



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 07:45 am GMT

PDB ID : 5K0N  
Title : Crystal Structure of COMT in complex with 4-[5-[1-(4-methoxyphenyl)cyclopropyl]-1H-pyrazol-3-yl]-1,3-dimethylpyrazole  
Authors : Ehler, A.; Rodriguez-Sarmiento, R.M.  
Deposited on : 2016-05-17  
Resolution : 1.99 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

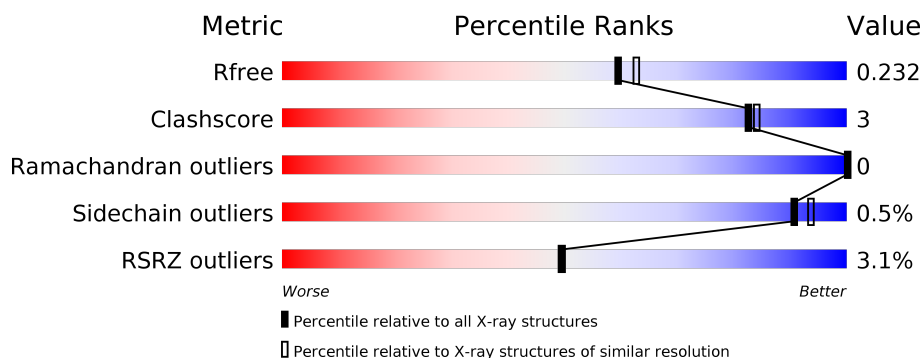
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.99 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	220	<div> <div>4%</div> <div>89%</div> <div>11%</div> </div>
1	B	220	<div> <div>3%</div> <div>95%</div> <div>5%</div> </div>
1	C	220	<div> <div>3%</div> <div>93%</div> <div>7%</div> </div>
1	D	220	<div> <div>2%</div> <div>90%</div> <div>10%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EDO	A	301	-	-	-	X
2	EDO	D	301	-	-	-	X
3	MG	A	302	-	-	-	X
6	K	D	306	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7717 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Catechol O-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	3	0
			1735	1102	287	334	12			
1	B	220	Total	C	N	O	S	0	1	0
			1724	1093	286	333	12			
1	C	220	Total	C	N	O	S	0	1	0
			1725	1094	287	332	12			
1	D	220	Total	C	N	O	S	0	2	0
			1730	1097	286	335	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	91	ILE	MET	engineered mutation	UNP P22734
A	95	CYS	TYR	engineered mutation	UNP P22734
B	91	ILE	MET	engineered mutation	UNP P22734
B	95	CYS	TYR	engineered mutation	UNP P22734
C	91	ILE	MET	engineered mutation	UNP P22734
C	95	CYS	TYR	engineered mutation	UNP P22734
D	91	ILE	MET	engineered mutation	UNP P22734
D	95	CYS	TYR	engineered mutation	UNP P22734

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).

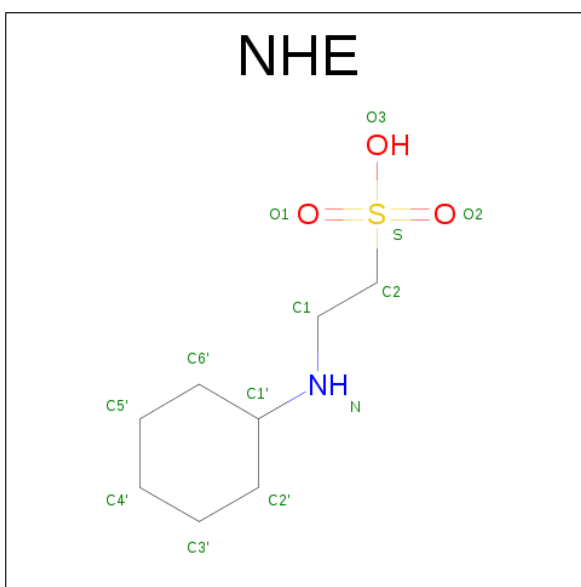


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

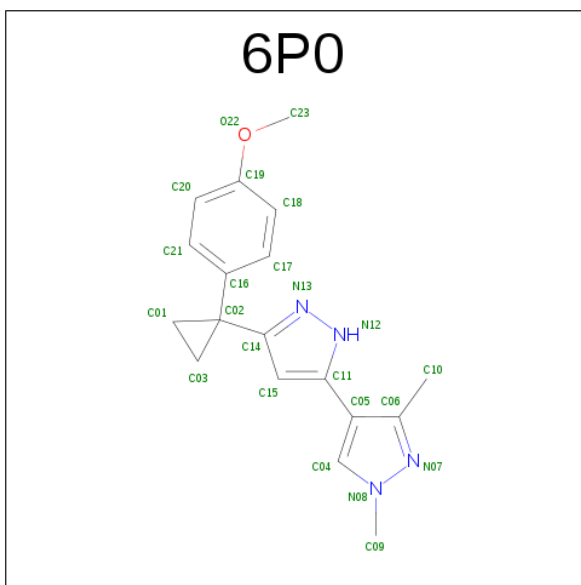
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (three-letter code: NHE) (formula: C<sub>8</sub>H<sub>17</sub>NO<sub>3</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
4	B	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
4	C	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
4	C	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
4	D	1	Total	C	N	O	S	0	0
			13	8	1	3	1		
4	D	1	Total	C	N	O	S	0	0
			13	8	1	3	1		

- Molecule 5 is 5-[1-(4-methoxyphenyl)cyclopropyl]-1',3'-dimethyl-1'H,2H-3,4'-bipyrazole (three-letter code: 6P0) (formula: C<sub>18</sub>H<sub>20</sub>N<sub>4</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			23	18	4	1		
5	B	1	Total	C	N	O	0	0
			23	18	4	1		
5	C	1	Total	C	N	O	0	0
			23	18	4	1		
5	D	1	Total	C	N	O	0	0
			23	18	4	1		

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	K	0	0
			1	1		
6	A	1	Total	K	0	0
			1	1		
6	D	1	Total	K	0	0
			1	1		
6	C	1	Total	K	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	134	Total	O	0	0
			134	134		

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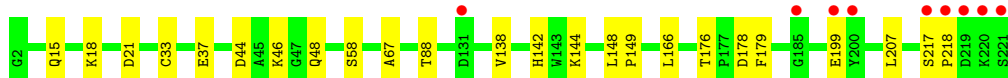
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	147	Total 147	O 147	0	0
7	C	165	Total 165	O 165	0	0
7	D	171	Total 171	O 171	0	0



### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

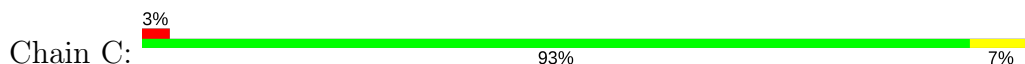
- Molecule 1: Catechol O-methyltransferase



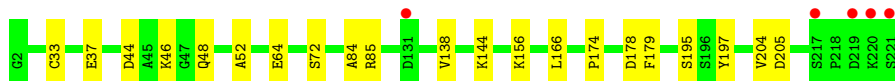
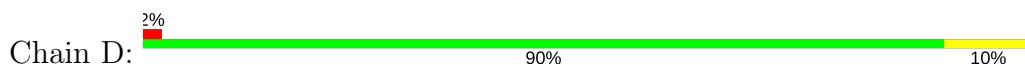
- Molecule 1: Catechol O-methyltransferase



- Molecule 1: Catechol O-methyltransferase



- Molecule 1: Catechol O-methyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.02Å 69.89Å 104.10Å 90.00° 94.09° 90.00°	Depositor
Resolution (Å)	45.42 – 1.99 45.42 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.42-1.99) 89.9 (45.42-1.99)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.10 (at 1.98Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.184 , 0.233 0.185 , 0.232	Depositor DCC
$R_{free}$ test set	3887 reflections (5.15%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.0	Xtrriage
Anisotropy	0.133	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 44.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7717	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.99 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.5231e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NHE, MG, K, 6P0, EDO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.38	0/1776	0.52	0/2407
1	B	0.39	0/1759	0.53	0/2384
1	C	0.40	0/1760	0.52	0/2385
1	D	0.40	0/1768	0.54	0/2396
All	All	0.39	0/7063	0.53	0/9572

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1735	0	1745	14	0
1	B	1724	0	1726	6	0
1	C	1725	0	1730	9	0
1	D	1730	0	1732	14	0
2	A	4	0	6	0	0
2	D	4	0	6	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	1	0	0	0	0
4	A	13	0	17	0	0
4	B	13	0	17	0	0
4	C	26	0	34	0	0
4	D	26	0	34	1	0
5	A	23	0	0	0	0
5	B	23	0	0	0	0
5	C	23	0	0	0	0
5	D	23	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	134	0	0	2	0
7	B	147	0	0	1	0
7	C	165	0	0	2	0
7	D	171	0	0	0	0
All	All	7717	0	7047	41	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (41) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:LYS:HE2	1:B:21:ASP:HB2	1.61	0.82
1:A:46:LYS:HG3	1:A:207:LEU:HD11	1.71	0.72
1:D:46:LYS:NZ	1:D:205:ASP:OD2	2.23	0.70
1:C:169:ASP:OD2	7:C:401:HOH:O	2.16	0.60
1:A:15:GLN:NE2	7:A:403:HOH:O	2.36	0.57
1:A:138:VAL:HB	1:A:166:LEU:HD22	1.88	0.55
1:D:138:VAL:HB	1:D:166:LEU:HD22	1.89	0.54
1:C:138:VAL:HB	1:C:166:LEU:HD22	1.90	0.52
1:A:44:ASP:O	1:A:48:GLN:HG2	2.12	0.49
1:A:148:LEU:HB3	1:A:149:PRO:HD3	1.94	0.49
1:A:144:LYS:HB3	1:A:176:THR:HG22	1.95	0.49
1:D:174:PRO:HD3	4:D:303:NHE:HC11	1.95	0.48
1:B:138:VAL:HB	1:B:166:LEU:HD22	1.94	0.48
1:C:201:MET:HG3	1:C:203:VAL:HG12	1.96	0.48
1:C:49:ILE:HG12	1:D:195:SER:HB2	1.97	0.47
1:D:144:LYS:HG3	1:D:174:PRO:HG2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:84:ALA:O	1:D:85:ARG:HD3	2.15	0.46
1:B:67:ALA:HB2	1:B:88:THR:OG1	2.15	0.46
1:B:84:ALA:O	1:B:85:ARG:HD3	2.15	0.46
1:D:156:LYS:HE2	1:D:156:LYS:HB3	1.74	0.45
1:D:44:ASP:O	1:D:48:GLN:HG2	2.16	0.45
1:A:18:LYS:HG2	1:A:21:ASP:HB3	1.99	0.45
1:D:33:CYS:HA	1:D:37:GLU:O	2.17	0.45
1:C:220:LYS:O	1:C:221:SER:HB2	2.17	0.45
1:A:33:CYS:HA	1:A:37:GLU:O	2.18	0.44
1:C:147:TYR:CD2	1:C:176:THR:HG21	2.53	0.43
1:A:67:ALA:HB2	1:A:88:THR:OG1	2.17	0.43
1:C:197:TYR:CD2	1:D:52:ALA:HB1	2.53	0.43
1:D:197:TYR:CZ	1:D:204:VAL:HG22	2.54	0.43
1:A:58:SER:O	7:A:401:HOH:O	2.21	0.43
1:B:33:CYS:HA	1:B:37:GLU:O	2.19	0.43
1:C:11:ARG:NH2	7:C:409:HOH:O	2.45	0.43
1:A:178:ASP:OD1	1:A:179:PHE:N	2.52	0.42
1:A:18:LYS:HG2	1:A:21:ASP:CB	2.49	0.42
1:A:199:GLU:HG2	1:A:199:GLU:H	1.60	0.41
1:C:144:LYS:HG3	1:C:174:PRO:HG2	2.01	0.41
1:D:64:GLU:OE2	1:D:72:SER:HB2	2.20	0.41
1:D:44:ASP:OD2	1:D:48:GLN:NE2	2.54	0.41
1:A:217:SER:HA	1:A:218:PRO:HD3	1.95	0.40
1:B:45:ALA:HB3	7:B:510:HOH:O	2.21	0.40
1:D:178:ASP:OD1	1:D:179:PHE:N	2.55	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	221/220 (100%)	214 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	219/220 (100%)	210 (96%)	9 (4%)	0	100	100
1	C	219/220 (100%)	212 (97%)	7 (3%)	0	100	100
1	D	220/220 (100%)	212 (96%)	8 (4%)	0	100	100
All	All	879/880 (100%)	848 (96%)	31 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	192/189 (102%)	191 (100%)	1 (0%)	91	93
1	B	190/189 (100%)	189 (100%)	1 (0%)	91	93
1	C	190/189 (100%)	187 (98%)	3 (2%)	68	72
1	D	191/189 (101%)	191 (100%)	0	100	100
All	All	763/756 (101%)	758 (99%)	5 (1%)	91	90

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	142	HIS
1	B	142	HIS
1	C	100[A]	GLN
1	C	100[B]	GLN
1	C	142	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 8 are monoatomic - leaving 12 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	EDO	A	301	-	3,3,3	0.51	0	2,2,2	0.33	0
4	NHE	A	303	-	13,13,13	1.04	1 (7%)	15,17,17	2.08	3 (20%)
5	6P0	A	304	-	24,26,26	2.09	7 (29%)	25,39,39	2.59	7 (28%)
4	NHE	B	302	-	13,13,13	1.06	1 (7%)	15,17,17	2.11	3 (20%)
5	6P0	B	303	-	24,26,26	2.16	7 (29%)	25,39,39	2.44	8 (32%)
4	NHE	C	302	3	13,13,13	1.24	2 (15%)	15,17,17	2.45	4 (26%)
4	NHE	C	303	-	13,13,13	0.99	0	15,17,17	2.77	3 (20%)
5	6P0	C	304	-	24,26,26	2.08	6 (25%)	25,39,39	2.32	7 (28%)
2	EDO	D	301	-	3,3,3	0.50	0	2,2,2	0.42	0
4	NHE	D	303	3	13,13,13	1.14	2 (15%)	15,17,17	2.80	4 (26%)
4	NHE	D	304	-	13,13,13	0.98	0	15,17,17	2.04	3 (20%)
5	6P0	D	305	-	24,26,26	2.07	6 (25%)	25,39,39	2.50	9 (36%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical

component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	A	301	-	-	0/1/1/1	0/0/0/0
4	NHE	A	303	-	-	0/7/15/15	0/1/1/1
5	6P0	A	304	-	-	0/8/22/22	0/3/4/4
4	NHE	B	302	-	-	0/7/15/15	0/1/1/1
5	6P0	B	303	-	-	0/8/22/22	0/3/4/4
4	NHE	C	302	3	-	0/7/15/15	0/1/1/1
4	NHE	C	303	-	-	0/7/15/15	0/1/1/1
5	6P0	C	304	-	-	0/8/22/22	0/3/4/4
2	EDO	D	301	-	-	0/1/1/1	0/0/0/0
4	NHE	D	303	3	-	0/7/15/15	0/1/1/1
4	NHE	D	304	-	-	0/7/15/15	0/1/1/1
5	6P0	D	305	-	-	0/8/22/22	0/3/4/4

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	303	6P0	N07-N08	-6.35	1.31	1.37
5	D	305	6P0	N07-N08	-5.85	1.31	1.37
5	A	304	6P0	N07-N08	-5.66	1.31	1.37
5	C	304	6P0	N07-N08	-5.13	1.32	1.37
5	C	304	6P0	N12-N13	-3.95	1.30	1.37
5	D	305	6P0	N12-N13	-3.85	1.30	1.37
5	A	304	6P0	N12-N13	-3.47	1.31	1.37
5	B	303	6P0	N12-N13	-3.34	1.31	1.37
5	D	305	6P0	C09-N08	-2.85	1.43	1.47
5	C	304	6P0	C09-N08	-2.80	1.43	1.47
5	A	304	6P0	C09-N08	-2.14	1.44	1.47
5	B	303	6P0	C09-N08	-2.14	1.44	1.47
5	A	304	6P0	C15-C11	2.04	1.43	1.40
5	A	304	6P0	C15-C14	2.05	1.42	1.39
5	D	305	6P0	C15-C11	2.06	1.43	1.40
5	D	305	6P0	O22-C19	2.07	1.42	1.37
4	B	302	NHE	O1-S	2.08	1.51	1.45
4	A	303	NHE	O2-S	2.12	1.51	1.45
5	B	303	6P0	C15-C11	2.20	1.44	1.40
4	D	303	NHE	O1-S	2.20	1.51	1.45
4	D	303	NHE	O2-S	2.32	1.51	1.45
4	C	302	NHE	O2-S	2.35	1.52	1.45
4	C	302	NHE	O1-S	2.45	1.52	1.45
5	C	304	6P0	O22-C19	2.46	1.42	1.37
5	B	303	6P0	O22-C19	2.58	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	304	6P0	O22-C19	2.59	1.43	1.37
5	B	303	6P0	C15-C14	2.80	1.43	1.39
5	C	304	6P0	C15-C14	2.92	1.43	1.39
5	D	305	6P0	C05-C06	4.66	1.43	1.38
5	C	304	6P0	C05-C06	4.96	1.44	1.38
5	B	303	6P0	C05-C06	5.12	1.44	1.38
5	A	304	6P0	C05-C06	5.53	1.44	1.38

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	303	NHE	O3-S-O1	-4.10	101.97	111.37
4	C	302	NHE	O3-S-O2	-4.05	102.08	111.37
4	D	303	NHE	O2-S-O1	-3.73	100.93	113.86
4	B	302	NHE	O2-S-O1	-3.47	101.83	113.86
5	A	304	6P0	C15-C14-N13	-3.33	106.80	111.51
5	C	304	6P0	C15-C14-N13	-3.24	106.93	111.51
4	A	303	NHE	O3-S-O1	-3.21	104.02	111.37
5	D	305	6P0	C15-C14-N13	-3.11	107.10	111.51
4	D	304	NHE	O2-S-O1	-2.88	103.87	113.86
5	B	303	6P0	C15-C14-N13	-2.77	107.59	111.51
5	C	304	6P0	C15-C11-C05	-2.59	125.84	129.44
5	D	305	6P0	C15-C11-C05	-2.50	125.97	129.44
5	B	303	6P0	C15-C11-C05	-2.23	126.34	129.44
5	D	305	6P0	C18-C17-C16	-2.00	118.57	121.26
5	B	303	6P0	C17-C16-C21	2.02	121.01	117.94
5	D	305	6P0	C09-N08-N07	2.16	123.05	120.59
5	A	304	6P0	C03-C02-C01	2.22	59.95	58.59
5	A	304	6P0	C09-N08-N07	2.48	123.43	120.59
5	A	304	6P0	C05-C11-N12	2.50	124.84	120.96
5	A	304	6P0	C10-C06-N07	2.53	125.25	119.78
5	D	305	6P0	C03-C02-C01	2.56	60.16	58.59
5	B	303	6P0	C05-C11-N12	2.56	124.93	120.96
5	D	305	6P0	C10-C06-N07	2.58	125.34	119.78
5	B	303	6P0	C10-C06-N07	2.78	125.79	119.78
5	C	304	6P0	C09-N08-N07	2.88	123.88	120.59
5	C	304	6P0	C05-C11-N12	2.90	125.46	120.96
5	B	303	6P0	C09-N08-N07	2.91	123.91	120.59
5	D	305	6P0	C05-C11-N12	2.94	125.52	120.96
5	C	304	6P0	C10-C06-N07	2.99	126.24	119.78
4	D	303	NHE	O3-S-C2	3.04	109.80	106.06
4	A	303	NHE	O1-S-C2	3.29	109.61	106.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	302	NHE	O1-S-C2	3.56	109.85	106.79
4	C	302	NHE	O3-S-C2	4.10	111.10	106.06
5	C	304	6P0	C02-C14-N13	4.42	125.20	120.63
5	B	303	6P0	C02-C14-N13	4.43	125.22	120.63
4	D	304	NHE	O3-S-C2	4.65	111.78	106.06
4	B	302	NHE	O3-S-C2	4.69	111.83	106.06
5	D	305	6P0	C02-C14-N13	4.75	125.55	120.63
4	C	303	NHE	O1-S-C2	4.83	110.94	106.79
5	A	304	6P0	C02-C14-N13	4.98	125.78	120.63
4	D	304	NHE	O1-S-C2	5.06	111.14	106.79
4	B	302	NHE	O1-S-C2	5.08	111.15	106.79
4	D	303	NHE	O2-S-C2	5.10	111.17	106.79
4	C	302	NHE	O2-S-C2	6.13	112.06	106.79
4	A	303	NHE	O2-S-C2	6.33	112.23	106.79
5	C	304	6P0	C06-N07-N08	7.42	110.66	104.52
4	D	303	NHE	O1-S-C2	7.93	113.60	106.79
4	C	303	NHE	O2-S-C2	8.13	113.77	106.79
5	D	305	6P0	C06-N07-N08	8.43	111.49	104.52
5	B	303	6P0	C06-N07-N08	8.69	111.71	104.52
5	A	304	6P0	C06-N07-N08	9.30	112.22	104.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	303	NHE	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	220/220 (100%)	-0.14	9 (4%) 38 38	20, 30, 50, 82	0
1	B	220/220 (100%)	-0.13	7 (3%) 48 48	21, 28, 46, 66	0
1	C	220/220 (100%)	-0.15	6 (2%) 55 54	20, 27, 47, 64	0
1	D	220/220 (100%)	-0.25	5 (2%) 61 60	20, 27, 42, 59	0
All	All	880/880 (100%)	-0.16	27 (3%) 49 49	20, 28, 47, 82	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	200	TYR	7.9
1	C	221	SER	6.4
1	D	221	SER	6.1
1	B	221	SER	5.3
1	C	220	LYS	5.2
1	B	200	TYR	4.5
1	A	221	SER	4.2
1	C	219	ASP	4.2
1	B	220	LYS	3.9
1	B	217	SER	3.9
1	A	219	ASP	3.4
1	D	217	SER	3.3
1	A	220	LYS	3.3
1	D	219	ASP	3.1
1	A	199	GLU	2.9
1	D	131[A]	ASP	2.9
1	C	131	ASP	2.9
1	D	220	LYS	2.9
1	C	217	SER	2.7
1	B	219	ASP	2.6
1	C	218	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	131[A]	ASP	2.3
1	B	2	GLY	2.2
1	B	218	PRO	2.1
1	A	218	PRO	2.1
1	A	217	SER	2.0
1	A	185	GLY	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	EDO	D	301	4/4	0.90	0.24	20.43	37,39,42,43	0
2	EDO	A	301	4/4	0.92	0.13	2.98	42,43,43,45	0
6	K	D	306	1/1	0.99	0.21	2.92	47,47,47,47	0
3	MG	A	302	1/1	0.59	0.14	2.63	41,41,41,41	0
3	MG	B	301	1/1	0.92	0.13	1.69	35,35,35,35	0
4	NHE	D	304	13/13	0.98	0.12	1.63	22,28,31,32	0
4	NHE	C	303	13/13	0.98	0.12	1.52	27,29,31,33	0
6	K	A	305	1/1	0.86	0.18	1.13	53,53,53,53	0
5	6P0	D	305	23/23	0.97	0.11	0.95	18,22,27,36	0
4	NHE	C	302	13/13	0.95	0.13	0.84	37,44,49,51	0
5	6P0	B	303	23/23	0.97	0.11	0.84	17,22,31,36	0
5	6P0	C	304	23/23	0.97	0.12	0.84	18,23,31,39	0
4	NHE	A	303	13/13	0.98	0.12	0.79	25,26,36,36	0
6	K	C	305	1/1	0.96	0.17	0.77	48,48,48,48	0
4	NHE	B	302	13/13	0.97	0.12	0.69	26,28,37,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	6P0	A	304	23/23	0.96	0.10	0.32	16,23,32,40	0
6	K	B	304	1/1	0.97	0.13	-0.02	49,49,49,49	0
4	NHE	D	303	13/13	0.97	0.09	-0.38	29,36,38,38	0
3	MG	D	302	1/1	0.89	0.09	-0.83	29,29,29,29	0
3	MG	C	301	1/1	0.89	0.13	-	34,34,34,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.