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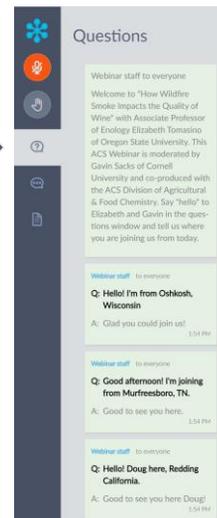
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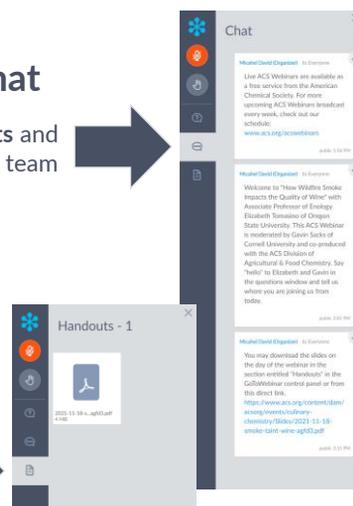
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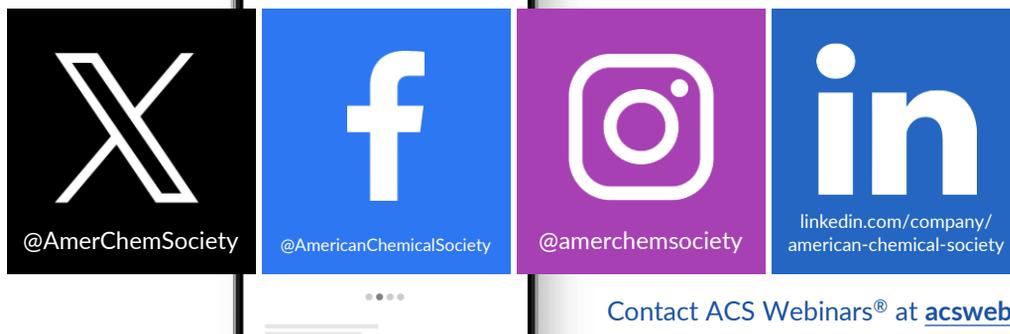


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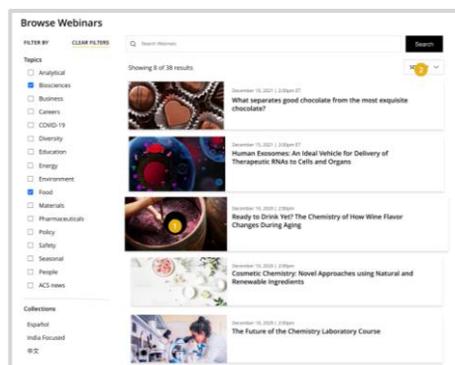
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ACS Career Resources



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Personal Career Consultations

Jim Tung

Assistant
Lacamas Laboratories

S.L. Biochemistry, University of Oregon
Ph.D., Organic Chemistry, University of Notre Dame

Jim Tung works at Lacamas Laboratories in Portland, OR, currently as a business development manager. He has been with Lacamas for 10 years, working on developing new chemical manufacturing projects. Before that, he was a senior research chemist at Orlite Research in Champaign, IL, performing kilo-scale organic chemistry.

An Oregon native, Jim got his B.S. in biochemistry from the University of Oregon, his Ph.D. in organic chemistry from the University of Notre Dame, with postdoctoral experience at Pfizer's laboratories in La Jolla, CA. He is past chair of the Portland Section of the American Chemical Society and was 2019 general co-chair of NORM 2019. He has interests in process chemistry, labor economics, social media outreach and encouraging career exploration and development for younger chemists.

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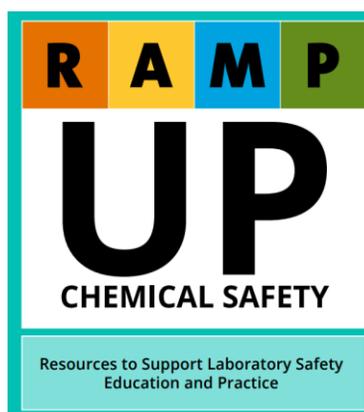
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A complete listing of ACS Safety Programs and Resources



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<p>ACS Publications DEIR Hub See what ACS Publications is doing for fostering inclusivity in scholarly publishing</p>	<p>ACS Volunteer and ACS Meetings Code of Conduct Fostering a positive and welcoming environment for attendees, volunteers and staff.</p>
<p>C&EN Trailblazers C&EN highlights scientists from different backgrounds who are making an impact in chemistry.</p>	<p>NEW! Download DEIR Educational Resources Download this educational guide for additional recommendations on videos, articles, books, podcasts, and more on diversity, inclusion, and related topics.</p>
<p>Quick Guide: Inclusion Moments Learn more about what Inclusion Moments are and see ideas to host them during your meetings.</p>	<p>Quick Guide: How to host inclusive in-person events Recommendations and best practices to ensure that your events can accommodate everyone.</p>

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Fungal Foes: Understanding the Challenges of Fungal Infections and New Treatment Options



HONGMIN LI, PhD

Professor, R. Ken and Donna Coit Endowed
Chair in Drug Discovery, Department of
Pharmacology and Toxicology, College of
Pharmacy, University of Arizona, Tucson



SEAN EKINS, PhD, D.Sc.

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The Prp8 Intein as a novel Target for Inhibition of Pathogenic Fungi

Hongmin Li

Professor, R. Ken and Donna Coit Endowed Chair in Drug Discovery

Department of Pharmacology and Toxicology

College of Pharmacy



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- Background
- High throughput screening assay
- Inhibition of the prp8 intein by cisplatin
- Inhibition of *C. neoformans* by Prp8-inhibitors

Li et al. (2019), *Emerging microbes & infections*, 8(1): 895–908

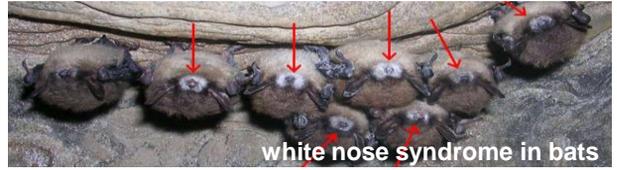
Green et al (2019), *Plos Biol*, doi.org/10.1371/journal.pbio.3000104

Li et al. (2021), *PNAS*, **118** (2), e2008815118

Anil et al. (2022), *ACS Infect Dis*, 8, 1851-68

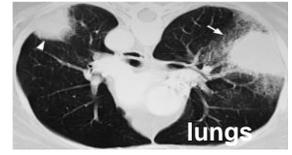
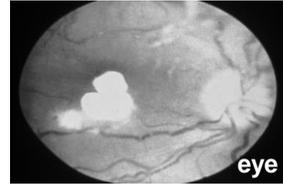
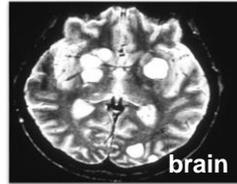


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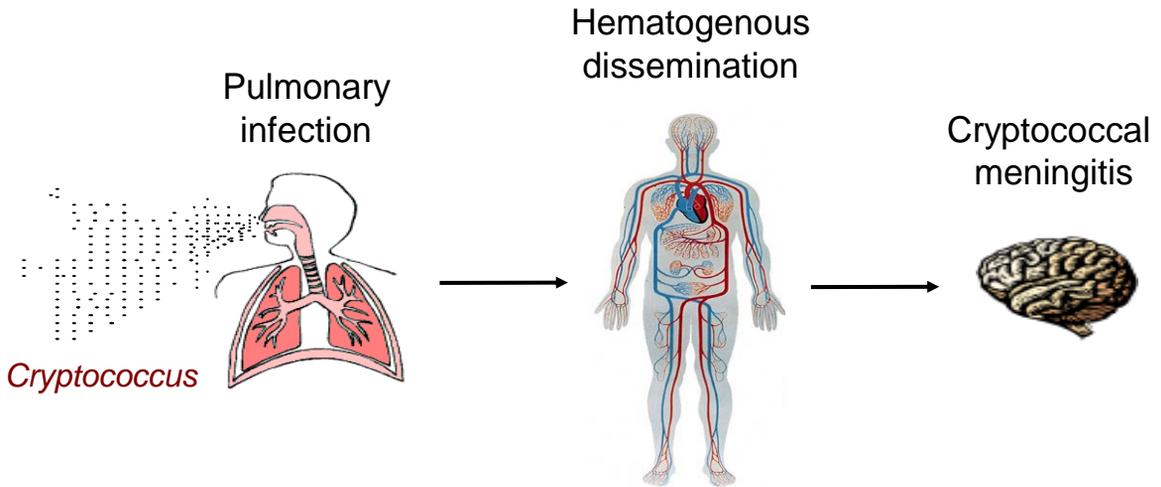
Fungal Infections

Cryptococcus



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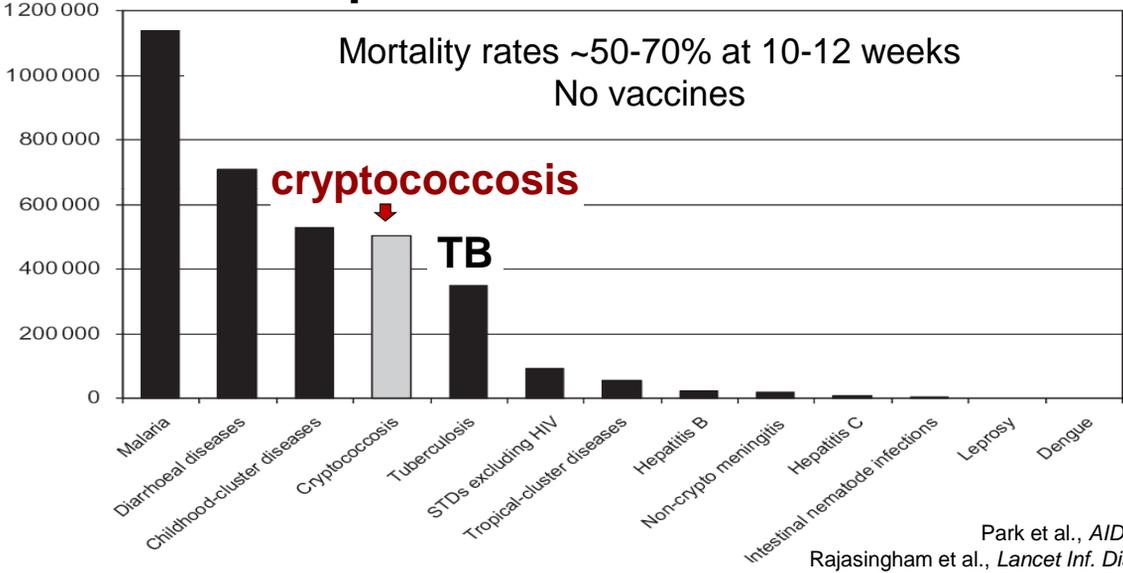
Cryptococcus infection



Lin and Heitman, *Ann Rev Microbiol* 2006, 60, 69-105

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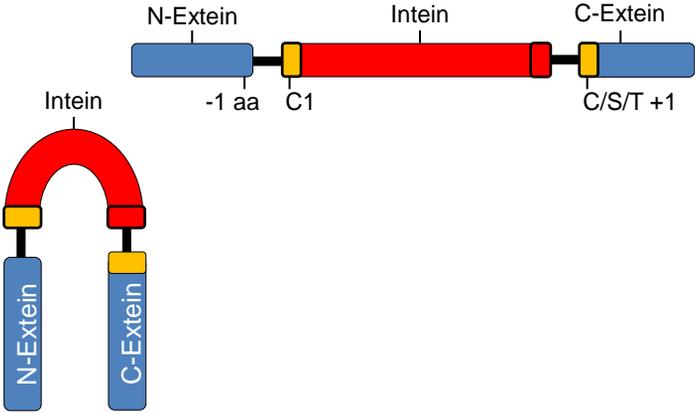
Cryptococcosis causes 15% of deaths in AIDS patients worldwide



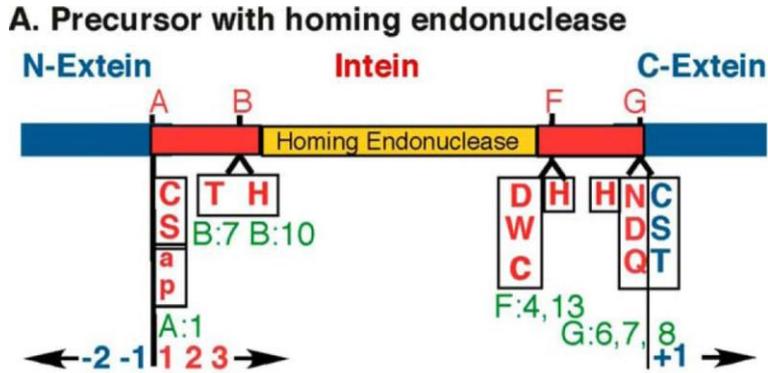
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Microbial inteins as drug target

Intein is a mobile self-splicing element within a host protein similar to an intron between exons



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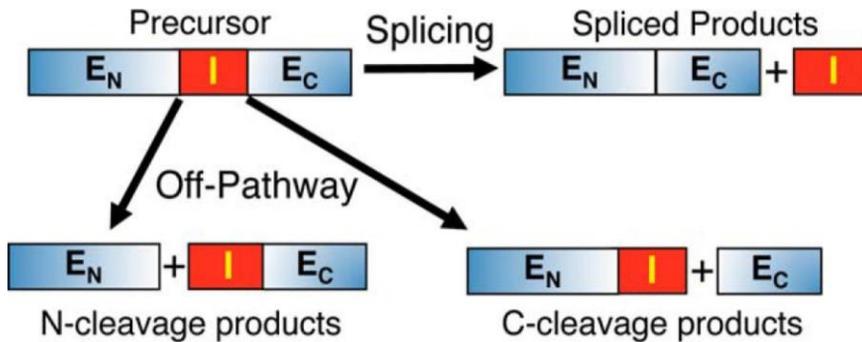


Mills et al (2014) JBC, 289, 14498-14505



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Potential intein reactions

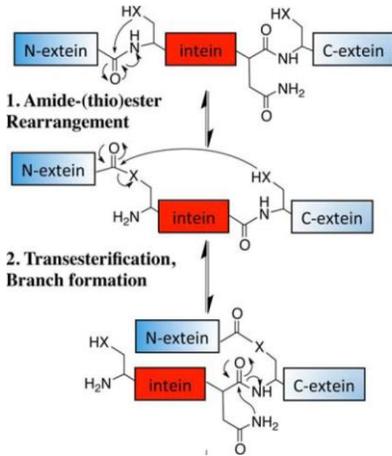


Mills et al (2014) JBC

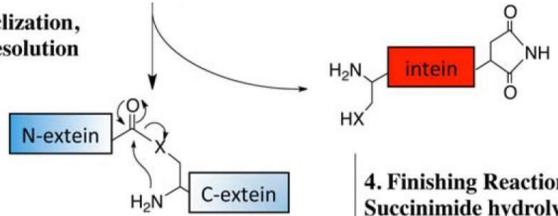


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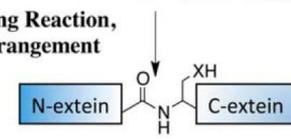
Class I intein splicing mechanism



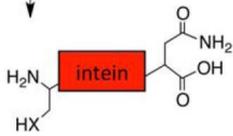
3. Asn cyclization, Branch resolution



4. Finishing Reaction, Acyl rearrangement



4. Finishing Reaction, Succinimide hydrolysis

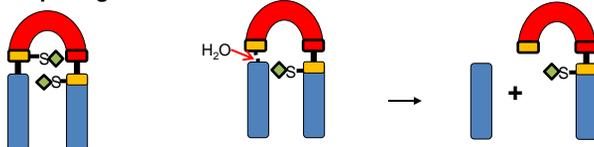


Mills et al (2014) JBC



Splicing mechanism and inhibition

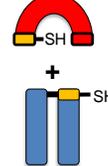
No Splicing



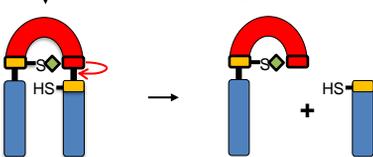
N-Terminal cleavage



Splicing



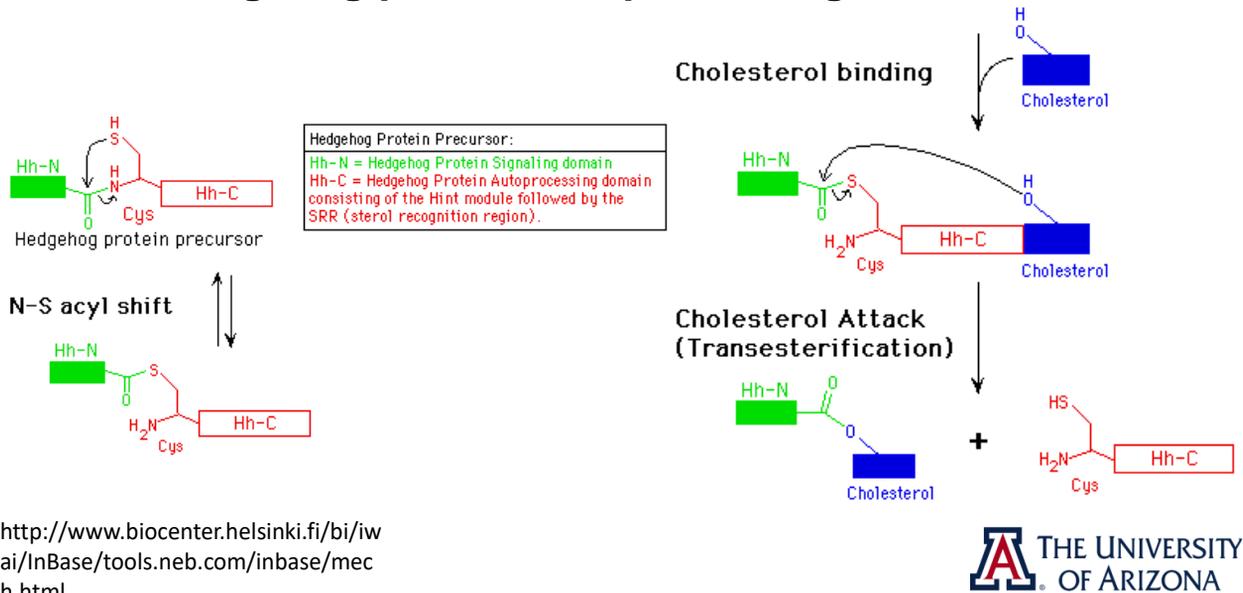
C-Terminal cleavage



- Intein
- Extein
- Cysteine
- Amide bond
- ⋮ Thioester bond
- ◆ Inhibition



Hedgehog protein autoprocessing mechanism



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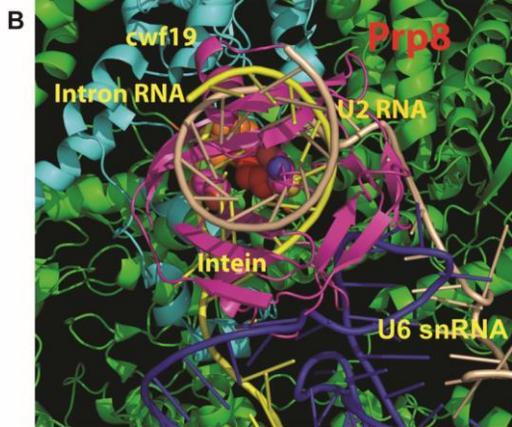
Pathogenic fungi contain the prp8 intein

- **Example Prp8 intein-containing pathogenic fungi:**
 - *Cryptococcus neoformans* and *C. gattii* - *Trichophyton rubrum*
 - *Aspergillus fumigatus* - *Blastomyces dermatitidis*
 - *Histoplasma capsulatum* - *Microsporium gypseum*
 - *Paracoccidioides brasiliensis* - *Trichosporon asahii*
 - *Neosartorya fischeri* - *Exophiala oligosperma*
 - *Microsporium canis* - *Fonsecaea pedrosoi*
 - *Botrytis cinerea* - *Rhinocladiella mackenziei*
 - *Emmonsia parva* (formerly *Chrysosporium parvum*)
- **Genes of human beings do not contain intein elements !**

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Prp8 is a critical component of the spliceosome

A Cga Prp8 WEKAC...intein...HNSGFE
 Cne Prp8 WEKAC...intein...HNSGFE
 Afu Prp8 WERAC...intein...HNSGFE
 Spo Prp8 WEKA-----SGFE



Schizosaccharomyces pombe (Spo)



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Cis-Pt is specific for intein prp8-containing *Cryptococcus* fungi

Table 1. Inhibition of pathogenic fungi by cisplatin. (MIC₅₀ and MIC₈₀ were defined as minimum inhibitory concentration required to kill fungus at 50% and 80% in µg/ml, respectively)

	Prp8 intein ?	Strain	Group	MIC ₅₀	MIC ₈₀
<i>C. neoformans</i>	Yes	NIH H99	VN I	0.92	2.6
		WM148	VN I	2.0	8.0
		WM626	VN II	1.4	7.9
<i>C. gattii</i>	Yes	NIH444	VG IIa	1.1	2.6
		WM276	VG I	1.9	15
		CA1222	VG IIIa	1.5	3.5
		VM779	VG IV	1.5	12
<i>Candida albicans</i>	No	ATCC90028		25	100

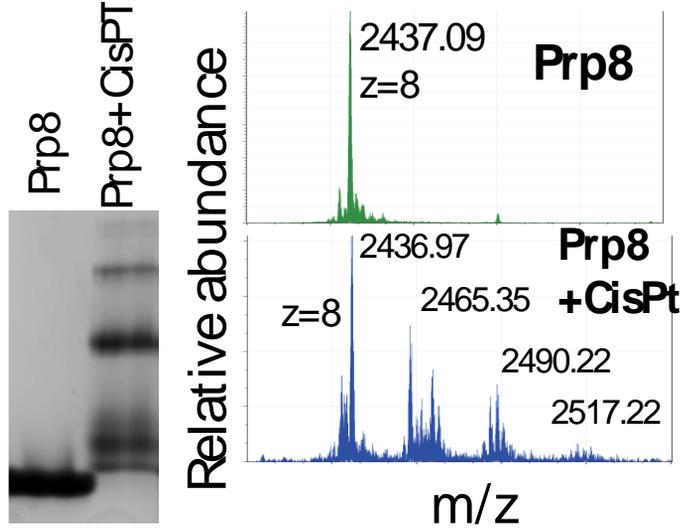
Photo courtesy of Dr. Lesley Moore, CDC



Li et al (2019) Emerging Microbes and Infection, 8(1): 895–908

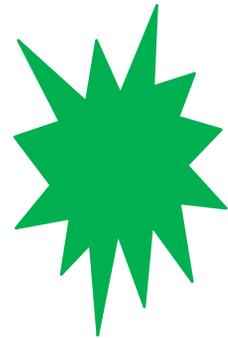
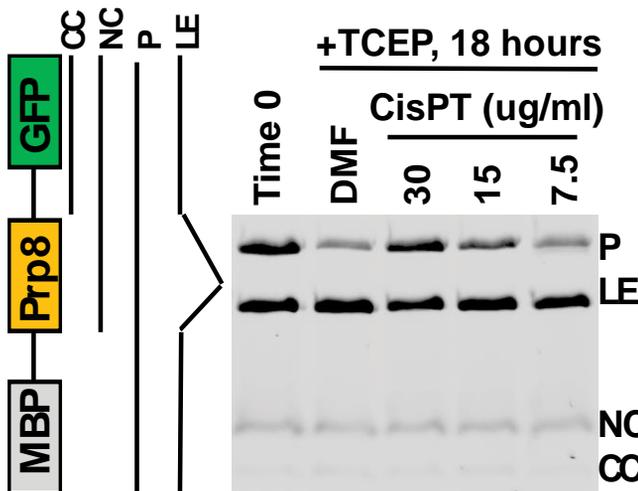
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Binding of CisPt to the Prp8 intein



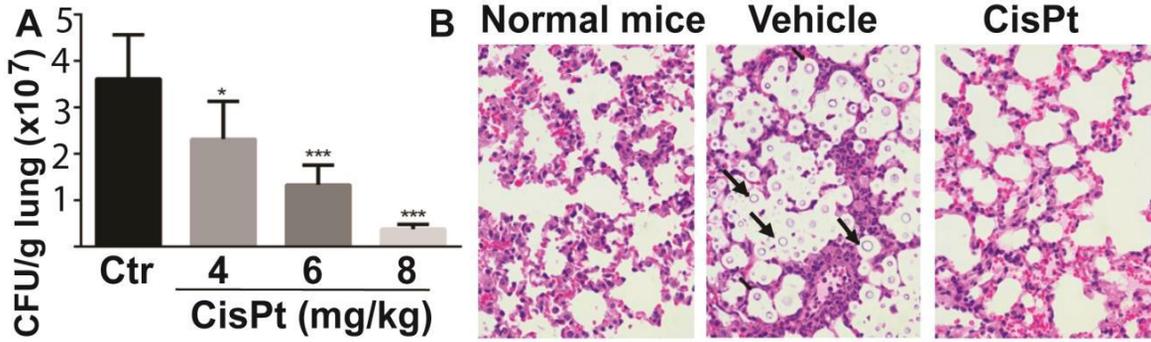
Li et al (2019) Emerging Microbes and Infection

Inhibition of in vitro splicing of the Prp8 intein by CisPt



Li et al (2019) Emerging Microbes and Infection

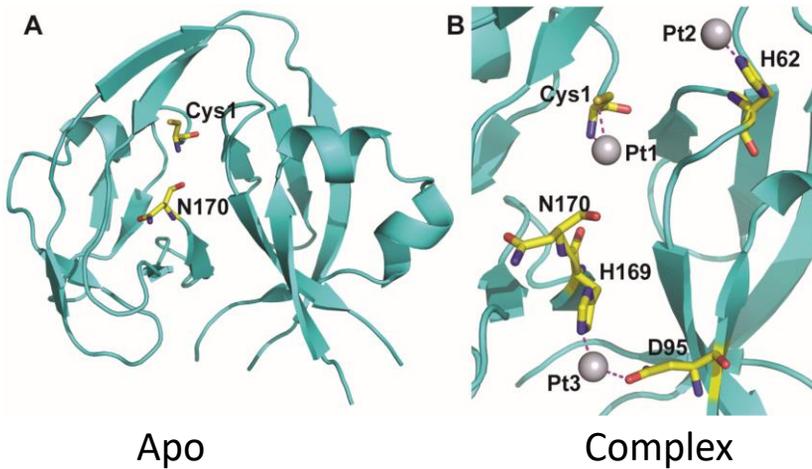
In vivo efficacy of CisPt in mouse model



Li et al (2019) Emerging Microbes and Infection



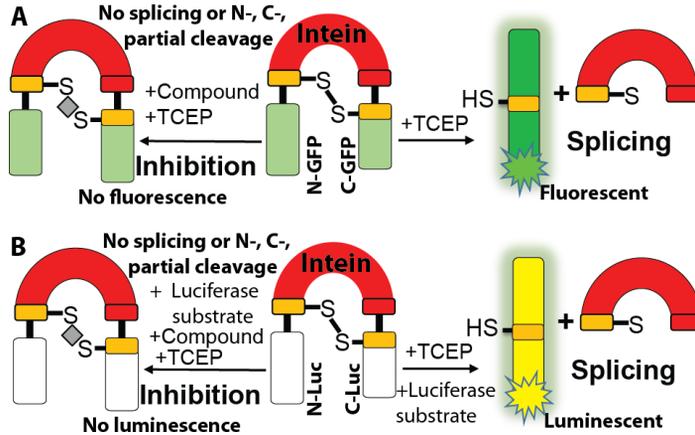
Cga Prp8-Cisplatin complex



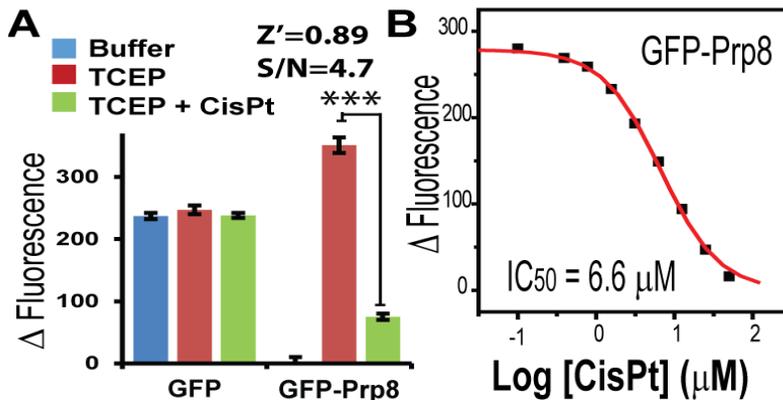
Li et al (2019) Emerging Microbes and Infection



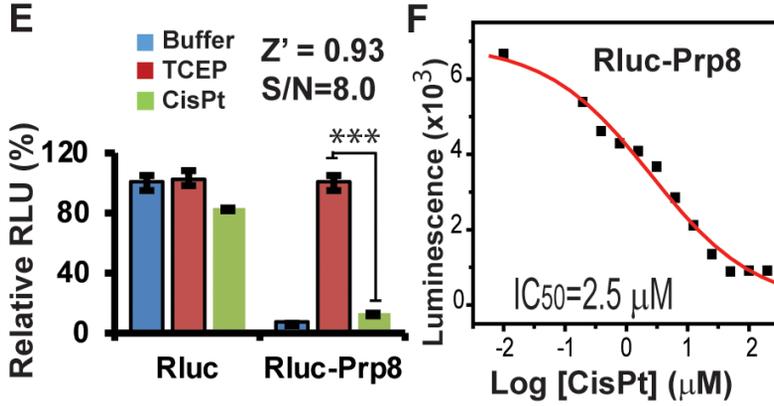
Development of split luciferase-based or GFP-based HTS assays



IC50 for cisplatin and HTS parameters



Split-Luc HTS assay

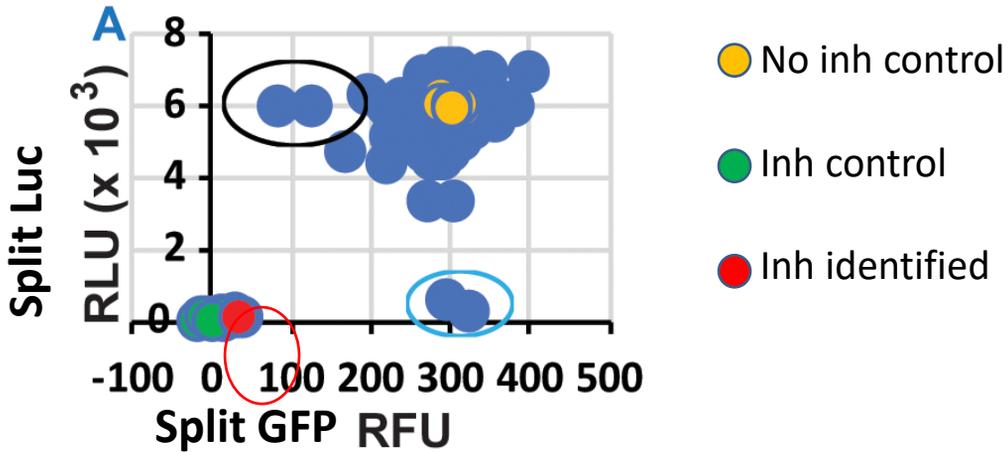


Li et al (2019) Emerging Microbes and Infection
Li et al (2021) PNAS, **118** (2), e2008815118



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Pilot screen

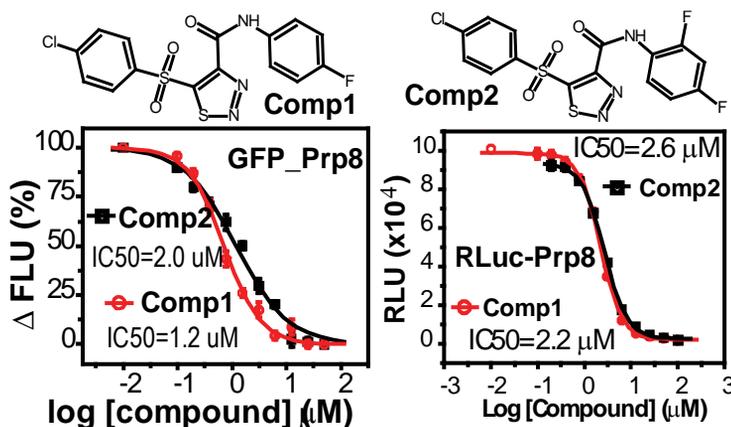


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Li et al (2021) PNAS, **118** (2), e2008815118



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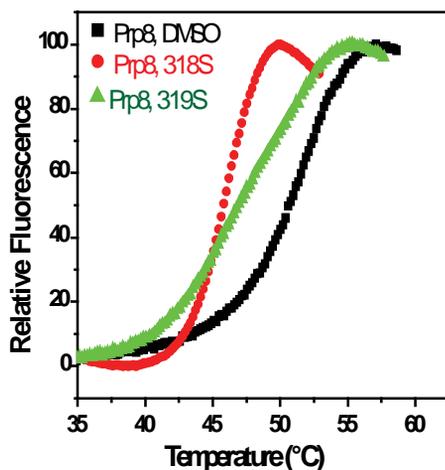
Inhibition of prp8 intein splicing by small molecule inhibitor



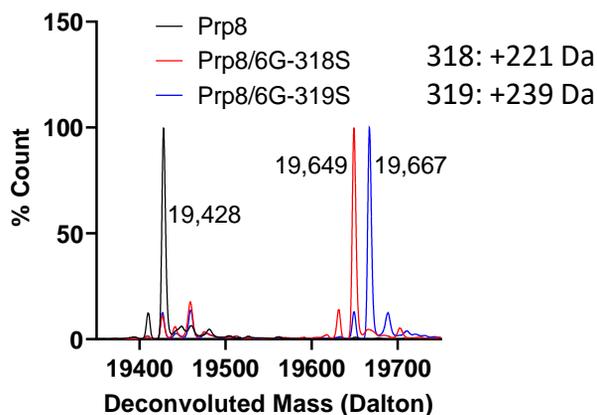
Li et al (2021) PNAS, **118** (2), e2008815118

47

Binding of small molecule to the prp8 intein



Protein thermal shift assay

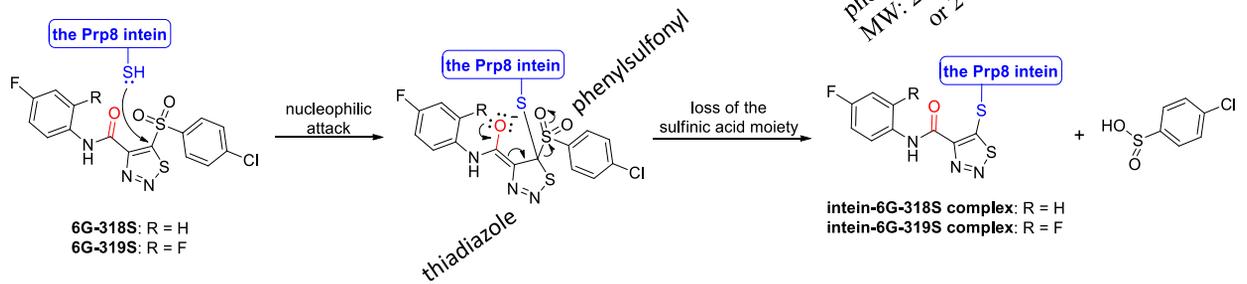


LC-MS/MS

Li et al (2021) PNAS, **118** (2), e2008815118

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Proposed chemistry

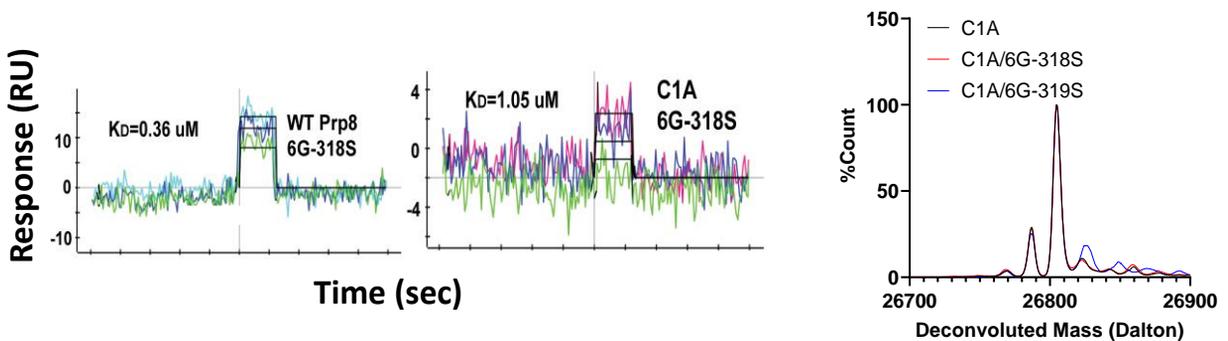


Li et al (2021) PNAS, **118** (2), e2008815118



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C1A mutation led to loss of binding of 6G-318S to the Prp8 intein



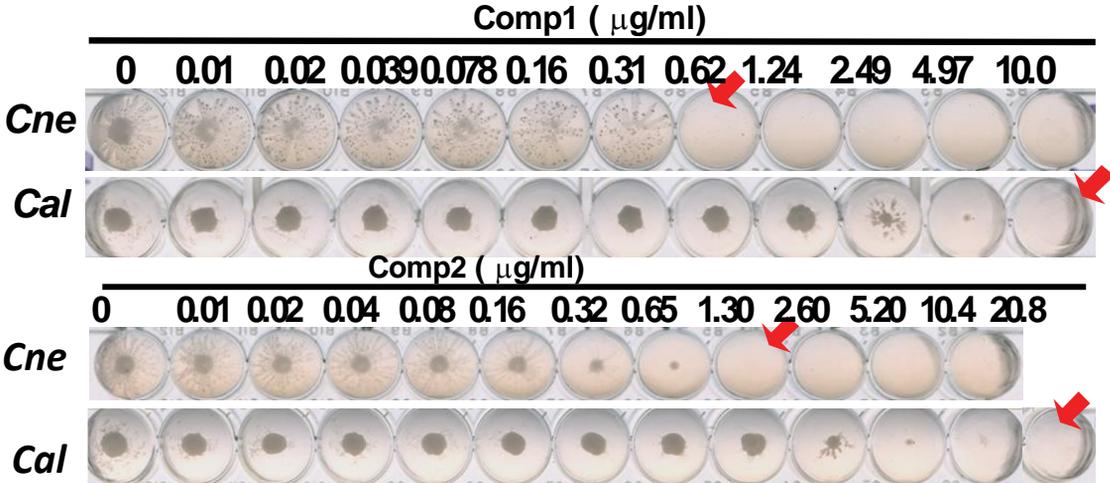
Surface plasmon resonance binding studies

Li et al (2021) PNAS, **118** (2), e2008815118



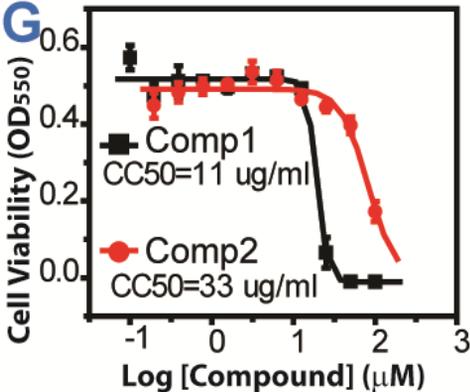
50

Inhibition of Prp8 intein-containing Cne but not *Candida albicans* (Cal) (no intein)



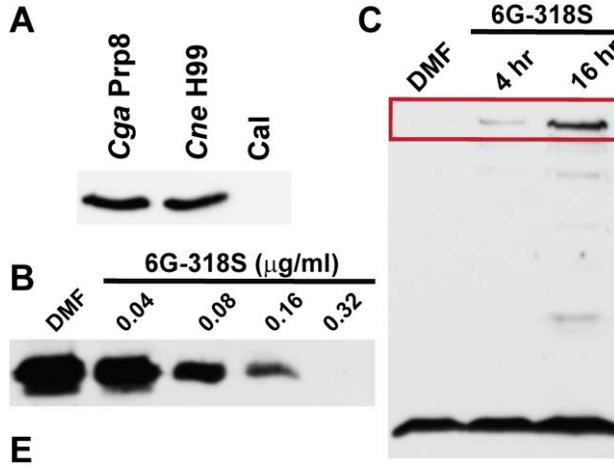
Li et al (2021) PNAS, 118 (2), e2008815118

Cell viability on A549 lung carcinoma cell



Li et al (2021) PNAS, 118 (2), e2008815118

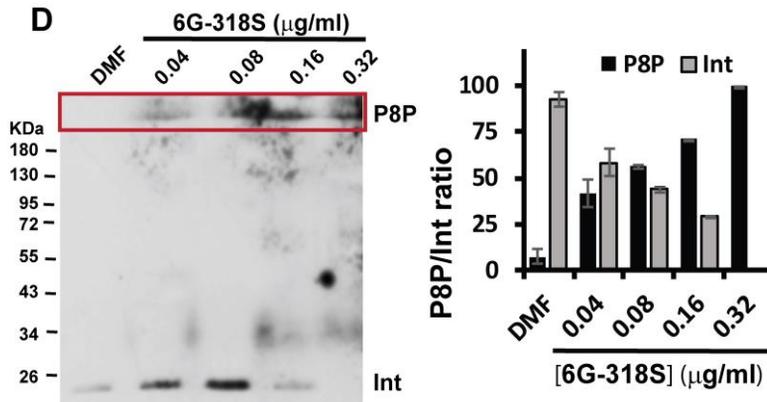
Inhibition of the Prp8 intein splicing *in vivo* by 6G-318S



Li et al (2021) PNAS, 118 (2), e2008815118



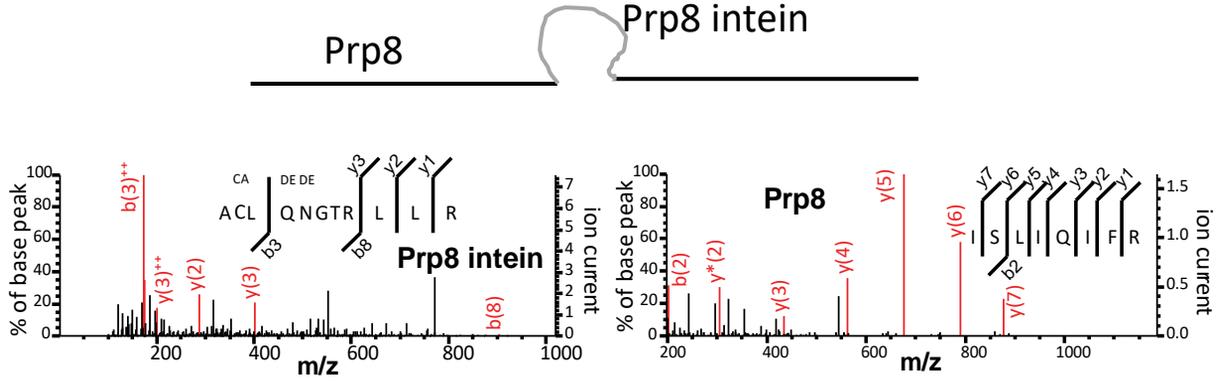
Dose-dependent inhibition of the Prp8 intein splicing *in vivo* by 6G-318S



Li et al (2021) PNAS, 118 (2), e2008815118



Identification of the Prp8 precursor by Mass Spectrometry

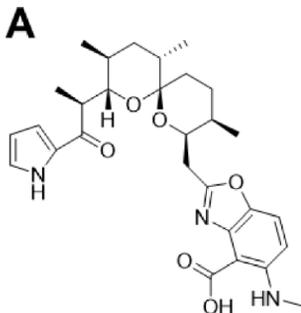


Li et al (2021) PNAS, 118 (2), e2008815118



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Calcimycin (CMN) specifically inhibits intein-containing but not intein-free *C. neoformans*



Species-Strain	MIC μM ($\mu\text{g/ml}$)
<i>C. neoformans</i> (Cneo-WT)	3.0 (1.5)
<i>C. neoformans</i> (Cneo-Mut)	>24 (12.0)
<i>C. gatti</i>	3.0 (1.5)
<i>C. amyloletus</i>	>50
<i>A. funigatus</i>	>25

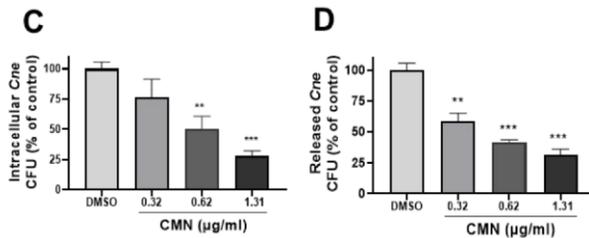
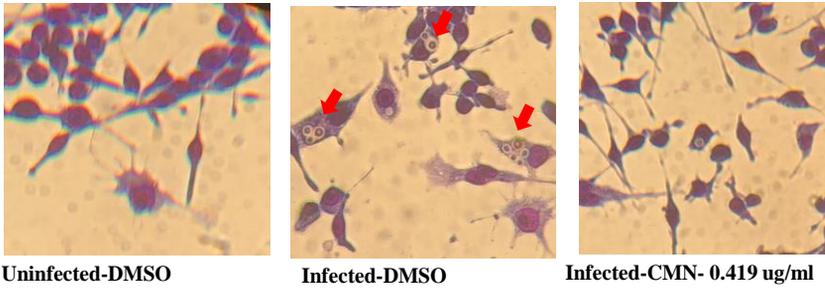
Calcimycin (CMN)

Anil et al. (2022), ACS Infect Dis, 8, 1851-68



56

CMN reduces macrophage intracellular infection of *C. neoformans*

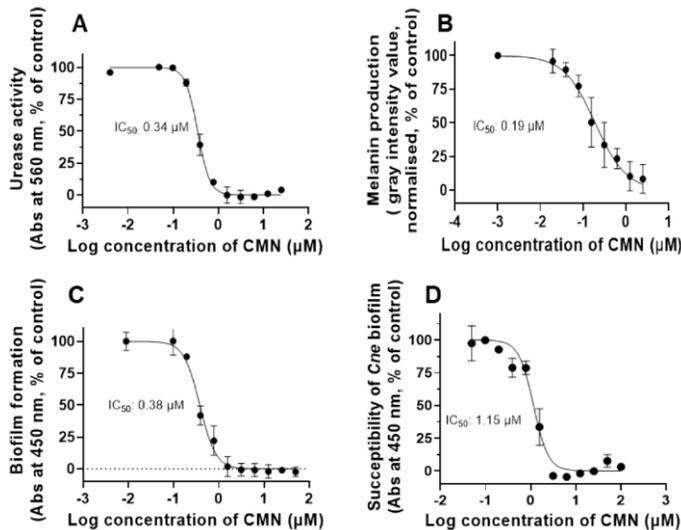


Anil et al. (2022), ACS Infect Dis, 8, 1851-68



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CMN reduces *Cne* virulent factors

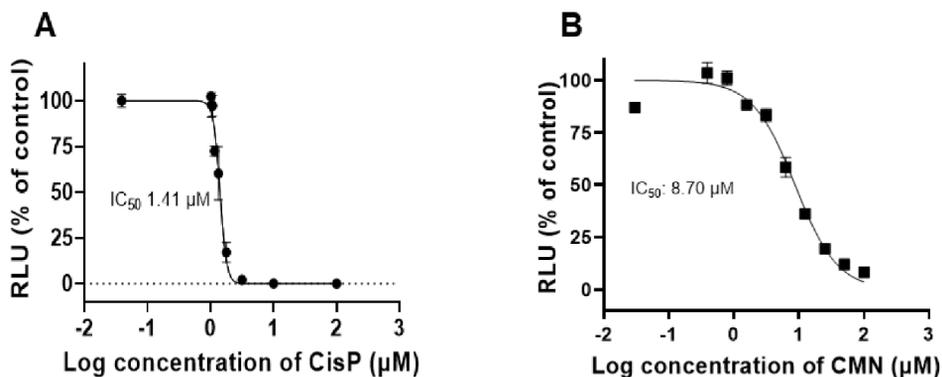


Anil et al. (2022), ACS Infect Dis, 8, 1851-68



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CMN reduces the Prp8 intein splicing

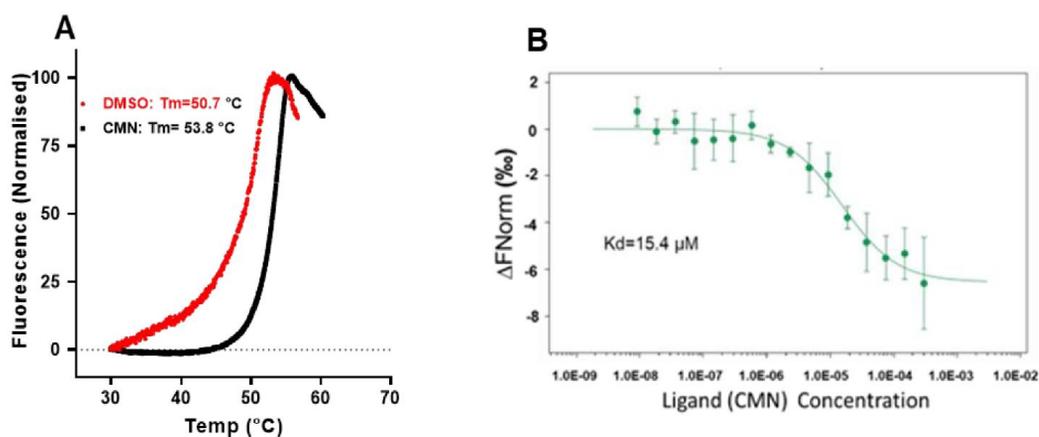


Anil et al. (2022), ACS Infect Dis, 8, 1851-68



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CMN directly binds the Prp8 intein

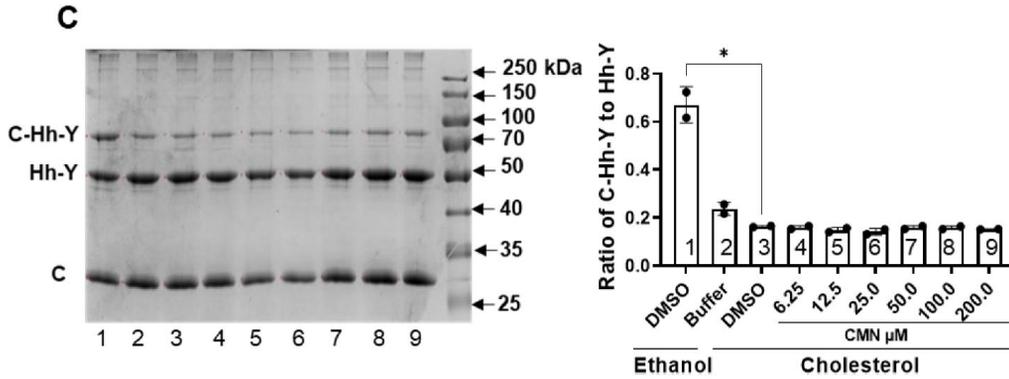


Anil et al. (2022), ACS Infect Dis, 8, 1851-68



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CMN does not interfere hedgehog cholysterolysis

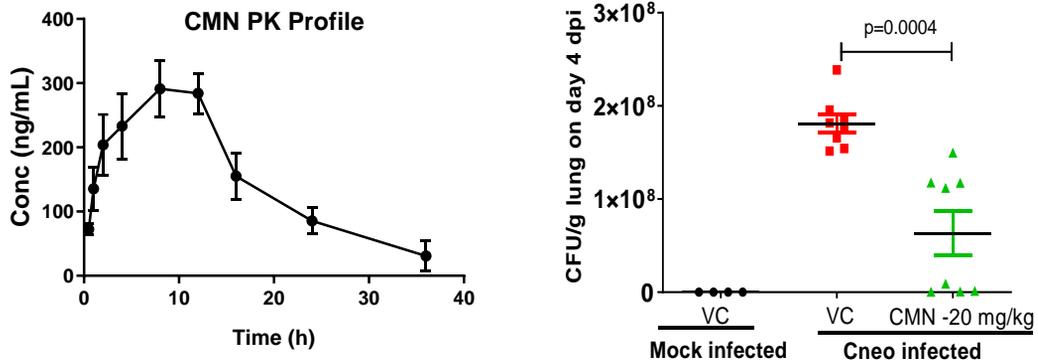


Anil et al. (2022), ACS Infect Dis, 8, 1851-68



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CMN treatment reduces fungal burden in the lung in mouse model



Anil et al. (2022), ACS Infect Dis, 8, 1851-68



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Acknowledgement

- Li's lab
 - Zhong Li
 - Jing Zhang
 - Fengshan Gao
 - Anil Tharappel
 - Qing-Yu Zhang's lab
 - Xiangmeng Wu
 - Sudha Chaturvedi
(Wadsworth Center)
- Marlene Belfort's lab
 - Cathleen Green
 - Hon Chan
 - Seth Pearson
 - Jia Zhou, UTMB
 - Jimin Xu
 - Guojian Liao, Southwest University
China
 - Bin Fu

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Drug discovery for *Cryptococcus neoformans* and *Cryptococcus gattii*

Sean Ekins Ph.D., D.Sc.
CEO

Collaborations Pharmaceuticals, Inc.

Raleigh, NC, USA

sean@collaborationspharma.com

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Collaborations Pharmaceuticals, Inc.

Founded in 2015

Pre-clinical stage company

Develops software for drug discovery and consumer product applications

>20 grants funded (~\$21.3M) since 2016

Private company

3 Labs ~2,000 sqft incubator space at NC State University

9 orphan drug designations for rare & neglected diseases

3 pediatric rare disease designations

1 patent issued, multiple patents filed, 7 trademarks

>150 publications



Our work has been highlighted by:



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OUR MISSION

Transforming Chemistry, Enriching Lives

We use real intelligence alongside artificial intelligence to develop clinical candidates for rare, neglected and unmet therapeutic needs, as well as new molecules for consumer product applications.

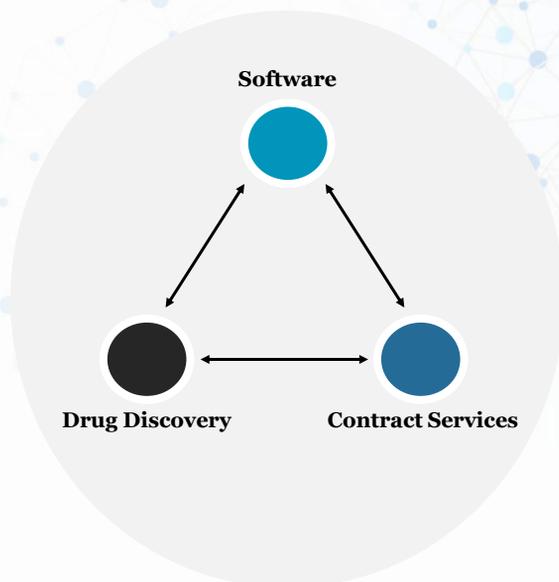
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Company overview

- **We are a molecule discovery company**
 - We use *artificial intelligence* to develop molecules for consumer product and therapeutic needs. e.g. molecule design, sustainable chemistry, toxicology applications
- **We are a software company**
 - We license our internally-developed suite of machine learning tools allowing for the generative design and evaluation of molecules and the building/validation of brand new models.
- **We are a contract services organization**
 - Using our machine learning tools, we bring our AI expertise to your enterprise. We do the work, you keep your data.



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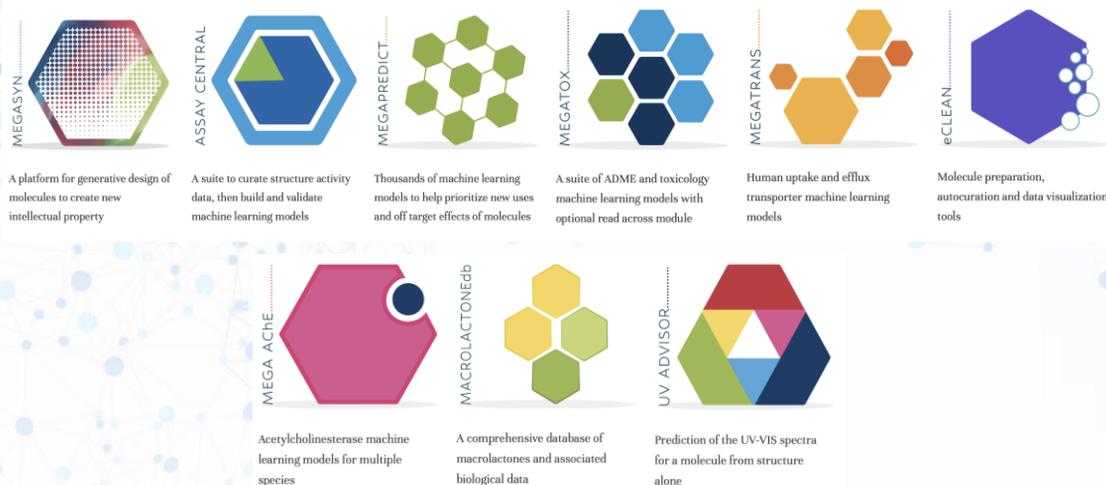


4

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Company Developed Software Tools

Our suite of machine learning and generative design tools is available for your molecule design needs



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Company Pipeline

Assets available for licensing, partnering, spin outs.

Category	Disease	Targets	Preclinical In vitro	Preclinical In vivo	Pre-IND	Clinical	Rare Disease Designation	Orphan Designation	IND/IND	Funding	Machine Learning	Patent Filing
Viruses	Ebola virus disease	Entry / Glycoprotein	██████████	██████████			***	*	*	*	*	*
	HIV-1	NHR1, CCR5	██████████	██████████							*	*
	Enteroviruses	Capsid	██████████	██████████							*	*
	COVID-19	PI ³ , Lysosome, Kinases (GAMK1, MELK)	██████████	██████████							*	*
	Hepatitis B disease	?	██████████	██████████							*	*
	Nipah virus disease	?	██████████	██████████							*	*
	Yellow Fever	?	██████████	██████████							*	*
	Chikungunya	?	██████████	██████████							*	*
	Marburgvirus disease	?	██████████	██████████							*	*
	HTN1	Neuraminidase	██████████	██████████							*	*
Rare Diseases	Malaria	Hemozoin Formation	██████████	██████████			*	**	*	*	*	*
	Chagas Disease	?	██████████	██████████							*	*
	S. aureus	?	██████████	██████████							*	*
	C. neoformans/gattii	?	██████████	██████████							*	*
	Tuberculosis	Various	██████████	██████████							*	*
	M. abscessus	?	██████████	██████████							*	*
	Neisseria gonorrhoeae	?	██████████	██████████							*	*
	Batten CLN1 (chaperone)	PPT1	██████████	██████████							*	*
	Sialidosis	Sialidase-1	██████████	██████████							*	*
	Batten CLN1 (ERT)	PPT1	██████████	██████████			*	*	*	*	*	*
Cancer	Pitt Hopkins Syndrome	Nav1.8	██████████	██████████			*	*	*	*	*	*
	Multiple Cancers	FLT3, KIT, LRRK2, CLK2	██████████	██████████			*	*	*	*	*	*
	Neuroblastoma	?	██████████	██████████							*	*
Various	Chordoma	?	██████████	██████████							*	*
	Alzheimer's Disease	AChE, BDNF, GSK3β	██████████	██████████							*	*
	Psychopostogens	5HT _{2A}	██████████	██████████							*	*
	Countermeasures	ACHE	██████████	██████████							*	*
Various	Stroke	CCBA	██████████	██████████							*	*

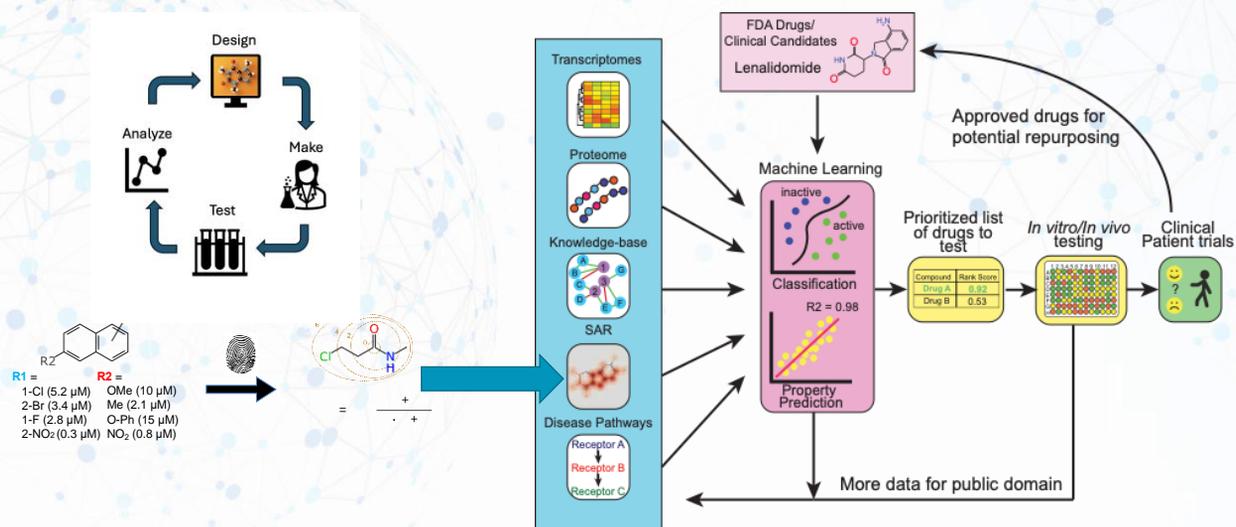
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Finding new molecules or repurposing using machine learning



Urbina, Puhl, Ekins et al., 2021 *Curr Opin Chem Biol*, 65:74-84

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Audience Survey Question

ANSWER THE QUESTION ON THE INTERACTIVE SCREEN IN ONE MOMENT

What is considered true about *Cryptococcus neoformans*?

(Select all that apply)

- Identified in the 1860s
- 3rd Leading cause of infections in solid organ transplant
- Currently not treatable
- None of the above

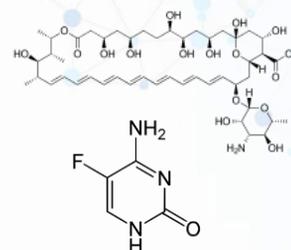
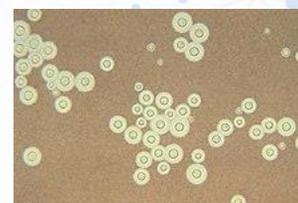
* If your answer differs greatly from the choices above **tell us in the chat!**

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Cryptococcus neoformans

- Identified in the 1960s
- 3rd leading cause of infections in solid organ transplant
- 3% develop in the 1st yr and mortality = 25-40%
- Remain susceptible for 5 yrs
- It is treatable with Amphotericin B (binds ergosterol) and Flucytosine (pyrimidine biosynthesis)
- Treatment is long and toxic
- Mortality 15-30% in those with HIV
- Sub-Saharan Africa: cryptococcal meningitis prevalence is 25-45%



Donlin et al., ACS Med. Chem. Lett. 2021, 12, 774–781

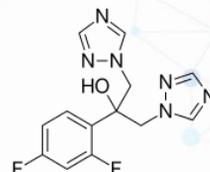
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Cryptococcus gattii

- Lives in soil and trees
- Affects lungs and nervous system
- Infects immunocompetent
- Endemic in tropical areas
- Antifungals are insufficient to cure it
- No new antifungals approved since 2003
- Need to be safe and effective
- Fluconazole is only fungi static – potential for relapse
- Newest class of molecules is echinocandins but they are not active against cryptococcus
- VT-1129 CYP51 inhibitor –
- Some repurposing and clinical studies – nothing promising.



Donlin et al., ACS Med. Chem. Lett. 2021, 12, 774–781

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Our collaborators



Dr. Vadim Makarov
Federal Research Centre "Fundamentals of Biotechnology" of the Russian Academy of Sciences (Research Centre of Biotechnology RAS)

Inventor of BTZ043 and PBTZ169 for TB. He is an expert in medicinal chemistry and rational drug design with special interest in developing antimicrobial and antiviral agents.

We have worked on several TB and antiviral projects (HIV, HepB, SARS-CoV-2, YFV, HepB, EV-D68)



Dr. Maureen Donlin
Saint Louis University School of Medicine

Studies the cell wall integrity signaling pathway in the human fungal pathogen *Cryptococcus neoformans*. Works on identification of small molecule antifungals.

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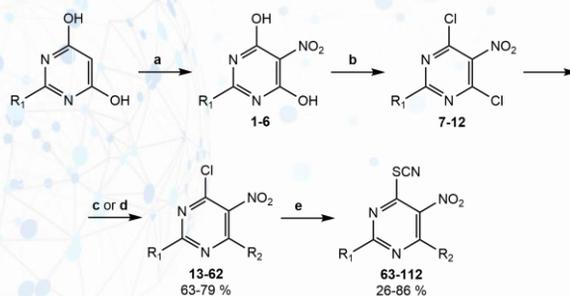


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General synthetic scheme of 5-nitro-6-thiocyanatopyrimidines

- Reagents and conditions: a) HNO_3 , $\text{H}_2\text{SO}_{4\text{cat}}$; b) POCl_3 , Et_3N , HCl ; c) corresponding amine solution, AcOH , dioxane or d) corresponding sodium alkoxide, alcohol; e) KSCN , alcohol



Donlin et al., ACS Med. Chem. Lett. 2021, 12, 774–781

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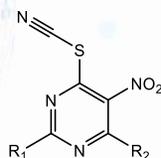
75

C. Neoformans & C. gattii

- Collaborated with Dr. Maureen J. Donlin, Saint Louis University School of Medicine
- Initially screened 121 compounds – Whole cell phenotypic assay
- Measured MIC_{80} against *C. neoformans* strain KN99
- 17 of the 121 compounds had $\text{MIC}_{80} < 50 \mu\text{M}$
- 5-nitro-6-thiocyanatopyrimidines were the most interesting
- Performed SAR

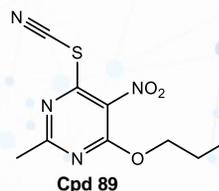


Core selection

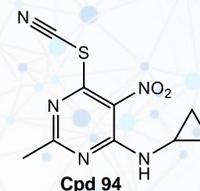


MIC_{80} s (*C. neoformans* KN99) ~ 12.5-50 μM

Hit 4-thiocyano-5-nitropyrimidines



MIC_{80} (*C. neoformans* KN99) ~ 0.6 μM
 MIC_{80} (*C. gattii*) ~ 0.78-1.56 μM
 MIC_{80} (FLC-resist. *C. neoformans*) ~ 0.78-1.56 μM



MIC_{80} (*C. neoformans* KN99) ~ 0.6 μM
 MIC_{80} (*C. gattii*) ~ 0.39-0.78 μM
 MIC_{80} (FLC-resist. *C. neoformans*) ~ 0.78-1.56 μM

Predicting with a machine learning model and *in vitro* testing

Donlin et al., ACS Med. Chem. Lett. 2021, 12, 774–781

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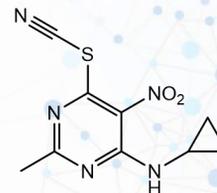


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Checkerboard assay and ADME properties

- Cpd 94 tested with Amphotericin B and flucytosine
- FICIs 1.25 and 1.5
- Indifference, but not antagonistic
- **Poor metabolic stability**



Hit compound – Cpd 94

MIC₈₀ (*C. neoformans* KD99) ~ 0.6 μM
 MIC₈₀ (*C. gattii*) ~ 0.39-0.78 μM
 MIC₈₀ (FLC-resist. *C. neoformans*) ~ 0.78-1.56 μM

In vitro ADME properties for compound 94

Solubility	< 0.2 μM pH 7.4
CYP inhibition	1A2 (4.78μM), 2C9 (40.2μM), 2C19 (50μM), 3A4 & 2D6 (>50μM)
Mouse liver microsomes	t _{1/2} <5 min, CL _{int} 277.3 μL/min/mg protein
Human liver microsomes	t _{1/2} <5 min, CL _{int} 277.3 μL/min/mg protein

Donlin et al., ACS Med. Chem. Lett. 2021, 12, 774–781

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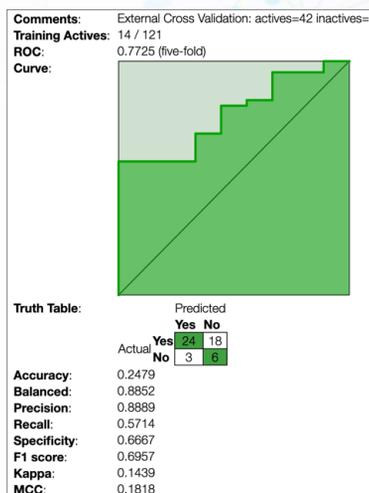
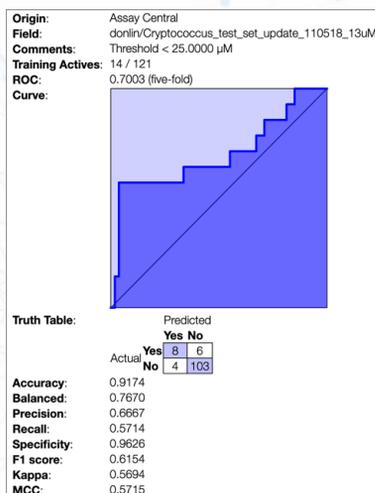


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Machine learning

- Early version of Assay Central was used
- Bayesian algorithm with ECFP6 fingerprints
- N= 121 cpds – active threshold MIC₈₀ 12.5-25μM
- Training 5 fold cross validation ROC 0.70
- Tested on additional 51 molecules
- ROC 0.77



Donlin et al., ACS Med. Chem. Lett. 2021, 12, 774–781

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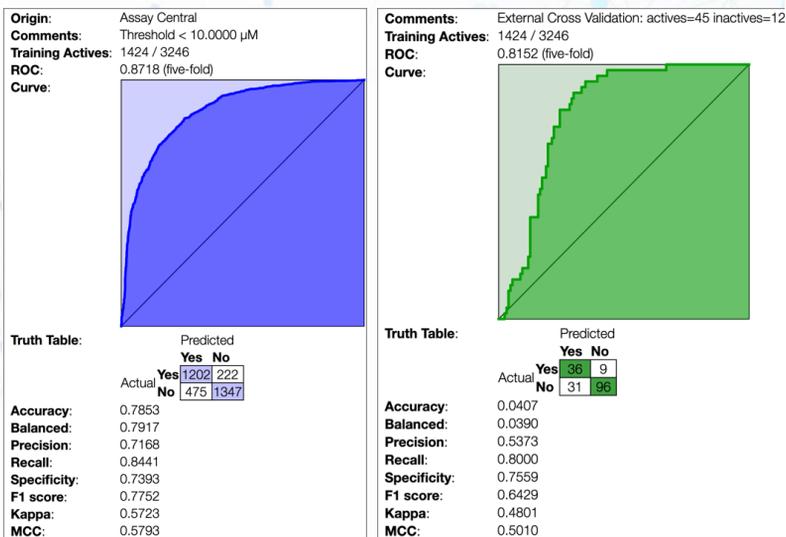


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Literature cryptococcus neoformans model

- Data from NIAID ChemDB HIV Opportunistic Infection and Tuberculosis Therapeutics Database
- Threshold MIC₈₀ 10 μ M – 5-fold ROC 0.87
- Use our data to test this model
- ROC 0.81
- Models were also developed with *C. gattii* data
- Models could be used for virtual screening



Donlin et al., ACS Med. Chem. Lett. 2021, 12, 774–781

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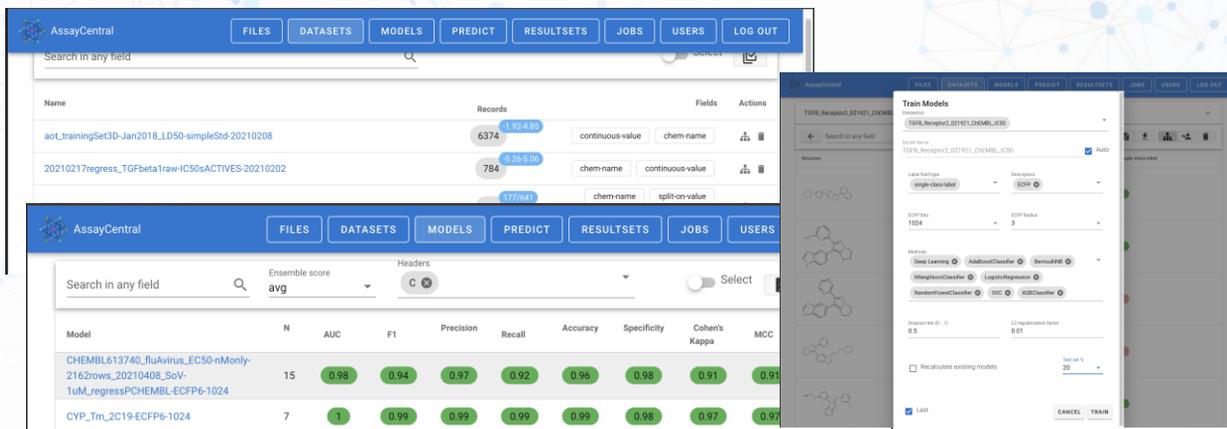


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- www.assaycentral.org
- Web-app based, QSAR model automated model-building platform (no code required)
- We can host on AWS, our servers or your own.



The screenshot displays the Assay Central web application interface. The top navigation bar includes buttons for FILES, DATASETS, MODELS, PREDICT, RESULTSETS, JOBS, USERS, and LOG OUT. Below the navigation bar, there is a search bar and a list of datasets. One dataset is highlighted, showing its name, number of records (6374), and fields (continuous-value, chem-name). Below the dataset list, there is a table of models with columns for Model, N, AUC, F1, Precision, Recall, Accuracy, Specificity, Cohen's Kappa, and MCC. The table shows two models with high performance metrics. On the right side, there is a 'Train Models' panel with options for selecting a model, choosing a learning method (Deep Learning, NeighborhoodClassifier, LogisticRegression, RandomForestClassifier, SVC, XGBClassifier), and setting parameters like Epochs and Learning Rate.

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New Assay Machine Learning Models

- More algorithms and all the data generated (191 compounds 53 active, 138 inactive)
- 10 μM MIC₈₀ cutoff 5-fold cross validation

Method	AUC	F1	Precision	Recall	Accuracy	Specificity	Cohen's Kappa	MCC
ada	0.9	0.7	0.66	0.76	0.82	0.84	0.57	0.58
bnb	0.92	0.74	0.72	0.83	0.84	0.84	0.63	0.66
knn	0.9	0.75	0.64	0.91	0.83	0.8	0.63	0.65
lreg	0.92	0.78	0.75	0.84	0.87	0.88	0.69	0.7
DL	0.89	0.73	0.66	0.83	0.83	0.83	0.61	0.62
rf	0.94	0.78	0.71	0.91	0.85	0.83	0.68	0.7
svc	0.94	0.79	0.68	0.95	0.85	0.82	0.68	0.71
xgb	0.92	0.73	0.72	0.76	0.84	0.88	0.62	0.63

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Assay Central Machine Learning Models

- 5 μM MIC₈₀ cutoff (191 compounds 33 active, 158 inactive)

Method	AUC	F1	Precision	Recall	Accuracy	Specificity	Cohen's Kappa	MCC
ada	0.88	0.24	0.31	0.21	0.83	0.96	0.19	0.2
bnb	0.87	0.53	0.52	0.55	0.83	0.89	0.43	0.43
knn	0.89	0.59	0.56	0.64	0.84	0.88	0.49	0.5
lreg	0.89	0.56	0.59	0.59	0.85	0.91	0.48	0.5
DL	0.89	0.3	0.34	0.28	0.84	0.96	0.24	0.24
rf	0.9	0.65	0.5	0.94	0.82	0.8	0.54	0.6
svc	0.9	0.66	0.51	0.94	0.83	0.8	0.56	0.61
xgb	0.89	0.64	0.7	0.67	0.88	0.92	0.57	0.6

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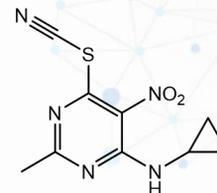


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Next steps

- Need to generate more ADME/Tox data, Caco-2, MDCK
- BBB penetration
- Identify target – identify genes
- Perform directed evolution studies and or gene deletion screening
- Develop alternative scaffolds as back ups
- Test versus other fungi such a *C. auris*
- Access to data in public domain is limited
- Could use generative AI approaches to develop analogs
- Could use our approach with other Fungi



Hit compound – Cpd 94

MIC₈₀ (*C. neoformans* KD99) ~ 0.6 μM
 MIC₈₀ (*C. gattii*) ~ 0.39-0.78 μM
 MIC₈₀ (FLC-resist. *C. neoformans*) ~ 0.78-1.56 μM

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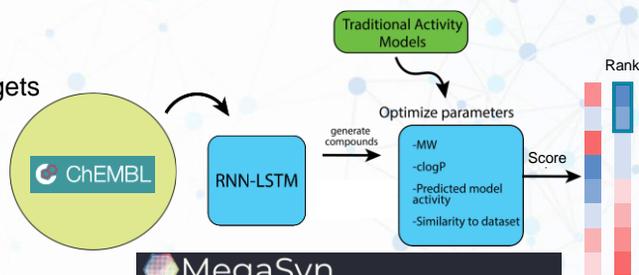


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MegaSyn- Generative AI

- Integrated ML models for targets and off-targets
- Property prediction
- An easy-to-use interface
- Also command line version
- Enables rapid molecule generation
- Starting point for run could be a target molecule or guided by optimal parameter scores



Urbina et al., ACS Omega 2022 May 27;7(22):18699-18713

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