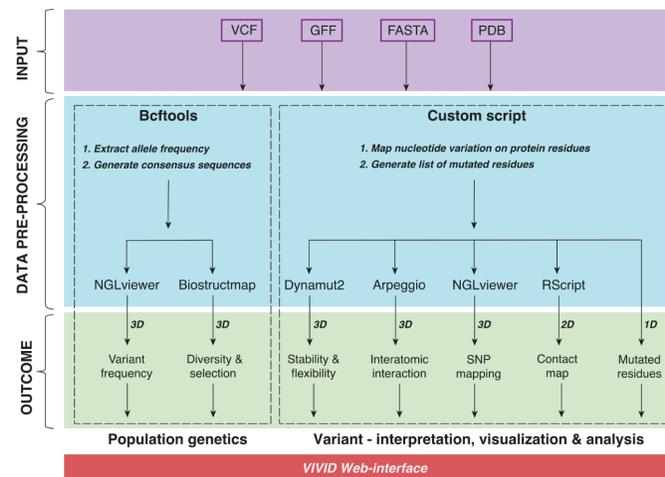


VIVID: a web application for variant interpretation and visualisation in multidimensional analyses

Swapnil Tichkule, Yoochan Myung, Myo T. Naung, Brendan R. E. Ansell, Andrew J. Guy, Namrata Srivastava, Somya Mehra, Simone M. Caccio, Ivo Mueller, Alyssa E. Barry, Cock van Oosterhout, Bernard Pope, David B. Ascher, Aaron R. Jex



Large-scale comparative genomics- and population genetics-based studies generate enormous amounts of polymorphism data in the form of DNA variants. The ultimate goal of these studies is to associate genetic variants with phenotypic outcomes. We introduce VIVID, an interactive, user-friendly web application that integrates a wide range of approaches for encoding genotypic to phenotypic information in any organism or disease, from an individual or population in three-dimensional (3D) space. It allows mutation mapping and annotation, calculation of interactions and conservation scores, prediction of harmful effects, population-scale genetic analyses and 3-dimensional (3D) visualisation of genotypic information encoded in Variant Call Format (VCF) on AlphaFold2 protein models. VIVID indeed offers a convenient way to rapidly assess genes of interest and accelerate research by prioritising targets for experimental validation.

About VIVID

VIVID is a user-friendly web server that allows users to visualise genomic mutations from single-individual to population-scale for their impact on protein structure, function, and evolution.

Read more here:

<https://doi.org/10.1101/2021.11.16.468904>

[Download example dataset 1](#)

Plasmodium falciparum: Erythrocyte binding antigen protein

[Download example dataset 2](#)

SARS-CoV-2: Spike protein

Biosig Lab 

Our group is interested in developing and experimentally validating novel computational methods to exploit this data, enhancing the impact of genome sequencing, structural genomics, and functional genomics on biology and medicine.



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[Source of example dataset 1] <https://www.malariagen.net/data/pf3k-5>

[Source of example dataset 2] <https://usegalaxy.org/u/carlosfarkas/h/snpeffsars-cov-2>



Run



Help



Contact



Acknowledgements

Genetic interpretation and analyses

Andrew J. Guy, Namrata Srivastava, Somya Mehra, David Pope, David B. Ascher, Aaron R. Jex

Large-scale comparative genomics- and population genetics-based studies generate enormous amounts of polymorphism data in the form of DNA variants. The ultimate goal of these studies is to associate genetic variants with phenotypic outcomes. We introduce VIVID, an interactive, user-friendly web application that integrates a wide range of approaches for encoding genotypic to phenotypic information in any organism or disease, from an individual or population in three-dimensional (3D) space. It allows mutation mapping and annotation, calculation of interactions and conservation scores, prediction of harmful effects, population-scale genetic analyses and 3-dimensional

Run Analysis

The job submission page for input files can be accessed via the menu item **Run** on the top bar menu.

Run Analysis

Provide following information

At this input step users have two options to provide a protein structure (PDB file):

(a) Upload a protein structure from the local system or access it via the RCSB PDB database.

 **VIVID**

a **Provide following information:**

I have my own PDB structure.
 I want to check available AlphaFold models.

1.Reference gene sequence (FASTA)

FASTA FILE _____ OR Complete nucleotide coding sequence

```
>CHUDEA6_1080
ATGAGATTGTCGCTCATTATCGTATTAC
TCTCCGTTATAGTCTCCGCTGTATTCT
CAGCCCCAGCCGTCCTCCACTCAGAGG
```

2.VCF file **3.Features & annotation file (GFF)**

VCF FILE _____ **GFF FILE** _____

Run Analysis

b I have my own PDB structure.
 I want to check available AlphaFold models.

1.Reference gene sequence (FASTA)

FASTA FILE PF3D7_0731500.1.fasta OR Complete nucleotide coding sequence

```
>CHUDEA6_1080
ATGAGATTGTCGCCTCATTATCGTATTAC
TCTCCGTTATAGTCTCCGCTGTATTCT
CAGCCCCAGCCGTCCTCCACTCAGAGG
```

CHECK AVAILABLE ALPHAFOLD MODEL:

c Use AlphaFold Model : Erythrocyte-binding antigen 175, Uniprot ID:P19214, length : 1442, percent identity : 85.3 bitscore : 2291.0, Average pLDDT : 60.7
 Provide a PDB

Provide following information

(b) Request through VIVID to check the availability of a protein structure in the AlphaFold Protein Structure Database. First, this is done by blasting the query sequence against the SWISS-PROT database to obtain the UniProt ID of the top blast search hit. Second, the UniProt ID is then searched in AlphaFold Protein Structure Database to obtain the protein structure. After this search, VIVID provides information such as UniProt ID, sequence identity, and average PLDDT score of the model structure to allow the user to decide whether to proceed with the analyses **(c)**.

Run Analysis

VIVID

Provide following information:

I have my own PDB structure.

I want to check available AlphaFold models.

1.Reference gene sequence (FASTA)

1a

OR

1b Complete nucleotide coding sequence

```
>CHUDEA6_1080
ATGAGATTGTCGCTCATTATCGTATTAC
TCTCCGTTATAGTCTCCGCTGTATTCT
CAGCCCCAGCCGTCCTCCACTCAGAGG
```

2.VCF file

3.Features & annotation file (GFF)

Reference gene sequence (FASTA)

The complete nucleotide coding sequence of a gene can be provided by either uploading the FASTA file from the local system **(1a)** or by pasting the sequence along with the gene id into the box **(1b)**.

Please note:

The header in a FASTA file should contain only '>gene_id' without any additional information such as delimiters ('|', 'space', 'tab', etc.) or annotation **(1b)**.

Run Analysis

VIVID [Run](#) [Help](#) [Contact](#) [Acknowledge](#)

2.VCF file

3.Features & annotation file (GFF)

4.Protein structure (PDB) OR PDB accession
Chain identifier

5.Genetic Code

6.Thresholds

Ångstrom threshold (for contact map)

Primary distance threshold (for contact map)

Radius Ångstrom

VCF file

Provide a VCF file that contains only bi-allelic SNPs. If the VCF file size is large (>500 Mb), we suggest users reduce the file size by selecting/keeping SNPs specific to the coding region of the query sequence to avoid lengthy processing times. If the VCF file is unavailable, SNP information can also be provided in a tabular format ([download example](#)).

Please note:

The nucleotide coding sequence should be from the same version of the reference genome used to call SNPs.

2.VCF file

VCF FILE

3

3.Features & annotation file (GFF)

GFF FILE

4.Protein structure (PDB)

PDB FILE

OR

PDB accession

4K2U

Chain identifier

A

5.Genetic Code

Standard Code

6.ThresholdsÅngstrom threshold
(for contact map)

10

Primary distance threshold
(for contact map)

6

Radius Ångstrom

15

Run Analysis

GFF file

Provide a GFF annotation file that should contain the “CDS” feature. If the GFF file is unavailable, CDS coordinates can also be provided in tabular format ([download example](#)).

Run Analysis

VIVID Run Help Contact Acknowledgements

2.VCF file
VCF FILE

3.Features & annotation file (GFF)
GFF FILE

4a **4. Protein structure (PDB)**
PDB FILE

4b Chain identifier
A

4c **OR** PDB accession
4K2U

5.Genetic Code
Standard Code

6.Thresholds

Ångstrom threshold (for contact map) 10

Primary distance threshold (for contact map) 6

Radius Ångstrom 15

Protein structure (PDB)

Provide a protein structure file (**4a or 4c**) and chain ID (**4b**) if you have your PDB structure. This can be provided by either uploading a PDB file from the local system (**4a**) or accessing it via the RCSB PDB by providing a PDB ID (**4c**). These details will be auto-filled if AlphaFold models are selected at the beginning.

2.VCF file

VCF FILE

3.Features & annotation file (GFF)

GFF FILE

4.Protein structure (PDB)

PDB FILE

OR

PDB accession

4K2U

Chain identifier

A

5

5.Genetic Code

Standard Code

6.ThresholdsÅngstrom threshold
(for contact map)

10

Primary distance threshold
(for contact map)

6

Radius Ångstrom

15

Run Analysis

Genetic code

Select the appropriate genetic code (default: 'Standard Code') from the drop-down menu used to translate queried coding sequence into amino acids.

Run Analysis

6

VIVID Run Help Contact Acknow

Standard Code

6.Thresholds

Ångstrom threshold (for contact map)

Primary distance threshold (for contact map)

Radius Ångstrom (for BioStructmap)

7.Email (optional)

Email

If you provide an e-mail, we will send a notice with the result link.

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Thresholds

These inputs are optional and are associated with “Contact Map” and “BioStructmap” analyses that display pairwise residue interactions and perform 3D sliding window population genetics analyses. Ångstrom (0.1 nanometres) is the standard unit of measurement for protein crystal structures.

Standard Code

6.Thresholds

6a

Ångstrom threshold
(for contact map)

10

6b

Primary distance threshold
(for contact map)

6

6c

Radius Ångstrom
(for BioStructmap)

15

7.Email (optional)

Email

your_email@email.com

If you provide an e-mail, we will send a notice with the result link.

RUN EXAMPLE

Run Analysis

Thresholds

Here, the **Ångstrom threshold (6a)** indicates the Euclidian distance in 3-dimensional space between alpha carbon atoms of amino acids (default: 10 Ångstrom) in the contact map. The **primary distance threshold (6b)** represents the number of amino acids apart in the primary sequence (default: 6 AA) in the contact map. **Radius Ångstrom (6c)** represents Euclidean distance from the alpha carbon atoms of the mutated residues (default: 15 Ångstrom), for which 3D sliding window population genetic analyses will be performed.

Run Analysis

Email

By providing an **Email** address, the user can receive a notification email after job completion.

Click **SUBMIT** to get your results

VIVID Run Help Contact Acknow

Standard Code

6.Thresholds

Ångstrom threshold (for contact map)

Primary distance threshold (for contact map)

Radius Ångstrom (for BioStructmap)

7.Email (optional)

Email

If you provide an e-mail, we will send a notice with the result link.

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7

Results

1

External Information

Go to Uniprot: [Q8IBE8](#)
Go to Pfam: [PF05424](#)

Protein Sequence Viewer

Starts with: 152

```

NEVLSNCREK RKG MKWDCKK KNDRSNYVCI PDRRIQLCIV NLSIIKTYTK ETMKDHFIEA 59
SKKESQLLLK KNDNKYNSKF CNDLKN SFLDYGH LAMGN DMDFGGYSTKAE NKIQEVFKGA 119
HGEISEHKIK NFRK KWWNEF REKLWEAMLS EHKNNINCK NIPQEELOIT QWIK EWHGEF 179
LLERDNR SKL PKSKCKNNTL YEACEKECID PCMKYRDWII RSKFEWHTLS KEYETQKVPK 239
ENAENYL IKI SENKND AKVS LLLNNCDAEY SKYCDCKHTT TLVKSVLNGN DNTIKEKREH 299
IDLDDFSKFG CDKNSVD TNT KVWECKRPYK LSTKDV CVPPRRQELCLGNI DRIYDKNLLM 359
IKEHILAIAI YESRILKRKY KNKDDKEVCK IINKTFADIR DIIGGTDYWN DLSNRKLVGK 419
INTNSQYVHR NKQNDK LFRD EWWKVIK KDV WNVISWVFKD KTVCKEDDIE NIPQFFRWF 479
EWGDDYQDK TKMIETL KVE CKEKPCEDDN CKRKCNSYKE WISKKKEEYN KQAKQYQ EY 539
KGNNYKMYSE FRK IKPEVYL KKYSEKCSNL NFEDEFKEEL HSDYKKNKCTM CPEV 593

```

Results

External Information

Provides a link for UniProt and Pfam databases to obtain additional biological information where users can render structural and functional domain information (e.g., conserved structural domains, active sites, etc.) on protein sequence and structure to identify mutational hotspots.

Please note:

The UniProt and Pfam IDs are obtained by performing a BLAST search of the nucleotide query sequence against the SWISSPROT database

Results

Results

Protein Sequence Viewer

The nucleotide coding sequence of a gene is encoded into amino acid residues of a protein where synonymous (purple) and non-synonymous (yellow) mutations are highlighted by default. Only residues present in the PDB file are represented in the primary sequence. This interactive panel can be used to select and highlight **External Information** from above, in primary sequence and 3D Visualisation.

2

External Information

Go to Uniprot: [Q8IBE8](#)
Go to Pfam: [PF05424](#)

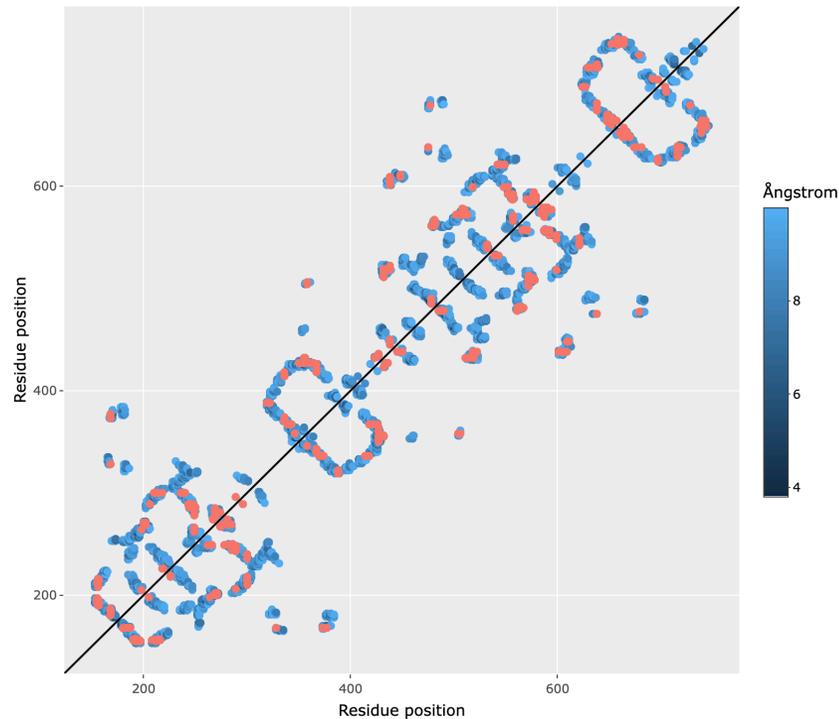
Protein Sequence Viewer

Starts with: 152

NEVLSNCREK RKGKWDCKK KNDRSNYVCI PDRRIQLCIV NLSIIKTYTK ETMKDHFIEA 59
 SKKESQLLLK KNDNKYNSKF CNDLKNFSLD YGHLAMGNDM DFGGYSTKAE NKIQEVFKGA 119
 HGEISEHKIK NFRKQWNEF REKLWEAMLS EHKNNINCK NIPQEELOIT QWIKKEWHGEF 179
 LLERDNRSKL PPSKCKNNTL YEACEKFCID PCMKYRDWII RSKFEWHTLS KEYETQKVPK 239
 ENAENYLIKI SENKNDKAVS LLLNNCDAEY SKYCDCKHTT TLVKSVLNGN DNTIKEKREH 299
 IDLDDFSKFG CDKNSVDNTNT KVWECKRPYK LSTKDVCVPP RRRQELCLGNI DRIYDKNLLM 359
 IKEHILAI AI YESRILKRKY KNKDDKEVCK IINKTFADIR DIIGGTDYWN DLSNRKLVGK 419
 INTNSNYVHR NKQNDKLFRE WVKVKKDV WNVISWVFKD KTVCKEDDIE NIPQFFRWFS 479
 EWGDDYCQDK TKMIETLKVE CKEKPCDDN CKRKCNSYKE WISKKKEEYN KQAKQYQEQ 539
 KGNNYKMYSE FRSIKPEVYL KKYSEKCSNL NFEDEFKEEL HSDYKKNKCTM CPEV 593

Contact Map

Angstrom distance lower threshold: 10
Sequence distance lower threshold: 6
Mutations are shown in pink.



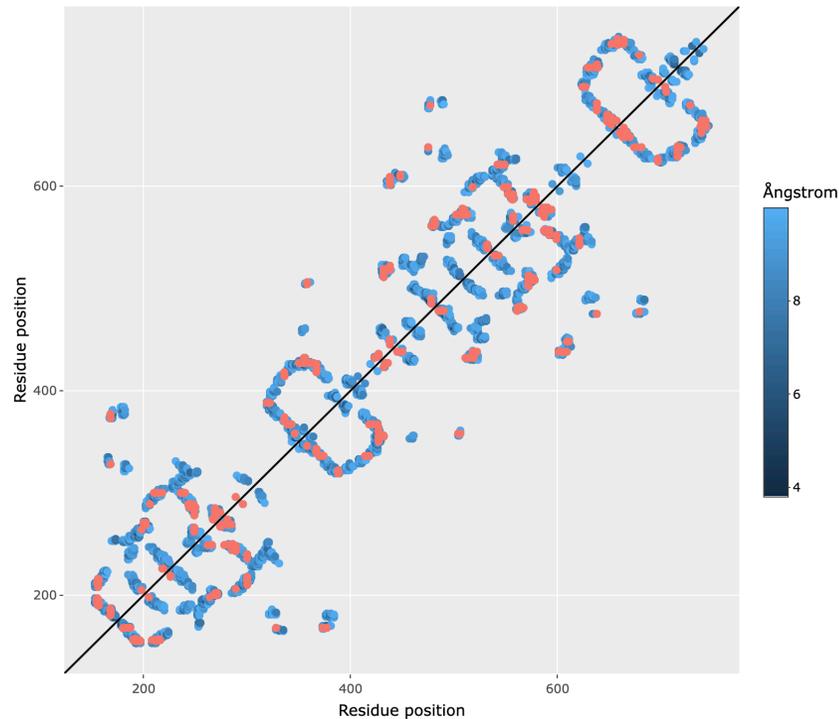
Results

Contact Map

This represents pairwise residue-residue interactions. Interactions within user-defined *Angular threshold* in 3D-space and found more than the *primary distance threshold* are shown in blue, where interactions involving mutated residues are highlighted in pink. This interactive panel allows users to *zoom in* by selecting a box. Also, users can *hover over* interactions to display details of interacting residues.

Contact Map

Angstrom distance lower threshold: 10
Sequence distance lower threshold: 6
Mutations are shown in pink.



Results

Contact Map

Please note:

If users want to display more long-range interactions in 2D space and avoid closely associated residues in the primary sequence, they can go back to the submission page and increase the Ångstrom threshold and Primary distance threshold.

VIVID Run Help Contact Acknowledgements

3D Visualisation

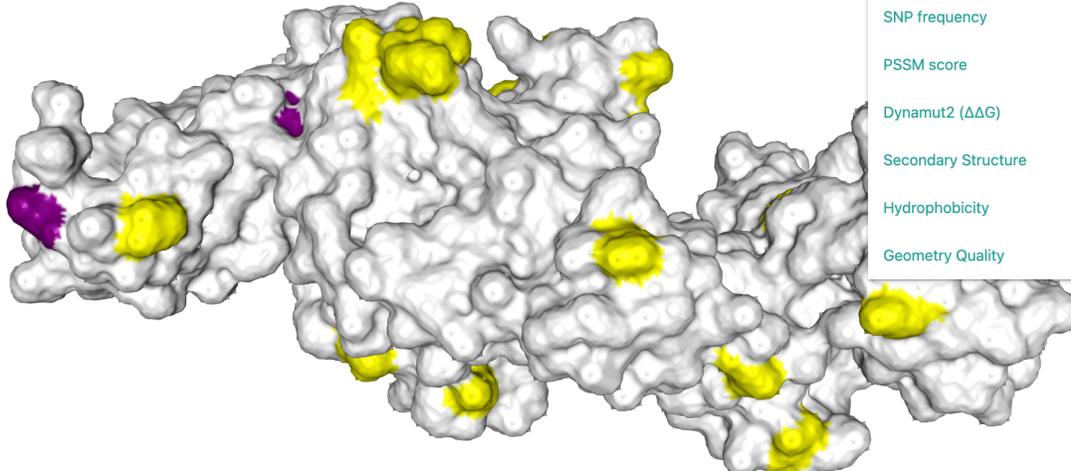
Background: White | Surface Transparency: 100% | Representation: surface | Color Scheme: Syn/non-synonymous mutations

Interactions

- Atom representation: Hide Show
- PI interaction: Hide Show
- Aromatic: Hide Show
- VDW: Hide Show
- Hydrophobic: Hide Show
- Hydrogen Bond: Hide Show
- Carbonyl: Hide Show

Color Scheme

- Syn/non-synonymous mutations
- Chain
- Element/CPK
- Residue
- Molecule Type
- Tajima's D
- Nucleotide diversity
- SNP frequency
- PSSM score
- Dynamut2 ($\Delta\Delta G$)
- Secondary Structure
- Hydrophobicity
- Geometry Quality



A 3D surface representation of a protein structure. The surface is primarily white, with several yellow patches scattered across it, indicating interactions. Two purple patches are also visible, representing mutations. The protein is shown in a complex, folded conformation.

Results

3D Visualisation

This panel shows interactive 3D viewer. Default view displays interatomic interactions between the wild-type residue and nearby residues.

4a

3D Visualisation

Background: White

Surface Transparency: 100%

Representation: surface

Color Scheme: Syn/non-synonymous mutations

Interactions:

- Atom representation: Hide Show
- PI interaction: Hide Show
- Aromatic: Hide Show
- VDW: Hide Show
- Hydrophobic: Hide Show
- Hydrogen Bond: Hide Show
- Carbonyl: Hide Show

Synonymous Nonsynonymous

4c

Color Scheme

- Syn/non-synonymous mutations
- Chain
- Element/CPK
- Residue
- Molecule Type
- Tajima's D
- Nucleotide diversity
- SNP frequency
- PSSM score
- Dynamut2 ($\Delta\Delta G$)
- Secondary Structure
- Hydrophobicity
- Geometry Quality

4b

ROTATE ON X-AXIS OF 90°

ROTATE ON Y-AXIS OF 90°

ROTATE ON Z-AXIS OF 90°

RESET VIEW ?

CLEAR SELECTION ?

SPIN ?

FULLSCREEN ?

SCREENSHOT ?

Results

3D Visualisation

Interactions can be hidden or displayed using the controls provided (4a). The viewer can be manipulated using buttons at the bottom of the panel (4b). VIVID allows users to perform multiple 3D renderings using the control panel by selecting options from the 'colour scheme' drop-down menu (4c). The default colour scheme is synonymous and non-synonymous mutations. Some interesting, informative visualisation in the 'colour scheme' could be Tajima's D, Nucleotide diversity, SNP frequency, PSSM score and Dynamut2 ($\Delta\Delta G$).

4a **3D Visualisation**

Background: White | Surface Transparency: 100% | Representation: surface | Color Scheme: Syn/non-synonymous mutations

Interactions:

- Atom representation: Hide Show
- PI interaction: Hide Show
- Aromatic: Hide Show
- VDW: Hide Show
- Hydrophobic: Hide Show
- Hydrogen Bond: Hide Show
- Carbonyl: Hide Show

4c

Color Scheme:

- Chain
- Element/CPK
- Residue
- Molecule Type
- Tajima's D
- Nucleotide diversity
- SNP frequency
- PSSM score
- Dynamut2 ($\Delta\Delta G$)
- Secondary Structure
- Hydrophobicity
- Geometry Quality

4b

Legend: Synonymous (purple) | Nonsynonymous (yellow)

ROTATE ON X-AXIS OF 90° | ROTATE ON Y-AXIS OF 90° | ROTATE ON Z-AXIS OF 90° | RESET VIEW ?

CLEAR SELECTION ? | SPIN ? | FULLSCREEN ? | SCREENSHOT ?

Results

3D Visualisation

Please note:

Population genetics indices such as Tajima's D and Nucleotide diversity are calculated with a 3D sliding window (default Radius Ångstrom = 15) analysis in the BioStructmap program. Depending on the size of the protein, the default value of Radius Ångstrom might not be sufficient; hence the user can go back to the submission page and increase/decrease the Radius Ångstrom threshold. For more details, please refer to the BioStructmap publication [1].

[1] Guy AJ, Irani V, Richards JS, Ramsland PA. 2018. BioStructMap: a Python tool for integration of protein structure and sequence-based features. Bioinformatics 34:3942-3944.

5

Mutational Analysis



Active	Chain	Wild	Position	Mutant	ΔΔG _{stability} ⓘ
<input checked="" type="checkbox"/>	A	S	156	N	-0.28
<input type="checkbox"/>	A	N	157	S	0.25
<input type="checkbox"/>	A	D	168	H	-0.69
<input type="checkbox"/>	A	S	176	R	-0.84
<input type="checkbox"/>	A	T	198	R	-1.57
<input type="checkbox"/>	A	K	226	E	-0.17
<input type="checkbox"/>	A	K	269	E	-0.32
<input type="checkbox"/>	A	A	271	D	-0.26
<input type="checkbox"/>	A	E	274	K	0.65
<input type="checkbox"/>	A	I	275	K	-0.69

Results

Mutational Analysis

This panel will be shown once Dynamut2 computations are completed. It displays predicted changes of folding free energy ($\Delta\Delta G$) of substituted amino acids on protein structure stability and flexibility using the Dynamut2 program.

Results

Mutational Analysis

5a



5b

Active	Chain	Wild	Position	Mutant	$\Delta\Delta G_{\text{stability}}$
<input checked="" type="checkbox"/>	A	S	156	N	-0.28
<input type="checkbox"/>	A	N	157	S	0.25
<input type="checkbox"/>	A	D	168	H	-0.69
<input type="checkbox"/>	A	S	176	R	-0.84
<input type="checkbox"/>	A	T	198	R	-1.57
<input type="checkbox"/>	A	K	226	E	-0.17
<input type="checkbox"/>	A	K	269	E	-0.32
<input type="checkbox"/>	A	A	271	D	-0.26
<input type="checkbox"/>	A	E	274	K	0.65
<input type="checkbox"/>	A	I	275	K	-0.69

$\Delta\Delta G$ values are represented in a bar chart (5a) and tabular format (5b). $\Delta\Delta G$ values can also be visualised in the 3D visualisation panel by clicking on a drop-down menu of 'colour scheme'. For more details about $\Delta\Delta G$ calculation, please refer to the Dynamut2 publication [2].

Arpeggio Results

The difference of Arpeggio interactions between wildtype and mutant structures.

Column visibility

Active	Mutation	WeakPolar	d_Donor-PI	d_Amide-Amide	d_PI-PI	d_Cation-PI	d_MetalSulphur-PI	d_Amide-Ring	d_Carbon-PI	Covalent
<input type="checkbox"/>	A156N	0	0	-2	0	0	0	0	0	0
<input type="checkbox"/>	A157S	1	0	2	0	0	0	0	0	0
<input type="checkbox"/>	A168H	2	-1	0	0	-1	0	0	0	0
<input type="checkbox"/>	A176R	1	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A198R	-2	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A226E	-1	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A269E	1	0	-1	0	0	0	0	0	0
<input type="checkbox"/>	A271D	0	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A274K	2	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A275K	1	0	0	2	0	0	0	0	0

Showing 1 to 10 of 38 entries

Previous 1 2 3 4 Next

Download

Dynamut2 result(csv) file

Arpeggio result(csv) file

Biosig Lab

Our group is interested in developing and experimentally validating novel computational methods to exploit this data, enhancing the impact of genome sequencing, structural genomics, and functional genomics on biology and medicine.



Results

Arpeggio Results

This panel displays information about interatomic interactions between the substituted residue and nearby residues in in protein structures. Mainly, it reports changes among 20 interatomic interactions when compared wildtype and mutant residues. Users can use this table to get information about lost and gained interaction after substitution in a protein structure.

Results

Arpeggio Results

By default, information about nine types of interactions is shown in the table (6a). Users can click on 'column visibility' (6b) to display additional interactions. For more details, please refer to the Arpeggio publication [3].

VIVID Run Help Contact Acknowledgements

Arpeggio Results

The difference of Arpeggio interactions between wildtype and mutant structures.

Column visibility

6a

Active	Mutation	WeakPolar	d_Donor-PI	d_Amide-Amide	d_PI-PI	d_Cation-PI	d_MetalSulphur-PI	d_Amide-Ring	d_Carbon-PI	Covalent
<input type="checkbox"/>	A156N	0	0	-2	0	0	0	0	0	0
<input type="checkbox"/>	A157S	1	0	2	0	0	0	0	0	0
<input type="checkbox"/>	A168H	2	-1	0	0	-1	0	0	0	0
<input type="checkbox"/>	A176R	1	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A198R	-2	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A226E	-1	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A269E	1	0	-1	0	0	0	0	0	0
<input type="checkbox"/>	A271D	0	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A274K	2	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A275K	1	0	0	2	0	0	0	0	0

Showing 1 to 10 of 38 entries Previous 1 2 3 4 Next

6b

Download

Dynamut2 result(csv) file Arpeggio result(csv) file

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institute

Arpeggio Results

The difference of Arpeggio interactions between wildtype and mutant structures.

Column visibility

Active	Mutation	WeakPolar	d_Donor-PI	d_Amide-Amide	d_PI-PI	d_Cation-PI	d_MetalSulphur-PI	d_Amide-Ring	d_Carbon-PI	Covalent
<input type="checkbox"/>	A156N	0	0	-2	0	0	0	0	0	0
<input type="checkbox"/>	A157S	1	0	2	0	0	0	0	0	0
<input type="checkbox"/>	A168H	2	-1	0	0	-1	0	0	0	0
<input type="checkbox"/>	A176R	1	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A198R	-2	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A226E	-1	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A269E	1	0	-1	0	0	0	0	0	0
<input type="checkbox"/>	A271D	0	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A274K	2	0	0	0	0	0	0	0	0
<input type="checkbox"/>	A275K	1	0	0	2	0	0	0	0	0

Showing 1 to 10 of 38 entries

Previous 1 2 3 4 Next

Download

 Dynamut2 result(csv) file

 Arpeggio result(csv) file

Biosig Lab [↗](#)

Our group is interested in developing and experimentally validating novel computational methods to exploit this data, enhancing the impact of genome sequencing, structural genomics, and functional genomics on biology and medicine.



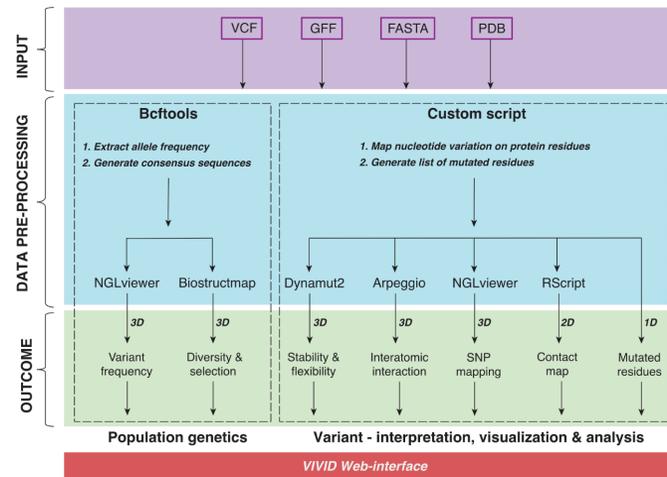
Results

Download

Users can download results of Dynamut2 $\Delta\Delta G$ values and Arpeggio interactions of substituted protein residues.

VIVID: a web application for variant interpretation and visualisation in multidimensional analyses

Swapnil Tichkule, Yoochan Myung, Myo T. Naung, Brendan R. E. Ansell, Andrew J. Guy, Namrata Srivastava, Somya Mehra, Simone M. Caccio, Ivo Mueller, Alyssa E. Barry, Cock van Oosterhout, Bernard Pope, David B. Ascher, Aaron R. Jex



Large-scale comparative genomics- and population genetics-based studies generate enormous amounts of polymorphism data in the form of DNA variants. The ultimate goal of these studies is to associate genetic variants with phenotypic outcomes. We introduce VIVID, an interactive, user-friendly web application that integrates a wide range of approaches for encoding genotypic to phenotypic information in any organism or disease, from an individual or population in three-dimensional (3D) space. It allows mutation mapping and annotation, calculation of interactions and conservation scores, prediction of harmful effects, population-scale genetic analyses and 3-dimensional (3D) visualisation of genotypic information encoded in Variant Call Format (VCF) on AlphaFold2 protein models. VIVID indeed offers a convenient way to rapidly assess genes of interest and accelerate research by prioritising targets for experimental validation.

Contact Us

In case you experience any trouble using VIVID or if you have any suggestions or comments, please do not hesitate in contacting us either via [email](#) or via our [Group website](#).

If you are are contacting regarding a job submission, please include details such as input information and the job identifier.

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