

Estimated model parameters using the patch-clamp technique

Rate Constant	Wild-type control	Wild-type FPL	IIS4N control	IIS4N FPL	A780T control	A780T FPL
α	0.27 ± 0.06	0.26 ± 0.01	0.16 ± 0.03	0.08 ± 0.02	0.24 ± 0.09	0.09 ± 0.04
β	0.21 ± 0.04	0.07 ± 0.03	0.31 ± 0.07	0.14 ± 0.02	0.61 ± 0.08	0.22 ± 0.05
γ	0.02 ± 0.01	0.002 ± 0.001	0.03 ± 0.01	0.003 ± 0.001	0.01 ± 0.01	0.014 ± 0.006
δ	2.09 ± 1.05	2.68 ± 1.00	2.48 ± 1.23	1.36 ± 0.81	1.85 ± 0.29	1.45 ± 0.12
x_0	1.65 ± 0.80	7.77 ± 3.41	1.35 ± 0.50	1.33 ± 0.38	2.81 ± 0.97	57.14 ± 14.63
y_0	0.21 ± 0.07	0.17 ± 0.09	0.16 ± 0.04	0.02 ± 0.003	0.0008 ± 0.0003	0.00018 ± 0.00003
k_x	12.39 ± 3.12	5.67 ± 0.82	10.42 ± 2.29	8.07 ± 0.74	16.84 ± 1.82	5.85 ± 0.20
k_y	51.61 ± 37.06	25.32 ± 5.31	74.70 ± 33.78	29.72 ± 4.32	7.08 ± 0.79	12.30 ± 0.90
G	19.68 ± 6.72	60.86 ± 9.90	22.47 ± 9.68	40.03 ± 9.32	108.24 ± 36.55	330.04 ± 92.47

FPL: In the presence of Calcium agonist FPL 64174 (1 μ M)

Reference: <https://pubmed.ncbi.nlm.nih.gov/25966699/>

****Rate constants of A \leftrightarrow O and R \leftrightarrow D transitions (in ms⁻¹), estimated using data from Hohaus et al. (2005). (shown below)**

Construct	α	β	γ	δ
Wild-type ^a	0.15 ± 0.11	0.24 ± 0.08	0.021 ± 0.021	1.39 ± 0.17
G770P	0.33 ± 0.31	0.31 ± 0.21	0.030 ± 0.073	0.56 ± 0.11
N771P ^a	0.95 ± 0.63	0.11 ± 0.07	0.111 ± 0.057	1.41 ± 0.23
F778P ^a	0.13 ± 0.12	0.28 ± 0.09	0.016 ± 0.026	0.70 ± 0.09
L779P ^a	1.79 ± 0.81	0.11 ± 0.02	0.002 ± 0.002	0.36 ± 0.09
A780P ^a	0.19 ± 0.03	0.0064 ± 0.0022	0.015 ± 0.005	0.14 ± 0.02
A780G	0.96 ± 0.62	0.27 ± 0.12	0.037 ± 0.022	2.10 ± 0.33
I781T ^a	1.95 ± 0.91	0.045 ± 0.012	0.009 ± 0.003	1.02 ± 0.26
I781P ^a	4.16 ± 1.86	0.034 ± 0.007	0.003 ± 0.001	0.74 ± 0.43
I781G	1.73 ± 0.81	0.036 ± 0.010	0.011 ± 0.003	0.78 ± 0.18
I781A ^a	1.72 ± 0.79	0.132 ± 0.028	0.003 ± 0.001	1.55 ± 0.44
I781V ^a	0.55 ± 0.30	0.22 ± 0.03	0.0003 ± 0.0002	2.01 ± 0.77
I781N ^a	2.17 ± 0.99	0.10 ± 0.02	0.003 ± 0.002	0.74 ± 0.20
A782P ^a	2.65 ± 1.23	0.111 ± 0.026	0.004 ± 0.002	0.94 ± 0.27
A782G	1.74 ± 0.97	0.32 ± 0.10	0.013 ± 0.009	1.96 ± 0.37
D784G	0.88 ± 0.53	0.34 ± 0.09	0.008 ± 0.006	1.62 ± 0.35

^a: Rate constants determined using data from Hohaus et al. (2005). <https://pubmed.ncbi.nlm.nih.gov/16157588/>

Reference: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2737230/>

The influence of IIS6 pore mutations on voltage-dependent gating of CaV1.2

Midpoints and slope factors of the activation curves and amount of channel inactivation during a 300-ms pulse (r_{300}) to the peak potentials of the I–V curve.

	Half-activation	Slope	r_{300}
	mV	mV	%
Co-expression of β^1^a			
Wild-type	-9.9 ± 1.1	6.3 ± 0.7	65 ± 4
I781T	-37.7 ± 1.2	7.2 ± 1.0	47 ± 3

I781P	-47.2 ± 1.1	6.3 ± 0.6	53 ± 6
I781L	-20.6 ± 1.2	6.1 ± 0.2	63 ± 7
I781A	-29.5 ± 0.6	7.9 ± 0.5	51 ± 4
I781N	-34.6 ± 1.6	9.1 ± 0.4	37 ± 6
I781Q	No currents	N/A	N/A
I781R	No currents	N/A	N/A
C769P	2.8 ± 0.8	4.9 ± 1.0	67 ± 7
G770P	-11.4 ± 1.3	5.8 ± 0.3	62 ± 4
N771P	-26.9 ± 1.1	4.9 ± 0.2	43 ± 4
Y772P	No currents	N/A	N/A
I773P	-14.2 ± 1.8	2.9 ± 0.6	65 ± 6
L774P	No currents	N/A	N/A
L775P	No currents	N/A	N/A
N776P	No currents	N/A	N/A
V777P	No currents	N/A	N/A
F778P	-9.3 ± 0.8	7.7 ± 0.3	23 ± 3
L779P	-29.78 ± 1.90	6.0 ± 0.4	3 ± 1
A780P	-37.1 ± 0.7	5.7 ± 0.8	2 ± 1
A782P	-35.7 ± 1.4	9.8 ± 0.3	30 ± 5
V783P	No currents	N/A	N/A
Co-expression of β^{2a}			
Wild-type	-13.8 ± 0.9	6.0 ± 0.5	16 ± 5
I781T	-44.9 ± 1.4	8.8 ± 1.0	25 ± 4
I781P	-52.3 ± 1.3	7.3 ± 0.8	27 ± 6

β^{1a} : β subunit of a DHP-sensitive calcium channel in skeletal muscle with the DNA sequence from Perez-Reyes et al. 1989 (<https://pubmed.ncbi.nlm.nih.gov/2549640/>)

β^{2a} : β subunit of a DHP-receptor/calcium channel in skeletal muscle with the DNA sequence from Perez-Reyes et al. 1992 (<https://pubmed.ncbi.nlm.nih.gov/1370480/>)

Reference: <https://pubmed.ncbi.nlm.nih.gov/16157588/>

Model parameters describing the R \leftrightarrow A transition

Rate constant	Estimated value
x0 (ms ⁻¹)	0.427 ± 0.029
kx (mV)	328.8 ± 447.4
y0 (ms ⁻¹)	0.216 ± 0.084
ky (mV)	9.04 ± 0.52

Reference: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2737230/>

Rate constants of pore opening and closure

	α	β	γ	δ
Wild-type	0.2	0.25	0.08	1.2
I781T	8.3	0.07	0.011	0.6
I781P	22	0.035	0.007	0.3

Parameters for voltage dependent rate constants x(V) and y(V)

Rate constant	Estimated value
x0 (ms ⁻¹)	0.38

kx (mV)	55
y0 (ms ⁻¹)	0.17
ky (mV)	8

Reference: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3196840/>

Midpoints and slope factors of the activation curve of CaV1.2 IIS6 mutants

Mutant	Half-activation <i>mV</i>	Slope <i>mV</i>
Wild-type ^a	-9.9 ± 1.1	6.3 ± 0.7
A780P ^a	-37.1 ± 0.7	5.7 ± 0.8
A780G	-19.3 ± 0.8	6.3 ± 0.6
I781P ^a	-47.2 ± 1.1	6.3 ± 0.6
I781G	-40.2 ± 0.8	7.5 ± 0.7
I781T ^a	-37.7 ± 1.2	7.2 ± 1.0
A782P ^a	-35.7 ± 1.4	9.8 ± 0.3
A782G	-22.2 ± 0.4	7.8 ± 0.4
V783G	No current	N/A
D784G	-15.6 ± 1.1	6.3 ± 0.6

a: Data from Hohaus et al. (2005). <https://pubmed.ncbi.nlm.nih.gov/16157588/>

Reference: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2737230/>

S4 Segments of Cav 1.2 Channels: Midpoints and slope factors (k) of the activation curves and estimated effective charge (αZ)

Mutant	V0.5, mV	<i>k act</i> , mV	αZ
Wild-type	-18.6 ± 0.8 (n = 7)	5.9 ± 0.9	4.27 ± 0.65
G432W ^b	-33.7 ± 0.6 (n = 8)	4.7 ± 0.4	5.36 ± 0.46
A780T ^b	-44.0 ± 0.6 (n = 5)	5.1 ± 0.6	4.94 ± 0.58
G1193T ^b	-49.8 ± 1.0 (n = 7)	5.1 ± 0.6	4.94 ± 0.58
A1503G ^b	-41.4 ± 0.8 (n = 5)	5.8 ± 0.5	4.34 ± 0.37
IS4 neutralisations			
IS4N	No detectable current		
K264Q/R267Q/R270Q/R273Q (IS4N+R276)	-33.1 ± 1.1 (n = 5)	8.5 ± 0.6	2.96 ± 0.21
K264Q/R267Q/R270Q (IS4N+R276+R273)	-16.3 ± 0.7 (n = 4)	9.9 ± 0.7	2.54 ± 0.18
G432W/R267Q	-11.9 ± 1.0 (n = 4)	8.5 ± 0.8	2.96 ± 0.28
G432W/IS4N+R276	No detectable current		
A780T/R267Q	-28.5 ± 1.3 (n = 4)	9.6 ± 0.7	2.62 ± 0.19
A780T/IS4N+R276	-42.7 ± 1.1 (n = 4)	11.9 ± 1.0	2.12 ± 0.18
A780T/K264Q/R267Q/R270Q (A780T/IS4N+R276+R273)	-33.5 ± 0.6 (n = 4)	11.5 ± 0.6	2.19 ± 0.11
G1193T/R267Q	-28.6 ± 0.9 (n = 5)	9.1 ± 0.5	2.77 ± 0.15
G1193T/IS4N+R276	No detectable current		
A1503G/R267Q	-28.5 ± 0.6 (n = 5)	9.1 ± 0.4	2.77 ± 0.12
A1503G/IS4N+R276	-41.1 ± 0.6 (n = 5)	8.7 ± 0.5	2.89 ± 0.17
IIS4 neutralisations			
IIS4N ^a	-17.5 ± 0.8 (n = 11)	6.7 ± 0.7	3.76 ± 0.39
R650Q/R653Q/R656Q/K659Q (IIS4N+R662)	-23.9 ± 1.0 (n = 6)	6.3 ± 0.7	4.00 ± 0.44

R650Q/R653Q/R656Q (IIS4N+R662+K659)	-18.2 ± 0.7 (n = 5)	7.2 ± 0.6	3.50 ± 0.29
R650Q/R653Q	-25.1 ± 0.9 (n = 5)	5.7 ± 0.6	4.42 ± 0.47
G432W/R656Q	-17.9 ± 0.9 (n = 5)	6.0 ± 0.7	4.20 ± 0.49
G432W/IIS4N+R662	-31.0 ± 0.6 (n = 5)	8.4 ± 0.8	3.00 ± 0.29
G432W/IIS4N ^a	-19.3 ± 0.7 (n = 8)	5.8 ± 0.7	4.34 ± 0.52
A780T/R650Q	-30.7 ± 0.3 (n = 4)	5.7 ± 0.3	4.42 ± 0.23
A780T/R653Q	-30.2 ± 0.6 (n = 5)	5.3 ± 0.3	4.75 ± 0.27
A780T/R656Q	-33.5 ± 0.5 (n = 5)	6.5 ± 0.3	3.88 ± 0.18
A780T/K659Q	-32.0 ± 1.3 (n = 4)	7.1 ± 0.8	3.55 ± 0.40
A780T/R662Q	-34.0 ± 0.7 (n = 5)	5.4 ± 0.3	4.67 ± 0.26
A780T/IIS4N+R662	-33.6 ± 0.6 (n = 4)	6.3 ± 0.3	4.00 ± 0.19
A780T/IIS4N+R650	-39.4 ± 0.8 (n = 4)	6.1 ± 0.6	4.13 ± 0.41
A780T/IIS4N ^a	-32.0 ± 0.7 (n = 10)	5.1 ± 0.7	4.94 ± 0.68
G1193T/R650Q	-39.0 ± 0.9 (n = 5)	6.8 ± 0.6	3.71 ± 0.33
G1193T/R653Q	-34.0 ± 0.6 (n = 6)	6.6 ± 0.5	3.82 ± 0.29
G1193T/R656Q	-38.3 ± 0.8 (n = 5)	5.0 ± 0.5	5.04 ± 0.50
G1193T/K659Q	-40.3 ± 0.9 (n = 4)	4.9 ± 0.5	5.14 ± 0.52
G1193T/R662Q	-40.2 ± 0.4 (n = 6)	5.7 ± 0.3	4.42 ± 0.23
G1193T/IIS4N+R662	-38.0 ± 0.8 (n = 5)	6.1 ± 0.6	4.13 ± 0.41
G1193T/IIS4N ^a	-20.8 ± 0.7 (n = 5)	7.5 ± 0.6	3.36 ± 0.27
A1503G/R656Q	-26.6 ± 0.7 (n = 5)	7.3 ± 0.5	3.45 ± 0.24
A1503G/IIS4N+R662	-25.3 ± 1.0 (n = 6)	7.7 ± 0.6	3.27 ± 0.25
A1503G/IIS4N ^a	-19.8 ± 0.7 (n = 6)	7.5 ± 0.7	3.36 ± 0.31
IIS4 neutralisations			
IIS4N	No detectable current		
K1025Q/R1028Q/R1031Q/R1034Q/R1037 (IIS4N+R1041)	No detectable current		
K1025Q/R1028Q/R1031Q/R1034Q (IIS4N+R1041+R1037)	-19.7 ± 0.9 (n = 5)	8.0 ± 0.5	3.15 ± 0.20
R1034Q	-23.4 ± 0.6 (n = 5)	6.5 ± 0.4	3.82 ± 0.23
A780T/K1025Q/R1028Q/R1031Q/R1034Q	-43.6 ± 0.6	9.3 ± 0.4	2.69 ± 0.12
A780T/K1025Q/R1028Q	-34.7 ± 0.5 (n = 7)	7.7 ± 0.3	3.29 ± 0.11
A780T/R1034Q	-33.5 ± 0.6 (n = 4)	6.1 ± 0.5	4.14 ± 0.31
G1193T/K1025Q/R1028Q/R1031Q/R1034Q	-41.8 ± 0.6	8.2 ± 0.6	3.09 ± 0.21
A1503G/R1034Q	-27.4 ± 0.5 (n = 4)	7.1 ± 0.3	3.56 ± 0.13
IVS4 neutralisations			
IVS4N	No detectable current		
R1359Q/R1362Q/R1365Q/K1368Q (IVS4N+R1372)	No detectable current		
R1359Q/R1362Q/R1365Q	No detectable current		
R1359Q/R1362Q	No detectable current		
R1359Q	-6.0 ± 1.0 (n = 5)	5.0 ± 0.6	5.04 ± 0.60
R1365Q	-5.8 ± 1.0 (n = 5)	5.6 ± 1.0	4.47 ± 0.79
G1193T/K1025Q/R1028Q	-35.8 ± 0.7 (n = 7)	8.7 ± 0.6	2.89 ± 0.20

^a: Data from Beyl et al. <https://pubmed.ncbi.nlm.nih.gov/22941337/>

^b: Data from Depil et al. <https://pubmed.ncbi.nlm.nih.gov/21685391/>

Reference: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5138263/>

Mutant	<i>V</i> _{act} , mV	<i>k</i> , mV ^a	Δ <i>G</i> , kcal/Mol	<i>I</i> _{max} , pA/pF
Wild-type	-18.6 ± 0.9 (n = 8)	5.9 ± 0.6		15.1 ± 2.8
IS6 segment				
L434A	-39.3 ± 0.9 (n = 5)	5.9 ± 0.8	-2.03 ± 0.57	13.3 ± 2.5
L434G	-32.3 ± 0.7 (n = 7)	7.6 ± 0.7	-0.63 ± 0.31	15.7 ± 2.8
L434N	-22.0 ± 0.8 (n = 6)	6.5 ± 0.7	-0.11 ± 0.30	12.3 ± 2.1
L434T	-30.8 ± 1.3 (n = 6)	6.9 ± 0.9	-0.76 ± 0.41	17.1 ± 3.0
L434V	-32.6 ± 0.8 (n = 5)	5.9 ± 0.7	-1.37 ± 0.44	12.6 ± 2.7
L434M	-23.0 ± 1.2 (n = 6)	4.6 ± 0.7	-1.08 ± 0.51	14.3 ± 3.2
L434S	-28.9 ± 0.7 (n = 6)	5.0 ± 0.5	-1.55 ± 0.42	13.7 ± 2.2
L434W	No current	N/A	N/A	N/A
L434P ^b	No current	N/A	N/A	N/A
IIS6 segment				
F1191T	-25.7 ± 1.0 (n = 6)	7.1 ± 0.8	-0.26 ± 0.32	9.6 ± 2.5
V1192T	-16.4 ± 0.9 (n = 7)	6.9 ± 0.9	0.45 ± 0.28	9.1 ± 2.2
G1193T	-49.8 ± 1.0 (n = 7)	5.1 ± 0.6	-3.89 ± 0.72	17.5 ± 3.2
G1193V	-38.1 ± 0.7 (n = 8)	5.6 ± 0.6	-2.14 ± 0.48	12.3 ± 2.7
G1193N	-46.5 ± 1.0 (n = 5)	5.6 ± 0.8	-2.99 ± 0.73	11.2 ± 2.9
G1193M	-33.6 ± 0.7 (n = 8)	6.4 ± 0.6	-1.22 ± 0.36	8.4 ± 2.0
G1193A	-12.1 ± 1.0 (n = 6)	5.7 ± 0.7	0.60 ± 0.28	9.3 ± 1.8
G1193Q	-39.2 ± 0.8 (n = 5)	7.0 ± 0.7	-1.42 ± 0.39	9.8 ± 2.1
G1193P	-37.7 ± 0.7 (n = 7)	6.3 ± 0.6	-1.63 ± 0.39	11.3 ± 2.7
G1193W	No current	N/A	N/A	N/A
F1194T	-16.5 ± 0.9 (n = 7)	7.8 ± 0.9	0.61 ± 0.26	17.3 ± 3.2
V1195T	-28.9 ± 0.7 (n = 7)	5.1 ± 0.7	-1.48 ± 0.51	18.7 ± 3.4
I1196T	-26.6 ± 0.6 (n = 9)	4.9 ± 0.6	-1.31 ± 0.44	18.4 ± 2.7

^a: in comparison to Wild-Type the changes of slope factors for mutated channels are statistically not significant (p > 0.05)

^b: Data from Kudrnac et al. (<https://pubmed.ncbi.nlm.nih.gov/19265197/>)

Reference: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3016219/>

S6 Segments: Coupled and Independent Contributions of Residues in IS6 and IIS6 to Activation Gating of CaV1.2

Mutant	<i>V</i> _{0.5, act}	<i>k</i> _{act}	<i>V</i> _{0.5, inact}	<i>k</i> _{inact}	<i>r</i> ₃₀₀
	mV	mV	mV	mV	%
Wild-type	-9.9 ± 1.1 (n = 8)	6.3 ± 0.7	-38.7 ± 1.0 (n = 3)	8.1 ± 0.9	65 ± 4
IS6 segment					
L429T	-16.5 ± 0.6 (n = 5)	7.5 ± 0.6	-42.5 ± 1.1 (n = 3)	7.9 ± 0.9	69 ± 6
L434T	-21.9 ± 1.3 (n = 5)	6.9 ± 0.9	-51.1 ± 1.1 (n = 3)	8.6 ± 1.0	63 ± 5
S435T	-11.3 ± 0.7 (n = 5)	6.1 ± 0.6	-40.1 ± 0.9 (n = 3)	7.7 ± 0.8	64 ± 6
S435A	-15.9 ± 0.6 (n = 6)	6.9 ± 0.5	-44.1 ± 0.9 (n = 4)	7.8 ± 0.9	70 ± 5
S435P	-35.8 ± 0.6 (n = 6)	8.8 ± 0.6	-65.7 ± 0.7 (n = 4)	7.3 ± 0.7	5 ± 4 ^a
IIS6 segment					
L779T	-18.6 ± 0.7 (n = 5)	6.4 ± 0.6	-50.5 ± 1.2 (n = 3)	7.1 ± 0.6	12 ± 5 ^a
I781T	-37.7 ± 1.2 (n = 7)	7.2 ± 1.0	-57.8 ± 0.7 (n = 3)	8.9 ± 0.5	47 ± 3 ^a
I781P	-47.2 ± 1.1 (n = 8)	6.3 ± 0.6	-68.7 ± 0.8 (n = 5)	5.8 ± 0.5	53 ± 6
Double mutants					
L429T/I781T	-44.0 ± 1.0 (n = 7)	8.3 ± 0.9	-61.2 ± 1.0 (n = 4)	8.7 ± 0.9	41 ± 5 ^a

L429T/L779T	-22.5 ± 0.8 (n = 5)	6.4 ± 0.7	-49.6 ± 1.3 (n = 3)	8.0 ± 0.7	12 ± 6 ^a
L434T/I781T	-50.3 ± 0.8 (n = 5)	5.4 ± 0.8	-70.0 ± 1.6 (n = 3)	8.5 ± 1.2	15 ± 4 ^a
L434T/L779T	-32.3 ± 0.8 (n = 7)	7.1 ± 0.7	-58.2 ± 0.8 (n = 5)	8.2 ± 0.9	52 ± 5
S435A/I781T	-35.3 ± 0.9 (n = 6)	8.7 ± 0.7	-59.1 ± 0.9 (n = 4)	8.1 ± 0.8	48 ± 4 ^a
S435P/I781T	-43.7 ± 0.9 (n = 5)	9.1 ± 0.9	-64.1 ± 1.1 (n = 3)	8.6 ± 1.0	44 ± 5 ^a
S435P/I781P	No current	N/A	N/A	N/A	N/A

^a: Data are statistically significantly different from wild type (p < 0.05). Data for wild type, I781T, and I781P are from Hohaus et al. (12). Mutations G422P, S423P, F424P, N428P, L429P, V430T/V430P, L431T/L431P, G432T/G432P, V433T/V433P, L434P, E437P, F438P, and S439P were not functional

Reference: <https://pubmed.ncbi.nlm.nih.gov/19265197/>

S6 Segments: Timothy Mutation Disrupts the Link between Activation and Inactivation in CaV1.2 Protein

Construct	V0.5 mV	kact mV	V0.5,inact mV	kinact mV	r3000
Wild-type					
	-18.4 ± 0.8 (n = 9)	6.0 ± 0.7	-41.5 ± 0.9 (n = 5)	6.4 ± 0.9	0.35 ± 0.03
IS6 G432a					
G432A	-14.2 ± 0.6 (n = 7)	6.2 ± 0.5			0.77 ± 0.05
G432M	-23.2 ± 0.6 (n = 7)	7.7 ± 0.6			0.68 ± 0.07
G432N	-34.4 ± 0.4 (n = 7)	6.5 ± 0.5			0.72 ± 0.04
G432S	-19.2 ± 0.7 (n = 7)	5.9 ± 0.7			0.74 ± 0.07
G432V	-12.0 ± 0.6 (n = 6)	5.7 ± 0.5			0.86 ± 0.04
G432W	-33.7 ± 0.6 (n = 8)	4.7 ± 0.4			0.58 ± 0.04
IIS6 A780					
A780G	-29.4 ± 0.6 (n = 5)	6.2 ± 0.6	-54.4 ± 1.3 (n = 4)	6.2 ± 1.1	0.11 ± 0.06
A780N	-43.8 ± 1.0 (n = 7)	6.8 ± 0.9	-67.4 ± 0.7 (n = 4)	4.6 ± 0.9	0.25 ± 0.04
A780P	-45.0 ± 0.7 (n = 5)	5.9 ± 0.8	-39.4 ± 1.2 (n = 4)	5.2 ± 1.9	0.34 ± 0.07
A780T	-44.0 ± 0.6 (n = 5)	5.1 ± 0.6	-59.8 ± 0.9 (n = 4)	7.5 ± 0.9	0.24 ± 0.04
A780V	-34.6 ± 0.8 (n = 8)	6.6 ± 0.7	-54.3 ± 0.8 (n = 4)	4.8 ± 0.8	0.10 ± 0.05
A780W	-49.3 ± 0.6 (n = 7)	5.9 ± 0.5	-68.0 ± 0.8 (n = 4)	6.3 ± 0.9	0.16 ± 0.05
IIIS6 G1193b					
G1193A	-12.1 ± 1.0 (n = 6)	5.7 ± 0.7	-25.2 ± 1.1 (n = 6)	8.8 ± 0.9	0.27 ± 0.07
G1193M	-33.6 ± 0.7 (n = 8)	6.4 ± 0.6	-52.8 ± 1.0 (n = 4)	6.1 ± 0.9	0.34 ± 0.08
G1193N	-46.5 ± 1.0 (n = 5)	5.6 ± 0.8	-61.3 ± 0.9 (n = 4)	6.9 ± 0.9	0.38 ± 0.08
G1193P	-37.7 ± 0.7 (n = 7)	6.3 ± 0.6	-64.6 ± 1.0 (n = 4)	6.1 ± 0.8	0.18 ± 0.07
G1193Q	-39.2 ± 0.8 (n = 5)	7.0 ± 0.7	-64.4 ± 1.2 (n = 4)	8.4 ± 1.1	0.29 ± 0.08
G1193T	-49.8 ± 1.0 (n = 7)	5.1 ± 0.6	-70.0 ± 1.1 (n = 5)	5.4 ± 1.1	0.16 ± 0.07
G1193V	-38.1 ± 0.7 (n = 8)	5.6 ± 0.6	-60.4 ± 0.8 (n = 5)	7.5 ± 0.6	0.14 ± 0.08
IVS6 A1503					
A1503G	-41.4 ± 0.8 (n = 5)	5.8 ± 0.5	-54.0 ± 1.0 (n = 4)	4.9 ± 0.8	0.31 ± 0.07
A1503M	-29.2 ± 0.7 (n = 8)	5.9 ± 0.7	-60.1 ± 1.0 (n = 4)	5.5 ± 1.0	0.26 ± 0.08
A1503N	-31.5 ± 0.7 (n = 5)	6.3 ± 0.6	-45.1 ± 1.1 (n = 4)	6.0 ± 1.0	0.32 ± 0.09
A1503T	-17.9 ± 0.8 (n = 7)	8.7 ± 0.8	-38.0 ± 1.2 (n = 4)	6.9 ± 1.1	0.29 ± 0.09
A1503V	-11.4 ± 0.8 (n = 5)	7.2 ± 0.6	-37.2 ± 1.2 (n = 4)	6.8 ± 1.2	0.24 ± 0.06
A1503W	-16.9 ± 0.6 (n = 9)	6.6 ± 0.6	-38.9 ± 1.3 (n = 4)	7.5 ± 0.8	0.33 ± 0.09
A1503P	No current	N/A	N/A	N/A	N/A
Double mutation					

G432S/S435G	-19.8 ± 0.9 (n = 5)	6.3 ± 0.7	-39.2 ± 1.2 (n = 4)	5.7 ± 1.1	0.54 ± 0.07
-------------	-------------------------	---------------	-------------------------	---------------	-----------------

Reference: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3173108/>