



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 04:19 am BST

PDB ID : 5WCW  
Title : Phosphotriesterase variant S4  
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Deposited on : 2017-07-02  
Resolution : 1.46 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

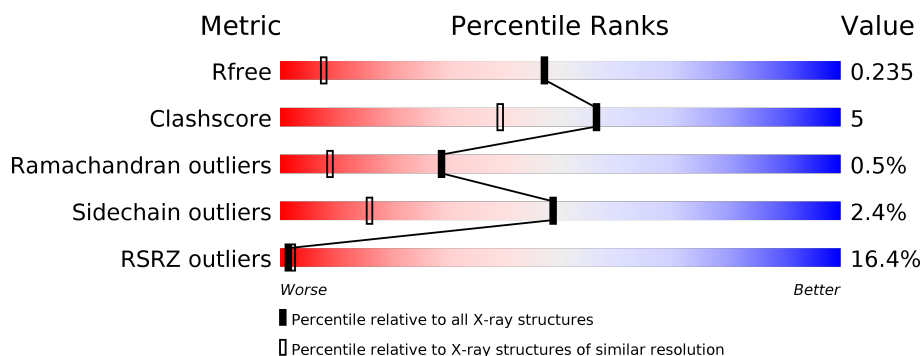
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.46 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))
$R_{free}$	130704	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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 respectively. 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	333	<div> <div>4%</div> <div>85%</div> <div>9%</div> <div>7%</div> </div>
1	G	333	<div> <div>27%</div> <div>80%</div> <div>13%</div> <div>6%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MPD	G	2403	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5103 atoms, of which 6 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 Phosphotriesterase variant PTE-R1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	0	5	0
			2417	1527	435	449	6			
1	G	313	Total	C	N	O	S	0	3	0
			2412	1526	429	451	6			

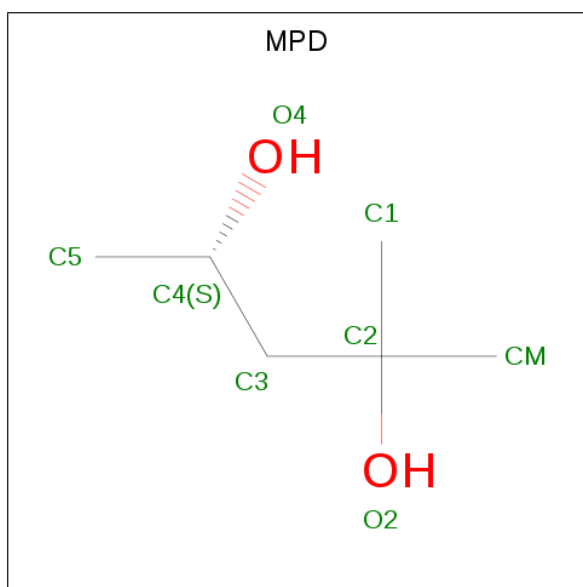
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	233	ALA	ASP	conflict	UNP A0A060GZX0
A	254	SER	ARG	conflict	UNP A0A060GZX0
A	271	HIS	LEU	conflict	UNP A0A060GZX0
A	293	THR	MET	conflict	UNP A0A060GZX0
A	306	ILE	PHE	conflict	UNP A0A060GZX0
G	233	ALA	ASP	conflict	UNP A0A060GZX0
G	254	SER	ARG	conflict	UNP A0A060GZX0
G	271	HIS	LEU	conflict	UNP A0A060GZX0
G	293	THR	MET	conflict	UNP A0A060GZX0
G	306	ILE	PHE	conflict	UNP A0A060GZX0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

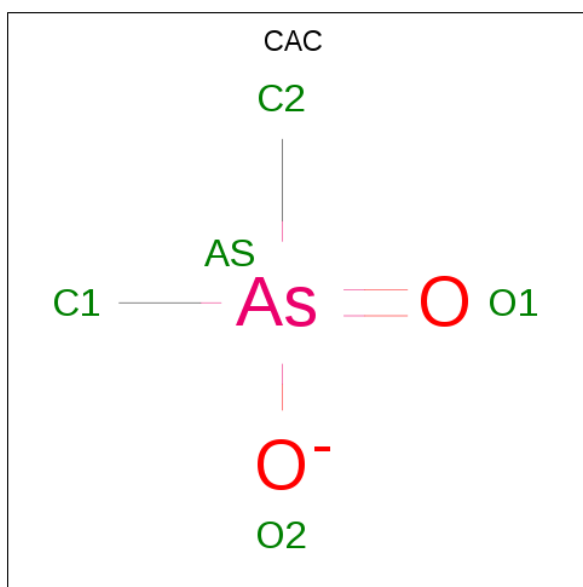
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	G	1	Total	C	O	0	0
			8	6	2		

- Molecule 4 is CACODYLATE ION (three-letter code: CAC) (formula:  $C_2H_6AsO_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	As	C	O	0	0
			5	1	2	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	G	1	Total	As	C	H	O	0	0
			11	1	2	6	2		

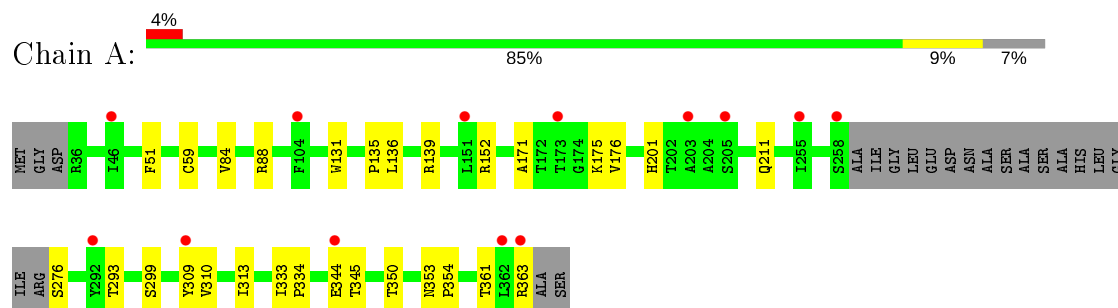
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	137	Total	O	0	0
			137	137		
5	G	93	Total	O	0	0
			93	93		

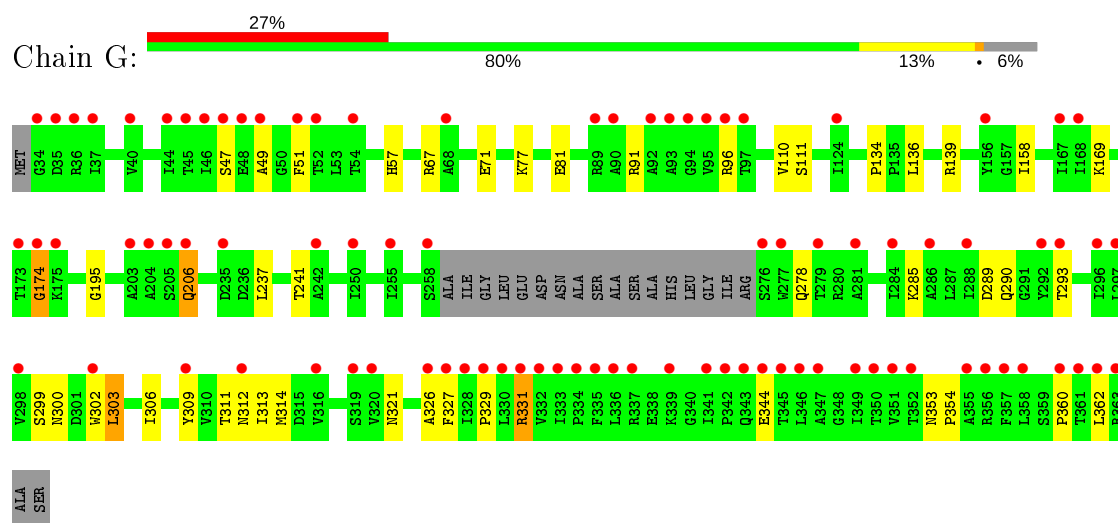
### 3 Residue-property plots [i](#)

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: Phosphotriesterase variant PTE-R1



#### • Molecule 1: Phosphotriesterase variant PTE-R1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.51Å 85.89Å 88.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.25 – 1.46 44.19 – 1.46	Depositor EDS
% Data completeness (in resolution range)	99.4 (39.25-1.46) 99.4 (44.19-1.46)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.71 (at 1.46Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, $R_{free}$	0.208 , 0.234 0.209 , 0.235	Depositor DCC
$R_{free}$ test set	5683 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.0	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.016 for -h,l,k 0.017 for -l,-k,-h 0.019 for k,h,-l 0.007 for k,l,h 0.007 for l,h,k	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5103	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% of the height of the origin peak. No significant pseudotranslation is detected.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CAC, ZN, MPD, KCX

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	0.44	0/2448	0.64	0/3324
1	G	0.35	0/2443	0.57	0/3318
All	All	0.39	0/4891	0.61	0/6642

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

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	2417	0	2447	18	1
1	G	2412	0	2436	27	1
2	A	2	0	0	0	0
2	G	2	0	0	0	0
3	A	16	0	28	4	0
3	G	8	0	14	1	0
4	A	5	0	0	1	0
4	G	5	6	0	1	0
5	A	137	0	0	1	0
5	G	93	0	0	3	0
All	All	5097	6	4925	49	1

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 5.

All (49) 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:G:136[A]:LEU:HD13	1:G:139:ARG:NH2	1.94	0.81
1:G:278:GLN:HG2	5:G:2591:HOH:O	1.83	0.79
1:A:131:TRP:HE1	4:A:2405:CAC:C2	1.97	0.77
3:A:2403:MPD:O4	3:A:2403:MPD:O2	2.05	0.73
3:A:2404:MPD:O2	3:A:2404:MPD:O4	2.10	0.60
1:G:174:GLY:HA2	1:G:206:GLN:HG2	1.83	0.60
1:G:77:LYS:NZ	1:G:81:GLU:OE2	2.34	0.60
1:G:136[A]:LEU:HD13	1:G:139:ARG:HH21	1.69	0.58
1:G:293:THR:HG22	5:G:2586:HOH:O	2.05	0.57
1:A:361:THR:HG22	1:A:363:ARG:H	1.70	0.56
1:G:71[B]:GLU:H	1:G:71[B]:GLU:CD	2.10	0.55
1:A:136:LEU:HG	1:A:139:ARG:NH2	2.21	0.55
1:G:195:GLY:O	1:G:360:PRO:HA	2.08	0.54
1:G:49:ALA:O	1:G:96:ARG:HB2	2.10	0.52
1:A:175:LYS:HA	1:A:211:GLN:NE2	2.24	0.52
1:G:353:ASN:HB2	1:G:354:PRO:HD3	1.92	0.51
1:A:333:ILE:HB	1:A:334:PRO:HD3	1.93	0.51
1:G:306:ILE:HG22	1:G:314:MET:HB2	1.94	0.50
3:G:2403:MPD:H12	5:G:2561:HOH:O	2.11	0.50
1:A:353:ASN:HB2	1:A:354:PRO:HD3	1.93	0.49
1:A:59:CYS:HB3	5:A:2602:HOH:O	2.13	0.49
1:A:175:LYS:HA	1:A:211:GLN:HE21	1.77	0.49
1:A:293:THR:HG21	1:A:345:THR:HG23	1.95	0.49
1:G:285:LYS:NZ	1:G:289:ASP:OD2	2.40	0.49
1:A:350:THR:OG1	3:A:2403:MPD:H52	2.14	0.47
1:G:306:ILE:HG21	1:G:313:ILE:HG23	1.96	0.47
1:A:309:TYR:CD2	1:A:310:VAL:HG22	2.50	0.46
1:G:67:ARG:NH2	1:G:111[A]:SER:OG	2.49	0.46
1:G:300:ASN:OD1	1:G:327:PHE:HB3	2.15	0.46
1:G:57:HIS:O	1:G:303:LEU:HA	2.15	0.46
1:A:135:PRO:O	1:A:139:ARG:HG3	2.15	0.45
1:A:309:TYR:CD2	1:A:313:ILE:HG12	2.51	0.45
1:A:344:GLU:H	1:A:344:GLU:CD	2.18	0.45
1:G:331:ARG:HA	1:G:331:ARG:HD3	1.75	0.45
1:G:302:TRP:CH2	1:G:321:ASN:HB3	2.52	0.44
1:G:309:TYR:HB3	1:G:313:ILE:HG21	1.99	0.44
1:G:110:VAL:HG11	1:G:158:ILE:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:169:KCX:OQ2	4:G:2404:CAC:O2	2.35	0.44
1:G:326:ALA:C	1:G:329:PRO:HD2	2.37	0.44
1:G:110:VAL:HG11	1:G:158:ILE:CD1	2.49	0.43
1:A:171:ALA:CB	1:A:201:HIS:HB3	2.49	0.43
1:G:237:LEU:O	1:G:241:THR:HG23	2.18	0.42
3:A:2403:MPD:HM1	3:A:2403:MPD:H53	2.01	0.42
1:A:84:VAL:O	1:A:88[A]:ARG:HG3	2.20	0.41
1:A:313:ILE:HD12	1:A:313:ILE:HA	1.95	0.41
1:G:314:MET:HA	1:G:314:MET:CE	2.51	0.41
1:G:311:THR:O	1:G:312:ASN:HB2	2.21	0.40
1:A:136:LEU:CD2	1:A:139:ARG:NH2	2.84	0.40
1:G:134:PRO:O	1:G:139:ARG:HD3	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:THR:OG1	1:G:344:GLU:OE2[1_556]	2.02	0.18

## 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	311/333 (93%)	303 (97%)	7 (2%)	1 (0%)	41	18
1	G	311/333 (93%)	300 (96%)	9 (3%)	2 (1%)	25	7
All	All	622/666 (93%)	603 (97%)	16 (3%)	3 (0%)	29	9

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	176	VAL

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Mol	Chain	Res	Type
1	G	362	LEU
1	G	174	GLY

### 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	255/265 (96%)	251 (98%)	4 (2%)	62	31
1	G	254/265 (96%)	246 (97%)	8 (3%)	40	9
All	All	509/530 (96%)	497 (98%)	12 (2%)	49	16

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	PHE
1	A	152	ARG
1	A	276	SER
1	A	299	SER
1	G	47	SER
1	G	51	PHE
1	G	91	ARG
1	G	206	GLN
1	G	290	GLN
1	G	299	SER
1	G	303	LEU
1	G	331	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z  > 2$
1	KCX	A	169	1,2	7,11,12	1.93	1 (14%)	4,12,14	1.16	1 (25%)
1	KCX	G	169	1,2	7,11,12	0.69	0	4,12,14	0.96	0

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
1	KCX	A	169	1,2	-	0/7/10/12	-
1	KCX	G	169	1,2	-	0/7/10/12	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	169	KCX	CE-NZ	4.85	1.55	1.45

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	KCX	CE-NZ-CX	2.00	126.34	122.95

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
1	G	169	KCX	1	0

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	$\# Z  > 2$
3	MPD	G	2403	-	7,7,7	0.62	0	9,10,10	0.28	0
3	MPD	A	2403	-	7,7,7	0.64	0	9,10,10	0.35	0
3	MPD	A	2404	-	7,7,7	0.61	0	9,10,10	0.46	0
4	CAC	G	2404	2	0,4,4	0.00	-	0,6,6	0.00	-
4	CAC	A	2405	2	0,4,4	0.00	-	0,6,6	0.00	-

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
3	MPD	G	2403	-	-	3/5/5/5	-
3	MPD	A	2403	-	-	1/5/5/5	-
3	MPD	A	2404	-	-	3/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	2403	MPD	O2-C2-C3-C4
3	A	2404	MPD	O2-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
3	A	2404	MPD	C2-C3-C4-O4
3	G	2403	MPD	C1-C2-C3-C4
3	G	2403	MPD	CM-C2-C3-C4
3	A	2403	MPD	CM-C2-C3-C4
3	A	2404	MPD	C2-C3-C4-C5

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	2403	MPD	1	0
3	A	2403	MPD	3	0
3	A	2404	MPD	1	0
4	G	2404	CAC	1	0
4	A	2405	CAC	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	310/333 (93%)	0.75	13 (4%)	36 39	13, 22, 38, 62	1 (0%)
1	G	312/333 (93%)	1.51	89 (28%)	0 0	16, 38, 57, 74	0
All	All	622/666 (93%)	1.13	102 (16%)	1 2	13, 29, 54, 74	1 (0%)

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	362	LEU	23.7
1	G	34	GLY	7.7
1	G	320	VAL	6.7
1	G	363	ARG	6.1
1	G	330	LEU	5.7
1	G	44	ILE	5.5
1	A	362	LEU	5.3
1	G	173	THR	5.2
1	G	204	ALA	4.9
1	G	49	ALA	4.9
1	G	328	ILE	4.8
1	G	46	ILE	4.8
1	G	51	PHE	4.5
1	G	337	ARG	4.4
1	G	360	PRO	4.4
1	G	37	ILE	4.3
1	G	255	ILE	4.1
1	G	329	PRO	3.9
1	G	327	PHE	3.6
1	G	95	VAL	3.6
1	G	334	PRO	3.6
1	G	35	ASP	3.6
1	G	89	ARG	3.5
1	G	347	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
1	G	277	TRP	3.5
1	G	312	ASN	3.4
1	A	363	ARG	3.4
1	G	335	PHE	3.4
1	G	349	ILE	3.3
1	G	361	THR	3.3
1	G	336	LEU	3.3
1	G	326	ALA	3.2
1	G	355	ALA	3.2
1	G	350	THR	3.2
1	G	351	VAL	3.2
1	G	288	ILE	3.1
1	G	333	ILE	3.1
1	G	156	TYR	3.1
1	G	174	GLY	3.0
1	G	205	SER	3.0
1	G	296	ILE	3.0
1	G	293	THR	3.0
1	G	48	GLU	3.0
1	G	36	ARG	2.9
1	G	358	LEU	2.9
1	G	284	ILE	2.9
1	G	332	VAL	2.9
1	A	309	TYR	2.8
1	G	346	LEU	2.8
1	A	205	SER	2.8
1	G	52	THR	2.8
1	G	175	LYS	2.7
1	G	235	ASP	2.7
1	A	292	TYR	2.7
1	G	286	ALA	2.7
1	G	342	PRO	2.7
1	G	331	ARG	2.6
1	G	97	THR	2.6
1	G	339	LYS	2.5
1	G	93	ALA	2.5
1	G	206	GLN	2.5
1	G	352	THR	2.5
1	G	357	PHE	2.5
1	G	40	VAL	2.5
1	A	344	GLU	2.5
1	G	343	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	173	THR	2.4
1	G	356	ARG	2.4
1	G	297	LEU	2.4
1	G	92	ALA	2.4
1	G	258	SER	2.3
1	A	255	ILE	2.3
1	G	302	TRP	2.3
1	A	151	LEU	2.3
1	G	316	VAL	2.3
1	G	276	SER	2.2
1	G	90	ALA	2.2
1	A	46	ILE	2.2
1	G	345	THR	2.2
1	G	96	ARG	2.2
1	G	250	ILE	2.2
1	G	344	GLU	2.2
1	G	45	THR	2.2
1	G	279	THR	2.2
1	G	242	ALA	2.2
1	G	309	TYR	2.2
1	G	68	ALA	2.1
1	G	281	ALA	2.1
1	G	341	ILE	2.1
1	A	258	SER	2.1
1	G	54	THR	2.1
1	A	203	ALA	2.1
1	G	94	GLY	2.1
1	G	319	SER	2.0
1	G	124	ILE	2.0
1	G	168	ILE	2.0
1	G	298	VAL	2.0
1	G	47	SER	2.0
1	A	104	PHE	2.0
1	G	167	ILE	2.0
1	G	292	TYR	2.0
1	G	203	ALA	2.0

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

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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
1	KCX	G	169	12/13	0.77	0.13	25,27,29,32	0
1	KCX	A	169	12/13	0.92	0.12	12,13,14,15	0

### 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MPD	G	2403	8/8	0.26	0.41	43,44,46,47	8
3	MPD	A	2404	8/8	0.47	0.25	40,44,45,45	0
3	MPD	A	2403	8/8	0.68	0.26	43,44,46,46	8
4	CAC	G	2404	5/5	0.94	0.41	33,37,40,40	11
2	ZN	G	2401	1/1	0.98	0.08	30,30,30,30	0
4	CAC	A	2405	5/5	0.98	0.12	14,15,18,20	5
2	ZN	G	2402	1/1	0.99	0.07	31,31,31,31	0
2	ZN	A	2402	1/1	1.00	0.08	16,16,16,16	0
2	ZN	A	2401	1/1	1.00	0.11	14,14,14,14	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.