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INV  KDTIVANGSDA I TLTATVTDAYGNPVPGG--EVTFSPVSDGATLFSNGTA-----TTDANGIA--TVTLTSTKAGTIVTASLEND
C030 QTSIFLAG-NAYNITLTLLDSVGDPTCVLY--DPLLSV--SCPSSSSNGRDFCSLQLSPLYNGVYNIKVIPQTL--WGGHTVWPPPYSD
C276 LPQEVFAG--IPVSLTLQAMDIMSNPTRLVDP--ESYQP--FGQQ-PDNKTLQVRLVT-VDSGALQPNVVAIPTNTTGACSWSIIT-FF
C392 LPEIGFAG--TTLTYVTPRDLMGNITAPLANN--DLSIGL--TGST-FFHSFI----PVEPVKGDYSVYSLTTE--AGLVVSIQLHND
C501 APTPLVAG--EQVYLRVFKDLYGNTIQADKVVDLNIVG--PGQV-LMNMSM-----LPSCAF--EVIYQPIV-AGLVVSIQLHND
C598 VDDYIVAG--EASSFKLAFHDSVGNAAASSG--EASVVVFKYGGESLSFPL-----NLSGKFIIEELPFRLMH-SGLVAFSIS-VND
G033 PEGPVVAG--RPYNFS I LLRDNDLQPVNLY--DPLLAV--GCPNSFNE NLCTTYSLRPLGDGVYVVSLLVLLTF-K-GAHEPWPQYND
G280 SNTQIVAG--SLYHVTVQSRDRFSNPTPLS--DPAQY-TTWLEQVQNSS-LVTMSLSS---GHVQLEPIV NAT I SPGGLAOWHIRFR
C399 IKDTFEAG--PLLLVARFADEWGNPTLGS--ANVYV-SELKNGAQLL-----PSFRAVYVQEVVYSVNIIFRAGAVVIRISLGA
C509 GPTPVVAG--VQYSVWVHAYDIVGNQLHK--DSNCCG-LQIGGAPTA----NTDIEEDTQKLG--FSYNIIVTSGNVMSLATTE
G607 FSTAVVAG--MSFYATVEFTDSFGNPAVPTG--VLSV IITG-GVQHTTEV-----AMNGDCNATIISLQLQVAST-VAAAYGY-MND

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Figure S7. Invasin/intimin immunoglobulin (Ig)-like repeats found in both

***Chlamydomonas reinhardtii* and *Gonium pectorale* FUS1 based on Misamore**

et al. (2003). FUS1 domains and the bacterial invasin/ intimin Ig-like consensus

sequence are aligned. “INV” is a consensus sequence based on 25 different,

invasin-related BID1, bacterial Ig-like (group 1) domains (accession numbers:

1F00_I, 1CWV_A, gi12513096, gi12516151, gi12519346, gi1706558, gi2125981,

gi124714, gi3257750, gi11044949, and gi7462086). The remaining ten sequences,

whose positions are indicated by the numbers at the left, are derived from FUS1 (C

for CrFUS1; G for GpFUS1). The alignment was manually edited. Identical and

similar amino acids are represented by blocked and shaded backgrounds,

respectively.