AT4G21670.1

CPL1

ATGTATAGTAATAATAGAGTAGAAGTGTTTCATGGTGATGGAAGACTTGGAGAATTGGAGATATACCCTTCAAGGGAATTGAATCAGCAACAAGATGATGTGATGAAGCAGAGGAAGAAGAAACAGAGGGAAGTAATGGAGCTAGCCAAGATGGGAATCAGAATAAGCCACTTTTCTCAATCTGGCGAGAGGTGTCCTCCTCTTGCAATACTTACTACAATTTCATCTTGTGGCCTTTGTTTCAAATTAGAAGCTTCACCTTCTCCAGCTCAGGAGTCACTCAGTTTATTCTACTCGTCCTGTCTCAGGGACAACAAGACAGCAGTAATGCTCTTGGGTGGAGAAGAGCTCCATTTGGTTGCTATGTACTCGGAAAATATCAAGAATGACCGTCCTTGTTTCTGGGCATTTAGTGTTGCTCCTGGAATTTACGATTCCTGTCTTGTTATGTTGAATCTTAGATGTCTGGGTATTGTCTTTGATCTTGATGAAACCCTTGTAGTGGCGAATACCATGCGCTCATTTGAGGATAAGATTGACGGGTTTCAGCGGAGAATAAACAACGAGATGGACCCTCAACGCCTTGCCGTTATAGTGGCTGAGATGAAGCGTTATCAAGATGACAAAAATCTATTGAAGCAATATATTGAAAGTGACCAGGTTGTTGAAAACGGGGAGGTGATAAAGGTGCAATCTGAAATTGTTCCTGCCTTGTCTGACAACCATCAGCCTCTTGTTCGCCCTCTGATAAGGTTGCAAGAGAAGAATATTATTCTGACTCGCATTAACCCAATGATTCGTGATACAAGTGTTCTTGTGAGAATGAGGCCCTCATGGGAGGAACTTCGAAGCTATTTGACAGCAAAAGGGCGTAAGCGTTTTGAAGTATATGTTTGCACGATGGCTGAAAGAGATTACGCCTTAGAGATGTGGAGGCTCCTTGATCCAGAAGGGAATTTGATAAACACAAATGACTTGCTTGCTCGCATCGTTTGTGTGAAATCTGGTTTTAAAAAGTCACTGTTCAATGTGTTTCTCGATGGAACCTGCCATCCAAAGATGGCATTGGTAATTGATGATCGATTGAAAGTTTGGGATGAGAAGGATCAGCCGAGGGTACATGTGGTTCCTGCATTCGCTCCCTATTATTCTCCTCAAGCTGAAGCTGCTGCAACACCAGTACTATGTGTTGCCAGGAACGTTGCCTGTGGTGTCAGAGGTGGATTTTTCAGGGATTTTGATGATAGTCTGCTACCAAGGATTGCTGAAATTTCTTATGAGAATGATGCTGAGGATATTCCTTCTCCGCCTGATGTCAGCCATTATTTGGTGTCGGAGGATGATACATCGGGTTTAAATGGGAACAAAGATCCACTTTCCTTTGACGGGATGGCTGATACTGAAGTGGAGAGAAGACTGAAGGAGGCAATTTCTGCATCTTCAGCTGTCCTTCCGGCGGCAAATATAGATCCGAGGATAGCTGCTCCCGTTCAGTTCCCCATGGCTTCTGCTTCTTCTGTTTCAGTTCCAGTACCAGTACAAGTCGTGCAACAAGCAATACAACCTTCAGCTATGGCCTTTCCAAGTATTCCATTTCAACAACCTCAACAACCGACATCAATAGCTAAACACTTGGTTCCTTCAGAACCAAGCTTGCAGAGTTCTCCTGCTAGAGAGGAAGGTGAGGTACCTGAATCAGAATTAGATCCAGATACTAGGAGGAGACTCCTCATATTGCAGCATGGACAAGATACTAGGGATCCTGCTCCAAGTGAACCTTCATTTCCTCAGAGACCTCCAGTTCAAGCTCCACCCTCACATGTGCAATCAAGAAATGGCTGGTTTCCTGTTGAGGAGGAGATGGATCCTGCTCAAATTCGTCGAGCAGTCTCAAAAGAATATCCGTTGGATTCTGAAATGATTCATATGGAAAAGCACAGGCCTCGTCATCCATCATTTTTTTCTAAGATTGATAACTCAACTCAGTCTGACAGGATGCTTCATGAGAATCGCAGGCCGCCAAAGGAGTCTCTCCGGAGAGATGAACAGTTACGTTCAAATAACAATCTACCTGACTCTCATCCTTTCTATGGGGAGGATGCGTCTTGGAATCAATCTTCCTCTAGGAACAGTGATCTTGACTTCCTACCTGAACGAAGTGTCTCAGCAACGGAGACTTCAGCTGATGTTCTACACGGAATTGCTATCAAATGTGGAGCTAAGGTGGAGTACAAACCAAGTTTAGTTTCTAGTACAGATTTGCGGTTCTCTGTTGAGGCTTGGCTTTCTAATCAAAAAATTGGAGAAGGGATTGGCAAATCGAGAAGAGAAGCCCTGCATAAGGCTGCTGAAGCTTCTATACAGAATTTAGCTGATGGATATATGCGTGCAAATGGTGACCCAGGGCCCAGCCACAGAGATGCTACCCCCTTCACCAATGAAAATATAAGTATGGGAAACGCAAATGCGCTTAATAATCAGCCATTTGCTAGAGATGAAACAGCGTTGCCAGTTTCTTCTAGACCTACAGATCCGAGATTAGAAGGTTCTATGAGGCACACTGGCTCCATTACTGCACTCAGGGAATTGTGTGCATCGGAGGGTCTTGAGATGGCTTTTCAATCTCAGCGTCAGCTTCCATCTGACATGGTCCACAGAGATGAATTACATGCTCAGGTTGAAATAGATGGGCGTGTTGTAGGGGAAGGAGTTGGATCGACATGGGACGAAGCTAGAATGCAGGCTGCTGAGAGAGCACTGTCCAGTGTGAGATCAATGCTTGGTCAACCTCTGCATAAACGACAAGGATCTCCACGATCATTTGGTGGGATGTCAAACAAGCGATTAAAGCCGGACTTTCAACGGTCTCTGCAACGGATGCCATCTTCGGGAAGATACTCTTAA

MYSNNRVEVFHGDGRLGELEIYPSRELNQQQDDVMKQRKKKQREVMELAKMGIRISHFSQSGERCPPLAILTTISSCGLCFKLEASPSPAQESLSLFYSSCLRDNKTAVMLLGGEELHLVAMYSENIKNDRPCF**W**AFSVAPGIYDSCLVMLNLRCLGIVFDLDETLVVANTMRSFEDKIDGFQRRINNEMDPQRLAVIVAEMKRYQDDKNLLKQYIESDQVVENGEVIKVQSEIVPALSDNHQPLVRPLIRLQEKNIILTRINPMIRDTSVLVRMRPSWEELRSYLTAKGRKRFEVYVCTMAERDYALEMWRLLDPEGNLINTNDLLARIVCVKSGFKKSLFNVFLDGTCHPKMALVIDDRLKVWDEKDQPRVHVVPAFAPYYSPQAEAAATPVLCVARNVACGVRGGFFRDFDDSLLPRIAEISYENDAEDIPSPPDVSHYLVSEDDTSGLNGNKDPLSF**D**GMADTEVERRLKEAISASSAVLPAANIDPRIAAPVQFPMASASSVSVPVPVQVVQQAIQPSAMAFPSIPFQQPQQPTSIAKHLVPSEPSLQSSPAREEGEVPESELDPDTRRRLLILQHGQDTRDPAPSEPSFPQRPPVQAPPSHVQSRNGWFPVEEEMDPAQIRRAVSKEYPLDSEMIHMEKHRPRHPSFFSKIDNSTQSDRMLHENRRPPKESLRRDEQLRSNNNLPDSHPFYGEDASWNQSSSRNSDLDFLPERSVSATETSADVLHGIAIKCGAKVEYKPSLVSSTDLRFSVEAWLSNQKIGEGIGKSRREALHKAAEASIQNLADGYMRANGDPGPSHRDATPFTNENISMGNANALNNQPFARDETALPVSSRPTDPRLEGSMRHTGSITALRELCASEGLEMAFQSQRQLPSDMVHRDELHAQVEIDGRVVGEGVGSTWDEARMQAAERALSSVRSMLGQPLHKRQGSPRSFGGMSNKRLKPDFQRSLQRMPSSGRYS

EMS07 - G405A, or W135\*

EMS07 – G1384A, or D462N

EMS02 – C905T, or A302V (this is cpl1-7)

(over 900 AA long)

Pfam:

135 – nothing (but, stop codon).

302 – FCP1 homology domain, 151 - 401

462 - nothing

(Also has two double-stranded RNA binding domains at C terminus)

W135 – very high confidence; beta sheet. H bond to Val120;

D462 – very low confidence; a bend in structure. H bond to Met464, Ser460,

A302V – very high confidence; a bend in structure. H bond to Cys332, Thr300,

Maybe ask them to examine this structure and rank the likelihood that the three mutations would result in a change in protein function that could explain the mutant phenotypes. Could also ask them to describe how to test whether same gene causes phenotype in EMS07 and EMS02.

Pfam

https://www.ebi.ac.uk/interpro/result/InterProScan/#table

FCP1 domain, 151 – 401; dsRNA binding domains, 727 – 792 and 855 – 925