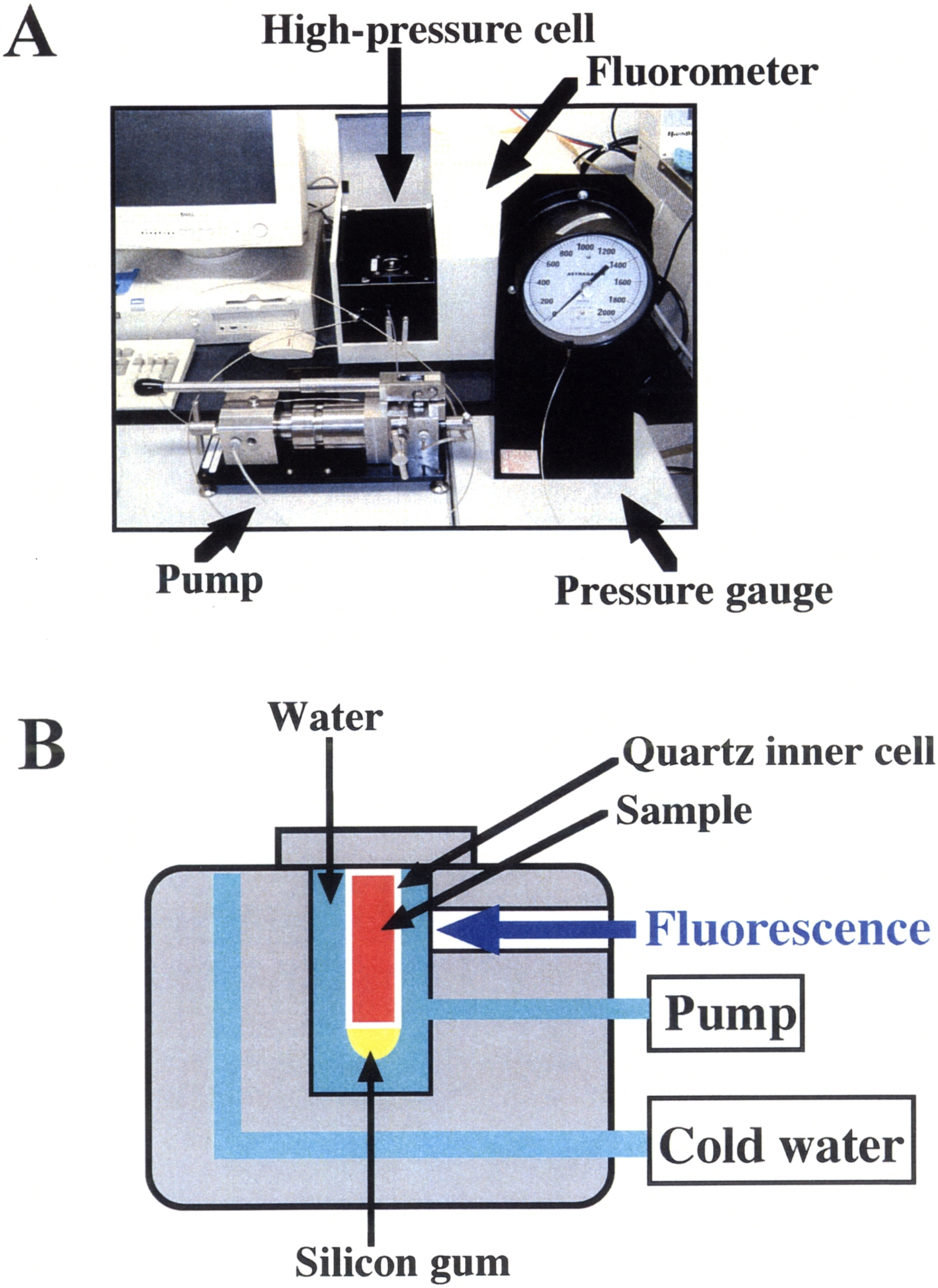

Fig. 2-1. High-pressure measurement system. (A) Component of high-pressure measurement system. A high-pressure cell is set in a fluorometer. High-pressure is generated with a hand pump. (B) A high-pressure cell. A sample is put in the quartz inner cell. High-pressure generated with the pump is conveyed by the water medium. The water medium pushes up the silicon gum and the sample in the inner cell is compressed. The whole cell is cooled with cold water.

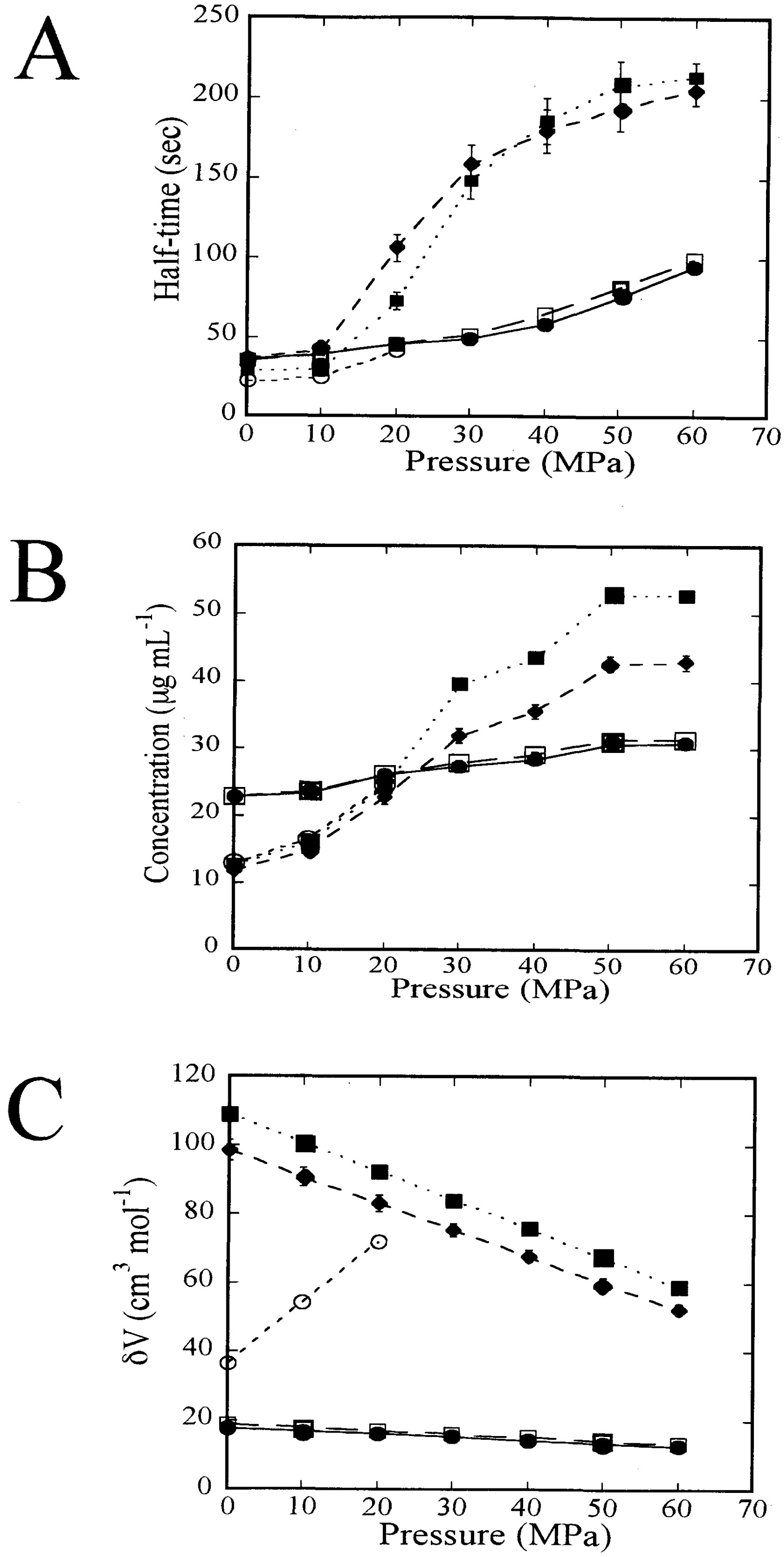

Fig. 2-2. Effects of pressure on actin polymerization. (A) Half-time to steady state in polymerization of actin. (B) Critical concentration of actin at various pressures. (C) Volume change (δV) associated with polymerization of actin at various pressures. Symbols are as follows: *C. yaquinae* (●); *C. armatus* (□); Chicken (◆); carp (O); *C. acrolepis* (■). Values are means ± S.D. of four independent experiments. Errors for several experiments are too small to show error bars.

```
                  -49
C.acrolepis-1      TTGGGTCTT TCTCTCTCCA AGCCGCAGAC ACTCACCTAA GAAAGCCATC
C.acrolepis-2a       TTAC... GT.....GAT CC..CGGAG. TAC..A..G. AT...T..A.
C.cinereus-1                                                   G........
C.cinereus-2a                                                    ..T..A.
C.armatus-2a                          T CC..CGGAG. TAC..A..G. AT...T..A.
C.armatus-2b                      ..... .......... .......... .G.....T..
C.yaquinae-2a                         T CC..CGGAG. TAC..A..G. AT...T..A.
C.yaquinae-2b                     ..... .......... .......... .G.....T..

                   START                                                50
C.acrolepis-1      ATGTGTGACG ATGAGGAGAC TACCGCCCTT GTGTGCGACA ACGGCTCCGG
C.acrolepis-2a     .......... .C..A..... C........C .......... ..........
C.cinereus-1       .......... .......... .......... .......... ..........
C.cinereus-2a      .......... .C..A..... C........C .......... ..........
C.armatus-2a       .......... .C..A..... C........C .......... ..........
C.armatus-2b       .......... .......... .......... .......... ..........
C.yaquinae-2a      .......... .C..A..... C........C .......... ..........
C.yaquinae-2b      .......... .......... .......... .......... ..........

                                                                       100
C.acrolepis-1      CCTGGTGAAG GCTGGGTTCG CCGGAGACGA TGCCCCCAGG GCTGTCTTCC
C.acrolepis-2a     ...C...... .....C.... .......... C..A...... ..C.......
C.cinereus-1       .......... .......... .......... .......... ..........
C.cinereus-2a      ...C...... .....C.... .......... C..A...... ..C.......
C.armatus-2a       ...C...... .....C.... .......... C..A...... ..C.......
C.armatus-2b       ...C...... .......... .......T.. C..G...... ..........
C.yaquinae-2a      ...C...... .....C.... .......... C..A...... ..C.......
C.yaquinae-2b      ...C...... .......... .......T.. C..G...... ..........

                                                                       150
C.acrolepis-1      CCTCCATCGT CGGCCGCCCC CGTCACCAGG GTGTCATGGT CGGTATGGGT
C.acrolepis-2a     .A........ .........T .......... .C........ G..C.....G
C.cinereus-1       .......... .......... .......... .......... ..........
C.cinereus-2a      .A........ .........T .......... .C........ G..C.....G
C.armatus-2a       .A........ .........T .......... .C........ G..C.....G
C.armatus-2b       .A........ ..........            .......... A..C.....G
C.yaquinae-2a      .A........ .........T .......... .C........ G..C.....G
C.yaquinae-2b      .A........ .......... .......... .......... A..C.....G

                                                                       200
C.acrolepis-1      CAGAAAGACT CCTACGTCGG CGACGAGGCC CAGAGCAAGA GAGGTATCTT
C.acrolepis-2a     .....G.... .......G.. .......... .......... ........C.
C.cinereus-1       .....G.... .......... .......... .......... ..........
C.cinereus-2a      .....G.... .......G.. .......... .......... .G......C.
C.armatus-2a       .....G.... .......G.. .......... .......... .G..C...C.
C.armatus-2b       .....G.... ......CG.. .......... .......... .G......C.
C.yaquinae-2a      .....G.... .......G.. .......... .......... .G..C...C.
C.yaquinae-2b      .....G.... .......G.. .......... ........A. .G......C.

                                                                       250
C.acrolepis-1      GACTCTTAAG TACCCCATTG AGCACGGCAT CATCACCAAC TGGGACGACA
C.acrolepis-2a     ...C..C... ........C. .......... .......... ..........
C.cinereus-1       .......... .......... .......... .......... ..........
C.cinereus-2a      ...C..C... ........C. .......... .......... ..........
C.armatus-2a       ...C..C... ........C. .......... .......... ..........
C.armatus-2b       ...C..C... .......... .......... .........T ..........
C.yaquinae-2a      ...C..C... ........C. .......... .......... ..........
C.yaquinae-2b      ...C.CC... .......... .......... .........T ..........
```

Fig. 2-3. Comparison of cDNA nucleotide sequences encoding α-actin 1, α-actin 2a and α-actin 2b. The dot indicates an identical nucleotide with that of *C. acrolepis* α-actin 1. 5' primer-2, 3, 5' primer-4, 5 and polyadenylation signals are indicated by red, blue and boldfaced letters, respectively. These sequences are available from the DDBJ/EMBL/GenBank databases. The accession numbers are AB021649, AB021650, AB021651, AB021652, AB086240, AB086241, AB086242, and AB086242 from the top.

```
                                                                       300
C.acrolepis-1   TGGAGAAGAT CTGGCACCAC ACCTTCTACA ATGAGCTGCG CGTGGCCCCC
C.acrolepis-2a  .......... .......... .......... .C........ T.........
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   .......... .......... .......... .C........ T.........
C.armatus-2a    .......... .......... .......... .C........ T.........
C.armatus-2b    .......... .......... .......... .C........ ..........
C.yaquinae-2a   .......... .......... .......... .C........ T.........
C.yaquinae-2b   .......... .......... .......... .C........ ..........

                                                                       350
C.acrolepis-1   GAGGAGCACC CCACCCTGCT CACTGAGGCC CCCCTGAACC CCAAGGCTAA
C.acrolepis-2a  .......... .......... ...C...... .....C.... .......C..
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   .......... .......... ...C...... .....T.... .......C..
C.armatus-2a    .......... .....T.... ...C...... .....C.... .......C..
C.armatus-2b    .......... .......... .......... .....C.... ..........
C.yaquinae-2a   .......... .......... ...C...... .....C.... .......C..
C.yaquinae-2b   .......... .......... .......... .....C.... ..........

                                                                       400
C.acrolepis-1   CCGTGAAAAG ATGACCCAGA TCATGTTTGA GACCTTCAAC GTCCCCGCCA
C.acrolepis-2a  .A.G..G... .......... .......C.. .......... ..G.......
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   .A.G..G... .......... .......C.. .......... ..G.......
C.armatus-2a    .A.G..G... .......... .......C.. .......... ..G.......
C.armatus-2b    .A....G... .....A.... .......... .......... ..G.......
C.yaquinae-2a   .A.G..G... .......... .......C.. .......... ..G.......
C.yaquinae-2b   .A....G... .....A.... .......... .......... ..G.......

                                                                       450
C.acrolepis-1   TGTATGTGGC CATCCAGGCT GTGCTGTCCC TGTACGCTTC CGGCCGTACC
C.acrolepis-2a  ....C..... .........C .......... .......C.. ..........
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   ....C..... .........C .......... .......C.. ..........
C.armatus-2a    ....C..... .........C .......... .......C.. ..........
C.armatus-2b    .......... ....A....C .......... .......... ......C...
C.yaquinae-2a   ....C..... .........C .......... .......C.. ..........
C.yaquinae-2b   ......C... ....A....C .......... .......... ...A..C...

                                                                       500
C.acrolepis-1   ACCGGTATTG TGCTGGATGC TGGTGATGGT GTCACCCACA ACGTCCCAGT
C.acrolepis-2a  ..T.....C. .......CT. C.....C... ..G....... ....G..G..
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   ..T.....C. .......CT. C.....C... ..G....... ....G..G..
C.armatus-2a    ..T.....C. .......CT. C.....C... ..G....... ....G..G..
C.armatus-2b    ..T.....C. .......CT. C..G..C... ..G.....T. ....G..G..
C.yaquinae-2a   ..T.....C. .......CT. C.....C... ..G....... ....G..G..
C.yaquinae-2b   ..A.....C. .......CT. C..G..C... ..G.....T. .......C..

                                                                       550
C.acrolepis-1   GTATGAGGGT TACGCCCTGC CCCACGCCAT CATGCGTCTT GACCTGGCTG
C.acrolepis-2a  .........C .....G.... .......... ......C..G ........C.
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   .........C .....G.... .......... ......C..G ........C.
C.armatus-2a    ...C.....C .....G.... .......... ......C..G ........C.
C.armatus-2b    ...C...... .....T.... .......... ....A.G..G ...T....C.
C.yaquinae-2a   ...C.....C .....G.... .......... ......C..G ........C.
C.yaquinae-2b   A..C.....C .....T.... .......... ....A.GT.G ...T....C.

                                                                       600
C.acrolepis-1   GTCGCGACCT GACCGACTAC CTGATGAAGA TCCTGACCGA GCGTGGCTAC
C.acrolepis-2a  .C........ C......... ..C....... ....C..... ...C..A...
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   .C........ C......... ..C....... ....C..... ...C..A...
C.armatus-2a    .C........ C......... ..C....... ....C..... ...C..A...
C.armatus-2b    .......... C......... ..C....... ....C..... .A.G..G...
C.yaquinae-2a   .C........ C......... ..C....... ....C..... ...C..A...
C.yaquinae-2b   ....G..... C..A...... ..C....... .......... .A.G......
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Fig. 2-3. *Continued.*

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                                                                        650
C.acrolepis-1    TCTTTCGTTA CCACCGCCGA GCGTGAGATC GTGCGCGACA TCAAGGAGAA
C.acrolepis-2a   ..C.....C. .......... .......... .......... ..........
C.cinereus-1     .......... .......... .......... .......... ..........
C.cinereus-2a    ..C.....C. .......... .......... .......... .......A..
C.armatus-2a     ..C.....C. .......... ...G...... .......... ..........
C.armatus-2b     ........C. .......... .......... .......... ..........
C.yaquinae-2a    ..C.....C. .......... ...G...... .......... ..........
C.yaquinae-2b    AG......C. .......... .......... .......... ..........

                                                                        700
C.acrolepis-1    GCTGTGCTAT GTGGCTCTGG ACTTCGAGAA CGAGATGGCC ACCGCCGCCT
C.acrolepis-2a   .........C ..C..C.... .......... .........A ..........
C.cinereus-1     .......... .......... .......... .......... ..........
C.cinereus-2a    .........C ..C..C.... .......... .........A ..........
C.armatus-2a     .........C ..C..C.... .......... .........G ..........
C.armatus-2b     .......... .....G.... .......... .........G ........G.
C.yaquinae-2a    .........C ..C..C.... .......... .........G ..........
C.yaquinae-2b    .......... .....G.... .......... .........G ........T.

                                                                        750
C.acrolepis-1    CCTCCTCCTC CCTGGAGAAG AGCTACGAGC TTCCCGACGG TCAGGTCATC
C.acrolepis-2a   .......... .......... .....T.... .G........ ..........
C.cinereus-1     .......... .........A .......... .......... ..........
C.cinereus-2a    .......... .......... .......... .G........ ..........
C.armatus-2a     .......... .......... .......... .G........ ..........
C.armatus-2b     .......A.. T......... .......... .G........ ..........
C.yaquinae-2a    .......... .......... .......... .G........ ..........
C.yaquinae-2b    .......A.. .......... ..T....... .G........ ..........

                                                                        800
C.acrolepis-1    ACCATAGGAA ACGAGCGTTT CCGTTGCCCT GAGACCCTCT TCCAGCCTTC
C.acrolepis-2a   .....C..C. .......G.. ...C.....C .......... .......C..
C.cinereus-1     .....C.... .......... .......... .......... ..........
C.cinereus-2a    .....C..C. .......C.. ...C.....C .......... .......C..
C.armatus-2a     .....C..C. .......C.. ...C.....C .......... .......C..
C.armatus-2b     ........C. .......C.. ...C...... .......... ..........
C.yaquinae-2a    .....C..C. ....A..C.. ...C.....C .......... .......C..
C.yaquinae-2b    ........C. .......C.. ...C...... .......... ..........

                                                                        850
C.acrolepis-1    CTTCATCGGA ATGGAGTCCG CCGGTATCCA TGAGACCGCC TACAACAGCA
C.acrolepis-2a   .........C ........T. ....C..... C......... ..........
C.cinereus-1     .......... .......... .......... .......... ..........
C.cinereus-2a    .........C ........T. ....C..... C......... ..........
C.armatus-2a     .........C .......... ....C..... C......... ..........
C.armatus-2b     .........T .......... .......... .......... ..........
C.yaquinae-2a    .........C .......... ....C..... C......... ..........
C.yaquinae-2b    .........T ........G. .......... .......... ..........

                                                                        900
C.acrolepis-1    TCATGAAGTG CGACATTGAC ATCCGCAAGG ACCTGTACGC CAACAACGTG
C.acrolepis-2a   .......... ......C... .......... .......... ..........
C.cinereus-1     .......... .......... .......... .......... ..........
C.cinereus-2a    .......... ......C... .......... .......... ..........
C.armatus-2a     .......... ......C... .......... .......... ..........
C.armatus-2b     .......... ......C... .......... .......... .........T
C.yaquinae-2a    .......... ......C... .......... .......... ..........
C.yaquinae-2b    .......... ......C... .......... .......... ..........

                                                                        950
C.acrolepis-1    CTCTCCGGTG GTACCACCAT GTACCCTGGT ATTGCTGACC GTATGCAGAA
C.acrolepis-2a   ..G.....C. C......... .......... .......... .C........
C.cinereus-1     .......... .......... .......... .......... ..........
C.cinereus-2a    ..G.....C. .C........ .......... ..C....... .C........
C.armatus-2a     ..G.....C. .C........ ......C... ..C....... .C........
C.armatus-2b     ..G....... .......... .......... ..C....... ..........
C.yaquinae-2a    ..G.....C. .C........ ......C... ..C....... .C........
C.yaquinae-2b    ..G....... .......... ......G... ..C..C.... ..........
```

Fig. 2-3. *Continued.*

```
                                                                     1000
C.acrolepis-1   GGAGATCACC GCCCTGGCCC CATCCACCAT GAAGATCAAG ATCATTGCTC
C.acrolepis-2a  .......... ........G. .T........ .......... .....C..C.
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   .......... ........G. .T........ .......... .....C..C.
C.armatus-2a    .......... ........G. .T........ .......... .....C..C.
C.armatus-2b    .......... ........A. .C........ .......... ..........
C.yaquinae-2a   .......... ........G. .T........ .......... .....C..C.
C.yaquinae-2b   .........A ........A. .G........ .......... ..........

                                                                     1050
C.acrolepis-1   CCCCCGAGAG GAAGTACTCC GTCTGGATCG GTGGCTCCAT CCTGGCTTCC
C.acrolepis-2a  ....A..... .........T .......... .A........ ......C...
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   ....A..... .........T .......... .A........ ......C...
C.armatus-2a    ....A..... .........T .......... .A........ ......C...
C.armatus-2b    ....A..... .......... .......... .......... ..........
C.yaquinae-2a   ....A..... .........T ..G....... .A........ ......C...
C.yaquinae-2b   ....A..... .......... .......... .......... ..........

                                                                     1100
C.acrolepis-1   CTGTCCACCT TCCAGCAGAT GTGGATCTCC AAGCAGGAGT ACGACGAGGC
C.acrolepis-2a  .......... .......... .......AG. .......... ..........
C.cinereus-1    ........A. .......... .......... .......... ..........
C.cinereus-2a   .......... .......... .......AG. .......... ..........
C.armatus-2a    .......... .......... .......AG. .......... ..........
C.armatus-2b    .......... .......... .......... .......... ..........
C.yaquinae-2a   .......... .......... .......AG. .......... ..........
C.yaquinae-2b   .......... .......... .......... .......... ..........

                                                      STOP           1150
C.acrolepis-1   AGGCCCCAGC ATTGTCCACA GGAAGTGCTT CTAAATCCTC AACATTTGTC
C.acrolepis-2a  C......TC. ..C....... .......... .......AC. C..CCAGCGT
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   C......TC. ..C....... .......... .......AC. C..CCAGCGT
C.armatus-2a    C......TC. ..C....... .......... .......AC. C..CCAGCGT
C.armatus-2b    .......... .......... .......... .......AC. CG.CCAGCGT
C.yaquinae-2a   C......TC. ..C....... .......... .......AC. C..CCAGCAT
C.yaquinae-2b   .......... .......... .......... .......AC. CG.CCAGCGT

                                                                     1200
C.acrolepis-1   TCCATCATTT TCGCCATCAC CATCATCACC ACCTGTCACC AGGAGATCGG
C.acrolepis-2a  CTGC..TCAG GACA..A.CA ACCGG.GG.A CGAC.G.G.. .CCCAGGA.C
C.cinereus-1    .......... .......... ...T...... .......... ..........
C.cinereus-2a   CTGC..TCAG GACA..A.CA ACCGG.GG.A CGAC.G.G.. .CCCAGGA.C
C.armatus-2a    CTGC..TCAG GACA..A.CA ACCGG.GG.A CGAC.G.G.. .CCCAGGA.C
C.armatus-2b    CTGC..TCAG GACA..A.CA ACCGG.GG.A CGAC.G.G.. .CCCAGGG.C
C.yaquinae-2a   CTGC..TCAG GACA..A.CA ACCGG.GG.A CGAC.G.G.. .CCCAGGA.C
C.yaquinae-2b   CTGC..TCAG GACA..A.CA ACCGG.GG.A CGAC.G.G.. .CCCAGGA.C

                                                                     1250
C.acrolepis-1   GCGAGGAGGA GGACCACCCC ATGCGGCACA GCGACACCCT GCTGCTCATA
C.acrolepis-2a  CGCCTAGT.G AC.TTTTGTT G.TGTTGTTG TT.TTGTGGA TG..G.AG..
C.cinereus-1    .......... .......... .......... .......... ..........
C.cinereus-2a   CGCCTAGT.G AC.TTTTGTT G.TGTTGTTG TT.TGGATG. .G.AG.AG.T
C.armatus-2a    CGCCTA.T.G AC.TTTTGTT G.TGTTGTTG TT.TTGTGGA TG..G.AG..
C.armatus-2b    CGCCTAGT.G AC.TTTTGTT G.TGTTGTTG TT.TTGTGGA TG..G.AG..
C.yaquinae-2a   CGCCTAGT.G AC.TTTTGTT G.TGTTGTTG TT.TTGTGGA TG..G.AG..
C.yaquinae-2b   CGCCTAGT.G AC.TTTTGTT G.TGTTGTTG TT.TGGATG. .G.AG.AG.T

                                                                     1300
C.acrolepis-1   TGCATTTTTT TTTATGATTC TTGAATCTGC ATATCGTACT GGCTGTCTGT
C.acrolepis-2a  GTTG..G..G ..GTG.TAGT GGA.GAAGTG T.TGGTGGTG T.G.CAACCG
C.cinereus-1    .......... .......... ..AG...... .....TCT.. ..........
C.cinereus-2a   GTTG..G..G .GGTG.TGGA AGAGG.G.TT GGTGGTGTGG TCACCGAA.C
C.armatus-2a    GTTG..G..G ..GTG.TACT GGA.GAAGTG T.TGGTGGTG T.G.CA.C.A
C.armatus-2b    GTTG..G..G .GGTG.TGGT GA...GG..T T.TGG.CTG. .TTG...ACC
C.yaquinae-2a   GTTG..G..G ..GTG.TACT GGA.GAAGTG T.TGGTGGTG T.G.CAACCG
C.yaquinae-2b   GTTG..G.GG .GGTG.TGGA GGAGG.G.TT GGCGGTGTG. TCACCGAA.C
```

Fig. 2-3. *Continued.*

					1350
C.acrolepis-1	TGTCTGTGTT	GTGCGGAGAA	CAAGCTGTGA	ACAAACAACA	CTGAACCATG
C.acrolepis-2a	AAG.GCAAG.	...TA.C.C.	A.CCGGAGCG	.GC.G.GGGG	GGCG.G..G.
C.cinereus-1	....	........G.	....	.........G	A.........
C.cinereus-2a	GCAAGTGTG.	AGCGCA.ACC	GG...GAGC.	G.GGGGGG.G	AGC.GGG.G.
C.armatus-2a	A.CGCAA..G	TGTA.CGC..	.CG.AGCGA.	CAGCGGGGGG	.GAGCAAGGA
C.armatus-2b	GAAGC.CAAG	CGTGTACCGC	A.CCGGAGCG	.AC.CGGGGG	GG.GGAGCA.
C.yaquinae-2a	AAG.GCAAG.	...TA.C.C.	A.CCGGA.CG	CGGGGGGGGG	GG.G.G..G.
C.yaquinae-2b	GCAAGCGTG.	AGCGCA.CCG	G.GCGA.CAG	.AC.CGGCGG	GC.G.G..GT

					1400
C.acrolepis-1	CATCTAACCC	CCAAAAAATT	**AATAAA**AAAA	TCAAAACAAA	AAAAAAAAAA
C.acrolepis-2a	G.GG.C.G.A	.GTG..CGCG	TGA.G..CTG	.AC.T.TG.T	T.TTT.TTG.
C.cinereus-1	....C.....	....	....	ATC...AC..	C.........
C.cinereus-2a	TCAGC.CGTG	AACGCGTGAA	G.ACTGT.C.	.ATG.TT.TT	T.TTG.TT.T
C.armatus-2a	AG..AGCA.G	TG..CGCT.G	..AG...CTG	.AC.T.ATG.	.T.TTT.TTG
C.armatus-2b	TGAGGTCAG.	A.GTG..GAA	.CA.C.....	.A....ACC.	CC........
C.yaquinae-2a	G.AG.C.G.A	..TG..CGCG	TGA.G..CTG	.AC.T.TG..	T.TTT.TTG.
C.yaquinae-2b	G.GG.C.G.A	.GTG..G.AA	C.AC.....T	AA.....C.C	C.........

					1450
C.acrolepis-1	AAAAA				
C.acrolepis-2a	TT.TGCAGGC	CTACATGGAG	GGATTGTTTT	GTAAGGACAG	GGGCCCGTGG
C.cinereus-1	.....AAAAA	A			
C.cinereus-2a	GC.GGCCTAC	ATGGAGGGAT	TGTTTTGTAA	GGACAGGGGC	CCGTGGCCCC
C.armatus-2a	.TT.TGCAGG	CCTACATGGA	AGGATGTTTG	TTAGAACGGG	GGCCCCACGG
C.armatus-2b	.				
C.yaquinae-2a	TT.TGCAGGC	CTACATGGAG	GGATTGTTAG	AAAAGGGGCC	CACGGCCCCG
C.yaquinae-2b	.				

					1500
C.acrolepis-1					
C.acrolepis-2a	CCCCGCAGGC	GATGAGTTGG	CTGTTGGCTT	CGAGGTCGAG	GAAAACCCCG
C.cinereus-1					
C.cinereus-2a	GCAGGCGATG	AGTTGGCTGT	TGGCTTCGAG	GTCGAGGAAA	ACCCCGAACA
C.armatus-2a	CCCCGCAGGA	GACGAGTTGG	CTGTTGGCTT	CGAGGTCGAG	GAAAACCCCG
C.armatus-2b					
C.yaquinae-2a	CAGGAGACGA	GTTGGCTGTT	GGCTTCGAGG	TCGAGGAAAA	CCCCGAACAA
C.yaquinae-2b					

					1550
C.acrolepis-1					
C.acrolepis-2a	AACAAAGAAA	TGAAAAAGAC	CAACAAAAAA	AAAAGAACAA	AGCA**AATAAA**
C.cinereus-1					
C.cinereus-2a	AAGAAATGAA	AAAGACCAAC	AAAAAAAAAA	AAGAACAAAG	CA**AATAAA**AT
C.armatus-2a	AACAAAGAAA	TGAAAAAGAC	CAACAAAAAA	AAAAAAGAAC	AAAGC**AAATA**
C.armatus-2b					
C.yaquinae-2a	AGAAATGAAA	AAGACCAACA	AAAAAAAAAA	AGAACAAAGC	A**AATAAA**ATA
C.yaquinae-2b					

				1587
C.acrolepis-1				
C.acrolepis-2a	ATAATTTATT	TTCTAAAAAA	AAAAAAAAAA	AAAAAA
C.cinereus-1				
C.cinereus-2a	AATTTATTTT	CAAAAAAAAA	AAAAAAAA	
C.armatus-2a	**A**AATAATTTA	TTTTCAAAAA	AAAAAAAAAA	AAAAAAA
C.armatus-2b				
C.yaquinae-2a	ATTTATTTTC	AAAAAAAAAA	AAAAAAAAAA	AA
C.yaquinae-2b				

Fig. 2-3. *Continued.*

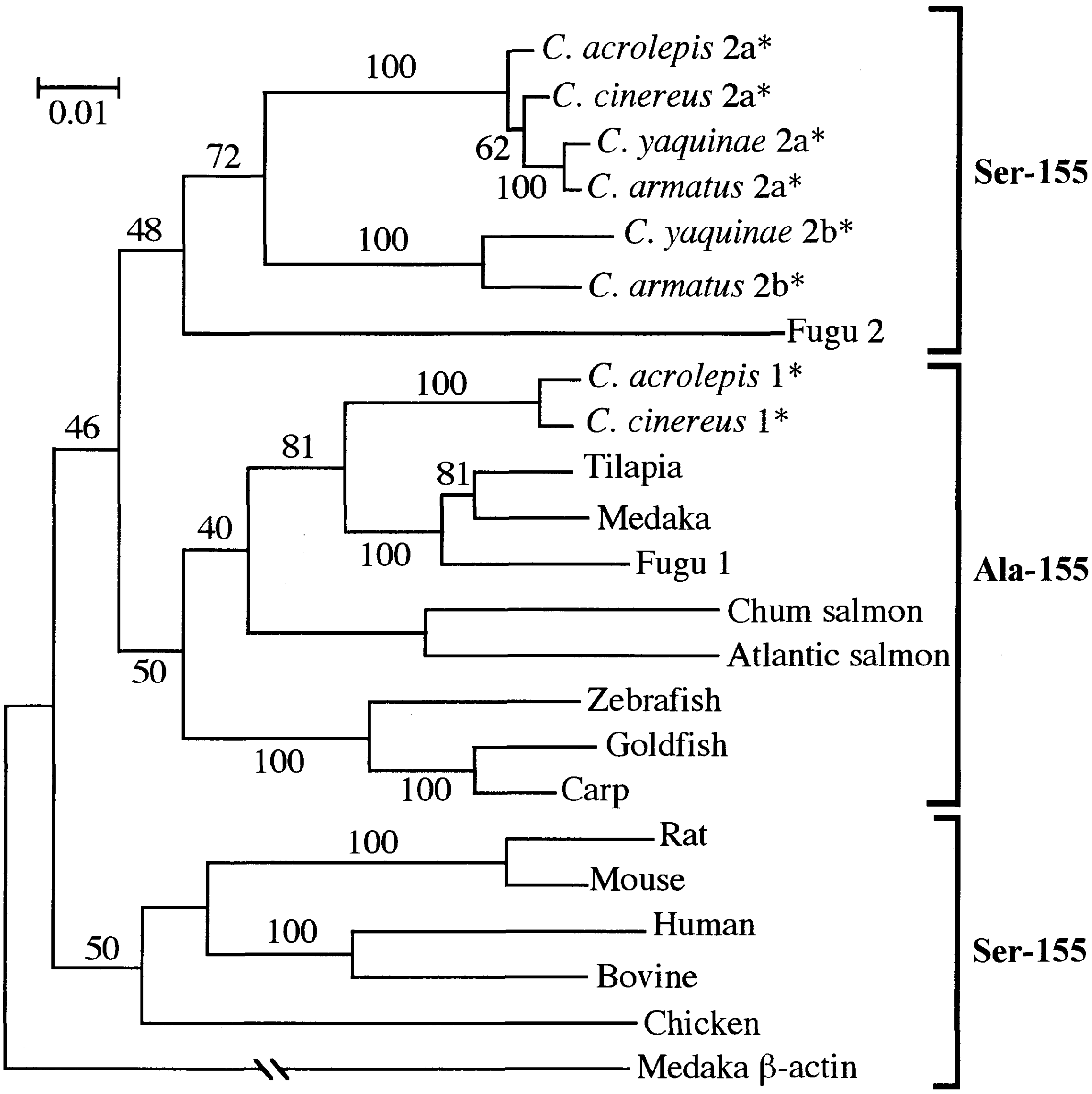

Fig. 2-4. Molecular phylogentic tree constructed by neighbor-joining method based on nucleotide sequences in the coding regions of actin cDNA from various species. Numbers at internal branches denote the bootstrap percentages of 1000 replicates. The scale indicates the evolutionary distance of the base substitution per site, estimated by the Kimura two-parameter method. The Medaka β-actin gene was used as the outgroup gene. Asterisks indicate the cDNAs that were cloned in this study.

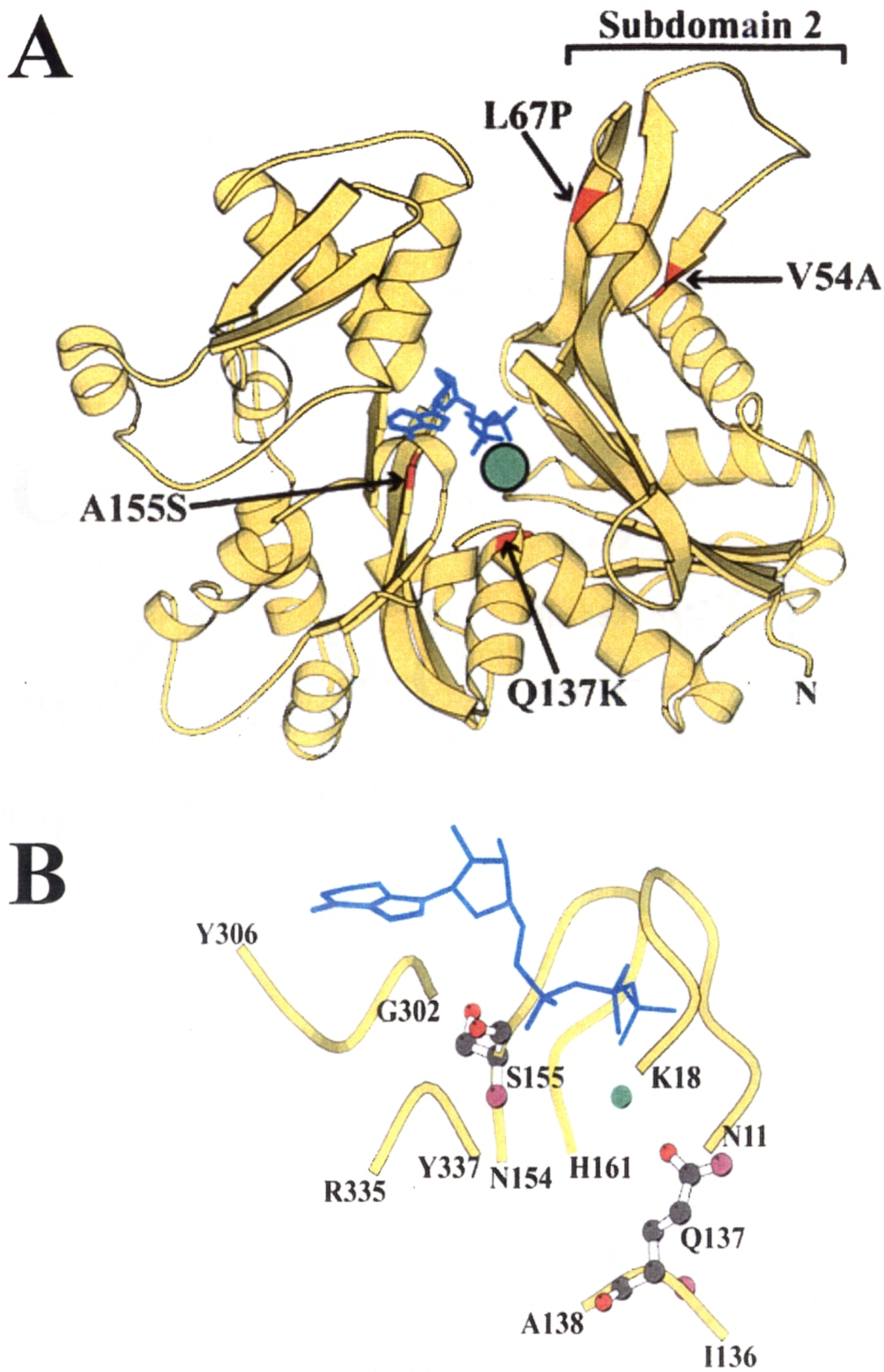

Fig. 2-5. The structure of the actin bound to ATP and Ca^{2+}. Blue sticks and a greenball represent ATP and Ca^{2+}, respectively. (A) Ribbon drawing of actin (Kabsch et al., 1990). The substitutions found in this study are colored red. (B) Environment of ATP and Ca^{2+} bound to the actin. Gln-137 and Ser-155 are represented by ball and stick. Atoms C, O and N are colored grey, red and purple, respectively. Images A and B are created using MOLSCRIPT (Kraulis, 1991). (C) Schematic drawing for interactions of ATP with actin and Ca^{2+} (Kabsch et al., 1990). Distances between atoms are given in Å. Amino acids of actin are specified near the circular segment in the left part of the drawing from a pocket covering the adenine.

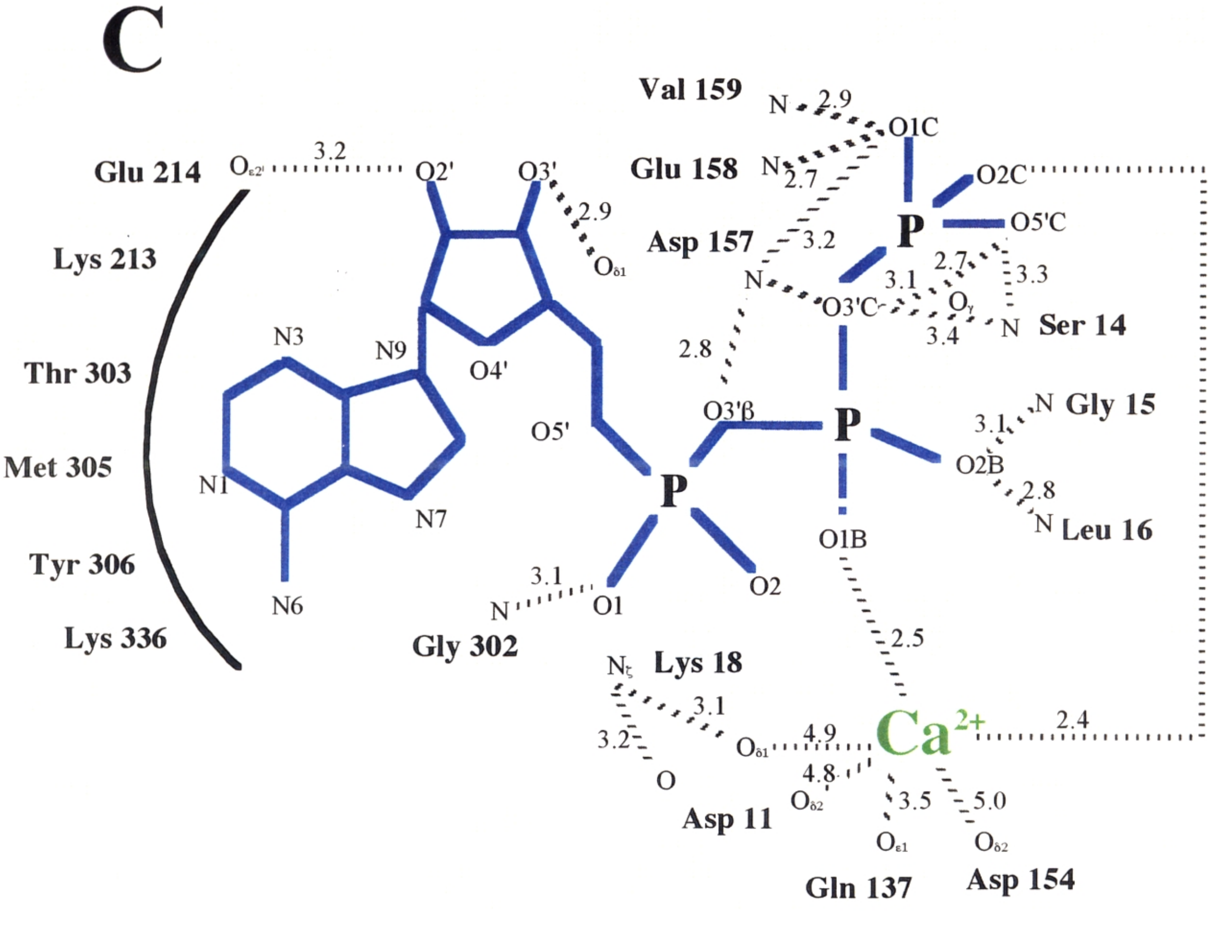

Fig. 2-5. *Continued.*

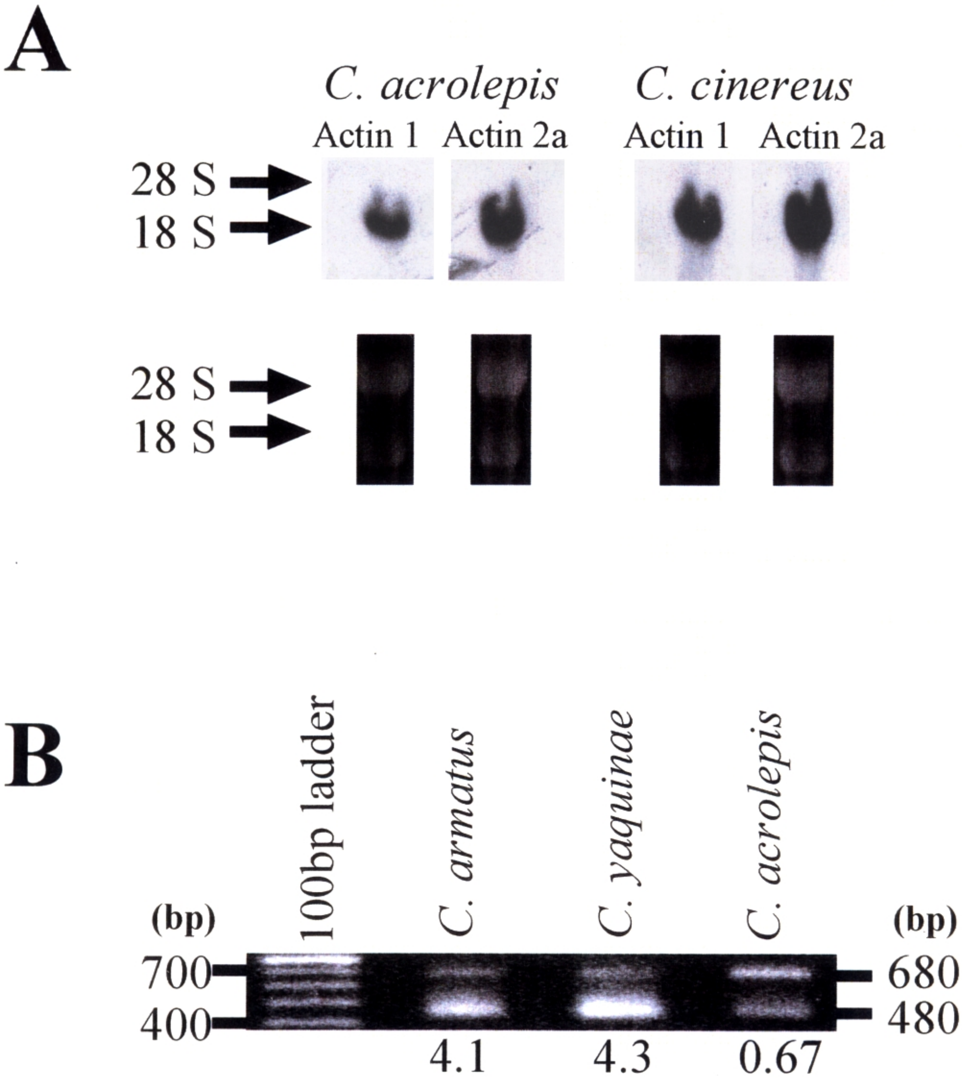

Fig. 2-6. Northern blot analysis and quantification of actin isoform mRNAs. (A) Northern blot analysis of *C. acrolepis* and *C. cinereus* α-skeletal actin isoform mRNA. The ethidium bromide-stained gels show 28S and 18S rRNA (lower panel), and the separated RNA bands were blotted onto nylon membranes and hybridized with the specific probe for α-skeletal actin 1 and α-skeletal actin 2a (upper panel). (B) RT-PCR analysis for the actin genes from *C. armatus, C. yaquinae* and *C. acrolepis*. Numbers indicate the ratios of actin 2b to actin 2a for *C. armatus* and *C. yaquinae,* and actin 1 to actin 2a for *C. acrolepis*.

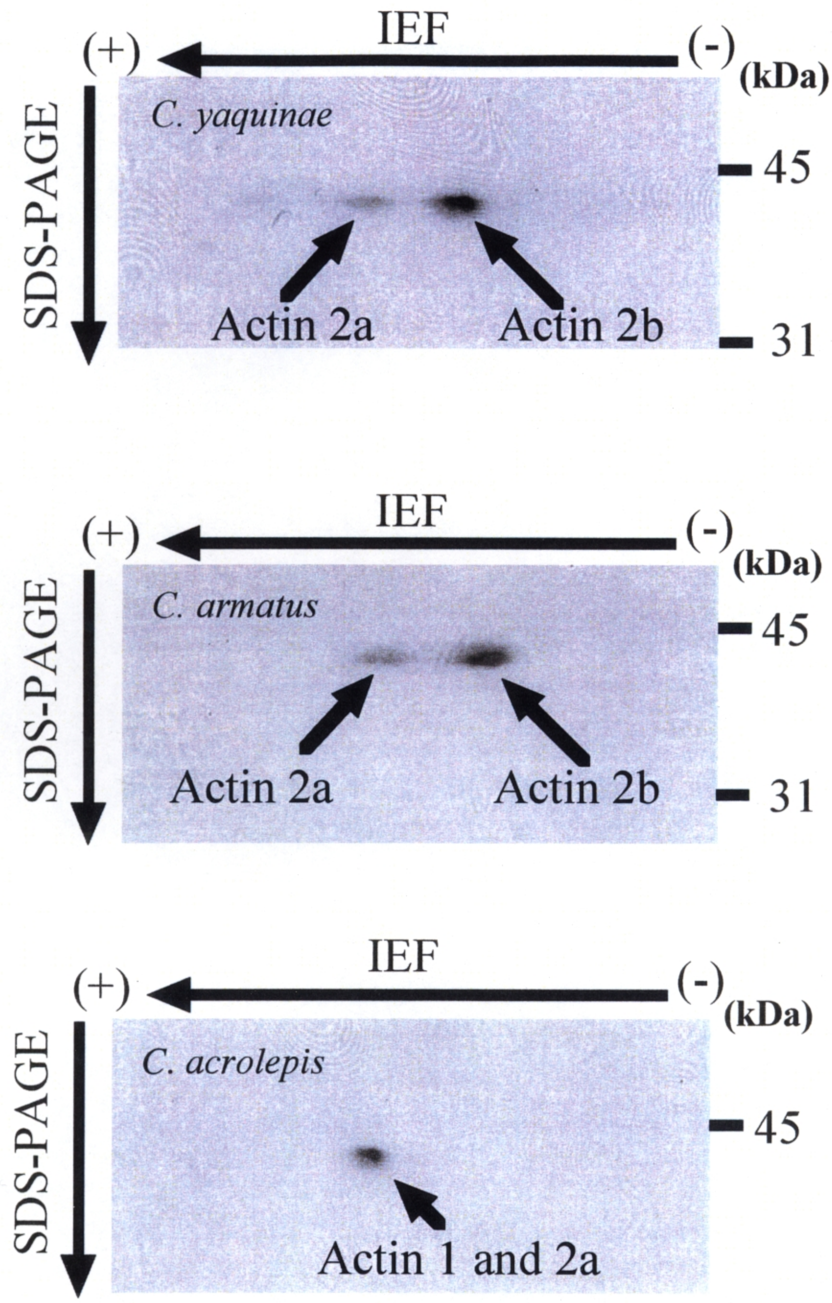

Fig. 2-7. Quantification of actin isoforms. Two-dimensional electrophoretic patterns of actin from *C. yaquinae*, *C. armatus* and *C. acrolepis* .

```
-2++++                     ++  +           #  ######
MCDDEETTALVC DNGSGLVKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK 50

    54       #### 67                            + +
  DSYVGDEAQS KRGILTLKYP IEHGIITNWD DMEKIWHHTF YNELRVAPEE 100

         # ##                          137
  HPTLLTEAPL NPKANREKMT QIMFETFNVP AMYVAIQAVL SLYASGRTTG 150

     155          ####  # #                       ##
  IVLDSGDGVT HNVPVYEGYA LPHAIMRLDL AGRDLTDYLM KILTERGYSF 200

   ####                                         ###
  VTTAEREIVR DIKEKLCYVA LDFENEMATA ASSSSLEKSY ELPDGQVITI 250

                 ###### ###            #####
  GNERFRCPET LFQPSFIGME SAGIHETAYN SIMKCDIDIR KDLYANNVLS 300

                         ####           +
  GGTTMYPGIA DRMQKEITAL APSTMKIKII APPERKYSVW IGGSILASLS 350

                        #
  TFQQMWISKQ EYDEAGPSIV HRKCF 375
```

Fig. 2-8. Amino acid sequences of Coryphaenoides actin 1. Symbols # and + represent the binding sites to other actin monomers and myosin, respectively. Amino acid residues constructing subdomains 1,2, 3 and 4 are indicated by red, blue, green and orange characters, respectively.

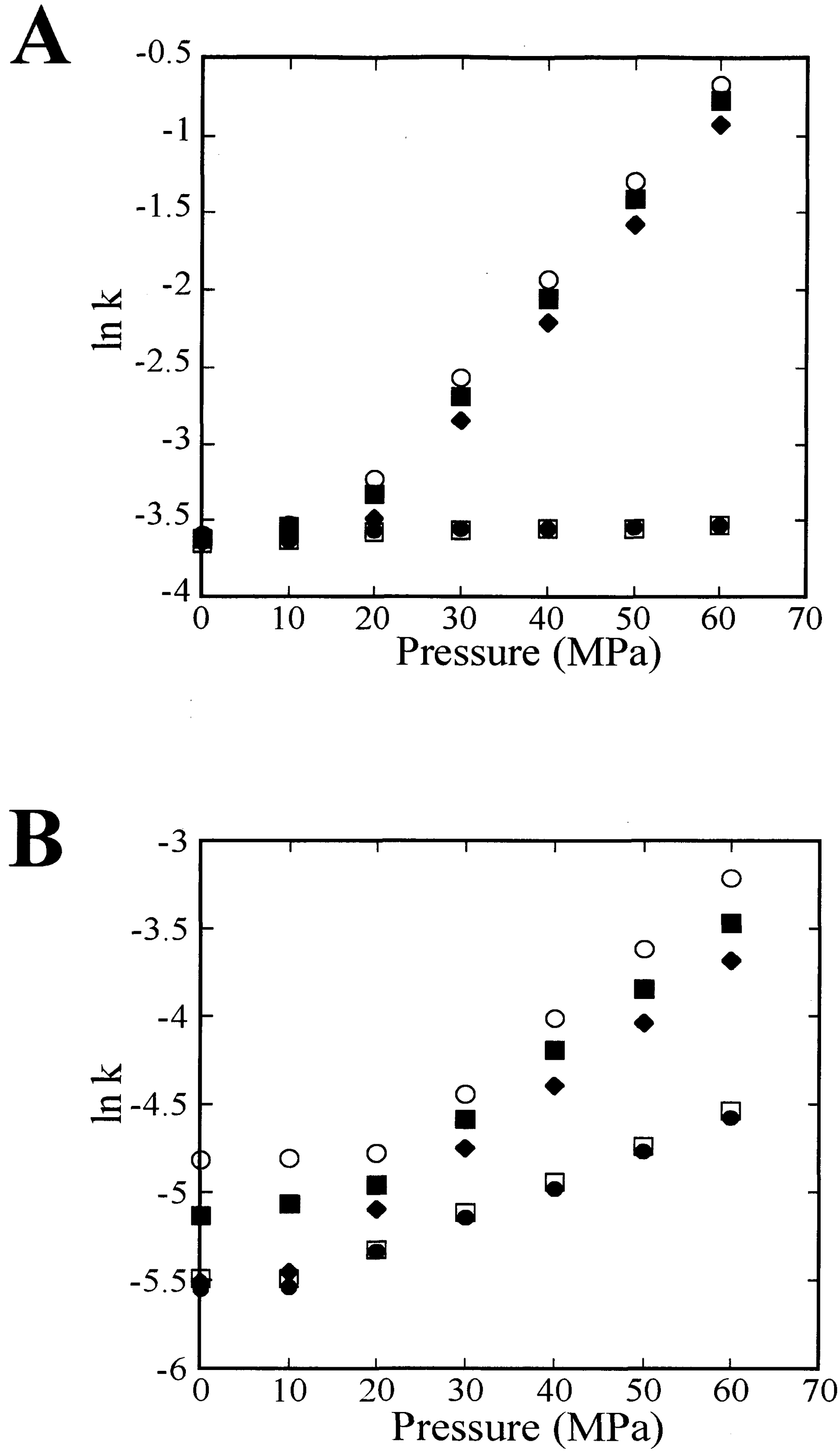

Fig. 3-1. Logarithmic plots of the dissociation rate constant of Ca^{2+} (A) and ATP (B) in actin at various pressures. Symbols are as follows: abyssal *C. yaquinae* (●); abyssal *C. armatus* (□); chicken (◆); carp (○); non-abyssal *C. acrolepis* (■). Values are means ± S.D. of four independent experiments. Errors for all experiments are too small to show error bars.

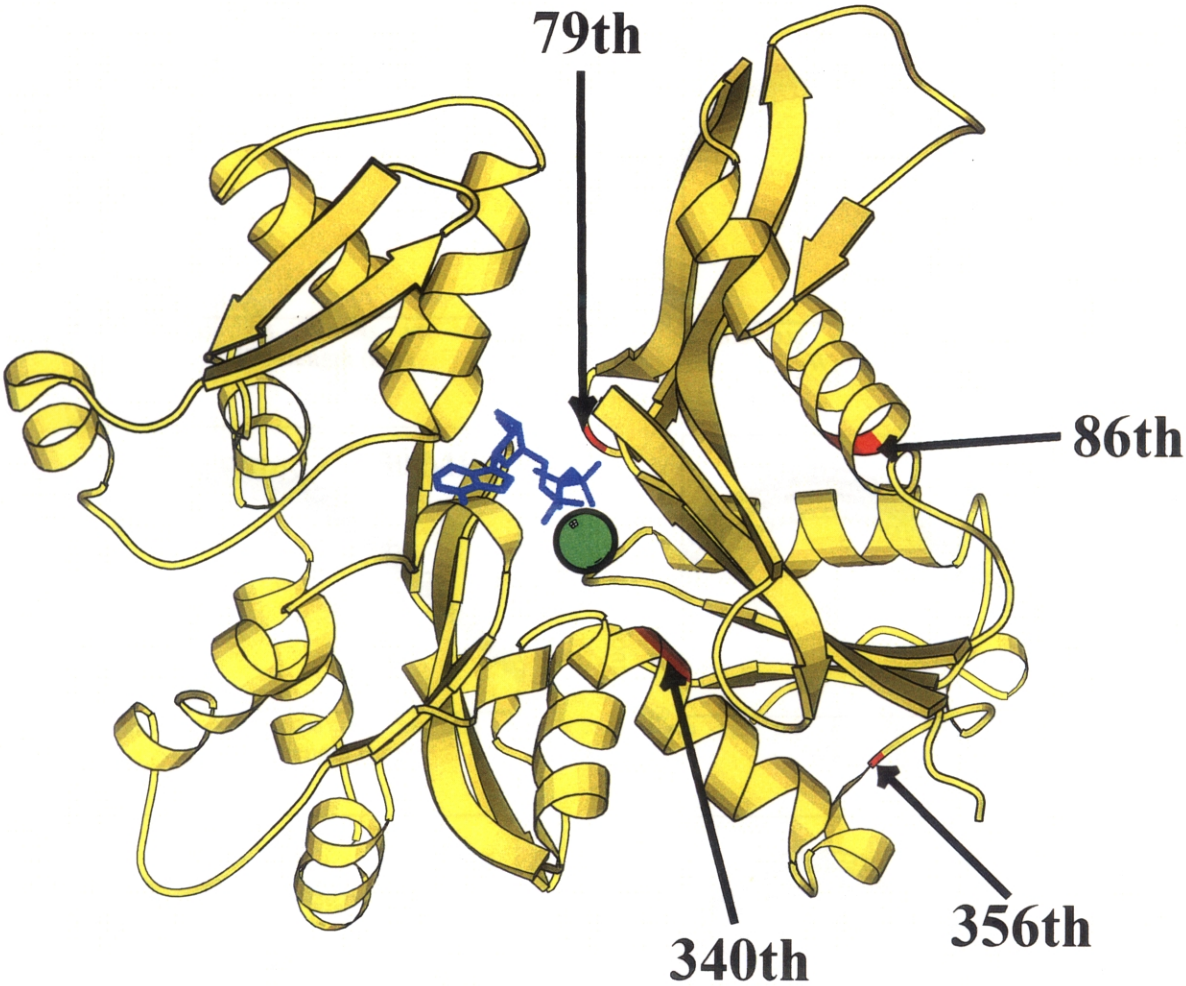

Fig. 3-2. The positions of tryptophan residues in G-actin.
Tryptophan residues at 79, 86, 340, and 356 are colored by red.
Blue bars indicate ATP, and a green ball does Ca.

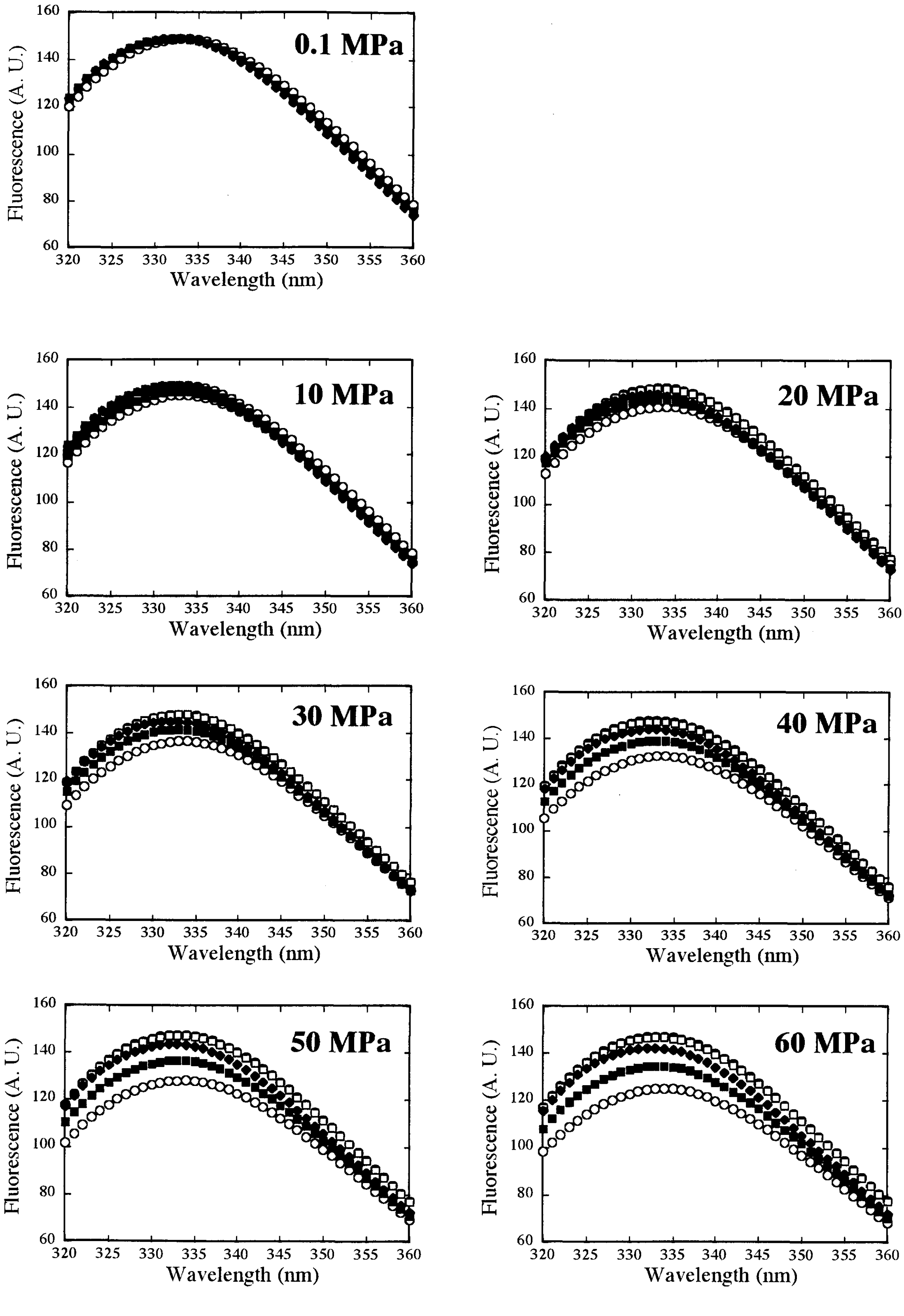

Fig. 3-3. Effects of pressures from 0.1 MPa to 60 MPa on the intrinsic tryptophan fluorescence spectrum of Ca^{2+}-G-actins. Symbols are as follows: abyssal *C. yaquinae* (●); abyssal *C. armatus* (□); chicken (◆); carp (○); non-abyssal *C. acrolepis* (■).

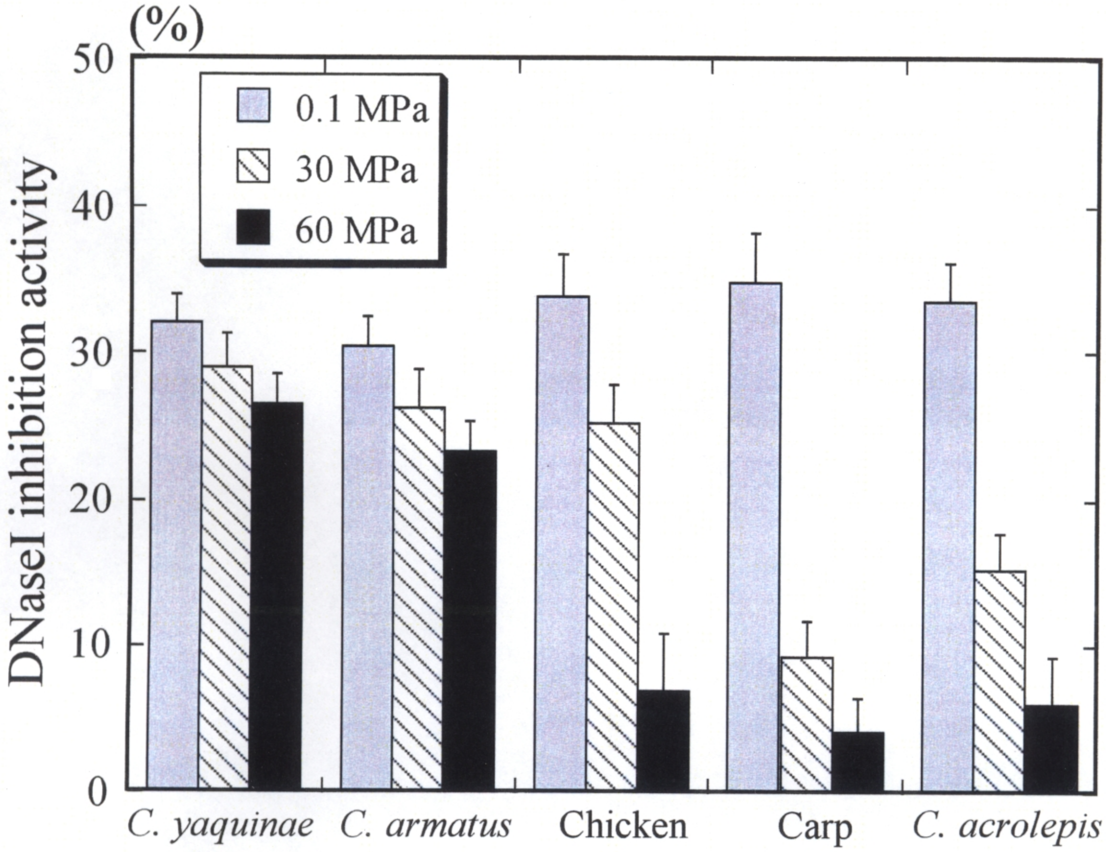

Fig. 3-4. Effects of pressures on the DNaseI inhibition activity of G-actin. The experiments for each actin were performed at the same ratios of actin/DNaseI at every pressure. Values are means ± S.D. of four independent experiments.

IA		β1 β2		β3		α1
Actin	8	LVCDNGSGLVKAGFA	29	AVFP	78	NWDDMEKIWHHTFYNELRVA
Hexokinase	83	LAIDLGGTNLRVVLV	109	QSKY	123	NPDELWEFIADSLKAFIDEQ
GK	7	VALDQGTTSSRAVMD	31	SQRE	48	DPMEIWATQSSTLVEVLAKA
Hsc70	7	VGIDLGTTYSCVGVF	36	RTTP	116	PEEVSSMVLTKMKEIAEAYL
		β-hairpin				

		β4		α2		β5 α3
Actin	102	PTLLTEA	114	ANREKMTQI	132	MYVAIQAVLSLYASG
Hexokinase	152	PLGFTFS	189	VPMLQKQIS	206	VALINDTTGTLVASY
GK	76	AIGITNQ	165	VDTWLIWKM	240	SGIAGDQQAALFGQL
Hsc70	141	NAVTVPY	157	ATKDAGTIA	170	LRIINEPTAAAIAYG

IIA		β1 β2		β3		α1
Actin	150	GOVLDSGDGVTHNVP	175	TMRL	274	IHETTYNSIM
Hexokinase	227	KMGVIFGT-GVNGAY	267	NCEY	397	VCGIAAICQK
GK	260	MAKNTYGT-GCFMLM	303	EGAV	388	TRDVLEAMQA
Hsc70	195	VLIFDLGGGTFDVSI	222	TAGD	313	TLDPVEKALR
		β-hairpin				

		β4		α2		β5		α3
Actin	297	NVMSGG	311	DRMQKE	328	KIIA	337	YSVWIGGSILASL
Hexokinase	414	IAADGS	427	FKEKAA	452	KIVP	458	DGSGAGAAVIAAL
GK	406	LRVDGG	420	QFQSDI	429	RVER	437	EVTALGAAYLAGL
Hsc70	334	IVLVGG	348	KLLQDF	358	ELNK	367	EAVAYGAAVQAAI

Fig. 3-5. Sequences of structurally conserved regions of actin related superfamily members (Hurley, 1996). The hexokinase sequence is numbered according to the translated gene sequence of yeast hexokinase B. The alignment is based solely on three-dimensional structural equivalence. Only regions that are equivalent structurally in all four proteins are shown. Red residues are either identical in all sequences or have structurally equivalent roles in the nucleotide binding site.