A view of the structure along **a** is given in Fig. 2. The structure is characterized by a strong hydrogen-bonded network, details of which are given in Table 2.

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Structure of DL-Selenomethionine, $C_5H_{11}NO_2Se$

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Abstract. $M_r = 196{\cdot}1$, monoclinic, $P2_1/a$, $a = 9{\cdot}893\ (1)$, $b = 4{\cdot}713\ (2)$, $c = 17{\cdot}082\ (4)$ Å, $\beta = 101{\cdot}63\ (1)°$, $V = 780{\cdot}0\ (7)$ Å^3, $Z = 4$, $D_m = 1{\cdot}67$, $D_x = 1{\cdot}76$ g cm^{-3}, λ(Cu $K\alpha$) $= 1{\cdot}5418$ Å, $\mu = 61{\cdot}8$ cm^{-1}, $F(000) = 392$, $T = 294$ K. Final $R = 0{\cdot}079$ for 1391 observed reflections. The crystal structure is found to be isomorphous to that of the α-form of DL-methionine. The two Se–C bond lengths are 1·938 (4) and 1·907 (8) Å, and the C–Se–C angle is 98·9 (3)°, slightly smaller than the C–S–C angle.

Introduction. Selenium is an important component of several biologically important macromolecules and is essential in trace amounts, though it is toxic in large quantities. For example, selenium is found to be a component of several enzymes, some proteins whose role in biological systems is not yet known and some bacterial aminoacyl transfer nucleic acids (Stadtman, 1980). Formate dehydrogenase, glycine reductase, nicotinic acid hydroxylase, xanthine dehydrogenase and glutathione peroxidase are some of the naturally occurring selenoproteins. Glutathione peroxidase is a selenium-dependent enzyme found in mammalian cells; this enzyme contains selenium in the form of selenocysteines (Forstrom, Zakowski & Tappel, 1978). Recently, there has been some evidence for the occurrence of selenium as selenomethionine in *Clostridium kluyveri* (Hartmanis & Stadtman, 1982). Naturally, the question arises, why is selenium preferred over sulfur in these proteins? This preference may be due to differences in the chemical and stereochemical properties of amino acids that contain selenium instead of sulfur. Some possible chemical reasons for the preference to selenium over sulfur in biological catalysts are (Stadtman, 1980): (i) At biological pH, selenols (*R*SeH), in contrast to thiols (*R*SH) are largely ionized in enzymes and are charged. (ii) Selenols have lower redox potentials than thiols (*e.g.* selenocysteine *vs* cysteine); this may be the reason for the occurrence of selenols in redox catalysts, *e.g.* formate dehydrogenase and glycine reductase which are found in anaerobic bacteria. (iii) Seleno-organic compounds are generally more reactive than the corresponding sulfur compounds. (iv) Selenols are good nucleophiles and serve as good leaving groups. A comparison of the stereochemical features of the biologically active molecules containing sulfur with those containing selenium will throw some light on the question: What stereochemical feature (if any) favors the selection of selenium over sulfur in some proteins? In this context, we decided to compare the crystal structures and conformation of methionine (I) with selenomethionine (SeM) (II).

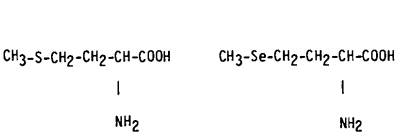

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Table 1. *Positional and isotropic thermal parameters with their e.s.d.'s in parentheses*

$B_{eq} = \frac{4}{3}\sum_i\sum_j \beta_{ij} a_i a_j$.

	x	y	z	B_{eq}/B_{iso}(Å^2)
Se	−0·16218 (7)	−0·0699 (2)	0·13038 (4)	5·35 (2)
O(1)	−0·5030 (3)	−0·0532 (9)	0·3779 (3)	3·27 (7)
O(2)	−0·3257 (3)	−0·3250 (8)	0·4355 (2)	2·76 (6)
N(2)	−0·1396 (4)	0·0574 (10)	0·4098 (2)	2·41 (7)
C(5)	−0·3409 (10)	0·0285 (34)	0·0714 (6)	8·5 (3)
C(4)	−0·1746 (7)	0·0980 (15)	0·2322 (4)	4·3 (1)
C(3)	−0·2750 (5)	−0·0494 (13)	0·2746 (3)	2·82 (9)
C(2)	−0·2795 (4)	0·0625 (11)	0·3574 (3)	2·20 (8)
C(1)	−0·3767 (4)	−0·1194 (9)	0·3950 (3)	2·03 (7)
H1(N2)	−0·142 (4)	0·091 (9)	0·452 (3)	0·8 (8)
H2(N2)	−0·087 (6)	0·179 (15)	0·385 (4)	4·5 (15)
H3(N2)	−0·101 (7)	−0·092 (15)	0·410 (4)	4·5 (17)
H(C2)	−0·302 (6)	0·168 (15)	0·353 (4)	2·8 (14)
H1(C3)	−0·255 (5)	−0·232 (14)	0·274 (3)	3·2 (13)
H2(C3)	−0·360 (8)	−0·024 (18)	0·251 (4)	5·3 (17)
H1(C4)	−0·096 (9)	0·175 (20)	0·259 (5)	8·7 (22)
H2(C4)	−0·219 (7)	0·296 (17)	0·218 (4)	5·6 (18)
H1(C5)	−0·324 (10)	−0·008 (24)	0·034 (5)	8·1 (24)
H2(C5)	−0·366 (9)	−0·082 (19)	0·081 (5)	7·4 (24)
H3(C5)	−0·373 (7)	0·282 (17)	0·091 (4)	5·8 (17)

Experimental. Title compound (Sigma) was crystallized earlier by Dr C. S. Chen in our laboratory. Crystals of (II) are very soft and grow as thin, flat plates; density measured by flotation (bromoform/benzene); accurate unit-cell parameters on a CAD-4 diffractometer using 25 reflections with $12 < \theta < 57°$; a crystal of dimensions 1·2 × 0·35 × 0·10 mm used for three-dimensional data (up to $2\theta = 150°$ for Cu $K\alpha$ radiation) by $\omega/2\theta$ scan; scan widths calculated using expression $(0{\cdot}75 + 0{\cdot}15\tan\theta)°$, aperture widths using equation $(4{\cdot}0 + 1{\cdot}2\tan\theta)$ mm; maximum time spent on any reflection measurement 100 s, faster scan used for strong reflections. Intensities of three reflections monitored after every hour of exposure, variation in intensity <1·6% during complete data collection; orientation matrix checked every 100 reflections; 1810 unique reflections measured (range of *hkl*: 0–12, 0–5, −21 to 20), out of which 1391 significant ($\geq 2\sigma$). Lorentz and polarization corrections applied, intensities of three reflections at $\chi \sim 90°$ measured for all values of φ from 0 to 360° and resultant curve of transmission as a function of φ used to calculate the anisotropy of absorption for all reflections, average transmission factor 0·80. Structure solved by heavy-atom method; position of Se atom determined from a three-dimensional Patterson map; rest of structure recovered from Se-phased Fourier syntheses. Refinements with individual anisotropic thermal parameters led to R 0·09; difference electron-density maps computed at this stage revealed positions of H atoms in the structure; final cycles of refinement with anisotropic thermal parameters for non-H atoms, isotropic thermal parameters for H atoms and extinction-parameter refinement led to R 0·079 for the 1391 reflections, $R_w = 0{\cdot}105$, $S = 3{\cdot}22$; quantity minimized $\sum w(|F_o| - 1/k|F_c|)^2$ where $w = 4|F_o|^2/\sigma(|F_o|^2)^2$ and $\sigma(|F_o|)^2 = [\sigma(I)^2 + 0{\cdot}05I^2]^{1/2}/\mathrm{Lp}$ where $\sigma(I)$ is the standard deviation of intensity I based upon counting statistics and k is the scale factor. $(\Delta/\sigma)_{max}$ 0·15. Programs and atomic scattering factors as in Enraf–Nonius *SDP* (1979); Fourier and torsion-angle programs by Dr S. T. Rao and *ORTEP* by Johnson (1965).

Discussion. The final positional parameters for all atoms are given in Table 1.* A comparison of the unit-cell dimensions of α-DL-methionine (Taniguchi, Takaki & Sakurai, 1980) with those of SeM indicates that these two crystal structures are isomorphous (Table 2); the structure determination proved that these structures, indeed, are isomorphous. The SeM molecule exists, as expected, as a zwitterion in the crystal. The bond distances and bond angles are given in Fig. 1 for bonds not involving H atoms. Bond angles involving H atoms are in the usual range for X-ray determination.

The bond distances and angles in SeM may be compared to those found in DL-methionine (Taniguchi *et al.*, 1980), L-methionine (Torii & Iitaka, 1973), L-methionyl-L-methionine (Stenkamp & Jensen, 1975) and DL-alanyl-LD-methionine (Stenkamp & Jensen, 1974), remembering, however, that the Se–C bond lengths are longer, since the covalent radius of the Se

* Lists of structure factors and anisotropic thermal parameters have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 39032 (10 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 5 Abbey Square, Chester CH1 2HU, England.

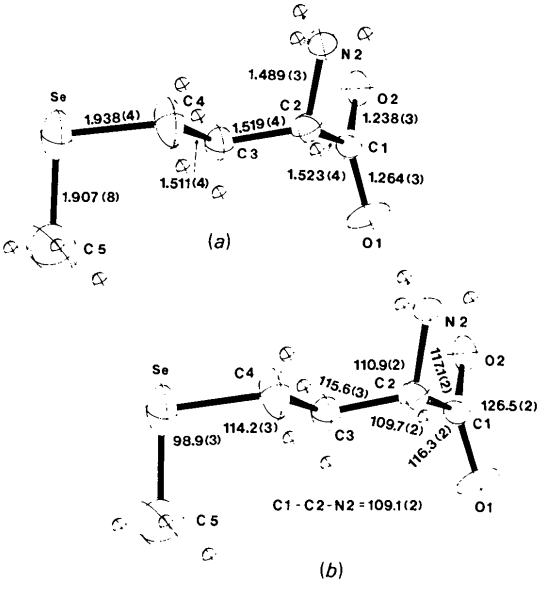

Fig. 1. (*a*) Covalent bond distances (Å) for bonds not involving H atoms. The quantities in parentheses denote e.s.d.'s for bond lengths. (*b*) Covalent bond angles (°) for bonds not involving H atoms. The quantities in parentheses denote e.s.d.'s for bond angles.

Table 2. *Comparison of the unit-cell dimensions of* α- *and* β-DL-*methionine with* DL-*selenomethionine*

Compound	Temperature	a(Å)	b(Å)	c(Å)	β(°)	Space group	Z	Reference
α-DL-Methionine	RT	9·76	4·70	16·70	102	$P2_1/a$	4	Mathieson (1952)
α-DL-Methionine	333 K	9·89 (2)	4·70 (2)	16·74 (3)	102·3 (7)	$P2_1/a$	4	Taniguchi *et al.* (1980)
β-DL-Methionine	293 K	9·912 (5)	4·700 (7)	33·13 (2)	106·3 (3)	$I2/a$	4	
DL-Selenomethionine	294 K	9·893 (1)	4·713 (2)	17·082 (4)	101·63 (1)	$P2_1/a$	4	Present study

Table 3. *Comparison of torsion angles* (°) *of* DL-*selenomethionine with other similar molecules whose structures have been studied previously*

Molecule		N(2)–C(2)–C(3)–C(4) χ^1	O(2)–C(1)–C(2)–N(2) ψ^2	C(1)–C(2)–C(3)–C(4)	C(2)–C(3)–C(4)–Se/S χ^2	C(3)–C(4)–Se/S–C(5) χ^3
DL-Selenomethionine[a]		∓55·3 (7)	∓30·8 (6)	∓175·8 (7)	±175·5 (7)	±68·7 (7)
DL-Methionine[a,b,c]	α	∓59·8 (8)	∓29·3 (7)	∓178·6 (8)	±177·4 (8)	±68·9 (9)
	β	∓54·4 (5)	∓31·0 (4)	∓174·4 (5)	∓179·3 (5)	∓174·4 (5)
L-Methionine[b,d]	*A*	−166 (2)	−17 (2)	+71 (2)	+174 (2)	+180 (2)
	B	−166 (3)	−34 (2)	+74 (2)	+74 (2)	+74 (2)

Notes: (*a*) The sign '±' refers to the two enantiomorphs in the structure, with the upper sign designating the conformation of the molecule in Table 1.
(*b*) The standard deviations in torsion angles were calculated by us from the published standard deviations in atomic coordinates using a program *DSCAN* written by Dr S. T. Rao.
(*c*) The structure of DL-methionine was first solved by Mathieson (1952) and then re-refined by Taniguchi *et al.* (1980).
(*d*) Torii & Iitaka (1973).

atom is larger than that of S. The Se–C bond lengths in SeM are found to be comparable to the weighted average value of 1·98 (2) Å, calculated by Hope, Knobler & McCullough (1970) from eight non-aromatic compounds. The shortening of the Se–C(5) bond as compared to the C(4)–Se bond might be due to the large thermal vibrations of C(5), the terminal atom (see also Torii & Iitaka, 1973).

The C–C bond lengths in SeM are quite different from the normal single-bond value of 1·542 Å. This departure from the normal value increases as we go along the chain from C(1) to C(4), parallel to the increase in B_{eq} (Table 1). The reason for the increase in B_{eq} from C(1) to C(4) may be due to the hydrogen bonding to the carboxyl group, which stabilizes the C(1) end while the terminal atoms are held in place by weaker forces only. The least-squares plane through the atoms C(2), C(1), O(1) and O(2) is given by the equation $-0{\cdot}018X-0{\cdot}587Y+0{\cdot}809Z=5{\cdot}089$, where the coefficients of X, Y and Z are the direction cosines of the normal to the plane relative to **a**, **b** and **c***. X, Y any Z are Cartesian coordinates in Å. The N(2) atom is about 0·67 Å away from the carboxylate plane, a feature observed in many amino acids (Marsh & Donohue, 1967).

The torsion angles for the SeM molecule are listed in Table 3 along with those obtained for DL- and L-methionine. The amino group in SeM is g^- to C(4), *i.e.* the torsion angle N(2)–C(2)–C(3)–C(4) is −55·3 (7)°, as observed in the case of DL-methionine. In L-methionine, however, the conformation of the amino group is *t* to C(4). Torsion angles for the SeM molecule correspond very closely to those for the α-form of DL-methionine and fall in the preferred

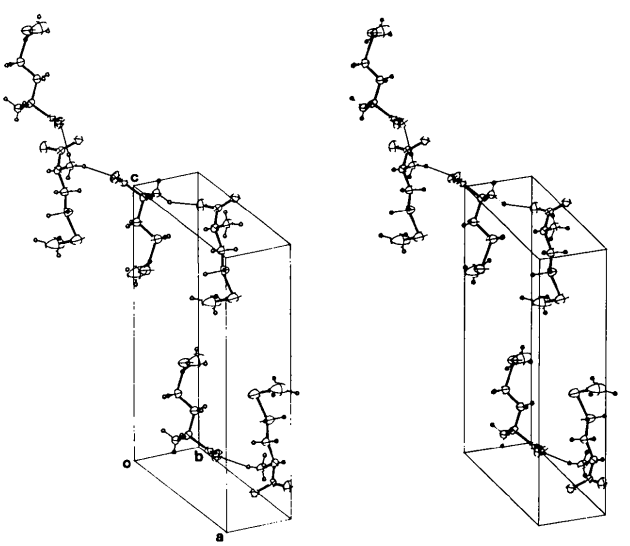

Fig. 2. Stereoview illustrating hydrogen-bonding interactions and crystal packing.

regions in the distribution of conformation angles for the methionine residues (Chen & Parthasarathy, 1977). That the conformation of methionine and SeM molecules in these crystals is nearly identical indicates that there is no conformational reason for selecting the selenium analog over methionine in proteins.

The molecular arrangement and hydrogen-bonding interactions are depicted in Fig. 2. All three H atoms of the amino N are intermolecularly hydrogen-bonded to carboxyl O atoms forming a distorted tetrahedral arrangement around N(2). The distances H1(N2)···O(2), H2(N2)···O(1) and H3(N2)···O(1)

are 2·05 (4), 1·96 (7) and 2·05 (7) Å respectively and the respective angles N–H···O are 173 (4), 149 (6) and 164 (7)°. Such $COO^-\cdots H_3N^+$ hydrogen bonds are found in all amino acids. There are, however, no short contacts with the Se atom, though selenides have been shown to form short contacts with electrophiles and nucleophiles (Ramasubbu & Parthasarathy, 1983) as in the case of sulfides (Rosenfield, Parthasarathy & Dunitz, 1977).

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Structure of 2,4-Diamino-5-(3,4,5-trimethoxybenzyl)pyrimidinium Benzoate (Trimethoprim Monobenzoate), $C_{14}H_{19}N_4O_3^+.C_7H_5O_2^-$

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Abstract. $M_r = 412{\cdot}4$, monoclinic, $P2_1/n$, $a = 11{\cdot}295$ (1), $b = 28{\cdot}266$ (2), $c = 6{\cdot}543$ (1) Å, $\beta = 100{\cdot}97$ (1)°, $V = 2050{\cdot}8$ (4) Å^3, $Z = 4$, $D_m = 1{\cdot}36$, $D_x = 1{\cdot}336$ Mg m^{-3}, Cu $K\alpha$, $\lambda = 1{\cdot}5418$ Å, $\mu = 0{\cdot}81$ mm^{-1}, $F(000) = 872$, $T = 296$ K, $R = 0{\cdot}039$ for 1895 observed reflections. The interaction compound is formed by the trimethoprim N(1) cation and the benzoate anion. Two interionic hydrogen bonds lead to the formation of an eight-membered pseudo ring. Cyclic dimers *via* pairs of hydrogen bonds across centers of symmetry are formed by the ions of the title compound.

Introduction. Binary systems in which the antifolate drug trimethoprim [2,4-diamino-5-(3,4,5-trimethoxybenzyl)pyrimidine, TMP] is involved have been investigated by some of us both for phase equilibria and for thermal behavior. TMP and sulfamethoxazole (SMZ), components of widely used antibacterial formulations (*e.g.* BACTRIM^R), give a 1:1 molecular compound, TSC, with a congruent melting point (Giordano, Bettinetti, La Manna & Ferloni, 1977). This compound, totally dissociated in the melt (Margheritis & Sinistri, 1978), is a hydrogen-bonded complex (Giuseppetti, Tadini, Bettinetti, Giordano & La Manna, 1980). TMP and benzoic acid (BA) form in the solid phase two congruent melting intermediate compounds, BA–TMP and $(BA)_2$–TMP, which show only partial dissociation in the melt (Bettinetti, Caramella, Giordano, La Manna, Margheritis & Sinistri, 1983). The high stability of these interaction compounds suggests a bond pattern stronger than that found by us in the TMP–SMZ complex.

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