Coronavirus Screening Tools

Cayman has developed a SARS-CoV-2 Screening Library in which over 70,000 unique drugs and small molecules have been screened *in silico* for binding to SARS-CoV-2 targets including the spike glycoprotein, proteases, and non-structural proteins (nsps), and human angiotensin-converting enzyme 2 (ACE2). These are available as both a data pack and a library of the chemical entities in a 96-well format.



Cayman's unique set of compounds

FDA-approved drugs

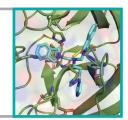
Diverse commercial compounds



Virtual screening against SARS-CoV-2 targets

Hit selection criteria:

- · Docking scores
- · Intermolecular hydrogen bonds within the amino acid residues of the binding pockets





Library Data Package

| Parameter | HTS02812 | JFD03677 |
|-------------------------|---------------|---------------|
| GlideScore/Glide Emodel | -9.38/-85.955 | -9.60/-98.831 |
| MW | 369.463 | 452.509 |
| Number of H Donors | 3 | 4 |
| Number of H Acceptors | 7.4 | 6 |
| PSA | 82.08 | 97.04 |
| ClogS | -2.18 | -5.376 |
| ClogPo/w | 2.57 | 4.867 |
| ClogBB | -0.56 | -1.69 |
| ClogHERG | -6.29 | -7.64 |

Docking score units are in kcal/mol.

Library Preparation



- Can be customized to your selected compounds/targets
- · Supplied in a 96-well Matrix™ format



Hit-to-Lead and Lead Optimization Services

- · In vitro/In vivo Screening
- · SBDD/MedChem

SARS-CoV-2 Screening Library

Item No. 9003509

The SARS-CoV-2 Screening Library is a custom, made-to-order library that features a diverse set of FDA-approved and drug-like compounds identified from *in silico* modeling using Maestro (Schrödinger Suite) software. Choose from the entire library of 2,000+ compounds or a custom built library to your preferred target and specifications. The data package for all SARS-CoV-2 targets is also available. SARS-CoV-2 targets include:

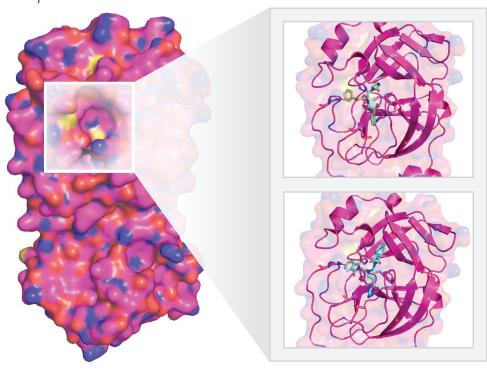
- Main protease (M^{pro}), also known as 3C-like protease (3CL^{pro}; nsp5)
- · Spike glycoprotein
- · ACE2 (human)
- RNA-dependent RNA polymerase (RdRp; nsp12)
- Endoribonuclease (nsp15)

- Guanine-N7 methyltransferase (Guanine-N7 MTase; nsp14)
- Exoribonuclease domain (ExoN domain; nsp14)
- Papain-like protease (PL^{pro}; nsp3)
- · ADP-ribose phosphatase (ADRP; nsp3)
- Nucleocapsid protein

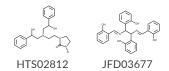
SARS-CoV-2 Library Data Package

The SARS-CoV-2 Library Data Package includes compound characteristics, docking scores (per target), and predicted physicochemical properties for ten SARS-CoV-2 targets. It is available for purchase, and the cost can be applied towards your next screening, lead optimization, or compound synthesis project with Cayman.

Sample Data:



Key Residues in M^{pro} SARS-CoV-2: His41 motif, His163-Glu166 motif, and catalytic Cys145



Parameter HTS02812 JFD03677 -9.38/ -9.60/ GlideScore/ Glide Emodel -85.955 -98.831 MW 369.463 452.509 Number of H Donors Number of 7.4 6 H Acceptors PSA 82.08 97.04 -2.18 -5.376 ClogS ClogPo/w 2.57 4.867 ClogBB -0.56 -1.69 ClogHERG -6.29 -7.64

Docking score units are in kcal/mol.

To learn more about our Medicinal Chemistry & Structural Biology services, visit www.caymanchem.com/medchem

M^{pro} (PDB ID 6LU7)