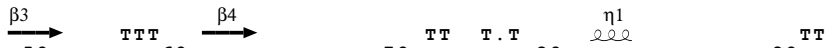


UBE2D2



UBE2D2

consensus

- 1c1|Glyma.04G089600_33-128
1c1|Glyma.06G091400_33-128
1c1|Glyma.02G199700_17-143
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1c1|Glyma.19G197500_17-154
1c1|Glyma.03G113100_5-108
1c1|Glyma.15G189500_8-136
1c1|Glyma.05G235000_15-150
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1c1|Glyma.07G168100_15-150
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1c1|Glyma.01G043600_7-145
1c1|Glyma.02G020000_7-145
1c1|Glyma.04G173300_7-145
1c1|Glyma.05G028800_7-145
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1c1|Glyma.18G124600_7-111
1c1|Glyma.10G212200_39-178
1c1|Glyma.20G178900_39-174
1c1|Glyma.11G095700_39-155
1c1|Glyma.12G021800_39-176
1c1|Glyma.05G091100_9-153
1c1|Glyma.17G169700_9-153
1c1|Glyma.11G053300_8-150
1c1|Glyma.01G188900_8-150
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1c1|Glyma.04G199200_6-145
1c1|Glyma.06G166300_6-145
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1c1|Glyma.13G040500_3-143
1c1|Glyma.06G124900_3-142
1c1|Glyma.14G124300_3-142
1c1|Glyma.03G255400_3-142
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1c1|Glyma.12G153900_92-241
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1c1|Glyma.17G034400_40-142
1c1|Glyma.07G046200_7-157
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1c1|Glyma.07G240600_12-127
1c1|Glyma.17G032800_12-151
1c1|Glyma.15G141200_12-127
1c1|Glyma.09G036300_12-127
1c1|Glyma.11G099100_34-153

Sequence alignment of UBE2D2 protein variants. The alignment shows conserved regions across different Glyma accessions. Key motifs are highlighted: beta3 (TTT), beta4 (TT, T.T), and eta1 (222). Residue positions 50, 60, 70, 80, and 90 are indicated. The alignment includes amino acid sequences for each accession, with some residues highlighted in red to indicate conservation or specific mutations.

