WHAT IS CLAIMED IS:

1. A method of preventing or reducing nuclear localisation of a SETDB1 polypeptide, the method comprising contacting the SETDB1 polypeptide and/or an IMPα polypeptide to an agent that inhibits binding of the SETDB1 polypeptide to the IMPα polypeptide.

2. Use of an agent in the manufacture of a medicament for the treatment or prevention of cancer in a subject, wherein the agent inhibits binding of a SETDB1 polypeptide to an IMPα polypeptide.

3. The method of claim 1 or the use of claim 2, wherein the agent inhibits the binding of the SETDB1 polypeptide to the IMPα polypeptide, but does not inhibit the binding of any other polypeptide to the IMPα polypeptide, optionally wherein the agent directly binds to the IMPα polypeptide.

4. The method or use of any one of claims 1 to 3, wherein the agent reduces the amount of SETDB1 polypeptide that is present in the cell nucleus, and optionally wherein the agent reduces the ratio of nuclear SETDB1 polypeptide to cytoplasmic SETDB1 polypeptide.

5. The method or use of any one of claims 1 to 4, wherein the agent is a proteinaceous molecule comprising, consisting, or consisting essentially of an amino acid sequence corresponding to the nuclear localisation sequence (NLS) of a SETDB1 polypeptide, and optionally wherein the proteinaceous molecule comprises, consists, or consists essentially of the amino acid sequence set forth in any of SEQ ID NOs: 1-6, or a at least 85% sequence identity to the sequence set forth in any one of SEQ ID NOs: 1-6.

6. The use according to any one of claims 2 to 5, wherein one or more further cancer therapies (e.g., a chemotherapeutic agent or immunotherapy) are to be administered to the subject.

7. The method or use according to any one of claims 1-6, wherein the proteinaceous molecule comprises, consists or consists essentially of an amino acid sequence corresponding to residues 206 to 232 of the full length human SETDB1 protein, optionally wherein the proteinaceous molecule is a fragment of a nuclear localisation sequence (NLS), and/or optionally wherein the proteinaceous molecule comprises 50 amino acid residues or less, and/or optionally wherein the proteinaceous molecule is distinguished from SETDB1 by the addition, deletion and/or substitution of at least one (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 etc.) amino acid corresponding to residues 206 to 232 of the full length human SETDB1 protein.

8. An isolated or purified proteinaceous molecule represented by Formula I:

$$Z_1GKKRX_1KX_2WHX_3GTLIX_4IQTVGPGKKX_5KVKZ_2$$

wherein:

Z_1 and Z_2 are independently absent or are independently selected from at least one of a proteinaceous moiety comprising from about 1 to about 50 amino acid residues (and all integer residues in between), and a protecting moiety;

X_1 is selected from Thr, Arg, and modified forms thereof;

X_2 is selected from Thr, Leu, and modified forms thereof;

X_3 is selected from Lys, Gly, and modified forms thereof;

X_4 is selected from Ala, Pro, and modified forms thereof; and

X_5 is selected from Tyr, Lys, and modified forms thereof.

9. The proteinaceous molecule according to claim 8, wherein Z_1 is absent.

10. The proteinaceous molecule according to claim 8 or 9, wherein Z_2 is absent.

11. The proteinaceous molecule of any one of claims 8 to 10, wherein X_1 is Thr, and/or X_2 is Thr, and/or X_3 is Lys, and/or X_4 is Ala, and/or X_5 is Tyr.

12. The proteinaceous molecule of any one of claims 8 to 10, wherein X_1 is Arg, and/or X_2 is Leu, and/or X_3 is Gly, and/or X_4 is Pro, and/or X_5 is Lys.

13. The proteinaceous molecule according to claim 12, wherein the proteinaceous molecule of Formula I comprises, consists, or consists essentially of, an amino acid sequence represented by any one of SEQ ID NO: 1 or 2:

SEQ ID NO: 1	GKKRTKTWHKGTLIAIQTVGPGKKYKVK
SEQ ID NO: 2	GKKRRKLWHGGTLIPIQTVGPGKKKKVK

14. The proteinaceous molecule according to any one of claims 16 to 21, wherein the proteinaceous molecule of Formula I further comprises at least one membrane permeating moiety (e.g., a lipid moiety and/or a myristoyl group).

15. A SETDB1 bicyclic peptide mimetic comprising a polypeptide that comprises at least three cysteine residues, separated by at least two loop sequences, and a molecular scaffold which forms covalent bonds with the cysteine residues of the polypeptide such that at least two polypeptide loops are formed on the molecular scaffold, wherein the SETDB1 bicyclic peptide mimetic comprises an amino acid sequence of Formula (II):

$$Z_1X_1C_1GKKRTKTWHC_2KGTLIAIQTVGX_2GC_3KKYKVKZ_2$$

Formula (II)

or a modified derivative, or pharmaceutically acceptable salt, thereof.

wherein:

C_1, C_2, and C_3 represent first, second and third cysteine residues, respectively;

Z_1 and Z_2 are independently absent or are independently selected from at least one of a proteinaceous moiety comprising from about 1 to about 50 amino acid residues (and all integer resides in between), and a protecting moiety;

X_1 is absent or alanine; and

X_2 is selected from any nonpolar/neutral amino acid residue (e.g., proline, leucine, alanine, glycine, isoleucine, methionine, phenylalanine, tryptophan, valine, and norleucine).

16. The SETDB1 bicyclic peptide mimetic of claim 15, comprising the amino acid sequence: CGKKRTKTWHCKGTLIAIQTVGPGCKKYKV [SEQ ID NO: 8].

17. The SETDB1 bicyclic peptide mimetic of claim 15 or claim 16, wherein the molecular scaffold is 1,3,5-(tribroMoMethyl)benzene) or TBAB.

18. The SETDB1 bicyclic peptide mimetic of any one of claims 15 to 17, wherein the modified derivative comprises one or more D-amino acid, optionally wherein substantially all of the amino acids except glycine are D-amino acids.

19. The SETDB1 bicyclic peptide mimetic of any one of claims 15 to 18, wherein all of the amino acids are in retro-inverso form.

20. The SETDB1 bicyclic peptide mimetic of claim 19, the amino acid sequence set forth in SEQ ID NO: 11 (vkykkcGpgvtqisiltGkchwtktrkkcG).