final test trial was 3.95 for condition A and 2.20 for condition B. The difference is significant statistically, t being 2.8.

These results suggest that the very general conclusions formulated by Rock (*1*) are unwarranted. The logical design of the present experiments differs from Rock's only in that items are discarded as soon as they are responded to correctly. Under this condition the probability of responding correctly to a previously missed item is clearly greater than the probability of getting an entirely new item correct. It appears, from these data and from Dotson's (*5*), that the difficulty of a previously missed item is greater in the presence of previously correct items than in the presence of unpracticed items or no other items. Therefore, until the necessary experiments have been done to control differential interactions among items, conclusions about the central theoretical problem of the role of repetition in the formation of associative bonds cannot be made with confidence (*6*).

ALFRED B. KRISTOFFERSON
Department of Psychology, University of Cincinnati, Cincinnati, Ohio

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2. ———, *Sci. American* **199**, 2 (Aug. 1958).
3. ———, and W. Heimer, *Am. J. Psychol.* **72**, 1 (1959); L. L. Clark, T. G. Lansford, K. M. Dallenbach, *ibid.* **73**, 1 (1960). I have repeated the basic experiment also and obtained results similar to those reported in these references.
4. W. K. Estes, *Psychol. Rev.* **67**, 4 (1960).
5. J. M. Dotson, unpublished M.A. thesis, University of Cincinnati (1961).
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Recommendations for the Nomenclature of Hemoglobins

There is now general agreement on the naming of the peptide chains of the major components of normal adult and fetal hemoglobins as the α, β, and γ chains; for example, adult hemoglobin is written as $\alpha_2^A\beta_2^A$ and fetal hemoglobin as $\alpha_2^A\gamma_2^F$. The superscripts A and F refer to the fact that the particular chain is the one found in the human adult and fetal hemoglobins. It is recommended that this practice be continued and that the symbols α, β, and γ, without superscripts, be reserved for those occasions when reference is being made to, for example, α chains in general.

Information concerning the structure of the chains of hemoglobin A_2 is now sufficient to indicate that one of the chains is identical with the α^A chain, whereas the second differs in a number of residues from the three foregoing chains. In addition, there is evidence (see, for example, *1*) to indicate that the genetic control of this unique chain is independent of the genes of the α, β, and γ chains. It is therefore recommended that this chain be designated as δ^{A_2}; Hb A_2 is then written as $\alpha_2^A\delta_2^{A_2}$. Again, one could refer simply to δ chains in the general case.

The simplest method of naming the tryptic peptides of a chain is to number them in the order in which they occur in the chain, beginning with the NH_2-terminus. The symbol for the chain is included as a part of the designation. The letters Tp are included to identify that these are the peptides obtainable by tryptic digestion. For example, the third tryptic peptide of the α chain would be αTpIII in this system. Where a lysyl bond is not attacked under the conditions used, the symbol for the resultant "dipeptide" or "double peptide" would contain the numbers appropriate to both tryptic peptides, for example αTpI,II. From the published structure of the α and β chains (*2*) and from the amino acid composition, it is evident that the α chain will contain the tryptic peptides αTpI to αTpXIV and the β chain the tryptic peptides βTpI and βTpXV. It so happens that the tryptic "peptides" αTpVIII and βTpVIII are lysine. In addition, the present methods of tryptic cleavage do not break the bond separating the expected tryptic peptides αTpXII and αTpXIII, nor the bond between the expected peptides βTpX and βTpXI. In view of the possibility that these bonds might be split in some experiments at a later date, it is felt that the numbering system should correspond with the theoretical number of tryptic peptides.

When the complete sequence of the chains is determined beyond question and is published, then a more specific designation involving residue numbers should be adopted. Thus, βTpI can be designated as βTp1–8.

An ideal nomenclature system for the abnormal hemoglobins would provide for adequate designation of the chemical structure at each stage of the investigation. The following system is an attempt to meet this requirement.

When only the chain in which the abnormality resides is known, then the hemoglobin may be written as $\alpha_2^A\beta_2^S$, or $\alpha_2^A\beta_2^{D_{Punjab}}$. When the abnormality has been located in a particular tryptic peptide, as by fingerprinting, then the designation should be, for example, $\alpha_2^A\beta_2^{TpI}$. When the amino acid composition of the tryptic peptide indicates a particular amino acid substitution, then this will be indicated as $\alpha_2^A\beta_2^{TpI(Glu\rightarrow Val)}$ for Hb S. Finally, when the amino acid interchange has been located at a particular residue position in the chain, the fully descriptive formula, as in the case of Hb S, would be in the form: $\alpha_2^A\beta_2^{6Val}$.

Presumably, for use in formulas describing experiments such as reassociation, it will be necessary to define in a given paper a one-letter designation for a particular hemoglobin. For example, the formula $\alpha_2^I\beta_2^S$ could be used, provided that wherever possible the individual hemoglobins have been defined, as, for example, Hb I as $\alpha_2^{16Asp}\beta_2^A$ and Hb S as $\alpha_2^A\beta_2^{6Val}$.

It is strongly urged that no further letters be assigned to abnormal hemoglobins. Newly discovered hemoglobins, prior to their chemical identification, should be known by the letter designation of the previously described hemoglobin whose electrophoretic mobility they most nearly resemble. To the letter should be attached a subscript indicating the geographic origin of the new hemoglobin.

Proposals similar to the above originated during the Hemoglobin Structure Workshop held in Boston, 14–16 December 1960. These proposals have been modified at the suggestion of other workers in the protein structure field. In their present form they represent a compromise between the views of these two groups (*3*).

P. S. GERALD
Children's Hospital Medical Center, and Harvard Medical School, Boston, Massachusetts

V. M. INGRAM
Division of Biochemistry, Department of Biology, Massachusetts Institute of Technology, Cambridge

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