syringe. The Nessler results after 8 h hydrolyses were the same as the 20 h micro-Kjeldahl.

As Kendrew [5] has mentioned in *Structure and function in myoglobins and other proteins*, "myoglobins from different species have amino acid compositions which are broadly similar, but differ in detail". We may only confirm his statement by comparing the compositions of the purified myoglobins which are presently available, namely sperm whale [6], seal and horse [7] myoglobin. The results show that these myoglobins differ only in details.

The amino acid analysis of Mb II, Mb III, Mb IV and Mb V are in progress using the procedure of Moore and Stein.

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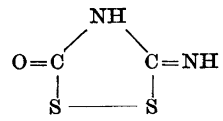
Structure of Rhodan Hydrate

ASBJÖRN HORDVIK

Chemical Institute, University of Bergen, Bergen, Norway

So far X-ray structure determinations of two unsaturated five-membered cyclic disulphides have been reported [1,2]. Observed bond lengths in the thiuret ion [1] and in 4 - methyl - 1,2 - dithia - 4 - *cyclo*pentene - 3 - thione [2] indicate that the five-membered ring has some aromatic character. This seems to explain the relatively high stability of unsaturated five-membered cyclic disulphides as contrasted with saturated ones. It is hoped that a determination of the molecular structure of rhodan hydrate will give further information that can be used to test this idea. The rhodan hydrate molecule has, according to Söderbäck [3], the following structure:



The preparation of rhodan hydrate has been described by Söderbäck [3,4], and the unit cell and space group have been reported by Foss [5]. The crystals are monoclinic, $a = 12.50$ Å, $b = 5.24$ Å, $c = 14.67$ Å,

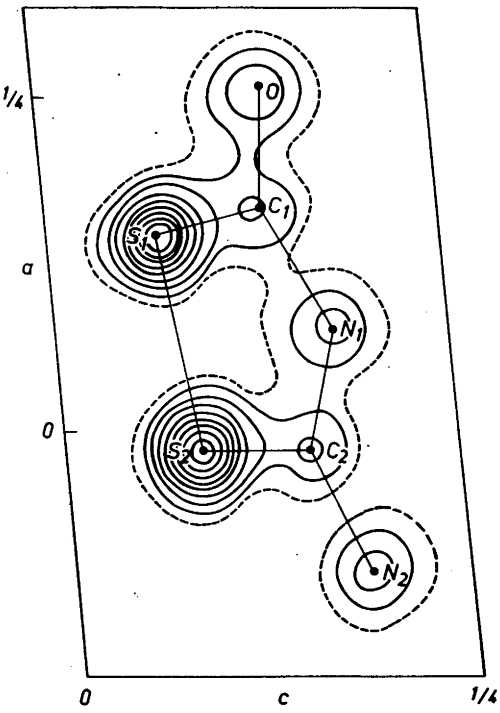


Fig. 1. Electron density projection of rhodan hydrate along the *b*-axis showing one asymmetric unit. Plane group *p*2 and origin in center of symmetry in the projection. Contours at arbitrary but equal intervals.

Table 1. Atomic coordinates, in fractions of corresponding cell edges.

	x	z
S_1	0.1470	0.0695
S_2	−0.0150	0.0865
C_1	0.1635	0.1365
C_2	−0.0135	0.1550
N_1	0.0760	0.1750
N_2	−0.1060	0.1885
O	0.2585	0.1450

$\beta = 95\ 1/2°$. Preliminary results of a complete crystal structure determination of rhodan hydrate are given here.

The space group of rhodan hydrate was found to be either $C2/c$ or C/c. The morphology of the crystals indicates [5] the presence of a twofold axis and thus the correctness of the centrosymmetric space group. The "average test" and "zero moment test" [6] also indicated centrosymmetry.

Attempts to solve the structure from Patterson projections did not succeed, and the solution was then sought by means of Harker Kasper inequalities and the "multiplication rule" [7]. This led to three possible sets of signs for the 35 strongest reflections in the b-axis projection. The molecule was recognised in one of the corresponding Fourier maps, and after three Fourier-refinements the reliability factor R was 0.115. The electron density map is reproduced in Fig. 1. The map shows that the cyclic form of rhodan hydrate, anticipated by Söderbäck [3], is correct. Further refinement will be carried out by means of $(F_o - F_c)$-technique.

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The σ-Phase Ta_2Al

LARS-ERIK EDSHAMMAR and BO HOLMBERG

Institute of Inorganic and Physical Chemistry, University of Stockholm, Stockholm, Sweden

In the course of a study of the tantalum-aluminium system recently started at this Institute, the existens of a σ-type phase has been observed in samples of the approximate composition Ta_2Al prepared by arc-melting in an argon atmosphere.

The dimensions of the tetragonal unit cell obtained from a Guinier powder pattern were found to be:

$a = 9.828$ Å $\qquad c = 5.232$ Å

The axial ratio $c/a = 0.532$ is similar to that found for other σ-phases such as the one occurring in the nickel-vanadium system studied by Kasper and Waterstrat [1] using neutron diffraction techniques. Since the ratios of the atomic radii r_{Ta}/r_{Al} and r_V/r_{Ni} are comparable, the atomic distribution reported for the nickel-vanadinium phase was tentatively adopted for Ta_2Al:

Space-group: $D_{4h}^{14}-P4/mnm$.

Unit cell content: 10 Ta_2Al.

Table 1. The Guinier powder pattern of Ta_2Al ($CuK\alpha_1$ radiation).

hkl	$\sin^2\Theta_{obs}$	$\sin^2\Theta_{calc}$	I_{obs}	I_{calc}
110	0.01228	0.01228	vw	0.5
200	—	0.02457	—	0.0
101	0.02782	0.02781	st	5.5
210	0.03068	0.03071	st *	2.5
111	0.03396	0.03396	w	2.0
220	0.04911	0.04914	vw	0.8
211	0.05238	0.05238	vw	0.8
310	0.06142	0.06142	vw	1.0
221	—	0.07081	—	0.0
301	0.07696	0.07695	w	2.2
320	0.07982	0.07985	vw	1.1
311	0.08311	0.08310	m	4.5
002	0.08670	0.08668	vw	0.7
400	0.09831	0.09828	vw	1.5
112	0.09898	0.09897	vw	1.3
321	0.10153	0.10152	vvw	0.6
410	0.10443	0.10442	vst	10.7
330	0.11059	0.11057	st	5.8
202	0.11130	0.11125	st	6.8
212	0.11739	0.11739	vst	10.0
420	0.12285	0.12285	vvw	0.5
411	0.12603	0.12609	vst	9.5
331	0.13224	0.13224	m	4.0

* Line overlaps line of neighbouring phase.