Legend to Supplementary Figures

Figure S1 Predicted secondary structural elements for the sequence of sperm Whale myoglobin N-Butyl isocyanide [PDB-id: 105M].

Figure S2 The schematic diagram represents the comparison of secondary structures predicted (CSSP) by the proposed server and the correct secondary structural elements (PDB) obtained from the three-dimensional structure of sperm Whale myoglobin N-Butyl isocyanide [PDB-id: 105M].

Figure S3 The consensus secondary structure predicted by CSSP for the sequence of Mannose-specific agglutinin (Lectin) from *Glanthus Nivalis* [PDB-id: 1JPC].

Figure S4 The diagram represents the comparison of secondary structures predicted (CSSP) and the secondary structures observed (PDB) in the three-dimensional structure of Mannose-specific agglutinin from *Glanthus Nivalis* [PDB-id: 1JPC].

Figure S1

```
                       10        20        30        40        50
                       |         |         |         |         |
AA Sequence : VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLK
DSC         : CCCCCCCHHHHHHHHHCCCCCCCCCCHHHHHHHHCCCCHHHHHHHHHHHH
GOR IV      : CCCCCCCHHHHHHHHHHHHHHHCCCHHHHHHHHHCCCHHHHHHHHHHHHH
Predator    : CCCCCHHHHHHHHHHHHHHHHCCCCHHHHHHHHHHCHHHHHHCCHHHHHH
SIMPA96     : CCCCHHHHHHHHHHHHHHHHHCCCHHHHHHHHHHCCHHHHHHHHHHHHHH
PSIPRED     : CCCHHHHHHHHHHHHHHHHCCHHHHHHHHHHHHHHCHHHHHHHHHCCCCC
PROFphd     : CCCCCHHHHHHHHHHHHHHHHHCCHHHHHHHHHHCCHHHHHHHCHHHHHC
Consensus   : CCCCCHHHHHHHHHHHHHHHHHCCHHHHHHHHHHCCHHHHHHHHHHHHHH

                       60        70        80        90       100
                       |         |         |         |         |
AA Sequence : TEAEMKASEDLKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIP
DSC         : HHHHHHHHHHHHCCCCEEEHHHHHHHHHHCCCCCCCCHHHHHHCCCCCCC
GOR IV      : HHHHHHHHHHHHHCCEEEHHHHHHHHHHHCCHHHHHHHHHHHHHHCCCCC
Predator    : HHHHHHHHHHHHCCCCHHHHHHHHHHHHCCCCCCCHHHHHHHHHHHCCCC
SIMPA96     : HHHHHHHHHHHHHCCCCHHHHHHHHHHHCCCCHHHHHHHHHHHHCCCCCH
PSIPRED     : CHHHCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHCCCCC
PROFphd     : HHHHHHHHHHHHHCCCHHHHHHHHHHHHCCCCHHHCCHHHHHHHHCCCCC
Consensus   : HHHHHHHHHHHHHCCCHHHHHHHHHHHHHCCCHHHHHHHHHHHHHCCCCC

                      110       120       130       140       150
                       |         |         |         |         |
AA Sequence : IKYLEFISEAIIHVLHSRHPGDFGADAQGAMNKALELFRKDIAAKYKELG
DSC         : CHHHHHHHHHHHHEECCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHC
GOR IV      : HHHHHHHHHHHHHHHHCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHC
Predator    : CHHHHHHHHHHHHHHHHCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHH
SIMPA96     : HHHHHHHHHHHHHHHHCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHC
PSIPRED     : HHHHHHHHHHHHHHHHHHHCCCCCHHHHHHHHHHHHHHHHHHHHHHHHCC
PROFphd     : HHHHHHHHHHHHHHHHCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHC
Consensus   : HHHHHHHHHHHHHHHHCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHC


AA Sequence : YQG
DSC         : CCC
GOR IV      : EEC
Predator    : CCC
SIMPA96     : CCC
PSIPRED     : CCC
PROFphd     : CCC
Consensus   : CCC

Percentage of alpha helix predicted = 79.084969
Percentage of beta sheet predicted = 0.000000
```

Figure S2

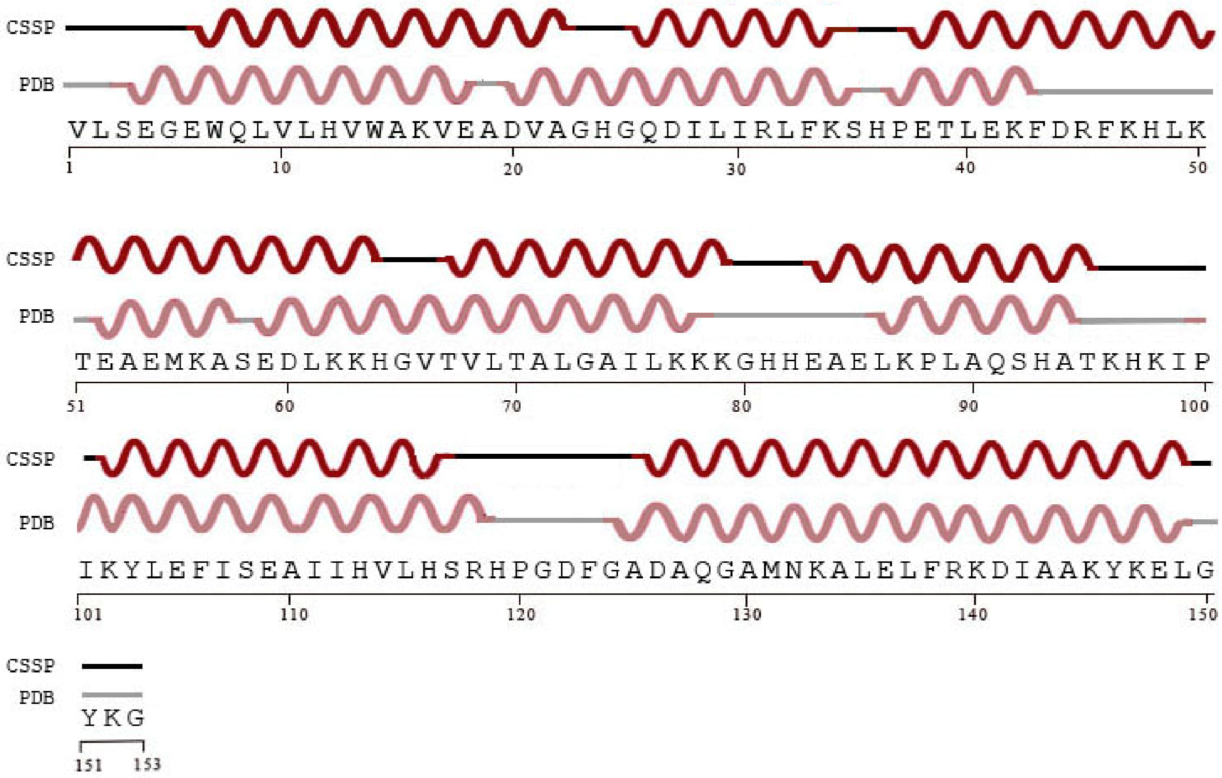

CSSP
PDB
VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLK
1
10
20
30
40
50
CSSP
PDB
TEAEMKASEDLKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIP
51
60
70
80
90
100
CSSP
PDB
IKYLEFISEAIIHVLHSRHPGDFGADAQGAMNKALELFRKDIAAKYKELG
101
110
120
130
140
150
CSSP
PDB
YKG
151
153

Figure S3

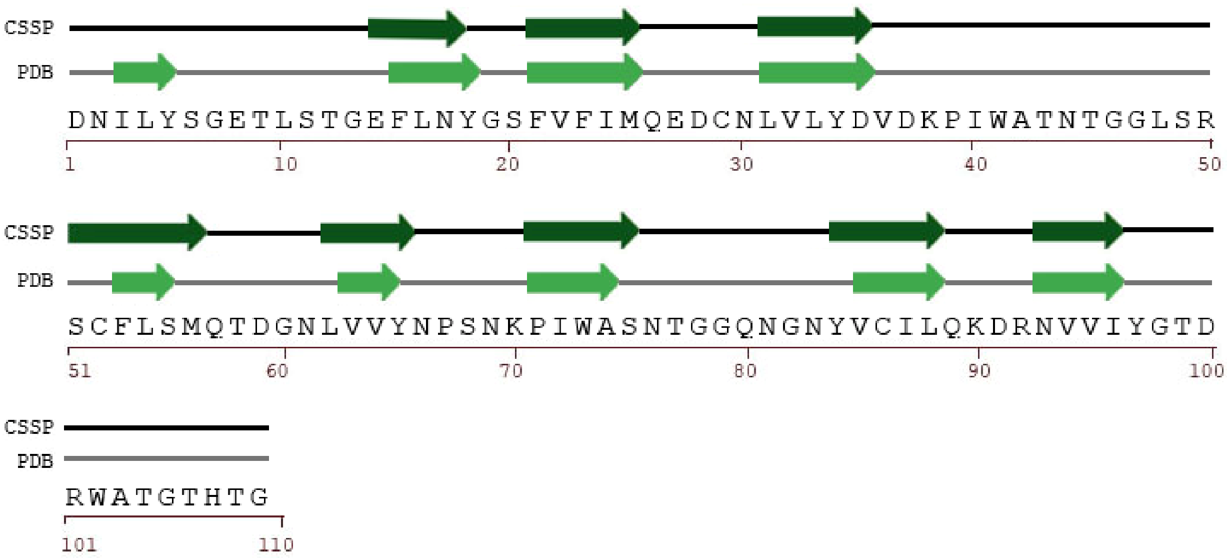
```
                         10        20        30        40        50
                         |         |         |         |         |
AA Sequence  : DNILYSGETLSTGEFLNYGSFVFIMQEDCNLVLYDVDKPIWATNTGGLSR
DSC          : CCEEEECCCCCEEEEECCCCEEEEEECCCCEEEECCCCCEEEECCCCCCE
GOR IV       : CCCCCCCCCCCCCCCCCCCCEEEEEECCCCEEEEECCCCEEEECCCCCCC
Predator     : CCEEECCEEECCCEEEEECCEEEEECCCCCEEEEECCEEEEECCCCCCCC
SIMPA96      : CEEEECCCCCCCCCCCCCCCEEEEECCCCCEEEECCCCCEEECCCCCCCC
PSIPRED      : CCEECCCCEECCCCEEEECCEEEEECCCCCEEEEECCCEEEECCCCCCCC
PROFphd      : CCEEEECEECCCCEEEECCEEEEEEECCCCEEEEECCCCEEEECCCCCCE
Consensus    : CCCCCCCCCCCCCEEEECCCEEEEECCCCCEEEEECCCCCCCCCCCCCCC

                         60        70        80        90       100
                         |         |         |         |         |
AA Sequence  : SCFLSMQTDGNLVVYNPSNKPIWASNTGGQNGNYVCILQKDRNVVIYGTD
DSC          : EEEEEECCCCEEEEECCCCCEEEEEECCCCCCCEEEEECCCCEEEEEEEC
GOR IV       : EEEEECCCCCCEEEECCCCCCEEEECCCCCCCCEEEEECCCCCEEEEECC
Predator     : CCEEEECCCCCEEEECCCCCEEEECCCCCCCCCCEEEECCCCCEEEECCC
SIMPA96      : EEEEEECCCCCEEEECCCCCEEEEECCCCCCCEEEEEECCCCEEEEECCC
PSIPRED      : CCEEEECCCCCEEEECCCCCEEEEECCCCCCCCEEEEECCCCCEEEECCC
PROFphd      : EEEEEEECCCCEEEECCCCCEEEEECCCCCCCEEEEEEEECCCEEEEEEC
Consensus    : EEEEEECCCCCEEEECCCCCEEEEECCCCCCCCEEEEECCCCCEEEECCC


AA Sequence  : RWATGTHTG
DSC          : EEEEECCCC
GOR IV       : CEEEEEEEC
Predator     : CCCCCCCCC
SIMPA96      : CCCCCCCCC
PSIPRED      : CCCCCCCCC
PROFphd      : CCCCCCCCC
Consensus    : CCCCCCCCC

Percentage of alpha helix predicted = 0.000000
Percentage of beta sheet predicted = 34.862385
```

Figure S4


CSSP
PDB
DNILYSGETLSTGEFLNYGSFVFIMQEDCNLVLYDVDKPIWATNTGGLSR
1
10
20
30
40
50
CSSP
PDB
SCFLSMQTDGNLVVYNPSNKPIWASNTGGQNGNYVCILQKDRNVVIYGTD
51
60
70
80
90
100
CSSP
PDB
RWATGTHTG
101
110