

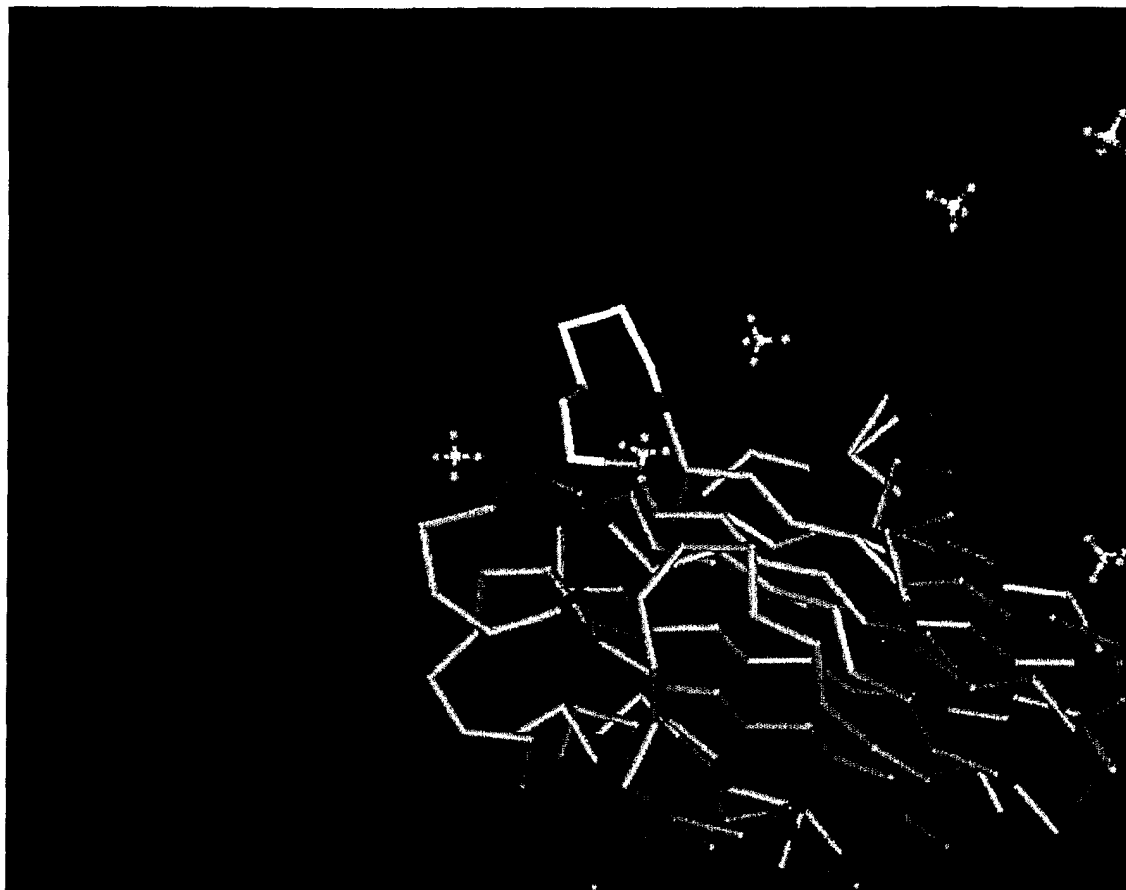


Figure 1: 1GWY Chain A, Crystal Structure Of The Water-Soluble Pore-Forming Cytolysin StxH

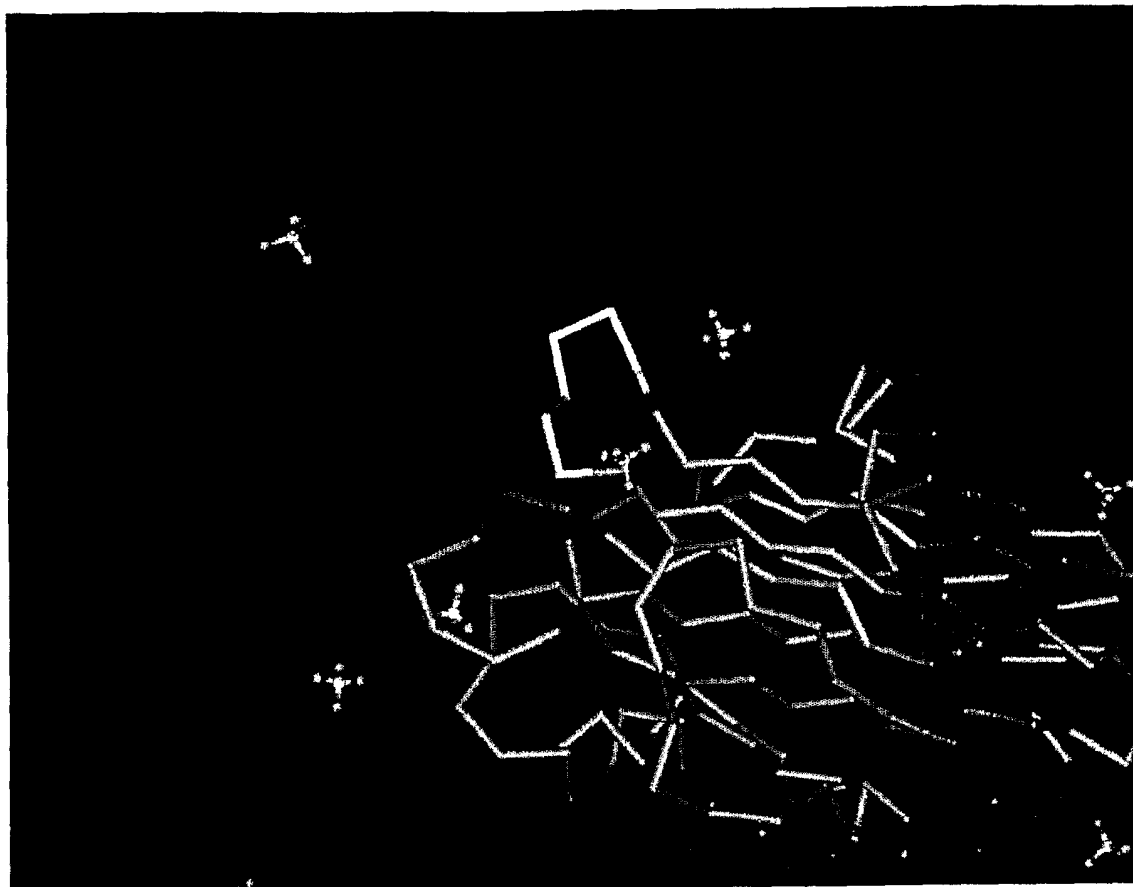


Figure 2: 1GWY Chain B, Crystal Structure Of The W State Of The Pore- Forming Cytolysin Sticholysin II

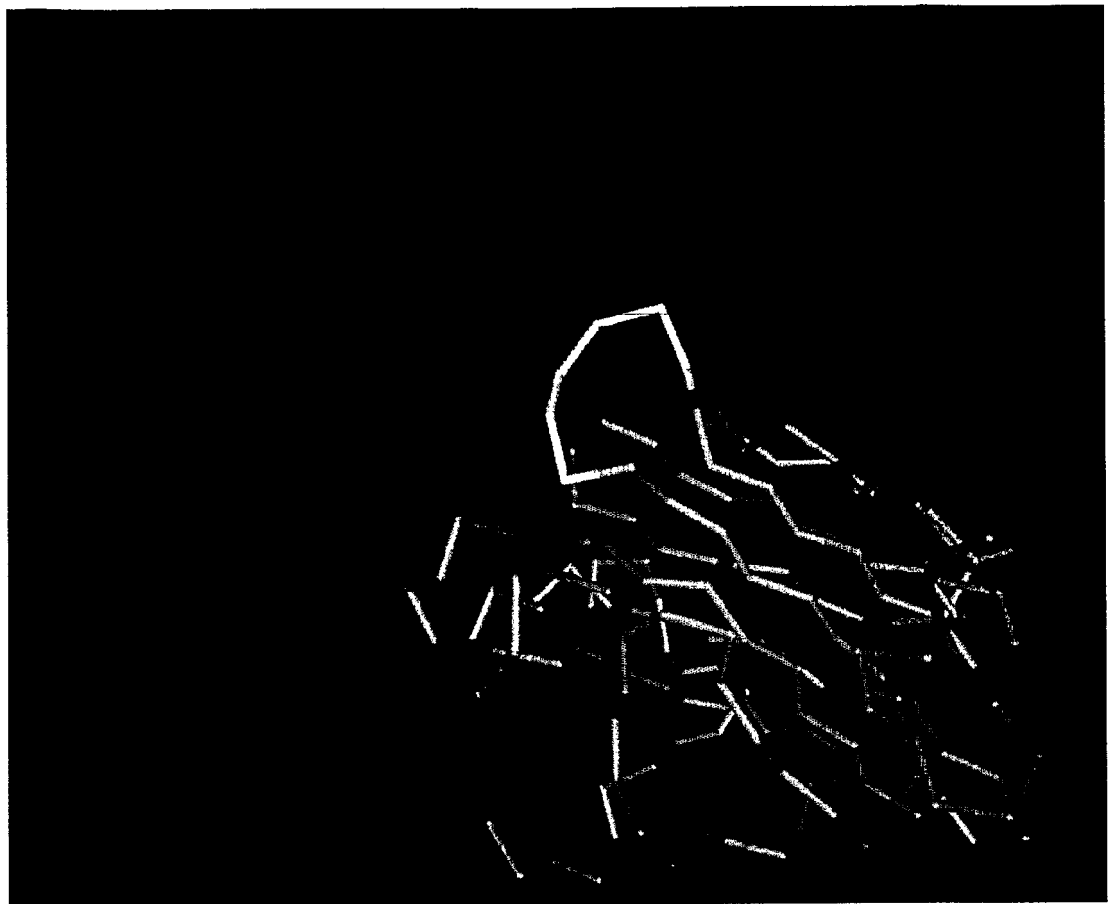


Figure 3: 1KD6 Chain A, Solution Structure Of The E Pore-Forming Cytolysin Equinatoxin Ii

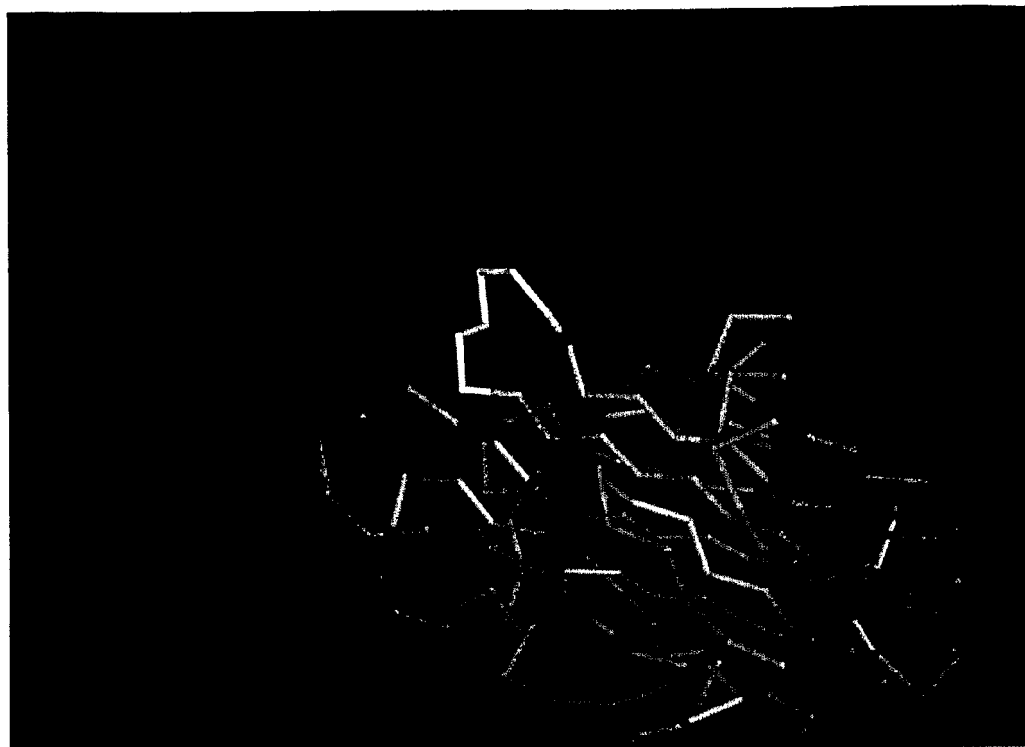
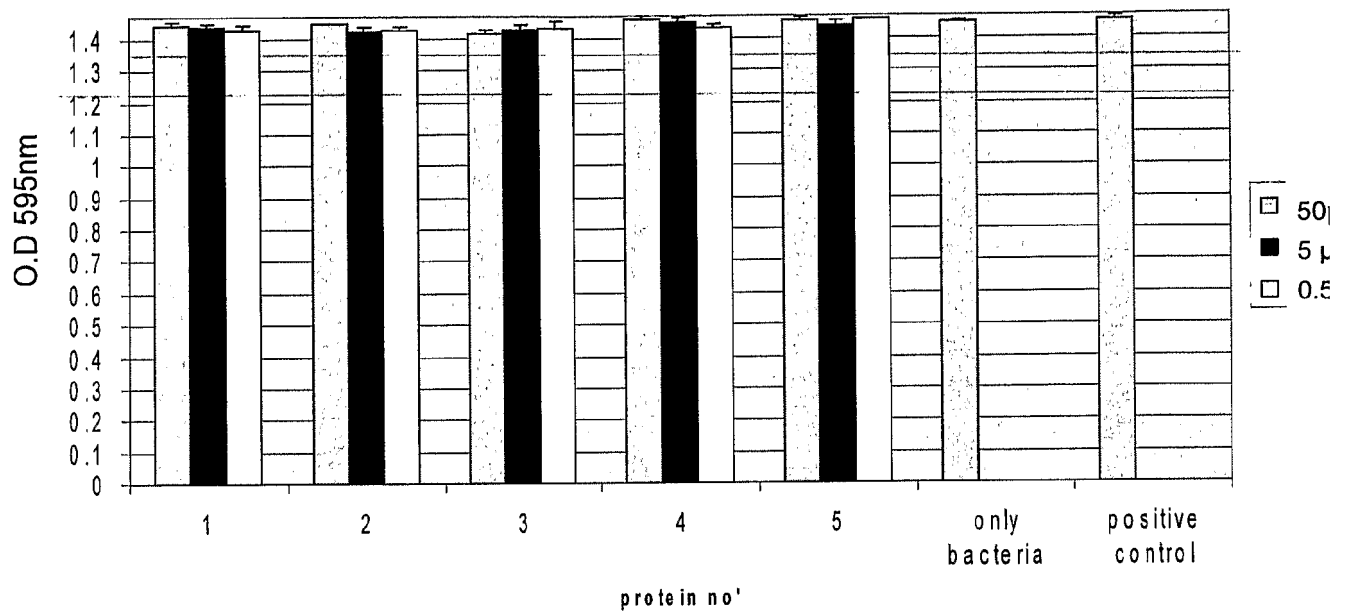
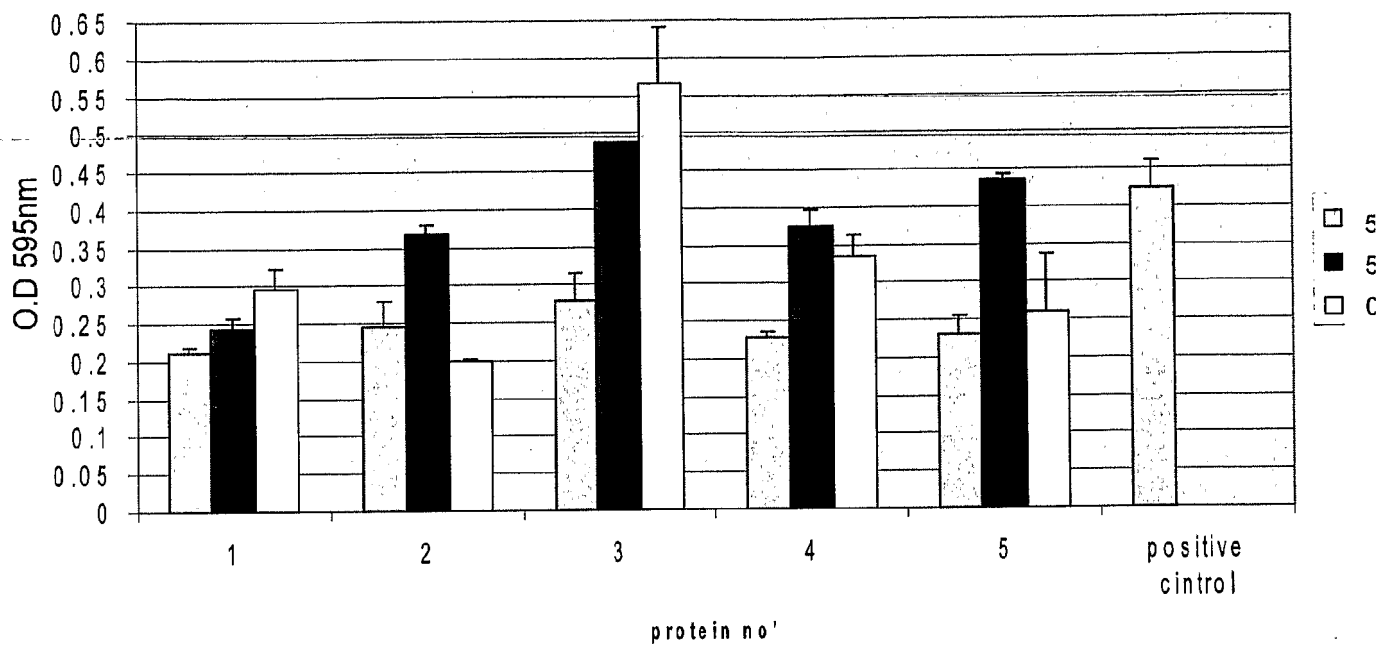


Figure 4: 1TZQ Chain A, Crystal Structure Of The Equinatoxin li 8-69 Double Cysteine Mutant

Figure 5***Pseudomonas aeruginosa* ATCC 27853 growth 24h**

- 1- AbacZ-17C
- 2- AbacZ-17
- 3- AbacZ-16C
- 4- AbacZ-6
- 5- AbacZ-8C

Figure 6**Prevention of *Pseudomonas aeruginosa* ATCC 27853 biofilm**

- 1- AbacZ-17C
- 2- AbacZ-17
- 3- AbacZ-16C
- 4- AbacZ-6
- 5- AbacZ-8C

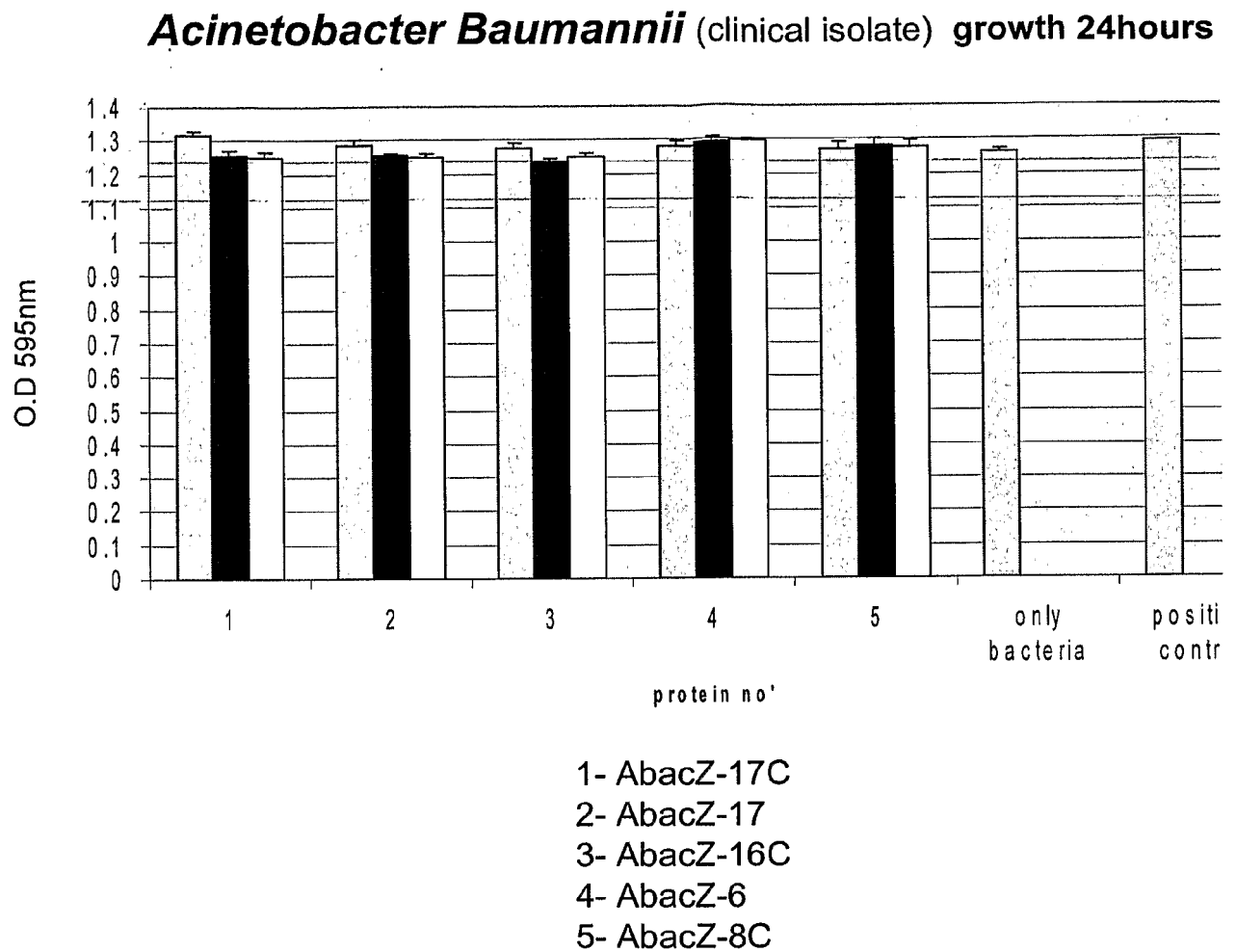
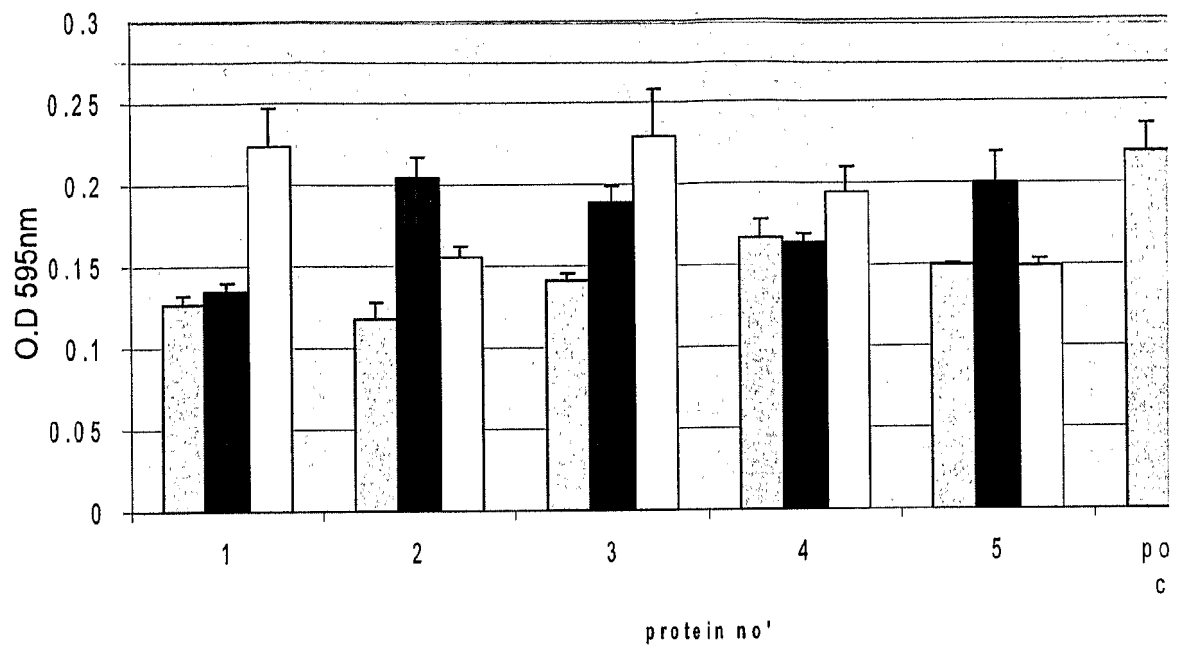
Figure 7

Figure 8**Prevention of *Acinetobacter Baumannii* (clinical isolate) biofilm**

- 1- AbacZ-17C
- 2- AbacZ-17
- 3- AbacZ-16C
- 4- AbacZ-6
- 5- AbacZ-8C

Figure 9
Prevention of *Actinetobacter baumannii* biofilm formation by equine fractions

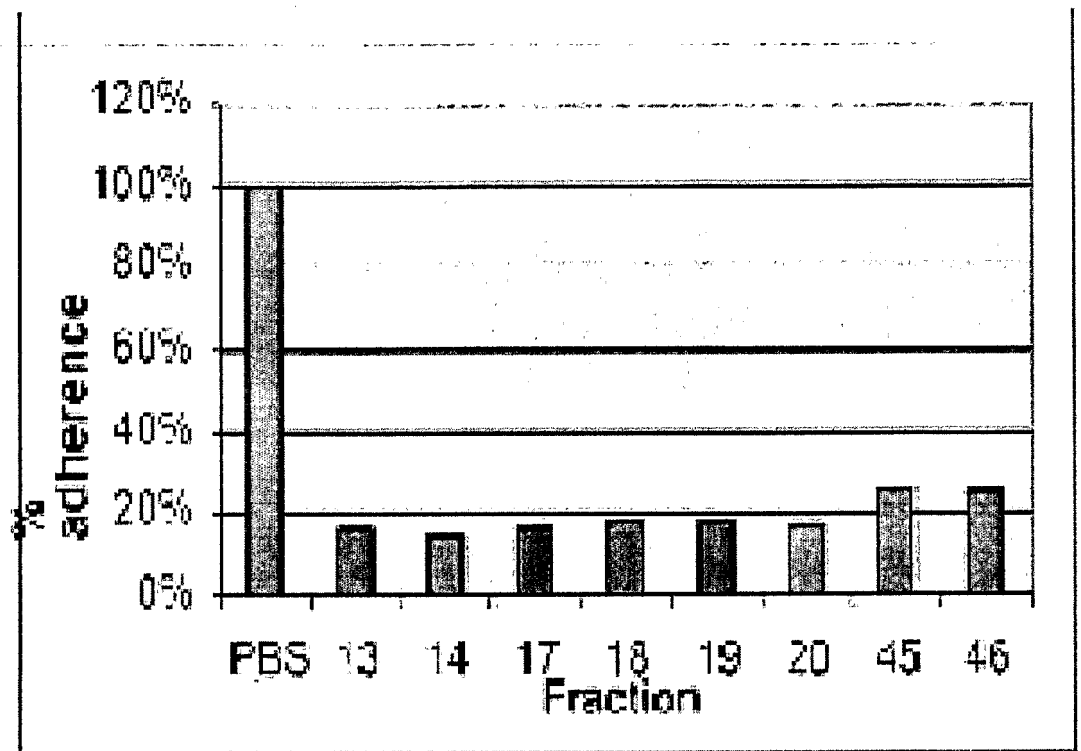
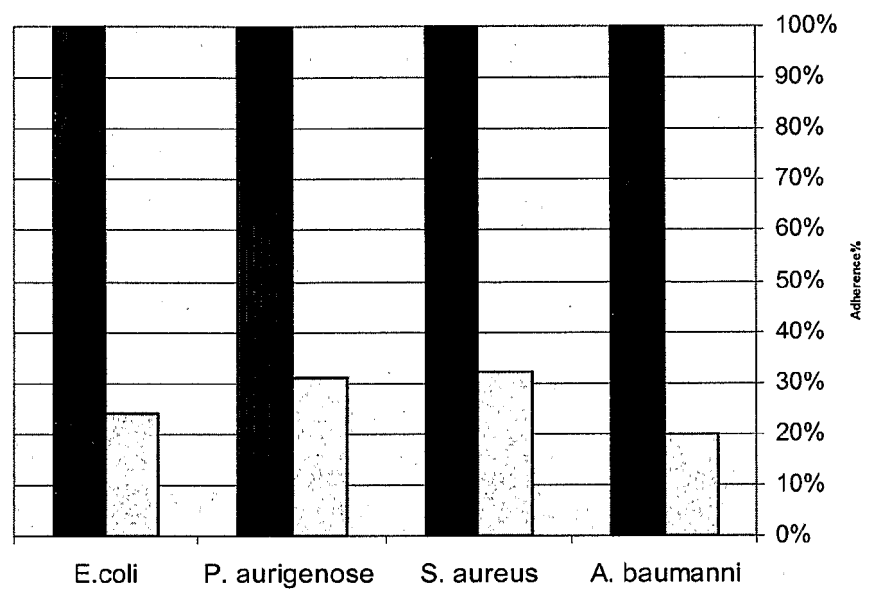


Figure 10
Prevention of biofilm formation by fraction 13



Prevention of *Pseudomonas aeruginosa* biofilm formation by *Anemonia*, *Aiptasia* and *Physcomitrella* (Moss)

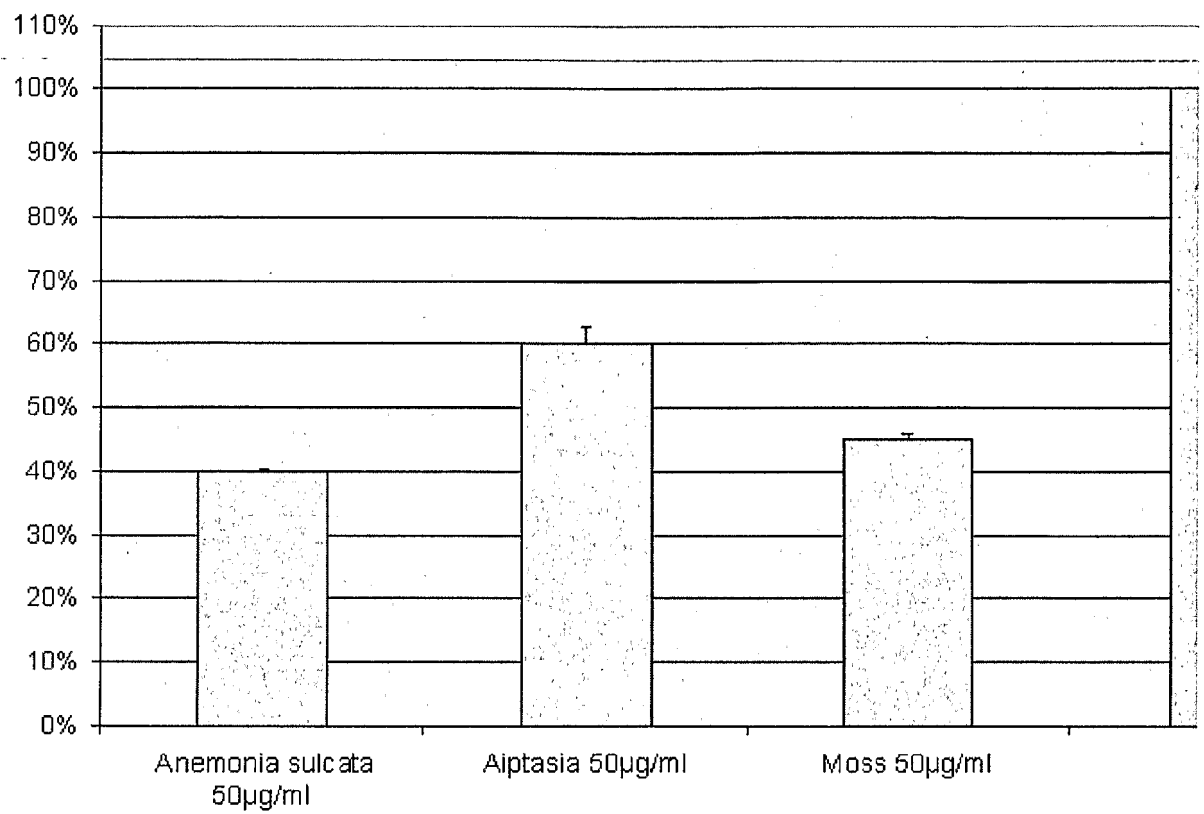


Figure 11

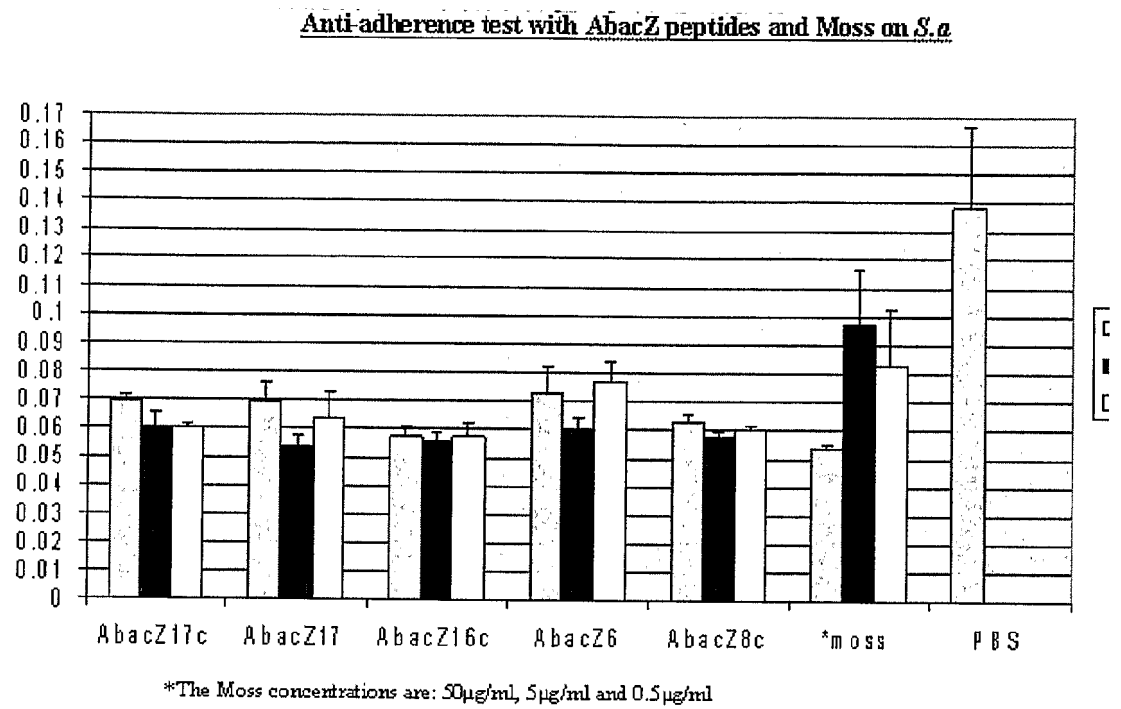
Figure 12

Figure 13

Fig. 8

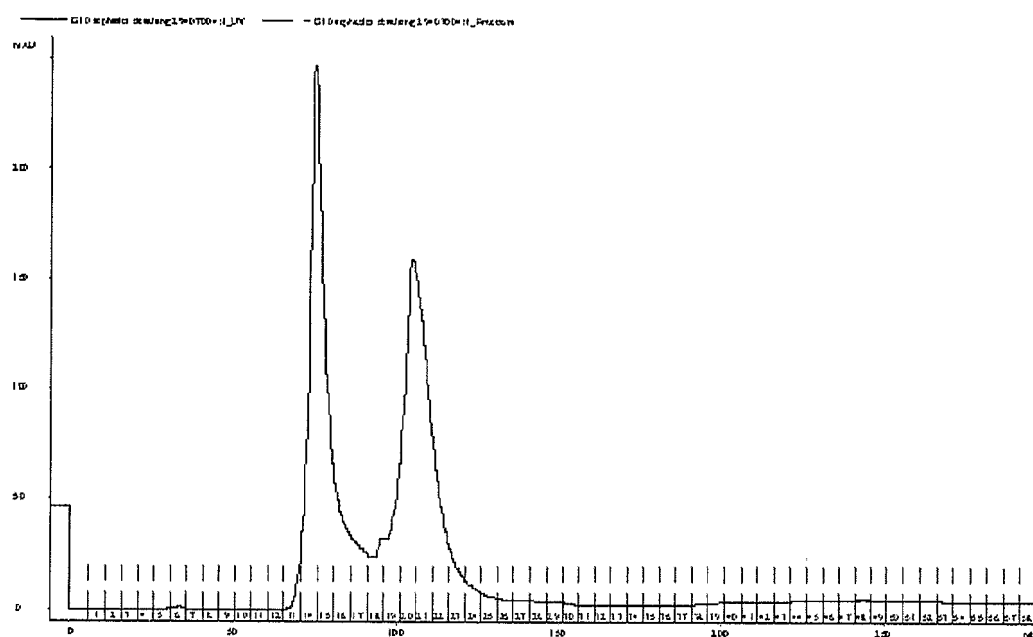


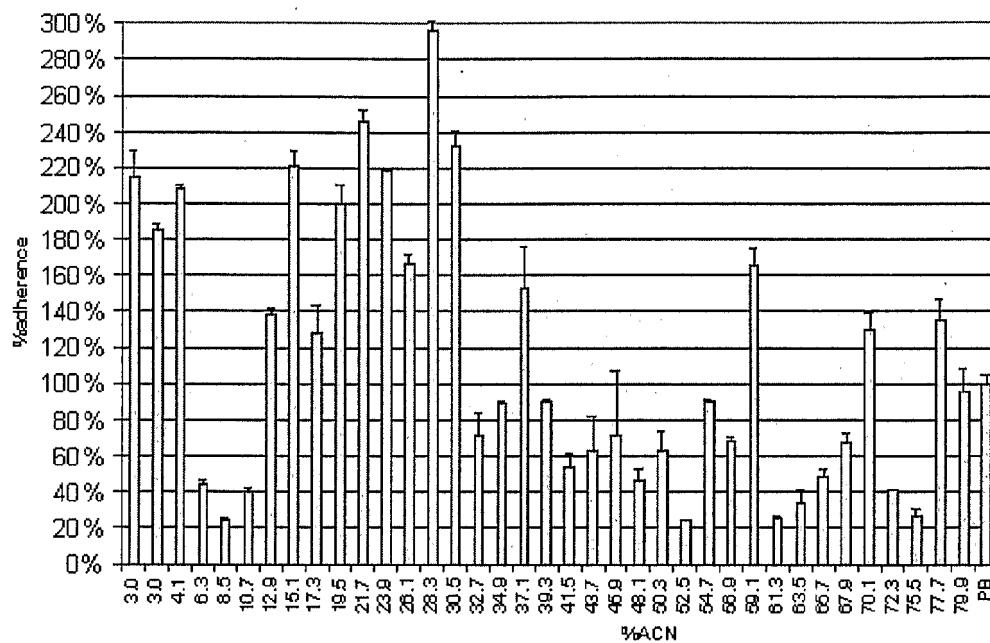
Figure 15

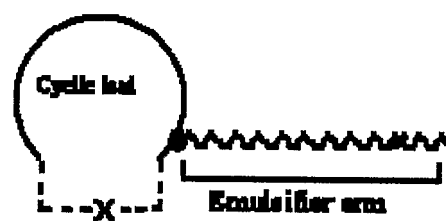
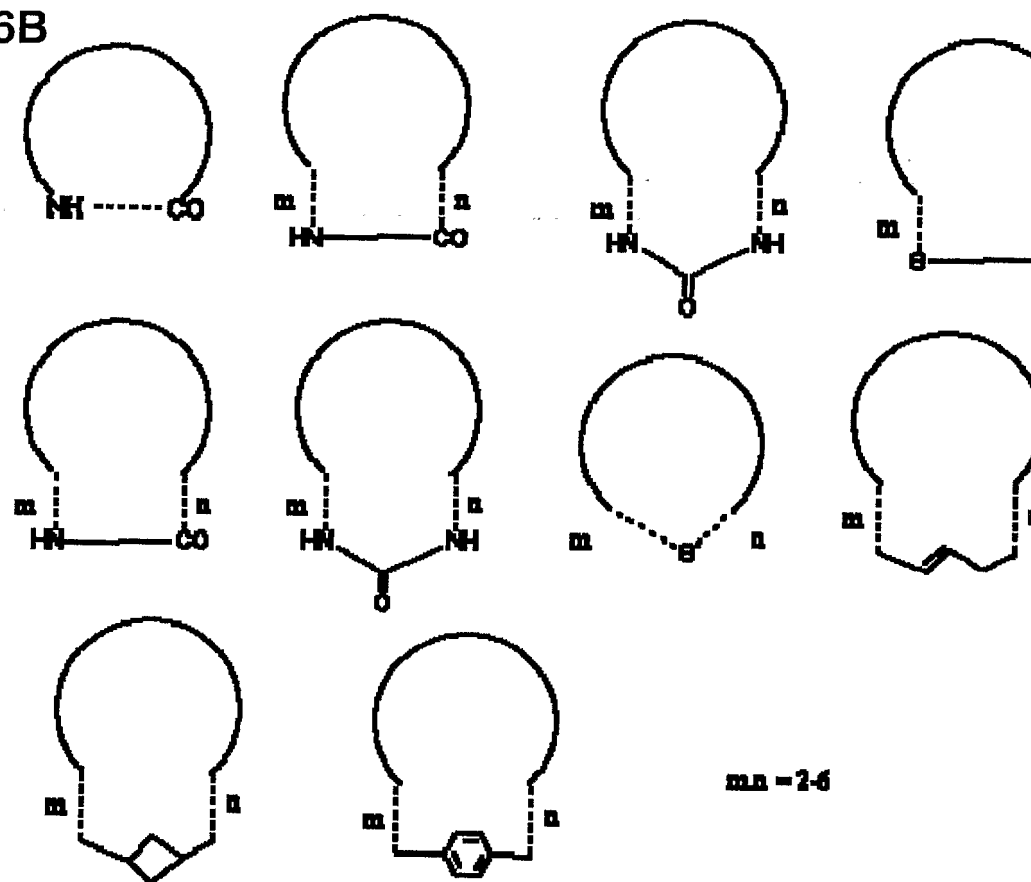
Figure 16A**Scheme 1. General structure of the cyclic lead with emulsifier arm**

Figure 16B



mn = 2-6

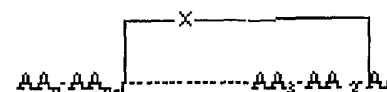
Scheme 2. Cyclization strategies:

FLOW CHART FOR DEVELOPMENT OF CYCLIC PEPTIDE EMULSIFYING ARM

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Figure 17

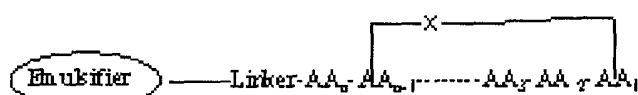
1. Parallel assembly and cyclization of the peptide hit
SPPS (Fmoc chemistry)



X = amide, urea, S-S, S, cyclobutane, Ph, etc.

2. Bio-screening of cyclic peptides for defining of the
cyclization mode

3. Parallel and sequential addition of emulsifying linker:



4. Resubmission to the bio-test and absorption experi

5. Evaluation of the results.