

The effect of Fc region affinity of protein-based antibody-recruiting molecules on antibody-dependent cellular cytotoxicity

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Supporting Information

A-Z (381 bp, 127 aa)

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10      20      30      40      50      60      70      80      90     100
1 ATGTTGATAATAAATTCACAAAGAGATGCGCAACGCGTATTGGGAGATTGCTTTGCTTCCAAACCTTAACAACCAGCAGAAACGGGCCTTTATCCGTT 100
  M V D N K F N K E M R N A Y W E I A L L P N L N N Q Q K R A F I R S
      110     120     130     140     150     160     170     180     190     200
101 CCCTGTACGATGACCCCTCACAGAGCGCCAACCTTATTGGCAGAGGCGAAGAACTGAACGACGCTCAAGCACCTAAATCGTCTTCTCCGGAATCGATAA 200
  L Y D D P S Q S A N L L A E A K K L N D A Q A P K S S S S G V D N
      210     220     230     240     250     260     270     280     290     300
201 TAAGTTTAAACAAGGAACAACAAAACGCCTTCTATGAGATCCTTCACCTGCCGAACCTTAATGAAGAACAACGGAACGCTTTCATACAATCTCTGAAGGAC 300
  K F N K E Q Q N A F Y E I L H L P N L N E E Q R N A F I Q S L K D
      310     320     330     340     350     360     370     380
301 GACCCATCGCAGAGTGCAAACCTTACTTGGGAGGCTAAAAAATTAATGATGCTCAAGCTCCGAAGCATCATCATCACCATCAC 384
  D P S Q S A N L L A E A K K L N D A Q A P K H H H H H H H
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A-ZZ (585 bp, 195 aa)

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10      20      30      40      50      60      70      80      90     100
1 ATGTTGATAATAAATTCACAAAGAGATGCGCAACGCGTATTGGGAGATTGCTTTGCTTCCAAACCTTAACAACCAGCAGAAACGGGCCTTTATCCGTT 100
  M V D N K F N K E M R N A Y W E I A L L P N L N N Q Q K R A F I R S
      110     120     130     140     150     160     170     180     190     200
101 CCCTGTACGATGACCCCTCACAGAGCGCCAACCTTATTGGCAGAGGCGAAGAACTGAACGACGCTCAAGCACCTAAATCGTCTTCTCCGGAAGTAGCAG 200
  L Y D D P S Q S A N L L A E A K K L N D A Q A P K S S S S G S S S
      210     220     230     240     250     260     270     280     290     300
201 TTCGGGGTCTCCTCAAGCGGCATCGATAATAAGTTTAAACAAGGAACAACAAAACGCCTTCTATGAGATCCTTCACCTGCCGAACCTTAATGAAGAACA 300
  S G S S S G V D N K F N K E Q Q N A F Y E I L H L P N L N E E Q
      310     320     330     340     350     360     370     380     390     400
301 CGGAACGCTTTCATACAATCTCTGAAGGACGACCCATCGCAGAGTGCAAACCTTACTTGGGAGGCTAAAAAATTAATGATGCTCAAGCTCCGAAGGTCCG 400
  R N A F I Q S L K D D P S Q S A N L L A E A K K L N D A Q A P K V D
      410     420     430     440     450     460     470     480     490     500
401 ATAATAAGTTTAAACAAGGAACAACAAAACGCCTTCTATGAGATCCTTCACCTGCCGAACCTTAATGAAGAACAACGGAACGCTTTCATACAATCTCTGAA 500
  N K F N K E Q Q N A F Y E I L H L P N L N E E Q R N A F I Q S L K
      510     520     530     540     550     560     570     580
501 GGACGACCCATCGCAGAGTGCAAACCTTACTTGGGAGGCTAAAAAATTAATGATGCTCAAGCTCCGAAGCATCATCATCACCATCAC 588
  D D P S Q S A N L L A E A K K L N D A Q A P K H H H H H H H
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Fig. S1 Codon sequences and amino acid sequences of Fc-ARMs.

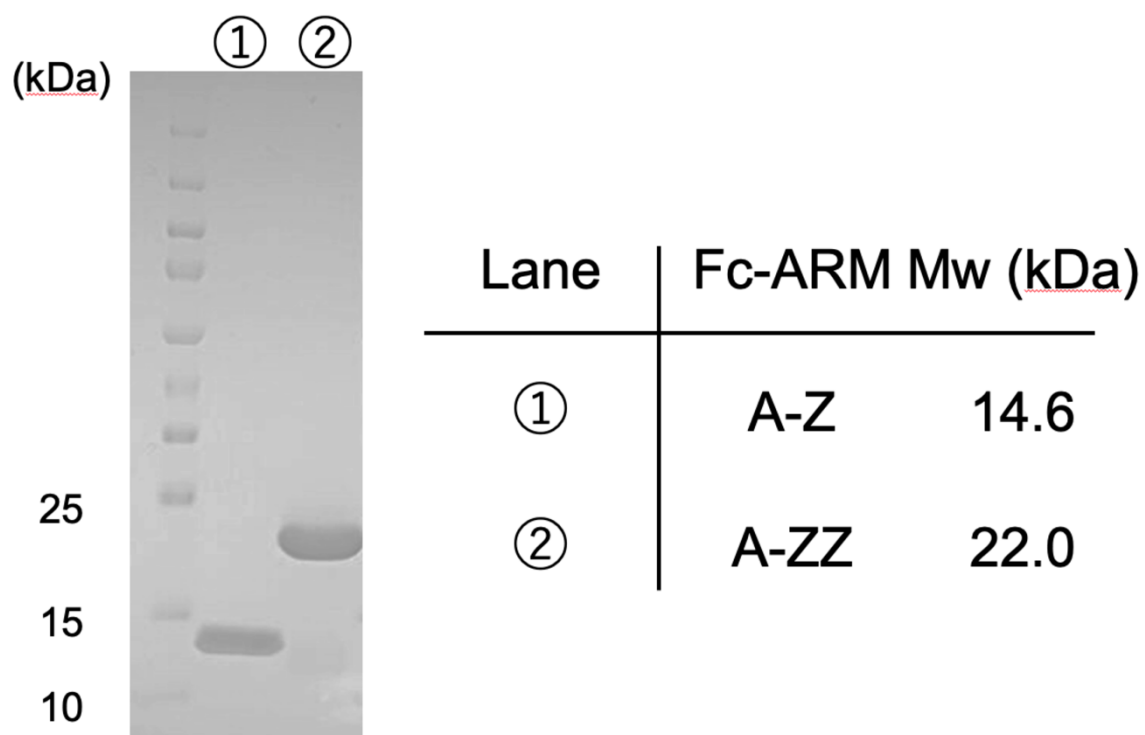


Fig. S2 SDS-PAGE of each Fc-ARM after purification and their calculated molecular weights: 1: A-Z, and 2:A-ZZ.

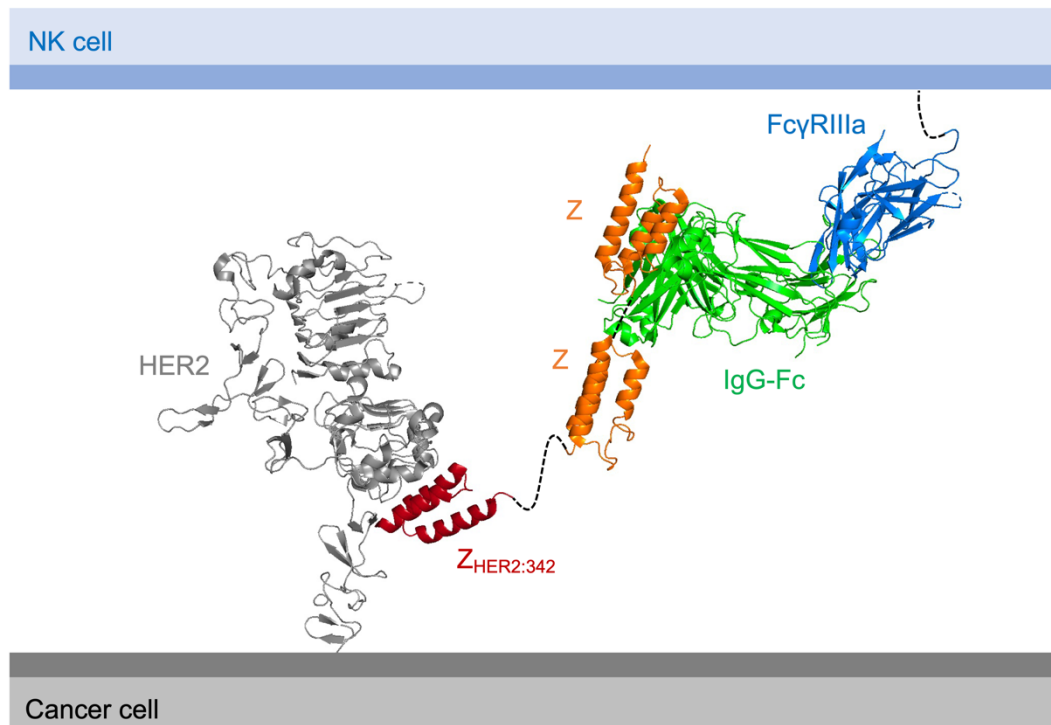


Fig. S3 A complex model of HER2/Fc-ARM/IgG/FcγRIIIa generated based on the crystal structures of HER2/Z_{HER2 342} (PDB ID: 3MZW), Z/Fc (PDB ID: 1FCC), and Fc/FcγRIIIa (PDB ID: 5VU0).

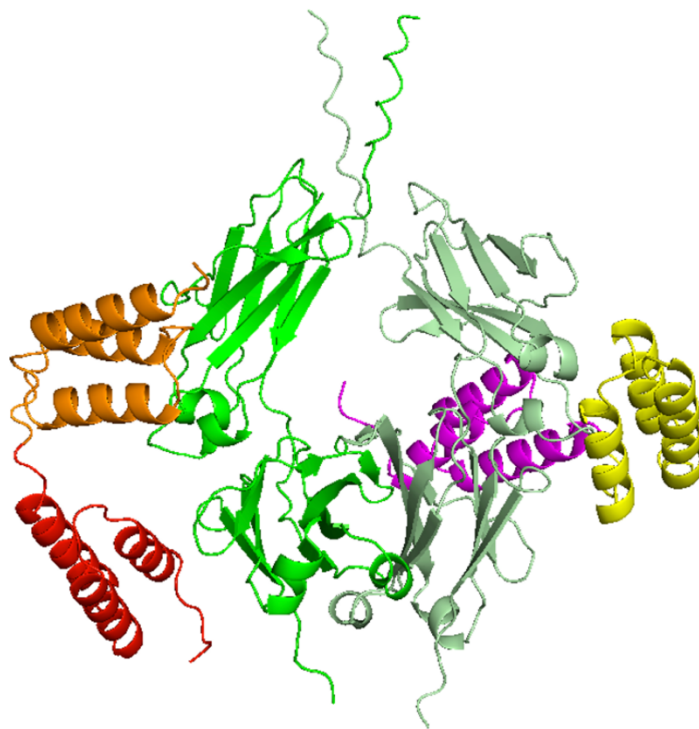


Fig. S4 The complex between ZZ (red and orange, or magenta and yellow) and IgG Fc (light green and pale green) predicted by Alphafold2 and generated by PyMOL.