



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 06:49 AM BST

PDB ID : 6BH7  
Title : Phosphotriesterase variant R18+254S  
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Deposited on : 2017-10-30  
Resolution : 1.40 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 : 2.13.1  
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) : 2.13.1

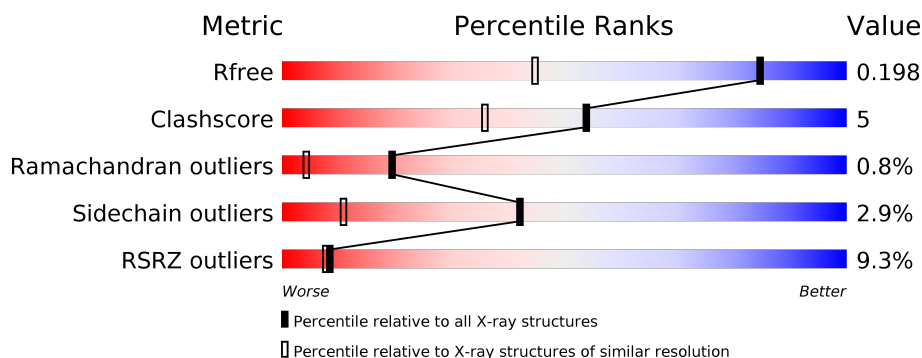
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.40 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	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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>10%</div> <div>80%</div> <div>10%</div> <div>8%</div> </div>
1	G	333	<div> <div>8%</div> <div>88%</div> <div>9%</div> <div>••</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
1	KCX	G	169	X	-	-	-
3	MPD	A	2404	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12826 atoms, of which 6356 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.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	308	Total	C	H	N	O	S	251	107	0
			6209	1948	3155	549	549	8			
1	G	328	Total	C	H	N	O	S	33	94	0
			6194	1941	3131	545	569	8			

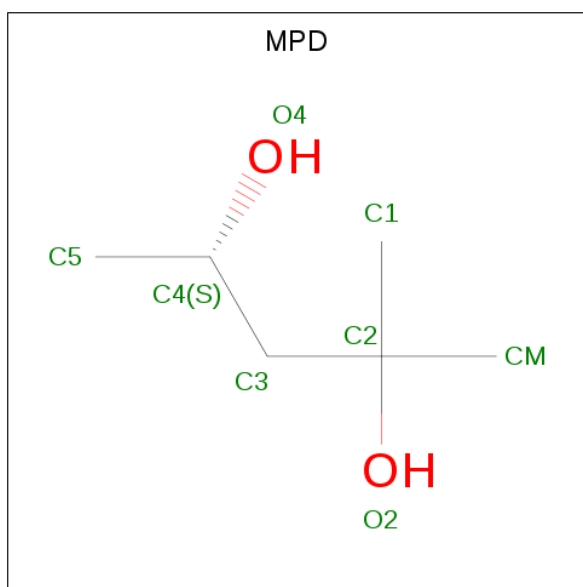
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	254	SER	ARG	conflict	UNP A0A060GYS7
G	254	SER	ARG	conflict	UNP A0A060GYS7

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

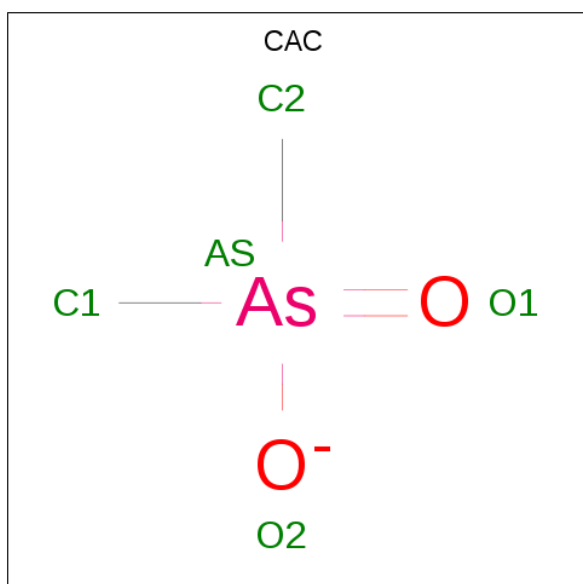
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		

- 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	H	O	0	0
			22	6	14	2		
3	A	1	Total	C	H	O	0	0
			22	6	14	2		
3	A	1	Total	C	H	O	0	0
			22	6	14	2		
3	G	1	Total	C	H	O	0	0
			22	6	14	2		
3	G	1	Total	C	H	O	0	0
			22	6	14	2		

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



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

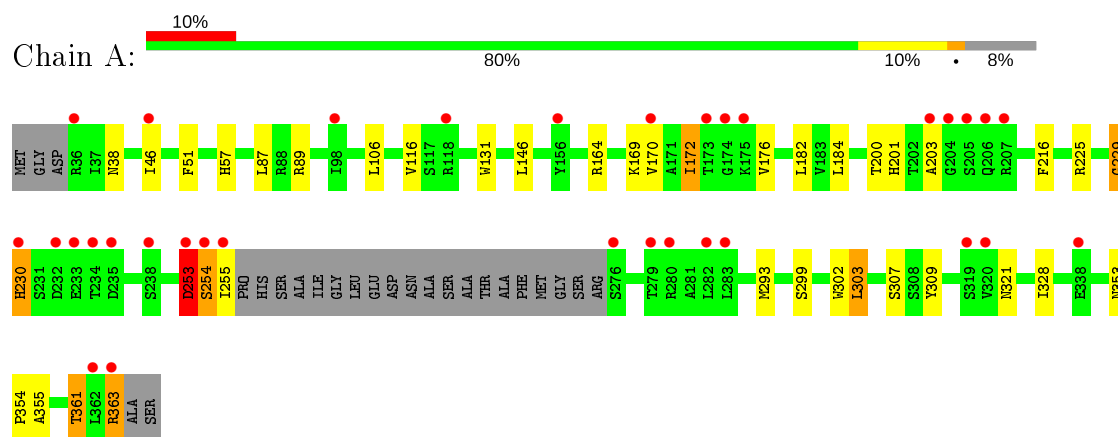
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	150	Total	O	0	0
			150	150		
5	G	154	Total	O	0	0
			154	154		

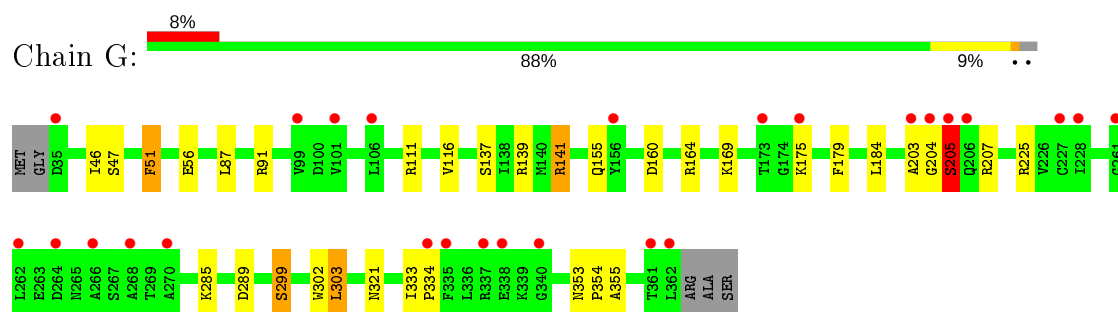
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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



#### • Molecule 1: Phosphotriesterase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.67Å 86.01Å 88.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.04 – 1.40 29.04 – 1.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.04-1.40) 100.0 (29.04-1.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.51 (at 1.40Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.166 , 0.198 0.167 , 0.198	Depositor DCC
$R_{free}$ test set	6399 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.8	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 44.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.011 for -h,l,k 0.013 for -l,-k,-h 0.013 for k,h,-l 0.002 for k,l,h 0.002 for l,h,k	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	12826	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% 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	0.49	0/3294	0.71	2/4467 (0.0%)
1	G	0.50	0/3307	0.70	1/4485 (0.0%)
All	All	0.49	0/6601	0.71	3/8952 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	2
1	G	1	1
All	All	2	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	225	ARG	NE-CZ-NH1	-5.69	117.45	120.30
1	G	225	ARG	NE-CZ-NH1	-5.36	117.62	120.30
1	A	225	ARG	NE-CZ-NH2	5.01	122.81	120.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	230	HIS	CA
1	G	169	KCX	CA

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	229	GLY	Peptide
1	A	253[B]	ASP	Peptide
1	G	203[A]	ALA	Peptide

## 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	3054	3155	2984	36	0
1	G	3063	3131	2948	28	0
2	A	2	0	0	0	0
2	G	2	0	0	0	0
3	A	24	42	42	1	0
3	G	16	28	28	1	0
4	G	5	0	0	0	0
5	A	150	0	0	7	0
5	G	154	0	0	2	0
All	All	6470	6356	6002	62	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 5.

All (62) 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:A:307:SER:O	1:G:141[A]:ARG:NH2	2.15	0.79
1:A:309:TYR:O	1:G:141[A]:ARG:NH2	2.18	0.76
1:A:307:SER:O	1:G:141[C]:ARG:NH2	2.20	0.74
1:A:172[A]:ILE:HD11	1:A:184[A]:LEU:HD11	1.71	0.72
1:A:146[B]:LEU:HD12	1:A:182:LEU:CD2	2.21	0.70
1:A:253[A]:ASP:OD2	5:A:2501:HOH:O	2.08	0.69
1:A:230:HIS:CD2	5:A:2515:HOH:O	2.49	0.65
1:A:230:HIS:ND1	1:A:253[A]:ASP:OD1	2.31	0.64
1:A:89[C]:ARG:NH2	5:A:2502:HOH:O	2.29	0.62
1:A:201:HIS:NE2	5:A:2501:HOH:O	2.18	0.60
1:G:87[A]:LEU:HD12	1:G:116:VAL:HG12	1.84	0.59
1:G:155[A]:GLN:O	1:G:164[A]:ARG:NE	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:GLY:CA	1:A:230:HIS:HD2	2.17	0.57
1:A:253[C]:ASP:OD2	5:A:2501:HOH:O	2.18	0.56
1:G:111[C]:ARG:NH2	1:G:160:ASP:OD1	2.37	0.56
1:A:230:HIS:ND1	1:A:253[C]:ASP:OD1	2.39	0.56
1:G:139[C]:ARG:NH1	5:G:2504:HOH:O	2.39	0.55
1:G:46[B]:ILE:HG23	1:G:355:ALA:HB1	1.89	0.54
1:G:137:SER:O	1:G:141[C]:ARG:NE	2.42	0.53
1:A:146[B]:LEU:HD12	1:A:182:LEU:HD23	1.90	0.52
1:A:229:GLY:HA3	1:A:230:HIS:HD2	1.75	0.52
1:A:170[A]:VAL:CG2	1:A:200:THR:HG22	2.39	0.51
1:A:200:THR:O	1:A:229:GLY:HA3	2.10	0.51
1:G:285:LYS:NZ	1:G:289:ASP:OD2	2.42	0.51
1:A:57[B]:HIS:O	1:A:303:LEU:HA	2.12	0.50
1:G:205[A]:SER:CB	1:G:207[A]:ARG:H	2.24	0.50
1:G:204[B]:GLY:CA	1:G:205[B]:SER:CB	2.90	0.49
1:A:106[B]:LEU:HG	1:A:131[B]:TRP:CD2	2.47	0.49
1:A:230:HIS:ND1	1:A:253[B]:ASP:HB2	2.28	0.48
1:A:254[A]:SER:O	1:A:255[A]:ILE:CB	2.62	0.48
1:A:361:THR:HG22	1:A:363:ARG:H	1.78	0.48
1:G:204[A]:GLY:HA3	1:G:205[A]:SER:C	2.33	0.48
1:A:302:TRP:CH2	1:A:321:ASN:HB3	2.49	0.48
1:G:205[A]:SER:CA	1:G:207[A]:ARG:H	2.28	0.47
1:A:254[A]:SER:OG	1:A:328:ILE:HD11	2.15	0.46
1:G:51:PHE:HE2	3:G:2405:MPD:H11	1.80	0.46
1:A:87:LEU:HD12	1:A:116[A]:VAL:HG12	1.97	0.46
1:A:203:ALA:HB2	5:A:2628:HOH:O	2.17	0.45
1:A:230:HIS:N	1:A:230:HIS:CD2	2.84	0.45
1:G:353:ASN:HB2	1:G:354:PRO:HD3	1.99	0.45
1:A:38:ASN:HD21	1:A:164[B]:ARG:CZ	2.29	0.44
1:A:230:HIS:CE1	1:A:253[B]:ASP:OD1	2.70	0.44
1:A:172[A]:ILE:HD11	1:A:184[A]:LEU:CD1	2.45	0.44
1:A:46[B]:ILE:HG13	1:A:355:ALA:HB1	2.00	0.44
3:A:2403:MPD:HM1	3:A:2403:MPD:O4	2.18	0.43
1:A:57[B]:HIS:HB2	1:A:303:LEU:HB3	1.99	0.43
1:A:353:ASN:HB2	1:A:354:PRO:HD3	2.00	0.43
1:G:333:ILE:HB	1:G:334:PRO:HD3	1.99	0.43
1:G:91[C]:ARG:NH2	5:G:2506:HOH:O	2.50	0.43
1:G:139[C]:ARG:HA	1:G:179:PHE:CE1	2.53	0.43
1:G:139[B]:ARG:HA	1:G:179:PHE:CE1	2.54	0.42
1:A:229:GLY:CA	1:A:230:HIS:CD2	2.99	0.42
1:G:302:TRP:CH2	1:G:321:ASN:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89[C]:ARG:NH1	5:A:2502:HOH:O	2.53	0.41
1:A:184[C]:LEU:HD22	1:A:216:PHE:CZ	2.56	0.41
1:G:155[A]:GLN:HA	1:G:164[A]:ARG:HE	1.85	0.41
1:G:205[A]:SER:HB3	1:G:207[A]:ARG:H	1.85	0.41
1:G:56[A]:GLU:OE2	1:G:299[A]:SER:OG	2.27	0.41

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	414/333 (124%)	395 (95%)	12 (3%)	7 (2%)	9	1
1	G	420/333 (126%)	407 (97%)	11 (3%)	2 (0%)	29	9
All	All	834/666 (125%)	802 (96%)	23 (3%)	9 (1%)	19	2

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	HIS
1	A	254[A]	SER
1	A	254[B]	SER
1	G	205[A]	SER
1	G	205[B]	SER
1	A	176	VAL
1	A	253[A]	ASP
1	A	253[B]	ASP
1	A	253[C]	ASP

### 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	342/268 (128%)	332 (97%)	10 (3%)	42	11
1	G	341/268 (127%)	329 (96%)	12 (4%)	36	7
All	All	683/536 (127%)	661 (97%)	22 (3%)	42	9

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51[B]	PHE
1	A	51[C]	PHE
1	A	172[A]	ILE
1	A	172[B]	ILE
1	A	293	MET
1	A	299[A]	SER
1	A	299[C]	SER
1	A	303	LEU
1	A	361	THR
1	A	363	ARG
1	G	47[B]	SER
1	G	47[C]	SER
1	G	51	PHE
1	G	141[A]	ARG
1	G	141[C]	ARG
1	G	175	LYS
1	G	184	LEU
1	G	205[A]	SER
1	G	205[B]	SER
1	G	299[A]	SER
1	G	299[B]	SER
1	G	303	LEU

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	G	169	1,2	7,11,12	3.96	2 (28%)	4,12,14	0.60	0
1	KCX	A	169	1,2	7,11,12	3.37	1 (14%)	4,12,14	1.06	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	G	169	1,2	1/1/3/4	2/7/10/12	-
1	KCX	A	169	1,2	-	2/7/10/12	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	169	KCX	CA-N	-9.97	1.18	1.48
1	A	169	KCX	CA-N	-8.74	1.21	1.48
1	G	169	KCX	CB-CA	2.95	1.57	1.53

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	G	169	KCX	CA

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	G	169	KCX	C-CA-CB-CG
1	G	169	KCX	CA-CB-CG-CD
1	A	169	KCX	C-CA-CB-CG
1	A	169	KCX	CA-CB-CG-CD

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	A	2405	-	7,7,7	0.35	0	9,10,10	0.66	0
3	MPD	G	2405	-	7,7,7	0.35	0	9,10,10	0.30	0
3	MPD	G	2404	-	7,7,7	0.34	0	9,10,10	0.31	0
3	MPD	A	2404	-	7,7,7	0.39	0	9,10,10	0.31	0
3	MPD	A	2403	-	7,7,7	0.35	0	9,10,10	0.59	0
4	CAC	G	2403	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	2405	-	-	2/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MPD	A	2405	-	-	2/5/5/5	-
3	MPD	A	2403	-	-	2/5/5/5	-
3	MPD	A	2404	-	-	0/5/5/5	-
3	MPD	G	2404	-	-	1/5/5/5	-

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	2405	MPD	C2-C3-C4-C5
3	G	2405	MPD	C2-C3-C4-O4
3	A	2403	MPD	C2-C3-C4-O4
3	A	2405	MPD	O2-C2-C3-C4
3	G	2404	MPD	O2-C2-C3-C4
3	A	2405	MPD	C2-C3-C4-C5
3	A	2403	MPD	C2-C3-C4-C5

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	2405	MPD	1	0
3	A	2403	MPD	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	307/333 (92%)	0.55	33 (10%) <b>6</b> <b>5</b>	12, 19, 47, 91	0
1	G	327/333 (98%)	0.54	26 (7%) <b>12</b> <b>11</b>	14, 24, 39, 71	0
All	All	634/666 (95%)	0.55	59 (9%) <b>8</b> <b>8</b>	12, 22, 41, 91	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	204[A]	GLY	14.2
1	A	204	GLY	10.3
1	A	203	ALA	10.1
1	G	362	LEU	9.2
1	G	203[A]	ALA	7.2
1	A	235	ASP	6.1
1	A	255[A]	ILE	5.9
1	G	173	THR	5.8
1	G	35	ASP	5.8
1	G	205[A]	SER	5.7
1	A	206	GLN	5.5
1	A	205	SER	5.2
1	A	175	LYS	5.1
1	A	254[A]	SER	4.4
1	G	337	ARG	4.4
1	A	230	HIS	4.3
1	G	175	LYS	4.2
1	A	233	GLU	4.2
1	G	261	GLY	4.1
1	G	264	ASP	4.1
1	G	101	VAL	4.1
1	A	282	LEU	4.0
1	A	46[B]	ILE	3.8
1	A	232	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	174	GLY	3.7
1	A	253[A]	ASP	3.7
1	A	338	GLU	3.6
1	A	207	ARG	3.4
1	A	118[A]	ARG	3.3
1	A	173	THR	3.2
1	A	276	SER	3.2
1	G	262	LEU	3.0
1	A	279	THR	2.9
1	G	268	ALA	2.9
1	A	280	ARG	2.8
1	G	340	GLY	2.7
1	G	99	VAL	2.7
1	G	206[A]	GLN	2.7
1	G	266	ALA	2.6
1	G	228	ILE	2.6
1	G	156[A]	TYR	2.6
1	G	338	GLU	2.6
1	A	320	VAL	2.5
1	G	334	PRO	2.4
1	A	363	ARG	2.4
1	G	106[A]	LEU	2.4
1	G	227	CYS	2.3
1	A	238	SER	2.3
1	G	335	PHE	2.3
1	A	36	ARG	2.2
1	A	98[B]	ILE	2.2
1	A	170[A]	VAL	2.2
1	A	362	LEU	2.2
1	A	234	THR	2.1
1	A	283	LEU	2.1
1	G	361	THR	2.1
1	A	156	TYR	2.1
1	G	270	ALA	2.1
1	A	319	SER	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	0.90	0.16	16,18,22,22	0
1	KCX	A	169	12/13	0.94	0.14	13,17,21,22	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides 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	A	2404	8/8	0.31	0.53	87,105,106,106	0
3	MPD	A	2403	8/8	0.54	0.28	50,60,61,63	0
3	MPD	G	2404	8/8	0.66	0.30	53,64,66,66	0
3	MPD	G	2405	8/8	0.68	0.25	62,74,75,75	0
3	MPD	A	2405	8/8	0.79	0.17	56,68,69,69	0
2	ZN	A	2402	1/1	0.99	0.08	25,25,25,25	1
4	CAC	G	2403	5/5	0.99	0.12	16,18,19,19	5
2	ZN	G	2401	1/1	1.00	0.07	18,18,18,18	0
2	ZN	G	2402	1/1	1.00	0.07	18,18,18,18	1
2	ZN	A	2401	1/1	1.00	0.08	14,14,14,14	0

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

There are no such residues in this entry.