

Figure 1

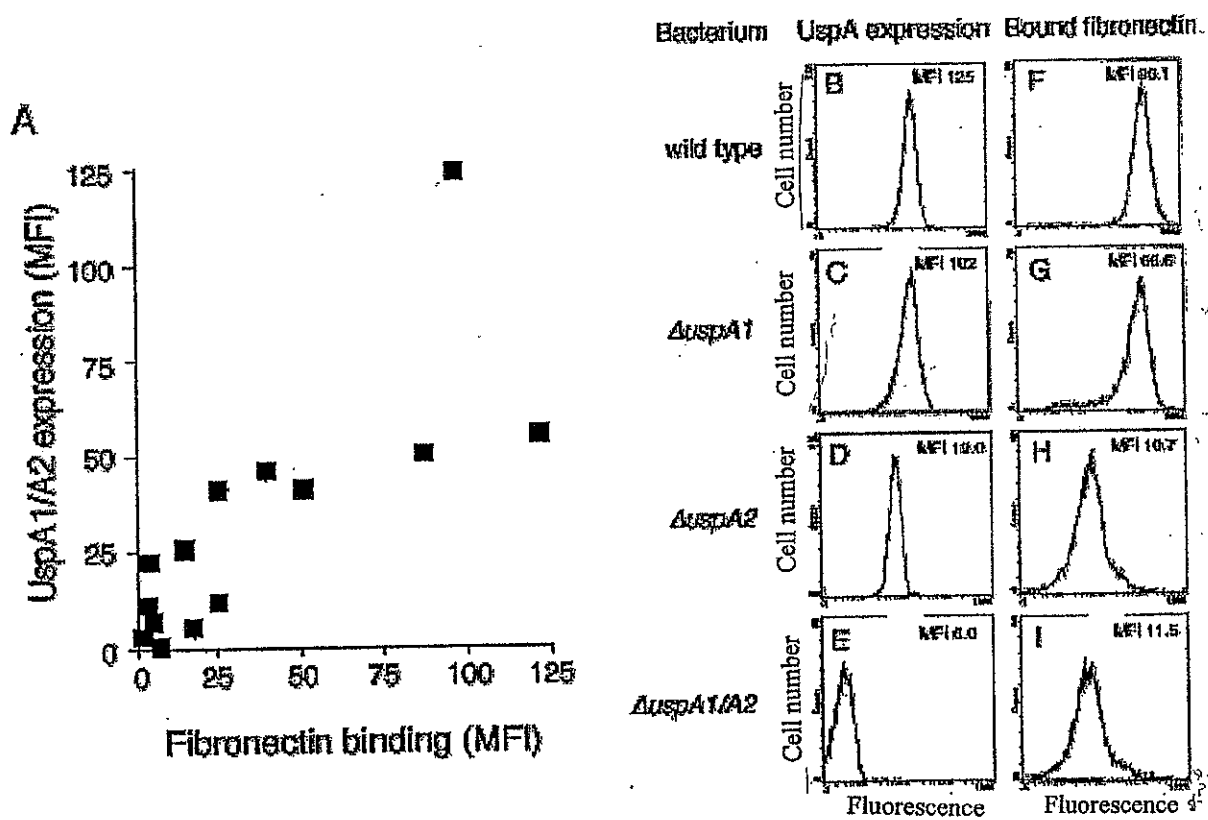


Figure 2

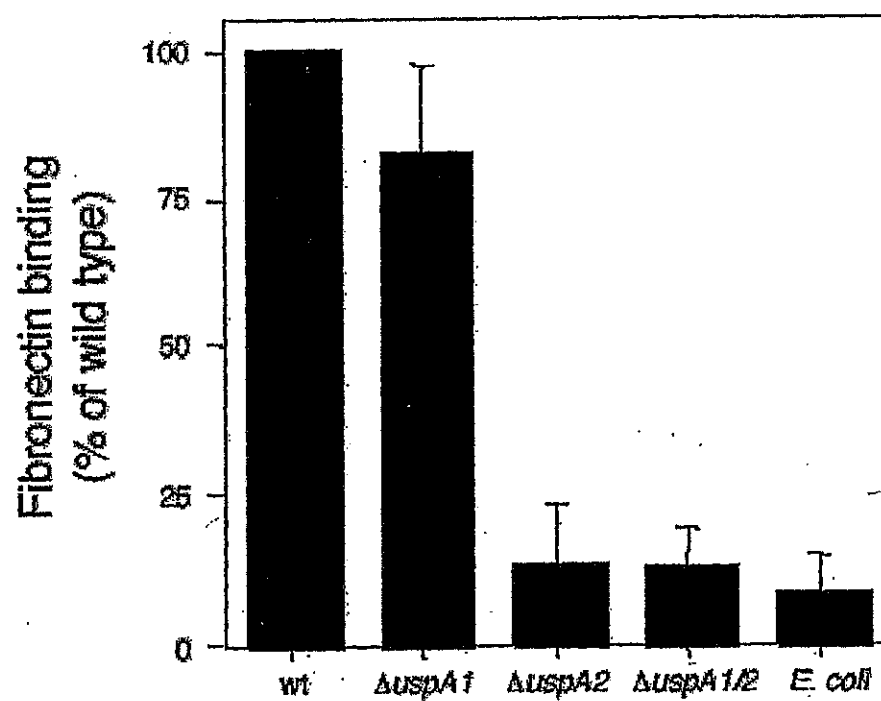
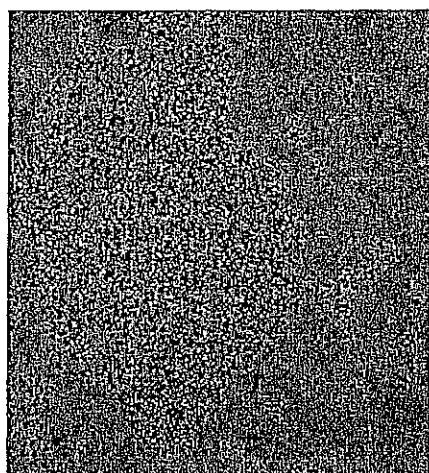
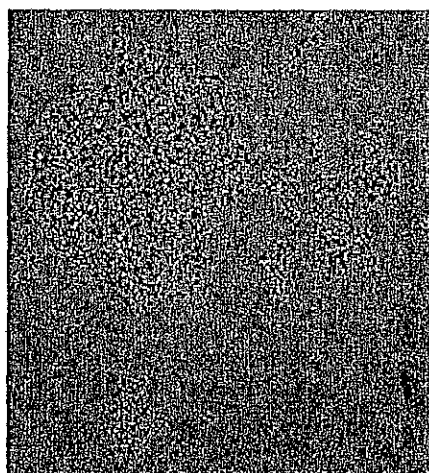


Figure 3

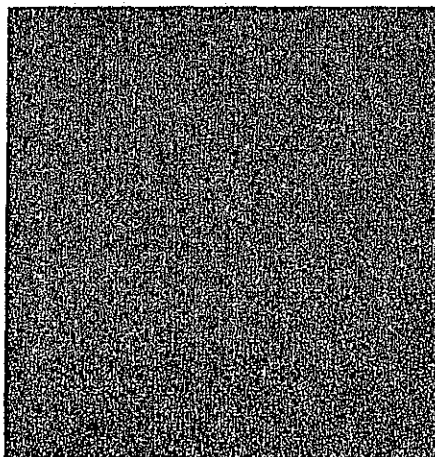
A. *M. catarrhalis* wild type



B. $\Delta uspA1$ mutant



C. $\Delta uspA2$ mutant



D. $\Delta uspA1/A2$ double mutant

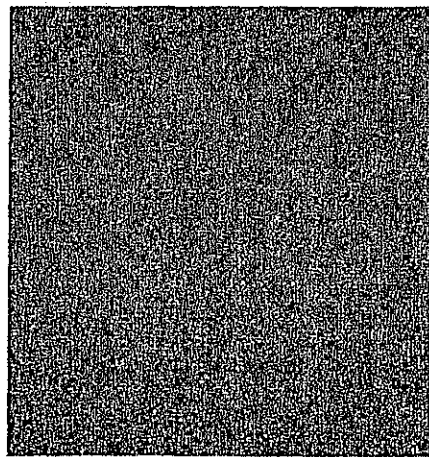


Figure 4

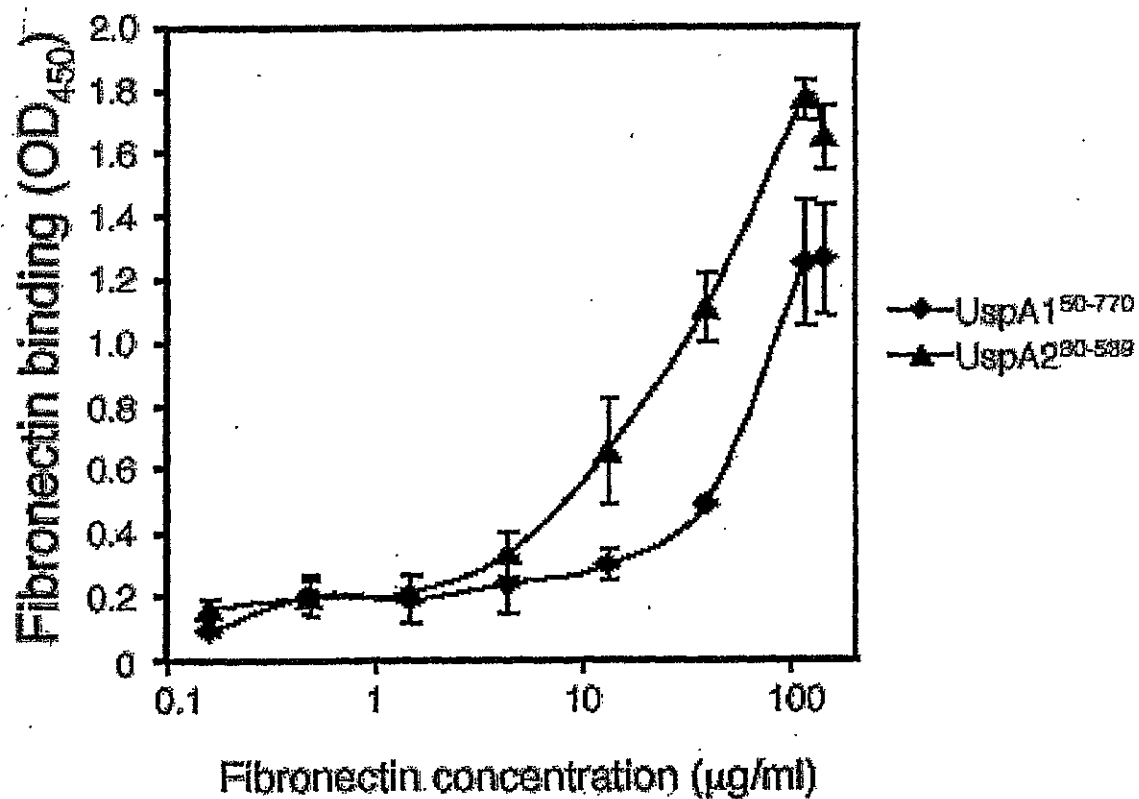


Figure 5

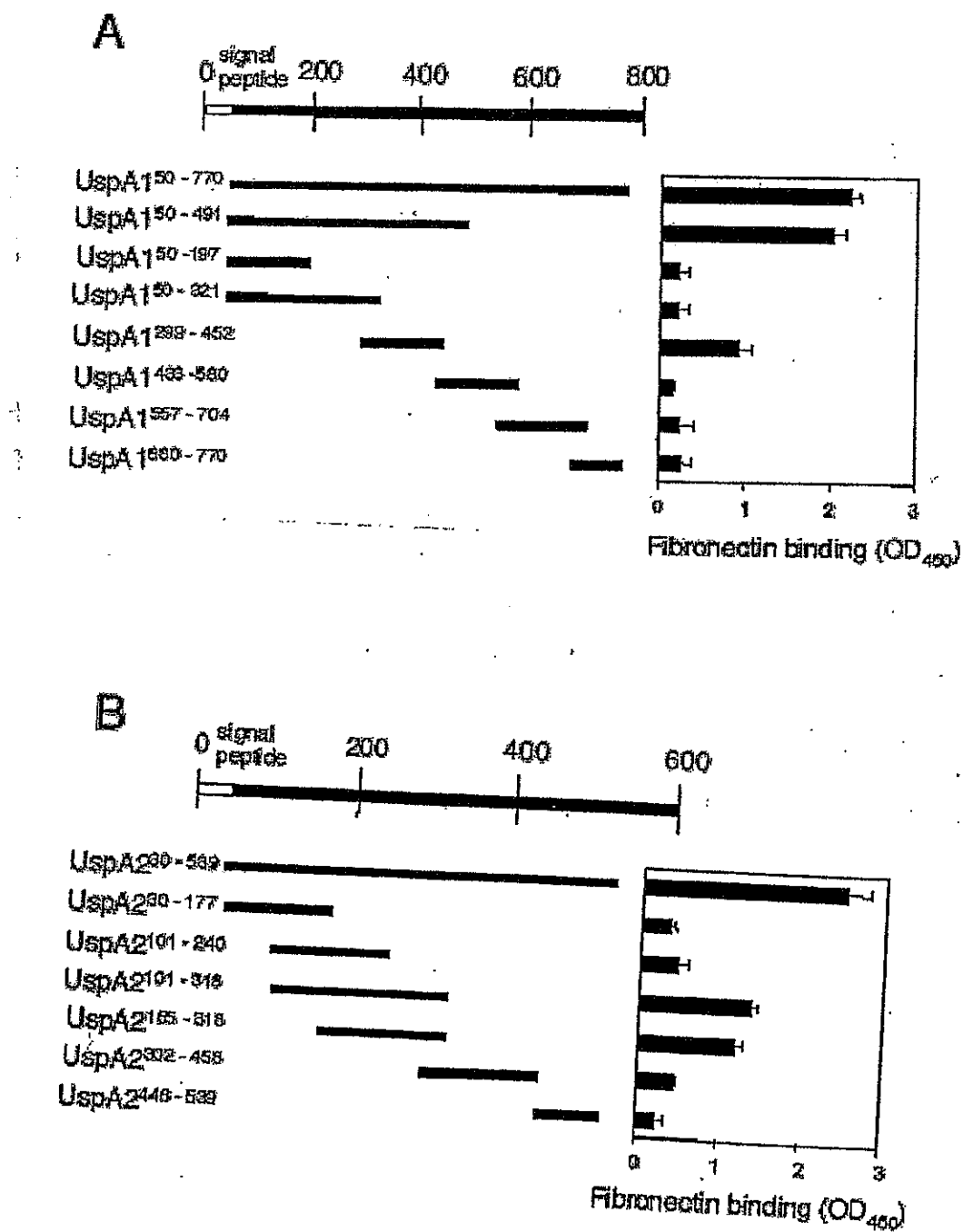


Figure 6

UspA1 299-452	TGNGTVSVGKKGKERQIVHVGAGEISDTST
UspA2 165-318	- -KDAIAKNNE SIED - LYDFGH - EVAES - -
UspA1 299-452	DAYNGSQLHVLATVVAQNKADIEDLDDRYG
UspA2 165-318	- - - IG - EIAHNN - - EAQNET - - - -LK - - - G
UspA1 299-452	LLGEEINSLEGEIFNNQDAIAKNQADIKTL
UspA2 165-318	LI - - - TNSIE - - NTNN - - - ITKNKADIQAL
UspA1 299-452	ESNVEEGLLDL SGRLLDQKADIDNNINNIY
UspA2 165-318	ENNVVEELFNL SGRLIDQKADIDNNINNIY
UspA1 299-452	ELAQQQDQHSSDIKTLKKNVVEEGLLDLSCR
UspA2 165-318	ELAQQQDQHSSDIKTLKKNVVEEGLLLELSDH
UspA1 299-452	LIDQ - - - - -
UspA2 165-318	IIDQKTDIAQNQANIQDLATYNELQDQYAAQ
UspA1 299-452	-
UspA2 165-318	K

Figure 7

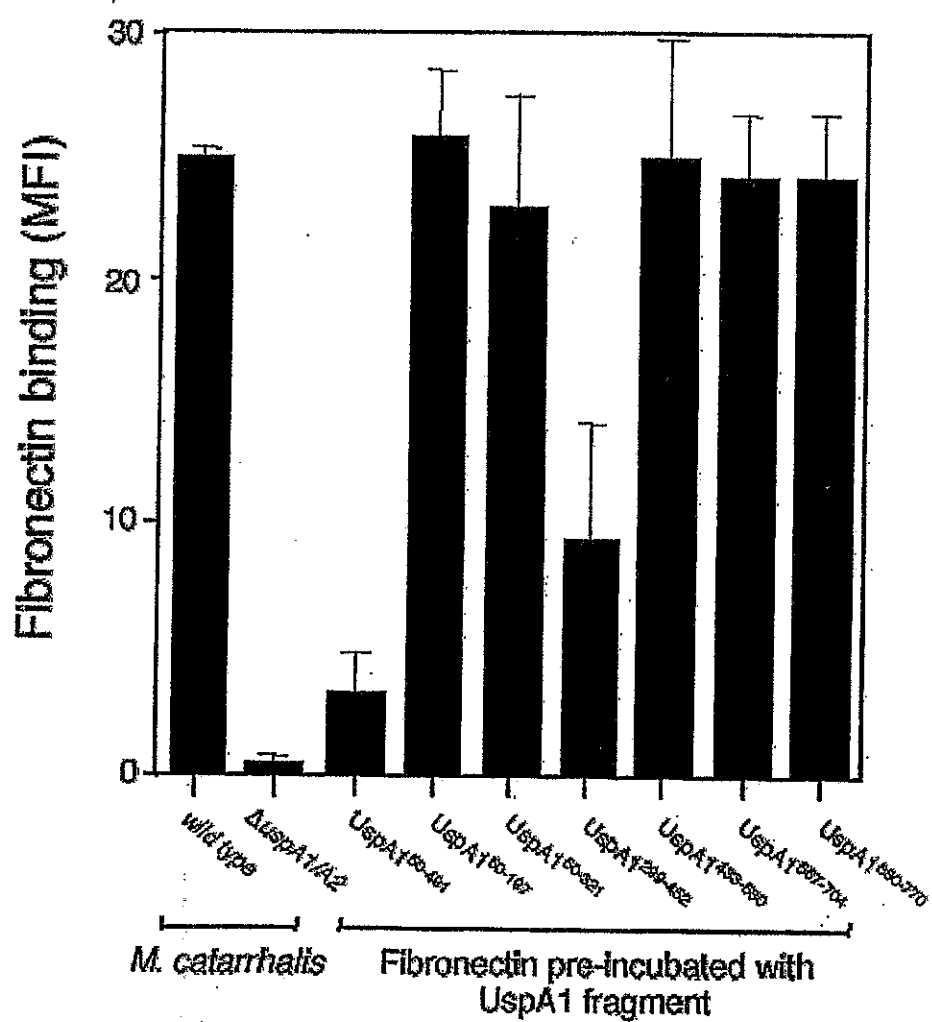
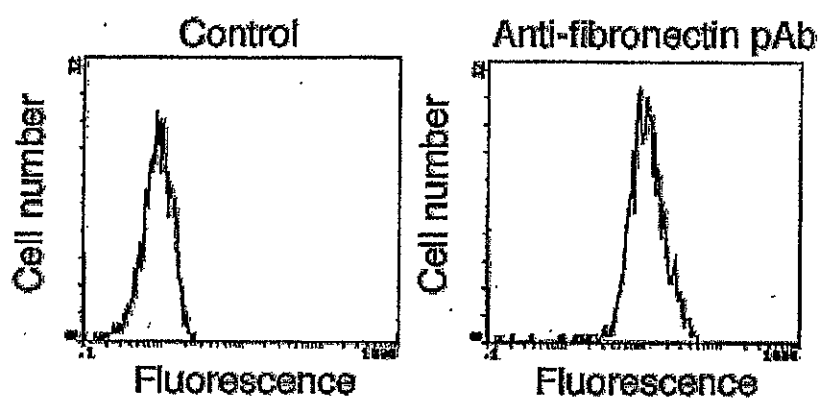
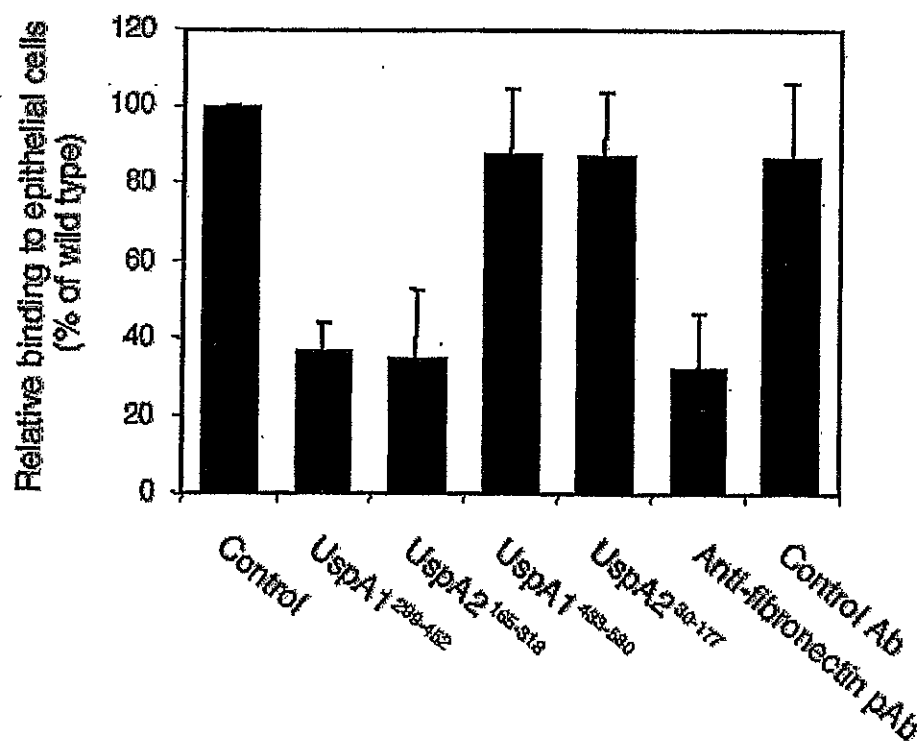


Figure 8

A



B



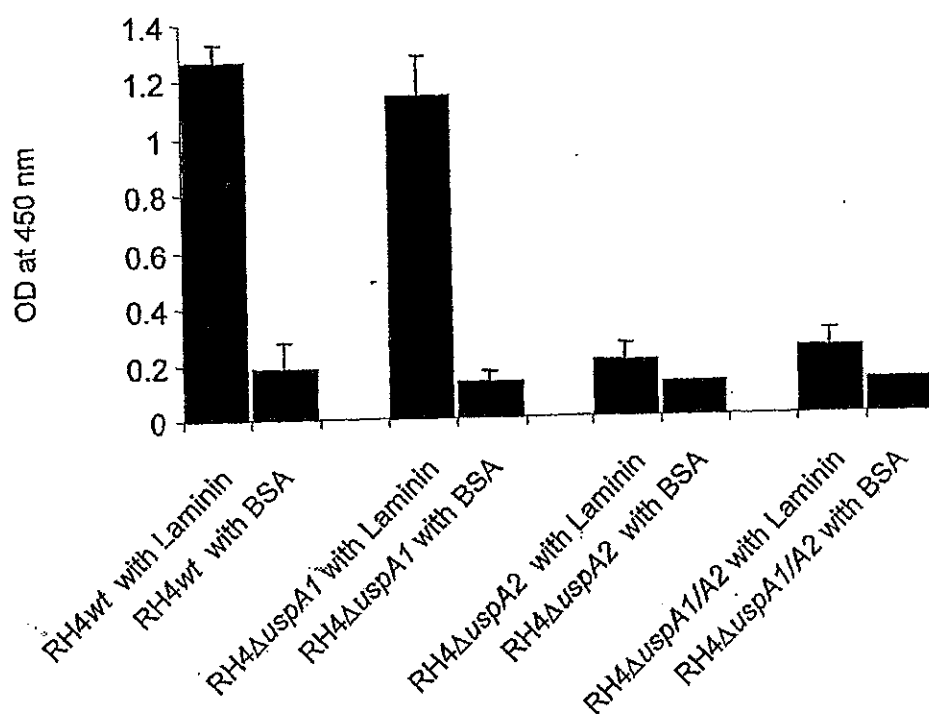


Figure 9A.

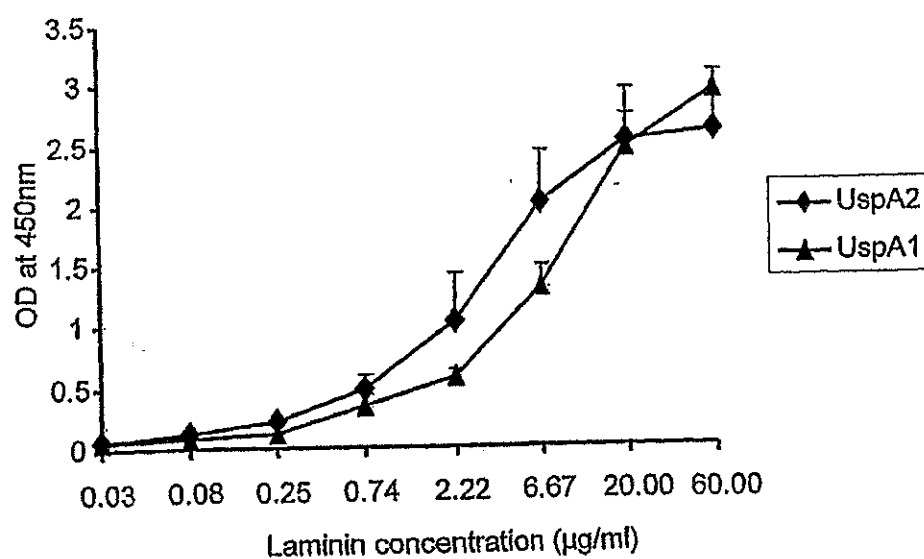


Figure 9B.

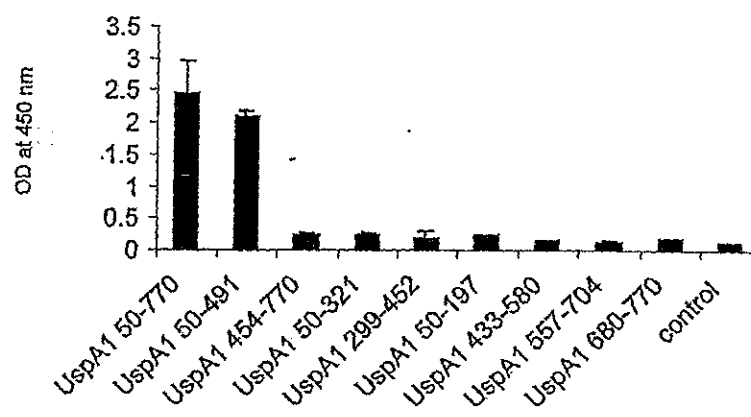


Figure 10A.

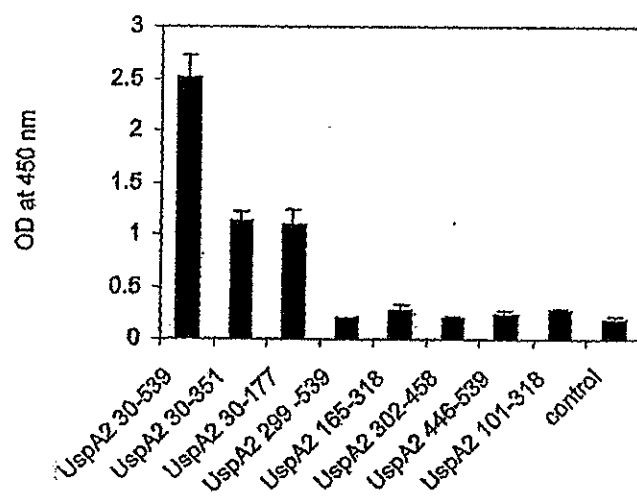


Figure 10B.

Figure 11

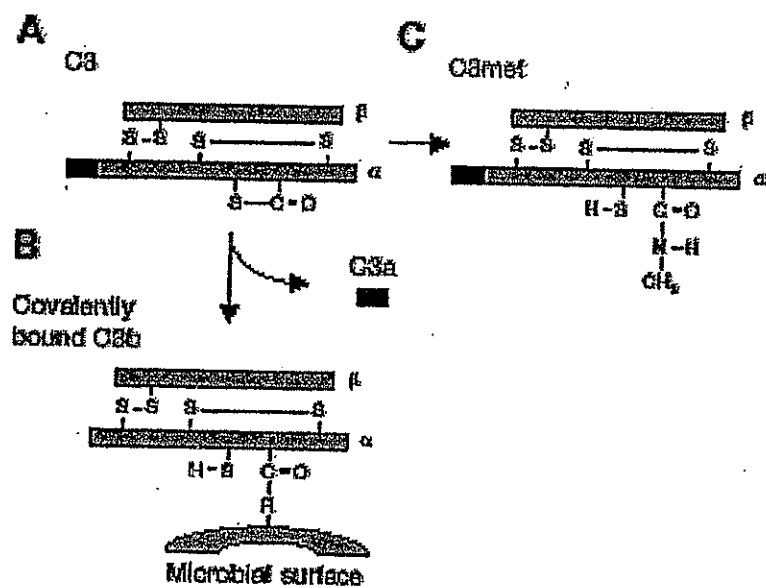


Figure 12

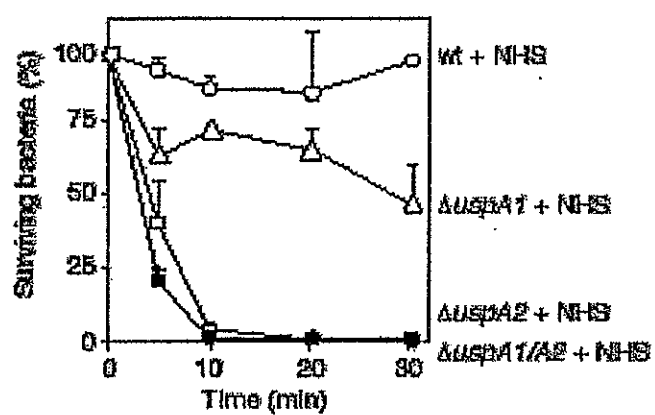
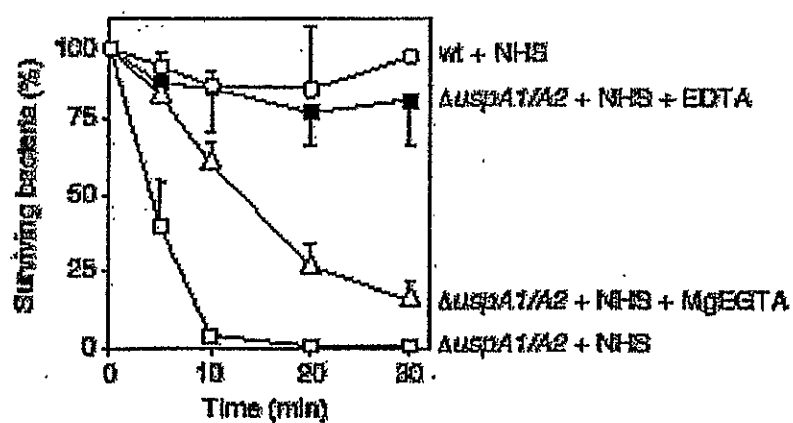
A**B**

Figure 13

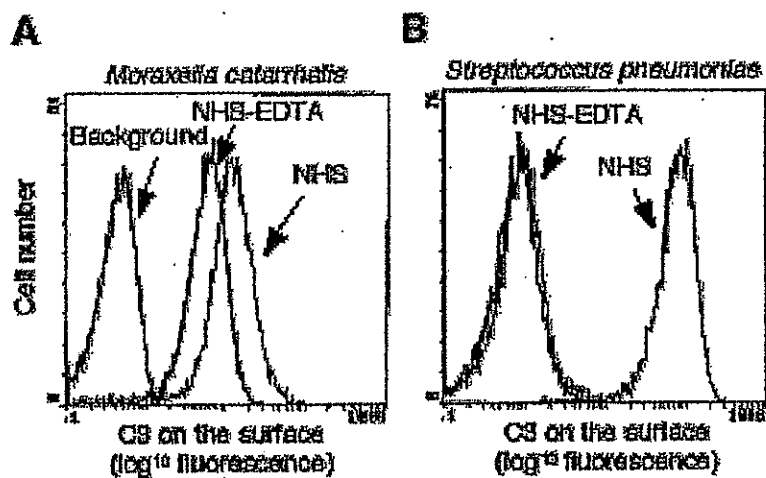


Figure 14

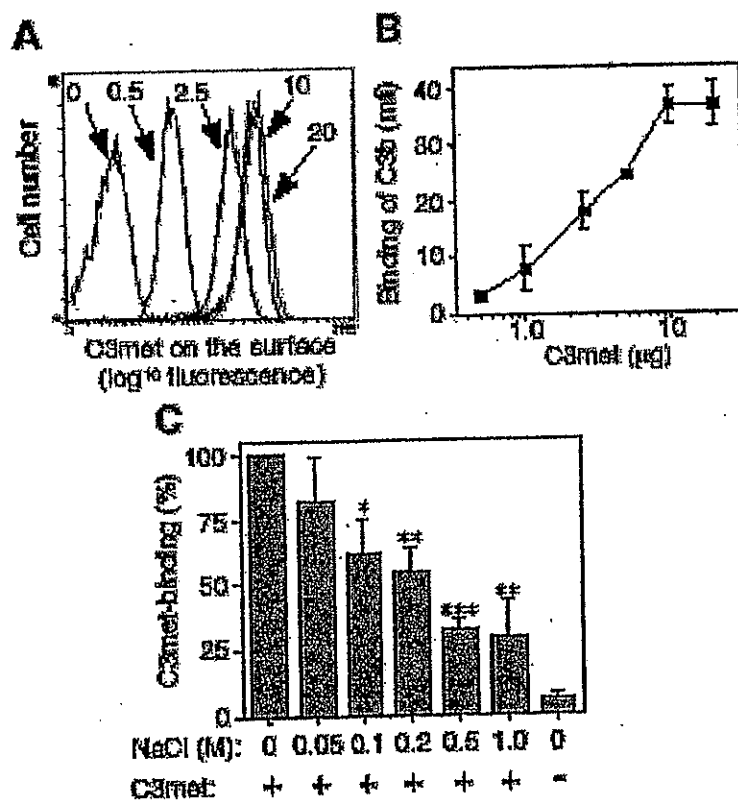


Figure 15

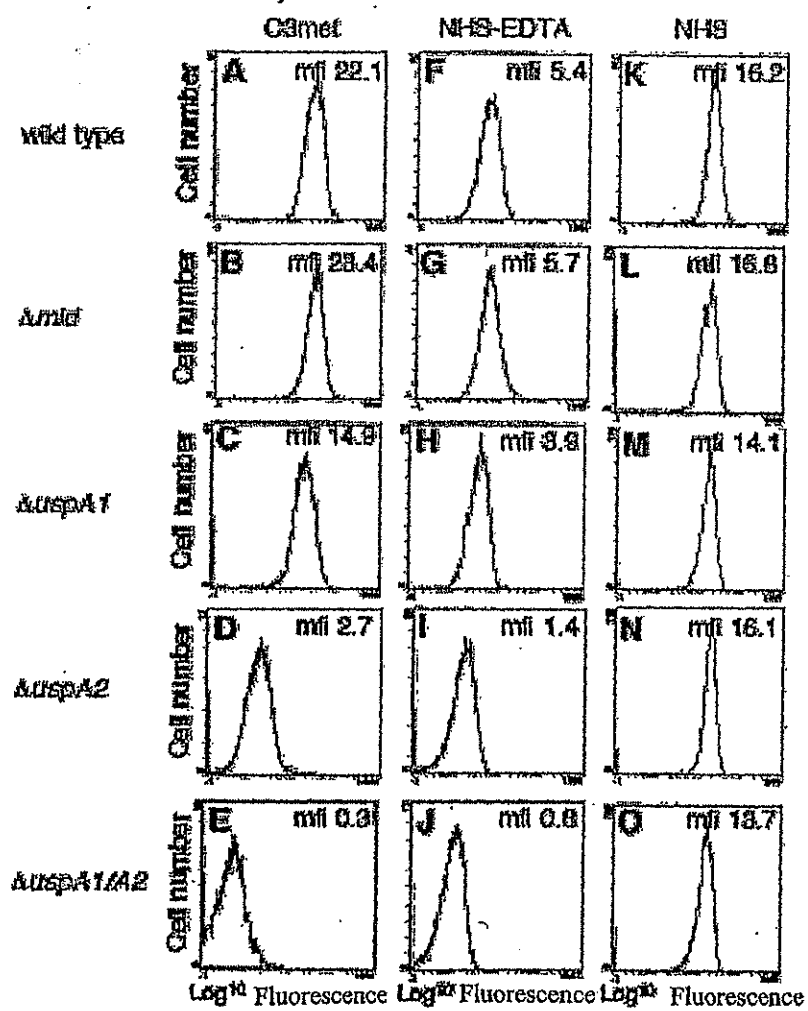


Figure 16

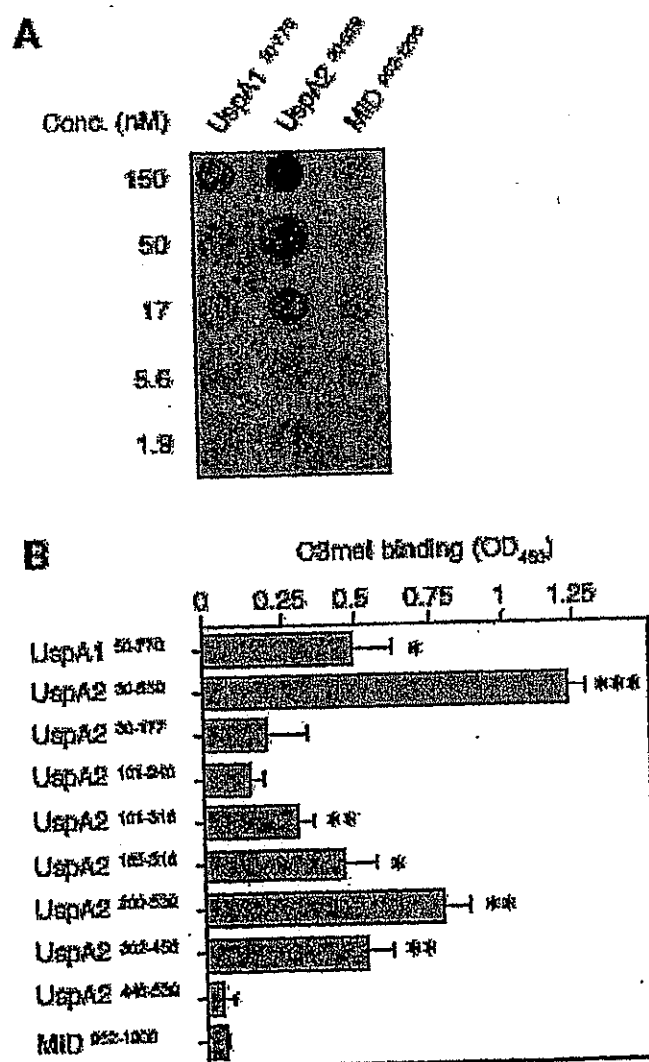


Figure 17

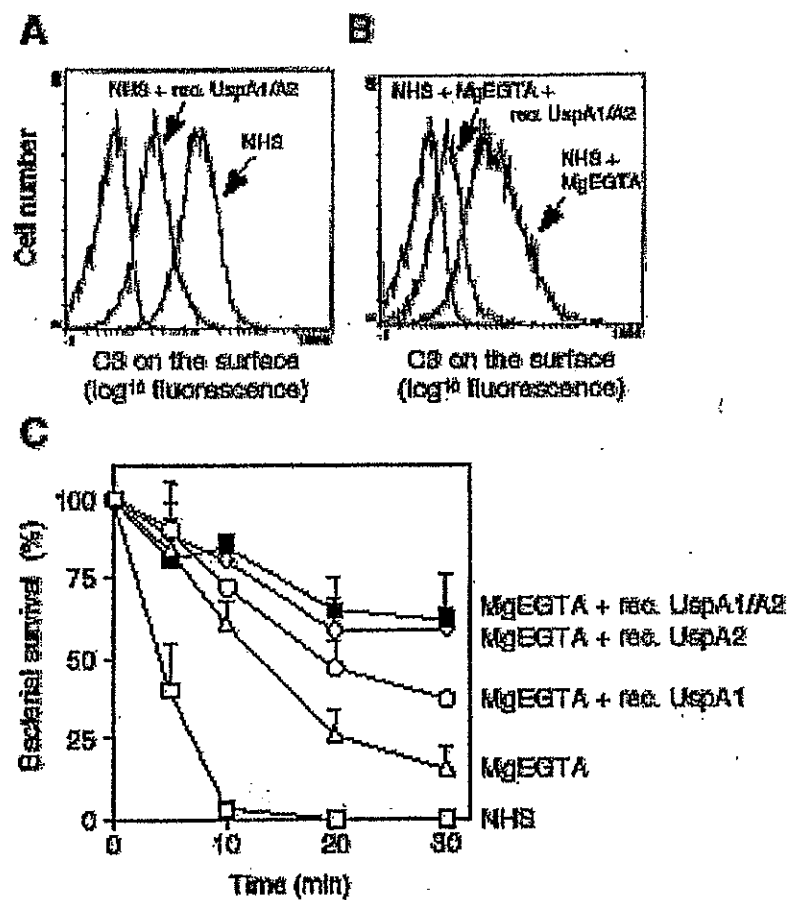


Figure 18

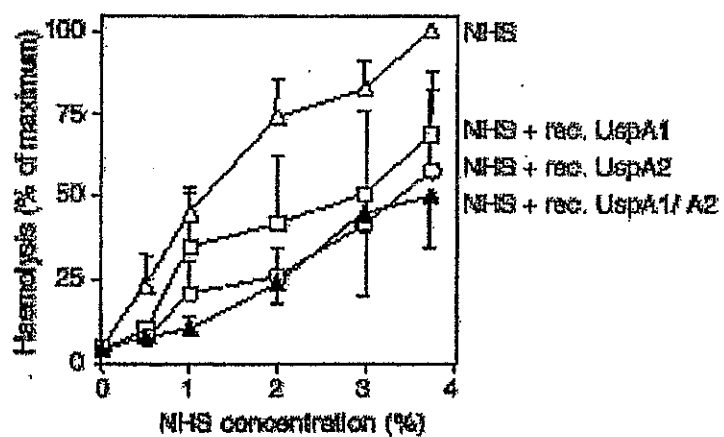


Fig. 19

Pileup – beginning and end of the fibronectin binding domain marked with { and }

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      *           20           *           40           *
USPA1_O12E : MNKIYKVKKNAAGHLVACSEFAKGHTKKAVLGSLLIVGHLGMATTASAO : 49
USPA1_P44 : MNKIYKVKKNAAGHLVACSEFAKGHTKKAVLGSLLIVGHLGMATTASAO : 49
USPA1_ATCC : MNKIYKVKKNAAGHLVACSEFAKGHTKKAVLGSLLIVGHLGMATTASAO : 49
USPA1_O46E : MNKIYKVKKNAAGHLVACSEFAKGHTKKAVLGSLLIVGHLGMATTASAO : 49
USPA1_TTA3 : MNKIYKVKKNAAGHLVACSEFAKGHTKKAVLGSLLIVGHLGMATTASAO : 50
USPA1_O35E : MNKIYKVKKNAAGHLVACSEFAKGHTKKAVLGSLLIVGHLGMATTASAO : 49
USPA1_TTA2 : MNKIYKVKKNAAGHLVACSEFAKGHTKKAVLGSLLIVGHLGMATTASAO : 49
USPA1_V117 : MNKIYKVKKNAAGHLVACSEFAKGHTKKAVLGSLLIVGHLGMATTASAO : 49

      60           *           80           *           100
USPA1_O12E : ----KAANTTNQASGRHT-----YVGGGDNQATCMGFFGCGFFNQ : 87
USPA1_P44 : ----AIN-----TGQGT-----VVDQ-NGEAIENMTASCGGDNQ : 80
USPA1_ATCC : ----KVGKATNKISGGDNNTANGTYLTIGGGDYKTKCRMTTGGGLFNE : 95
USPA1_O46E : --ATKGTGKHVVDN--KDNKAKGDYSTASGGKDLEAKENMTVGGGDNE : 95
USPA1_TTA3 : TIARQKGKMHSTIIGGGNDNEANGDYSTVSGGDYLEAKDSMTTGGGYNE : 100
USPA1_O35E : ----ATNS-----KGTGAHLGVNNNNE : 67
USPA1_TTA2 : ----MATTPSAQVVKTN-----KKNCTHPFLGGGDNNT : 79
USPA1_V117 : ----QNNQ-----KSKCPFLGGGNN : 68

      *           120           *           140           *
USPA1_O12E : ATGNHLTICCGSSANQAKGNYSITLGGGDNETTCTHSTLGGGDS----- : 130
USPA1_P44 : AKGNYSITASCGSGNTAEKNYSTASGGLGNTAEKNYSTASGGLG----- : 123
USPA1_ATCC : ATNYSITLGGSGGYNAKAKRYSTLGGGGYNEATNQSTLGGGDN----- : 138
USPA1_O46E : AKGNYSITLGGSSNTAKGKSTLGGGDTNDANGTSTLGGG----- : 136
USPA1_TTA3 : ANGDSITLGGGFYNDAKGESITLGGGDNNSATCMSTLGGGDNNSATGRY : 150
USPA1_O35E : APGDSITLGGSGGYNAKGRYSALGGGLFNKATNESTLGGGY----- : 110
USPA1_TTA2 : TKGNYSITLGGGHNDAECNYSITVGGGFTNEAIGKNSTVGGGFT----- : 122
USPA1_V117 : VDKNYSITLGGGLNDAECKYPLTGGGAHNKANETSTLGGGSY----- : 111

      160           *           180           *           200
USPA1_O12E : -----NKAECTHSTLGGGYDNTAKGTHSTIVGGRKNRAEGNYSITVAG : 172
USPA1_P44 : -----NTAKCKYSTVAGGANNQAKGDYSTASGGSGNTAEKNYSTVAG : 165
USPA1_ATCC : -----NTAKGRYSTLGGGYNEATIENTSTLGGGGYNQAKGRNSTVAG : 180
USPA1_O46E : -----YYSRAIGDSSTLGGGYNQATLEKSTLGGGRNNQATGNNSTVAG : 180
USPA1_TTA3 : STIAGGWLNQATGHSSTVAGGWLNQATNENSTLGGGRFNQATGRNSTVAG : 200
USPA1_O35E : -----NKAEGRYSTLGGGSNNEATNEYSTIVGGDDNKATGRYSTIGG : 152
USPA1_TTA2 : -----NEAMGEYSTVAGGANNQAKGNYSTLGGGNGKATENNSTVVG : 164
USPA1_V117 : -----NEAMGEKSTLGGGDNNTAKGNHSTVGGYKNEATGKYSTVGC : 153

      *           220           *           240           *
USPA1_O12E : GDNQNAATGNNSTVVGSKNQATGAGSFAAGVNNQAKTENAVAGKNNITG : 222
USPA1_P44 : GKNQNAATGLNSTVAGGSDNQATGIGSFAAGVNNANAEAVAGKNNITG : 215
USPA1_ATCC : GYNNAATGTDSTIAGGRKNQATGKCSFAAGIDNANADNAVAGKNNITG : 230
USPA1_O46E : GSYNQAAAGNNSTVACGSHNQATGEGSFAAGVNNANANNAVAGKNNITG : 230
USPA1_TTA3 : GYKNKATGVDSTIAGGRNNQANGIGSFAAGIDNANANNITVAGKNNITG : 250
USPA1_O35E : GDNNTAEYYSTVAGGKNNQBTGTSFAAGVNNANAEAVAGKNNITG : 202
USPA1_TTA2 : GSNQAKSEHSTIAGGKNNQATGNGSFAAGVNNADANNAVAGKNNITG : 214
USPA1_V117 : GSNKKECTDSTIAGGKNNQAKGEGSFAAGVNNANAEAVAGKNNITG : 203

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                260          *          280          *          300
USPA1_O12E : GTNSVAIGSNNTWEDKQDVFIILGSN--ITNEISGGSVLLGNNTSGKKAATA : 270
USPA1_P44 : GENSVAIGSNNTWETGKENVFIILGSG--ITGVTSNSVLLGNNTAGKKAATA : 263
USPA1_ATCC : GENSVAIGSNNTWKKQONVFIILGSNTDTNNAKNGSVLLGNNTAGKKAATI : 280
USPA1_O46E : GDNSVAIGSNNTIDSKQNVFIILGSSTNTNNAKNGSVLLGNNTAGKKAATA : 280
USPA1_TTA3 : GKDSVAIGSNNTWETGKENVFIILGS--NTKDAHSNSVLLGNNTETGKKAATT : 298
USPA1_O35E : GENSVAIGSENNTKTEHKNVFIILGS--GTGVTNSVLLGNNTETAGKKAATT : 250
USPA1_TTA2 : GTNSVAIGSNNTWETGKENVFIILGSNTNTNNAKNGSVLLGNNTAGKKAATT : 264
USPA1_V117 : GKDSVAIGSENNTWENNKQNVFIILGS--KTSGAGNSVLLGNNTETGKKAATT : 251

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                *          320          *          340          *
USPA1_O12E : VSSATVGRKLEKIFAGVSOANQA-NSGIVSVGSANSEERQIVNVGAGQISA : 319
USPA1_P44 : VNDATVNGILTLEKIFAGVSKT----GNCIVSVGSENHERQIVNVGAGKISA : 309
USPA1_ATCC : VNSAEVGLSLLEKIFAGSKT----GNCIVSVGKKKQERQIVNVGAGETSD : 326
USPA1_O46E : VSSAKVNGILTLEKIFAGSKTGT----NCIVSVGSENNERQIVNVGAGNISA : 326
USPA1_TTA3 : VENAKVGLSLLEKIFVGSKANT--NNGIVSVGKQEKERQIVNVGAGQISA : 346
USPA1_O35E : VKNAEVGLSLLEKIFAGESKEN----GVSVSGSEKGERQIVNVGAGQISD : 296
USPA1_TTA2 : VNNAEVNGILTLEKIFAGSKANANN-ICIVSVGSENNERQIVNVGAGQISA : 313
USPA1_V117 : VENAEVGLSLLEKIFGSKANANANI-ILSVSGSEKGERQIVNVGAGQISA : 301

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                360          *          380          *          400
USPA1_O12E : LSTDAVNGSQLHALATAVSAQ-----QDNILTNRVDIQETK : 355
USPA1_P44 : DSTDAVNGSQLHALATVAKNK-----SDITKNQAETLVNRVNIETE : 352
USPA1_ATCC : LSTDAVNGSQLHALATVAAQ-----KADIKDLD : 355
USPA1_O46E : DSTDAVNGSQLHALATAKAD-----ADENFRALT : 356
USPA1_TTA3 : DSTDAVNGSQLHALATAV-----DAEFRILT : 372
USPA1_O35E : LSTDAVNGSQLHALATVDDQYDIVNNRADILNNQDDIKDLQKEVGLD : 346
USPA1_TTA2 : LSTDAVNGSQLHALATAKAK-----KSDIKGLNKGVELD : 349
USPA1_V117 : LSTDAVNGSQLHALASTIDEE-----VDILG : 327

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                *          420          *          440          *
USPA1_O12E : RKQENDIKEVVEMQNAIAEADID--NKNHIDAKAQLAGVAVMEEEDK : 402
USPA1_P44 : RKQENDIKEVVEMQNAIAEADK--NKNHIDAKAQLAGVTVMEEENK : 399
USPA1_ATCC : DEVG-----LLG----- : 362
USPA1_O46E : KTQN-----TLIEAGE-----AQDALIAQNOT : 378
USPA1_TTA3 : QTQN-----ALIEAGEA--INQELEGLADYTNQAQDEKILKNQT : 408
USPA1_O35E : NEVGELSRDINSLHDDVTDNQQD-----DKELKRGVKELDNEVGVSER : 389
USPA1_TTA2 : KEVGLSRDINSLHDDVADNQDSIAKNKADKGENKEVKELDKEVGVSER : 399
USPA1_V117 : EEINSLEGEIFNNQDAIAKNQA-----DIAATNKTNIETNGSKITNCT : 370

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                460          *          480          *          500
USPA1_O12E : HVEDLYETNENLDKESQLDGAVFNNNTQNIEDLAAYNELQDAYAKQQTFA : 452
USPA1_P44 : HVEDLYETNDNLDKESQLDGAVFN----- : 424
USPA1_ATCC : -----EEINSLEGEIFN----- : 374
USPA1_O46E : DITANKTIERNFNRTVVNGFEIEK----- : 403
USPA1_TTA3 : DITANKTIEQNFNRTVTNGFEIEK----- : 433
USPA1_O35E : DINSLHDDVADNQDDIAKADIKGLNKEVKELDKEVG-----VLSRD : 432
USPA1_TTA2 : DIGSLHDDVADNQDSIAKNKADIKGLNKEVKELDKEVG-----VLSRD : 442
USPA1_V117 : LYATVTKAVGNNTOGVAAAKADITKNKADIQDLDDVEG-----VLSQD : 413

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                *          520          *          540          *
USPA1_O12E : IDALNKASSENTQNIAKNSNHIITLESNVVEELLNLSGRLLDQKADIDNN : 502
USPA1_P44 : -----NTQNIAKNSNHIITLENNVVEELLNLSGRLLDQKADIDNN : 464
USPA1_ATCC : -----NDAIAKNQADITLESNVVEELLNLSGRLLDQKADIDNN : 414
USPA1_O46E : -----NKAGIAKNQADITLENNVVEELLNLSGRLLDQKADIDNN : 443
USPA1_TTA3 : -----NKAGIAKNQADITLENDVGEKLLNLSGRLLDQKADIDNN : 473

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USPA1_035E : IGS LHDDVATNQADIAKNSAPITKLENNVEEELL LSGRLIDQKADIDNN : 482
USPA1_TTA2 : IGS LHDDVATNQADIAKNSAPITKLENNVEEELL LSGRLIDQKADIDNN : 492
USPA1_V117 : IGS LHDDVATNQADIAKNSAPITKLENNVEEELL LSGRLIDQKADIDNN : 463

560 * 580 * 600
USPA1_012E : INN IYELAQQQDOHSSDIKTLK : 525
USPA1_P44 : INN IYELAQQQDOHSSDIKTLK : 514
USPA1_ATCC : INN IYELAQQQDOHSSDIKTLK : 464
USPA1_046E : INN IYELAQQQDOHSSDIKTLK : 493
USPA1_TTA3 : INN IYELAQQQDOHSSDIKTLK : 523
USPA1_035E : INN IYELAQQQDOHSSDIKTLK : 505
USPA1_TTA2 : INN IYELAQQQDOHSSDIKTLK : 542
USPA1_V117 : INN IYELAQQQDOHSSDIKTLK : 513

* 620 * 640 *
USPA1_012E : --NVEEGLLDLSGRLIDQKADIANKNOADIAQNOQDIQDLAAYNELOQAYA : 573
USPA1_P44 : --NVEEGLLDLSGRLIDQKADIANKNOADIAQNOQDIQDLAAYNELOQAYA : 564
USPA1_ATCC : --NVEEGLLDLSGRLIDQKADIANKNOADIAQNOQDIQDLAAYNELOQAYA : 514
USPA1_046E : --NVEEGLLDLSGRLIDQKADIANKNOADIAQNOQDIQDLAAYNELOQAYA : 543
USPA1_TTA3 : --NVEEGLLDLSGRLIDQKADIANKNOADIAQNOQDIQDLAAYNELOQAYA : 566
USPA1_035E : --NVEEGLLDLSGRLIDQKADIANKNOADIAQNOQDIQDLAAYNELOQAYA : 553
USPA1_TTA2 : KNNVEEGLLDLSGRLIDQKADIANKNOADIAQNOQDIQDLAAYNELOQAYA : 592
USPA1_V117 : --NVEEGLLDLSGRLIDQKADIANKNOADIAQNOQDIQDLAAYNELOQAYA : 563

660 * 680 * 700
USPA1_012E : KOOTEAIDALNKASSENTDRITAFALGTAENKKDAQTAQAQANENKKGTA : 623
USPA1_P44 : KOOTEAIDALNKASSENTDRITAFALGTAENKKDAQTAQAQANENKKGTA : 614
USPA1_ATCC : KOOTEAIDALNKASSENTDRITAFALGTAENKKDAQTAQAQANENKKGTA : 564
USPA1_046E : KOOTEAIDALNKASSENTDRITAFALGTAENKKDAQTAQAQANENKKGTA : 593
USPA1_TTA3 : KOOTEAIDALNKASSENTDRITAFALGTAENKKDAQTAQAQANENKKGTA : 616
USPA1_035E : KOOTEAIDALNKASSENTDRITAFALGTAENKKDAQTAQAQANENKKGTA : 572
USPA1_TTA2 : KOOTEAIDALNKASSENTDRITAFALGTAENKKDAQTAQAQANENKKGTA : 642
USPA1_V117 : KOOTEAIDALNKASSENTDRITAFALGTAENKKDAQTAQAQANENKKGTA : 613

* 720 * 740 *
USPA1_012E : KNOADTOLHDKKTINLEGLHSMVARAVGNNTQGYATNKADIAKNOADIAN : 673
USPA1_P44 : KNOADTOLHDKKTINLEGLHSMVARAVGNNTQGYATNKADIAKNOADIAN : 664
USPA1_ATCC : KNOADTOLHDKKTINLEGLHSMVARAVGNNTQGYATNKADIAKNOADIAN : 614
USPA1_046E : KNOADTOLHDKKTINLEGLHSMVARAVGNNTQGYATNKADIAKNOADIAN : 643
USPA1_TTA3 : KNOADTOLHDKKTINLEGLHSMVARAVGNNTQGYATNKADIAKNOADIAN : 624
USPA1_035E : KNOADTOLHDKKTINLEGLHSMVARAVGNNTQGYATNKADIAKNOADIAN : 583
USPA1_TTA2 : KNOADTOLHDKKTINLEGLHSMVARAVGNNTQGYATNKADIAKNOADIAN : 692
USPA1_V117 : KNOADTOLHDKKTINLEGLHSMVARAVGNNTQGYATNKADIAKNOADIAN : 663

760 * 780 * 800
USPA1_012E : NIKNIYELAQQQDOHSSDIKTLAKVSAANTDRIAKNKAEDASFETLTKN : 723
USPA1_P44 : NIKNIYELAQQQDOHSSDIKTLAKVSAANTDRIAKNKAEDASFETLTKN : 714
USPA1_ATCC : NIKNIYELAQQQDOHSSDIKTLAKVSAANTDRIAKNKAEDASFETLTKN : 664
USPA1_046E : NIKNIYELAQQQDOHSSDIKTLAKVSAANTDRIAKNKAEDASFETLTKN : 693
USPA1_TTA3 : NIKNIYELAQQQDOHSSDIKTLAKVSAANTDRIAKNKAEDASFETLTKN : 674
USPA1_035E : NIKNIYELAQQQDOHSSDIKTLAKVSAANTDRIAKNKAEDASFETLTKN : 633
USPA1_TTA2 : NIKNIYELAQQQDOHSSDIKTLAKVSAANTDRIAKNKAEDASFETLTKN : 742
USPA1_V117 : NIKNIYELAQQQDOHSSDIKTLAKVSAANTDRIAKNKAEDASFETLTKN : 713

* 820 * 840 *

USPA1_O12E : QNTLIEQGEALVEQNKAINQELLEGFAAHADVODKQILONQADITTNKTAI : 773
 USPA1_P44 : QNTLIEQGEALVEQNKAINQELLEGFAAHADVODKQILONQADITTNKTAI : 764
 USPA1_ATCC : QNTLIEQGEALVEQNKAINQELLEGFAAHADVODKQILONQADITTNKTAI : 714
 USPA1_O46E : QNTLIEQGEALVEQNKAINQELLEGFAAHADVODKQILONQADITTNKTAI : 743
 USPA1_TTA3 : QNTLIEQGEALVEQNKAINQELLEGFAAHADVODKQILONQADITTNKTAI : 724
 USPA1_O35E : QNTLIEQGEALVEQNKAINQELLEGFAAHADVODKQILONQADITTNKTAI : 683
 USPA1_TTA2 : QNTLIEQGEALVEQNKAINQELLEGFAAHADVODKQILONQADITTNKTAI : 792
 USPA1_V117 : QNTLIEQGEALVEQNKAINQELLEGFAAHADVODKQILONQADITTNKTAI : 763

860 * 880 * 900
 USPA1_O12E : EQNINRTVANGFEIEKNKAGIATNKQELILODRLNINETNNHODQKID : 823
 USPA1_P44 : EQNINRTVANGFEIEKNKAGIATNKQELILODRLNINETNNHODQKID : 814
 USPA1_ATCC : EQNINRTVANGFEIEKNKAGIATNKQELILODRLNINETNNHODQKID : 764
 USPA1_O46E : EQNINRTVANGFEIEKNKAGIATNKQELILODRLNINETNNHODQKID : 793
 USPA1_TTA3 : EQNINRTVANGFEIEKNKAGIATNKQELILODRLNINETNNHODQKID : 774
 USPA1_O35E : EQNINRTVANGFEIEKNKAGIATNKQELILODRLNINETNNHODQKID : 733
 USPA1_TTA2 : EQNINRTVANGFEIEKNKAGIATNKQELILODRLNINETNNHODQKID : 842
 USPA1_V117 : EQNINRTVANGFEIEKNKAGIATNKQELILODRLNINETNNHODQKID : 813

* 920 * 940 *
 USPA1_O12E : QLGVALKEQGQHFNRRISAVERTAGGIANATAIATLPSPSRAGEHHVLE : 873
 USPA1_P44 : QLGVALKEQGQHFNRRISAVERTAGGIANATAIATLPSPSRAGEHHVLE : 864
 USPA1_ATCC : QLGVALKEQGQHFNRRISAVERTAGGIANATAIATLPSPSRAGEHHVLE : 814
 USPA1_O46E : QLGVALKEQGQHFNRRISAVERTAGGIANATAIATLPSPSRAGEHHVLE : 843
 USPA1_TTA3 : QLGVALKEQGQHFNRRISAVERTAGGIANATAIATLPSPSRAGEHHVLE : 824
 USPA1_O35E : QLGVALKEQGQHFNRRISAVERTAGGIANATAIATLPSPSRAGEHHVLE : 783
 USPA1_TTA2 : QLGVALKEQGQHFNRRISAVERTAGGIANATAIATLPSPSRAGEHHVLE : 892
 USPA1_V117 : QLGVALKEQGQHFNRRISAVERTAGGIANATAIATLPSPSRAGEHHVLE : 863

960 * 980 *
 USPA1_O12E : GSGYHNGQAAVSLGAAGLSDTGKSTYKIGLSWSDAGGLSGGVGGSYRWK : 922
 USPA1_P44 : GSGYHNGQAAVSLGAAGLSDTGKSTYKIGLSWSDAGGLSGGVGGSYRWK : 913
 USPA1_ATCC : GSGYHNGQAAVSLGAAGLSDTGKSTYKIGLSWSDAGGLSGGVGGSYRWK : 863
 USPA1_O46E : GSGYHNGQAAVSLGAAGLSDTGKSTYKIGLSWSDAGGLSGGVGGSYRWK : 892
 USPA1_TTA3 : GSGYHNGQAAVSLGAAGLSDTGKSTYKIGLSWSDAGGLSGGVGGSYRWK : 873
 USPA1_O35E : GSGYHNGQAAVSLGAAGLSDTGKSTYKIGLSWSDAGGLSGGVGGSYRWK : 832
 USPA1_TTA2 : GSGYHNGQAAVSLGAAGLSDTGKSTYKIGLSWSDAGGLSGGVGGSYRWK : 941
 USPA1_V117 : GSGYHNGQAAVSLGAAGLSDTGKSTYKIGLSWSDAGGLSGGVGGSYRWK : 912

Fig. 20

PileUp multiple alignment of full length UspA2 protein sequences

```

               *      20      *      40      *
q848s1_morca : MNKIYKVKKNAAGHSVACSEFAKGHTKKAVLGSLLI VGALGMATTASAC-L
: 50
q91961_morca : MNKIYKVKKNAAGHLVACSEFAKGHTKKAVLGSLLI VGALGMATTASACQL
: 51
q8rtb2_morca : ~~~~~~
: -
q91963_morca : ~~~~~~
: -
o54407_morca : ~~~~~~
: -
q9xd51_morca : ~~~~~~
: -
q58xp4_morca : ~~~~~~
: -
q8gh86_morca : ~~~~~~
: -
q91962_morca : ~~~~~~ MNKIYKVKKR
: 10
forsgren_uspa2 : ~~~~~~
: -
q9xd55_morca : ~~~~~~
: -
q848s2_morca : ~~~~~~
: -
q9xd53_morca : ~~~~~~
: -

               60      *      80      *      100
q848s1_morca : VSTQENIDYRSTTIGNNIGSSWSIIGAGHDNIVRSANSGILSGYKNIV
: 101
q91961_morca : VSTNKE-----NOOVKPTNSIIGAGFNNVGGSAHSGILSGYKNIV
: 93
q8rtb2_morca : ~~~~~~
: -
q91963_morca : ~~~~~~
: -
o54407_morca : ~~~~~~
: -
q9xd51_morca : ~~~~~~
: -
q58xp4_morca : ~~~~~~
: -
q8gh86_morca : ~~~~~~
: -
q91962_morca : AAGHSVACSEFAKGHTKKAVLGSLLI VGALGMATTASAC GSTNAANGNLI
: 61
forsgren_uspa2 : ~~~~~~
: -
q9xd55_morca : ~~~~~~
: -
q848s2_morca : ~~~~~~
: -

```

```

*               120               *               140               *
q848s1_morca : NCSTSAIVGGYDNETKCKYTFVGGGYKNLAEGCHSDIGGGYENNAEGDNAT
: 152
q91961_morca : NCNTSAIVGGYGNETKGDYTFVGGGYKNLAKGNYPFVGGGYKNLAEGDNAT
: 144
q8rtb2_morca : ~~~~~~
: -
q91963_morca : ~~~~~~
: -
c54407_morca : ~~~~~~
: -
q9xd51_morca : ~~~~~~
: -
q58xp4_morca : ~~~~~~
: -
q8gh86_morca : ~~~~~~
: -
q91962_morca : SGVGAIVGGGYINQAKKNYPFVGGGLINRAKGNYSVISGGGLINQAKCHST
: 112
forsgren_uspa2 : ~~~~~~
: -
q9xd55_morca : ~~~~~~
: -
q848s2_morca : ~~~~~~
: -
q9xd53_morca : ~~~~~~
: -

```

```

160          *          180          *          200
q848s1_morca : TAGGFTNEAAGNLSAIGGGYANAECHDATIAGGFTENRAEGNLSAEGGGAA
: 203
q91961_morca : TAGGFTNLAAGNATIAGGFTENRAEGTDSMVEGGYANQANIGGSSTVAGGSN
: 195
q8rtb2_morca : ~~~~~
: -
q91963_morca : ~~~~~
: -
o54407_morca : ~~~~~
: -
q9xd51_morca : ~~~~~
: -
q58xp4_morca : ~~~~~
: -
q8gh86_morca : ~~~~~
: -
q91962_morca : TAGGTSNGATGCTNSTVAGGNNNOAGTGSTVAGGNNNOAGGCTNSTVAGGCTN
: 163
forsgren_uspa2 : ~~~~~
: -
q9xd55_morca : ~~~~~
: -
q848s2_morca : ~~~~~
: -
q9xd53_morca : ~~~~~
: -

```

```

      *           220           *           240           *
q848s1_morca : NFAAGDETFWGGCENHAGNQSAIGGGYANLAEGDNATIAGGENAKGE
: 254
q91961_morca : NLAEGSSAIGGGCRONEASGDRSTVSGGYNNLAEGKSSAIGGGENLAGN
: 246
q8rtb2_morca : ~~~~~~
: ~~~~~~
q91963_morca : ~~~~~~
: ~~~~~~
o54407_morca : ~~~~~~
: ~~~~~~
q9xd51_morca : ~~~~~~
: ~~~~~~
q58xp4_morca : ~~~~~~
: ~~~~~~
q8gh86_morca : ~~~~~~
: ~~~~~~
q91962_morca : QANTDNAMPLGKNNENGNNAPSSENTNNNGKNNATIGSNTNAQSGS
: 214
forsgren_uspa2 : ~~~~~~
: ~~~~~~
q9xd55_morca : ~~~~~~
: ~~~~~~
q848s2_morca : ~~~~~~
: ~~~~~~
q9xd53_morca : ~~~~~~
: ~~~~~~

      260           *           280           *           300
q848s1_morca : NSVSSGGYANGARGESSTFAGG-----FENREGIDSVVSGCTANDAMTAW
: 300
q91961_morca : NATISGGCRONEASGNSTVAFG-----FONQAIGKYSTEGCRNEASSDDR
: 292
q8rtb2_morca : ~MKTMKLLPLKIAVTSAMIGLGAASTANAG-----AMETFLPNLDNDY
: 44
q91963_morca : ~MKTMKLLPLKIAVTSAMVGLGAASTANAGQOKSPKETFLPNLDNDN
: 49
o54407_morca : ~MKTMKLLPLKIAVTSAMIVLGASTYNAG-----VVEETFPNTEEN
: 44
q9xd51_morca : ~MKTMKLLPLKIAVTSAMIVLGASTYNAG-----VVEETFPNTEEN
: 44
q58xp4_morca : ~MKTMKLLPLKIAVTSAMIVLGAASTANAGQOKETFLPNLDYNDY
: 49
q8gh86_morca : ~MKTMKLLPLKIAVTSAMIVLGASTANAGVASPANOKI-----QOK
: 42
q91962_morca : VLGCGESSGEATAVSRARNGLILKNEGCVETQEDGVSV-----QSE
: 258
forsgren_uspa2 : ~MKTMKLLPLKIAVTSAMIGLGAASTANAGAKN-----DI-----T
: 36
q9xd55_morca : ~MKTMKLLPLKIAVTSAMIGLGAASTANAGAKN-----DI-----T
: 36
q848s2_morca : ~MKTMKLLPLKIAVTSAMIVLGASTNAQAQSRSEDOI-----QTK
: 42
q9xd53_morca : ~MKTMKLLPLKIAVTSAMIGLGAASTANAGSRSEEDI-----QDS
: 42

      *           320           *           340           *
q848s1_morca : -SVAGVYNQATESSTIAGSNQATVQTAGVENMADANATA

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q8rtb2_morca : EQSAYSRGIGDIDDLNANKENNRLEHGDITANEESVOYLNKEVOIN
 : 191
 q91963_morca : -NSAYSRGIGDIDDLNANKENNRLEHGDITANEESVOYLNREVOIN
 : 196
 o54407_morca : EQSAYSRGIGDIDDLNDEEVNFKAHDYNEKOTEADALNKAESAN
 : 196
 q9xd51_morca : EQSAYSRGIGDIDDLNDEEVNFKAHDYNEKOTEADATNKASAN
 : 196
 q58xp4_morca : D-SAYSRGIGDIDDLNDEMFLNHEETSLYDNTANQDDIKGLKKVKD
 : 201
 q8gh86_morca : -----IGSLNDEEALNYTEIDNYTDILNCAANTAKNODITEKN
 : 155
 q91962_morca : -----IGSLNDEEAL-----NCAATAKN
 : 344
 forsgren_uspa2 : ENED-CGLADIVEGEGEGLONFYSIKKNDORNLVNGFETEKNKDATAKN
 : 171
 q9xd55_morca : ENED-CGLADIVEGEGEGLONETSIKKNDORNLVNGFETEKNKDATAKN
 : 171
 q848s2_morca : ERRTAQNQAD-IOLENNVVEELFW-----SDRLIDQKEDIKNEADIAQN
 : 181
 q9xd53_morca : ERRTAQNQAD-IOLENNVVEELFW-----SDRLIDQKEDIK-----N
 : 167

0 * 480 * 500 *
 q848s1_morca : EVHVGAGELISNDSTDAVNGSGLMALAAVEMNODIEKNODDIEKIRGV-
 : 488
 q91961_morca : EVHVGAGELISNDSTDAVNGSGLMALAAVEMNODIEKNODDIAKNADIA
 : 483
 q8rtb2_morca : ENNI-HEL---AQQDQSSDIKELKKNVEGLLELSCH---LIAQKEDIA
 : 235
 q91963_morca : ENNI-HEL---AQQDQSSDIKELKKNVEGLLELSCH---LIAQKEDIA
 : 240
 o54407_morca : ENRI-ETA---EETIDKNEYDIKALENVVEGLLELSCH---LIDQKADET
 : 240
 q9xd51_morca : ENRI-ETA---EETIDKNEYDIKALENVVEGLLELSCH---LIDQKADET
 : 240
 q58xp4_morca : KKGV-KEL---NKKELKELDKELGVLSRSG---SINDD---VAQNNESLE
 : 241
 q8gh86_morca : QEDT-KEL---DKREVGLSREIGSLNDEV-----ADNEDIA
 : 188
 q91962_morca : KENI-KEL---DKEMNVLSREIVSLNDEV-----ADNADIA
 : 377
 forsgren_uspa2 : NESI-ELYDFEHEVAESIGEITHANEACNETLKGLITN---SIENNNININ
 : 218
 q9xd55_morca : NESI-ELYDFEHEVAESIGEITHANEACNETLKGLITN---SIENNNININ
 : 218
 q848s2_morca : NESI-ELYDFEHEVAEKGEITHAYTEVNKTLODLITN---SWANNININ
 : 228
 q9xd53_morca : NASI-ELYDFEHEVAERTGEITHAYTEVNKTLENLITN---SWANTONED
 : 214

520 * 540 * 560
 q848s1_morca : -----KELDKEMLVLSRDVSLNDEV-----ACNQ-----SD
 : 515
 q91961_morca : KNQADIQTLENVVKELINISGRLLIDQKADIDNNINHIYELAQQQDQHSDD
 : 534
 q8rtb2_morca : QNQIDIOELATYNEI-----QDQMAOKQWEAIDALNKASSENTONIAKNSNH
 : 282
 q91963_morca : QNQIDIOELATYNEI-----QDQMAOKQWEAIDALNKASSENTONIAKNSNH

```

: 287
o54407_morca : KD-----
: 242
q9xd51_morca : KD-----
: 242
q58xp4_morca : MDPSQEVASGE-----ENKAKNETODNTNSMENTNTERKAD
: 288
q8gh86_morca : KNOADIQTLENNVEEGLELSGHLIDOKADIDNNINNIYELAQQODQHSSD
: 239
q91962_morca : KNOADIKTLENNVEEGLELSGRLIDOKADIDNNINNIYELAQQODQHSSD
: 428
forsgren_uspa2 : KKNADIQALENNVVEELNLSGRLIDOKADIDNNINNIYELAQQODQHSSD
: 269
q9xd55_morca : KKNADIQALENNVVEELNLSGRLIDOKADIDNNINNIYELAQQODQHSSD
: 269
q848s2_morca : KN-----KADIDNNINNIYELAQQODQHSSD
: 254
q9xd53_morca : KN-----KADIDNNINNIYELAQQODQHSSD
: 240

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*          580          *          600          *
q848s1_morca : IKTLKNNVEEGLELSGHLIDOKADLTCDIKALENNVEEGLLD-----
: 558
q91961_morca : IKTLKNNVEEGLELSGHLIDOKADLTCDIKALESNVEEGLLD-----
: 577
q8rtb2_morca : IKTLENNVEEGLELSGHLIDOKADLTCDIKALESNVEEGLLD-----
: 325
q91963_morca : IKTLENNVEEGLELSGHLIDOKADLTCDIKALESNVEEGLLD-----
: 330
o54407_morca : IKALENNVEEGLELSGHLIDOKADLTCDIKALESNVEEGLLD-----
: 285
q9xd51_morca : IKALENNVEEGLELSGHLIDOKADLTCDIKALESNVEEGLLD-----
: 285
q58xp4_morca : IQALENNVMEELNLSGHLIDOKADLTCDIKALESNVEEGLLD-----
: 331
q8gh86_morca : IKTLKNNVEEGLELSGHLIDOKDTDAONCANEDDTATYNEIDQYAEQOT
: 290
q91962_morca : IKTLKNNVEEGLELSGHLIDOKADTAQOQDIDQDLATYNEIDQYAEQOT
: 479
forsgren_uspa2 : IKTLKNNVEEGLELSGHLIDOKEDTAON-----C-----
: 299
q9xd55_morca : IKTLKNNVEEGLELSGHLIDOKEDTAON-----C-----
: 299
q848s2_morca : IKTLKNNVEEGLELSGHLIDOKADLTCDIKALE-----
: 288
q9xd53_morca : IKTLKNNVEEGLELSGHLIDOKADLTCDIKALE-----
: 274

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```

          620          *          640          *          660
q848s1_morca : -----LSGRLIDOKADIKNQAD
: 576
q91961_morca : -----LSGRLIDOK-----AD
: 588
q8rtb2_morca : -----LSGRLIDOKADIKNQAD
: 343
q91963_morca : -----LSGRLIDOK-----AD
: 341
o54407_morca : -----LSGRLIDOKADIKNQAD
: 303

```

q9xd51_morca : -----LSGRLIDOKADIADNQCAN
 : 303
 q58xp4_morca : -----LSGHLIDOKADIAKNOQAD
 : 349
 q8gh86_morca : EALDALNKASSENTQNT-----AKNSNRLEALE-----SN
 : 320
 q91962_morca : EALDALNKASSENTQNTIEDLAAYNELODAYAKOOTEALDALNKASSENTQNT
 : 530
 forsgren_uspa2 : -----AN
 : 301
 q9xd55_morca : -----AN
 : 301
 q848s2_morca : -----NN
 : 290
 q9xd53_morca : -----SN
 : 276

* 680 * 700 *
 q848s1_morca : I-----
 : 577
 q91961_morca : I-----
 : 589
 q8rtb2_morca : I-----AQNOTIQLDLAAYNELODAYAK
 : 366
 q91963_morca : I-----AENQANIQLDLAAYNELODAYAK
 : 364
 o54407_morca : I-----
 : 304
 q9xd51_morca : IQLDLAAYNELODAYAKOOTEALDALNKASSENTQNTIEDLAAYNELODAYAK
 : 354
 q58xp4_morca : I-----
 : 350
 q8gh86_morca : VEEGLLELSGHLIDOKADLTKDKALESNVEEGLLELSGHLID
 : 363
 q91962_morca : IEDLAAYNELODAYAKOOTEALDALNKASSENTQNTIEDLAAYNELODAYAK
 : 581
 forsgren_uspa2 : IQD-----LATANELODQAS-----KOTHAIDAL
 : 326
 q9xd55_morca : IQD-----LATANELODQAS-----KOTHAIDAL
 : 326
 q848s2_morca : VEEGLLDLSGRLIDOKAD-----IN
 : 312
 q9xd53_morca : VEEGLLDLSGRLIDOKADLTKDKALESNVEEGLLDLSGRLID
 : 319

720 * 740 * 760
 q848s1_morca : -----AQNOTIQLDLAAYNELODAYAKOOTEALDALNKASSENTQNT
 : 615
 q91961_morca : -----AQNOTIQLDLAAYNELODAYAKOOTEALDALNKASSENTQNT
 : 627
 q8rtb2_morca : QOTEALDALNKASSENTQNTIEDLAAYNELODAYAKOOTEALDALNKASSENTQNT
 : 417
 q91963_morca : QOTEALDALNKASSENTQNTIEDLAAYNELODAYAKOOTEALDALNKASSENTQNT
 : 415
 o54407_morca : -----AQNOTD-----
 : 310
 q9xd51_morca : QOTEALDALNKASSENTQNTIEDLAAYNELODAYAKOOTEALDALNKASSENTQNT
 : 405
 q58xp4_morca : -----AQNOANIQLDLAAYNELODAYAKOOTEALDALNKASSENTQNT

: 388
q8gh86_morca : QKADI-----AQNQANIQDLAAYNELODYAKQOTEALDALNKASSEN
: 406
q91962_morca : QOTEALDALNKASSENTONIQDLAAYNELODAYAKQOTEALDALNKASSEN
: 632
forsgren_uspa2 : NKAS-----SENTONIEDLAAYNELODAYAKQOTEALDALNKASSEN
: 368
q9xd55_morca : NKAS-----SENTONIEDLAAYNELODAYAKQOTEALDALNKASSEN
: 368
q848s2_morca : QADI-----AQNQDIQDLAAYNELODYAKQOTEALDALNKASSEN
: 354
q9xd53_morca : QKADI-----AQNQDIQDLAAYNELODYAKQOTEALDALNKASSEN
: 362

* 780 * 800 *

q848s1_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 666
q91961_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 678
q8rtb2_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 468
q91963_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 466
o54407_morca : ---IQDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 358
q9xd51_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 456
q58xp4_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 439
q8gh86_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 457
q91962_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 683
forsgren_uspa2 : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 419
q9xd55_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 419
q848s2_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 405
q9xd53_morca : TONIEDLAAYNELODAYAKQOTEALDALNKASSENTONIAKNQADIANNIN
: 413

820 * 840 * 860

q848s1_morca : NIYELAQQQDOHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
: 717
q91961_morca : NIYELAQQQDOHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
: 729
q8rtb2_morca : NIYELAQQQDOHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
: 519
q91963_morca : NIYELAQQQDOHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
: 517
o54407_morca : NIYELAQQQDOHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
: 409
q9xd51_morca : NIYELAQQQDOHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
: 507
q58xp4_morca : NIYELAQQQDOHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
: 490
q8gh86_morca : NIYELAQQQDOHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
: 508

q91962_morca : NIYELAQOODQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
 : 734
 forsgren_uspa2 : NIYELAQOODKHRSDIKTLAKTSAANTDRIAKNKADDDASFETLTKNQNTL
 : 470
 q9xd55_morca : NIYELAQOODQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
 : 470
 q848s2_morca : NIYELAQOODQHSSDIKTLAKASAANTDRIAKNKADADASFETLTKNQNTL
 : 456
 q9xd53_morca : NIYELAQOODQHSSDIKTLAKASAANTNRI-----ATAFHTAENKKDZQ
 : 458

* 880 * 900 * 9
 q848s1_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 768
 q91961_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 780
 q8rtb2_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 570
 q91963_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 568
 o54407_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 460
 q9xd51_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 558
 q58xp4_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 541
 q8gh86_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 559
 q91962_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 785
 forsgren_uspa2 : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 521
 q9xd55_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 521
 q848s2_morca : IEKDKEHDKLITANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 507
 q9xd53_morca : IEKAOAN-----ANKTAIDANKASADTKFAATADAITKNGNAITKNAKSIT
 : 504

20 * 940 * 960
 q848s1_morca : DLGTVKVDGFDGRVT-----ALDTKVNAFDGRITALDSKVENGMAAQAAL
 : 812
 q91961_morca : DLGTVKVDGFDGRVT-----ALDTKVNAFDGRITALDSKVENGMAAQAAL
 : 824
 q8rtb2_morca : DLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAAL
 : 621
 q91963_morca : DLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAAL
 : 619
 o54407_morca : DLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAAL
 : 511
 q9xd51_morca : DLGTVKVDGFDGRVTALDTKVNALDTKVNAFDGRITALDSKVENGMAAQAAL
 : 609
 q58xp4_morca : DLGTVKVDGFDGRVT-----ALDTKVNAFDGRITALDSKVENGMAAQAAL
 : 585
 q8gh86_morca : DLGTVKVDGFDGRVT-----ALDTKVNAFDGRITALDSKVENGMAAQAAL
 : 603
 q91962_morca : DLGTVKVDGFDGRVT-----ALDTKVNAFDGRITALDSKVENGMAAQAAL
 : 829
 forsgren_uspa2 : DLGTVKVDGFDGRVT-----ALDTKVNAFDGRITALDSKVENGMAAQAAL

```

: 565
q9xd55_morca : DLGTVKVDGFDGRVT-----ALDTKVNAFDGRITALDSKVENGMAAQAAL
: 565
q848s2_morca : DLGTVKVDGFDGRVT-----ALDTKVNAFDGRITALDSKVENGMAAQAAL
: 551
q9xd53_morca : DLGTVKVDGFDGRVT-----ALDTKVNAFDGRITALDSKVENGMAAQAAL
: 548

```

```

*          980          *          1000          *          1020
q848s1_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 863
q91961_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 875
q8rtb2_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 672
q91963_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 670
o54407_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 562
q9xd51_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 660
q58xp4_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 636
q8gh86_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 654
q91962_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 880
forsgren_uspa2 : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 616
q9xd55_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 616
q848s2_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 602
q9xd53_morca : SGLFQPYSVGKFNATAALGGYGSKSAVAIGAGYRVNPNLAFKAGAAINTSG
: 599

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*
q848s1_morca : NKKGSYNIGVNYEF : 877
q91961_morca : NKKGSYNIGVNYEF : 889
q8rtb2_morca : NKKGSYNIGVNYEF : 686
q91963_morca : NKKGSYNIGVNYEF : 684
o54407_morca : NKKGSYNIGVNYEF : 576
q9xd51_morca : NKKGSYNIGVNYEF : 674
q58xp4_morca : NKKGSYNIGVNYEF : 650
q8gh86_morca : NKKGSYNIGVNYEF : 668
q91962_morca : NKKGSYNIGVNYEF : 894
forsgren_uspa2 : NKKGSYNIGVNYEF : 630
q9xd55_morca : NKKGSYNIGVNYEF : 630
q848s2_morca : NKKGSYNIGVNYEF : 616
q9xd53_morca : NKKGSYNIGVNYEF : 613

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Fig. 21

% identity in regions identified on Forsgren sequence

	30-177 laminin binding	165-318 fibronectin binding	302-458 C3-binding
q848s1_morca	8	19	74
q9l961_morca	6	41	73
q8rtb2_morca	9	22	67
q9l963_morca	10	23	68
o54407_morca	10	17	53
q9xd51_morca	10	19	66
q58xp4_morca	10	16	75
q8gh86_morca	18	43	69
q9l962_morca	9	36	64
q9xd55_morca	99	98	96
q848s2_morca	35	54	74
q9xd53_morca	29	52	64