What is claimed is:

1. A polypeptide complex comprising, from N-terminus to C-terminus, a Fab domain operably linked to a hinge region, wherein the Fab domain and the hinge region or part thereof, are derived from different IgG isotypes; wherein said hinge region or part thereof is of human IgG1 isotype or human IgG4 type.
2. The polypeptide complex of claim 1, wherein the hinge region comprises a sequence having the following formula (I):

   X_1 X_2 X_3 X_4 X_5 X_6 X_7 X_8 X_9 X_{10} CPPCP (I)

   wherein, X_1=null or E; X_2=null or P; X_3= null or K; X_4= null or S or E; X_5= null or C or S, preferably null; X_6= D or K; X_7= K or Y; X_8= T or G; and/or X_9X_{10}=HT, HP, PT or PP, preferably PT or PP.

3. The polypeptide complex of claim 1, wherein the hinge region comprises a sequence having the following formula (II):

   EPKx_1C x_2 x_3 x_4 x_5 x_6 x_7 x_8 CPPCP (II)

   wherein, x_1 = null or S; x_2 = null or E or S, preferably null; x_3 = null or S or C; x_4 = null or K or D; x_5 = Y or K; x_6 = G or T; and/or x_7x_8 = PP, PT, HP or HT.

4. The polypeptide complex of claim 1, wherein the hinge region or part thereof comprises (a) the sequence as set forth in DKTHTCPPCP (SEQ ID NO: 1), or

   (b) a sequence having at least 85% of identity to (a), or

   (c) a variant of (a) or (b), wherein the variant has a mutation or mutations being selected from the group consisting of insertion, deletion and substitution, or the variant comprises a non-naturally occurring amino acid residue or non-naturally occurring amino acid residues.
5. The polypeptide complex of claim 4, wherein the hinge region or part thereof comprises (a) the sequence as set forth in EPKSDKTHTCPPCP (SEQ ID NO: 2) or EPKDKTHTCPPCP (SEQ ID NO: 3), or

   (b) a sequence having at least 85% of identity to (a), or

   (c) a variant of (a) or (b), wherein the variant has a mutation or mutations being selected from the group consisting of insertion, deletion and substitution, or the variant comprises a non-naturally occurring amino acid residue or non-naturally occurring amino acid residues.
6. The polypeptide complex of claim 1, wherein the hinge region or part thereof comprises (a) the sequence as set forth in any one of SEQ ID NOs: 12 to 14;

(b) a sequence having at least 85% of identity to (a), or

(c) a variant of (a) or (b), wherein the variant has a mutation or mutations being selected from the group consisting of insertion, deletion and substitution, or the variant comprises a non-naturally occurring amino acid residue or non-naturally occurring amino acid residues.

7. The polypeptide complex of claim 1, wherein the hinge region, or part thereof, comprises (a) the sequence as set forth in EPKSCESKYGPPCPPCP (SEQ ID NO: 4), or

(b) a sequence having at least 85% of identity to (a), or

(c) a variant of (a) or (b), wherein the variant has a mutation or mutations being selected from the group consisting of insertion, deletion and substitution, or the variant comprises a non-naturally occurring amino acid residue or non-naturally occurring amino acid residues.

8. The polypeptide complex of claim 7, wherein the hinge region, or part thereof, comprises (a) the sequence as set forth in EPKSCSKYGPPCPPCP (SEQ ID No. 5), or EPKSCKYGPPCPPCP (SEQ ID No. 6), or EPKSCYGPPCPPCP (SEQ ID No. 7), or EPKSCSKYGHTCPPCP (SEQ ID No. 8), or EPKSCSKYGHPCPPCP (SEQ ID No. 9), or EPKSCSKYGPTCPPCP (SEQ ID No. 10), or

(b) a sequence having at least 85% of identity to (a), or

(c) a variant of (a) or (b), wherein the variant has a mutation or mutations being selected from the group consisting of insertion, deletion and substitution, or the variant comprises a non-naturally occurring amino acid residue or non-naturally occurring amino acid residues.

9. The polypeptide complex of claim 3, wherein the hinge region or part thereof comprises (a) the sequence as set forth in SEQ ID NO: 11, or

(b) a sequence having at least 85% of identity to (a), or

(c) a variant of (a) or (b), wherein the variant has a mutation or mutations being selected from the group consisting of insertion, deletion and substitution, or the variant comprises a non-naturally occurring amino acid residue or non-naturally occurring amino acid residues.

10. The polypeptide complex of claim 1, wherein the hinge region or part thereof comprises (a) the sequence as set forth in any one of SEQ ID NOs: 15-17, or

(b) a sequence having at least 85% of identity to (a), or

(c) a variant of (a) or (b), wherein the variant has a mutation or mutations being selected from the group consisting of insertion, deletion and substitution, or the variant comprises a non-naturally occurring amino acid residue or non-naturally

occurring amino acid residues.

11. The polypeptide complex of claim 1, wherein the polypeptide complex further comprises a Fc polypeptide which is operably linked to the hinge region, or wherein the polypeptide complex further comprises an additional polypeptide which is operably linked to the hinge region.
12. The polypeptide complex of claim 11, wherein the Fc polypeptide is a human IgG1, IgG2, IgG3 or IgG4 Fc polypeptide, preferably wherein the Fc polypeptide is a human IgG1 or IgG4 Fc polypeptide.
13. The polypeptide complex of claim 1, comprising
    (i) a light chain comprising the sequence of SEQ ID NO: 20 and a heavy chain comprising he sequence of SEQ ID NO: 21;
    (ii) a light chain comprising the sequence of SEQ ID NO: 22 and a heavy chain comprising he sequence of SEQ ID NO: 23;
    (iii) a light chain comprising the sequence of SEQ ID NO: 24 and a heavy chain comprising he sequence of SEQ ID NO: 25;
    (iv) a light chain comprising the sequence of SEQ ID NO: 26 and a heavy chain comprising he sequence of SEQ ID NO: 27;
    (v) a light chain comprising the sequence of SEQ ID NO: 28 and a heavy chain comprising he sequence of SEQ ID NO: 29; or
    (vi) a light chain comprising the sequence of SEQ ID NO: 30 and a heavy chain comprising he sequence of SEQ ID NO: 31.
14. An antibody drug conjugate comprising a polypeptide complex according to any one of claims 1-13.
15. A pharmaceutical composition comprising an antibody drug conjugate according to claim 14 and a pharmaceutically acceptable carrier or excipient.
16. A method of preparing the antibody drug conjugate of claim 14, comprising:
    providing the polypeptide complex of any one of claims 1-13;
    reacting a maleimido or haloacetyl moiety with free thiol group in cysteine residue generated by reduction of interchain disulfide bonds via Michael addition reaction.
17. The method of claim 16, wherein the free thiol group is generated by partial reduction of interchain disulfide bonds with mild reducing reagent such as TCEP or DTT, preferably the partial reduction is carried out in a buffer with pH range from 4.0 to 8.0, with reducing agent /mAb ratio from 3 to 10, reaction temperature from 4 ^{o}C to 37 ^{o}C, and reduction time from 1hr to 24hr.
18. The method of claim 17, wherein the partial reduction is carried out with TCEP /mAb ratio from 3 to 10.

19. The method of claim 17, wherein the conjugation is carried out in a buffer with pH range from 4.0 to 8.0, organic additive from 0.0% to 20.0% by weight, drug/mAb ratio from 7 to 20, reaction temperature from 4 ^{o}C to 37 ^{o}C, and conjugation time from 1hr to 4hr.
20. Use of the polypeptide complex of any of claims 1-13 for manufacturing an antibody drug conjugate.