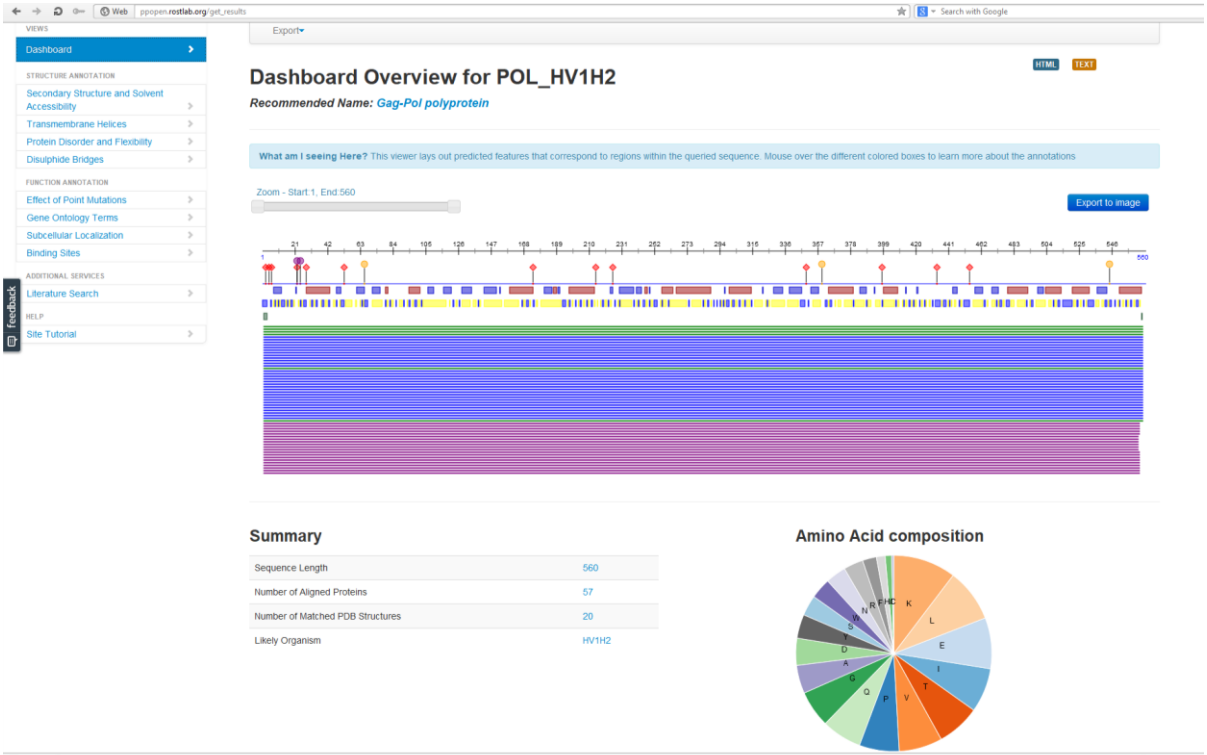
Dashboard
Secondary Structure and Solvent Accessibility
Transmembrane Helices
Protein Disorder and Flexibility
Disulphide Bridges
Effect of Point Mutations
Gene Ontology Terms
Subcellular Localization
Binding Sites
Literature Search
Site Tutorial
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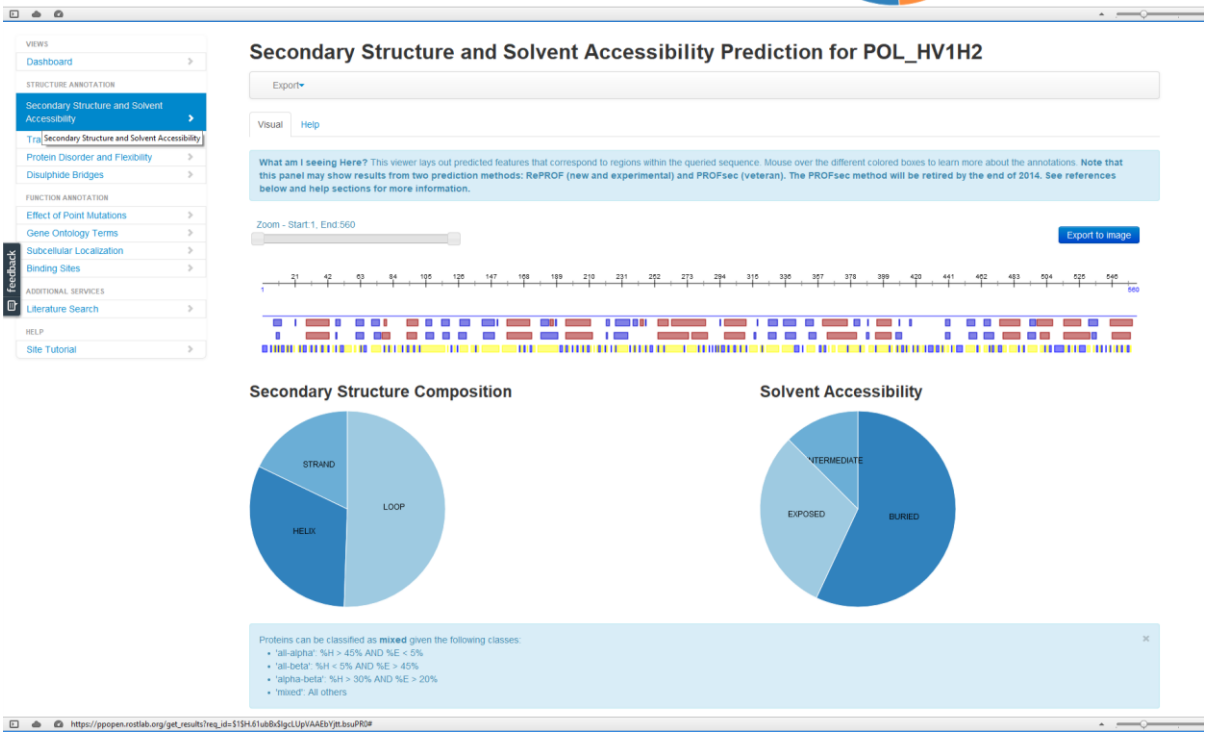
TEXT
Dashboard Overview for POL_HV1H2
Recommended Name: Gag-Pol polyprotein
What am I seeing Here? This viewer lays out predicted features that correspond to regions within the queried sequence. Mouse over the different colored boxes to learn more about the annotations
Zoom - Start:1, End:560
Export to image
Summary
Sequence Length 560
Number of Aligned Proteins 57
Number of Matched PDB Structures 20
Likely Organism HV1H2
Amino Acid composition


Secondary Structure and Solvent Accessibility Prediction for POL_HV1H2
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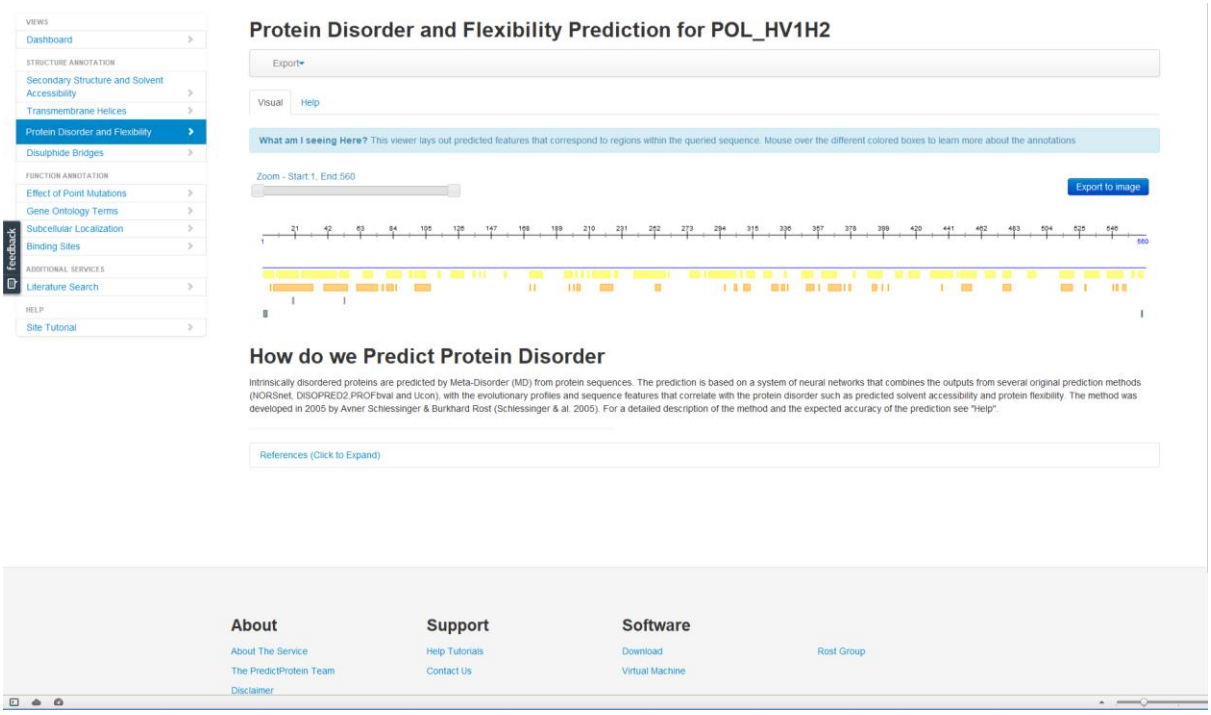
What am I seeing Here? This viewer lays out predicted features that correspond to regions within the queried sequence. Mouse over the different colored boxes to learn more about the annotations. Note that this panel may show results from two prediction methods: RePROF (new and experimental) and PROFsec (veteran). The PROFsec method will be retired by the end of 2014. See references below and help sections for more information.
Zoom - Start:1, End:560
Export to image
Secondary Structure Composition
STRAND
LOOP
HELIX
Solvent Accessibility
INTERMEDIATE
EXPOSED
BURIED
Proteins can be classified as mixed given the following classes:
'all-alpha': %H > 45% AND %E < 5%
'all-beta': %H < 5% AND %E > 45%
'alpha-beta': %H > 30% AND %E > 20%
'mixed': All others


VIEWS
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What am I seeing Here? This viewer lays out predicted features that correspond to regions within the queried sequence. Mouse over the different colored boxes to learn more about the annotations
Zoom - Start:1, End:560
Export to image
How do we Predict Protein Disorder
Intrinsically disordered proteins are predicted by Meta-Disorder (MD) from protein sequences. The prediction is based on a system of neural networks that combines the outputs from several original prediction methods (NORSnet, DISOPRED2,PROFbval and Ucon), with the evolutionary profiles and sequence features that correlate with the protein disorder such as predicted solvent accessibility and protein flexibility. The method was developed in 2005 by Avner Schlessinger & Burkhard Rost (Schlessinger & al. 2005). For a detailed description of the method and the expected accuracy of the prediction see "Help".
References (Click to Expand)

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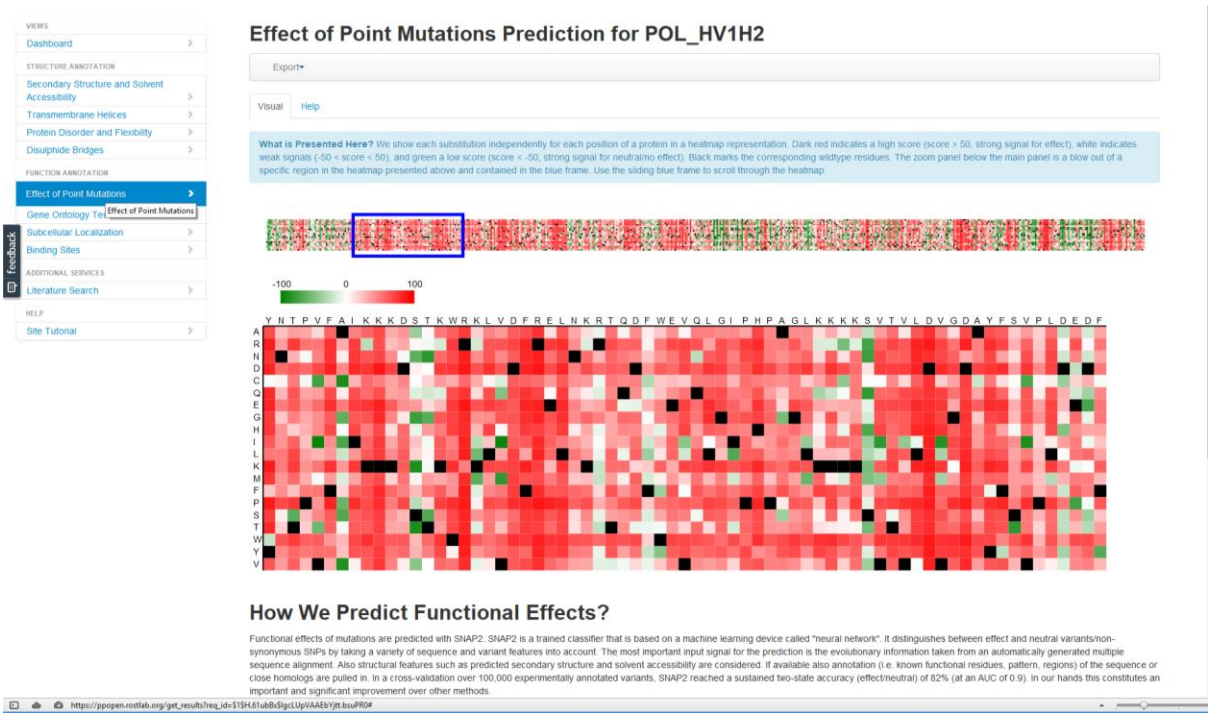
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What is Presented Here? We show each substitution independently for each position of a protein in a heatmap representation. Dark red indicates a high score (score > 50, strong signal for effect), white indicates weak signals (-50 < score < 50), and green a low score (score < -50, strong signal for neutral/no effect). Black marks the corresponding wildtype residues. The zoom panel below the main panel is a blow out of a specific region in the heatmap presented above and contained in the blue frame. Use the sliding blue frame to scroll through the heatmap.
-100
0
100
How We Predict Functional Effects?
Functional effects of mutations are predicted with SNAP2. SNAP2 is a trained classifier that is based on a machine learning device called "neural network". It distinguishes between effect and neutral variants/non-synonymous SNPs by taking a variety of sequence and variant features into account. The most important input signal for the prediction is the evolutionary information taken from an automatically generated multiple sequence alignment. Also structural features such as predicted secondary structure and solvent accessibility are considered. If available also annotation (i.e. known functional residues, pattern, regions) of the sequence or close homologs are pulled in. In a cross-validation over 100,000 experimentally annotated variants, SNAP2 reached a sustained two-state accuracy (effect/neutral) of 82% (at an AUC of 0.9). In our hands this constitutes an important and significant improvement over other methods.