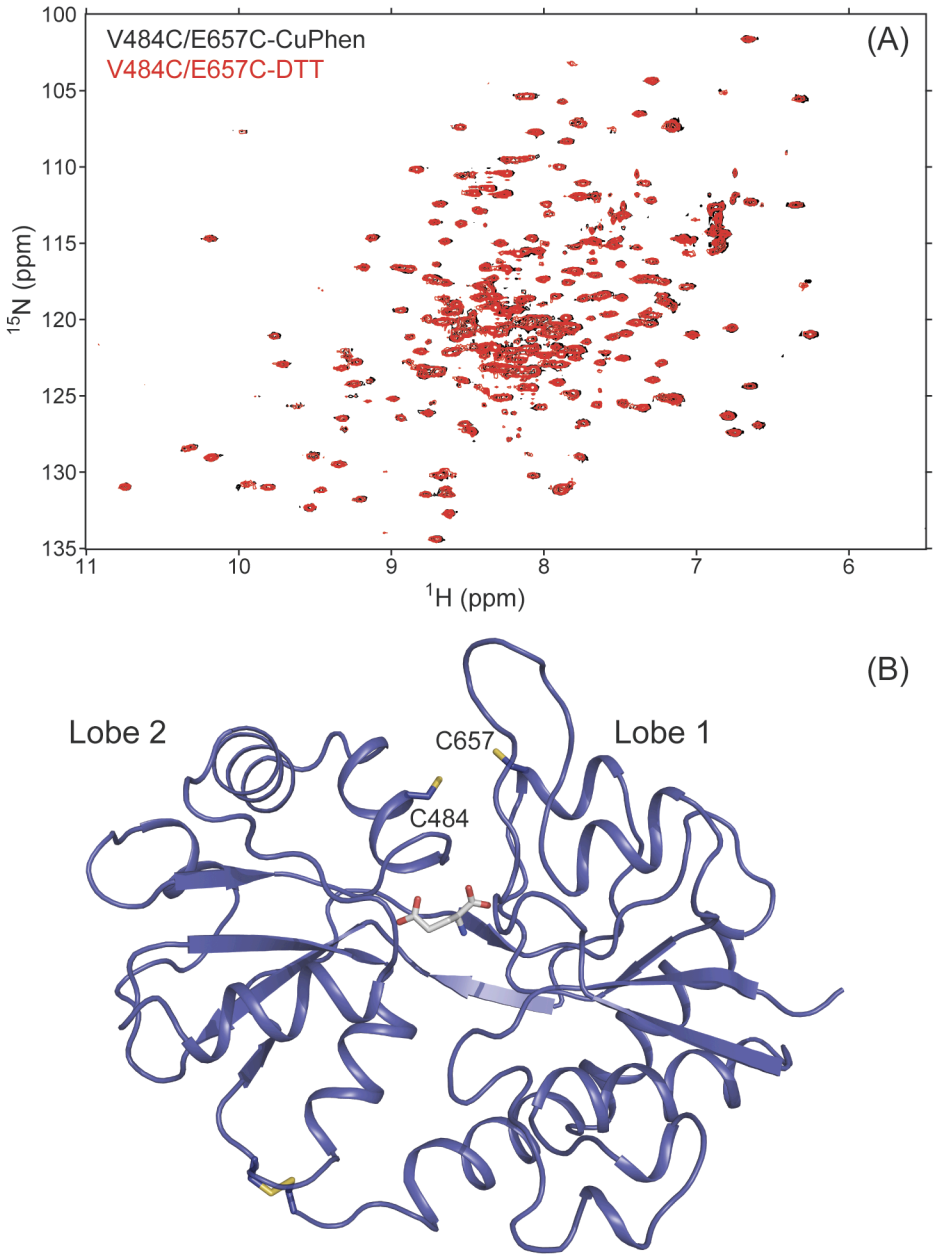
Supplementary Figure 1



Supplemental Figure 1

Legend to Supplementary Figure 1. **(A)** ^{1}H,^{15}N-HSQC spectrum of the V484C/E657C mutation of the GluA2 LBD bound to glutamate. The reduced (DTT) and oxidized (CuPhen) spectra were identical. **(B)** The crystal structure (1.82 Å, R/R_{free} = 20.8/25.5) of the double mutation clearly showed that the disulfide bond was not formed under oxidizing conditions.

Supplemental Table 1

Structural Statistics of Oxidized Forms

Structure	**Glutamate A452C/S652C**	**IW A452C/S652C**	**Kainate A452C/S652C**	**CNQX A452C/S652C**
Space Group	$P22_12_1$	$P22_12_1$	$P22_12_1$	$P2_12_12$
Unit Cell (Å)	a=47.6 b=114.3 c=163.8	a=47.8 b=114.4 c=163.5	a=47.8 b=113.9 c=164.8	a=114.7 b=165.2 c=47.7
X-ray source	CHESS (A1)	CHESS (A1)	CHESS (A1)	CHESS (A1)
Wavelength (Å)	0.977	0.977	0.977	0.977
Resolution (Å)	50-1.9 (1.93-1.90)	50-1.87 (1.90-1.87)	50.0-2.05 (2.05-2.02)	50.0-1.97 (2.00-1.97)
Measured reflections (#)	361048	512266	379373	388141
Unique reflections (#)	66721	69972	55053	56778
Data redundancy	5.2 (5.0)	6.8 (5.4)	6.3 (6.1)	6.4 (4.8)
Completeness (%)	98.3 (98.6)	99.9 (100.0)	99.9 (100.0)	92.8 (98.0)
R_{sym} (%)	8.3 (44.3)	12.2 (87.3)	11.3 (95.7)	5.0 (16.5)
I/σ_i	22.1 (3.2)	29.2 (2.3)	26.1 (2.12)	47.6 (9.8)
PDB ID	3T93	3T96	3T9H	3T9U
Current Model Refinement Statistics				
Phasing	MR	MR	MR	MR
Molecules/AU	3	3	3	3
R_{work}/R_{free} (%)	18.1/22.9	18.3/21.9	18.7/23.5	16.8/22.2
Free R test set size (#/%)	1938 (2.9)	1868 (2.7)	1832 (3.3)	3039 (5.1)
Number of protein atoms	6022	6038	6028	5918
Number of heteroatoms	35	50	50	56
Rmsd bond length (Å)	.015	.007	.015	.022
Rmsd bond angles (°)	1.54	1.10	1.52	1.83

Supplemental Table 2

Structural Statistics

Structure	**CNQX A452C/S652C (red)**	**Glutamate V484C/E657C**
Space Group	P2	$P22_12_1$
Unit Cell (Å)	a=49.2 b=58.7 c=96.1 α=90.0, β=93.4, γ=90.0	a=47.2 b=114.2 c=163.8
X-ray source	CHESS (A1)	CHESS (A1)
Wavelength (Å)	0.977	0.977
Resolution (Å)	50-1.97 (2.00-1.99)	50-1.82 (1.85-1.82)
Measured reflections (#)	137661	314725
Unique reflections (#)	37055	74434
Data redundancy	3.6 (2.6)	4.1 (3.5)
Completeness (%)	99.6 (96.0)	95.5 (99.8)
R_{sym} (%)	9.7 (28.7)	7.3 (30.9)
I/σ_i	14.0 (2.4)	33.6 (4.1)
PDB ID	3T9V	3T9X
Current Model Refinement Statistics		
Phasing	MR	MR
Molecules/AU	2	3
R_{work}/R_{free} (%)	17.8/23.8	19.9/24.0
Free R test set size (#/%)	1932 (5.2)	1953 (2.6)
Number of protein atoms	4029	6007
Number of heteroatoms	38	35
Rmsd bond length (Å)	.014	.008
Rmsd bond angles (°)	1.46	1.10