Figure S4: Sequence alignments of the SQDAR 69-73 segment.

This sequence alignment shows how the residues highlighted in yellow are well conserved in the CRT groups 1 and 2; less conserved in groups 3 and 4; and not conserved in the group 5. The following F74 (green) is found in most of the CRT-like sequences, except for the plant group 4. It is not present in the CNX-like group 5 sequences. Details corresponding to the sequence names are given in Figure S2.

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GROUP_1
human_GB_CRT        GLQTSQDARFYAL
SPT_A8E4J9_9ACAR    GIQTSEDARFYGL
SPT_Q64K99_9ACAR    GLQTSEDARFYGI
SPT_B5X0V5_SALSA    GLQTSQDARFYAL
SW_CALR_RABIT       GLQTSQDARFYAL
SPT_Q64K76_IXOPE    GIQTSEDARFYGL
SPT_Q7ZXY3_XENLA    GLQTSQDARFYAM
SPT_Q68HD1_IXOSC    GIQTSEDARFYGL
SPT_B5X207_SALSA    GLQTSQDAHFYSS
SPT_Q64K83_9ACAR    GIQTSEDARFYGL
SW_CALR_MACFA       GLQTSQDARFYAL
SPT_Q9U6S0_STRPU    GIQTSQDAKFYGL
SPT_A5D7J6_BOVIN    GLQTSQDARFYAL
SPT_A1YB06_EISFO    GLQTTQDARFYGI
SPT_Q98984_RANRU    GLQTSQDAKFYAH
SPT_B3S3X6_TRIAD    GIQTSQDARFYAV
SPT_Q6NVT6_XENTR    GLQTSQDARFYAL
SPT_A5LGG9_CRAGI    GIQTSQDAKFYGI
SW_CALR_CRIGR       GLQTSQDARFYAL
SPT_A6YIE3_PINFU    GIQTSQDAKFYGI
SPT_Q6WSQ2_RHISA    GLQTSEDARFYGI
SPT_Q64K91_DERAN    GLQTSEDARFYGI
SPT_Q64K92_9ACAR    GLQTSEDARFYGI
SPT_Q0VJ74_9BILA    GLKTSQDAKFYSR
SPT_Q64K89_DERVA    GLQTSEDARFYGI
SPT_O97372_DIRIM    GLKTTQDAKFYSI
SPT_Q9PUC1_DANRE    GLQTSQDARFYAL
SPT_C5MRN9_9BILA    GLKTAQDARFYSI
SPT_Q26268_APLCA    IQTSQDARFYGL
SW_CALR_ONCVO       GLKTTQDAKFYSI
SPT_A9C3S5_DANRE    GLQTSQDAHFYAM
SPT_B8K275_FENCH    GIQTGQDARFYGL
SPT_Q8IS63_COTRU    GIQTTEDARFYAL
SPT_Q8WR36_ANOGA    GLQTSQDARFYAL
SPT_Q17MI1_AEDAE    GLQTSQDARFYAA
SPT_C1BVC1_9MAXI    GIQTSQDARFYAL
SPT_D3TM69_GLOMM    GLQTSQDARFYAI

GROUP_2
SPT_Q7Y140_ORYSJ    GIQTSEDYRFYAI
SPT_A9SCB3_PHYPA    GIQTSTDSRYYAI
SW_CALR_BERST       GIQTSEDYRFYAI
SPT_C4PB36_CARPA    GIQTSEDYRFYAI
SW_CALR1_ARATH      GIQTSEDYRFYAI
SPT_A9NS22_PICSI    GIQTHPDARFFAI
SPT_Q5MCL9_WHEAT    GIQTSEDYRFYAI
SPT_O22502_BRANA    RPARTTDSTPSQL
SPT_B9F6V5_ORYSJ    GIQTSEDYRFYAI
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GROUP_3
SPT_Q4R3W0_MACFA    GLQTTQNGRFYAI
SPT_B1Q2L7_MOUSE    GLQTTQNSRFYAI
SW_CALR3_HUMAN      GLQTTQNGRFYAI
SPT_Q3TQS0_MOUSE    GLQTTEDAKFYAL
SPT_D3ZYM6_RAT      GLQTTEDAKFYAL
SPT_C1N041_9CHLO    GIQTSADARFYAL
SPT_O45034_SCHJA    GLKTTQDARFYGI
SPT_C4Q5I7_SCHMA    GLKTTQDARFYGI
SPT_C8XTL8_9EUKA    GIMTTQDAKFYAL
SPT_D3BIF1_POLPA    GIQTSPDARFYAI
SW_CALR_EUGGR       GIQTSQDAKFYAI
SPT_C4M296_ENTHI    GLQTSEDNKFYIA
SPT_B7GDH4_PHATR    GIQTSVDARFFGI
SPT_Q967S4_TRYCO    GLRLTEDARFYAL
SPT_A4HJP8_LEIBR    GVKLTEDSKFYAI
SPT_Q4Q601_LEIMA    GLKLMEDAKFYAV
SPT_Q4CPZ0_TRYCR    GLRLTEDARFYAL
SPT_C8CIJ1_9TRYP    GLQLTQDARFYAV
SPT_Q9XYF8_TRYCR    GLRLTEDARFYAL
SPT_C5L9W8_9ALVE    GLKTAEDHRYYAY
SPT_C5LE92_9ALVE    GLKTAEDHRYYAY
SPT_C5LZP6_9ALVE    GLKTAEDHRYYAY
SPT_D0NR25_PHYIN    AIKTSEDARFYAL
SPT_A8PEL1_BRUMA    GLTTTEDVKNYAI

GROUP_4
SPT_C6TCW1_SOYBN    GIQTSSDAKHFAI
SPT_B6TA28_MAIZE    GIQTTIDARHFAI
SPT_C5XET1_SORBI    GIQTTMDARHFAI
SPT_B8LRK0_PICSI    GIQTYPDARHYAI
SPT_B4FUA8_MAIZE    GIQTTIDARHFAI
SPT_C5Z0S1_SORBI    GIQTTGDAKHFAI
SPT_Q8GUI1_ARATH    GIQTYNDAKHYAI
SPT_B9MY68_POPTR    GIQTYNDAKHFAI
SPT_Q8LJ85_ORYSJ    GIQTTLDARHFAI
SPT_B8AZS4_ORYSI    GIQTTSDAKHFAI

GROUP_5
SPT_B5M4U3_9STRA    GLVLDKPARHYGL
SPT_A9PHA6_POPTR    GLLVSEPAKKYAI
SW_CALX_PEA         GLLVSEPARKYAI
SW_CALX_RAT         GLVLMSRAKHHAI
SPT_B4R3M8_DROSI    GLVLKSKAKHAAI
SPT_Q9TVF3_SCHJA    ALVLKSKAKHHAV
SPT_A2E253_TRIVA    LFKMKAASKYYGA
SPT_A8K454_HUMAN    GLVLKSRAKHHAI
SPT_Q80YU3_MOUSE    GLVLKSKAKHHAI
SPT_Q7Q9V3_ANOGA    GLVLKSKAKHAAI
SPT_B4JYJ8_DROGR    GLVLKSKAKHAAI
SPT_D1ZZU8_TRICA    GLVLKSKAKHAAI
SPT_Q0KHZ9_DROME    GLVLKSKAKHAAI
SPT_Q9I7S9_DROME    GLVLKSKAKHAAI
SPT_B4IF87_DROSE    GLVLKSKAKHAAI
SPT_Q6ZP56_HUMAN    GLVLMSRAKHHAI
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