AT1G09700.1

ATGACCTCCACTGATGTTTCCTCTGGTGTTTCCAATTGCTATGTTTTCAAAAGTCGGTTGCAGGAGTATGCTCAGAAGTACAAGCTCCCAACGCCTGTTTATGAGATCGTTAAAGAAGGCCCTTCACACAAATCTTTATTTCAATCGACTGTGATACTGGATGGTGTCAGATATAATTCTTTGCCTGGATTCTTCAATCGTAAGGCTGCAGAGCAATCAGCTGCCGAGGTTGCTCTCCGGGAATTAGCAAAATCCAGTGAGCTAAGCCAATGTGTTTCACAACCTGTTCACGAAACGGGATTATGCAAGAACCTACTTCAAGAATACGCTCAAAAGATGAATTACGCGATTCCATTGTATCAGTGCCAGAAGGTCGAAACTCTTGGGAGAGTTACACAATTCACATGTACTGTAGAGATTGGAGGCATAAAGTACACAG**G**AGCTGCAACAAGAACTAAAAAAGATGCTGAGATTAGCGCTGGGAGAACTGCTCTTTTAGCGATCCAGTCAGACACTAAAAACAACCTTGCCAACTACAACACTCAGCTTACTGTACTTCCTTGTGAGAAGAAGACAATACAGGCAGCTATCCCGCTTAAAGAAACCGTCAAGACTCTTAAAGCCAGGAAGGCTCAGTTCAAGAAGAAAGCTCAGAAAGGAAAACGCACAGTAGCTAAAAATCCTGAAGATATTATCATCCCTCCTCAACCTACTGATCATTGTCAAAACGATCAGTCAGAGAAAATTGAGACAACGCCAAATCTGGAACCTTCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAACCTCCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAACCTCCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAACCTTCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAACCTCCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAATCTTCTTCATGCATGAGCGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAAGCAAGCCACGCATAA

MTSTDVSSGVSNCYVFKSRLQEYAQKYKLPTPVYEIVKEGPSHKSLFQSTVILDGVRYNSLPGFFNRKAAEQSAAEVALRELAKSSELSQCVSQPVHETGLCKNLLQEYAQKMNYAIPLYQCQKVETLGRVTQFTCTVEIGGIKYT**G**AATRTKKDAEISAGRTALLAIQSDTKNNLANYNTQLTVLPCEKKTIQAAIPLKETVKTLKARKAQFKKKAQKGKRTVAKNPEDIIIPPQPTDHCQNDQSEKIETTPNLEPSSCMNGLKEAAFGSVETEKIETTPNLEPPSCMNGLKEAAFGSVETEKIETTPNLEPPSCMNGLKEAAFGSVETEKIETTPNLEPSSCMNGLKEAAFGSVETEKIETTPNLEPPSCMNGLKEAAFGSVETEKIETTPNLESSSCMSGLKEAAFGSVETEASHA-

Mutations = GtoA at position 440

ATGACCTCCACTGATGTTTCCTCTGGTGTTTCCAATTGCTATGTTTTCAAAAGTCGGTTGCAGGAGTATGCTCAGAAGTACAAGCTCCCAACGCCTGTTTATGAGATCGTTAAAGAAGGCCCTTCACACAAATCTTTATTTCAATCGACTGTGATACTGGATGGTGTCAGATATAATTCTTTGCCTGGATTCTTCAATCGTAAGGCTGCAGAGCAATCAGCTGCCGAGGTTGCTCTCCGGGAATTAGCAAAATCCAGTGAGCTAAGCCAATGTGTTTCACAACCTGTTCACGAAACGGGATTATGCAAGAACCTACTTCAAGAATACGCTCAAAAGATGAATTACGCGATTCCATTGTATCAGTGCCAGAAGGTCGAAACTCTTGGGAGAGTTACACAATTCACATGTACTGTAGAGATTGGAGGCATAAAGTACACAG**A**AGCTGCAACAAGAACTAAAAAAGATGCTGAGATTAGCGCTGGGAGAACTGCTCTTTTAGCGATCCAGTCAGACACTAAAAACAACCTTGCCAACTACAACACTCAGCTTACTGTACTTCCTTGTGAGAAGAAGACAATACAGGCAGCTATCCCGCTTAAAGAAACCGTCAAGACTCTTAAAGCCAGGAAGGCTCAGTTCAAGAAGAAAGCTCAGAAAGGAAAACGCACAGTAGCTAAAAATCCTGAAGATATTATCATCCCTCCTCAACCTACTGATCATTGTCAAAACGATCAGTCAGAGAAAATTGAGACAACGCCAAATCTGGAACCTTCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAACCTCCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAACCTCCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAACCTTCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAACCTCCTTCATGCATGAACGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAGAAAATTGAGACAACGCCAAATCTGGAATCTTCTTCATGCATGAGCGGGTTAAAGGAGGCAGCATTTGGGAGTGTGGAGACAGAAGCAAGCCACGCATAA

MTSTDVSSGVSNCYVFKSRLQEYAQKYKLPTPVYEIVKEGPSHKSLFQSTVILDGVRYNSLPGFFNRKAAEQSAAEVALRELAKSSELSQCVSQPVHETGLCKNLLQEYAQKMNYAIPLYQCQKVETLGRVTQFTCTVEIGGIKYT**E**AATRTKKDAEISAGRTALLAIQSDTKNNLANYNTQLTVLPCEKKTIQAAIPLKETVKTLKARKAQFKKKAQKGKRTVAKNPEDIIIPPQPTDHCQNDQSEKIETTPNLEPSSCMNGLKEAAFGSVETEKIETTPNLEPPSCMNGLKEAAFGSVETEKIETTPNLEPPSCMNGLKEAAFGSVETEKIETTPNLEPSSCMNGLKEAAFGSVETEKIETTPNLEPPSCMNGLKEAAFGSVETEKIETTPNLESSSCMSGLKEAAFGSVETEASHA-

EXPASY: reading frame = 5’3’ frame 1

G to E at amino acid **147** (419 AA total)

Pfam:

double-stranded RNA binding domain is from amino acids 101 - 170

Alphafold for AT1G09700.1 nope

AT1G09700. Nope

Arabidopsis HYL1 = yes

https://alphafold.ebi.ac.uk/entry/A0A178W466

Residue 147 G147E

Is this in a region with a high level of model confidence?

Yes, very high

Is this in a region with a predicted secondary structure? If so, what type?

Kind of the end of a beta sheet.

What is approximate predicted aligned error (PAE)? Between 0 and 5 angstroms (maybe skip this one). Although it does demonstrate 147 is within a predicted well-folded region.

<https://alphafold.ebi.ac.uk/entry/O04492> H bond to Cys 136.

DynaMut - <https://biosig.lab.uq.edu.au/dynamut/results_prediction/169690416508>

DynaMut results: <https://biosig.lab.uq.edu.au/dynamut/results_prediction/169690416508>

Not really that useful for me.

Pfam:

https://www.ebi.ac.uk/interpro/result/InterProScan/iprscan5-R20231010-052651-0946-25848996-p1m/

dsRBD domain, 15-84 and 101-170;

HYL1 –

Interesting structure from alphafold.

Residues 256 - 419. Low confidence, but very regular. Not listed as anything in Pfam

Higher confidence domain from 11 – 90, (pfam: 15 -84 is dsRBD)

and from 99 – 176 (pfam: dsRBD)

mutation = G147E

Score is very high: 92.6

H bond to Cys 146;

Looks like part of a beta sheet adjacent to an alpha helix