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**DEPARTMENT OF BIOINFORMATICS**

**CERTIFICATE**

This is to certify that Mr. **Shalmon N Anandas** of M.Sc. Part I Bioinformatics has satisfactorily completed the practical semester II course prescribed by the university of Mumbai during the academic year 2021-2022

**TEACHER IN CHARGE**

**HEAD OF DEPARTMENT**

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## WEBLEM 1

### SECONDARY STRUCTURE PREDICTION

#### **Introduction:**

- ➔ Secondary structure prediction is relatively accurate, and is in fact much easier to solve than three-dimensional structure prediction. The accuracy of assigning strand, helix or loops to a certain residue can go up to 80% with the most reliable methods. Typically, these methods use periodicity in the sequence combined with phi and psi angle preferences of certain amino acids types to come to accurate predictions. The real challenge lies in assembling the secondary structure element in a correct topology. Nevertheless, secondary structure prediction may be used to assess the quality of model built with a structure prediction method. Many methods also incorporated secondary structure information during homology detection.

#### **Secondary structure prediction has three generations:**

##### **1. First Generation: Chou and Fasman**

- ➔ CFSSP (Chou & Fasman Secondary Structure Prediction Server) is an online protein secondary structure prediction server. This server predicts regions of secondary structure from the protein sequence such as alpha helix, beta sheet, and turns from the amino acid sequence. The output of predicted secondary structure is also displayed in linear sequential graphical view based on the probability of occurrence of alpha helix, beta sheet, and turns. The method implemented in CFSSP is Chou-Fasman algorithm, which is based on analyses of the relative frequencies of each amino acid in alpha helices, beta sheets, and turns based on known protein structures solved with X-ray crystallography. CFSSP is freely accessible via ExPASy server.

##### **2. Second Generation: GOR IV**

- ➔ The GOR method is based on information theory and was developed by J.Garnier, D.Osguthorpe and B.Robson (J.Mol.Biol.120,97, 1978). The present version, GOR IV, uses all possible pair frequencies within a window of 17 amino acid residues and is reported by J. Garnier, J.F. Gibrat and B.Robson in Methods in Enzymology, vol 266, p 540-553 (1996). After cross validation on a data base of 267 proteins, the version IV of GOR has a mean accuracy of 64.4% for a three-state prediction (Q3). The program gives two outputs, one eye-friendly giving the sequence and the predicted secondary structure in rows, H=helix, E=extended or beta strand and C=coil; the second gives the probability values for each secondary structure at each amino acid position. The predicted secondary structure is the one of highest probability compatible with a predicted helix segment of at least four residues and a predicted extended segment of at least two residues.

##### **3. Third Generation: PSIPRED**

- ➔ The PSIPRED Workbench provides a range of protein structure prediction methods. The site can be used interactively via a web browser or programmatically via our REST API. For high- throughput analyses, downloads of all the algorithms are available. Amino acid sequences enable: secondary structure prediction, including regions of disorder and transmembrane helix packing; contact analysis; fold recognition; structure modelling; and prediction of domains and function. In addition, PDB Structure files allow prediction of protein-metal ion contacts, protein-protein hotspot residues, and membrane protein orientation.

#### **References:**

- ➔ Protein Secondary Structure - an overview | ScienceDirect Topics. (2016). Science Direct. <https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/protein-secondary-structure>
- ➔ Edwards, Y. J., and Cottage, A. 2003. Bioinformatics methods to predict protein structure and function. A

- practical approach. Mol. Biotechnol. 23:139-66.
- ➔ Ashok Kumar, T. (2013). CFSSP: Chou and Fasman Secondary Structure Prediction server. WIDE SPECTRUM: Research Journal. 1(9):15-19.
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  - ➔ Moller, S., Croning, M. D. R., and Apweiler, R. 2001. Evaluation of methods for the prediction of membrane spanning regions. Bioinformatics 17:646-53.

## WEBLEM 1A

### SECONDARY STRUCTURE PREDICTION

**Aim:**

- Secondary Structure prediction for CAD13\_HUMAN (Cadherin) using various tools (CF, GOR IV, PSIPRED)

**Introduction:**

- Secondary Structure prediction has three generations:

**1. First Generation: Chou and Fasman**

- CFSSP (Chou & Fasman Secondary Structure Prediction Server) is an online protein secondary structure prediction server. This server predicts regions of secondary structure from the protein sequence such as alpha helix, beta sheet, and turns from the amino acid sequence. The output of predicted secondary structure is also displayed in linear sequential graphical view based on the probability of occurrence of alpha helix, beta sheet, and turns.

**2. Second Generation: GOR IV**

- The GOR method is based on information theory and was developed by J.Garnier, D.Osguthorpe and B.Robson. After cross validation on a data base of 267 proteins, the version IV of GOR has a mean accuracy of 64.4% for a three-state prediction. The program gives two outputs, one eye-friendly giving the sequence and the predicted secondary structure in rows, H=helix, E=extended or beta strand and C=coil; the second gives the probability values for each secondary structure at each amino acid position.

**3. Third Generation: PSIPRED**

- The PSIPRED Workbench provides a range of protein structure prediction methods. The site can be used interactively via a web browser or programmatically via our REST API. For high- throughput analyses, downloads of all the algorithms are available. Amino acid sequences enable: secondary structure prediction, including regions of disorder and transmembrane helix packing; contact analysis; fold recognition; structure modelling; and prediction of domains and function

**Cadherin:**

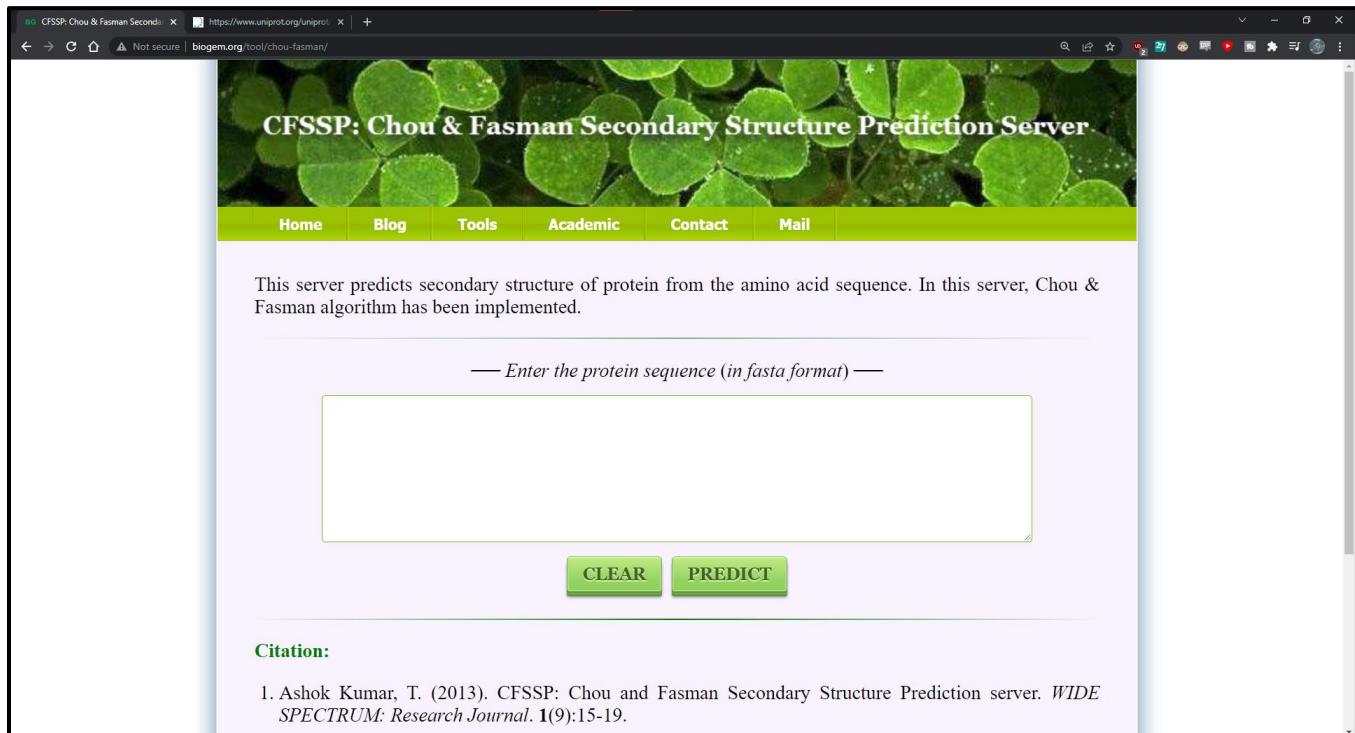
- Cadherins are a large family of cell-cell adhesion molecules acting in a homotypic, homophilic manner that play an important role in the maintenance of tissue integrity. In the human kidney several members of the cadherin family are expressed in a controlled spatiotemporal pattern. Cadherin-16 also called kidney-specific cadherin, is exclusively expressed in epithelial cells of the adult kidney.

**Methodology:**

- Open Homepage of (CF, GOR IV, PSIPRED)
- Enter the query Cadherin Fasta sequence in the search bar.
- Open the Result page.
- Interpret the Results.

## Observations:

### → First Generation: Chou and Fasman



The screenshot shows the homepage of the CFSSP: Chou & Fasman Secondary Structure Prediction Server. The header features a green banner with the text "CFSSP: Chou & Fasman Secondary Structure Prediction Server" and a background image of green leaves. Below the banner is a navigation menu with links to "Home", "Blog", "Tools", "Academic", "Contact", and "Mail". A text area below the menu states: "This server predicts secondary structure of protein from the amino acid sequence. In this server, Chou & Fasman algorithm has been implemented." A large input field is labeled "Enter the protein sequence (in fasta format)". Below the input field are two buttons: "CLEAR" and "PREDICT". At the bottom of the page, there is a "Citation" section with the following text: "1. Ashok Kumar, T. (2013). CFSSP: Chou and Fasman Secondary Structure Prediction server. *WIDE SPECTRUM: Research Journal*. 1(9):15-19."

**Fig1: Homepage of Chou and fasman**



The screenshot shows a browser window displaying the FASTA sequence of CAD13\_HUMAN Cadherin. The sequence is as follows:

```
>sp|P55290|CAD13_HUMAN Cadherin-13 OS=Homo sapiens OX=9606 GN=CDH13 PE=1 SV=1
MQPRTPLVLCVLLSQVLLTSAEDLDCTPGFQQKVFHINQPAEFIEDQSILNLTFSCKG
NDKLRYEVSSPYFKVNSDGLVALRNITAVGKTLFVHARTPHAEDEMAEVIVGGKDIQGS
LQDIFKFARTSPVPRQKRSIVSPILIPENQRQPFPRDVGKVVDSRPERSKFRLTGKGV
DQEPKGIFRINENTGSVSVTRTLDREVIAVYQLFVETTDVNGKTLEGPVPLEVIVIDQND
NRPIFREGPYIGHVMEGSPTGTTVRMTAFDADDPATDNALLRYNIRQQTPDKPSPNMFY
IDPEKGDIVTVVSPALLDRETLENPKYELIIEAQDMAGLDVGLTGTATATIMIDDKNDHS
PKFTKKEFQATVEEGAVGVIVNLTVEDKDDPTTGAWRAAYTIINGNPGQSFEIHTNPQTN
EGMLSVVKPLDYEISAFHTLLIKVENEDPLVPDVSYGPSSTATVHITVLDVNEGPPVFPD
PMMVTRQEDLSVGSVLLTVNATDPDSLQHQTIRYSVYKDPAGWLNNPINGTVDTTAVLD
RESPFVDNSVYTALFLAIDSGNPPATGTGTLITLEDVNDNAPFIYPTVAEVCDAAKNLS
VVLGASDKDLHPNTDPFKFEIHKQAVPDVKWKISKINNTHALVSSLQNLNKANYNLPI
VTDSGKPPMTNITDLRVQVCSRNSKVDNAAGALRFLPSVLLSLFSLACL
```

**Fig2. FASTA sequence of CAD13\_HUMAN Cadherin**

CFSSP: Chou & Fasman Secondary Structure Prediction Server

This server predicts secondary structure of protein from the amino acid sequence. In this server, Chou & Fasman algorithm has been implemented.

— Enter the protein sequence (in fasta format) —

```
>sp|P55290|CAD13_HUMAN Cadherin-13 OS=Homo sapiens OX=9606 GN=CDH13 PE=1
SV=1
MQPRTPLVLCVLLSQVLLTSAEDLDCTPGFQQKVFHINQPAEFIEDQSILNLTFSDCKG
NDKLRYEVSSPYFKVNSDGGLVALRNITAVGKTLFVHARTPHAEDEMAELVIVGGKDIQGS
LQDIFKFARTSPVPRKRSIVVSPILIPENQRQPFPRDVKGKVVDSDRPERSKFRLTGKGV
DQEPKGIFRINENTGSVSVTRTLDRREVIAVYQLFVETTDVNGKTLEGPVPLEVIVIDQND
NRPIFREGPYIGHVMEGSPPTGTTVMMRMTAFDADDPATDNA LLRNYIRQQTPDKPSPNMFY
```

**Citation:**

1. Ashok Kumar, T. (2013). CFSSP: Chou and Fasman Secondary Structure Prediction server. *WIDE SPECTRUM: Research Journal.* 1(9):15-19.

**Fig3. Search bar with FASTA sequence of CAD13\_HUMAN Cadherin**

CFSSP: Chou & Fasman Secondary Structure Prediction Server

Target Sequence:

```

10          20          30          40          50          60          70
MQPRTPLVLC VLLSQVLLT SAEDLDCTPG FQQKVFHINQ PAEFIEDQSI LNLTFSDCKG NDKLRYEVSS
80          90          100         110         120         130         140
PYFKVNSDGG LVALRNITAV GKTTLFVHART PHAEDMAELV IVGGKDIQGS LQDIFKFART SPVPRKRSI
150         160         170         180         190         200         210
VVSPILIPEN QRQPFPRDVG KVVDSDRPER SKFRLTGKGV DQEPKGIFR NENTGSVSVT RTLDRREVIAV
220         230         240         250         260         270         280
YQLFVETTDV NGKTLEGPVPL LEVIVIDQND NRPIFREGPY IGHVMEGSPT GTTVMMRMTAF DADDPATDNA
290         300         310         320         330         340         350
LLRNYIRQQT PDKPSPNMFY IDPEKGDIYT VVSPALLDRE TLENPKYELI IEAQDMAGLD VGLTGTATAT
360         370         380         390         400         410         420
IMIDDKNHIS PKFTKKEFQA TVEEGAVGVI VNLTVEKD PTTGAWRAAY TIINGNPGQS FEIHTNPQTN
430         440         450         460         470         480         490
EGMLSVVKPL DYEISAFHTL LIKVENEEDPL VPDVSYGPSS TATVHITVLD VNEGPFYFPD PMMVTRQEDL
500         510         520         530         540         550         560

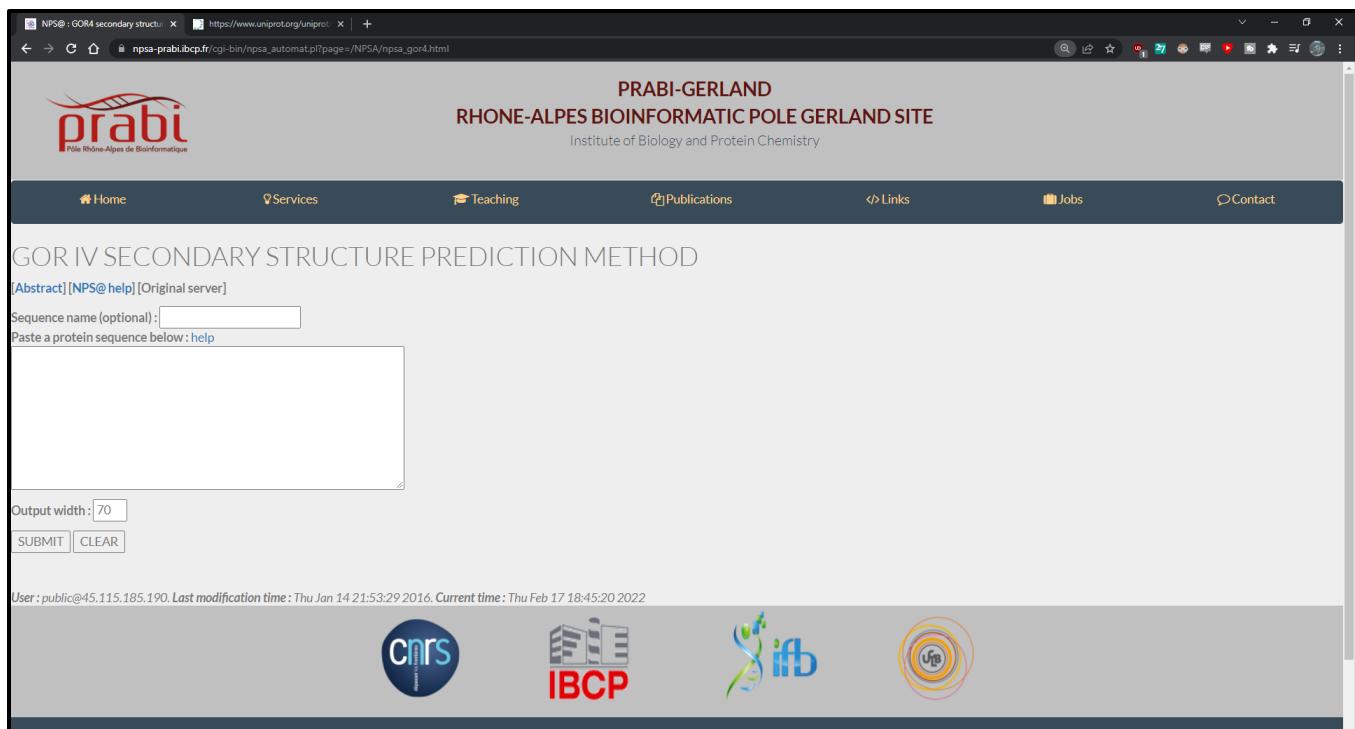
```

**Fig4. Result page of Cadherin showing target sequence**



## Fig5. Result page of Cadherin showing Secondary structure

## → Secondary Generation: GOR IV



**Fig1. Homepage of GOR IV**

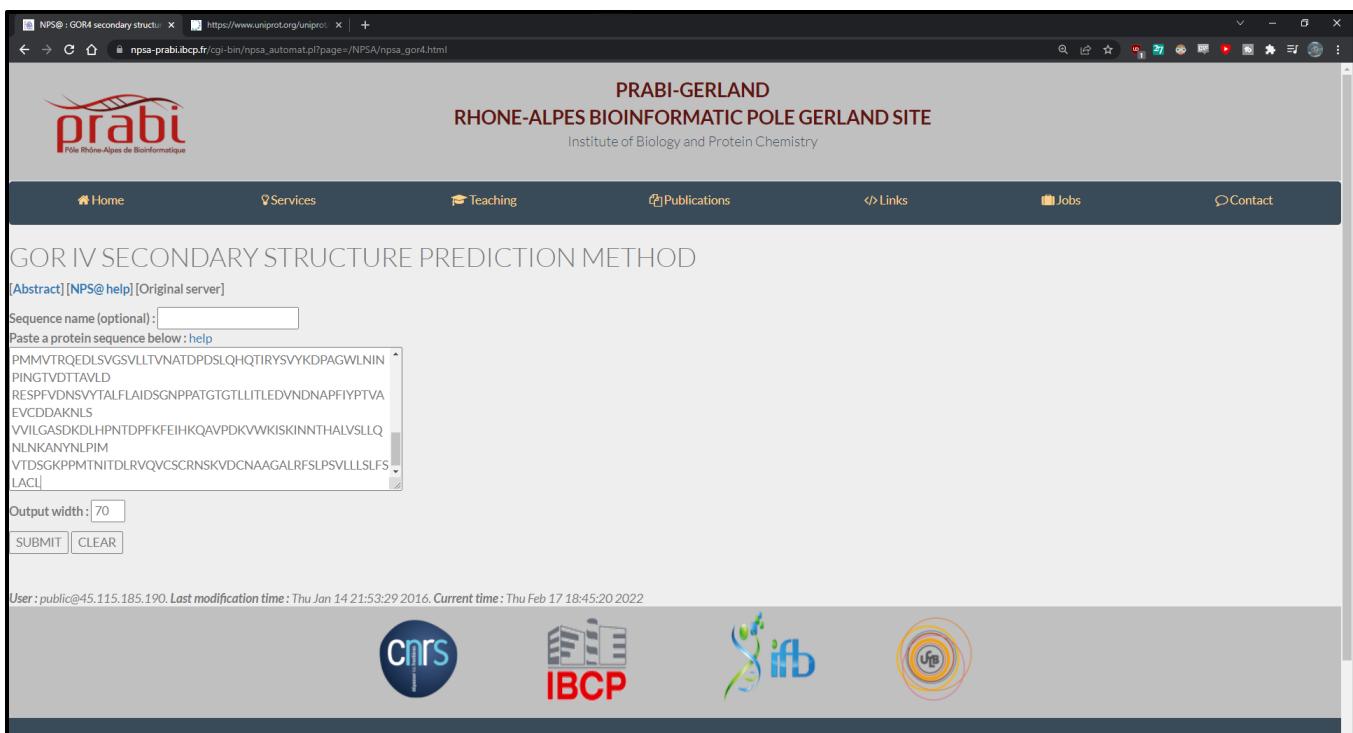


```

>sp|P55290|CAD13_HUMAN Cadherin-13 OS=Homo sapiens OX=9606 GN=CDH13 PE=1 SV=1
MQPRTPLVLCVLLSQVLLTSAEDLDCTPGFQQKVFHINQPAEFIEDQSILNLTFSDCKG
NDKLRYEVSSPYFKVNSDGGVALRNITAVGKTLFVHARTPHAEDEMAELVIVGGKDIQGS
LQDIFKFARTSPVPRQRSTIVSPILIPENQRQPFPRDVGVKVVSDRPERSKFRLTGKV
DQEPKGIFRINENTGSVSVTRTLDREVIAVYQLFVETTDVNKGTLLEGPVPLEVIVIDQND
NRPIFREGPYIGHVMEGSPTGTTVMRMTAFDADDPATDNALLRYNIRQQTPDKPSPNMFY
IDPEKGDIVTVVSPALLDRETLENPKYELIIEAQDMAGLDVGLTGTATATIMIDDKNDHS
PKFTKKEFQATVEEGAVGVIVNLTVEDKDDPTTGAWRRAAYTIINGNPGQSFEIHTNPQTN
EGMLSVVKPLDYEISAFHTLLIKVENEDPLVPDVSYGPPSTATVHITVLDVNEGPFYPD
PMMVTRQEDLSVGSVLLTVNATDPDSLQHQQTIRYSVYKDPAGWLNNPINGTVDTTAVLD
RESPFVNDNSVYTALFLAIDSGNPPATGTGTLITLEDVNDNAPFIYPTVAEVCDAAKNLS
VVLGASDKDLHPNTDPFKFEIHKQAVPDKVWKISKINNTHALVSSLQNLNKANYNLPI
VTDSGKPPMTNITDLRVQVCSCRNSKVDNAAGALRFSLPSVLLSLFSLACL

```

**Fig2. FASTA sequence of CAD13\_HUMAN Cadherin**



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Institute of Biology and Protein Chemistry

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GOR IV SECONDARY STRUCTURE PREDICTION METHOD

[Abstract] [NPS@ help] [Original server]

Sequence name (optional):

Paste a protein sequence below :

Output width : 70

User : public@45.115.185.190. Last modification time : Thu Jan 14 21:53:29 2016. Current time : Thu Feb 17 18:45:20 2022

**Fig3. Search bar with FASTA sequence of cadherin**

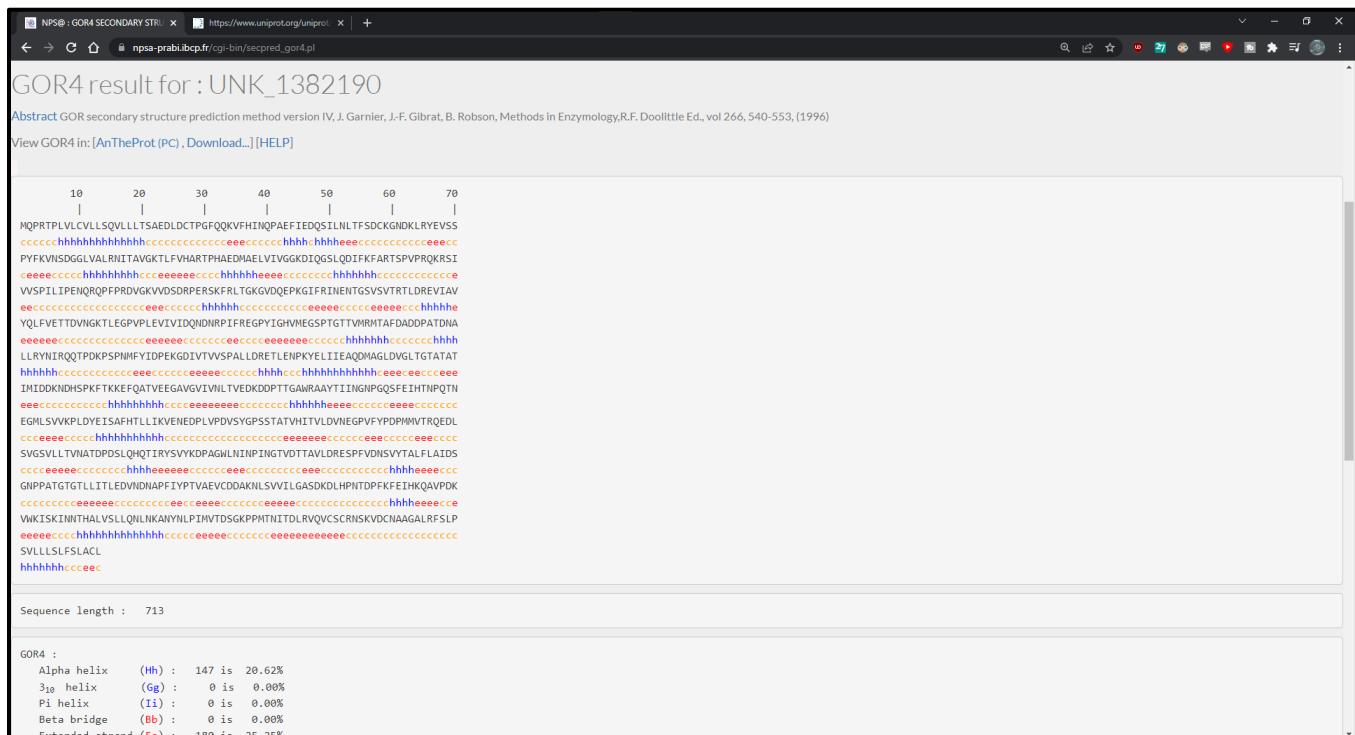


Fig4. Result page of GOR IV for Cadherin

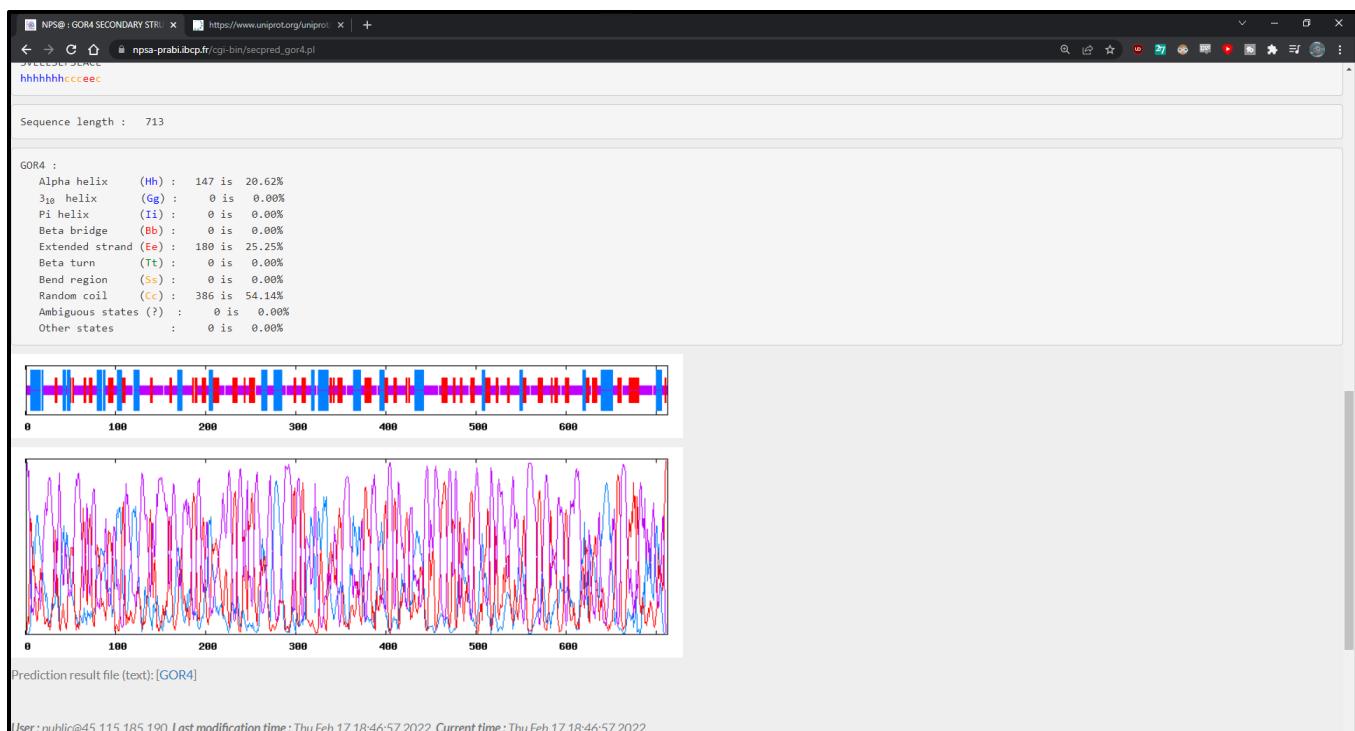


Fig5. Frequency graph for Cadherin

## → Third Generation: PSIPRED

The PSIPRED Workbench provides a range of protein structure prediction methods. The site can be used interactively via a web browser or programmatically via our REST API. For high-throughput analyses, downloads of all the algorithms are available.

Amino acid sequences enable: secondary structure prediction, including regions of disorder and transmembrane helix packing; contact analysis; fold recognition; structure modelling; and prediction of domains and function. In addition PDB Structure files allow prediction of protein-metal ion contacts, protein-protein hotspot residues, and membrane protein orientation.

**Data Input**

Select input data type

Sequence Data  PDB Structure Data

Choose prediction methods (hover for short description)

Popular Analyses

PSIPRED 4.0 (Predict Secondary Structure)  DISOPRED3 (Disopred Prediction)  
 MEMSAT-SVM (Membrane Helix Prediction)  pGenTHREADER (Profile Based Fold Recognition)

Contact Analysis

DeepMetaPSICOV 1.0 (Structural Contact Prediction)  MEMPACK (TM Topology and Helix Packing)

Fold Recognition

GenTHREADER (Rapid Fold Recognition)  nDomTHREADER (Protein Domain Fold Recognition)

Fig1. Homepage for PSIPRED

>sp|P55290|CAD13\_HUMAN Cadherin-13 OS=Homo sapiens OX=9606 GN=CDH13 PE=1 SV=1

MQPRTPLVLCVLLSQVLLTSAEDLDCTPGFQQKVFHINQPAEFIEDQSIILNLTFSDCKG

NDKLRYEVSSPYFKVNSDGGVALRNITAVGKTLFVHARTPHAEDEMAELVIVGGKDIQGS

LQDIFKFARTSPVPRQKRSIVVSPILIPENQRQPFPRDVGVKVVDSDRPERSKFRLTGKGV

DQEPKGIFRINENTGSVSVTRLDREVIAVYQLFVETTDVNGKTLEGPVPLEVIVIDQND

NRPIFREGPYIGHVMEGSPTGTTVMRMTAFDADDPATDNALLRYNIRQQTPDKPSPNMFY

IDPEKGDIVTVVSPALLDRETLENPKYELIIEAQDMAGLDVGLTGTATATIMIDDKNDHS

PKFTKKEFQATVEEGAVGVIVNLTVEDKDDPTTGAWRAYTIINGNPGQSFEIHTNPQTN

EGMLSVVKPLDYEISAFHTLLIKVENEDPLVPDVSYGPSSTATVHITVLDVNEGPVFPYD

PMVVTRQEDLSVGSVLLTVNATDPDSLQHQTIRYSVYKDPAGWLNNPINGTVDTTAVLD

RESPFVDNSVYTALFLAIDSGNPATGTGTLITLEDVNDNAPFIYPTVAEVCDAAKNLS

VVILGASDKDLHPNTDPFKFEIHKQAVPDKVWKISKINNTHALVSSLQNLNKANYNLPIV

VTDSGKPPMTNITDLRVQVCSRCNSKVDNAAGALRFSLPSVLLSLFSLACL

Fig2. FASTA sequence of CAD13\_HUMAN Cadherin

Fig3. Search bar of PSIPRED with FASTA sequence of Cadherin

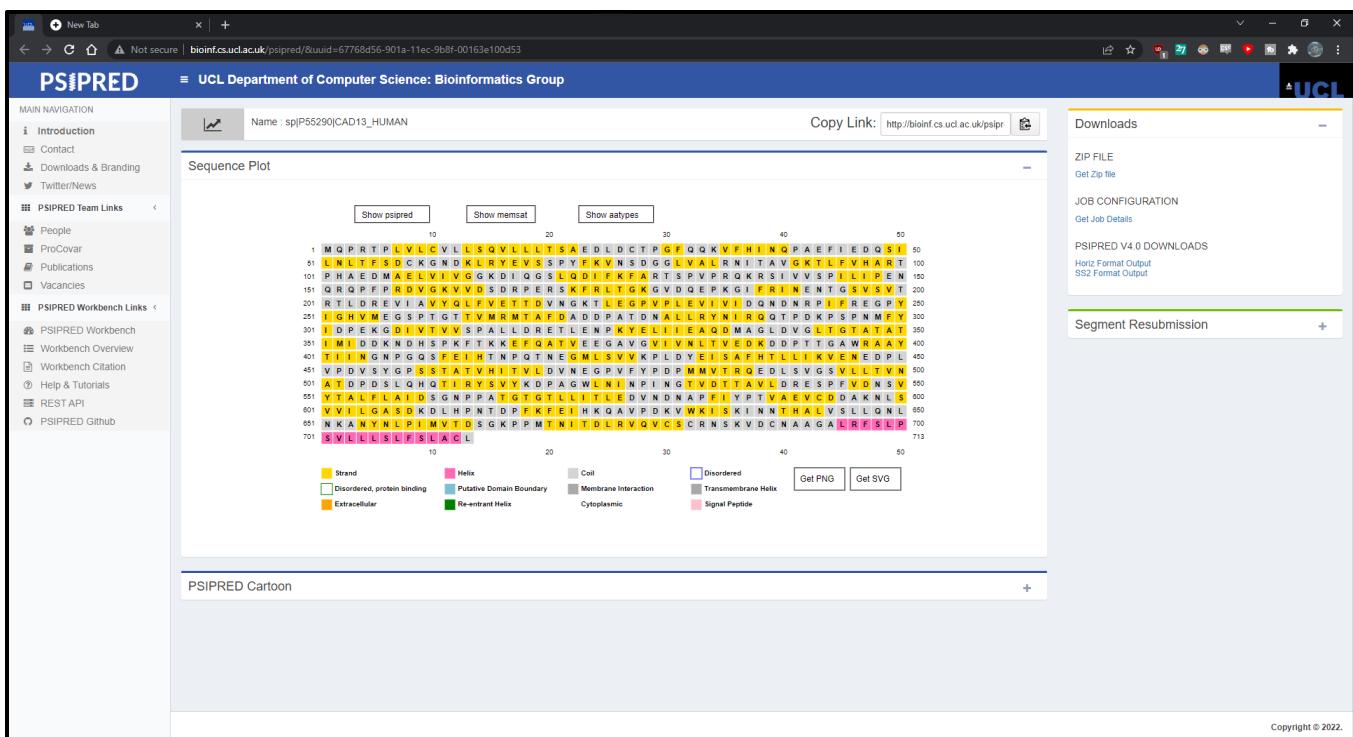
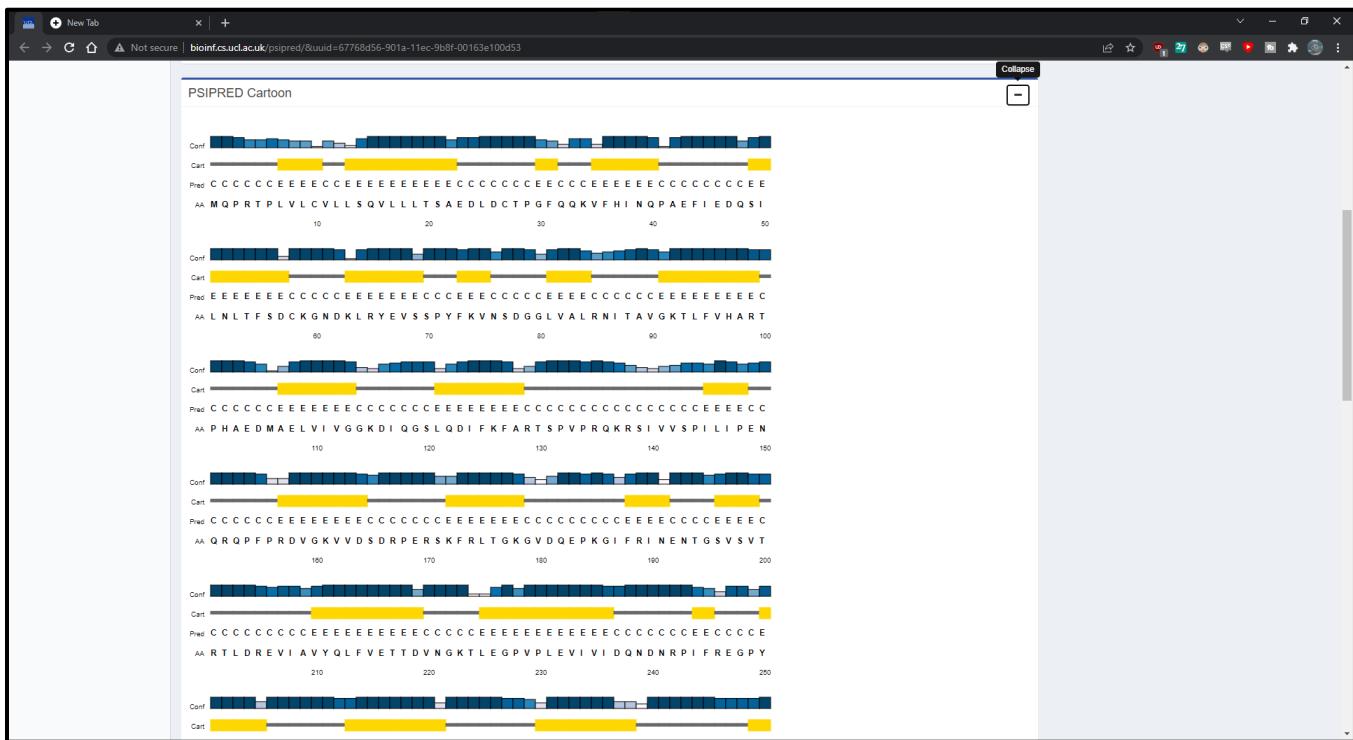


Fig4. Sequence plot of CAD13\_HUMAN Cadherin in PSIPRED



**Fig5. Legend of Cadherin in PSIPRED**

## Results:

### → First Generation: Chou and Fasman

- In secondary structure prediction using Chou and Fasman tools. The FASTA Sequence length of query Cadherin is 713 and their total residues are H: 455; E: 470; T:95; and the percentage is H: 63.8; E: 65.9; T:13.3;

### → Second Generation: GOR IV

- In secondary structure prediction using GOR IV tools. The FASTA Sequence length of query Cadherin is 713 and total residues are Alpha helix: 147 (20.62%); Extended Strand: 180 (25.25%); Random coil: 386 (54.14%).

### → Third Generation: PSIPRED

- In secondary structure prediction using PSIPRED tools. The FASTA sequence length of query Cadherin is 713. Here the maximum helix residues are predicted and we can find legend of confidence of prediction, 3-state assignment cartoon and target sequence.

## Conclusion:

- The secondary structure of the protein is Alpha helix and Beta sheet. Protein structure plays a key role in its function. Secondary structure prediction is important from the structural and functional point of view. Secondary structure is local interactions between stretches of a polypeptide chain and include alpha helix and beta pleated sheet structures.

**References:**

- ➔ Ranscht, B. (2010). Cadherin Regulation of Adhesive Interactions. *Handbook of Cell Signaling*, 1975–1988. <https://doi.org/10.1016/b978-0-12-374145-5.00242-4>
- ➔ CHOU-FASMAN. (2022, February 12). CHOU-FASMAN. Retrieved February 14, 2022, from <http://www.biogem.org/tool/chou-fasman/index.php>
- ➔ Ashok Kumar, T. (2013). CFSSP: Chou and Fasman Secondary Structure Prediction server. *WIDE SPECTRUM: Research Journal*. 1(9):15-19.
- ➔ GOR IV. (2022, February 12). GOR IV. Retrieved February 14, 2022, from [https://npsa-prabi.ibcp.fr/cgi-bin/npsa\\_automat.pl?page=/NPSA/npsa\\_gor4.html](https://npsa-prabi.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_gor4.html)
- ➔ PSIPRED. (2016, September 12). <Http://Bioinf.Cs.Ucl.Ac.Uk/Psipred>. Retrieved February 14, 2022, from <http://bioinf.cs.ucl.ac.uk/psipred>

## WEBLEM 2

### INTRODUCTION TO PROTEIN CLASSIFICATION

#### **Introduction:**

One of the applications of protein structure comparison is structural classification. The ability to compare protein structure allows classification of the structure data and identification of relationships among structures. The reason to develop a protein structure classification system is to establish hierarchical relationships among protein structures and to provide a comprehensive and evolutionary view of known structure. Once a hierarchical classification system is established, a newly obtained protein structure can find its place in a proper category. As a result, its functions can be better understood based on association with other proteins.

#### **CATH:**

CATH ([www.biochem.ucl.ac.uk/bsm/cath\\_new/index.html](http://www.biochem.ucl.ac.uk/bsm/cath_new/index.html)) classifies proteins based on the automatic structural alignment program SSAP as well as manual comparison. Structural domain separation is carried out also as a combined effort of a human expert and computer programs. Individual domain structures are classified at five major levels: class, architecture, fold/topology, homologous superfamily, and homologous family. In the CATH release version 2.5.1 (January 2004), there are 4 classes, 37 architectures, 813 topologies, 1,467 homologous superfamilies, and 4,036 homologous families. The definition for class in CATH is similar to that in SCOP, and is based on secondary structure content. Architecture is a unique level in CATH, intermediate between fold and class. This level describes the overall packing and arrangement of secondary structures independent of connectivity between the elements. The topology level is equivalent to the fold level in SCOP, which describes overall orientation of secondary structures and takes into account the sequence connectivity between the secondary structure elements. The homologous superfamily and homologous family levels are equivalent to the superfamily and family levels in SCOP with similar evolutionary definitions, respectively.

#### **SCOPe:**

Structural Classification of Proteins-extended (SCOPe, <http://scop.berkeley.edu>) is a database of protein structural relationships that extends the SCOP database. SCOP is a manually curated ordering of domains from the majority of proteins of known structure in a hierarchy according to structural and evolutionary relationships. Development of the SCOP 1.x series concluded with SCOP 1.75. The ASTRAL compendium provides several databases and tools to aid in the analysis of the protein structures classified in SCOP, particularly through the use of their sequences. SCOPe extends version 1.75 of the SCOP database, using automated curation methods to classify many structures released since SCOP 1.75. We have rigorously benchmarked our automated methods to ensure that they are as accurate as manual curation, though there are many proteins to which our methods cannot be applied. SCOPe is also partially manually curated to correct some errors in SCOP. SCOPe aims to be backward compatible with SCOP, providing the same parseable files and a history of changes between all stable SCOP and SCOPe releases. SCOPe also incorporates and updates the ASTRAL database. The latest release of SCOPe, 2.03, contains 59 514 Protein Data Bank (PDB) entries, increasing the number of structures classified in SCOP by 55% and including more than 65% of the protein structures in the PDB.

#### **References:**

1. Berman, H. M. (2000). The Protein Data Bank. *Nucleic Acids Research*, 28(1), 235–242. <https://doi.org/10.1093/nar/28.1.235>
2. Murzin, A. G. (1995). *Journal of Molecular Biology*, 247(4), 536–540. <https://doi.org/10.1006/jmbi.1995.0159>

## WEBLEM 2A

(URL:<https://www.cathdb.info/>)

### Aim:

To study the structural classification of proteins (Leucine) using CATH and SCOPe database.

### Introduction:

- **CATH:**

- CATH ([www.biochem.ucl.ac.uk/bsm/cath\\_new/index.html](http://www.biochem.ucl.ac.uk/bsm/cath_new/index.html)) classifies proteins based on the automatic structural alignment program SSAP as well as manual comparison. Structural domain separation is carried out also as a combined effort of a human expert and computer programs. Individual domain structures are classified at five major levels: class, architecture, fold/topology, homologous superfamily, and homologous family. In the CATH release version 2.5.1 (January 2004), there are 4 classes, 37 architectures, 813 topologies, 1,467 homologous superfamilies, and 4,036 homologous families. The definition for class in CATH is similar to that in SCOP, and is based on secondary structure content. Architecture is a unique level in CATH, intermediate between fold and class.

- **SCOPe:**

- Structural Classification of Proteins-extended (SCOPe, <http://scop.berkeley.edu>) is a database of protein structural relationships that extends the SCOP database. SCOP is a manually curated ordering of domains from the majority of proteins of known structure in a hierarchy according to structural and evolutionary relationships. Development of the SCOP 1.x series concluded with SCOP 1.75. The ASTRAL compendium provides several databases and tools to aid in the analysis of the protein structures classified in SCOP, particularly through the use of their sequences. SCOPe extends version 1.75 of the SCOP database, using automated curation methods to classify many structures released since SCOP 1.75.

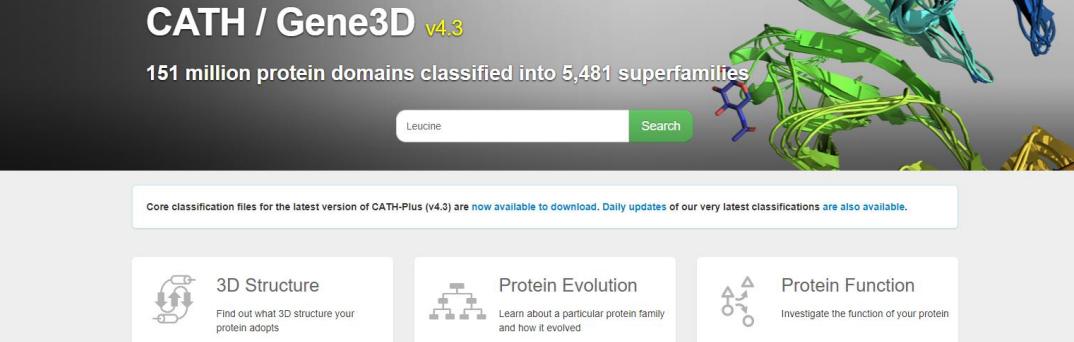
- **Leucine:**

- Leucine is one of nine essential amino acids in humans (provided by food). Leucine is important for protein synthesis and many metabolic functions. Leucine contributes to regulation of blood-sugar levels; growth and repair of muscle and bone tissue; growth hormone production; and wound healing. Leucine also prevents breakdown of muscle proteins after trauma or severe stress and may be beneficial for individuals with phenylketonuria. Leucine is available in many foods and deficiency is rare.

- **Methodology:**

- Open Homepage of CATH and SCOPe
- Enter the query Leucine in the search bar
- Open the result page of each category
- Interpret the results.

## Observation:



The image shows the homepage of the CATH / Gene3D v4.3 website. At the top, there is a navigation bar with the CATH logo, Home, Search, Browse, Download, About, and Support links. To the right of the navigation bar is a search bar with the placeholder "Search CATH by keywords or ID". Below the navigation bar, the main title "CATH / Gene3D v4.3" is displayed in large, bold, white text. Below the title, a subtitle "151 million protein domains classified into 5,481 superfamilies" is shown. A search bar with the text "Leucine" and a "Search" button is located below the subtitle. To the right of the search bar is a 3D ribbon model of a protein structure, colored in green, blue, and yellow. Below the main title and subtitle, a message states: "Core classification files for the latest version of CATH-Plus (v4.3) are now available to download. Daily updates of our very latest classifications are also available." Below this message, there are six cards arranged in a 2x3 grid, each with an icon and a title. The cards are: "3D Structure" (3D structure icon), "Protein Evolution" (tree icon), "Protein Function" (triangle icon), "Conserved Sites" (down arrow icon), "Download Data" (down arrow icon), and "Learn more" (question mark icon). Each card has a "Find out more" button and a "Go" button.

## Fig1. Homepage of CATH database with query Leucine

C A T H
[Home](#)
[Search](#)
[Browse](#)
[Download](#)
[About](#)
[Support](#)

Search CATH

Clear
Search

**Search CATH by text or ID**  
Type in general text or biological identifiers in the box and click "search" to perform a general text search on CATH data.

Examples: "protease", "1cux"

Search by Text or ID
Search by Sequence
Search by Structure

### Results

Currently displaying the top ranked hits from three separate search queries: CATH Superfamilies, CATH domains and PDB entries. Click "View all entries" to expand each section and show all the hits. Use the panel on the right to add additional filters to this query.

**21 Matching CATH Superfamilies**

**1.10.10.10**  
"winged helix" repressor DNA binding domain

putative development, Methionine aminopeptidase 2, 2,7-dihydroxy-5-methyl-1-naphthalene 7-O-methyltransferase, CST complex, Protein STN1, telomere capping, Neck appendage protein, Transcriptional regulator, GtrR family, HTH-type transcriptional regulator TsP, endo-alpha(2,6)-sialidase activity, Protein mbo, protein N-terminus binding, DNA-directed RNA polymerase III complex, DNA dealkylation involved in DNA repair, positive regulation of double-strand break repair, Possible MafB-transcriptional regulator, ATP-dependent DNA helicase activity, ATP-dependent helicase activity, Bloom syndrome protein, G-quadruplex DNA unwinding, Four-way junction DNA binding, methyl G2 DNA damage checkpoint, Complement protein subunit, peptid NCTC 11169 + ATCC 700919, Probable HTH type II

[View all entries](#)

**3344 Matching CATH Domains**

**3basA00**  
PDB code 3bas, chain A, domain 00  
Superfamily: 1.20.5.340

sequence-specific DNA binding, positive regulation of transcription initiation from RNA polymerase II promoter, General control protein GCNA, nucleus, identical protein binding, Argoprotein Iridians, Myosin heavy chain, striated muscle, transcription factor activity, RNA polymerase II transcription factor recruiting, negative regulation of transcription from RNA polymerase II promoter, transcription factor activity, sequence-specific DNA binding, protein self-association, transcriptional repressor activity, RNA polymerase II transcription factor binding, chromatin binding, nucleic acid binding, positive regulation of RNA polymerase II transcription, transcription factor

[View all entries](#)

### Current Search Filters

Remove search filters by clicking on the 'X'

Leucine X

### Filter by Keyword / CATH ID

Start typing and press 'enter' to add a new filter

### Top Keywords

Click a keyword to filter results

+ -L - a acid activity also amino and are binding but cell complex cytosol dimeric domain ec family formerly from homo human in ion is leucine leucine-rich monomeric hom-polymer not of on or polymer polypeptide() positive process protein regulation repeat residues response sapiens the to transferase water zinc

**Fig2. Result page for leucine in CATH database**

[C](#) [A](#) [T](#) [U](#) Home Search Browse Download About Support

Search CATH by keywords or ID

**Filter by Keyword / CATH ID**  
Start typing and press "enter" to add a new filter

**Top Keywords**  
Click a keyword to filter results

+ -l - = acid activity also amino an and are binding but cell complex cytosol dimeric domain ec family formerly from homo human in ion is leucine leucine-rich monomeric non- polymer not of or on polymer polypeptide(l) positive process protein regulation repeat residues response sapiens the to transferase water zinc

**3basA00**  
Matching CATH Domains

PDB code 3bas, chain A, domain 00  
Superfamily: 1.20.5.340

sequence-specific DNA binding, positive regulation of transcription initiation from RNA polymerase II promoter, General control protein GCN4 nucleus, identical protein binding, Aggregation inhibitor, Myosin heavy chain, striated muscle, transcription factor activity, RNA polymerase II transcription factor recruiting, negative regulation of transcription from RNA polymerase II promoter, transcription factor activity, sequence-specific DNA binding, protein self-association, transcriptional repressor activity, RNA polymerase II transcription factor binding, transcriptional repressor, positive binding, positive regulation of RNA polymerase II transcriptional process

**1a05**  
Matching PDB Structures

PDB code 1a05

3-ISOPROPYLALATE DEHYDROGENASE, polymer, MAGNESIUM ION, non-polymer, 3-ISOPROPYLALIC ACID, non-polymer, water, water, poly(peptide(L)), Acidithiobacillus, API-19-3, LEUB, Acidithiobacillus ferrooxidans, dimeric, OXIDOREDUCTASE, OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE BIOSYNTHESIS, 3-ISOPROPYLALATE DEHYDROGENASE, polymer, MAGNESIUM ION, non-polymer, 3-ISOPROPYLALIC ACID, non-polymer, water, water, poly(peptide(L)), Acidithiobacillus, API-19-3, LEUB, Acidithiobacillus ferrooxidans, dimer, OXIDOREDUCTASE, OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE BIOSYNTHESIS, 3-ISOPROPYLALATE DEHYDROGENASE, polymer, MAGNESIUM ION, non-polymer, 3-ISOPROPYLALIC ACID, non-polymer, water, water, poly(peptide(L)), Acidithiobacillus, API-19-3, LEUB, Acidithiobacillus ferrooxidans, dimer, OXIDOREDUCTASE, OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE BIOSYNTHESIS

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CATH-GENE3D is a Core Data Resource within ELIXIR and ELIXIR-UK Learn more

### Fig3. Available CATH Superfamilies for leucine

**CATH Superfamily 1.10.10.10**

Winged helix-like DNA-binding domain superfamily/Winged helix DNA-binding domain

[View in Gene3D](#)

---

[Home](#) / [Superfamily 1.10.10.10](#)

**SUPERFAMILY LINKS**

**Summary**

[Superfamily Superposition](#)

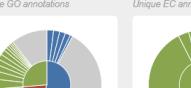
[Classification / Domains](#)

[Functional Families](#)

[Structural Neighbourhood](#)

**GO Diversity**

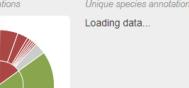
Unique GO annotations



3134 Unique GO terms

**EC Diversity**

Unique EC annotations



11 Unique EC terms

**Species Diversity**

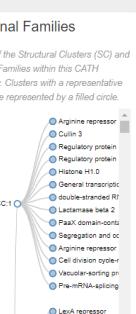
Unique species annotations

Loading data...

30308 Unique species

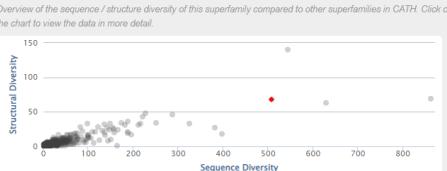
**Functional Families**

Overview of the Structural Clusters (SC) and Functional Families within this CATH Superfamily. Clusters with a representative structure are represented by a filled circle.



**Sequence/Structure Diversity**

Overview of the sequence / structure diversity of this superfamily compared to other superfamilies in CATH. Click on the chart to view the data in more detail.



Structural Diversity

Sequence Diversity

All Superfamilies 1.10.10.10

**Superfamily Summary**

A general summary of information for this superfamily.

**Structures**

Domains:	3444
Domain clusters (>95% seq id):	768
Domain clusters (>35% seq id):	524
Unique PDBs:	1604

**Alignments**

Structural Clusters (5A):	84
Structural Clusters (9A):	42
FunFam Clusters:	2121

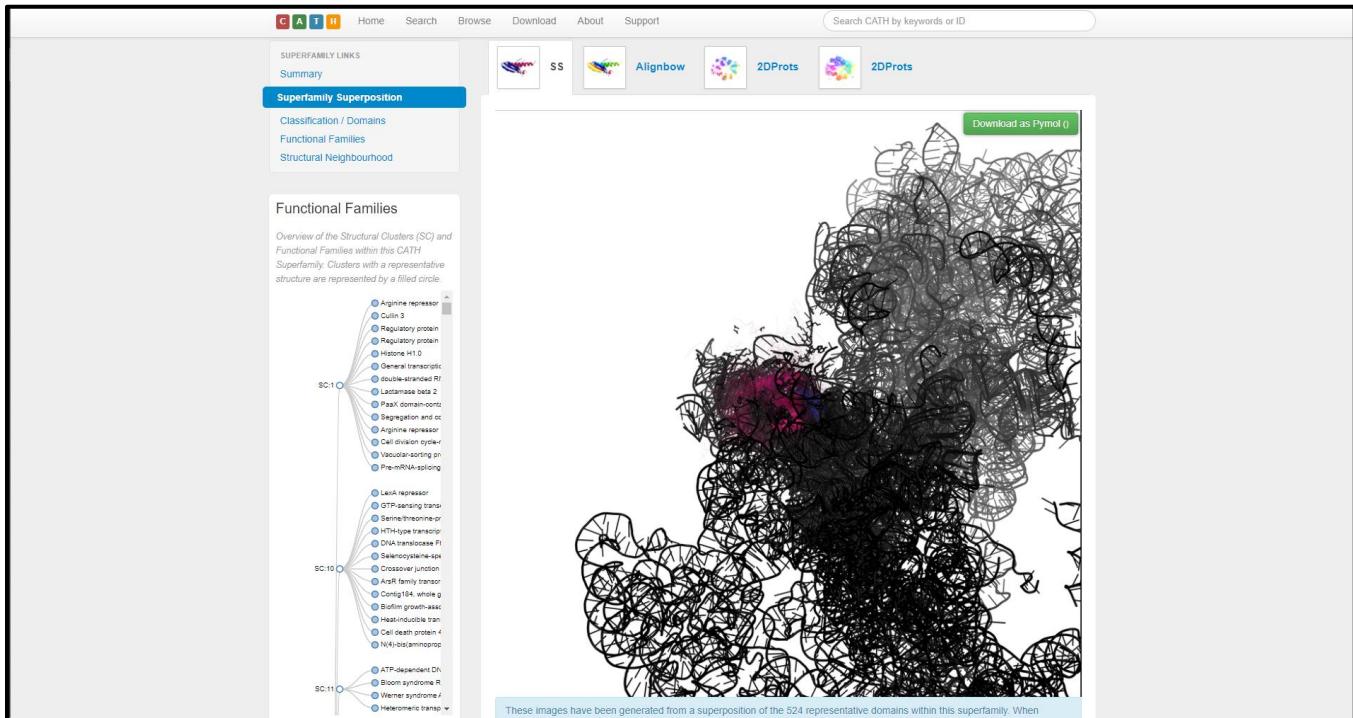
**Function**

Unique EC:	77
Unique GO:	3134

**Taxonomy**

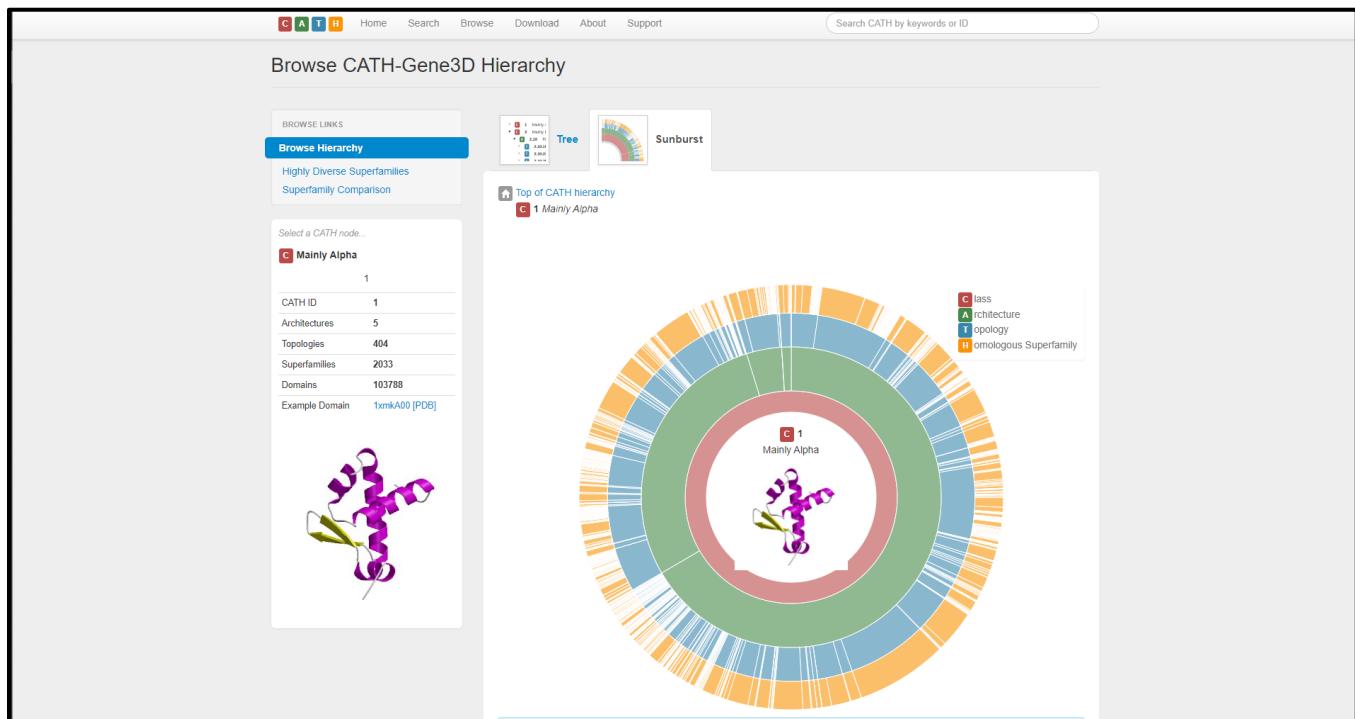
Unique Species:	30308
-----------------	-------

### Fig3.1. Summary of CATH superfamily for Leucine

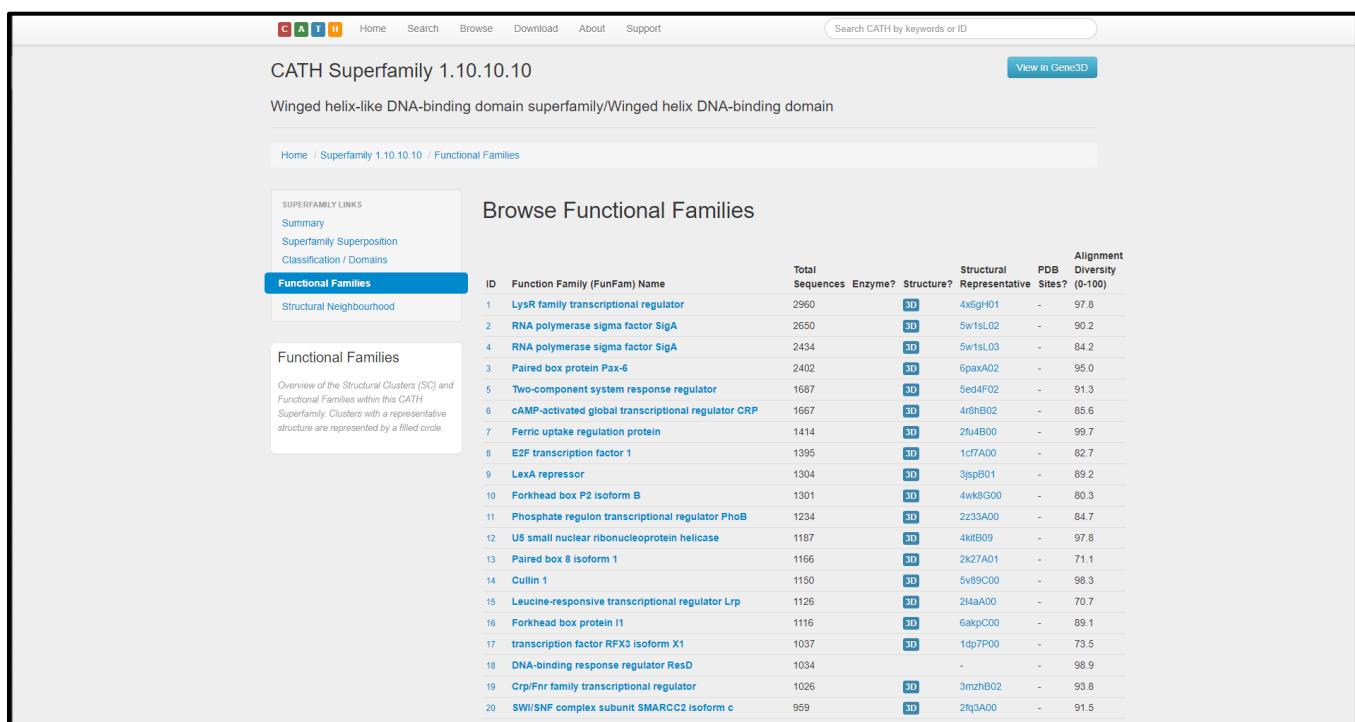


**Fig3.2. Superfamily superposition under CATH superfamily for leucine**

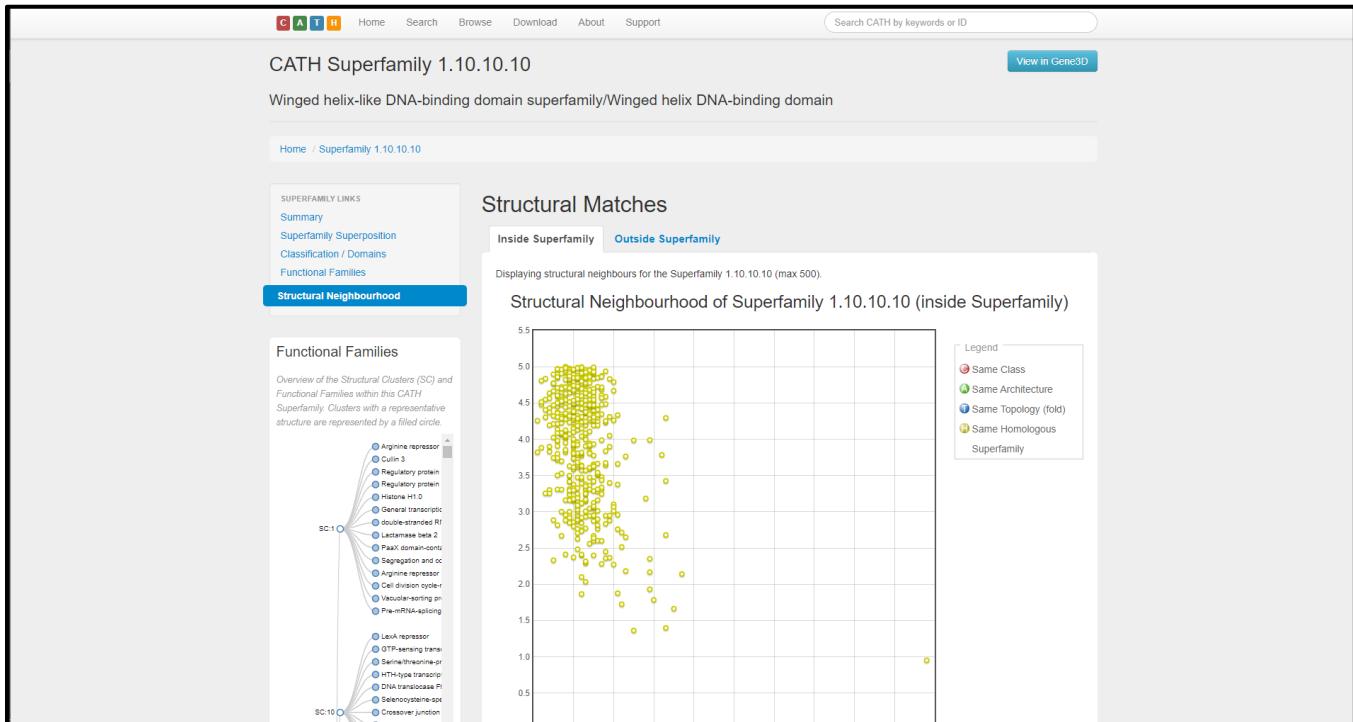
**Fig3.3. Classification / Domain of CATH superfamilies for Leucine**



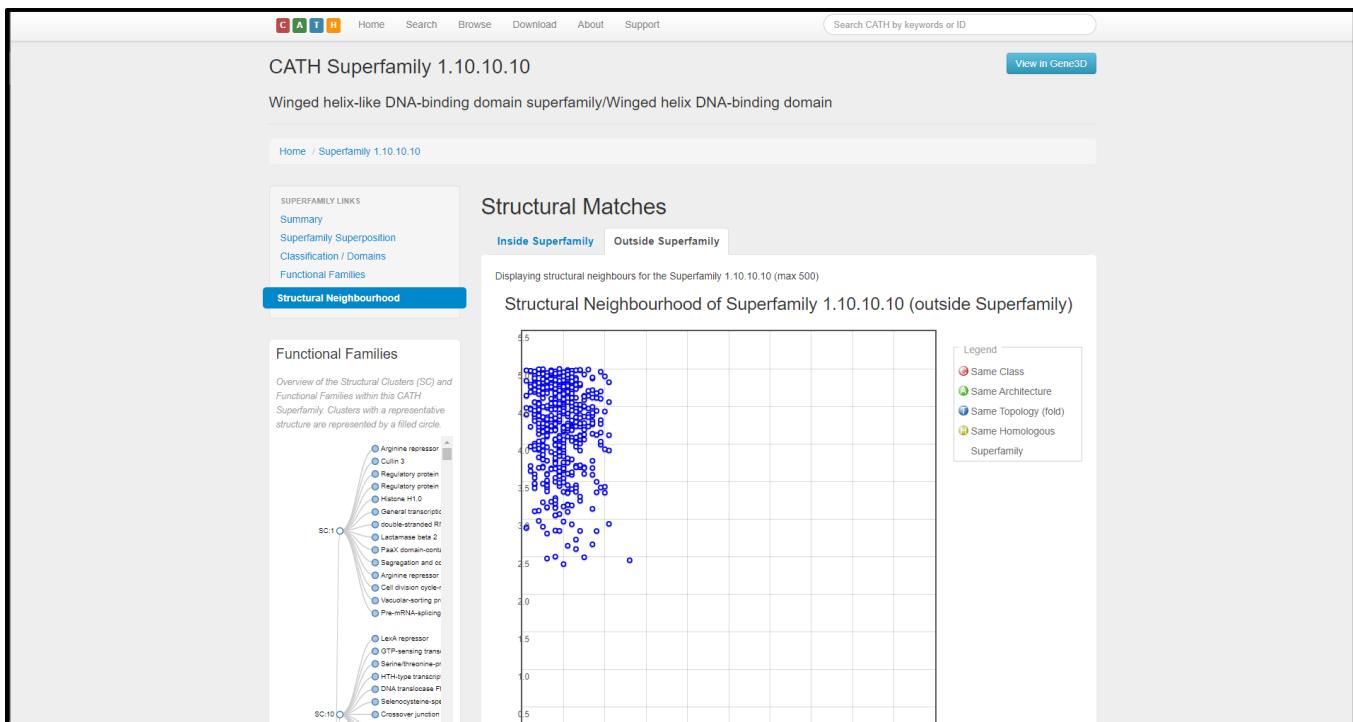
**Fig3.4. Sunburst diagram of Alpha domain of CATH superfamilies for leucine**



**Fig3.5. Functional Families of CATH superfamilies for leucine**



**Fig3.6. Structural neighborhood of CATH superfamilies for leucine (Inside Superfamily)**



**Fig3.7. Structural neighborhood of CATH superfamilies for leucine (Outside Superfamily)**

**CATH** Home Search Browse Download About Support Search CATH by keywords or ID

**71 Matching CATH Superfamilies**

**1.10.10.10**

**"winged helix" repressor DNA binding domain**

putamen development, Methionine aminopeptidase 2, 2,7-dihydroxy-5-methyl-1-naphthoate 7-O-methyltransferase, CST complex, Protein STN1, telomere capping, Neck spenner protein, Transcriptional regulator, GnrR family, HTH-type transcriptional regulator TsrR, endo-alpha-2,8-sialidase activity, Protein mtc, protein N terminus binding, DNA-directed RNA polymerase III complex, DNA deacetylation involved in DNA repair, positive regulation of double-strand break repair, Possible MsrB-transcriptional regulator, ATP-dependent DNA helicase activity, ATP-dependent helicase activity, Bloom syndrome protein, G-quadruplex DNA unwinding, four-way junction DNA binding, mifc02

DMC1, Dmc1, RecQL, Complement factor I, subunit, jejunum NC\_011168 + ATCC 270519, Probable HTLV-type

**View all entries**

**3344 Matching CATH Domains**

**3basA00**

PDB code 3bas, chain A, domain 00  
Superfamily: 1.20.5.340

**View all entries**

**383 Matching PDB Structures**

**1a05**

PDB code 1a05

3-ISOPROPYLALATE DEHYDROGENASE, polymer, MAGNESIUM ION, non-polymer, 3-ISOPROPYLALIC ACID, non-polymer, water, water, poly(peptide)(L), Acidithiobacillus, AP19-3, LEUB, Acidithiobacillus ferrooxidans, dimeric, OXIDOREDUCTASE, OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE BIOSYNTHESIS, 3-ISOPROPYLALATE DEHYDROGENASE, polymer, MAGNESIUM ION, non-polymer, 3-ISOPROPYLALIC ACID, non-polymer, water, water, poly(peptide)(L), Acidithiobacillus, AP19-3, LEUB, Acidithiobacillus ferrooxidans, dimeric, OXIDOREDUCTASE, OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE BIOSYNTHESIS, 3-ISOPROPYLALATE DEHYDROGENASE, polymer, MAGNESIUM ION, non-polymer, 3-I

**View all entries**

**Filter by Keyword / CATH ID**  
Start typing and press 'enter' to add a new filter

**Top Keywords**  
Click a keyword to filter results

+ -I = a acid activity also amino an and are binding but cell complex cytosol dimeric domain ec family formerly from homo human in ioh is leucine leucine-rich monomer non-polymer not of on or polymer polypeptide(l) positive process protein regulation repeat residues response sapiens the t0 transferase water zinc

#### Fig4. Matching CATH domains for Leucine

CATH Home Search Browse Download About Support Search CATH by keywords or ID 1 keywords

## CATH Domain 3basA00

Home / Superfamily 1.20.5.340 / Domain 3basA00

DOMAIN LINKS

**Summary**

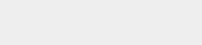
Structure  
Sequence  
Neighbourhood

CATH Classification

Level	CATH Code	Description
1	Mainly Alpha	
1.20	Up-down Bundle	
1.20.5	Single alpha-helices involved in coiled-coils or other helix-helix interfaces	
1.20.5.340		

Domain Context

View Domain in Chain



3bas (A)

PDB 3BAS

External Links • PDBsum • Proteopedia

Method X-RAY DIFFRACTION

Organism Escherichia

Primary An unstable head-rod junction may promote folding into the compact off-state conformation of regulated myosins.

Citation Brown, J.H., Yang, Y., Reshetnikova, L., Gourinath, S., Suveges, D., Kardos, J., Hobor, F., Reutzel, R., Nyitrai, L., Cohen, C. *J. Mol. Biol.*

**Fig4.1. Summary of matching CATH domains for Leucine**

CATH Domain 3basA00

Home / Superfamily 1.20.5.340 / Domain 3basA00

DOMAIN LINKS

Summary

**Structure**

Sequence

Neighbourhood

View Domain in Chain

3bas (A)

Domain	Start	Stop	Length
3basA00	840	919	79

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**Fig4.2. Structure of matching CATH domains for Leucine**

CATH Domain 3basA00

Home / Superfamily 1.20.5.340 / Domain 3basA00

ATOM Sequence

The ATOM sequence is based on the residues observed in the ATOM records of the PDB file for this structure.

```
>cath:4_3_0|3basA00/10-89 PDB=840-919
ARQEENHEEQLKQCNQKEDLANTERIPELEKEQNVILLEQKNDLFGSMQEDPVVEELL
```

COMBS Sequence

The COMBS sequence is based on the residues observed in the SEQRES records of the PDB file for this structure. This can sometimes contain extra residues that were not able to be resolved in the 3D co-ordinates.

```
>cath:4_3_0|3basA00/10-89 PDB=840-919
GSRNIDLLSIANQEENHEEQLKQCNQKEDLANTERIPELEKEQNVILLEQKNDLFGSMQEDPVVEELL
```

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**Fig4.3. ATOM and COMBS sequence of matching CATH domains for Leucine**

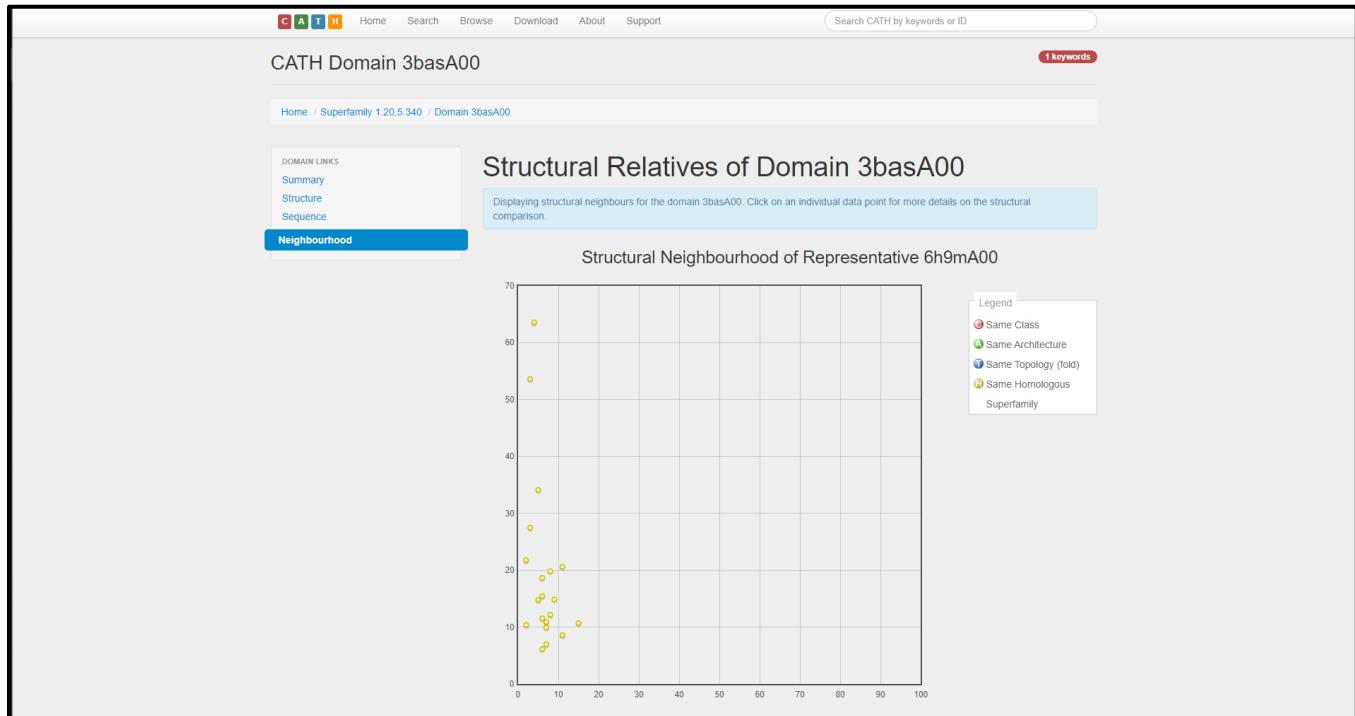


Fig4.4. Structural relatives of matching CATH domains for leucine

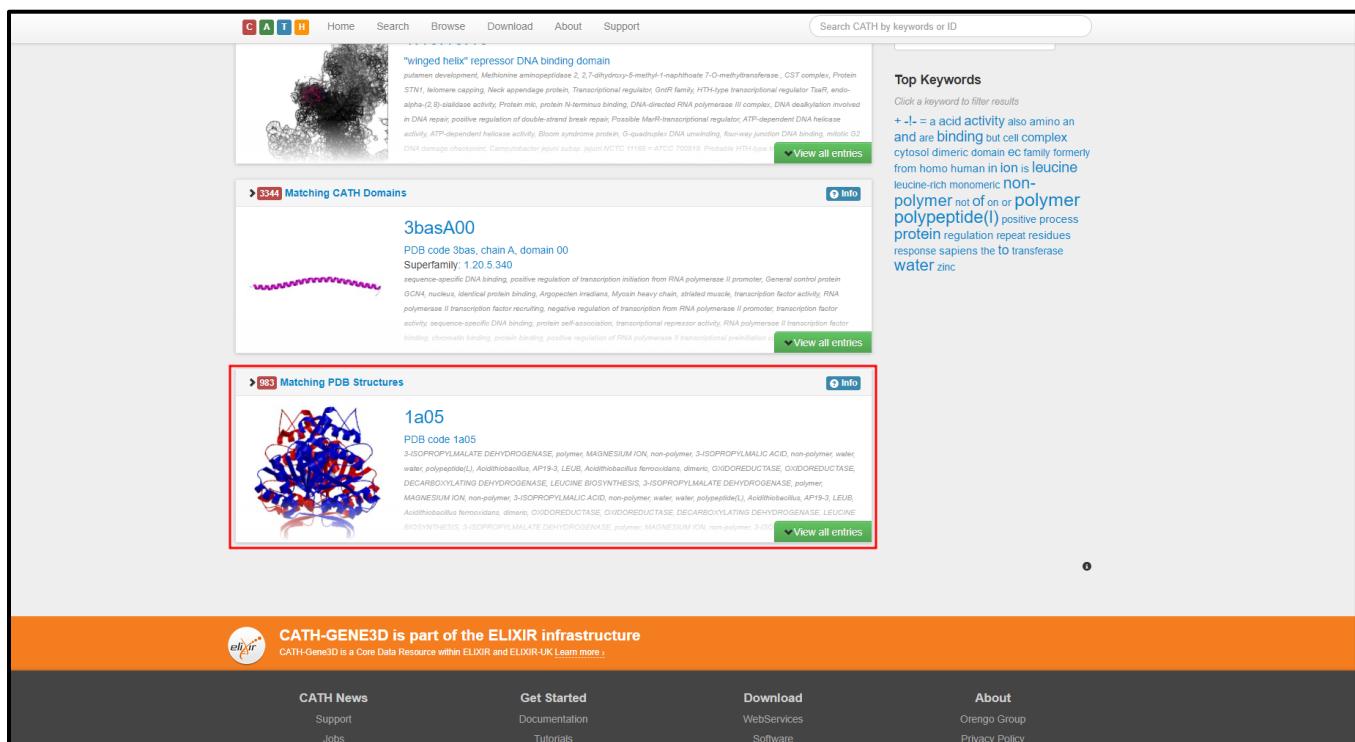


Fig5. Matching PDB structure for leucine

PDB 1a05

PDB LINKS Overview PDB Information

**PDB 1a05**  
Method X-RAY DIFFRACTION  
Host Organism Escherichia coli  
Gene Source Acidithiobacillus ferrooxidans  
Primary Citation Structure of 3-isopropylmalate dehydrogenase in complex with 3-isopropylmalate at 2.0 Å resolution: the role of Glu88 in the unique substrate-recognition mechanism.  
Imada, K., Inagaki, K., Matsunami, H., Kawaguchi, H., Tanaka, H., Tanaka, N., Namba, K.  
Structure  
Header Oxidoreductase  
Released 1997-12-09  
Resolution 2.000  
CATH Insert Date 05 Mar, 2006

PDB Prints

PDB Chains (2)

Chain ID	Date inserted into CATH	CATH Status
A	05 Mar, 2006	Chopped ⓘ
B	05 Mar, 2006	Chopped ⓘ

CATH Domains (2)

Domain ID	Date inserted into CATH	Superfamily	CATH Status
1a05A00	05 Mar, 2006	3.40.718.10	Assigned ⓘ
1a05B00	05 Mar, 2006	3.40.718.10	Assigned ⓘ

PDB Images (5)

PDB 1a05 PDB 1a05

Fig5.1. Overview of matching PDB structures for leucine

Tanaka, N., Namba, K.  
Structure  
Header Oxidoreductase  
Released 1997-12-09  
Resolution 2.000  
CATH Insert Date 05 Mar, 2006

PDB Prints

PDB Chains (2)

Chain ID	Date inserted into CATH	CATH Status
A	05 Mar, 2006	Chopped ⓘ
B	05 Mar, 2006	Chopped ⓘ

CATH Domains (2)

Domain ID	Date inserted into CATH	Superfamily	CATH Status
1a05A00	05 Mar, 2006	3.40.718.10	Assigned ⓘ
1a05B00	05 Mar, 2006	3.40.718.10	Assigned ⓘ

UniProtKB Entries (2)

Accession	Gene ID	Taxon	Description
Q56268	LEU3_ACIFR	Acidithiobacillus ferrooxidans	3-isopropylmalate dehydrogenase
Q56268	LEU3_ACIFR	Acidithiobacillus ferrooxidans	3-isopropylmalate dehydrogenase

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Fig5.2. Prints, Chains, CATH domains and UniProtKB entries for matching PDB structure for leucine

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Welcome to **SCOPe**!

**SCOPe** (Structural Classification of Proteins – extended) is a database developed at the Berkeley Lab and UC Berkeley to extend the development and maintenance of SCOP. SCOP was conceived at the MRC Laboratory of Molecular Biology, and developed in collaboration with researchers in Berkeley. Work on SCOP (version 1) concluded in June 2009 with the release of SCOP 1.75. **SCOPe** classifies many newer structures through a combination of automation and manual curation, and corrects some errors in SCOP, aiming to have the same accuracy as the hand-curated SCOP releases. **SCOPe** also incorporates and updates the **ASTRAL** database.

[About SCOPe](#) [Stats & Prior Releases](#)

**News**

2022-01-07: We published a paper describing the new features in **SCOPe 2.08-stable**. [\[PDF\]](#).

2021-09-20: **SCOPe 2.08-stable** has been released, with nearly 20,000 new **PDB** entries added since the last stable release. Important features include **genetic variant** search tools and annotations of structural heterogeneity and repeat units. Click either the [About](#) or [Stats & History](#) links for more details on what's new!

2018-11-30: We published a paper describing **updates to SCOPe**, focusing on our findings from classifying large structures. [\[PDF\]](#).

**Classes in SCOPe 2.08:**

1. a: All alpha proteins [46456] (290 folds)
2. b: All beta proteins [48724] (180 folds)
3. c: Alpha and beta proteins (a/b) [51349] (148 folds)
4. d: Alpha and beta proteins (a+b) [53931] (396 folds)
5. e: Multi-domain proteins (alpha and beta) [56572] (74 folds)
6. f: Membrane and cell surface proteins and peptides [56835] (69 folds)
7. g: Small proteins [56992] (100 folds)
8. h: Coiled coil proteins [57942] (7 folds)

Fig6. Homepage of SCOPe Database with query leucine

**SCOPe** [Browse](#) [Stats & History](#) [Downloads](#) [Help](#)

**Folds found:**

- c.10: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) [52046] (3 superfamilies)  
2 curved layers, a/b; parallel beta-sheet; order 1234...N; there are sequence similarities between different superfamilies
- k.11: Retro-GCN4 leucine zipper [58851] (1 superfamily)

**Superfamilies found:**

- h.1.3: Leucine zipper domain [57959] (2 families)
- k.11.1: Retro-GCN4 leucine zipper [58852] (1 family)

**Families found:**

- a.118.1.5: Leucine-rich repeat variant [48396] (1 protein)  
this is a repeat family; one repeat unit is 1rv A:123-147 found in domain
- c.10.2.6: Leucine rich effector protein YopM [69433] (1 protein)  
this is a repeat family; one repeat unit is 1gu A:139-161 found in domain
- c.50.1.1: Leucine aminopeptidase (Aminopeptidase A), N-terminal domain [52950] (1 protein)
- c.56.5.3: Leucine aminopeptidase, C-terminal domain [53201] (2 proteins)  
automatically mapped to Pfam PF00883
- c.66.1.37: Leucine carboxy methyltransferase Ppm1 [102569] (1 protein)
- c.66.1.57: ML2640-like [159694] (2 proteins)
- Pfam PF02409; O-methyltransferase N-terminus (DUF142); most similar structure to the Leucine carboxy methyltransferase Ppm1 family
- h.1.3.1: Leucine zipper domain [57960] (17 proteins)
- k.11.1.1: Retro-GCN4 leucine zipper [58853] (1 protein)

**Proteins found:**

- Leucine-rich repeat variant [48397] from a.118.1.5: Leucine-rich repeat variant (1 species)  
contains a FeS4 centre
- Max protein [47461] from a.38.1.1: HLH, helix-loop-helix DNA-binding domain (2 species)  
BHLHZ region; contains leucine-zipper motif
- Homeobox-leucine zipper protein Homez [116778] from a.4.1.1: Homeodomain (1 species)
- Leucine rich effector protein YopM [69434] from c.10.2.6: Leucine rich effector protein YopM (1 species)
- Leucine dehydrogenase [51890] from c.2.1.7: Aminoacid dehydrogenase-like, C-terminal domain (1 species)
- Leucine aminopeptidase (Aminopeptidase A), N-terminal domain [52951] from c.50.1.1: Leucine aminopeptidase (Aminopeptidase A), N-terminal domain (2 species)
- Leucine aminopeptidase, C-terminal domain [53202] from c.56.5.3: Leucine aminopeptidase, C-terminal domain (2 species)
- Leucine dehydrogenase [53231] from c.58.1.1: Aminoacid dehydrogenases (1 species)
- Leucine carboxy methyltransferase Ppm1 [102570] from c.66.1.37: Leucine carboxy methyltransferase Ppm1 (1 species)  
involved in the regulation of protein phosphatase 2a activity
- Leucine-isoleucine-valine-binding (LIV) protein [53841] from c.93.1.1: L-arabinose binding protein-like (1 species)
- Leucine-binding protein [53843] from c.93.1.1: L-arabinose binding protein-like (1 species)
- Retro-GCN4 leucine zipper [58854] from k.11.1.1: Retro-GCN4 leucine zipper (1 species)
- Designed heterodimeric leucine zipper [58825] from k.6.1.1: Designed heterodimeric coiled-coil (1 species)

Fig7. Result page of SCOPe for query leucine

**SCOPe** [Browse](#) [Stats & History](#) [Downloads](#) [Help](#)  

Lineage for **Fold c.10: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)**

1. Root: SCOPe 2.08
2.  Class c: Alpha and beta proteins (a/b) [51349] (148 folds)
3.  Fold c.10: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) [52046] (3 superfamilies)
  - 2 curved layers, a/b; parallel beta-sheet; order 1234..N; there are sequence similarities between different superfamilies

Superfamilies:

1.  c.10.1: RNI-like [52047] (4 families) 
  - regular structure consisting of similar repeats
2.  c.10.2: L domain-like [52058] (9 families) 
  - less regular structure consisting of variable repeats
3.  c.10.3: Outer arm dynein light chain 1 [52075] (1 family) 
  - (beta-beta-alpha)n superhelix

More info for **Fold c.10: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)**

Timeline for **Fold c.10: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)**:

- Fold c.10: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) first appeared (with stable ids) in SCOP 1.55
- Fold c.10: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix) appears in SCOPe 2.07

SCOPe: Structural Classification of Proteins — extended. Release 2.08 (September 2021)  
 References: Fox NK, Brenner SE, Chandonia JM. 2014. *Nucleic Acids Research* 42:D304-309. doi: 10.1093/nar/gkt1240.  
 Chandonia JM, Guan L, Lin S, Yu C, Fox NK, Brenner SE. 2022. *Nucleic Acids Research* 50:D553–559. doi: 10.1093/nar/gkab1054. (citing information)  
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 scope@compbio.berkeley.edu

**Fig8. Random result from “Folds found” of SCOPe database for leucine**

**SCOPe** [Browse](#) [Stats & History](#) [Downloads](#) [Help](#)  

Lineage for **Superfamily h.1.3: Leucine zipper domain**

1. Root: SCOPe 2.08
2.  Class h: Coiled coil proteins [57942] (7 folds)
3.  Fold h.1: Parallel coiled-coil [57943] (41 superfamilies)
  - this is not a true fold; includes oligomers of shorter identical helices
4.  Superfamily h.1.3: Leucine zipper domain [57959] (2 families) 

Families:

1.  h.1.3.1: Leucine zipper domain [57960] (17 proteins)
2.  h.1.3.0: automated matches [338702] (1 protein)
  - not a true family

More info for **Superfamily h.1.3: Leucine zipper domain**

Timeline for **Superfamily h.1.3: Leucine zipper domain**:

- Superfamily h.1.3: Leucine zipper domain first appeared (with stable ids) in SCOP 1.55
- Superfamily h.1.3: Leucine zipper domain appears in SCOPe 2.07

SCOPe: Structural Classification of Proteins — extended. Release 2.08 (September 2021)  
 References: Fox NK, Brenner SE, Chandonia JM. 2014. *Nucleic Acids Research* 42:D304-309. doi: 10.1093/nar/gkt1240.  
 Chandonia JM, Guan L, Lin S, Yu C, Fox NK, Brenner SE. 2022. *Nucleic Acids Research* 50:D553–559. doi: 10.1093/nar/gkab1054. (citing information)  
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**Fig8. Random result from “Superfamilies” of SCOPe database for leucine**

**SCOPe** [Browse](#) [Stats & History](#) [Downloads](#) [Help](#)

Lineage for **Family a.118.1.5: Leucine-rich repeat variant**

1. Root: SCOPe 2.08
2. Class a: All alpha proteins [46456] (290 folds)
3. Fold a.118: alpha-alpha superhelix [48370] (28 superfamilies)  
multihelical; 2 (curved) layers: alpha/alpha; right-handed superhelix
4. Superfamily a.118.1: ARM repeat [48371] (28 families)
5. Family a.118.1.5: Leucine-rich repeat variant [48396] (1 protein)  
*this is a repeat family; one repeat unit is 1lrv A:123-147 found in domain*

**Protein:**

Leucine-rich repeat variant [48397] (1 species)  
 contains a FeS4 centre  
 Species *Azotobacter vinelandii* [TaxId:354] [48398] (1 PDB entry)

More info for **Family a.118.1.5: Leucine-rich repeat variant**

Timeline for Family a.118.1.5: Leucine-rich repeat variant:

- Family a.118.1.5: Leucine-rich repeat variant first appeared (with stable ids) in SCOP 1.55
- Family a.118.1.5: Leucine-rich repeat variant appears in SCOPe 2.07

SCOPe: Structural Classification of Proteins — extended. Release 2.08 (September 2021)  
 References: Fox NK, Brenner SE, Chandonia JM. 2014. *Nucleic Acids Research* 42:D304-309. doi: 10.1093/nar/gkt1240.  
 Chandonia JM, Guan L, Lin S, Yu C, Fox NK, Brenner SE. 2022. *Nucleic Acids Research* 50:D553–559. doi: 10.1093/nar/gkab1054. (citing information)  
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**Fig9. Random result from “Families” of SCOPe database for leucine**

**SCOPe** [Browse](#) [Stats & History](#) [Downloads](#) [Help](#)

Lineage for **Protein: Leucine-rich repeat variant**

1. Root: SCOPe 2.08
2. Class a: All alpha proteins [46456] (290 folds)
3. Fold a.118: alpha-alpha superhelix [48370] (28 superfamilies)  
multihelical; 2 (curved) layers: alpha/alpha; right-handed superhelix
4. Superfamily a.118.1: ARM repeat [48371] (28 families)
5. Family a.118.1.5: Leucine-rich repeat variant [48396] (1 protein)  
*this is a repeat family; one repeat unit is 1lrv A:123-147 found in domain*
6. Protein Leucine-rich repeat variant [48397] (1 species)  
 contains a FeS4 centre

**Species:**

*Azotobacter vinelandii* [TaxId:354] [48398] (1 PDB entry)  
 Domain for 1lrv:  
 Domain d1lrv\_a: 1lrv A: [19146]

More info for **Protein Leucine-rich repeat variant from a.118.1.5: Leucine-rich repeat variant**

Timeline for **Protein Leucine-rich repeat variant from a.118.1.5: Leucine-rich repeat variant**:

- Protein Leucine-rich repeat variant from a.118.1.5: Leucine-rich repeat variant first appeared (with stable ids) in SCOP 1.55
- Protein Leucine-rich repeat variant from a.118.1.5: Leucine-rich repeat variant appears in SCOPe 2.07

SCOPe: Structural Classification of Proteins — extended. Release 2.08 (September 2021)  
 References: Fox NK, Brenner SE, Chandonia JM. 2014. *Nucleic Acids Research* 42:D304-309. doi: 10.1093/nar/gkt1240.  
 Chandonia JM, Guan L, Lin S, Yu C, Fox NK, Brenner SE. 2022. *Nucleic Acids Research* 50:D553–559. doi: 10.1093/nar/gkab1054. (citing information)  
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**Fig10. Random result from “Proteins found” of SCOPe database for leucine**

SCOPe [Browse](#) [Stats & History](#) [Downloads](#) [Help](#) [Search \(click for examples\)](#) [\[Feedback\]](#)

## Lineage for Species: Human (*Homo sapiens*) [TaxId: 9606]

1. Root: SCOPe 2.08

2. Class a: All alpha proteins [46456] (290 folds)

3. Fold a.38: HLH-like [47458] (2 superfamilies)

4. Superfamily a.38.1: HLH, helix-loop-helix DNA-binding domain [47459] (2 families)

5. Family a.38.1.1: HLH, helix-loop-helix DNA-binding domain [47460] (9 proteins)

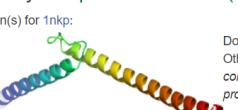
6. Protein Myc proto-oncogene protein [81750] (1 species)

7. Species Human (*Homo sapiens*) [TaxId:9606] [81751] (1 PDB entry)

**BHLHZ region; contains leucine-zipper motif**

## PDB entry in Species: Human (*Homo sapiens*) [TaxId: 9606]:

Domain(s) for 1nkp:

1.  Domain d1nkp1: 1nkp A:900-984 [80573]  
Other proteins in same PDB: d1nkp2, d1nkp2\_, d1nkp2, d1nkp\_e\_...  
complexed with *Max*  
protein/DNA complex

2.  Domain d1nkp2: 1nkp D:500-581 [80575]  
Other proteins in same PDB: d1nkp2, d1nkp2\_, d1nkp2, d1nkp\_e\_...  
complexed with *Max*  
protein/DNA complex

## More info for Species Human (*Homo sapiens*) [TaxId:9606] from a.38.1.1 Myc proto-oncogene protein

Timeline for Species Human (*Homo sapiens*) [TaxId:9606] from a.38.1.1 Myc proto-oncogene protein:

- Species Human (*Homo sapiens*) [TaxId:9606] from a.38.1.1 Myc proto-oncogene protein first appeared in SCOP 1.63, called Species Human (*Homo sapiens*) [TaxId:9606] from a.38.1.1 Myc proto-oncogene protein
- Species Human (*Homo sapiens*) [TaxId:9606] from a.38.1.1 Myc proto-oncogene protein appears in SCOPe 2.07

**Fig11. Random result from “Species found” of SCOPe database for leucine**

Lineage for d1gk6a\_ (1gk6 A:)

1. Root: SCOPe 2.08
2. Class h: Coiled coil proteins [57942] (7 folds)
3. Fold h.1: Parallel coiled-coil [57943] (41 superfamilies)
  - this is not a true fold; includes oligomers of shorter identical helices*
4. Superfamily h.1.20: Intermediate filament protein, coiled coil region [64593] (2 families)
5. Family h.1.20.1: Intermediate filament protein, coiled coil region [64594] (3 proteins)
  - C-terminal part of Pfam PF00038*
6. Protein Vimentin coil [64595] (1 species)
7. Species Human (Homo sapiens) [TaxId:9606] [64596] (3 PDB entries)
- 8.

Search (click for examples)

Domain d1gk6a\_: 1gk6 A: [70210]  
coil 2B fragment linked to GCN4 leucine zipper



**Details for d1gk6a\_**

**PDB Entry:** 1gk6 (more details), 1.9 Å

**PDB Description:** human vimentin coil 2b fragment linked to gcn4 leucine zipper (z2b)

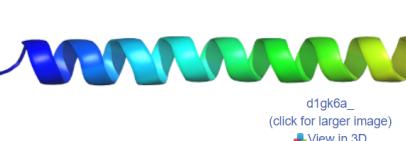
**PDB Compounds:** (A:) vimentin

**SCOPe Domain Sequences for d1gk6a\_:**  
 Sequence; same for both **SEQRES** and **ATOM** records: (download)  
 >d1gk6a\_h.1.20.1 (A:) Vimentin coil (Human (Homo sapiens) [TaxId: 9606])  
 mkgledkvee11sknyhlnenavarKK1vgd1lnvkmaldieatyrrkleeges

**SCOPe Domain Coordinates for d1gk6a\_:**  
 Click to download the PDB-style file with coordinates for d1gk6a\_...  
 (The format of our PDB-style files is described [here](#).)

**Timeline for d1gk6a\_:**

- d1gk6a\_ first appeared in SCOPe 1.61
- 14-Nov-2002, 2002-0-07

**d1gk6a\_ in context of PDB**  
  
[View in 3D](#)  
 Domains from other chains: (mouse over for more information)

**Fig11. Random result from “Domains found” of SCOPe database for leucine**

## Results:

### CATH:

- ➔ In protein classification using CATH database for query leucine. It shows,
  - ➔ 71 matching CATH superfamilies.
  - ➔ 3344 matching CATH Domains
  - ➔ 983 matching PDB structures
- ➔ For CATH superfamilies we saw the Winged helix-like DNA-binding domain superfamily.
- ➔ For CATH Domains we saw CATH Domain 3basA00
- ➔ For PDB structures we saw PDB 1A05 from Escherichia Coli

### SCOPe:

- ➔ In SCOPe database the result was divided into 6 sections:
  - ➔ Folds found [Fold c.10: Leucine-rich repeat, LRR (right-handed beta-alpha superhelix)]
  - ➔ Superfamilies found [Superfamily h.1.3: Leucine zipper domain]
  - ➔ Family found [Family a.118.1.5: Leucine-rich repeat variant]
  - ➔ Protein Found [Protein: Leucine-rich repeat variant]
  - ➔ Species found [Species: Human (Homo sapiens) [TaxId: 9606]]
  - ➔ Domains found [d1gk6a\_ (1gk6 A:)]

## Conclusions:

- ➔ The CATH database is valuable for biologists and bioinformaticians alike.
- ➔ For biologists with very specific tasks, browsing for individual domains is made easy by the user-friendly web interface.
- ➔ For bioinformaticians with a focus on large-scale analyses can find complete datasets available for downloading.
- ➔ Thus, working with CATH is remarkably uncomplicated.
- ➔ Updates are frequent, and, given the significant upcoming extension with horizontal layers complementary to the hierarchical structure, CATH is likely to become an even more valuable resource in the future.
- ➔ Since it was created, the development of SCOPe has been always guided by its user's feedback and needs.
- ➔ The automation in crystallography and advances in cryo-electron microscopy open a new era in structural biology and with it come new demands for data suitable for modelling of large proteins and protein complexes.
- ➔ In addition to a range of new annotations, SCOPe has introduced new functionalities that support relatively easy retrieval and assembly of independently determined, structurally characterized parts of proteins of interest.
- ➔ They will continue updating the database and providing regular releases while working on steadily increasing the coverage of structural data and adding new functionalities to the web interface.

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## WEBLEM 3

### Introduction to tertiary structure prediction

Proteins are involved in many cell activities (e.g., molecular transport, mechanical functions, message exchange) thus **knowing their 3D structure is crucial** in order to understand their function. **Protein tertiary structure prediction** is a research field which aims to **create models and software tools** able to predict the **three-dimensional shape of protein molecules** by describing the spatial disposition of each of its atoms starting from the sequence of its amino acids. There exist exact methods to **resolve the molecular structure with high precision**, but they are both time and resource consuming. **Computational based software techniques** can predict the tertiary structure of a protein with **acceptable precision** for many applications with high efficiency allowing for **genome-wide investigations**, otherwise not feasible.

Having a **computer-generated three-dimensional model** of a protein of interest has many ramifications, assuming it is reasonably correct. It may be of use for the **rational design of biochemical experiments**, such as **site-directed mutagenesis, protein stability, or functional analysis**. In addition to serving as a **theoretical guide to design experiments** for protein characterization, the model can help to **rationalize the experimental results** obtained with the protein of interest. In short, the modelling study helps to advance our **understanding of protein functions**.

### **METHODS:**

There are **three computational approaches** to protein three-dimensional structural modelling and prediction. They are **homology modelling, threading, and ab initio prediction**.

### **HOMOLOGY MODELLING:**

As the name suggests, **homology modelling** predicts protein structures based on **sequence homology** with known structures. It is also known as comparative modelling. The principle behind it is that if two proteins share a **high enough sequence similarity**, they are likely to have very **similar three-dimensional structures**. If one of the protein sequences has a **known structure**, then the structure **can be copied to the unknown protein** with a high degree of confidence. Homology modelling produces an **all-atom model** based on **alignment with template proteins**.

The overall homology modelling procedure consists of six steps.

1. **Template Selection** which involves identification of homologous sequences in the protein structure database to be used as templates for modelling
2. **Alignment** of target and template sequences.
3. **Building a framework structure** for the target protein consisting of main chain atoms.
4. **Refine and optimize** the entire model according to energy criteria.
5. **Evaluation** of the overall quality of the model obtained.

A number of **comprehensive modelling programs** are able to perform the complete procedure of homology modelling in an automated fashion. The **automation requires assembling a pipeline** that includes **target selection, alignment, model generation, and model evaluation**.

### **MODELLER:**

**MODELLER** is a computer program for **comparative protein structure modelling**. In the simplest case, the input is an **alignment of a sequence** to be modelled with the **template structures**, the atomic coordinates of the templates, and a simple script file. **MODELLER** then automatically **calculates a model** containing all **non-hydrogen atoms**, within minutes on a modern PC and with no user intervention. Apart from model building, **MODELLER** can perform additional auxiliary tasks, including **fold assignment, alignment of two protein sequences or their profiles, multiple alignment of protein sequences and/or structures, calculation of phylogenetic trees, and de novo modelling of loops** in protein structures.

### **THREADING AND FOLD RECOGNITION:**

There are only **small number of protein folds available** (<1,000), compared to millions of protein sequences. This means that protein structures tend to be **more conserved** than protein sequences. Consequently, many proteins can share a **similar fold** even in the absence of **sequence similarities**. This allowed the development of computational methods to predict protein structures **beyond sequence similarities**. To determine whether a **protein sequence adopts** a known **three-dimensional structure** fold relies on **threading and fold recognition** methods. By definition, threading or structural fold recognition predicts the **structural fold** of an **unknown protein sequence** by fitting the sequence into a **structural database** and selecting the **best-fitting fold**. The comparison emphasizes matching of **secondary structures**, which are most evolutionarily conserved. Therefore, this approach can **identify structurally similar proteins** even without detectable sequence similarity.

The algorithms can be classified into two categories, **pairwise energy based** and **profile based**. The pairwise energy-based method was originally referred to as **threading** and the profile-based method was originally defined as **fold recognition**. However, the two terms are now often used **interchangeably without distinction** in the literature. A number of threading and fold recognition programs are available using **either or both prediction strategies**.

### **I-TASSER:**

**I-TASSER** server is an on-line platform that implements the **I-TASSER based algorithms** for protein structure and function predictions. It allows academic users to **automatically generate high-quality model predictions** of 3D structure and **biological function** of protein molecules from their amino acid sequences. When user submits an amino acid sequence, the server **first tries to retrieve template proteins of similar folds** (or super-secondary structures) from the PDB library by LOMETS, a locally installed meta-threading approach.

In the **second step**, the continuous fragments excised from the PDB templates are reassembled into full-length models by **replica-exchange Monte Carlo simulations** with the threading unaligned regions (mainly loops) built by **ab initio modelling**. In cases where no appropriate template is identified by **LOMETs**, **I-TASSER** will build the whole structures by ab initio modelling. The low free-energy states are identified by **SPICKER** through clustering the simulation decoys.

In the **third step**, the fragment assembly simulation is performed again starting from the **SPICKER cluster centroids**, where the spatial restraints collected from **both** the **LOMETs** templates and the **PDB** structures by TM-align are used to **guide the simulations**. The purpose of the **second iteration** is to **remove the steric clash** as well as to **refine the global topology** of the cluster centroids. The decoys generated in the second simulations are then clustered and the lowest energy structures are selected. The **final full-atomic models** are obtained by **REMO** which builds the atomic details from the selected I-TASSER decoys through the optimization of the **hydrogen-bonding network**.

For **predicting the biological function** of the protein, the I-TASSER server matches the **predicted 3D models** to the **proteins in 3 independent libraries** which consist of proteins of known **enzyme classification (EC) number**, **gene ontology (GO) vocabulary**, and **ligand-binding sites**. The final results of function predictions are deduced from the consensus of **top structural matches** with the function scores calculated based on the confidence score of the I-TASSER structural models, the **structural similarity** between model and templates as **evaluated by TM-score**, and the sequence identity in the structurally aligned regions.

#### **1. What is C-score?**

**C-score** is a **confidence score** for estimating the quality of predicted models by I-TASSER. It is calculated based on the **significance of threading template alignments** and the **convergence parameters** of the structure assembly simulations. C-score is typically in the **range of [-5,2]**, where a C-score of **higher value** signifies a model with a **high confidence** and vice-versa.

#### **2. What is TM-score?**

**TM-score** is a recently proposed scale for measuring the **structural similarity between two structures**. The purpose of proposing TM-score is to **solve** the problem of **RMSD** which is sensitive to the local error. Because RMSD is an **average distance** of all residue pairs in **two structures**, a **local error** (e.g., a misorientation of the tail) will arise a **big RMSD value** although the global topology is correct. In TM-score, however, the **small distance is weighted stronger than the big distance** which makes the score **insensitive to the local modelling error**. A **TM-score >0.5** indicates a model of correct topology and a **TM-score<0.17** means a random similarity. These cut-off does not depend on the protein length.

### 3. What is difference and relationship between C-score and TM-score?

**TM-score** (or **RMSD**) is a known **standard** for measuring **structural similarity** between two structures which are usually used to measure the **accuracy of structure modelling** when the native structure is known, while **C-score** is a metric that I-TASSER developed to **estimate the confidence of the modelling**. In case where the native structure is not known, it becomes necessary to predict the quality of the modelling prediction, i.e., what is the distance between the predicted model and the native structures? To answer this question, we tried **predicting the TM-score and RMSD** of the predicted models relative the native structures based on the **C-score**.

In a benchmark test set of 500 non-homologous proteins, we found that C-score is highly correlated with TM-score and RMSD. Correlation coefficient of C-score of the first model with TM-score to the native structure is 0.91, while the coefficient of C-score with RMSD to the native structure is 0.75. These data lay the base for the reliable prediction of the TM-score and RMSD using C-score. In the output section, I-TASSER only reports the quality prediction (TM-score and RMSD) for the first model, because it was found that the correlation between C-score and TM-score is weak for lower rank models. However, the C-score is listed for all models just for a reference.

## AB INITIO PROTEIN STRUCTURAL PREDICTION

The limited knowledge of protein folding forms the basis of ab initio prediction. As the name suggests, the ab initio prediction method attempts to produce all-atom protein models based on sequence information alone without the aid of known protein structures. The perceived advantage of this method is that predictions are not restricted by known folds and that novel protein folds can be identified. However, because the physicochemical laws governing protein folding are not yet well understood, the energy functions used in the ab initio prediction are at present rather inaccurate. The folding problem remains one of the greatest challenges in bioinformatics today.

Current ab initio algorithms are not yet able to accurately simulate the protein folding process. They work by using some type of heuristics. Because the native state of a protein structure is near energy minimum, the prediction programs are thus designed using the energy minimization principle. These algorithms search for every possible conformation to find the one with the lowest global energy. However, searching for a fold with the absolute minimum energy may not be valid in reality. This contributes to one of the fundamental flaws of this approach. In addition, searching for all possible structural conformations is not yet computationally feasible. It has been estimated that, by using one of the world's fastest supercomputers (one trillion operations per second), it takes 10-20 years to sample all possible conformations of a 40-residue protein. Therefore, some type of heuristics must be used to reduce the conformational space to be searched. Some recent ab initio methods combine fragment search and threading to yield a model of an unknown protein. The following web program is such an example using the hybrid approach.

## ROBETTA:

The ROBETTA server provides automated tools for protein structure prediction and analysis. For structure prediction, sequences submitted to the server are parsed into putative domains and structural models are generated using either comparative modelling or *novo* structure prediction methods. If a confident

match to a protein of known structure is found using BLAST, PSI-BLAST, FFAS03 or 3D-Jury, it is used as a template for comparative modelling. If no match is found, structure predictions are made using the de novo Rosetta fragment insertion method. Experimental nuclear magnetic resonance (NMR) constraints data can also be submitted with a query sequence for RosettaNMR de novo structure determination. Other current capabilities include the prediction of the effects of mutations on protein–protein interactions using computational interface alanine scanning. The Rosetta protein design and protein–protein docking methodologies will soon be available through the server as well.

## **INPUT AND OUTPUT:**

### Registration:

Users must register (<http://robetta.bakerlab.org/register.jsp>) before submitting jobs to Robetta.

### Structure prediction server:

Sequences submitted to the structure prediction server must be in one-letter amino acid format. They can either be pasted into the submission form, or uploaded from a file. Users have the option to submit a sequence for either domain identification or full structure prediction. A user also has the option to specify the PDB id and chain for comparative modeling. For RosettaNMR submissions, a user must upload experimental NMR constraints data (chemical shifts, NOE data and/ or residual dipolar couplings). The required input format for each type of data is described at [http://robetta.bakerlab.org/documents/data\\_formats.jsp](http://robetta.bakerlab.org/documents/data_formats.jsp).

Results for a specific job are provided through the web interface by clicking on the job id listed in the queue table (<http://robetta.bakerlab.org/queue.jsp>). For full structure predictions, coordinates are also emailed to the user. For added insight, the following results are displayed along with the predicted models:

1. The prediction of transmembrane helices using TMHMM.
2. Low-complexity regions assigned by the program SEG
3. Coiled-coils prediction using COILS
4. The prediction of disordered regions using DISOPRED
5. Secondary structure predictions using PSIPRED, SAM-T99, Jufo and Jufo3D
6. The results listed above, domain predictions and the NR PSI-BLAST multiple sequence alignment used
7. For the last step in the domain prediction protocol condensed into an image to help corroborate the domain prediction results
8. Domain repeats prediction using REPRO predicted boundaries are given if repeats are detected
9. The top NR PSI-BLAST results and annotations for the top 20 species determined by lowest E-values.

The models for the full query are displayed as images at the bottom of the page. The coordinates for these models can be downloaded from the web site by clicking on the icons represented below each model image. Specific results are also provided for each domain by clicking on the domain number listed in the Ginzu domain prediction results table. For comparative models, the KSync alignment used for modelling is displayed. For de novo models, the Mammoth structure-model comparison results are displayed for the top 10 matches with Z-scores  $>4.5$ . The actual Mammoth structure-model alignment can be downloaded by clicking on the Z-score and viewed for further inspection using a molecular viewer such as RasMol. Users can download domain models by clicking on the icons below each domain model image.

Thus, modeller, I-TASSER and Robetta can be used to predict tertiary structures of proteins. These tools give faster results than x-ray or NMR techniques and can be used by researchers to understand protein functions.

## **REFERENCES:**

1. Xiong, J. (2008). Tertiary structure prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 214-228.

2. Tradigo, Giuseppe (2018). Reference Module in Life Sciences || Algorithms for Structure Comparison and Analysis: Prediction of Tertiary Structures of Proteins. , (), -. doi:10.1016/B978-0-12-809633-8.20483-4
3. Bateman, Alex; Pearson, William R.; Stein, Lincoln D.; Stormo, Gary D.; Yates, John R. (2002). Current Protocols in Bioinformatics || Comparative Protein Structure Modeling Using MODELLER. , (), 5.6.1–5.6.37. doi:10.1002/cpbi.3
4. Tutorial. (n.d.). Salilab.org. Retrieved March 8, 2022, from <https://salilab.org/modeller/tutorial/basic.html>
5. I-TASSER server for protein structure and function prediction. (n.d.). Zhanggroup.org. Retrieved March 8, 2022, from <https://zhanggroup.org/I-TASSER/about.html>
6. Kim, D. E.; Chivian, D.; Baker, D. (2004). Protein structure prediction and analysis using the Robetta server. , 32(0), 0–0. doi:10.1093/nar/gkh468

**WEBLEM 3a**  
**MODELLER**  
**([URL:https://salilab.org/modeller/](https://salilab.org/modeller/))**

**AIM:**

To perform tertiary structure prediction by comparative Modelling/Homology Modelling method using Modeller for query Rhodopsin

**INTRODUCTION:**

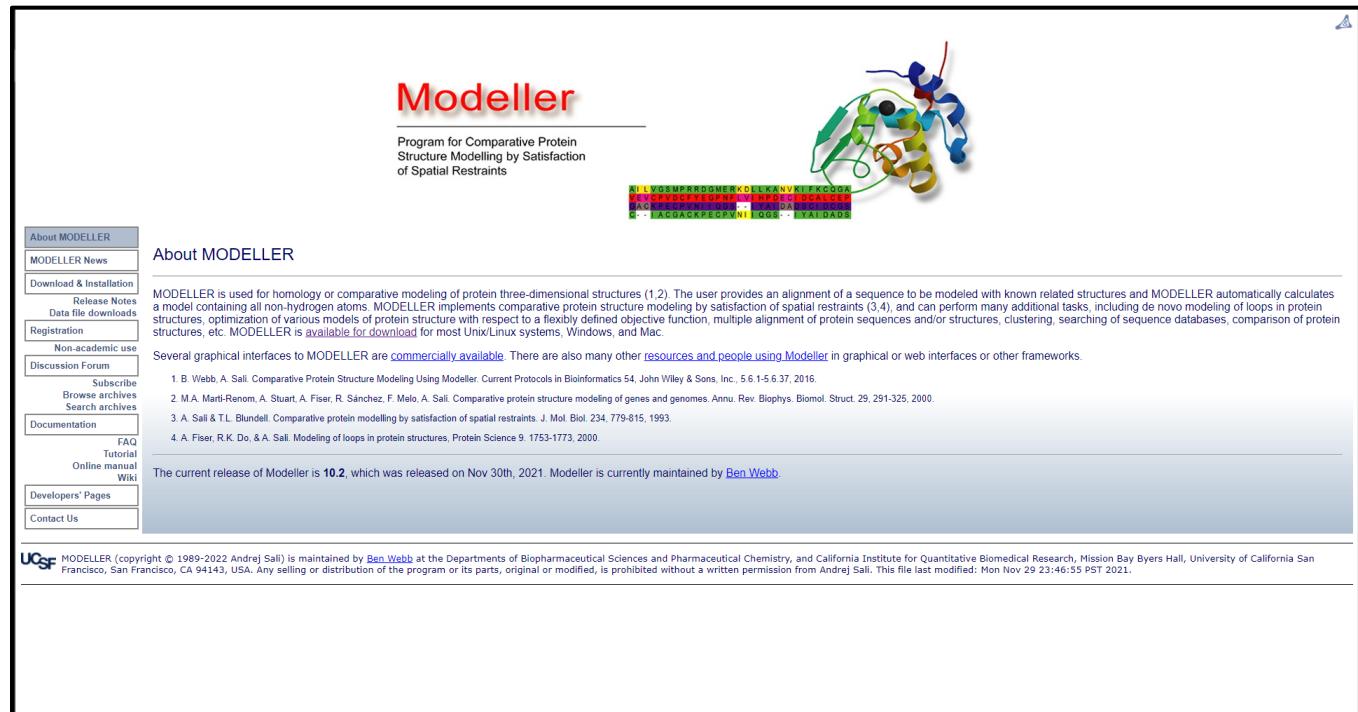
Rhodopsin, also called visual purple, pigment-containing sensory protein that converts light into an electrical signal. Rhodopsin is found in a wide range of organisms, from vertebrates to bacteria. In many seeing animals, including humans, it is required for vision in dim light and is located in the retina of the eye—specifically, within the tightly packed disks that make up the outer segment of the retina's photoreceptive rod cells, which are specially adapted for vision under low-light conditions.

**MODELLER** is a computer program for **comparative protein structure modelling**. In the simplest case, the input is an **alignment of a sequence** to be modelled with the **template structures**, the atomic coordinates of the templates, and a simple script file. **MODELLER** then automatically **calculates a model** containing all **non-hydrogen atoms**, within minutes on a modern PC and with no user intervention. Apart from model building, **MODELLER** can perform additional auxiliary tasks, including **fold assignment**, **alignment of two protein sequences** or their profiles, **multiple alignment** of protein sequences and/or structures, **calculation of phylogenetic trees**, and **de novo modelling of loops** in protein structures.

**METHODOLOGY:**

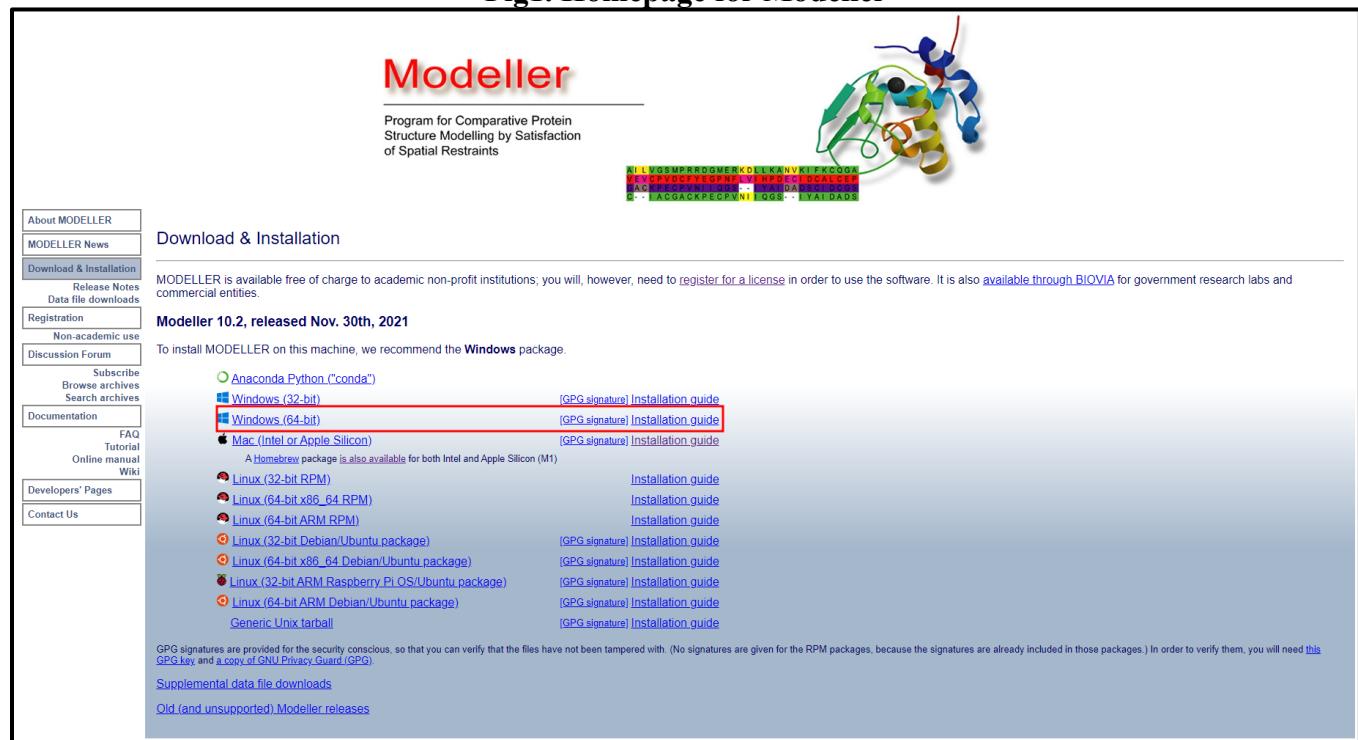
1. Install modeller. (URL: <https://salilab.prg/modeller>)
2. Retrieve FASTA sequence for enzyme rhodopsin
3. Follow the steps given in the tutorial section.
4. Run scripts for searching for structures related to query, selecting template target-template alignment and model building/
5. Observe and interpret the results.

## OBSERVATION:



The screenshot shows the official Modeller website. At the top, the word "Modeller" is written in a large, stylized red font. Below it, a sub-header reads "Program for Comparative Protein Structure Modelling by Satisfaction of Spatial Restraints". To the right of the text is a 3D ribbon model of a protein structure. Below the main title, there is a "About MODELLER" section with a list of links: "About MODELLER", "MODELLER News", "Download & Installation" (which is currently selected), "Release Notes", "Data file downloads", "Registration", "Non-academic use", "Discussion Forum", "Subscribe", "Browse archives", "Search archives", "Documentation", "FAQ", "Tutorial", "Online manual", and "Wiki". The "Download & Installation" section contains a "Release Notes" link, a "Data file downloads" link, and a "Registration" link. Below these are several bibliographic references. A note at the bottom states: "The current release of Modeller is 10.2, which was released on Nov 30th, 2021. Modeller is currently maintained by [Ben Webb](#)". At the very bottom, there is a copyright notice: "UCSF MODELLER (copyright © 1989-2022 Andrey Sali) is maintained by [Ben Webb](#) at the Departments of Biopharmaceutical Sciences and Pharmaceutical Chemistry, and California Institute for Quantitative Biomedical Research, Mission Bay Byers Hall, University of California San Francisco, San Francisco, CA 94143, USA. Any selling or distribution of the program or its parts, original or modified, is prohibited without a written permission from Andrey Sali. This file last modified: Mon Nov 29 23:46:55 PST 2021."

Fig1. Homepage for Modeller



This screenshot shows the "Download & Installation" section of the Modeller website. The "Modeller" logo and sub-header are at the top. Below is the "About MODELLER" section with the same list of links as the homepage. The "Download & Installation" section is expanded, showing a list of download options. The "Windows (64-bit)" link is highlighted with a red box. To the right of each link are "GPG signature" and "Installation guide" links. The list includes: "Anaconda Python ("conda")", "Windows (32-bit)", "Windows (64-bit)" (highlighted), "Mac (Intel or Apple Silicon)", "Linux (32-bit RPM)", "Linux (64-bit x86\_64 RPM)", "Linux (64-bit ARM RPM)", "Linux (32-bit Debian/Ubuntu package)", "Linux (64-bit x86\_64 Debian/Ubuntu package)", "Linux (32-bit ARM Raspberry Pi OS/Ubuntu package)", "Linux (64-bit ARM Debian/Ubuntu package)", and "Generic Unix tarball". A note at the bottom states: "A Homebrew package is also available for both Intel and Apple Silicon (M1)". Below the download links, there is a note about GPG signatures, a link to "Supplemental data file downloads", and a link to "Old (and unsupported) Modeller releases".

Fig2. Page to install Modeller

UniProtKB - P02699 (OPSD\_BOVIN)

Display Help video BLAST Align Format Add to basket History

UniProtKB The new UniProt website is here! Take me to UniProt BETA

Entry Protein Rhodopsin Gene RHO Organism Bos taurus (Bovine) Status Reviewed - Annotation score: 5/5 - Experimental evidence at protein level<sup>1</sup>

Function<sup>1</sup> Photoreceptor required for image-forming vision at low light intensity. Required for photoreceptor cell viability after birth (By similarity). Light-induced isomerization of 11-cis to all-trans retinal triggers a conformational change that activates signaling via G-proteins (PubMed:10926528, PubMed:12044163, PubMed:11972040, PubMed:16908857, PubMed:16586416, PubMed:17060607, PubMed:17449675, PubMed:18818650, PubMed:21389983, PubMed:22198838, PubMed:23579341, PubMed:25205354, PubMed:27458239). Subsequent receptor phosphorylation mediates displacement of the bound G-protein alpha subunit by the arrestin SAG and terminates signaling (PubMed:1396673, PubMed:15111114).

By similarity 5 Publications 11 Publications

Sites

Feature key	Position(s)	Description	Actions	Graphical view	Length
Site <sup>1</sup>	113	Plays an important role in the conformation switch to the active conformation	3 Publications	1	
Metal binding <sup>1</sup>	201 Zinc	Combined sources	2 Publications	1	
Metal binding <sup>1</sup>	279 Zinc	Combined sources	2 Publications	1	

GO - Molecular function<sup>1</sup>

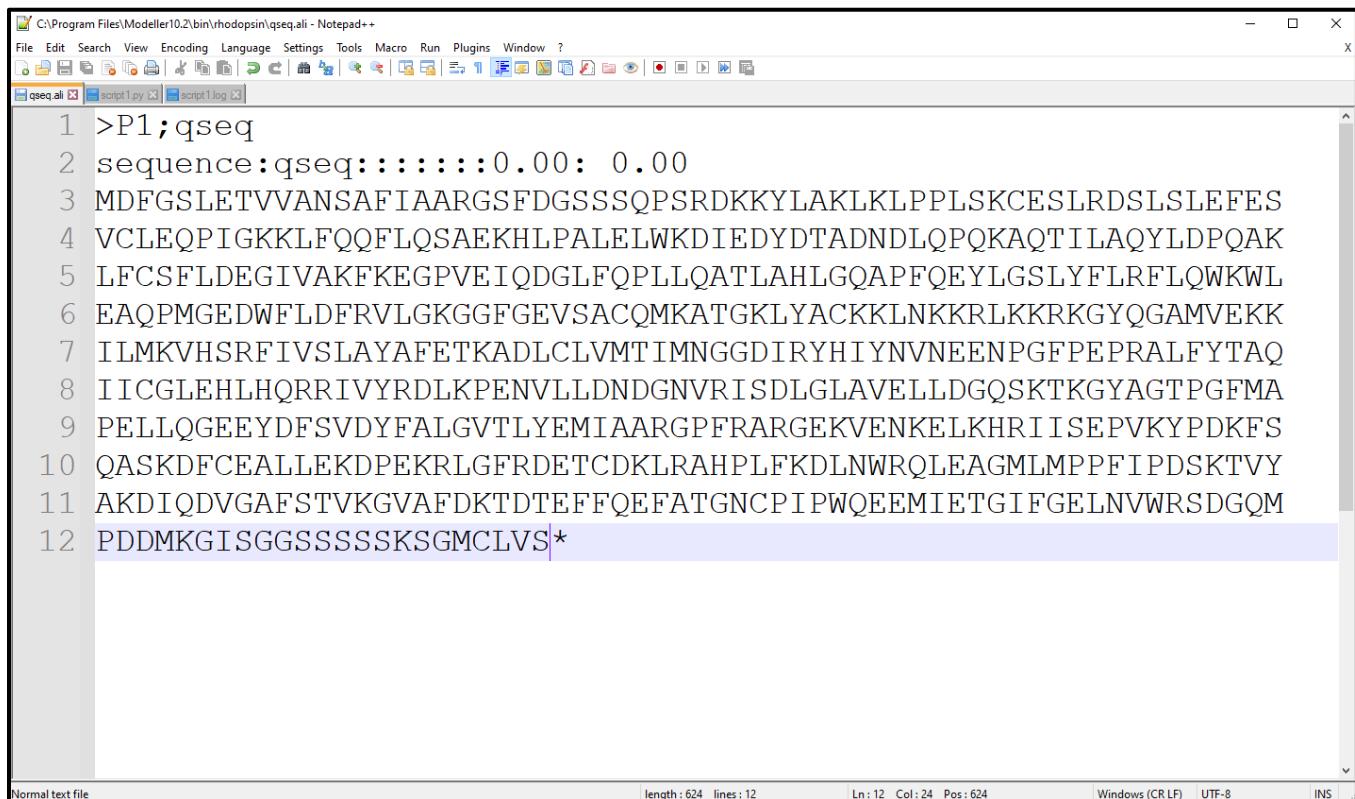
- 11-cis retinal binding Source: UniProtKB
- arrestin family protein binding Source: CAFA
- G-protein alpha-subunit binding Source: CAFA
- G-protein-coupled photoreceptor activity Source: UniProtKB
- guanyl-nucleotide exchange factor activity Source: UniProtKB
- identical protein binding Source: IntAct
- opsin binding Source: CAFA
- zinc ion binding Source: CAFA

Complete GO annotation on QuickGO ...

Fig3. Result page for Rhodopsin in UniProt database

```
>sp|Q15835|GRK1_HUMAN Rhodopsin kinase GRK1 OS=Homo sapiens OX=9606 GN=GRK1 PE=1
SV=1
MDFGSLETVVANSAFIAARGSFDGSSQPSRDKYLAALKLPLSKCESLRDLSLSLEFES
VCLEQPIGKKLFQQFLQSAEKHLPALELWKDIEDYDTADNDLQPQKAQTILAQYLDPQAK
LFCFLDEGIVAKFKEGPVEIQDGLFQPLLQATLAHLGQAPFQEYLGSYFLRFLQWKWL
EAQPMGEDWFLDFRVLGKGGEV SACQMKATGKLYACKKLNKKRKGYYQGAMVEKK
ILMKVHSRFIVSLAYAFETKADLCLVMTIMNGGDIRYHIYNVNEENPGFPEPRALFYTAQ
IICGLEHLHQRRIVYRDLKPENVLLNDGNVRISDLGLAVERLDGQSCKGYAGTPGFMA
PELLQGEYDFSVDYFALGVTLYEMIAARGPFRARGEKVENKELKRIISEPVKYPDKFS
QASKDFCEALLEKDPEKRLGFRDETCDKLRAHPLFKDNLWRQLEAGMLMPPFIPDSKTVY
AKDIQDVGAFSTVKVGAFDKTDTEFFQEATGNCPPIPQEEMIETGIFGELNVWRSDGQM
PDDMKGISGGSSSSSKSGMCLVS
```

Fig4. FASTA sequence for Rhodopsin

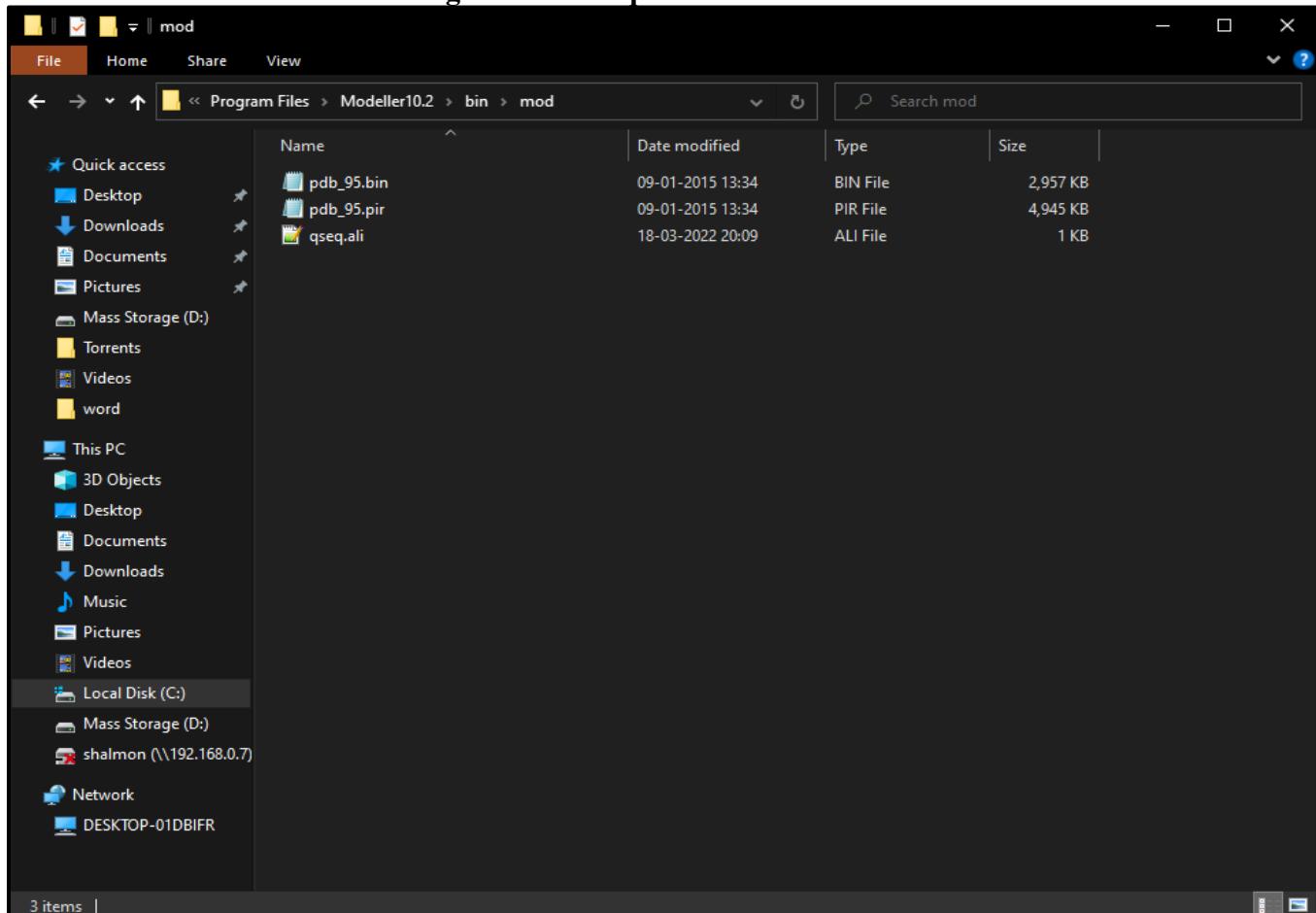


```

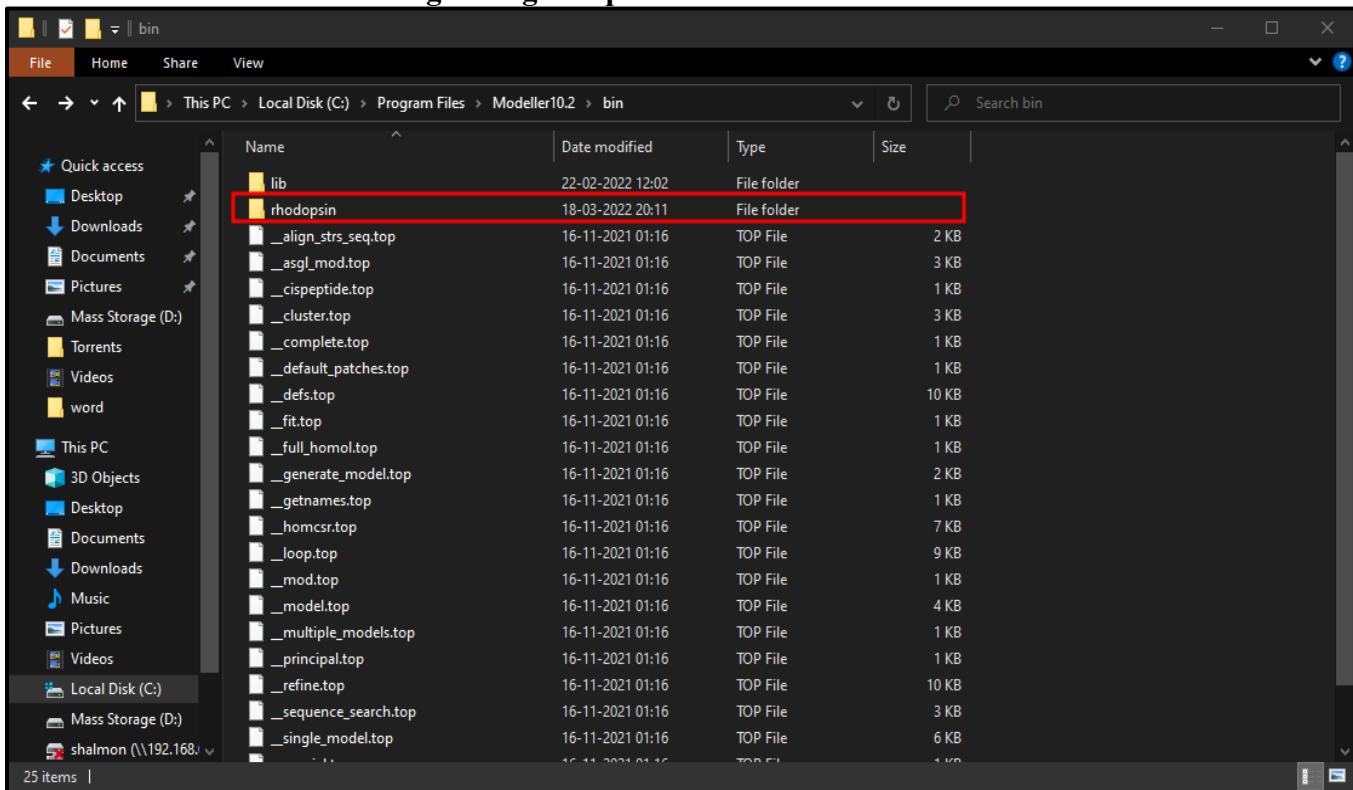
C:\Program Files\Modeller10.2\bin\hodopsin\qseq.ali - Notepad++
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?
qseq.ali script1.pir script1.log
1 >P1;qseq
2 sequence:qseq::::::::::0.00: 0.00
3 MDFGSLETVVANSAFIAARGSFDGSSQPSRDKYLAKLKLPLSKCESLRDSLSEFES
4 VCLEQPIGKKLFQQFLQSAEKHLPALEWKDIEDYDTADNDLQPQKAQTILAQYLDPQAK
5 LFCSFLDEGIVAKFKEGPVEIQDGLFQPLLQATLAHLGQAPFQEYLGSLYFLRFLQWKWL
6 EAQPMGEDWFLDFRVLGKGGFGEVSACQMKATGKLYACKKLNKKRKGYQGAMVEKK
7 ILMKVHSRFIVSLAYAFETKADLCLVMTIMNGGDIRYHIYNVNEENPGFPEPRALFYTAQ
8 IICGLELHQRRIVYRDLKPENVLLNDGNVRISDLGLAVELLDGQSKTKGYAGTPGFMA
9 PELLQGEEYDFSVDYFALGVTLYEMIAARGPFRARGEKVENKELKHRIISEPVKYPDKFS
10 QASKDFCEALLEKDPEKRLGFRDETCDKLRAHPLFKDLNWRQLEAGMLMPPFIPDSKTVY
11 AKDIQDVGAFSTVKVAFDKTDTEFFQEFA...GELNVWRSDGQM PDDMKGISGGSSSSKSGMCLVS*

```

Fig5. FASTA sequence in PIR format



**Fig6. Target sequence saved in .ali format**

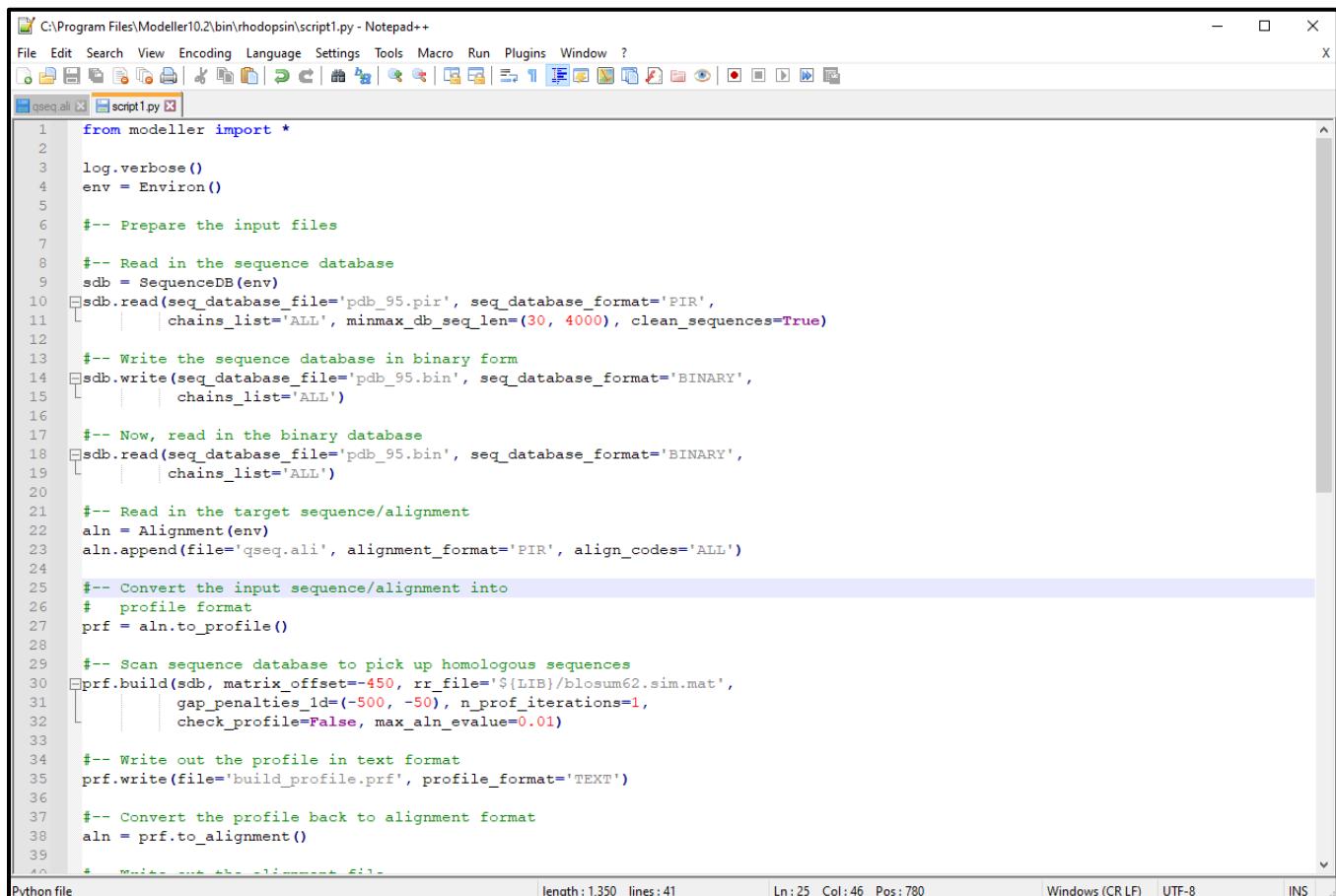


**Fig7. Rhodopsin folder saved in the bin folder of modeller**

A screenshot of a Modeller command line interface. The text shows the working directory being set:

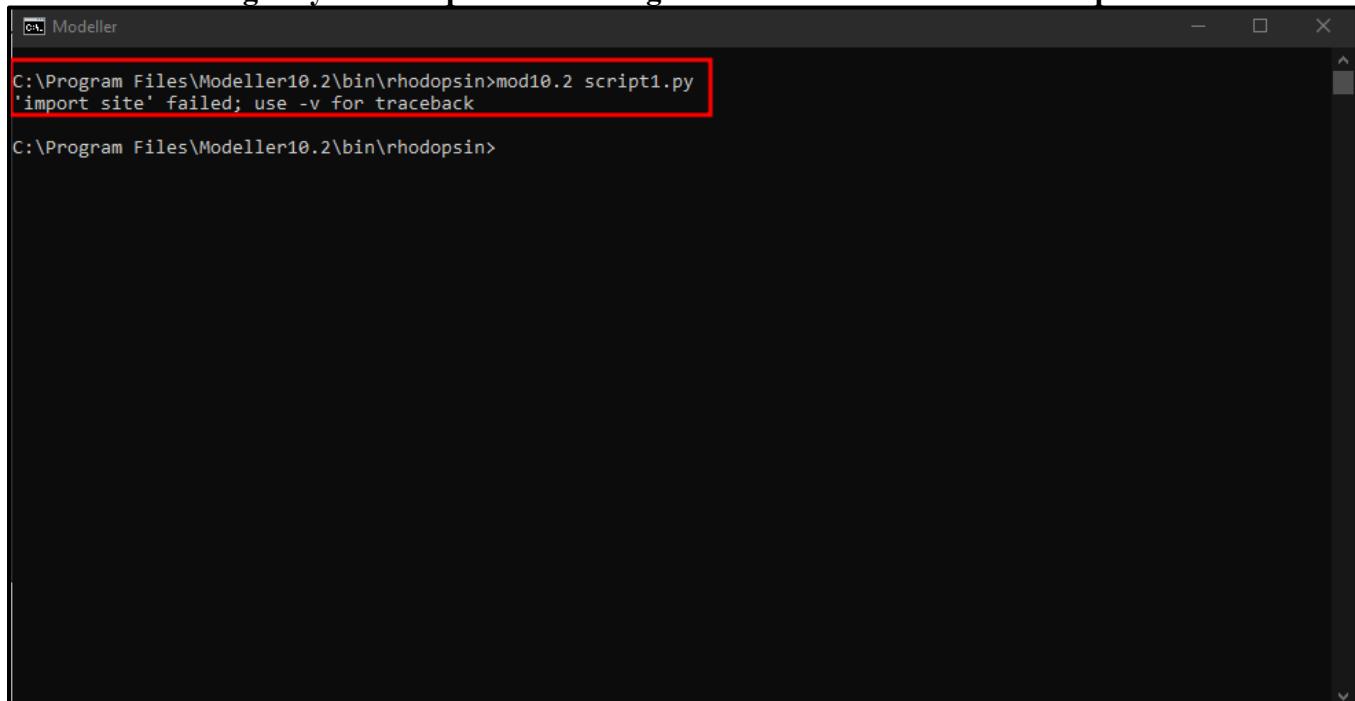
```
C:\Program Files\Modeller10.2>cd bin/rhodopsin
C:\Program Files\Modeller10.2\bin\rhodopsin>
```

**Fig8. Setting Working directory in Modeller command line**



```
C:\Program Files\Modeller10.2\bin\rhodopsin>script1.py - Notepad++  
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?  
qseq.ali script1.py  
1  from modeller import *  
2  
3  log.verbose()  
4  env = Environ()  
5  
6  #-- Prepare the input files  
7  
8  #-- Read in the sequence database  
9  sdb = SequenceDB(env)  
10 sdb.read(seq_database_file='pdb_95.pir', seq_database_format='PIR',  
11           chains_list='ALL', minmax_db_seq_len=(30, 4000), clean_sequences=True)  
12  
13  #-- Write the sequence database in binary form  
14 sdb.write(seq_database_file='pdb_95.bin', seq_database_format='BINARY',  
15           chains_list='ALL')  
16  
17  #-- Now, read in the binary database  
18 sdb.read(seq_database_file='pdb_95.bin', seq_database_format='BINARY',  
19           chains_list='ALL')  
20  
21  #-- Read in the target sequence/alignment  
22 aln = Alignment(env)  
23 aln.append(file='qseq.ali', alignment_format='PIR', align_codes='ALL')  
24  
25  #-- Convert the input sequence/alignment into  
26  # profile format  
27 prf = aln.to_profile()  
28  
29  #-- Scan sequence database to pick up homologous sequences  
30 prf.build(sdb, matrix_offset=-450, rr_file='${LIB}/blosum62.sim.mat',  
31           gap_penalties_1d=(-500, -50), n_prof_iterations=1,  
32           check_profile=False, max_aln_evalue=0.01)  
33  
34  #-- Write out the profile in text format  
35 prf.write(file='build_profile.prf', profile_format='TEXT')  
36  
37  #-- Convert the profile back to alignment format  
38 aln = prf.to_alignment()  
39  
40  #-- Write out the alignment in PIR format  
41 aln.write(file='script1.ali', alignment_format='PIR')  
Python file length: 1,350 lines: 41 Ln: 25 Col: 46 Pos: 780 Windows (CR LF) UTF-8 INS
```

Fig9. Python script for searching for structures relation to rhodopsin



```
C:\ Modeller  
C:\Program Files\Modeller10.2\bin\rhodopsin>mod10.2 script1.py  
'import site' failed; use -v for traceback  
C:\Program Files\Modeller10.2\bin\rhodopsin>
```

Fig10. Running script1.py

```
C:\Program Files\Modeller10.2\bin\rhodopsin\script1.log - Notepad++
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?
req.all script1.py script1.log

1
2           MODELLER 10.2, 2021/11/15, r12267
3
4           PROTEIN STRUCTURE MODELLING BY SATISFACTION OF SPATIAL RESTRAINTS
5
6
7           Copyright(c) 1989-2021 Andrey Sali
8           All Rights Reserved
9
10          Written by A. Sali
11          with help from
12          B. Webb, M.S. Madhusudhan, M-Y. Shen, G.Q. Dong,
13          M.A. Marti-Renom, N. Eswar, F. Alber, M. Topf, B. Oliva,
14          A. Fiser, R. Sanchez, B. Yerkovich, A. Badretdinov,
15          F. Melo, J.P. Overington, E. Feyfant
16          University of California, San Francisco, USA
17          Rockefeller University, New York, USA
18          Harvard University, Cambridge, USA
19          Imperial Cancer Research Fund, London, UK
20          Birkbeck College, University of London, London, UK
21
22
23 Kind, OS, HostName, Kernel, Processor: 4, Windows Vista build 9200, DESKTOP-01DBIFR, SMP, unknown
24 Date and time of compilation      : 2021/11/15 19:44:35
25 MODELLER executable type        : x86_64-w64
26 Job starting time (YY/MM/DD HH:MM:SS): 2022/03/18 21:01:53
27
28 open__224-> Open      $ (LIB)/restyp.lib
29 open__224-> Open      $ (MODINSTALL10v2)/modlib/resgrp.lib
30 rdresgr_266-> Number of residue groups: 2
31 openf__224-> Open      $ (MODINSTALL10v2)/modlib/sstruc.lib
32
33 Dynamically allocated memory at amaxlibraries [B,KiB,MiB]: 191566 187.076 0.183
34
35 Dynamically allocated memory at amaxlibraries [B,KiB,MiB]: 192094 187.592 0.183
36 openf__224-> Open      $ (MODINSTALL10v2)/modlib/resdih.lib
37
38 Dynamically allocated memory at amaxlibraries [B,KiB,MiB]: 240694 235.053 0.230
39 rdrdih_263-> Number of dihedral angle types      : 9
40
```

Fig11. Log file for script1.py

```
C:\Program Files\Modeller10.2\bin\rhodopsin\script1.log - Notepad++
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?
qseq_all script1.py script1.log
271 Z: 1 8.05000 0.00000 0.00002
272
273 HITS FOUND IN ITERATION: 1
274
275
276 Dynamically allocated memory at amaxprofile [B,KiB,MiB]: 1088666 1063.150 1.038
277 > 1a06 1 43 14050 279 563 36.29 0.0 2 233 179 453 1 237
278 > 1ywrA 1 270 7950 338 563 28.57 0.43E-10 3 193 196 412 26 228
279 > 1qcfA 1 347 7600 449 563 26.87 0.39E-09 4 262 92 386 108 375
280 > 1fgkA 1 421 6800 278 563 26.74 0.15E-07 5 258 184 451 3 275
281 > 1rdqE 1 609 22200 340 563 36.69 0.0 6 275 188 477 33 310
282 > 1g28A 1 624 10300 290 563 27.94 0.0 7 246 196 458 10 281
283 > 1vjyA 1 907 6200 299 563 27.92 0.40E-06 8 178 196 385 11 207
284 > 2BfxA 1 1121 13950 270 563 29.69 0.0 9 254 194 471 12 267
285 > 1blkxA 1 1187 9100 305 563 25.61 0.0 10 249 196 458 15 299
286 > 2bikB 1 1204 7600 272 563 26.40 0.21E-09 11 243 195 458 11 260
287 > 1uu3A 1 1206 18450 277 563 34.65 0.0 12 253 194 463 14 267
288 > 1mq4A 1 1316 13100 261 563 29.55 0.0 13 243 189 443 3 249
289 > 1bygA 1 1510 5050 246 563 25.43 0.14E-03 14 171 194 392 13 185
290 > 1ck1A 1 1804 5550 292 563 24.27 0.12E-04 15 228 194 430 13 251
291 > 1cm8A 1 1847 8000 327 563 27.55 0.32E-10 16 233 212 459 36 300
292 > 1csn 1 1943 5000 293 563 26.62 0.23E-03 17 127 300 433 109 247
293 > 1om1A 1 2136 7500 325 563 30.53 0.45E-09 18 178 194 392 37 226
294 > 1pme 1 2878 8100 333 563 25.42 0.20E-10 19 261 200 477 17 315
295 > 1f3mC 1 3067 10600 287 563 28.70 0.0 20 225 193 438 25 254
296 > 1fmk 1 3385 5600 437 563 26.01 0.15E-04 21 220 196 441 192 414
297 > 1fotA 1 3435 20600 299 563 31.58 0.0 22 283 190 486 6 290
298 > 1cpjA 1 3450 6600 287 563 26.49 0.46E-07 23 182 196 385 25 209
299 > 1fvrA 1 3525 6950 299 563 27.54 0.75E-08 24 188 188 390 8 214
300 > 1ir3A 1 3719 8350 300 563 25.18 0.49E-11 25 259 194 460 20 293
301 > 1gjoA 1 3818 7000 280 563 26.23 0.53E-08 26 232 196 435 21 264
302 > 1j1bA 1 3869 9500 354 563 31.19 0.0 27 194 190 392 22 223
303 > 1o61A 1 4037 25450 316 563 38.97 0.0 28 271 194 474 11 282
304 > 1oiuC 1 4061 10750 265 563 29.84 0.0 29 245 196 458 11 258
305 > 1un1A 1 4075 7250 292 563 23.30 0.15E-08 30 249 196 457 10 288
306 > 1q8yA 1 4291 5450 351 563 23.90 0.26E-04 31 162 285 457 118 322
307 > 1i5oA 1 4562 11650 322 563 30.71 0.0 32 260 190 466 1 267
```

### Fig11.1. Hits found for similar structures

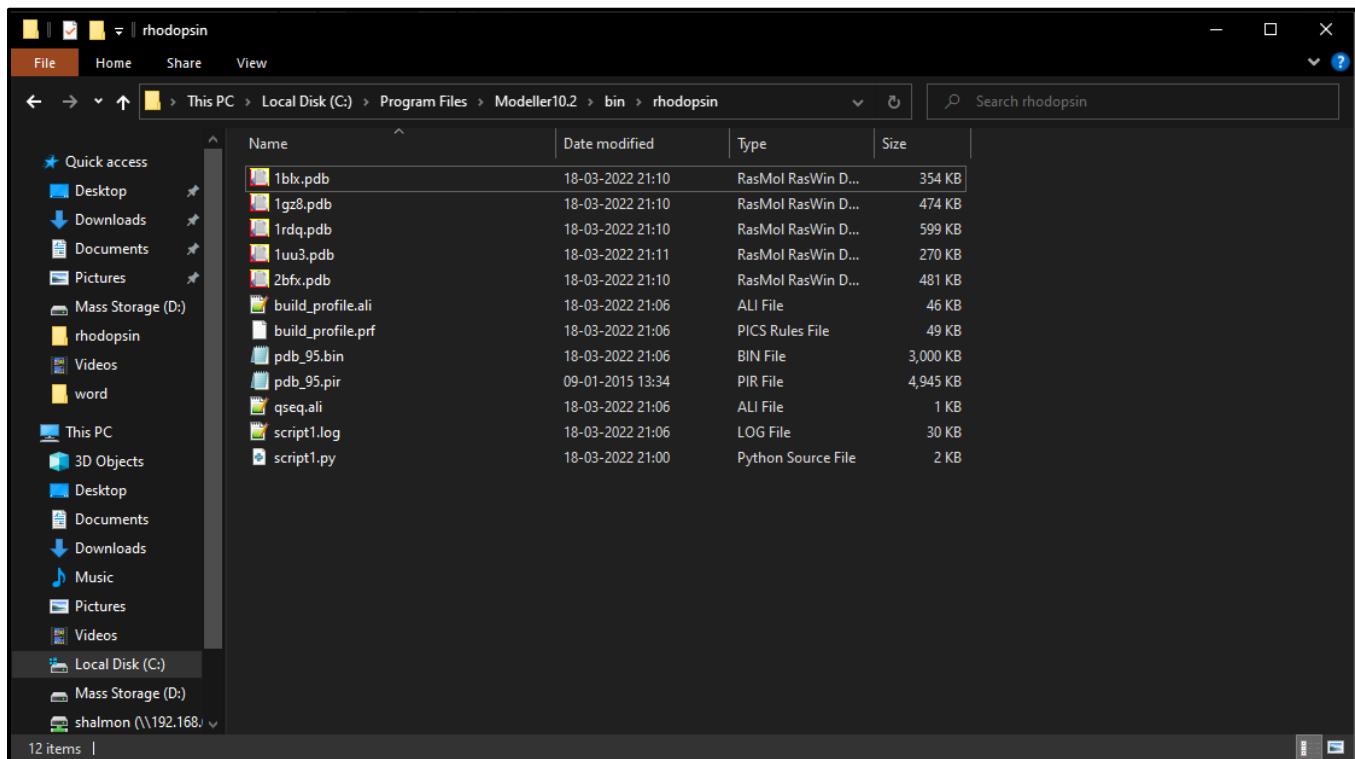


Fig12. Five structure download in PDB format

```

1  from modeller import *
2
3  env = Environment()
4  aln = Alignment(env)
5  for (pdb, chain) in (('1rdq', 'E'), ('1g28', 'A'), ('2bfx', 'A'),
6  ('1blx', 'A'), ('1uu3', 'A')):
7      m = Model(env, file=pdb, model_segment=('FIRST:'+chain, 'LAST:'+chain))
8      aln.append_model(m, atom_files=pdb, align_codes=pdb+chain)
9  aln.align()
10 aln.malign3d()
11 aln.compare_structures()
12 aln.id_table(matrix_file='family.mat')
13 env.dendrogram(matrix_file='family.mat', cluster_cut=-1.0)

```

Fig13. Python script for selecting a template

```
Modeller
C:\Program Files\Modeller10.2\bin\rhodopsin>mod10.2 script2.py
'import site' failed; use -v for traceback
C:\Program Files\Modeller10.2\bin\rhodopsin>
```

**Fig14. Running script2.py**

C:\Program Files\Modeller10.2\bin\rhodopsin\script2.log - Notepad++

File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?

File1.py script1.log script2.py script2.log

```
1 MODELLER 10.2, 2021/11/15, r12267
2
3 PROTEIN STRUCTURE MODELLING BY SATISFACTION OF SPATIAL RESTRAINTS
4
5
6
7 Copyright(c) 1989-2021 Andrey Sali
8 All Rights Reserved
9
10
11 Written by A. Sali
12 with help from
13 B. Webb, M.S. Madhusudhan, M-Y. Shen, G.Q. Dong,
14 M.A. Marti-Renom, N. Eswar, F. Alber, M. Topf, B. Oliva,
15 A. Fiser, R. Sanchez, B. Yerkovich, A. Badretdinov,
16 F. Melo, J.P. Overington, E. Feyfant
17 University of California, San Francisco, USA
18 Rockefeller University, New York, USA
19 Harvard University, Cambridge, USA
20 Imperial Cancer Research Fund, London, UK
21 Birkbeck College, University of London, London, UK
22
23 Kind, OS, HostName, Kernel, Processor: 4, Windows Vista build 9200, DESKTOP-01DBIFR, SMP, unknown
24 Date and time of compilation : 2021/11/15 19:44:35
25 MODELLER executable type : x86_64-w64
26 Job starting time (YY/MM/DD HH:MM:SS): 2022/03/18 21:15:40
27
28
29 Multiple dynamic programming alignment (MALIGN):
30 Residue-residue metric : $(LIB)/asl.sim.mat
31 ALIGN_BLOCK : 1
32 Gap introduction penalty: -900.0000
33 Gap extension penalty : -50.0000
34 Length of alignment : 353
```

**Fig15. Log file for script2**

```

C:\Program Files\Modeller10.2\bin\rhodopsin\script2.log - Notepad++
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?
qseq.all script1.py script1.log script2.py script2.log script2.log

3327 2bfxa @1 22 19 270 50 68
3328 1blxa @1 17 41 19 305 53
3329 1uu3a @1 34 23 25 19 277
3330
3331
3332 Weighted pair-group average clustering based on a distance matrix:
3333
3334
3335
3336
3337
3338
3339
3340
3341
3342
3343
3344
3345
3346
3347
3348
3349
3350
3351 Total CPU time [seconds] : 0.73
3352

Normal text file length: 179471 lines: 3352 Ln: 20 Col: 65 Pos: 908 Windows (CR LF) UTF-8 INS

```

Fig15.1 Structure selected with low x-ray crystallography value and high NMR value

```

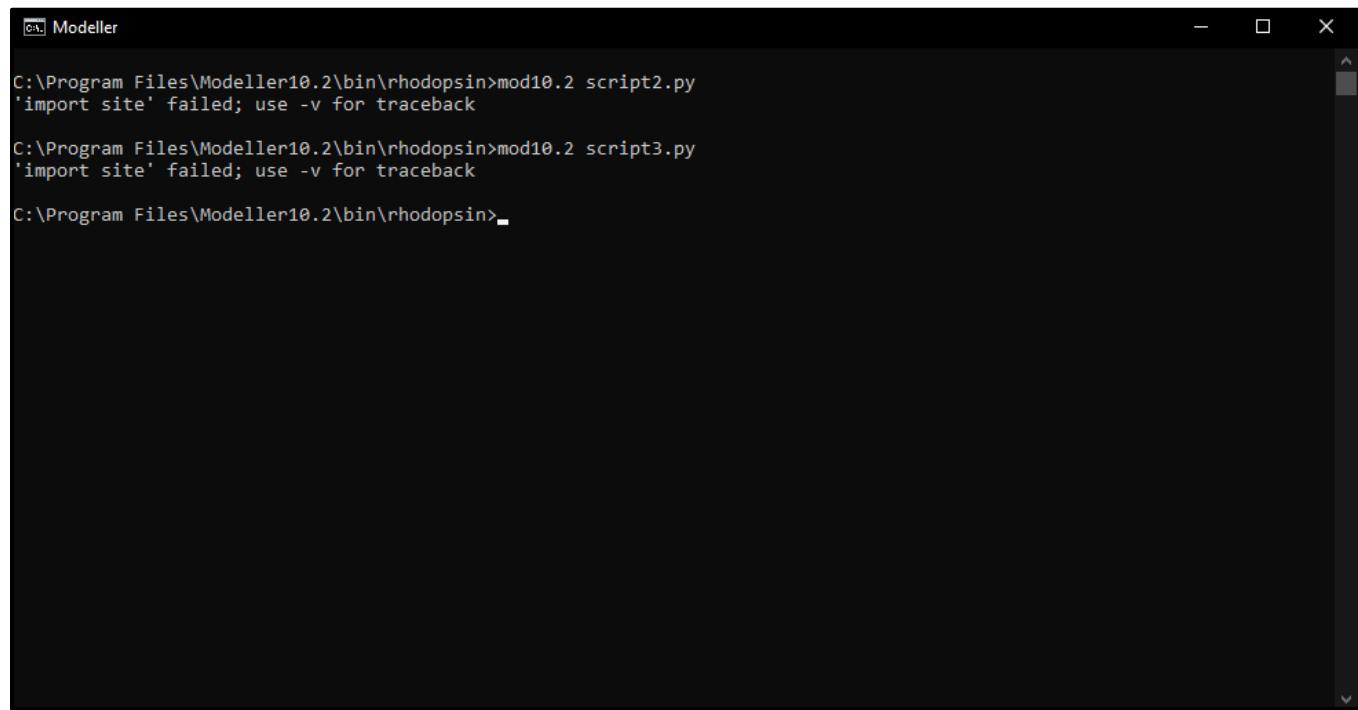
C:\Program Files\Modeller10.2\bin\rhodopsin\script3.py - Notepad++
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?
qseq.all script1.py script1.log script2.py script2.log script3.py

1 from modeller import *
2
3 env = Environ()
4 aln = Alignment(env)
5 mdl = Model(env, file='2bfxa', model_segment=('FIRST:A','LAST:A'))
6 aln.append_model(mdl, align_codes='2bfxa', atom_files='2bfxa.pdb')
7 aln.append(file='qseq.ali', align_codes='qseq')
8 aln.align2d(max_gap_length=50)
9 aln.write(file='qseq-2bfxa.ali', alignment_format='PIR')
10 aln.write(file='qseq-2bfxa.pap', alignment_format='PAP')

Python file length: 394 lines: 10 Ln: 10 Col: 57 Pos: 395 Windows (CR LF) UTF-8 INS

```

Fig16. Python script for aligning query with the template

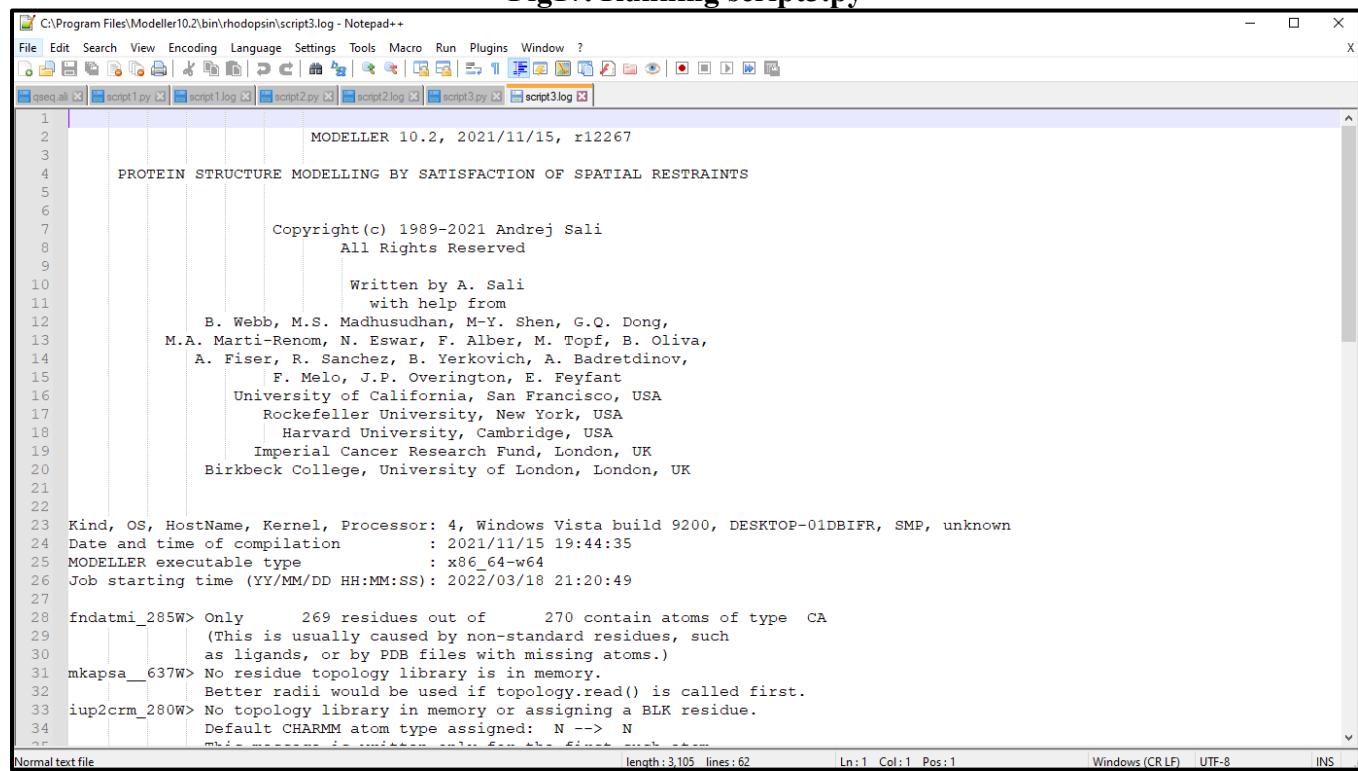


```
C:\Program Files\Modeller10.2\bin\rhodopsin>mod10.2 script2.py
'import site' failed; use -v for traceback

C:\Program Files\Modeller10.2\bin\rhodopsin>mod10.2 script3.py
'import site' failed; use -v for traceback

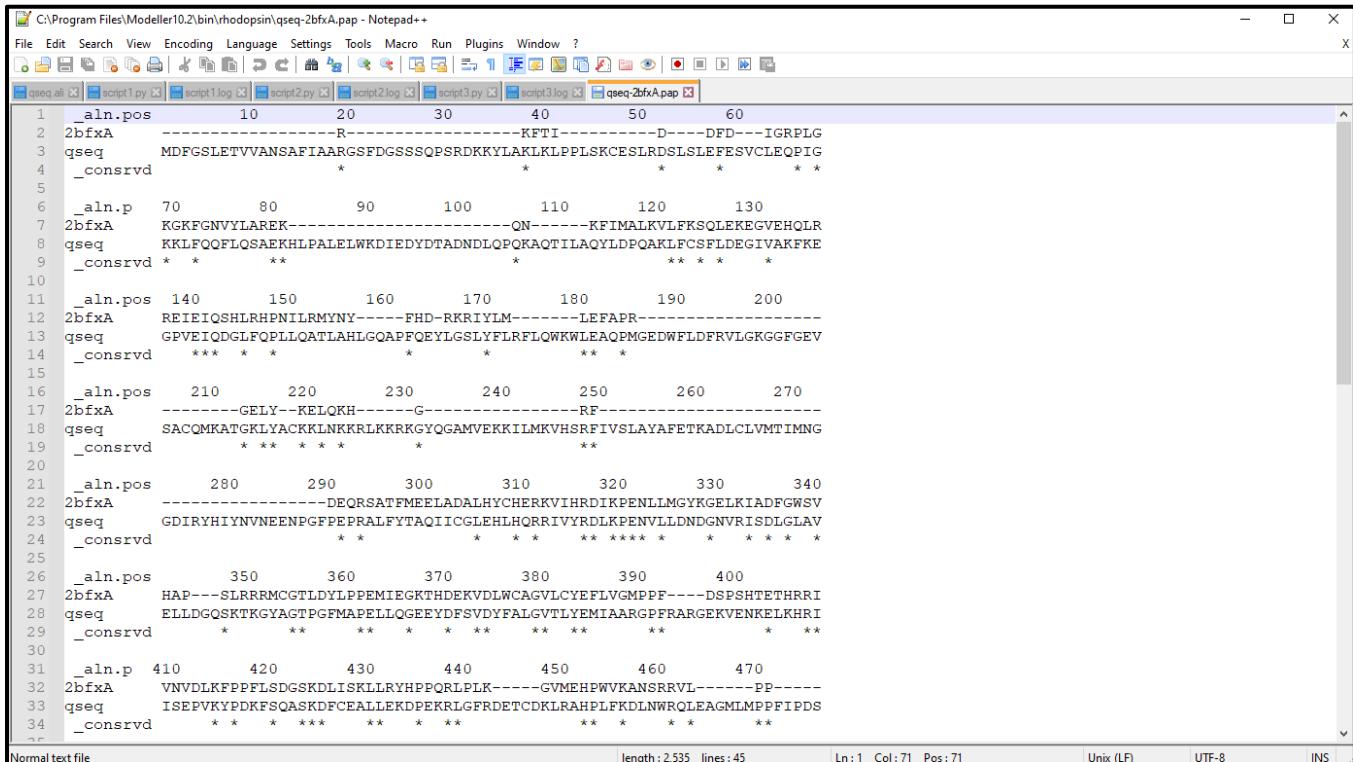
C:\Program Files\Modeller10.2\bin\rhodopsin>-
```

Fig17. Running script3.py



```
1 MODELLER 10.2, 2021/11/15, r12267
2
3 PROTEIN STRUCTURE MODELLING BY SATISFACTION OF SPATIAL RESTRAINTS
4
5
6
7 Copyright(c) 1989-2021 Andrey Sali
8 All Rights Reserved
9
10 Written by A. Sali
11 with help from
12 B. Webb, M.S. Madhusudhan, M-Y. Shen, G.Q. Dong,
13 M.A. Marti-Renom, N. Eswar, F. Alber, M. Topf, B. Oliva,
14 A. Fiser, R. Sanchez, B. Yerkovich, A. Badretdinov,
15 F. Melo, J.P. Overington, E. Feyfant
16 University of California, San Francisco, USA
17 Rockefeller University, New York, USA
18 Harvard University, Cambridge, USA
19 Imperial Cancer Research Fund, London, UK
20 Birkbeck College, University of London, London, UK
21
22
23 Kind, OS, HostName, Kernel, Processor: 4, Windows Vista build 9200, DESKTOP-01DBIFR, SMP, unknown
24 Date and time of compilation : 2021/11/15 19:44:35
25 MODELLER executable type : x86_64-w64
26 Job starting time (YY/MM/DD HH:MM:SS): 2022/03/18 21:20:49
27
28 fndatmi_285W> Only 269 residues out of 270 contain atoms of type CA
29 (This is usually caused by non-standard residues, such
30 as ligands, or by PDB files with missing atoms.)
31 mkapsa_637W> No residue topology library is in memory.
32 Better radii would be used if topology.read() is called first.
33 iup2crm_280W> No topology library in memory or assigning a BLK residue.
34 Default CHARMM atom type assigned: N --> N
```

Fig18. Log file for script3



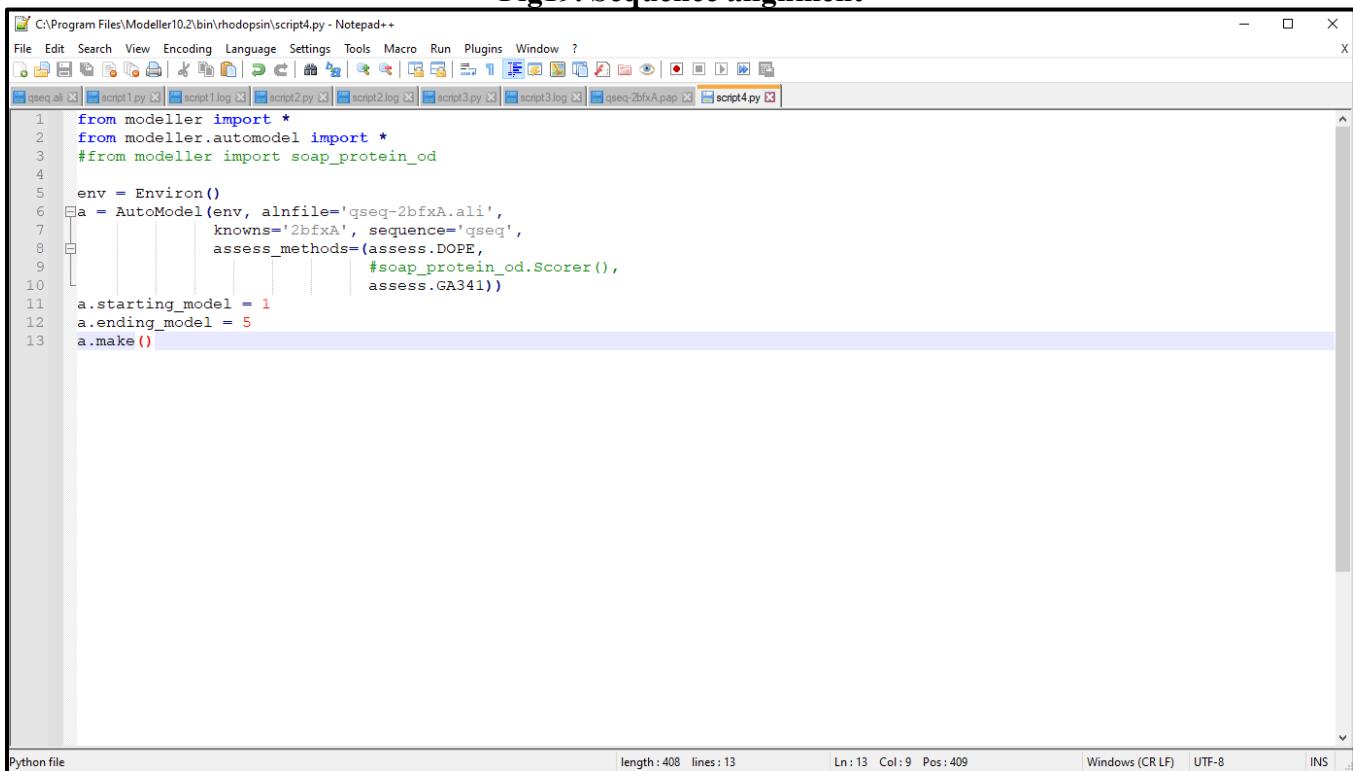
```

C:\Program Files\Modeller10.2\bin\rhodopsin\qseq-2bfxA.pap - Notepad++
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?
seq.all script1.py script1.log script2.py script2.log script3.py script3.log qseq-2bfxA.pap

1 _aln.pos 10 20 30 40 50 60
2 2bfxA -----R-----KFTI-----DFD--IGRPLG
3 qseq MDFGSLETVVANSAFIAARGSF DGS QPSRDKKYLARKLKPPLSKCESLRD SLSLEFESV CLEQPIG
4 _consrvd * * * * * *
5
6 _aln.p 70 80 90 100 110 120 130
7 2bfxA KGKFGNVYLAREK-----QN-----KFIMALVLFKSQLEKEGV EHQRL
8 qseq KKLFQQFLQS A EKHLPALELWKDIEDYDTADNDLQPKA Q TILA QYLD PQA KLFCSFL D E GIVAKFKE
9 _consrvd * * * * * *
10
11 _aln.pos 140 150 160 170 180 190 200
12 2bfxA REIEIQSHL RHPN IILRMYN -----FHD-RKRIYLM-----LEFAPR
13 qseq G V E I Q D G L F Q P Q L L Q A T L A H L G Q A P F Q E Y L G S L Y F L R F L Q W K W L E A Q P M G E D W F L D F R V L G K G G F E V
14 _consrvd * * * * * *
15
16 _aln.pos 210 220 230 240 250 260 270
17 2bfxA -----G E L Y --K E L Q K H -----G-----R F -----
18 qseq S A C Q M K A T G K L Y A C K K L N K K R L K R K G Y Q G A M V E K K I L M K V H S R P I V S L A Y A F E T K A D L C L V M T I M N G
19 _consrvd * * * * * *
20
21 _aln.pos 280 290 300 310 320 330 340
22 2bfxA -----D E Q R S A T F M E E L A D A L H Y C H E R K V I H R D I K P E N I L M G Y K G E L K I A D F G W S V
23 qseq G D I R Y H I Y N V N E E N P G F F E P R A L F Y T A Q I I C G L E H L H Q R R I V Y R D L K P E N V L L D N D G N V R I S D L G L A V
24 _consrvd * * * * * * * * * *
25
26 _aln.pos 350 360 370 380 390 400
27 2bfxA H A P -----S L R R M C G T L D Y L P P E M I E G K T H D E K V D L W C A G V L C Y E F L V G M P P F -----D S P S H T E T H R R I
28 qseq E L L D G Q S K T K G Y A G T P G F M A P E L L Q G E E Y D F S V D Y F A L G V I Y Y E M I A A R G P F R A R G E K V E N K E L K R I
29 _consrvd * * * * * * * * * *
30
31 _aln.p 410 420 430 440 450 460 470
32 2bfxA V N V D L K F P P F L S D G S K D L I S K L R Y H P P Q R L P L K -----G V M E H P W V K A N S R R V L -----P P -----
33 qseq I S E P V K Y P D K F S Q A S K D F C E A L L E K D P E K R L G F R D E T C D K L R A H P L F K D L N W R O L E A G M L M P P F I P D S
34 _consrvd * * * * * * * * * *

```

Fig19. Sequence alignment



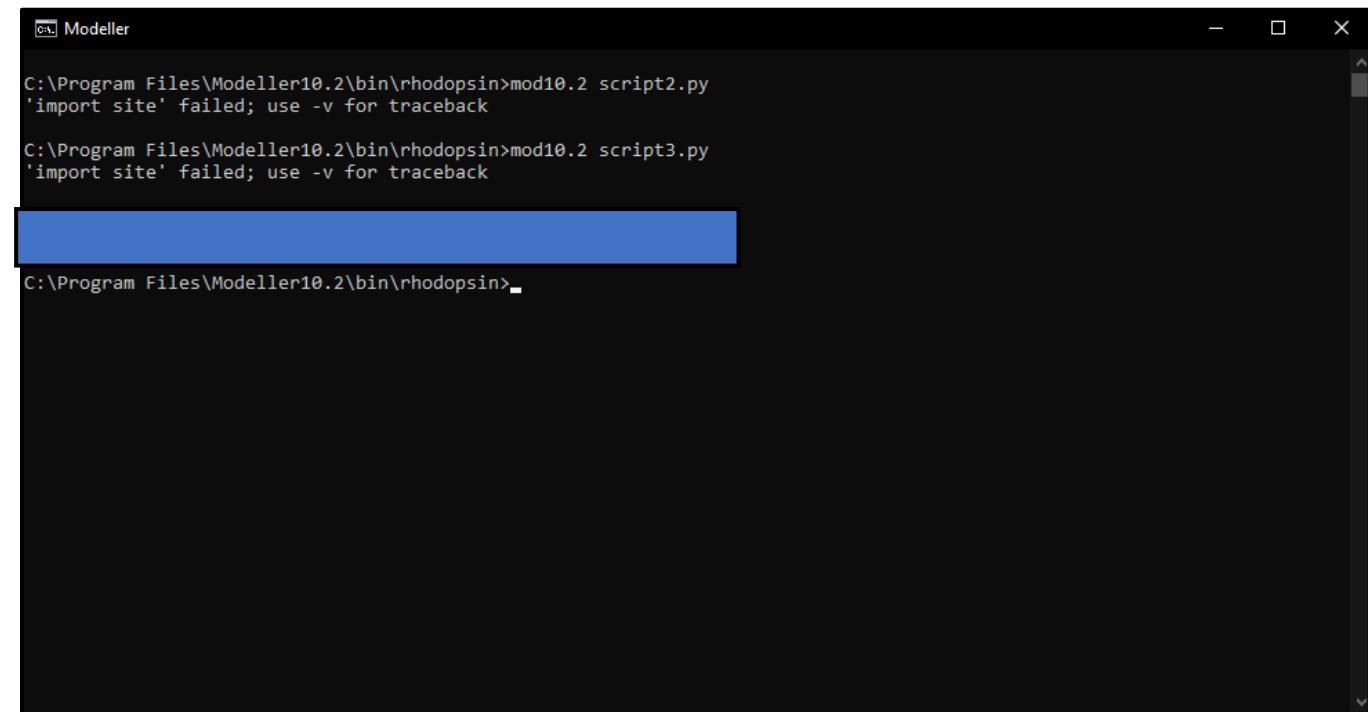
```

C:\Program Files\Modeller10.2\bin\rhodopsin\script4.py - Notepad++
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?
seq.all script1.py script1.log script2.py script2.log script3.py script3.log qseq-2bfxA.pap script4.py

1 from modeller import *
2 from modeller import *
3 #from modeller import soap_protein_od
4
5 env = Environ()
6 a = AutoModel(env, alnfile='qseq-2bfxA.ali',
7                 knowns='2bfxA', sequence='qseq',
8                 assess_methods=(assess.DOPE,
9                                  #soap_protein_od.Scorer(),
10                                 assess.GA341))
11 a.starting_model = 1
12 a.ending_model = 5
13 a.make()

```

Fig20. Python script for model building

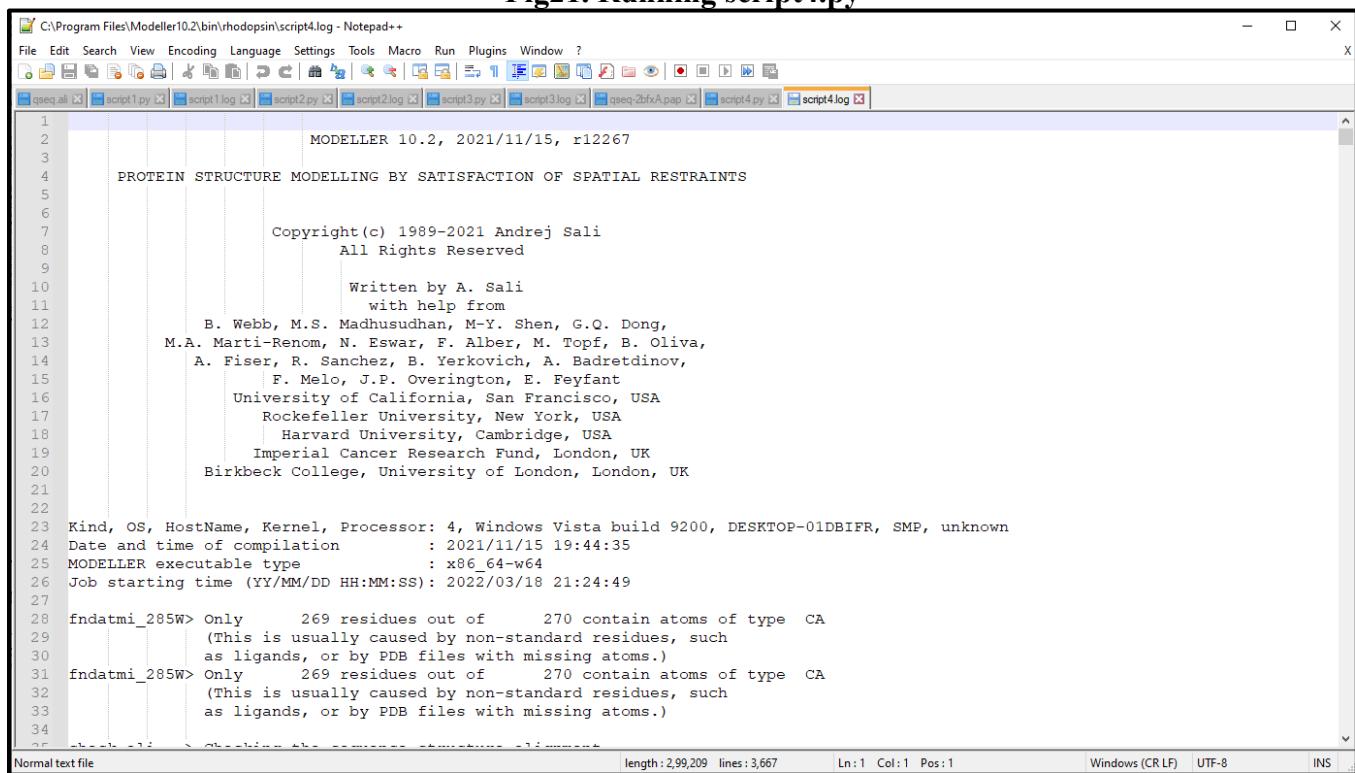


```
C:\Program Files\Modeller10.2\bin\rhodopsin>mod10.2 script2.py
'import site' failed; use -v for traceback

C:\Program Files\Modeller10.2\bin\rhodopsin>mod10.2 script3.py
'import site' failed; use -v for traceback

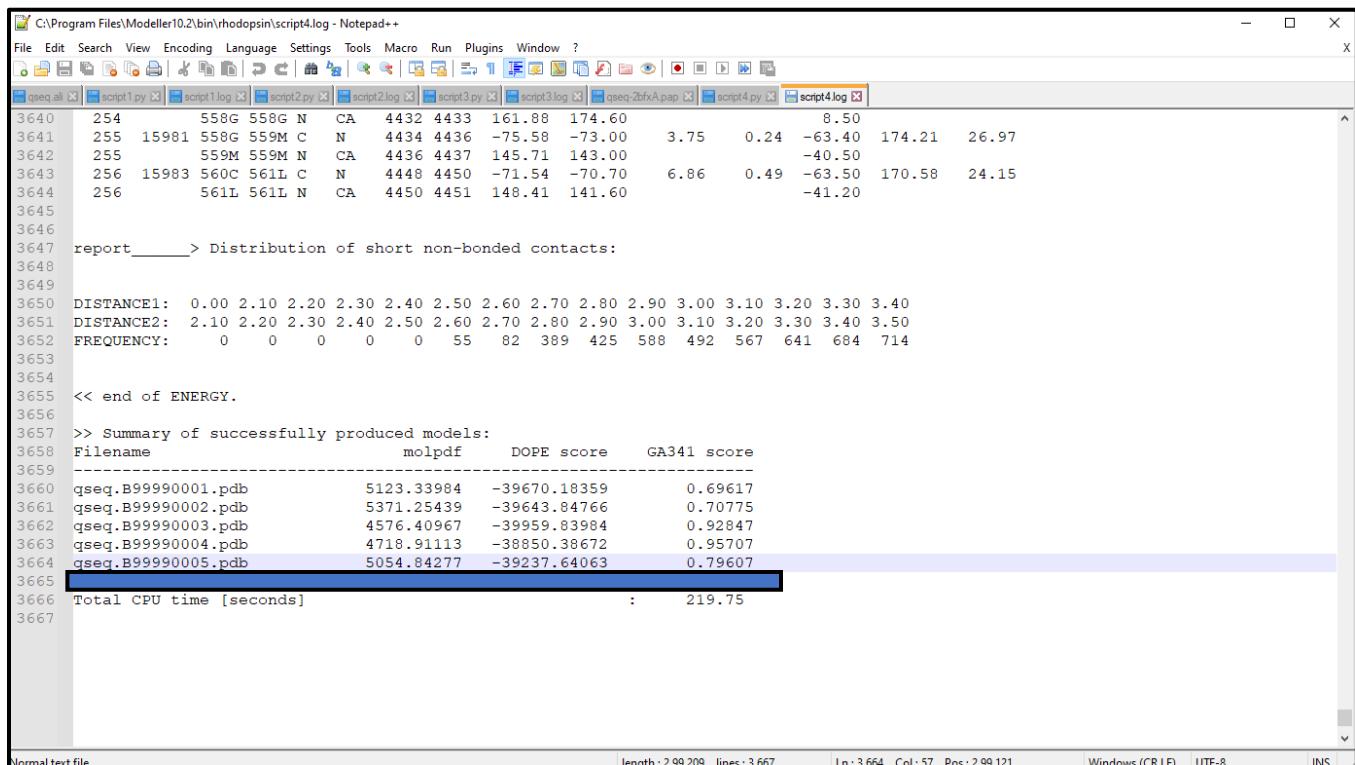
C:\Program Files\Modeller10.2\bin\rhodopsin>
```

Fig21. Running script4.py



```
1 MODELLER 10.2, 2021/11/15, r12267
2
3 PROTEIN STRUCTURE MODELLING BY SATISFACTION OF SPATIAL RESTRAINTS
4
5
6 Copyright(c) 1989-2021 Andrej Sali
7 All Rights Reserved
8
9 Written by A. Sali
10 with help from
11 B. Webb, M.S. Madhusudhan, M.-Y. Shen, G.Q. Dong,
12 M.A. Marti-Renom, N. Eswar, F. Alber, M. Topf, B. Oliva,
13 A. Fiser, R. Sanchez, B. Yerkovich, A. Badretdinov,
14 F. Melo, J.P. Overington, E. Feyfant
15 University of California, San Francisco, USA
16 Rockefeller University, New York, USA
17 Harvard University, Cambridge, USA
18 Imperial Cancer Research Fund, London, UK
19 Birkbeck College, University of London, London, UK
20
21
22 Kind, OS, HostName, Kernel, Processor: 4, Windows Vista build 9200, DESKTOP-01DBIFR, SMP, unknown
23 Date and time of compilation : 2021/11/15 19:44:35
24 MODELLER executable type : x86_64-w64
25 Job starting time (YY/MM/DD HH:MM:SS): 2022/03/18 21:24:49
26
27
28 fndatmi_285W> Only 269 residues out of 270 contain atoms of type CA
29 (This is usually caused by non-standard residues, such
30 as ligands, or by PDB files with missing atoms.)
31 fndatmi_285W> Only 269 residues out of 270 contain atoms of type CA
32 (This is usually caused by non-standard residues, such
33 as ligands, or by PDB files with missing atoms.)
34
```

Fig22. Log file for script4



```

C:\Program Files\Modeller10.2\bin\rhodopsin\script4.log - Notepad++
File Edit Search View Encoding Language Settings Tools Macro Run Plugins Window ?
qseq.al1 script1.py script1.log script2.py script2.log script3.py script3.log qseq2bfkA.pap script4.py script4.log

3640 254 558G 558G N CA 4432 4433 161.88 174.60 8.50
3641 255 15981 558G 559M C N 4434 4436 -75.58 -73.00 3.75 0.24 -63.40 174.21 26.97
3642 255 559M 559M N CA 4436 4437 145.71 143.00 -40.50
3643 256 15983 560C 561L C N 4448 4450 -71.54 -70.70 6.86 0.49 -63.50 170.58 24.15
3644 256 561L 561L N CA 4450 4451 148.41 141.60 -41.20
3645
3646
3647 report_____> Distribution of short non-bonded contacts:
3648
3649
3650 DISTANCE1: 0.00 2.10 2.20 2.30 2.40 2.50 2.60 2.70 2.80 2.90 3.00 3.10 3.20 3.30 3.40
3651 DISTANCE2: 2.10 2.20 2.30 2.40 2.50 2.60 2.70 2.80 2.90 3.00 3.10 3.20 3.30 3.40 3.50
3652 FREQUENCY: 0 0 0 0 55 82 389 425 588 492 567 641 684 714
3653
3654
3655 << end of ENERGY.
3656
3657 >> Summary of successfully produced models:
3658 Filename molpdf DOPE score GA341 score
3659 -----
3660 qseq.B99990001.pdb 5123.33984 -39670.18359 0.69617
3661 qseq.B99990002.pdb 5371.25439 -39643.84766 0.70775
3662 qseq.B99990003.pdb 4576.40967 -39959.83984 0.92847
3663 qseq.B99990004.pdb 4718.91113 -38850.38672 0.95707
3664 qseq.B99990005.pdb 5054.84277 -39237.64063 0.79607
3665
3666 Total CPU time [seconds] : 219.75
3667

```

**Fig23. Structure with lowest DOPE score selected as final model**

## RESULT:

Modeller was used to predict the tertiary structure of Rhodopsin

## CONCLUSION:

Thus, modeller can be used to predict tertiary structures of proteins by comparative protein structure modelling. These tools give faster results than x-ray or NMR techniques and can be used by researchers to understand protein functions and drug designing.

## REFERENCES:

1. Xiong, J. (2008). Tertiary structure prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 214-228.
2. Encyclopædia Britannica, inc. (n.d.). *Rhodopsin*. Encyclopædia Britannica. Retrieved March 18, 2022, from <https://www.britannica.com/science/rhodopsin>
3. Uniprot. (n.d.). Retrieved March 18, 2022, from <https://www.uniprot.org/uniprot/Q15835.fasta>

## **WEBLEM 3b**

### **I-TASSER**

**(URL: <https://zhanggroup.org/I-TASSER/>)**

#### **AIM:**

To perform tertiary structure prediction by threading approach using I-TASSER server for query rhodopsin.

#### **INTRODUCTION:**

Rhodopsin, also called visual purple, pigment-containing sensory protein that converts light into an electrical signal. Rhodopsin is found in a wide range of organisms, from vertebrates to bacteria. In many seeing animals, including humans, it is required for vision in dim light and is located in the retina of the eye—specifically, within the tightly packed disks that make up the outer segment of the retina's photoreceptive rod cells, which are specially adapted for vision under low-light conditions.

I-TASSER server is an on-line platform that implements the I-TASSER based algorithms for protein structure and function predictions. It allows academic users to automatically generate high-quality model predictions of 3D structure and biological function of protein molecules from their amino acid sequences.

#### **METHODOLOGY:**

1. Open homepage for I-TASSER. (URL: <https://zhanggroup.org/I-TASSER/>)
2. Complete registration.
3. Submit FASTA sequence for kinase.
4. Observe and interpret results.

#### **OBSERVATION:**

UniProtKB - P02699 (OPSD\_BOVIN)

Display Help video BLAST Align Format Add to basket History

UniProtKB The new UniProt website is here! Take me to UniProt BETA

Entry

Protein Rhodopsin  
Gene RHO  
Organism *Bos taurus (Bovine)*  
Status Reviewed - Annotation score: 5/5 - Experimental evidence at protein level<sup>1</sup>

Function<sup>1</sup>

Photoreceptor required for image-forming vision at low light intensity. Required for photoreceptor cell viability after birth (By similarity).

Light-induced isomerization of 11-cis to all-trans retinal triggers a conformational change that activates signaling via G-proteins (PubMed:10926528, PubMed:12044163, PubMed:11972040, PubMed:16908857, PubMed:16586416, PubMed:17060607, PubMed:17449675, PubMed:18818650, PubMed:21389983, PubMed:22198838, PubMed:23579341, PubMed:25205354, PubMed:27458239).

Subsequent receptor phosphorylation mediates displacement of the bound G-protein alpha subunit by the arrestin SAG and terminates signaling (PubMed:1396673, PubMed:15111114).

By similarity 5 Publications 11 Publications

Sites

Feature key	Position(s)	Description	Actions	Graphical view	Length
Site <sup>1</sup>	113	Plays an important role in the conformation switch to the active conformation 3 Publications 1 Publication			1
Metal binding <sup>1</sup>	201 Zinc	Combined sources 2 Publications			1
Metal binding <sup>1</sup>	279 Zinc	Combined sources 2 Publications			1

GO - Molecular function<sup>1</sup>

- 11-cis retinal binding Source: UniProtKB
- arrestin family protein binding Source: CAFA
- G-protein alpha-subunit binding Source: UniProtKB
- G-protein-coupled photoreceptor activity Source: UniProtKB
- guanyl-nucleotide exchange factor activity Source: UniProtKB
- identical protein binding Source: IntAct
- opsin binding Source: CAFA

[View all biological processes](#)

Fig1. Result page for Rhodopsin in UniProt database

```
>sp|P02699|OPSD_BOVIN Rhodopsin OS=Bos taurus OX=9913 GN=RHO PE=1 SV=1
MNGTEGPNFYVPFSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLIMLGFPINFLTLY
VTQHKKLRTPLNYILLNLAVADLFMVFGGFTTLYTSLHGYFVFGPTGCNLEGFFATLG
GEIALWSLVLAIERYVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIP
EGMQCSCGIDYYTPHEETNNESFVIYMFVVFIIPLIVIFFCYGQLVFTVKEAAAQQQES
ATTQKAKEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTS
YNPVIYIMMNQFRNCMVTLCCGKNPLGDEASTVSKTETSQVAPA
```

Fig2. FASTA sequence for Rhodopsin

**Zhang Lab** 

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(The server completed predictions for 676386 proteins submitted by 163852 users from 159 countries)  
(The template library was updated on 2022/03/14)

**I-TASSER** (Iterative Threading ASSEmby Refinement) is a hierarchical approach to protein structure prediction and structure-based function annotation. It first identifies structural templates from the PDB by multiple threading approach **LOMETS**, with full-length atomic models constructed by iterative template-based fragment assembly simulations. Function insights of the target are then derived by re-threading the 3D models through protein function database **BioLP**. I-TASSER (as Zhang-Server) was ranked as the No 1 server for protein structure prediction in recent community-wide CASP7, CASP8, CASP9, CASP10, CASP11, CASP12, CASP13, and CASP14 experiments. It was also ranked the best for function prediction in CASP9. The server is in active development with the goal to provide the most accurate protein structure and function predictions using state-of-the-art algorithms. The server is only for non-commercial use. Please report problems and questions at [I-TASSER message board](#) and our developers will study and answer the questions accordingly. ([More about the server](#)...)

**Structure models for the SARS-CoV2 Coronavirus genome by C-I-TASSER**

[Queue] [Forum] [Download] [Search] [Registration] [Statistics] [Remove] [Potential] [Decoys] [News] [Annotation] [About] [FAQ]

**I-TASSER On-line Server** ([View an example of I-TASSER output](#)):

Copy and paste your sequence within [10, 1500] residues in FASTA format. [Click here for a sample input](#).

Or upload the sequence from your local computer:  
 [Choose File] [No file chosen]

Email: (mandatory, where results will be sent to)

Password: (mandatory, please click [here](#) if you do not have a password)

ID: (optional, your given name of the protein)

► [Option I: Assign additional restraints & templates to guide I-TASSER modeling](#).  
 ► [Option II: Exclude some templates from I-TASSER template library](#).  
 ► [Option III: Specify secondary structure for specific residues](#).

Keep my results public (uncheck this box if you want to keep your job private, and a key will be assigned for you to access the results. We received numerous requests from users who loss their key to access result. To save your time, please keep results public, or ensure you remember the key if you choose to keep job private)

[Run I-TASSER] [Clear form]  
 (Please submit a new job only after your old job is completed)

Waiting for www.google...

Fig3. Homepage for I-TASSAR

**Zhang Lab** 

Home Research COVID-19 Services Publications People Teaching Job Opening News Forum Lab Only

**I-TASSER**  
 Protein Structure & Function Predictions

(The server completed predictions for 676386 proteins submitted by 163852 users from 159 countries)  
(The template library was updated on 2022/03/14)

**I-TASSER** (Iterative Threading ASSEmby Refinement) is a hierarchical approach to protein structure prediction and structure-based function annotation. It first identifies structural templates from the PDB by multiple threading approach **LOMETS**, with full-length atomic models constructed by iterative template-based fragment assembly simulations. Function insights of the target are then derived by re-threading the 3D models through protein function database **BioLP**. I-TASSER (as Zhang-Server) was ranked as the No 1 server for protein structure prediction in recent community-wide CASP7, CASP8, CASP9, CASP10, CASP11, CASP12, CASP13, and CASP14 experiments. It was also ranked the best for function prediction in CASP9. The server is in active development with the goal to provide the most accurate protein structure and function predictions using state-of-the-art algorithms. The server is only for non-commercial use. Please report problems and questions at [I-TASSER message board](#) and our developers will study and answer the questions accordingly. ([More about the server](#)...)

**Structure models for the SARS-CoV2 Coronavirus genome by C-I-TASSER**

[Queue] [Forum] [Download] [Search] [Registration] [Statistics] [Remove] [Potential] [Decoys] [News] [Annotation] [About] [FAQ]

**I-TASSER On-line Server** ([View an example of I-TASSER output](#)):

Copy and paste your sequence within [10, 1500] residues in FASTA format. [Click here for a sample input](#).

Or upload the sequence from your local computer:  
 [Choose File] [No file chosen]

Email: (mandatory, where results will be sent to)  
 [gm.shamoni.anandas@gnhaisa.edu.in]

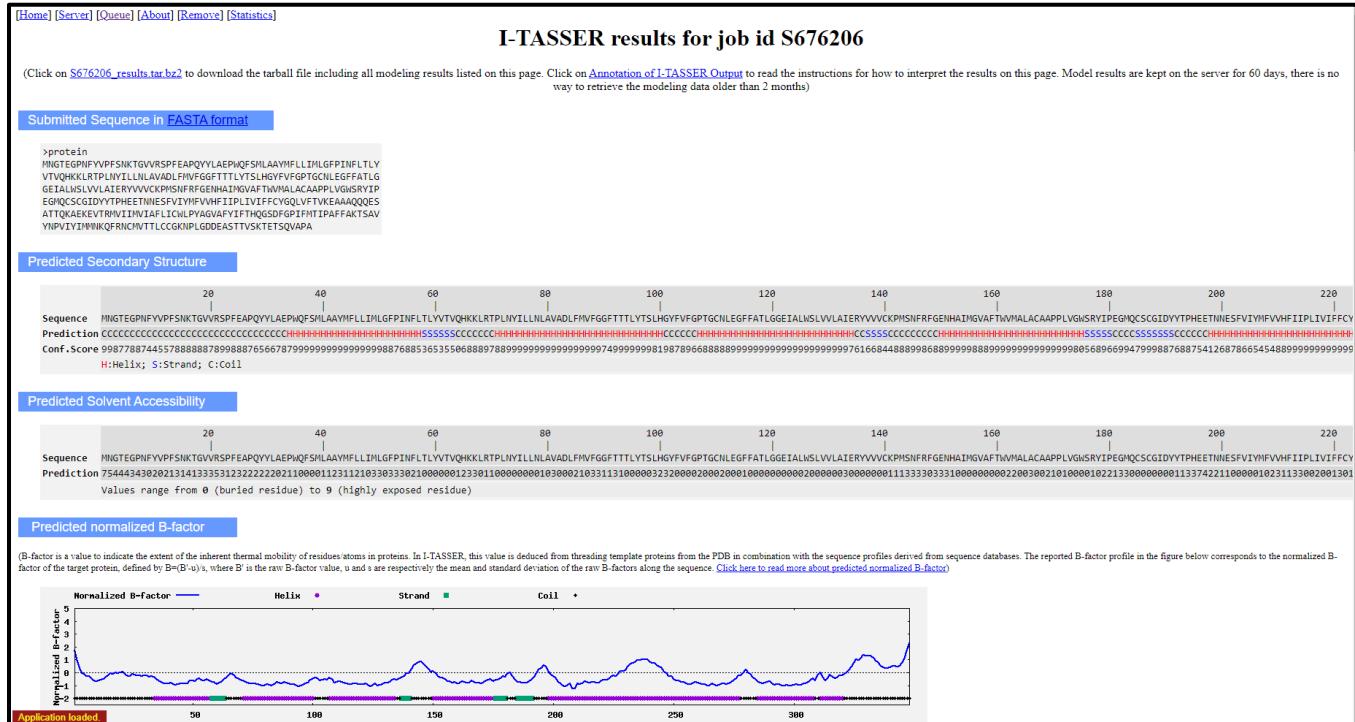
Password: (mandatory, please click [here](#) if you do not have a password)

ID: (optional, your given name of the protein)  
 [OPSD\_BOVIN]

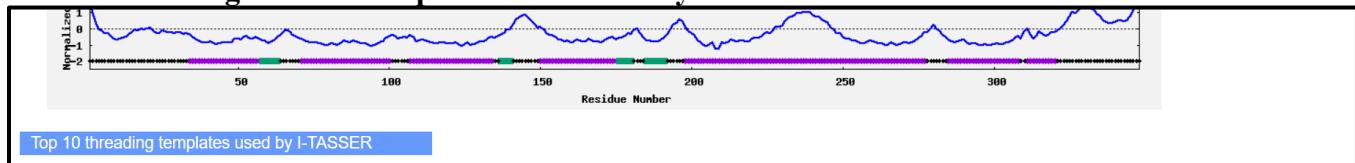
► [Option I: Assign additional restraints & templates to guide I-TASSER modeling](#).  
 ► [Option II: Exclude some templates from I-TASSER template library](#).  
 ► [Option III: Specify secondary structure for specific residues](#).

Keep my results public (uncheck this box if you want to keep your job private, and a key will be assigned for you to access the results. We received numerous requests from users who loss their key to access result. To save your time, please keep results public, or ensure you remember the key if you choose to keep job private)

Fig4. Submission of query



**Fig5. Result for predicted secondary structure and normalized B-factor**



Top 10 threading templates used by I-TASSER

(I-TASSER modeling starts from the structure templates identified by LOMETS from the PDB library. LOMETS is a meta-server threading approach containing multiple threading programs, where each threading program can generate tens of thousands of template alignments. I-TASSER only uses the templates of the highest significance in the threading alignments, the significance of which are measured by the Z-score, i.e. the difference between the raw and average scores in the unit of standard deviation. The templates in this section are the 10 best templates selected from the LOMETS threading programs. Usually, one template of the highest Z-score is selected from each threading program, where the threading programs are sorted by the average performance in the large-scale benchmark test experiments.)

Rank	PDB	Iden1	Iden2	Cov	Norm.	Download	20	40	60	80	100	120	140	
	Hit				Z-score	Align.								
<b>Sec.Str</b>														
<b>Seq</b>														
1	1gzmA	1.00	0.94	0.94	4.81	<a href="#">Download</a>	RNGTEGPNFYVPSNKTGVRSPEAQPOYYLAEPWQPSFLAAYMFLILMLQGFLPINTLTYLTVTQVHKKLRTPLNYLNLAVADLFMVGGFTTLLYTSLGHGYVFGPTGNCLEGFFATLGEGTALWSLVVLATERYVVKCPNSNFRGEH							
2	7gkR	0.19	0.19	0.83	1.89	<a href="#">Download</a>	-----DAFPNCEIDNGYDVLRLVNLINLAIAGNITLVLTSRYKLTVPRFLMCLFLSFADECGLYLLLIAVSQ-OTKQGYYNGSG-STAGEFTVFASELSVYTLTVTLEWHTIITYHQLKRLR							
3	2g87	1.00	1.00	1.00	1.24	<a href="#">Download</a>	RNGTEGPNFYVPSNKTGVRSPEAQPOYYLAEPWQPSFLAAYFLLILQGFLPINTLTYLTVTQVHKKLRTPLNYLNLAVADLFMVGGFTTLLYTSLGHGYVFGPTGNCLEGFFATLGEGTALWSLVVLATERYVVKCPNSNFRGEH							
4	2ped	1.00	1.00	1.00	0.77	<a href="#">Download</a>	RNGTEGPNFYVPSNKTGVRSPEAQPOYYLAEPWQPSFLAAYFLLILQGFLPINTLTYLTVTQVHKKLRTPLNYLNLAVADLFMVGGFTTLLYTSLGHGYVFGPTGNCLEGFFATLGEGTALWSLVVLATERYVVKCPNSNFRGEH							
5	2g87A	1.00	1.00	1.00	2.84	<a href="#">Download</a>	RNGTEGPNFYVPSNKTGVRSPEAQPOYYLAEPWQPSFLAAYFLLILQGFLPINTLTYLTVTQVHKKLRTPLNYLNLAVADLFMVGGFTTLLYTSLGHGYVFGPTGNCLEGFFATLGEGTALWSLVVLATERYVVKCPNSNFRGEH							
6	2ped	1.00	1.00	1.00	1.25	<a href="#">Download</a>	RNGTEGPNFYVPSNKTGVRSPEAQPOYYLAEPWQPSFLAAYFLLILQGFLPINTLTYLTVTQVHKKLRTPLNYLNLAVADLFMVGGFTTLLYTSLGHGYVFGPTGNCLEGFFATLGEGTALWSLVVLATERYVVKCPNSNFRGEH							
7	5wqDp	0.92	0.90	0.97	7.31	<a href="#">Download</a>	RNGTEGPNFYVPSNKTGVRSPEAQPOYYLAEPWQPSFLAAYFLLILQGFLPINTLTYLTVTQVHKKLRTPLNYLNLAVADLFMVGGFTTLLYTSLGHGYVFGPTGNCLEGFFATLGEGTALWSLVVLATERYVVKCPNSNFRGEH							
8	2g87A	1.00	1.00	1.00	3.21	<a href="#">Download</a>	RNGTEGPNFYVPSNKTGVRSPEAQPOYYLAEPWQPSFLAAYFLLILQGFLPINTLTYLTVTQVHKKLRTPLNYLNLAVADLFMVGGFTTLLYTSLGHGYVFGPTGNCLEGFFATLGEGTALWSLVVLATERYVVKCPNSNFRGEH							
9	7mRg	0.23	0.21	0.82	2.84	<a href="#">Download</a>	RNGTEGPNFYVPSNKTGVRSPEAQPOYYLAEPWQPSFLAAYFLLILQGFLPINTLTYLTVTQVHKKLRTPLNYLNLAVADLFMVGGFTTLLYTSLGHGYVFGPTGNCLEGFFATLGEGTALWSLVVLATERYVVKCPNSNFRGEH							
10	5wqDp	0.87	0.90	1.00	4.79	<a href="#">Download</a>	RNGTEGPNFYVPSNKTGVRSPEAQPOYYLAEPWQPSFLAAYFLLILQGFLPINTLTYLTVTQVHKKLRTPLNYLNLAVADLFMVGGFTTLLYTSLGHGYVFGPTGNCLEGFFATLGEGTALWSLVVLATERYVVKCPNSNFRGEH							

### Top 5 final models predicted by I-TASSER

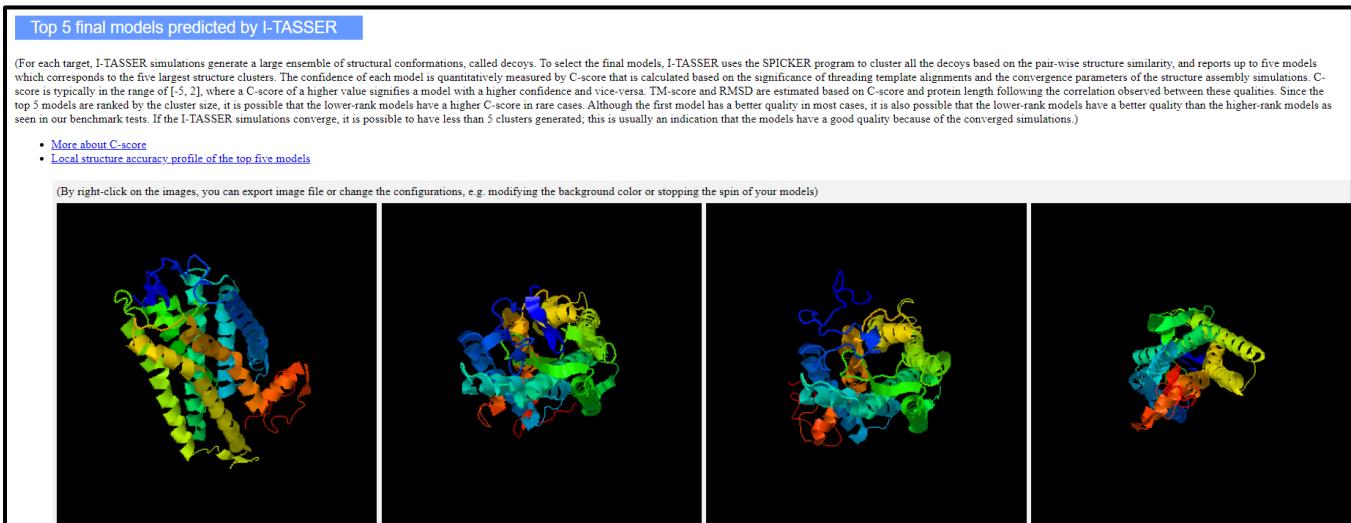
(For each target, I-TASSER simulates a large ensemble of structural conformations, called decoys. To select the final models, I-TASSER uses the SPICKER program to cluster all the decoys based on the pair-wise structure similarity, and reports up to five models which correspond to the five largest structure clusters. The confidence of each model is quantitatively measured by C-score, which is calculated based on the significance of threading template alignments and the convergence parameters of the structure assembly simulations. C-score is a measure of the quality of the predicted structure, where higher values indicate higher quality.)

Fig7. Result for top 10 threading templates

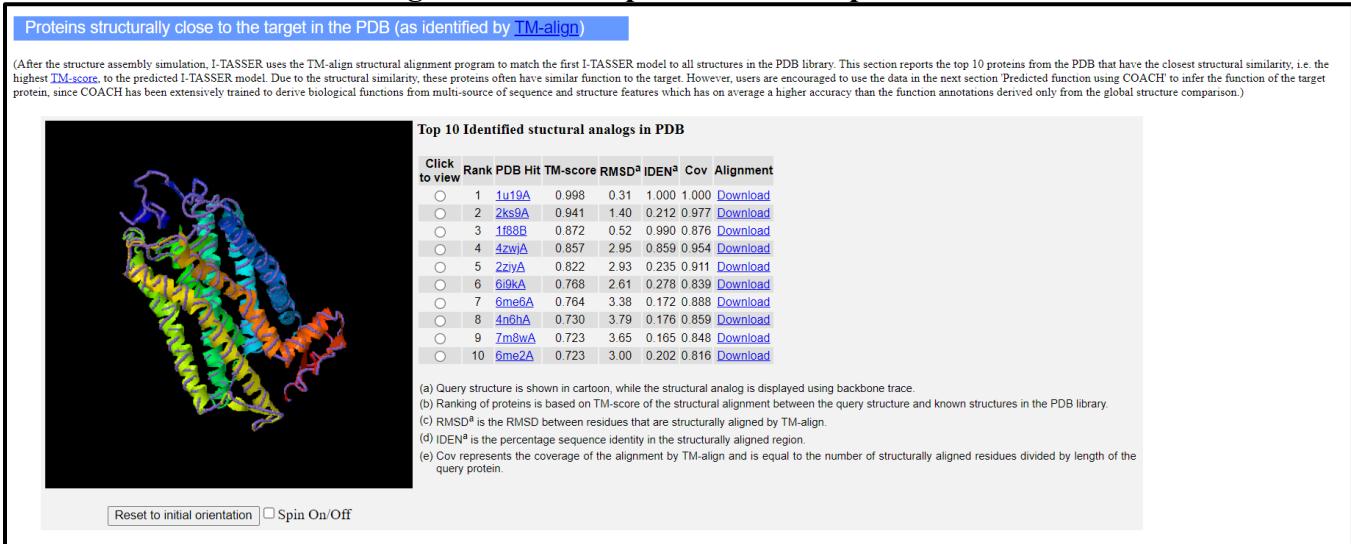
- Fig.4. Result for top 10 threading templates

  - a. All the residues are coloured in black; however, those residues in template which are identical to the residue in the query sequence are highlighted in colour. Colouring scheme is based on the property of amino acids, where polar are brightly coloured while non-polar residues are coloured in dark shade. (More about the colours used)
  - b. Rank of templates represents the top ten threading templates used by I-TASSER.
  - c. Iden1 is the percentage sequence identity of the templates in the threading aligned region with the query sequence.

- d. Iden2 is the percentage sequence identity of the whole template chains with query sequence.
- e. Cov represents the coverage of the threading alignment and is equal to the number of aligned residues divided by the length of query protein.
- f. Norm. Z-score is the normalized Z-score of the threading alignments. Alignment with a Normalized Z-score >1 mean a good alignment and vice versa.
- g. Download Align. provides the 3D structure of the aligned regions of the threading templates.
- h. The top 10 alignments reported above (in order of their ranking) are from the following threading programs: 1: FFAS-3D 2: SPARKS-X 3: HHSEARCH2 4: HHSEARCH I 5: Neff-PPAS 6: HHSEARCH 7: pGenTHREADER 8: wdPPAS 9: PROSPECT2 10: SP3



**Fig8. Result for top 5 final models predicted**



**Fig9. Result for proteins that are structurally close to target**

- a. Query structure is shown in cartoon, while the structural analog is displayed using backbone trace.
- b. Ranking of proteins is based on TM-score of the structural alignment between the query structure and known structures in the PDB library
- c. RMSDa is the RMSD between residues that are structurally aligned by TM-align
- d. IDENa is the percentage sequence identity in the structurally aligned region.

- e. Cov represents the coverage of the alignment by TM-align and is equal to the number of structurally aligned residues divided by length of the query protein.

**Predicted function using COFACTOR and COACH**

(This section reports biological annotations of the target protein by COFACTOR and COACH based on the iTASSER structure prediction. While COFACTOR deduces protein functions (ligand-binding sites, EC and GO) using structure comparison and protein-protein networks, COACH is a meta-server approach that combines multiple function annotation results (on ligand-binding sites) from the COFACTOR, TM-SITE and S-SITE programs.)

**Ligand binding sites**

Click to view Rank C-score Cluster size PDB Hit Lig Name Download Complex Ligand Binding Site Residues

<input checked="" type="radio"/>	1	0.64	89	3oaxB	RET	Rep. Mult	113,117,118,121,122,186,187,188,189,191,207,212,261,265,268,269,292,296
<input type="radio"/>	2	0.06	7	1gzmA	CBE	Rep. Mult	40,43,267,290,291,294
<input type="radio"/>	3	0.04	9	4a4mA	PEPTIDE	Rep. Mult	71,135,138,230,238,239,245,310,311,312
<input type="radio"/>	4	0.04	20	3zgqA	Y01	Rep. Mult	69,74,78,81,119,150,154,157,161
<input type="radio"/>	5	0.03	7	4ldeA	1WV	Rep. Mult	44,47,98,289,293

Download the residue-specific ligand binding probability, which is estimated by SVM.  
Download the all possible binding ligands and detailed prediction summary.  
Download the templates clustering results.

(a) C-score is the confidence score of the prediction. C-score ranges [0-1], where a higher score indicates a more reliable prediction.  
(b) Cluster size is the total number of templates in a cluster.  
(c) Lig Name is name of possible binding ligand. Click the name to view its information in the BioLiP database.  
(d) Rep is a single complex structure with the most representative ligand in the cluster, i.e., the one listed in the Lig Name column.  
Mult is the complex structures with all potential binding ligands in the cluster.

Reset to initial orientation  Spin On/Off

**Fig10. Result for predicted fuctions**

- C-score is the confidence score of the prediction. C-scores ranges [0-1], where a higher score indicated a more reliable prediction.
- Cluster size is the total number of templates in a cluster.
- Lig Name is name of possible binding ligand. Click the name to view its information in the BioLiP database.
- Rep is a single complex structure with the most representative ligand in the cluster, i.e., the one listed in the Lig Name column. Mult is the complex structures with all potential binding ligands in the cluster.

**Enzyme Commission (EC) numbers and active sites**

Click to view Rank Cscore<sup>EC</sup> PDB Hit TM-score RMSD<sup>a</sup> IDEN<sup>a</sup> Cov EC Number Active Site Residues

<input type="radio"/>	1	0.348	3d4sA	0.690	3.34	0.212	0.787	<a href="#">3.2.1.17</a>	NA
<input type="radio"/>	2	0.254	2occN	0.456	5.90	0.051	0.695	<a href="#">1.9.3.1</a>	NA
<input type="radio"/>	3	0.254	1xmeA	0.472	5.83	0.051	0.727	<a href="#">1.9.3.1</a>	NA
<input type="radio"/>	4	0.253	1occA	0.456	5.89	0.048	0.695	<a href="#">1.9.3.1</a>	NA
<input type="radio"/>	5	0.242	1m56A	0.473	5.13	0.038	0.649	<a href="#">1.9.3.1</a>	NA

Click on the radio buttons to visualize predicted active site residues.

(a) Cscore<sup>EC</sup> is the confidence score for the EC number prediction. Cscore<sup>EC</sup> values range in between [0-1], where a higher score indicates a more reliable EC number prediction.  
(b) TM-score is a measure of global structural similarity between query and template protein.  
(c) RMSD<sup>a</sup> is the RMSD between residues that are structurally aligned by TM-align.  
(d) IDEN<sup>a</sup> is the percentage sequence identity in the structurally aligned region.  
(e) Cov represents the coverage of global structural alignment and is equal to the number of structurally aligned residues divided by length of the query protein.

Reset to initial orientation  Spin On/Off

**Fig11. Enzyme commission (EC) numbers and active sites**

- Cscore<sup>EC</sup> is the confidence score for the EC number prediction. Cscore<sup>EC</sup> values range in between [0-1]; where a higher score indicates a more reliable EC number prediction.
- TM-score is a measure of global structural similarity between query and template protein.

- c. RMSDa is the RMSD between residues that are structurally aligned by TM-align.
- d. IDENa is the percentage sequence identity in the structurally aligned region.
- e. Cov represents the coverage of global structural alignment and is equal to the number of structurally aligned residues divided by length of the query protein.

Gene Ontology (GO) terms							
Top 10 homologous GO templates in PDB							
Rank	Cscore <sup>GO</sup>	TM-score	RMSD <sup>a</sup>	IDEN <sup>a</sup>	Cov	PDB Hit	Associated GO Terms
1	0.74	0.9980	0.31	1.00	1.00	1u19A	GO:0018298 GO:0046872 GO:0004930 GO:0007601 GO:0009583 GO:0001750 GO:0009881 GO:0007602 GO:0050953 GO:0016021 GO:0050896 GO:0007165 GO:0004871 GO:0007186 GO:0004872 GO:0005515 GO:0009416 GO:0005886 GO:0016020 GO:0060342 GO:0042622 GO:0006468 GO:0001917
2	0.61	0.8715	0.52	0.99	0.88	1f88B	GO:0046872 GO:0018298 GO:0007186 GO:0050953 GO:0004872 GO:0009583 GO:0005515 GO:0016021 GO:0009416 GO:0009881 GO:0005886 GO:0050896 GO:0016020 GO:0007601 GO:0060342 GO:0007165 GO:0042622 GO:0007602 GO:0006468 GO:0004871 GO:0001917 GO:0001750 GO:0004930
3	0.47	0.6974	3.16	0.19	0.80	2y0B	GO:0004935 GO:0007186 GO:0016021 GO:0071875 GO:0004940
4	0.45	0.9412	1.40	0.21	0.98	2ks9A	GO:0004995 GO:0005886 GO:0007186 GO:0016021
5	0.41	0.8215	2.93	0.23	0.91	2zjyA	GO:0004871 GO:0016021 GO:0007601 GO:0018298 GO:0007186 GO:0007602 GO:0004872 GO:0009881 GO:0007165 GO:0004930 GO:0050896 GO:0016020
6	0.40	0.6716	3.20	0.21	0.77	3p0gA	GO:0016998 GO:0016787 GO:0003824 GO:0009253 GO:0003796 GO:0016798 GO:0008152 GO:0042742 GO:0019835 GO:0007186 GO:0016021
7	0.37	0.6573	3.46	0.18	0.78	2vdA	GO:0001609 GO:0001973 GO:0007186 GO:0016021
8	0.36	0.6969	2.76	0.19	0.78	3rzaE	GO:0005737 GO:0004872 GO:0007186 GO:0016021 GO:0010894 GO:0042742 GO:0008152 GO:0016798 GO:0003796 GO:0019835 GO:0003824 GO:0009253 GO:0016787 GO:0016998 GO:0004930 GO:0009629 GO:0045907 GO:0005887 GO:0045429 GO:0006954 GO:0005730 GO:0004969 GO:0051381 GO:0007165 GO:0007200 GO:0004871 GO:0005634 GO:0016020 GO:0005624 GO:0007288 GO:0005886
9	0.35	0.6937	3.31	0.20	0.80	2rh1A	GO:0003796 GO:0007186 GO:0009253 GO:0016021 GO:0016998 GO:0042742 GO:0008152 GO:0016798 GO:0003824 GO:0019835 GO:0003796 GO:0009253 GO:0042742 GO:0007186 GO:0016021
10	0.34	0.6847	3.01	0.27	0.77	3pb1A	GO:0019835 GO:0016998 GO:0016787 GO:0008152 GO:0003824 GO:0003796 GO:0009253 GO:0042742 GO:0007186 GO:0016021

**Fig12. Gene Ontology (GO) terms**

- a. CscoreGO is a combined measure for evaluating global and local similarity between query and template protein. It's range is [0-1] and higher values indicate more confident predictions.
- b. TM-score is a measure of global structural similarity between query and template protein.
- c. RMSDa is the RMSD between residues that are structurally aligned by TM-align.
- d. IDENa is the percentage sequence identity in the structurally aligned region.
- e. Cov represents the coverage of global structural alignment and is equal to the number of structurally aligned residues divided by length of the query protein.
- f. The second table shows a consensus GO terms amongst the top scoring templates. The GO-Score associated with each prediction is defined as the average weight of the GO term, where the weights are assigned based on CscoreGO of the template.

## RESULT:

I-TASSER was used to predict the tertiary structure of Kinase based on threading approach. The information regarding solvent accessibility, normalized B-factor, top 10 threading templates, top 5 final models, proteins that are structurally close to target, functions and active sites were predicted.

## CONCLUSION:

Thus, I-TASSER can be used to predict tertiary structures of proteins by threading method. These tools give faster results than x-ray or NMR techniques and can be used by researchers to understand protein functions and drug designing.

## REFERENCES:

1. Xiong, J. (2008). Tertiary structure prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 214-228.
2. kinase | Definition, Biology, & Function. (n.d.). Encyclopedia Britannica. Retrieved March 8, 2022, from <https://www.britannica.com/science/kinase>
3. I-TASSER server for protein structure and function prediction. (n.d.-b). Zhanggroup.org. Retrieved March 8, 2022, from <https://zhanggroup.org/I-TASSER/>

4. I-TASSER results. (n.d.). Zhanggroup.org. Retrieved March 8, 2022, from <https://zhanggroup.org/I-TASSER/output/S673761/>

**WEBLEM 3c**  
**ROBETTA**  
(URL: <https://robbetta.bakerlab.org/>)

**AIM:**

To perform tertiary structure prediction by Ab-Initio approach using ROBETTA server for query Rhodopsin.

**INTRODUCTION:**

Rhodopsin, also called visual purple, pigment-containing sensory protein that converts light into an electrical signal. Rhodopsin is found in a wide range of organisms, from vertebrates to bacteria. In many seeing animals, including humans, it is required for vision in dim light and is located in the retina of the eye—specifically, within the tightly packed disks that make up the outer segment of the retina's photoreceptive rod cells, which are specially adapted for vision under low-light conditions.

The Robetta server provides automated tools for protein structure prediction and analysis. For structure prediction, sequences submitted to the server are parsed into putative domains and structural models are generated using either comparative modeling or de novo structure prediction methods. If a confident match to a protein of known structure is found using BLAST, PSI-BLAST, FFAS03 or 3D-Jury, it is used as a template for comparative modeling. If no match is found, structure predictions are made using the de novo Rosetta fragment insertion method. Experimental nuclear magnetic resonance (NMR) constraints data can also be submitted with a query sequence for RosettaNMR de novo structure determination. Other current capabilities include the prediction of the effects of mutations on protein–protein interactions using computational interface alanine scanning. The Rosetta protein design and protein–protein docking methodologies will soon be available through the server as well.

**METHODOLOGY:**

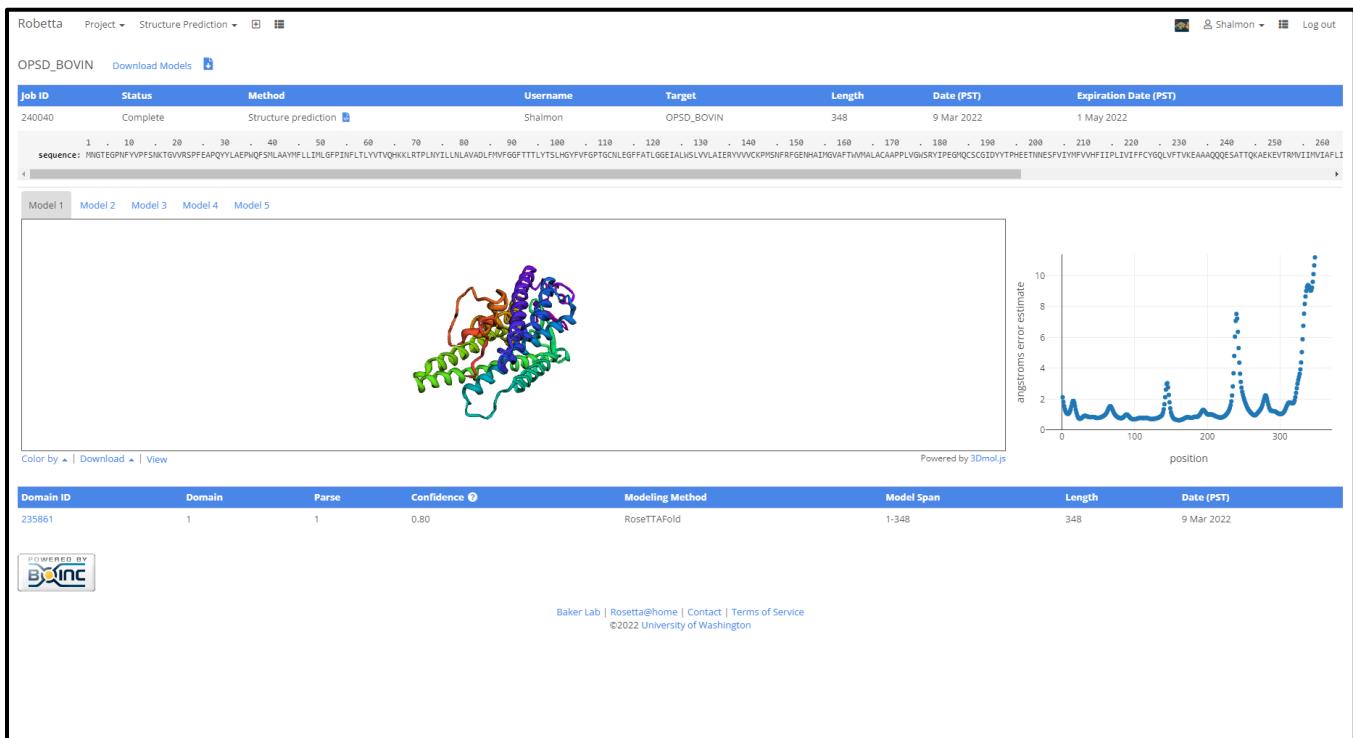
1. Open homepage for Robetta (URL: <https://robbetta.bakerlab.org/>)
2. Complete registration
3. Submit FASTA sequence for kinase.
4. Observe and interpret results.

## OBSERVATION:

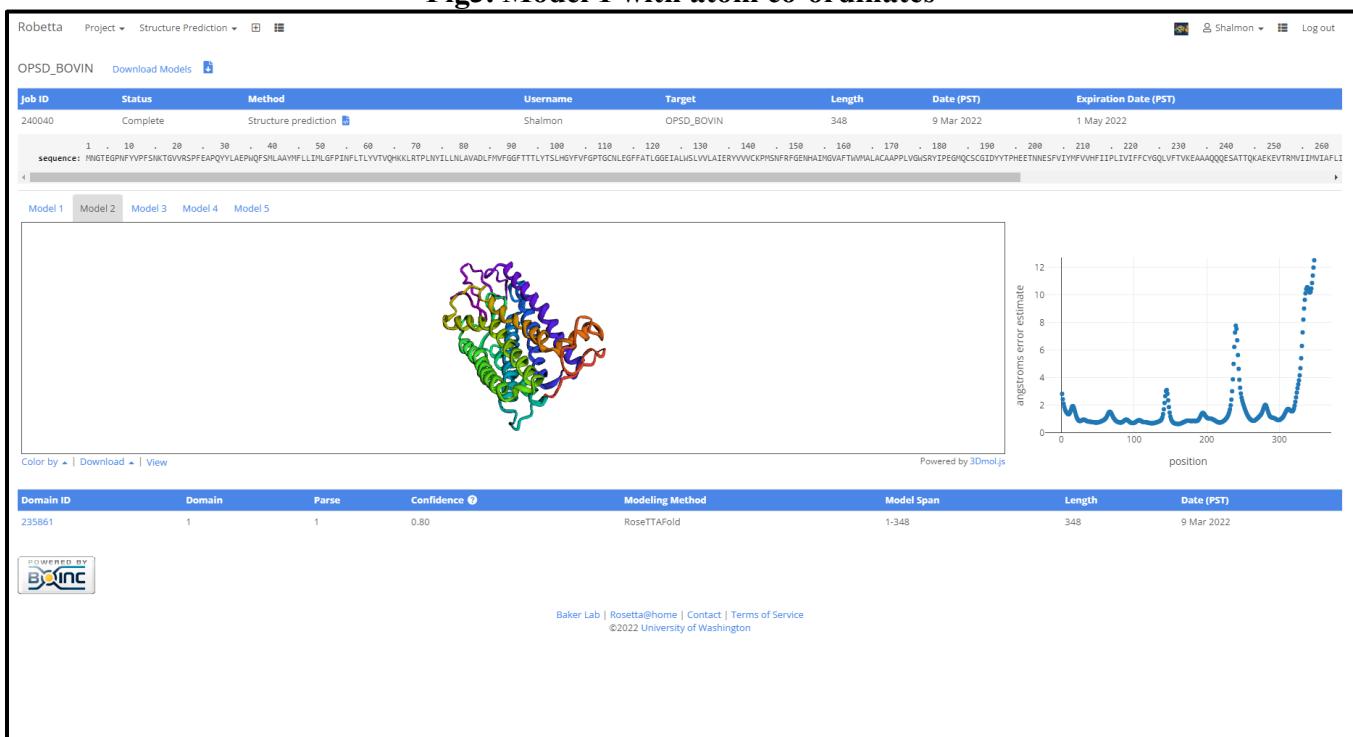
Fig1. Result page for Rhodopsin in UniProt database

```
>sp|P02699|OPSD_BOVIN Rhodopsin OS=Bos taurus OX=9913 GN=RHO PE=1 SV=1
MNGTEGPNFYVPFSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLIMLGFPINFLTLY
VTQHQKKLRTPLNYILLNLAVADLFMVFGGFTTLYTSLHGYFVFGPTGCNLEGFFATLG
GEIALWSLVLAIERYVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIP
EGMQCSCGIDYYTPHEETNNESFVIYMFVVFIIPLIVIFFCYGQLVFTVKEAAAQQQES
ATTQKAEKEVTRMVIIMVIAFLICWLPHYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAV
YNPVIYIMMNKQFRNCMVTLCCGKNPLGDEASTTVSKTETSQVAPA
```

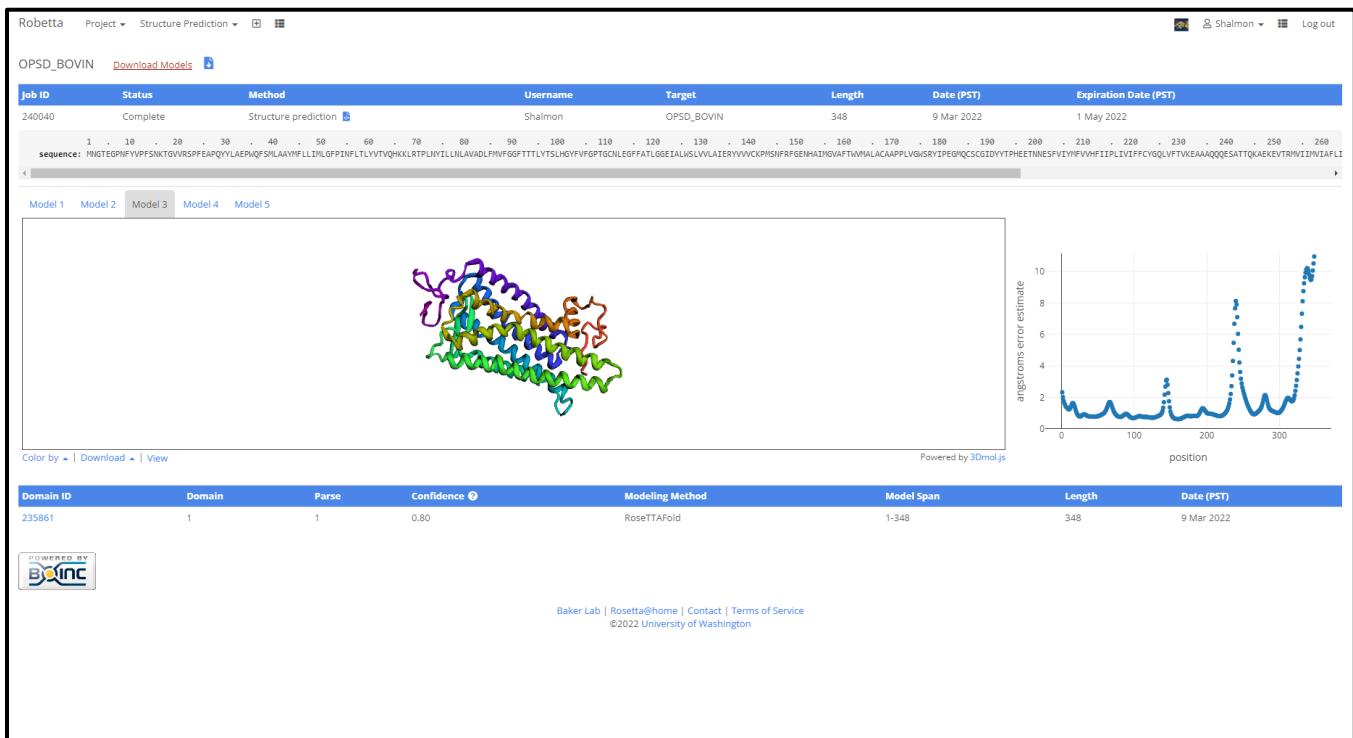
Fig2. FASTA sequence for Rhodopsin



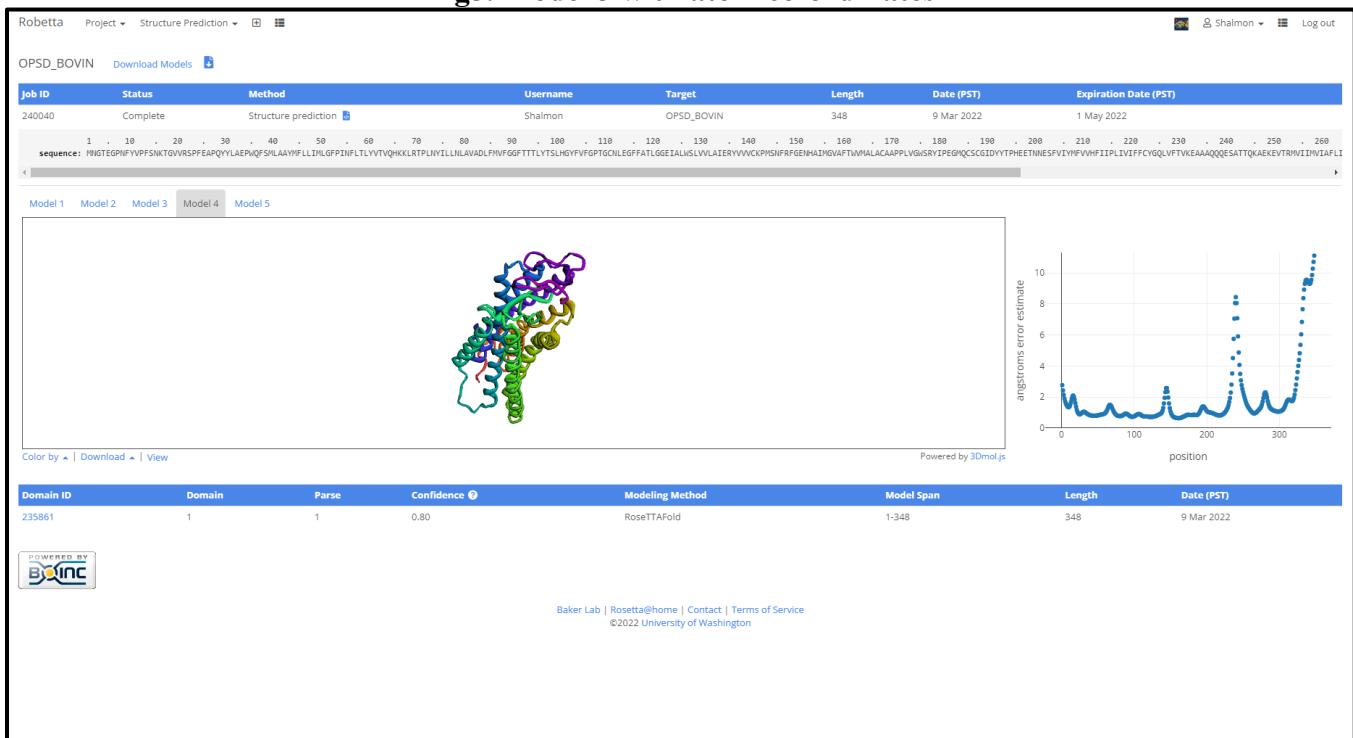
**Fig3. Model 1 with atom co-ordinates**



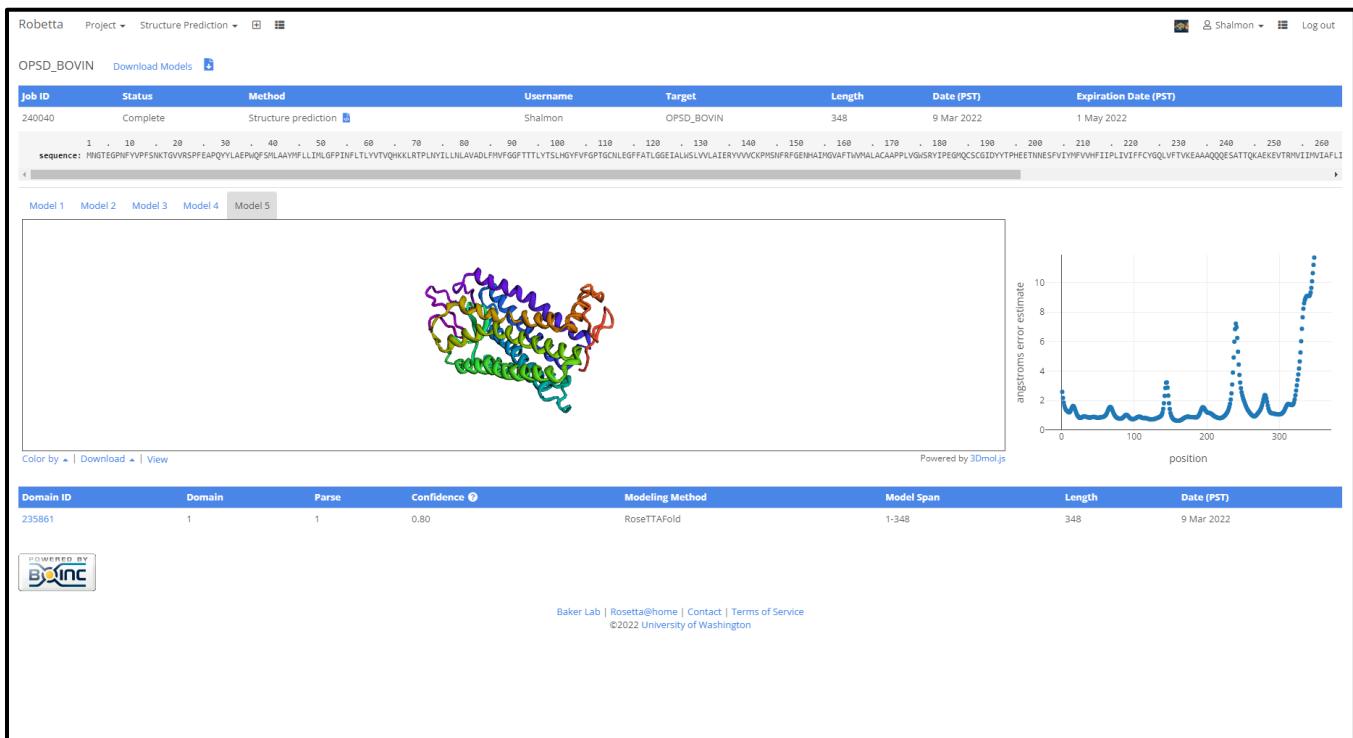
**Fig4. Model 2 with atom co-ordinates**



**Fig5. Model 3 with atom co-ordinates**



**Fig6. Model 4 with atom co-ordinates**



**Fig7. Model 5 with atom co-ordinates**

## RESULT:

Robetta was used to predict the tertiary structure of Rhodopsin based on ab-initio approach.

## CONCLUSION:

Thus, Robetta can be used to predict tertiary structures of proteins by ab-initio method. These tools give faster results than x-ray or NMR techniques and can be used by researchers to understand protein functions and drug designing.

## REFERENCES:

1. Xiong, J. (2008). Tertiary structure prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 214-228.
2. Encyclopædia Britannica, inc. (n.d.). *Rhodopsin*. Encyclopædia Britannica. Retrieved March 18, 2022, from <https://www.britannica.com/science/rhodopsin>
3. Robetta (2021b). Bakerlab.org. Retrieved March 18, 2022, from <https://robbetta.bakerlab.org/results.php?id=240040>

## WEBLEM 4

### Introduction to Validation server – SAVES server

Homology model, threading method and ab-initio method of tertiary structure prediction all have to be evaluated to make sure that the structural features of the model are consistent with the physicochemical rules. This involves checking anomalies in  $\phi$ - $\psi$  angles, bond lengths, close contacts, and so on. Another way of checking the quality of a protein model is to implicitly take these stereochemical properties into account. This is a method that detects errors by compiling statistical profiles of spatial features and interaction energy from experimentally determined structures. By comparing the statistical parameters with the constructed model, the method reveals which regions of a sequence appear to be folded normally and which regions do not. If structural irregularities are found, the region is considered to have errors and has to be further refined.

#### **SAVES server:**

SAVES server contains various tools for structure validation that are all integrated in one single server. The tool available are:

#### **ERRAT:**

A novel method for differentiating between correctly and incorrectly determined regions of protein structures based on characteristic atomic interaction is described. Different types of atoms are distributed nonrandomly with respect to each other in proteins. Errors in model building lead to more randomized distributions of the different atom types, which can be distinguished from correct distributions by statistical methods. Atoms are classified in one of three categories: carbon (C), nitrogen (N), and oxygen (O). This leads to six different combinations of pairwise noncovalently bonded interactions (CC, CN, CO, NN, NO, and OO). A quadratic error function is used to characterize the set of pairwise interactions from nine-residue sliding windows in a database of 96 reliable protein structures. Regions of candidate protein structures that are mistraced or misregistered can then be identified by analysis of the pattern of nonbonded interactions from each window.

Errat is a program for verifying protein structures determined by crystallography. Error values are plotted as a function of the position of a sliding 9-residue window. The error function is based on the statistics of non- bonded atom-atom interactions in the reported structure (compared to a database of reliable high-resolution structures).

A plot of an initial model and a final model is retrieved. Regions of the structure that can be rejected at the 95% confidence level are yellow; 5% of a good protein structure is expected to have an error value above this level. Regions that can be rejected at the 99% level are shown in red. Generally speaking, the method is sensitive to smaller errors than 3-D Profile analysis.

#### **Verify3D:**

It is another server using the statistical approach. It uses a precomputed database containing eighteen environmental profiles based on secondary structures and solvent exposure, compiled from high-resolution protein structures. To assess the quality of a protein model, the secondary structure and solvent exposure propensity of each residue are calculated. It determines the compatibility of an atomic model (3D) with its own amino acid sequence (1D) by assigning a structural class based on its location and environment (alpha, beta, loop, polar, nonpolar etc) and comparing the results to good structures. If the parameters of a residue fall within one of the profiles, it receives a high score, otherwise a low score. The result is a two-dimensional graph illustrating the folding quality of each residue of the protein structure. The threshold value is normally set at zero. Residues with scores below zero are considered to have an unfavourable environment.

#### **PROVES:**

It calculates the volumes of atoms in macromolecules using an algorithm which treats the atoms like hard spheres and calculates a statistical Z-score deviation for the model from highly resolved (2.0 Å or better) and refined (R-factor of 0.2 or better) PDB-deposited structures.

Standard ranges of atomic and residue volumes are computed in 64 highly resolved and well-refined protein crystal structures using the classical Voronoi procedure. Deviations of the atomic volumes from the standard values, evaluated as the volume Z-scores, are used to assess the quality of protein crystal structures. To score a structure globally, we compute the volume Z-score root mean square deviation (Z-score rms), which measures the average magnitude of the volume irregularities in the structure. We find that the Z-score rms decreases as the resolution and R-factor improve, consistent with the fact that these improvements generally reflect more accurate models. From the Z-score rms distribution in structures with a given resolution or R-factor, we determine the normal limits in Z-score rms values for structures solved at that resolution or R-factor. Structures whose Z-score rms exceeds these limits are considered as outliers. Such structures also exhibit unusual stereochemistry, as revealed by other analyses. Absolute Z-scores of individual atoms are used to identify problems in specific regions within a protein model. These Z-scores correlate fairly well with the atomic B-factors, and atoms having absolute Z-scores  $> 3$ , occur at or near regions in the model where programs such as PROCHECK identify unusual stereochemistry. Atomic volumes, themselves not directly restrained in crystallographic refinement, can thus provide an independent, rather sensitive, measure of the quality of a protein structure.

### **WHAT\_CHECK:**

Derived from a subset of protein verification tools from the WHAT IF program, this does extensive checking of many stereochemical parameters of the residues in the model. WHAT IF is a comprehensive protein analysis server that validates a protein model for chemical correctness. It has many functions, including checking of planarity, collisions with symmetry axes (close contacts), proline puckering, anomalous bond angles, and bond lengths. It also allows the generation of Ramachandran plots as an assessment of the quality of the model.

### **PROCHECK:**

It is a UNIX program that is able to check general physicochemical parameters such as  $\phi$ - $\psi$  angles, chirality, bond lengths, bond angles, and so on. It checks the stereochemical quality of a protein structure by analyzing residue-by-residue geometry and overall structure geometry. The parameters of the model are used to compare with those compiled from well-defined, high-resolution structures. If the program detects unusual features, it highlights the regions that should be checked or refined further.

### **CRYST:**

This program searches the Protein Data Bank for entries that have a unit cell similar to your input file. CRYST1 record required. Use the standalone CRYST server for more options.

The assessment results can be different using different verification programs. Because no single method is clearly superior to any other, a good strategy is to use multiple verification methods and identify the consensus between them. It is also important to keep in mind that the evaluation tests performed by these programs only check the stereochemical correctness, regardless of the accuracy of the model, which may or may not have any biological meaning. Thus, SAVES server is an excellent platform that provides various validation methods to accurately validate the structures.

### **REFERENCES:**

1. SAVESv6.0 - Structure Validation Server. (n.d.-b). Saves.mbi.ucla.edu. Retrieved March 8, 2022, from <https://saves.mbi.ucla.edu/>
2. ERRAT – UCLA-DOE Institute. (n.d.). Retrieved March 8, 2022, from <https://www.doembi.ucla.edu/errat/>
3. Chris Colovos; Todd O. Yeates (1993). Verification of protein structures: Patterns of nonbonded atomic interactions. , 2(9), 1511–1519. doi:10.1002/pro.5560020916

4. Xiong, J. (2008). Tertiary structure prediction. *Essential bioinformatics*. Cambridge: Cambridge University Press. 220-222.
5. Joan Pontius; Jean Richelle; Shoshana J. Wodak (1996). Deviations from Standard Atomic Volumes as a Quality Measure for Protein Crystal Structures. , 264(1), 0–136. doi:10.1006/jmbi.1996.0628

DATE: 10-03-22

## WEBLEM 4a SAVES server (URL: <https://saves.mbi.ucla.edu/>)

## AIM:

To validate structure qseq.B99990005 generated from modeller.

## Introduction:

qseq.B99990005 is the structure predicted using homology modelling using modeller. The structure has to be evaluated to make sure that the structural features of the model are consistent with the physicochemical rules. This can be done using SAVES server.

SAVES is a structure validation server that has various tools like Errat, Verify3D, Prove, Whatcheck, Procheck, and Cryst integrated in one single platform. This involves checking anomalies in  $\phi$ - $\psi$  angles, bond lengths, close contacts, and so on. Another way of checking the quality of a protein model is to implicitly take these stereochemical properties into account. This is a method that detects errors by compiling statistical profiles of spatial features and interaction energy from experimentally determined structures. By comparing the statistical parameters with the constructed model, the method reveals which regions of a sequence appear to be folded normally and which regions do not. If structural irregularities are found, the region is considered to have errors and has to be further refined.

## METHODOLOGY:

1. Open homepage for SAVES server. (URL: <https://saves.mbi.ucla.edu/>)
  2. Upload structure retrieved from Modeller in PDB format.
  3. Obtain results for Errat, Verify3D, Prove, Whatcheck and Procheck.
  4. Observe and interpret the results.

## OBSERVATION:

**UCLA-DOE LAB — SAVES v6.0**

To run any or all programs:  
upload your structure, in PDB format only

No file chosen

---

## References

ERRAT

- Reference: Verification of protein structures: patterns of nonbonded atomic interactions, Colovos C and Yeates TO, 1993.
- C++ software

VERIFY 3D

- Profile Search Software [Bowie et al., 1991, Luehly et al., 1992].
- DSSP original and Wikipedia

PROVE

- Reference: Deviations from standard atomic volumes as a quality measure for protein crystal structures, Pontius J, Richelle J, Wodak SJ. 1996

PROCHECK

- PROCHECK source information
- Result analysis

Fig1. Homepage for SAVES server

## UCLA-DOE LAB — SAVES v6.0

UCLA

To run any or all programs:  
upload your structure, in PDB format only

qseq.B99990005.pdb

Customize job name:

qseq.B99990005.pdb

### References

#### ERRAT

- Reference: Verification of protein structures: patterns of nonbonded atomic interactions, Colovos C and Yeates TO, 1993.
- C++ software

#### VERIFY 3D

- Profile Search Software [Bowie et al., 1991, Luethy et al., 1992].
- DSSP original and Wikipedia

#### PROVE

- Reference: Deviations from standard atomic volumes as a quality measure for protein crystal structures, Pontius J, Richelle J, Wodak SJ, 1996

#### PROCHECK

**Fig2. Structure from Modeller for validation**

## UCLA-DOE LAB — SAVES v6.0

UCLA

Job 937164 has been created

**job #937164: qseq.B99990005.pdb [job link] [3D Viewer]**

**ERRAT** Complete

Overall Quality Factor

**16.1491**

**VERIFY** Complete

51.33% of the residues have averaged 3D/1D score  $\geq 0.2$

**Fail**

**PROVE** Complete

Buried outlier protein atoms total from 1 Model: 11.2%

**fail**

**WHATCHECK** Complete

1 2 3 4 5 6 7 8 9 10 11 12 13  
14 15 16 17 18 19 20 21 22 23  
24 25 26 27 28 29 30 31 32 33  
34 35 36 37 38 39 40 41 42 43  
44 45 46 47

**PROCHECK** Complete

Out of 8 evaluations

- Errors: 5
- Warnings: 1
- Pass: 2

Almost ready, check back soon

### References

**Fig3. Result page for structure validation for various servers**

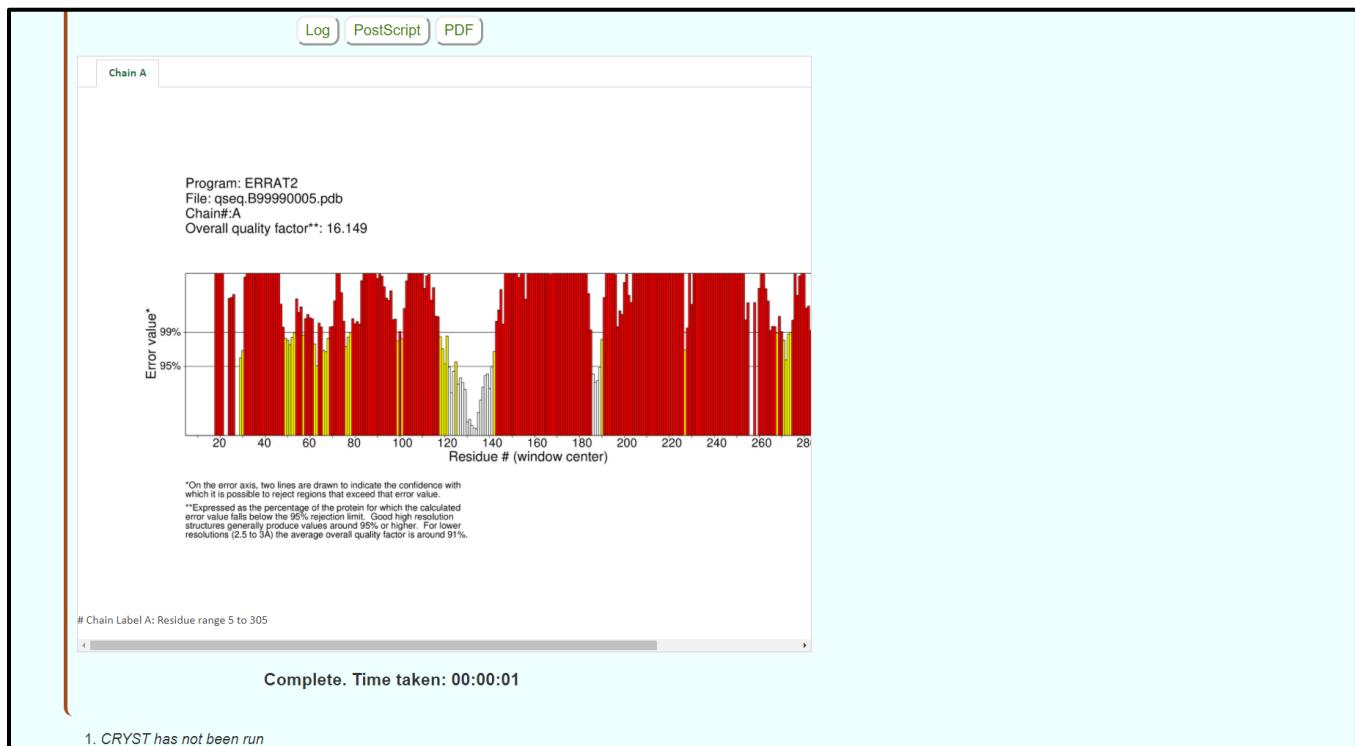


Fig4. Result page for ERRAT

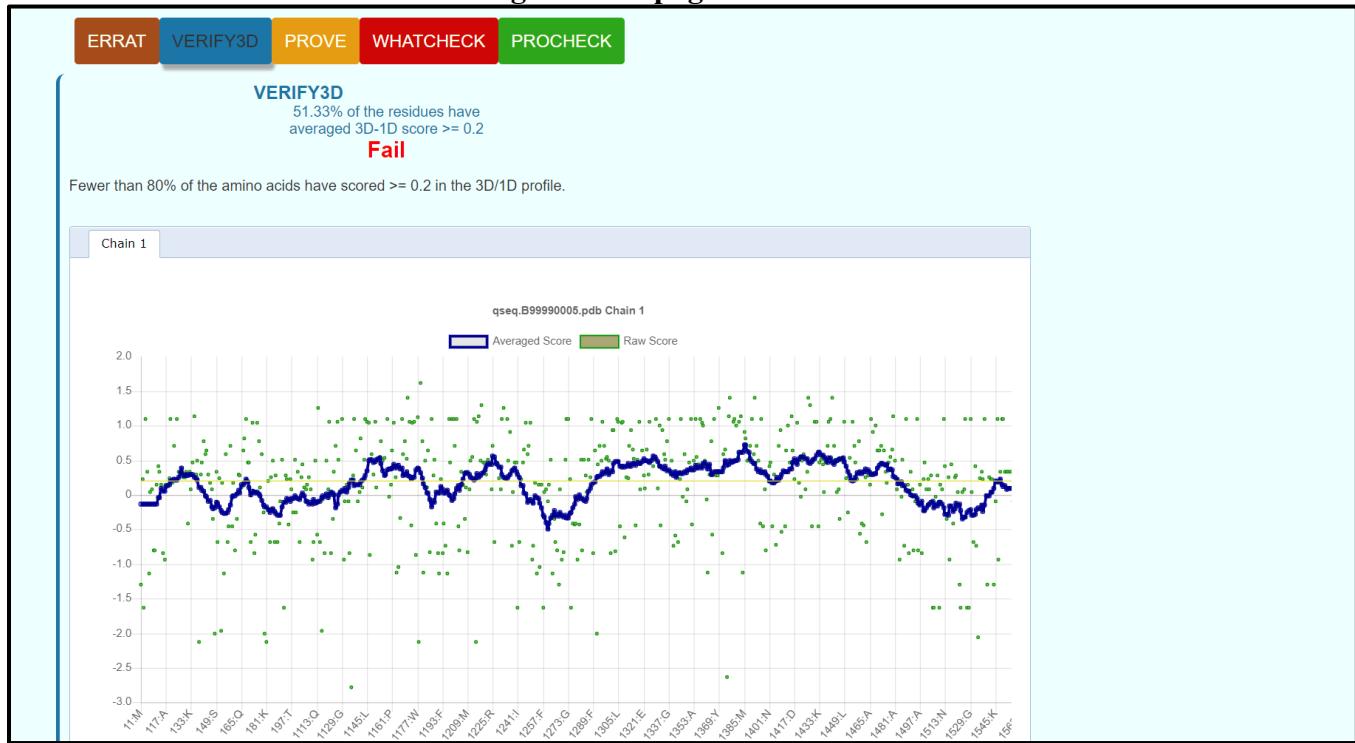
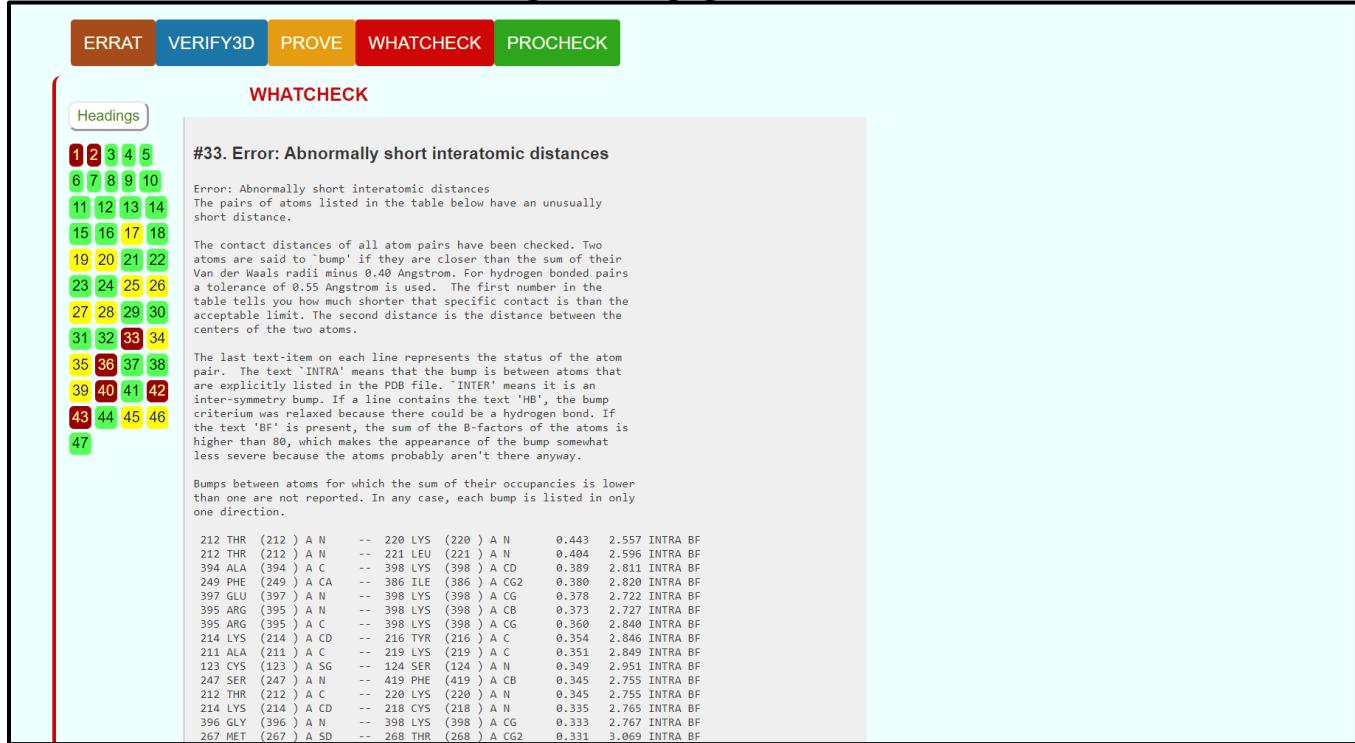


Fig5. Result page for Verify3D



**Fig6. Result page for Prove**



**Fig7. Result page for Whatcheck**

**PROCHECK**

Out of 8 evaluations

- Errors: 5
- Warning: 1
- Pass: 2

*The evaluations are the '+' (Warning) and '\*\*\*' (Error) in the summary. The categories on the left do not always correspond in number due to PROCHECK output documents.*

Summary	
Ramachandran plot	Error
All Ramachandrans	Error
Chi1-chi2 plots	Pass
Main-chain params	
Side-chain params	Error
Residue properties	Pass
Bond len/angle	Pass
M/c bond lengths	
M/c bond angles	
Planar groups	Pass
Program output	

```
-----<<< P R O C H E C K   S U M M A R Y >>>-----
/var/www/SAVES/Jobs/937164/saves.pdb  1.5          563 residues
* Ramachandran plot: 79.6% core 14.5% allow 4.1% gener 1.8% disall
* All Ramachandrans: 50 labelled residues (out of 563)
* Chi1-chi2 plots: 11 labelled residues (out of 362)
* Side-chain params: 5 better 0 inside 0 worse
* Residue properties: Max.deviation: 6.4      Bad contacts: 32
*                                Bond len/angle: 13.2      Morris et al class: 1 1 2
* G-factors          Dihedrals: -0.17      Covalent: -0.73      Overall: -0.36
* Planar groups: 100.0% within limits 0.0% highlighted
-----+
+ May be worth investigating further. * Worth investigating further.
```

Summary file

Complete. Time taken: 00:00:21

**Fig8. Result page for procheck**

**Main Ramachandran plot**

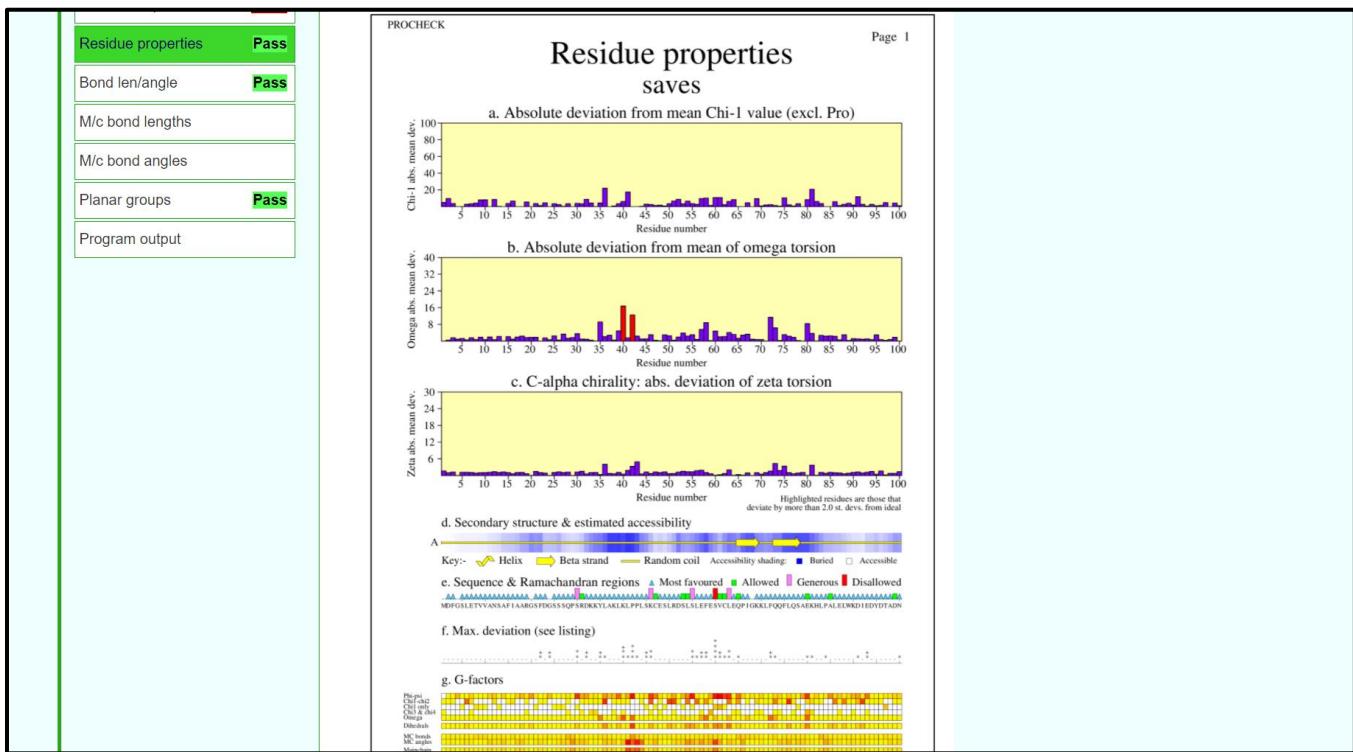
- Page 1
- PDF
- PostScript

**PROCHECK**

**Ramachandran Plot**

saves

**Fig9. Result page for Ramachandran plot**



**Fig10. Result page for residue properties**

## RESULT:

The structure predicted for enzyme kinase by homology modelling using modeller was validated using SAVES server.

## CONCLUSION:

SAVES is an integrated server containing various tools on a single platform that can be used for tertiary structure validation. The predicted structure for rhodopsin by modeller failed the validation thus, I-TASSER based on threading approach will be used to predict a better structure and will be validated again using SAVES server.

## REFERENCES:

1. Xiong, J. (2008). Tertiary structure prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 220-222.
2. SAVESv6.0 - Structure Validation Server. (n.d.). Saves.mbi.ucla.edu. Retrieved March 8, 2022, from <https://saves.mbi.ucla.edu/>
3. SAVESv6.0 - Structure Validation Server. (n.d.). Saves.mbi.ucla.edu. Retrieved March 8, 2022, from <https://saves.mbi.ucla.edu/?job=924086>

**WEBLEM 4b**  
**SAVES server**  
**(URL:<https://saves.mbi.ucla.edu/>)**

**AIM:**

To validate structure model1 generated from I-TASSER server.

**INTRODUCTION:**

Model1 is the structure predicted using threading approach using I-TASSER. The structure has to be evaluated to make sure that the structural features of the model are consistent with the physicochemical rules. This can be done using SAVES server.

SAVES is a structure validation server that has various tools like Errat, Verify3D, Prove, Whatcheck, Procheck, and Cryst integrated in one single platform. This involves checking anomalies in  $\phi$ - $\psi$  angles, bond lengths, close contacts, and so on. Another way of checking the quality of a protein model is to implicitly take these stereochemical properties into account. This is a method that detects errors by compiling statistical profiles of spatial features and interaction energy from experimentally determined structures. By comparing the statistical parameters with the constructed model, the method reveals which regions of a sequence appear to be folded normally and which regions do not. If structural irregularities are found, the region is considered to have errors and has to be further refined.

**METHODOLOGY:**

1. Open homepage for SAVES server. (URL: <https://saves.mbi.ucla.edu/>)
2. Upload structure retrieved from I-TASSER in PDB format.
3. Obtain results for Errat, Verify3D, Prove, Whatcheck and Procheck.
4. Observe and interpret the results.

**OBERSERVATION:**

**UCLA-DOE LAB — SAVES v6.0**



To run any or all programs:  
upload your structure, in PDB format only

No file chosen

**References**

ERRAT

- Reference: Verification of protein structures: patterns of nonbonded atomic interactions, Colovos C and Yeates TO, 1993.
- C++ software

VERIFY 3D

- Profile Search Software [Bowie et al., 1991, Luethy et al., 1992].
- DSSP original and Wikipedia

PROVE

- Reference: Deviations from standard atomic volumes as a quality measure for protein crystal structures, Pontius J, Richelle J, Wodak SJ. 1996

PROCHECK

- PROCHECK source information
- Result analysis
- Protein PDB

**Fig1. Homepage for SAVES server**

## UCLA-DOE LAB — SAVES v6.0

UCLA

To run any or all programs:  
upload your structure, in PDB format only

Choose File model1.pdb

Customize job name:

model1.pdb

Run programs

### References

#### ERRAT

- Reference: Verification of protein structures: patterns of nonbonded atomic interactions, Colovos C and Yeates TO, 1993.
- C++ software

#### VERIFY 3D

- Profile Search Software [Bowie et al., 1991, Luethy et al., 1992].
- DSSP original and Wikipedia

#### PROVE

- Reference: Deviations from standard atomic volumes as a quality measure for protein crystal structures, Pontius J, Richelle J, Wodak SJ. 1996

#### PROCHECK

Fig2. Structure from Modeller for validation

## UCLA-DOE LAB — SAVES v6.0

UCLA

Job 937181 has been created

New Job

job #937181: model1.pdb [job link] [3D Viewer]

#### ERRAT Complete

Overall Quality Factor

**97.0588**

[Results](#)

#### VERIFY Complete

75.86% of the residues have averaged 3D-1D score  $\geq 0.2$

**Fail**

Fewer than 80% of the amino acids have scored  $\geq 0.2$  in the 3D/1D profile.

[Results](#)

#### PROVE Complete

Buried outlier protein atoms total from 1 Model: 4.2%

**Warning**

[Results](#)

#### WHATCHECK Complete



[Results](#)

#### PROCHECK Complete

Out of 8 evaluations

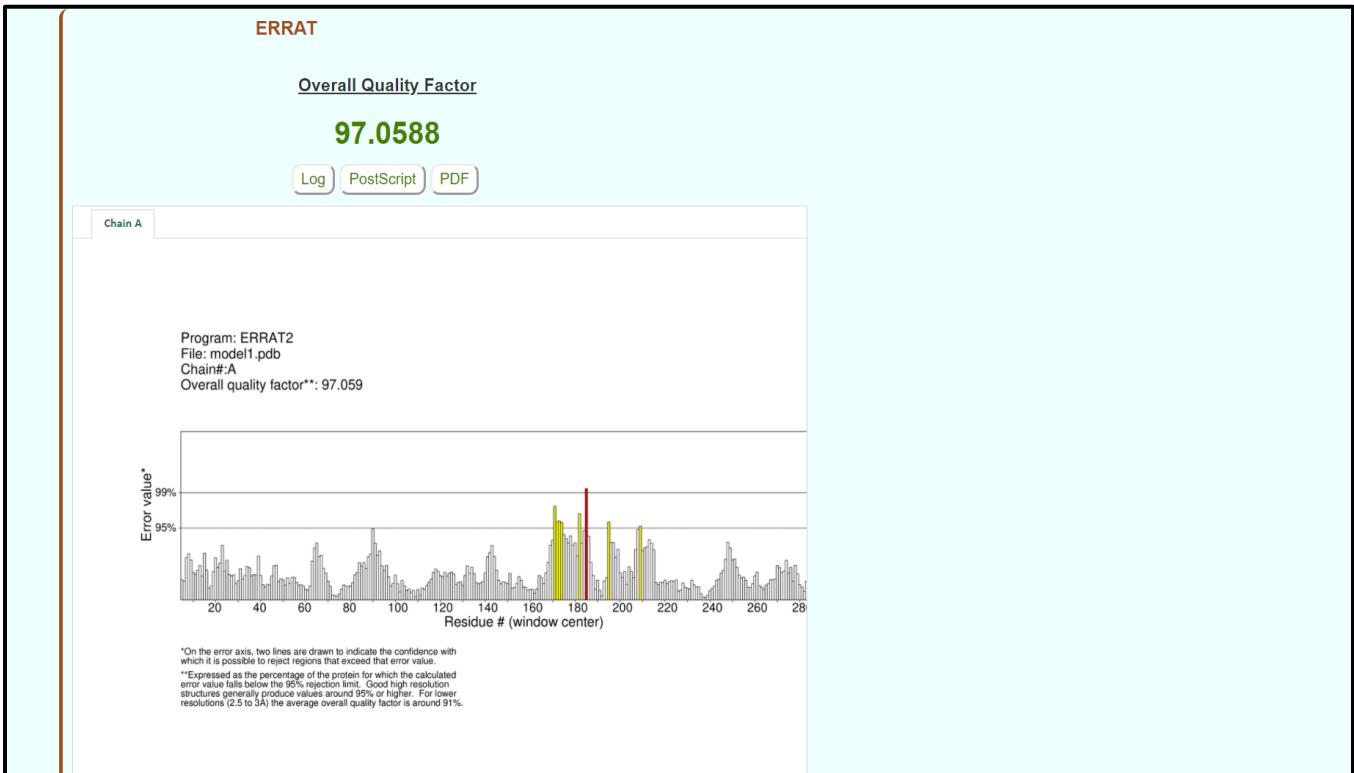
- Errors: 6
- Warning: 0
- Pass: 2

[Results](#)

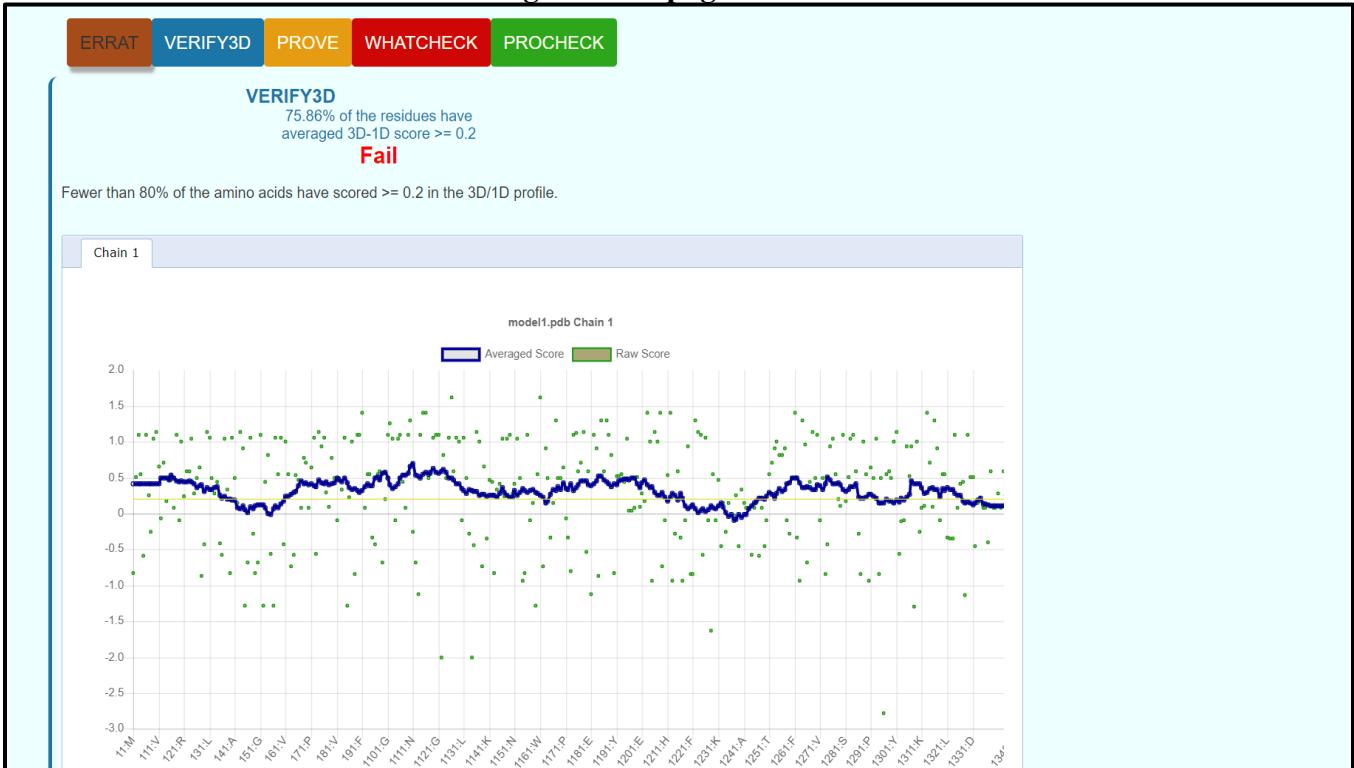
Almost ready, check back soon

### References

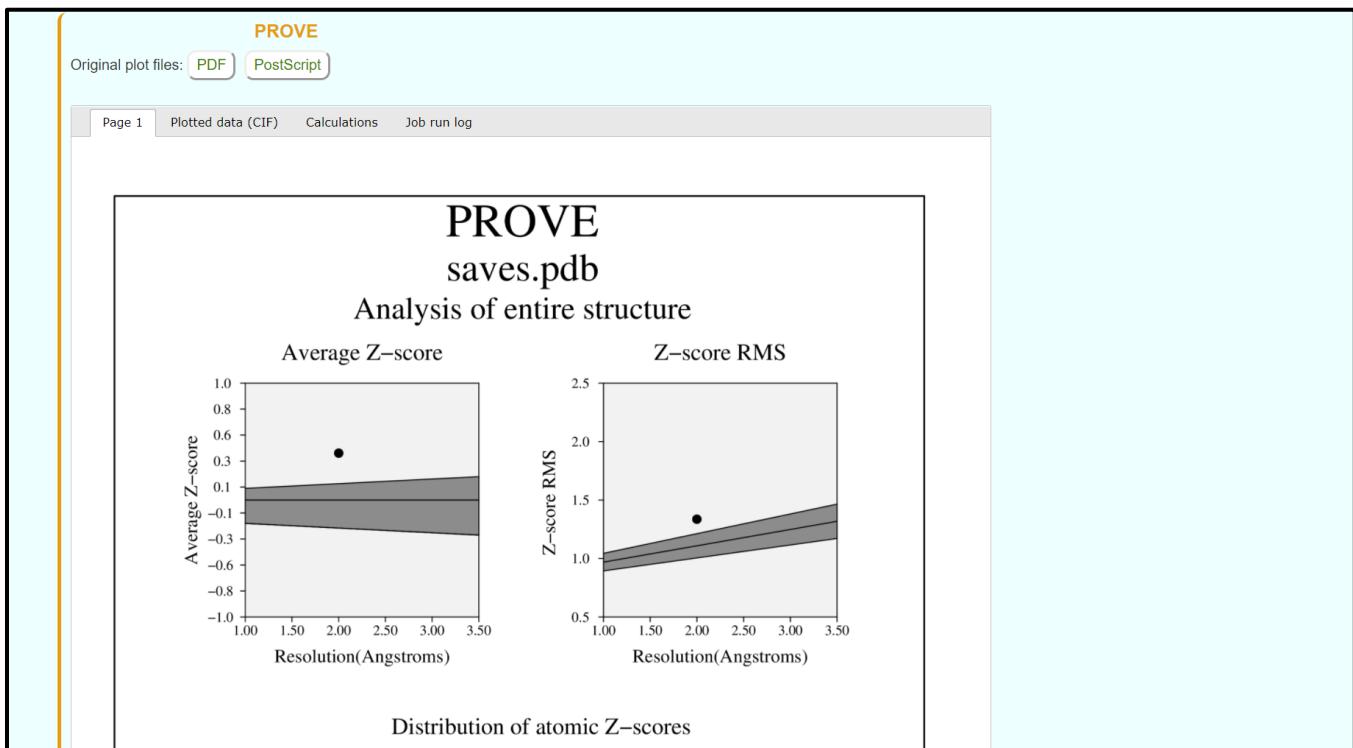
Fig3. Result page for structure validation for various servers



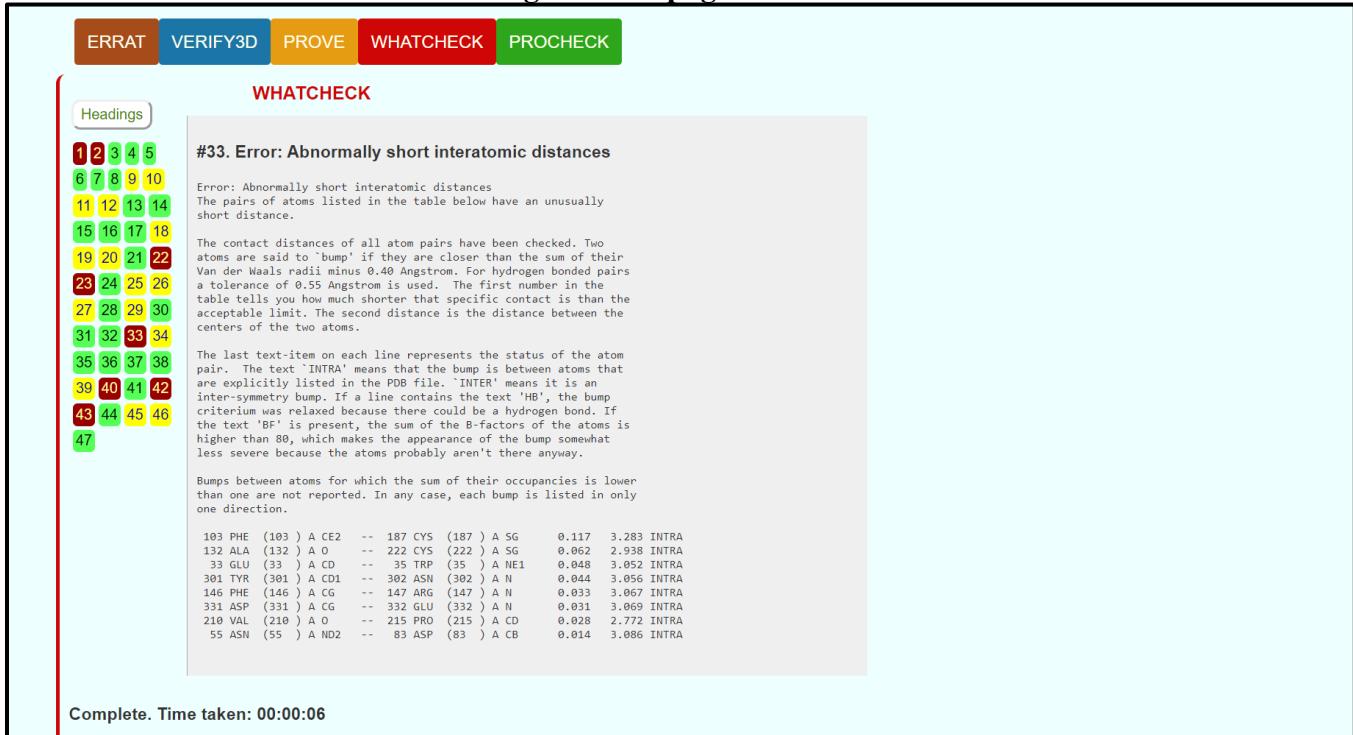
#### Fig4. Result page for Errat



## Fig5. Result page for Verify3D



**Fig6. Result page for Prove**



**Fig7. Result page for Whatcheck**

**PROCHECK**

Out of 8 evaluations

- Errors: 6
- Warning: 0
- Pass: 2

The evaluations are the '+' (Warning) and '\*' (Error) in the summary. The categories on the left do not always correspond in number due to PROCHECK output documents.

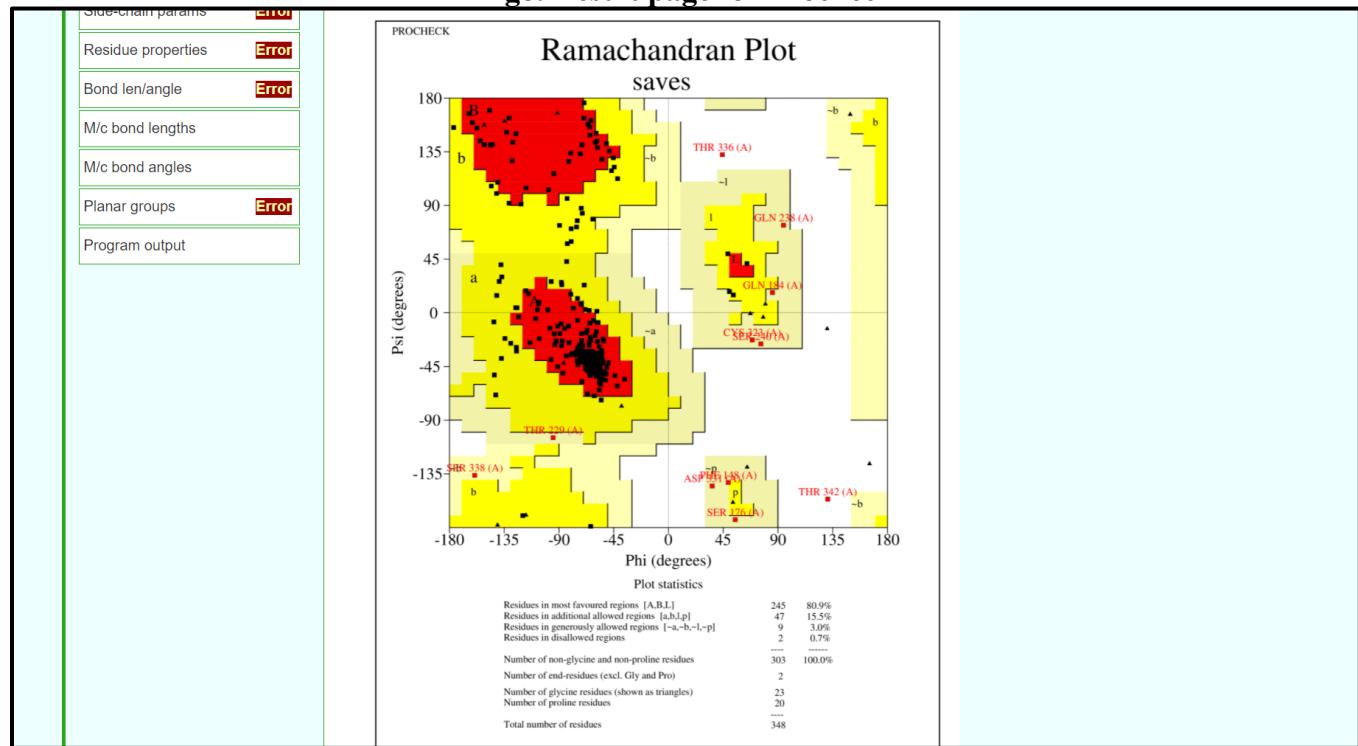
Summary	
Ramachandran plot	Error
All Ramachandrans	Error
Chi1-chi2 plots	Pass
Main-chain params	
Side-chain params	Error
Residue properties	Error
Bond len/angle	Error
M/c bond lengths	
M/c bond angles	
Planar groups	Error
Program output	

```
+-----<<< P R O C H E C K S U M M A R Y >>>-----+
/var/www/SAVES/Jobs/937181/saves.pdb 1.5 348 residues
*| Ramachandran plot: 80.9% core 15.5% allow 3.0% gener 0.7% disall
*| All Ramachandrans: 21 labelled residues (out of 348)
*| Chi1-chi2 plots: 6 labelled residues (out of 195)
Side-chain params: 5 better 0 inside 0 worse
*| Residue properties: Max.deviation: 10.6 Bad contacts: 0
*| Bond len/angle: 5.4 Morris et al class: 1 2 1
G-factors Dihedrals: -0.42 Covalent: 0.09 Overall: -0.20
*| Planar groups: 87.9% within limits 12.1% highlighted 3 off graph
+-----+
+ May be worth investigating further. * Worth investigating further.
```

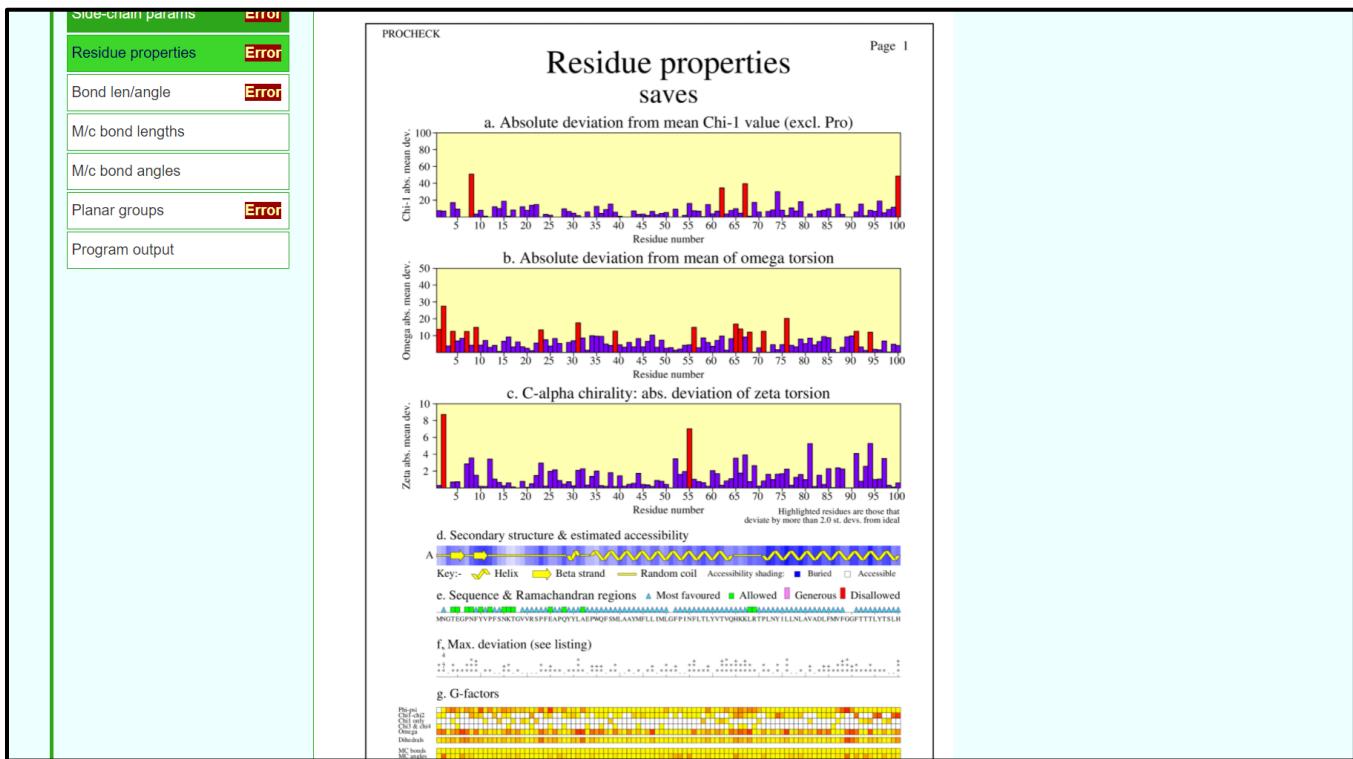
Summary file

Complete. Time taken: 00:00:19

**Fig8. Result page for Procheck**



**Fig9. Result page for Ramachandran plot**



**Fig10. Result page for residue properties**

## RESULT:

The structure predicted for enzyme kinase by threading approach using I-TASSER was validated using SAVES server.

## CONCLUSION:

SAVES is an integrated server containing various tools on a single platform that can be used for tertiary structure validation. The predicted structure for kinase by I-TASSER passed only for ERRAT and did not give required results for the rest. Even though I-TASSER gave better predicted structure than modeller, Robetta based on ab-initio approach will be used to predict a better structure and will be validated again using SAVES server.

## REFERENCES:

1. Xiong, J. (2008). Tertiary structure prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 220-222.
2. SAVESv6.0 - Structure Validation Server. (n.d.). Saves.mbi.ucla.edu. Retrieved March 8, 2022, from <https://saves.mbi.ucla.edu/>
3. SAVESv6.0 - Structure Validation Server. (n.d.). Saves.mbi.ucla.edu. Retrieved March 8, 2022, from <https://saves.mbi.ucla.edu/?job=924117>

**WEBLEM 4c**  
**SAVES server**  
**(URL: <https://saves.mbi.ucla.edu/>)**

**AIM:**

To validate structure 240040 generated from Robetta server.

**INTRODUCTION:**

240040 is the structure predicted using Ab-initio approach using Robetta. The structure has to be evaluated to make sure that the structural features of the model are consistent with the physicochemical rules. This can be done using SAVES server.

SAVES is a structure validation server that has various tools like Errat, Verify3D, Prove, Whatcheck, Procheck and Cryst integrated in one single platform. This involves checking anomalies in  $\phi$ - $\psi$  angles, bond lengths, close contacts, and so on. Another way of checking the quality of a protein model is to implicitly take these stereochemical properties into account. This is a method that detects errors by compiling statistical profiles of spatial features and interaction energy from experimentally determined structures. By comparing the statistical parameters with the constructed model, the method reveals which regions of a sequence appear to be folded normally and which regions do not. If structural irregularities are found, the region is considered to have errors and has to be further refined.

**METHODOLOGY:**

1. Open homepage for SAVES server. (URL: <https://saves.mbi.ucla.edu/>)
2. Upload structure retrieved from Robetta in PDB format.
3. Obtain results for Errat, Verify3D, Prove, Whatcheck and Procheck.
4. Observe and interpret the results.

**OBSERVATION:**

**UCLA-DOE LAB — SAVES v6.0**

**UCLA**

To run any or all programs:  
upload your structure, in PDB format only

Choose File No file chosen

Run programs

**References**

**ERRAT**

- Reference: Verification of protein structures: patterns of nonbonded atomic interactions, Colovos C and Yeates TO, 1993.
- C++ software

**VERIFY 3D**

- Profile Search Software [Bowie et al., 1991, Luethy et al., 1992].
- DSSP original and Wikipedia

**PROVE**

- Reference: Deviations from standard atomic volumes as a quality measure for protein crystal structures, Pontius J, Richelle J, Wodak SJ. 1996

**PROCHECK**

- PROCHECK source information
- Result analysis
- Protein PDB

**Fig1. Homepage for SAVES server**

## UCLA-DOE LAB — SAVES v6.0

UCLA

To run any or all programs:  
upload your structure, in PDB format only

robetta\_mo...\_240040.pdb

Customize job name:

robetta\_models\_240040.pdb

### References

#### ERRAT

- Reference: Verification of protein structures: patterns of nonbonded atomic interactions, Colovos C and Yeates TO, 1993.
- C++ software

#### VERIFY 3D

- Profile Search Software [Bowie et al., 1991, Luethy et al., 1992].
- DSSP original and Wikipedia

#### PROVE

- Reference: Deviations from standard atomic volumes as a quality measure for protein crystal structures, Pontius J, Richelle J, Wodak SJ. 1996

#### PROCHECK

Fig2. Structure from Modeller for validation

## UCLA-DOE LAB — SAVES v6.0

UCLA

Job 937186 has been created

job #937186: robetta\_models\_240040.pdb [\[job link\]](#) [\[3D Viewer\]](#)

#### ERRAT Complete

Error(s) found.

Check full results for more information

#### Overall Quality Factor

#### WHATCHECK Complete



#### VERIFY Processing results

Error(s) found.

Check full results for more information

#### PROVE Complete

Buried outlier protein atoms total  
from 1 Model: 4.6%

**warning**

#### PROCHECK Complete

Out of 9 evaluations

- Errors: 3
- Warning: 2
- Pass: 4

Almost ready, check back  
soon

### References

Fig3. Result page for structure validation for various servers

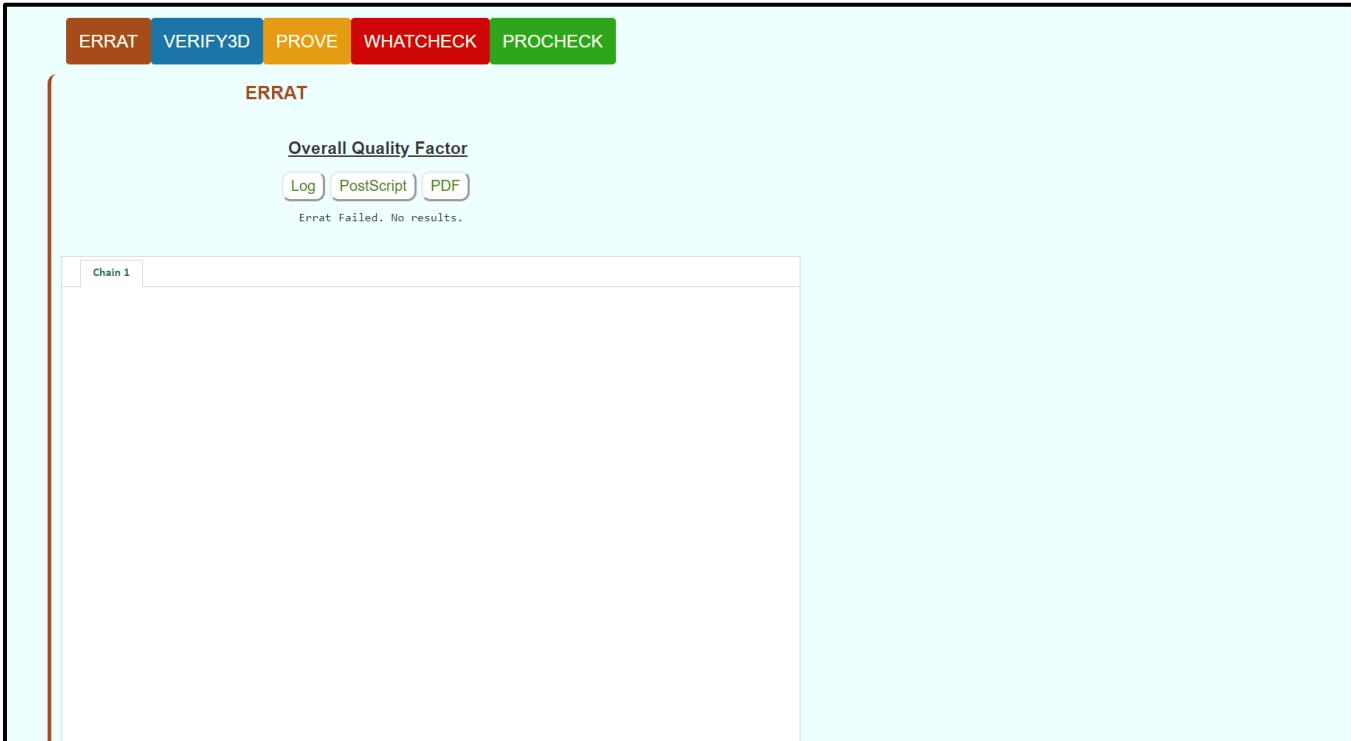


Fig4. Result page for Errat

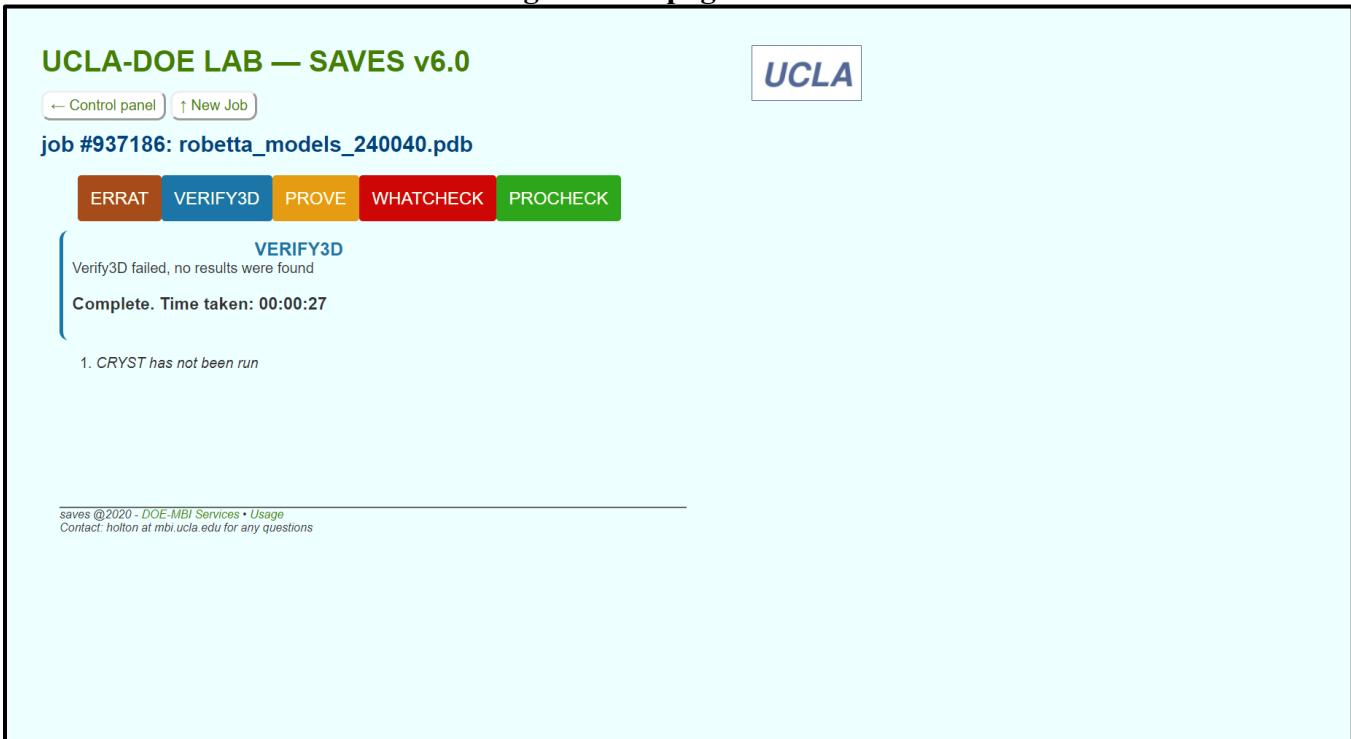


Fig5. Result page for Verify3D

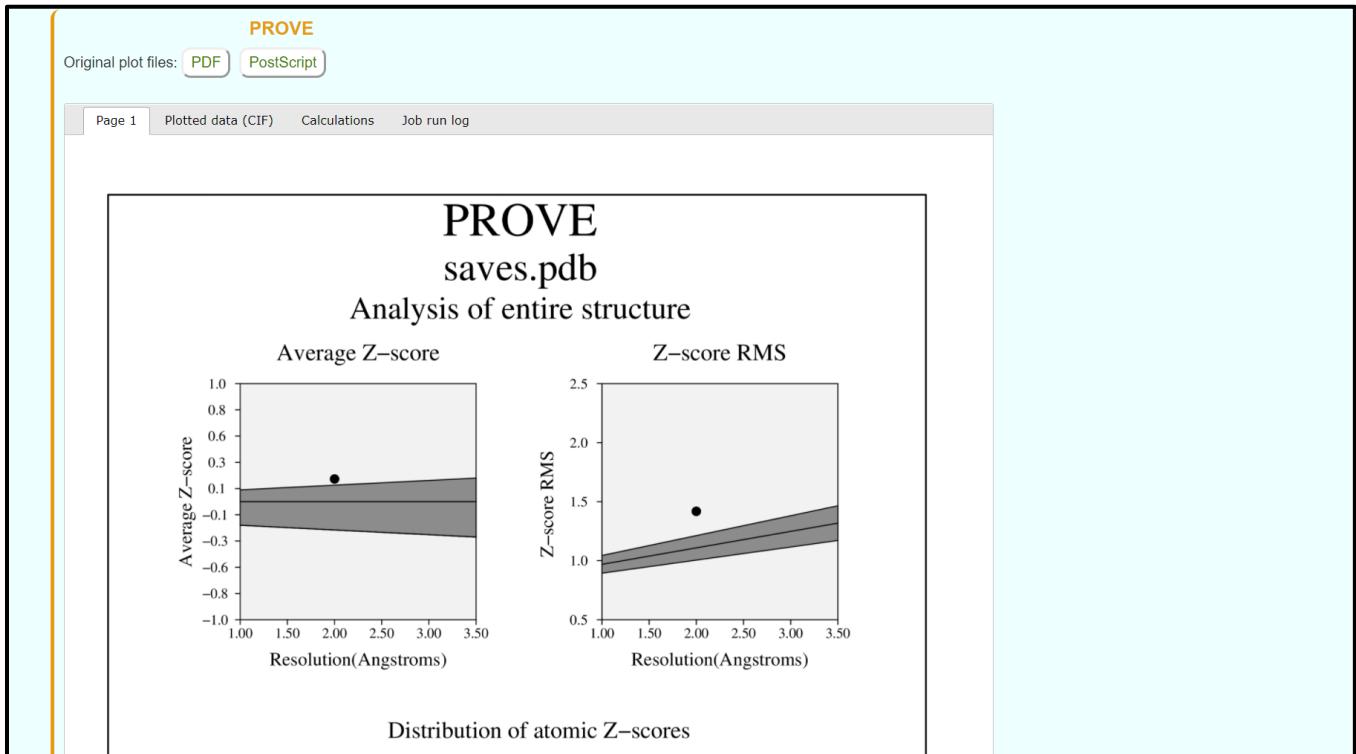


Fig6. Result page for PROVE

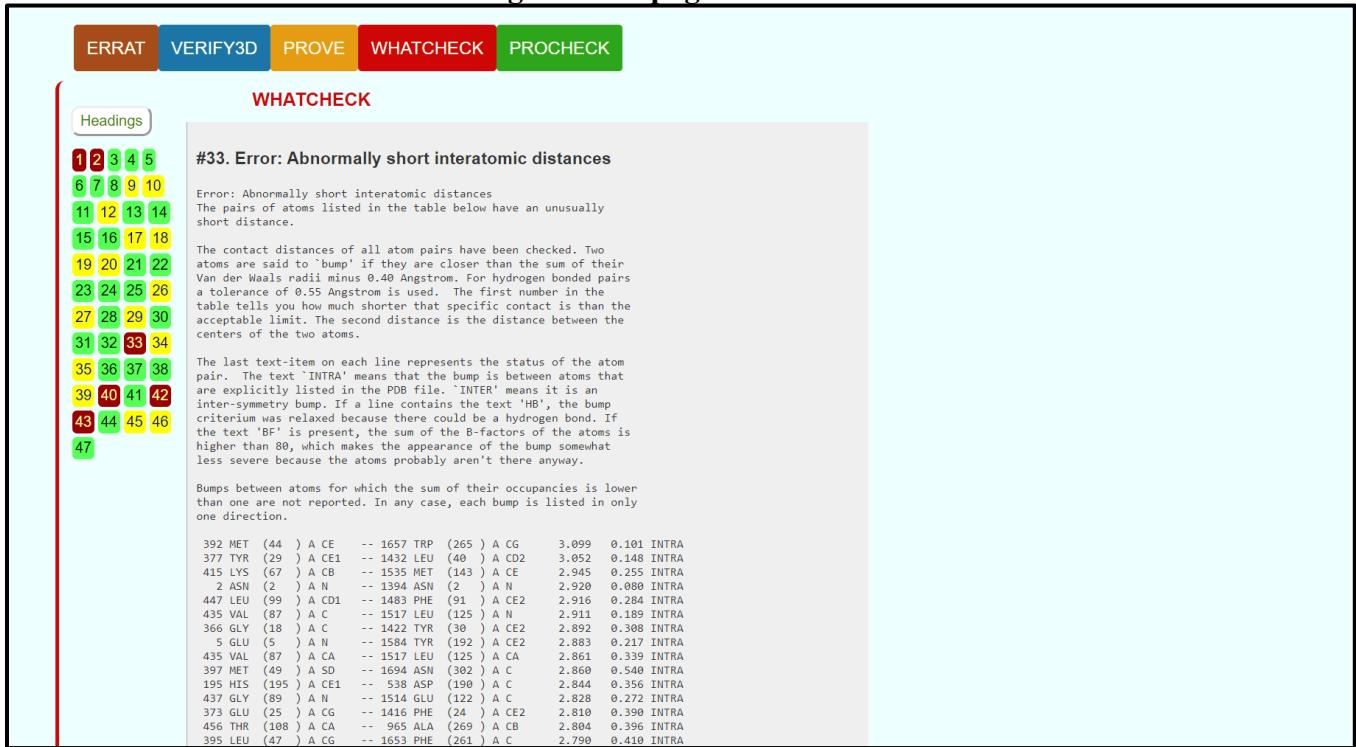


Fig7. Result page for Whatcheck

Summary

Ramachandran plot **Warning**

All Ramachandrans **Pass**

Chi1-chi2 plots **Pass**

Main-chain params

Side-chain params **Error**

Residue properties **Pass**

Bond len/angle **Pass**

M/c bond lengths

M/c bond angles

Planar groups **Pass**

Program output

```
+-----<<< P R O C H E C K S U M M A R Y >>>-----+
| /var/www/SAVES/Jobs/937186/saves.pdb 1.5 348 residues
*| Ramachandran plot: 89.1% core 9.6% allow 0.3% gener 1.0% disall
+| All Ramachandrans: 10 labelled residues (out of 346)
| Chi1-chi2 plots: 0 labelled residues (out of 195)
| Side-chain params: 5 better 0 inside 0 worse
*| Residue properties: Max.deviation: 12.4 Bad contacts: 1
*| Bond len/angle: 11.8 Morris et al class: 1 1 1
+| 1 cis-peptides
| G-factors Dihedrals: 0.33 Covalent: 0.34 Overall: 0.35
| Planar groups: 100.0% within limits 0.0% highlighted
+-----+
+ May be worth investigating further. * Worth investigating further.
```

Summary file

Complete. Time taken: 00:00:19

1. CRYST has not been run

saves @2020 - DOE-MBI Services • Usage  
Contact: holton at mbi ucla edu for any questions

Fig8. Result page for Procheck

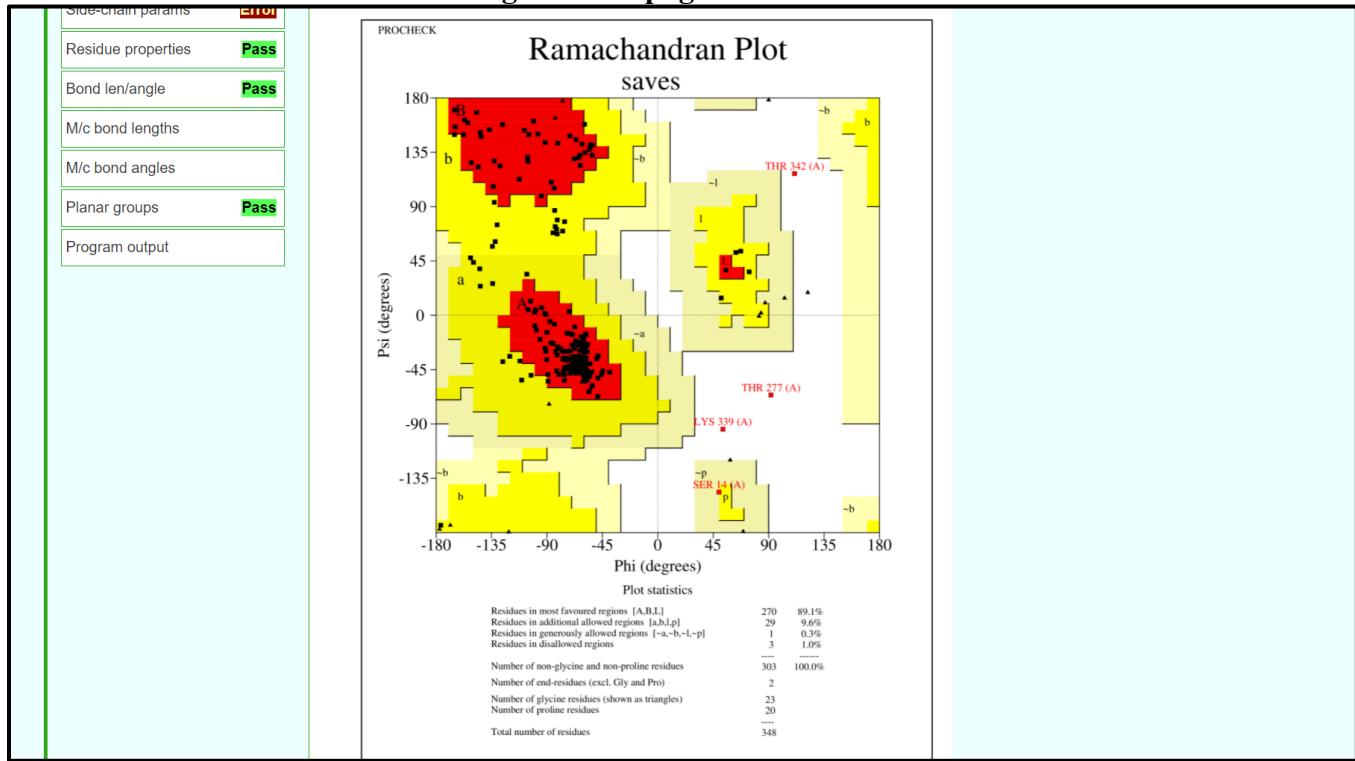
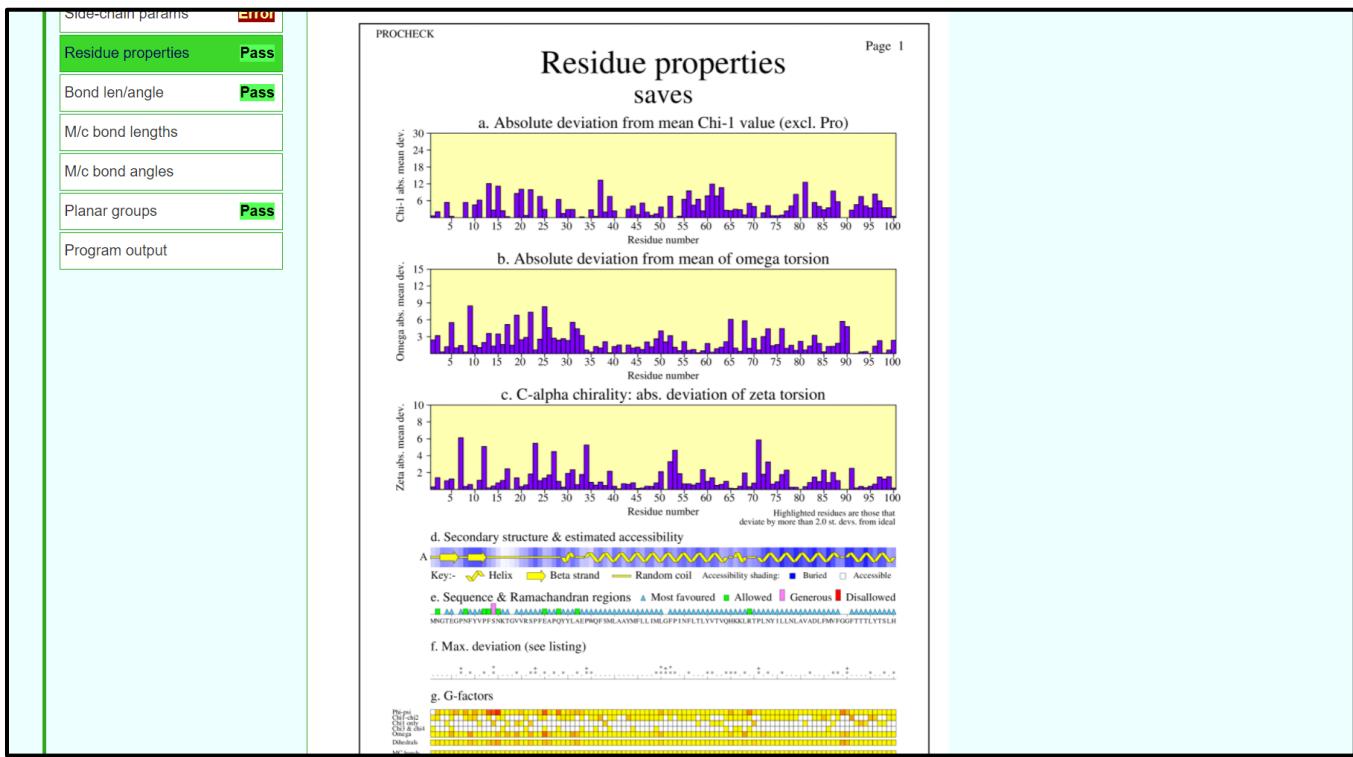


Fig9. Result page for Ramachandran plot



**Fig10. Result page for residue properties**

## RESULT:

The structure predicted for enzyme kinase by abi-initio approach using Robetta was validated using SAVES server.

## CONCLUSION:

SAVES is an integrated server containing various tools on a single platform that can be used for tertiary structure validation. The predicted structure for Rhodopsin by Robetta passed maximum requirements of validation. Hence, it can be concluded that the structure predicting by Robetta was the most accurate out of all three methods used for prediction.

## REFERENCES:

1. Xiong, J. (2008). Tertiary structure prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 220-222.
2. SAVESv6.0 - Structure Validation Server. (n.d.). Saves.mbi.ucla.edu. Retrieved March 8, 2022, from <https://saves.mbi.ucla.edu/>
3. SAVESv6.0 - Structure Validation Server. (n.d.). Saves.mbi.ucla.edu. Retrieved March 8, 2022, from <https://saves.mbi.ucla.edu/?job=928054>

## WEBLEM 5

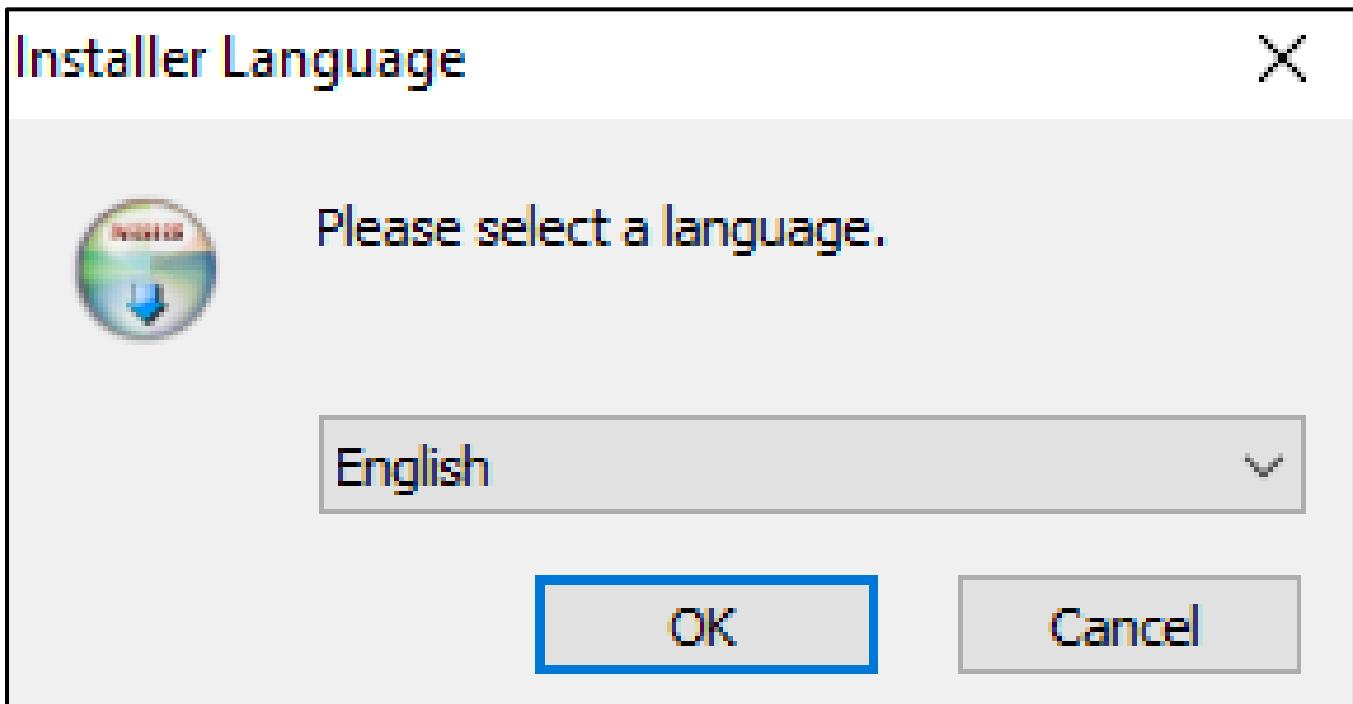
### Introduction to Visualization of Tertiary structure using RASMOL & PyMOL

We can obtain all the available information about the 3D structure of this enzyme by browsing through the links or download the PDB file to a local directory in our computer and work with our preferred molecular modelling and visualization package.

#### RasMol:

RasMol is a computer program written for molecular graphics visualization intended and used primarily for the depiction and exploration of biological macromolecule structures, such as those found in the Protein Data Bank. It was originally developed by Roger Sayle in the early 90s. Historically, it was an important tool for molecular biologists since the extremely optimized program allowed the software to run on (then) modestly powerful personal computers. Before RasMol, visualization software ran on graphics workstations that, due to their expense, were less accessible to scholars. RasMol has become an important educational tool as well as continuing to be an important tool for research in structural biology.

#### Installation:



Select language and proceed

**License Agreement**

Please review the license terms before installing RasMol -- RasWin 2.7.5.2.



Press Page Down to see the rest of the agreement.

## COPYING

This version is based in large part on RasMol 2.7.4.2, RasMol 2.7.4.1, RasMol 2.7.3, RasMol version 2.7.2.1.1, Rasmol version 2.7.2, RasMol version 2.7.1.1 and RasTop version 1.3 and indirectly on the RasMol 2.5-ucb and 2.6-ucb versions and version 2.6\_CIF.2, RasMol 2.6x1 and RasMol\_2.6.4.

RasMol 2.7.5 may be distributed under the terms of the GNU General Public License (the GPL), see

<http://www.gnu.org/licenses/gpl.txt>

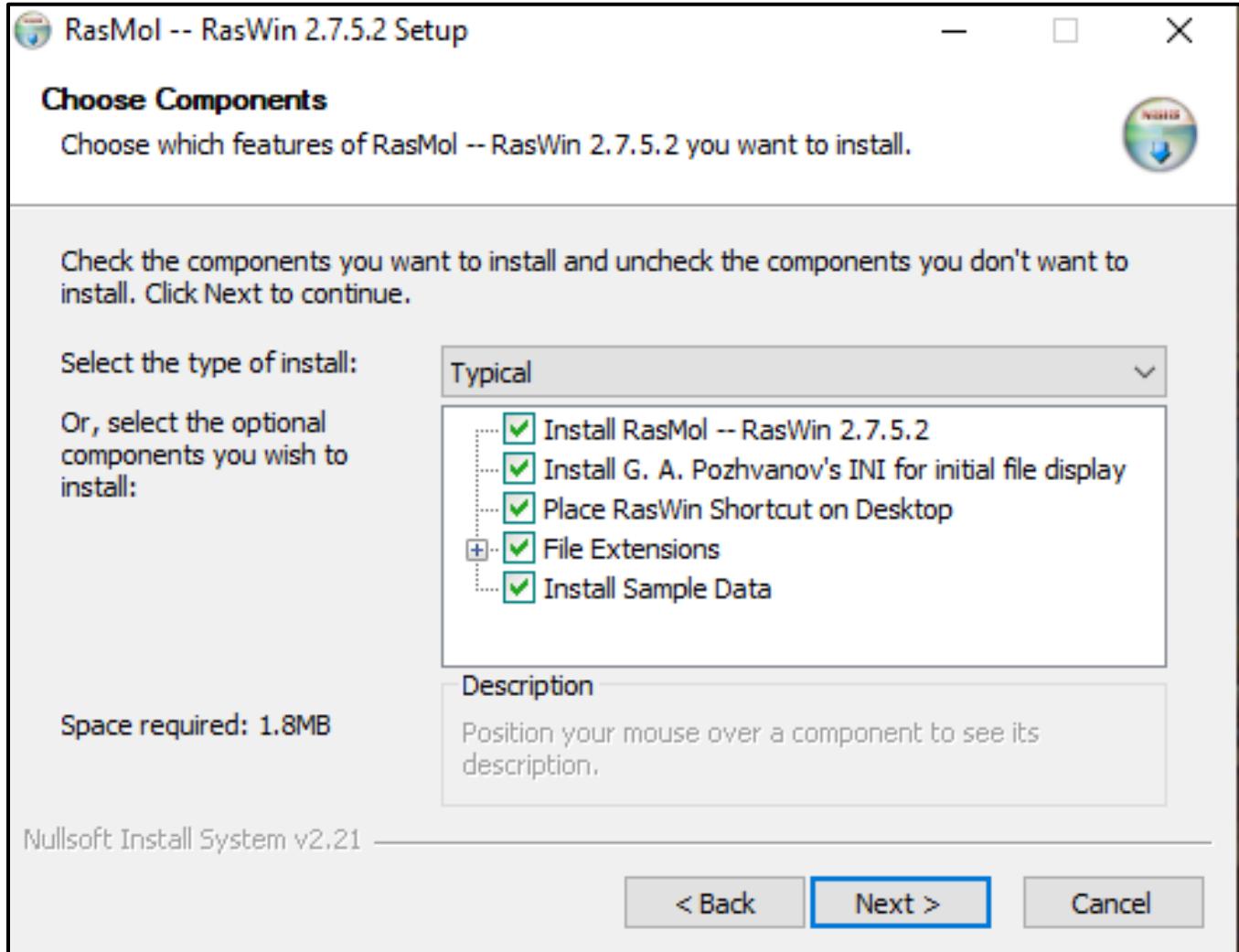
If you accept the terms of the agreement, click I Agree to continue. You must accept the agreement to install RasMol -- RasWin 2.7.5.2.

Nullsoft Install System v2.21

I Agree

Cancel

**Read the License Agreement and click "I Agree" to proceed**



Select the components of RasMol you want to install and click “Next” to proceed



### Choose Install Location

Choose the folder in which to install RasMol -- RasWin 2.7.5.2.



Setup will install RasMol -- RasWin 2.7.5.2 in the following folder. To install in a different folder, click Browse and select another folder. Click Install to start the installation.

Destination Folder

C:\Program Files (x86)\RasWin

[Browse...](#)

Space required: 1.8MB

Space available: 65.3GB

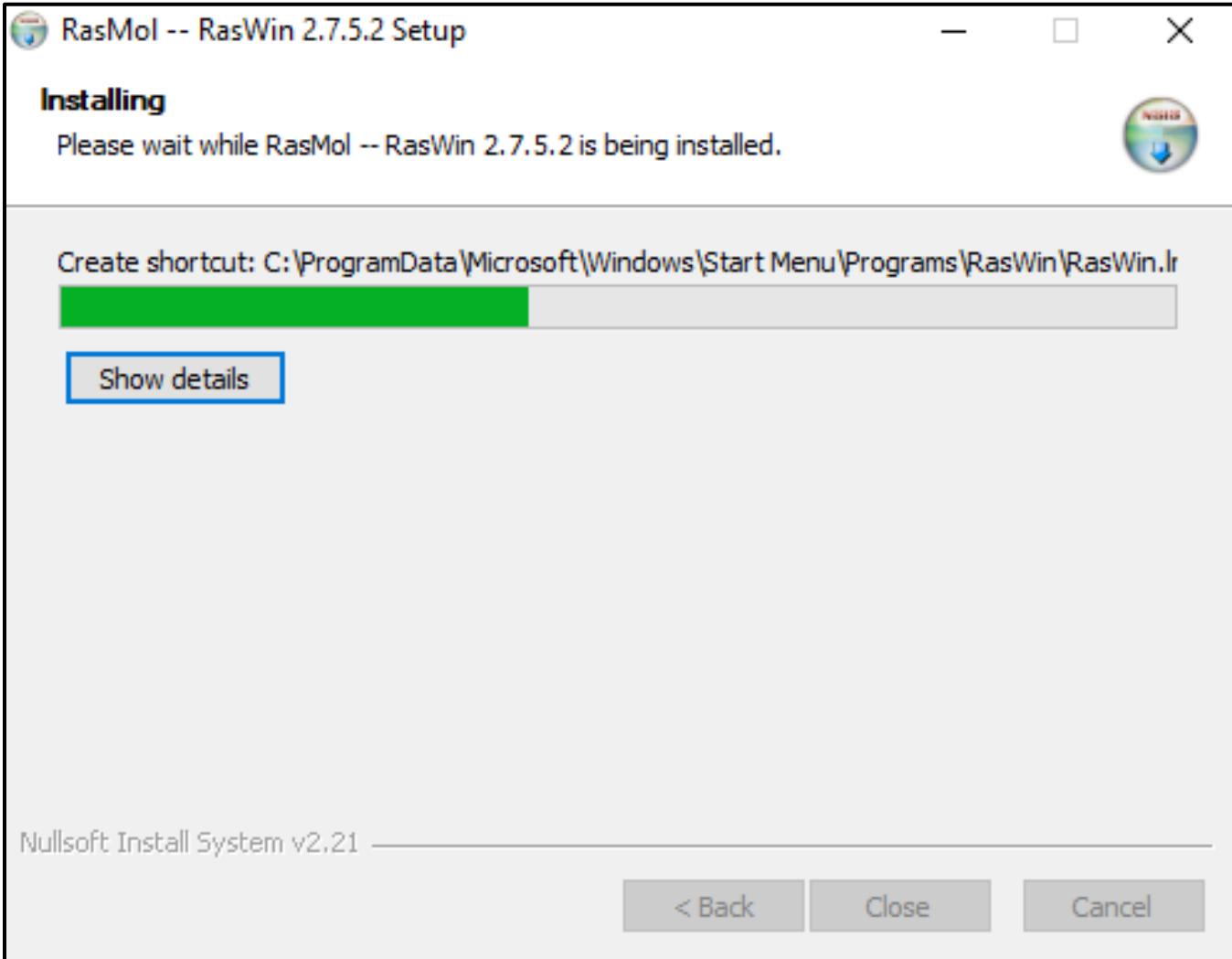
Nullsoft Install System v2.21

[< Back](#)

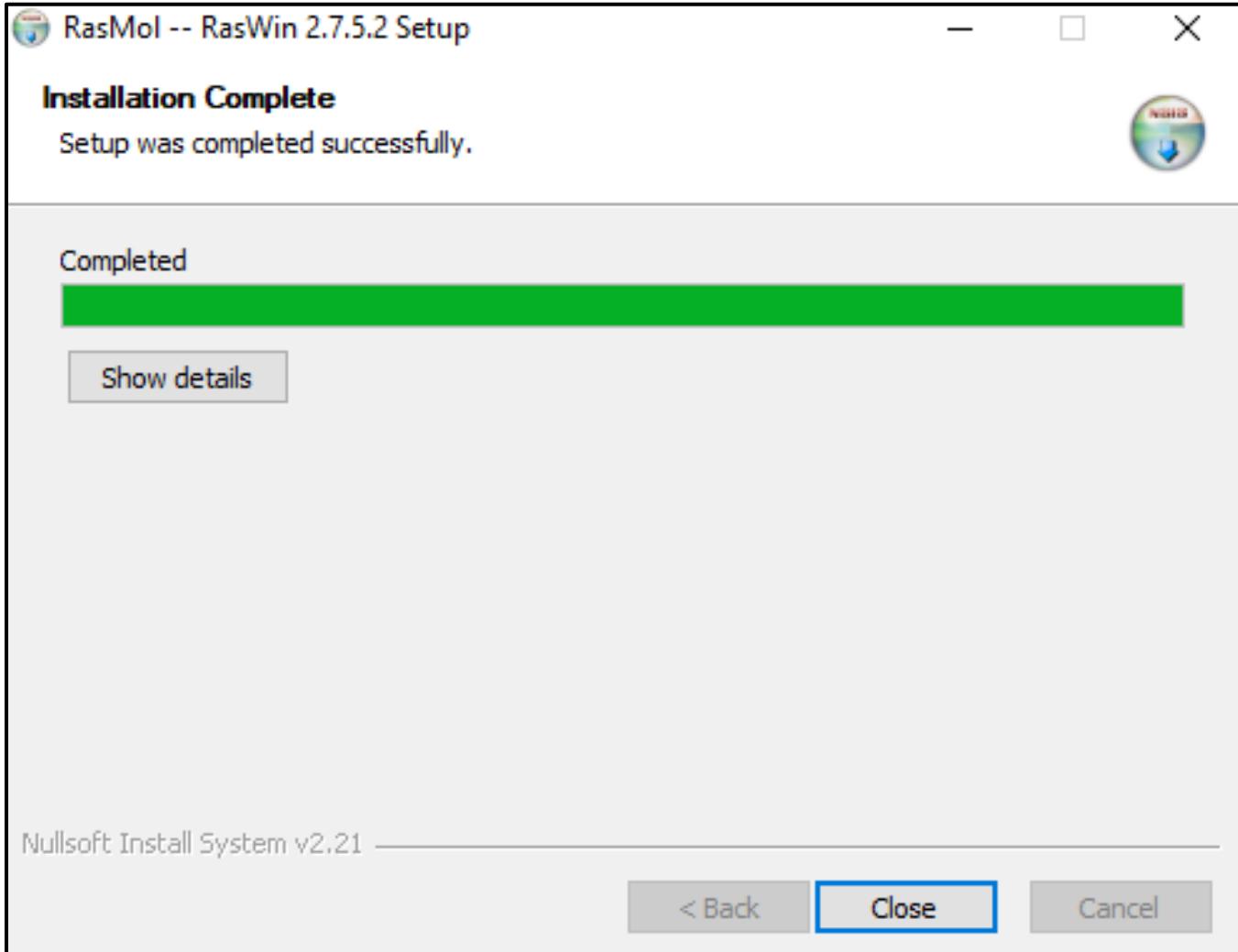
[Install](#)

[Cancel](#)

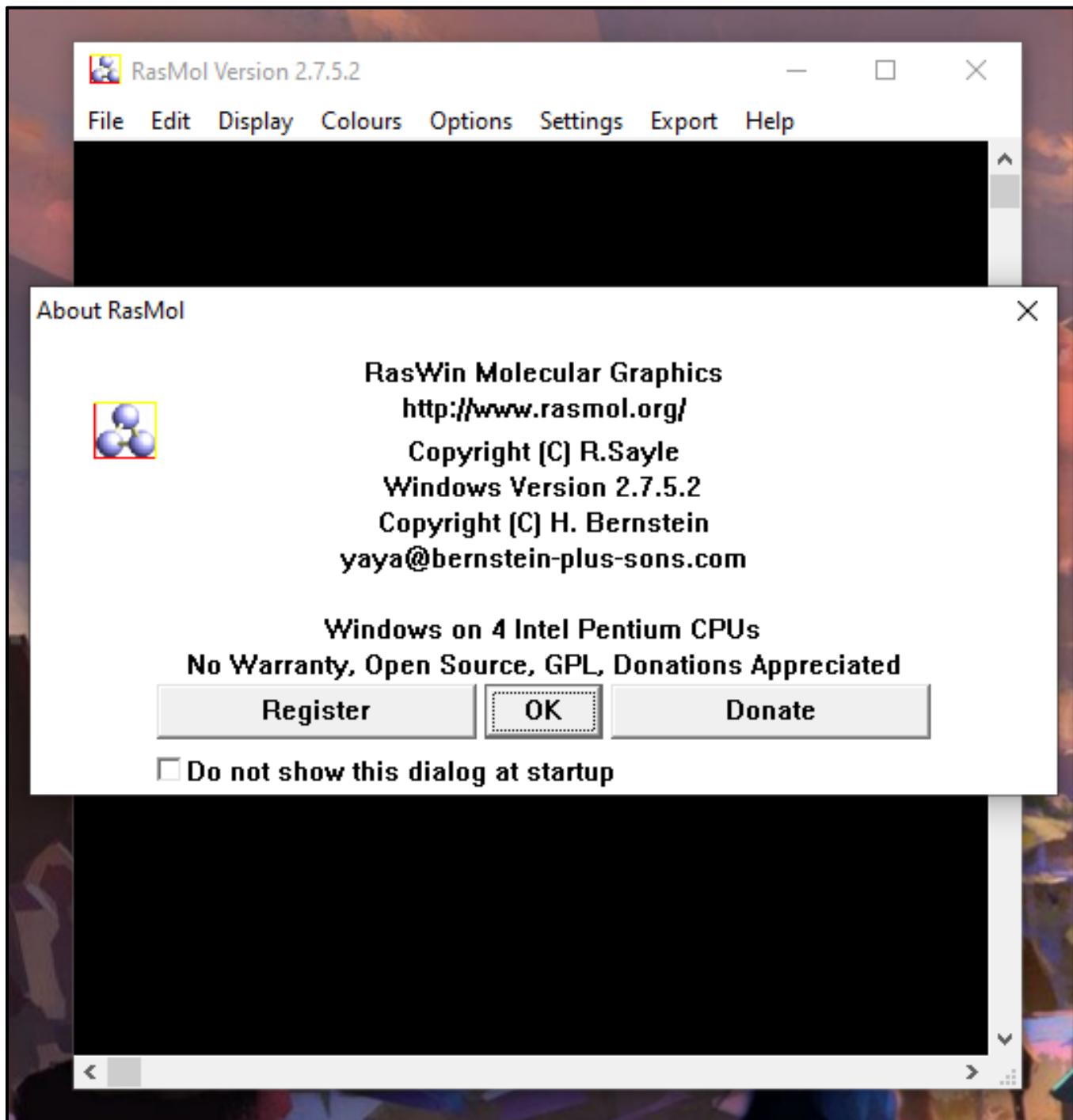
Select the directory in which you want to install RasMol and click "Install" to proceed



**The software will now install**



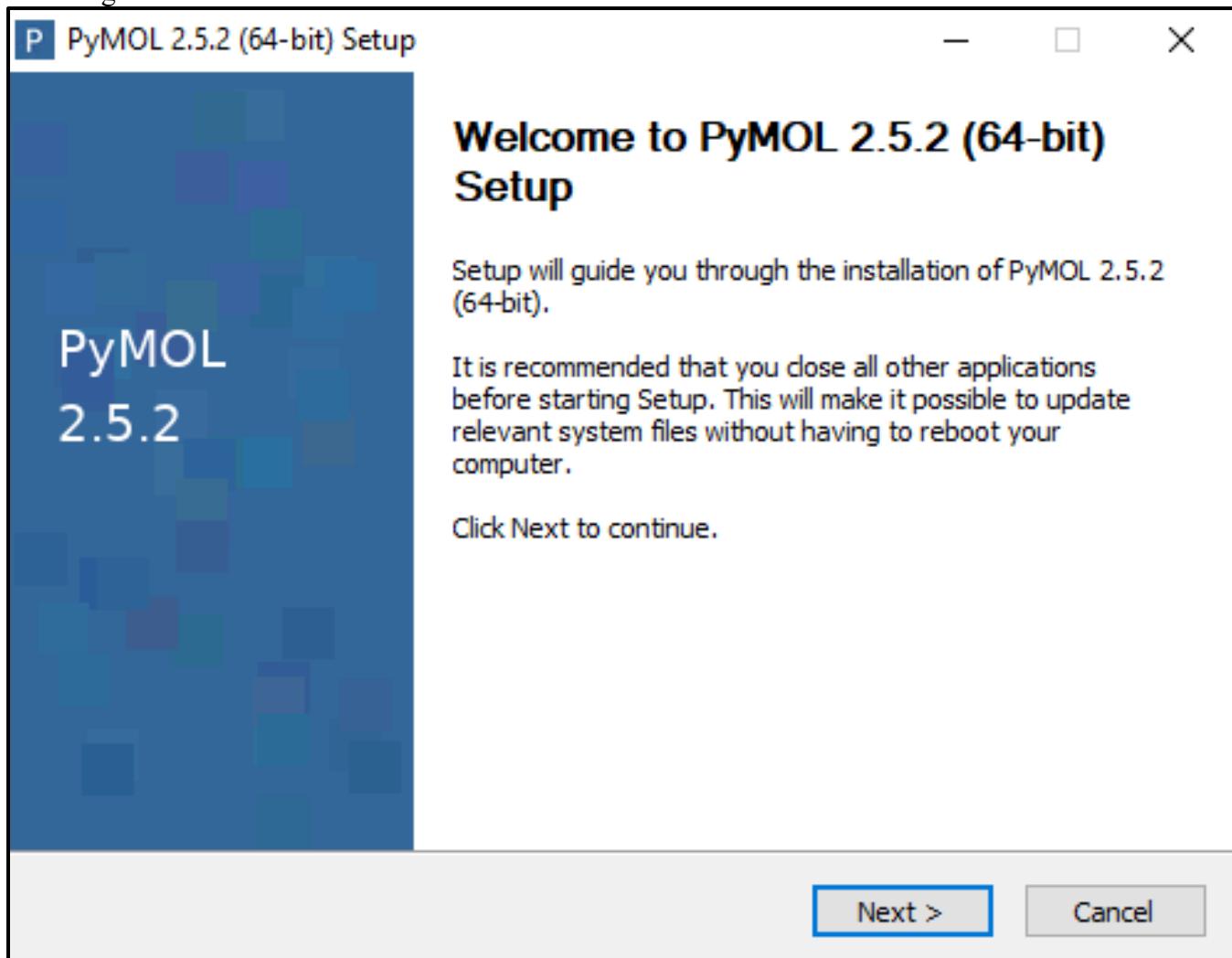
**Close the installer after the install is completed**



RasMol is now installed

## PyMol

PyMOL, a cross-platform molecular graphics tool, has been widely used for three-dimensional (3D) visualization of proteins, nucleic acids, small molecules, electron densities, surfaces, and trajectories. It is also capable of editing molecules, ray tracing, and making movies. This Python-based software, alongside many Python plugin tools, has been developed to enhance its utilities and facilitate the drug design in PyMOL. To gain an insightful view of useful drug design tools and their functions in PyMOL, we present an extensive discussion on various molecular modeling modules in PyMOL, covering those for visualization and analysis enhancement, protein–ligand modeling, molecular simulations, and drug screening.



Download and run the installer. Click next to proceed

# PyMOL

## License Agreement

Please review the license terms before installing PyMOL 2.5.2 (64-bit).

Press Page Down to see the rest of the agreement.

By using this software, you agree to:

(1) The Schrodinger End-User License Agreement (Schrodinger EULA):

<https://www.schrodinger.com/salesagreements>

(2) Licenses of all third party components bundled with PyMOL:

<https://pymol.org/PyMOLThird-PartySoftwareLibrariesandUtilities.pdf>

If you accept the terms of the agreement, click I Agree to continue. You must accept the agreement to install PyMOL 2.5.2 (64-bit).

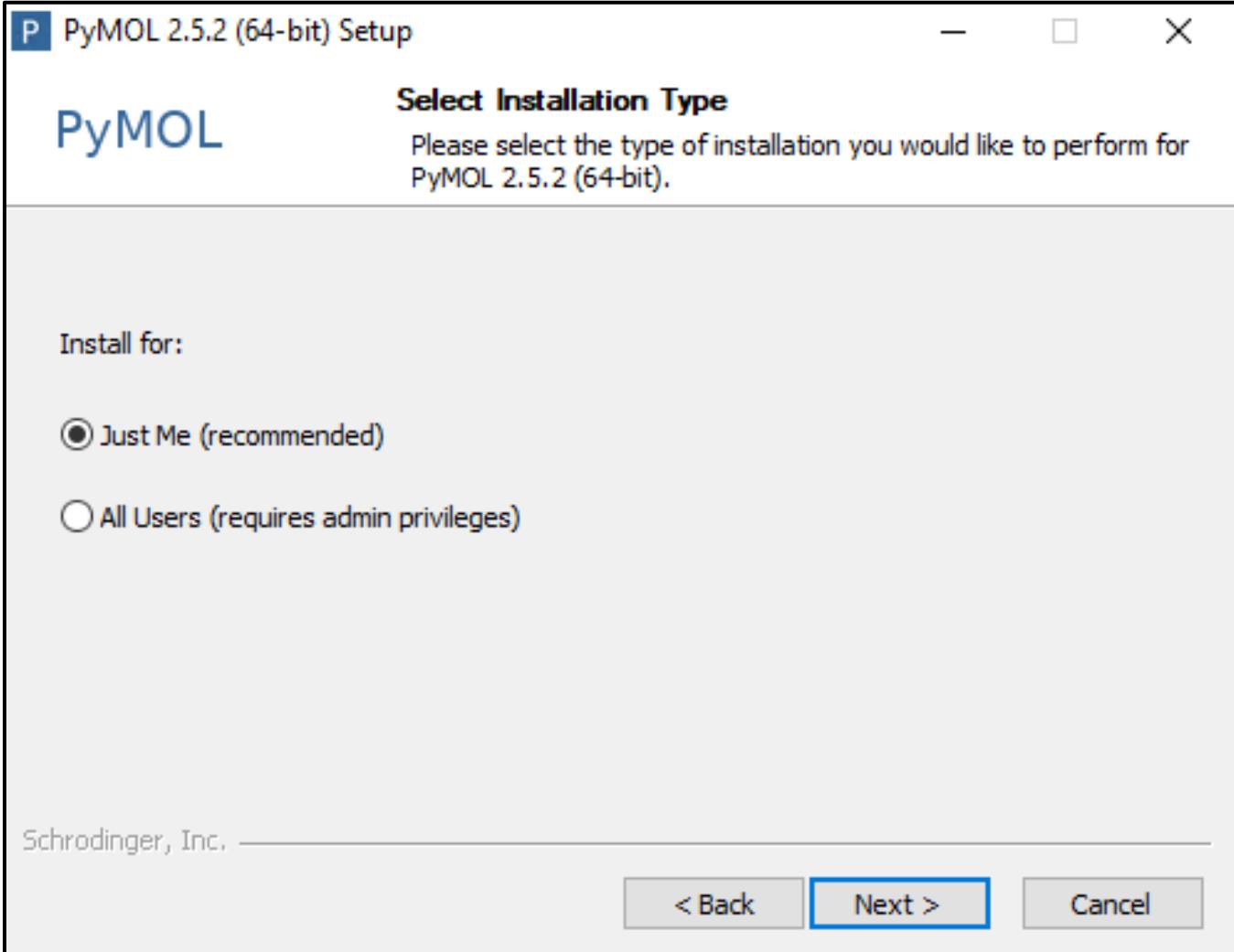
Schrodinger, Inc. \_\_\_\_\_

< Back

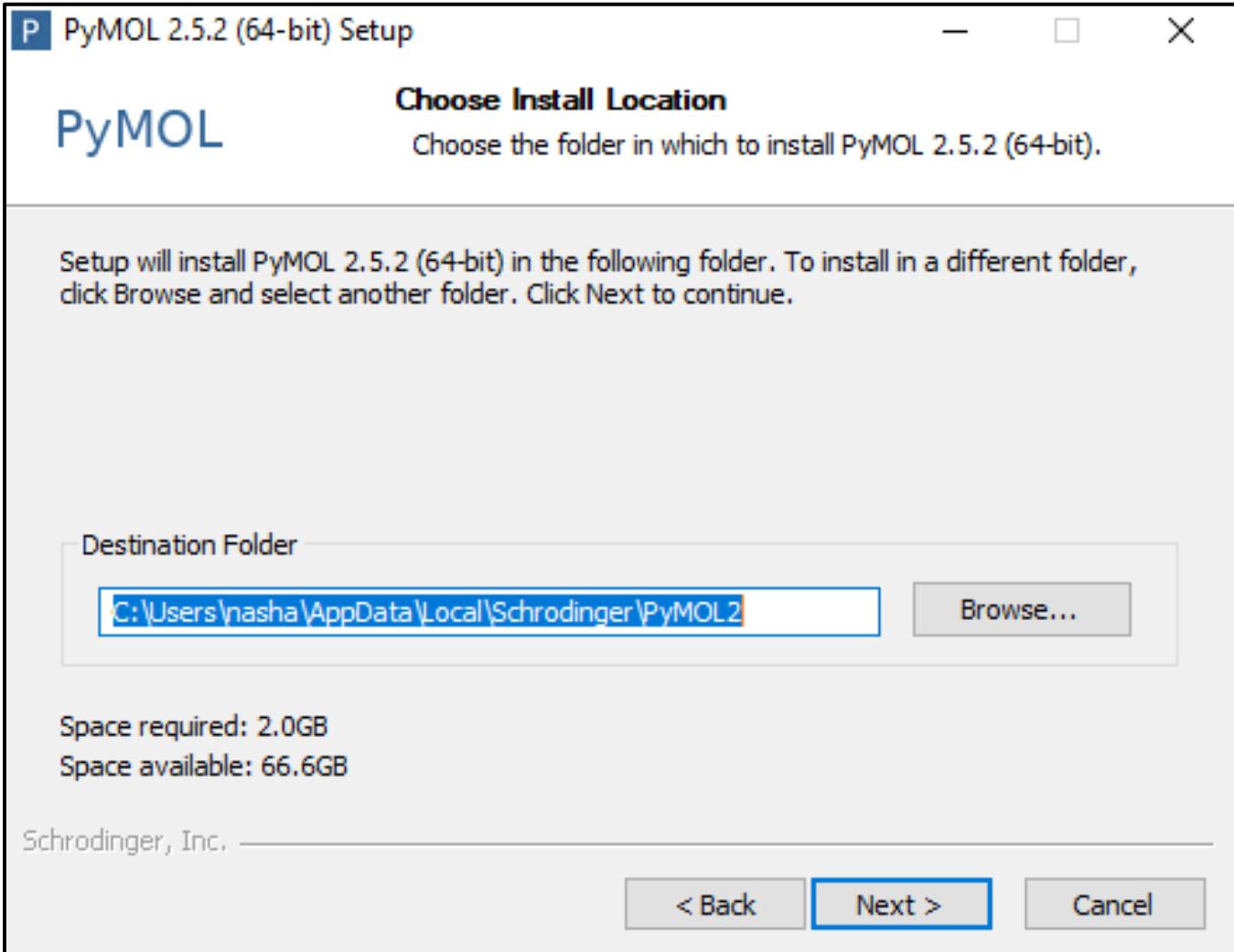
I Agree

Cancel

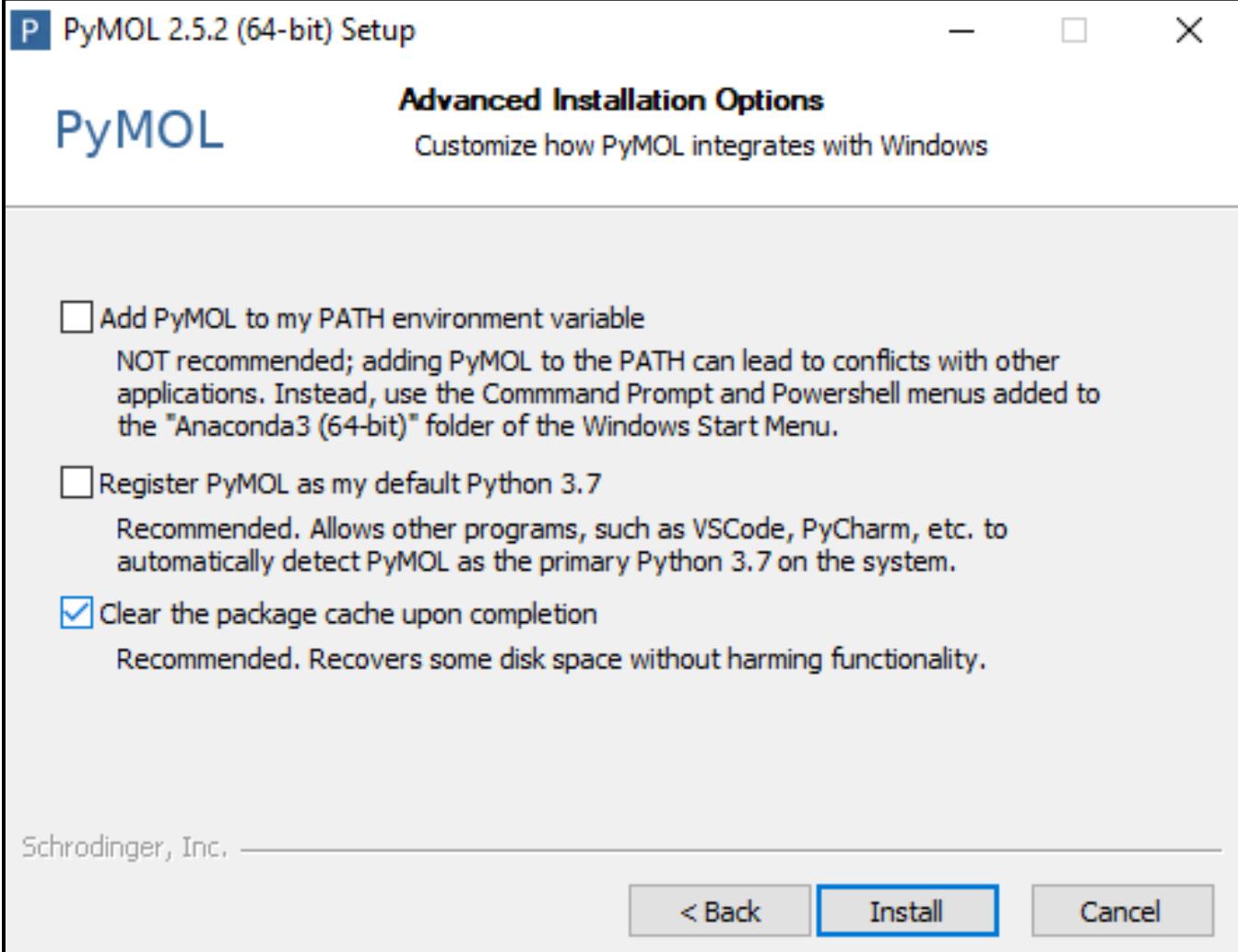
Read the License Agreement and click “I Agree” to proceed



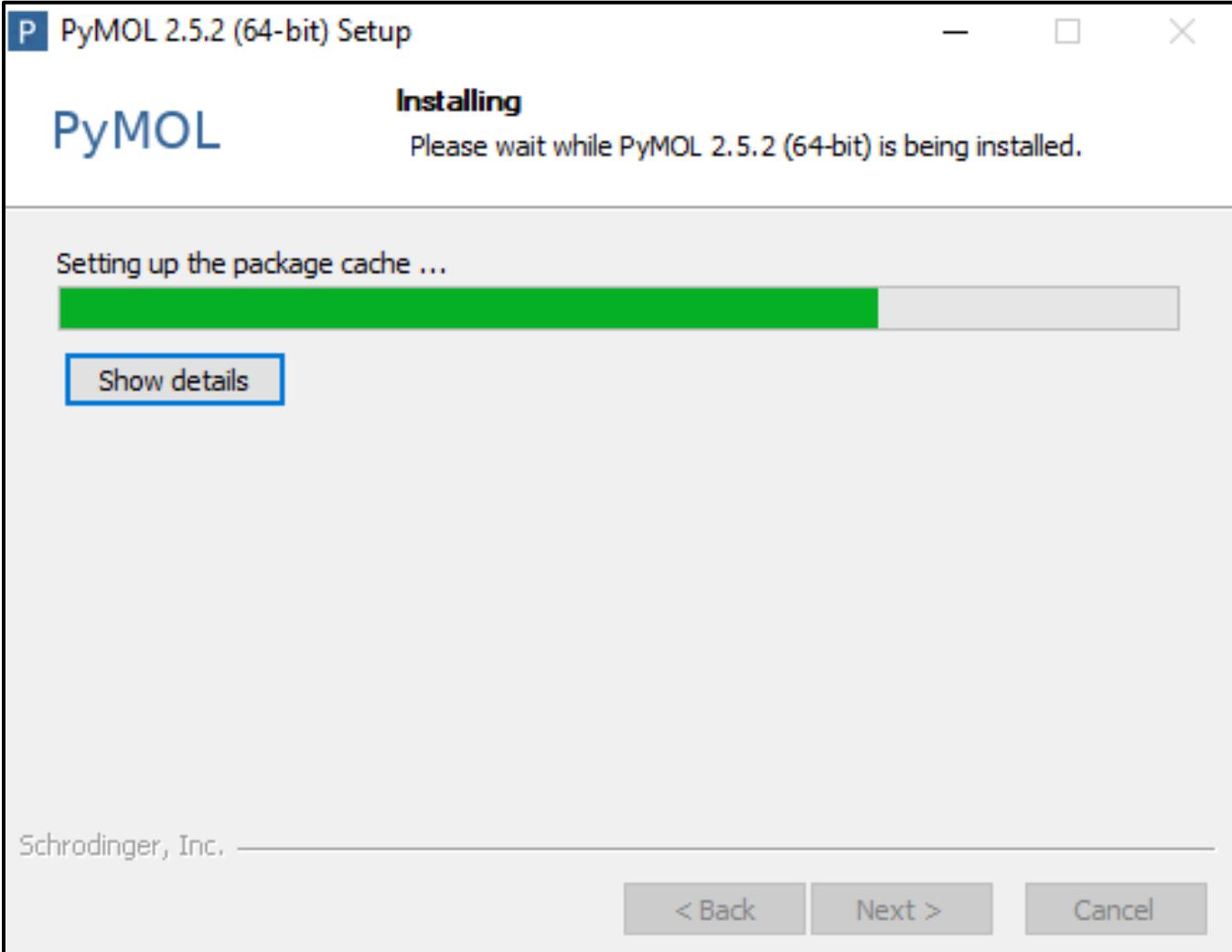
Select the Installation type and click “Next” to proceed



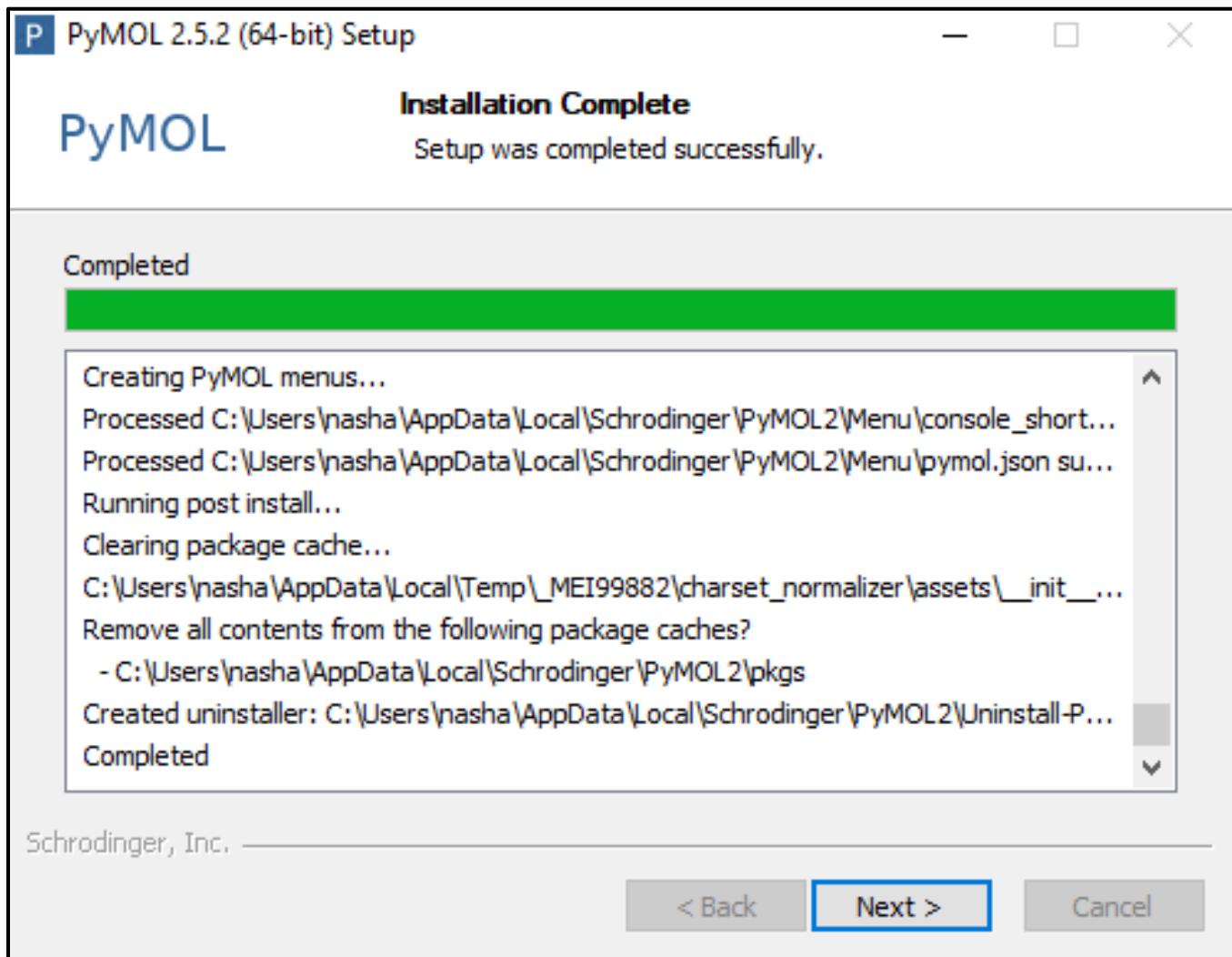
Select the Directory in which you want to install PyMol



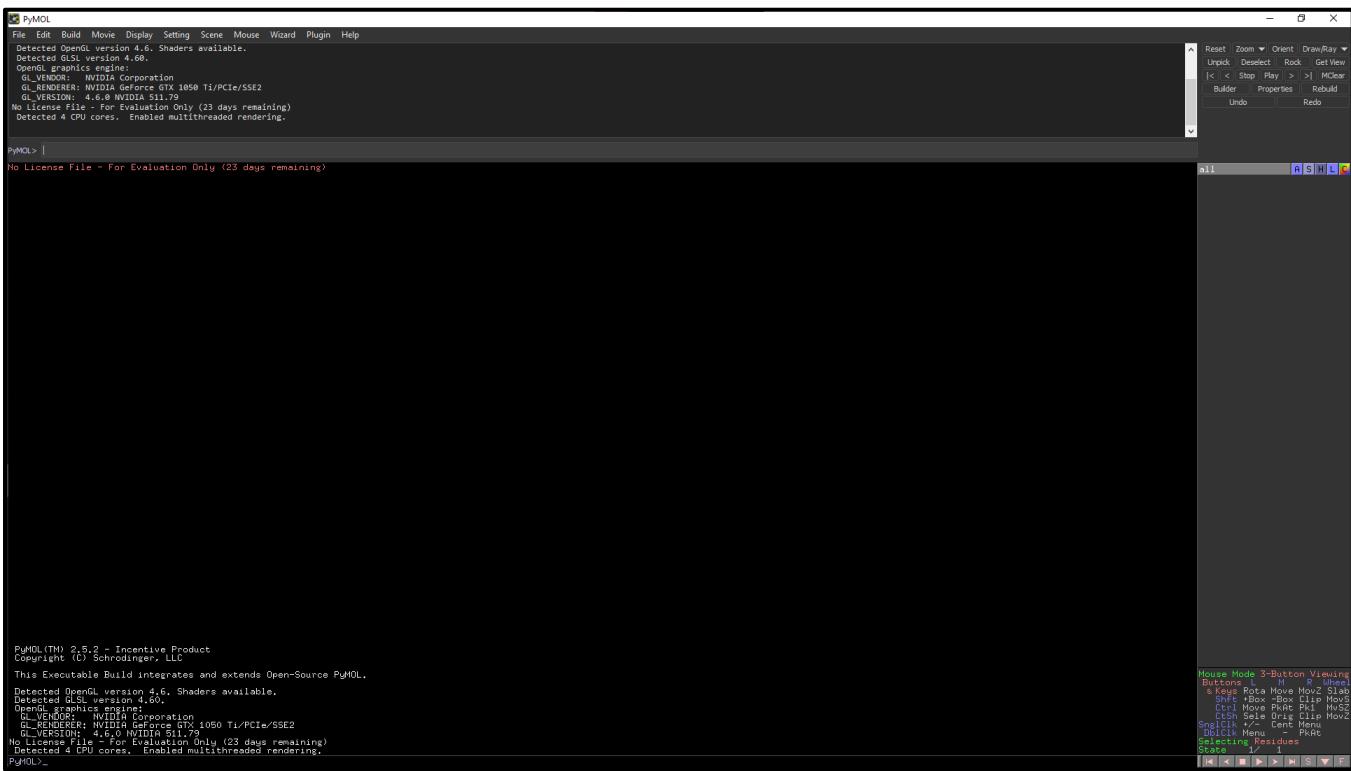
Select the additional options if you want to and click "Install" to start the installation of PyMol



Let the installer install PyMol



After completion click on “Next” to finalize installation



### Pymol is now installed

Thus, RASMOL and PyMOL tools can be used for protein structure visualisation which is helpful in understanding protein–ligand modeling, molecular simulations, and drug screening. It provides an essential support for presenting results, reasoning on and formulating hypotheses related to molecular structure. It also helps to analyze and compare protein structures to gain insight to functions of the proteins.

## REFERENCES:

1. Xiong, J. (2008). Protein Structure Visualization, Comparison, and Classification. Essential bioinformatics. Cambridge: Cambridge University Press. 187-188.
2. Yuan, S., Chan, H. C. S., & Hu, Z. (2017). Using PyMOL as a platform for computational drug design. *WIREs Computational Molecular Science*, 7(2). <https://doi.org/10.1002/wcms.1298>
3. RasMol and OpenRasMol. (n.d.). [Www.openrasmol.org.](http://www.openrasmol.org/) Retrieved March 4, 2022, from <http://www.openrasmol.org/>
4. PyMOL | pymol.org. (2019). [Pymol.org.](https://pymol.org/2/) Retrieved March 4, 2022, from <https://pymol.org/2/>

## WEBLEM 6A

To visualize 3D structure of Hemoglobin (1SI4) using RASMOL & PyMOL tool

RASMOL:

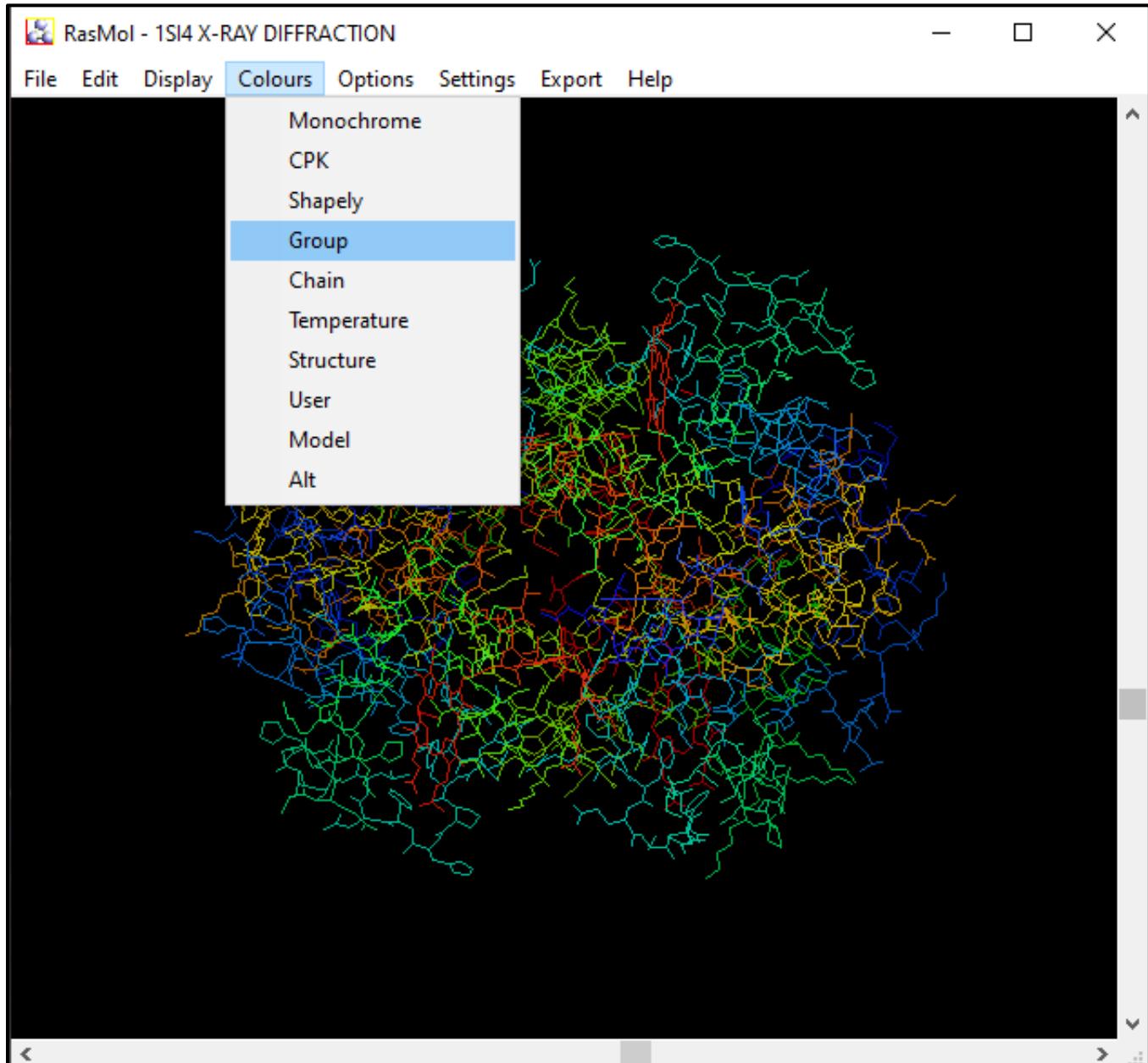


Fig1. PDB Structure of Hemoglobin (1SI4) loaded in RasMol to show it in 3D space with the colour scheme set to Groups

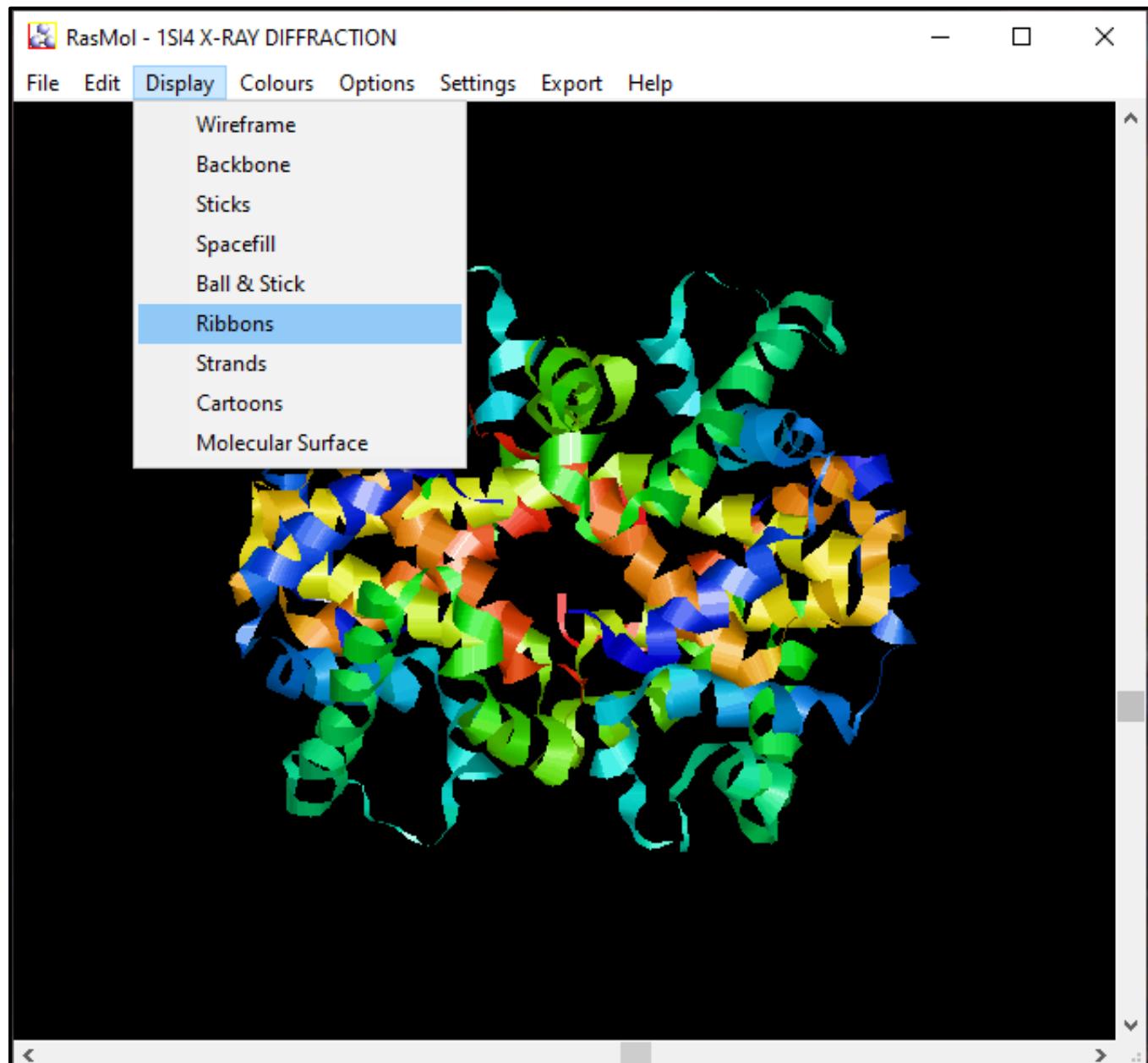


Fig2. PDB structure of Hemoglobin (1SI4) Shown with the display mode set to ribbons

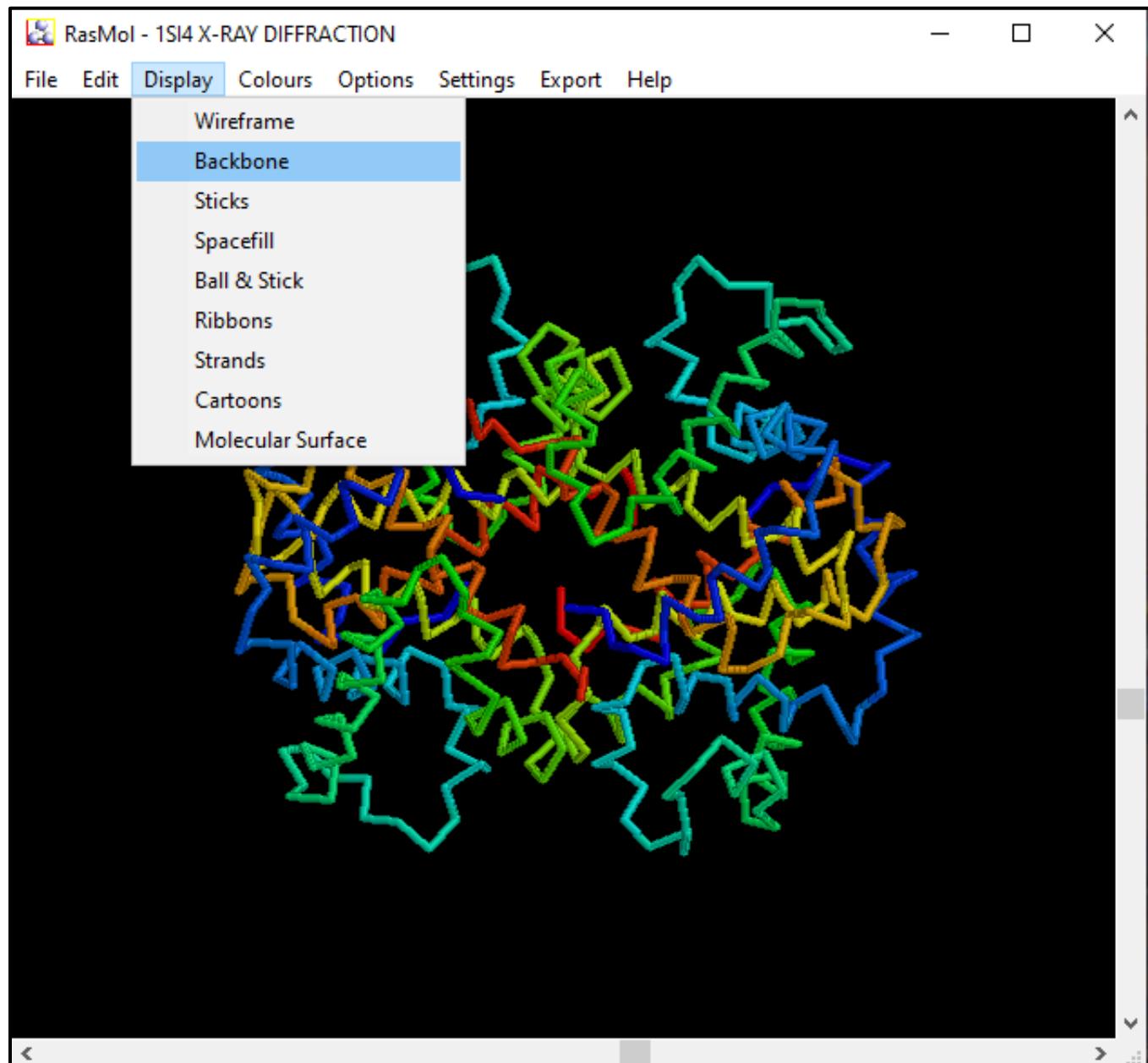


Fig3. PDB structure of Hemoglobin (1SI4) shown with display type set to Backbone

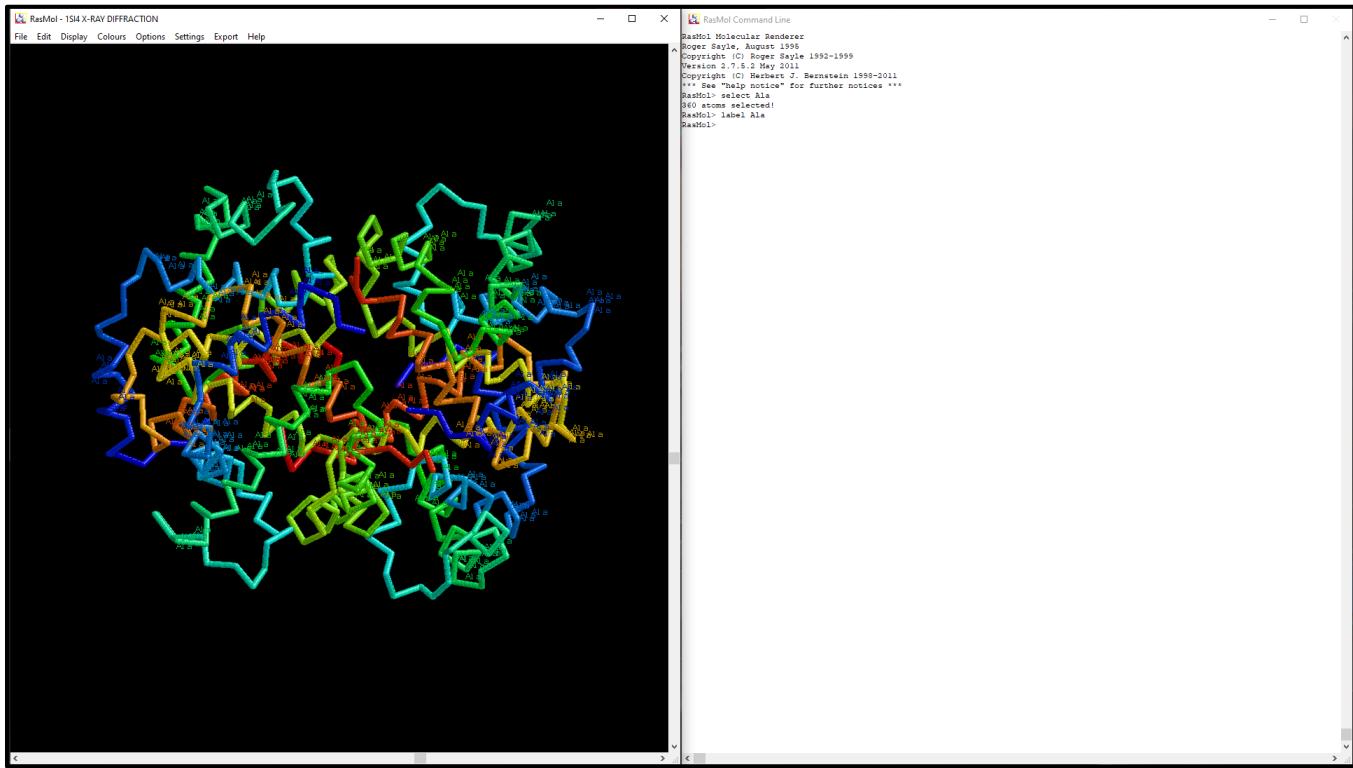


Fig.4 PDB Structure of Hemoglobin (1SI4) visualizing Alanine in the structure.

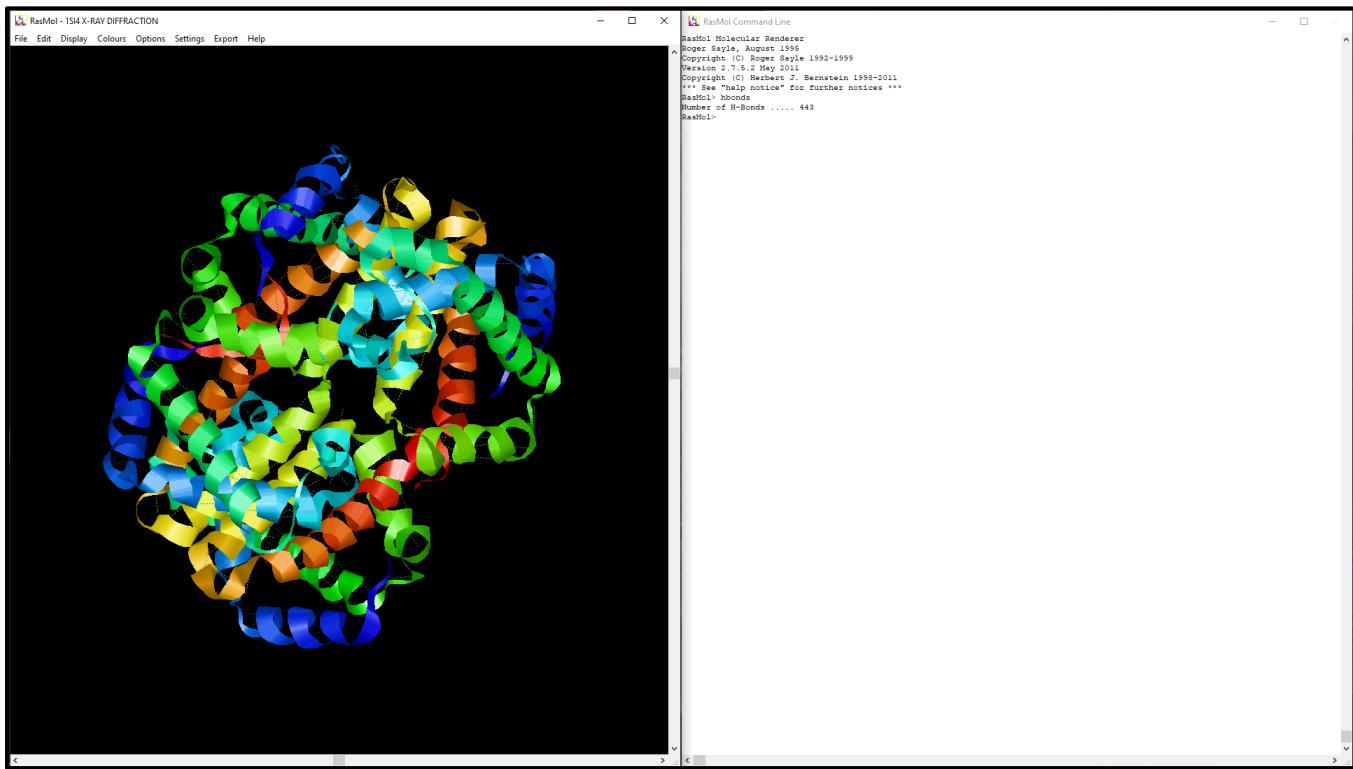


Fig5. PDB structure of Hemoglobin (1SI4) with Hydrogen Bonds visualized

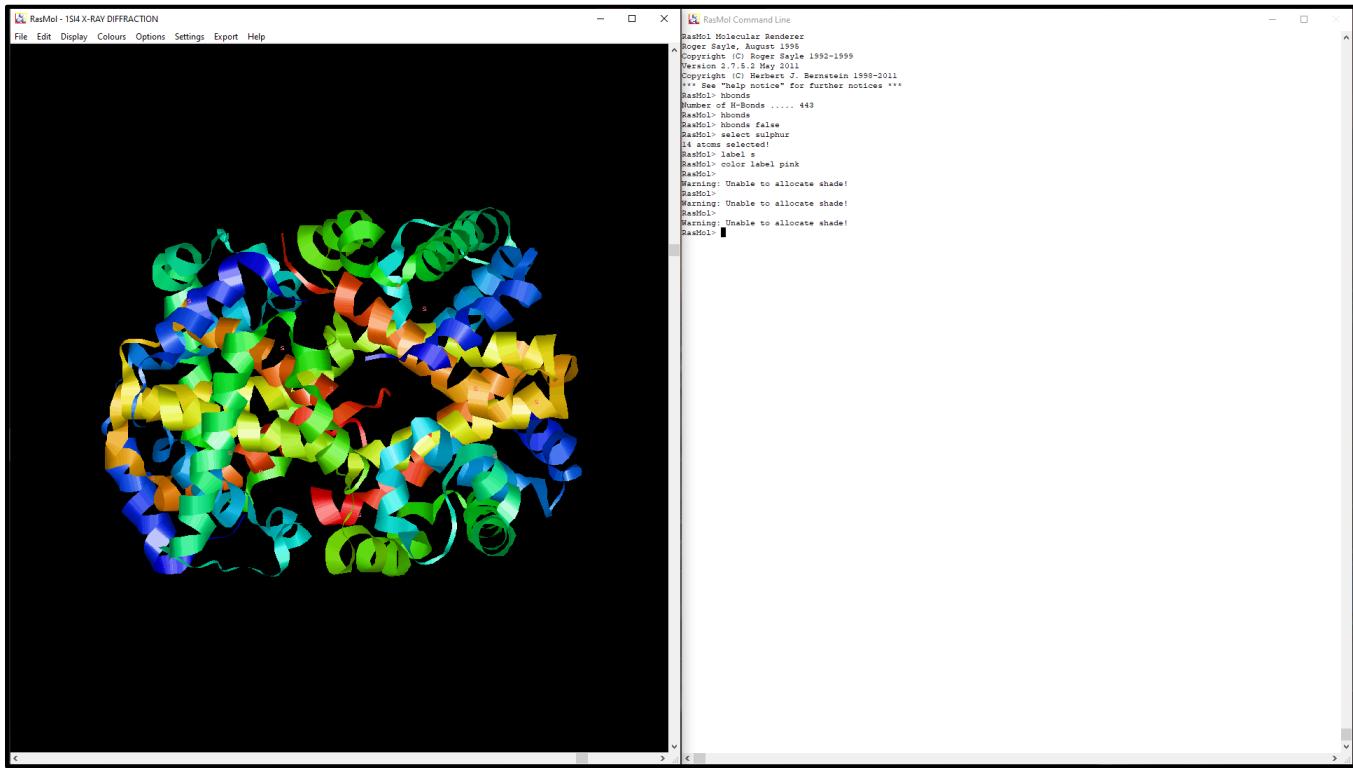


Fig6. PDB structure of Hemoglobin (1SI4) with sulphur atoms visualized with label “s”

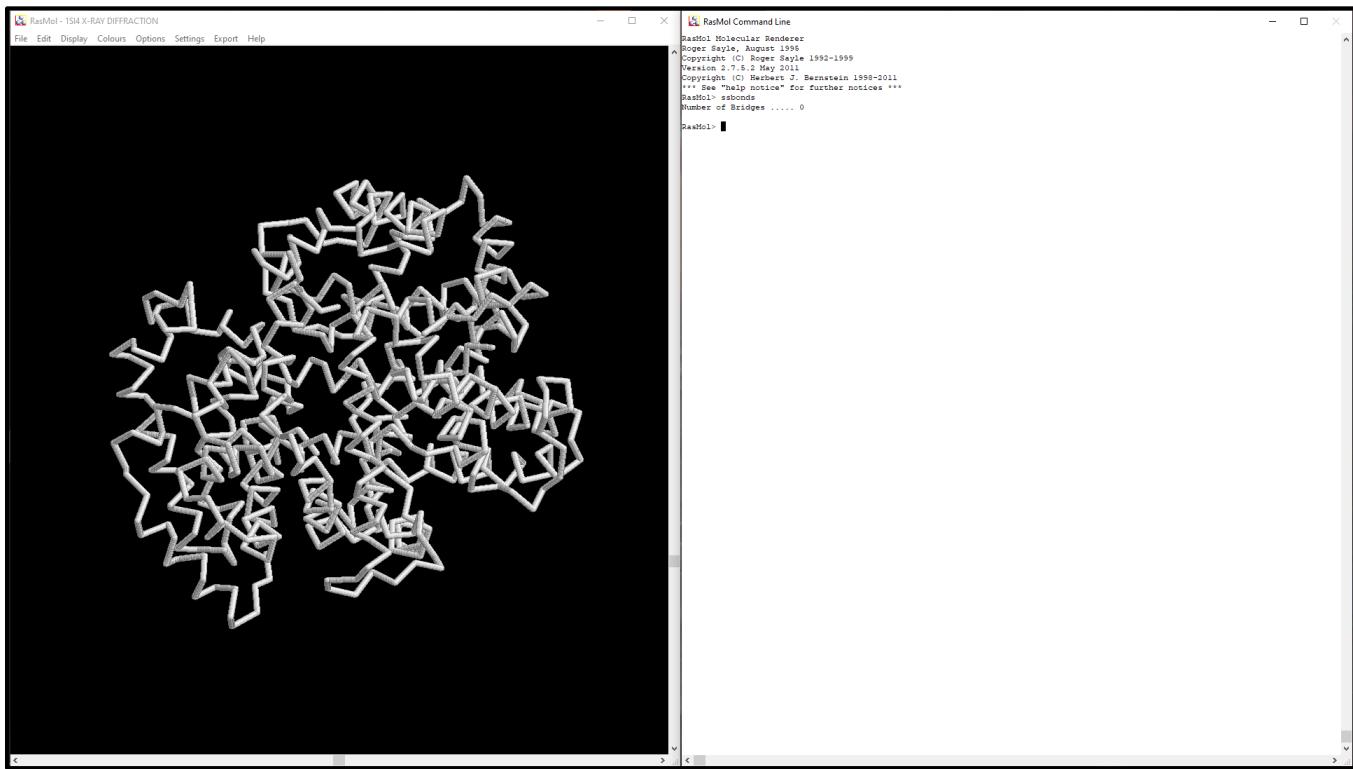
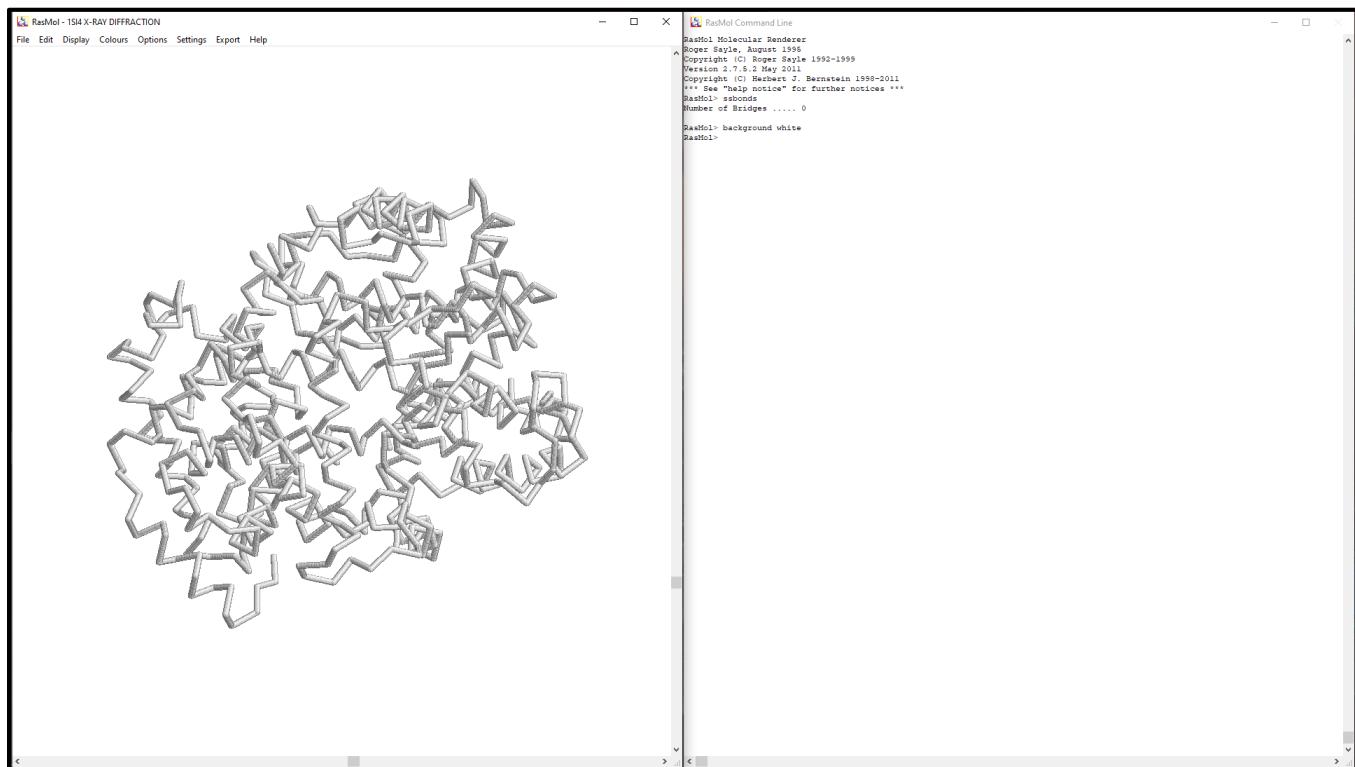
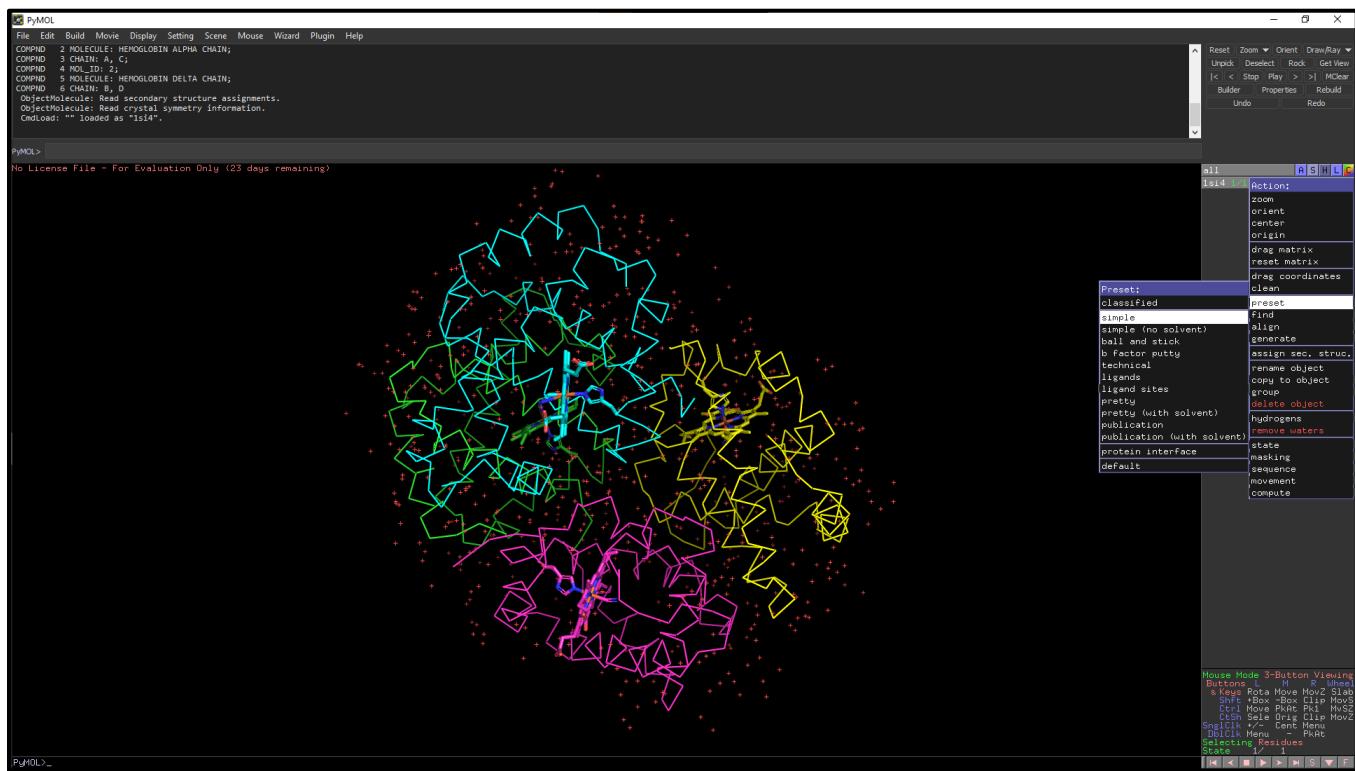


Fig7. PDB structure of Hemoglobin (1SI4) visualizing sulphuer-sulphur bonds (0 in this case)



**Fig8. PDB structure of Hemoglobin (1SI4) with the background color set to white to clearly see the sulphur-sulphur bonds (0 in this case)**

## PYMOL:



**Fig9. PDB structure Hemoglobin (1SI4) loaded in PyMol and set to simple view preset**

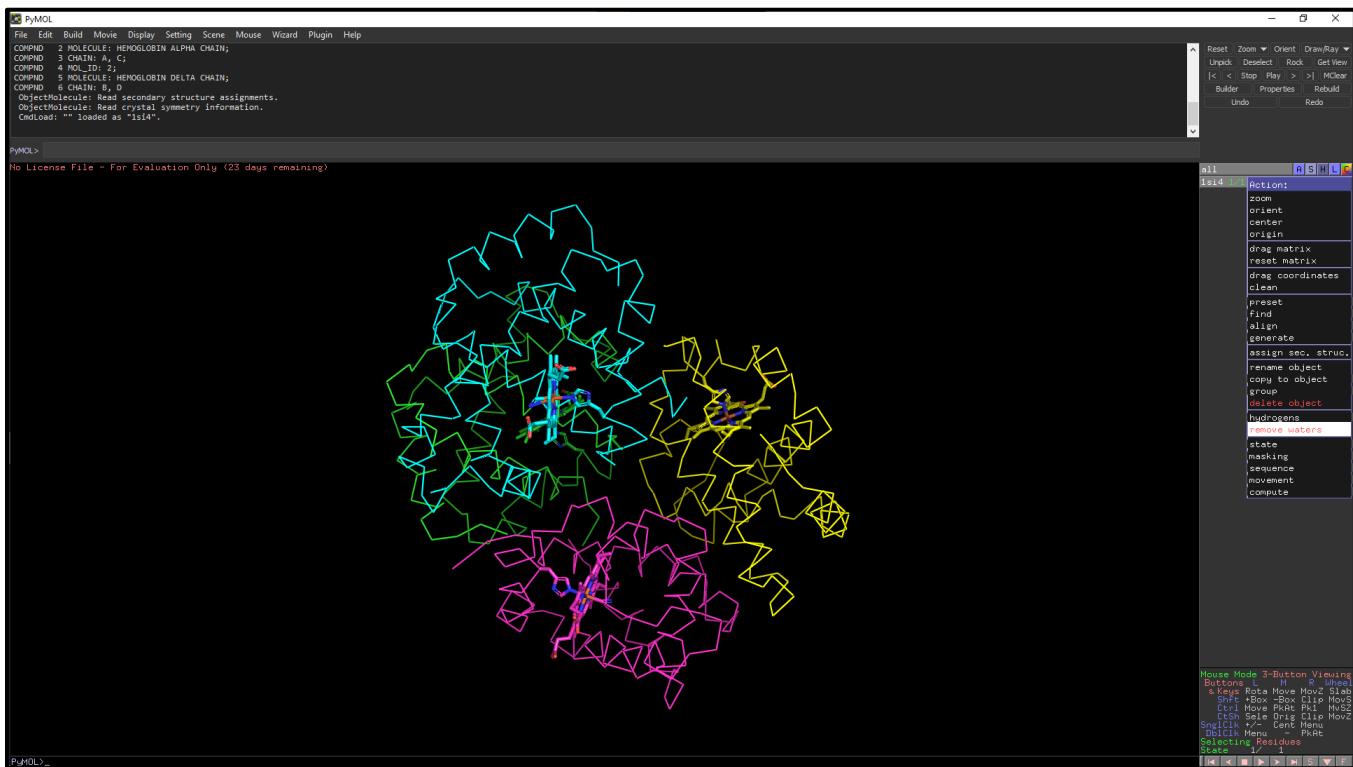


Fig10. PDB structure of Hemoglobin (1SI4) with waters removed

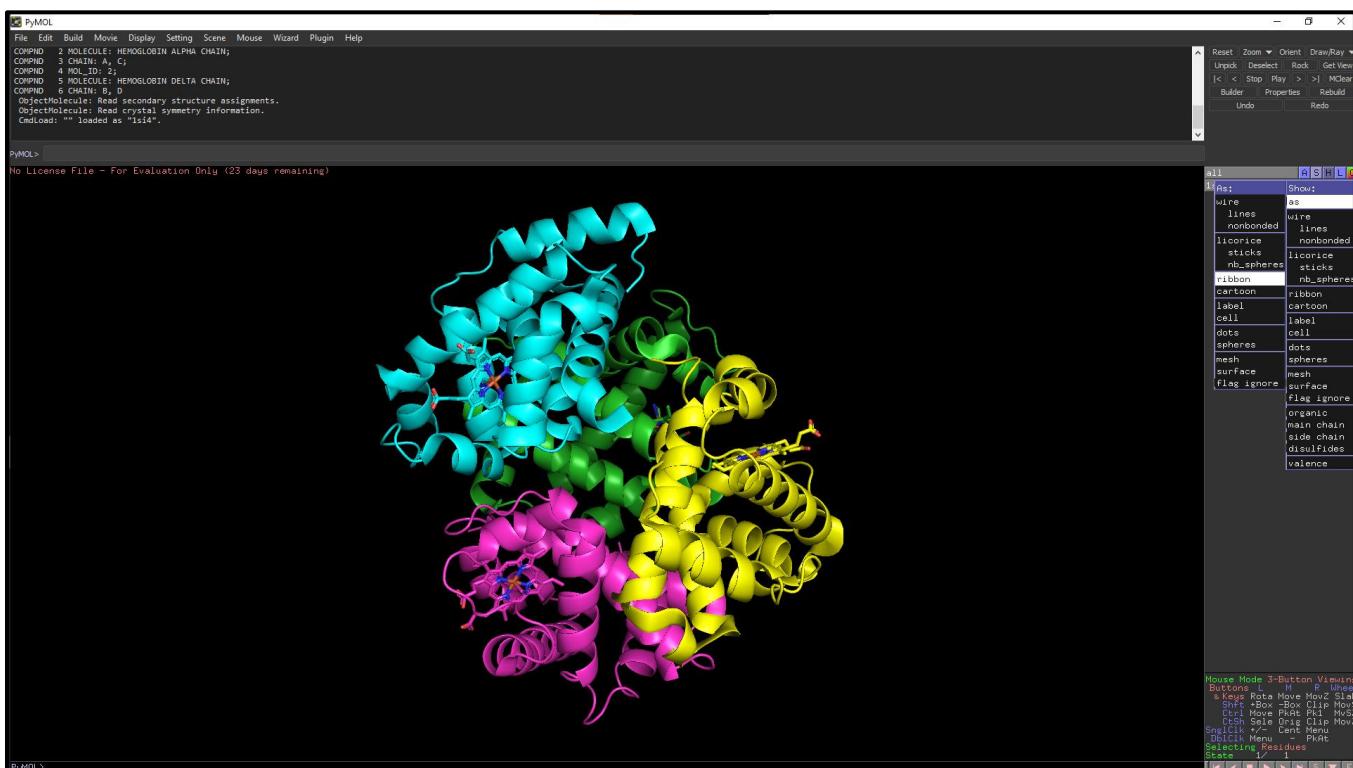
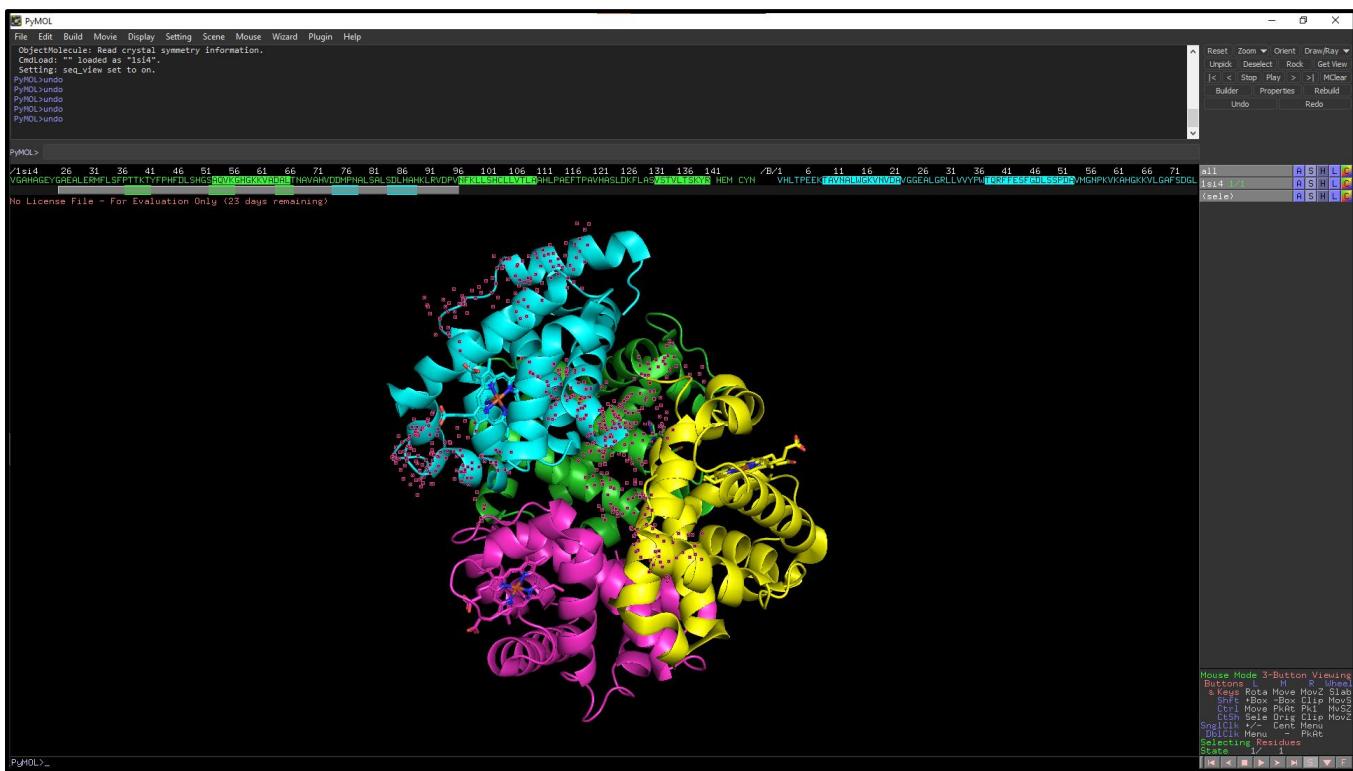


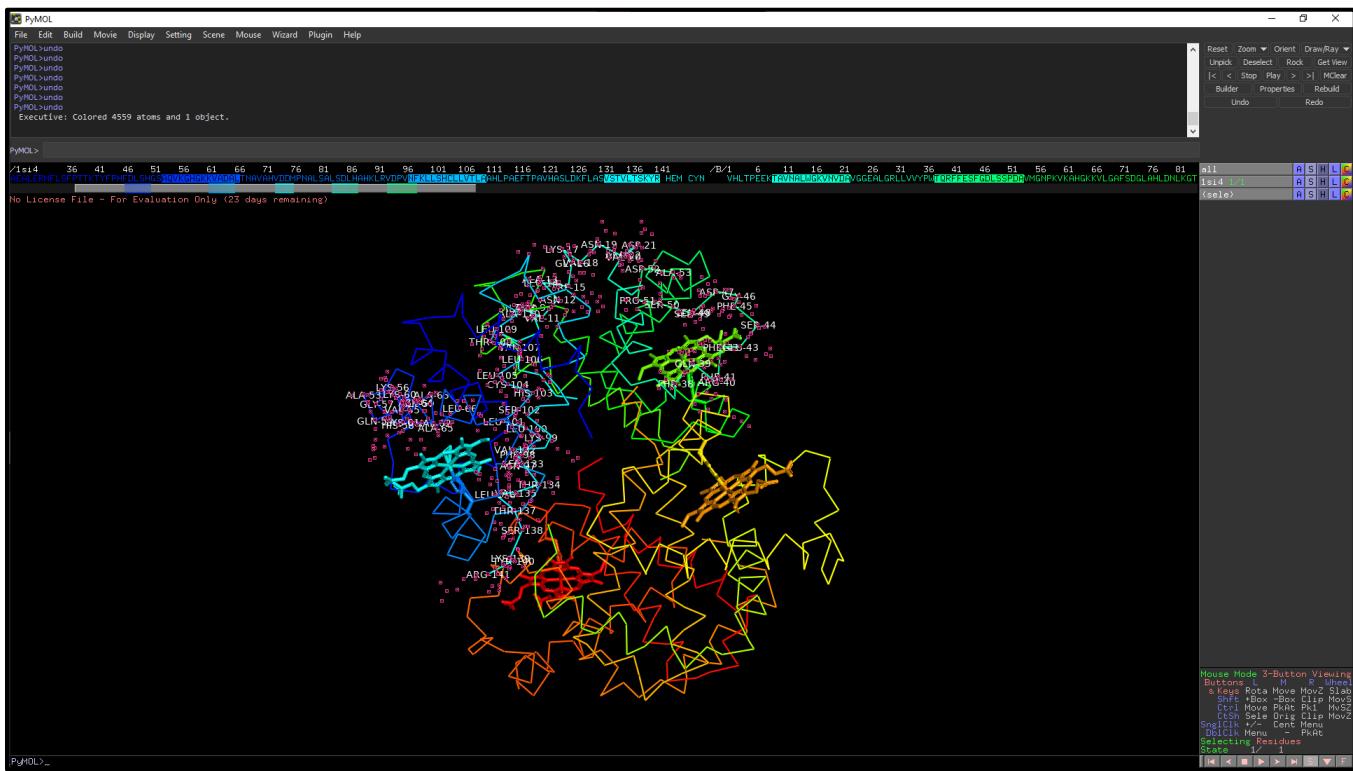
Fig11. PDB structure of Hemoglobin (1SI4) with visual style set to ribbon



**Fig12. PDB structure of Hemoglobin (1SI4) with the sequence displayed**



**Fig13. PDB structure of Hemoglobin (1SI4) with random segments from sequence selected and visualized**



**Fig14. PDB structure of Hemoglobin (1SI4) with the residues of the randomly selected segments from sequence visualized**

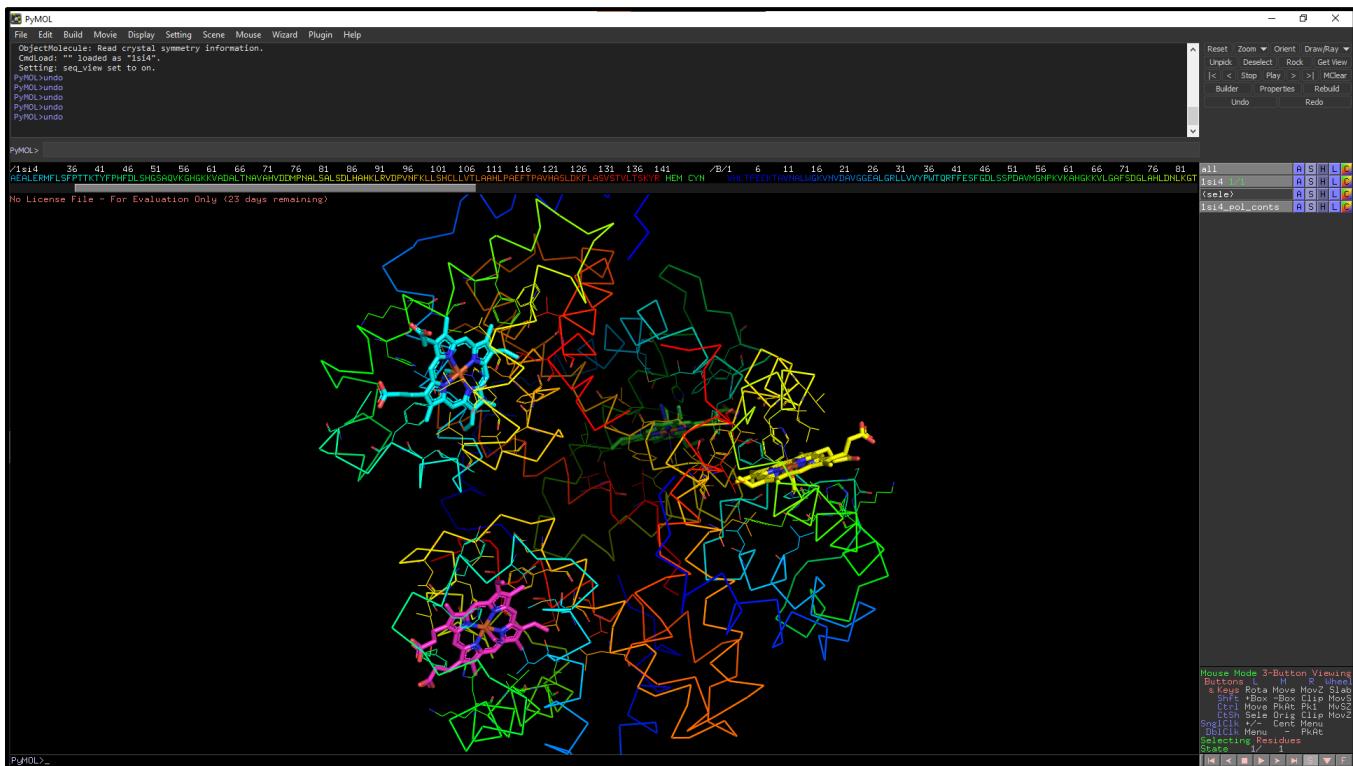


Fig15. PDB structure of Hemoglobin (1SI4) with it set to preset ligand view

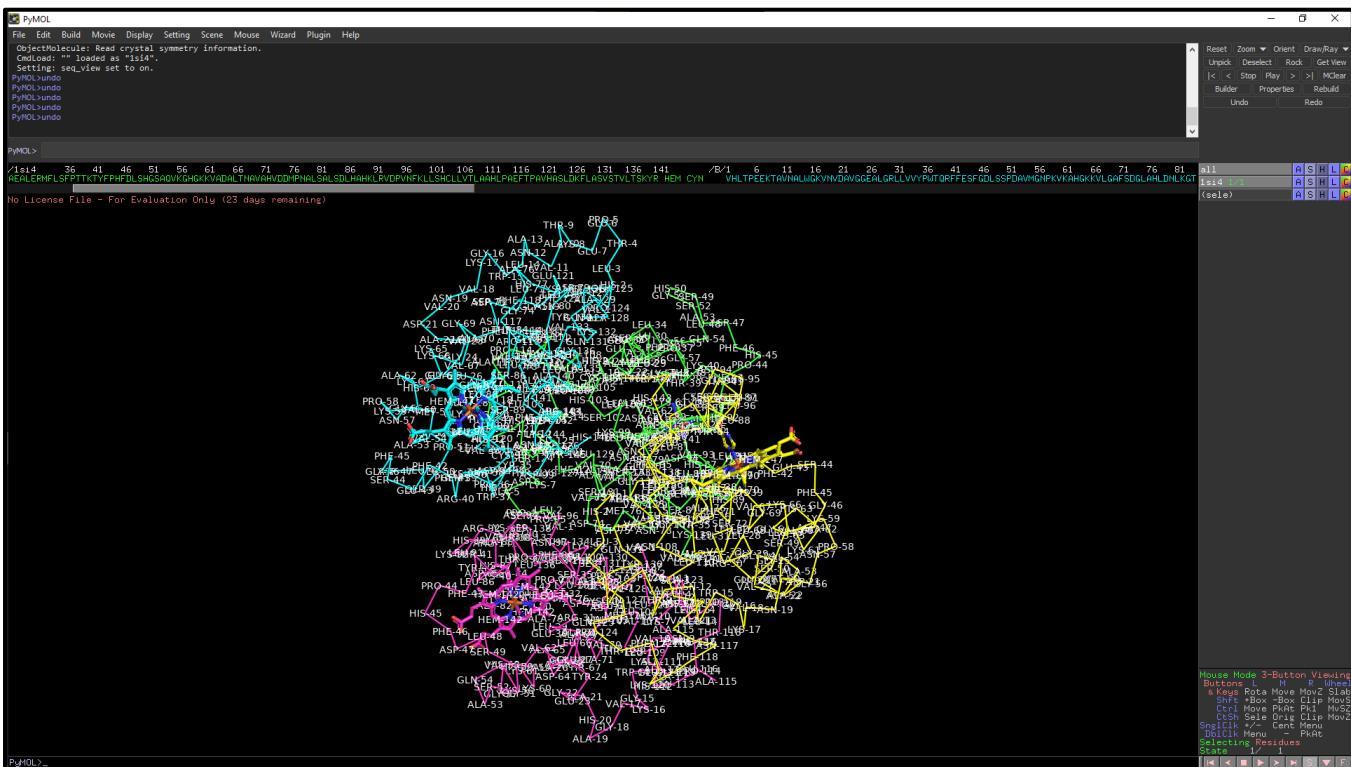


Fig16. PDB structure of Hemoglobin (1SI4) with all its residues labelled

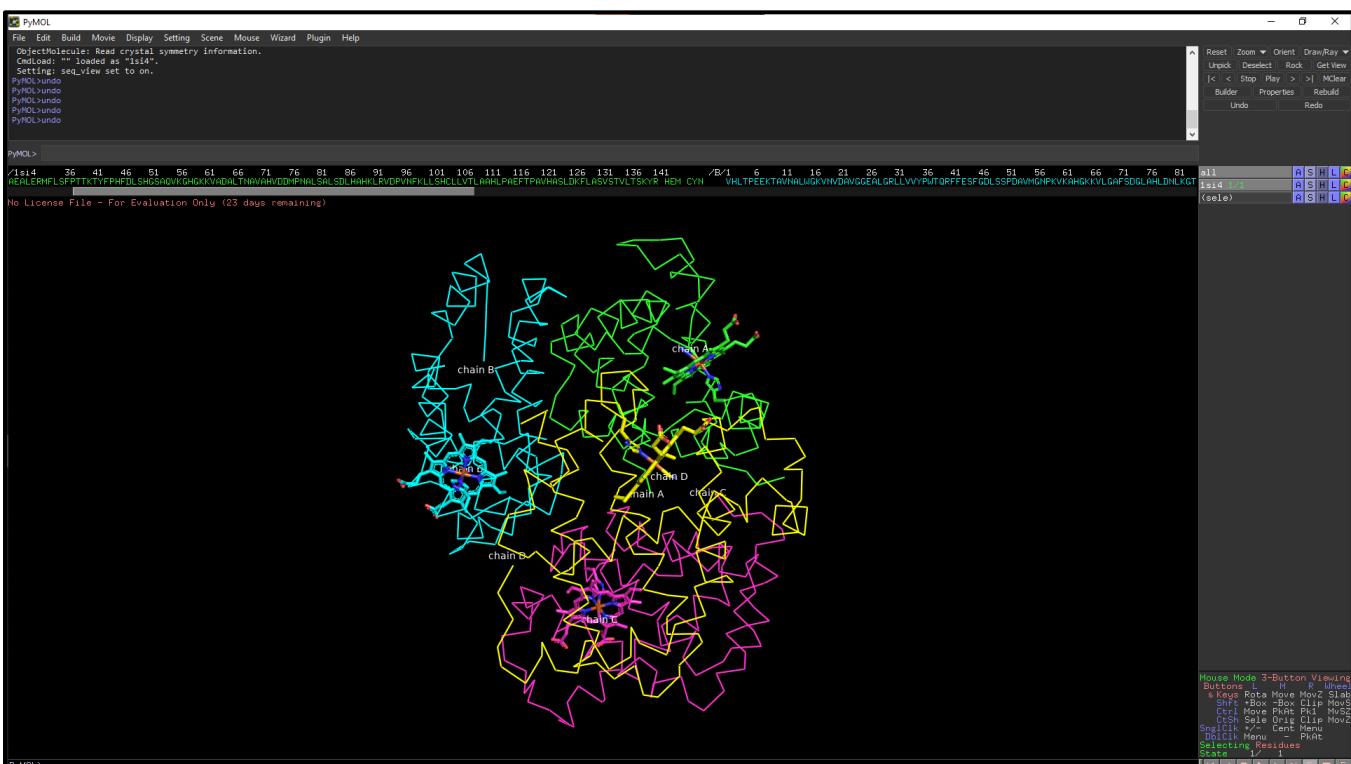
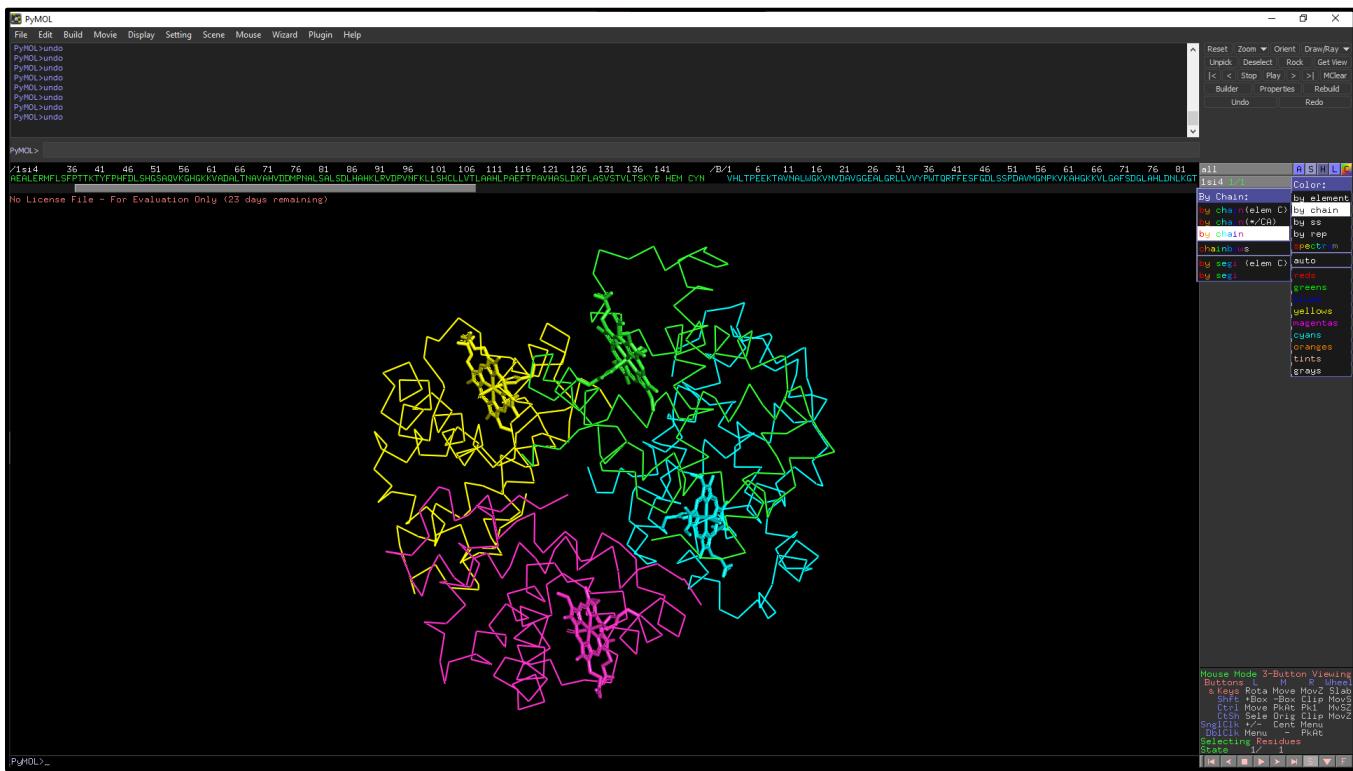


Fig17. PDB structure of Hemoglobin (1SI4) with all its chains labelled



**Fig18. PDB structure of Hemoglobin (1SI4) visualized with the chain color scheme set to rainbow**

## RESULT:

Hemoglobin structure was visualised with various formats along with its residues, bonds and chains using RASMOL and PyMOL tools.

## CONCLUSION:

RASMOL and PyMOL tools can be used for protein structure visualisation which is helpful in understanding protein–ligand modeling, molecular simulations, and drug screening. It provides an essential support for presenting results, reasoning on and formulating hypotheses related to molecular structure. It also helps to analyze and compare protein structures to gain insight to functions of the proteins.

## REFERENCES:

1. The Editors of Encyclopedia Britannica. (2018). Fibrin | biochemistry. In Encyclopædia Britannica. Retrieved March 4, 2022, from <https://www.britannica.com/science/fibrin>
2. Yuan, S., Chan, H. C. S., & Hu, Z. (2017). Using PyMOL as a platform for computational drug design. *WIREs Computational Molecular Science*, 7(2). <https://doi.org/10.1002/wcms.1298>
3. RasMol and OpenRasMol. (n.d.). [Www.openrasmol.org.](http://www.openrasmol.org/) Retrieved March 4, 2022, from <http://www.openrasmol.org/>
4. PyMOL | pymol.org. (2019). [Pymol.org.](https://pymol.org/2/) Retrieved March 4, 2022, from <https://pymol.org/2/>

**WEBLEM 6****Introduction to binding pocket prediction of protein w.r.t to PTM studies**

Protein structures are complex and are sculpted with numerous surface pockets, internal cavities and cross channels. These topographic features provide structural basis and micro-environments for proteins to carry out their functions such as ligand binding, DNA interaction and enzymatic activity. Identification and quantification of these topographic features of proteins are therefore of fundamental importance for understanding the structure–function relationship of proteins, in engineering proteins for desired properties and in developing therapeutics against protein targets.

**CASTp:**

- The CASTp server aims to provide comprehensive and detailed quantitative characterization of topographic features of proteins. Since its release 15 years ago, the CASTp server has ~45,000 visits and fulfills ~33,000 calculation requests annually. It has been proven to be a useful tool for a wide range of studies, including investigations of signaling receptors, discoveries of cancer therapeutics, understanding of mechanism of drug actions, studies of immune disorder diseases, analysis of protein–nanoparticle interactions, inference of protein functions and development of high-throughput computational tools.
- The CASTp server takes protein structures in the PDB format and a probe radius as input for topographic computation. Through the intuitive interface, users can either search for pre-computed results using a four-letter PDB ID, or submit their own protein structures to request customized computation. For pre-computed results, a default probe radius of 1.4 Å is used, which is the standard value for computing solvent accessible surface area. For customized computation request, users can specify any probe radius desired.
- The CASTp server identifies all surface pockets, interior cavities and cross channels in a protein structure and provides detailed delineation of all atoms participating in their formation. It also measures their exact volumes and areas, as well as sizes of the mouth openings if exist. These metrics are calculated analytically, using both the solvent accessible surface model (Richards' surface) and the molecular surface model (Connolly's surface). In addition, the CASTp server also provides imprints of topographic features. These results can be directly downloaded from CASTp server, which can be visualized using either the UCSF Chimera or our PyMOL plugin, CASTpPyMOL.

**NetOGlyc – 4.0**

- Glycosylation is the most abundant and diverse posttranslational modification of proteins. While several types of glycosylation can be predicted by the protein sequence context, and substantial knowledge of these glycoproteomes is available, our knowledge of the GalNAc-type O-glycosylation is highly limited. This type of glycosylation is unique in being regulated by 20 polypeptide GalNAc-transferases attaching the initiating GalNAc monosaccharides to Ser and Thr (and likely some Tyr) residues.
- The finding of unique subsets of O-glycoproteins in each cell line provides evidence that the O-glycoproteome is differentially regulated and dynamic. The greatly expanded view of the O-glycoproteome should facilitate the exploration of how site-specific O-glycosylation regulates protein function.
- The output conforms to the GFF version 2 format. For each input sequence the server prints a list of potential glycosylation sites, showing their positions in the sequence and the prediction confidence scores. Only the sites with scores higher than 0.5 are predicted as glycosylated and marked with the string "#POSITIVE" in the comment field.

**NetPhos - 3.1**

- Protein phosphorylation at serine, threonine or tyrosine residues affects a multitude of cellular signaling processes. How is specificity in substrate recognition and phosphorylation by protein kinases achieved?

- In addition, serine and threonine residues in p300/CBP that can be modified by O-linked glycosylation with N-acetylglucosamine are identified. Glycosylation may prevent phosphorylation at these sites, a mechanism named yin-yang regulation.
- The results can be interpreted as:
  - **Sequence** - the sequence name;
  - **#** - the position of the residue in the sequence;
  - **x** - the residue in one-letter code;
  - **Context** - the sequence context of the residue, shown as a 9-residue subsequence centered on the residue;
  - **Score** - the prediction score (a value in the range [0.000-1.000]; the scores above **0.500** indicate positive predictions);
  - **Kinase** - the active kinase or the string "unsp" for non-specific prediction (as in NetPhos 2.0);
  - **Answer** - the string "**YES**" for positive predictions, else a dot.

## References:

- Tian, W., Chen, C., Lei, X., Zhao, J., & Liang, J. (2018). CASTp 3.0: Computed atlas of surface topography of proteins. *Nucleic Acids Research*, 46(W1). <https://doi.org/10.1093/nar/gky473> Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology.
- Steenroft C, Vakhrushev SY, Joshi HJ, Kong Y, Vester-Christensen MB, Schjoldager KT, Lavrsen K, Dabelsteen S, Pedersen NB, Marcos-Silva L, Gupta R, Bennett EP, Mandel U, Brunak S, Wandall HH, Levery SB, Clausen H. *EMBO J*, 32(10):1478-88, May 15, 2013. (doi: 10.1038/emboj.2013.79. Epub 2013 Apr 12)
- Sequence- and structure-based prediction of eukaryotic protein phosphorylation sites. Blom, N., Gammeltoft, S., and Brunak, S. *Journal of Molecular Biology*: 294(5): 1351-1362, 1999.

## WEBLEM 6A

### To predict binding pocket of protein Glutamine using Castp server.

#### Introduction:

- The CASTp server aims to provide comprehensive and detailed quantitative characterization of topographic features of proteins. Since its release 15 years ago, the CASTp server has ~45,000 visits and fulfills ~33,000 calculation requests annually. It has been proven to be a useful tool for a wide range of studies.
- **Glutamine**
  - Glutamine is the most abundant and versatile amino acid in the body. In health and disease, the rate of glutamine consumption by immune cells is similar or greater than glucose. For instance, in vitro and in vivo studies have determined that glutamine is an essential nutrient for lymphocyte proliferation and cytokine production, macrophage phagocytic plus secretory activities, and neutrophil bacterial killing. Glutamine release to the circulation and availability is mainly controlled by key metabolic organs, such as the gut, liver, and skeletal muscles.

#### Methodology:

- Take a PDB id from a protein structure of Glutamine
- Enter the PDB id on the webpage of CASTp
- Interpret the results

#### Observation:

The screenshot shows the RCSB PDB website interface. At the top, there is a navigation bar with links for Deposit, Search, Visualize, Analyze, Download, Learn, More, Documentation, and Careers. A search bar is located at the top right. Below the header, the RCSB PDB logo is displayed, along with a map of the world and links for PDB-101, Worldwide PDB, EMDataResource, and the Worldwide Protein Data Bank Foundation.

The main content area is titled "2BVC" and describes the "Crystal structure of Mycobacterium tuberculosis glutamine synthetase in complex with a transition state mimic". It provides the PDB DOI (10.2210/pdb2BVC/pdb), classification (LIGASE), organism (Mycobacterium tuberculosis H37Rv), expression system (Escherichia coli BL21), and mutation information. The structure is shown as a 3D ribbon model of a protein dimer.

On the left, there are links for "3D View", "Annotations", "Experiment", "Sequence", "Genome", "Ligands", and "Versions". On the right, there are buttons for "Display Files" and "Download Files".

The "Experimental Data Snapshot" section includes details about the method (X-RAY DIFFRACTION), resolution (2.10 Å), and R-value metrics (Free: 0.230, Work: 0.191, Observed: 0.193). The "wwPDB Validation" section provides a summary of validation metrics and percentile ranks relative to all X-ray structures and similar resolution structures.

Fig1. PDB page for query Glutamine

CASTp

Computed Atlas of Surface Topography of proteins

CASTp Calculation Background Plugin FAQ

Please cite this paper if you publish or present results using CASTp analysis:

Tian et al., Nucleic Acids Res. 2018. PMID: 29860391 DOI: 10.1093/nar/gky473.

For questions and bugs, please contact uic.lianglab(at)gmail.com.

SHOW POCKETS DOWNLOAD

PDB or job ID: 2BVC

2R7G

Structure of the retinoblastoma protein pocket domain in complex with adenovirus E1A CR1 domain

PocID	Area (SA)	Volume (SA)
1	1297.018	1555.051

Fig2. CASTp page with the PDB id of my query entered

2BVC

Crystal structure of Mycobacterium tuberculosis glutamine synthetase in complex with a transition state mimic

PocID	Area (SA)	Volume (SA)
1	9854.746	50255.524

PocID	Chain	SeqID	AA	Atom
1	A	17	LYS	CD
1	A	17	LYS	CE
1	A	17	LYS	NZ
1	A	19	GLU	CB
1	A	19	GLU	CG
1	A	19	GLU	CD

Fig3. Result of my query on CASTp

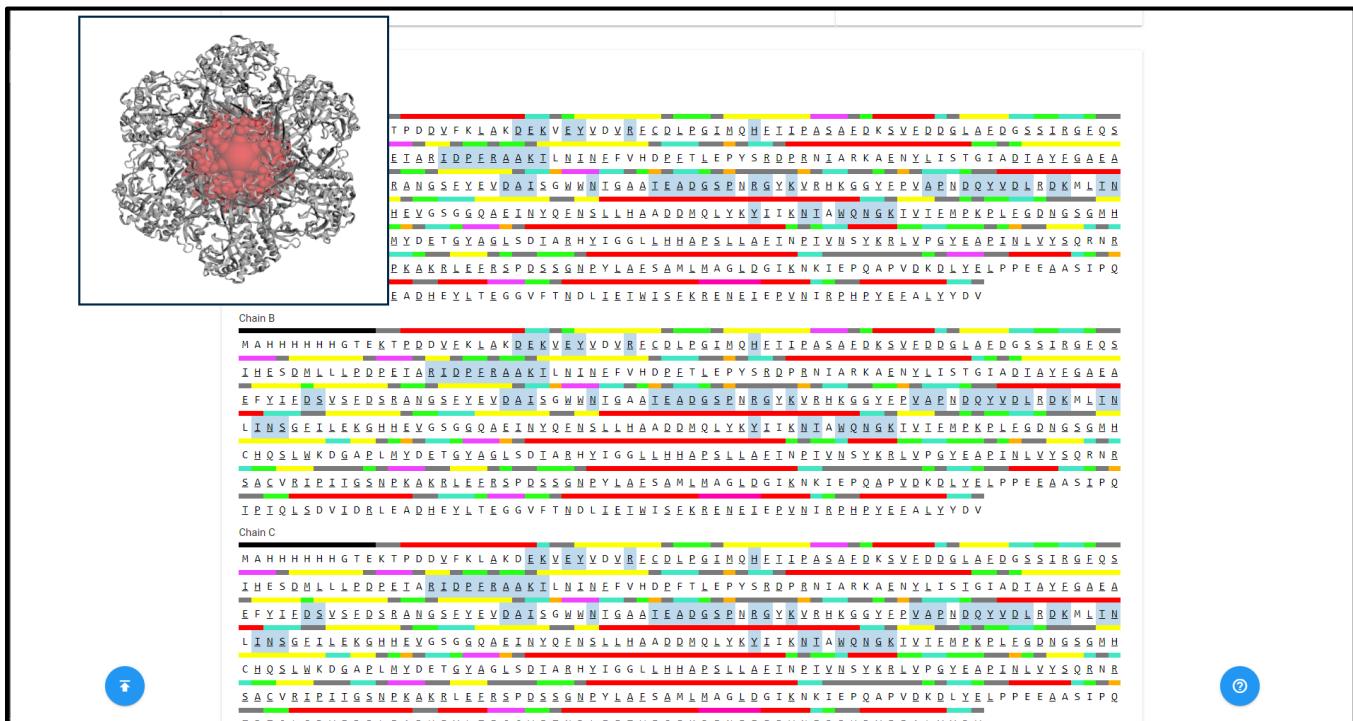


Fig4. Sequence data of the query on CASTp

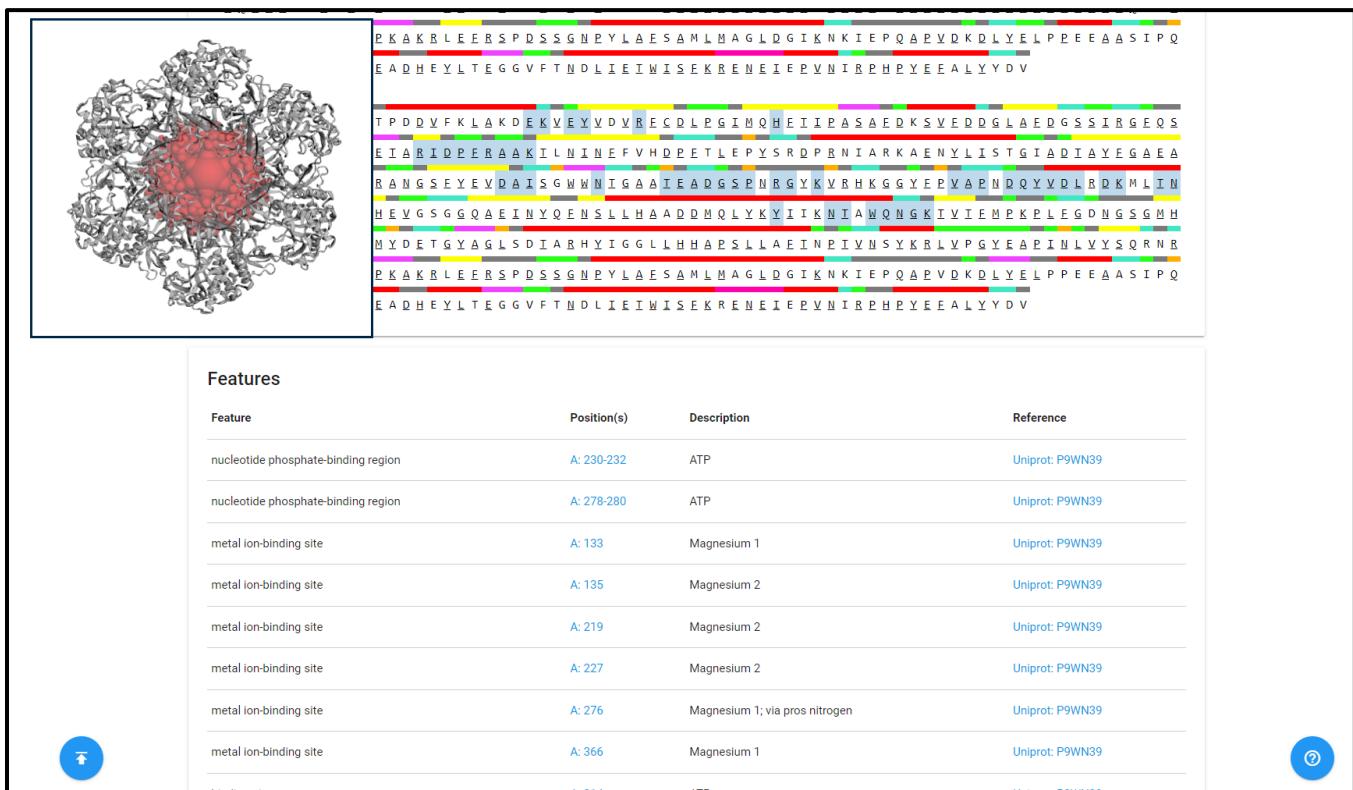
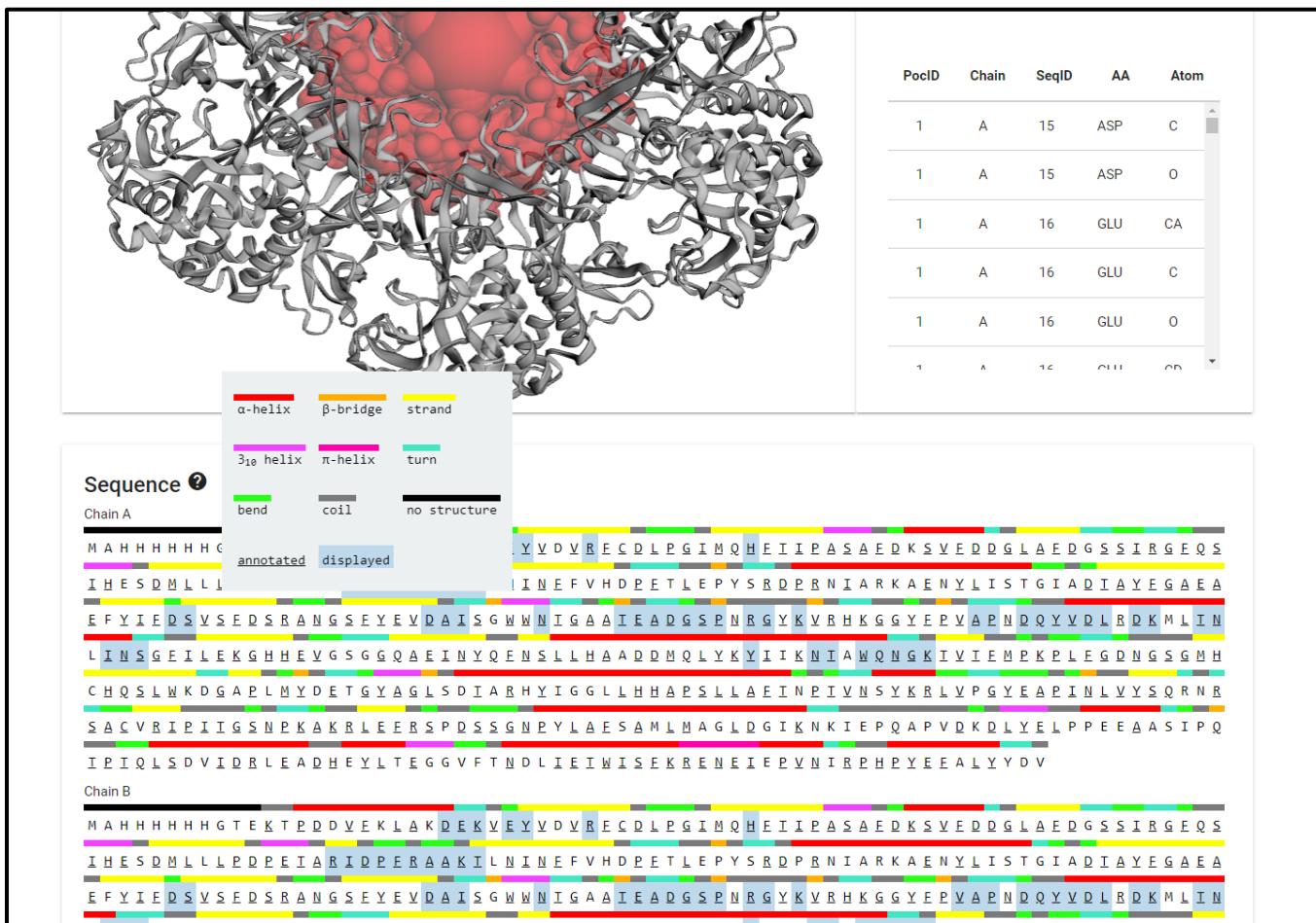
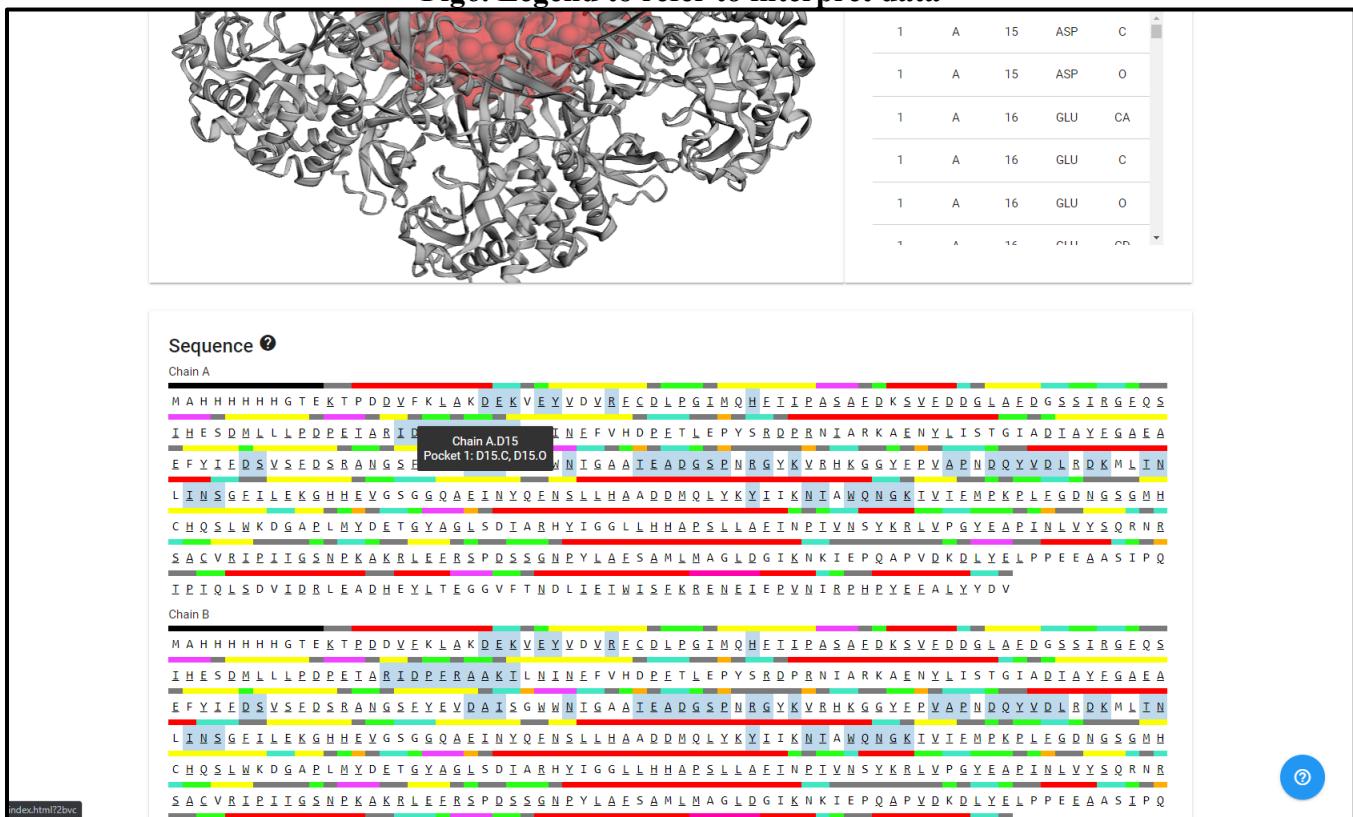


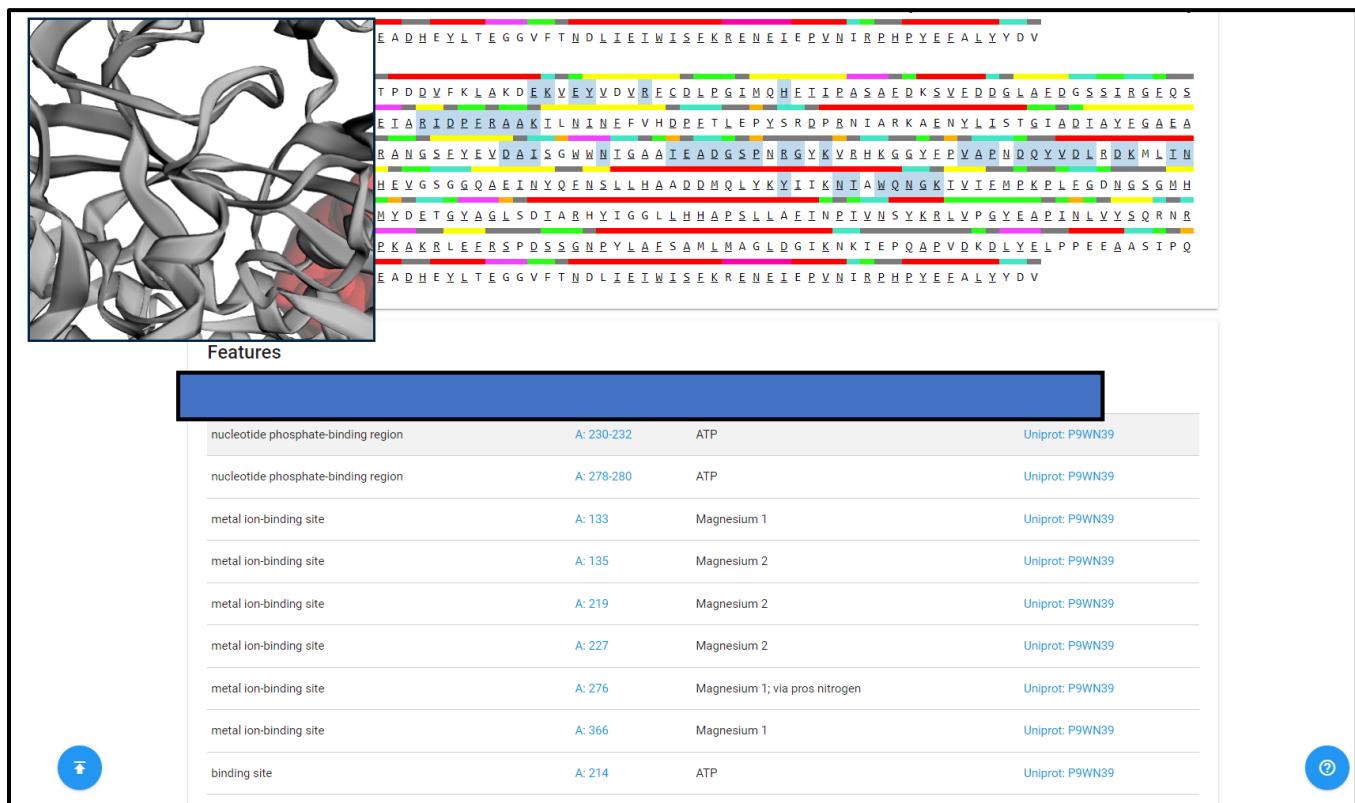
Fig5. Features data of my query on CASTp



### Fig6. Legend to refer to interpret data



**Fig7. Pocket info for Chain A.D15, Pocket 1: D15.C, D15.O**



**Fig8. Position in 3D space of nucleotide phosphate binding region A:230-232**

Please cite this paper if you publish or present results using CASTp analysis:

Tian et al., Nucleic Acids Res. 2018. PMID: 29860391 DOI: 10.1093/nar/gky473.

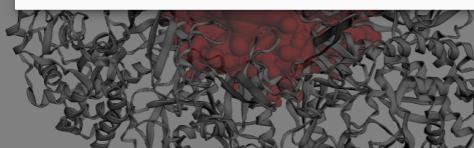
For questions and bugs, please contact us: baigled@gmail.com

Configure the visualization of pockets

Show	Pocket ID	Area (SA)	Volume (SA)	Negative Volume Color	Representation Style
<input checked="" type="checkbox"/>	1	9854.746	50255.524	Red	Cartoon
<input checked="" type="checkbox"/>	2	33.830	16.244	Blue	Cartoon
<input checked="" type="checkbox"/>	3	12.760	1.458	Green	Cartoon
<input checked="" type="checkbox"/>	4	17.884	3.260	Yellow	Cartoon
<input type="checkbox"/>	5	37.389	16.648	Red	Cartoon
<input type="checkbox"/>	6	26.462	5.897	Red	Cartoon
<input type="checkbox"/>	7	29.620	6.403	Red	Cartoon

Volume and/or surface rendering for large pockets may cause high usage of memory and CPU.

CANCEL UPDATE



Atom	Element	Atom	Element	Atom	Element
1	A	15	ASP	C	O
1	A	15	ASP	O	
1	A	16	GLU	CA	

**Fig9. Customizing the visualization of pocket in CASTp**

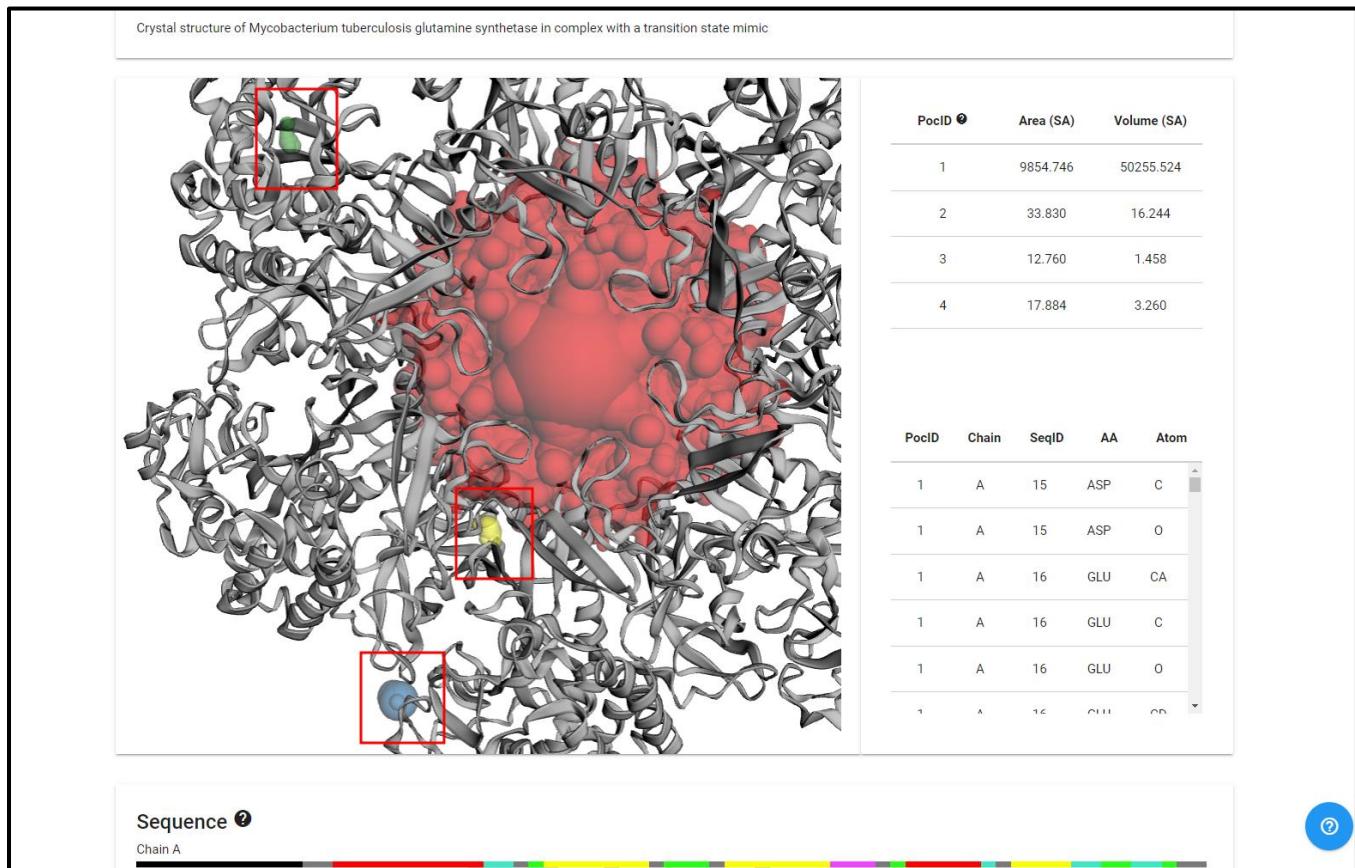


Fig10. Customized view of pockets for query in CASTp

## Result:

1. The Results are categorically divided:
  - a. **Structure:** Here we can customize the visualization of the protein structure.
  - b. **Sequence:** Here we can see the amino acid sequences of the given protein structure.
  - c. **Features:** Here we see the features of the provided protein structure
2. In the given structure the Area is 9854.746 SA and the volume is 50255.524 SA

## Observation:

- Castp is a great tool to find out the specific sites on the protein in 3D space.
- The colors of the site can be changed according to us and be seen clearly and boldly.

## References:

- Bank, R. C. S. B. P. D. (n.d.). 2BVC: *Crystal structure of mycobacterium tuberculosis glutamine synthetase in complex with a transition state mimic*. RCSB PDB. Retrieved March 3, 2022, from <https://www.rcsb.org/structure/2BVC>
- CASTp 3.0: Computed atlas of surface topography of proteins. (n.d.). Retrieved March 3, 2022, from <http://sts.bioe.uic.edu/castp/index.html?2bvc>
- Cruzat, V., Macedo Rogero, M., Noel Keane, K., Curi, R., & Newsholme, P. (2018). Glutamine: Metabolism and immune function, supplementation and clinical translation. *Nutrients*, 10(11), 1564. <https://doi.org/10.3390/nu10111564>



## WEBLEM 6B

### To predict binding pocket for Glycosylation sites in (query name) using NetOGlyc 4.0 Server

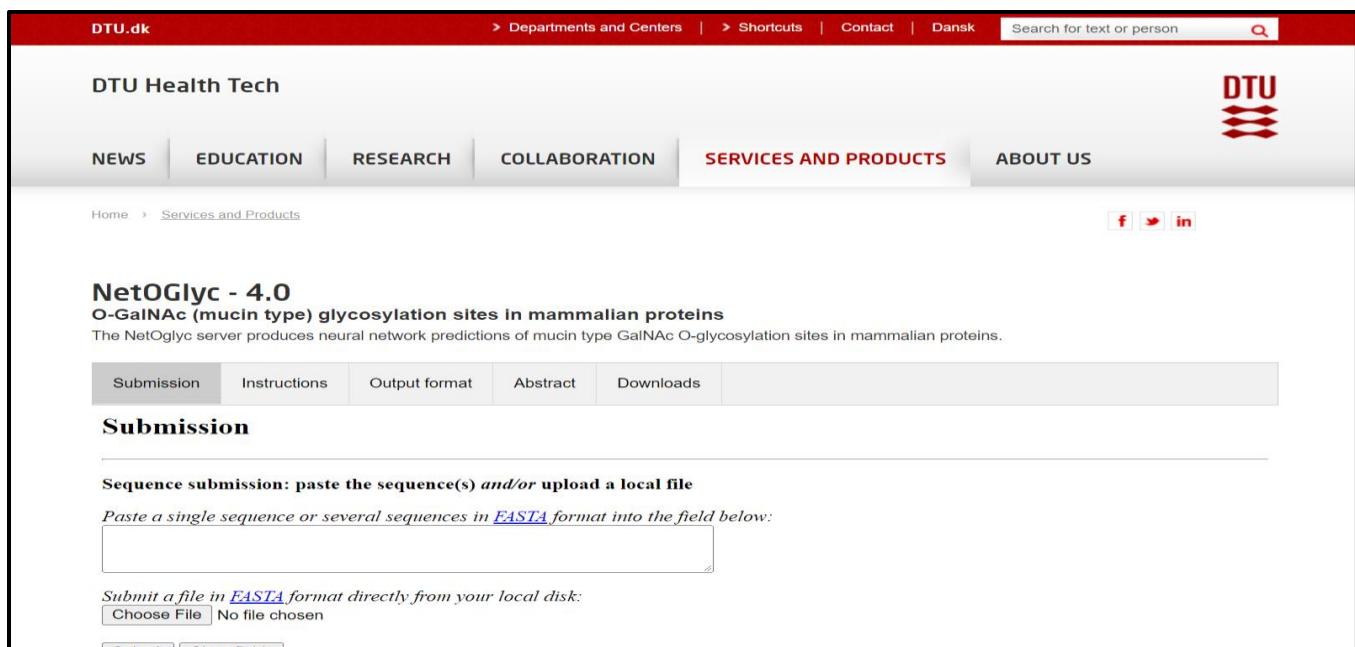
#### **Introduction:**

- Glycosylation is the most abundant and diverse posttranslational modification of proteins.
- The output conforms to the GFF version 2 format. For each input sequence the server prints a list of potential glycosylation sites, showing their positions in the sequence and the prediction confidence scores. Only the sites with scores higher than 0.5 are predicted as glycosylated and marked with the string "#POSITIVE" in the comment field.
- **Glutamine**
  - Glutamine is the most abundant and versatile amino acid in the body. In health and disease, the rate of glutamine consumption by immune cells is similar or greater than glucose. For instance, in vitro and in vivo studies have determined that glutamine is an essential nutrient for lymphocyte proliferation and cytokine production, macrophage phagocytic plus secretory activities, and neutrophil bacterial killing. Glutamine release to the circulation and availability is mainly controlled by key metabolic organs, such as the gut, liver, and skeletal muscles.

#### **Methodology:**

- Take a FASTA sequence from uniprot
- Enter the sequence into the submission box
- Interpret the result according to the output tab

#### **Observation:**



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DTU Health Tech

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Home > Services and Products

f  

### NetOGlyc - 4.0

O-GalNAc (mucin type) glycosylation sites in mammalian proteins

The NetOGlyc server produces neural network predictions of mucin type GalNAc O-glycosylation sites in mammalian proteins.

Submission Instructions Output format Abstract Downloads

#### Submission

Sequence submission: paste the sequence(s) and/or upload a local file

Paste a single sequence or several sequences in [FASTA](#) format into the field below:

Submit a file in [FASTA](#) format directly from your local disk:  
Choose File No file chosen

Clear file Clear all

**Fig1. Homepage of NetOGlyc – 1.0**

```

>sp|P21980|TGM2_HUMAN Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens
OX=9606 GN=TGM2 PE=1 SV=2
MAEELVLERCDLELETNGRDHHTADLCREKLVRRGQPFWLTLHFEGRNYEASVDSLTF
VVTGPAPSQEAGTKARFPLRDAVEEGDWTATVVDQQDCTLSQLTPANAPIGLYRLSLE
ASTGYQGSSFVLGHFILLFNAWCADAVYLDSEERQEYVLQQGFIYQGSAKFIKNIPW
NFGQFEDGILDICLILLDVNPKFLKNAGRDCSRRSSPVYVGRVSGMVNCNDQGVLLGR
WDNNYGDGVSPMSWIGSVDILRRWKNHGCQRVKYQGCWVFAAVACTVLRCLGIPTRVVTN
YNSAHDQNSNLIEYFRNEFGEIQGDKSEMIWNFHCWESWMTRPDLQPGYEGWQALDPT
PQEKESEGTYCCGPVPVRAIKEGDLSTKYDAPFVFAEVNADVVWDWIQQDDGSVHKSINRSL
IVGLKISTKSGVRDEREDITHTYKYPEGSSEERAFTRANHLNKLAKEETGMAMRIRVG
QSMNMGSDFDVFAHITNNTAEEYVCRLLCARTVSYNGILGPECGTKYLLNLNLEPFSEK
SVPLCILYEKYRDCLTESNLIKVRALLVEPVINSYLLAERDLYLENPEIKIRILGEPKQK
RKLVAEVSLQNPPLPVALEGCTTVEGAGLTEEQKTVEIPDPVEAGEEVKVRMDLLPLHMG
LHKLVNFESDKLKAVKGFRNVIIGPA

```

**Fig2. FASTA Sequence for query Glutamine**

## NetOGlyc - 4.0

### O-GalNAc (mucin type) glycosylation sites in mammalian proteins

The NetOGlyc server produces neural network predictions of mucin type GalNAc O-glycosylation sites in mammalian proteins.

[Submission](#) [Instructions](#) [Output format](#) [Abstract](#) [Downloads](#)

### Submission

**Sequence submission: paste the sequence(s) and/or upload a local file**

*Paste a single sequence or several sequences in [FASTA](#) format into the field below:*

```

SVPLCILYEKYRDCLTESNLIKVRALLVEPVINSYLLAERDLYLENPEIKIRILGEPKQK
RKLVAEVSLQNPPLPVALEGCTTVEGAGLTEEQKTVEIPDPVEAGEEVKVRMDLLPLHMG
LHKLVNFESDKLKAVKGFRNVIIGPA

```

*Submit a file in [FASTA](#) format directly from your local disk:*

No file chosen

**Note:** Please allow 2-3 minutes of processing time per input sequence.

**Restrictions:** At most 50 sequences and 200,000 amino acids per submission; each sequence not more than 4,000 amino acids.

**Confidentiality:** The sequences are kept confidential and will be deleted after processing.

### CITATIONS

For publication of results, please cite:

**Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology.**

Steentoft C, Vakhrushev SY, Joshi HJ, Kong Y, Vester-Christensen MB, Schjoldager KT, Larsen K, Dabelsteen S, Pedersen NB, Marcos-Silva L,

**Fig3. Homepage of NetOGlyc with the FASTA sequence of query pasted in the search box**

## NetOGlyc - 4.0

### O-GalNAc (mucin type) glycosylation sites in mammalian proteins

The NetOGlyc server produces neural network predictions of mucin type GalNAc O-glycosylation sites in mammalian proteins.

Submission Instructions Output format Abstract Downloads

### NetOGlyc-4.0 Server Output - DTU Health Tech

```
##gff-version 2
##source-version NetOGlyc 4.0.0.13
##date 22-3-3
##Type Protein
#seqname source feature start end score strand frame comment
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 16 16 0.0787162 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 23 23 0.137768 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 42 42 0.0592758 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 53 53 0.033419 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 56 56 0.0444774 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 58 58 0.0335661 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 60 60 0.203501 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 63 63 0.285525 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 68 68 0.352325 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 73 73 0.355121 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 89 89 0.051151 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 91 91 0.086065 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 99 99 0.0260473 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 101 101 0.0235857 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 105 105 0.0208268 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 106 106 0.0140802 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 118 118 0.0247396 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 122 122 0.0498245 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 123 123 0.0239158 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 128 128 0.0189996 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 129 129 0.0207258 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 152 152 0.00668514 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 162 162 0.0333635 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 171 171 0.0196308 .
SP_P21980_TGM2_HUMAN netOGlyc-4.0.0.13 CARBOHYD 212 212 0.226317 .
```

Fig4. Result page of NetNGlyc showing the submission data for query

## NetOGlyc - 4.0

### O-GalNAc (mucin type) glycosylation sites in mammalian proteins

The NetOGlyc server produces neural network predictions of mucin type GalNAc O-glycosylation sites in mammalian proteins.

Submission Instructions Output format Abstract Downloads

### Output format

#### DESCRIPTION

The output conforms to the [GFF version 2](#) format. For each input sequence the server prints a list of potential glycosylation sites, showing their positions in the sequence and the prediction confidence scores. Only the sites with scores higher than 0.5 are predicted as glycosylated and marked with the string "#POSITIVE" in the comment field.

The example below shows the output for human granulocyte-macrophage colony-stimulating factor, The example below shows the output for human granulocyte-macrophage colony-stimulating factor, taken from the [UniProt](#) entry [CSF2\\_HUMAN](#). Currently, 4 sites have been experimentally annotated for this protein, and NetOGlyc predicts that two of these are glycosylated. Additionally, it predicts an additional site is glycosylated at site 108. Occupancy of O-glycosylation sites can vary in-vivo depending on the cells that are expressing the protein. The interactions between sites of initial O-Glycosylation with subsequent sites of glycosylation are yet to be fully elucidated, while our capability to precisely predict the substrate specificity of individual GalNAc-Ts remains limited. The combination of these factors mean that although NetOGlyc will attempt to predict individual sites of glycosylation, a safe interpretation of a positive prediction is that the protein in that local region is more likely to carry O-GalNAc modifications.

#### EXAMPLE OUTPUT

```
##gff-version 2
##source-version NetOGlyc 4.0.0.12
##date 13-7-15
##Type Protein
#seqname source feature start end score strand frame comment
CSF2_HUMAN netOGlyc-4.0.0.12 CARBOHYD 5 5 0.04656 .
```

## **Fig5. Output format for NetOGlyc used to refer to interpret the results of our query**

### **Result:**

- After submitting the FASTA sequence for query Glutamine it gives 3 potential glycolysis sites.
- This interpretation can be made by looking at the scores higher than 0.5 and a comment that has #POSITIVE

### **Conclusion:**

- To conclude NetOGlyc is a great source to gather data about the potential Glycolysis sites quickly and accurately
- We can submit one or multiple sequences upto 50 sequences and 200,000 amino acids at once which makes the processing of sequences more efficient

### **References:**

- Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology. Steentoft C, Vakhrushev SY, Joshi HJ, Kong Y, Vester-Christensen MB, Schjoldager KT, Lavrsen K, Dabelsteen S, Pedersen NB, Marcos-Silva L, Gupta R, Bennett EP, Mandel U, Brunak S, Wandall HH, Levery SB, Clausen H. *EMBO J*, 32(10):1478-88, May 15, 2013. (doi: 10.1038/emboj.2013.79. Epub 2013 Apr 12)
- Uniprot. (n.d.). Retrieved March 3, 2022, from <https://www.uniprot.org/uniprot/P21980.fasta>
- Cruzat, V., Macedo Rogero, M., Noel Keane, K., Curi, R., & Newsholme, P. (2018). Glutamine: Metabolism and immune function, supplementation and clinical translation. *Nutrients*, 10(11), 1564. <https://doi.org/10.3390/nu10111564>

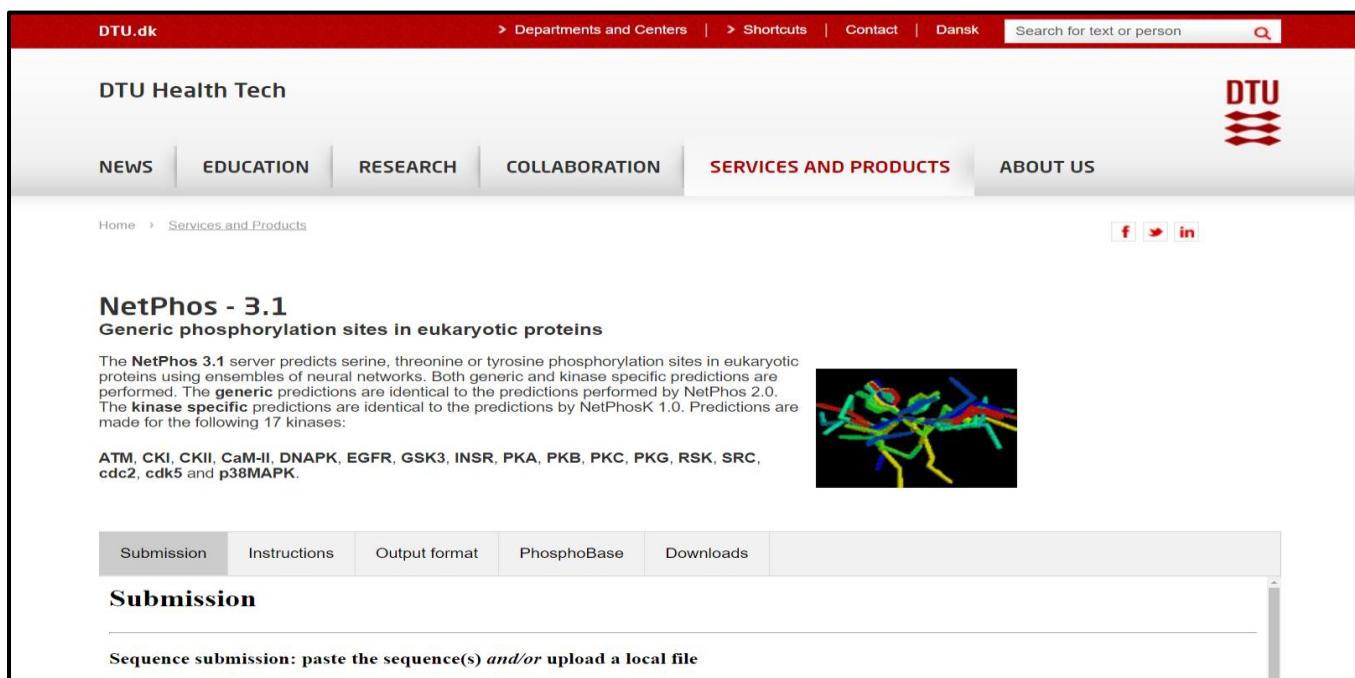
**WEBLEM 6C**  
**To predict binding pocket for Phosphorylation site in (query name) using NetPhos**  
**3.1 server**

**Introduction:**

- Protein phosphorylation at serine, threonine or tyrosine residues affects a multitude of cellular signaling processes. How is specificity in substrate recognition and phosphorylation by protein kinases achieved? In addition, serine and threonine residues in p300/CBP that can be modified by O-linked glycosylation with N-acetylglucosamine are identified. Glycosylation may prevent phosphorylation at these sites, a mechanism named yin-yang regulation.
- **Glutamine**
  - Glutamine is the most abundant and versatile amino acid in the body. In health and disease, the rate of glutamine consumption by immune cells is similar or greater than glucose. For instance, in vitro and in vivo studies have determined that glutamine is an essential nutrient for lymphocyte proliferation and cytokine production, macrophage phagocytic plus secretory activities, and neutrophil bacterial killing. Glutamine release to the circulation and availability is mainly controlled by key metabolic organs, such as the gut, liver, and skeletal muscles.

**Methodology:**

- Take FASTA sequence from uniprot
- Enter it in the submission box for NetPhos
- Interpret the result according to the output page of NetPhos



DTU.dk > Departments and Centers | > Shortcuts | Contact | Dansk Search for text or person

DTU Health Tech

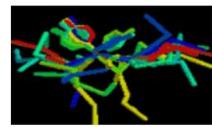
NEWS EDUCATION RESEARCH COLLABORATION **SERVICES AND PRODUCTS** ABOUT US

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**NetPhos - 3.1**  
Generic phosphorylation sites in eukaryotic proteins

The NetPhos 3.1 server predicts serine, threonine or tyrosine phosphorylation sites in eukaryotic proteins using ensembles of neural networks. Both generic and kinase specific predictions are performed. The **generic** predictions are identical to the predictions performed by NetPhos 2.0. The **kinase specific** predictions are identical to the predictions by NetPhosK 1.0. Predictions are made for the following 17 kinases:

ATM, CK1, CKII, CaM-II, DNAPK, EGFR, GSK3, INSR, PKA, PKB, PKC, PKG, RSK, SRC, cdc2, cdk5 and p38MAPK.



Submission Instructions Output format PhosphoBase Downloads

**Submission**

Sequence submission: paste the sequence(s) and/or upload a local file

**Fig1. Homepage of NetPhos 3.1**

```
>sp|P21980|TGM2_HUMAN Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens
OX=9606 GN=TGM2 PE=1 SV=2
MAEELVLERCDLELETNGRDHHTADLCREKLVRRGQPFWTLHFEGRNYEASVDSLTF
VVTGPAPSQEAGTKARFPLRDAVEEGDWTATVVDQQDCTLSQLTTPANAPIGLYRLSLE
ASTGYQGSSFVLGHFILLFNAWCPADAVYLDSEERQEYVLTQQGFIYQGSAKFIKNIPW
NFGQFEDGILDICLILLDVNPKFLKNAGRDCSRRSSPVYGRVSGMVNCNDDQGVLLGR
WDNNYGDGVSPMSWIGSVDILRRWKNHGCQRVKYQQCWVFAAVACTVLRCLGIPTRVVNT
YNSAHDQNSNLIEYFRNEFGEIQGDKSEMIWNFHCVVESMTRPDLQPGYEGWQALDPT
PQEKGEGTYCCGPVPVRAIKEGDLSTKYDAPFVFAEVNADVVWDWIQQDDGSVHKSI
RSLIVGLKISTKSVGRDEREDITHTYKYPEGSSEEREAFTRANHNLKAEKEETGMAMRIRVG
QSMNMGSDFDVFAHITNNTAEYVCRLLCARTVSYNGILGPECGTKYLLNLNLEPFSEK
SVPLCILYEKYRDCLTESNLIKVRALLVEPVINSYLLAERDLYLENPEIKIRILGEPKQK
RKLVAEVSLQNPPLPVALEGCTFTVEGAGLTEEQKTVEIPDPVEAGEEVKVRMDLLPLHMG
LHKLVNFESDKLKAVKGFRNVIIGPA
```

**Fig2. FASTA Sequence for Query Glutamine**

Submission	Instructions	Output format	PhosphoBase	Downloads
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### Submission

---

**Sequence submission:** paste the sequence(s) *and/or* upload a local file

*Paste a single sequence or several sequences in [FASTA](#) format into the field below:*

*Submit a file in [FASTA](#) format directly from your local disk:*

**Residues to predict**  serine  threonine  tyrosine  all three

**For each residue display only the best prediction**

**Display only the scores higher than**

**Output format**  classical  GFF

**Generate graphics**

---

**Restrictions:**  
At most 2000 sequences and 200,000 amino acids per submission; each sequence not less than 15 and not more than 4,000 amino acids.

**Confidentiality:**  
The sequences are kept confidential and will be deleted after processing.

**Fig3. FASTA sequence pasted in the submission box on NetPhos 3.1**

## NetPhos-3.1 Server Output - DTU Health Tech

```
>sp_P21980_TGM2_HUMAN 687 amino acids
#
# netphos-3.1b prediction results
#
# Sequence      # x  Context      Score  Kinase   Answer
#
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.486 CKII
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.461 GSK3
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.432 CaM-II
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.411 cdc2
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.367 CKI
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.342 DNAPK
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.302 p38MAPK
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.267 PKC
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.240 ATM
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.237 PKG
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.192 RSK
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.171 cdk5
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.088 PKA
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.085 PKB
# sp_P21980_TGM2_HUMAN 16 T LELETNGRD 0.029 unsp
#
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.568 CKII YES
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.452 CaM-II
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.448 GSK3
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.388 cdc2
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.361 CKI
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.343 PKG
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.342 DNAPK
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.325 p38MAPK
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.260 ATM
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.224 PKA
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.201 RSK
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.153 cdk5
# sp_P21980_TGM2_HUMAN 23 T RDHHTADLC 0.098 PKC
```

Fig4. Server output for the FASTA sequence showing amino acid prediction results

```
%
%1 .....S.T....T....S....T.....T.....# 100
%1 S....T.....S....ST....S.....Y. # 150
%1 .S.....Y.T....S.....# 200
%1 .....S....S....Y....S.....Y....S # 250
%1 .S.....# 300
%1 .S.....S.....# 350
%1 .....T....S....Y.....ST.....# 400
%1 .....S....S....S....S....T....SS # 450
%1 .....# 500
%1 ..Y.....S.....Y.....S....S.....# 550
%1 .....S.....S....Y.....# 600
%1 .....T....T.....# 650
%1 .....
```

NetPhos 3.1a: predicted phosphorylation sites in sp\_P21980\_TGM2\_HUMAN

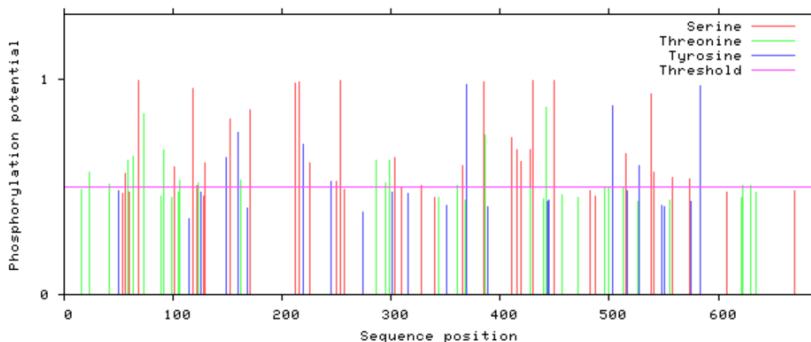


Fig5. Predicted phosphorylation sites in the sequence according to NetPhos 3.1

## Output format

### Classical format

For each input sequence the following is shown (see the example below):

- **FASTA-like header line:** a line showing the sequence name and length.
- **Prediction lines:** one line per residue and kinase, with six columns in the form:
  1. **Sequence** - the sequence name;
  2. **#** - the position of the residue in the sequence;
  3. **x** - the residue in one-letter code;
  4. **Context** - the sequence context of the residue, shown as a 9-residue subsequence centered on the residue;
  5. **Score** - the prediction score (a value in the range [0.000-1.000]; the scores above **0.500** indicate positive predictions);
  6. **Kinase** - the active kinase or the string "unsp" for non-specific prediction (as in NetPhos 2.0);
  7. **Answer** - the string "YES" for positive predictions, else a dot.
- **Sequence** - the input sequence as processed by NetPhos, with an overview of the positions of the predicted sites.
- **Graphics** - a plot of scores illustrating the predictions. NOTE: for each residue only the highest score is shown.

### GFF

The output in GFF ([GFF version 2](#)) provides essentially the same information as the classical format described above. The only differences, apart from the syntax, are as follows:

- the sequence context of the residues is not provided

the sequence context is provided in the sequence line (e.g. 11-127-11-128-11-129-11-130-11-131)

**Fig6. Output format of NetPhos 3.1 used to interpret results for query accordingly**

### Result:

- After submitting the result we can determine that there are 56 potential phosphorylation sites in the given protein sequence
- This interpretation was made on the basis that 56 results have a score about 0.5 and answer is YES
- The active kinase is also given and for non-specific prediction it is "unsp"

### Observation:

- NetPhos is a great tool to find the phosphorylation sites of a given protein sequence.
- Multiple sequences can be submitted at once and the results can be interpreted in bulk making it easier to interpret.

### References:

- Uniprot. (n.d.). Retrieved March 3, 2022, from <https://www.uniprot.org/uniprot/P21980.fasta>
- Sequence- and structure-based prediction of eukaryotic protein phosphorylation sites. Blom, N., Gammeltoft, S., and Brunak, S. *Journal of Molecular Biology*: 294(5): 1351-1362, 1999.
- Cruzat, V., Macedo Rogero, M., Noel Keane, K., Curi, R., & Newsholme, P. (2018). Glutamine: Metabolism and immune function, supplementation and clinical translation. *Nutrients*, 10(11), 1564. <https://doi.org/10.3390/nu10111564>

## WEBLEM 7

### Introduction to Structural Blast – VAST and DALI

The protein structures that populate the PDB have provided crucial insights at the atomic level as to the molecular mechanisms that underlie protein function. Indeed, structural studies have had, and continue to have, a significant and sometimes revolutionary impact in all areas of biology. However, structural biology has tended to focus on single proteins or biological systems and, despite significant advances in the general area of structural bioinformatics, the horizontal integration of the vast quantity of structural information available in the PDB has had little or no impact in the larger biological community. This is in contrast to protein sequence information, which is more routinely, automatically and broadly used. Given that structure is more conserved than sequence, structural similarity has the potential to yield a great deal of functional information that sequence relationships cannot provide and to identify relationships between many more pairs of proteins. In this article we argue that the exploitation of statistical and machine learning techniques combined with the vast amount of high-throughput experimental data constantly being generated enable a significant expansion in the scale and diversity of application of structural information to biological problems.

The ultimate potential impact of both global and local structural relationships in inferring function is highlighted by the observation that, given a suitably “loose” definition of structural similarity, the repertoire of structures currently in the structural databases is nearly complete at the domain level. Thus, it can be expected that most newly solved protein structures will have both near and remote structural neighbors which can provide clues as to their function. Programs such as BLAST use local sequence relationships to quickly scan sequence databases. Since structure-based scans of protein structural databases can be carried out very quickly with current technology (typically minutes for a database of tens of thousands of structures), a similar strategy can be used for structural relationships as well, essentially defining a “structural BLAST”

Comparative analyses of protein sequences and structures play a fundamental role in understanding proteins and their functions. Assuming an evolutionary continuity of structure and function, describing the structural similarity relationships between protein structures allows scientists to infer the functions of newly discovered proteins. The most widespread purpose of structural alignment has been to identify homologous residues (encoded by the same codon in the genome of a common ancestor). Mutations manifest in plastic deformations, shifts and rotations of the secondary structure elements (SSEs). A wide spectrum of structural alignment methods exist, which differ in their treatment of structural variations, scoring functions and optimization algorithms.

There are aware of half a dozen web servers that provide structure comparisons against the current weekly updated Protein Data Bank (PDB). Each server is unique because they employ different structure comparison methods.

#### VAST:

The VAST search database and database of precomputed structure alignments have been maintained as complete and redundant collections since their launch, with automated updates occurring on a weekly basis. This was made possible by implementing a fast heuristic that uses a model for the statistical significance of initial alignments of secondary structure vectors (which can be computed quickly), so that the database searches can avoid costly alignment refinements for the large majority of insignificant and uninteresting similarities. The drawbacks are that a heuristic will miss some potentially interesting similarities. The VAST algorithm will not, for example, report similarities between structures deemed to have secondary structure elements. Searches for structural similarity can and should be complemented with searches for sequence similarity, as flexibility of molecular structure and limitations of the structure comparison method may preclude the detection of matches between structures of homologous polypeptides. In general, though, structure comparison methods will pick up many subtle similarities that evade detection by sequence

comparison strategies, and there is no natural cutoff point for a ranked list of similar structures, unlike in the sequence comparison scenario, where matches to non-homologous gene products are considered accidental and uninformative, for the most part.

Results computed by the VAST algorithm have been compared against other approaches a number of times. Although there are subtle differences in retrieval sensitivity and alignment accuracy, it appears fair to state that the large majority of extensive structural similarities, which are indicative of common evolutionary descent and could be used to infer functional similarities, are reported by VAST (and by most if not all of the alternative approaches to detect common substructures).

As structure similarity search strategies have been developed to also detect distant relationships that might not be evident from sequence analysis, most if not all of the current approaches have been implemented so that they use a single protein molecule or rather a single domain as the unit of comparison. This has been true for VAST, in particular. However, the Protein Data Bank is continuing to accumulate structures of larger macromolecular complexes and has started to provide data on what constitutes functionally or biologically relevant macromolecular complexes or biological assemblies. Such assemblies range from simple homo-oligomers to intricate arrangements of many different components, revealing details on specific molecular interactions and on how these might constrain sequence variation. A small number of approaches have been published in the past few years that examine structural similarity of macromolecular complexes. Here we present a simple strategy that builds on the existing database of pairwise structure alignments computed by VAST and supports the first (to our knowledge) comprehensive and regularly updated collection of macromolecular complex similarities.

### **VAST+ as an extension to existing protein structure comparison**

As information characterizing biological assemblies in macromolecular structure data has become available, it seemed that the biological assembly would be a convenient and informative unit of comparison between individual entries in the structure database. If the goal is to list structures most similar to any particular query, one would have to consider that the query itself may contain a macromolecular complex with a given stoichiometry, and that matching complexes with matching stoichiometry might be more informative ‘structure neighbors’ than, for example, the structures that happen to contain molecules with the strongest local similarity to the query, irrespective of the context.

VAST+ builds on the existing VAST database to generate such a report of structure neighbors. Its goal is to find the largest set of pairs of matching macromolecules between two biological assemblies and to characterize that match and compute instructions for a global superimposition that can be used to visualize the structural similarity. For each pair of structures in MMDDB, VAST+ examines pre-computed structure alignments stored in the VAST database that were computed for the full-length protein molecule components of the default biological assemblies. If such pairwise alignments are found, the alignments between individual protein components of the biological assemblies are compared with each other for compatibility, and compatible/matching alignments are clustered into sets of alignments that together constitute a biological assembly match. Pairwise alignments are compatible (i) if they do not share the same macromolecules, i.e. a protein molecule from one assembly cannot be aligned to two molecules from the other assembly at the same time and (ii) if they generate similar instructions (spatial transformation matrices) for the superpositions of coordinate sets. A simple distance metric can be used to compare transformation matrices and it lends itself to cluster alignment sets efficiently.

Each set of compatible pairwise alignments can be characterized by (i) the number of pairwise matches, i.e. the total number of pairs of protein molecules from the query and subject biological assemblies, that are simultaneously aligned with each other; (ii) the RMSD of the superposition obtained from considering all alignments in the set; (iii) the total length of all pairwise alignments, i.e. the total number of amino acids that are aligned in 3D space; and (iv) percentage of identical residues in the alignments. For each pairwise comparison of two biological assemblies, only the match with the highest number of aligned molecules and the highest number of aligned residues is recorded and reported.

Currently, 53% of polypeptide-containing structures in MMDB have >1 polypeptide chain. The histogram plotted in Figure 1 breaks down the numbers by oligomer size and indicates that large fractions of the oligomeric assemblies have, in general, structure neighbors that match the entire assemblies. It should be noted that the fractions might be somewhat exaggerated, as exact duplicates of a structure would be counted as biological assembly matches, and no attempt was made to remove redundant structures or classify biological assembly matches as informative versus uninformative.

### **DALI:**

The Dali server is a network service for comparing protein structures in 3D. You submit the coordinates of a query protein structure and Dali compares them against those in the Protein Data Bank (PDB). In favourable cases, comparing 3D structures may reveal biologically interesting similarities that are not detectable by comparing sequences.

User can perform three types of database searches:

- Heuristic PDB search - compares one query structure against those in the Protein Data Bank
- Exhaustive PDB25 search - compares one query structure against a representative subset of the Protein Data Bank
- Hierarchical AF-DB search - compares one query structure against a species subset of the AlphaFold Database

There are two types of structure comparisons of user selected structures:

- Pairwise structure comparison - compares one query structure against those specified by the user
- All against all structure comparison - returns a structural similarity dendrogram for a set of structures specified by the user

## **DESCRIPTION OF THE SERVER**

### **Inputs**

The input to the server is one or two protein structures in PDB format. The query structure can be specified as a PDB identifier plus chain identifier, or a PDB file uploaded by the user. There are three cross-linked query forms for the Dali server, Dali Database and pairwise comparison, respectively. For example, the entry point to the Dali server is [http://ekhidna.biocenter.helsinki.fi/dali\\_server](http://ekhidna.biocenter.helsinki.fi/dali_server).

All backbone atoms (N, CA, C, O) are required and the minimum chain length is 30 amino acids. Backbone atoms may be reconstructed from a CA trace using the MaxSprout server at

External links to the Dali database should use , where 1nnn represents a PDB identifier and chainid is optional. Meta-servers may link to, which directly returns the match list and alignment data as plain text.

### **Processing**

Queries to the Dali Database and pairwise comparison are processed interactively; the result is usually returned within a minute. The Dali server processes up to eight PDB searches in parallel, others are queued. Most PDB- search queries are processed in less than an hour. Results are stored on the server for two weeks. The results of identical queries are retrieved instantly from cache.

The Dali server and Dali database return only the best match of the query to each PDB structure. The pairwise comparison returns also suboptimal matches. The pairwise comparison is based on a systematic branch-and- bound search that returns non-overlapping solutions in decreasing order of alignment score. Suboptimal matches can be of interest in cases of internal symmetries or repeated domains.

Dali Database is updated twice a year and contains precomputed structural alignments of PDB90 against the full PDB. The query structure is mapped to the closest representative in PDB90 and the structure comparison scores are recomputed using the transitive alignment via the representative.

The Dali server aims to retrieve a list of 500 structural neighbors of the query structure with the highest Z-scores. Most query structures have strong similarity to a structure already in the PDB. We use fast filters to identify a shortlist of about 100 promising candidates. If these produce strong matches, the search proceeds

by walking. Otherwise, the query structure is compared with PDB90 in one versus all fashion, followed by a walk to collect matches to redundant PDB structures (which are over 90% sequence identical to PDB90 representatives).

Walking selects targets for structural comparison from the neighbours of neighbours found so far. The second shell of neighbors is known because all structures in the PDB are stored in a precomputed network of similarities. The pairwise alignments (Q,P) and (P,R) induce a transitive alignment (Q,R), which is used as the starting point of refinement rather than optimizing the alignment from scratch. There are many possible choices of intermediate structure P en route from Q to R. We select the ‘high road’, in other words, the minimum of the Z-scores  $Z(Q,P)$  and  $Z(P,R)$  should be as high as possible. The ‘high road’ may change as more structures are added to the first neighbour shell. To avoid redundant comparisons, we only test induced alignments which are longer than previously obtained ones. When the alignment (Q,R) has been refined, R is added to the first neighbour shell. The walk ends when either there are no new neighbours in the second shell, a specified number of hits (1000) have been reported, or a maximum number of comparisons (1000) have been performed.

## Outputs

The Dali server, Dali Database and pairwise comparison use a common output format and share interactive analysis tools.

The result consists of (i) a list of structural neighbours, ranked by Z-score, and (ii) the alignment data. The results are presented as plain text for downloading by downstream application, and as hypertext for interactive analysis. The default results page reports the top 500 matches to all chains in the PDB. A subset of matches to PDB90, filtered at 90% sequence identity, is provided for convenience.

Selected subsets of matches can be visualized (i) as multiple sequence alignments, or (ii) in multiple 3D superimposition. While sophisticated tools with integrated sequence alignment and structure superimposition views are available, we have chosen Jmol, an open source Java viewer for molecular graphics, because it was most easily accessible to the casual user. Each neighbour is aligned (superimposed) against the query structure in a star-like tree topology. Active sites can be recognized by clusters of conserved residues and ligands. Sequence and structure conservation are calculated within the selected subset of matches.

VAST and DALI are thus very useful structure similarity BLAST tool. VAST provides user with similar structures to their query along with its molecular components and chemicals and non-standard biopolymers, aligned sequences and 3D structure superimposition information which includes information regarding H-bonds, interactions, buried surface area, 2D interaction network and much more. DALI provides user with similar structures to their query along with its pairwise alignment, coordinates information, 3Dsuperimposition results. Describing the structural similarity relationships between protein structures allows scientists to infer the functions of newly discovered proteins.

## REFERENCES:

1. Dey, Fabian; Cliff Zhang, Qiangfeng; Petrey, Donald; Honig, Barry (2013). Toward a “Structural BLAST”: Using structural relationships to infer function. *Protein Science*, 22(4), 359– 366. doi:10.1002/pro.2225
2. Madej, T.; Lanczycki, C. J.; Zhang, D.; Thiessen, P. A.; Geer, R. C.; Marchler-Bauer, A.; Bryant, S. H. (2014). MMDB and VAST+: tracking structural similarities between macromolecular complexes. *Nucleic Acids Research*, 42(D1), D297–D303. doi:10.1093/nar/gkt1208
3. Dali server. (n.d.). Ekhidna2.Biocenter.helsinki.fi. Retrieved March 14, 2022, from <http://ekhidna2.biocenter.helsinki.fi/dali/>
4. Holm, L.; Rosenstrom, P. (2010). Dali server: conservation mapping in 3D. *Nucleic Acids Research*, 38(Web Server), W545–W549. doi:10.1093/nar/gkq366

**WEBLEM 7a****VAST**

(URL: <https://www.ncdi.nlm.nih.gov/Structure/vastplus/vastplus.cgi>)

**AIM:**

To perform structure BLAST for tubulin using VAST tool.

**INTRODUCTION:**

Tubulin is the protein that polymerizes into long chains or filaments that form microtubules, hollow fibers which serve as a skeletal system for living cells. Microtubules have the ability to shift through various formations which is what enables a cell to undergo mitosis or to regulate intracellular transport.

The computational detection of similarities between protein 3D structures has become an indispensable tool for the detection of homologous relationships, the classification of protein families and functional inference. Consequently, numerous algorithms have been developed that facilitate structure comparison, including rapid searches against a steadily growing collection of protein structures. To this end, NCBI's Molecular Modeling Database (MMDB), which is based on the Protein Data Bank (PDB), maintains a comprehensive and up-to- date archive of protein structure similarities computed with the Vector Alignment Search Tool (VAST). These similarities have been recorded on the level of single proteins and protein domains, comprising in excess of 1.5 billion pairwise alignments. VAST+, an extension to the existing VAST service, which summarizes and presents structural similarity on the level of biological assemblies or macromolecular complexes. VAST+ simplifies structure neighboring results and shows, for macromolecular complexes tracked in MMDB, lists of similar complexes ranked by the extent of similarity. VAST+ replaces the previous VAST service as the default presentation of structure neighboring data in NCBI's Entrez query and retrieval system.

**METHODOLOGY:**

1. Open homepage for VAST. (URL: <https://www.ncbi.nlm.nih.gov/Structure/vastplus/vastplus.cgi>)
2. Retrieve PDB ID for Albumin.
3. Search for similar structures on VAST for the PDB ID.
4. Observe and interpret the results.

## OBSERVATION:

**VAST+ Similar Structures** 3D structural similarities among biological assemblies

**COVID-19 Information**

**VAST+** is a tool designed to identify macromolecules that have similar 3-dimensional structures, with an emphasis on finding those with similar biological assemblies ("biological units" or "biounits"). The similarities are calculated using purely geometric criteria, and therefore can identify distant homologs that cannot be recognized by sequence comparison.

Input a valid PDB ID or MMDB ID:  PDB ID or MMDB ID  ?

To use VAST+, enter the PDB ID or MMDB ID of any structure that is currently in the Molecular Modeling Database (MMDB). VAST+ will display a list of similar structures, ranking them by the extent of their similarity to the query structure's biological unit. [more...](#)

**Citing VAST**

- Gibrat JF, Madej T, Bryant SH. "Surprising similarities in structure comparison." *Curr Opin Struct Biol*. 1996 Jun;6(3): 377-85.
- Madej T, Lanczycki CJ, Zhang D, Thiessen PA, Geer RC, Marchler-Bauer A, Bryant SH. "MMDB and VAST+: tracking structural similarities between macromolecular complexes." *Nucl. Acids Res.* 2014 Jan;42(Database issue):D297-303.
- Thomas Madej, Aron Marchler-Bauer, Christopher Lanczycki, Dachuan Zhang, Stephen H Bryant. "Biological Assembly Comparison With VAST" *Methods Mol. Biol.* 2020(2112):175-186

You are here: NCBI > Computational Biology Branch > Structure Group > VAST+ Write to the Help Desk

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Fig1. Homepage for VAST

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Structure Summary 3D View Annotations Experiment Sequence Genome Ligands Versions

**Biological Assembly 1** 1Z2B

Tubulin-colchicine-vinblastine: stathmin-like domain complex

**PDB DOI:** 10.2210/pdb1Z2B/pdb

**Classification:** CELL CYCLE  
**Organism(s):** Bos taurus, Rattus norvegicus  
**Expression System:** Escherichia coli BL21(DE3)  
**Mutation(s):** No

**Deposited:** 2005-03-08 **Released:** 2005-05-31  
**Deposition Author(s):** Gigant, B., Wang, C., Ravelli, R.B.G., Roussi, F., Steinmetz, M.O., Curmi, P.A., Sobel, A., Knossow, M.

**Experimental Data Snapshot**

**Method:** X-RAY DIFFRACTION  
**Resolution:** 4.10 Å  
**R-Value Free:** 0.269  
**R-Value Work:** 0.209  
**R-Value Observed:** 0.212

**wwPDB Validation** [?](#) [3D Report](#) [Full Report](#)

Metric Percentile Ranks Value

Fig2. Tubulin PDB structure

**NCBI** National Center for Biotechnology Information

**VAST+ Similar Structures** 3D structural similarities among biological assemblies

**COVID-19 Information**  
Public health information (CDC) | Research information (NIH) | SARS-CoV-2 data (NCBI) | Prevention and treatment information (HHS) | Español

**VAST+** is a tool designed to identify macromolecules that have similar 3-dimensional structures, with an emphasis on finding those with similar biological assemblies ("biological units" or "biounits"). The similarities are calculated using purely geometric criteria, and therefore can identify distant homologs that cannot be recognized by sequence comparison.

Input a valid PDB ID or MMDB ID:

To use VAST+, enter the PDB ID or MMDB ID of any structure that is currently in the Molecular Modeling Database (MMDB). VAST+ will display a list of similar structures, ranking them by the extent of their similarity to the query structure's biological unit. [more...](#)

**Citing VAST**

Gibrat JF, Madej T, Bryant SH. "Surprising similarities in structure comparison.", *Curr Opin Struct Biol*.1996 Jun;6(3): 377-85.  
Madej T, Lanczycki CJ, Zhang D, Thiessen PA, Geer RC, Marchler-Bauer A, Bryant SH. "MMDB and VAST+: tracking structural similarities between macromolecular complexes." *Nucl. Acids Res.* 2014 Jan;42(Database issue):D297-303.  
Thomas Madej, Aron Marchler-Bauer, Christopher Lanczycki, Dachuan Zhang, Stephen H Bryant. "Biological Assembly Comparison With VAST" *Methods Mol. Biol.* 2020(2112):175-186

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8600 Rockville Pike, Bethesda MD, 20894 USA

Fig3. Search for tubulin PDB structure

**NCBI** National Center for Biotechnology Information

**VAST+ Similar Structures** 3D structural similarities among biological assemblies

**1Z2B : Tubulin-Colchicine-Vinblastine: Stathmin-Like Domain Complex**

Biological unit 1: pentameric  
Source organism: *Rattus norvegicus*, ▼  
Number of proteins: 5 (RB3 STATHMIN-LIKE DOMAIN 4, TUBULIN ALPHA CHAIN... ▼)  
Number of chemicals: 9 (Magnesium Ion (2),2-Mercapto-N-[1,2,3,10-Tetram... ▼)

**Similar Structures (3038)**

**All matching molecules superposed** **Invariant substructure superposed**

**▲ Hide filters**

**Filter by number of matching molecules**

Complete match, 5 proteins (114)

Partial match, 4 proteins (44)

Partial match, 3 proteins (2)

Partial match, 2 proteins (95)

Partial match, 1 protein (2783)

**Filter by taxonomy**

Eukaryota (1154)

Bacteria (1686)

Archaea (137)

Viruses (10)

Others (51)

**Apply Filter Selection**

**Showing 1 to 10 out of 3038 selected structures**

		Search within results: PDB ID or search word				
PDB ID	Description	Taxonomy	Aligned Protein	RMSD	Aligned Residues	Sequence Identity
1    3N2G	Tubulin-Nsc 613863: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.89 Å	1814	99%

Fig4. Hit page for Tubulin

**Filter by number of matching molecules**

Complete match, 5 proteins (114)

Partial match, 4 proteins (44)

Partial match, 3 proteins (2)

Partial match, 2 proteins (95)

Partial match, 1 protein (2783)

**Filter by taxonomy**

Eukarya (1154)

Bacteria (1686)

Archaea (137)

Viruses (10)

Others (51)

**Apply Filter Selection**

**Showing 1 to 10 out of 112 selected structures**

**Search within results:** PDB ID or search word **Go** **Reset**

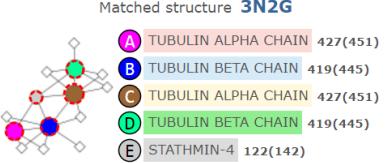
PDB ID	Description	Taxonomy	Aligned Protein	RMSD	Aligned Residues	Sequence Identity
1 3N2G	Tubulin-Nsc 613863: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.89 Å	1814	100%
2 3HCK	Tubulin-Abt751: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.92 Å	1814	100%
3 3N2K	Tubulin-Nsc 613862: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.77 Å	1813	100%
4 3HKE	Tubulin-T138067: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.77 Å	1813	100%
5 3HKD	Tubulin-Tn16 : Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.81 Å	1812	100%
6 3E22	Tubulin-Colchicine-Soblidotin: Stathmin-Like Domain Complex	Bos taurus/Rattus norvegicus	5	0.79 Å	1810	99%
7 3HKB	Tubulin: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.92 Å	1808	100%
8 5KX5	Crystal Structure Of Tubulin-stathmin-ttl-compound 11 Complex	Gallus gallus/Ovis aries/Rattus norvegicus	5	1.66 Å	1808	100%
9 1SA0	Tubulin-Colchicine: Stathmin-Like Domain Complex	Bos taurus/Rattus norvegicus	5	0.73 Å	1807	99%
10 1SA1	Tubulin-Podophyllotoxin: Stathmin-Like Domain Complex	Bos taurus/Rattus	5	0.91 Å	1806	99%

**Fig5. Hit page after applying filter**

**Showing 1 to 10 out of 112 selected structures**

**Search within results:** PDB ID or search word **Go** **Reset**

**Apply Filter Selection**

PDB ID	Description	Taxonomy	Aligned Protein	RMSD	Aligned Residues	Sequence Identity
1 3N2G	Tubulin-Nsc 613863: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.89 Å	1814	100%
<b>Aligned Molecules</b>						
Query structure 1Z2B						
						
Matched structure 3N2G						
						
*Select schematic circles or highlighted molecule names to view matches						
<a href="#">Visualize 3D structure superposition</a> <a href="#">View aligned sequences</a>						
2 3HCK	Tubulin-Abt751: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.92 Å	1814	100%
3 3N2K	Tubulin-Nsc 613862: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.77 Å	1813	100%
4 3HKE	Tubulin-T138067: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.77 Å	1813	100%
5 3HKD	Tubulin-Tn16 : Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.81 Å	1812	100%
6 3E22	Tubulin-Colchicine-Soblidotin: Stathmin-Like Domain Complex	Bos taurus/Rattus norvegicus	5	0.79 Å	1810	99%
7 3HKB	Tubulin: Rb3 Stathmin-Like Domain Complex	Ovis aries/Rattus norvegicus	5	0.92 Å	1808	100%

**Fig6. Result for aligned molecules**

139

## 3N2G: Tubulin-Nsc 613863: Rb3 Stathmin-Like Domain Complex

Citation: [?](#)

**Stathmin and interfacial microtubule inhibitors recognize a naturally curved conformation of tubulin dimers**

Barbier P, Dorléans A, Devred F, Sanz L, Allegro D, Alfonso C, Knossow M, Peyrot V, Andreu JM

*J Biol Chem* (2010) **285** p.31672-81

### Abstract

Tubulin is able to switch between a straight microtubule-like structure and a curved structure in complex with the stathmin-like domain of the RB3 protein (T2)RB3. GTP hydrolysis following microtubule assembly induces protofilament curvature and disassembly. The conformation of the labile tubulin heterodimers is unknown. One important question is whether free GDP-tubulin dimers... [read more](#)

**PDB ID:** 3N2G [Download](#) [?](#)  
**MMDB ID:** 83668 [?](#)  
**PDB Deposition Date:** 2010/5/18 [?](#)  
**Updated in MMDB:** 2012/11 [?](#)  
**Experimental Method:** x-ray diffraction [?](#)  
**Resolution:** 4 Å [?](#)  
**Source Organism:** *Rattus norve...* [?](#)  
**Similar Structures:** [VAST+](#) [?](#)  
[Download sequence data](#) [?](#)

### Biological Unit

### Asymmetric Unit

[?](#)

Biological Unit for 3N2G: pentameric; determined by author and by software (PISA) [?](#)

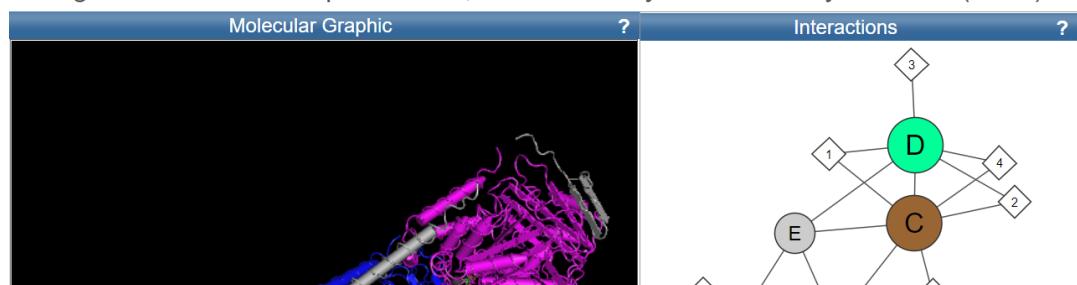


Fig7. Result page for structure (3N2G) similar to Tubulin

### Molecular Components in 3N2G [?](#)

Label	Count	Molecule
<b>Proteins (5 molecules)</b>		
<b>A</b> <b>C</b>	2	<b>Tubulin Alpha Chain</b> 2 Proteins 3D Domains Domain Families Specific Hits Super Families 1 100 200 300 400 451 1 2 1
<b>B</b> <b>D</b>	2	<b>Tubulin Beta Chain</b> 2 Proteins Domain Families Specific Hits Super Families 1 100 200 300 400 445 PLN00220 PLN00220 superfamily
<b>E</b>	1	<b>Stathmin-4</b> 1 Protein 3D Domains 1 100 142
<b>Chemicals and Non-standard biopolymers (9 molecules)</b>		
<b>1</b>	2	<b>Guanosine-5'-Triphosphate</b>
<b>2</b>	3	<b>Magnesium Ion</b>

Fig8. Molecular components and chemical and non-standard biopolymers for 1N5U

Aligned Sequences [Close](#)

[Visualize 3D structure superposition](#)

**1Z2B\_A: TUBULIN ALPHA CHAIN**  
**3N2G\_A: TUBULIN ALPHA CHAIN**

**1Z2B\_A** 2 RECISIHVQAGVQIGNACWELYCLEHGIQPDGQMPsdktigggdDSFNTFFSETGAGKH 61  
**3N2G\_A** 2 RECISIHVQAGVQIGNACWELYCLEHGIQPDGQMPsdktigggdDSFNTFFSETGAGKH 61

**1Z2B\_A** 62 VPRAVFVDELEPTVIDEVRTGTYRQLFHPQLITGKEDAANNYARGHHTIGKEIIDLVLDR 121  
**3N2G\_A** 62 VPRAVFVDELEPTVIDEVRTGTYRQLFHPQLITGKEDAANNYARGHHTIGKEIIDLVLDR 121

**1Z2B\_A** 122 IRKLAQCTGLQGFLVFHSGGGTGSFTSLLMERLSDYGGKSKLEFSIYPAPQVSTAV 181  
**3N2G\_A** 122 IRKLAQCTGLQGFLVFHSGGGTGSFTSLLMERLSDYGGKSKLEFSIYPAPQVSTAV 181

**1Z2B\_A** 182 VEPVNSILTTTLEHSDCAFMDNEAIYDICRRNLDIERPTTYTNLNRLQIVSSITAS 241  
**3N2G\_A** 182 VEPVNSILTTTLEHSDCAFMDNEAIYDICRRNLDIERPTTYTNLNRLQIVSSITAS 241

**1Z2B\_A** 242 LRFDGALINVDTTEFQTNLVPYPRIHFPPLATYAPVISAEKAYHEQLSVAEITNACFEPANO 301  
**3N2G\_A** 242 LRFDGALINVDTTEFQTNLVPYPRIHFPPLATYAPVISAEKAYHEQLSVAEITNACFEPANO 301

**1Z2B\_A** 302 MVKCDPRHGKYMACCLLYRGDVPKDVNAAIATIKTKR1QFVWDHCPGFKVGINYQPPT 361  
**3N2G\_A** 302 MVKCDPRHGKYMACCLLYRGDVPKDVNAAIATIKTKR1QFVWDHCPGFKVGINYQPPT 361

**1Z2B\_A** 362 VVPGGDALKVQRAVCMNSNTTAIAEAWARLDHKFDLHYAKRAFVHNVYGEGMEEGEFSEA 421  
**3N2G\_A** 362 VVPGGDALKVQRAVCMNSNTTAIAEAWARLDHKFDLHYAKRAFVHNVYGEGMEEGEFSEA 421

**1Z2B\_A** 422 REDMAALEKDYEEVGI 437  
**3N2G\_A** 422 REDMAALEKDYEEVGI 437

[Visualize 3D structure superposition](#)

**1Z2B\_B: TUBULIN BETA CHAIN**  
**3N2G\_B: TUBULIN BETA CHAIN**

**1Z2B\_B** 2 REIVHIQAGQCGNQIGAKFWEVISDEHGDPTGSYHGSIDLQLERINVYYNEATGNKYV 61

**Fig9. Result page for aligned sequences**

File | Select | View | Style | Color | Analysis | Help | Toolbar - |   ?

**Select residues in aligned sequences**

Structure Alignment of **1Z2B** and **3N2G** from VAST+

**1Z2B\_A** **3N2G\_A** TUBULIN ALPHA CHAIN TUBULIN ALPHA CHAIN

**1Z2B\_A** 2 RECISIHVQAGVQIGNACWELYCLEHGIQPDGQMPsdktigggdDSFNTFFSETGAGKH 61  
**3N2G\_A** 2 RECISIHVQAGVQIGNACWELYCLEHGIQPDGQMPsdktigggdDSFNTFFSETGAGKH 61

**1Z2B\_B** **3N2G\_B** TUBULIN BETA CHAIN TUBULIN BETA CHAIN

**1Z2B\_B** 4 REIVHIQAGQCGNQIGAKFWEVISDEHGDPTGSYHGSIDLQLERINVYYNEATGNKYV 61  
**3N2G\_B** 4 REIVHIQAGQCGNQIGAKFWEVISDEHGDPTGSYHGSIDLQLERINVYYNEATGNKYV 61

**1Z2B\_C** **3N2G\_C** TUBULIN ALPHA CHAIN TUBULIN ALPHA CHAIN

**1Z2B\_C** 2 RECISIHVQAGVQIGNACWELYCLEHGIQPDGQMPsdktigggdDSFNTFFSETGAGKH 61  
**3N2G\_C** 2 RECISIHVQAGVQIGNACWELYCLEHGIQPDGQMPsdktigggdDSFNTFFSETGAGKH 61

**1Z2B\_D** **3N2G\_D** TUBULIN BETA CHAIN TUBULIN BETA CHAIN

**1Z2B\_D** 2 RECISIHVQAGVQIGNACWELYCLEHGIQPDGQMPsdktigggdDSFNTFFSETGAGKH 61  
**3N2G\_D** 2 RECISIHVQAGVQIGNACWELYCLEHGIQPDGQMPsdktigggdDSFNTFFSETGAGKH 61

```
> load alignment 52185,1,83668,1 | parameters &showalignseq=1&align=52185,1,83668,1&atype=0
>
```

**Fig10. Result page for 3D structure superimposition**

File Select View Style Color Analysis Help All atoms | Toolbar | one-letter seq. | Search ?

**Structure Alignment of 1Z2B and 3N2G from VAST+**

**Hydrogen bonds/Interactions between two sets of atoms**

1. Choose interaction types and their thresholds:

Hydrogen Bonds: 3.8 Å |  Salt Bridge/Ionic: 6 Å |  Contacts/Interaction

Halogen Bonds: 3.8 Å |  π-Cation: 6 Å |  π-Stacking: 5 Å

2. Select the first set: **selected** 1Z2B, 1Z2B\_A, 1Z2B\_B, 1Z2B\_C

3. Select the second set: **non-selected** selected 1Z2B, 1Z2B\_A, 1Z2B\_B

4. Cross Structure Interactions: No

3D Display Interactions

Highlight Interactions in Table | Sort Interactions on: Set 1 | Set 2

2D Interaction Network | to show interactions between two lines of residue nodes

2D Interaction Map | to show interactions as map

2D Graph(Force-Directed) | to show interactions with strength parameters in 0-200:

Helix or Sheet: 100 | Coil or Nucleotide: 50 | Disulfide Bond: 50

Hydrogen Bond: 50 | Salt Bridge/Ionic: 50 | Contacts: 25

Halogen Bonds: 50 | π-Cation: 50 | π-Stacking: 50

(Note: you can also adjust thresholds at #1 to add/remove interactions.)

**Buried solvent accessible surface area in the interface**

Calculate solvent accessible surface area in the interface:

Set 1: 1Z2B, Surface: 56097.10 Å<sup>2</sup>  
 Set 2: non-selected, Surface: 10143.75 Å<sup>2</sup>  
 Total Surface: 56170.29 Å<sup>2</sup>  
 Buried Surface for Set 1: 526.39 Å<sup>2</sup>  
 Buried Surface for Set 2: 8433.20 Å<sup>2</sup>

Fig11. Buried surface information

File Select View Style Color Analysis Help Selection | Toolbar | one-letter seq. | Search ?

**Structure Alignment of**

**1Z2B\_A 3N2G\_A** TUBULIN ALPHA CHAIN TUBULIN ALPHA CHAIN

10 20 30

1Z2B\_A 3N2G\_A 2 REC I S I H V G Q A G V Q I G N A C W E L Y C L E H G I Q P D G Q M P S C

1Z2B\_A 3N2G\_A 2 REC I S I H V G Q A G V Q I G N A C W E L Y C L E H G I Q P D G Q M P S C

**1Z2B\_B 3N2G\_B** TUBULIN BETA CHAIN TUBULIN BETA CHAIN

10 20 30

1Z2B\_B 3N2G\_B 4 R E I V H I Q A G Q C G N Q I G A K F W E V I S D E H G I D P T G S Y H G C

1Z2B\_B 3N2G\_B 4 R E I V H I Q A G Q C G N Q I G A K F W E V I S D E H G I D P T G S Y H G C

**1Z2B\_C 3N2G\_C** TUBULIN ALPHA CHAIN TUBULIN ALPHA CHAIN

10 20 30

1Z2B\_C 3N2G\_C 2 R E C I S I H V G Q A G V Q I G N A C W E L Y C L E H G I Q P D G Q M P S C

1Z2B\_C 3N2G\_C 2 R E C I S I H V G Q A G V Q I G N A C W E L Y C L E H G I Q P D G Q M P S C

**1Z2B\_D 3N2G\_D** TUBULIN BETA CHAIN TUBULIN BETA CHAIN

10 20 30

1Z2B\_D 3N2G\_D 2 R E C I S I H V G Q A G V Q I G N A C W E L Y C L E H G I Q P D G Q M P S C

1Z2B\_D 3N2G\_D 2 R E C I S I H V G Q A G V Q I G N A C W E L Y C L E H G I Q P D G Q M P S C

> display interaction 3d | 1Z2B non-selected | hbonds,salt bridge,interactions,halogen,pi-cation,pi-stacking | false | threshold 3.8 6 4 3.8 6 5.5

Fig12. Result for itneractions

1. Choose interaction types and their thresholds:

- Hydrogen Bonds: 3.8 Å A
- Salt Bridge/Ionic: 6 Å A
- Contacts/Interactions: 25
- Halogen Bonds: 3.8 Å A
- π-Cation: 6 Å A
- π-Stacking: 50

2. Select the first set: selected 1Z2B, 1Z2B\_A, 1Z2B\_B, 1Z2B\_C

3. Select the second set: non-selected 1Z2B, 1Z2B\_A, 1Z2B\_B

4. Cross Structure Interactions: No

5. Reset and select new sets

3872 hydrogen bond pairs:

Atom 1	Atom 2	Distance(Å)	Highlight in 3D
ARG \$1Z2B.A:2@NE	GLU \$1Z2B.A:3@OE2	3.8	Highlight
GLU \$1Z2B.A:3@O	GLN \$1Z2B.A:133@N	2.9	Highlight
GLU \$1Z2B.A:3@OE2	ARG \$1Z2B.A:2@NE	3.8	Highlight
GLU \$1Z2B.A:3@OE2	THR \$1Z2B.A:130@OG1	3.7	Highlight
CYS \$1Z2B.A:1@N	THR \$1Z2B.A:1@O	3.2	Highlight

6. The interfaces are:  
 interface\_1 Highlight in 3D  
 interface\_2 Highlight in 3D

Note: Each checkbox below selects the corresponding residue. You can click "Save Selection" in the "Select" menu to save the selection and click on "Highlight" button to clear the checkboxes.

Fig13. Result for interactions

Structure Alignment of 4L8U and 1N5U from VAST+

Show interactions between two lines of residue nodes

Hold Ctrl key to select multiple nodes/lines.

Green: H-Bonds; Cyan: Salt Bridge/Ionic; Grey: contacts  
 Magenta: Halogen Bonds; Red: π-Cation; Blue: π-Stacking

Scale: 1

Line graph interaction pairs | 1N5U selected | hbonds,salt bridge,interactions,halogen,pi-cation,pi-stacking | true | threshold 3.8 6 4 3.8 6 5.5

Fig14. Result for 2D interaction network

## RESULT:

PDB ID for tubulin structure was searched in structure similarity BLAST tool, VAST and 152 similar structures were retrieved.

## CONCLUSION:

VAST is a useful structure similarity BLAST tool which provides user with similar structures to their query along with its molecular components and chemicals and non-standard biopolymers, aligned sequences and 3D structure superimposition information which includes information regarding H-bonds, interactions, buried surface area, 2D interaction network and much more. Describing the structural similarity relationships between protein structures allows scientists to infer the functions of newly discovered

proteins.

## REFERENCES:

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2. Tubulin: Mystery of vital cell protein solved after 30 years. (n.d.). Retrieved March 19, 2022, from <https://www2.lbl.gov/Science-Articles/Archive/3D-tubulin.html#:~:text=Tubulin%20is%20the%20protein%20that,or%20to%20regulate%20intracellular%20transport>.
3. Similar Protein Structure Assemblies. (2014). Nih.gov. Retrieved March 19, 2022, from <https://www.ncbi.nlm.nih.gov/Structure/vastplus/vastplus.cgi>
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7. iCn3D: Web-based 3D Structure Viewer. (n.d.). [Www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov). Retrieved March 19, 2022, from <https://www.ncbi.nlm.nih.gov/Structure/icn3d/full.html?showalignseq=1&align=112122>

**WEBLEM 7b**  
**DALI**  
**(URL: <http://ekhidna2.biocenter.helsinki.fi/dali/>)**

**AIM:**

To perform structural blast for tubulin using DALI tool

**Introduction:**

Tubulin is the protein that polymerizes into long chains or filaments that form microtubules, hollow fibers which serve as a skeletal system for living cells. Microtubules have the ability to shift through various formations which is what enables a cell to undergo mitosis or to regulate intracellular transport.

The DALI server is a network service for comparing protein structures in 3D. You submit the coordinates of a query protein structure and DALI compares them against those in the Protein Data Bank (PDB). In favourable cases, comparing 3D structures may reveal biologically interesting similarities that are not detectable by comparing sequences.

User can perform three types of database searches:

- **Heuristic PDB search** - compares one query structure against those in the Protein Data Bank
- **Exhaustive PDB25 search** - compares one query structure against a representative subset of the Protein Data Bank
- **Hierarchical AF-DB search** - compares one query structure against a species subset of the AlphaFold Database

**METHODOLOGY:**

1. Open homepage for DALI. (URL: <http://ekhidna2.biocenter.helsinki.fi/dali/>)
2. Enter Albumin PDB ID.
3. Observe similar structures matches against PDB25, PDB50, PDB90 and all PDB structures.
4. Interpret the results.

# DALI

## PROTEIN STRUCTURE COMPARISON SERVER

About PDB search PDB25 AF-DB search Pairwise All against all Gallery References Statistics Download

The DALI server is a network service for comparing protein structures in 3D. You submit the coordinates of a query protein structure and DALI compares them against those in the Protein Data Bank (PDB). In favourable cases, comparing 3D structures may reveal biologically interesting similarities that are not detectable by comparing sequences.

Check queue status [here](#). Megausers please consider downloading the standalone program.

You can perform three types of database searches:

- Heuristic [PDB search](#) - compares one query structure against those in the Protein Data Bank
- Exhaustive [PDB25](#) search - compares one query structure against a representative subset of the Protein Data Bank
- Hierarchical [AF-DB](#) search - compares one query structure against a species subset of the AlphaFold Database

and two types of structure comparisons of user selected structures:

- [Pairwise](#) structure comparison - compares one query structure against those specified by the user
- [All against all](#) structure comparison - returns a structural similarity dendrogram for a set of structures specified by the user

Citation:

1. Holm L (2020) Using DALI for protein structure comparison. Methods Mol. Biol.

Fig1. Homepage for DALI

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**RCSB PDB** 188431 Biological Macromolecular Structures Enabling Breakthroughs in Research and Education

PDB Archive Advanced Search | Browse Annotations Help

PDB-101 Worldwide Protein Data Bank EMDataResource Worldwide Protein Data Bank Foundation

Structure Summary 3D View Annotations Experiment Sequence Genome Ligands Versions

1Z2B

Tubulin-colchicine-vinblastine: stathmin-like domain complex

PDB DOI: 10.2210/pdb1Z2B/pdb

Classification: CELL CYCLE  
Organism(s): Bos taurus, Rattus norvegicus  
Expression System: Escherichia coli BL21(DE3)  
Mutation(s): No

Deposited: 2005-03-08 Released: 2005-05-31  
Deposition Author(s): Gigant, B., Wang, C., Ravelli, R.B.G., Roussi, F., Steinmetz, M.O., Curmi, P.A., Sobel, A., Knossow, M.

3D View: Structure | 1D-3D View | Electron Density | Validation Report | Ligand Interaction

Pseudo Symmetry: Asymmetric - C1

Experimental Data Snapshot

Method: X-RAY DIFFRACTION  
Resolution: 4.10 Å  
R-Value Free: 0.269  
R-Value Work: 0.209  
R-Value Observed: 0.212

wwPDB Validation

Metric	Percentile Ranks	Value
Rfree	40	0.276
Clashscore	9.8%	
Ramachandran outliers	36.1%	
Sidechain outliers	1.7%	
RSRZ outliers		
Worse		
Better		

Fig2. Tubulin PDB structure

**DALI**  
PROTEIN STRUCTURE COMPARISON SERVER

About PDB search PDB25 AF-DB search Pairwise All against all Gallery References Statistics Download

**PDB search**

Compare query structure against Protein Data Bank.

STEP 1 - Enter your query protein structure

Structures may be specified by concatenating the PDB identifier (4 characters) and a chain identifier (1 character) or, alternatively, you may upload a PDB file.

OR upload file  No file chosen

Job title:

E-mail:

STEP 3 - Submit your job

If the same structure has been submitted recently, you will be redirected to the result page of the previous instance.

**Fig3. PDB search for tubulin**

## Results: Imao

### Chain: 1z2bA

- [Matches against PDB25](#). [Correlation matrix](#)
- [Matches against PDB50](#)
- [Matches against PDB90](#)
- [Matches against full PDB](#)
- [Download matches against PDB25](#)
- [Download matches against PDB50](#)
- [Download matches against PDB90](#)
- [Download matches against full PDB](#)

Results will be deleted after one week.

**Fig4. Result page of Tubulin**

## Matches against PDB25:

## Results: Imao

## Query: 1z2bA

MOLECULE: TUBULIN ALPHA CHAIN;

Select neighbours (check boxes) for viewing as multiple structural alignment or 3D superimposition. The list of neighbours is sorted by Z-score. Similarities with a Z-score lower than 2 are spurious. Each neighbour has links to pairwise structural alignment with the query structure, and to the PDB format coordinate file where the neighbour is superimposed onto the query structure.

Structural Alignment  Expand gaps 3D Superimposition (PV) SANS PANZ Pfam Reset Selection

## Summary

No:	Chain	Z	rmsd	lali	nres	%id	PDB	Description
□ 1:	7m2w-A	47.6	1.8	408	453	30	PDB	MOLECULE: TUBULIN GAMMA CHAIN;
□ 2:	3zid-A	32.4	2.7	317	360	16	PDB	MOLECULE: TUBULIN/FTSZ, GTPASE;
□ 3:	1w59-A	24.7	3.1	291	350	12	PDB	MOLECULE: CELL DIVISION PROTEIN FTSZ HOMOLOG 1;
□ 4:	4xcq-A	23.9	3.5	280	303	11	PDB	MOLECULE: TUBZ;
□ 5:	4eit-A	23.6	4.0	313	382	11	PDB	MOLECULE: PLASMID REPLICATION PROTEIN REPX;
□ 6:	2xka-F	23.2	3.8	313	414	12	PDB	MOLECULE: FTSZ/TUBULIN-RELATED PROTEIN;
□ 7:	3zbq-A	19.8	3.5	263	315	13	PDB	MOLECULE: PHIKZ039;
□ 8:	4fkz-A	7.8	3.9	174	384	10	PDB	MOLECULE: UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE;
□ 9:	4zht-A	7.3	3.7	167	384	9	PDB	MOLECULE: BIFUNCTIONAL UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE/

### Fig5. Result for similar structures

## Pairwise Structural Alignments

Notation: three-state secondary structure definitions by DSSP (reduced to H=helix, E=sheet, L=coil) are shown above the amino acid sequence. Structurally equivalent residues are in uppercase, structurally non-equivalent residues (e.g. in loops) are in lowercase. Amino acid identities are marked by vertical bars.

No 1: Query=1z2bA Sbjct=7m2wA Z-score=47.6

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## Fig6. Results for pairwise structural alignment

```

REMARK Coordinates of 7m2w rotated and translated as follows:
REMARK | 0.40520 0.53216 -0.74338 | | x | | 173.000 |
REMARK | -0.07305 -0.79168 -0.60655 | * | y | + | 510.000 |
REMARK | -0.91131 0.30008 -0.28191 | | z | | 313.000 |
REMARK
REMARK HOH and TIP residues excluded. Only first MODEL passed through.
REMARK
HEADER CELL CYCLE 17-MAR-21 7M2W
TITLE ENGINEERED DISULFIDE CROSS-LINKED CLOSED CONFORMATION OF THE YEAST
TITLE 2 GAMMA-TURC(SS)
COMPND MOL_ID: 1;
COMPND 2 MOLECULE: TUBULIN GAMMA CHAIN;
COMPND 3 CHAIN: B, A, C, D;
COMPND 4 SYNONYM: GAMMA-TUBULIN;
COMPND 5 ENGINEERED: YES;
COMPND 6 MUTATION: YES;
COMPND 7 MOL_ID: 2;
COMPND 8 MOLECULE: SPINDLE POLE BODY COMPONENT SPC97;
COMPND 9 CHAIN: E, G;
COMPND 10 ENGINEERED: YES;
COMPND 11 MOL_ID: 3;
COMPND 12 MOLECULE: SPINDLE POLE BODY COMPONENT SPC98;
COMPND 13 CHAIN: F, H;
COMPND 14 ENGINEERED: YES;
COMPND 15 MOL_ID: 4;
COMPND 16 MOLECULE: SPINDLE POLE BODY COMPONENT 110;
COMPND 17 CHAIN: U, K, X, Y;
COMPND 18 SYNONYM: EXTRAGENIC SUPPRESSOR OF CMD1-1 MUTANT PROTEIN 1, NUCLEAR
COMPND 19 FILAMENT-RELATED PROTEIN 1, SPINDLE POLE BODY SPACER PROTEIN SPC110;
COMPND 20 ENGINEERED: YES
AUTHOR A.F.BRILOT,A.S.LYON,A.ZELTER,S.VISWANATH,A.MAXWELL,M.J.MACCOSS,
AUTHOR 2 E.G.MULLER,A.SALI,T.N.DAVIS,D.A.AGARD

```

**Fig7. Result for coordinates of similar structure**

Matches against PDB50:

## Results: lmao

### Query: 1z2bA

MOLECULE: TUBULIN ALPHA CHAIN;

Select neighbours (check boxes) for viewing as multiple structural alignment or 3D superimposition. The list of neighbours is sorted by Z-score. Similarities with a Z-score lower than 2 are spurious. Each neighbour has links to pairwise structural alignment with the query structure, and to the PDB format coordinate file where the neighbour is superimposed onto the query structure.

Structural Alignment  Expand gaps  3D Superimposition (PV)  SANS  PANZ  Pfam  Reset Selection

### Summary

No:	Chain	Z	rmsd	lali	nres	%id	PDB	Description
1:	2btq-A	54.0	1.5	410	436	38	<a href="#">PDB</a>	MOLECULE: TUBULIN BTUBA;
2:	7pqc-B	54.0	1.6	426	451	99	<a href="#">PDB</a>	MOLECULE: TUBULIN BETA CHAIN;
3:	2btq-B	53.5	1.8	388	391	41	<a href="#">PDB</a>	MOLECULE: TUBULIN BTUBA;
4:	7pqc-A	51.5	1.8	418	445	41	<a href="#">PDB</a>	MOLECULE: TUBULIN BETA CHAIN;
5:	3cb2-A	51.4	1.8	407	432	32	<a href="#">PDB</a>	MOLECULE: TUBULIN GAMMA-1 CHAIN;
6:	7m2w-A	47.6	1.8	408	453	30	<a href="#">PDB</a>	MOLECULE: TUBULIN GAMMA CHAIN;
7:	7anz-B	44.6	1.8	375	410	28	<a href="#">PDB</a>	MOLECULE: TUBULIN GAMMA CHAIN;
8:	3zid-A	32.4	2.7	317	360	16	<a href="#">PDB</a>	MOLECULE: TUBULIN/FTSZ, GTPASE;
9:	4b46-A	30.6	2.7	307	330	18	<a href="#">PDB</a>	MOLECULE: CELL DIVISION PROTEIN FTSZ;

**Fig8. Result for similar structures**

## Pairwise Structural Alignments

Notation: three-state secondary structure definitions by DSSP (reduced to H=helix, E=sheet, L=coil) are shown above the amino acid sequence. Structurally equivalent residues are in uppercase, structurally non-equivalent residues (e.g. in loops) are in lowercase. Amino acid identities are marked by vertical bars.

**No 1: Query=1z2bA Sbjct=2btqA Z-score=54.0**

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### Fig9. Result for similar structures

```

REMARK Coordinates of 2btq rotated and translated as follows:
REMARK | 0.28475 -0.95786 0.03764 | * | x | | 92.000 |
REMARK | -0.37807 -0.07614 0.92264 | * | y | + | 137.000 |
REMARK | -0.88090 -0.27695 -0.38382 | | z | | 57.000 |
REMARK
REMARK HOH and TIP residues excluded. Only first MODEL passed through.
REMARK
HEADER STRUCTURAL PROTEIN 06-JUN-05 2BTQ
TITLE STRUCTURE OF BTUBAB HETERO-DIMER FROM PROSTHECOBACTER DEJONGEII
COMPND MOL_ID: 1;
COMPND 2 MOLECULE: TUBULIN BTUBA;
COMPND 3 CHAIN: A;
COMPND 4 ENGINEERED: YES;
COMPND 5 MOL_ID: 2;
COMPND 6 MOLECULE: TUBULIN BTUBB;
COMPND 7 CHAIN: B;
COMPND 8 ENGINEERED: YES
AUTHOR D.SCHLIEPER,J.LOWE
HELIX 1 1 GLY A 12 GLY A 31 1
HELIX 2 2 GLU A 74 SER A 85 1
HELIX 3 3 ASN A 90 ALA A 92 5
HELIX 4 4 ASN A 104 LEU A 110 1
HELIX 5 5 GLY A 111 LYS A 130 1
HELIX 6 6 GLY A 146 TYR A 163 1
HELIX 7 7 SER A 176 SER A 180 5
HELIX 8 8 THR A 184 ALA A 200 1
HELIX 9 9 ASN A 208 ARG A 217 1
HELIX 10 10 THR A 225 PHE A 246 1
HELIX 11 11 SER A 255 VAL A 264 1
HELIX 12 12 GLY A 291 PHE A 300 1
HELIX 13 13 SER A 310 GLY A 314 5
HELIX 14 14 ASP A 329 LEU A 344 1

```

**Fig10. Result for coordinates of similar structure**

## Query: 1z2bA

## MOLECULE: TUBULIN ALPHA CHAIN;

Select neighbours (check boxes) for viewing as multiple structural alignment or 3D superimposition. The list of neighbours is sorted by Z-score. Similarities with a Z-score lower than 2 are spurious. Each neighbour has links to pairwise structural alignment with the query structure, and to the PDB format coordinate file where the neighbour is superimposed onto the query structure.

Structural Alignment  Expand gaps  3D Superimposition (PV)  SANS  PANZ  Pfam  Reset Selection

## Summary

No:	Chain	Z	rmsd	lali	nres	%id	PDB	Description
□ 1:	5w3f-A	55.4	1.5	424	440	74	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA-1 CHAIN;
□ 2:	2btq-A	54.0	1.5	410	436	38	<a href="#">PDB</a>	MOLECULE: TUBULIN BTUBA;
□ 3:	7pqc-B	54.0	1.6	426	451	99	<a href="#">PDB</a>	MOLECULE: TUBULIN BETA CHAIN;
□ 4:	2btq-B	53.5	1.8	388	391	41	<a href="#">PDB</a>	MOLECULE: TUBULIN BTUBA;
□ 5:	5ubq-A	52.2	1.7	425	441	87	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
□ 6:	5mlv-C	52.0	1.7	418	430	40	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA-1 CHAIN;
□ 7:	7pqc-A	51.5	1.8	418	445	41	<a href="#">PDB</a>	MOLECULE: TUBULIN BETA CHAIN;
□ 8:	3cb2-A	51.4	1.8	407	432	32	<a href="#">PDB</a>	MOLECULE: TUBULIN GAMMA-1 CHAIN;
□ 9:	5w3f-B	51.3	1.7	416	427	40	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA-1 CHAIN;
□ 10:	7m2w-A	47.6	1.8	408	453	30	<a href="#">PDB</a>	MOLECULE: TUBULIN GAMMA CHAIN;
□ 11:	6v5v-g	45.8	1.6	356	369	33	<a href="#">PDB</a>	MOLECULE: TUBULIN GAMMA-1 CHAIN;
□ 12:	7zpq-B	44.6	1.8	375	410	28	<a href="#">PDB</a>	MOLECULE: TUBULIN GAMMA CHAIN;

**Fig11. Result for similar structures**

## Pairwise Structural Alignments

Notation: three-state secondary structure definitions by DSSP (reduced to H=helix, E=sheet, L=coil) are shown above the amino acid sequence. Structurally equivalent residues are in uppercase, structurally non-equivalent residues (e.g. in loops) are in lowercase. Amino acid identities are marked by vertical bars.

No 1: Query=1z2bA Sbjct=5w3fA Z-score=55.4

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## Fig12. Result for pairwise structural alignment

```

REMARK Coordinates of 5w3f rotated and translated as follows:
REMARK | 0.39885 -0.50887 0.76286 | | x | | -11.000 |
REMARK | -0.13412 0.79058 0.59749 | * | y | + | -390.000 |
REMARK | -0.90715 -0.34062 0.24708 | | z | | 366.000 |
REMARK
REMARK HOH and TIP residues excluded. Only first MODEL passed through.
REMARK
HEADER HYDROLASE 07-JUN-17 5W3F
TITLE YEAST TUBULIN POLYMERIZED WITH GTP IN VITRO
COMPND MOL_ID: 1;
COMPND 2 MOLECULE: TUBULIN ALPHA-1 CHAIN;
COMPND 3 CHAIN: A;
COMPND 4 MOL_ID: 2;
COMPND 5 MOLECULE: TUBULIN BETA CHAIN;
COMPND 6 CHAIN: B;
COMPND 7 SYNONYM: BETA-TUBULIN
AUTHOR S.C.HOWES, E.A.GEYER, B.LAFRANCE, R.ZHANG, E.H.KELLOGG, S.WESTERMANN,
AUTHOR 2 L.M.RICE, E.NOGALES
HELIX 1 AA1 GLY A 10 HIS A 28 1 19
HELIX 2 AA2 GLU A 72 ASN A 81 1 10
HELIX 3 AA3 TYR A 84 PHE A 88 5 5
HELIX 4 AA4 HIS A 89 GLU A 91 5 3
HELIX 5 AA5 ASN A 103 HIS A 108 1 6
HELIX 6 AA6 VAL A 111 GLU A 114 5 4
HELIX 7 AA7 ILE A 115 CYS A 130 1 16
HELIX 8 AA8 GLY A 144 TYR A 162 1 19
HELIX 9 AA9 VAL A 183 ALA A 199 1 17
HELIX 10 AB1 ASN A 207 ASN A 217 1 11
HELIX 11 AB2 SER A 224 VAL A 239 1 16
HELIX 12 AB3 THR A 240 ARG A 244 5 5
HELIX 13 AB4 ASN A 254 VAL A 261 1 8
HELIX 14 AB5 SER A 288 GLU A 298 1 11

```

**Fig13. Result for coordinates of similar structure**

### Query: 1z2bA

MOLECULE: TUBULIN ALPHA CHAIN;

Select neighbours (check boxes) for viewing as multiple structural alignment or 3D superimposition. The list of neighbours is sorted by Z-score. Similarities with a Z-score lower than 2 are spurious. Each neighbour has links to pairwise structural alignment with the query structure, and to the PDB format coordinate file where the neighbour is superimposed onto the query structure.

Structural Alignment  Expand gaps  3D Superimposition (PV)  SANS  PANZ  Pfam  Reset Selection

### Summary

No:	Chain	Z	rmsd	lali	nres	%id	PDB	Description
<input type="checkbox"/> 1:	1z2b-A	75.0	0.0	427	427	100	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
<input type="checkbox"/> 2:	1sa0-A	69.5	0.3	427	427	99	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
<input type="checkbox"/> 3:	3hkc-A	69.1	0.5	426	426	100	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
<input type="checkbox"/> 4:	3hke-A	69.0	0.5	427	427	100	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
<input type="checkbox"/> 5:	3n2k-A	68.9	0.5	427	428	100	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
<input type="checkbox"/> 6:	3e22-A	68.9	0.5	427	427	98	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA-1C CHAIN;
<input type="checkbox"/> 7:	3hkb-A	68.6	0.5	427	427	100	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
<input type="checkbox"/> 8:	1z2b-C	68.5	0.6	420	427	99	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
<input type="checkbox"/> 9:	1sa0-C	68.5	0.5	421	421	99	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
<input type="checkbox"/> 10:	3ed1-F	68.4	0.5	421	421	99	<a href="#">PDB</a>	MOLECULE: ALPHA-TUBULIN;
<input type="checkbox"/> 11:	3n2g-A	68.1	0.5	427	428	100	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;
<input type="checkbox"/> 12:	3hkd-A	68.1	0.5	427	428	100	<a href="#">PDB</a>	MOLECULE: TUBULIN ALPHA CHAIN;

**Fig14. Result for similar structures**

## Pairwise Structural Alignments

Notation: three-state secondary structure definitions by DSSP (reduced to H=helix, E=sheet, L=coil) are shown above the amino acid sequence. Structurally equivalent residues are in uppercase, structurally non-equivalent residues (e.g. in loops) are in lowercase. Amino acid identities are marked by vertical bars.

No 1: Query=1z2bA Sbjct=1z2bA Z-score=75.0

[back to top](#)

DSSP	LLLHHHHHHLLLLLHHHEEELLL	LLLHHHHHLLHHHHHHHHHHHHLLL
Query	EPTVIDEVRTGTYRQLFHPQLITGKEDAANNYARGHYTIGKEIDLVLDIRKLADQCT	120
ident		
Sbjct	EPTVIDEVRTGTYRQLFHPQLITGKEDAANNYARGHYTIGKEIDLVLDIRKLADQCT	120
DSSP	LLLHHHHHHLLLLLHHHEEELLL	LLLHHHHHLLHHHHHHHHHHHHLLL

### Fig15. Result for pairwise structural alignment

```

REMARK Coordinates of 1z2b rotated and translated as follows:
REMARK | 1.00000 0.00000 -0.00000 | | x | | -0.000 |
REMARK | -0.00000 1.00000 0.00000 | * | y | + | 0.000 |
REMARK | 0.00000 -0.00000 1.00000 | | z | | 0.000 |
REMARK
REMARK HOH and TIP residues excluded. Only first MODEL passed through.
REMARK
HEADER CELL CYCLE 08-MAR-05 1Z2B
TITLE TUBULIN-COLCHICINE-VINBLASTINE: STATHMIN-LIKE DOMAIN COMPLEX
COMPND MOL_ID: 1;
COMPND 2 MOLECULE: TUBULIN ALPHA CHAIN;
COMPND 3 CHAIN: A, C;
COMPND 4 MOL_ID: 2;
COMPND 5 MOLECULE: TUBULIN BETA CHAIN;
COMPND 6 CHAIN: B, D;
COMPND 7 MOL_ID: 3;
COMPND 8 MOLECULE: RB3 STATHMIN-LIKE DOMAIN 4;
COMPND 9 CHAIN: E;
COMPND 10 SYNONYM: STATHMIN-LIKE PROTEIN B3, RB3-SLD;
COMPND 11 ENGINEERED: YES
AUTHOR B.GIGANT,C.WANG,R.B.G.RAVELLI,F.ROUSSI,M.O.STEINMETZ,P.A.CURMI,
AUTHOR 2 A.SOBEK,M.KNOSSOW
HELIX 1 1 GLY A 10 GLY A 29 1 20
HELIX 2 2 THR A 73 ARG A 79 1 7
HELIX 3 3 HIS A 88 GLU A 90 5 3
HELIX 4 4 ASN A 102 TYR A 108 1 7
HELIX 5 5 ILE A 110 ALA A 126 1 17
HELIX 6 6 GLY A 143 TYR A 161 1 19
HELIX 7 7 VAL A 182 GLU A 196 1 15
HELIX 8 8 ASP A 205 ASN A 216 1 12
HELIX 9 9 THR A 223 ALA A 240 1 18
HELIX 10 10 ALA A 240 ASP A 245 1 6

```

**Fig16. Result for coordinates of similar structure**

## RESULT:

PDB ID for albumin structure was searched in structure similarity BLAST tool, DALI and similar structures matches against PDB25, PDB50, PDB90 and all PDB structures were retrieved.

## CONCLUSION:

DALI is a useful structure similarity BLAST tool which provides user with similar structures to their query along with its pairwise alignment, coordinates information, 3D superimposition results. Describing the

structural similarity relationships between protein structures allows scientists to infer the functions of newly discovered proteins.

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## WEBLEM 8

### Introduction to Gene Prediction and various elements in Prokaryotes and Eukaryotes

With the rapid accumulation of genomic sequence information, there is a pressing need to use computational approaches to accurately predict gene structure. Computational gene prediction is a prerequisite for detailed functional annotation of genes and genomes. The process includes detection of the location of open reading frames (ORFs) and delineation of the structures of introns as well as exons if the genes of interest are of eukaryotic origin. The ultimate goal is to describe all the genes computationally with near 100% accuracy. The ability to accurately predict genes can significantly reduce the amount of experimental verification work required.

### **CATEGORIES OF GENE PREDICTION PROGRAMS**

The current gene prediction methods can be classified into two major categories, ab initio-based and homology-based approaches. The ab initio-based approach predicts genes based on the given sequence alone. It does so by relying on two major features associated with genes. The first is the existence of gene signals, which include start and stop codons, intron splice signals, transcription factor binding sites, ribosomal binding sites, and polyadenylation (poly-A) sites. In addition, the triplet codon structure limits the coding frame length to multiples of three, which can be used as a condition for gene prediction. The second feature used by ab initio algorithms is gene content, which is statistical description of coding regions. It has been observed that nucleotide composition and statistical patterns of the coding regions tend to vary significantly from those of the noncoding regions. The unique features can be detected by employing probabilistic models such as Markov models or hidden Markov models to help distinguish coding from noncoding regions.

The homology-based method makes predictions based on significant matches of the query sequence with sequences of known genes. For instance, if a translated DNA sequence is found to be similar to a known protein or protein family from a database search, this can be strong evidence that the region codes for a protein. Alternatively, when possible exons of a genomic DNA region match a sequenced cDNA, this also provides experimental evidence for the existence of a coding region.

Some algorithms make use of both gene-finding strategies. There are also a number of programs that actually combine prediction results from multiple individual programs to derive a consensus prediction. This type of algorithms can therefore be considered as consensus based.

### **Gene Prediction Using Markov Models and Hidden Markov Models**

Markov models and HMMs can be very helpful in providing finer statistical description of a gene. A Markov model describes the probability of the distribution of nucleotides in a DNA sequence, in which the conditional probability of a particular sequence position depends on  $k$  previous positions. In this case,  $k$  is the order of a Markov model. A zero-order Markov model assumes each base occurs independently with a given probability. This is often the case for noncoding sequences. A first-order Markov model assumes that the occurrence of a base depends on the base preceding it. A second-order model looks at the preceding two bases to determine which base follows, which is more characteristic of codons in a coding sequence. The use of Markov models in gene finding exploits the fact that oligonucleotide distributions in the coding regions are different from those for the noncoding regions. These can be represented with various orders of Markov models. Since a fixed-order Markov chain describes the probability of a particular nucleotide that depends on previous  $k$  nucleotides, the longer the oligomer unit, the more non randomness can be described for the coding region. Therefore, the higher the order of a Markov model, the more accurately it can predict a gene.

FGENESB is a web-based program that is also based on fifth-order HMMs for detecting coding regions. The program is specifically trained for bacterial sequences. It uses the Viterbi algorithm to find an optimal match for the query sequence with the intrinsic model. A linear discriminant analysis (LDA) is used to

further distinguish coding signals from noncoding signals.

#### **Step-by-Step Description of FGENESB annotation.**

**STEP 1.** Finds all potential ribosomal RNA genes using BLAST against bacterial and/or archaeal rRNA databases, and masks detected rRNA genes.

**STEP 2.** Predicts tRNA genes using tRNAscan-SE program (Washington University) and masks detected tRNA genes.

**STEP 3.** Initial predictions of long ORFs that are used as a starting point for calculating parameters for gene prediction. Iterates until stabilizes. Generates parameters such as 5th-order in-frame Markov chains for coding regions, 2nd-order Markov models for region around start codon and upstream RBS site, Stop codon and probability distributions of ORF lengths.

**STEP 4.** Predicts operons based only on distances between predicted genes.

**STEP 5.** Runs BLASTP for predicted proteins against COG database, cog.pro.

**STEP 6.** Uses information about conservation of neighboring gene pairs in known genomes to improve operon prediction.

**STEP 7.** Runs BLASTP against NR for proteins having no COGs hits.

**STEP 8.** Predicts potential promoters (BPROM program) or terminators (BTERM) in upstream and downstream regions, correspondingly, of predicted genes. BTERM is the program predicting bacterial - independent terminators with energy scoring based on discriminant function of hairpin elements.

**STEP 9.** Refines operon predictions using predicted promoters and terminators as additional evidences.

#### **Prediction Using Discriminant Analysis.**

Some gene prediction algorithms rely on discriminant analysis, either LDA or quadratic discriminant analysis (QDA), to improve accuracy. LDA works by plotting a two-dimensional graph of coding signals versus all potential 3\_ splice site positions and drawing a diagonal line that best separates coding signals from noncoding signals based on knowledge learned from training data sets of known gene structures. QDA draws a curved line based on a quadratic function instead of drawing a straight line to separate coding and noncoding features. This strategy is designed to be more flexible and provide a more optimal separation between the data points.

FGENES is a web-based program that uses LDA to determine whether a signal is an exon. In addition to FGENES, there are many variants of the program. Some programs, such as FGENESH, make use of HMMs. There are others, such as FGENESH C, that are similarity based. Some programs, such as FGENESH+, combine both ab initio and similarity-based approaches.

#### **Output format:**

- G - predicted gene number, starting from start of sequence
- Str - DNA strand (+ for direct or - for complementary)
- Feature - type of coding sequence: CDSf - First (Starting with Start codon), CDSi - internal (internal exon), CDSl - last coding segment, ending with stop codon)
- TSS - Position of transcription start (TATA-box position and score)
- TSS - position of transcription start
- TATA - position of TATA-box
- wTATA - Discriminant function score for TATA box
- Start and End - Position of the Feature
- Weight - Discriminant function score for the feature
- ORF - start/end positions where the first complete codon starts and the last codon ends

An issue related to gene prediction is promoter prediction. Promoters are DNA elements located in the vicinity of gene start sites (which should not be confused with the translation start sites) and serve as binding sites for the gene transcription machinery, consisting of RNA polymerases and transcription

factors. Therefore, these DNA elements directly regulate gene expression. Promoters and regulatory elements are traditionally determined by experimental analysis. The process is extremely time consuming and laborious. Computational prediction of promoters and regulatory elements is especially promising because it has the potential to replace a great deal of extensive experimental analysis.

### **PREDICTION ALGORITHMS**

Current algorithms for predicting promoters and regulatory elements can be categorized as either *ab initio* based, which make *de novo* predictions by scanning individual sequences; or similarity based, which make predictions based on alignment of homologous sequences; or expression profile based using profiles constructed from a number of co-expressed gene sequences from the same organism. The similarity type of prediction is also called phylogenetic foot-printing.

### **PREDICTION FOR PROKARYOTES**

One of the unique aspects in prokaryotic promoter prediction is the determination of operon structures, because genes within an operon share a common promoter located upstream of the first gene of the operon. Thus, operon prediction is the key in prokaryotic promoter prediction. Once an operon structure is known, only the first gene is predicted for the presence of a promoter and regulatory elements, whereas other genes in the operon do not possess such DNA elements.

There are a number of methods available for prokaryotic operon prediction. The most accurate is a set of simple rules developed by Wang et al. This method relies on two kinds of information: gene orientation and intergenic distances of a pair of genes of interest and conserved linkage of the genes based on comparative genomic analysis. A scoring scheme is developed to assign operons with different levels of confidence. This method is claimed to produce accurate identification of an operon structure, which in turn facilitates the promoter prediction.

This newly developed scoring approach is, however, not yet available as a computer program. The prediction can be done manually using the rules, however. The few dedicated programs for prokaryotic promoter prediction do not apply the Wang et al. rule for historical reasons. The most frequently used program is BPROM.

BPROM is a web-based program for prediction of bacterial promoters. It uses a linear discriminant function combined with signal and content information such as consensus promoter sequence and oligonucleotide composition of the promoter sites. This program first predicts a given sequence for bacterial operon structures by using an intergenic distance of 100 bp as basis for distinguishing genes to be in an operon. This rule is more arbitrary than the Wang et al. rule, leading to high rates of false positives. Once the operons are assigned, the program is able to predict putative promoter sequences. Because most bacterial promoters are located within 200 bp of the protein coding region, the program is most effectively used when about 200 bp of upstream sequence of the first gene of an operon is supplied as input to increase specificity.

#### **Output format:**

- First line - name of your sequence;
- Second and Third lines - LDF threshold and the length of presented sequence
- 4th line - The number of predicted promoters
- Next lines - positions of predicted promoters, and their scores with 'weights' of two conserved promoter boxes. Promoter position assign to the first nucleotide of the transcript (Transcription Start Site position).
- After that we present elements of Transcriptional factor binding sites for each predicted promoter (if they found).

### **PREDICTION FOR EUKARYOTES**

The *ab initio* method for predicting eukaryotic promoters and regulatory elements also relies on searching the input sequences for matching of consensus patterns of known promoters and regulatory elements. The consensus patterns are derived from experimentally determined DNA binding sites which are compiled into

profiles and stored in a database for scanning an unknown sequence to find similar conserved patterns. However, this approach tends to generate very high rate of false positives owing to nonspecific matches with the short sequence patterns. Furthermore, because of the high variability of transcription factor binding sites, the simple sequence matching often misses true promoter sites, creating false negatives.

To increase the specificity of prediction, a unique feature of eukaryotic promoter is employed, which is the presence of CpG islands. It is known that many vertebrate genes are characterized by a high density of CG dinucleotides near the promoter region overlapping the transcription start site. By identifying the CpG islands, promoters can be traced on the immediate upstream region from the islands. By combining CpG islands and other promoter signals, the accuracy of prediction can be improved. Several programs have been developed based on the combined features to predict the transcription start sites in particular.

The eukaryotic transcription initiation requires cooperation of a large number of transcription factors. Cooperativity means that the promoter regions tend to contain a high density of protein-binding sites. Thus, finding a cluster of transcription factor binding sites often enhances the probability of individual binding site prediction. TSSW is a web program that distinguishes promoter sequences from non-promoter sequences based on a combination of unique content information such as hexamer/trimer frequencies and signal information such the TATA box in the promoter region. The values are fed to a linear discriminant function to separate true motifs from background noise.

#### **Output format:**

- First line - name of your sequence;
- Second and Third lines - LDF threshold and the length of presented sequence
- 4th line - The number of predicted promoter regions
- Next lines - positions of predicted sites, their 'weights' and TATA box position (if found)
- Position shows the first nucleotide of the transcript (TSS position)
- After that functional motifs are given for each predicted region; (+) or (-) reflects the direct or complementary chain; S... means a particular motif identifier from the Wingender data base.
- Lower cased letters mean non-conserved nucleotides in the site consensus
- The letters except (A,T,G,C) describe ambiguous sites in a given DNA sequence motif, where a single character may represent more than one nucleotide using Standard IUPAC Nucleotide code.

#### **ORF finder:**

ORF finder searches for open reading frames (ORFs) in the DNA sequence you enter. The program returns the range of each ORF, along with its protein translation. Use ORF finder to search newly sequenced DNA for potential protein encoding segments, verify predicted protein using newly developed SMART BLAST or regular BLASTP. This web version of the ORF finder is limited to the sub range of the query sequence up to 50 kb long. Stand-alone version, which doesn't have query sequence length limitation.

Thus, TSSW and BPROM are a useful tool for the recognition promoter region and start of transcription. Understanding the regulation of gene expression is an important aspect of understanding the gene function, thus this tool will be useful in elucidating regulation and expression mechanisms of genes and may even shed light on the function of novel and uncharacterized genes with the help of knowledge of promoters. FGENESB tool is useful for prediction of bacterial operon and gene and FGENES for prediction of exons. Identifying the genes that are grouped together into operons may enhance our knowledge of gene regulation and function, and such information is an important addition to genome annotation. All this can be done with the help of FGENESB. ORF finder can be used to predict open reading frames in the genome. This information of long ORFs are often used, along with other evidence, to initially identify candidate protein-coding regions or functional RNA-coding regions in a DNA sequence. Small Open Reading Frames (small ORFs/sORFs/smORFs) are important sources of putative peptides previously dismissed as being non-functional or junk DNA.

#### **REFERENCES:**

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## WEBLEM 8a

## TSSW

(URL: <http://www.softberry.com/berry.phtml?topic=tssw&group=programs&subgroup=promoter>)

**AIM:**

To recognize the *Saccharomyces cerevisiae* kinase and start of transcription using TSSW tool.

**INTRODUCTION:**

kinase, an enzyme that adds phosphate groups ( $\text{PO}_4^{3-}$ ) to other molecules. A large number of kinases exist—the human genome contains at least 500 kinase-encoding genes. Included among these enzymes' targets for phosphate group addition (phosphorylation) are proteins, lipids, and nucleic acids. *Saccharomyces cerevisiae* kinase and start of transcription can be recognized using TSSW.

TSSW is a web program that distinguishes promoter sequences from non-promoter sequences based on a combination of unique content information such as hexamer/trimer frequencies and signal information such as the TATA box in the promoter region. The values are fed to a linear discriminant function to separate true motifs from background noise.

**METHODOLOGY:**

1. Open homepage for softberry. (URL: <http://www.softberry.com/>)
2. Under search for promotor/functional motifs select TSSW. (URL: <http://www.softberry.com/berry.phtml?topic=tssw&group=programs&subgroup=promoter>)
3. Retrieve nucleotide FASTA sequence for protease from GenBank.
4. Process the FASTA sequence on TSSW.
5. Observe and interpret the results.

**OBSERVATION:**

**Saccharomyces cerevisiae kinase (RIM11) gene, complete cds**

GenBank: L29284.2

[FASTA](#) [Graphics](#)

[Go to: ▾](#)

**LOCUS** YSCRIM11A 1920 bp DNA linear PLN 19-JUL-2018

**DEFINITION** *Saccharomyces cerevisiae* kinase (RIM11) gene, complete cds.

**ACCESSION** L29284

**VERSION** L29284.2

**KEYWORDS** RIM11 gene; kinase.

**SOURCE** *Saccharomyces cerevisiae* (baker's yeast)

**ORGANISM** *Saccharomyces cerevisiae*

Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

**REFERENCE** 1 (bases 1 to 1920)

**AUTHORS** Bowdish, K.S., Yuan, H.E. and Mitchell, A.P.

**TITLE** Analysis of RIM11, a yeast protein kinase that phosphorylates the meiotic activator IME1

**JOURNAL** Mol. Cell. Biol. 14 (12), 7909-7919 (1994)

**PUBMED** [7969131](#)

**COMMENT** On Jul 19, 2018 this sequence version replaced [L29284.1](#). Original source text: *Saccharomyces cerevisiae* (strain S288C) (library: YCP50 library of M. Rose) DNA.

**FEATURES**

source Location/Qualifiers

1..1920 /organism="Saccharomyces cerevisiae" /mol\_type="genomic DNA" /db="Saccharomyces"

**Related information**

Protein

PubMed

Taxonomy

Full text in PMC

PubMed (Weighted)

**LinkOut to external resources**

Dryad Digital Repository [Dryad Digital Repository]

Fig1. GenBank result for Human kinase

## Saccharomyces cerevisiae kinase (RIM11) gene, complete cds

GenBank: L29284.2

[GenBank](#) [Graphics](#)

>L29284.2 Saccharomyces cerevisiae kinase (RIM11) gene, complete cds  
 GTCAAATGAGTGGCTACCGGAGAAGGTATTGATAACCTGGGTGACCGCTCTGGTGAATCTGGCATT  
 TTACCCAATACGTCTAACAGATGTGAGCACCATATAAAACTTAAATAATGTCAGTTTATAGCGTGA  
 TAGTTCAATTACCGGAGACTGTGGCATTCTGGCTACTCCGGATAATAATACCAAGGG  
 TCTTCGTAAGGCTTGGGGTTACAAAGCACGGGTTCATTGAAAGATCTTACACAAAGAAGGAGTGTAGGAAG  
 ACCAGCAGATTTCCTAACGCGTCTGGCATTGTTTCTGGCGATTGCGATT  
 AACACCTTTTCCAGAATAGCCAAACCCGGAGCTGATTACACATTACTGGGAAAGATCTTGACAT  
 AGCATTACATTACAAACGGCAACACTAATCACGCAAGCGTAGAACTCGGGAGGATGAATATTCAAAGC  
 AATAATTCCGAATCTCAGTATAACATAGTGTCAAAACAGGTTACTACGCCATCTCCACCTACGA  
 TAGAGCTTCAAGGATCTGGGAGATCTGGGAGACTGGGATTTGGGAGTGTGGTTGGT  
 GGTTGGCACTGTATTCAAGAAACTAATGAAAAGTCTGATTAAAGAAAGTCTGAAAGATAAACG  
 TTCAAGAACAGAGCTGGAAATAATGAAAATCTGAGTGTGAGTCATAAAATATAGATCTGAAGTACTTT  
 TCTATGAGAAAGGACTCCAAAGATGAGATTATTTAAATTGATACTAGAAATACATGCCAACATTGTA  
 CCAGGTTTACGTCTTCGTCATCACGCGATGTCAAGATTGGAAATAAAGTACTACATGTT  
 CAATTGTTCAAGTCTGAAATTCTCATCTTGGGAGCTGTCTGATAGAGACATTAAAGCTCAA  
 ATTATGAGTGTGAGACTGGTCTTAAACTGTGGGATTTGGGAGTGTGCAAGAACGAAATTGAAACC  
 TACTGAACCTAACGTTCTATATTGTCAGGTATAGAGCACCAAGCTAACTTGGGGCAACA  
 AATTATACCAACCAAATGCACATATGGCTCTGGCTGTAATGGCGAACTGTATTGGGCAACCAA  
 TGTTCCCTGGAGAAAGTGGTATTGATCAACTAGTGGAAATCATTAAATCTAGGTTACTCCATCAAAGCA  
 AGAAATTGCTCTATGAATCCCAATTATATGGGACATAAGTCCCGCAAATTAAACCAATCATTGTA  
 CGTGTGTTCAAGAAAGAGTATGCAACTGTGGAAATTCTAGCTGAGTTGAATATGATCCTAG  
 AAAGATTAAATGCTCACAACTGCTGTGAGTAACTAAACCTGTGAGCTGAAAC  
 AAATCAAATACAACGTTAAATTGCTAGAGTTGATGAAAATGTCGAATTGGCCCATCTATCTCCC  
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 GCAAGAATAATGGGAGAAGGAAACATATAGCTATGTCATTTTTAGTATTAACTGTTAT  
 ATTATGAGTATTGTTTACCATATCTTCAATTAGTAACTGTTAGTAAAGCTTATGTTTAC  
 GCAATTCACTCGAATTGTATAAAAGCGTATTGCAAGTCAAAACTATTAAATGACACCTT  
 TACTTAAACGGGTAACAACTCTTAAAT

Customize view

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Related information

Protein

PubMed

Taxonomy

Full text in PMC

PubMed (Weighted)

LinkOut to external resources

Dryad Digital Repository

[Dryad Digital Repository]

Recent activity

Turn Off Clear

Saccharomyces cerevisiae kinase (RIM11) gene, complete cds Nucleotide

Human male germ cell-associated kinase (mak) gene, exon N Nucleotide

K... [774125]

Fig2. Nucleotide FASTA sequence for Protease

Softberry

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Computational methods to empower basic and applied research

Cloud computing services

Annotation of Animal Genomes

Alignment and Genome comparison

Next generation

Annotation of Plant Genomes

Protein structure and functions

Annotation of Bacterial Genomes

Genome regulation analysis

RNA structure and functions

Fig3. Homepage for Softberry



Softberry

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Home

Gene finding in Eukaryota

Gene finding with similarity

Operon and Gene Finding in Bacteria

Gene Finding in Viral Genomes

Next Generation

Alignment (sequences and genomes)

Genome visualization tools

**Search for promoters/functional motifs**

Deep learning recognition

Protein Location

RNA structures

Protein structure

Pathway prediction

Protein/DNA 3D-Visual Works

Manipulations with sequences

Multiple alignments

Synteny from genome contigs

Analysis of gene expression data

Plant Promoter Database

## Services Test Online

### Search for promoters/functional motifs

The programs usage in Scientific publications

**List of Plant Regsite database factors used in TSSP and Nsite-PL programs**

**FPROM** / Human promoter prediction [[Help](#)] [[Example](#)]

**PATTERN** / pattern search [[Help](#)] [[Example](#)]

**TSSP** / Prediction of PLANT Promoters (Using RegSite Plant DB, Softberry Inc.) [[Help](#)] [[Example](#)]

**TSSPlant** / Search for RNA polymerase II promoters (TSSs) in plant DNA sequences [[Help](#)] [[Example](#)]

**TSSG** / Recognition of human PolII promoter region and start of transcription [[Help](#)] [[Example](#)]

**TSSW** / Recognition of human PolII promoter region and start of transcription (Transfac DB, Biobase GmbH, ONLY for academic use) [[Help](#)] [[Example](#)]

**Nsite-PL** / Recognition of PLANT Regulatory motifs with statistics (RegsitePL DB) [[Help](#)] [[Example](#)]

**NsiteM-PL** / Recognition of PLANT Regulatory motifs conserved in several sequences (RegsitePL DB) [[Help](#)] [[Example](#)]

**PlantPromDB\_Blast** / BLAST search in sequences of [PlantPromDB](#) [[Example](#)]

**Nsite** / Recognition of Regulatory motifs (for RE Sets derived from ooTFD, RegsiteAN DB and RegsitePL DB) [[Help](#)] [[Example](#)]

**NsiteM** / Recognition of Conserved Regulatory motifs (for RE Sets derived from ooTFD, RegsiteAN DB and RegsitePL DB) [[Help](#)] [[Example](#)]

**NsiteH** / Search for functional motifs conserved in a pair of orthologous sequences (for RE Sets derived from ooTFD, Regsite AN DB and RegsitePL DB) [[Help](#)] [[Example](#)]

**POLYAH** / Recognition of 3'-end cleavage and polyadenylation region [[Help](#)] [[Example](#)]

**BPROM** / Prediction of bacterial promoters [[Help](#)] [[Example](#)]

**PromH(G)** / Promoter prediction using orthologous sequences in eukaryotic genomes [[Help](#)] [[Example](#)]

**PromH(W)** / Promoter prediction using orthologous sequences in eukaryotic genomes (only for academic usage) [[Help](#)] [[Example](#)]

**CpGFinder** / GC-Islands finding [[Help](#)] [[Example](#)]

**ScanWM-P** / Search for weight matrix patterns of plant regulatory sequences [[Help](#)] [[Example](#)]

**Motif Explorer** / Motif and promoter visualization

**Fig4. Tools for promoters/functional motifs**

Softberry

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Services Test Online

## TSSW

**Reference:** Solovyev VV, Shahmuradov IA, Salamov AA. (2010) Identification of promoter regions and regulatory sites. Computational Biology of Transcription Factor Binding, Volume 674 of the series *Methods in Molecular Biology*, 57-83.

**TSSW / Recognition of human PolII promoter region and start of transcription**

Paste nucleotide sequence here:

Alternatively, load a local file with sequence in Fasta format:  
Local file name:  
 No file chosen

[\[Help\]](#) [\[Example\]](#)

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Last modification date: 24 Jun 2016

Fig5. Homepage for TSSW

Softberry

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## TSSW

**Reference:** Solovyev VV, Shahmuradov IA, Salamov AA. (2010) Identification of promoter regions and regulatory sites. Computational Biology of Transcription Factor Binding, Volume 674 of the series *Methods in Molecular Biology*, 57-83.

**TSSW / Recognition of human PolII promoter region and start of transcription**

Paste nucleotide sequence here:  

```
>M35863.1 Human male germ cell-associated kinase (mak) gene, exon N
TTTTTTCTCCGTATATCATCAAGGCTTTTCTAGGGCATGAAACCGAGAAAATTGCTTGATGGG
TCCAGAGCTTGAAATTGCTGATTGGACTTGCAGAGAATTAAAGTCACAGCCACCATACACTGA
```

Alternatively, load a local file with sequence in Fasta format:  
Local file name:  
 No file chosen

[\[Help\]](#) [\[Example\]](#)

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Last modification date: 24 Jun 2016

Fig6. Search for protease nucleotide FASTA sequence

>L29284.2 <i>saccharomyces cerevisiae</i> kinase (RIM11) gene, complete cds		SoftBerry	SoftBerry
Length of sequence - 1920			
Thresholds for TATA- promoters - 0.45, for TATA-/enhancers - 3.70			
[3 promoter/enhancer(s) are predicted]			
Enhancer Pos: 1391 LDF- 5.79			
Promoter Pos: 1390 LDF- 5.84			
Promoter Pos: 1870 LDF- 0.84 TATA box at 1841 21.05			
Transcription factor binding sites:			
for promoter at position - 1391			
1187 (+) HS\$BAC_03	CCAT	SoftBerry	SoftBerry
1281 (+) HS\$BAC_03	CCAT	SoftBerry	SoftBerry
1316 (+) HS\$BAC_03	CCAT	SoftBerry	SoftBerry
1181 (-) HS\$BAC_03	CCAT	SoftBerry	SoftBerry
1289 (-) CHICK\$BAC_	TATAA	SoftBerry	SoftBerry
1127 (-) CHICK\$BAC_	TATAA	SoftBerry	SoftBerry
1208 (-) Y\$CYC1_09	TCC	SoftBerry	SoftBerry
1195 (-) Y\$CYC1\$BU_2	ACCGAT	SoftBerry	SoftBerry
1314 (+) RATS\$AL\$BU_2	ACCGAT	SoftBerry	SoftBerry
1327 (+) Y\$CFPES_01	GTCAGCTG	SoftBerry	SoftBerry
1177 (+) MOUSES\$A21C	ATTGG	SoftBerry	SoftBerry
1320 (-) MOUSES\$A21C	ATTGG	SoftBerry	SoftBerry
1285 (-) MOUSES\$A21C	ATTGG	SoftBerry	SoftBerry
1191 (-) MOUSES\$A21C	ATTGG	SoftBerry	SoftBerry
1164 (+) MOUSES\$A21C	gccacagccctccATTGGggagacg	SoftBerry	SoftBerry
1333 (-) MOUSES\$A21C	gccacagccctccATTGGggagacg	SoftBerry	SoftBerry
1298 (-) MOUSES\$A21C	gccacagccctccATTGGggagacg	SoftBerry	SoftBerry
1204 (-) MOUSES\$A21C	gccacagccctccATTGGggagacg	SoftBerry	SoftBerry
1201 (-) Y\$CYC1_09	ctatatttggcgccATTGGG	SoftBerry	SoftBerry
1146 (-) Y\$CYC1_09	ctatatttggcgccATTGGG	SoftBerry	SoftBerry
1297 (-) AD\$E3_06	ggggcagggtATAAAactccactga	SoftBerry	SoftBerry
1135 (-) AD\$E3_06	ggggcagggtATAAAactccactga	SoftBerry	SoftBerry
1203 (-) AD\$E3_16	ACGAA	SoftBerry	SoftBerry
1215 (-) HS\$IGF1_15	TCTAT	SoftBerry	SoftBerry
1378 (-) RATS\$E1_09	TCTAG	SoftBerry	SoftBerry
1283 (-) Y\$GALL_02	ActTATAT	SoftBerry	SoftBerry
1290 (-) Y\$GRLL_12	ATATAA	SoftBerry	SoftBerry
1110 (-) HSSBG_05	AGAGATAG	SoftBerry	SoftBerry
1239 (-) MOUSES\$BMG	cagtagtTGTATTggaca	SoftBerry	SoftBerry
1099 (+) MOUSES\$BMG	aggggcaAACTTgtc	SoftBerry	SoftBerry
1231 (+) MOUSES\$BMG	aggggcaAACTTgtc	SoftBerry	SoftBerry
1187 (+) HS\$GG_17	CCAAATag	SoftBerry	SoftBerry
1281 (+) HS\$GG_17	CCAAATag	SoftBerry	SoftBerry
1316 (+) HS\$GG_17	CCAAATag	SoftBerry	SoftBerry
1181 (-) HS\$GG_17	CCAAATag	SoftBerry	SoftBerry
1286 (+) RATS\$GLU_04	TATAT	SoftBerry	SoftBerry
1231 (+) HS\$CMC\$SP_0	CAATA	SoftBerry	SoftBerry
1163 (-) HS\$CMC\$SP_0	CAATA	SoftBerry	SoftBerry
1389 (-) HS\$CMC\$SP_0	TATTT	SoftBerry	SoftBerry
1210 (-) HS\$HO_01	atggccACGTGACccgc	SoftBerry	SoftBerry
1231 (-) HSSH\$H4_01	GATTTC	SoftBerry	SoftBerry
1146 (+) HSSH\$H4_02	GGTC	SoftBerry	SoftBerry
1335 (-) HSSH\$H4_02	gttCTGTAgttagggccg	SoftBerry	SoftBerry
1137 (-) HS\$IGH_04	ATTTCgtT	SoftBerry	SoftBerry
1229 (-) HS\$IGH_01	TTTCCA	SoftBerry	SoftBerry
1223 (+) RATS\$INS_01	GTGGAAA	SoftBerry	SoftBerry

**Fig7. Result for recognised promoter regions**

## RESULT:

Nucleotide FASTA sequence for *Homo sapiens* neutral protease of length 3298bps was submitted. With LDF threshold of 0.45 for promoters and 3.70 for enhancers, 3 promoters at position 809, 323 and 2884 with 9.40, 6.96 and 3.70 LDF values were recognised. 1 enhancer at position 319 with 7.38 LDF was also recognised.

## CONCLUSION:

TSSW is a useful tool for the recognition of human Pol III promoter region and start of transcription. Understanding the regulation of gene expression is an important aspect of understanding the gene function, thus this tool will be useful in elucidating regulation and expression mechanisms of genes and may even shed light on the function of novel and uncharacterized genes with the help of knowledge of promoters.

## REFERENCE:

1. Xiong, J. (2008). Promoter and Regulatory Element Prediction. Essential bioinformatics. Cambridge Cambridge University Press. 113-119.
2. PROTEOLYTIC ENZYMES (PROTEASES): Overview, Uses, Side Effects, Precautions, Interactions Dosing and Reviews. (n.d.). [Www.webmd.com](http://www.webmd.com). Retrieved March 18, 2022, from [https://www.webmd.com/vitamins/ai/ingredientmono-1623/proteolytic-enzymes-proteases#:~:text=Proteolytic%20enzymes%20\(proteases\)%20are%20enzymes](https://www.webmd.com/vitamins/ai/ingredientmono-1623/proteolytic-enzymes-proteases#:~:text=Proteolytic%20enzymes%20(proteases)%20are%20enzymes)
3. *Homo sapiens* neutral protease alpha subunit gene, complete cds. (2016). NCBI Nucleotide. Retrieved March 18, 2022, from <https://www.ncbi.nlm.nih.gov/nuccore/AH001431.2?report=genbank>
4. Softberry Home Page. (n.d.). [Www.softberry.com](http://www.softberry.com). Retrieved March 18, 2022, from <http://www.softberry.com/>
5. TSSW - Recognition of human PolII promoter region and start of transcription. (n.d.). [Www.softberry.com](http://www.softberry.com). Retrieved March 18, 2022, from <http://www.softberry.com/berry.phml?topic=tssw&group=programs&subgroup=promoter>

6. Softberry - TSSW result. (n.d.). [Www.softberry.com](http://www.softberry.com/cgi-bin/programs/promoter/tssw.pl). Retrieved March 18, 2022, from <http://www.softberry.com/cgi-bin/programs/promoter/tssw.pl>

## WEBLEM 8b

### B PROM

(URL: <http://www.softberry.com/berry.phtml?topic=bprom&group=programs&subgroup=gfindb>)

#### AIM:

To predict bacterial promoter for *Enterococcus Alcedinis* using BPROM tool.

#### INTRODUCTION:

Two Gram-positive, catalase-negative bacterial strains were isolated from the cloaca of common kingfishers (*Alcedo atthis*). Repetitive sequence-based PCR fingerprinting using the (GTG)5 primer grouped these isolates into a single cluster separated from all known enterococcal species. The two strains revealed identical 16S rRNA gene sequences placing them within the genus *Enterococcus* with *Enterococcus aquimarinus* LMG 16607(T) as the closest relative (97.14 % similarity).

B PROM is a web-based program for prediction of bacterial promoters. It uses a linear discriminant function combined with signal and content information such as consensus promoter sequence and oligonucleotide composition of the promoter sites. This program first predicts a given sequence for bacterial operon structures by using an intergenic distance of 100 bp as basis for distinguishing genes to be in an operon. This rule is more arbitrary than the Wang et al. rule, leading to high rates of false positives. Once the operons are assigned, the program is able to predict putative promoter sequences. Because most bacterial promoters are located within 200 bp of the protein coding region, the program is most effectively used when about 200 bp of upstream sequence of the first gene of an operon is supplied as input to increase specificity.

#### METHODOLOGY:

1. Open homepage for softberry. (URL: <http://www.softberry.com/>)
2. Under operon and gene finding select BPROM. (URL:<http://www.softberry.com/berry.phtml?topic=bprom&group=programs&subgroup=gfindb>)
3. Retrieve bacterial nucleotide FASTA sequence from GenBank.
4. Process the FASTA sequence on BPROM.
5. Observe and interpret the results.

## OBSERVATION:

NCBI Resources How To Sign in to NCBI

Nucleotide Nucleotide Advanced Search Help

GenBank ▾ Send to: ▾ Change region shown

## Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence

GenBank: JX948102.1

FASTA Graphics PopSet

Go to: ▾

LOCUS JX948102 1260 bp DNA linear BCT 01-MAR-2016

DEFINITION Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence.

ACCESSION JX948102

VERSION JX948102.1

KEYWORDS .

SOURCE Enterococcus alcedinis

ORGANISM [Enterococcus alcedinis](#)

Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus.

REFERENCE 1 (bases 1 to 1260)

AUTHORS Frolikova,P., Svec,P., Sedlacek,I., Maslanova,I., Cernohlavkova,J., Ghosh,A., Zurek,L., Radimersky,T. and Literak,I.

TITLE Enterococcus alcedinis sp. nov., isolated from common kingfisher (Alcedo atthis)

JOURNAL Int. J. Syst. Evol. Microbiol. 63 (PT 8), 3069-3074 (2013)

PUBMED [23416573](#)

REFERENCE 2 (bases 1 to 1260)

AUTHORS Frolikova,P.

TITLE Direct Submission

JOURNAL Submitted (09-OCT-2012) Department of Biology and Wildlife Diseases, University of Veterinary and Pharmaceutical Sciences Brno, Palackeho, Brno 61242, Czech Republic

COMMENT

Send to: ▾ Change region shown

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Find in this Sequence

Related information

PubMed

Taxonomy

BioCollections

PopSet

LinkOut to external resources

Enterococcus alcedinis

[BacDive]

Ribosomal Database Project II

[Ribosomal Database Project II]

### Fig1. GenBank result for *Neisseria gonorrhoeae*

NCBI Resources ▾ How To ▾ Sign in to NCBI

Nucleotide Nucleotide ▾ | Advanced Search Help

FASTA ▾ Send to: ▾ Change region shown ▾

Customize view ▾

## Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence

GenBank: JX948102.1

[GenBank](#) [Graphics](#) [PopSet](#)

```
>JX948102.1 Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence
AGAAAAGAAGTGGCGGACGGGTAGATAACACGTGGTAACCTGCGCTTACGGGGGGATAACACTTGA
AACAGTGTAAACCGATAACTTTTCTCGATGAGAGAAAAGTAAAGACGCTTTGGCTACTA
GAGGATGACCGCGCTGCATTAGCTAGTTGGTGGAGTCAACCAAGGCCAGATGCATAGCCGA
CTGGAGGGTGTACGGCACACTGGACTGAGACACGCCAGACTCTACGGGAGGCAGCTAGGGGA
ATCTCGGCAATGGACGAAAGTCTACGCCGAAACGGCTGAGTGAAGAAGGTTTCCGATCTAAAAA
CTCTGTGTTAGAAGAAGATAAGGTAGAGATGAGATGTTCATCCTTGACGGTATCTAACCGAAAACC
ACGGCTAACACTGTGCCAGCAGCCCGTAATCGTAGGGCAAGCGTGTCCGATTATTGGCGTA
AAGCGAGGCCAGCGGTTTAAAGTCTGATGTAAGACGCCCGCTTAACCGGGAGGGTATTGGAAA
CTGGTACATTGAGTGTAGAGAAGGGAGGTGAATTCCATGTTAGCGGTGAAATCGTAGATATGGA
GAAACACCGTGGCAAGGGCAGACTCTGGCTGAACTGACGCTGAGGCTGAAAGCGTGGGAGCGAA
CAGGATTAGATACCCCTGGTAGTCACGGCTAAACGATGAGTCTAAAGTGTGGAGGGTTCCGCCCTTC
AGTCTGCAAGCAACCGCTTAAGACACTGCCCTGGGAGTAGGTCAGACTGAAACTCAAAGGAATT
GACGGGGGCCGCACAGCGTGGAGCATGTTAACTGAAAGCACCGCAAGAGAACCTTACAGGTCT
TGACATCTTGGACTCTAGAGATGAGACTTCCCTGGGAGAACAGTGCACGGTGTGCGATGGTTG
TGCTCAGCTGGCTGTTAGATGTTGGTTAAAGTCCGGCAAGGGCAACCCCTTATTGTTAGTGGCAT
CATTCACTGGGACTCTAGCGAGACTGCCGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCAT
CATGCCCTTATGACTCTGGCTACACAGCTGTCACAAATGGAAAGTACAACGAGTCGCAAAAGTGGGAGGC
TAAGCTAATCTTAAACCTCTCGTGGATTGAGCTGCAACTGCCTACATGAAGGCCGAAATC
```

Analyze this sequence

Run BLAST

Pick Primers

Highlight Sequence Features

Related information

PubMed

Taxonomy

BioCollections

PopSet

LinkOut to external resources

Enterococcus alcedinis

[BacDive]

Ribosomal Database Project II

[Ribosomal Database Project II]

SILVA SSU Database

[SILVA]

## Fig2. Nucleotide FASTA sequence

Fig3. Homepage for softberry

Fig4. Tools for bacterial promoter, operon and gene finding

Softberry

Run Programs Online ▾

Home  
Gene finding in Eukaryota  
Gene finding with similarity  
**Operon and Gene Finding in Bacteria**  
Gene Finding in Viral Genomes  
Next Generation  
Alignment (sequences and genomes)  
Genome visualization tools  
Search for promoters/functional motifs  
Deep learning recognition  
Protein Location  
RNA structures  
Protein structure  
Pathway prediction  
Protein/DNA 3D-Visual Works  
Manipulations with sequences  
Multiple alignments  
Synteny from genome contigs  
Analysis of gene expression data  
Plant Promoter Database

**Services Test Online**

**BPROM**

Used in more than 800 publications.

**Reference:** V. Solovyev, A. Salamov (2011) Automatic Annotation of Microbial Genomes and Metagenomic Sequences. In Metagenomics and its Applications in Agriculture, Biomedicine and Environmental Studies (Ed. R.W. Li), Nova Science Publishers, p. 61-78

**BPROM** - Prediction of bacterial promoters

BPROM is bacterial sigma70 promoter recognition program with about 80% accuracy and specificity. It is best used in regions immediately upstream from ORF start for improved gene and operon prediction in bacteria.

Paste nucleotide sequence here (plain or in fasta format):

Alternatively, load a local file with sequence:

Local file name:  No file chosen

[\[Help\]](#) [\[Example\]](#)

Return to page with other programs of group: [Operon and gene finding in bacteria](#)

---

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Last modification date: 24 Oct 2016

**Fig5. Homepage for BPROM**

Softberry

Run Programs Online ▾

Home  
Gene finding in Eukaryota  
Gene finding with similarity  
**Operon and Gene Finding in Bacteria**  
Gene Finding in Viral Genomes  
Next Generation  
Alignment (sequences and genomes)  
Genome visualization tools  
Search for promoters/functional motifs  
Deep learning recognition  
Protein Location  
RNA structures

**Services Test Online**

**BPROM**

Used in more than 800 publications.

**Reference:** V. Solovyev, A. Salamov (2011) Automatic Annotation of Microbial Genomes and Metagenomic Sequences. In Metagenomics and its Applications in Agriculture, Biomedicine and Environmental Studies (Ed. R.W. Li), Nova Science Publishers, p. 61-78

**BPROM** - Prediction of bacterial promoters

BPROM is bacterial sigma70 promoter recognition program with about 80% accuracy and specificity. It is best used in regions immediately upstream from ORF start for improved gene and operon prediction in bacteria.

Paste nucleotide sequence here (plain or in fasta format):

```
>JX948102.1 Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence
AGAAAGAAGAGTGGCGGACGGGTGAGTAACACGTGGTAACCTGCCCTTAG
```

Alternatively, load a local file with sequence:

Local file name:  No file chosen

[\[Help\]](#)

**Fig6. Homepage for nucleotide FASTA sequence**

```

>JX948102.1 Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial s
Length of sequence- 1260
Threshold for promoters - 0.20
Number of predicted promoters - 2
Promoter Pos: 1165 LDF- 3.90
-10 box at pos. 1150 TGCTACAAT Score 72
-35 box at pos. 1131 ATGACC Score 14
Promoter Pos: 394 LDF- 3.11
-10 box at pos. 379 GAGTAGAAT Score 60
-35 box at pos. 356 TTGTTA Score 45

Oligonucleotides from known TF binding sites:

For promoter at 1165:
rpoD19: ACGTGCTA at position 1147 Score - 12
rpoD17: GCTACAAT at position 1151 Score - 8
For promoter at 394:
rpoD17: AGTAGAAT at position 380 Score - 11

```

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**Fig7. Result for predicted promoters and known TF binding sites**

## RESULT:

Nucleotide FASTA sequence for Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence with length 1260 was submitted. With threshold LDF value of 0.20, 9 promoters were predicted using BPROM with their TF binding sites.

## CONCLUSION:

BPROM is a useful tool for the recognition of bacterial promoter region. Understanding the regulation of gene expression is an important aspect of understanding the gene function, thus this tool will be useful in elucidating regulation and expression mechanisms of genes and may even shed light on the function of novel and uncharacterized genes with the help of knowledge of promoters.

## REFERENCES:

1. Xiong, J. (2008). Promoter and Regulatory Element Prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 113-119.
2. Neisseria gonorrhoeae - an overview | ScienceDirect Topics. (n.d.). [Www.sciencedirect.com](https://www.sciencedirect.com/topics/medicine-and-dentistry/neisseria-gonorrhoeae#:~:text=Neisseria%20gonorrhoeae%20is%20a%20bacterial). Retrieved March 18, 2022, from <https://www.sciencedirect.com/topics/medicine-and-dentistry/neisseria-gonorrhoeae#:~:text=Neisseria%20gonorrhoeae%20is%20a%20bacterial>
3. Neisseria gonorrhoeae strain NG\_869 plasmid pNG869\_3, whole genome shotgun sequence. (2022).NCBI Nucleotide. Retrieved March 18, 2022, from [https://www.ncbi.nlm.nih.gov/nuccore/NZ\\_CM003348.1](https://www.ncbi.nlm.nih.gov/nuccore/NZ_CM003348.1)
4. Softberry Home Page. (n.d.). [Www.softberry.com](http://www.softberry.com). Retrieved March 18, 2022, from <http://www.softberry.com/>
5. BPROM - Prediction of bacterial promoters. (n.d.). [Www.softberry.com](http://www.softberry.com). Retrieved March 18, 2022, from <http://www.softberry.com/berry.phtml?topic=bprom&group=programs&subgroup=gfindb>
6. Softberry - BPROM result. (n.d.). [Www.softberry.com](http://www.softberry.com). Retrieved March 18, 2022, from <http://www.softberry.com/cgi-bin/programs/gfindb/bprom.pl>



## WEBLEM 8c

### FGENESB

(URL:

<http://www.softberry.com/berry.phtml?topic=fgenesb&group=programs&subgroup=gfindb>

#### AIM:

To predict bacterial operon and gene for *Enterococcus alcedinis* using FGENESB tool.

#### INTRODUCTION:

Two Gram-positive, catalase-negative bacterial strains were isolated from the cloaca of common kingfishers (*Alcedo atthis*). Repetitive sequence-based PCR fingerprinting using the (GTG)5 primer grouped these isolates into a single cluster separated from all known enterococcal species. The two strains revealed identical 16S rRNA gene sequences placing them within the genus *Enterococcus* with *Enterococcus aquimarinus* LMG 16607(T) as the closest relative (97.14 % similarity).

FGENESB is a web-based program that is also based on fifth-order HMMs for detecting coding regions. The program is specifically trained for bacterial sequences. It uses the Viterbi algorithm to find an optimal match for the query sequence with the intrinsic model. A linear discriminant analysis (LDA) is used to further distinguish coding signals from noncoding signals.

#### METHODOLOGY:

1. Open homepage for softberry. (URL: <http://www.softberry.com/>)
2. Under operon and gene finding in bacteria select FGENESB. (URL:<http://www.softberry.com/berry.phtml?topic=fgenesb&group=programs&subgroup=gfindb>)
3. Retrieve bacterial nucleotide FASTA sequence from GenBank.
4. Process the FASTA sequence on FGENESB.
5. Observe and interpret the results.

#### OBSERVATION:

Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence

GenBank: JX948102.1

FASTA Graphics PopSet

Go to: ▾

LOCUS JX948102 1260 bp DNA linear BCT 01-MAR-2016

DEFINITION Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence.

ACCESSION JX948102

VERSION JX948102.1

KEYWORDS .

SOURCE Enterococcus alcedinis

ORGANISM [Enterococcus alcedinis](#)  
Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus.

REFERENCE 1 (bases 1 to 1260)

AUTHORS Frolkova,P., Svec,P., Sedlacek,I., Maslanova,I., Cernohlavkova,J., Ghosh,A., Zurek,L., Radimersky,T. and Literak,I.

TITLE Enterococcus alcedinis sp. nov., isolated from common kingfisher (*Alcedo atthis*)

JOURNAL Int. J. Syst. Evol. Microbiol. 63 (PT 8), 3069-3074 (2013)

PUBMED 23416573

REFERENCE 2 (bases 1 to 1260)

AUTHORS Frolkova,P.

TITLE Direct Submission

JOURNAL Submitted (09-OCT-2012) Department of Biology and Wildlife Diseases, University of Veterinary and Pharmaceutical Sciences Brno, Palackeho, Brno 61242, Czech Republic

COMMENT JX948102.1 is part of STREPUM

Related information

PubMed

Taxonomy

BioCollections

PopSet

LinkOut to external resources

Enterococcus alcedinis

[BacDive]

Ribosomal Database Project II

[Ribosomal Database Project II]

**Fig1. GenBank result for *Enterococcus alcedinis***

Advanced Help

FASTA ▾

Send to: ▾ Change region shown ▾

Customize view ▾

**Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence**

GenBank: JX948102.1

GenBank Graphics PopSet

>JX948102.1 Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence

AGAAAGAAGAGTGGCGGACGGGTGAGTAACACGTGGTAACCTGCCCTTAGCGGGGATAACACTTGGAAACAGGTGCTAAATACCGCAATATTCTTCGCGATGAGAGAAAAGTGAAGACGCTTTGCGTCACTAAGGGATGGCAGCCGCGCTGATTAGCTAGTTGGTGAAGGTAATGGCTCACCAAGGCCACGATGCATAGCGAAGCTGGAGAGGGTGAACGGCACACTGGGACTGAGACACGGCCAGACTCTACGGGAAGGCAGAGTGGGAATCTGGGAGGGTGAAGGTTTCGATCGTAAAGCTCTGGTGAAGAAGGGTGGGAATTCTCATGTGATGGTGAAGGTTTCGATCTAACAGAAAGCCACGGCTAACACTGTCAGCCAGCAGCCGCGCTGATTAGCTAGTTGGTGAAGGCTGGTCCGGGATTTATGGCGTAAGCGAGGGCAGGGCGTTTATTAAAGCTGATGTTGAAGGAAAGCCTCCGCTTAACCGGGGAGGGTATTGGAAAATGGTAGACTTGGTGAAGAAGGGAGAGTGGAAATTCTCATGTGATGGTGAAGGTTTCGATCTAACAGAAAGCCAGGATTAGATAACCTGTAGTCCAGGCCGTAACAGATGAGCTTAAGTGTGAGGGTTTCGCCCTTCAGTGCTGAGCAACGCCGATTAAGCAGACTCCGCGCTGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGGCCGCAACAGCGGTGGAGCATGTTGTTAAATTCGAAGCACAAGCGGAAGAACCTTACAGGTCTTGACATGTTGTCGTCAGCTGTGCTGAGATGGTGGGTTAAAGTCCCGAACAGGCAACGGCAACCCCTATTGTTAGTGGCCATCATTAGTGGGACTCTAGCGAGACTGCGGTTGACAACGGAGGGTGGGGATGAGCTCAATCATGCTGAGACAGGAGTGCAGGAAAGTCCGGAGGCATGCTGAGTGGGTTAAAGTCCCGAACAGGCAACCCCTATTGTTAGTGGCCATCATGCCCTTATGACTGGCTACACACGTGCTACAAACGGAGTACACAGGAGTGCAGGAAAGTCCGGAGGCATAAGCTTAATCTCTCACTGGATTGAGGCTGCAACTCGCCTACATGAAGCCGGATC

Analyze this sequence ▾

Run BLAST

Pick Primers

Highlight Sequence Features

Related information ▾

PubMed

Taxonomy

BioCollections

PopSet

LinkOut to external resources ▾

Enterococcus alcedinis [BacDive]

Ribosomal Database Project II [Ribosomal Database Project II]

SILVA SSU Database [SILVA]

Recent activity ▾

**Fig2. Nucleotide FASTA sequence**

Softberry Run Programs Online ▾

Annotation of Plant Genomes

Cloud computing services

Annotation of Animal Genomes

Next generation

Annotation of Bacterial Genomes

Genome regulation analysis

About Downloads Products Services In publications Management Contacts

**Fig3. Homepage for softberry**

Softberry

Run Programs Online ▾

Home  
Gene finding in Eukaryota  
Gene finding with similarity  
**Operon and Gene Finding in Bacteria**  
Gene Finding in Viral Genomes  
Next Generation  
Alignment (sequences and genomes)  
Genome visualization tools  
Search for promoters/functional motifs  
Deep learning recognition  
Protein Location  
RNA structures

**Services Test Online**

## Bacterial Promoter, Operon and Gene Finding

Solovyev V, Salamov A. (2011) Automatic Annotation of Microbial Genomes and Metagenomic Sequences. In Metagenomics and its Applications in Agriculture, Biomedicine and Environmental Studies (Ed. R.W. Li), Nova Science Publishers, p.61-78.

**The programs usage in Scientific publications**

**fgenesB** - Pattern/Markov chain-based bacterial operon and gene prediction [[Help](#)] [[Example](#)]  
**BPROM** - Prediction of bacterial promoters [[Help](#)] [[Example](#)]  
**AbSplit** - Separating archaea and bacterial genomic sequences [[Help](#)] [[Example](#)]  
**FindTerm** - Finding Terminators in bacterial genomes [[Help](#)] [[Example](#)]  
**Visualization of FgenesB annotation using CGView** [[Example](#)]  
**Bacterial GenomeSequence Explorer** - Visualization of Bacterial genomes information [[Help](#)]  
**All bacteria genomes annotations**  
**General scheme of bacterial genome annotation** -(automatic pipeline - Fgenesb\_annotator)  
**Human Microbiome gene prediction**  
**Softberry Microbiome Annotation Database**

**FGENESB** is the fastest (*E.coli* genome is annotated in ~14 sec) and most accurate *ab initio* bacterial operon and gene prediction program available - for more details, see [FGENESB help](#). It uses genome-specific parameters learned by **FgenesB-train script**, which requires only DNA sequence from genome of interest as an input. It automatically creates a file with gene prediction

**Fig4. Tools for bacterial promoter, operon and gene finding**

Softberry

Run Programs Online ▾

Home  
Gene finding in Eukaryota  
Gene finding with similarity  
**Operon and Gene Finding in Bacteria**  
Gene Finding in Viral Genomes  
Next Generation  
Alignment (sequences and genomes)  
Genome visualization tools  
Search for promoters/functional motifs  
Deep learning recognition  
Protein Location  
RNA structures

**Services Test Online**

## FGENESB: Bacterial Operon and Gene Prediction

Used in more than 330 publications

**Reference:** V. Solovyev, A. Salamov (2011) Automatic Annotation of Microbial Genomes and Metagenomic Sequences. In Metagenomics and its Applications in Agriculture, Biomedicine and Environmental Studies (Ed. R.W. Li), Nova Science Publishers, p. 61-78

FGENESB is a suite of bacterial operon and gene prediction programs: its detailed description is given [here](#). Presented on this page is gene finding portion of FGENESB, which is pattern/Markov chain-based and is the fastest (*E.coli* genome is annotated in appr. 14 sec) and most accurate *ab initio* bacterial gene prediction program available - for more details, see [FGENESB help](#). FGENESB uses genome-specific parameters learned by **FgenesB-train script**, which requires only DNA sequence from genome of interest as an input. It automatically creates a file with gene prediction parameters for analyzed genome. It took only a few minutes to create such file for *E.coli* genome using its sequence. If you need parameters for your new bacteria, please contact Softberry - we can include them in the web list.

Annotation portion of FGENESB consumes a lot computer resources and is therefore not available at our web site.

Paste nucleotide sequence here (plain or in fasta format):

Alternatively, load a local file with sequence:

Local file name:

**Fig5. Homepage for FGENESB**

Softberry

Run Programs Online ▾

Home  
Gene finding in Eukaryota  
Gene finding with similarity  
**Operon and Gene Finding in Bacteria**  
Gene Finding in Viral Genomes  
Next Generation  
Alignment (sequences and genomes)  
Genome visualization tools  
Search for promoters/functional motifs  
Deep learning recognition  
Protein Location  
RNA structures

## Services Test Online

### FGENESB: Bacterial Operon and Gene Prediction

Used in more than 330 publications

**Reference:** V. Solovyev, A. Salamov (2011) Automatic Annotation of Microbial Genomes and Metagenomic Sequences. In Metagenomics and its Applications in Agriculture, Biomedicine and Environmental Studies (Ed. R.W. Li), Nova Science Publishers, p. 61-78

FGENESB is a suite of bacterial operon and gene prediction programs: its detailed description is given [here](#). Presented on this page is gene finding portion of FGENESB, which is pattern/Markov chain-based and is the fastest (E.coli genome is annotated in appr. 14 sec) and most accurate *ab initio* bacterial gene prediction program available - for more details, see [FGENESB help](#). FGENESB uses genome-specific parameters learned by [FgenesB-train script](#), which requires only DNA sequence from genome of interest as an input. It automatically creates a file with gene prediction parameters for analyzed genome. It took only a few minutes to create such file for *E.coli* genome using its sequence. If you need parameters for your new bacteria, please contact Softberry - we can include them in the web list.

Annotation portion of FGENESB consumes a lot computer resources and is therefore not available at our web site.

Paste nucleotide sequence here (plain or in fasta format):  
>JX948102.1 Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence  
AGAAAGAAGAGTGGCGGACGGGTGAGTAACACGTGGTAACCTGCCCTTAG

Alternatively, load a local file with sequence:

Local file name:

**Fig6. Search for nucleotide FASTA sequence**

Prediction of potential genes in microbial genomes  
Time: Tue Jan 1 00:00:00 2005  
Seq name: JX948102.1 Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial s  
Length of sequence - 1260 bp  
Number of predicted genes - 0

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**Fig7. Result for predicted bacterial operon and genes**

## RESULT:

Nucleotide FASTA sequence for Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence with length of 1260 was submitted and 9 genes, 5 transcriptional units and 2 operons were predicted using FGENESB.

## **CONCLUSION:**

FGENESB tool is useful for prediction of bacterial operon and gene. Gene prediction information is a prerequisite for detailed functional annotation of genes and genomes. Identifying the genes that are grouped together into operons may enhance our knowledge of gene regulation and function, and such information is an important addition to genome annotation. All this can be done with the help of FGENESB.

## **REFERENCES:**

1. Xiong, J. (2008). Gene Prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 97111.
2. Neisseria gonorrhoeae - an overview | ScienceDirect Topics. (n.d.). [Www.sciencedirect.com.Retrieved](https://www.sciencedirect.com/topics/medicine-and-dentistry/neisseria-gonorrhoeae#:~:text=Neisseria%20gonorrhoeae%20is%20a%20bacterial) March 18, 2022, from <https://www.sciencedirect.com/topics/medicine-and-dentistry/neisseria-gonorrhoeae#:~:text=Neisseria%20gonorrhoeae%20is%20a%20bacterial>
3. Neisseria gonorrhoeae strain NG\_869 plasmid pNG869\_3, whole genome shotgun sequence. (2022). NCBI Nucleotide. Retrieved March 18, 2022, from [https://www.ncbi.nlm.nih.gov/nuccore/NZ\\_CM003348.1](https://www.ncbi.nlm.nih.gov/nuccore/NZ_CM003348.1)
4. Softberry Home Page. (n.d.). [Www.softberry.com.](http://www.softberry.com/) Retrieved March 18, 2022, from <http://www.softberry.com/>
5. FGENESB - Bacterial Operon and Gene Prediction. (n.d.). [Www.softberry.com.](http://www.softberry.com/berry.phtml?topic=fgenesb&group=programs&subgroup=gfindb) Retrieved March 18, 2022, from <http://www.softberry.com/berry.phtml?topic=fgenesb&group=programs&subgroup=gfindb>
6. Softberry - fgenesB results. (n.d.). [Www.softberry.com.](http://www.softberry.com/cgi-bin/programs/gfindb/fgenesb.pl) Retrieved March 18, 2022, from <http://www.softberry.com/cgi-bin/programs/gfindb/fgenesb.pl>

## WEBLEM 8d

### FGENES

(URL: <http://www.softberry.com/berry.phtml?topic=fgenes&group=programs&subgroup=gfind>)

#### AIM:

To predict exon signals in Kinase using FGENES tool.

#### INTRODUCTION:

**Kinase**, an enzyme that adds phosphate groups ( $\text{PO}_4^{3-}$ ) to other molecules. A large number of kinases exist—the human genome contains at least 500 kinase-encoding genes. Included among these enzymes' targets for phosphate group addition (phosphorylation) are proteins, lipids, and nucleic acids. *Saccharomyces cerevisiae* kinase and start of transcription can be recognized using FGENES.

FGENES is a web-based program that uses LDA to determine whether a signal is an exon. In addition to FGENES, there are many variants of the program. Some programs, such as FGENESH, make use of HMMs. There are others, such as FGENESH C, that are similarity based. Some programs, such as FGENESH+, combine both ab initio and similarity-based approaches.

#### METHODOLOGY:

1. Open homepage for softberry. (URL: <http://www.softberry.com/>)
2. Under Gene for Eukaryotes select FGENES. (URL: <http://www.softberry.com/berry.phtml?topic=fgenes&group=programs&subgroup=gfind>)
3. Retrieve nucleotide FASTA sequence for protease from GenBank.
4. Process the FASTA sequence on FGENES.
5. Observe and interpret the results.

#### OBSERVATION:

**Saccharomyces cerevisiae kinase (RIM11) gene, complete cds**

GenBank: L29284.2

[FASTA](#) [Graphics](#)

[Go to: ▾](#)

**LOCUS** YSCRIM11A 1920 bp **DNA** linear **PLN** 19-JUL-2018

**DEFINITION** *Saccharomyces cerevisiae* kinase (RIM11) gene, complete cds.

**ACCESSION** L29284

**VERSION** L29284.2

**KEYWORDS** RIM11 gene; kinase.

**SOURCE** *Saccharomyces cerevisiae* (baker's yeast)

**ORGANISM** *Saccharomyces cerevisiae*

Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

**REFERENCE** 1 (bases 1 to 1920)

**AUTHORS** Bowdish,K.S., Yuan,H.E. and Mitchell,A.P.

**TITLE** Analysis of RIM11, a yeast protein kinase that phosphorylates the meiotic activator IME1

**JOURNAL** Mol. Cell. Biol. 14 (12), 7909-7919 (1994)

**PUBMED** 7969131

**COMMENT** On Jul 19, 2018 this sequence version replaced [L29284.1](#). Original source text: *Saccharomyces cerevisiae* (strain S288C) (library: Ycp50 library of M. Rose) DNA.

**FEATURES**

**source**

- Location/Qualifiers
- 1..1920
- /organism="Saccharomyces cerevisiae"
- /mol\_type="genomic DNA"
- /strand="+"; "genomic DNA"

**Related information**

Protein

PubMed

Taxonomy

Full text in PMC

PubMed (Weighted)

**LinkOut to external resources**

Dryad Digital Repository

[Dryad Digital Repository]

Fig1. GenBank result for *Saccharomyces cerevisiae* kinase

**Saccharomyces cerevisiae kinase (RIM11) gene, complete cds**

GenBank: L29284.2

[GenBank](#) [Graphics](#)

```
>L29284.2 Saccharomyces cerevisiae kinase (RIM11) gene, complete cds
GTCAAATGTAGTGGGT TACCGGAGAAAGTTATGATAACCTGGGTGACCGCTGGTGGAAATCTGCCATT
TTACCCAATATCGTCTAAGATGTGAGCACCATATAAAAACCTTAAATAATGTCAGTTTATAGCTGA
TAGTTCAATTACCGGCACTGTGGCATTCTGCTACTCCGGATAATAACTACCAAGGGG
TCTGTAAAGGCTTGGGGTTACAAAGCACGGGTCATTGAAGATTTACACAAGAAGGGAGTGTAGGAAG
ACCAGCAGATTTCCTAACGTCGTGTCATTGCTTCTGGCGATTGCGATTTC
AACACCTTTTCCAGAATAGCCAAACACCGAGCTGATTACACATTACTGGCAAGATCTTGACAT
AGCATTACATTACACAGGCAACACTAATCGCAAGCTGAGAATCTGGCAGGGTGAATATTCAAAGC
AATAATTCGAACTCTGAATAACATAGTCAGAACAGGTTTACAGCCCATCTCACCTACGA
TAGACCCGAATGTCGGTCAAGATACTTCCACCCGAAGTGTGGGATGTTGTTGGTGT
GGTATTGGCACTGTATTCAAGAAACTATGAAAAGTGTCTTAAAGAAGATCTGCAAGATAAACGA
TTCAGAAACAGAGCTGAAAATAGTCAAGATGACATAAAATAATGATCTGAAGTACTTTT
TCTATGAAAGGACTCCAAAGATGAGATTTTAAATGATACTAGAATACATGCCACAATCTTGTA
CCAGAGGTTACGTCATTGCTCATCACTGAGCTACGGAGTCAAGATTGAAATAAAGTACTACATGTTT
CAATTGTTCAAGTCATTGAAATTACCTCATATTGCGAACGCTGTCTAGATAGAGACATTAAGGCCAAA
ATTATTAGTAGATCTGAGACCGGCTCTAAACTGTGCGATTGCGAGTGCAAAGCAATTGAAACC
TACTGAACGTTCTTATTTGTCACGGTACTAGAGCACCAGAGCTAATCTGGCGCAACA
AATTATACCAACCAAAATCGACATATGGTCTCTGGCTGTAATGGCGAACTGCTATTGGCCCAACCAA
TGTCCCTGGAGAAAGTGGTATTGATCAACTAGTGGAAATCATTAAATCTAGGTACTCCATCAAAGCA
AGAAATGCTTATGAACTCCAAATTATGGAGCATAAAGTCCCGCAAATTAAACCAATACATTGTC
CGTGTGTTCAAGAAAGAGATGATCAAACCTGTGAAATTCTAGCTGAGTTTGAATATGATCCACTAG
AAAGATTTAAATGCTCTACAATGGCTGTAGTCATATTGATGAACAAACTTGTAGCGGAAAT
AAATCAAATACAAACTGATTAAATTGTCAGAGCTGATGAAAATGTCGAATTGGCCATCTATCTCC
GATGAACTATCATCTGAAAAAAAGACTATCCGAAAGCTTAAGTAATGATAGCACCAGGGAGGCCA
GGCAAGAATATGGAGAAGAGGAGAACATATAGTGTCTTTTTAGTACTATTACTGTTAT
TATTATGAGTATTGTTTGTATTACCATCATTTCTTATCATTATTAGTAAAGCTTATTGTTATC
ATTACTGTTATAATGAATACAATTATGAAAAAAATAGTAAAGGCAAAATAAATTGTAACTTTTAT
GCCATTCTCGAATTATGATAAAAGCGTATTCTTGGCAGTAGAAACTATTAAATGACACCTT
TACTTAAACCGGTTAACAACTTCCCTAAAT
```

**Analyze this sequence**

Customize view

Run BLAST

Pick Primers

Highlight Sequence Features

**Related information**

Protein

PubMed

Taxonomy

Full text in PMC

PubMed (Weighted)

**LinkOut to external resources**

Dryad Digital Repository

[Dryad Digital Repository]

**Recent activity**

Saccharomyces cerevisiae kinase (RIM11) gene, complete cds Nucleotide

kinase (7718105) Nucleotide

Turn Off Clear

Fig2. Nucleotide FASTA sequence for *Saccharomyces cerevisiae* kinase

**Softberry**

**Annotation of Plant Genomes**

Run Programs Online ▾

**MOLQUEST**

About Downloads Products Services In publications Management Contacts

**Cloud computing services**  
Data analysis using Softberry, public or clients' own pipelines in AWS cloud. Adopting pipelines to run on cloud computer clusters.

**Annotation of Animal Genomes**  
Gene identification, HMM Fgenesh gene finder and Fgenesh++ genome annotation pipeline, building gene

**Next generation**  
Genome and transcripts assembling, Reads Mapping, Alternative transcripts (Transomics pipeline), Snp discovery and evaluation, visualization

**Annotation of Plant Genomes**  
Gene identification, Fgenesh gene finder and Fgenesh++ genome annotation pipeline, 42 custom

**Annotation of Bacterial Genomes**  
Bacterial gene, promoters, terminators, operons identification, metagenomics, Fgenesb pipeline. Microbiome sequence analysis and annotation.

**Genome regulation analysis**  
De novo finding regulatory motifs, search for non-random occurrence of functional motifs, plant and

Fig3. Homepage for softberry

Softberry

Run Programs Online ▾

Home

Gene finding in Eukaryota

Gene finding with similarity

Operon and Gene Finding in Bacteria

Gene Finding in Viral Genomes

Next Generation

Alignment (sequences and genomes)

Genome visualization tools

Search for

## Services Test Online

### Gene Finding: Gene models construction, splice sites, protein-coding exons

Total 506 genome-specific parameters are available for genefinders of FGENESH suite  
The programs usage in Scientific publications

FGENESH is the fastest and most accurate *ab initio* gene prediction program available - for more details, see [FGENESH help](#). Its variants that use similarity information: FGENESH+ (similar protein), FGENESH\_C (similar cDNA), FGENESH-2 (two homologous genomic sequences) greatly improve accuracy of gene prediction when such similarity information is available. These programs can be accessed [here](#).

To find genes in Bacterial sequences click [here](#).

Our two best gene finders cannot be accessed at our site due to computing resources limitations. These two are FGENESH++ (automated version of FGENESH+) and FGENESH++C, which maps known mRNA/EST sequences from RefSeq and then performs FGENESH++-like gene prediction, resulting in fully automatic annotation of quality similar to that of manual annotation.

FGENES, FGENES-M, FGENESH\_GC and SPLM can be used on human sequences only.  
BESTORF and Fsplice can be used with 296 organisms sequences.

Fig4. Tools for gene finding in Eukaryota

Softberry

Run Programs Online ▾

Home

Gene finding in Eukaryota

Gene finding with similarity

Operon and Gene Finding in Bacteria

Gene Finding in Viral Genomes

Next Generation

Alignment (sequences and genomes)

Genome visualization tools

Search for

## Services Test Online

### FGENES

Pattern based human gene structure prediction (multiple genes, both chains)

Paste nucleotide sequence here:

Alternatively, load a local file with sequence in Fasta format:

Local file name:

No file chosen

[\[Help\]](#) [\[Example\]](#)

Return to page with other programs of group: [Gene finding](#)

Fig5. Homepage for FGENES

Softberry

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Home

Gene finding in Eukaryota

Gene finding with similarity

Operon and Gene Finding in Bacteria

Gene Finding in Viral Genomes

Next Generation

Alignment (sequences and genomes)

Genome visualization tools

softberry.com search for

**Services Test Online**

## FGENES

Pattern based human gene structure prediction (multiple genes, both chains)

Paste nucleotide sequence here:

```
>L29284.2 Saccharomyces cerevisiae kinase (RIM11) gene, complete cds
GTCAAATGAGTGGCGTTACCGGAGAAGGTATTGATAACCTGCGTGACCGTCT
GGTGGAATCCTGCCATT
```

Alternatively, load a local file with sequence in Fasta format:

Local file name:  No file chosen

[\[Help\]](#) [\[Example\]](#)

Return to page with other programs of group: [Gene finding](#)

**Fig6. Search for kinase nucleotide FASTA sequence**

[Show picture of predicted genes in PDF file](#)

FGENES 1.6 Prediction of multiple genes in genomic DNA  
 Time: 17:45:22 Date: Sat Mar 19 2022  
 Seq name: >L29284.2 Saccharomyces cerevisiae kinase (RIM11) gene, comp  
 Length of sequence: 1920 GC content: 0.38 Zone: 1  
 Number of predicted genes: 1 In +chain: 1 In -chain: 0  
 Number of predicted exons: 1 In +chain: 1 In -chain: 0  
 Positions of predicted genes and exons:

G	Str	Feature	Start	End	Weight	ORF-start	ORF-end		
1	+	CDS	476	-	1588	6.92	476	-	1588
1	+	PolA	1800			4.06			

Predicted proteins:

```
>FGENES 1.6 >L29284.2 Sacch 1 Single exon g. 476 - 1588 370 a Ch+
MNIQSNNSPNLNSNNIVSKQVYYAHPPPTIDPNPDVQISFPTTEVVGHGSFGVVFATVIQE
TNEKVAIKKVLQDKERFKNRELEIMKMLSHINIDLKYFFYERDSQDEIYLNLILEYMPQS
LYQRLRFVHQRTPMRLEIKYMFQLFKSLNLYLHHFANVCHRDIKPQNLVLPETWSLK
LCDFGSAKQLKPKTEPNSVSYICSRYYRAPELIFGATNYTNQIDIWSSGCVMAELLLGQPMF
PGESGIDQLVEIIKLLGTPSKQEICSMNPNYMEHKFPQIKPILSRVFKKEDDQTVFELA
DVLKYDPLERFNALQCLCSPYFDELKDDGKINQITTDLKLEFDENVELGHLSPELSS
VKKKLYPKSK
```

**Fig7. Result for predicted exon signals**

## RESULT:

Nucleotide FASTA sequence Saccharomyces cerevisiae kinase of length 1260 was submitted. With GC content of 0.57, 1 gene and 10 exons were predicted on the + chain. ORF start and end of each exon was predicted.

## CONCLUSION:

FGENES tool is useful for prediction of exon signals. Exon prediction information can be used to predict genes and annotate genomes. It can help in understanding the gene function.

## REFERENCES:

1. Xiong, J. (2008). Gene Prediction. Essential bioinformatics. Cambridge: Cambridge University Press. 97-111.
2. PROTEOLYTIC ENZYMES (PROTEASES): Overview, Uses, Side Effects, Precautions, Interactions, Dosing and Reviews. (n.d.). [www.webmd.com](https://www.webmd.com/vitamins/ai/ingredientmono-1623/proteolytic-enzymes-proteases#:~:text=Proteolytic%20enzymes%20(proteases)%20are%20enzymes). Retrieved March 18, 2022, from [https://www.webmd.com/vitamins/ai/ingredientmono-1623/proteolytic-enzymes-proteases#:~:text=Proteolytic%20enzymes%20\(proteases\)%20are%20enzymes](https://www.webmd.com/vitamins/ai/ingredientmono-1623/proteolytic-enzymes-proteases#:~:text=Proteolytic%20enzymes%20(proteases)%20are%20enzymes)
3. Homo sapiens neutral protease alpha subunit gene, complete cds. (2016). NCBI Nucleotide. Retrieved March 18, 2022, from <https://www.ncbi.nlm.nih.gov/nuccore/AH001431.2?report=genbank>
4. Softberry Home Page. (n.d.). [www.softberry.com](http://www.softberry.com/). Retrieved March 18, 2022, from <http://www.softberry.com/>
5. FGENES - pattern-based gene structure prediction. (n.d.). [www.softberry.com](http://www.softberry.com/berry.phtml?topic=fgenes&group=programs&subgroup=gfind). Retrieved March 18, 2022, from <http://www.softberry.com/berry.phtml?topic=fgenes&group=programs&subgroup=gfind>
6. Softberry - FGENES result. (n.d.). [www.softberry.com](http://www.softberry.com/cgi-bin/programs/gfind/fgenes.pl). Retrieved March 18, 2022, from <http://www.softberry.com/cgi-bin/programs/gfind/fgenes.pl>

**WEBLEM 8e**  
**ORF finder-NCBI**  
**(URL: <https://www.ncbi.nlm.nih.gov/orffinder/>)**

**AIM:**

To search for ORF region in *Neisseria gonorrhoeae* using ORF finder tool.

**INTRODUCTION:**

Two Gram-positive, catalase-negative bacterial strains were isolated from the cloaca of common kingfishers (*Alcedo atthis*). Repetitive sequence-based PCR fingerprinting using the (GTG)5 primer grouped these isolates into a single cluster separated from all known enterococcal species. The two strains revealed identical 16S rRNA gene sequences placing them within the genus *Enterococcus* with *Enterococcus aquimarinus* LMG 16607(T) as the closest relative (97.14 % similarity).

ORF finder searches for open reading frames (ORFs) in the DNA sequence you enter. The program returns the range of each ORF, along with its protein translation. Use ORF finder to search newly sequenced DNA for potential protein encoding segments, verify predicted protein using newly developed SMART BLAST or regular BLASTP. This web version of the ORF finder is limited to the subrange of the query sequence up to 50 kb long. Stand-alone version, which doesn't have query sequence length limitation.

**METHODOLOGY:**

1. Open homepage for ORF finder in NCBI. (URL: <https://www.ncbi.nlm.nih.gov/orffinder/>)
2. Retrieve nucleotide FASTA sequence for *Neisseria gonorrhoeae* from GenBank.
3. Submit the FASTA sequence.
4. Observe and interpret the results.

**OBSERVATION:**

The screenshot shows the NCBI ORF finder results for the Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence. The sequence details include:

- GenBank:** JX948102.1
- FASTA:** Graphics PopSet
- GO to:** Go to
- LOCUS:** JX948102
- DEFINITION:** Enterococcus alcedinis strain L34 16S ribosomal RNA gene, partial sequence.
- ACCESSION:** JX948102
- VERSION:** JX948102.1
- KEYWORDS:** Enterococcus alcedinis
- SOURCE:** Enterococcus alcedinis
- ORGANISM:** Enterococcus alcedinis; Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus.
- REFERENCE:** 1 (bases 1 to 1260)
- AUTHORS:** Frolkova, P., Svec, P., Sedlacek, I., Maslanova, I., Cernohlavkova, J., Ghosh, A., Zurek, L., Radimersky, T. and Literak, I.
- TITLE:** Enterococcus alcedinis sp. nov., isolated from common kingfisher (*Alcedo atthis*)
- JOURNAL:** Int. J. Syst. Evol. Microbiol. 63 (PT 8), 3069-3074 (2013)
- PUBMED:** 23416573
- REFERENCE:** 2 (bases 1 to 1260)
- AUTHORS:** Frolkova, P.
- TITLE:** Direct Submission
- JOURNAL:** Submitted (09-OCT-2012) Department of Biology and Wildlife Diseases, University of Veterinary and Pharmaceutical Sciences Brno, Palackeho, Brno 61242, Czech Republic

On the right side, there are various links and options:

- Analyze this sequence:** Run BLAST, Pick Primers, Highlight Sequence Features, Find in this Sequence.
- Related information:** PubMed, Taxonomy, BioCollections, PopSet.
- LinkOut to external resources:** Enterococcus alcedinis, Ribosomal Database Project II, [Ribosomal Database Project II].

**Fig1. Result for Enterococcus alcedinis**

## Fig2. Nucleotide FASTA sequence for *Enterococcus alcedinis*


**National Library of Medicine**  
*National Center for Biotechnology Information*

[Log in](#)

## COVID-19 Information

[Public health information \(CDC\)](#) | [Research information \(NIH\)](#) | [SARS-CoV-2 data \(NCBI\)](#) | [Prevention and treatment information \(HHS\)](#) | [Español](#)

### Open Reading Frame Finder

ORF finder searches for open reading frames (ORFs) in the DNA sequence you enter. The program returns the range of each ORF, along with its protein translation. Use ORF finder to search newly sequenced DNA for potential protein encoding segments, verify predicted protein using newly developed SMART BLAST or regular BLAST.

This web version of the ORF finder is limited to the subrange of the query sequence up to 50 kb long. Stand-alone version, which doesn't have query sequence length limitation, is available for Linux x64.

Examples (click to set values, then click Submit button):

- NC\_011604 *Salmonella enterica* plasmid pWES-1; genetic code: 11; 'ATG' and alternative initiation codons; minimal ORF length: 300 nt
- NM\_000059; genetic code: 1; start codon: 'ATG only'; minimal ORF length: 150 nt

Enter Query Sequence

Enter accession number, gi, or nucleotide sequence in FASTA format:

```
GACGGGGGCCGCCACAAAGGGTGGAGCATGGTTAACTGGAGCAACGGGAAGAACCTTACCA
TGACATCTTGGACACTTAGAGATAGAGCTTCCCTTCGGGGAAAGTGCACAGGGTGGCAT
TCGTCAGCTGGTGTGGAGATGGTTAAAGTCCCACAGGGCAACCCCTTATTGTAGTT
CATTCAAGTTGGGCACTCTAGCGAGAGCTGCCGGTGCAAAACCGGGAGGTGGGGATAGCTCAA
CATGCCCTTATGACTCTGGGCACACAGCTGCACAAATGGGAAGTCAACGGAGTCGCAAAGTGGC
TAAGCTAATCTTAAACCTCTCTAGTTGGATTGTAAGGCTGCAACTCGCCTACATGAAGCCG
```

<

From:  To:

Choose Search Parameters

Minimal ORF length (nt):

Genetic code:

ORF start codon to use:

"ATG" only

"ATG" and alternative initiation codons

Any sense codon

Ignore nested ORFs:

### Fig3. Search for Nucleotide FASTA sequence

Enter Query Sequence

Enter accession number, gi, or nucleotide sequence in FASTA format:

```
GACGGGGGCCGACAAAGCGTGGAGCATGTGGTTAATTGCAAGCAACGGGAAGAACCTTACCA ^  
TGACATCCTTGGACACTCTAGAGATAGCCTTCCCTTGGGGACAAAGTGCAGGTGGTGCAT  
TGTCAGCTGTTGAGATGGTTAAGTCGGCAACGCCAACCCCTATTGTTAGTT  
CATTCAAGCTGGGACACTAGCGAGACTGCCGTGACAACACGGAGGAAGGTGGGATGACGCTAA  
CATGCCCTTATGACCTGGCTACACACGTCTACAATGGAAAGTACAACGAGTCGAAAGTGC  
TAAGCTAATCTTAAACCTCTCAGTCGGATTGAGGTGCAACTCGCCTACATGAAGCCG
```

From: \_\_\_\_\_ To: \_\_\_\_\_

Choose Search Parameters

Minimal ORF length (nt): 75

Genetic code: 1. Standard

ORF start codon to use:

- "ATG" only
- "ATG" and alternative initiation codons
- Any sense codon

Ignore nested ORFs:

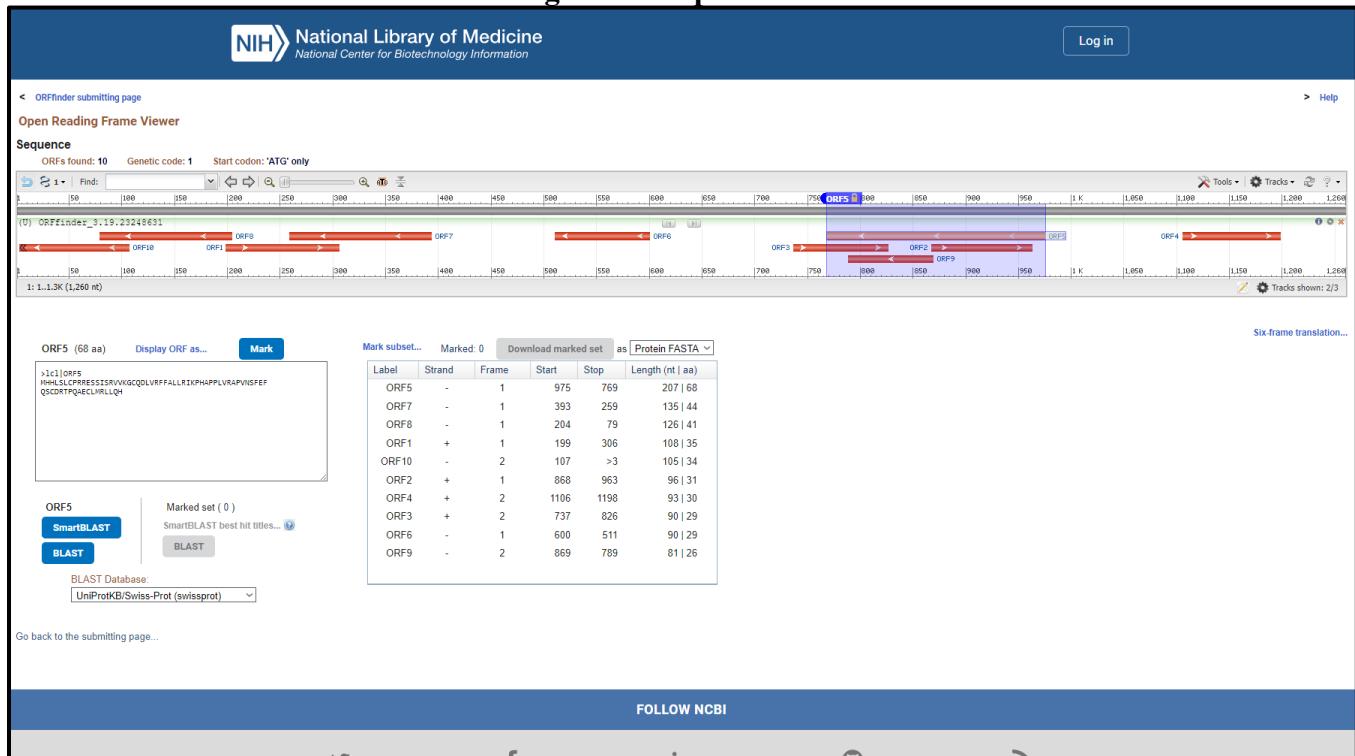
Start Search / Clear

**Submit** **Clear**

FOLLOW NCBI

Twitter  Facebook  LinkedIn  Google+  RSS 

**Fig4. Search parameters**



**Fig5. Result for recognised ORFs and tracks information**

## Results:

After submitting nucleotide FASTA sequence for complete genome of *Enterococcus alcedinis* on NCBI's ORF finder, 360 ORFs were predicted.

## **CONCLUSION:**

ORF finder can be used to predict open reading frames in the genome. This information of long ORFs are often used, along with other evidence, to initially identify candidate protein-coding regions or functional RNA- coding regions in a DNA sequence. Small Open Reading Frames (small ORFs/sORFs/smORFs) are important sources of putative peptides previously dismissed as being non-functional or junk DNA.

## **REFERENCES:**

1. Neisseria gonorrhoeae - an overview | ScienceDirect Topics. (n.d.). [Www.sciencedirect.com](https://www.sciencedirect.com/topics/medicine-and-dentistry/neisseria-gonorrhoeae#:~:text=Neisseria%20gonorrhoeae%20is%20a%20bacterial).Retrieved March 18, 2022, from <https://www.sciencedirect.com/topics/medicine-and-dentistry/neisseria-gonorrhoeae#:~:text=Neisseria%20gonorrhoeae%20is%20a%20bacterial>
2. Neisseria gonorrhoeae strain NJ189125 chromosome, complete genome. (2022). NCBI Nucleotide. Retrieved March 18, 2022, from [https://www.ncbi.nlm.nih.gov/nuccore/NZ\\_CP041586.1](https://www.ncbi.nlm.nih.gov/nuccore/NZ_CP041586.1)
3. Home - ORFfinder - NCBI. (2019). Nih.gov. Retrieved March 18, 2022, from <https://www.ncbi.nlm.nih.gov/orffinder/>

## WEBLEM 9

### Introduction to Genomics & its various browser (UCSC, ENSEMBL, GDV)

**Genomics** is the **study of genomes**. Genomic studies are characterized by **simultaneous analysis of a large number of genes** using **automated data gathering tools**. The topics of **genomics range** from **genome mapping sequencing**, and **functional genomic analysis** to **comparative genomic analysis**. The **advent of genomics** and the ensuing explosion of **sequence information** are the main driving force behind the **rapid development** of bioinformatics today.

Genomic study can be **tentatively divided** into **structural genomics** and **functional genomics**. Structural genomics refers to the **initial phase of genome analysis**, which includes construction of **genetic and physical maps** of a genome, identification of genes, **annotation of gene features**, and **comparison of genome structures**. Functional genomics refers to the analysis of **global gene expression** and gene functions in a genome.

Genome browsers are resources that **integrate data at the genomic level**, thereby allowing visualization of related **genomic information** in one space. These data can **include genes, noncoding elements** that regulate **gene expression, genetic variation** and the results of **comparative genomics analyses**, among other forms of annotation. Commonly used genome **browsers include Ensembl, the UCSC Genome Browser and GDV**.

#### 1. UCSC Genome Browser

The **University of California Santa Cruz (UCSC) Genome Browser** (genome.ucsc.edu) is a popular **Web-based tool** for quickly displaying a requested **portion of a genome** at any scale, accompanied by a series of **aligned annotation “tracks”**. The annotations generated by the **UCSC Genome Bioinformatics Group** and external collaborators display **gene predictions, mRNA and expressed sequence tag alignments, simple nucleotide polymorphisms, expression and regulatory data, phenotype and variation data, and pairwise and multiple-species comparative genomics data**. All **information relevant** to a region is presented **in one window**, facilitating **biological analysis and interpretation**. The database tables **underlying the Genome Browser tracks** can be **viewed, downloaded, and manipulated** using another **Web-based application**, the UCSC Table Browser. Users can upload data as **custom annotation tracks** in both browsers for research or educational use. The **vast size** of vertebrate genome data sets **presents challenges** in **efficient data storage and retrieval**. In addition, the **burgeoning number** of versions of a **particular genome** demands a process that can **rapidly integrate new data** and annotations into the database while **implementing creative solutions** for maintaining and **enhancing views of the data**. Through **software algorithmic refinements** and optimizations to **both the database and hardware**, the UCSC Genome Browser viewer maintains the **same interactive response time** on the **large Homo sapiens** and **Mus musculus** genomes that its predecessor had on the **much smaller Caenorhabditis elegans** genome.

**Sequence and annotation** data for each genome assembly are **stored in a MySQL relational database**, which is **quite efficient at retrieving data** from indexed files. The **database is loaded** in large batches and is used **primarily as a read-only database**. To improve performance, each of the Genome Browser web servers has a **copy of the database on its local disk**. UCSC **generates several annotations** based on **mRNA alignments**. The **mRNA and EST sequences** are extracted from GenBank, and are **aligned** against the genome **using the BLAST-like Alignment Tool (BLAT)**, a fast sequence alignment tool developed by Jim Kent. The **data is filtered based on percentage identity** and **near best** in genome to select only those alignments that **best match the sequence**. The **spliced EST annotation** is computed from the **filtered data by analyzing** the EST alignments for **evidence of splicing**.

## 2. ENSEMBL gene browser

The Ensembl project was initially launched in 1999 with the aim of **developing methodologies** for **automatic annotation** of (human) **genomic sequence** with genes and their **constituent transcripts**. Since that time, the project has broadened substantially in scope; the **Ensembl Genome Browser**, which came online in 2000, now includes **reference genomic sequence** and **annotation** for nearly **100 chordate organisms**. Ensembl is **rapidly incorporating** new data, including **whole clades** of new species' genomes and reference sequence for **multiple strains of existing species**, such as mouse. In addition, existing annotation is **regularly augmented** by the **inclusion of new data sets**. Ensembl's sister site, **Ensembl Genomes**, provides access to **nonvertebrate genomes** through dedicated portals for **Bacteria, Fungi, Plants, Metazoa, and Protists**.

Ensembl data, annotations, and analyses are updated every 2–3 months, alongside **software updates** to both the **public-facing website** and the **underlying databases**. A dedicated site is also maintained for the **GRCh37 reference human genome assembly**, which is annotated with **new data on a limited basis**; partial data from **ongoing genome annotation** can be accessed via the preview Pre! site.

Data from Ensembl can be **accessed at multiple scales**. Data can be accessed through the browser web pages and **via BioMart**, a web-based tool that **allows customized retrieval** of data from the **Ensembl databases**. However, data can also be **accessed programmatically** via our **Perl and REST APIs**. Files containing **genome-wide data** are available for all species **represented in Ensembl** via an **FTP site**; data from all releases of **Ensembl** can be **retrieved** from the **FTP site**, or from our databases via the **Perl APIs, in perpetuity**.

## 3. Genome Data Viewer

GDV is composed of an **embedded instance of SV** that displays **sequence and track data**, along with **additional page elements** that allow a user to **search within an entire genome assembly** and **efficiently narrow in on their chromosome, sequence, region, or gene of interest**. GDV replaced the NCBI Map Viewer, NCBI's **previous** tool for whole-genome display. Researchers using GDV **can go directly** to the **NCBI BLAST** service from the browser and **load BLAST** results as alignment tracks that can be viewed **side by side** with **gene annotation** and other data. Variation Viewer, a related browser **associated with NCBI's variation resources**, is **functionally similar to GDV** and also **incorporates an instance of SV** but is **configured with features specifically intended for analyzing human variation data**. GDV and Variation Viewer can both **display the same types of NCBI variation track data**.

The GDV **can be accessed** from its own **home page** and can also be **found via links** from other **NCBI resources, including gene, assembly, GEO, and dbGaP record pages**. GDV provides users a graphical gateway to data at the NCBI, especially **RefSeq** and **refSNP annotation**. Below, we highlight **some of the functions** of GDV and other instances of the NCBI SV and provide context for **GDV's features** with respect to the **broader collection** of publicly available **genome browsers**, including the UCSC and Ensembl genome browsers, JBrowse, and IGV. GDV was designed specifically to **support visualization and analysis** of the wide range of genomes and assemblies annotated at the NCBI. **RefSeq gene annotation** data tracks are shown by default in the **graphical view** for these assemblies. **NCBI refSNP data tracks** are also shown by default for **human assemblies**. **Gene and SNP tracks** are **automatically updated** in GDV and SV embedded instances upon **new releases** of the NCBI databases, so that **users of the NCBI graphical viewers** always have immediate access to the **latest versions of RefSeq and SNP annotation**.

GDV offers users the ability to **customize the displays of individual tracks**. Users can **hide** or **configure** tracks from the **track configuration panel** or by using the icons at the right end of each track. Different **public genome browsers** provide **conceptually similar**, but somewhat **distinct options**, for **visualizing gene, graphical, and alignment data**. In this section, we highlight **track data**

**visualizations** in the GDV browser and other instances of the **SV graphical** view component that support various **analysis scenarios**.

## REFERENCES:

1. Xiong, J. (2008). Genome Mapping, Assembly, and Comparison. Essential bioinformatics. Cambridge: Cambridge University Press. 243.
2. Baxevanis, Andreas D.; Petsko, Gregory A.; Stein, Lincoln D.; Stormo, Gary D. (2002). Current Protocols in Bioinformatics || The UCSC Genome Browser. , (), -. doi:10.1002/0471250953.bi0104s28
3. Karolchik, D. (2003). The UCSC Genome Browser Database. , 31(1), 51–54. doi:10.1093/nar/gkg129
4. Birney, E. (2004). An Overview of Ensembl. Genome Research, 14(5), 925–928. doi:10.1101/gr.1860604
5. Kollmar, Martin (2018). [Methods in Molecular Biology] Eukaryotic Genomic Databases Volume 1757 || The Ensembl Genome Browser: Strategies for Accessing Eukaryotic Genome Data. , 10.1007/978-1-4939-7737-6(Chapter 6), 115–139. doi:10.1007/978-1-4939-7737-6\_6
6. Rangwala, S. H., Kuznetsov, A., Ananiev, V., Asztalos, A., Borodin, E., Evgeniev, V., Joukov, V., Lotov, V., Pannu, R., Rudnev, D., Shkeda, A., Weitz, E. M., & Schneider, V. A. (2020). Accessing NCBI data using the NCBI Sequence Viewer and Genome Data Viewer (GDV). Genome Research, gr.266932.120. <https://doi.org/10.1101/gr.266932.120>

**WEBLEM 9a**  
**UCSC Genome Browser**  
**(URL: <https://genome.ucsc.edu/>)**

**AIM:**

To explore UCSC genome browser in order to understand the gene, its related studies & protein level information.

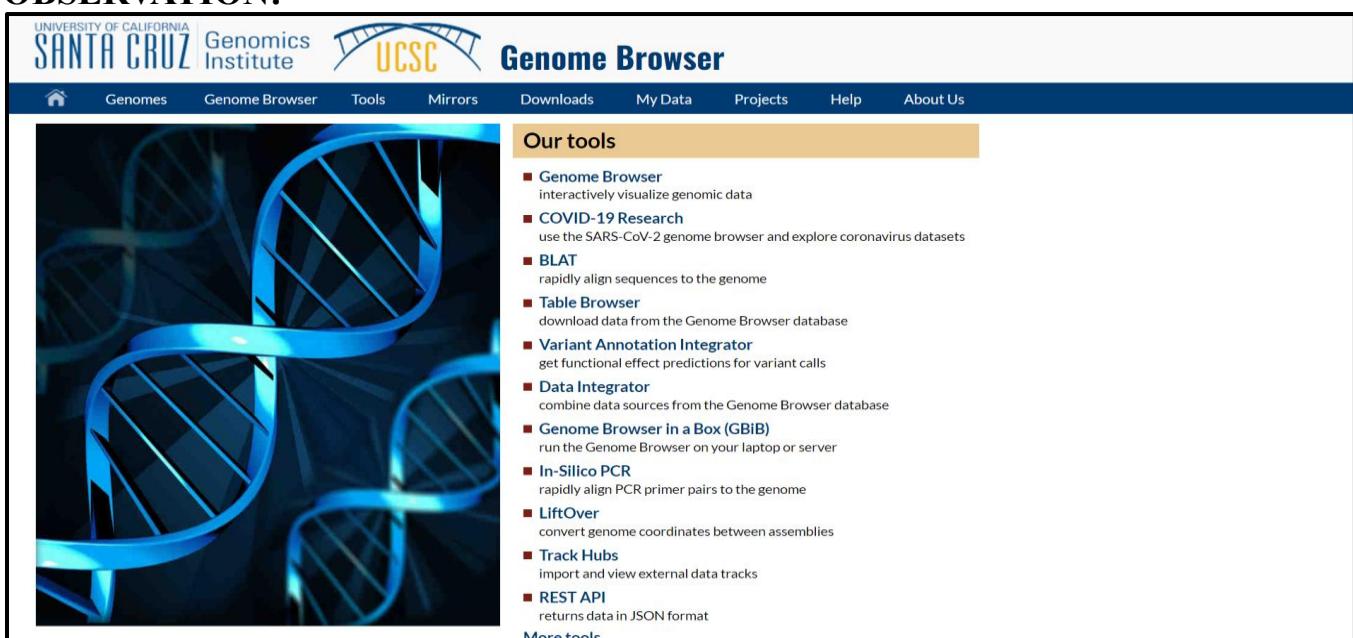
**INTRODUCTION:**

The **University of California Santa Cruz (UCSC) Genome Browser** (genome.ucsc.edu) is a popular **Web-based tool** for quickly displaying a requested **portion of a genome** at any scale, accompanied by a series of **aligned annotation “tracks”**. The annotations generated by the **UCSC Genome Bioinformatics Group** and external collaborators display **gene predictions, mRNA and expressed sequence tag alignments, simple nucleotide polymorphisms, expression and regulatory data, phenotype and variation data, and pairwise and multiple-species comparative genomics data**. All **information relevant** to a region is presented in **one window**, facilitating **biological analysis and interpretation**. The database tables **underlying the Genome Browser tracks** can be **viewed, downloaded, and manipulated** using another **Web-based application**, the UCSC Table Browser. Users can upload data as **custom annotation tracks** in both browsers for research or educational use.

**METHODOLOGY:**

1. Open homepage for UCSC browser (URL: <https://genome.ucsc.edu/>)
2. Select genome browser.
3. Select human assembly (GRCh3/hg38)
4. Navigate results through gene name, SNP id, Ref\_Seq, OMIM id, coordinates and cytological band.
5. Use tools for zooming tracks in and out, configuration by right click, drag and select and various option available at bottom of the page.
6. Observer and interpret the results.

**OBSERVATION:**



**Fig1. Homepage of UCSC browser**

**UNIVERSITY OF CALIFORNIA SANTA CRUZ Genomics Institute** **UCSC** **Genome Browser Gateway**

Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us

**Browse>Select Species**

**POPULAR SPECIES**

Human Mouse Rat Zebrafish Froglet Worm Yeast

Enter species, common name or assembly ID

Can't find a genome assembly?

**REPRESENTED SPECIES**

UCSC Genome Browser assembly ID: hg38  
Sequencing/Assembly provider ID: Genome Reference Consortium Human GRCh38.p13 (GCA\_000001405.28)  
Assembly date: Dec. 2013 initial release; Dec. 2017 patch release 13  
Assembly accession: GCA\_000001405.28  
NCBI Genome ID: 51 (Homo sapiens (human))  
NCBI Assembly ID: GCF\_000001405.39 (GRCh38.p13, GCA\_000001405.28)  
BioProject ID: PRJNA31257

**Find Position**

Human Assembly Dec. 2013 (GRCh38/hg38)

Position/Search Term Enter position, gene symbol or search terms

Current position: chrX:15,560,138-15,602,945

GO

**Human Genome Browser - hg38 assembly**

view sequences

**Search the assembly:**

- By position or search term: Use the "position or search term" box to find areas of the genome associated with many different attributes, such as a specific chromosomal coordinate range; mRNA, EST, or STS marker names; or keywords from the GenBank description of an mRNA. [More information](#), including sample queries.
- By gene name: Type a gene name into the "search term" box, choose your gene from the drop-down list, then press "submit" to go directly to the assembly location associated with that gene. [More information](#).
- By track type: Click the "track search" button to find Genome Browser tracks that match specific selection criteria. [More information](#).

**Download sequence and annotation data:**

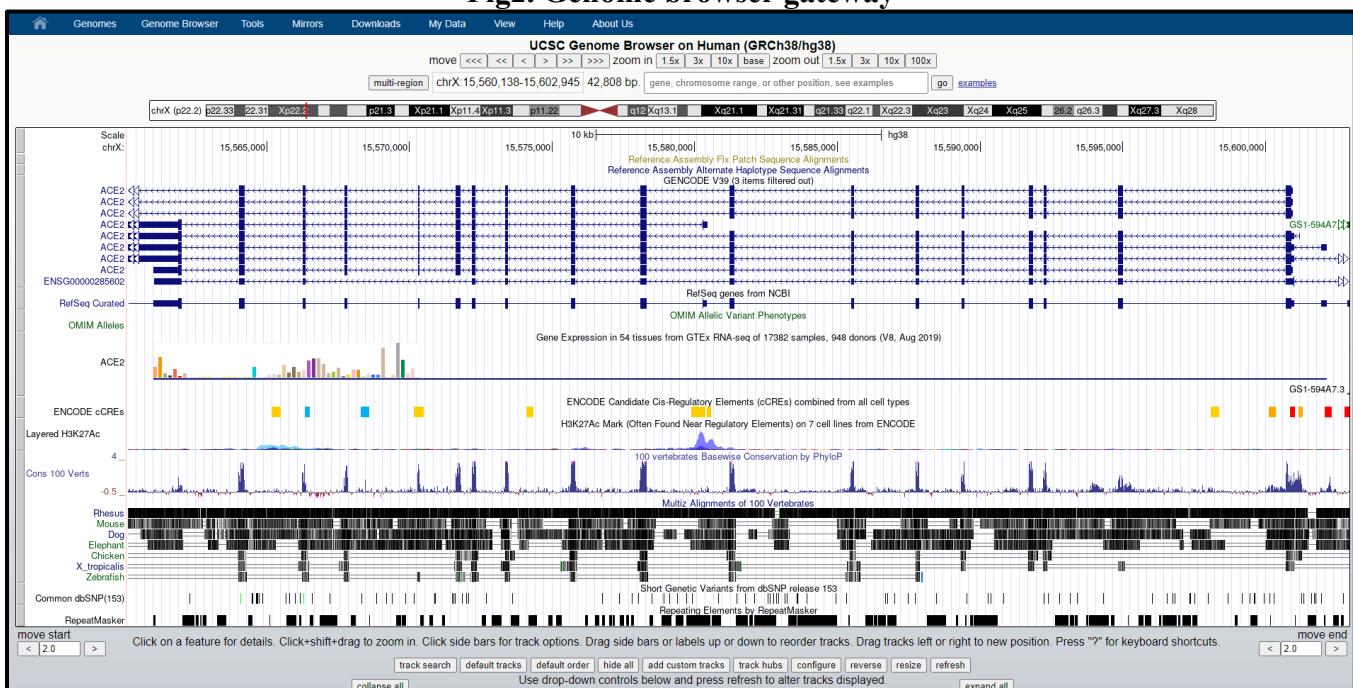
- Using rsync (recommended)
- Using HTTP
- Using FTP
- Data use conditions and restrictions
- Acknowledgments

**Assembly Details**

The GRCh38 assembly is the first major revision of the human genome released in more than four years. As with the previous GRCh37 assembly, the Genome Reference Consortium (GRC) is now the primary source for human genome assembly data submitted to GenBank. Beginning with this release, the UCSC Genome Browser version numbers for the human assemblies now match those of the GRC to minimize version confusion. Hence, the GRCh38 assembly is referred to as "hg38" in the Genome Browser datasets and documentation. For a glossary of assembly-related terms, see the [GRC Assembly Terminology page](#).

GRCh38 hg38

**Fig2. Genome browser gateway**



**Fig3. UCSC genome browser on human (GRCh38/hg38)**

track search | default tracks | default order | hide all | add custom tracks | track hubs | configure | reverse | resize | refresh | collapse all | expand all | Use drop-down controls below and press refresh to alter tracks displayed | Tracks with lots of items will automatically be displayed in more compact modes.

**Mapping and Sequencing**

- Base Position: *ET3 Fix Patches*, *ET3 Alt Haplotypes Assembly*, *Centromeres*, *Chromosome Band*
- Clone Ends: *Exome Probesets*, *FISH Clones*, *Gap*, *GC Percent*
- GRC Incident: *Hg19 Diff*, *INSDC*, *Gap*, *GC Percent*
- RefSeq Acc: *Restr Enzymes*, *Scaffolds*, *Short Match*, *STS Markers*
- UniProt: *hide*

**Genes and Gene Predictions**

- GENCODE V39: *hide*, *All*, *GENCODE*, *CCDS*, *CRISPR Targets*, *IKMC Genes Mapped*
- NCBI RefSeq: *dense*, *hide*, *Non-coding RNA*, *Old UCSC Genes*, *ORFeome Clones*
- LRG Transcripts: *hide*, *hide*, *hide*, *hide*
- Other RefSeq: *hide*, *Pfam in GENCODE*, *Prediction Archive*, *RetroGenes V9*, *TransMap V5*, *UCSC Alt Events*
- UniProt: *hide*

**Phenotype and Literature**

- OMIM Alleles: *CADD*, *Cancer Gene Expr*, *ClinGen*, *Deprecated ClinGen*, *OMIM Cyto Loci*, *Gene Interactions*, *GeneReviews*, *GWAS Catalog*
- Coriell CNVs: *COSMIC Regions*, *Development Delay*, *Gene Interactions*, *GeneReviews*, *GWAS Catalog*
- HGMD Variants: *LOVD Variants*, *OMIM Genes*, *Orphanet*, *REVEL Scores*
- SNPedia: *TCGA Pan-Cancer*, *UniProt Variants*, *Variants in Papers*

**COVID-19**

- COVID GWAS v4: *hide*, *Rare Harmful Vars*
- COVID GWAS v3: *hide*, *hide*

**Single Cell RNA-seq**

- Colon Wang: *Rectum Wang*, *Blood (PBMC) Wang*, *Cortex Wang*, *Fetal Wang*, *Gene Atlas Wang*
- Heart Cell Atlas: *Heart Cell Atlas*, *Liver MacParland*, *Lung Travaglini*, *Muscle De Michel*, *Pancreas Baron*

Fig4. Options for customization

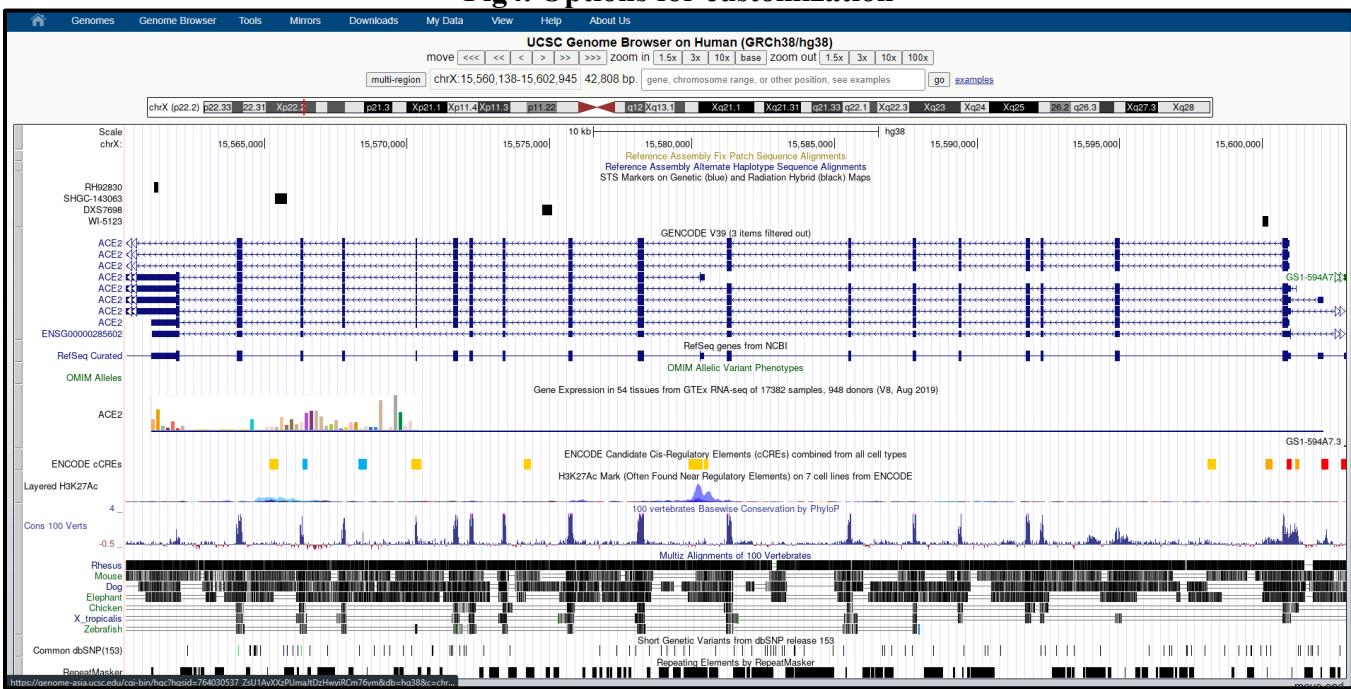


Fig5. Results after customization

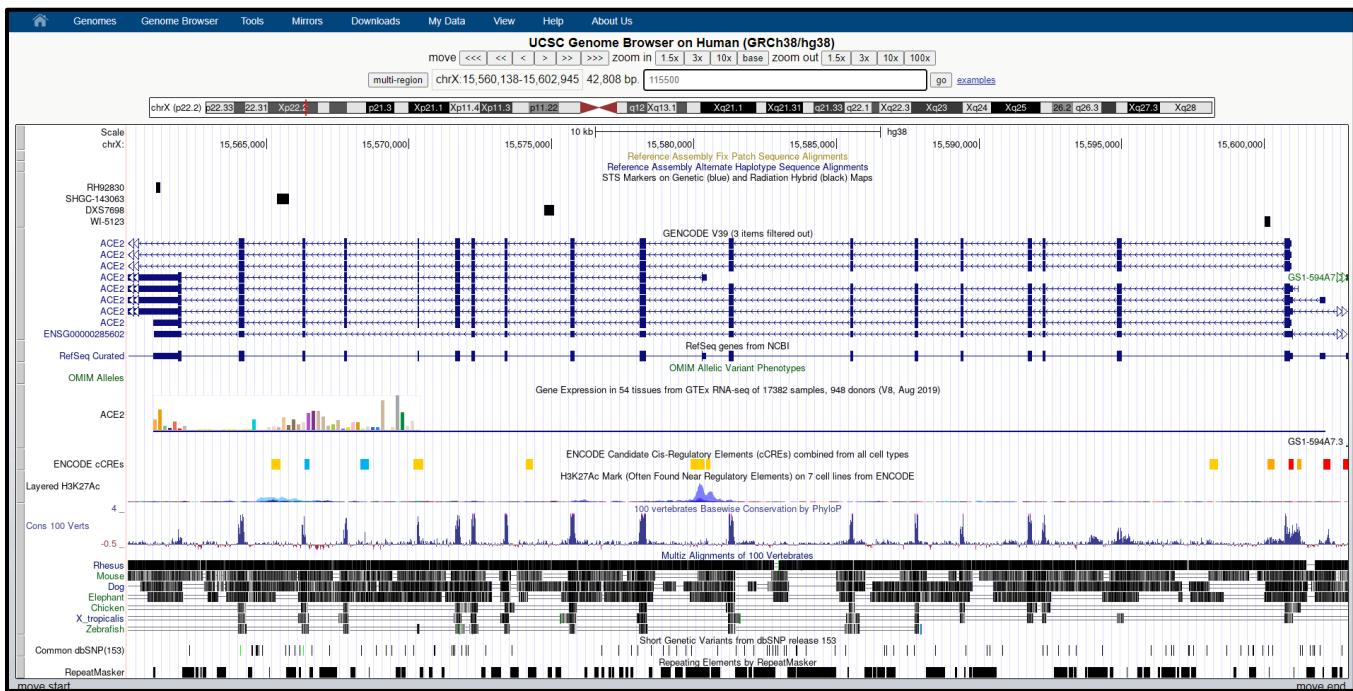


Fig6. Navigation by OMIM id: 115500

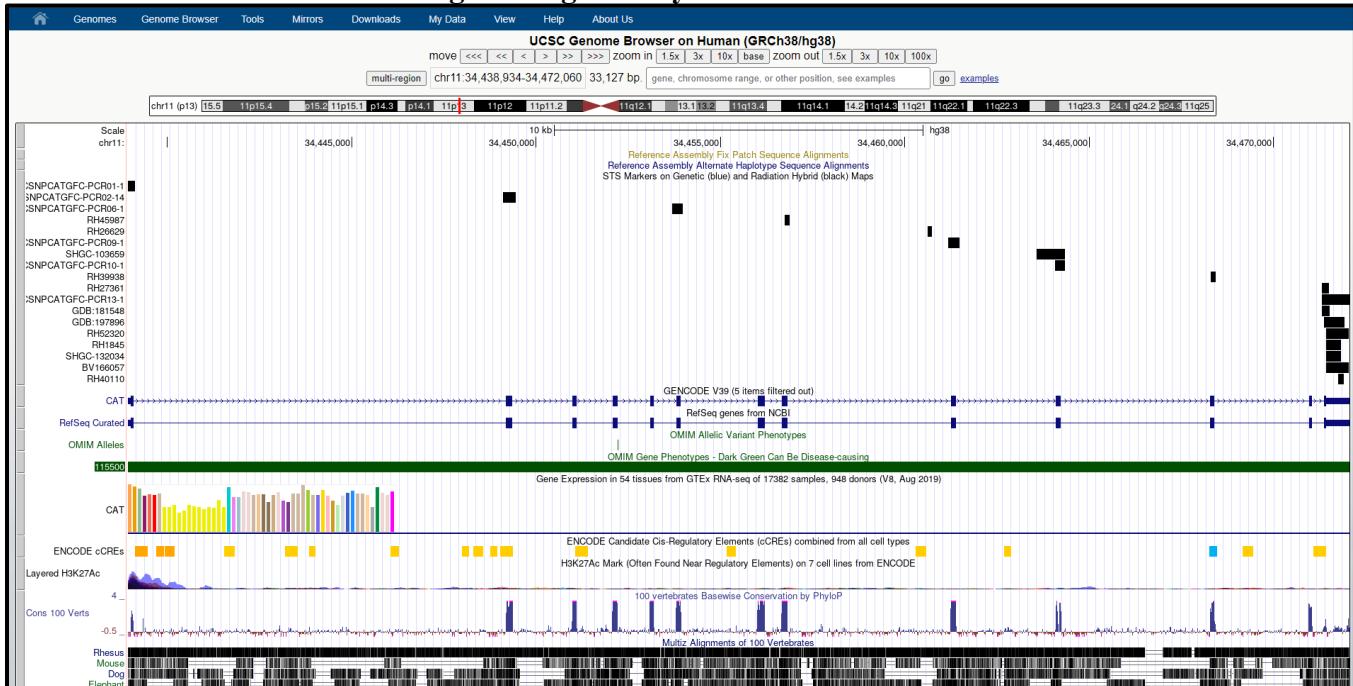


Fig7. Results for OMIM id: 115500

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**OMIM genes - 115500**

MIM gene number: [115500](#)  
HGNC-approved symbol: CAT — Catalase

Position: [chr11:34438934-34472060](#)  
Band: 11p13  
Genomic Size: 33127  
Alternative symbols: CAT  
RefSeq Gene(s): [NM\\_001752](#)  
Related Transcripts: [ENST00000241052.5](#)

Phenotype	Phenotype MIM Number	Inheritance	Phenotype Key
Acatalasemia	<a href="#">614097</a>		3 - molecular basis of the disease is known

[View table schema](#)  
[Go to OMIM Genes track controls](#)

Data last updated at UCSC: 2022-03-23

**Description**

**NOTE:**  
OMIM is intended for use primarily by physicians and other professionals concerned with genetic disorders, by genetics researchers, and by advanced students in science and medicine. While the OMIM database is open to the public, users seeking information about a personal medical or genetic condition are urged to consult with a qualified physician for diagnosis and for answers to personal questions. Further, please be sure to click through to [omim.org](#) for the very latest, as they are continually updating data.

**NOTE ABOUT DOWNLOADS:**  
OMIM is the property of Johns Hopkins University and is not available for download or mirroring by any third party without their permission. Please see [OMIM](#) for downloads.

OMIM is a compendium of human genes and genetic phenotypes. The full-text, referenced overviews in OMIM contain information on all known Mendelian disorders and over 12,000 genes. OMIM is authored and edited at the McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, under the direction of Dr. Ada Hamosh. This database was initiated in the early 1960s by Dr. Victor A. McKusick as a catalog of Mendelian traits and disorders, entitled Mendelian Inheritance in Man (MIM).

The OMIM data are separated into three separate tracks:

[OMIM Alleles](#)

## Fig8. Description for OMIM gene

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**Human Gene CAT (ENST00000241052.5) from GENCODE V39**

Description: Homo sapiens catalase (CAT), mRNA. (from RefSeq NM\_001752)

RefSeq Summary (NM\_001752): This gene encodes catalase, a key antioxidant enzyme in the bodies defense against oxidative stress. Catalase is a heme enzyme that is present in the peroxisome of nearly all aerobic cells. Catalase converts the reactive oxygen species hydrogen peroxide to water and oxygen and thereby mitigates the toxic effects of hydrogen peroxide. Oxidative stress is hypothesized to play a role in the development of many chronic or late-onset diseases such as diabetes, asthma, Alzheimer's disease, systemic lupus erythematosus, rheumatoid arthritis, and cancers. Polymorphisms in this gene have been associated with decreases in catalase activity but, to date, acatalasemia is the only disease known to be caused by this gene. [provided by RefSeq, Oct 2009]

Gene ID: [ENSG00000241052.5](#)  
Gene Code: [ENSG00000241052.5](#)  
Transcript (including UTRs):  
Position: hg38 chr11:34,438,934-34,472,060 Size: 33,127 Total Exon Count: 13 Strand: +  
Coding Region  
Position: hg38 chr11:34,439,014-34,471,433 Size: 32,420 Coding Exon Count: 13

Page Index	Sequence and Links	UniProtKB Comments	MalaCards	CTD	RNA-Seq Expression
Microarray Expression	RNA Structure	Protein Structure	Other Species	GO Annotations	mRNA Descriptions
Pathways	Other Names	Methods			

Data last updated at UCSC: 2022-01-18 01:30:34

**Sequence and Links to Tools and Databases**

Genomic Sequence (chr11:34,438,934-34,472,060)	mRNA (may differ from genome)	Protein (527 aa)			
Gene Sorter	Genome Browser	Other Species FASTA	VisiGene	Gene interactions	Table Schema
BioGPS	CGAP	Ensembl	Entrez Gene	ExonPrimer	Gencode
GeneCards	HGNC	HPRD	Lynx	MGI	neXtProt
OMIM	PubMed	Reactome	UniProtKB	Wikipedia	

**Comments and Description Text from UniProtKB**

ID: [CATA\\_HUMAN](#)  
DESCRIPTION: RecName: Full=Catalase; EC=1.11.1.6.  
FUNCTION: Occurs in almost all aerobically respiring organisms and serves to protect cells from the toxic effects of hydrogen peroxide. Promotes growth of cells including T-cells, B-cells, myeloid leukemia cells, melanoma cells, mastocytoma cells and normal and transformed fibroblast cells.  
CATALYTIC ACTIVITY: 2 H<sub>2</sub>O<sub>2</sub> = O<sub>2</sub> + 2 H<sub>2</sub>O.  
COFACTOR: Heme group.  
COFACTOR: NADP.  
SUBUNIT: Homotetramer.  
SUBCELLULAR LOCATION: Peroxisome.  
PTM: The N-terminus is blocked.  
DISEASE: Defects in CAT are the cause of acatalasemia (ACATLAS) [MIM:614097]. A metabolic disorder characterized by absence of catalase activity in red cells and is often associated with ulcerating oral lesions.  
SIMILARITY: Catalase, catalase family  
WEB RESOURCE: Name=Wikipedia, Note=Catalase entry, URL="http://en.wikipedia.org/wiki/Catalase";  
WEB RESOURCE: Name=SeattleSNPs, URL="http://pga.gs.washington.edu/data/cat";

**MalaCards Disease Associations**

MalaCards Gene Search: [CAT](#)

## Fig9. Related transcripts information



Fig10. Navigation by gene name: INS

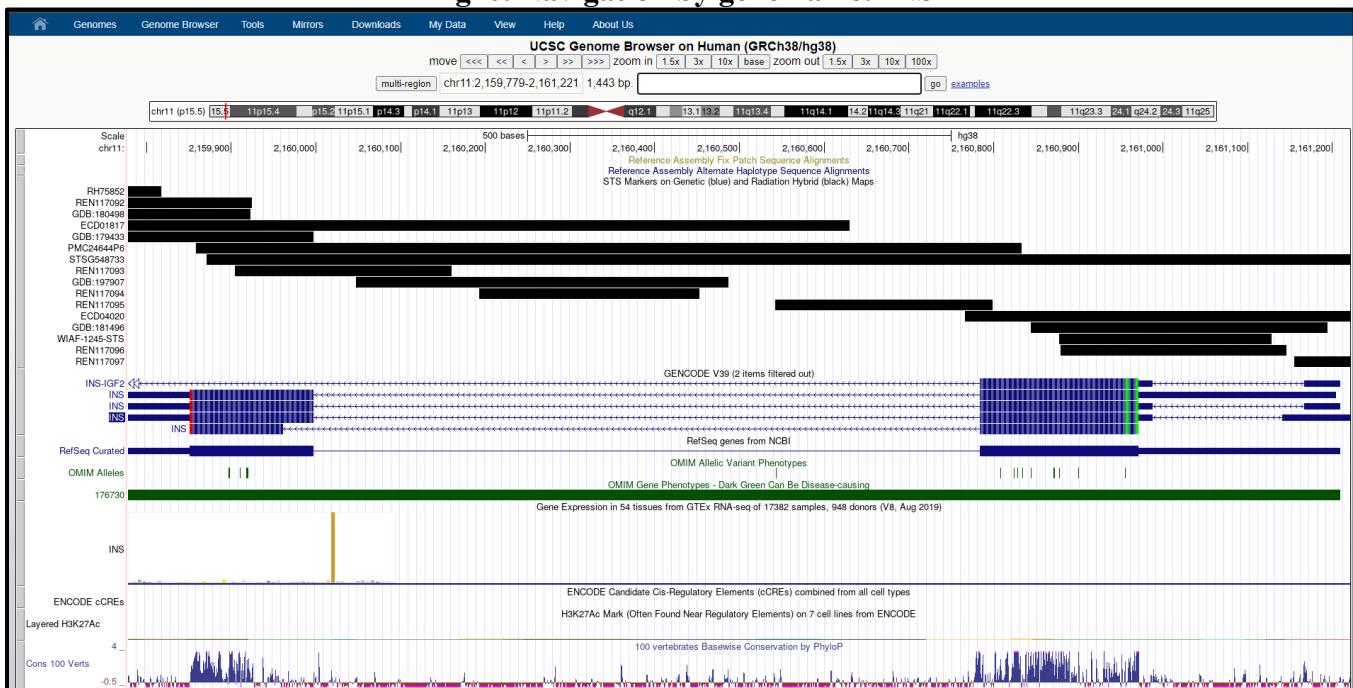


Fig11. Result for INS gene



Fig12. Option to configure tracks

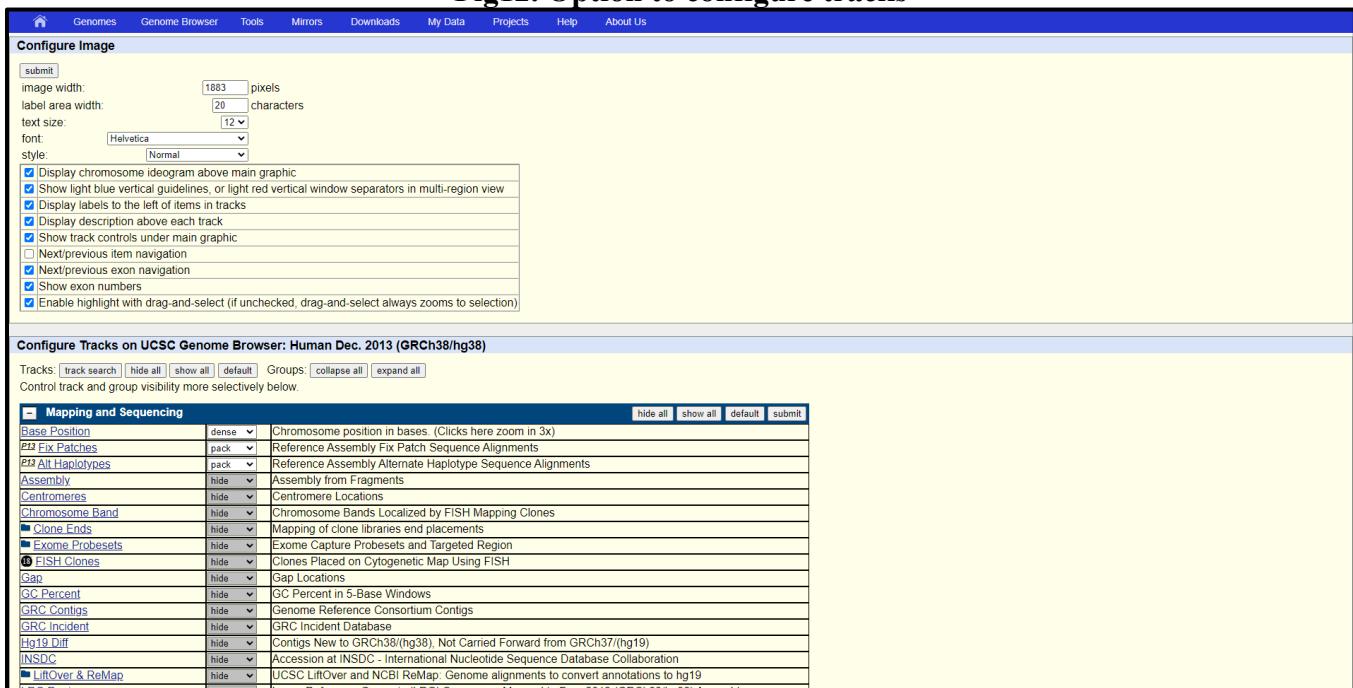


Fig13. Configuration settings

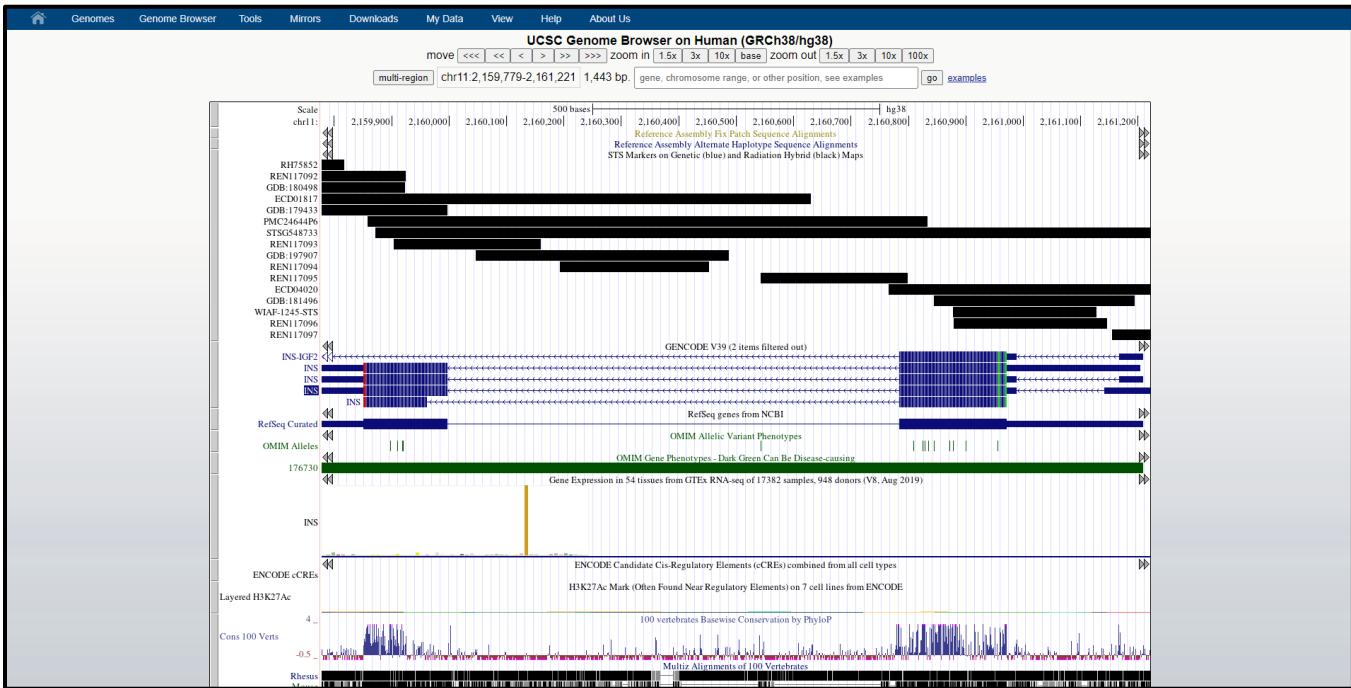


Fig14. Configured tracks

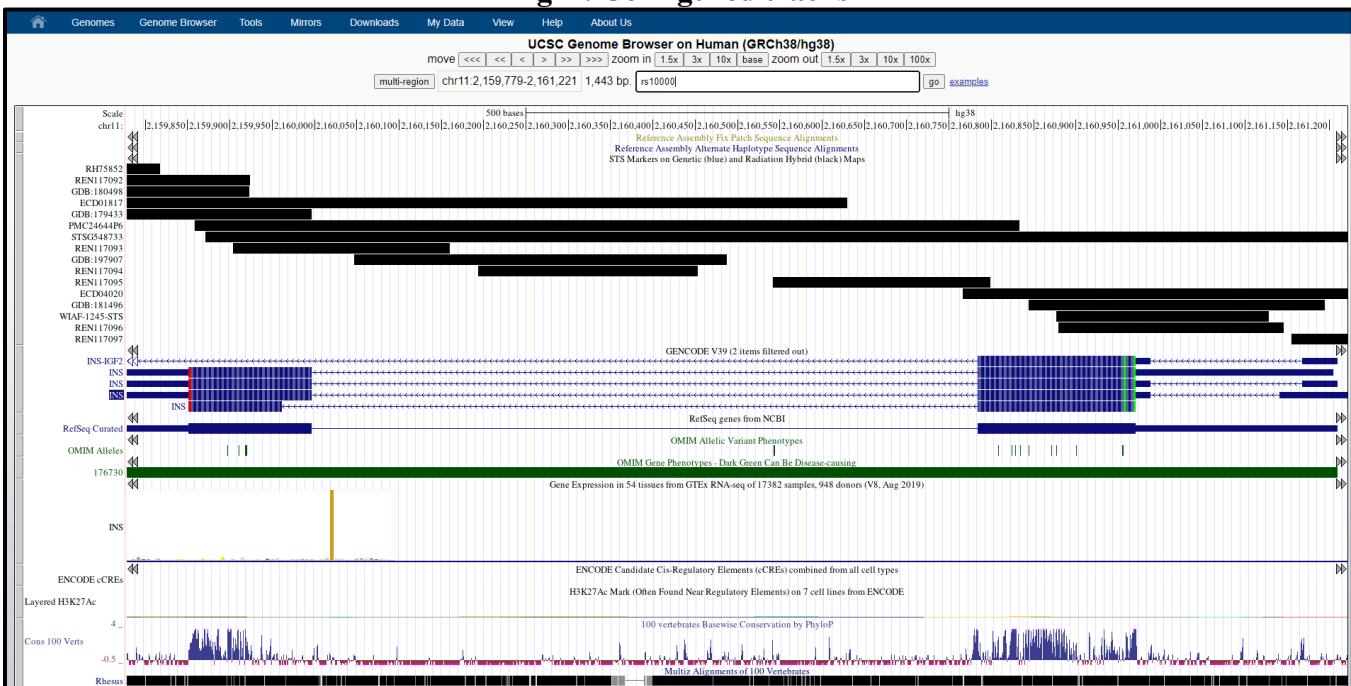


Fig15. Navigation by SNP id: rs10000

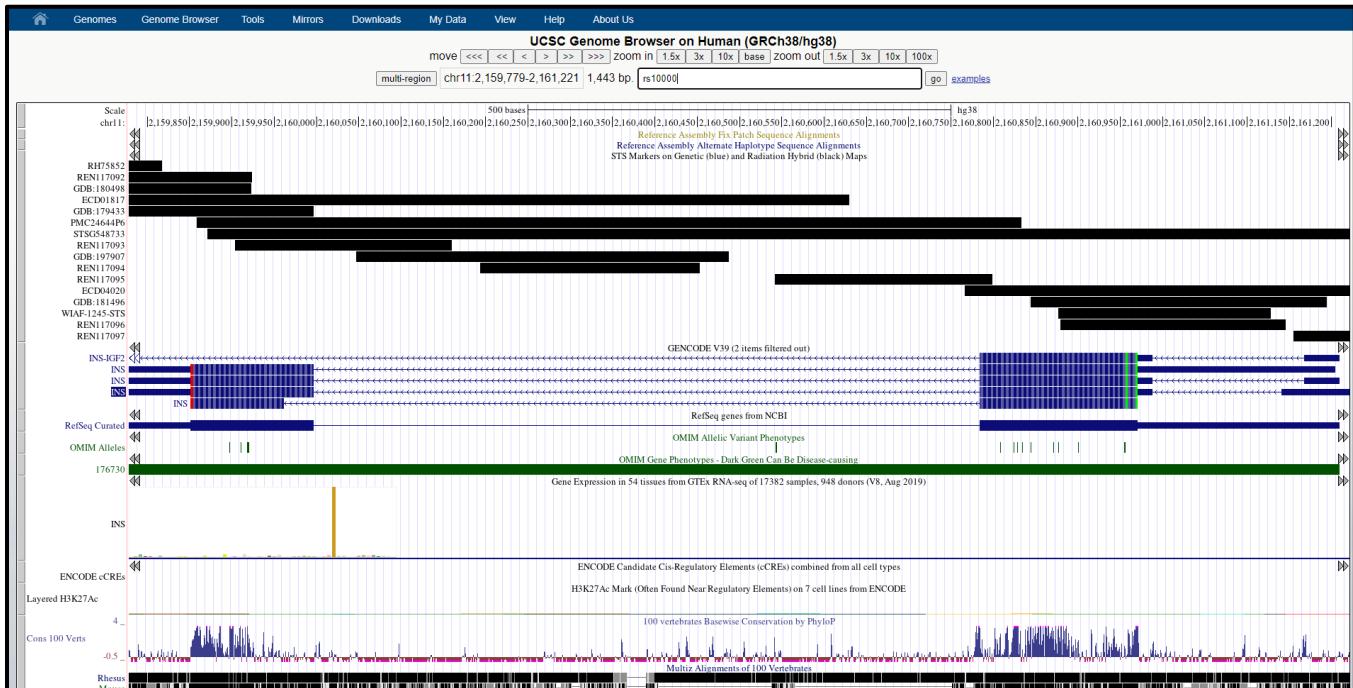


Fig16. Result for SNP id: rs10000

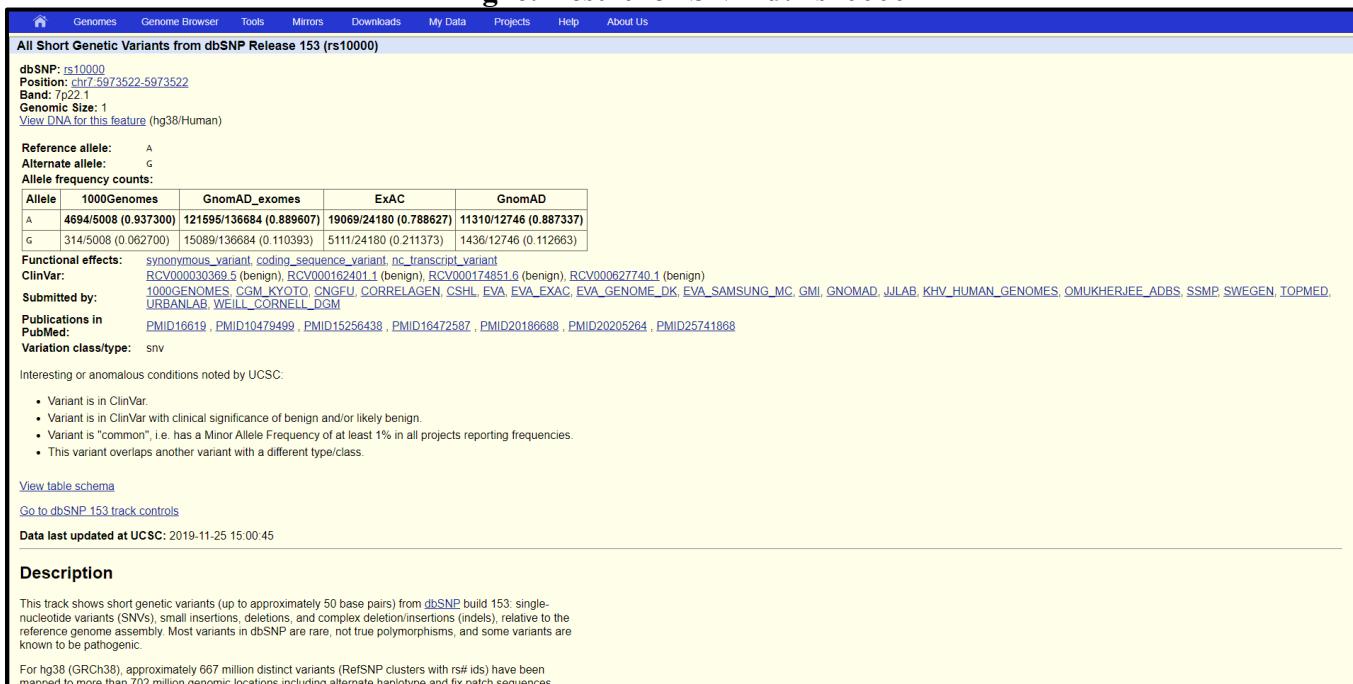


Fig17. Description for SNP id: rs10000



Fig18. Configuration option by right click

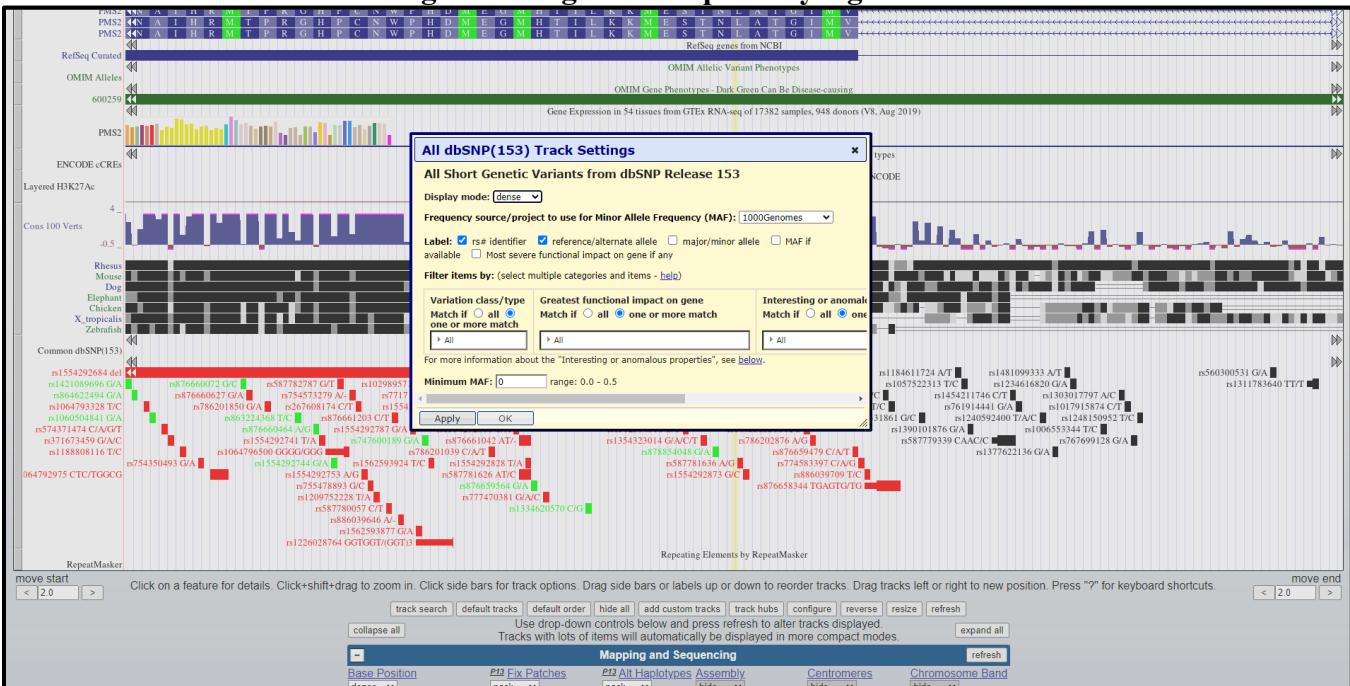


Fig19. Configuration applied

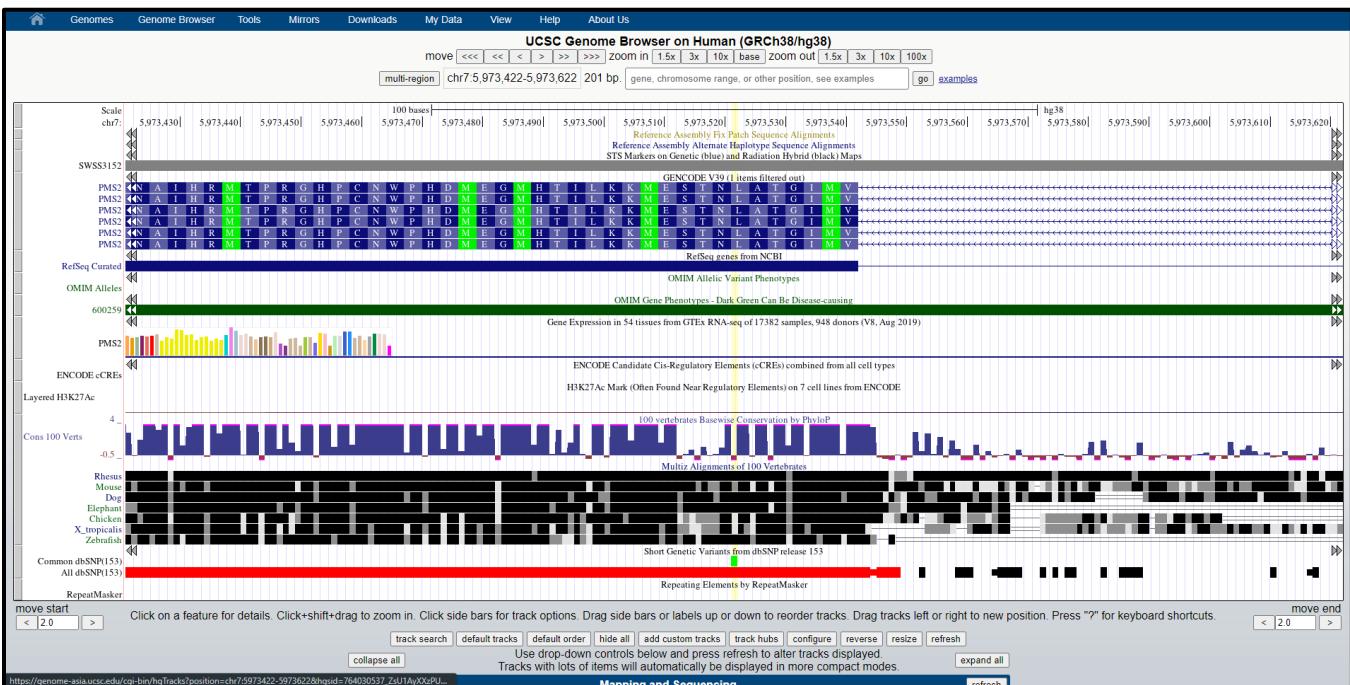


Fig20. Result after configuration

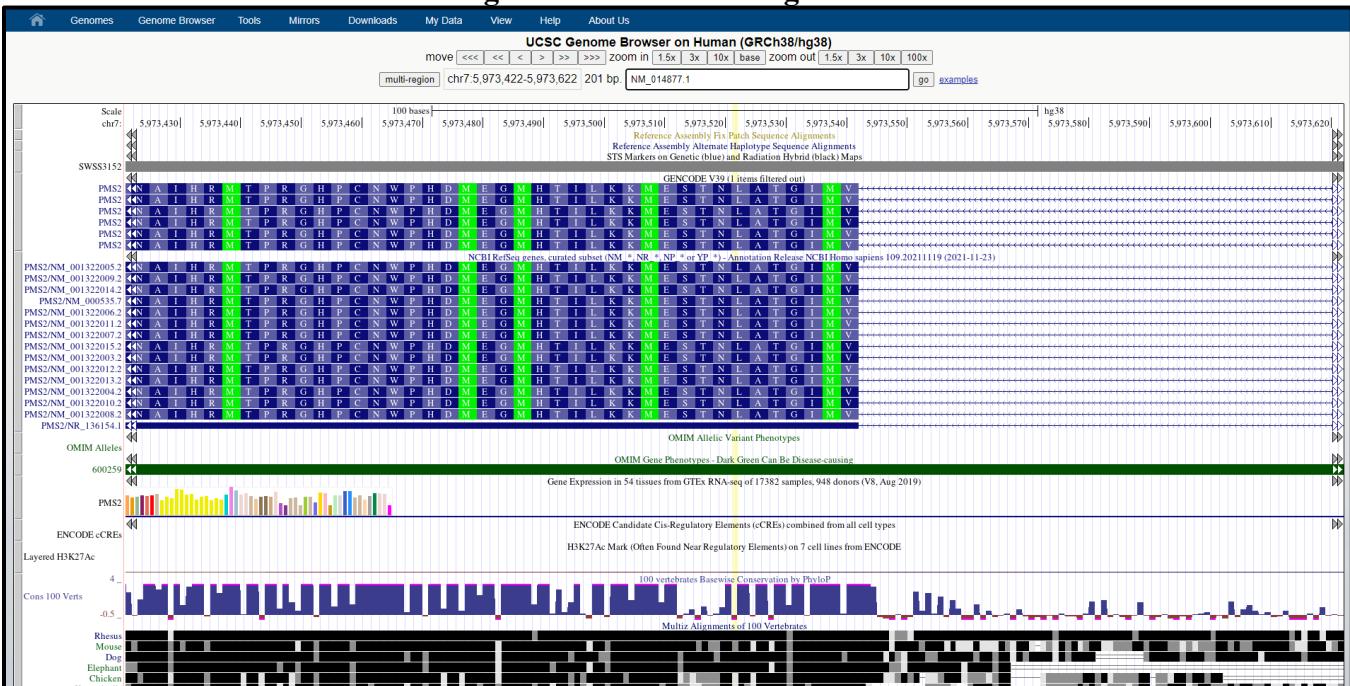


Fig21. Navigation by Ref\_Seq: NM\_014877.1 (HEL gene)



Fig22. Result for Ref Seq: NM\_014877.1 (HELZ gene)

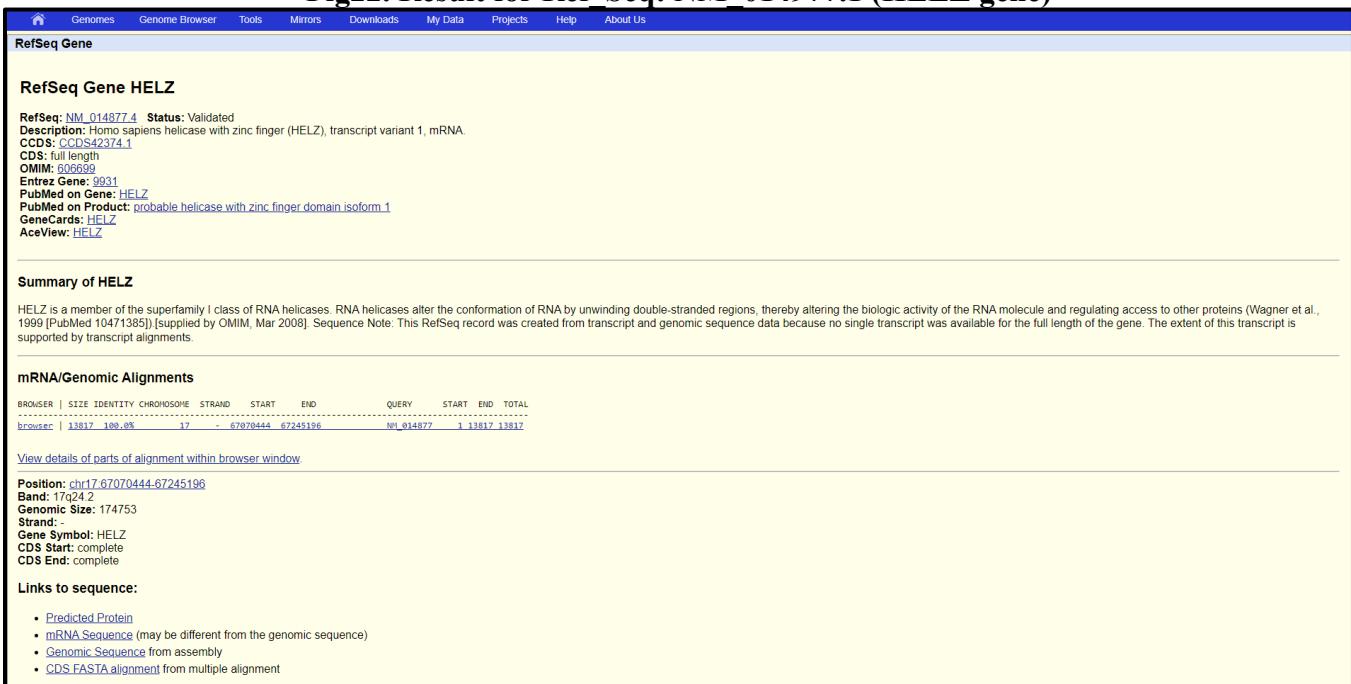


Fig23. Description for Gene HELZ

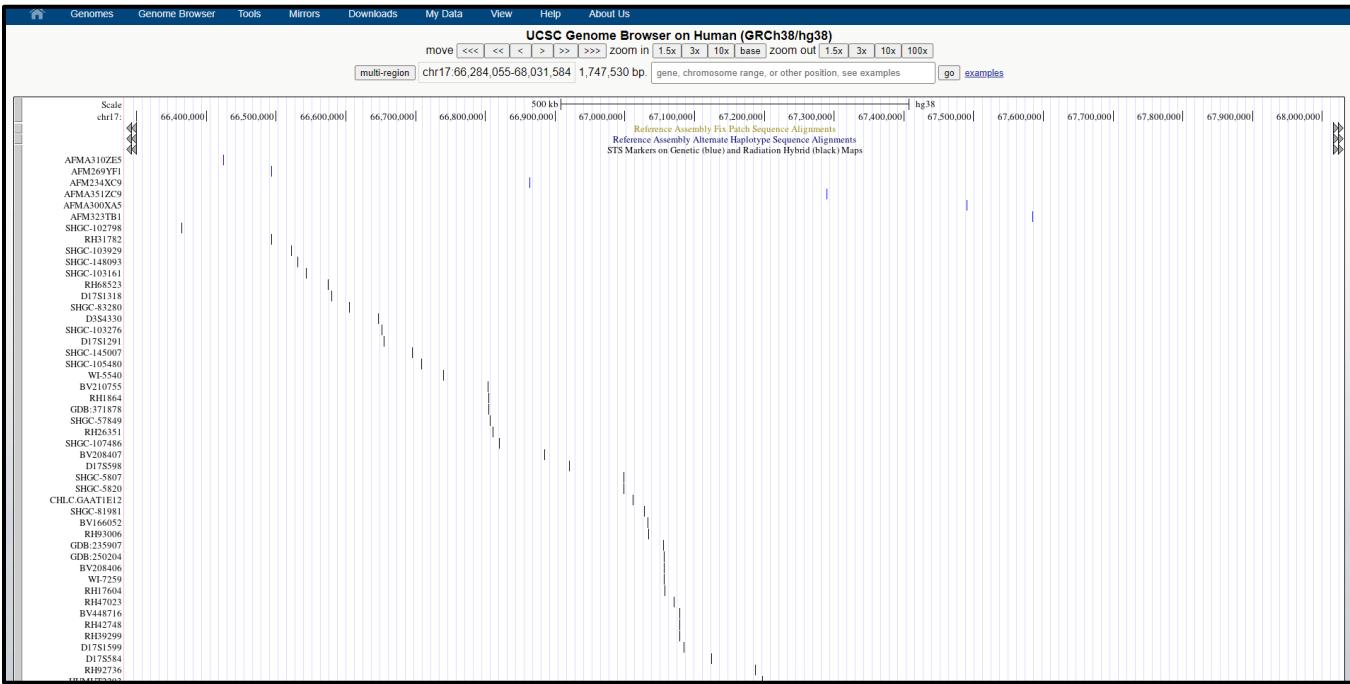


Fig24. Result after zooming 10x

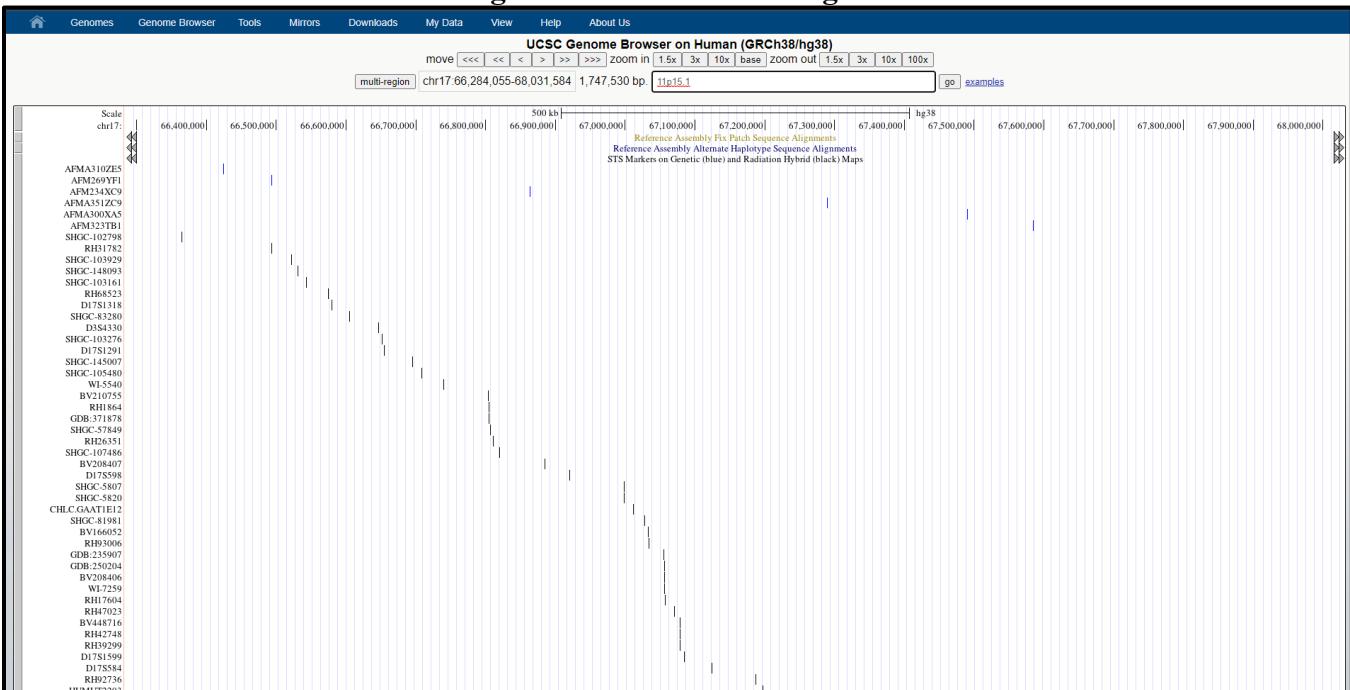


Fig25. Navigation by cytological band: 11p15.1

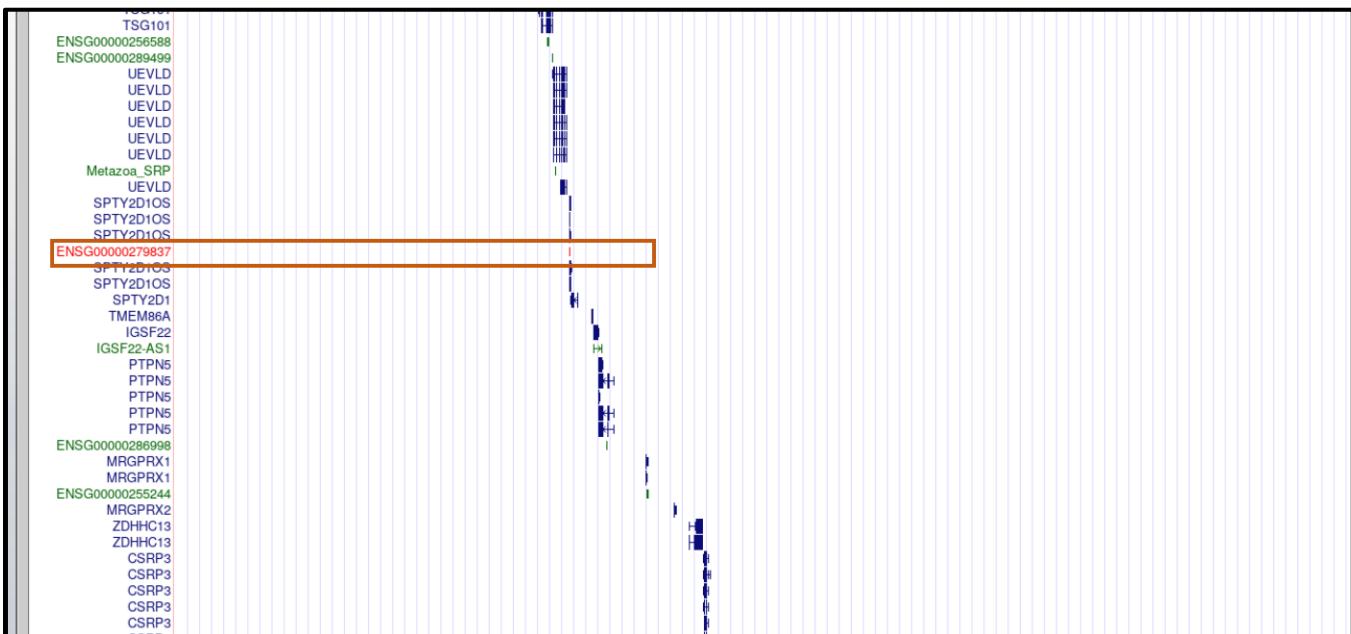


Fig26. Result for cytological band

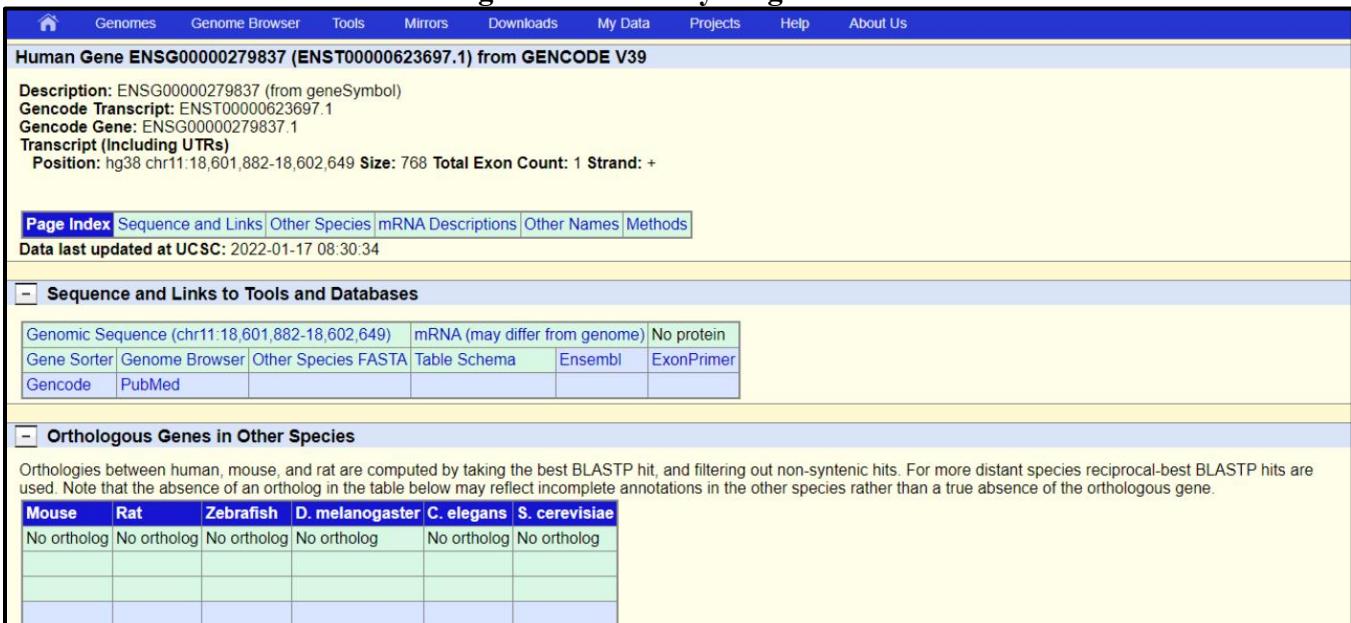


Fig27. Description for cytological band: 11p15.1

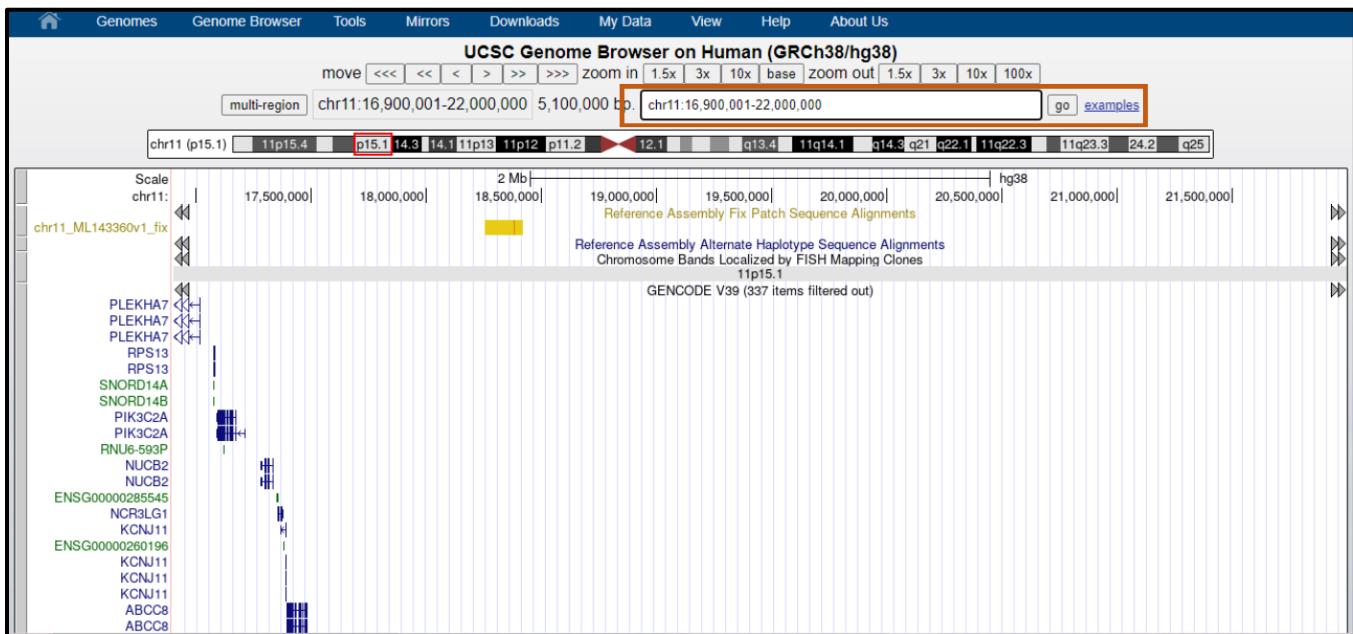


Fig28. Navigation by coordinates

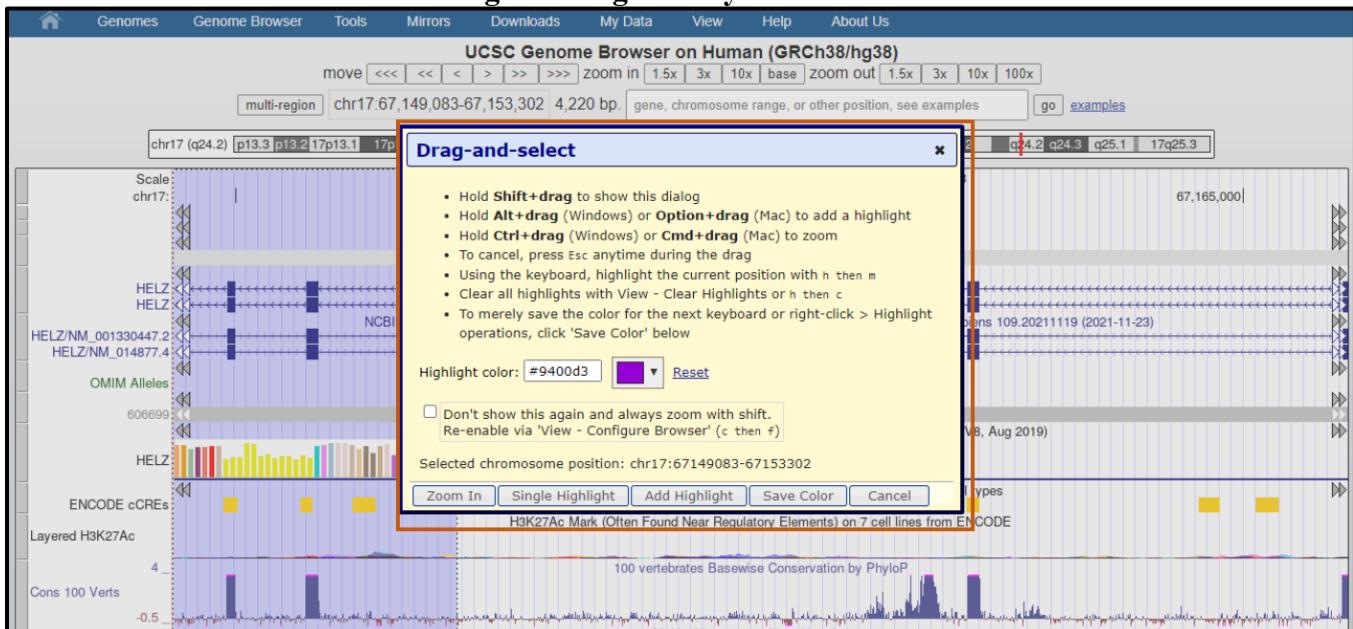


Fig29. Drag and select option for configuration

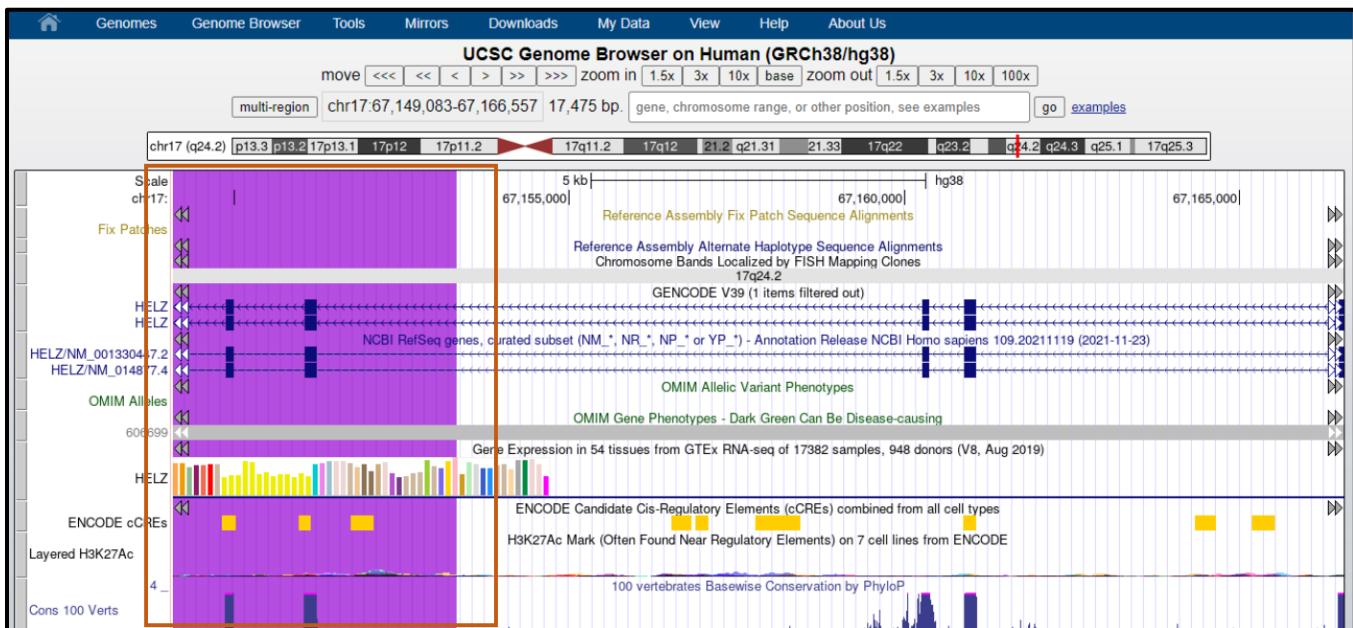


Fig30. Result after configuration

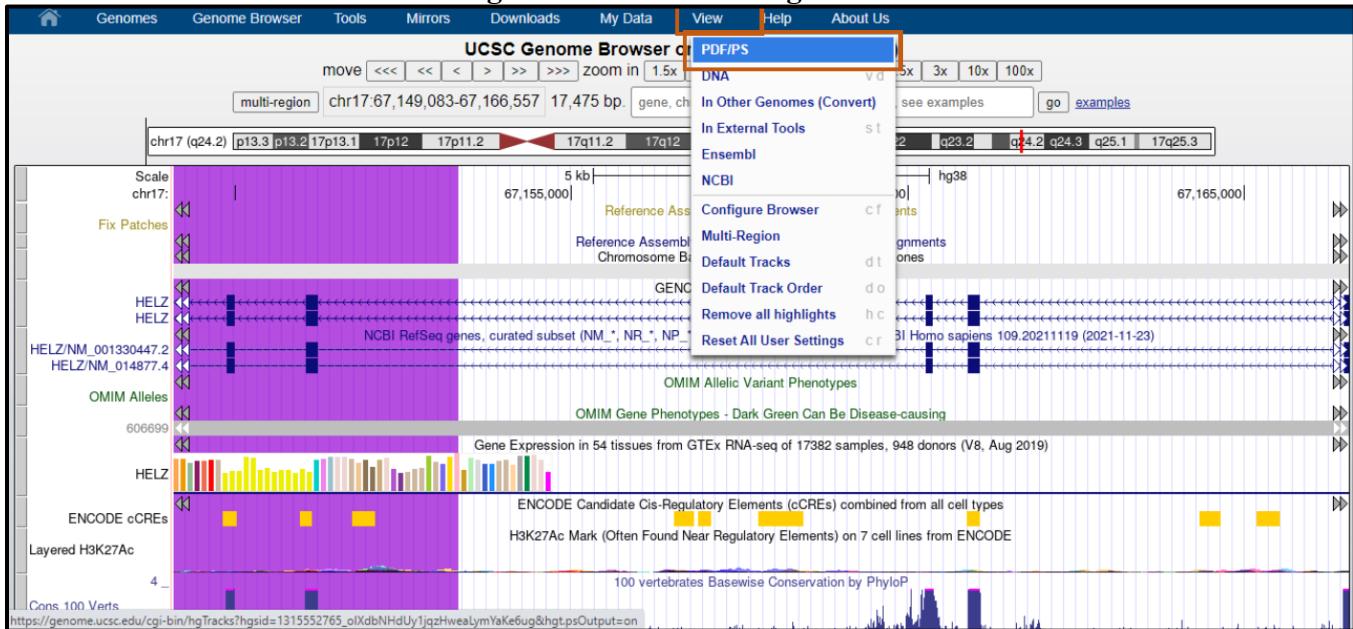


Fig32. Steps to export result as PDF

Genomes   Genome Browser   Tools   Mirrors   Downloads   My Data   View   Help   About Us

## PDF Output

PDF images can be printed with Acrobat Reader and edited by many drawing programs such as Adobe Illustrator or Inkscape.

- Download [the current browser graphic in PDF](#)
- Download [the current chromosome ideogram in PDF](#)

EPS (Postscript) images are a variant of PDF and easier to import into some drawing programs.

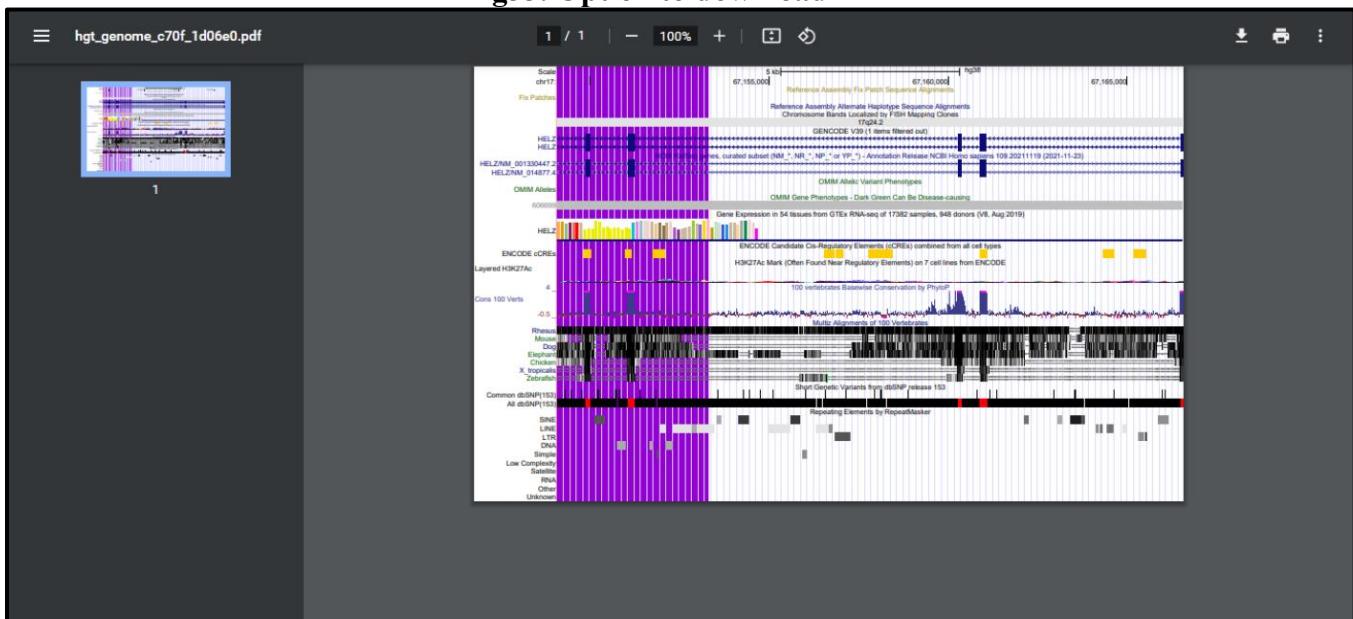
- Download [the current browser graphic in EPS](#)
- Download [the current chromosome ideogram in EPS](#)

Tips for producing quality images for publication:

- Add assembly name and chromosome range to the image on the [configuration page of the base position track](#).
- If using the UCSC Genes track, consider showing only one transcript per gene by turning off splice variants on the track configuration page.
- Increase the font size and remove the light blue vertical guidelines in the [image configuration menu](#).
- In the image configuration menu, change the size of the image, to make it look more square.

[Return to Browser](#)

**Fig33. Option to download PDF**



**Fig34. Result in PDF format**

## RESULT:

UCSC genome browser was used for setting for GRCH/hg38 browser and search option used were:

- Navigation by gene name
- Navigation by SNP id
- Navigation by Ref\_Seq: NM\_014877.4
- Navigation by OMIM Id: 115500
- Navigation by cytological band: 11p15.1

Various options for configuration of tracks, zooming in and out the results, saving results in PDF format, etc were also used.

## CONCLUSION:

UCSC genome browser can be used for gene predictions, mRNA and expressed sequence tag alignments,

simple nucleotide polymorphisms, expression and regulatory data, phenotype and variation data, and pairwise and multiple-species comparative genomics data. All information relevant to a region is presented in one window, facilitating biological analysis and interpretation. It also provides various tools for configuration of tracks and refining the results. Options are available for zooming in and out the results and downloading the results in PDF format.

## REFERENCES:

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2. UCSC Genome Browser Home. (2019). Ucsc.edu. Retrieved March 28, 2022, from <https://genome.ucsc.edu/>
3. UCSC Genome Browser Gateway. (2018). Ucsc.edu. Retrieved March 28, 2022, from <https://genome.ucsc.edu/cgi-bin/hgGateway>
4. Human hg38 chr11%3A34438934%2D34472060 UCSC Genome Browser v428. (n.d.). Genome.ucsc.edu. Retrieved March 28, 2022, from [https://genome.ucsc.edu/cg/bin/hgTracks?db=hg38&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr11%3A34438934%2D34472060&hgsid=1315552765\\_oIXdbNHdUy1jqzHweaLymYaKe6ug](https://genome.ucsc.edu/cg/bin/hgTracks?db=hg38&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr11%3A34438934%2D34472060&hgsid=1315552765_oIXdbNHdUy1jqzHweaLymYaKe6ug)
5. **Navigation by OMIM id:** OMIM genes - 115500. (n.d.). Genome.ucsc.edu. Retrieved March 28, 2022, from [https://genome.ucsc.edu/cgi-bin/hgc?hgsid=1315629613\\_43o3KD070AuOsLgYd19FgktiKt2H&db=hg38&c=chr11&l=34438933&r=34472060&o=34438933&t=34472060&g=omimGene2&i=115500](https://genome.ucsc.edu/cgi-bin/hgc?hgsid=1315629613_43o3KD070AuOsLgYd19FgktiKt2H&db=hg38&c=chr11&l=34438933&r=34472060&o=34438933&t=34472060&g=omimGene2&i=115500)
6. **Navigation by SNP id:** All Short Genetic Variants from dbSNP Release 153 (rs10000). (n.d.). Genome.ucsc.edu. Retrieved March 28 2022, from [https://genome.ucsc.edu/cgi-bin/hgc?hgsid=1315552765\\_oIXdbNHdUy1jqzHweaLymYaKe6ug&db=hg38&c=chr7&l=5973421&r=5973622&o=5973521&t=5973522&g=dbSnp153&i=rs10000](https://genome.ucsc.edu/cgi-bin/hgc?hgsid=1315552765_oIXdbNHdUy1jqzHweaLymYaKe6ug&db=hg38&c=chr7&l=5973421&r=5973622&o=5973521&t=5973522&g=dbSnp153&i=rs10000)
7. **Navigation by Ref\_Seq:** NCBI RefSeq genes, curated subset (NM\_\*, NR\_\*, NP\_\* or YP\_\*) - NM\_014877.4. (n.d.). Genome.ucsc.edu. Retrieved March 28, 2022, from [https://genome.ucsc.edu/cgibin/hgc?hgsid=1315552765\\_oIXdbNHdUy1jqzHweaLymYaKe6ug&db=hg38&c=chr17&l=67070443&r=67245196&o=67070443&t=67245196&g=ncbiRefSeqCurated&i=NM\\_014877.4](https://genome.ucsc.edu/cgibin/hgc?hgsid=1315552765_oIXdbNHdUy1jqzHweaLymYaKe6ug&db=hg38&c=chr17&l=67070443&r=67245196&o=67070443&t=67245196&g=ncbiRefSeqCurated&i=NM_014877.4)
8. **Navigation by Cytological band:** Human Gene ENSG00000279837 (ENST00000623697.1) from GENCODE V39. (n.d.)Genome.ucsc.edu. Retrieved March 28, 2022, from [https://genome.ucsc.edu/cgibin/hgGene?hgg\\_gene=ENST00000623697.1&hgg\\_chrom=chr11&hgg\\_start=18601881&hgg\\_end=18602649&hgg\\_type=knownGene&db=hg38](https://genome.ucsc.edu/cgibin/hgGene?hgg_gene=ENST00000623697.1&hgg_chrom=chr11&hgg_start=18601881&hgg_end=18602649&hgg_type=knownGene&db=hg38)

## WEBLEM 9b

### Ensembl Genome Browser

**(URL: <https://asia.ensembl.org/index.html>)**

#### AIM:

To explore Ensembl genome browser in order to gather information for annotated genes/genome/protein/transcript etc.

#### INTRODUCTION:

The Ensembl project was initially launched in **1999** with the aim of **developing methodologies for automatic annotation** of (human) **genomic sequence** with genes and their **constituent transcripts**. Since that time, the project has broadened substantially in scope; the **Ensembl Genome Browser**, which came online in **2000**, now includes **reference genomic sequence and annotation** for nearly **100 chordate organisms**. Ensembl is **rapidly incorporating** new data, including **whole clades** of new species' genomes and reference sequence for **multiple strains of existing species**, such as mouse. In addition, existing annotation is **regularly augmented** by the **inclusion of new data sets**. Ensembl's sister site, **Ensembl Genomes**, provides access to **nonvertebrate genomes** through dedicated portals for **Bacteria, Fungi, Plants, Metazoa, and Protists**.

#### METHODOLOGY:

1. Open homepage for Ensembl genome browser. (URL: <https://asia.ensembl.org/index.html>)
2. Select human (GRCh38.p13) genome assembly
3. Search for helad1 gene.
4. Observer the results.
5. Use the configuration tools for the tracks.
6. Interpret the results.

#### OBSERVATION:

**Fig1. Homepage for Ensembl**

**Ensembl** GENOME BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Human (GRCh38.p13) ▾

Search Human (Homo sapiens)

Search all categories ▾ Search... Go

e.g. BRCA2 or 17:63992802-64038237 or rs699 or osteoarthritis

Genome assembly: GRCh38.p13 (GCA\_000001405.28)

More information and statistics  
Download DNA sequence (FASTA)  
Convert your data to GRCh38 coordinates  
Display your data in Ensembl  
Other assemblies  
GRCh37 Full Feb 2014 archive with BLAST, VEP and BioMart ▾ Go

Comparative genomics

What can I find? Homologues, gene trees, and whole genome alignments across multiple species.  
More about comparative analysis  
Download alignments (EMF)

Regulation

What can I find? DNA methylation, transcription factor binding sites, histone modifications, and regulatory features such as enhancers and repressors, and microarray annotations.  
More about the Ensembl regulatory build and microarray annotation  
Experimental data sources  
Download all regulatory features (GFF)

Gene annotation

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.  
More about this genebuild  
Download FASTA files for genes, cDNAs, ncRNA, proteins  
Download GTF or GFF3 files for genes, cDNAs, ncRNA, proteins  
Update your old Ensembl IDs

Pax6 INS FGF2 DMD ssh Example gene  
ATCGAGCT ATCAGCT ATCGAGAT Example variant  
Example transcript

Variation

What can I find? Short sequence variants and longer structural variants, disease and other phenotypes.  
More about variation in Ensembl  
Download all variants (GVF)  
Variant Effect Predictor VelP

ATCGAGCT ATCAGCT ATCGAGAT Example variant  
Example phenotype  
Example structural variant

Ensembl release 105 - Dec 2021 © ENSEMBL-EBI

Permanent link - View in archive site

Fig2. Homepage for Human (GRCh38.p13) genome assembly

**Ensembl** GENOME BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Human (GRCh38.p13) ▾

Search Human (Homo sapiens)

Search all categories ▾ helad1 Go

e.g. BRCA2 or 17:63992802-64038237 or rs699 or osteoarthritis

Genome assembly: GRCh38.p13 (GCA\_000001405.28)

More information and statistics  
Download DNA sequence (FASTA)  
Convert your data to GRCh38 coordinates  
Display your data in Ensembl  
Other assemblies  
GRCh37 Full Feb 2014 archive with BLAST, VEP and BioMart ▾ Go

Comparative genomics

What can I find? Homologues, gene trees, and whole genome alignments across multiple species.  
More about comparative analysis  
Download alignments (EMF)

Regulation

What can I find? DNA methylation, transcription factor binding sites, histone modifications, and regulatory features such as enhancers and repressors, and microarray annotations.  
More about the Ensembl regulatory build and microarray annotation  
Experimental data sources  
Download all regulatory features (GFF)

Gene annotation

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.  
More about this genebuild  
Download FASTA files for genes, cDNAs, ncRNA, proteins  
Download GTF or GFF3 files for genes, cDNAs, ncRNA, proteins  
Update your old Ensembl IDs

Pax6 INS FGF2 DMD ssh Example gene  
ATCGAGCT ATCAGCT ATCGAGAT Example variant  
Example transcript

Variation

What can I find? Short sequence variants and longer structural variants, disease and other phenotypes.  
More about variation in Ensembl  
Download all variants (GVF)  
Variant Effect Predictor VelP

ATCGAGCT ATCAGCT ATCGAGAT Example variant  
Example phenotype  
Example structural variant

Ensembl release 105 - Dec 2021 © ENSEMBL-EBI

Permanent link - View in archive site

Fig3. Search for helad1 gene

Ensembl BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

New Search

Current selection: Only searching Human **helad1**

1 results match helad1 when restricted to species: Human

Restrict category to: Gene **1**

Human NAV2 (Human Gene) ENSG00000166833 11:19350724-20121601

Neuron navigator 2 [Source:HGNC Symbol:Acc:HGNC:15997]

Variant table • Phenotypes • Location • External Refs • Regulation • Orthologues • Gene tree

Per page: 10 25 50 100

Layout: Standard Table

**Tip:** Help and Documentation can be searched from the homepage! Just type in a term you want to know more about, like non-synonymous SNP

About Us Get help Our sister sites Follow us

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Contact us Adding custom tracks Ensembl Fungi Twitter

Citing Ensembl Downloading data Ensembl Plants Facebook

Privacy policy Video tutorials Ensembl Protists

Disclaimer Variant Effect Predictor Ensembl Metazoa (VEP)

Best gene match Human Gene Human NAV2 Human NAV2 (Human Gene) ENSG00000166833 11:19350724-20121601

Protein coding gene neuron navigator 2 HGNC Symbol: Acc:HGNC 15997

Ensembl release 105 - Dec 2021 © EMBL-EBI

Permanent link - View in archive site

Fig4. Hit page for helad1 gene

Ensembl BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Human (GRCh38.p13) ▾ Gene: NAV2

Location: 11:19,350,724-20,121,601

Gene-based displays

**Summary**

- Splice variants
- Transcript comparison
- Gene alleles
- Sequence
- Secondary Structure
- Comparative Genomics
- Genomic alignments
- Gene tree
- Gene gain/loss tree
- Orthologues
- Paralogs
- Ensembl protein families
- Ontologies
- GO: Biological process
- GO: Molecular function
- GO: Cellular component
- Phenotype
- Genetic Variation
- Variant table
- Variant image
- Structural variants
- Gene expression
- Pathway
- Regulation
- External references
- Supporting evidence
- ID History
- Gene history

**Configure this page**

**Custom tracks**

**Export data**

**Share this page**

**Bookmark this page**

Gene: NAV2 ENSG00000166833

neuron navigator 2 [Source:HGNC Symbol:Acc:HGNC:15997]

FLJ10633, FLJ11030, FLJ23707, HELAD1, KIAA1419, POMF1L2, RAINB1

Chromosome 11: 19,350,724-20,121,601 forward strand.

GRCh38.CM000673.2

This gene has 15 transcripts (splice variants), 209 orthologues and 2 paralogues.

Show transcript table

**Summary**

Name NAV2 (HGNC Symbol)

CCDS

UniProtKB

RefSeq

Ensembl version

Other assemblies

There is no unaligned mapping of this gene onto the GRCh37 assembly.

View this locus in the GRCh37 archive: ENSG00000166833

Protein coding

Annotation method

Annotation Attributes

Annotation for this gene includes both automatic annotation from Ensembl and Havana manual curation, see article.

overlapping locus [Definitions]

Go to Region in Detail for more tracks and navigation options (e.g. zooming)

Loading component

Ensembl release 105 - Dec 2021 © EMBL-EBI

Permanent link - View in archive site

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About us Using this website Ensembl Bacteria Blog

Fig5. Result for NAV2 gene

**Ensembl** beta BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

 Human (GRCh38.p13) ▾

Location 11:19,350,720-20,121,601 Gene: NAV2 Transcript: NAV2-201

Transcript-based displays

- Sequence
- cDNA
- Protein

Basic Information

- Protein summary
- Domains & features
- Variants

PDB 3D protein model

- Homology predicted model

Genetic Variation

- Variant table
- Variant Image
- Haplotypes
- Population comparison
- Comparison image

External References

- General identifiers
- Gene
- Protein
- Protein evidence
- Off-target evidence
- ID History
- Transcript history
- Protein history

Configure this page

Custom tracks

Export data

Share this page

Bookmark this page

Transcript: ENST00000349880.9 NAV2-201

Description: neuron navigator 2 [Source: HGNC Symbol; Acc: HGNC:15997] [Protein]

Gene Synonyms: FLJ10633, FLJ11030, FLJ22707, HELAD1, KIAA1419, POMF2L, RAINB1

Location: Chromosome 11: 19,721,837-20,121,601 forward strand

About this transcript: This transcript has 38 exons, is annotated with 68 domains and features, is associated with 110693 variant alleles and maps to 1154 oligo probes.

Gene: This transcript is a product of gene ENSG00000166833.23 [Hide transcript table](#)

Show/hide columns (1 hidden)

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	RefSeq Match	Flags
ENST00000349880.9	NAV2-201	11492	2429aa	Protein coding	CCDS7850#	Q8VL1-3#	NM_145117.5#	MANE Select v0.95 Ensembl Canonical GENCODE basic APPRIS P3 TSL.1
ENST00000360085.6	NAV2-203	11501	2432aa	Protein coding	CCDS7851#	Q8VL1-2#	-	GENCODE basic APPRIS ALT1 TSL.5
ENST00000360655.9	NAV2-202	10667	2365aa	Protein coding	CCDS53612#	Q8VL1-4#	-	GENCODE basic APPRIS ALT2 TSL.1
ENST00000360687.7	NAV2-204	7882	2486aa	Protein coding	CCDS58126#	Q8VL1-1#	-	GENCODE basic TSL.5
ENST00000353917.5	NAV2-212	5084	1493aa	Protein coding	CCDS4452#	Q8VL1-5#	-	GENCODE basic TSL.2
ENST00000352322.5	NAV2-206	2716	815aa	Protein coding	-	E9PNV5#	-	TSL.2 CDS 3' incomplete
ENST00000304081.9	NAV2-210	556	160aa	Protein coding	-	E9PLU3#	-	TSL.5 CDS 3' incomplete
ENST00000650578.1	NAV2-215	256	63aa	Protein coding	-	A0A3B3ISY2#	-	CDS 3' incomplete
ENST00000534279.1	NAV2-213	684	No protein	Processed transcript	-	-	-	TSL.3
ENST00000534299.5	NAV2-214	668	No protein	Processed transcript	-	-	-	TSL.5
ENST00000526675.1	NAV2-207	607	No protein	Processed transcript	-	-	-	TSL.5
ENST00000528008.1	NAV2-208	570	No protein	Processed transcript	-	-	-	TSL.4
ENST00000533746.1	NAV2-211	2289	No protein	Retained intron	-	-	-	TSL.2
ENST00000525025.1	NAV2-205	627	No protein	Retained intron	-	-	-	TSL.3
ENST00000528923.1	NAV2-209	563	No protein	Retained intron	-	-	-	TSL.2

**Summary** 

Statistics: Exons: 38, Coding exons: 38, Transcript length: 11,492 bps, Translation length: 2,429 residues

CCDS: This transcript is a member of the Human CCDS set: CCDS7850#

## Fig6. Result for NAV2-201

Summary

Name NAV2 (HGNC Symbol)

CCDS This gene is a member of the Human CCDS set: [CCDS44552.1](#), [CCDS93612.1](#), [CCDS58126.1](#), [CCDS7850.1](#), [CCDS7851.2](#)

UniProtKB This gene has proteins that correspond to the following UniProtKB identifiers: [Q8VLF](#)

RefSeq This Ensembl/Gencode gene contains transcript(s) for which we have [selected identical RefSeq transcript\(s\)](#). If there are other RefSeq transcripts available they will be in the [External references](#) table

Ensembl version ENSG00000166833.23

Other assemblies There is no ungapped mapping of this gene onto the GRCh37 assembly.

View this locus in the GRCh37 archive: [ENSG00000166833](#)

Gene type Protein coding

Annotation method Annotation for this gene includes both automatic annotation from Ensembl and Havana manual curation, see [article](#).

Annotation Attributes overlapping locus [Definitions](#)

Go to Region in Detail for more tracks and navigation options (e.g. zooming)

Fig7. Result for NAV2

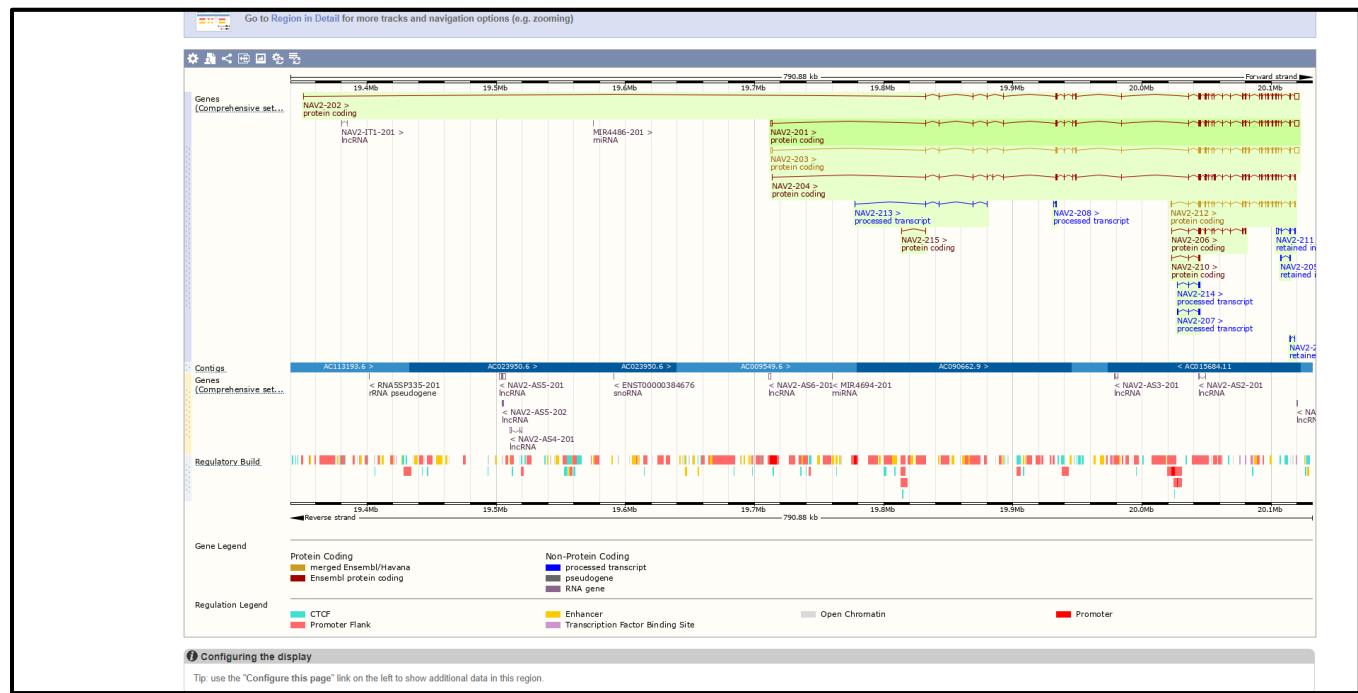


Fig6. Tracks information

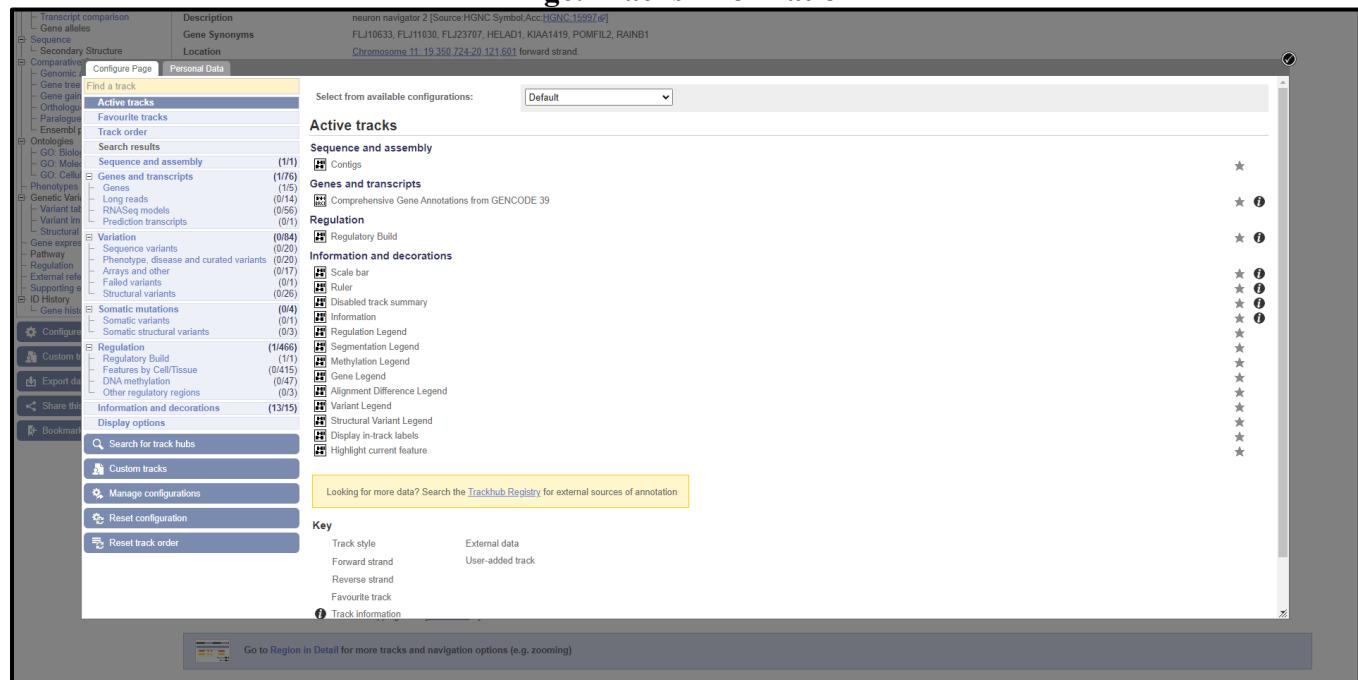


Fig7. Option for tracks configuration

neuron navigator 2 [Source:HGNC Symbol Acc:HGNC:15997@]  
FLJ10633, FLJ11030, FLJ23707, HELAD1, KIAA1419, POMF1L2, RAINB1  
Chromosome 11, 19,356,724-20,121,601 forward strand.

Select from available configurations:

**Active tracks**

**Sequence and assembly**

**Regulation**

**Information and decorations**

**Key**

Looking for more data? Search the [Trackhub Registry](#) for external sources of annotation

Fig8. Tracks configuration

neuron navigator 2 [Source:HGNC Symbol Acc:HGNC:15997@]  
FLJ10633, FLJ11030, FLJ23707, HELAD1, KIAA1419, POMF1L2, RAINB1  
Chromosome 11, 19,356,724-20,121,601 forward strand.

Select from available configurations:

**Genes and transcripts**

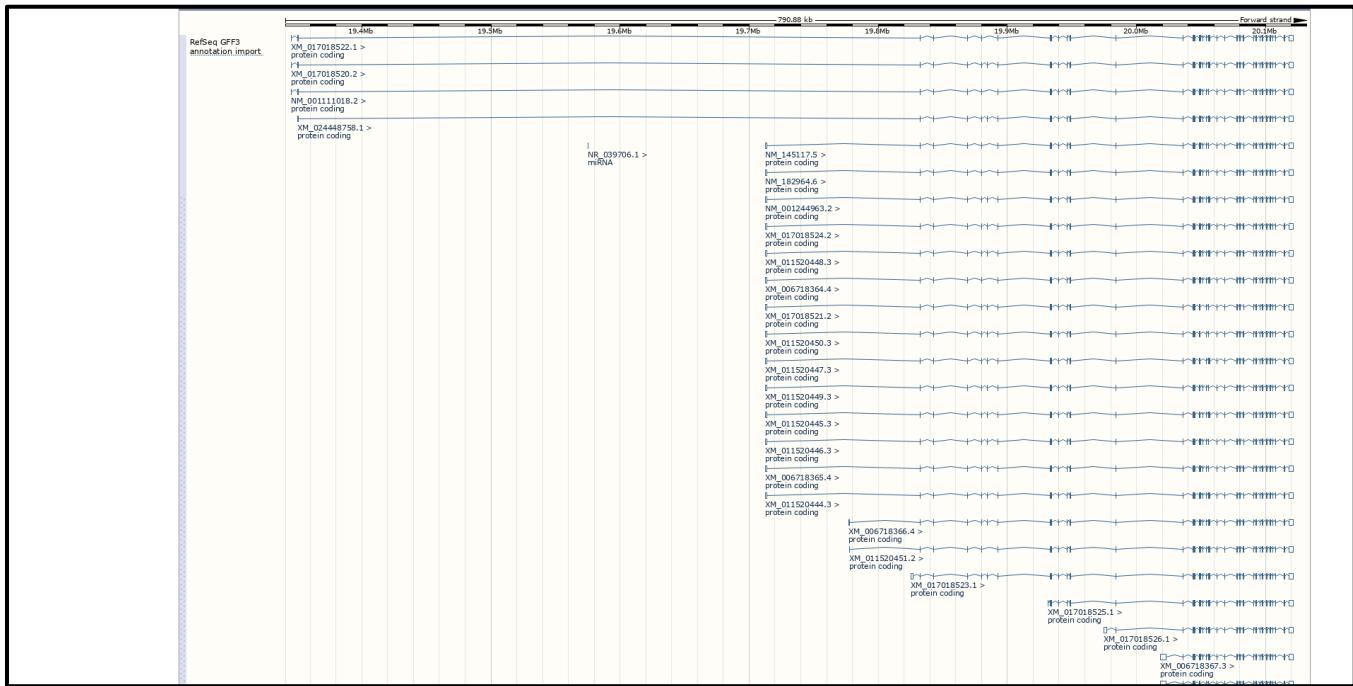
**Change track style**

**Configure RNASeq models**

**Prediction transcripts**

Looking for more data? Search the [Trackhub Registry](#) for external sources of annotation

Fig9. Tracks configuration



**Fig10. Updated results after track configuration**

## RESULT:

Emsembl genome browser was used to search for helad1 gene under human genome assembly and was explored for various tracks configuration options.

## CONCLUSION:

Ensembl genome browser provides annotation of (human) genomic sequence with genes and their constituent transcripts. Beyond providing access to data related to publicly available genome annotation, Ensembl integrates a number of tools designed to process or analyze your own data. Sequence alignment using BLAST and BLAT against Ensembl genes, genomes and proteins is also available, along with a suite of tools developed as part of the 1000 Genomes Project that can be accessed on the dedicated GRCh37 browser site.

## REFERENCES:

1. Karolchik, D. (2003). The UCSC Genome Browser Database. , 31(1), 51–54. doi:10.1093/nar/gkg129
2. Ensembl genome browser 100. (n.d.-b). Uswest.ensembl.org. Retrieved March 28, 2022, from <https://asia.ensembl.org/index.html>
3. Homo\_sapiens - Ensembl genome browser 104. (2014). Ensembl.org. Retrieved March 28, 2022, from [https://asia.ensembl.org/Homo\\_sapiens/Info/Index](https://asia.ensembl.org/Homo_sapiens/Info/Index)
4. helad1 - Search - Homo\_sapiens - Ensembl genome browser 105. (2021b). Ensembl.org. Retrieved March 28, 2022, from <https://asia.ensembl.org/Human/Search/Results?q=helad1>
5. Summary - Homo sapiens - Ensembl genome browser 100. (n.d.). Uswest.ensembl.org. Retrieved March 28, 2022, from [https://asia.ensembl.org/Homo\\_sapiens/Gene/Summary?db=core](https://asia.ensembl.org/Homo_sapiens/Gene/Summary?db=core)
6. Summary - Homo sapiens - Ensembl genome browser 100. (n.d.). Uswest.ensembl.org. Retrieved March 28, 2022, from [https://asia.ensembl.org/Homo\\_sapiens/Gene/Summary?db=core;g=ENSG00000166833;r=11:19350724-20121601;t=ENST00000349880](https://asia.ensembl.org/Homo_sapiens/Gene/Summary?db=core;g=ENSG00000166833;r=11:19350724-20121601;t=ENST00000349880)
7. Summary - Homo sapiens - Ensembl genome browser 100. (n.d.). Uswest.ensembl.org. Retrieved March 28, 2022, from [https://asia.ensembl.org/Homo\\_sapiens/Gene/Summary?db=core;g=XM\\_006718367.3](https://asia.ensembl.org/Homo_sapiens/Gene/Summary?db=core;g=XM_006718367.3)

DATE: 30-03-22

## WEBLEM 9c

### Genome Data Viewer

(URL: <https://www.ncbi.nlm.nih.gov/genome/gdv/>)

#### AIM:

To explore graphical displays of features on NCBI's assembly of human genomic sequence data as well as cytogenetic, genetic, physical, and radiation hybrid maps using Genome Data Viewer (GDV).

#### INTRODUCTION:

GDV is composed of an **embedded instance of SV** that displays **sequence and track data**, along with **additional page elements** that allow a user to **search within an entire genome** assembly and efficiently **narrow in on their chromosome, sequence, region, or gene of interest**. GDV replaced the NCBI Map Viewer, NCBI's previous tool for whole-genome display. Researchers using GDV **can go directly** to the NCBI BLAST service from the browser and **load BLAST results** as alignment tracks that can be viewed side by side with **gene annotation** and other data. **Variation Viewer**, a related browser associated with NCBI's variation resources, is **functionally similar** to GDV and also **incorporates an instance of SV** but is **configured with features specifically intended for analyzing human variation data**. GDV and Variation Viewer can both **display the same types** of NCBI variation track data.

#### METHODOLOGY:

1. Open homepage for GDV genome browser (URL: <https://www.ncbi.nlm.nih.gov/genome/gdv/>)
2. Select human genome assembly
3. Search for DNA repair in genome
4. Select BRCA1 gene
5. Observe the results
6. Use various configuration options
7. Interpret the results.

#### OBSERVATION:

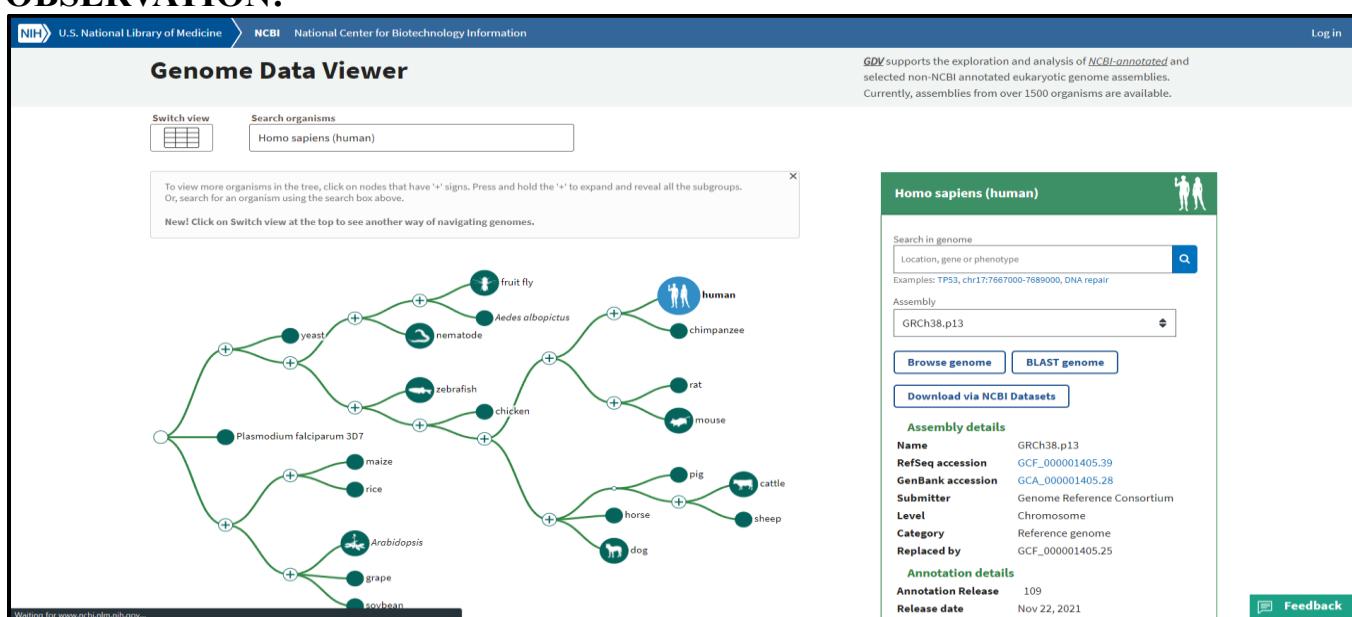


Fig1. Homepage for Genome Data Viewer

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Log in

## Genome Data Viewer

Switch view Search organisms Homo sapiens (human)

To view more organisms in the tree, click on nodes that have '+' signs. Press and hold the '+' to expand and reveal all the subgroups. Or, search for an organism using the search box above.

New! Click on Switch view at the top to see another way of navigating genomes.

**Homo sapiens (human)**

Search in genome DNA repair Examples: TP53, chr17:7667000-7689000, DNA repair

Assembly GRCh38.p13

Browse genome BLAST genome

Download via NCBI Datasets

**Assembly details**

Name GRCh38.p13  
RefSeq accession GCF\_000001405.39  
GenBank accession GCA\_000001405.28  
Submitter Genome Reference Consortium  
Level Chromosome  
Category Reference genome  
Replaced by GCF\_000001405.25

**Annotation details**

Annotation Release 109 ⓘ Release date Nov 22, 2021

Feedback

Fig2. Search for DNA repair in GRCh38.p13 assembly

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Log in

## Genome Data Viewer

Switch view Search organisms Homo sapiens (human)

To view more organisms in the tree, click on nodes that have '+' signs. Press and hold the '+' to expand and reveal all the subgroups. Or, search for an organism using the search box above.

New! Click on Switch view at the top to see another way of navigating genomes.

**Homo sapiens (human)**

Search in genome DNA repair Examples: TP53, chr17:7667000-7689000, DNA repair

Genes Other features

Name	Location
BRCA1	Chr7:43,044,295 - 43,125,364
ERCC2	Chr19:45,349,837 - 45,370,647
BRCA2	Chr13: 32,315,508 - 32,400,268
APEX1	Chr14:20,455,226 - 20,457,767
XRCC5	Chr2: 216,109,348 - 216,206,293
ERCC4	Chr16: 13,920,137 - 13,952,348
XRCC6	Chr22: 41,621,295 - 41,664,041
ERCC3	Chr2: 127,257,290 - 127,294,166

Assembly GRCh38.p13

Browse genome BLAST genome

Download via NCBI Datasets

**Assembly details**

Name GRCh38.p13

Feedback

Fig3. Results for DNA repair genes

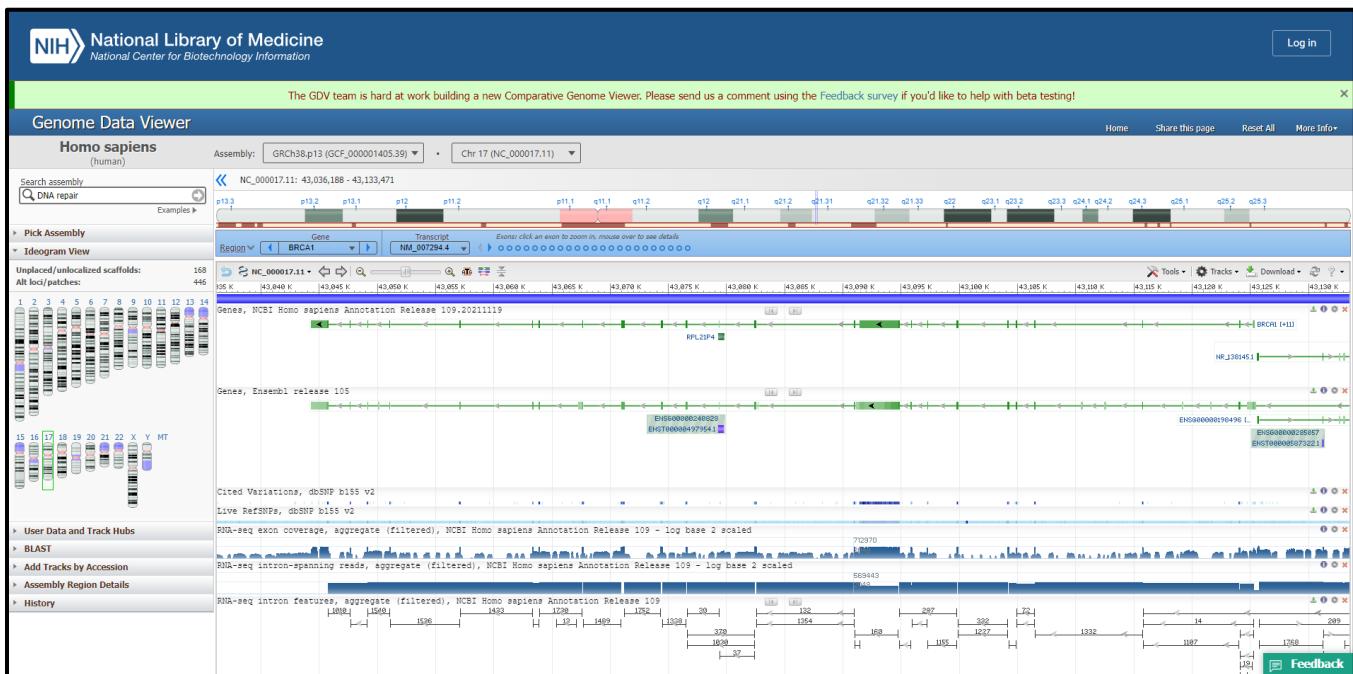


Fig4. Result for BRCA1 gene

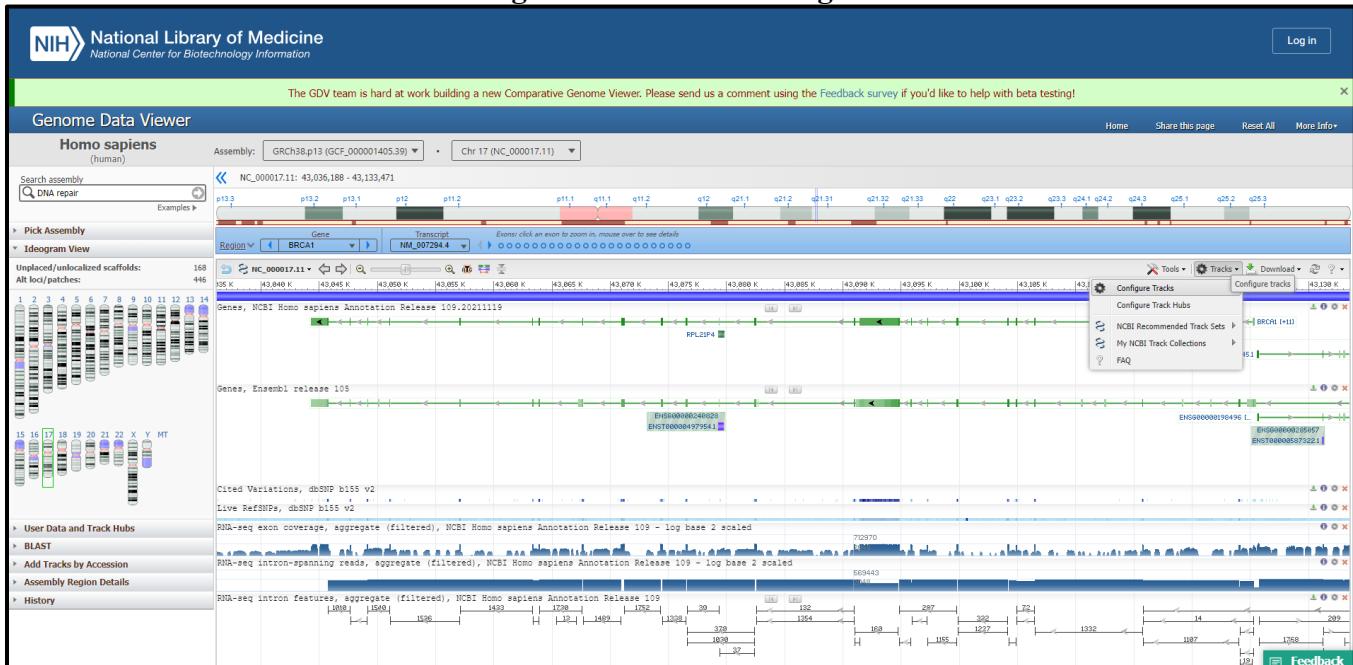


Fig5. Steps to configure tracks

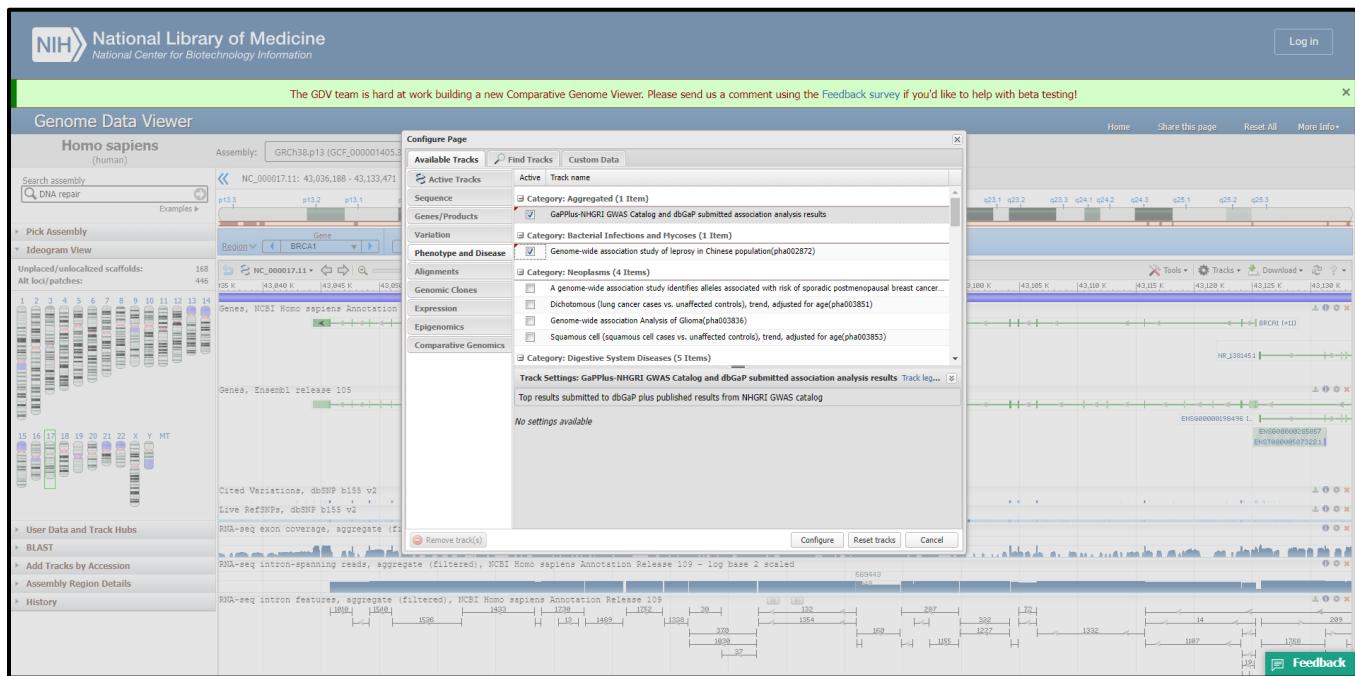


Fig6. Configuration page for phenotype and disease

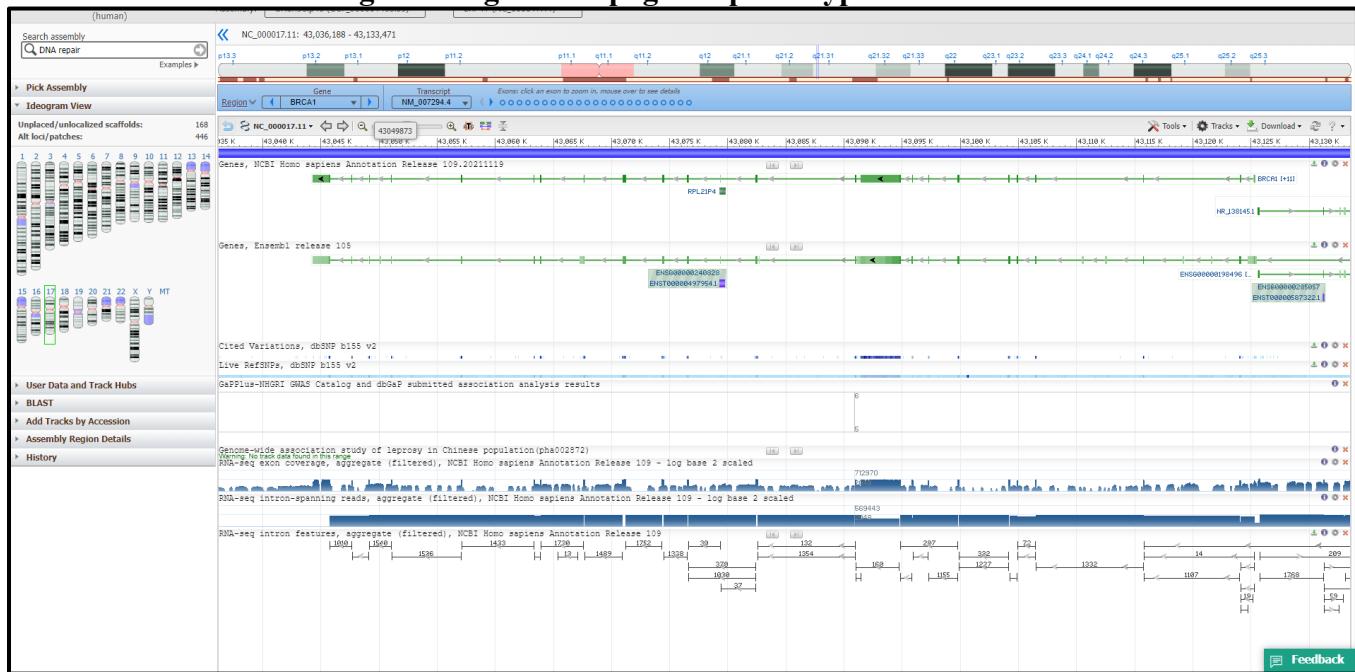


Fig7. Updated result after configuration

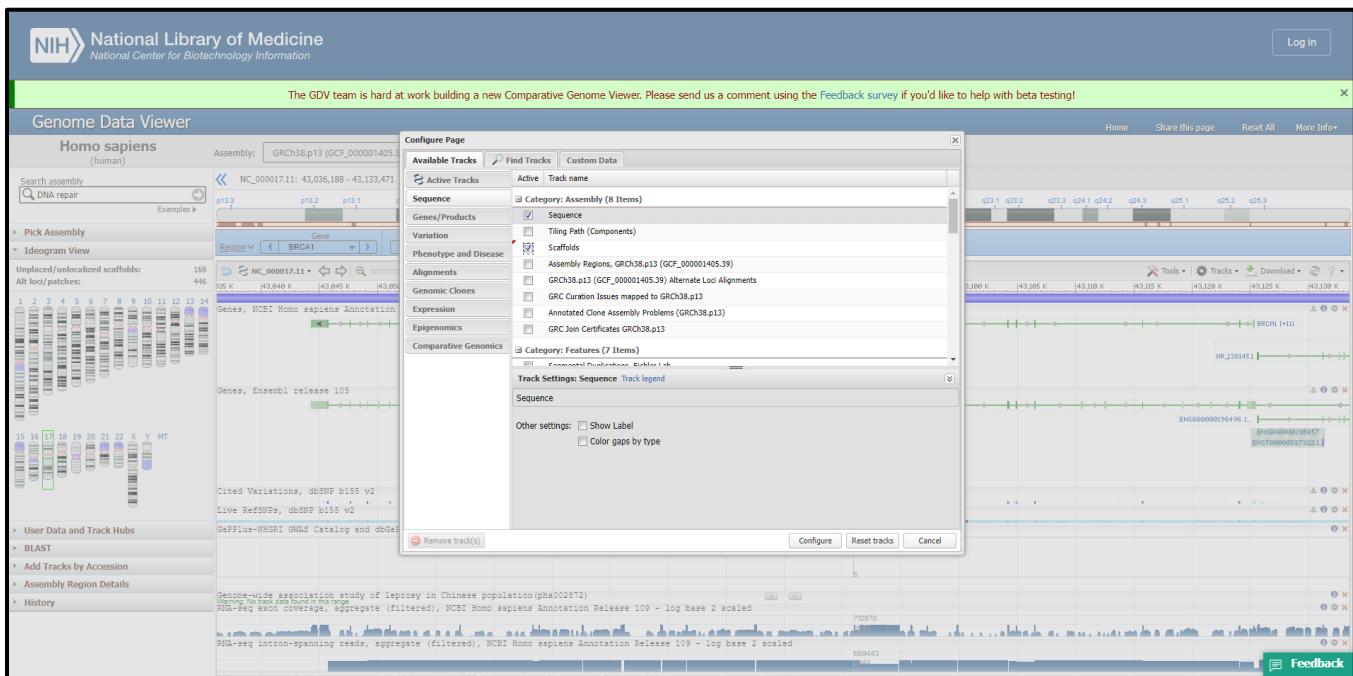


Fig8. Configuration page for sequence

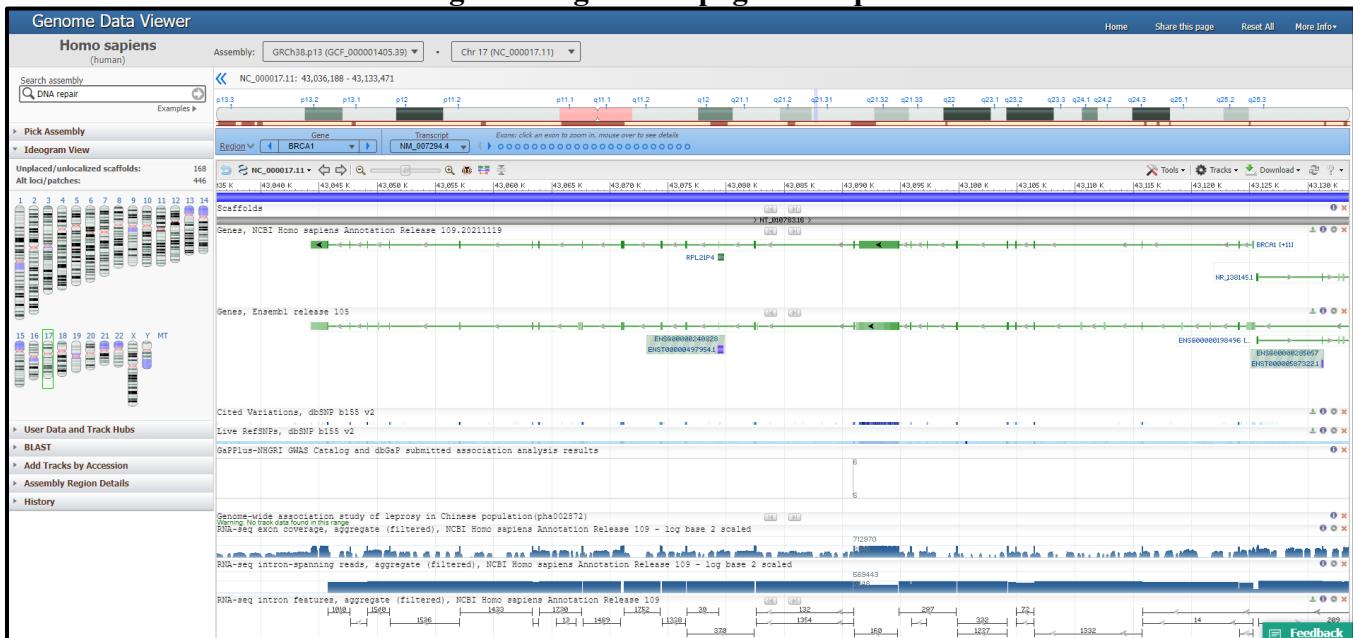
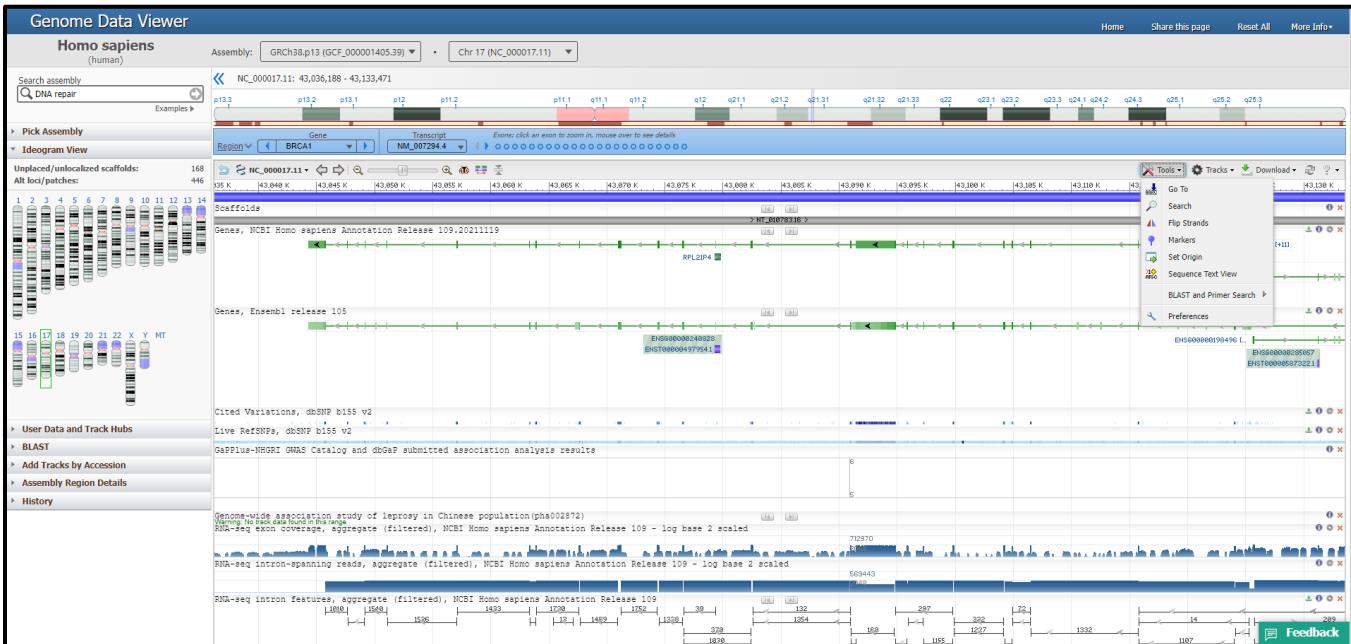
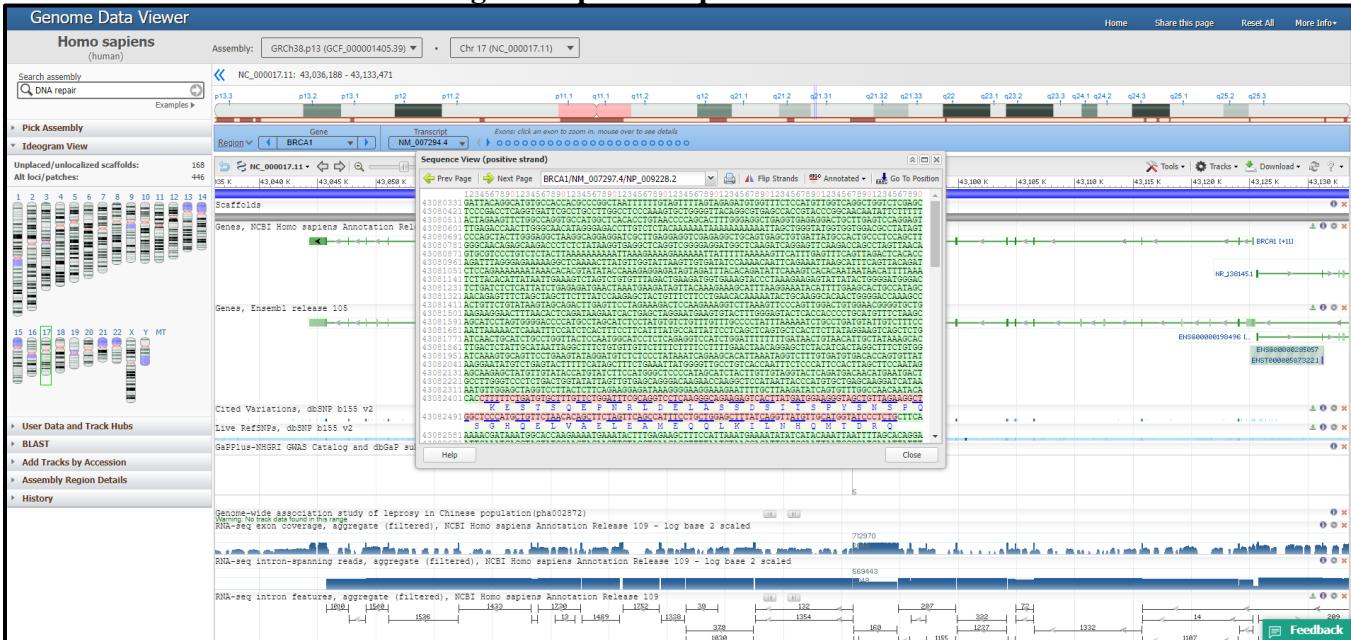


Fig9. Updated result after configuration



## **Fig10. Steps for sequence text view**



**Fig11. Result for sequence text view**

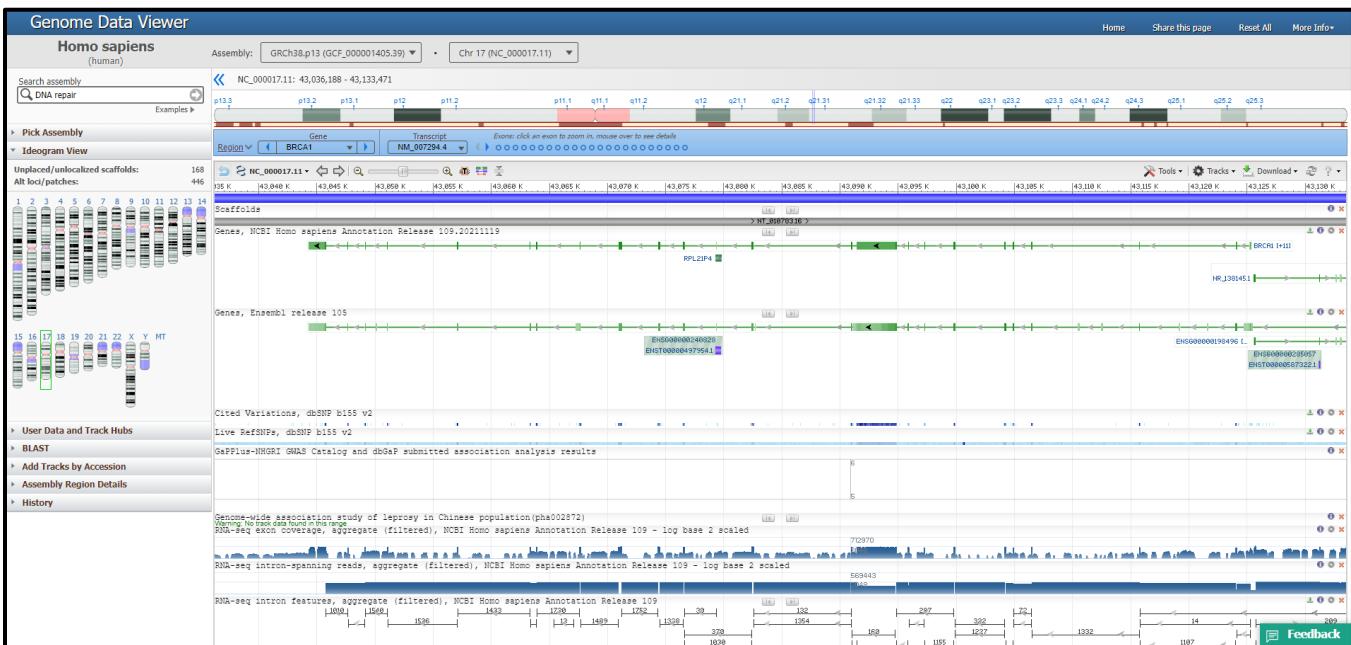


Fig12. Options to view exon information

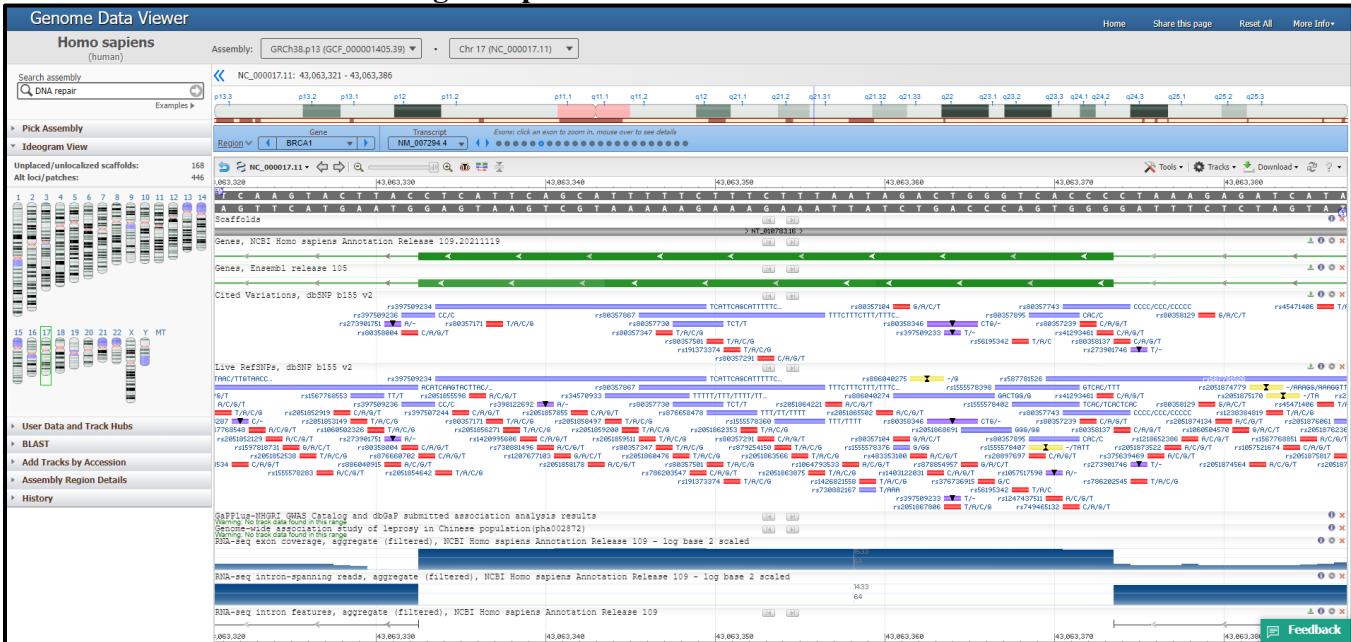


Fig13. Result for exon 18

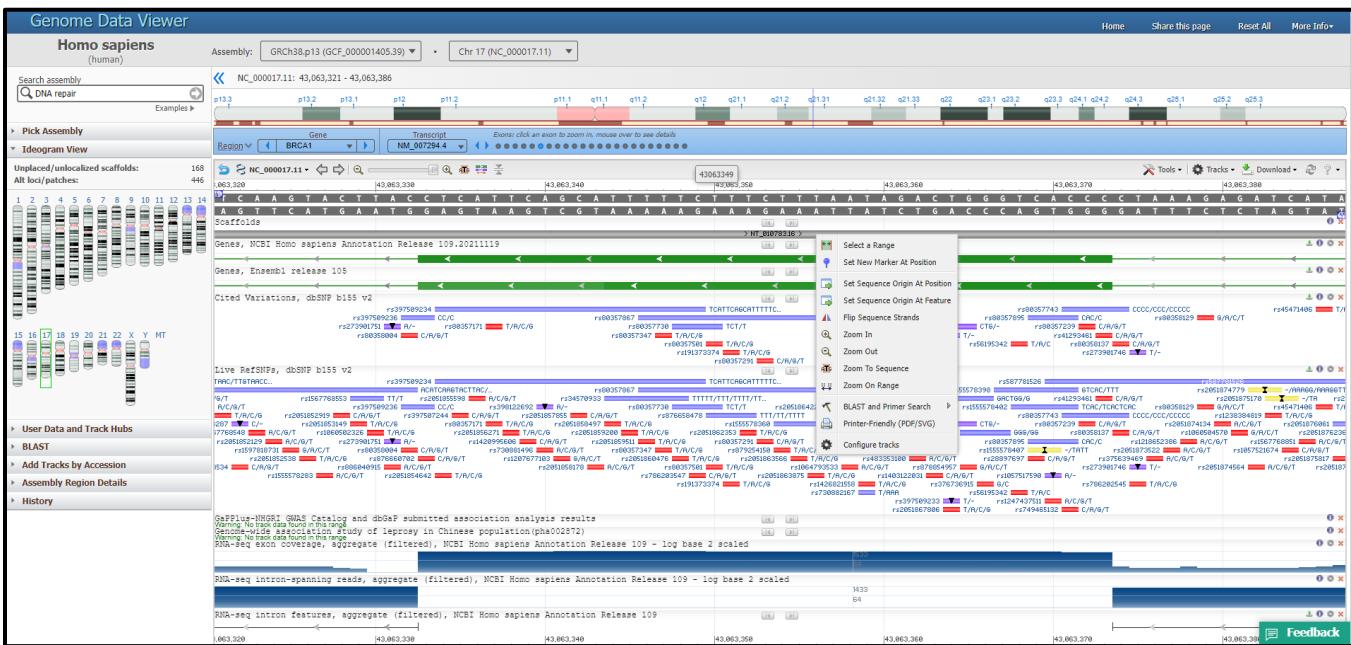


Fig14. Drag and select option for configuring tracks

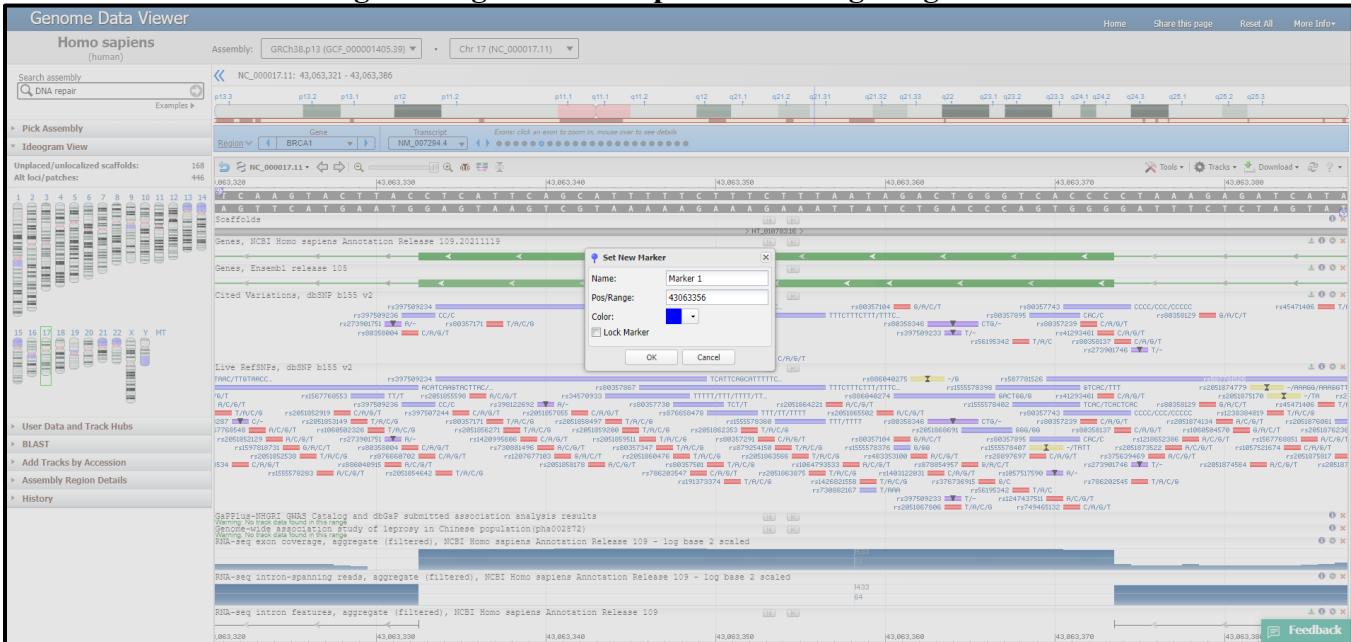


Fig15. Option to set new marker

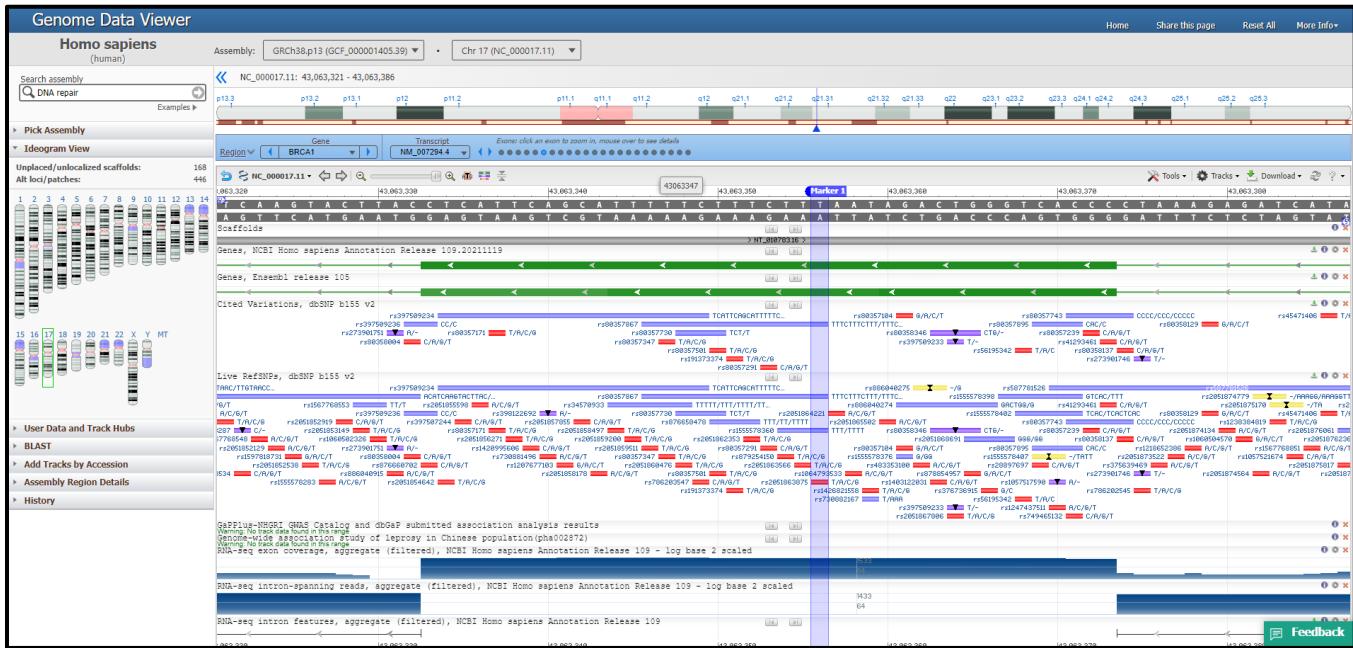


Fig16. Result for new marker

## RESULT:

GDV genome browser was used to search for DNA repair under human genome assembly and results were observed for BRCA1 gene. Various options for tracks configuration were explored and information regarding sequence and exons were also viewed.

## CONCLUSION:

GDV can be used for visualization and analysis of the wide range of genomes and assemblies annotated at the NCBI. RefSeq gene annotation data tracks are shown by default in the graphical view for these assemblies. NCBI ref SNP data tracks are also shown by default for human assemblies. GDV offers users the ability to customize the displays of individual tracks. Users can hide or configure tracks from the track configuration panel or by using the icons at the right end of each track.

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## WEBLEM 10

### A field guide to whole-genome sequencing, assembly and annotation

#### Introduction:

Genome sequencing projects were long confined to biomedical model organisms and required the concerted effort of large consortia. Rapid progress in high-throughput sequencing technology and the simultaneous development of bioinformatic tools have democratized the field. It is now within reach for individual research groups in the eco-evolutionary and conservation community to generate *de novo* draft genome sequences for any organism of choice. Because of the cost and considerable effort involved in such an endeavour, the important first step is to thoroughly consider whether a genome sequence is necessary for addressing the biological question at hand. Once this decision is taken, a genome project requires careful planning with respect to the organism involved and the intended quality of the genome draft.

The Steps involved in this are Genome Sequencing, Genome Assembly and Genome annotation. We will discuss these in detail ahead.

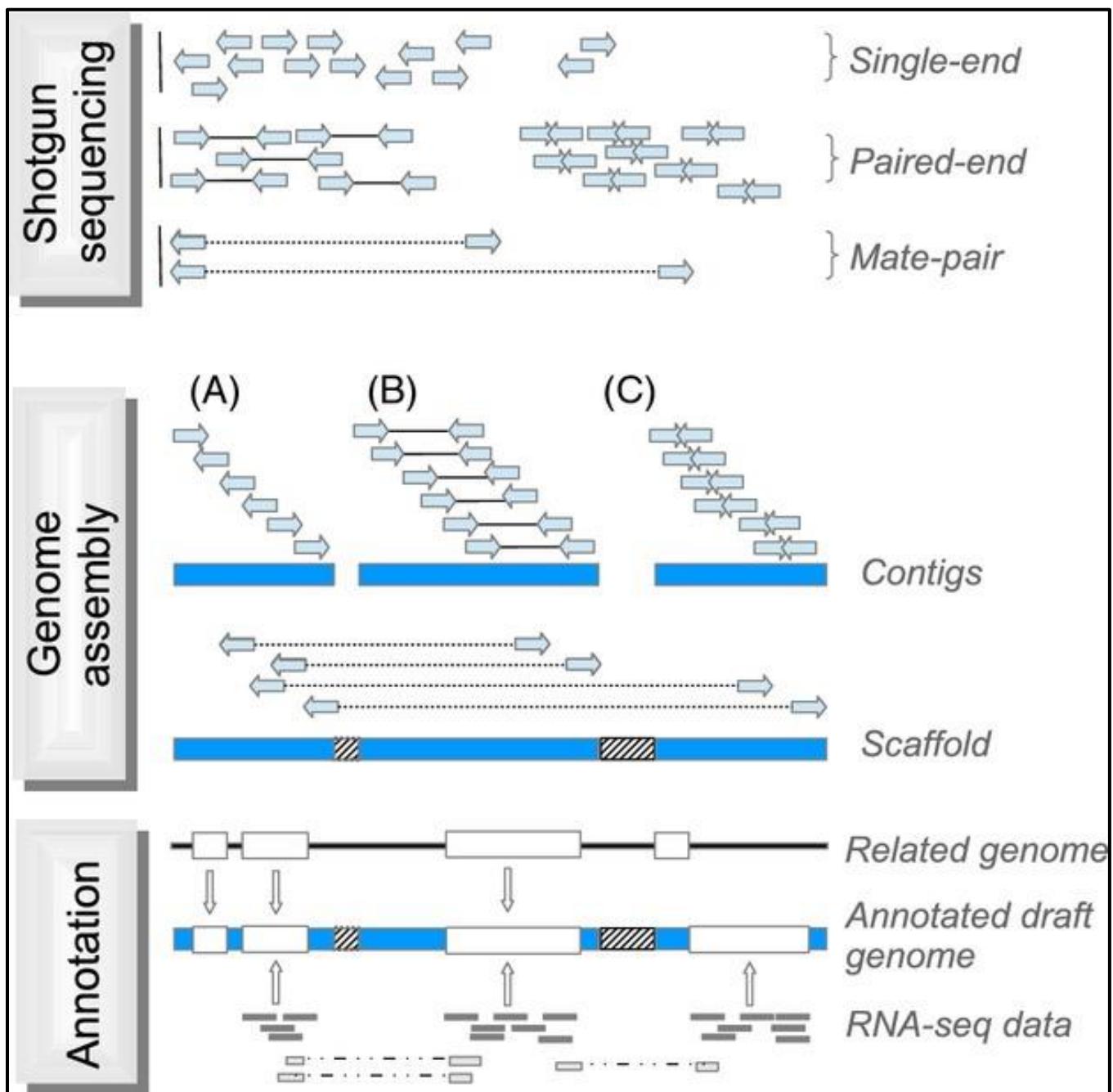
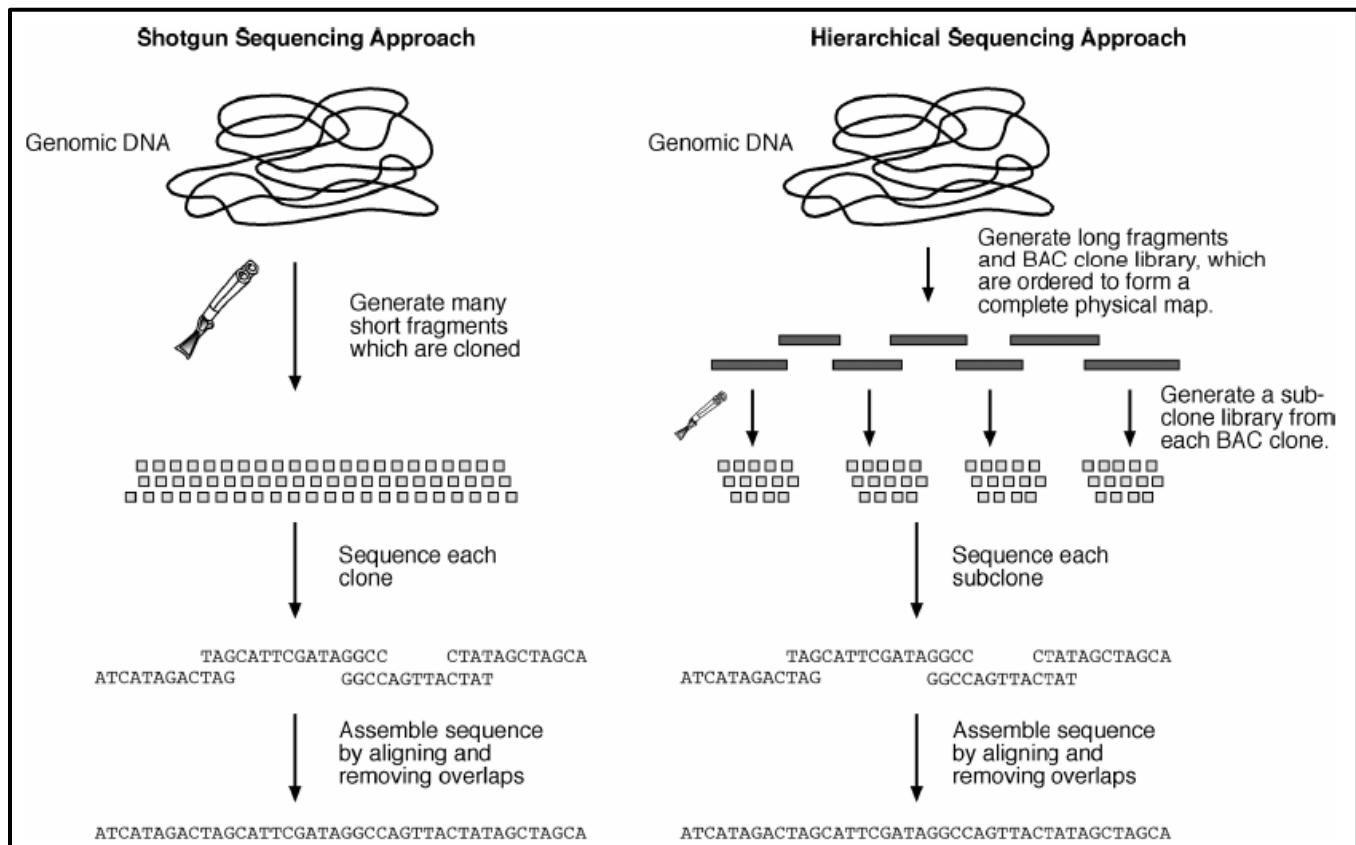


Fig1. Simplified illustration of the assembly process

### GENOME SEQUENCING:

- The highest resolution genome map is the genomic DNA sequence that can be considered as a type of physical map describing a genome at the single base-pair level.
- DNA sequencing is now routinely carried out using the Sanger method. This involves the use of DNA polymerases to synthesize DNA chains of varying lengths.
- There are two major strategies for whole genome sequencing:
  - Shotgun approach
    - The shotgun approach randomly sequences clones from both ends of cloned DNA. This approach generates a large number of sequenced DNA fragments.

- The number of random fragments has to be very large, so large that the DNA fragments overlap sufficiently to cover the entire genome.
  - This approach does not require knowledge of physical mapping of the clone fragments, but rather a robust computer assembly program to join the pieces of random fragments into a single, whole-genome sequence.
  - Generally, the genome has to be redundantly sequenced in such a way that the overall length of the fragments covers the entire genome multiple times.
  - This is designed to minimize sequencing errors and ensure correct assembly of a contiguous sequence.
  - Despite the multiple coverage, sometimes certain genomic regions remain unsequenced, mainly owing to cloning difficulties.
  - In such cases, the remainder gap sequences can be obtained through extending sequences from regions of known genomic sequences using a more traditional PCR technique, which requires the use of custom primers and performs genome walking in a stepwise fashion.
- Hierarchical approach
    - The hierarchical genome sequencing approach is similar to the shotgun approach, but on a smaller scale.
    - The chromosomes are initially mapped using the physical mapping strategy. Longer fragments of genomic DNA (100 to 300 kB) are obtained and cloned into a high-capacity bacterial vector called bacterial artificial chromosome (BAC).
    - Based on the results of physical mapping, the locations and orders of the BAC clones on a chromosome can be determined.
    - By successively sequencing adjacent BAC clone fragments, the entire genome can be covered. The complete sequence of each individual BAC clone can be obtained using the shotgun approach.
    - Overlapping BAC clones are subsequently assembled into an entire genome sequence.



**Fig2. Differences between Shotgun sequencing and hierarchical sequencing**

## GENOME ASSEMBLY:

- As described, initial DNA sequencing reactions generate short sequence reads from DNA clones. The average length of the reads is about 500 bases.
- To assemble a whole genome sequence, these short fragments are joined to form larger fragments after removing overlaps.
- These longer, merged sequences are termed contigs, which are usually 5,000 to 10,000 bases long. A number of overlapping contigs can be further merged to form scaffolds (30,000–50,000 bases, also called super contigs), which are unidirectionally oriented along a physical map of a chromosome.
- Overlapping scaffolds are then connected to create the final highest resolution map of the genome.
- Correct identification of overlaps and assembly of the sequence reads into contigs are like joining jigsaw puzzles, which can be very computationally intensive when dealing with data at the whole-genome level.
- The major challenges in genome assembly are sequence errors, contamination by bacterial vectors, and repetitive sequence regions. Sequence errors can often be corrected by drawing a consensus from an alignment of multiple overlapping sequences.
- Bacterial vector sequences can be removed using filtering programs prior to assembly. To overcome the problem of sequence repeats, programs such as RepeatMasker can be used to detect and mask repeats. Additional constraints on the sequence reads can be applied to avoid misassembly caused by repeat sequences.

- A commonly used constraint to avoid errors caused by sequence repeats is the so-called forward–reverse constraint.
- When a sequence is generated from both ends of a single clone, the distance between the two opposing fragments of a clone is fixed to a certain range, meaning that they are always separated by a distance defined by a clone length (normally 1,000 to 9,000 bases).
- When the constraint is applied, even when one of the fragments has a perfect match with a repetitive element outside the range, it is not able to be moved to that location to cause miss assembly.
- The first step toward genome assembly is to derive base calls and assign associated quality scores. The next step is to assemble the sequence reads into contiguous sequences.
- This step includes identifying overlaps between sequence fragments, assigning the order of the fragments and deriving a consensus of an overall sequence. Assembling all shotgun fragments into a full genome is a computationally very challenging step.
- There are a variety of programs available for processing the raw sequence data.
- The following is a selection of base calling and assembly programs commonly used in genome sequencing projects:
  - **Phred** (<https://www.phrap.org/>) is a UNIX program for base calling. It uses a Fourier analysis to resolve fluorescence traces and predict actual peak locations of bases
  - **Phrap** (<https://www.phrap.org/>) is a UNIX program for sequence assembly. It takes Phred base-call files with quality scores as input and aligns individual fragments in a pairwise fashion using the Smith–Waterman algorithm.
  - **VecScreen** (<https://www.ncbi.nlm.nih.gov/VecScreen/VecScreen.html>) is a web-based program that helps detect contaminating bacterial vector sequences.
  - **TIGR Assembler** (<https://www.tigr.org/>) is a UNIX program from TIGR for assembly of large shotgun sequence fragments. It treats the sequence input as clean reads without consideration of the sequence quality.
  - **ARACHNE** (<https://www.genome.wi.mit.edu/wga/>) is a free UNIX program for the assembly of whole-genome shotgun reads. Its unique features include using a heuristic approach similar to FASTA to align overlapping fragments, evaluating alignments using statistical scores, correcting sequencing errors based on multiple sequence alignment, and using forward–reverse constraints.
  - **EULER** (<http://nbcr.sdsc.edu/euler/>) is an assembly algorithm that uses a Eulerian Superpath approach, which is a polynomial algorithm for solving puzzles such as the famous “traveling salesman problem”: finding the shortest path of visiting a given number of cities exactly once and returning to the starting point.

## GENE ANNOTATION

- Before the assembled sequence is deposited into a database, it has to be analyzed for useful biological features. The genome annotation process provides comments for the features.
- This involves two steps:
  - Gene prediction.
  - Functional assignment.
- As a real-world example, gene annotation of the human genome employs a combination of theoretical prediction and experimental verification.
- Gene structures are first predicted by ab initio exon prediction programs such as GenScan or FgenesH.

- The predictions are verified by BLAST searches against a sequence database. The predicted genes are further compared with experimentally determined cDNA and EST sequences using the pairwise alignment programs such as GeneWise, Spidey, SIM4, and EST2Genome.
- All predictions are manually checked by human curators. Once open reading frames are determined, functional assignment of the encoded proteins is carried out by homology searching using BLAST searches against a protein database.
- Further functional descriptions are added by searching protein motif and domain databases such as Pfam and InterPro as well as by relying on published literature.

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