

UNIVERSITY OF CALIFORNIA SAN FRANCISCO

A Comprehensive Test to Diagnose Neurological Infections

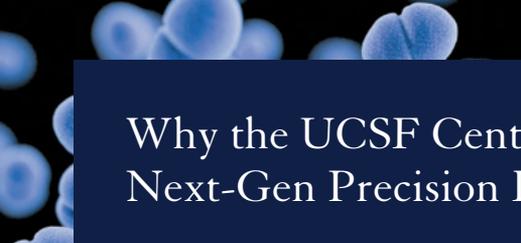


UCSF WAS THE FIRST IN THE WORLD

to provide metagenomic next-generation sequencing (mNGS) as a clinical test for diagnosis of neurological infections.

UCSF Center for Next-Gen
Precision Diagnostics





Why the UCSF Center for Next-Gen Precision Diagnostics?

Our clinicians and scientists are the original developers of clinical mNGS technologies.

WE ARE PART OF UCSF HEALTH – a clinical institution with widely acknowledged expertise in neurology, infectious disease and laboratory medicine – and a pioneer in the use of cutting-edge mNGS approaches for diagnosis of infections from patient samples.

As an institution that exists to serve the public good, all of our revenue goes directly into ongoing research and development efforts. This puts us in a unique position to optimize mNGS so it can save more lives and prevent more of the hardship associated with encephalitis and meningitis.

Why mNGS?

The mNGS assay offers clinicians with patients suffering from suspected infectious encephalitis or meningitis a single clinically validated test for identifying thousands of pathogens, including novel infectious agents and rare variants*. By testing for all organisms in an unbiased, hypothesis-free process, mNGS data placed in a clinical context tell a fact-based story that can help:

- Shorten the diagnostic journey for patients with rare or life-threatening conditions
- Eliminate unnecessary tests
- Accelerate time to treatment
- Avoid ineffective, expensive and potentially harmful treatments – including powerful antibiotics
- Decrease patient length of stay in high-acuity care settings

** mNGS testing results are intended to be used in the context of clinical, laboratory and radiologic findings to assist in the diagnosis of suspected infectious causes of meningitis and encephalitis.*

Meet our scientists

Charles Chiu, MD, PhD

Professor, Laboratory Medicine and Medicine/
Infectious Diseases

Director, UCSF-Abbott Viral Diagnostics &
Discovery Center

Assistant Director, UCSF Clinical Microbiology Laboratory

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Charles Chiu, MD, PhD, spearheaded the infectious disease program for the California Initiative to Advance Precision Medicine at UCSF, launching a multisite trial that made clinical mNGS for pathogen detection available to patients for the first time.

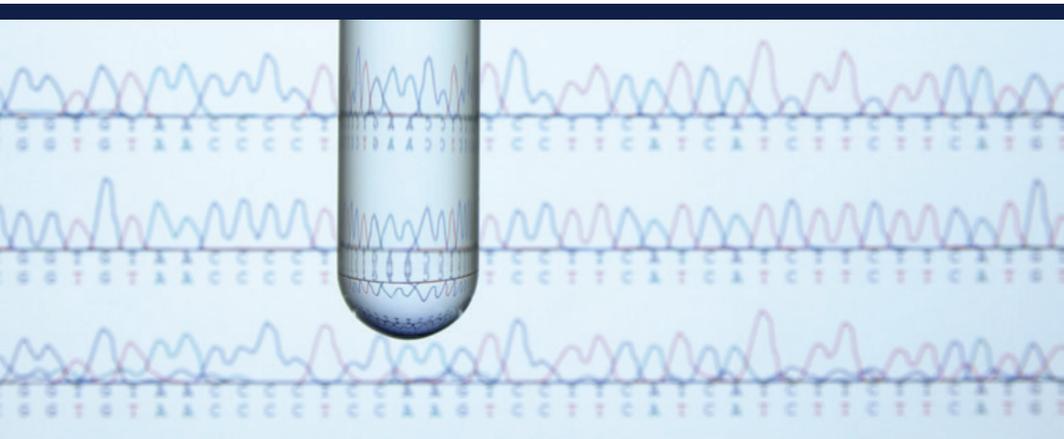


Steve Miller, MD, PhD

Associate Professor, Pathology & Laboratory Medicine
Director, UCSF Clinical Microbiology Laboratory

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Steve Miller, MD, PhD, together with Charles Chiu, MD, PhD, initiated validation of a lab-developed test at UCSF to detect all potential pathogens in one assay. He and Dr. Chiu established the UCSF Clinical Microbiology Laboratory as a leader in the field of metagenomic clinical sequencing for infectious disease.



Joe DeRisi, PhD

Professor, Biochemistry and Biophysics
Co-President, Chan Zuckerberg Biohub

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Since 2001, the DeRisi Lab has been at the forefront of the latest in genomic technology and bioinformatics to identify unusual and novel infectious diseases in humans and animals.

Ranging from SARS, malaria, zika, and challenging-to-diagnose conditions in humans, to novel viruses in birds, snakes, bees, even insects, the DeRisi Lab has established itself as a leader in the field of genomics and infectious disease.



Michael Wilson, MD

Assistant Professor, Neurology

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Michael Wilson, MD, a neurologist who trained in the DeRisi lab, launched his own lab by establishing an international research-patient network, advancing the development of novel technologies to elucidate the most challenging and often devastating neuroinflammatory diseases.



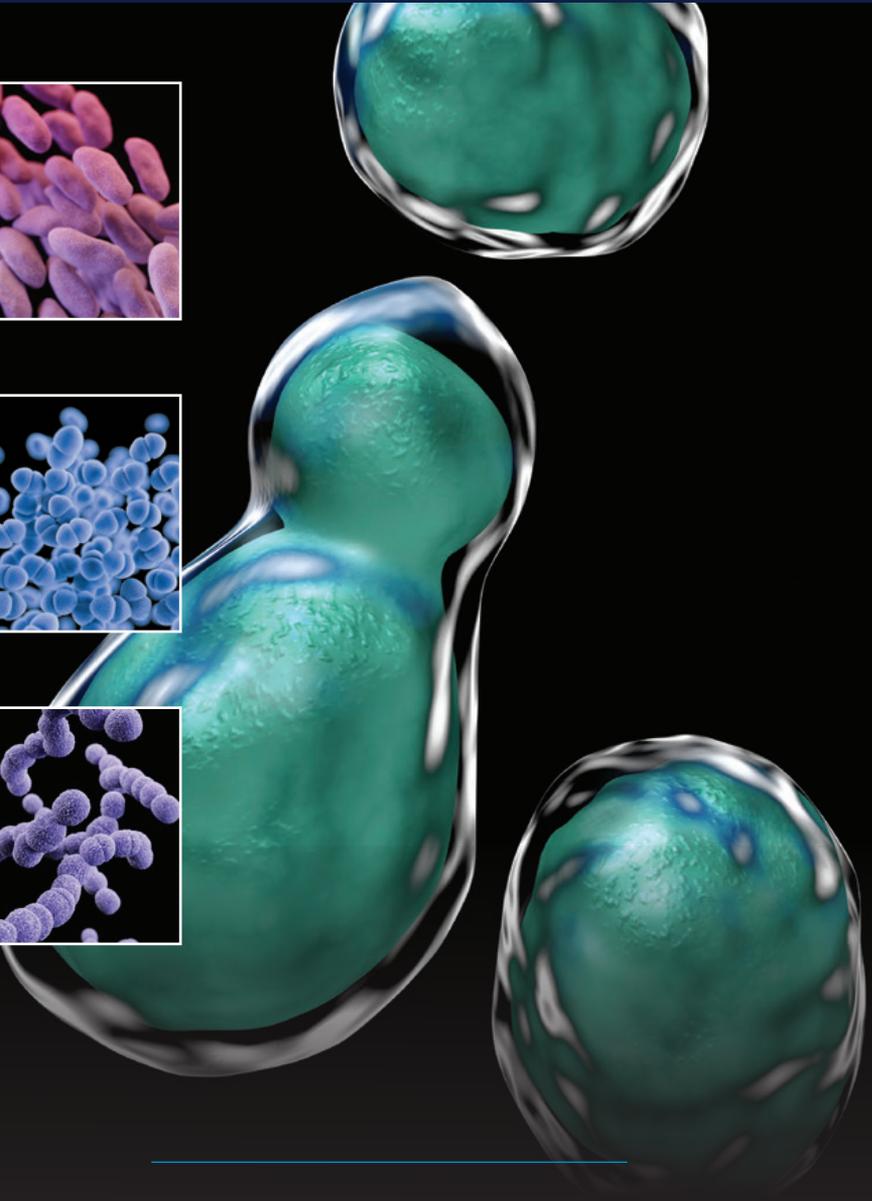
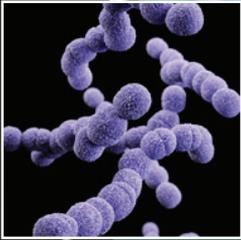
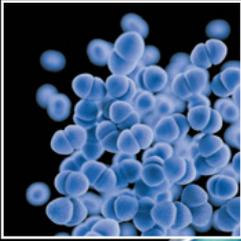
The need for improved diagnostic tools

Each year in the United States, approximately 40,000 patients arrive in hospitals with encephalitis or meningitis.



FAR TOO OFTEN, these patients undergo a traumatic diagnostic odyssey that comes up empty. The annual burden of disease includes more than a thousand deaths, potentially permanent neurological damage and billions of dollars in hospital costs.

The nation's top 10 hospitals use
UCSF's mNGS service for diagnosing
complex cases of meningitis and encephalitis.



Shorten the diagnostic odyssey
for patients with rare or
life-threatening conditions.

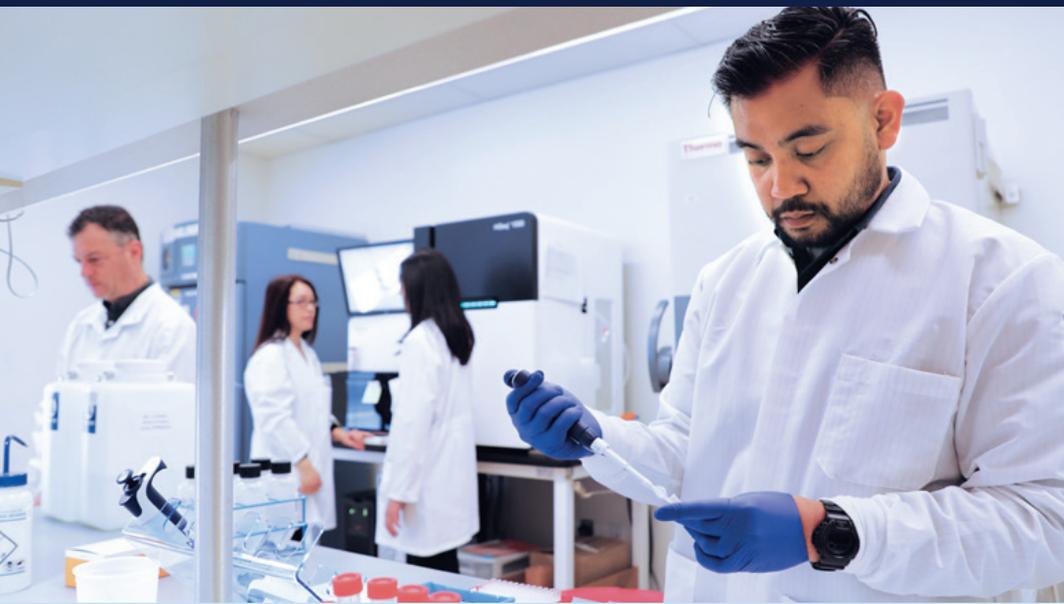


A single test paired with expert consultation

One clinically validated test identifies thousands of pathogens, including novel infectious agents and rare variants.

DEVELOPED BY RESEARCHERS AND CLINICIANS AT UCSF, our clinical metagenomic next-generation sequencing (mNGS) assay for encephalitis and meningitis has been validated in a licensed CLIA (Clinical Laboratory Improvement Amendments) diagnostic laboratory. The test sequences all of the DNA and RNA in a spinal fluid sample. Advanced bioinformatics are used to rapidly screen millions of reads for all potential pathogens, eliminating the need for serial, time-consuming testing based on incomplete clinical hypotheses. Our mNGS service includes:

- Comprehensive, unbiased sequencing of both DNA and RNA for identification of all pathogen types
- Advanced graphical visualization tailored for clinical use, which enables faster and more efficient analysis of data and results reporting
- Experts in laboratory medicine, neurology and infectious disease prepare a written interpretation of results, generally available within a week from receipt of the sample
- Patient-specific consultations available by teleconference to explain the results and place them in clinical context



We are leveraging mNGS so more lives can be saved, and more hardships associated with encephalitis and meningitis can be averted.



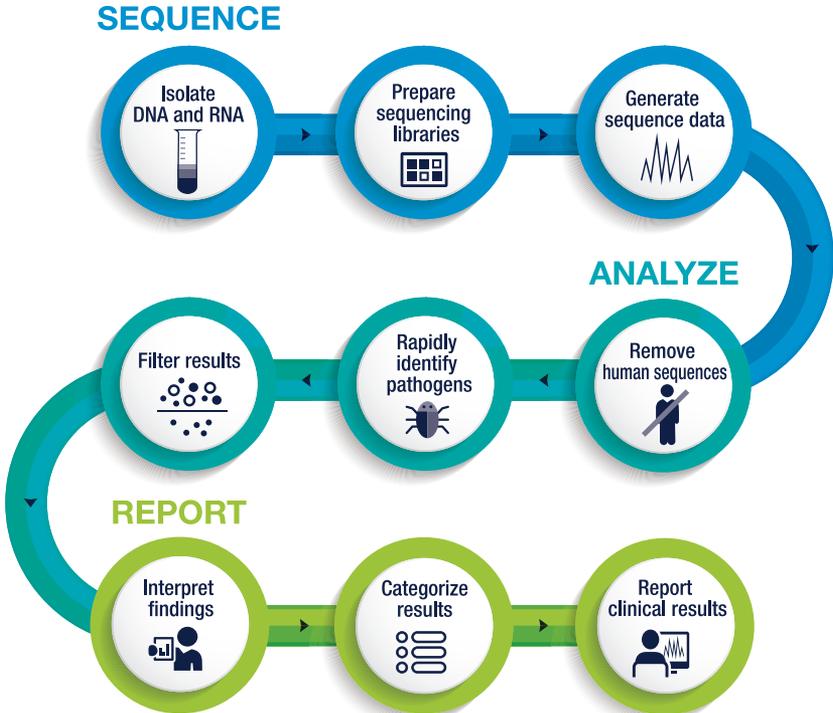
The bioinformatics advantage



SURPI+ IS A CLINICAL BIOINFORMATICS SOFTWARE PIPELINE

that can rapidly analyze mNGS data for all pathogenic microorganisms. Developed at UCSF in the Chiu lab and modeled after the published SURPI (sequence-based ultra-rapid pathogen identification) research pipeline, SURPI+ includes a patent-protected bioinformatics innovation, which screens out noise in the data prior to sequencing, thus increasing yield, improving accuracy and saving time.

How we use mNGS to diagnose infectious diseases





SURPI+ is a clinical bioinformatics software pipeline that can rapidly analyze mNGS data for all pathogenic microorganisms.



Four easy steps to begin testing at your institution

- 1 Create an account at nextgendiagnosics.ucsf.edu
- 2 Fill out a customized requisition form
- 3 Pack your 1-2 mL frozen CSF sample in dry ice, as per standard labeling and container requirements
- 4 Send the sample with the requisition form via overnight shipping

For more information, call us at 415-502-2632
or email us at NGDx@ucsf.edu