One Target and two drugs for SARS-CoV-2

By

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# Abstract

SARS-CoV-2, also known as COVID-19, is a virus that causes flu like symptoms including respiratory distress, in many cases requiring respirators to maintain oxygenation in patients. It is highly contagious, and is currently causing pandemic infection, with a fatality rate estimated between 2% and 3% [1]. Persons over 60 have may have much higher fatality rates [2].

A target repurposing strategy can provide drugs more quickly and cheaply than creating new drugs and finding new targets [3]. This strategy can produce treatments to ameliorate the disease until a vaccine becomes available, or in addition to the vaccine.

Using a paralog search pipeline, the author searched the ChEMBL 25 database, screening targets in it against the SARS-CoV-2 genome and found a high scoring target that has two known drugs [4-6]. The target that was found is an RNA polymerase from the viral genome used by the virus to reproduce.

These drugs were validated using docking simulations that showed high binding affinity to the RNA polymerase target.

# Introduction

ChEMBL provides a downloadable database that includes drug targets and drug information for those targets, as well as amino acid sequences of the protein targets [5, 6]. Drug targets tend to be proteins that are important enough to the organism to which they belong that they tend to be conserved [7].

Using **jackhmmer** to provide similarity reports, a pipeline imported scores showing sequence similarity. The target scores were loaded into a PostgreSQL database that also contains the ChEMBL data [8].

The data were analyzed, producing a report showing the target that had high similarity to the SARS-CoV-2 genome, and 3 drugs associated with that target.

The drugs were validated by simulated docking with the target by submitting queries to SwissDock, a web based docking server [9]. Two of these drugs had high affinity.

# Materials and Methods

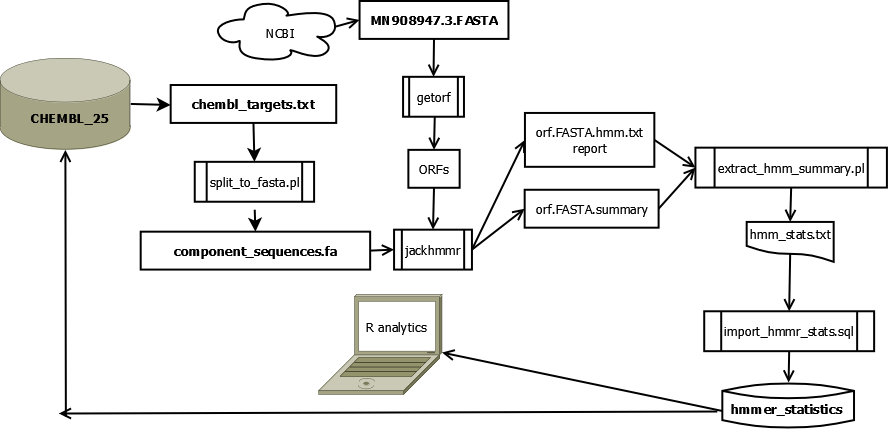


Figure : SARS-CoV-2 Genome analysis workflow

The nucleotide genome of SARS-CoV-2 was downloaded as MN908947.3.FASTA [10].

ORFs were translated using EMBOSS tools [11]. The orfs were translated rather than using curated protein sequences because the translation tool provides the amino acid FAST sequences in a form convenient for querying. While many ORFs may not be actual proteins, the query that uses these ORFs will eliminate them from consideration.

This command creates a file containing all the open reading frames (ORFs) found and translates the nucleotide sequences into amino acid sequences:

**getorf MN908947.3.FASTA**

This creates file MN908947.3.orf, which contains all the ORFs found for the .FASTA file.

Commands run in R Studio quantify how many ORFs are contained:

|  |
| --- |
| > aa=read.table(file="mn908947.orf",header = FALSE, sep='~', stringsAsFactors = FALSE)  > aa=aa[!is.na(aa[,1]),] # filter out NA  > aa=data.frame(lines=aa, stringsAsFactors = FALSE)  > orf\_headers=aa[substr(aa[,1],1,1)=='>' ,]  > length(orf\_headers)  [1] 1572 |
|  |
| |  | | --- | |  |   1572 ORFs were found. |

The set of target sequences comes from the **ChEMBL\_25** PostgreSQL database and was downloaded by a *psql* script (See 6.1. chembl\_25\_targets.sql) as file **chembl\_targets.txt**..

These targets are converted by a Perl script (See 6.2. split\_to\_fasta.pl) ) creating file **component\_sequences.fa**.

**Jackhmmer** was used to create reports and summaries of similarities with targets [8].

[osboxes@osboxes ~/genomes/MN908947.3 ] jackhmmer --domtblout orf.summary -o orf.hmm.txt mn908947.orf ~/hmmer\_targets/component\_sequences.fa

A Perl script (See 6.3. extract\_hmm\_summary.pl) extracts the similarity data from the **jackhmmer** report file, **orf.hmm.txt** and writes it to file **hmm\_stats.txt.**

From psql, the data were imported into the **chembl\_25** database:

[postgres@osboxes /home/osboxes/genomes] **psql -U postgres -d chembl\_25**

psql (9.2.24)

Type "help" for help.

chembl\_25=# **\i import\_hmmer\_statistics.sql**

TRUNCATE TABLE

INSERT 0 49

chembl\_25=# **update hmmer\_statistics set tax\_id=2697049, organism='SARS-CoV-2’ where tax\_id is null;**

(See appendix for 6.5. import\_hmmer\_statistics.sql).

49 ORFs had enough similarity to targets to participate in our analysis.

This histogram shows the distribution of scores:

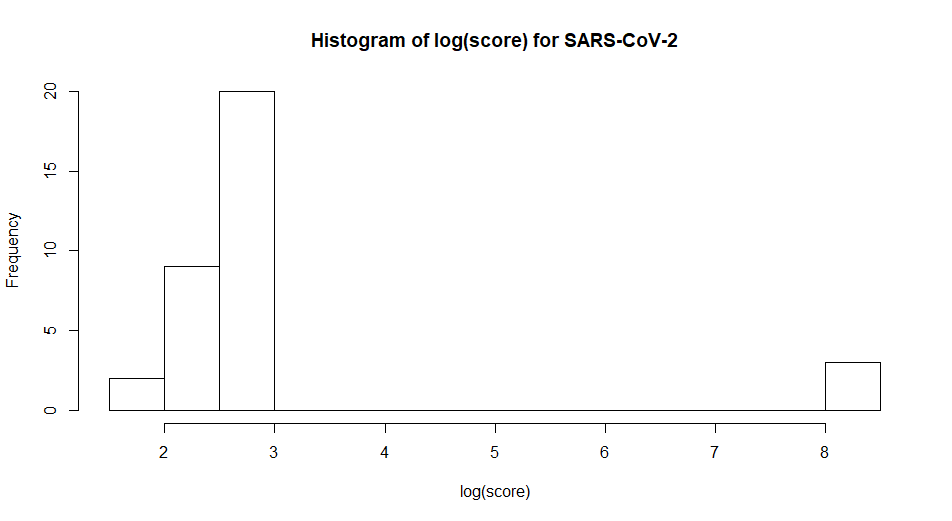


Figure : Target similarity score distribution of ORFs from SARS-CoV-2 genome.

Kmeans was used to identify the high scoring threshold.

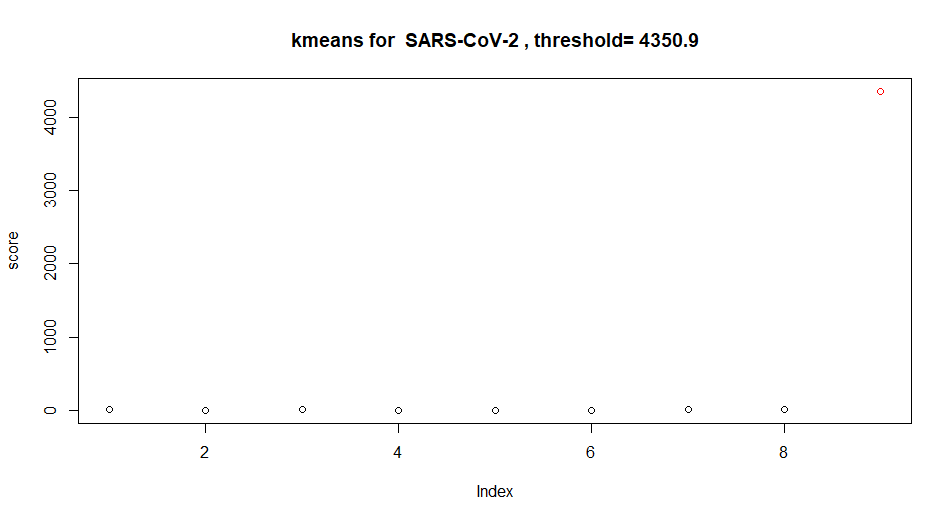


Figure : Kmeans showing high scoring group in red.

The threshold was used to select a report from the database identifying the target having high similarity to the SARS-CoV-2 genome, and drugs associated with it.

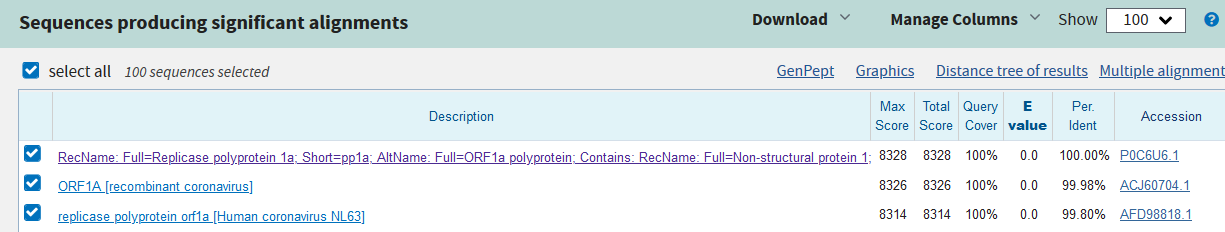
# Results and discussion

One target and three drugs were found.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **score** | **original tax id** | **orig\_organism** | **target\_type** | **target\_name** | **target\_chembl\_id** | **drug\_name** | **drug\_chembl\_id** |
| 4350.9 | 1773 | Mycobacterium tuberculosis | PROTEIN NUCLEIC-ACID COMPLEX | 70S ribosome | CHEMBL2363965 | VIOMYCIN SULFATE | CHEMBL3989823 |
| 4350.9 | 1773 | Mycobacterium tuberculosis | PROTEIN NUCLEIC-ACID COMPLEX | 70S ribosome | CHEMBL2363965 | CAPREOMYCIN SULFATE | CHEMBL2218913 |
| 4350.9 | 1773 | Mycobacterium tuberculosis | PROTEIN NUCLEIC-ACID COMPLEX | 70S ribosome | CHEMBL2363965 | PYRAZINAMIDE | CHEMBL614 |

In the ChEMBL database, a target may have multiple sequences. CHEMBL2363965 has 59 sequences. The high scoring sequence we chose has component\_id 8515.

NCBI BLASTP finds a 100% match:



[12, 13]

Although ChEMBL says that this is a Tuberculosis target, no match was found in the Tuberculosis genome. It may be that as part of treatment of Tuberculosis, a concurrent infection by a Carona virus also was treated by the drugs associated with this target.

The distance tree shows relations of this protein:

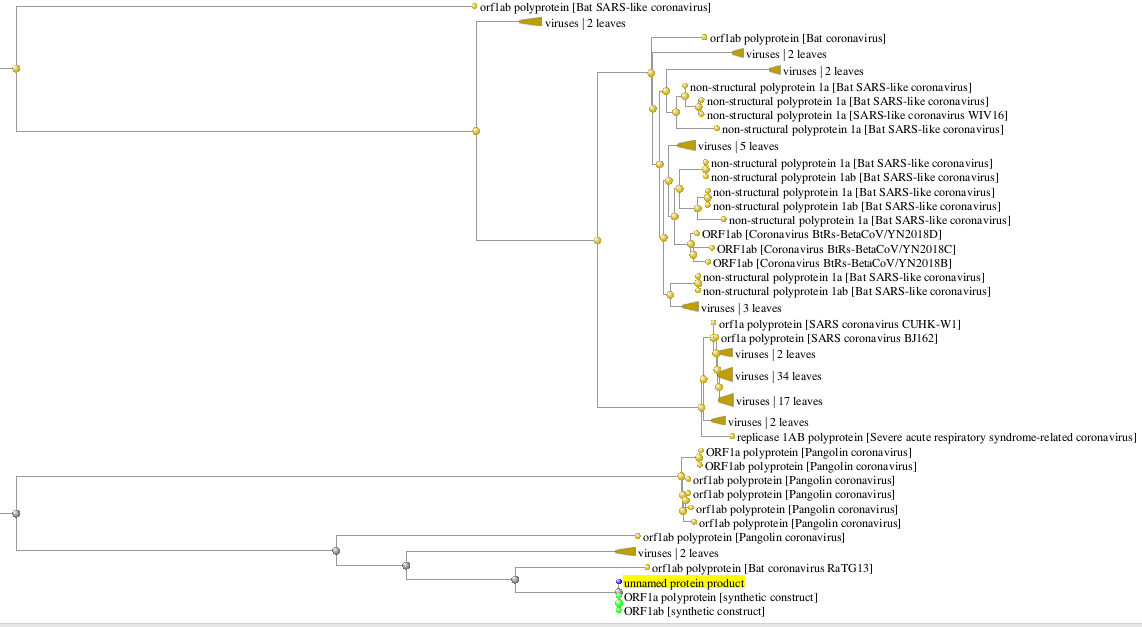
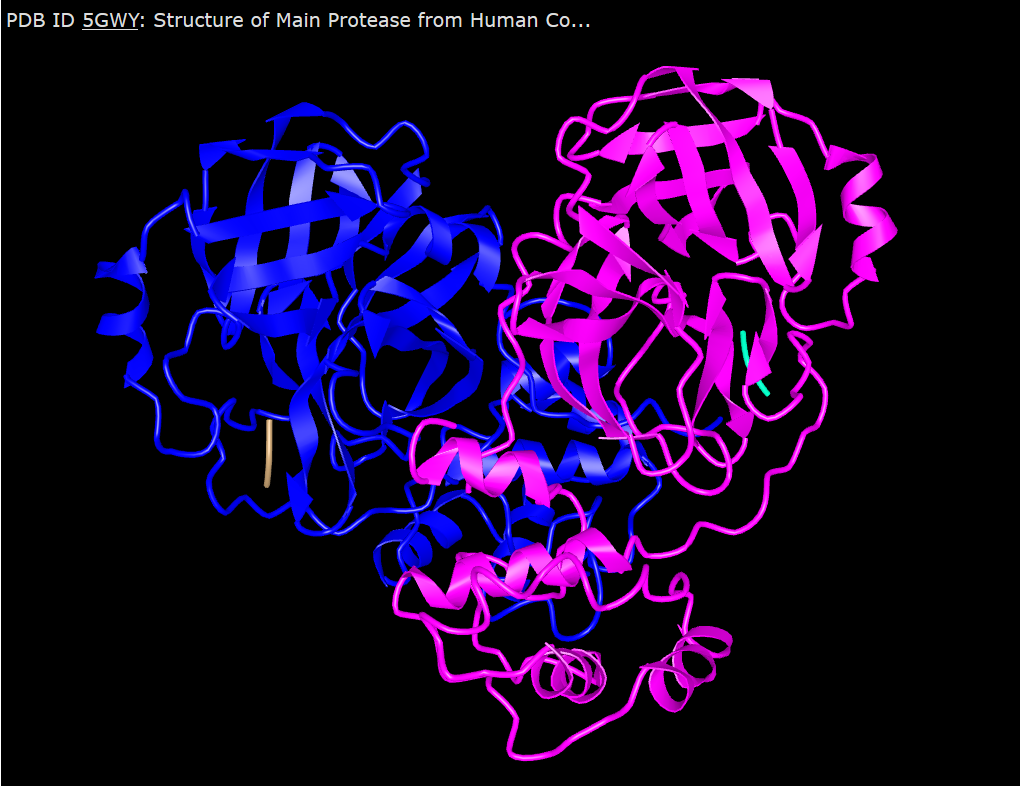


Figure : Distance tree for orf1a [12]

Link from accession [P0C6U6.1](https://www.ncbi.nlm.nih.gov/protein/P0C6U6.1?report=genbank&log$=prottop&blast_rank=1&RID=DCW398Y4014) gets us to the structural information:

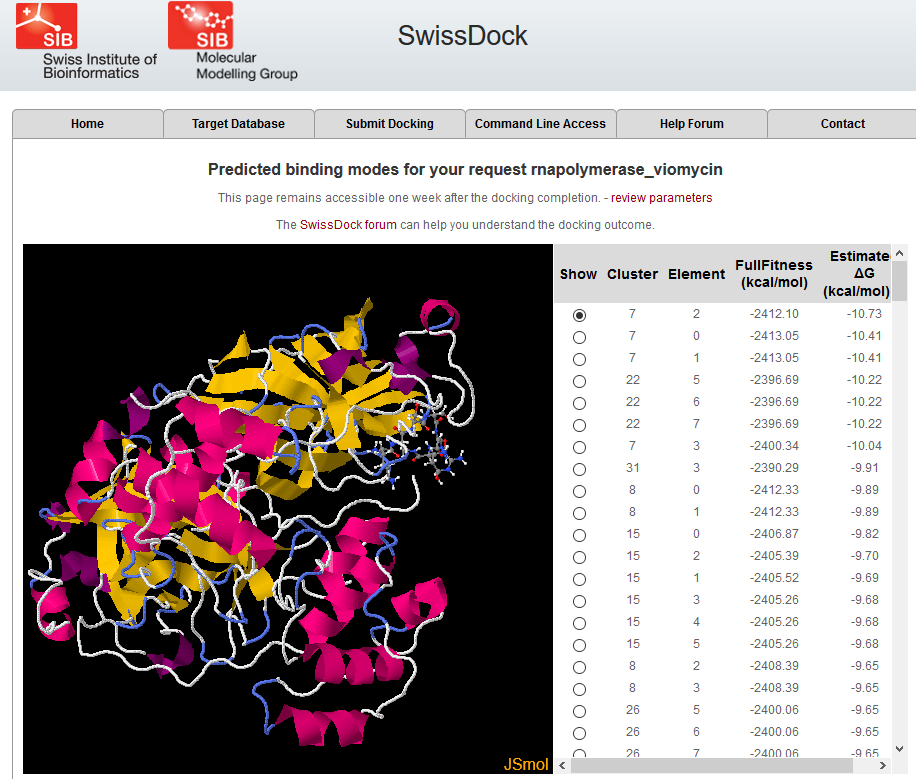


[14, 15]

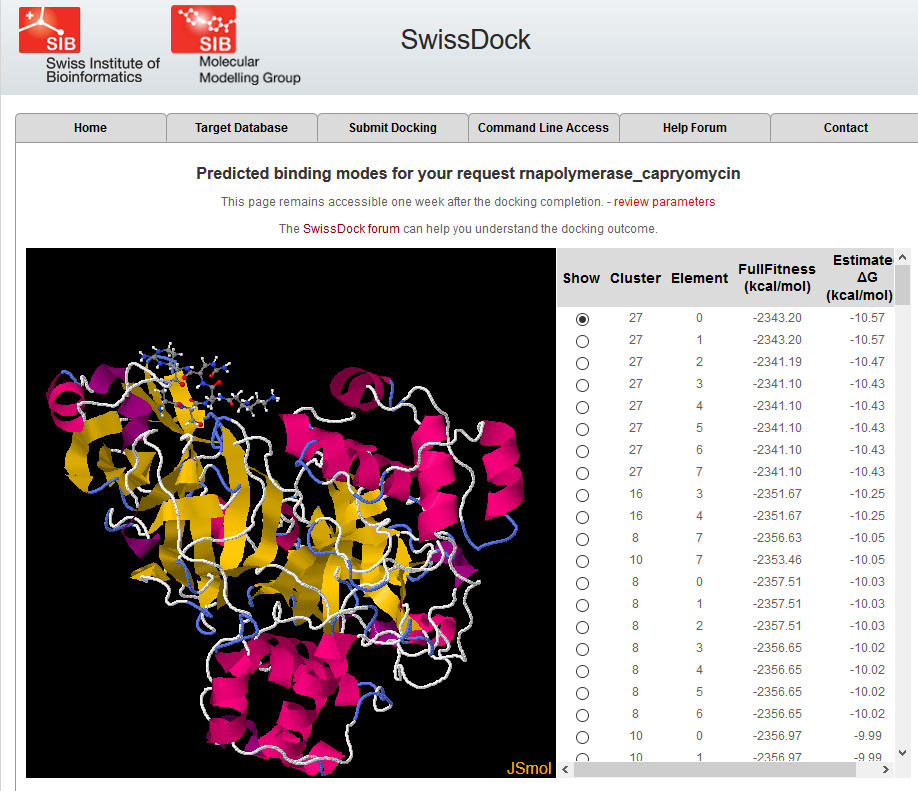
“The replicase polyprotein of coronaviruses is a multifunctional protein: it contains the activities necessary for the transcription of negative stranded RNA, leader RNA, sub genomic mRNAs and progeny virion RNA as well as proteinases responsible for the cleavage of the polyprotein into functional products [16].”

## Validating molecules with docking simulations

<http://www.swissdock.ch/docking/view/swissdockd_VHEkkw_H9B11C1W2BWGOB0D7H1Y>



<http://www.swissdock.ch/docking/view/swissdockd_LUH7ua_6VCTP9T7OL7HP95N5S60>



# Conclusions

Paralog searching the CHEMBL\_25 database with ORFs from the SARS-CoV-2 genome has found a target and two promising drugs that have already been used in the treatment of Tuberculosis.

Success with these drugs in Tuberculosis treatment may have been due to their affect in combination with other drugs to quell concurrent Corona virus infection.

Computational docking studies have found good docking affinity for two of the three drugs identified: capryomycin sulfphate, and viomycin sulphate.

# Appendix

## chembl\_25\_targets.sql

Run this script at the command line of psql connected as chembl\_25 in the blast\_targets directory.

This script creates **chembl\_targets.txt** file.

\copy (select td.chembl\_id, cs.sequence from target\_dictionary td join target\_components tc on td.tid = tc.tid join component\_sequences cs on tc.targcomp\_id=cs.component\_id) to chembl\_targets.txt

## split\_to\_fasta.pl

Run this script from the *bash* command line in the **blast\_targets** directory: **perl split\_to\_fasta.pl**

This script creates the **component\_sequences.fa**file.

#######################################

# split\_to\_fasta.pl

# input recs: <key><delim><sequence>

# output : rec1 = ><key>

# rec2 = <sequence>

#######################################

my $infile = 'chembl\_targets.txt';

my $outfile = 'component\_sequences.fa';

my $delim = '\t';

open(IN, $infile) or die("Unable to open $infile\n");

my @lines = <IN>;

close(IN);

open(OUT,">",$outfile) or die ("Unable to open $outfile\n");

foreach my $line(@lines)

{

my @rec = split($delim,$line);

if (scalar(@rec) > 1)

{

print OUT ">$rec[0]\n";

print OUT "$rec[1]\n";

}

}

close(OUT);

exit(0);

## extract\_hmm\_summary.pl

(in the ~/genomes directory.)

#!/bin/perl

use Switch;

if (scalar(@ARGV) < 1) {die "No filename passed.\n";}

my $text\_fn = $ARGV[0];

my $summary\_fn;

# print $text\_fn,"\n";

$summary\_fn = $text\_fn;

$summary\_fn =~ s/.hmm.txt/.summary/;

# print $summary\_fn,"\n";

my @lines;

open($IN, "<", $summary\_fn ) or die "Can't open $summary\_fn\n";

@lines = <$IN>;

close($IN);

# print "Lines: ",scalar(@lines), "\n";

my %target;

foreach my $line(@lines){

if ( $line =~ m/^(CHEMBL\S+)\s+(\S+)\s+(\S+)\s+(\S+)\s+(\S+)\s+(\S+)\s+(\S+)\s+(\S+)\s+/ ) {

if ( ! exists $target{$1} ) { # prevent duplicate line for a target match

print $1,"\t", $3, "\t", $4,"\t",$6, "\t", $7, "\t", $8, "\n";

$target{$1} = 1;

}

}

}

## import\_hmmer\_statistics.sql

Import this script from the psql command line as user *chembl\_25*.

This script is in **~/genomes**.

truncate table hmmer\_statistics\_import;

\copy hmmer\_statistics\_import from 'hmm\_stats.txt' delimiter E'\t' CSV HEADER

insert into hmmer\_statistics

( target, tlen, orf, qlen, evalue, score)

select target, tlen, orf, qlen, evalue, score

from hmmer\_statistics\_import;

# References

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