



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:30 PM UTC

PDB ID : 6BH7 / pdb_00006bh7
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

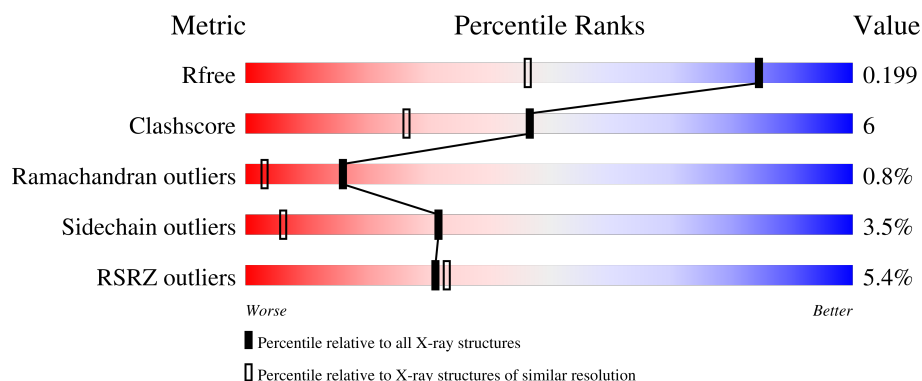
1 Overall quality at a glance

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}	180053	2563 (1.40-1.40)
Clashscore	190562	2660 (1.40-1.40)
Ramachandran outliers	187476	2611 (1.40-1.40)
Sidechain outliers	187428	2610 (1.40-1.40)
RSRZ outliers	180081	2561 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	
1	G	333	

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	-	-	-
4	CAC	G	2403	-	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			

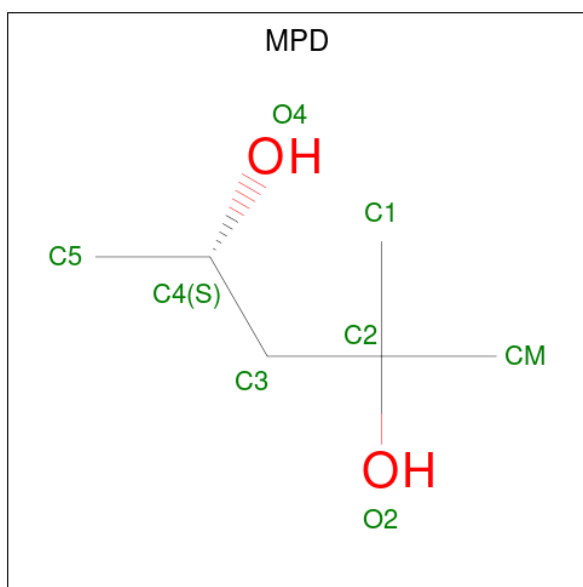
There are 2 discrepancies between the modelled and reference sequences:

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 (CCD ID: ZN) (formula: Zn).

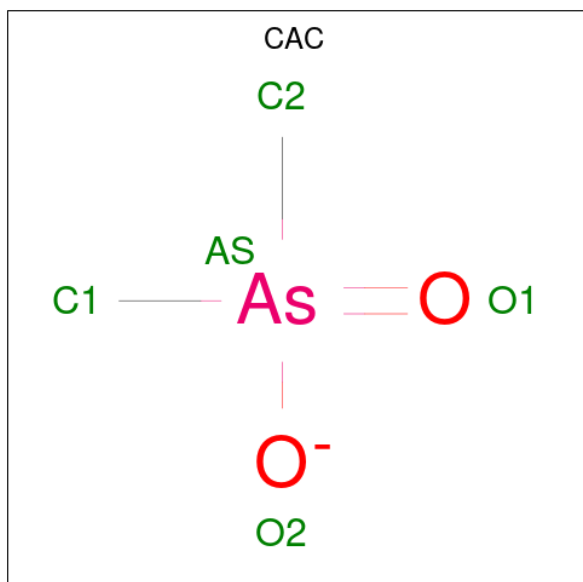
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	G	2	Total	Zn	0	0
			2	2		

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



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 (CCD ID: 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		

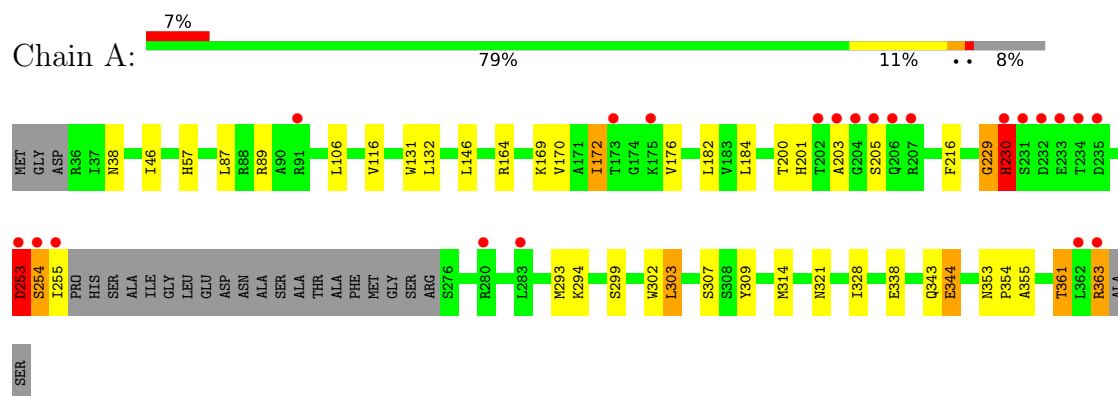
- Molecule 5 is water.

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

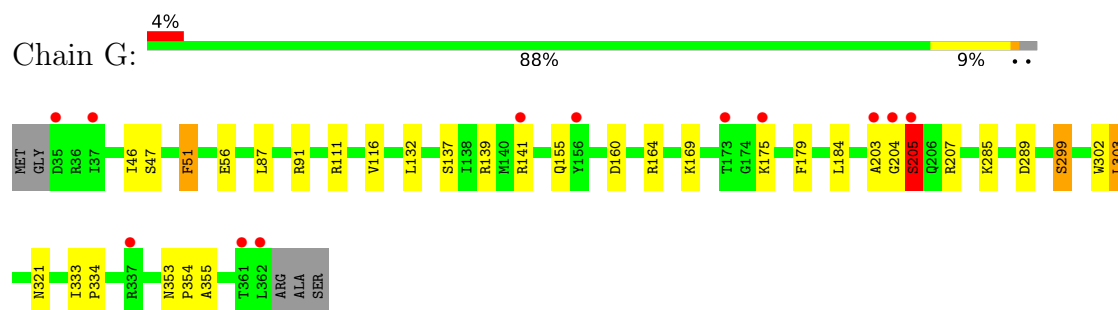
3 Residue-property plots [i](#)

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, α , β , γ	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) 99.9 (29.04-1.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 1.40Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.166 , 0.198 0.168 , 0.199	Depositor DCC
R_{free} test set	6401 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	16.8	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	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 ²)	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.*

¹Intensities estimated from amplitudes.

²Theoretical 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: ZN, MPD, KCX, CAC

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	0.54	0/3294	0.70	2/4467 (0.0%)
1	G	0.55	0/3307	0.71	0/4485
All	All	0.54	0/6601	0.71	2/8952 (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 (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	230	HIS	N-CA-C	6.13	123.86	110.80
1	A	205	SER	N-CA-C	5.11	117.08	108.96

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	39	0
1	G	3063	3131	2948	30	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	67	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 6.

All (67) 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:A:131[B]:TRP:CG	1:A:132[B]:LEU:H	2.26	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:G:204[A]:GLY:HA3	1:G:205[A]:SER:C	2.33	0.52
1:A:229:GLY:HA3	1:A:230:HIS:HD2	1.75	0.52
1:G:285:LYS:NZ	1:G:289:ASP:OD2	2.42	0.51
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: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: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:CD2	1:A:230:HIS:N	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:344:GLU:CD	1:A:344:GLU:H	2.25	0.44
1:A:46[B]:ILE:HG13	1:A:355:ALA:HB1	2.00	0.44
1:A:57[B]:HIS:HB2	1:A:303:LEU:HB3	1.99	0.43
3:A:2403:MPD:HM1	3:A:2403:MPD:O4	2.18	0.43
1:A:314:MET:HE3	1:A:314:MET:HA	2.01	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:139[B]:ARG:HA	1:G:179:PHE:CE1	2.54	0.42
1:G:204[A]:GLY:CA	1:G:205[A]:SER:C	2.91	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
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%)	7	0
1	G	420/333 (126%)	407 (97%)	11 (3%)	2 (0%)	24	7
All	All	834/666 (125%)	802 (96%)	23 (3%)	9 (1%)	16	1

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%)	328 (96%)	14 (4%)	27	4
1	G	341/268 (127%)	331 (97%)	10 (3%)	37	9
All	All	683/536 (127%)	659 (96%)	24 (4%)	32	6

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	172[A]	ILE
1	A	172[B]	ILE
1	A	230	HIS
1	A	293	MET
1	A	294[A]	LYS
1	A	294[B]	LYS
1	A	299[A]	SER
1	A	299[C]	SER
1	A	303	LEU
1	A	338	GLU
1	A	343	GLN
1	A	344	GLU
1	A	361	THR
1	A	363	ARG
1	G	47[B]	SER
1	G	47[C]	SER
1	G	51	PHE
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

Sometimes 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	2,1	10,11,12	3.12	1 (10%)	6,12,14	1.76	1 (16%)
1	KCX	G	169	2,1	10,11,12	3.75	4 (40%)	6,12,14	1.55	1 (16%)

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	2,1	-	2/9/10/12	-
1	KCX	G	169	2,1	1/1/3/4	2/9/10/12	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	169	KCX	CA-N	-10.72	1.18	1.48
1	A	169	KCX	CA-N	-9.40	1.21	1.48
1	G	169	KCX	CX-NZ	2.94	1.40	1.35
1	G	169	KCX	OQ1-CX	2.72	1.26	1.21
1	G	169	KCX	CB-CA	2.59	1.57	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	KCX	OQ1-CX-NZ	-3.92	118.97	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	169	KCX	OQ1-CX-NZ	-3.56	119.51	124.92

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	A	169	KCX	C-CA-CB-CG
1	G	169	KCX	C-CA-CB-CG
1	G	169	KCX	CA-CB-CG-CD
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 oligosaccharides 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	0.36	0	9,10,10	0.65	0
4	CAC	G	2403	2	2,4,4	2.77	2 (100%)	4,6,6	2.21	2 (50%)
3	MPD	A	2403	-	7,7,7	0.36	0	9,10,10	0.63	0
3	MPD	A	2404	-	7,7,7	0.41	0	9,10,10	0.32	0
3	MPD	G	2405	-	7,7,7	0.37	0	9,10,10	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MPD	G	2404	-	7,7,7	0.35	0	9,10,10	0.34	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
3	MPD	A	2405	-	-	2/5/5/5	-
3	MPD	A	2403	-	-	1/5/5/5	-
3	MPD	A	2404	-	-	0/5/5/5	-
3	MPD	G	2405	-	-	2/5/5/5	-
3	MPD	G	2404	-	-	0/5/5/5	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	2403	CAC	AS-C1	2.84	1.97	1.90
4	G	2403	CAC	AS-C2	2.69	1.96	1.90

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	2403	CAC	O1-AS-C2	-3.54	107.10	111.50
4	G	2403	CAC	O2-AS-C2	2.32	111.45	105.84

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2403	MPD	C2-C3-C4-O4
3	G	2405	MPD	C2-C3-C4-O4
3	G	2405	MPD	C2-C3-C4-C5
3	A	2405	MPD	C1-C2-C3-C4
3	A	2405	MPD	CM-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2403	MPD	1	0
3	G	2405	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, 95th 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 ²)	Q < 0.9
1	A	297/333 (89%)	-0.11	22 (7%)	20 21	5, 20, 53, 100	72 (24%)
1	G	327/333 (98%)	0.05	12 (3%)	45 47	7, 26, 41, 79	70 (21%)
All	All	624/666 (93%)	-0.03	34 (5%)	31 33	5, 23, 44, 100	142 (22%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	254[A]	SER	7.8
1	A	255[A]	ILE	7.3
1	G	156[A]	TYR	7.1
1	G	204[A]	GLY	6.9
1	G	205[A]	SER	6.9
1	G	362	LEU	6.7
1	A	204	GLY	5.9
1	A	232	ASP	5.9
1	A	230	HIS	5.8
1	G	203[A]	ALA	5.3
1	A	203	ALA	5.1
1	G	35	ASP	4.1
1	G	173	THR	4.1
1	A	207	ARG	3.8
1	A	362	LEU	3.7
1	A	253[A]	ASP	3.6
1	A	231	SER	3.6
1	A	205	SER	3.5
1	G	37[A]	ILE	3.5
1	A	233	GLU	3.5
1	A	363	ARG	3.2
1	A	234	THR	3.1
1	G	361	THR	3.0
1	G	337	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	235	ASP	2.5
1	A	206	GLN	2.4
1	A	280	ARG	2.3
1	A	175	LYS	2.3
1	A	91[B]	ARG	2.3
1	G	175	LYS	2.3
1	A	283	LEU	2.2
1	G	141[A]	ARG	2.1
1	A	202	THR	2.0
1	A	173	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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, 95th 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(Å ²)	Q<0.9
1	KCX	G	169	12/13	0.94	0.07	16,18,22,22	0
1	KCX	A	169	12/13	0.96	0.06	13,17,21,22	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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, 95th 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(Å ²)	Q<0.9
3	MPD	A	2404	8/8	0.45	0.32	87,105,106,106	0
3	MPD	G	2405	8/8	0.64	0.21	62,74,75,75	0
3	MPD	A	2403	8/8	0.65	0.25	50,60,61,63	0
3	MPD	G	2404	8/8	0.74	0.18	53,64,66,66	0
3	MPD	A	2405	8/8	0.74	0.19	56,68,69,69	0
2	ZN	A	2402	1/1	0.99	0.03	25,25,25,25	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	G	2402	1/1	1.00	0.01	18,18,18,18	1
2	ZN	A	2401	1/1	1.00	0.01	14,14,14,14	0
2	ZN	G	2401	1/1	1.00	0.02	18,18,18,18	0
4	CAC	G	2403	5/5	1.00	0.06	16,18,19,19	5

6.5 Other polymers [i](#)

There are no such residues in this entry.