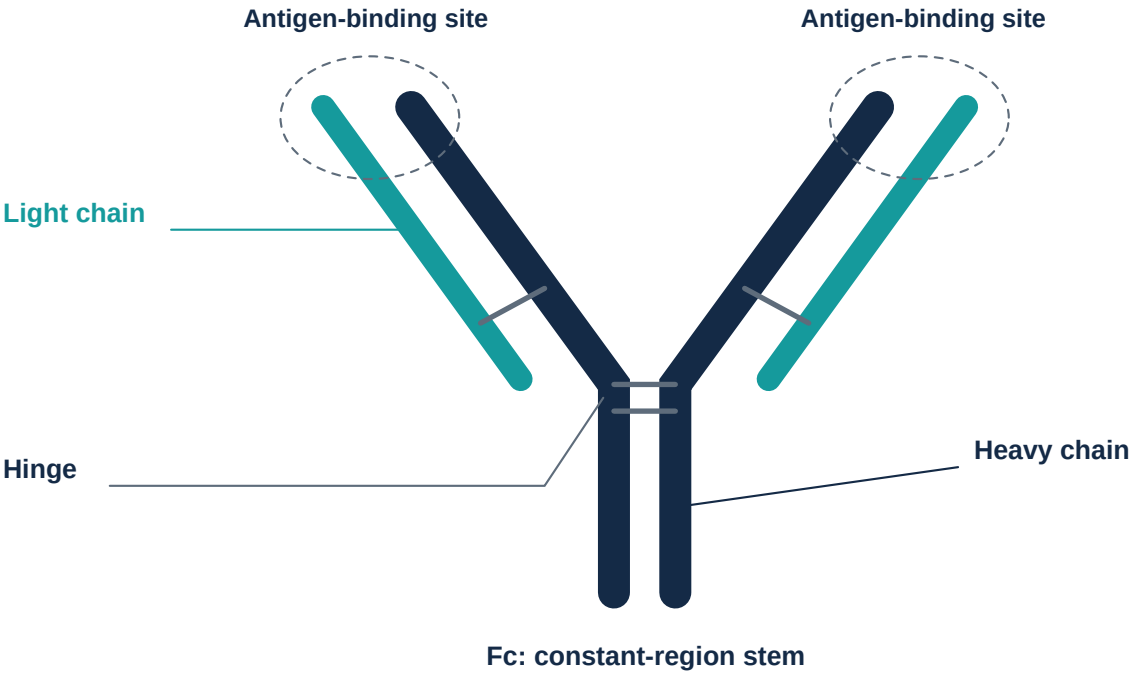
# Four chains, two binding sites

Antibodies (immunoglobulins) are globular glycoproteins secreted by plasma cells. Their molecular structure links specific antigen recognition to protective actions.

## 1. A SIMPLIFIED IgG ANTIBODY




Ovals: variable regions. Thin cross-links: disulfide bonds. Schematic; not to scale.

## 2. CHAIN ORGANISATION

One IgG molecule contains two identical heavy chains and two identical light chains. Disulfide bonds link the chains. Each binding site is formed by the variable regions of one heavy chain and one light chain.

## 3. NOT EVERY REGION IS VARIABLE

Both chain types contain variable and constant regions. The constant parts form much of the arms and the stem; constant region does not mean only the bottom of the Y.

IgG structure, chains and hinge: Immunobiology, NCBI Bookshelf.
Variable and constant regions: Molecular Biology of the Cell, NCBI Bookshelf.

Scope: Cambridge Biology 9700 syllabus, section 11.2, outcome 1, p. 31.

# How structure enables function

Follow the link from molecular feature to biological effect. The binding tips recognise the target; other regions help determine what happens after binding.

### 1. VARIABLE REGIONS: SPECIFICITY

Different amino acid sequences produce different three-dimensional binding surfaces. A complementary antigenic region (epitope) fits and binds through non-covalent interactions. The two sites on one typical IgG molecule recognise the same epitope.

### 2. TWO SITES: CROSS-LINKING

An antibody can bind matching epitopes on two separate particles. Many antibodies can build a network of linked particles. This helps explain agglutination: the formation of visible or microscopic clumps.

### 3. HINGE: FLEXIBILITY

Movement at the hinge lets the arms adopt different angles. The binding sites can therefore reach matching epitopes at different separations. Flexibility helps binding without changing the antibody's antigen specificity.

### 4. CONSTANT REGION: EFFECTOR INTERACTIONS

The exposed Fc region of bound antibody can interact with receptors on phagocytes. Suitable antibody classes can also recruit complement proteins. These interactions connect antigen recognition with removal or destruction.

Structure-function chain: amino acid sequence -> binding-site shape -> antigen recognition -> an appropriate protective mechanism.

Molecular specificity and antibody regions: Molecular Biology of the Cell.
Antibody-mediated protection: OpenStax, Microbiology 18.1.

Scope: Cambridge Biology 9700 syllabus, section 11.2, outcome 1, p. 31.

# What bound antibodies can do

Antibodies are not cells and do not engulf pathogens. Binding can block a harmful interaction or make a target easier for other immune mechanisms to remove.

### 1. NEUTRALISATION: BLOCK THE INTERACTION

Antibodies can bind a toxin or a viral surface molecule and obstruct attachment to a host-cell receptor. This prevents a harmful action or entry into cells; it does not mean an antibody digests the toxin or virus.

### 2. AGGLUTINATION: LINK PARTICLES

Antibodies cross-link cells or particles carrying matching epitopes into clumps. This can help trap targets and support their clearance. Clumping requires multiple binding interactions, not an antibody turning into a phagocyte.

### 3. OPSONISATION: MAKE ENGULFMENT EASIER

Antibody binding coats a pathogen. Receptors on phagocytes recognise exposed Fc regions, improving attachment and engulfment. Antigen-binding sites face the target; the phagocyte interacts with the antibody's constant region.

### 4. COMPLEMENT: RECRUIT PROTEIN DEFENCES

Some antigen-bound antibodies activate the complement cascade. Complement can enhance opsonisation and, on susceptible targets, help form membrane pores that cause lysis. The pores are formed by complement proteins, not antibodies themselves.

Keep the roles distinct: plasma cell makes antibody; antibody binds antigen; phagocyte engulfs; complement can help damage a target membrane.

Neutralisation, agglutination and opsonisation: OpenStax, Biology 2e, 42.3.
Antibody functions and complement: OpenStax, Microbiology 18.1.

Scope: Cambridge Biology 9700 syllabus, section 11.2, outcome 1, p. 31.