



MTSviewer User Guide

<https://neurobioinfo.github.io/MTSviewerR/>

Overview

The MTSviewer interface contains different tabs:

- (1) MTSviewer: the main platform whose utility will be explained
- (2) Human MTS mutations: a curated list of variants within human protein MTS's – derived from gnomAD v3.1 variants and sorted by increasing to decreasing iMTS value (from iMLP) for that matching residue
- (3) FAQ, Contact Us, Cite us

MTSviewer – brief notes

The MTSviewer user interface begins by selecting an organism (human or yeast) and a protein of interest.

For human proteins, you can choose a database for variant visualization (gnomAD v3.1 or ClinVar), and variants are overlaid onto an XY plot with the iMTS probability from protein N- to C-terminus.

Hovering over a variant dot on the XY plot reveals cursory details which are fully expanded in the variant table below.

For the structure viewer, two coloring schemes are toggleable: the iMTS score, or the AlphaFold per-residue confidence score (pLDDT). Users can investigate specific residues or variants by clicking either on the XY plot or on the protein structure, which will automatically zoom to highlight the interactions (ie. polar contacts) and residues in close proximity (5 Å) to the residue of interest.

Clicking on the iMTS plot will also highlight the residue of interest in the amino acid sequence in the box below. The XY plot also contains toggleable visualizations to highlight cleavage site predictions from the various MTS predictors and/or the experimentally determined N-terminomics sites.

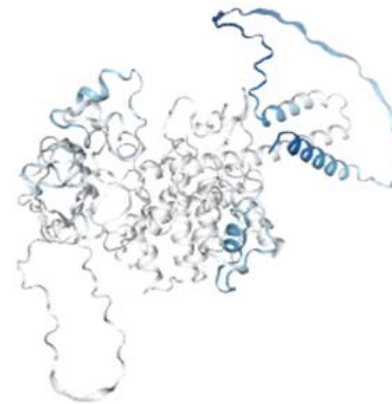
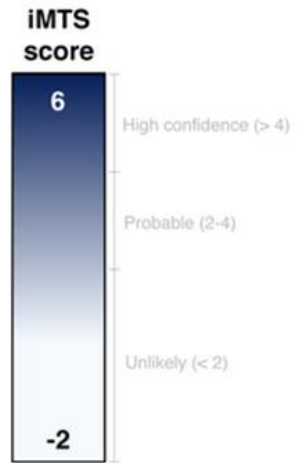
Aggregated comparisons of all targeting predictors are pooled in table format, and data frames are exportable as CSV files to facilitate downstream analyses.

1. Feature selection

PINK1 - Serine/threonine-protein kinase PINK1, mitochondrial (Q9BXM7)

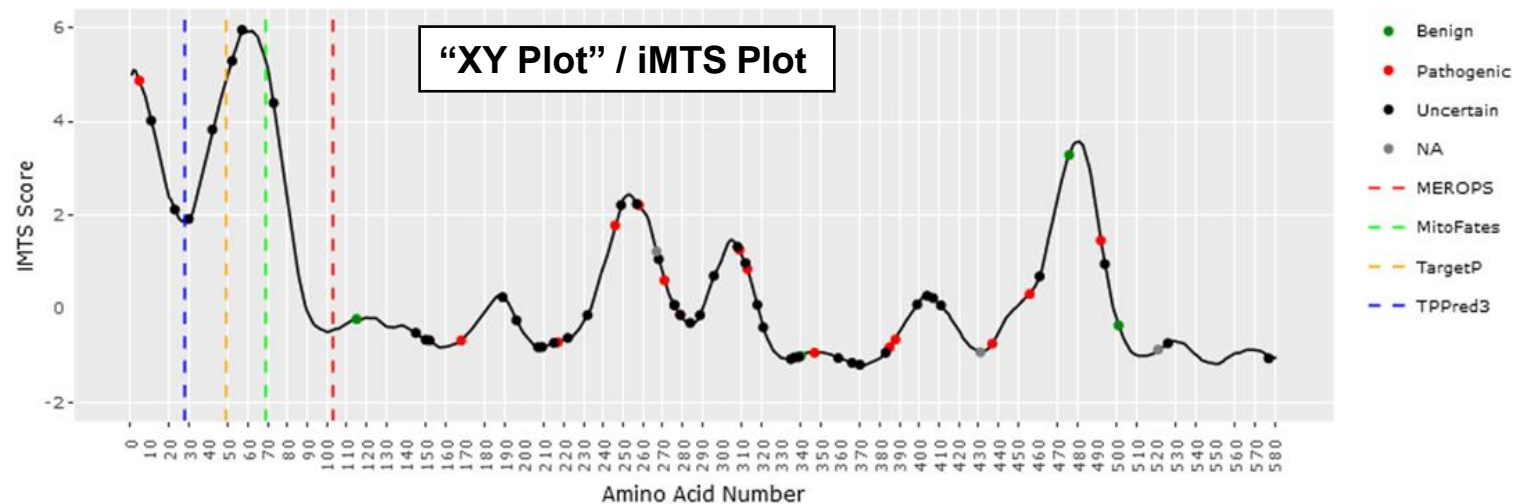
IMPI Class: Verified mitochondrial | IMPI SVM Score: 1

2. Structure viewer



3. iMTS scores + feature viewer

iMLP curves



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For human proteins, you can choose a database for variant visualization (gnomAD v3.1 or ClinVar), and variants are overlaid onto an XY plot with the iMTS probability from protein N- to C-terminus.

Organism
Human

Choose Genes
PINK1

Database
ClinVar

Colouring
iMTS

Type
cartoon

Show Variants?

Upload Variants
 No file selected

[Sample Variant File](#)

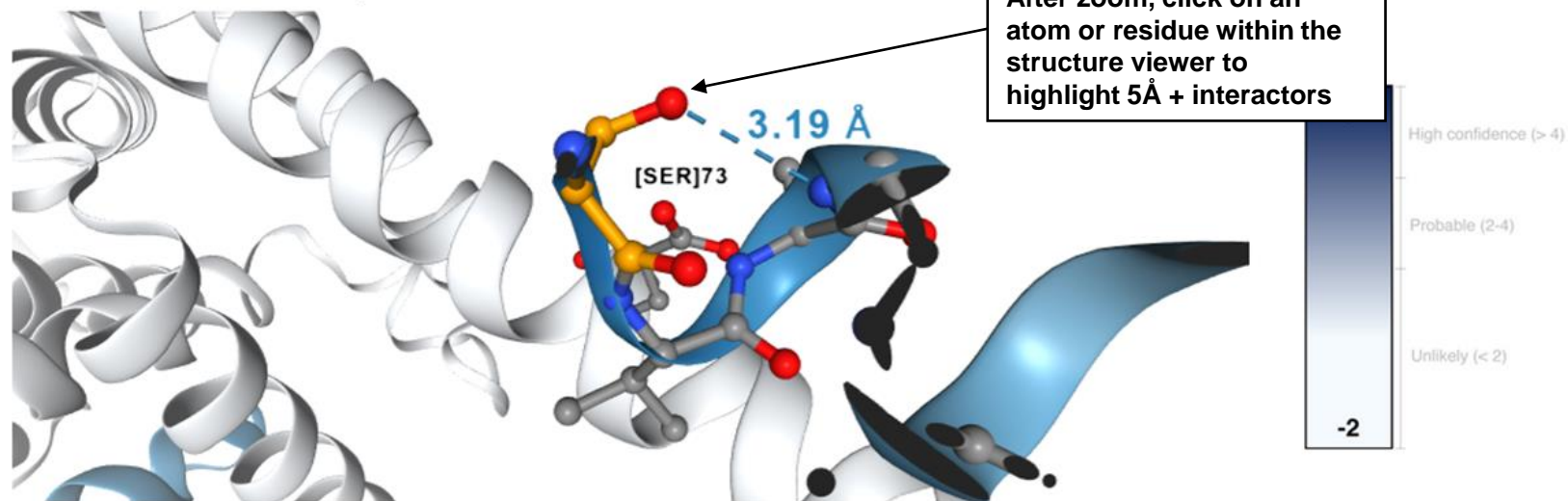
Hovering over a variant dot (e.g. Ser73Leu) on the XY plot reveals cursory details.

Clicking on the Ser73 dot will zoom into the structure at that location.

Clicking again on the residue within the structure viewer will highlight interactions and all residues within 5Å

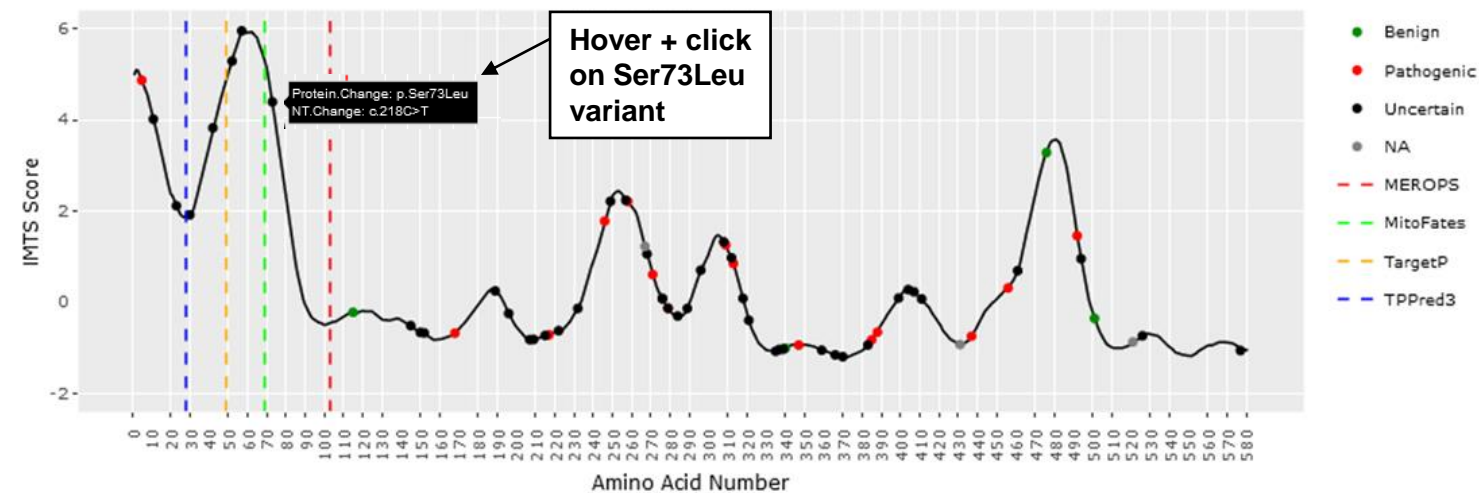
PINK1 - Serine/threonine-protein kinase PINK1, mitochondrial (Q9BXM7)

IMPI Class: Verified mitochondrial | IMPI SVM Score: 1



3. iMTS scores + feature viewer

iMLP curves



MTSviewer – uploading user variants

To visualize custom variant lists or datasets within MTSviewer, users can upload a custom CSV which will show up on the iMTS plot as “User” defined, and will be appended to the mutation list table.

The essential columns for the CSV upload are highlighted in **blue**:

Uniprot	amino.acid	HGVSp_VEP	Dataset?
Q9BXM7	480	p.Pro480Gly	Set 1
Q9BXM7	484	p.Gln484Lys	Set 2
Q9BXM7	488	p.Ala488Pro	Set 3

Important considerations:

(1) Multiple proteins (ie. Uniprot IDs) can be added in a single CSV upload (just add as extra rows underneath the same headers)

(2) In this current version of MTSviewer, all user uploaded Uniprot IDs must match Uniprot IDs that are already present in the MTSviewer database.

(3) To ensure matching, a list of all proteins + Uniprot IDs available in MTSviewer can be found here: <https://drive.google.com/file/d/17mmKTVpHwHZSi8juXL0BycBwoOmBrKBc/view?usp=sharing>

All other columns will get appended into the mutation list – in cases where the column name from the user upload matches one of the columns from dbNSFP (e.g. “CADD_raw”), the columns will be merged so that users can sort and compare their upload to the pre-existing gnomAD or ClinVar variants.

Currently, all user uploads will be coloured as purple on the iMTS plot. In later versions, we will try to include multiple colouring schemes.

The HGVSp_VEP column must be formatted properly (eg: p.Ala2Gly) in order for the upload to work.

MTSviewer – uploading user variants

Note: Protein matching is done based on Uniprot ID

Mismatches will return errors in the upload process

Format and upload variant list CSV of interest

Uniprot	amino.acid	HGVSp_VEP	Dataset?
Q9BXM7	480	p.Pro480Gly	Set 1
Q9BXM7	484	p.Gln484Lys	Set 2
Q9BXM7	488	p.Ala488Pro	Set 3

Proteins are matched based on Uniprot ID

“amino.acid” denotes the x-value for all plotting

“HGVSp_VEP” specifies the a.a. change for the hover over descriptions

Organism

Human

Choose Genes

PINK1

Database

ClinVar

Colouring

iMTS

Type

cartoon

Show Variants?

Upload Variants

Browse...

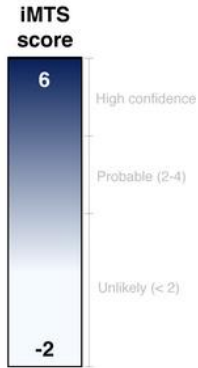
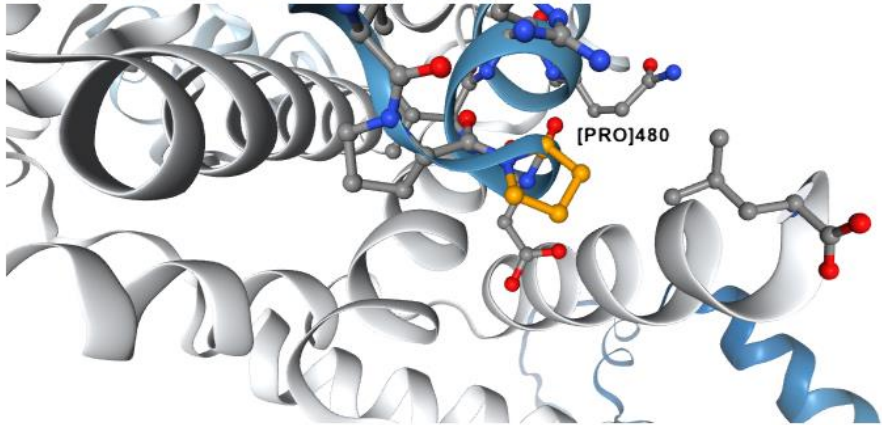
samplefile(6).csv

Upload complete

Sample Variant File (see FAQ)

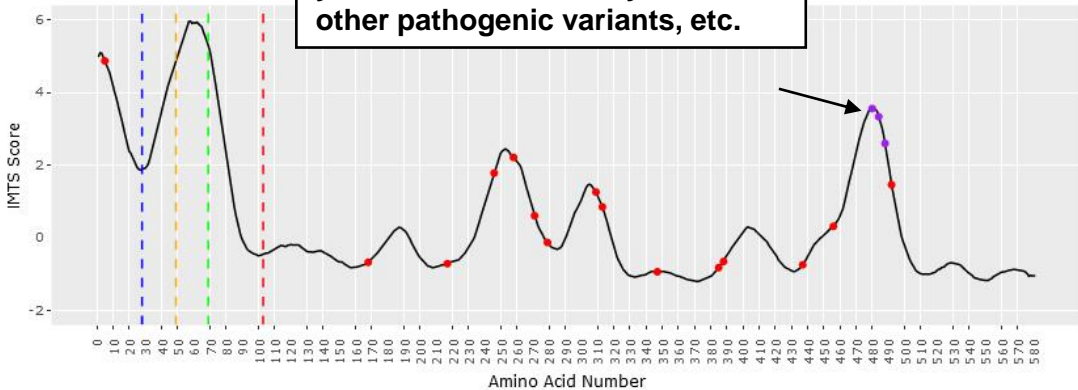
PINK1 - Serine/threonine-protein kinase PINK1, mitochondrial (Q9BXM7)

IMPI Class: Verified mitochondrial | IMPI SVM Score: 1



Reset View

iMLP curves



Visualize where on the iMTS plot your variants lie, if they cluster to other pathogenic variants, etc.

- Benign
- Pathogenic
- Uncertain
- User
- NA
- MEROPS
- MitoFates
- TargetP
- TPPred3

MTSviewer – suggestions and improvements

For all suggestions, bug reporting, or general feedback on our application, please feel free to contact:

mtsviewer.docs@gmail.com

