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Hydrogen-bond landscapes, geometry and energetics of squaric acid and its mono- and dianions: a Cambridge Structural Database, IsoStar and computational study

As part of a programme of work to extend central-group coverage in the Cambridge Crystallographic Data Centre's (CCDC) IsoStar knowledge base of intermolecular interactions, we have studied the hydrogen-bonding abilities of squaric acid (H₂SQ) and its mono- and dianions (HSQ⁻ and SQ²⁻) using the Cambridge Structural Database (CSD) along with dispersion-corrected density functional theory (DFT-D) calculations for a range of hydrogen-bonded dimers. The -OH and -C=O groups of H₂SO, HSO⁻ and SO²⁻ are potent donors and acceptors, as indicated by their hydrogenbond geometries in available crystal structures in the CSD, and by the attractive energies calculated for their dimers with acetone and methanol, which were used as model acceptors and donors. The two anions have sufficient examples in the CSD for their addition as new central groups in IsoStar. It is also shown that charge- and resonance-assisted hydrogen bonds involving H₂SQ and HSQ⁻ are similar in strength to those made by carboxylate COO⁻ acceptors, while hydrogen bonds made by the dianion SQ²⁻ are somewhat stronger. The study reinforces the value of squaric acid and its anions as cocrystal formers and their actual and potential importance as isosteric replacements for carboxylic acid and carboxylate functions.

1. Introduction

In the early 1960s West and co-workers (West et al., 1960; West & Powell, 1963) identified and studied a general series of D_{nh} symmetric, electron-delocalized oxocarbon dianions of the general formula $C_n O_n^{2-}$, representing a new class of aromatic substances. Thus, deltate (I), squarate (II), croconate (III) and rhodizonate (IV) are the dianions for n = 3-6, respectively, of the parent fully protonated compounds deltic, squaric, croconic and rhodizonic acids. While all of these parent acids and their simple derivatives, as well as their mono- and dianions, have attracted crystallographic interest, this interest has been heavily concentrated on the n = 4 homologue. Squaric acid [H₂SQ: 3,4-dihydroxycyclobut-3-ene-1,2-dione (V)] is a thermally stable, strained planar molecule and is highly acidic with $pK_1 = 1.2-1.7$ and $pK_2 = 3.2-3.5$ for the two O-H protons (Cohen et al., 1959; MacDonald, 1968). In this paper we denote the monoanion, hydrogen squarate (VI). as HSQ^{-} and the squarate dianion (II) as SQ^{2-} and, where necessary, refer to the whole grouping as SQ.

Our principal interest in squaric acid, its anions and derivatives arises from their applications, both actual and potential, as active pharmaceutical ingredients. Thus, the dibutylester of H_2SQ is used for the treatment of warts (see *e.g.* Silverberg *et al.*, 2000) and alopecia (Caserio, 1987), while Marson (2011) discusses the use of squarates as unusual



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scaffolds in medicinal chemistry. He notes that derivatives of H₂SO can act as isosteres of carboxylic acids, aminosquarate derivatives can mimic amino acids, while diamides of H₂SQ can act as phosphate isosteres and phosphate linkage mimics in DNA. Marson (2011) and Meanwell (2011) show several H₂SQ diamide derivatives that act as receptor antagonists, including the H₂SQ diamide derivative of a receptor antagonist (perzinfotel) that acts as a prodrug which increases the oral availability of perzinfotel by a factor of seven (Baudy et al., 2009). Squaric acid and its anions are also the basis of squaraine and squarylium dyestuffs, due to the formation of extended delocalized systems with aniline or other electronrich systems (see e.g. Sprenger & Ziegenbein, 1966), some of which are used as fluorescent biomarkers (Terpetschnig & Lakowicz, 1993). Some of these dyes present large second- and third-order nonlinear optical (NLO) responses and the NLO responses of these compounds and a number of other squarates, particularly pyridinium betaine derivatives, are an active research area (Spassova et al., 2000; Kolev et al., 2004). Squaric acid and its anions are also being investigated for their potential as organic ferroelectric materials (Horiuchi et al., 2007).



Historically, the major features of crystallographic structural interest in H_2SQ , HSQ^- and SQ^{2-} have been the effect of high strain and electron delocalization on the intramolecular geometry, and the patterns and geometry of the hydrogen bonds formed by the strong H-donors and Oacceptors (see *e.g.* Semmingsen *et al.*, 1977, 1995; Hollander *et al.*, 1977). It is the obvious ability of these molecules to form strong hydrogen bonds through charge- and resonance-assistance (CAHB, RAHB: see Gilli & Gilli, 2009 for an overview) that has led to applications in crystal engineering and their occurrence as cocrystal formers (see, *e.g.*, Bertolasi *et al.*, 2001; Gilli *et al.*, 2001; Mathew *et al.*, 2002).



An extensive knowledge of the hydrogen-bond landscapes of chemical functional groups is vital in many areas of research, and especially in guiding studies of protein–ligand interactions and protein–ligand docking in medicinal chemistry applications. To assist in these studies, the CSD system contains the comprehensive IsoStar library of intermolecular interaction information (Bruno *et al.*, 1997). IsoStar provides three-dimensional scatterplots of the distribution of 'contact groups', particularly hydrogen-bond donors, around a set of selected central groups, *i.e.* chemical functional groups and heterocyclic rings that are common in organic systems. IsoStar contains extensive numerical information on these interactions together with computational energy minima for selected interactions calculated using intermolecular perturbation theory (IMPT: Hayes & Stone, 1984; Stone, 1993).

In this paper we use the Cambridge Structural Database (CSD: Allen, 2002), including the generation of IsoStar plots, to analyse and map the intramolecular and hydrogen-bond geometries observed in crystal structures that contain H₂SQ, HSQ⁻ or SQ²⁻. The CSD and IsoStar analyses are augmented by DFT-D calculations to study the attractive energies of O– H···O hydrogen bonds formed by all three SQ moieties and a comparison of these data with energy values obtained previously for other hydrogen-bonded systems [see, *e.g.*, the IsoStar library (Bruno *et al.*, 1997) and elsewhere (Allen *et al.*, 2010, 2012)]. As a result of this work, intermolecular interaction information for HSQ⁻ and SQ²⁻ has been included in the November 2012 release of the IsoStar library so as to improve its coverage of groups that are important in medicinal chemistry and materials design.

2. Methodology

2.1. Cambridge Structural Database (CSD) analyses

Database analyses were carried out using CSD Version 5.34 (November 2012) plus its first distributed update, a total of

Table 1

Mean intramolecular geometry for H_2SQ , HSQ^- and SQ^{2-} determined from crystal structures retrieved from the CSD.

Atomic numbering is shown in the chemical formulae (II), (V) and (VI). Bond lengths (Å) and valence angles (°) are averaged over C_s symmetry for H₂SQ, C_1 symmetry for HSQ⁻ and D_{4h} symmetry for SQ²⁻. All numerical means (x) are given as $x(\sigma_s, n)$, where σ_s is the sample e.s.d. and n is the number of observations contributing to the mean. Symmetry-related mean values are shown in brackets, e.g. as [x].

Parameter	$H_2SQ(C_s)$	$\mathrm{HSQ}^{-}(C_1)$	$\mathrm{SQ}^{2-}\left(D_{4h}\right)$
C1-C2	1.497(7,10)	1.489(13,78)	1.459(11,184)
C2-C3	1.459(12,20)	1.487(11,78)	[1.459]
C3-C4	1.403(12,10)	1.428(15,63)	[1.459]
C4-C1	[1.459]	1.433(13,78)	[1.459]
C1-O1	1.231(11,20)	1.247(16,78)	1.254(11,184)
C2 - O2	[1.231]	1.226(8,78)	[1.259]
C3-O3	1.291(14,20)	1.252(13,78)	[1.259]
C4-O4	[1.291]	1.308(11,78)	[1.259]
C4-C1-C2	88.2(7,20)	89.0(9,78)	90.0(7,184)
C1-C2-C3	[88.2]	88.6(6,78)	[90.0]
C2-C3-C4	91.8(7,20)	89.2(8,78)	90.0
C3-C4-C1	[91.8]	93.1(6,78)	90.0
C2-C1-O1	135.8(6,20)	134.8(13,78)	135.0(11,368)
C4-C1-O1	136.4(7,20)	136.2(10,78)	[135.0]
C1-C2-O2	[136.4]	135.7(10,78)	[135.0]
C3-C2-O2	[135.8]	135.6(10,78)	[135.0]
C2-C3-O3	134.2(23,20)	134,5(11,78)	[135.0]
C4-C3-O3	134.1(23,20)	136.3(12,78)	[135.0]
C3-C4-O4	[134,1]	133.9(26,78)	[135.0]
C1-C4-O4	[134.2]	132.9(27,78)	[135.0]

586 977 structures. Substructure searches and the location of hydrogen bonds used the CSD system (CSDS) program *ConQuest* (Bruno *et al.*, 2002) with the following secondary search criteria: atomic coordinates error-free after CSD checks; no disorder in the crystal structure; no *catena* (polymeric) bonding; no powder studies; organic structures only according to CSD definitions; and a crystallographic *R* factor < 0.075 (unless stated otherwise).

The numbers of structures (N_s) and independent chemical fragments (N_f) available for detailed geometrical analysis were: H_2SQ ($N_s = 14$, $N_f = 14$), HSQ^- (69, 91) and SQ^{2-} (47,47). Hydrogen bonds involving N-H and O-H donors were located and geometrically characterized using neutronnormalized H-atom positions (Allen, 1986) with N-H and O-H bond distances of 1.015 and 0.993 Å, respectively, as determined from accurate neutron structures in the CSD (Allen & Bruno, 2010). Geometrical parameters used to characterize hydrogen bonds of the general form D(onor)- $H \cdots A(\text{cceptor}) - R$ were: the hydrogen-bond distance, d(HA)(Å), the angle at H, θ (DHA) (°), and where relevant the angle of approach to the acceptor-O, $\varphi(HAR)$ (°). Hydrogen bonds were defined as having d(HA) less than the sum of the van der Waals radii of H and A, and with $\theta(DHA) > 120^{\circ}$ (Wood *et al.*, 2009). All data analyses were carried out using the CSDS program Vista and its successor code (Sykes et al., 2011) incorporated within the CSDS Mercury program (Macrae et al., 2008).

2.2. IsoStar maps of intermolecular interactions

IsoStar (Bruno *et al.*, 1997) contains information about nonbonded interactions derived from the CSD and from proteinligand complexes in the Protein Data Bank (Berman *et al.*, 2000), together with IMPT energy minima for important interactions. The current distributed version of IsoStar (November 2012) covers more than 300 central groups and over 50 contact groups, which give rise to more than 20 000 scatterplots derived from the CSD and about 5500 scatterplots derived from PDB structures having a resolution better than 2 Å. *Ab initio* theoretical energy minima are included for more than 1500 key interactions. In this work we present IsoStar plots of the hydrogen-bond landscapes of HSQ⁻ and SQ²⁻ for which sufficient data exist in the CSD.

3. Mean intramolecular geometry

It is necessary to provide the computational procedures described later in this work with initial ground-state intramolecular geometry for model compounds, and this was determined for H₂SQ, HSQ⁻ and SQ²⁻ from the crystal structures retrieved from the CSD. Mean geometrical data are presented in Table 1, with the bond lengths and angles averaged over C_s symmetry for H₂SQ, C_1 symmetry for HSQ⁻ and D_{4h} symmetry for SQ²⁻. The numbering scheme for the C and O atoms is that shown in chemical diagrams (II), (V) and (VI). The bond-length data clearly show the effects of electron delocalization throughout the three systems, with squaric acid itself being trapezium shaped and the dianion a perfect square. A variety of computational results are available (see e.g. Lunelli et al., 1996; Zhou et al., 2000; Spassova et al., 2000), all of which show acceptable agreement with the experimental data in Table 1, but with variations due to the computational procedures or basis sets used. The hydroxy H atoms in parent H₂SQ can adopt one of three isomeric relationships: ZZ (VII), EZ (VIII) or EE (IX). Published computational studies on isolated molecules all agree that the ZZ isomer is the most energetically favoured, but that the EZ isomer is also within about $6-10 \text{ kJ mol}^{-1}$ of the minimum. The *EE* isomer has a higher relative energy, around 28 kJ mol^{-1} above the ZZ minimum (all energy data taken from Zhou et al., 2000). In the CSD, where the positions of the H atoms will adjust to hydrogen-bonding requirements in the condensed phase, two of the ten examples are ZZ, seven are EZ (including four independent redeterminations of either polymorph of H₂SQ itself), and only one example is *EE*.

4. Hydrogen bonding involving squaric acid and its anions

Parameter ranges and mean values derived from the CSD for d(HA), $\theta(DHA)$ and $\varphi(HAR)$ for hydrogen bonds involving the O—H donors and the terminal-O acceptors of squaric acid and its mono- and dianions are collected in Table 2. While it is valid to derive mean values for d(HA) and $\varphi(HAR)$ to assess the relative strengths of the various hydrogen bonds and their

Table 2

Mean geometry of hydrogen bonds involving O-H donors and terminal-O acceptors in squaric acid (H₂SQ) and its anions (HSQ⁻ and SQ²⁻).

Hydrogen bond lengths, d(HA), are in Å and relevant angles, $\theta(DHA)$ and $\varphi(HAR)$, are in degrees. All numerical means (x) are given as $x(\sigma_s, n)$, where σ_s is the sample e.s.d. and n is the number of observations contributing to the mean. Mean values for $\theta(DHA)$ are given as an indicator of the overall linearity of the hydrogen bonds included in the averaging process.

Hydrogen-bond type	$d(\mathrm{H}A)$ (Å)		$\theta(DHA)$ (°)		$\varphi(\text{HAR})$ (°)	
	Range	Mean	Range	Mean	Range	Mean
Squaric acid (H ₂ SQ)						
$O-H(H_2SQ)\cdots O=C(sq)$	1.42-1.62	1.54(5,18)	152-180	170(8,18)	112-136	121(7,18)
$N^+ - H \cdots O = C (H_2 SQ)^2$	1.88-2.25	2.06(15,4)	121–171	149(20,4)	125–137	132(6,4)
Hydrogen squarate (HSQ ⁻)						
$O-H(HSQ^{-})\cdots O=C(sq)$	1.44-1.67	1.55(5,65)	143-180	166(9,65)	109-142	126(10,65)
$O-H(HSQ^{-})\cdots N(bipy)$	1.59-1.65	1.63(2,6)	164-175	170(4,6)	-	-
$O-H(water) \cdots O = C(HSQ^{-})$	1.65-2.30	1.89(17,25)	120-179	159(15,25)	107-165	123(13,25)
$N^+(ar) - H \cdots O = C(HSQ^-)$	1.58 - 1.90	1.68(10,25)	144-177	165(9,25)	105-137	121(8,25)
$N^+ - H \cdots O = C(HSQ^-)$	1.71-2.41	1.98(18,79)	122-179	153(15,79)	95-147	123(11,79)
$N^0H \cdots O = C(HSQ^-)$	1.70-2.56	2.04(20,45)	124–179	157(15,45)	92-162	126(16,45)
Squarate dianion (SQ^{2-})						
$O-H(H_2SO)\cdots O=C(SO^{2-})$	1.53-1.55	1.54(1.3)	157-162	160(2,3)	120-129	125(4,3)
$CN-O-H(not sq)\cdots O=C(SQ^{2-})$	1.60-2.01	1.70(2.7)	139-175	162(12,7)	108-135	121(10,7)
$O-H(water)\cdots O = C(SQ^{2-})$	1.68 - 2.00	1.82(6,49)	147-179	166(8,49)	98-144	120(11,49)
$N^+(ar) - H \cdots O = C(SQ^{2-})$	1.52-1.73	1.62(6,11)	155-174	166(6,11)	110-132	119(7,11)
$N^+ - H \cdots O = C(SQ^{2-})$	1.67 - 2.08	1.83(10,41)	134-175	161(11,41)	102-144	119(9,41)
$N^0 - H \cdots O = C(SQ^{2-})$	1.65-2.28	1.87(14,39)	142–178	164(9,39)	88–175	124(15,39)
Comparison data						
$O - \dot{H}(COOH) \cdots O = C(COO^{-})$	1.44-1.91	1.57(7,1072)	119-180	169(8,1072)	95-177	121(9,1072)
O−H(COOH)···O=C(COOH)	1.48-2.19	1.67(5,2160)	122-180	171(7,2160)	105-176	124(8,2160)
$O-H(water) \cdots O = C(COO^{-})$	1.59-2.30	1.84(9,1929)	120-180	164(9,1929)	80-170	124(8,1929)
$N^+(ar) - H \cdots O = C(COO^-)$	1.50-1.93	1.67(9,410)	132-180	168(9,410)	83-167	117(9,410)
$N^+ - H \cdots O = C(COO^-)$	1.56-2.24	1.84(11,4090)	120-180	163(10,4090)	73-175	123(14,4090)
$N^0 - H \cdots O = C(COO^-)$	1.64-2.35	1.93(13,1144)	122–180	161(12,1144)	81–177	125(15,1144)

directionality of approach to O-acceptors, the mean values of $\theta(DHA)$ are included as an effective indicator of the overall hydrogen-bond linearity within a given distribution: the closer the mean $\theta(DHA)$ is to 180°, the greater the tendency for the distribution to approach linearity. A few of the O-H···O hydrogen bonds characterized in Table 2 involve the formal C=O acceptors of H₂SQ, HSQ⁻ and SQ²⁻ taken together; these acceptors are denoted collectively as O=C(sq) in Table 2 and in the ensuing discussion.

4.1. Squaric acid [H₂SQ (V)]

The O-H donors of the nine structures containing the parent squaric that pass the acceptance criteria of §2 are always used in hydrogen-bond formation, and these hydrogen bonds universally form to the O=C acceptors of squaric acid itself or to those of co-crystallized HSQ⁻ or SQ²⁻ anions. Thus these O-H(H₂SQ)···O=C(sq) hydrogen bonds are the only meaningful subset given for parent squaric acid in Table 2. As expected from the pK_a values (see §1), these bonds are short [mean d(HA) = 1.54 (5) Å], have a remarkably linear $\theta(DHA)$ distribution, and approach the O-acceptor along a lone-pair direction. These data should be compared with CSD averages for COOH···O=C(COO⁻) and COOH···O=C(COOH) hydrogen bonds presented in Table 2 for comparison

purposes. Clearly the $O-H(H_2SQ)\cdots O=C(sq)$ hydrogen bonds are of comparable length (strength) to the $COOH\cdots O=C(COO^{-})$ subset and are shorter (stronger) than the $COOH\cdots O(OH)C$ bonds. While the O=C acceptors of squaric acid are largely occupied by O-H donors from H_2SQ itself, they also form hydrogen bonds with four different N^+-H donors and the mean geometry for these bonds is also included in Table 2. Additionally, the O(hydroxy) of H_2SQ accepts hydrogen bonds from water (once, at a $H\cdots A$ distance of 2.18 Å) and from N^+-H donors (twice, at 2.36 and 2.57 Å) and with rather non-linear $\theta(DHA)$ values. It would appear that these bonds to O(hydroxy) are secondary to the much stronger $O-H(H_2SQ)\cdots O=C(sq)$ that define the structural frameworks in all squaric acid structures.

A 20-membered hydrogen-bonded ring motif, graph-set $R_4^4(20)$, is formed by four H₂SQ molecules in both the monoclinic and tetragonal polymorphs of the parent acid, as shown in Fig. 1 [see *e.g.* CSD reference code KECYBU11 (Semmingsen, 1973) and others in the KECYBU family (Semmingsen *et al.*, 1977, 1995; Hollander *et al.*, 1977)]. This motif is preserved in SOCLEC (Kolev *et al.*, 2008) and TURPOL (Mathew *et al.*, 2002), which are both ammonium salts of a co-crystal of H₂SQ with its monoanion (HSQ⁻); the ammonium ion, together with an additional water molecule in SOCLEC, serves to link the almost planar $R_4^4(20)$ rings in these

structures. Other squaric acid structures also contain HSQ⁻ and form dimers that are then linked by hydrogen bonds from N-containing counterions.

4.2. Hydrogen squarate monoanion [HSQ⁻ (VI)]

All of the O-H donors of the 78 independent HSQ⁻ fragments are involved in hydrogen bonding. The largest percentage (90%) form hydrogen bonds to O=C groups of HSQ⁻ ions or occasionally to O=C acceptors of H₂SQ or SQ²⁻ where they are also present in the structure. These 70 hydrogen bonds span a narrow distance range (1.42–1.62 Å) and are averaged together in Table 2 following removal of five obvious outliers. Two further O-H(HSQ⁻)···O bonds form to an amide O=C acceptor and to O-water. Only six hydrogen bonds are formed to N-acceptors, all to bipyridinium N atoms, for which the mean geometry is also shown in Table 2.

The C=O acceptors of HSQ- are topologically and chemically different: O1 and O3 are vicinal to the OH substituent and are topologically equivalent while O2, diagonally opposite to the OH substituent, is unique. As noted by Bertolasi et al. (2001), O1 and O3 are both able to carry the negative charge in Kekulé resonance forms of HSQ⁻, while this is not possible for O2. This factor is reflected in the CSD searches, where all 78 fragments form hydrogen bonds through one of the topologically equivalent O1 or O3 acceptors, while only 47 (60%) form hydrogen bonds using the unique O2 acceptor. However, these differences are not clearly reflected in the observed hydrogen-bond distances. The O1/O3 acceptors form 71 hydrogen bonds to squarate-OH ranging from 1.45–1.65 Å, with a mean d(HA) of 1.54(5,71) Å (in the nomenclature of Table 1). There are only seven hydrogen bonds involving squarate-OH donors and O2 (HSQ⁻) acceptors. Their range (1.54–1.63 Å) lies within the O1/O3 acceptor range and average to 1.58(3,7) Å. Thus, the three C=O acceptors of HSQ⁻ are treated as equivalent in generating the statistical data in Table 2.



Figure 1

The $R_4^4(20)$ hydrogen-bonded ring motif observed in parent squaric acid (*e.g.* the monoclinic KECYBU11: Semmingsen, 1973) and in other polymorphs.

A histogram of general $O-H \cdots O = C$ (HSQ⁻) hydrogen bonds is shown in Fig. 2. The distribution is bimodal, with the larger peak at shorter d(HA) (1.45–1.65 Å) arising from the $O-H(HSQ^{-})\cdots O=C(HSQ^{-})$ hydrogen bonds, together with a few $O-H(H_2SQ)\cdots O=C(HSQ^-)$ of very similar length, as discussed above. The mean $H \cdot \cdot \cdot O$ distance in these bonds is 1.55 (5) Å. This value is almost identical to the averages given in Table 2 for squaric acid O-H groups [O- $H(H_2SQ) \cdots O = C(sq)$ and for the unstrained comparator group $O-H(COOH) \cdots O = C(COO^{-})$. The second (and smaller) peak in Fig. 2 (bonds longer than 1.70 Å) arises from $O-H(water) \cdots O = C(HSQ^{-})$ hydrogen bonds. This peak has a long tail as reflected in the $H \cdot \cdot \cdot O$ distance range shown in Table 2, but there is no good chemical or statistical reason to exclude these longer bonds from the overall average $H \cdots O$ distance of 1.89 (17) Å. This value is comparable to the mean value for $O-H(water) \cdots O = C(COO^{-})$ hydrogen bonds of 1.84 (9) Å also given for comparison in Table 2.

In 95% of HSQ⁻ structures the counterion contains a protonated nitrogen (N⁺-H) donor; in addition 21 of these structures (30%) also contain amino-type N⁰-H donors (three-coordinate N with zero charge). Hence there is significant N-H···O=C(HSQ⁻) hydrogen bonding. These bonds form a broad overall distribution from 1.50 Å to around 2.40 Å, but inspection shows that those bonds involving N⁺(aromatic)-H donors occur at the shorter end of the distribution. The remainder of the distribution has been subdivided into bonds involving N⁺(non-aromatic)-H and amino-type N⁰-H donors (as defined above). The geometrical data provided in Table 2 suggests that the N⁺(aromatic)-H···O=C(HSQ⁻) bonds are stronger than those involving the other N-H donor types, which have comparable mean



Distances d(HA) (Å) for O-H(any)···O=C (HSQ⁻) hydrogen bonds showing the bimodal distribution arising from the shorter O-H(HSQ⁻)···O=C(HSQ⁻) bonds and the slightly longer O-H(water)···O=C(HSQ⁻) bonds (see text and Table 1).

d(HA) values. This trend of hydrogen-bond distances agrees well with comparison data (Table 2) generated for hydrogen bonds formed to COO⁻ by these three N-H donor types.

The hydroxy O atoms of HSQ⁻ also act as acceptors in a few structures, almost exclusively with N-H donors: only one O-H···O(hydroxy) hydrogen bond exists in structures with ordered O-H H atoms. This involves an O(water)-H donor at d(HA) = 2.21 Å. The nine N-H···O-H(HSQ⁻) bonds involve both N⁺-H and uncharged amino-type (N⁰-H) donors having a d(HA) range from 2.03 to 2.70 Å, and with $\theta(DHA)$ deviating quite significantly from linearity.

Almost half (47%) of the HSQ⁻ structures contain a dimer synthon (Desiraju, 1995). These dimers are almost always linked into chains or other extended structures via N-H···O hydrogen bonds from counterions, as in BOLFUD (Bock et al., 1998; Fig. 3a) where the counterion is pyrid-2-yl(2'-pyridinium)amine. As might be expected by analogy with the carboxylic acids, the other principal arrangement adopted by HSQ^{-} is the *catena* synthon (13/62 = 21%). Typical *catena* structures form in TIWWUR (Karle et al., 1996) with imidazolium counterions (Fig. 3b) and in LUVTOL (Mattes et al., 2003) with pyrimidinium counterions (Fig. 3c). All of these synthons use the C-O-H donor of HSQ⁻ and the dimers always use one of the topologically equivalent O1/O3 acceptor atoms (see above). The chains, though, can form using either an O1/O3 acceptor as in TIWWUR (Fig. 3b), or the topologically unique O2 acceptor (IV) as in LUVTOL (Fig. 3c). In fact, there are eight examples of chain formation via an O1/O3 acceptor and five examples of the use of O2. This factor contributes to the lower overall use of the O2 acceptor as discussed above. In a few structures that involve HSO⁻ cocrystallized with either H₂SQ or SQ²⁻ the $R_4^4(20)$ rings that are commonly found in H₂SQ structures (see above) are also observed.

4.3. Squarate dianion [SQ²⁻, (II)]

The SQ²⁻ dianion with four equivalent C=O acceptors relies on other co-crystallized components to provide Hdonors. Water molecules and molecules containing N⁺-H and uncharged amino-type (N⁰-H) donors commonly occur so that all SQ²⁻ are able to form hydrogen bonds. Rather few of these hydrogen bonds involve C-OH donors, with just three examples arising from co-crystallized examples of the parent acid, H_2SQ . Their d(HA) distances are closely comparable to other C–O–H(sq)···O=C(sq) distances; d(HA) values for $C-O-H \cdots O = C(SQ^{2-})$ where C-O-H is 'non-squarate' are slightly but significantly longer. The largest distribution of $O-H \cdots O = C(SO^{2-})$ bonds arises from O-H (water) donors where the hydrogen-bond geometry (Table 2) is highly comparable to that occurring in O-H(water)- $\cdots O = C(HSQ^{-})$ and in $O - H(water) \cdots O = C(COO^{-})$ systems. Hydrogen bonds from N⁺-H and uncharged aminotype $(N^0-H; Table 2)$ have again been subdivided as for the monoanion (HSQ⁻) and for the acyclic comparator COO⁻, and with similar overall results.

The most obvious feature of the packing of the aromatic SQ^{2-} dianions is the occurrence of stacked rings in 18 of the 46 structures. The stacking may be characterized by d_1 , the perpendicular distance between the ring planes, and d_2 , the distance between ring centroids, from which the offset from a







Dimer and *catena* synthons in the crystal structures of HSQ^- compounds: (*a*) the HSQ^- dimer synthon in BOLFUD (Bock *et al.*, 1998) where the counterion is pyrid-2-yl(2'-pyridinium)amine; (*b*) the HSQ^- *catena* synthon in TIWWUR (Karle *et al.*, 1996) where the counterion is imidazolium; (*c*) the HSQ^- *catena* synthon in LUVTOL (Mattes *et al.*, 2003) where the counterion is pyrimidinium.

(*c*)



(a)



Figure 4

Ring stacking in SQ²⁻ structures: (*a*) potassium diketocyclobutenediolate monohydrate (KKCBUO: Macintyre & Werkema, 1964) and (*b*) 3,3bis(imidazolium-2-yl)propionic acid squarate monohydrate (NEHKUH: Akhriff *et al.*, 2006).



Figure 5

Scatterplot of the inter-centroid distance (d_2) and the offset from perfect centroid overlay (d_3) in the 18 SQ²⁻ structures which exhibit ring stacking.

Propensities for single and multiple hydrogen-bond formation by the donor and acceptor O atoms of squaric acid (H₂SQ) and its anions (HSQ⁻ and SQ^{2^{-}}).

These data have been compiled by analysis of the November 2012 release of the CSD but using the structural acceptance criteria in §2. N_s is the number of structures exhibiting the structural feature described and P is the corresponding propensity. All hydrogen bonds considered involve O or N as an acceptor or donor.

	$N_{ m s}$	P (%)
H ₂ SQ (14 structures)		
At least one O-H donor used	14	100
Both O-H donors used	14	100
At least one C=O acceptor used	11	79
Both C=O acceptors used	9	64
HSQ ⁻ (70 structures)		
O-H donor used	70	100
C=O1 or C=O3 acceptor used	69	98
C=O2 acceptor used	41	59
Both C=O1 and C=O3 acceptors used	57	81
Only C=O1 or C=O3 used	9	13
Only C=O2 used	0	0
C=O3 or C=O3 and C=O2 used	41	49
C=O3 and C=O3 both used but not C=O2	19	27
SQ^{2-} (44 structures)		
C=O1 used (<i>i.e.</i> any C=O)	44	100
C=O1 and C=O2 used	41	93
C=O1 and C=O3 used	43	98
C=O1, C=O2 and C=O3 used	40	91
All four C=O acceptors used	35	80
Exactly three C=O acceptors used	5	11
Exactly two C=O acceptors used	4	9
Exactly 1 C=O acceptor used	0	0

perfect overlay of ring centroids, d_3 , can readily be calculated. The simplest example is KKCBUO (Macintyre & Werkema, 1964): potassium·SQ²⁻·H₂O illustrated in Fig. 4(*a*). Here, the SQ^{2-} stack is stabilized by $O(water) - H \cdots O = C(SQ^{2-})$ hydrogen bonds and there is almost perfect centroid overlay: $d_1 = 3.27$ Å, $d_2 = 3.30$ Å and $d_3 = 0.42$ Å. However, in this system the stacked rings are rotated with respect to each other by exactly 45°. Apart from SADREW (Ivanova & Spiteller, 2010), which has a ring rotation of 19° , all other systems have a stacked ring rotation of exactly 0° . A more complex structural example is provided by NEHKUH (Akhriff et al., 2006): 3,3bis(imidazolium-2-yl)propionic acid squarate monohydrate, where the SQ²⁻ stack is stabilized by hydrogen bonds from O(water)-H and N(imidazolium)-H, and is characterized by $d_1 = 3.17$ Å, $d_2 = 3.74$ Å and $d_3 = 1.98$ Å. The scatterplot of Fig. 5 shows the extent of the inter-centroid distance (d_2) and the offset from perfect centroid overlay (d_3) in the 18 SQ²⁻ structures which exhibit ring stacking.

4.4. Hydrogen-bond propensities

The analysis is extended in Table 3, which records the propensities for hydrogen-bond formation for various individual donor and acceptor O atoms and their combinations. Table 3 confirms that the O–H donors in H_2SQ and HSQ^- are highly potent and donate hydrogen bonds in 100% of cases, but the C=O acceptors in H_2SQ are slightly less potent

than those in HSQ⁻ and SQ²⁻ where propensities are 100% or close to it. For HSQ⁻, however, there is a clear decrease in the overall hydrogen-bond propensity of the unique C=O2 acceptor to 59%, and hydrogen bonds never form alone to this acceptor. These observations reflect the resonance effects referred to earlier. The SQ²⁻ dianion is notable for the multiple use of its C=O acceptors, with 80% of structures using all four acceptors in hydrogen-bond formation.

5. IsoStar representations of the hydrogen-bond landscapes

While insufficient data are available to derive useful plots using IsoGen for parent squaric acid (V), it has been possible to generate hydrogen-bond landscapes for both HSQ⁻ (VI) and SQ^{2-} (II). Fig. 6(*a*) shows the contoured distribution of H atoms from N-H and O-H donors around HSQ⁻. The peaks show strong hydrogen-bond density approaching the terminal O-acceptors along the lone-pair directions. It is visually clear also that the density of hydrogen bonds around the O2 atom (diagonally opposite the -OH ring-substituent) is lower than that around O1 and O3. Fig. 6(b) shows a similar contoured distribution of acceptor O atoms (defined as terminal O atoms connected to C via a single, double or delocalized double bond) around the OH donor of HSO⁻. Finally, Fig. 6(c) shows the distribution of N-H and O-H donors around the four equivalent O acceptors of SQ²⁻. The distribution has been symmetrized automatically within the IsoGen software and, again, the lone pair directionality of the N-H or O-H approach to acceptor-O is clearly displayed. We stress that the plots of Fig. 6 are selected two-dimensional static images: once generated by IsoGen these plots are fully interactive in terms of content, rotation and presentation. The plots in Fig. 6 do, however, show the importance of the IsoStar methodology in providing a rapid visual overview of information about nonbonded contacts that is vital in drug discovery and many other fields, and both HSQ⁻ and SQ²⁻ are now included in IsoStar as additional central groups from November 2012.

6. DFT-D and IMPT results

Initial models of the molecular structures of methanol, acetone, HSQ⁻, SQ²⁻ and the three isomers of H₂SQ [ZZ (VII), EZ (VIII), EE (IX)], were taken from X-ray crystal structures in the CSD. Isolated monomers were then fully optimized using the B97-D/cc-pVTZ model with GAUS-SIAN09 (Frisch et al., 2009). The basis-set superposition error correction was not applied, as recommended for the B97-D functional (Grimme, 2006). The relative energies of the H₂SQ isomers were found to be (in kJ mol⁻¹): ZZ (global minimum) = 0.0; EZ = 10.5, EE = 35.3, in good agreement with other published results (see e.g. Lunelli et al., 1996; Zhou et al., 2000; Spassova et al., 2000). Dimer geometries were generated from the gas-phase optimized monomers. Dimers were constructed keeping the interacting molecules (the EZ isomer of H_2SQ , HSQ^{-} or SQ^{2-} and methanol or acetone) coplanar and with θ (DHA) and φ (HAR) at their optimal values of 180 and 120°,

respectively. These dimer geometries were then allowed to fully optimize in the gas phase at the same level of theory. Interaction energies (E_{int}) for each AB dimer were calculated



(a)





Figure 6

Contoured IsoStar plots of (a) the distribution of N-H and O-H donors around the terminal-O acceptors of HSQ⁻, (b) the distribution of C=O acceptors around the O-H donor of HSQ⁻ and (c) the symmetrized distribution of N-H and O-H donors around the terminal-O acceptors of SQ²⁻.

Table 4

DFT-D energies $(E_{int}, kJ \text{ mol}^{-1})$ of optimized hydrogen-bonded dimers formed between the *EZ* isomer of H₂SQ, HSQ⁻ or SQ²⁻ (component *A*) and methanol or acetone (component *B*).

Data for the H₂SQ:H₂SQ cyclic dimer (X) are also included. Single-point IMPT energies (kJ mol⁻¹) for hydrogen bonds involving CH₃COO⁻, acetone and methanol (no values are available for CH₃COOH) are taken from IsoStar (Bruno *et al.*, 1997) and values for urea are taken from Wood *et al.* (2008); these data are included for comparison purposes. Hydrogen-bond distances [H to acceptor, d(HA)] are in Å.

Component A	Component B	$E_{\rm int}$	$d(\mathrm{H}A)$
H_2SQ (<i>E</i> hydroxy-H)	Acetone –C=O	-90	1.66
H_2SQ (Z hydroxy-H)	Acetone -C=O	-77	1.60
HSQ ⁻ (hydroxy-H)	Acetone –C=O	-71	1.75
H ₂ SQ (carbonyl-O)	Methanol –OH	-59	2.07
HSQ ⁻ (carbonyl-O1,O3)	Methanol – OH	-66	1.77
HSQ ⁻ (carbonyl-O2)	Methanol -OH	-61	1.83
SQ ²⁻ (carbonyl-O)	Methanol -OH	-140	1.59
H ₂ SQ	H_2SQ	-124	1.57
CH ₃ COO ⁻ (carbonyl-O)	Methanol –OH	-75	1.71†
CH ₃ COO ⁻ (carbonyl-O)	Water – OH	-72	1.92†
Acetone (carbonyl-O)	Methanol -OH	-25	1.94†
Urea (carbonyl-O)	Methanol -OH	-33	1.90^{+}

† IMPT values: dimer not optimized, d(HA) indicates the fixed point for the IMPT energy calculation.

as the difference between the optimized dimer energy (E_{AB}) and the energies of the monomers $(E_A \text{ and } E_B)$ using $E_{\text{int}} = E_{AB} - E_A - E_B$.

Interaction energies and optimized hydrogen-bond distances for a variety of dimers involving SQ species and acetone or methanol are collected in Table 4, which also includes similar data for the cyclic H₂SQ:H₂SQ dimer (X). Some comparison single-point IMPT hydrogen-bond energy data for CH₃COO⁻, acetone and methanol taken from IsoStar (Bruno *et al.*, 1997), and for hydrogen bonds from methanol-OH to urea-C=O (Wood *et al.*, 2008), are also included in Table 4. Obviously one cannot view the optimized DFT-D dimer energies as arising solely from their respective C=O···H-O bonds, but this bond is likely to make a major contribution to the attractive energy. Further, the DFT-D dimer energies cannot be compared with the single-point IMPT energies in a fully quantitative manner.

Despite these constraints it is clear that the C=O···H-O bonds involving SQ species are very strong. Thus, the OH donors in H₂SQ and HSQ⁻ form bonds to acetone with energies that are, even on a qualitative basis, much stronger than those arising from methanol-OH to the -C=O groups of acetone or urea: the 100% propensities for hydrogen-bond formation by SQ-OH (Table 3) is clearly reflected in the dimer energies of Table 4. Similarly, the bonds formed by SQ-C=O groups are also strong. The DFT-D dimer energies for the SQ-C=O···H-O (methanol) increase just a little in moving from H₂SQ to HSQ⁻, and the dimer energies here are at a level that is comparable with the IMPT energies obtained for COO⁻···H-O (methanol or water) hydrogen bonds. However, there is a much more dramatic increase in E_{int} in moving to the SQ²⁻ dianion, and the DFT-D calculations generate d(HA) values that decrease smoothly from 2.07 Å (H_2SQ) to 1.77–1.83 Å (HSQ^-) and then to the very short 1.59 Å for SQ²⁻. The difference between the E_{int} values for dimers formed through the 'resonance-preferred' O1,O3 of HSQ⁻ and dimers formed through the unique carbonyl (C=O2) is quite small at 5 kJ mol⁻¹, and there is only a very small concomitant elongation in the optimized hydrogen-bond distance, d(HA), from 1.77 to 1.83 Å. While resonance is clearly a factor here, it may be that steric effects also mitigate against the formation of hydrogen bonds to C=O2 and, hence, to its rather low hydrogen-bond propensity of 59% (Table 3). More structural data on HSQ⁻ compounds will be needed for a proper analysis of this issue.

The data for the H₂SQ:H₂SQ cyclic dimer (X) are in good agreement with the other calculations, with E_{int} being about double the value for dimers formed through a single hydrogen-bonded interaction. The optimized d(HA) value of 1.57 Å for this dimer may reflect the increased potency of the H₂SQ-OH donor by comparison with the methanol-OH used in the general calculations.

7. Conclusion

The primary objective of this work was to examine the available data for squaric acid and its anions, H₂SQ, HSQ⁻ and SO^{2-} , with a view to their inclusion as new central groups in IsoStar (Bruno et al., 1997), the knowledge base of intermolecular interactions, and this objective was accomplished in the November 2012 release of IsoStar, for the more populous anion datasets. While the IsoStar maps, exemplified in Fig. 6, define the landscape of nonbonded interactions, particularly their hydrogen-bonded interactions, the extended study has confirmed that SQ compounds are potent donors and acceptors, as defined by their hydrogen-bond geometries in available crystal structures and by the attractive energies calculated for their dimers with acetone and methanol as model acceptors and donors. Hydrogen bonds involving H₂SQ and HSQ⁻ are of similar strengths to those made by carboxylate COO⁻ acceptors, while hydrogen bonds made by the dianion SQ^{2-} are somewhat stronger. The study reinforces the value of SQ compounds as cocrystal formers (see, e.g., Bertolasi et al., 2001; Gilli et al., 2001; Mathew et al., 2002) and, particularly, as isosteric replacements for carboxylic acid and carboxylate functions (Meanwell, 2011; Marson, 2011). In the latter case, it is likely that the anionic species with the strongest hydrogenbonding abilities will predominate under physiological conditions.

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