**BDNF PREDICTION RESULTS**

1. **rs6265**

**MU PRO TOOL-**

Position: 66  
Original Amino Acid: V   
Substitute Amino Acid: M

Prediction Results:

1. Predicted both value and sign of energy change using SVM and sequence information only (Recommended)

detal delta G = -0.53414246 (DECREASE stability)

1. Prediction of the sign (direction) of energy change using SVM and neural network with a smaller sequence window

Method 1: Support Vector Machine, use sequence information only. Effect: INCREASE the stability of protein structure. Confidence Score: 0.46814845

Method 2: Neural Network, use sequence information only. Effect: INCREASE the stability of protein structure. Confidence Score: 0.6733155127013581

**I MUTANT TOOL-**

Position WT NEW DDG pH T

66 V M -0.49 7.0 25

WT: Amino Acid in Wild-Type Protein

NEW: New Amino Acid after Mutation

DDG: DG(NewProtein)-DG(WildType) in Kcal/mol

DDG<0: Decrease Stability

DDG>0: Increase Stability

T: Temperature in Celsius degrees

pH: -log[H+]

1. **rs1048218**

**MU PRO TOOL-**

Position: 75  
Original Amino Acid: Q  
Substitute Amino Acid: H  
  
**Prediction Results:**  
  
1. Predicted both value and sign of energy change using SVM and sequence information only (Recommended)  
  
detal delta G = -1.0011394 (DECREASE stability)  
  
2. Prediction of the sign (direction) of energy change using SVM and neural network with a smaller sequence window  
  
Method 1: Support Vector Machine, use sequence information only.  
Effect: DECREASE the stability of protein structure.  
Confidence Score: -0.89157392  
  
Method 2: Neural Network, use sequence information only.  
Effect: DECREASE the stability of protein structure.  
Confidence Score: -0.7873954620602

**I MUTANT TOOL-**

Position WT NEW DDG pH T

75 Q H -2.08 7.0 25

WT: Amino Acid in Wild-Type Protein

NEW: New Amino Acid after Mutation

DDG: DG(NewProtein)-DG(WildType) in Kcal/mol

DDG<0: Decrease Stability

DDG>0: Increase Stability

T: Temperature in Celsius degrees

pH: -log[H+]

1. **rs8192466**

**MU-PRO TOOL**

Position: 2  
Original Amino Acid: T  
Substitute Amino Acid: I  
  
**Prediction Results:**  
  
1. Predicted both value and sign of energy change using SVM and sequence information only (Recommended)  
  
detal delta G = 0.45217589 (INCREASE stability)  
  
2. Prediction of the sign (direction) of energy change using SVM and neural network with a smaller sequence window  
  
Method 1: Support Vector Machine, use sequence information only.  
Effect: INCREASE the stability of protein structure.  
Confidence Score: 0.85348803  
  
Method 2: Neural Network, use sequence information only.  
Effect: INCREASE the stability of protein structure.  
Confidence Score: 0.9813740091259998

Position: 2  
Original Amino Acid: T  
Substitute Amino Acid: N  
  
**Prediction Results:**  
  
1. Predicted both value and sign of energy change using SVM and sequence information only (Recommended)  
  
detal delta G = -0.72475555 (DECREASE stability)  
  
2. Prediction of the sign (direction) of energy change using SVM and neural network with a smaller sequence window  
  
Method 1: Support Vector Machine, use sequence information only.  
Effect: DECREASE the stability of protein structure.  
Confidence Score: -0.28739436  
  
Method 2: Neural Network, use sequence information only.  
Effect: DECREASE the stability of protein structure.  
Confidence Score: -0.772828284747498

**I MUTANT TOOL**

Position WT NEW DDG pH T

2 T I -0.23 7.0 25

WT: Amino Acid in Wild-Type Protein

NEW: New Amino Acid after Mutation

DDG: DG(NewProtein)-DG(WildType) in Kcal/mol

DDG<0: Decrease Stability

DDG>0: Increase Stability

T: Temperature in Celsius degrees

pH: -log[H+]

Position WT NEW DDG pH T

2 T N -0.82 7.0 25

WT: Amino Acid in Wild-Type Protein

NEW: New Amino Acid after Mutation

DDG: DG(NewProtein)-DG(WildType) in Kcal/mol

DDG<0: Decrease Stability

DDG>0: Increase Stability

T: Temperature in Celsius degrees

pH: -log[H+]