SUPPLEMENTARY DATA

PITRM1 interaction studies with amyloidogenic nonapeptide mutants of familial Alzheimer's disease

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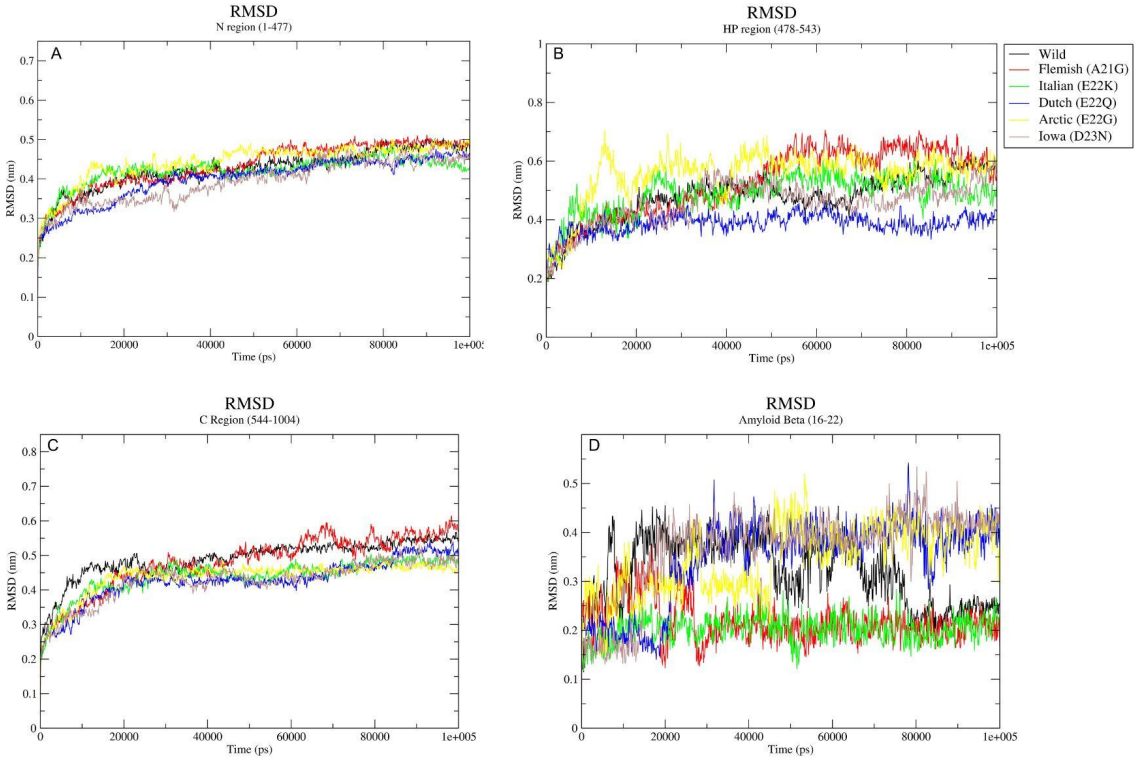

Figure S1: RMSD of 6 complex for a period of 100 ns. Black for native amyloid beta-PITRM complex, Green for Italian amyloid beta-PITRM complex, Blue for Dutch amyloid beta-PITRM complex, Yellow for Arctic amyloid beta-PITRM complex, Red for Flemish amyloid beta-PITRM complex and Brown for Iowa amyloid beta-PITRM complex. (A) RMSD of PITRM1-N region during interaction with Nonapeptide. (B) RMSD of PITRM1-HP region during interaction with Nonapeptide. (C) RMSD of PITRM1-C region during interaction with Nonapeptide. (D) RMSD of Nonapeptide alone..

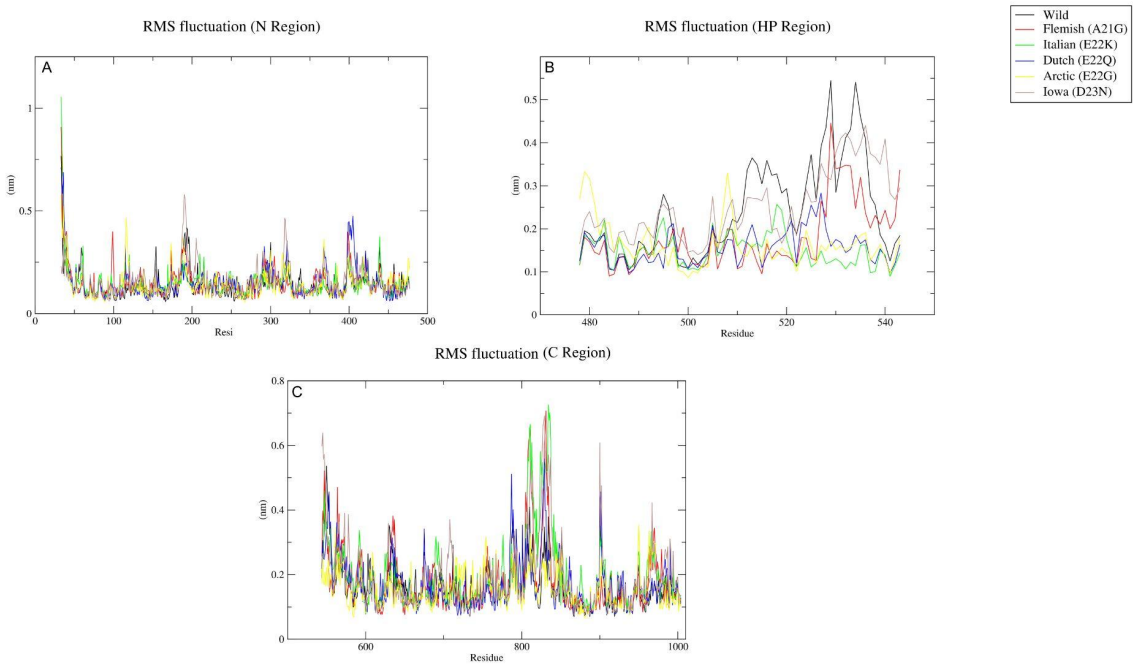

Figure S2: RMS fluctuations observed in PITRM1 during interaction with native and familial mutant amyloid beta (6 complex) for a period of 50 ns (last 50 ns of total 100ns). Black for native amyloid beta-PITRM complex, Green for Italian amyloid beta-PITRM complex, Blue for Dutch amyloid beta-PITRM complex, Yellow for Arctic amyloid beta-PITRM complex, Red for Flemish amyloid beta-PITRM complex and Brown for Iowa amyloid beta-PITRM complex. (A) RMS fluctuations of PITRM1-N region while interaction with amyloid beta. (B) RMS fluctuations of PITRM1-HP region while interaction with amyloid beta. (C) RMS fluctuations of PITRM1-C region while interaction with amyloid beta.

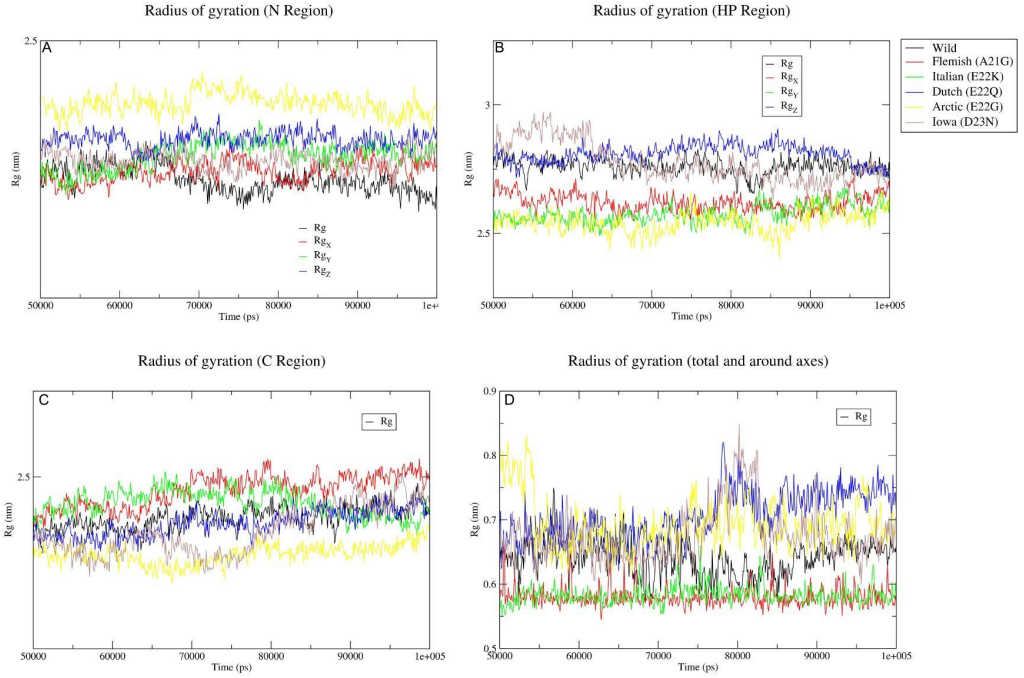

Figure S3: Radius of gyration observed in PITRM1 during interaction with native and familial mutant amyloid beta (6 complex) for a period of 50 ns (last 50 ns of total 100ns). Black for native amyloid beta-PITRM complex, Green for Italian amyloid beta-PITRM complex, Blue for Dutch amyloid beta-PITRM complex, Yellow for Arctic amyloid beta-PITRM complex, Red for Flemish amyloid beta-PITRM complex and Brown for Iowa amyloid beta-PITRM complex. (A) Radius of gyration of PITRM1-N region while interaction with amyloid beta. (B) Radius of gyration of PITRM1-HP region while interaction with amyloid beta. (C) Radius of gyration of PITRM1-C region while interaction with amyloid beta. (D) Radius of gyration of amyloid beta (native and familial mutants) while interaction with PITRM1.

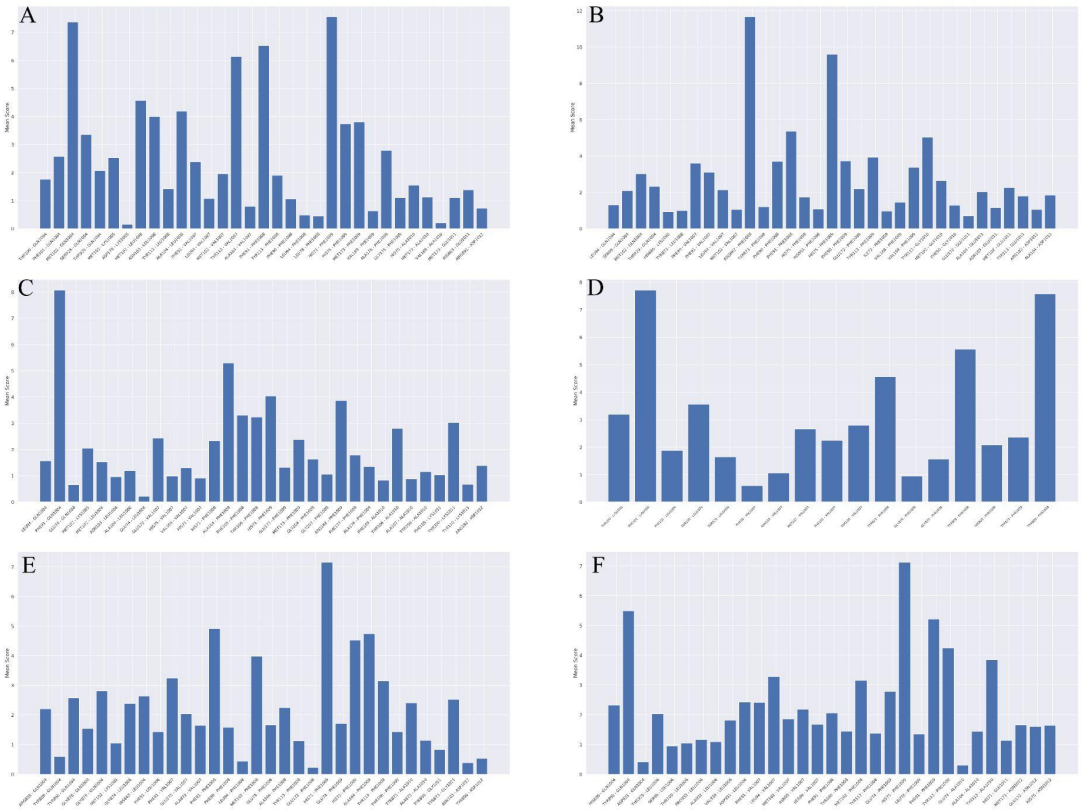

Figure S4:

Mean score of bond formation between PITRM1 and amyloid beta (wild and familial mutants) 6 complex for a period of 50 ns (last 50 ns of total 100ns).

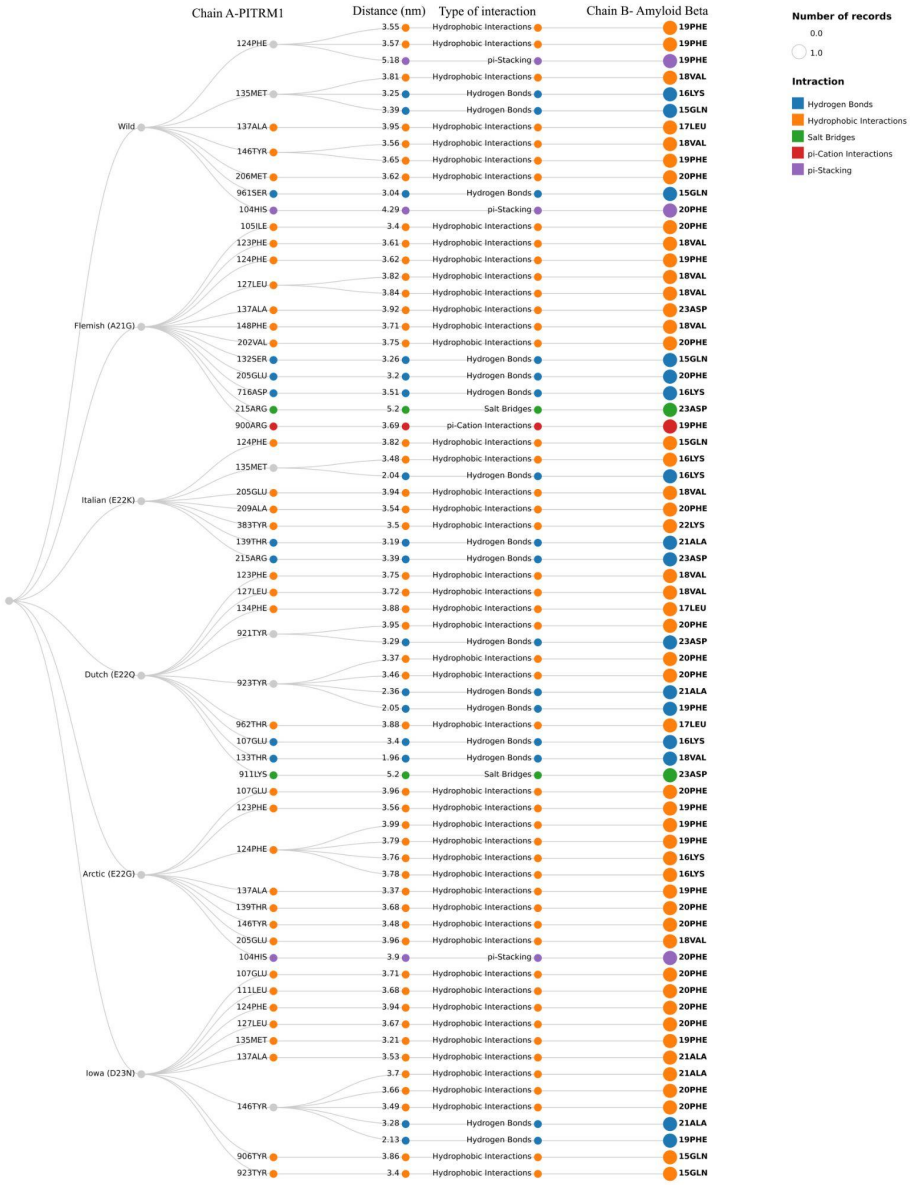

Figure S5: Distance and interaction between PITRM1 and amyloid beta of 6 MD simulated average complex.