



documentation

Prediction disease causing - long InDel

Model: complex_aae, prob: 0.999999956067277 (explain)

Summary

- amino acid sequence changed
- known disease mutation at this position (HGMD: CM940998)
- protein features (might be) affected
- splice site changes

[hyperlink](#)[illegible]

2.382 0.981
5.04 1
1.163 1
2.789 1
1.957 0.959
-2.568 0.008
2.011 0.081
0.648 0.078
-2.768 0
2.124 0.972
5.713 0.981
-0.18 0.015
0.033 0.008
1.538 0.021
-1.487 0.001
3.48 0.944
0.417 0.498
0.021 0.346
1.925 0.34
-0.456 0.09
0.068 0.11
5.367 0.431
0.67 0.215
-0.733 0.056
1.454 0.089
0.663 0.088
0.436 0.088
0.272 0.092
1.714 0.115
0.136 0.023
1.428 0.027
0.34 0.019
-0.027 0.019
1.47 0.982
2.661 0.981
-0.553 0.789
1.502 0.916
3.082 0.928
-0.794 0.742
2.991 0.99
1.586 0.99
0.634 0.979
0.377 0.969
0.713 0.967
0.138 0.962
2.32 0.968
0.444 0.937
0.153 0.916
1.679 0.916
1.779 0.748
-0.84 0.016
0.565 0.018
1.626 0.021
-4.166 0
2.13 0.969
2.183 0.975
0.357 0.946
-0.977 0.023
1.912 0.074
-0.471 0.07
3.839 0.949
2.187 0.946
-0.147 0.754
0.336 0.778
3.949 0.936
-0.635 0.313
5.731 0.952
1.117 0.881
-0.088 0.002
-0.454 0
0.504 0
-1.855 0
5.657 0.92
1.618 0.886
0.338 0.471
1.015 0.361
-1.194 0.021
0.469 0.076
0.245 0.069
0.245 0.062
-0.42 0
-0.075 0
-1.331 0
-1.88 0
3.069 0.962
2.359 0.966
0.232 0.897
2.208 0.985
1.4 0.978
-0.468 0.926
3.87 1
3.414 1
1.136 0.994
1.999 0.967
-0.072 0.29
-0.003 0.271
0.643 0.301
1.893 0.324
0.353 0.24
2.043 0.292
1.607 0.276
0.068 0.051
0.417 0.021
0.343 0.007
-2.808 0
-0.174 0.001
0.162 0.015
0.041 0.081
2.1 0.925
2.404 0.953
0.779 0.939
0.917 0.918
1.072 0.859
-0.246 0.62
2.304 0.641

AA/aa: amino acid; CDS: coding sequence; mu: mutated; NMD: nonsense-mediated mRNA decay; nt: nucleotide; wt: wildtype; TGP: 1000 Genomes Project