

Strontium dihydrogenphosphite

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Key indicators

Single-crystal X-ray study
 T = 293 K
 Mean $\sigma(\text{P}-\text{O}) = 0.006 \text{ \AA}$
 H-atom completeness 0%
 R factor = 0.068
 wR factor = 0.182
 Data-to-parameter ratio = 13.2

For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

The crystal structure of strontium dihydrogenphosphite, $\text{Sr}(\text{H}_2\text{PO}_3)_2$, contains eightfold-coordinated Sr ions connected by dihydrogenphosphite anions so that a layer structure is formed.

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Comment

Crystal structure analyses of alkaline-earth phosphites have been undertaken for several decades. The first one was $\text{MgHPO}_3 \cdot 6\text{H}_2\text{O}$ (Corbridge, 1956); this structure was later reinvestigated by neutron and X-ray diffraction (Powell *et al.*, 1994). $\text{Ca}(\text{H}_2\text{PO}_3)_2 \cdot \text{H}_2\text{O}$ was reported by Larbot *et al.* (1984).

We present here the crystal structure of $\text{Sr}(\text{H}_2\text{PO}_3)_2$ (Fig. 1). The framework of the title compound can be described as layers perpendicular to the crystallographic *c* axis (Fig. 2). Sr is coordinated by eight O atoms, with bond distances ranging from 2.489 (5) to 2.753 (6) Å. There are three different types of O atoms: O13 is bonded only to P; O11 and O21 are bonded to P and one Sr atom; O12, O22 and O23 are bonded to P and two different Sr atoms. The average P—O distance of 1.54 (5) Å is similar to those reported in other dihydrogenphosphites: 1.523 Å in $\text{Ca}(\text{H}_2\text{PO}_3)_2 \cdot \text{H}_2\text{O}$ or 1.513 Å in $\text{Zn}(\text{H}_2\text{PO}_3)_3 \cdot 0.333\text{H}_2\text{O}$ (Durand *et al.*, 1992).

Experimental

25 ml of $\text{SrCl}_2 \cdot 6\text{H}_2\text{O}$ (0.1 M) was added to a 25 ml aliquot of 1 M H_3PO_3 in water. The resulting solution was stirred for 8 h, at 333 K, before being left at room temperature. After a few days, large colourless block-shaped crystals were deposited. These were filtered off and washed with a solution of ethanol (80%).

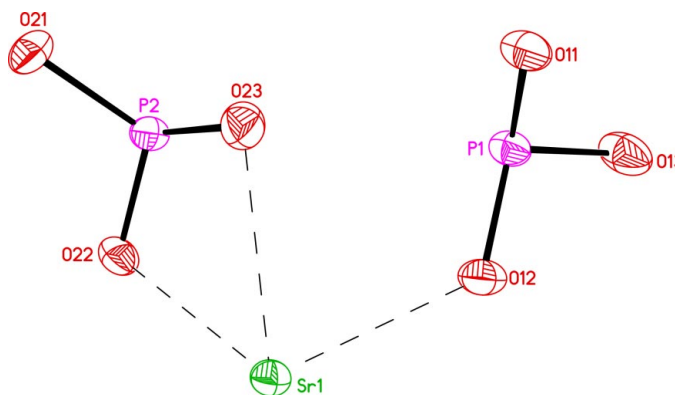


Figure 1

The asymmetric unit of the title compound with atom labelling and displacement ellipsoids drawn at the 50% probability level.

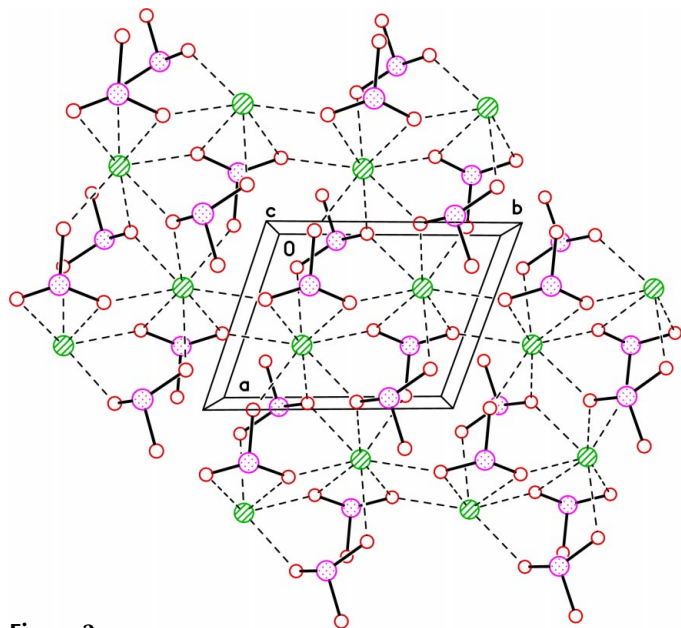


Figure 2
The crystal structure of $\text{Sr}(\text{H}_2\text{PO}_3)_2$, viewed perpendicular to the c axis. Key: Sr green, P violet and O red.

Crystal data

$\text{Sr}(\text{H}_2\text{PO}_3)_2$
 $M_r = 249.59$
Triclinic, $P\bar{1}$
 $a = 5.797$ (1) Å
 $b = 7.206$ (1) Å
 $c = 8.068$ (1) Å
 $\alpha = 97.87$ (1)°
 $\beta = 104.51$ (1)°
 $\gamma = 106.55$ (1)°
 $V = 304.78$ (8) Å³

$Z = 2$
 $D_x = 2.720$ Mg m⁻³
Mo $K\alpha$ radiation
Cell parameters from 688 reflections
 $\theta = 3.6$ – 28.2 °
 $\mu = 9.33$ mm⁻¹
 $T = 293$ (2) K
Block, colourless
 $0.30 \times 0.20 \times 0.10$ mm

Data collection

Stoe IPDS-II two-circle diffractometer
 ω scans
Absorption correction: multiscan (*MULABS*; Spek, 1990; Blessing, 1995)
 $T_{\min} = 0.121$, $T_{\max} = 0.394$

1079 measured reflections
1079 independent reflections
1045 reflections with $I > 2\sigma(I)$
 $\theta_{\max} = 25.0$ °
 $h = -6 \rightarrow 6$
 $k = -8 \rightarrow 8$
 $l = 0 \rightarrow 9$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.068$
 $wR(F^2) = 0.182$
 $S = 1.09$
1079 reflections
82 parameters
H atoms not located

$$w = 1/[\sigma^2(F_o^2) + (0.1484P)^2 + 0.2956P]$$

where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\max} < 0.001$
 $\Delta\rho_{\max} = 1.13 \text{ e \AA}^{-3}$
 $\Delta\rho_{\min} = -3.05 \text{ e \AA}^{-3}$

Table 1

Selected interatomic distances (Å).

Sr1—O23 ⁱ	2.489 (5)	Sr1—O21 ^{iv}	2.753 (6)
Sr1—O22 ⁱⁱ	2.513 (5)	P1—O12	1.504 (5)
Sr1—O12 ⁱⁱⁱ	2.537 (5)	P1—O11	1.502 (5)
Sr1—O12	2.593 (5)	P1—O13	1.591 (6)
Sr1—O11 ⁱ	2.682 (5)	P2—O22	1.495 (5)
Sr1—O23	2.687 (5)	P2—O23	1.515 (5)
Sr1—O22	2.723 (5)	P2—O21	1.608 (5)

Symmetry codes: (i) $1 - x, 1 - y, 1 - z$; (ii) $1 - x, 2 - y, 1 - z$; (iii) $-x, 1 - y, 1 - z$; (iv) $x - 1, y, z$.

The H atoms could not be located and were therefore not included in the refinement process.

Data collection: *X-Area* (Stoe & Cie, 2001); cell refinement: *X-Area*; data reduction: *X-Area*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *XP* in *SHELXTL-Plus* (Sheldrick, 1991).

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