

Supplementary File S

Analyzing Fourteen Deleterious nsSNPs of CFTR as a Promising Genetic Marker for Cancer Prognosis

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Table S1: nsSNPs data retrieved from Ensembl genome browser

Variant ID	Chr: bp	Alleles	AA	AA coord	sift_class	SIFT	polyphen_sort	polyphen_class	PolyPhen
rs1797976959	7:117480099	A/C	Q/P	2	deleterious - low confidence	0	767	possibly damaging	0.766
rs1052894635	7:117480102	G/T	R/M	3	deleterious - low confidence	0	472	possibly damaging	0.471
rs775329266	7:117480104	T/G	S/A	4	deleterious - low confidence	0.01	157	benign	0.156

rs397508173	7:117480105	C/A/T	S/L	4	deleterious - low confidence	0	16	benign	0.015
rs193922501	7:117480108	C/T	P/L	5	deleterious	0.01	997	probably damaging	0.996
rs1554373095	7:117480110	C/G	L/V	6	tolerated	1	2	benign	0.001
rs1327925872	7:117480111	T/G	L/R	6	tolerated	0.07	11	benign	0.01
rs121909045	7:117480113	G/C/T	E/Q	7	deleterious	0.03	489	possibly damaging	0.488
rs1204115625	7:117480117	A/G	K/R	8	tolerated	0.28	4	benign	0.003
rs949472192	7:117480120	C/T	A/V	9	deleterious	0.01	736	possibly damaging	0.735
rs762241850	7:117480123	G/A	S/N	10	tolerated	1	1	benign	0
rs1369001389	7:117480124	C/G/T	S/R	10	deleterious	0.02	112	benign	0.111
rs1800072	7:117480125	G/A/C	V/I	11	tolerated	0.13	1	benign	0
rs1800072	7:117480125	G/A/C	V/L	11	tolerated	0.21	1	benign	0
rs780188806	7:117480126	T/C	V/A	11	tolerated	0.1	1	benign	0
rs754221223	7:117480129	T/C	V/A	12	deleterious	0.03	8	benign	0.007
rs905181880	7:117480131	T/G	S/A	13	deleterious	0.02	991	probably damaging	0.99
rs397508635	7:117480132	C/A/T	S/Y	13	deleterious	0	1000	probably damaging	0.999
rs397508635	7:117480132	C/A/T	S/F	13	deleterious	0	1000	probably damaging	0.999
rs397508673	7:117480134	A/G/T	K/E	14	deleterious	0.02	2	benign	0.001
rs772774651	7:117480135	A/G/T	K/R	14	tolerated	0.58	2	benign	0.001
rs772774651	7:117480135	A/G/T	K/I	14	deleterious	0	100	benign	0.099
rs755405810	7:117480137	C/G/T	L/V	15	deleterious	0.02	31	benign	0.03
rs755405810	7:117480137	C/G/T	L/F	15	tolerated	0.35	2	benign	0.001

rs1562876459	7:117480138	T/C	L/P	15 deleterious	0	430 benign	0.429
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Table S2: The number of variants residing in different exons of CFTR

No. of Exons	Number of variants
1	29
2	47
3	54
4	113
5	41
6	76
7	41
8	105
9	36
10	76
11	103
12	58
13	58
14	220
15	34
16	6
17	114
18	43
19	61
20	101
21	45

	22	93
	23	68
.	24	32
	25	78
	26	36
	27	58

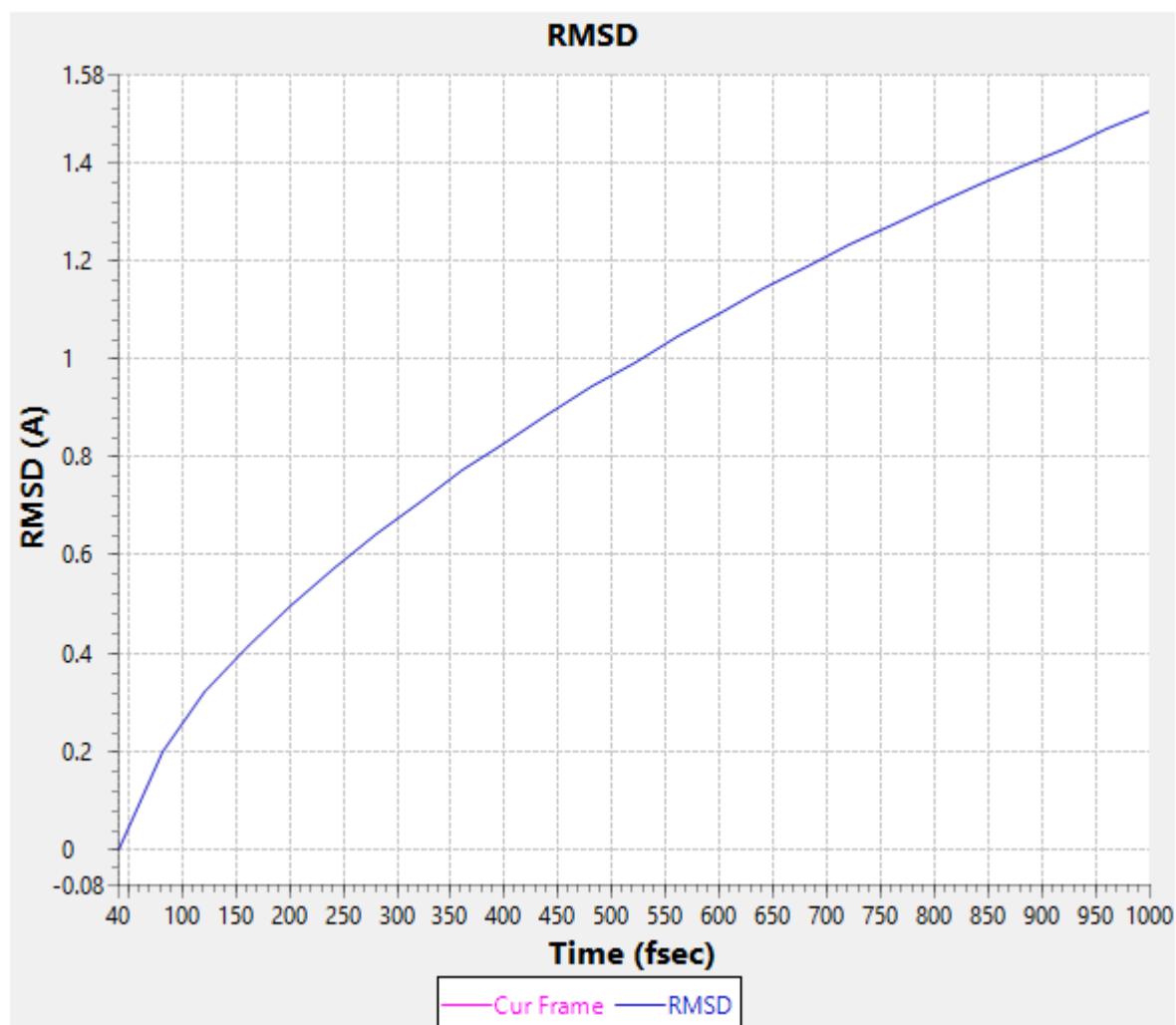


Figure S1a: RMSD plot for A9V

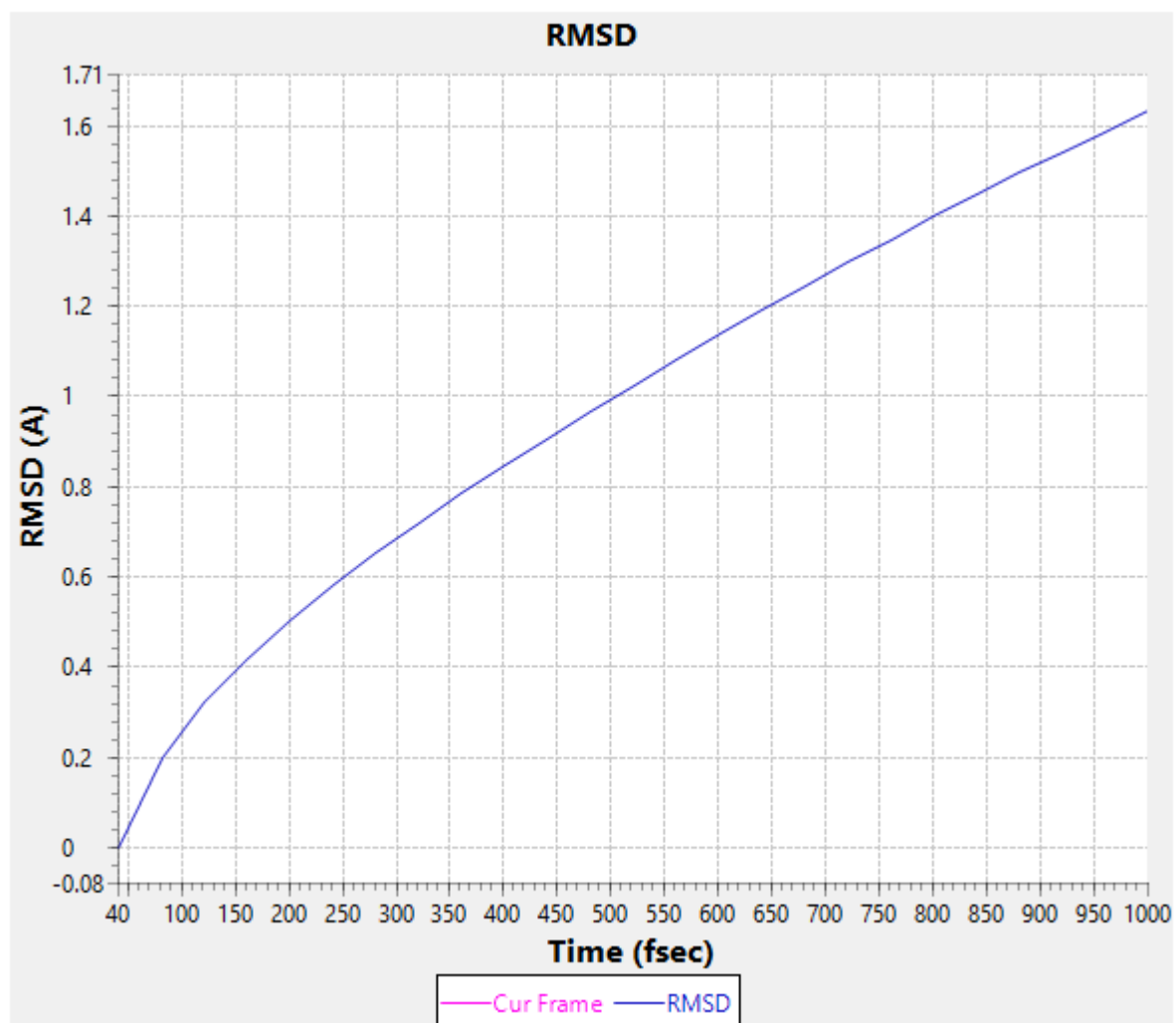


Figure S1b: RMSD plot for Q372R

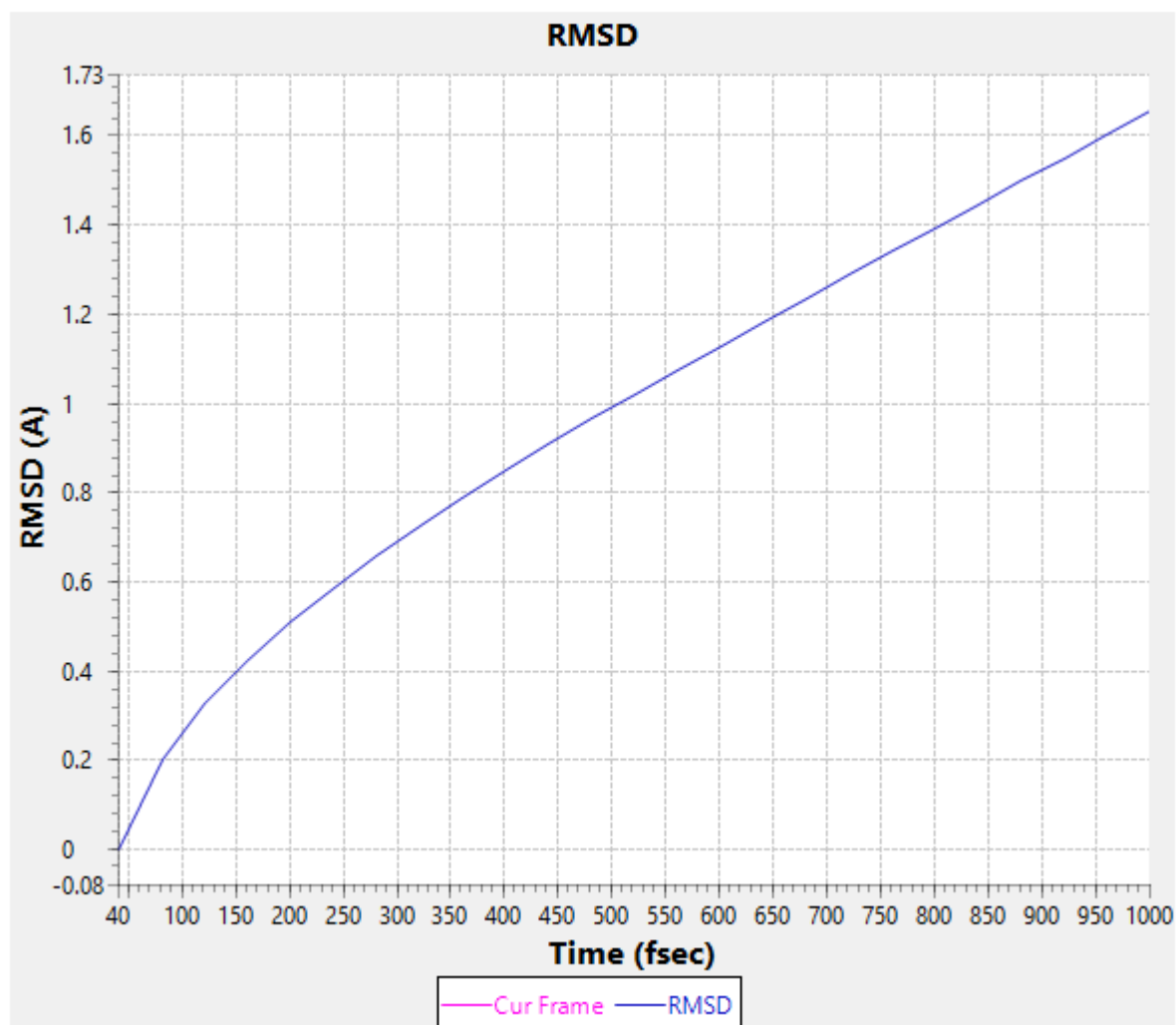


Figure S1c: RMSD plot for D373V

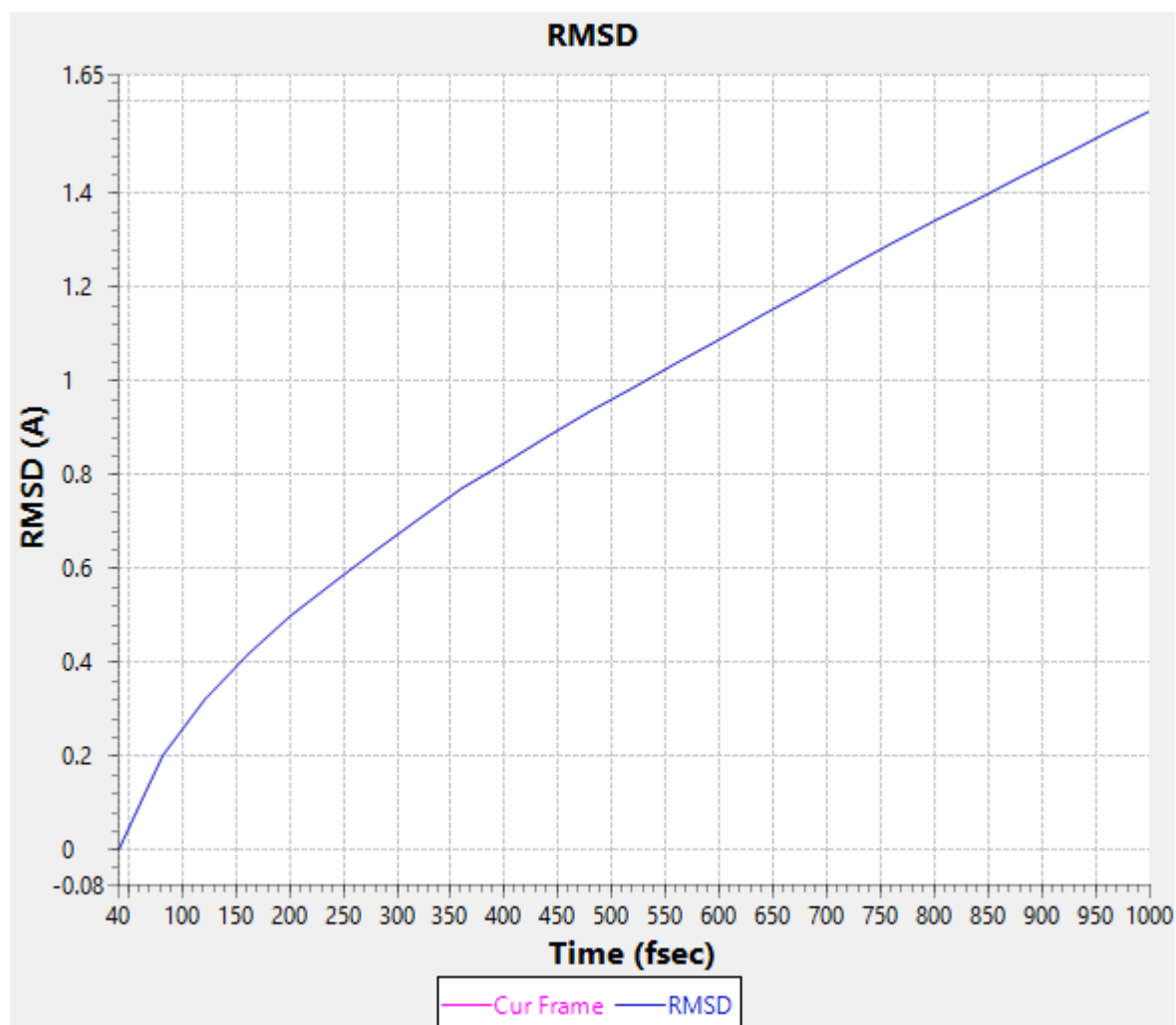


Figure S1d: RMSD plot for D373Y

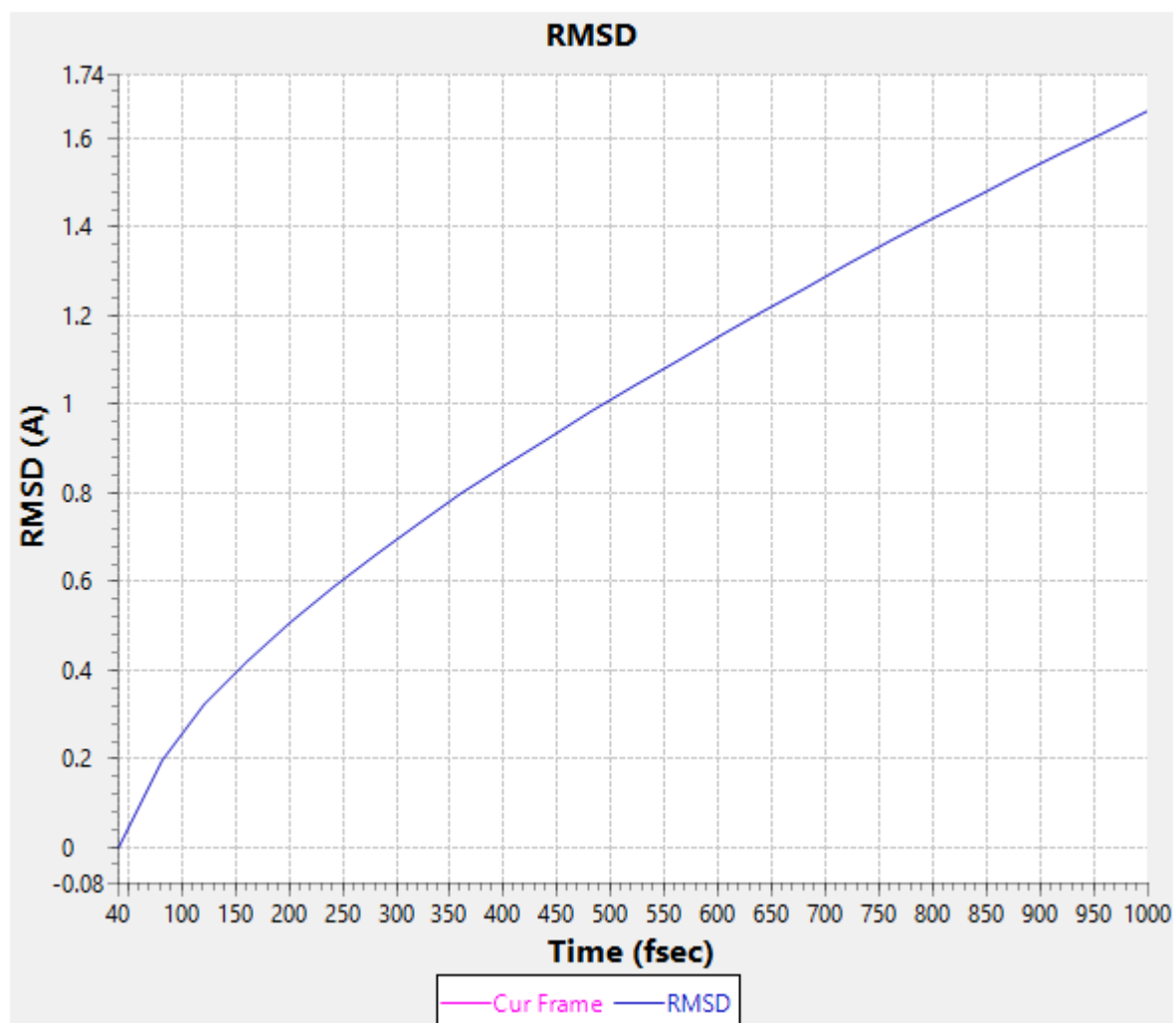


Figure S1e: RMSD plot for E528G

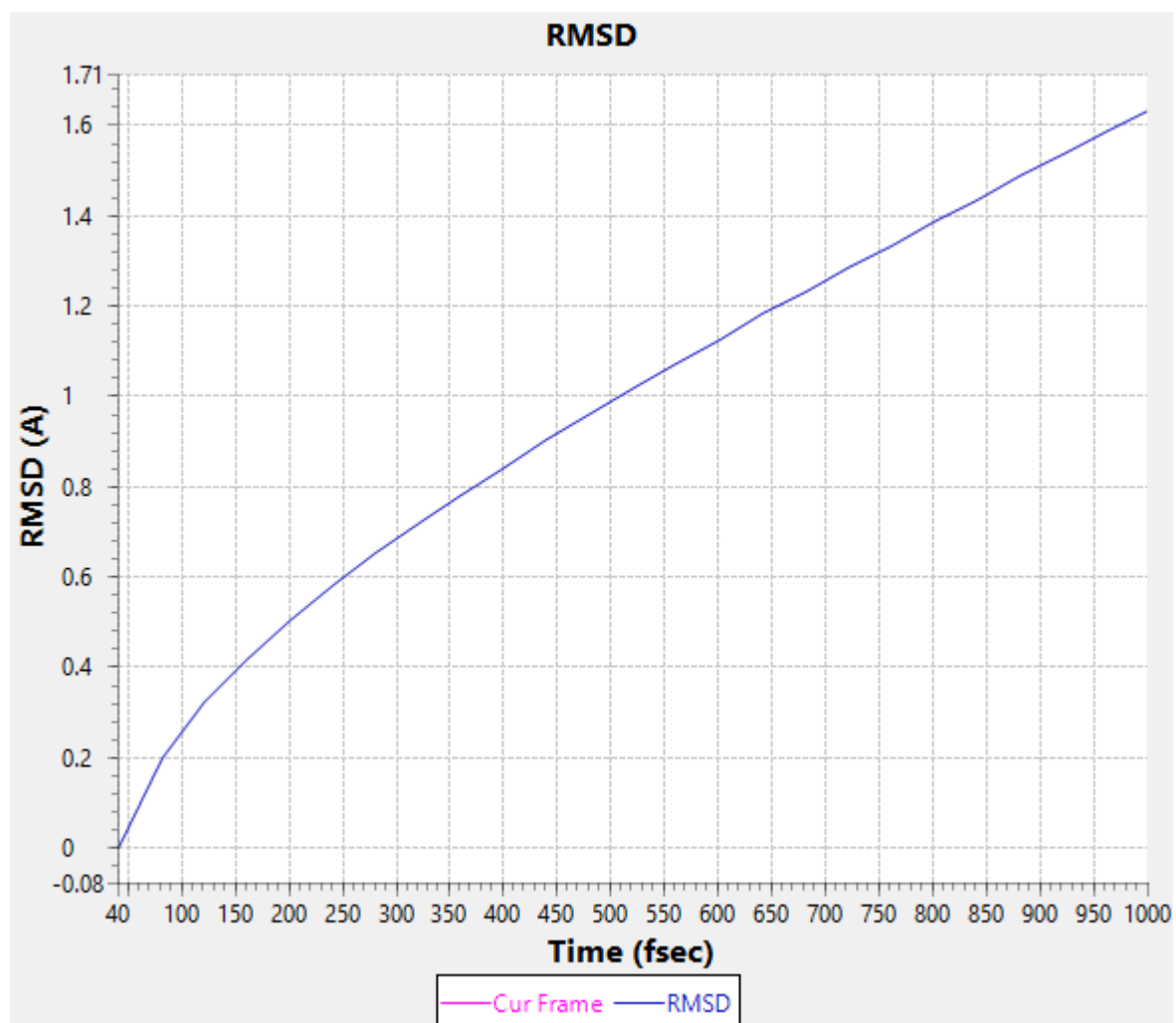


Figure S1f: RMSD plot for E588V

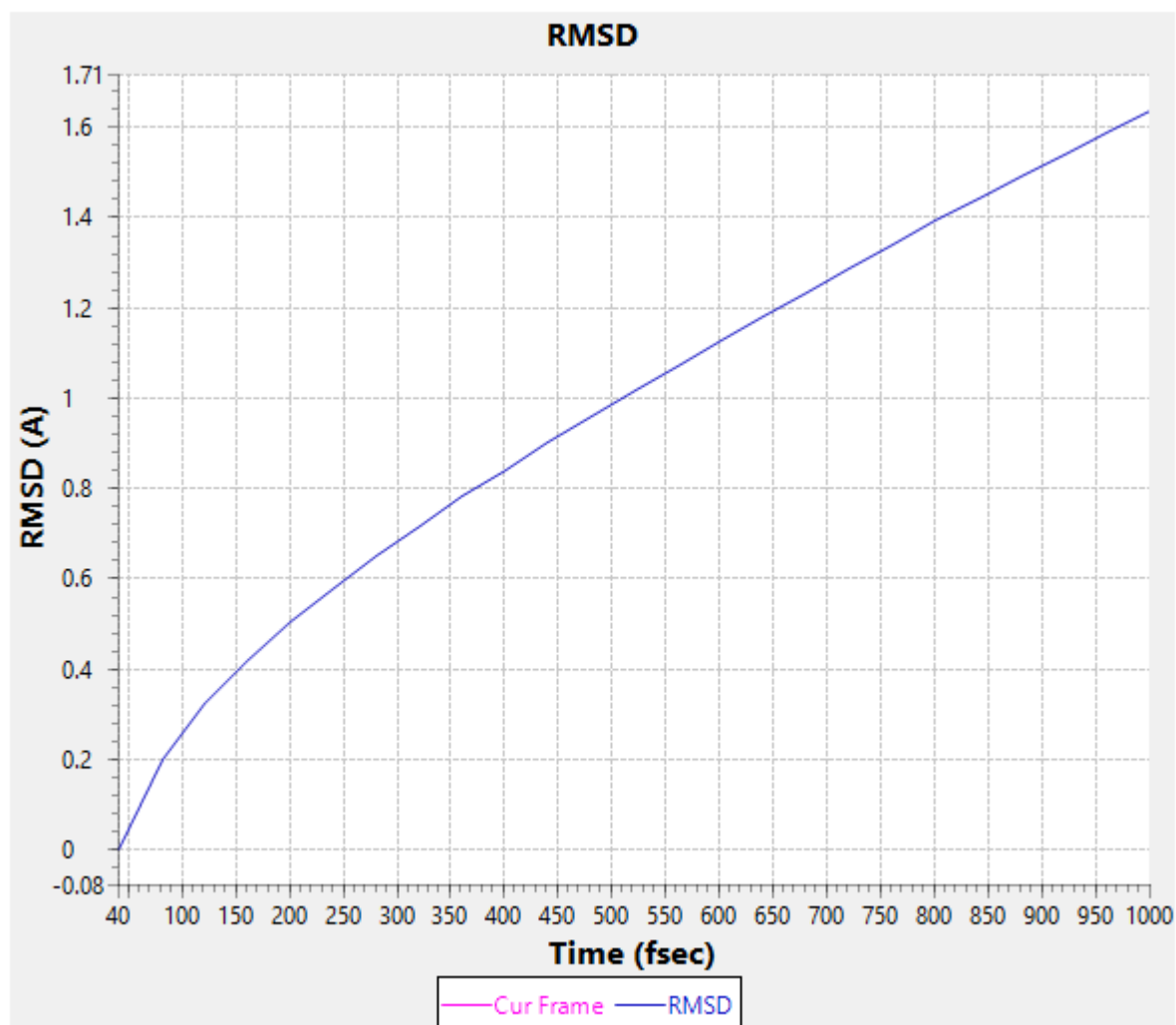


Figure S1g: RMSD plot for R487K

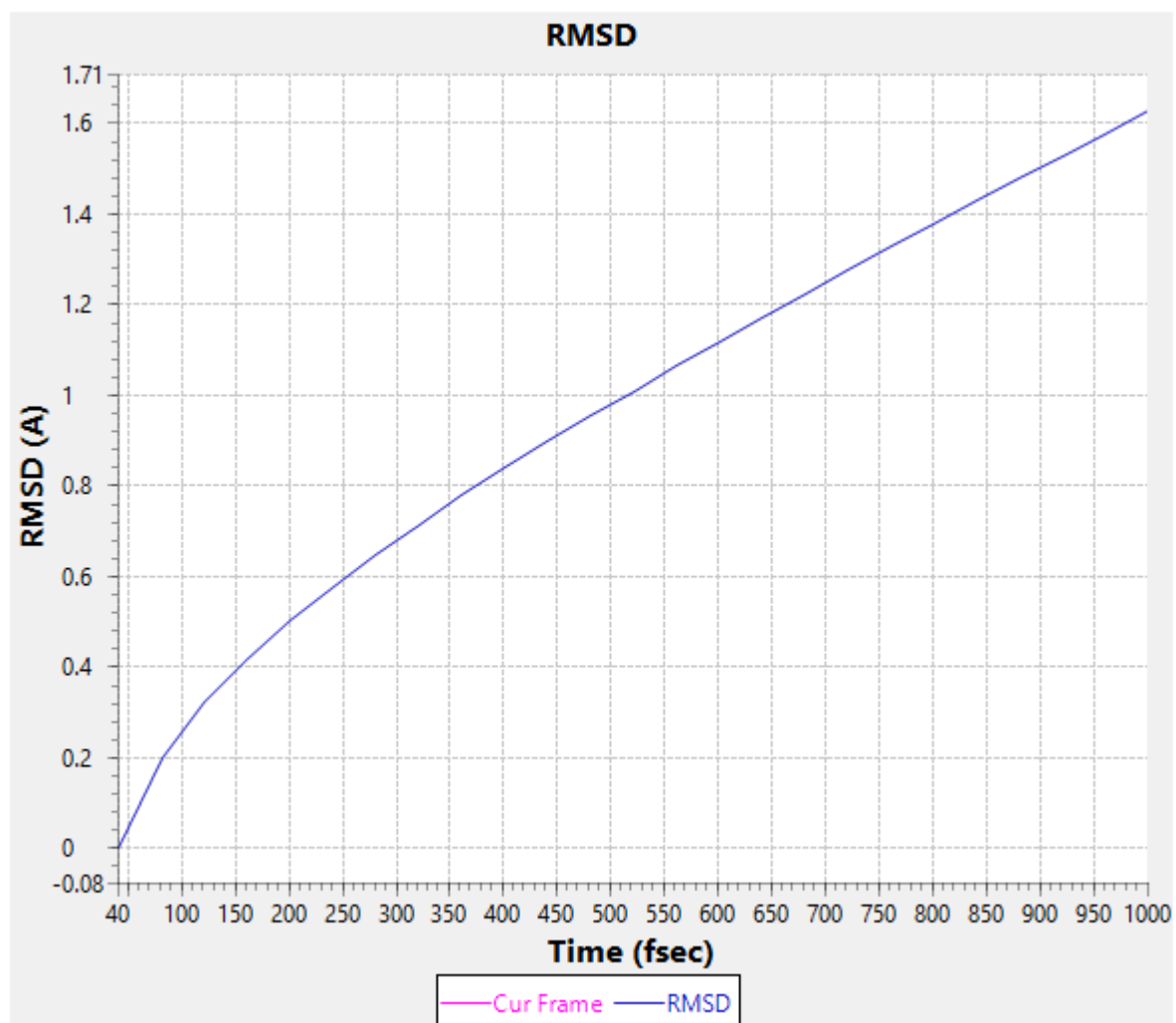


Figure S1h: RMSD plot for D984N

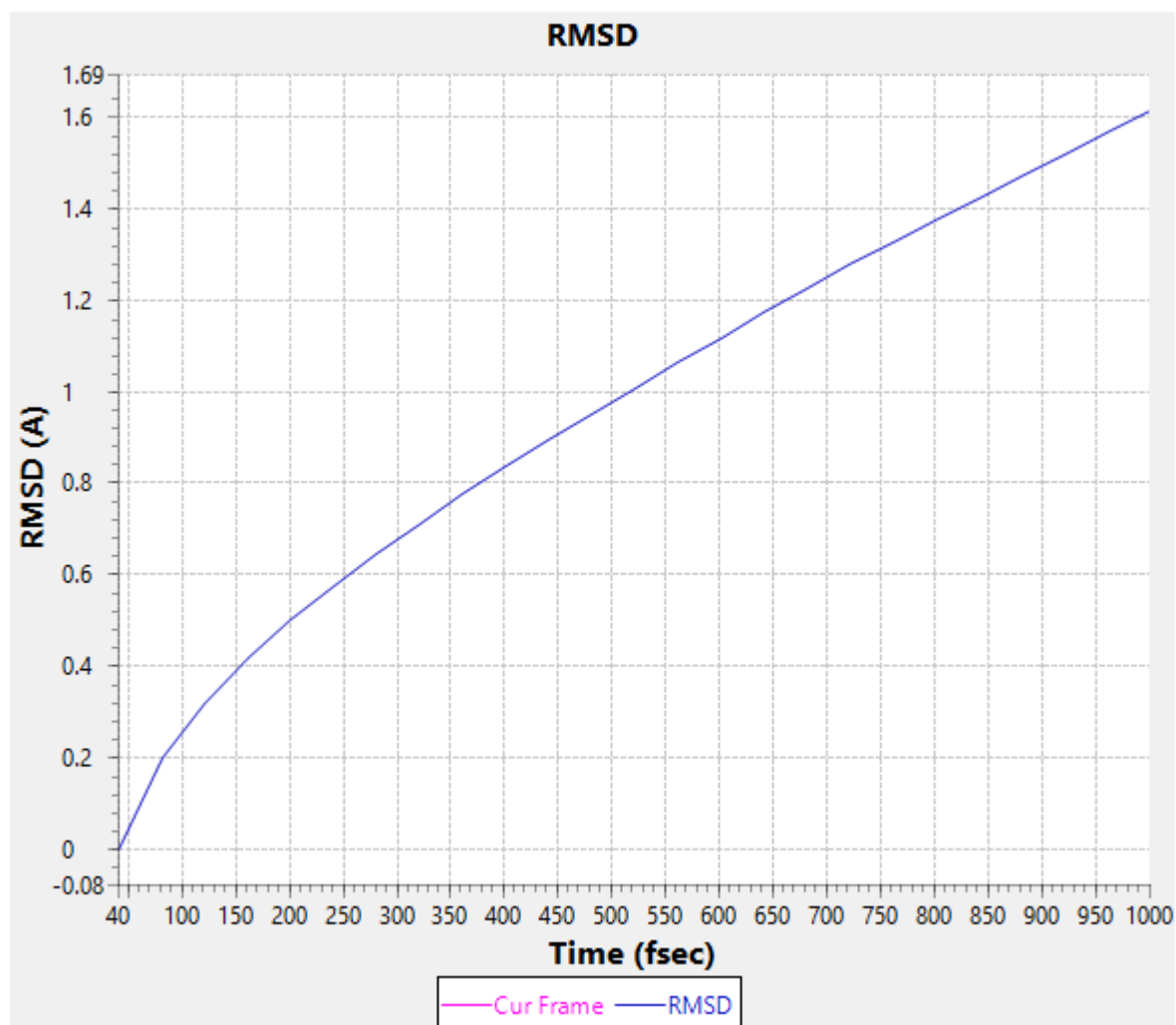


Figure S1i: RMSD plot for D985N

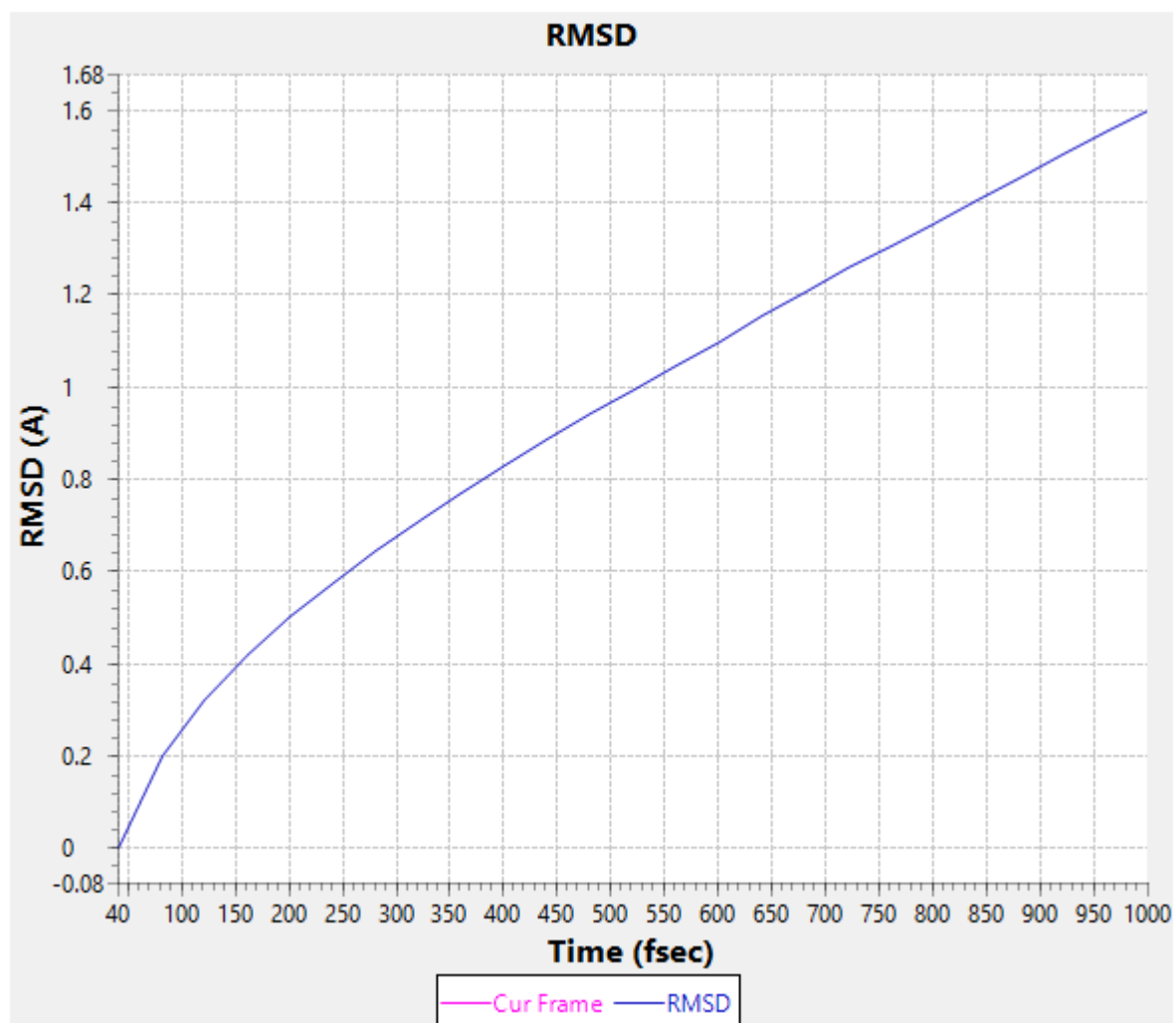


Figure S1j:RMSD plot for M1137I

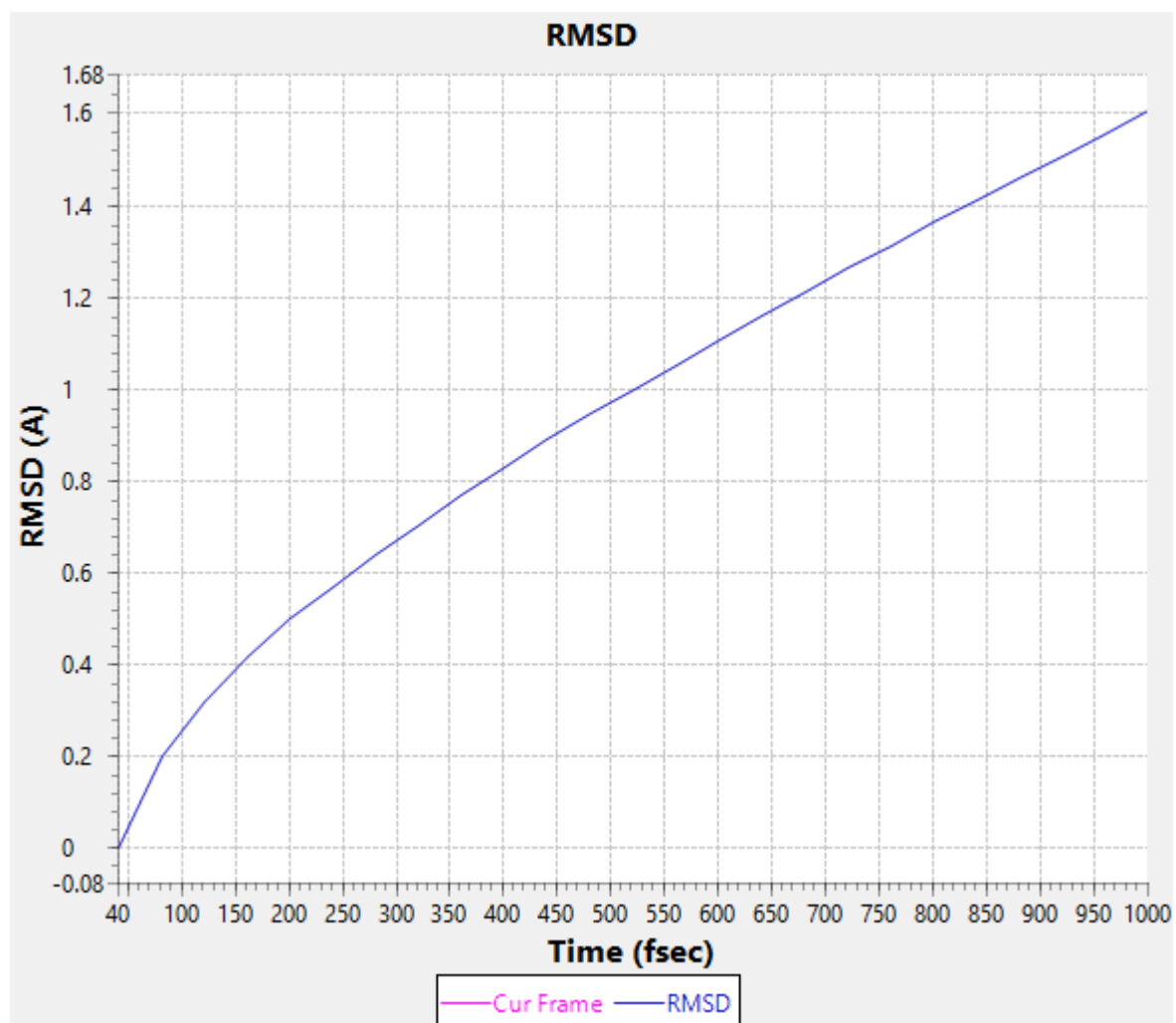


Figure S1k: RMSD plot for R1162L

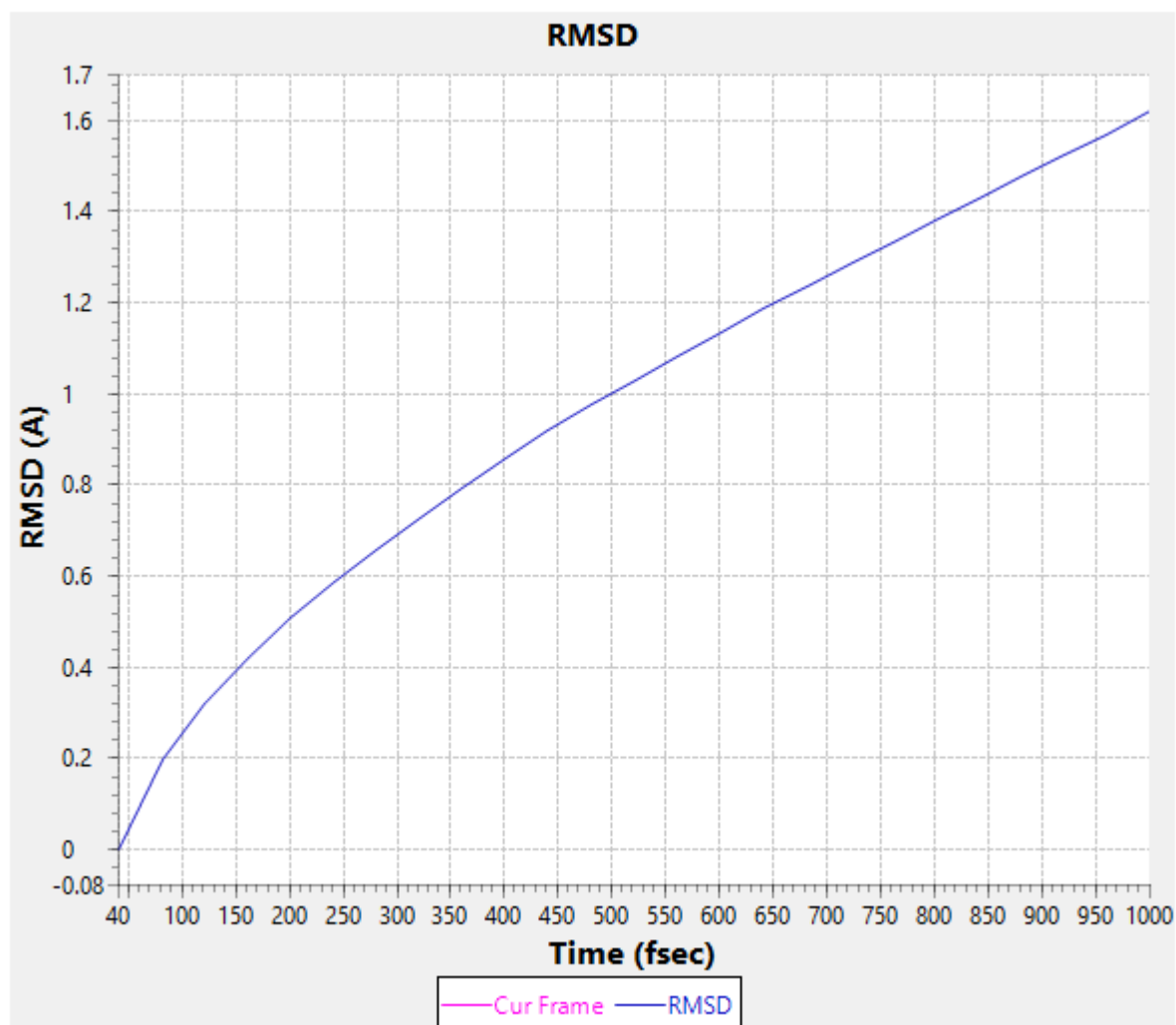


Figure S1l: RMSD plot for W1310G

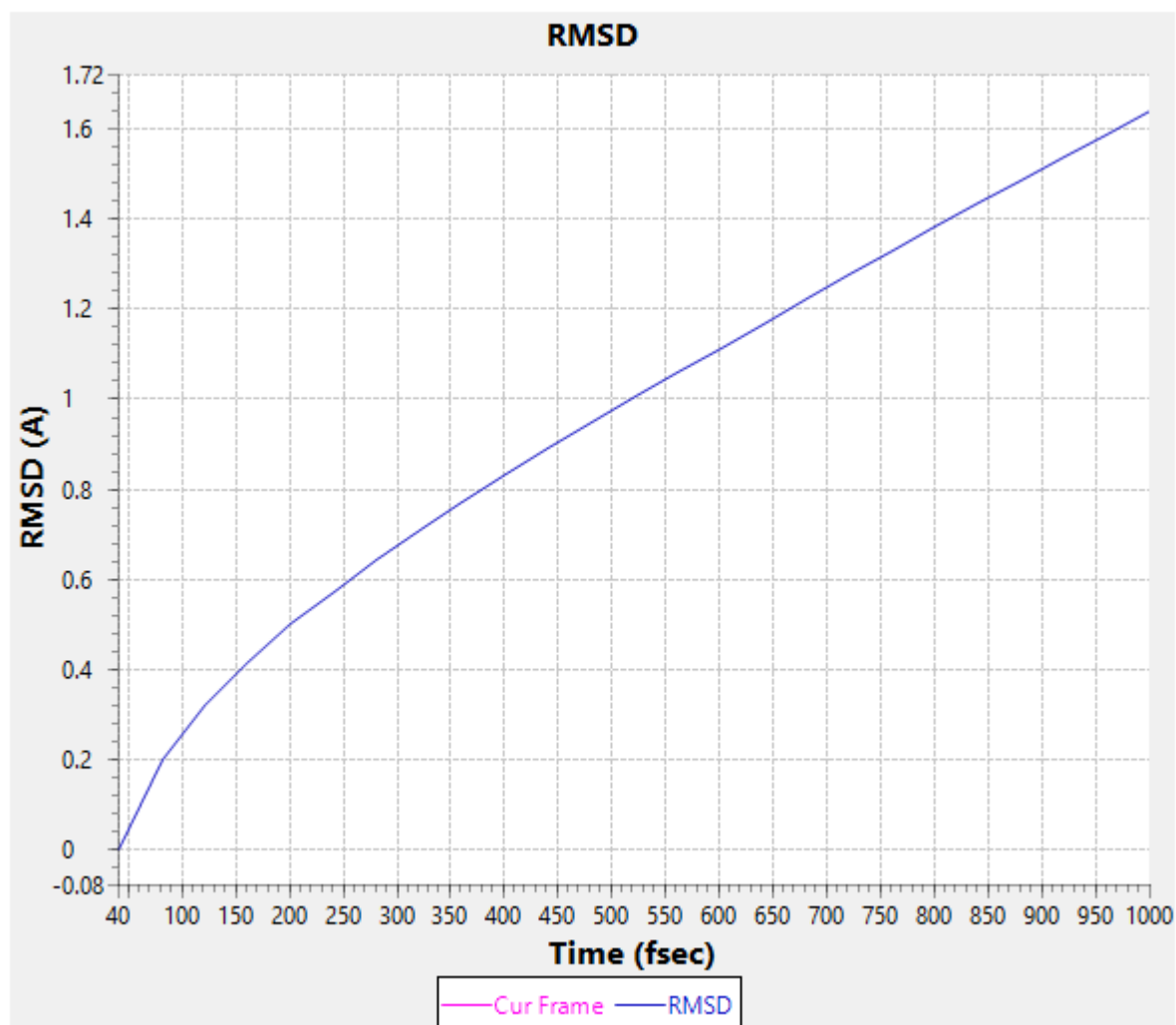


Figure S1m: RMSD plot for D1341G

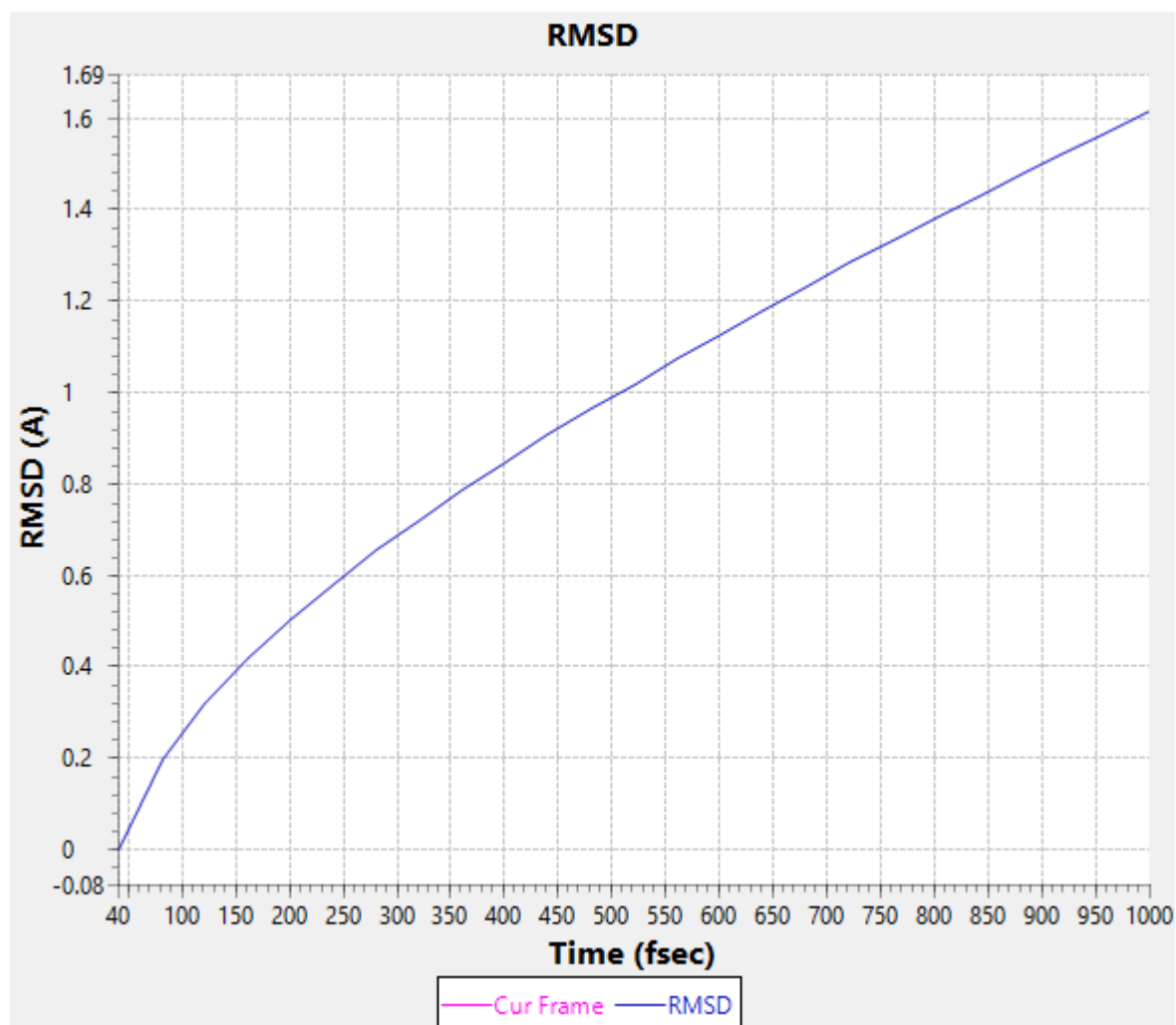


Figure S1n: RMSD plot for V1415G

Figure S1: RMSD plots for the Mutated variants

Table S3: Genotyping data as obtained through ARMS PCR

Patients						CONTROLS					
rs556880586(D373Y)			rs949472192			rs556880586(D373Y)			rs949472192		
AA	TT	AT	CC	TT	CT	AA	TT	AT	CC	TT	CT
-	-	+	-	+	-	+	-	-	-	+	-
-	-	+	-	+	-	+	-	-	-	+	-
-	-	+	+	-	-	+	-	-	-	+	-
-	-	+	-	+	-	-	-	+	-	+	-
-	-	+	-	+	-	+	-	-	-	+	-
-	-	+	-	+	-	-	-	+	+	-	-
-	+	-	+	-	-	+	-	-	+	-	-
-	-	+	-	-	+	+	-	-	-	+	-
-	-	+	-	+	-	-	-	+	+	-	-
-	-	+	-	+	-	+	-	-	+	-	-
-	-	+	-	+	-	+	-	-	+	-	-
-	-	+	-	+	-	+	-	-	+	-	-
-	+	-	-	+	-	+	-	-	-	-	+
-	-	+	-	+	-	+	-	-	+	-	-
-	+	-	-	+	-	+	-	-	+	-	-
-	-	+	-	-	+	+	-	-	-	+	-
-	-	+	+	-	-	+	-	-	+	-	-
-	+	-	-	-	+	-	-	+	+	-	-

-	-	+	-	-	+
-	-	+	-	+	-
-	-	+	-	+	-
-	-	+	-	+	-
-	-	+	-	+	-
-	-	+	+	-	-
-	-	+	-	+	-
-	+	-	-	-	+
-	+	-	-	-	+
-	-	+	+	-	-
-	+	-	-	-	+

-	-	+	-	+	-
+	-	-	+	-	-
-	-	+	-	-	+
+	-	-	+	-	-
+	-	-	-	+	-
+	-	-	-	+	-
-	-	+	+	-	-
-	-	+	-	-	+
-	+	-	-	-	+
+	-	-	-	+	-
-	-	+	-	-	+