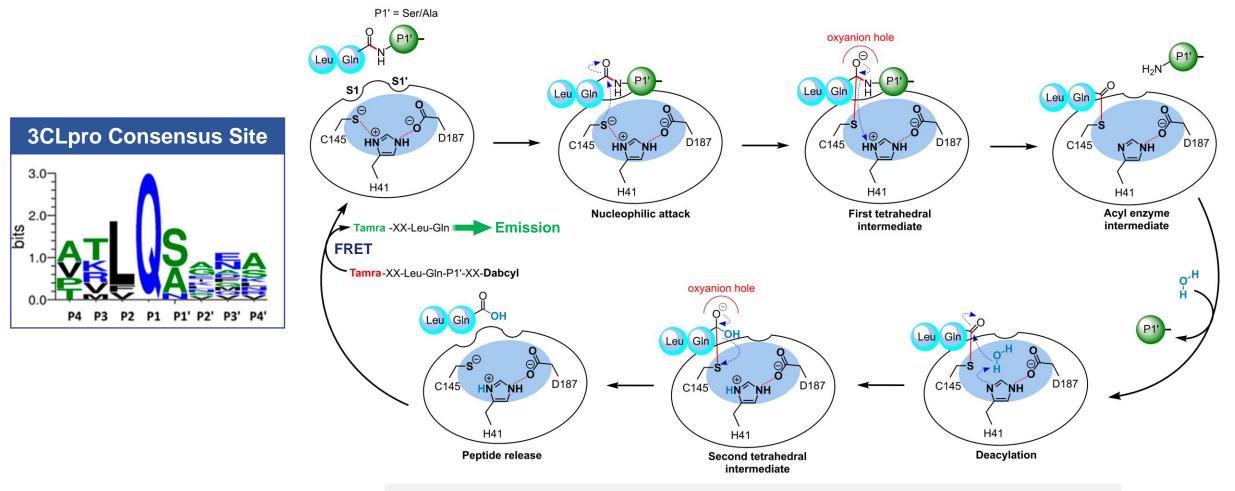
2022 Annual Meeting of ASBMB April 4th, 2022

SARS-CoV-2 life cycle and enzyme targets for antiviral development





Catalytic cycle of 3C-like protease from SARS-CoV-2

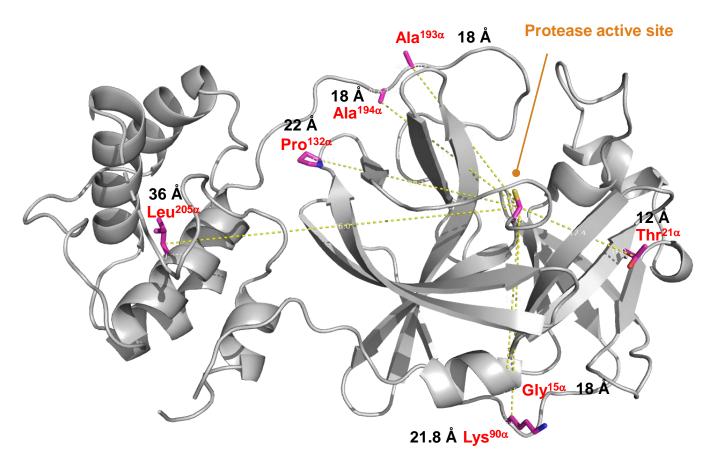


Catalytic activity monitored with FRET [fluorescence resonance energy transfer] assay

EDP-235 is a highly potent 3CLpro inhibitor and retains activity against SARS-CoV-2 variants



- 3CLpro is highly conserved across SARS-CoV-2 variants
- All variant enzymes were active in protease biochemical assays



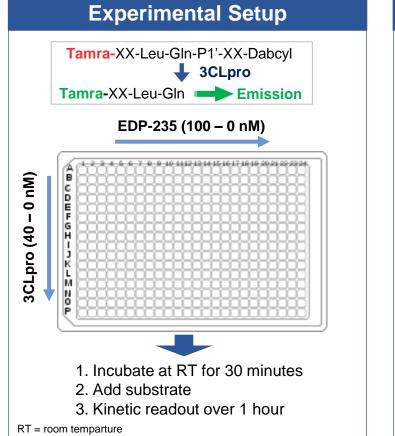
3CLpro Enzyme Assay				
SARS-CoV-2WHO3CLproLineageClassificationMutation		EDP-235 IC ₅₀ (nM)		
А	n/a	-	5.8 ± 3.7	
B.1.351	51 Beta K90R 2.8 ±		2.8 ± 0.9	
B.1.351.2	Beta	K90R/A193V	5.4 ± 1.0	
P.2	Zeta	L205V	3.4 ± 1.0	
B.1.617.3	n/a	A194S	5.7 ± 0.5	
B.1.1.318	n/a	T21I	2.0 ± 0.1	
C.36.3, C.37	n/a	G15S	4.7 ± 2.5	
B.1.1.529	Omicron	P132H	4.1 ± 0.8	

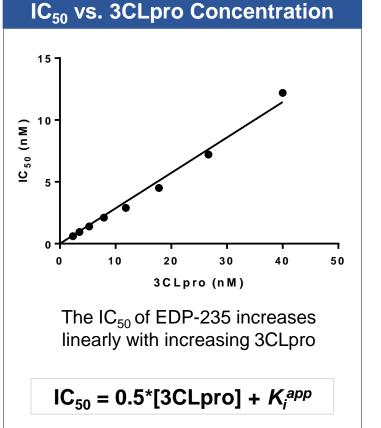
	Live \	/irus		
SARS-CoV-2 WHO Lineage Classification		3CLpro Mutation	EDP-235 EC ₅₀ (nM)	
А	n/a	-	5.1	
B.1.617.2	Delta	-	4.3	
B.1.1.529	Omicron	P132H	7.3	

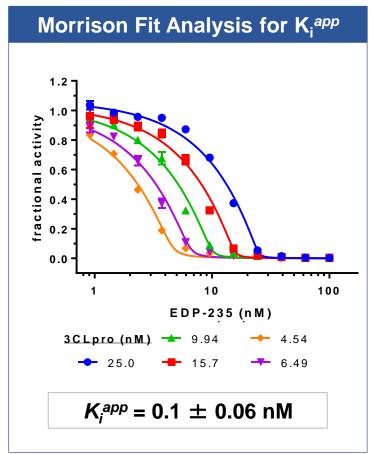
 IC_{50} = half-maximal inhibitory concentration. *The 3CLpro sequences for the ancestral A lineage and B.1.617.2 (Delta) variant are identical. Antiviral activity determined in the presence of a p-glycoprotein inhibitor.



EDP-235 is a tight-binding inhibitor of SARS-CoV-2 3CLpro

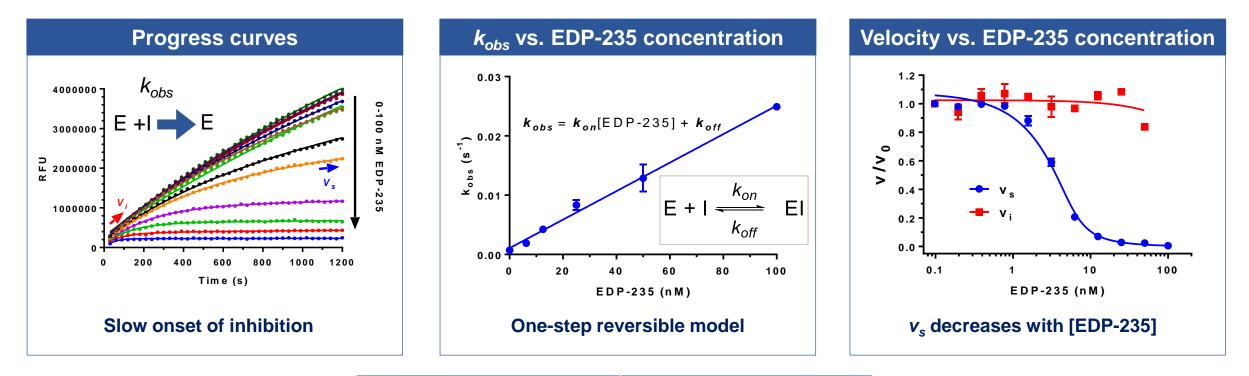








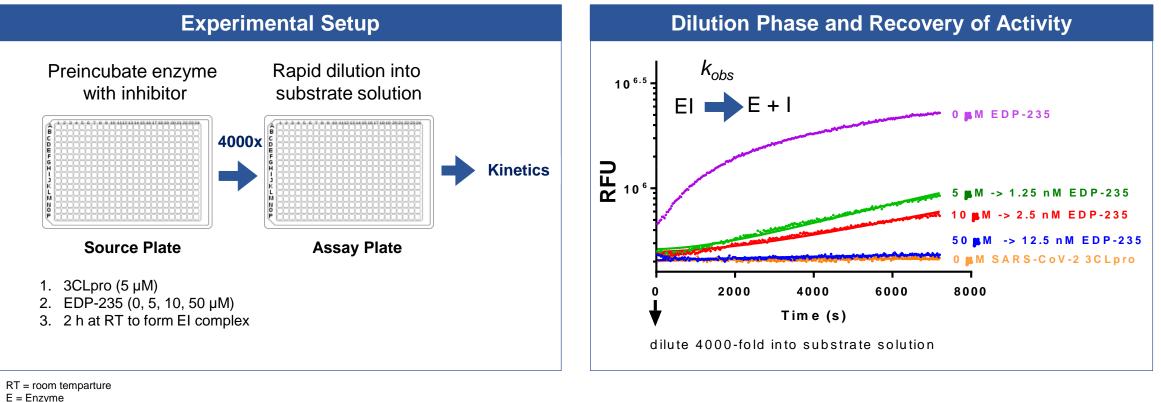
EDP-235 is a time-dependent inhibitor of SARS-CoV-2 3CLpro



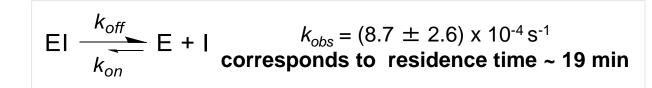
	Parameter	Value Mean ± SD, n=3	
	k _{on}	(2.6 ± 1.6) x 10 ⁵ M ⁻¹ s ⁻¹	$\sim k_{cat}/K_m = 2.1 \text{ x}10^5 \text{ M}^{-1}\text{s}^{-1}$
	k _{off}	(9 ± 1) x 10 ⁻⁴ s ⁻¹	
-	K_i^{app}	4.7 ± 2.4 nM	



EDP-235 is a reversible inhibitor of SARS-CoV-2 3CLpro



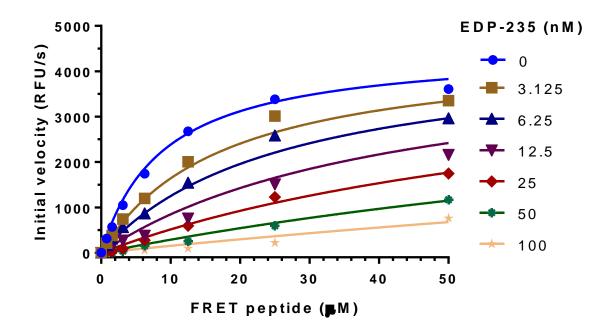
L = LinzyineI = Inhibitor



EDP-235 is a substrate competitive inhibitor of SARS-CoV-2 3CLpro



Kinetic Analysis with Respect to Substrate



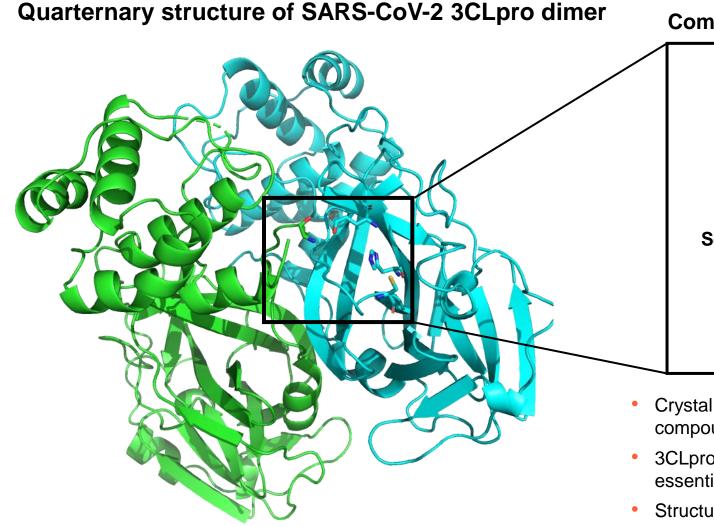
EDP-235 is a competitive inhibitor with respect
to the FRET peptide substrate

Summary of Kinetic Mechanism Characterization

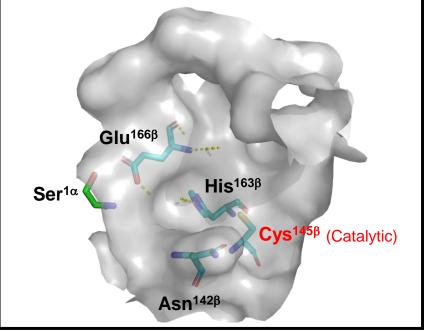
Parameter	Value	
IC ₅₀	5.8 nM	
K _i	$3.0 \pm 1.6 \text{ nM}$	
k _{on}	(2.6 \pm 1.6) x 10 ⁵ M ⁻¹ s ⁻¹	
k _{off}	$(8.7 \pm 2.6) \text{ x10}^{-4} \text{ s}^{-1}$	
Residence time	~ 19 min	
Kinetic Mechanism	Time-dependent, reversible, Substrate competitive inhibition	



EDP-235 analog binds at the active site of SARS-CoV-2 3CLpro



Compound binding site with key residues



- Crystal structures of apo 3CLpro and co-structures of key compounds were obtained at 2.5-2.8 Å.
- 3CLpro crystallized as a dimer and active site residues make essential polar contacts with compounds.
- Structures provide support for mechanism of inhibition of EDP-235.

EDP-235 shows antiviral activity against all human coronaviruses



Virus IC ₅₀ (nM)		Live Virus Assay					
			Cell Type	Endpoint	EC ₅₀ (nM)	CC ₅₀ (nM)	SI
	SARS-CoV-2	5.8	Vero E6*	CPE	5.1	>10,000	>1,960
	HCoV-229E	5.4	MRC-5	CPE	3.6	>50,000	>13,889
	HCoV-HKU1	3.8	-	-	-	-	-
	HCoV-NL63	1.8	LLC-MK2	RT-qPCR	6.1	-	-
	HCoV-OC43	3.4	HCT-8*	RT-qPCR	56	-	-
	SARS-CoV	1.9	Vero E6*	CPE	24	>3,000	>125
	MERS-CoV	70	Vero 76	CPE	150	>26,000	>173
				Viral Yield	130 [EC ₉₀]	>26,000	>200

*Assay performed in the presence of a P-glycoprotein inhibitor (CP-100356, 2 μ M) to prevent transporter-mediated efflux. CPE = cytopathic effect; P-gpi = P-glycoprotein inhibitor CP-100356 (2 μ M); qPCR = quantitative polymerase chain reaction. HCoV-229E, HCoV-HKU1, HCoV-OC43, HCoV-NL63 = human coronavirus 229E, HKU1, OC43, and NL63, respectively; SARS-CoV = severe acute respiratory syndrome; MERS-CoV = Middle East respiratory syndrome. Vero 76 and Vero E6 cells are derived from African green monkey kidney epithelia, MRC-5 are human lung fibroblasts, HCT-8 are derived from a human ileocecal adenocarcinoma, and LLC-MK2 are Rhesus monkey epithelial cells. pHAEC = primary human airway epithelial cells.

EDP-235 shows highly selective inhibition of 3CLpro compared to human proteases

Cysteine Proteases

- SARS CoV 2 PLpro, 3CLpro
- Caspases 1 11, 14

Cathepsins B, C, D, E, G, H, K, L, S, V

Papain, Calpain 1

Serine Proteases

- Trypsin
- TMPRSS 2
- Furin

Aspartyl protease

BACE1

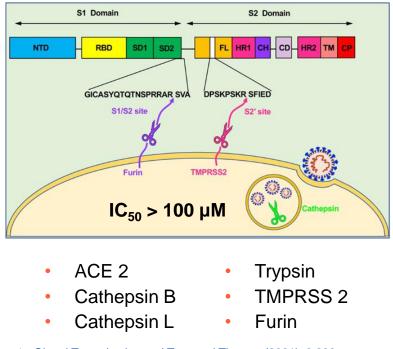
Zn metalloprotease

• ACE 1, 2

- Tested against 31 host proteases of diverse classes
- IC₅₀ > 100 µM against 23 out of 31 including host proteases relevant to viral infection

Target	EDP-235 IC ₅₀ (µM)		
Caspase 2	4.6		
Caspase 3	4.2		
Caspase 6	2		
Caspase 7	4.7		
Caspase 8	22.5		
Caspase 9	4.7		
Caspase 14	9		
Cathepsin K	18.5		
SARS-CoV-2 3CLpro	0.0058		
Selectivity Index	> 340		
Cysteine I	Proteases		

Host proteases in viral entry/fusion



Signal Transduction and Targeted Therapy (2021). 6:233
Int. J. Mol. Sci. (2020), 21(24), 9523

Molecular mechanism of EDP-235 action and its pharmacological effect



Molecular Observations	In vitro Pharmacology	Preclinical Properties		EDP-235 ¹
Time-dependence/on-target residence time	High potency and antiviral efficacy	Mechanisr	n	Protease Inhibitor
		Detensy	Enzyme IC ₅₀ (nM)	5.8
Substrate competitive /active site binder	Broad spectrum anti-coronaviral	Potency Vero Cell EC ₅₀ (nM)		5.1
Strong interactions with highly	High barrier to resistance	Oral Bioav	railability ²	95%
conserved active-site residues		Lung/Plasma ratio ³		4.1
High degree of selectivity over other mammalian proteases	On target pharmacology and low off-target effects	Projected Efficacious Dose		100 – 500mg QD
		1. Jiang <i>et al.,</i> IS	IRV Poster #120, Oct 19, 2021	

2. Oral bioavailability in rats for EDP-235

3. AUC lung to plasma ratio in rats for EDP-235



Acknowledgements

Virology
Archie Reyes
Nalini Bisht
Joyce Sweeney
Rachel Levene
Nicole McAllister
Tessa Cressey
Nathan Manalo
Miranda Crepeau
Michael Rhodin
Michael Vaine
Bryan Goodwin

Medicinal Chemistry Ruichao Shen Guoqiang Wang Joe Panarese Yat Sun Or

Program Management

Manami Shizuka





www.enanta.com

