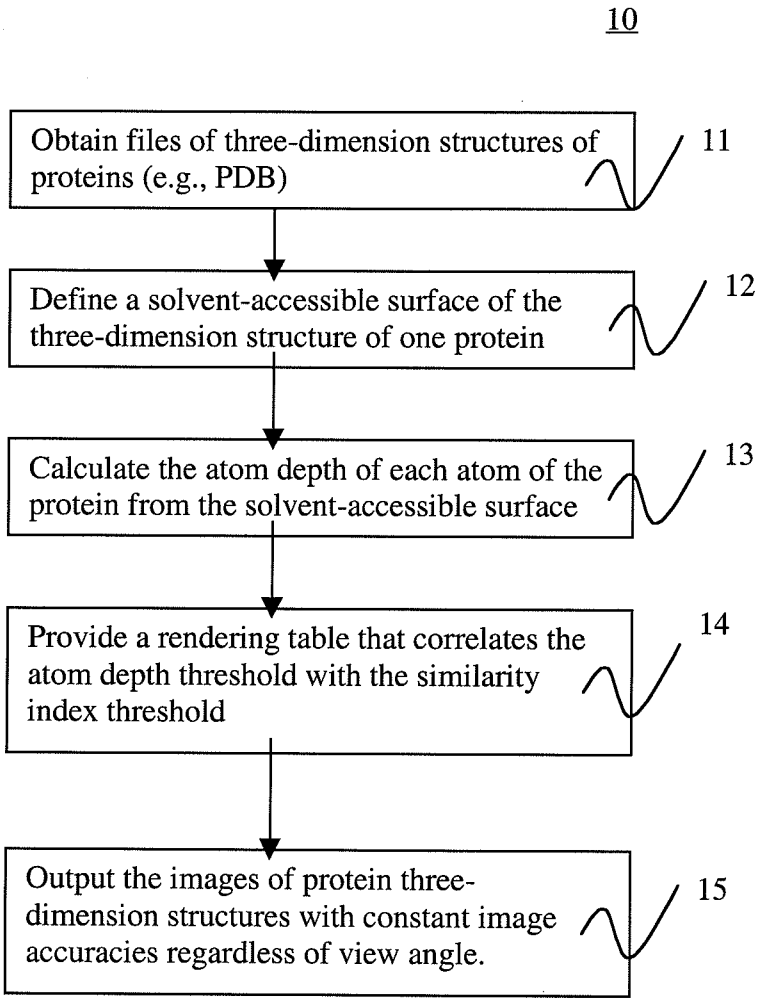

10
Obtain files of three-dimension structures of proteins (e.g., PDB)
11
Define a solvent-accessible surface of the three-dimension structure of one protein
12
Calculate the atom depth of each atom of the protein from the solvent-accessible surface
13
Provide a rendering table that correlates the atom depth threshold with the similarity index threshold
14
Output the images of protein three-dimension structures with constant image accuracies regardless of view angle.
15

FIG 1

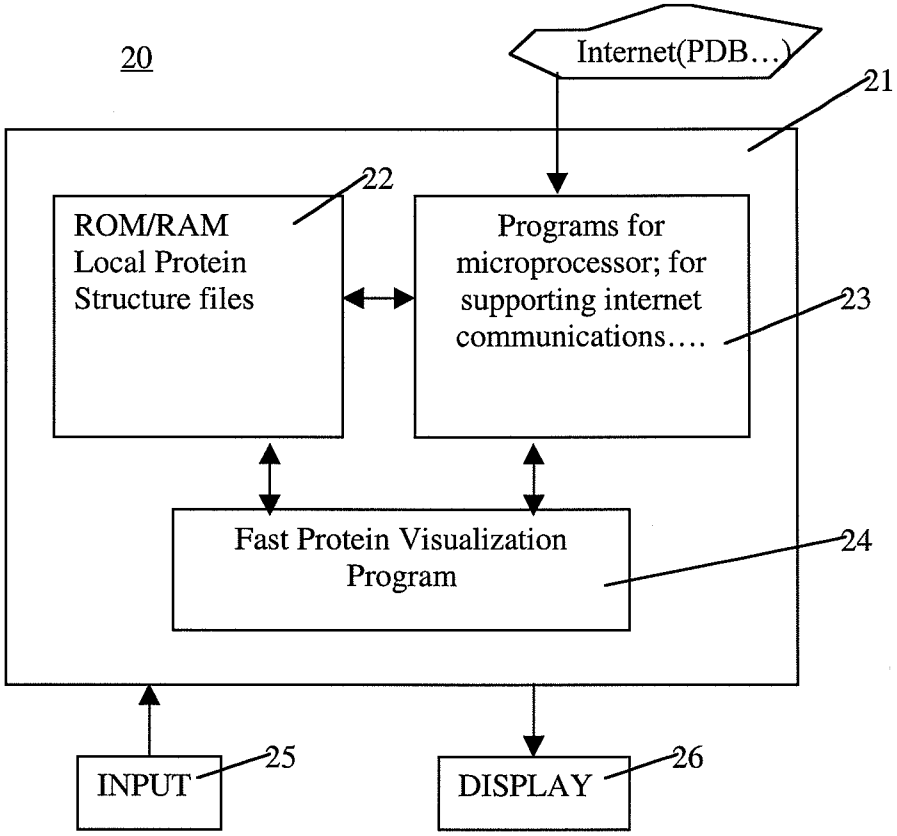
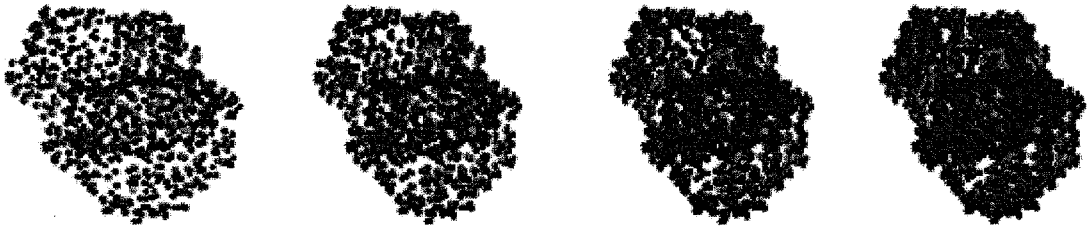

20
Internet(PDB…)
21
22
ROM/RAM
Local Protein
Structure files
Programs for
microprocessor; for
supporting internet
communications….
23
Fast Protein Visualization
Program
24
INPUT
25
DISPLAY
26

FIG 2

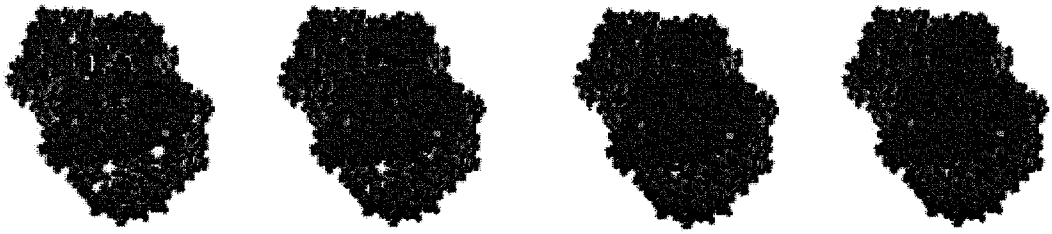
An Example Annotation

```
USER ATOMDEPTH     1         1.2
USER ATOMDEPTH     2         2.0
...
USER ATOMDEPTH     1000      2.7
USER XROTATION –90.0 0.0 90.0
USER YROTATION 0.0 180.0
USER RDATA 14.5  100.0  100.0  100.0  100.0  100.0 100.0  100.0 100.0 100.0 100.0 100.0 100.0
USER RDATA 14.0  99.8  99.7  100.0  99.4  98.2 100.0  100.0 100.0 100.0 100.0 100.0 100.0
...
USER RDATA 0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0  0.0
ATOM     1  C   ACE A  23     24.288  17.826  14.313  1.00 95.10      1OVA 378
ATOM     2  O   ACE A  23     24.917  18.906  14.298  1.00 59.40      1OVA 379
...
```

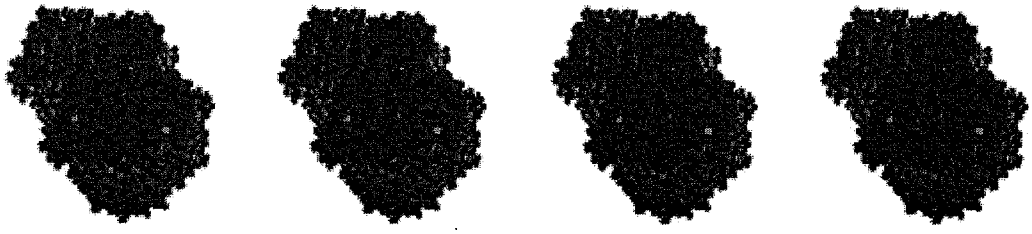
FIG 3



(a) Atom depth = 1.0 (b) Atom depth = 2.0 (c) Atom depth = 3.0 (d) Atom depth = 4.0

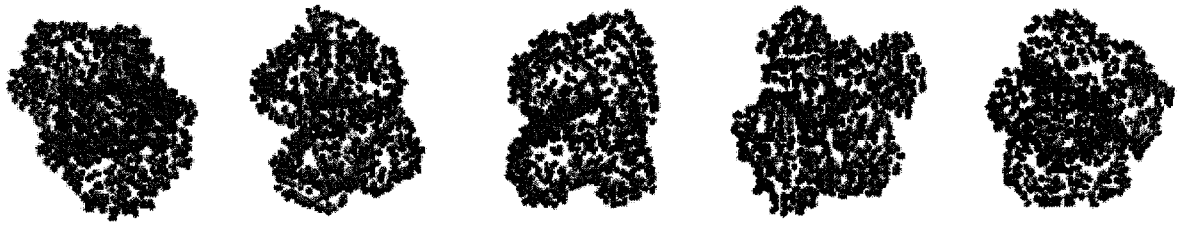


(e) Atom depth = 5.0 (f) Atom depth = 6.0 (g) Atom depth = 7.0 (h) Atom depth = 8.0



(i) Atom depth = 9.0 (j) Atom depth = 10.0 (k) Atom depth = 11.0 (l) Atom depth = 15.0

FIG 4



(a) view angle = 0 deg, atom depth =2.0 | (b) view angle = 45 deg, atom depth =2.0 | (c) view angle = 90 deg, atom depth =2.0 | (d) view angle = 135 deg, atom depth =2.0 | (e) view angle = 180 deg, atom depth =2.0

FIG 5

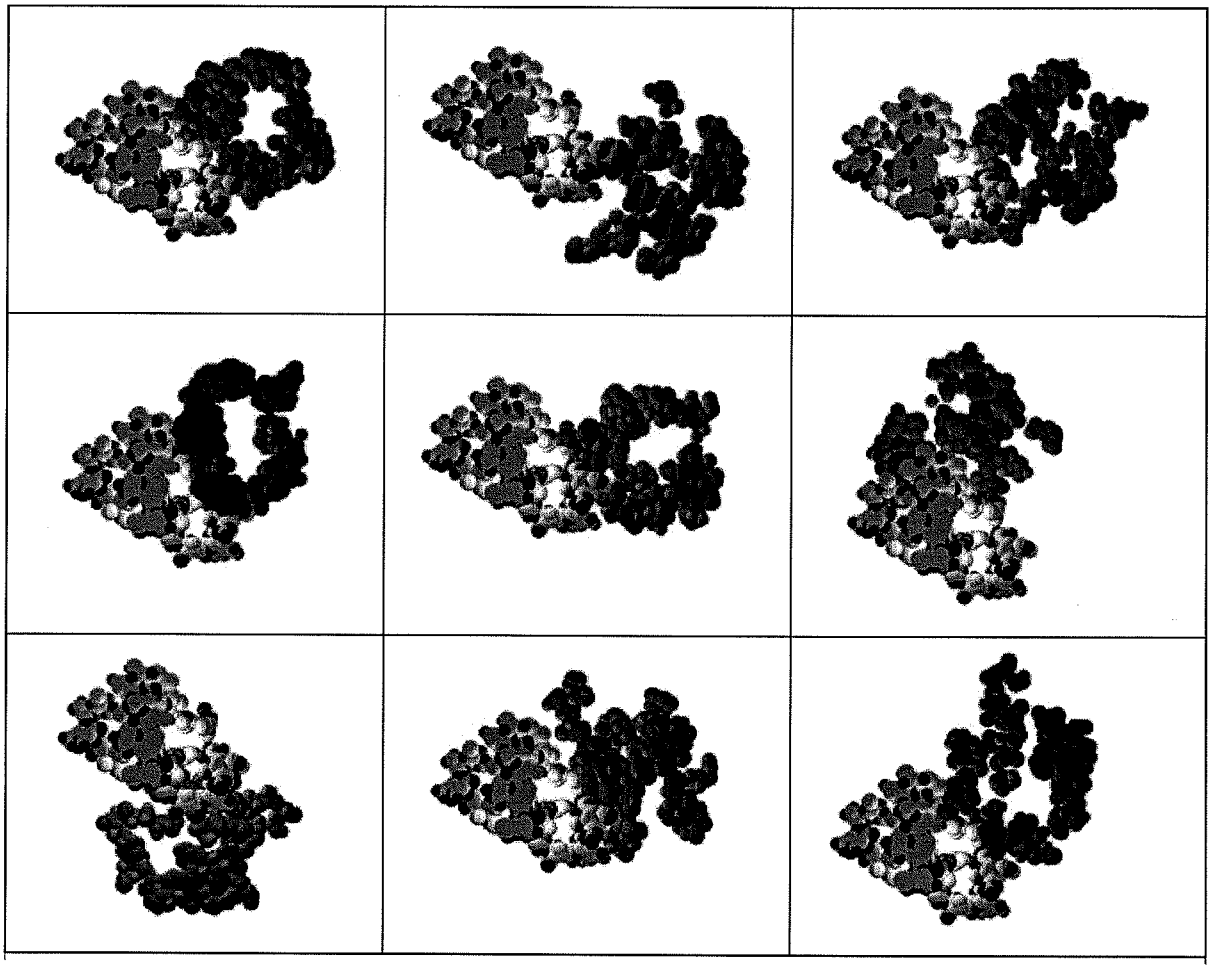


FIG 6