What is claimed is:

1. A crystalline recombinant interferon comprising the amino acid sequence of SEQ ID NO: 1.
2. The crystalline interferon of claim 1, wherein the space group of this crystal is $P3_121$.
3. The crystalline interferon of any one of claims 1-2, wherein the unit cell parameters of the crystal are a=b=77.92 Å, c=125.935 Å, $\alpha=\beta=90^{o}$, $\gamma=120^{o}$, with a variability of at most 5% in all cell parameters.
4. The crystalline interferon of any one of claims 1-3, wherein said crystal contains two molecules in an asymmetric unit.
5. The crystalline interferon of any one of claims 1-4, wherein the crystal further comprises covalently or non-covalently bound metal ions.
6. The crystalline interferon of any one of claims 1-5, wherein said recombinant interferon is encoded by the nucleotide sequence comprising SEQ ID NO: 2.
7. A composition comprising the crystalline interferon of any one of claims 1-6.
8. The composition of claim 7, wherein the composition is a pharmaceutical composition.
9. The composition of claim 8, further comprises a pharmaceutically acceptable carrier.
10. A computer-based method for identifying candidate compound that could interact with recombinant interferon, said method comprises the steps of:
    (a) providing a three-dimensional structure comprising atomic coordinate of recombinant interferon as shown in table 7, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms (Cα) of less than about 0.65 Å, or about 0.5 Å, or about 0.35 Å; and
    (b) selecting a candidate compound that comprises structural features capable of interacting with said three-dimensional structure or selected portion thereof, thereby identifying a candidate compound that could interact with said recombinant interferon.
11. The method of claim 10, wherein said structural features are selected from the group consisting of antigenic sites, hydrophilic properties, surface accessibility, and structural motifs.
12. The method of any one of claims 10-11, wherein the selection of candidate compound in step (b) comprises:
    (i) generating three-dimensional structures for a plurality of candidate compounds; and
    (ii) fitting each of the three-dimensional structures of step (i) against the

three-dimensional structure of step (a) or selected portion thereof to find the most energetically favorable interaction, thereby identifying a candidate compound that could interact with the recombinant interferon.

13. The method of any one of claims 10-12, further comprises the steps of:

(c) obtaining or synthesizing the candidate compound; and

(d) contacting the candidate compound with said recombinant interferon to determine the ability of the candidate compound to interact with said recombinant interferon.

14. The method of claim 13, wherein the step of determining the ability of the candidate compound to interact with said recombinant interferon further comprises measuring an activity of said recombinant interferon when contacted with the candidate compound.

15. The method of claim 14, wherein said activity is selected from the group consisting of antivirus activity, antitumor activity, anti-proliferation activity, natural killer cell activation, and immunomodulatory activity.

16. The method of any one of claims 10-15, wherein said candidate compound is a ligand bound to said recombinant interferon or selected portion thereof.

17. The method of claim 16, wherein said ligand is selected from the group consisting of receptor, modifier, agonist, antagonist, and said selected portion comprises one or more amino acid residues of amino acid residues 25-33 and/or 45-52 of said recombinant interferon.

18. The method of claim 17, wherein said selected portion comprises amino acid residues 25-33 and/or 44-52 of said recombinant interferon.

19. A computer-based method for designing a mimetic of a recombinant interferon, comprising the steps of:

(a) generating three-dimensional structures for a plurality of mimetics; and

(b) fitting each of the three-dimensional structures of step (a) against a three-dimensional structure comprising atomic coordinate of recombinant interferon as shown in table 7 or selected portion thereof to find the best fitting mimetic of said recombinant interferon, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms (Cα) of less than about 0.65 Å, or about 0.5 Å, or about 0.35 Å.

20. A computer-based method of rational drug design, comprising the steps of:

(a) providing a three-dimensional structure comprising atomic coordinate of recombinant interferon as shown in table 7, said atomic coordinates optionally have a variability of

root mean square deviation from the conserved backbone atoms (Cα) of less than about 0.65 Å, or about 0.5 Å, or about 0.35 Å;

(b) providing three-dimensional structures for a plurality of molecular fragments;

(c) fitting each of the three-dimensional structures of step (b) against the three-dimensional structure of step (a) or selected portion thereof; and

(d) assembling the selected molecular fragments into a molecule to form a candidate drug.

21. The method of claim 20, further comprises the following steps:

(e) obtaining or synthesizing the candidate drug; and

(f) contacting the candidate drug with said recombinant interferon to determine the ability of the candidate drug to interact with said recombinant interferon.

22. The method of any one of claims 10-21, wherein the selected portion of said three-dimensional structure comprises atomic coordinates of one or more amino acid residues of amino acid residues 25-33 and/or 45-52 of said recombinant interferon, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms (Cα) of less than about 0.65 Å, or about 0.5 Å, or about 0.35 Å.

23. The method of claim 22, wherein the selected portion of said three-dimensional structure comprises atomic coordinates of amino acid residues 25-33 and/or 45-52 in table 7, said atomic coordinates optionally have a variability of root mean square deviation from the conserved backbone atoms (Cα) of less than about 0.65 Å, or about 0.5 Å, or about 0.35 Å.

24. A mimetic of an interferon which comprises amino acid sequence as shown in SEQ ID NO: 4 and/or SEQ ID NO: 5.

25. The mimetic of claim 24, wherein after superimposition of the Cα-backbone of the three-dimensional structure of said interferon mimetic with the Cα-backbone of the three-dimensional structure of IFN-α2b protein using the least squares method, the location root-mean-square deviation of Cα in the 25-33 residues of said interferon mimetic and Cα in the corresponding residues of IFN-α2b protein is 3.63Å±5%.

26. The mimetic of claim 25, wherein in comparison with the corresponding residues of IFN-α2b, the deviations of α carbons of residues 25-33 of said mimetic are 3.291Å±5%, 4.779Å±5%, 5.090Å±5%, 3.588Å±5%, 2.567Å±5%, 2.437Å±5%, 3.526Å±5%, 4.820Å±5% and 2.756Å±5% respectively.

27. The mimetic of any one of claims 24-26, wherein after superimposition of the Cα-backbone of three-dimensional structure of said mimetic and the Cα-backbone of three-dimensional structure of IFN-α2b protein using the least squares method, the location root-mean-square deviation of Cα in the 44-52 residues of said mimetic and Cα in the corresponding residues of IFN-α2b protein is 2.90Å±5%.
28. The mimetic of claim 27, in comparison with the corresponding residues of IFN-α2b, the deviations of α carbons of residues 44-52 of said mimetic are 1.614Å±5%, 1.383Å±5%, 2.735Å±5%, 2.709Å±5%, 5.018Å±5%, 4.140Å±5%, 3.809Å±5%, 2.970Å±5%, and 0.881Å±5% respectively.
29. The mimetic of any one of claims 24-28, which is a functional mimetic or a structural mimetic.
30. The mimetic of any one of claims 24-29, wherein said interferon is recombinant interferon (rSIFN-co).
31. A composition comprising the mimetic of any one of claims 24-30.
32. The composition of claim 31, which is a pharmaceutical composition.
33. The composition of claim 32, further comprises a pharmaceutically acceptable carrier.
34. A method for the treatment of viral disease and/or tumor, said method comprises administering to the subject an effective amount of the crystal of any one of claims 1-6, mimetic of any one of claims 24-30 or composition of any one of claims 7-9 and 31-33.
35. Use of the crystal of any one of claims 1-6, mimetic of any one of claims 24-30 or composition of any one of claims 7-9 and 31-33 for preparation of medicament for treating viral diseases and/or tumors.
36. The method of claim 34 or use of claim 35, wherein said viral diseases include: hepatitis A, hepatitis B, hepatitis C, other types of hepatitis, viral infections caused by Epstein-Barr virus, human immunodeficiency virus (HIV), Ebola virus, severe acute respiratory syndrome (SARS) virus, influenza virus, cytomegalovirus, herpes simplex virus, or other types of herpes virus, papovavirus, pox virus, picornavirus, adenovirus, rhinovirus, human T-cell leukemia viruses type I, human T-cell leukemia viruses type II, or human T-cell leukemia virus type III.
37. The method of claim 34 or use of claim 35, wherein said tumor is cancerous.
38. The method of claim 34 or use of claim 35, wherein said tumor is solid tumor.
39. The method of claim 34 or use of claim 35, wherein said tumors include: skin cancer, basal cell carcinoma and malignant melanoma, renal cell carcinoma, liver cancer, thyroid

cancer, nasopharyngeal cancer, solid tumors, prostate cancer, stomach/abdominal cancer, esophageal cancer, rectal cancer, pancreatic cancer, breast cancer, ovarian cancer, superficial bladder cancer, hemangioma, epidermoid cancer, cervical cancer, non-small cell lung cancer, small cell lung cancer, glial stromal tumors, leukemia, acute leukemia, chronic leukemia, chronic myelogenous leukemia, hairy cell leukemia, lymphadenoma, multiple myeloma, polycythemia, Kaposi's sarcoma.

What is claimed is:

1. A crystalline recombinant interferon polypeptide consisting of the amino acid sequence of SEQ ID NO:1, wherein the space group of the crystal is $P3_121$, and the unit cell parameters of the crystal are a=b=77.92 Å, c=125.935 Å, $\alpha=\beta=90^\circ$, and $\gamma=120^\circ$.

2. The crystalline interferon of claim 1, wherein said crystal contains two molecules in an asymmetric unit.

3. The crystalline interferon of claim 1, wherein the crystal further comprises covalently or non-covalently bound metal ions.

4. A composition comprising the crystalline interferon of claim 1.

5. The composition of claim 4, wherein the composition is a pharmaceutical composition.

6. The composition of claim 5, further comprising a pharmaceutically acceptable carrier.