

VarMod

Variant Modeller

Modelling functional effects of non-synonymous variants

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Submission Details

Email: m.n.wass@kent.ac.uk

Unique
Submission identifier: vm53679ede56bbe

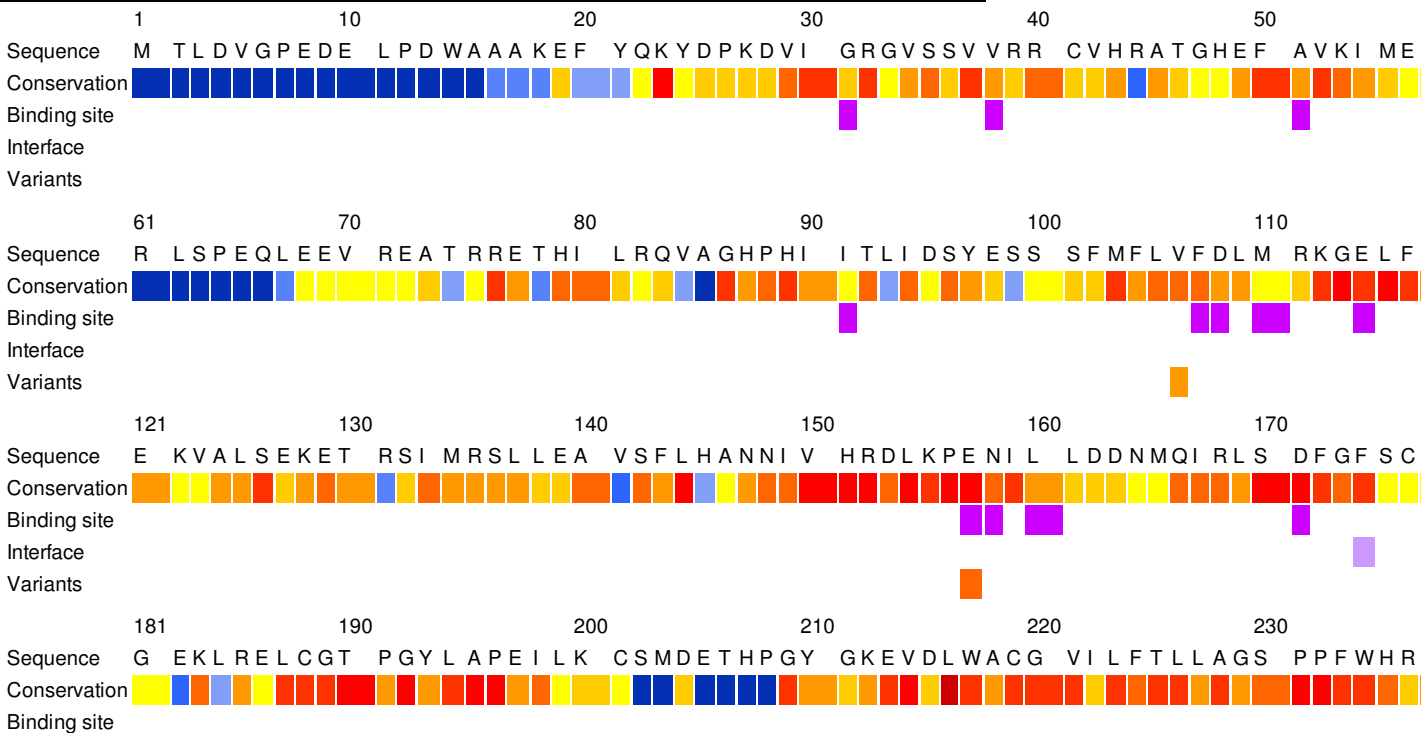
Description: P15735

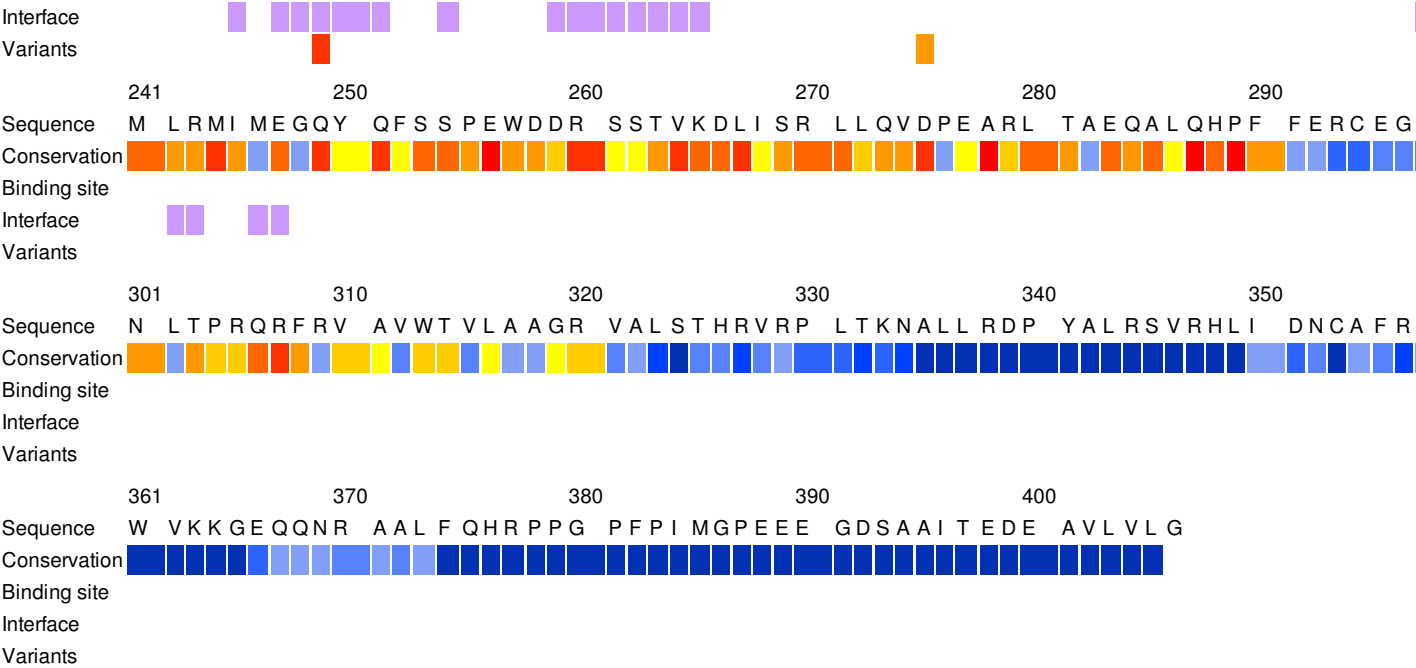
Uniprot
Accession: P15735

Query Seq: MTLDVGPEDELPDWAAAEFYQKYDPKDVIGRGVSSVVRRCVHRATGHEFAVKIMEVTAERLSPEQLEEV
REATRRETHILRQVAGHPHIITLDSYESSFMFLVFDLMRKGELFDYLTEKVALSEKETRSIMRSLLEA
VSFLHANNIVHRDLKPENILLDDNMQIRLSDFGFSCHLEPGEKLRCLGTPGYLAPEILKCSMDETHPGY
GKEVDLWACGVILFTLLAGSPPFWHRRQILMLRMIMEGQYQFSSPEWDDRSSTVKDLISRLQLQVDPEARL
TAEQALQHPFFERCEGSQPWNLTQRQFRVAVWTVLAAGRVALSTHRVRPLTKNALLRDPYALRSVRHLI
DNCAFRLYGHWVKKGEQQNRAALFQHRPPGPFPMGPPEEEGDSAAITEDEAVLVLG

The table below shows the machine learning VarMod prediction and a summary of the features used to make the prediction. They are colour coded to indicate how relevant each feature is likely to be when considering if the variant affects the protein function. The sections below provide detailed information relating to sequence conservation, ligand binding sites and protein-protein interactions. The structural data can be used to investigate the structural environment of the variants and consider how this may have an effect on protein function.

Variant	VarMod Probability	Interface	Binding site	Conservation	size	Charge	Func grp
V106E	0.693	0.448	0.002	0.630			
E157K	0.761	0.153	0.000	0.876			
G189K	0.800	0.000	0.305	0.771			
D215N	0.650	0.177	0.340	0.446			





Structural Templates

The details of the models generated for the protein are listed below. These include the structural templates used, the range of the protein sequence included and the variants present within each of the models

Model	Template	Sequence Range	Template probability	Variants present
1	2y7j_A	5-293	100	D215N, G189K, V106E, E157K Download model

In this section view the structural model and the ligand binding and interface sites. The jmol viewer displays the model of the protein with these regions mapped onto the structure. The control panel on the right can be used to modify the display of the protein, and the residues - variants, binding sites and interfaces

Structural Model

generate PNG image to disk

A dialog will appear to enter a file name of your choice, please ensure it ends with '.png'

This functionality will differ depending on browser:

- Chrome: will save the file to downloads
- Safari will open the image in a new tab, right click on the image to save it

Display Controls

Protein Model

Variants

Predicted Binding Site Residues

Protein-Protein interface Residues

View

Below is a list interaction partners in uniprot with the query protein. Models of the complex of these interactions are available. Click the relevant identifier to view the model in relation to the variants. They will be displayed in a separate window

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