order or at different rates. However, the induced exchange was reproducible when conditions were held constant so we were able to correct for it using the equation

$$\% \text{ exchange} = \frac{\% \text{ exchange (measured)} - \% \text{ exchange (induced)}}{100 - \% \text{ exchange (induced)}} (100)$$

The corrected values (always three or more excluding the value at zero time) obeyed the exponential exchange law.[3,4] The half-times for the exchange rates are summarized in Table I. As expected the exchange rate is not dependent on the method of separation when proper account is taken of the induced exchange.

TABLE I

Tl(I)-Tl(III) EXCHANGE RATES
0.0244 f. Tl(I), 0.0244 f. Tl(III)

Acid	Temperature	Method of separation	Exchange, half-time hr.
1.0 f. HNO_3	*ca.* 25°C.	Bromide	2.5 ± 0.2
1.5 f. HNO_3	24.8 ± 0.2°	Bromide	1.8 ± 0.
1.5 f. HNO_3	24.8 ± 0.2°	Hydroxide	1.6 ± 0.2
1.5 f. $HClO_4$	24.8 ± 0.2°	Hydroxide	36 ± 4
1.5 f. $HClO_4$	24.8 ± 0.2°	Bromide	35 ± 4
1.5 f. $HClO_4$	24.8 ± 0.2°	Bromide	33 ± 4
2.5 f. $HClO_4$	24.8 ± 0.2°	Bromide	45 ± 4
3.5 f. $HClO_4$	24.8 ± 0.2°	Bromide	67 ± 5

We are extending this work to determine the effect of temperature, ionic strength, and concentrations of the reactants on the exchange rate.

(3) H. A. C. McKay, *Nature*, **142**, 997 (1938).
(4) R. B. Duffield and M. Calvin, THIS JOURNAL, **68**, 557 (1946).

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RECEIVED DECEMBER 10, 1947

THE STRUCTURE OF THE DECABORANE MOLECULE

Sir:

We are studying the structure of crystalline decaborane, $B_{10}H_{14}$, by single crystal X-ray diffraction methods. We have established the approximate positions of the ten boron atoms and four of the hydrogen atoms, and have assigned probable positions to the remaining ten hydrogen atoms. (Hydrogen atoms are well resolved in fourier sections.)

The $B_{10}H_{14}$ molecule has the symmetry C_{2v}–mm2. The bond distances are as follows (see figure): B_1–B_1', B_1–B_4, B_2–B_3, B_2–B_4, B_3–B_4, are all 1.74 ±0.04 kX; B_1–B_2 and B_4–B_4' are 1.96 ± 0.04 kX; B_4–H_4 is 1.34 ± 0.04 kX,[1] and all other B–H distances are assumed the same, except B_6–H_6 which is assumed to be 1.54 ± 0.04 kX. (B_4–B_4''' and B_4'–B_4'' are 2.76 ± 0.04 kX and are not bond distances.) Each hydrogen atom, except H_6 and H_6' is bound to a single boron atom; H_6 and H_6' are each bound to two boron atoms. Each boron atom has three boron neighbors at 1.74 ± 0.04 kX and one hydrogen neighbor at 1.34 ± 0.04 kX. In addition, B_4, B_4', B_4'' and B_4''' each has a boron neighbor at 1.96 ± 0.04 kX and another hydrogen neighbor at 1.54 ± 0.04 kX; B_1, B_1', B_2, B_2', each has two boron neighbors at 1.96 ± 0.04 kX; B_3 and B_3', each has another hydrogen neighbor at 1.34 ± 0.04 kX.

(1) H_4, H_4', H_4'' and H_4''' were located on an electron density map; the positions of the other hydrogen atoms are assumed.

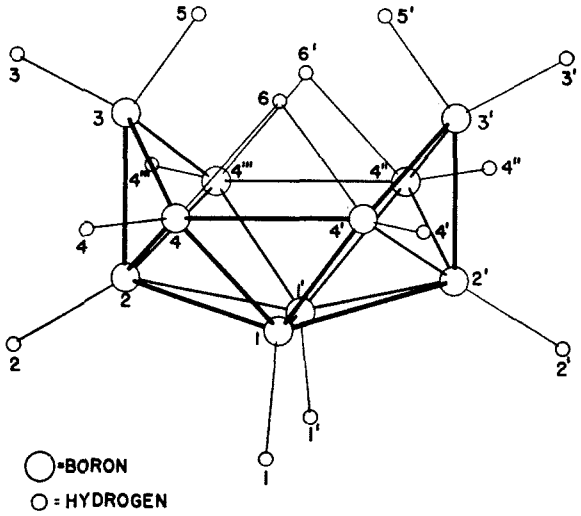

Fig. 1.

Each boron atom is bound to five or six other atoms, but the bonds are not all equivalent. Inasmuch as a bond distance of 1.96 kX has about half the "bond number"[2] of a bond distance of 1.74 kX, one can say that each boron forms five bonds of bond number 0.60. The corresponding radius, R(0.60) = 0.87 kX. Consequently, R(1) = 0.80 kX in agreement with Pauling.[2]

This structure for $B_{10}H_{14}$ gives excellent agreement with the observed X-ray diffraction intensities and also with the electron diffraction observations of S. Bauer.[3]

A detailed discussion of the determination of the structure of crystalline decaborane will be published soon.

(2) L. Pauling, THIS JOURNAL, **69**, 542 (1947).
(3) S. Bauer, *ibid.*, **70**, 115 (1948).

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RECEIVED JANUARY 21, 1948

HETEROGENEITY OF CRYSTALLINE BETA-LACTOGLOBULIN

Sir:

That crystalline β-lactoglobulin is not a homogeneous protein was indicated by the solubility measurements of Grönwall[1] and by the electrophoretic results of Li.[2] Our experiments with

(1) Grönwall, *Compt. rend. trav. lab. Carlsberg*, **24**, no. 8–11, 185 (1942).
(2) Li, THIS JOURNAL, **68**, 2746 (1946).