Science Journal Abstract rules:

Abstracts explain to the general reader why the research was done and why the results are important.

They should start with some brief BACKGROUND information: a sentence giving a broad introduction to the field comprehensible to the general reader, and then a sentence of more detailed background specific to your study.

This should be followed by the RESULTS, or if the paper is more methods/technique oriented an explanation of OBJECTIVES/METHODS and then the RESULTS.

The final sentence should outline the main CONCLUSIONS of the study, in terms that will be comprehensible to all our readers. The abstract should be 125 words or less. For Perspectives and Policy Forums, please include a one-sentence abstract.
In the paper *An Immunoglobulin Heavy Chain Variable Region Gene is Generated from Three Segments of DNA: \( V_H, D \) and \( J_H \) (1980)*, Hood and colleagues determined that there is a third germline gene segment, D, that joins between the \( V_H \) and \( J_H \) gene segments.

The authors isolated two germline clones, \( V_H \) and \( J_H \), from mouse sperm DNA and one clone, which contained the rearranged \( V_HC_\alpha \) gene from M603 myeloma DNA and determined the sequence for all three.

Their sequencing analysis revealed that there are blocks of conserved nucleotides 3′ to the V gene segment and 5′ to the J gene segment that are separated by a spacer containing either 11 or 22 non-conserved nucleotides and that germline D segments are located between the \( V_H \) and \( J_H \) segments so that they can be joined together to form the rearranged \( V_H \) gene.
Identification and nucleotide sequence of a diversity DNA segment (D) of immunoglobulin heavy-chain genes

Hitoshi Sakano, Yoshikazu Kurosawa, Martin Weigert & Susumu Tonegawa
Basel Institute for Immunology, 487 Grenzacherstrasse, Postfach, 4005 Basel 5, Switzerland
**Fig. 1** Southern blot analysis of mouse embryo and myeloma DNAs. Mouse DNAs were digested with *EcoRI*, separated in 0.8% agarose gels and blotted to nitrocellulose filters according to the method of Southern\(^\text{30}\). Filters were then incubated with the nick-translated \(J_H\) probe (1.1-kilobase *SacI*- *EcoRI* fragment, see ref. 11), essentially as described by Wahl et al.\(^\text{39}\). *HindIII* fragments of phage \(\lambda\) DNA were used as size markers (in kilobases, kb). For the cloning of a 5.2-kilobase Q52 fragment hybridizable with the \(J_H\) probe, *EcoRI* digest of the myeloma DNA was fractionated in a 0.8% agarose gel and DNA from the \(J_H\) probe-positive fraction was eluted as described previously\(^\text{40}\). Recombinant phages containing the mouse DNA were screened by *in situ* plaque hybridization\(^\text{41}\) with the \(J_H\) probe.
Fig. 2  A, Electron micrograph (a) and schematic interpretation (b) of a heteroduplex molecule formed between two EcoRI inserts, one from clone ME184-8 (embryonic J) and the other from clone Q52J (rearranged J from myeloma QUPCS2). Procedures used for the heteroduplex formation have been described previously. Clone ME184-8 was prepared by Richard Maki and contains, in a phage λ vector, the 6.4-kilobase EcoRI embryo DNA fragment carrying the four J₄ DNA segments whose sequences were determined previously using another DNA clone referred to as MEP203 (ref. 11). Numbers indicate lengths of various parts of the heteroduplex in kilobases. B, Restriction enzyme cleavage maps of the J-containing EcoRI fragments. a, 5.2-kilobase insert from the myeloma clone Q52J; b, 6.4-kilobase insert from the embryonic clone ME184-8. The broken line (Δ) in Ba represents a deletion in the myeloma clone; the bars in Bb indicate coding regions. The positions of four J₄ segments have been determined by R-loop mapping and DNA sequencing. The D segment is identified in the present study by DNA sequencing of the 5′ flanking region of J₄. Strategy of the sequencing is shown in Bc. Kbp, Kilobase pairs; bp, base pairs. The previously published BamHI sites have been corrected.
Fig. 3  Nucleotide sequence of the D–J structure in a myeloma clone, Q52J (b), and its germ-line sequences, J_{H2} (c) and D_{O52} (a). For the sequencing of b, a 110-base pair *Hind*I-*Hind* fragment containing a deletion was purified from a 600-base pair *Bgl*I–*Bam*II fragment (see Fig. 1Ba), both ends labelled with [α-^32^P]-nucleoside triphosphates, and the strand separated and sequenced in both directions according to the procedures described previously^32. The embryonic J_{H2} sequence (c) was taken from ref. 13. The embryonic D_{O52} region (a) was sequenced according to the strategy shown in Fig. 2Bc. Two blocks of conserved sequences,

\[
\text{GGTTTTTGT} \quad \text{and} \quad \text{CACCTGTG} \\
\text{CCAAAAACA} \quad \text{and} \quad \text{GTTGACAC}
\]

or their related sequences are boxed. Numbers indicate lengths of spacers separating the two conserved sequences in base pairs. Sequences in a and c contributing the coding region in b are underlined. The corresponding sequences in b are also underlined. Note that tetranucleotide AAGG in b between the two boundaries of D_{O52} and J_{H2} is not accounted for by either germ-line sequence. Vertical lines indicate possible recombination sites with D_{O52} and J_{H2}. Encoded amino acid sequences are in italics.
Fig. 4  Nucleotide sequence of the 5'-flanking region of J_{HI} DNA. Strategy for the sequencing is shown in Fig. 2C. The J_{HI} sequence and some of the 5'-flanking sequence have been published elsewhere\textsuperscript{12,13,43}. The D_{OS2} and J_{HI} segments are underlined. Two blocks of conserved sequences,

\[
\begin{align*}
\text{GGTTTTTGT} & \quad \text{and} \quad \text{CACTGTG} \\
\text{CCAAAAACA} & \quad \text{GTGACAC}
\end{align*}
\]

or their related sequences are boxed. Numbers indicate the lengths of the spacer separating the two conserved sequences in nucleotide bases.
CACAGTG  and  CACCGTG
GTGTCAC  and  GTGGCAC

and further flanked by A + T-rich nonamers,

GGTTTTTGAC  and  ACAAAAAACC
CCAAAAACTG  and  TGTTTTTGG
Synthesis of Multiple Immunoglobulin Classes by Single Lymphocytes

B. Pernis, L. Forni and A. L. Luzzati
Basel Institute for Immunology, CH-4058 Basel, Switzerland