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## DECLARATION OF NATHANIEL E FRANK-WHITE

1. I am a Records Request Processor at the Internet Archive. I make this declaration of my own personal knowledge.
2. The Internet Archive is a website that provides access to a digital library of Internet sites and other cultural artifacts in digital form. Like a paper library, we provide free access to researchers, historians, scholars, and the general public. The Internet Archive has partnered with and receives support from various institutions, including the Library of Congress.
3. The Internet Archive has created a service known as the Wayback Machine. The Wayback Machine makes it possible to browse more than 450 billion pages stored in the Internet Archive's web archive. Visitors to the Wayback Machine can search archives by URL (i.e., a website address). If archived records for a URL are available, the visitor will be presented with a display of available dates. The visitor may select one of those dates, and begin browsing an archived version of the Web. Links on archived files in the Wayback Machine point to other archived files (whether HTML pages or other file types), if any are found for the URL indicated by a given link. For instance, the Wayback Machine is designed such that when a visitor clicks on a hyperlink on an archived page that points to another URL, the visitor will be served the archived file found for the hyperlink's URL with the closest available date to the initial file containing the hyperlink.
4. The archived data made viewable and browseable by the Wayback Machine is obtained by use of web archiving software that automatically stores copies of files available via the Internet, each file preserved as it existed at a particular point in time.
5. The Internet Archive assigns a URL on its site to the archived files in the format `http://web.archive.org/web/[Year in yyyy][Month in mm][Day in dd][Time code in hh:mm:ss]/[Archived URL]` aka an "extended URL". Thus, the extended URL `http://web.archive.org/web/19970126045828/http://www.archive.org/` would be the URL for the record of the Internet Archive home page HTML file (`http://www.archive.org/`) archived on January 26, 1997 at 4:58 a.m. and 28 seconds (1997/01/26 at 04:58:28). The date indicated by an extended URL applies to a preserved instance of a file for a given URL, but not necessarily to any other files linked therein. Thus, in the case of a page constituted by a primary HTML file and other separate files (e.g., files with images, audio, multimedia, design elements, or other embedded content) linked within that primary HTML file, the primary HTML file and the other files will each have their own respective extended URLs and may not have been archived on the same dates.
6. Attached hereto as Exhibit A are true and accurate copies of screenshots of the Internet Archive's records of the archived files for the URLs and the dates specified in the attached coversheet of each printout.



7. I declare under penalty of perjury under the laws of the United States of America that the foregoing is true and correct.

DATE: Feb 22, 2022

*Nathaniel E Frank-White*  
Nathaniel E Frank-White

# EXHIBIT A

<https://web.archive.org/web/20081118174453/http://blocks.fhcrc.org/sift/SIFT.html>

# Sorting Intolerant From Tolerant



at the [Fred Hutchinson Cancer Research Center](#).  
Brought to you by the [Blocks WWW server](#).

SIFT predicts whether an amino acid substitution affects protein function based on sequence homology and the physical properties of amino acids. SIFT can be applied to naturally occurring nonsynonymous polymorphisms and laboratory-induced missense mutations.

Given a protein sequence, SIFT will return predictions for what amino acid substitutions will affect protein function.

SIFT is a multistep procedure that:

- (1) searches for and chooses similar sequences
- (2) makes an alignment of these sequences
- (3) calculates scores based on the amino acids appearing at each position in the alignment.

You can:

- submit a [dbSNP id](#) (SNPs from multiple proteins, 2 minutes)
- or- submit a [GI #](#) (2 minutes)
- or- submit a [protein sequence](#) (10-15 minutes)
- or- submit a [query sequence along with related sequences](#) (< 1 minute)
- or- submit [alignment of your query sequence with related sequences](#) (< 1 minute)
- or submit a [block](#)

SIFT for in-house use (version 3.0, released March 21, 2008):

[Copyright code & exe \(Sun, Linux\)](#) [Report bugs](#)

[Prediction on human SNPs](#) (*Genome Research* **12**: 436-446 [pdf](#))

Initial training/test sets for SIFT: [LacI](#), [Lysozyme](#), [HIV protease](#)

Other prediction tools for amino acid substitutions: [PolyPhen](#), [MAPP](#), [SNPs3D](#), [PMut](#)

*Many prediction tools have been developed since SIFT was first published in 2001. MAPP, SNPs3D, and PMut are three methods that have been shown to perform better than SIFT in their published results.*

- SNPs3D is great for fast retrieval of predictions of nsSNPs from dbSNP
- MAPP is great if you only have one or two proteins to predict on

Our review "[Predicting the Effects of Amino Acid Substitutions on Protein Function](#)" in *Annual Review of Genomics and Human Genetics*:

[Chapter](#)

[Supplementary Table 1](#)

[Citation](#)

Referencing SIFT

[version 1](#) (pdf), [version 2](#) (pdf)

[SIFT help page](#)

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