

## Crystal Structure of Pyrimidine-2-one

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The crystal structure of pyrimidine-2-one has been determined by X-ray crystallographic methods and refined to  $R=0.055$ . The space group is  $P4_12_12$ . The intensities of 518 reflections were measured on an automatic diffractometer using  $MoK\alpha$  radiation. The estimated standard deviation in bond lengths involving non-hydrogen atoms is 0.003–0.004 Å. The structure is compared with those of pyrimidine and cytosine.

Pyrimidine-2-one (2-hydroxy-pyrimidine) may be considered the parent substance of the biologically important pyrimidine bases and it would appear to be of considerable interest to know its structure. The structure of the pyrimidines of the nucleic acids,<sup>1-3</sup> as well as that of pyrimidine itself,<sup>4</sup> has been determined by X-ray crystallographic methods.

### STRUCTURE DETERMINATION

A sample of pyrimidine-2-one was kindly supplied by professor S. G. Laland. Crystals were grown by evaporating an ethylacetate solution. Needles (up to 5 cm long) extended along  $c$  were obtained. The space group is  $P4_12_12$  ( $P4_32_12$ ). The unit cell dimensions were measured on a manual diffractometer and found to be  $a=b=8.571\pm 0.003$  Å,  $c=12.406\pm 0.003$  Å. Flotation gave a density of 1.37 g/cm<sup>3</sup>. The calculated density is 1.40 g/cm<sup>3</sup>.

A crystal of dimensions 0.28 × 0.20 × 0.20 mm was used to measure the intensities on a Picker automatic diffractometer using  $MoK\alpha$  radiation ( $\lambda=0.71069$  Å). The  $\omega/2\theta$  scan technique (rate 2°/min) was employed. Out of the 1300 reflections with  $2\theta < 75^\circ$  only 518 had intensities greater than twice the standard deviation. Absorption correction was not applied.

The structure was solved by Patterson and trial-error methods and refined by full matrix least squares to  $R=0.067$ . The weighting scheme was based on standard deviation from counter statistics and 2% fluctuation in diffractometer stability. Secondary extinction correction and further refinement gave a final  $R$ -value of 0.055 ( $R_w=0.034$ ). In Table 1 the observed and calculated structure factors are listed. The atomic parameters were then corrected for thermal effects, assuming the molecule to be rigid.<sup>5</sup> The root mean square

Table 1. Observed and calculated structure factors.

h	k	l	F <sub>o</sub>	F <sub>c</sub>	h	k	l	F <sub>o</sub>	F <sub>c</sub>	h	k	l	F <sub>o</sub>	F <sub>c</sub>
0	0	4	277	279	10	0	0	179	171	8	1	5	32	33
0	0	8	48	50	10	0	1	39	39	8	1	6	56	55
0	0	12	405	407	10	0	11	46	43	8	1	7	45	66
0	0	16	58	58	10	0	12	74	69	8	1	10	36	21
1	0	1	65	62	11	0	4	40	30	8	1	11	38	38
1	0	2	735	735	11	0	5	46	40	8	1	12	59	50
1	0	3	205	204	12	0	0	37	9	8	1	14	56	39
1	0	4	189	193	12	0	6	42	30	8	1	15	47	35
1	0	5	294	298	1	1	0	118	119	9	1	1	112	110
1	0	6	56	91	1	1	1	454	414	9	1	2	90	30
1	0	7	24	92	1	1	2	556	518	9	1	4	39	38
1	0	8	167	167	1	1	3	289	283	9	1	11	81	61
1	0	9	54	55	1	1	4	242	251	10	1	0	31	54
1	0	11	124	120	1	1	5	112	112	10	1	1	48	45
1	0	12	85	77	1	1	6	158	155	10	1	2	50	45
1	0	13	106	103	1	1	7	20	16	10	1	3	34	35
1	0	14	143	142	1	1	8	126	125	10	1	6	54	42
2	0	1	150	169	1	1	9	183	185	8	10	8	41	31
2	0	2	55	33	1	1	10	140	144	10	1	14	50	21
2	0	3	20	19	1	1	11	213	214	11	1	4	49	37
2	0	4	226	219	1	1	12	29	24	11	1	5	39	16
2	0	5	445	453	1	1	13	57	55	11	1	8	42	18
2	0	6	123	126	1	1	14	69	70	11	1	11	50	24
2	0	7	354	368	2	1	0	46	40	2	2	0	683	660
2	0	8	166	187	2	1	0	701	700	2	2	1	150	153
2	0	9	82	81	2	1	1	434	428	2	2	2	284	280
2	0	10	117	116	2	1	2	643	644	2	2	3	350	345
2	0	11	53	58	2	1	3	512	517	2	2	4	162	165
2	0	12	46	48	2	1	4	62	37	2	2	5	85	69
2	0	14	40	37	2	1	6	135	134	2	2	6	17	23
2	0	15	37	34	2	1	7	300	297	2	2	7	53	55
3	0	2	301	296	2	1	8	33	31	2	2	8	56	68
3	0	3	259	255	2	1	9	127	126	2	2	9	29	29
3	0	5	113	113	2	1	10	145	145	2	2	10	27	21
3	0	6	162	166	2	1	11	100	101	2	2	12	97	90
3	0	7	110	107	2	1	12	119	118	2	2	13	49	50
3	0	8	33	31	2	1	14	55	61	2	2	14	49	49
3	0	9	26	28	2	1	15	65	62	2	2	15	70	66
3	0	10	25	23	2	1	16	54	54	2	2	16	57	48
3	0	11	28	25	3	1	1	252	251	3	2	1	48	47
3	0	13	43	41	3	1	2	130	126	3	2	2	125	124
3	0	14	49	31	3	1	3	295	294	3	2	3	156	152
3	0	15	59	45	3	1	4	185	181	3	2	4	23	31
4	0	1	138	139	3	1	5	244	242	3	2	5	202	203
4	0	2	103	99	3	1	6	135	137	3	2	6	97	97
4	0	3	58	56	3	1	7	105	104	3	2	6	92	92
4	0	4	182	179	3	1	8	35	37	3	2	7	107	107
4	0	5	153	153	3	1	9	83	85	3	2	8	186	190
4	0	6	41	45	3	1	10	64	63	3	2	9	86	92
4	0	7	28	24	3	1	11	51	50	3	2	10	132	131
4	0	8	65	64	3	1	14	30	25	3	2	11	58	60
4	0	9	53	50	3	1	15	57	50	3	2	12	37	31
4	0	10	43	43	4	1	2	125	125	3	2	14	41	43
4	0	12	35	35	4	1	3	82	82	4	2	0	80	82
4	0	13	37	33	4	1	4	180	180	4	2	1	155	153
5	0	2	24	25	4	1	5	166	164	4	2	2	95	92
5	0	3	65	65	4	1	6	24	22	4	2	3	156	155
5	0	4	30	30	4	1	7	113	112	4	2	5	95	97
5	0	5	25	27	4	1	8	72	69	4	2	7	28	29
5	0	7	25	28	4	1	9	52	47	4	2	8	135	129
5	0	8	39	42	4	1	10	74	82	4	2	9	24	22
5	0	9	46	38	4	1	10	74	82	4	2	10	40	41
5	0	11	22	17	4	1	11	78	78	4	2	11	38	45
6	0	1	148	145	5	1	1	157	158	4	2	12	53	55
6	0	2	88	86	5	1	2	79	76	4	2	13	55	52
6	0	3	29	29	5	1	3	95	99	4	2	14	41	32
6	0	4	112	112	5	1	5	27	22	4	2	15	48	38
6	0	5	129	128	5	1	6	19	12	5	2	0	411	409
6	0	6	104	105	5	1	7	47	44	5	2	1	67	66
6	0	7	51	55	5	1	8	29	26	5	2	2	102	103
6	0	8	51	60	5	1	9	38	27	5	2	3	213	214
6	0	10	47	54	5	1	12	29	13	5	2	4	123	122
6	0	11	62	72	5	1	13	35	33	5	2	5	42	42
7	0	1	111	110	5	1	14	38	39	5	2	6	23	14
7	0	3	75	80	6	1	1	33	40	5	2	8	25	17
7	0	4	65	65	6	1	2	33	35	5	2	9	56	60
7	0	7	65	62	6	1	3	75	79	5	2	10	25	20
7	0	11	34	39	6	1	4	70	73	5	2	11	49	51
7	0	13	53	45	6	1	5	22	27	5	2	12	83	84
7	0	16	44	25	6	1	7	41	43	6	2	0	22	16
8	0	0	82	81	6	1	8	49	52	6	2	1	112	114
8	0	1	81	81	6	1	9	55	70	6	2	2	70	58
8	0	2	72	68	6	1	10	64	66	6	2	3	155	167
8	0	3	129	126	6	1	11	38	33	6	2	4	137	140
8	0	4	32	35	7	1	0	53	52	6	2	5	72	77
8	0	5	66	66	7	1	1	39	34	6	2	6	61	39
8	0	6	34	28	7	1	3	57	59	6	2	7	27	29
8	0	7	67	66	7	1	4	36	35	6	2	8	82	82
8	0	8	62	50	7	1	5	56	55	6	2	9	48	48
8	0	9	37	38	7	1	6	59	63	6	2	10	30	26
8	0	10	51	51	7	1	9	65	65	6	2	15	40	40
9	0	2	53	44	7	1	10	42	45	7	2	1	50	54
9	0	3	44	36	7	1	15	36	40	7	2	2	75	73
9	0	9	36	21	7	1	0	182	182	7	2	3	93	97
9	0	11	55	50	8	1	1	121	118	7	2	4	139	138
9	0	12	51	46	8	1	2	105	106	7	2	5	85	88
9	0	13	56	48	8	1	3	100	101	10	3	0	35	25

Table 1. Continued.

h	k	l	F <sub>o</sub>	F <sub>c</sub>	h	k	l	F <sub>o</sub>	F <sub>c</sub>	h	k	l	F <sub>o</sub>	F <sub>c</sub>	h	k	l	F <sub>o</sub>	F <sub>c</sub>
10	3	4	39	25	6	4	5	100	99	5	5	9	35	30	6	6	7	103	104
4	4	0	229	226	6	4	6	37	31	6	5	0	91	92	6	6	9	60	57
4	4	1	24	26	6	4	7	144	146	6	5	1	74	77	6	6	12	46	43
4	4	2	77	76	6	4	8	65	66	6	5	2	37	37	7	6	0	36	35
4	4	3	113	116	6	4	9	57	57	6	5	3	98	97	7	6	1	30	23
4	4	4	93	92	6	4	10	34	15	6	5	4	103	105	7	6	2	35	37
4	4	5	95	97	6	4	11	40	40	6	5	5	35	28	7	6	3	31	14
4	4	6	22	19	6	4	12	38	46	6	5	6	62	55	7	6	4	39	37
4	4	7	244	247	7	4	0	55	55	6	5	7	49	38	7	6	5	35	28
4	4	8	42	46	7	4	1	81	89	6	5	8	12	38	7	6	6	36	20
4	4	9	80	78	7	4	2	81	83	6	5	9	13	39	7	6	7	37	34
4	4	10	38	40	7	4	3	74	78	6	5	10	45	28	7	6	8	47	4
4	4	11	30	19	7	4	4	37	37	7	5	1	38	38	8	6	1	35	29
4	4	12	49	40	7	4	5	33	25	7	5	2	53	41	8	6	2	35	34
4	4	17	45	22	7	4	6	32	27	7	5	3	55	37	7	7	0	41	35
5	4	0	49	51	7	4	11	46	35	7	5	4	38	42	7	7	1	39	45
5	4	1	34	32	8	4	0	59	67	7	5	5	55	51	7	7	2	32	45
5	4	2	73	76	8	4	1	32	27	7	5	6	50	45	7	7	3	37	45
5	4	3	44	46	8	4	2	44	43	7	5	7	45	34	7	7	4	32	30
5	4	4	174	179	8	4	3	33	27	7	5	8	55	42	8	7	1	32	17
5	4	5	265	267	8	4	4	28	31	7	5	9	45	44	8	7	2	38	41
5	4	6	191	190	8	4	5	39	31	8	5	0	89	92	8	7	3	35	43
5	4	7	198	199	9	4	0	34	36	8	5	1	30	24	8	7	4	42	41
5	4	8	94	94	10	4	2	37	17	8	5	2	47	49	8	7	5	47	39
5	4	9	84	84	10	4	3	36	11	8	5	3	44	29	10	7	3	37	7
5	4	10	74	72	11	4	1	32	30	8	5	4	49	36	9	8	0	48	28
5	4	12	42	28	5	5	1	58	59	6	6	0	122	128	10	8	1	45	14
6	4	0	125	122	5	5	2	78	77	6	6	1	55	53	10	8	2	39	18
6	4	1	63	63	5	5	3	23	24	6	6	2	52	56	11	8	3	42	6
6	4	2	81	78	5	5	4	25	40	6	6	3	95	96	9	9	1	54	51
6	4	3	69	71	5	5	5	125	125	6	6	4	70	64	9	9	2	45	24
6	4	4	60	63	5	5	6	63	69	6	6	5	97	94					

Table 2. Positional parameters for the atoms. E.s.d.'s in parentheses. The corrections of the parameters for rigid-body libration are also listed.

	<i>x</i>	<i>y</i>	<i>z</i>
O2	-.05917 (19) -105	.34962 (21) 94	.22186 (11) 6
N1	.15123 (25) 35	.23443 (24) 52	.29738 (15) 64
C2	.04015 (28) -62	.24486 (29) 51	.21805 (16) -2
N3	.04465 (24) 62	.14012 (26) -36	.13617 (15) -63
C4	.15697 (36) 20	.03622 (34) -95	.13582 (23) -59
C5	.27314 (37) 102	.02523 (38) -85	.21401 (21) 5
C6	.26601 (31) 108	.12748 (34) -17	.29621 (21) 53
H1	.1500 (26) 3	.3055 (36) 8	.3512 (18) 8
H4	.1556 (29) 1	-.0337 (28) -11	.0715 (22) -7
H5	.3629 (37) 12	.0494 (34) -9	.2101 (23) -1
H6	.3379 (30) 11	.1274 (28) 1	.3587 (20) 7

Table 3. Temperature parameters and estimated standard deviations.

Atom	$B_{11}$ (B)	$B_{22}$	$B_{33}$	$B_{12}$	$B_{13}$	$B_{23}$
O2	.01419 (32)	.01376 (30)	.00543 (13)	.00706 (57)	-.00196 (37)	-.00052 (37)
N1	.01183 (36)	.01207 (36)	.00383 (14)	-.00202 (67)	-.00232 (39)	-.00252 (42)
C2	.00949 (39)	.01170 (41)	.00341 (15)	-.00414 (69)	-.00053 (46)	.00154 (50)
N3	.01389 (40)	.01529 (38)	.00407 (14)	.00431 (66)	-.00232 (41)	-.00310 (44)
C4	.01848 (57)	.01759 (53)	.00522 (19)	.00633(108)	-.00147 (63)	-.00624 (61)
C5	.01608 (57)	.02026 (62)	.00705 (21)	.01235 (97)	-.00262 (67)	-.00579 (67)
C6	.01159 (46)	.01867 (57)	.00621 (22)	.00420 (91)	-.00471 (55)	-.00065 (63)
H1	2.8 (6)					
H4	4.6 (6)					
H5	6.8 (8)					
H6	4.3 (6)					

Table 4. Bond lengths (Å) and angles (°). (a) This investigation, uncorrected values. (b) Estimated standard deviations. (c) This investigation, libration corrected values. (d) Cytosine (uncorrected values).<sup>1</sup> (e) Pyrimidine (uncorrected values).<sup>4</sup>

	(a)	(b)	(c)	(d)	(e)
N1-C2	1.372	0.003	1.384	1.374	1.313
C2-N3	1.356	0.003	1.367	1.364	1.317
N3-C4	1.311	0.003	1.320	1.337	1.332
C4-C5	1.393	0.004	1.403	1.424	1.387
C5-C6	1.346	0.004	1.355	1.342	1.358
C6-N1	1.345	0.003	1.353	1.357	1.343
C2-O2	1.238	0.003	1.244	1.238	
N1-C2-N3	118.3	0.2	118.3	118.1	128.2
C2-N3-C4	118.2	0.2	118.1	119.9	115.1
N3-C4-C5	124.6	0.3	124.7	122.2	122.5
C4-C5-C6	116.8	0.3	116.9	117.3	116.3
C5-C6-N1	119.0	0.3	119.1	120.1	122.7
C6-N1-C2	123.0	0.3	123.0	122.7	115.2
N1-C2-O2	119.8	0.2	119.8	119.8	
N3-C2-O2	121.9	0.2	121.9	122.2	
N1-H1	0.903	0.024	C2-N1-H1	118.5	1.4
C4-H4	0.998	0.026	C6-N1-H1	118.4	1.4
C5-H5	1.002	0.032	N3-C4-H4	113.7	1.4
C6-H6	0.990	0.026	C5-C4-H4	121.6	1.4
			C4-C5-H5	123.9	1.7
			C6-C5-H5	119.2	1.7
			C5-C6-H6	124.4	1.4
			C5-C6-H6	116.6	1.4

## Bond lengths and angles involving hydrogen bonds.

N1-H1...O2	2.796	0.003	C2-O2...H1	113.1	0.6
H1...O2	1.894	0.025	C2-O2...N1	113.8	0.2
C6-H6...O2	3.250	0.003	C2-O2...H6	111.3	0.6
H6...O2	2.289	0.026	C2-O2...C6	113.2	0.2
C2-N1...O2	120.8	0.2	N1...O2...C6	113.2	0.1
C6-N1...O2	116.2	0.2	N1...O2...H6	117.9	0.6
N1-C6...O2	106.6	0.2	H1...O2...C6	114.7	0.6
C5-C6...O2	133.6	0.2	H1...O2...H6	119.3	0.8



spond in general to a redistribution of bonding electrons in favour of the pairing scheme



It is also of interest to note the changes which occur when an amino group is introduced at C4 in pyrimidine-2-one to give cytosine, the structure of which is well known.<sup>1</sup> Significant changes take place at C4, the bonds C4-N3

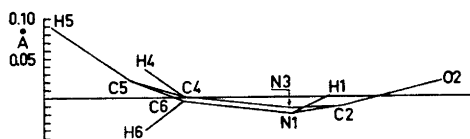
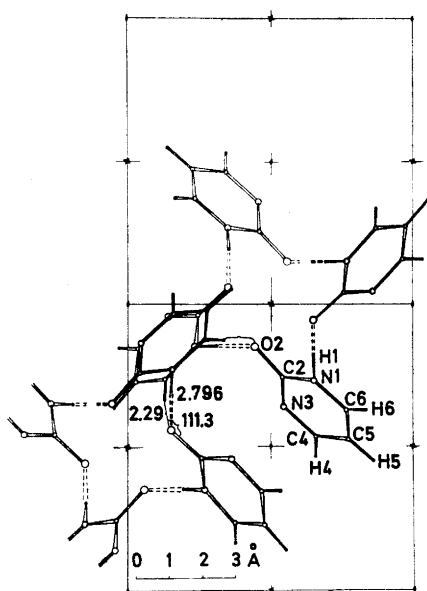


Fig. 2. The *c* projection of the structure. Fig. 3. Deviations from the least squares plane.

and C4-C5 becoming longer by about 0.02 Å and the ring angle at C4 correspondingly smaller (by 2.4°) when the amino group is introduced. The rest of the molecule is left practically unchanged, apart from small adjustments of the ring angles at N3 and C5.

Deviations from the least squares plane through all non-hydrogen atoms are shown in Fig. 3. Although the molecule is essentially planar, the largest displacements from the plane (0.02 Å) are probably significant. The molecule has a slightly curved, boat-shaped structure, as has been found also in a number of crystal structures of other pyrimidines, for instance cytosine monohydrate.<sup>9</sup> The least squares plane forms an angle of 58.7° with (001) and the distance between neighbouring planes is 3.42 Å.

The arrangement of the molecules in the crystal is shown in Fig. 2. They are linked together by hydrogen bonds  $N1-H1\cdots O2$  of length 2.796 Å in spirals up the four-fold screw axes. The bond is nearly linear and forms an angle of  $114^\circ$  with  $C2-O2$ . Neighbouring atoms  $O2$  and  $N1$ , to which the molecule is linked by hydrogen bonds, lie close to the molecular plane (to within 0.05 Å). The distance between  $O2$  and  $H6$  in a neighbouring molecule is also rather short, 2.29 Å; between  $O2$  and  $C6$  3.25 Å. This contact  $C6-H6\cdots O2$  has the stereochemistry of a hydrogen bond, the arrangement being nearly linear, and the angles  $C2-O2\cdots H6$  and  $H1\cdots O2\cdots H6$  having the values of  $111.3^\circ$  and  $119.3^\circ$ , respectively.

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