VarMod

Variant Modeller

Modelling functional effects of non-synonymous variants

Submission Details

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

Unique Submission identifier: vm53679eaef042c

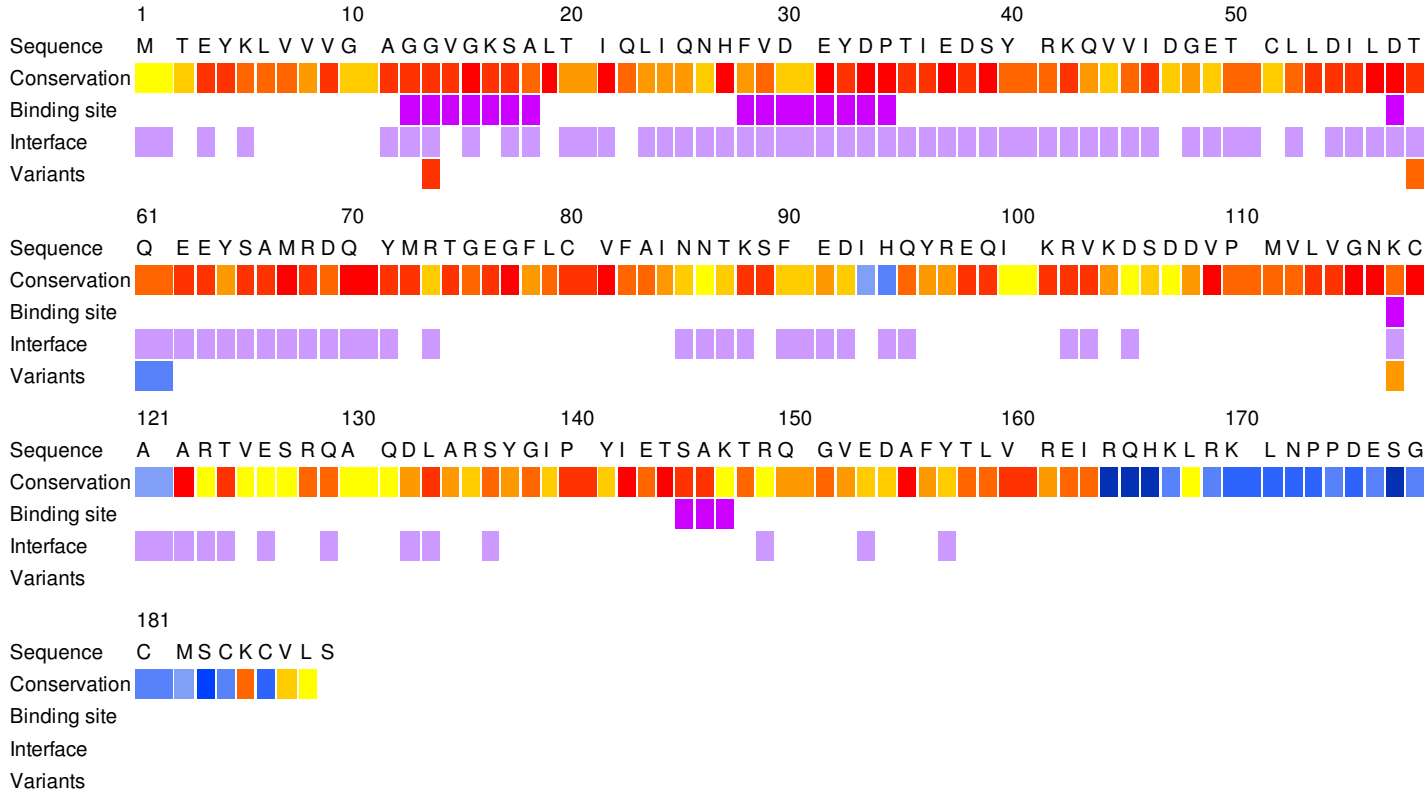
Description: RAS

Uniprot Accession: P01112

Query Seq:
MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAGQEEYSAMRDQ
YMRTGEGFLCVFAINNTKSFEDIHQYREQIKRVKDSDDVPMVLVGNKCDLAARTVESRQAQDLARSYGIP
YIETSAKTRQGVEDAFYTLVREIRQHKLRKLNPPDESGPGCMSCKCVLS

The table below shows the machine learning VarMod prediction and a summary of the features used to make the predictionThey are colour coded to indicate how relevant each feature is likely to be when considering if the variant affects the protein functionThe 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 mayhave an effect on protein function.

Variant	VarMod Probability	Interface	Binding site	Conservation	size	Charge	Func grp
G13R	0.819	0.000	0.000	0.763			
T58I	0.764	0.000	0.000	0.767			
Q61K	0.378	0.000	0.147	0.688			
K117R	0.692	0.000	0.000	0.633			



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 includedand the variants present within each of the models

Model	Template	Sequence Range	Template probability	Variants present	
1	2ce2_X	1-166	100	Q61K, K117R, G13R, T58I	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

Q9NZL6 P21359 P11233 O15211
P04049 Q9NS23 P15056 P10398
P20936 P01112 Q12967 Q07889
Q8WWW0 Q07890 Q9P212 P48736