



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 5WCW / pdb_00005wcw
Title : Phosphotriesterase variant S3
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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

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

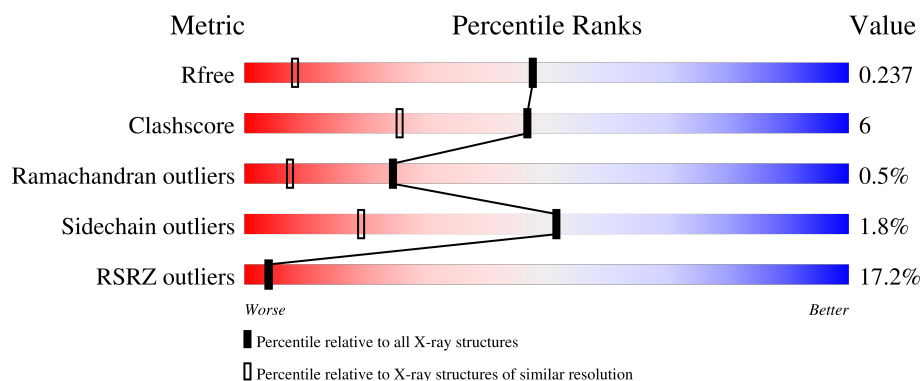
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.46 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}	180053	1756 (1.46-1.46)
Clashscore	190562	1795 (1.46-1.46)
Ramachandran outliers	187476	1776 (1.46-1.46)
Sidechain outliers	187428	1776 (1.46-1.46)
RSRZ outliers	180081	1756 (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 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
4	CAC	G	2404	-	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.

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

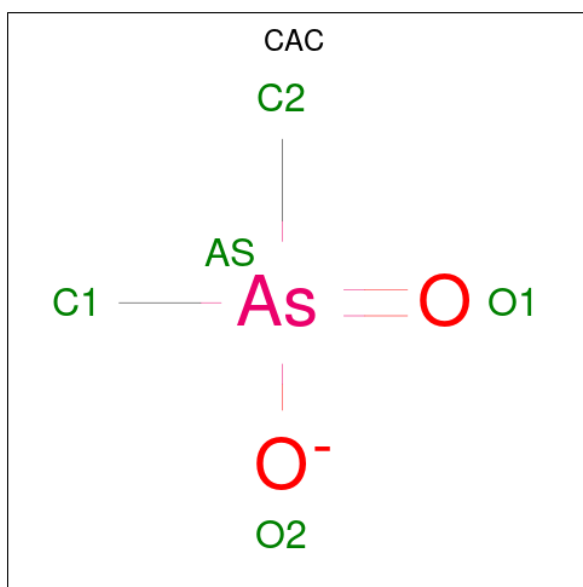
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	G	2	Total	Zn	0	0
			2	2		

- 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	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 (CCD ID: 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		

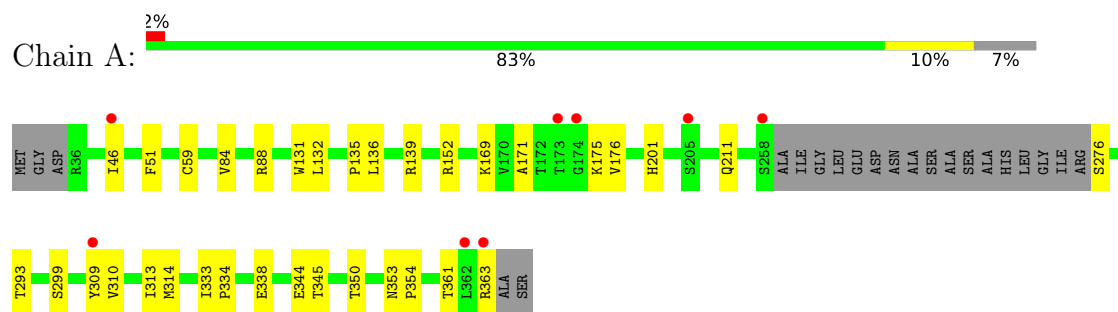
- Molecule 5 is water.

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

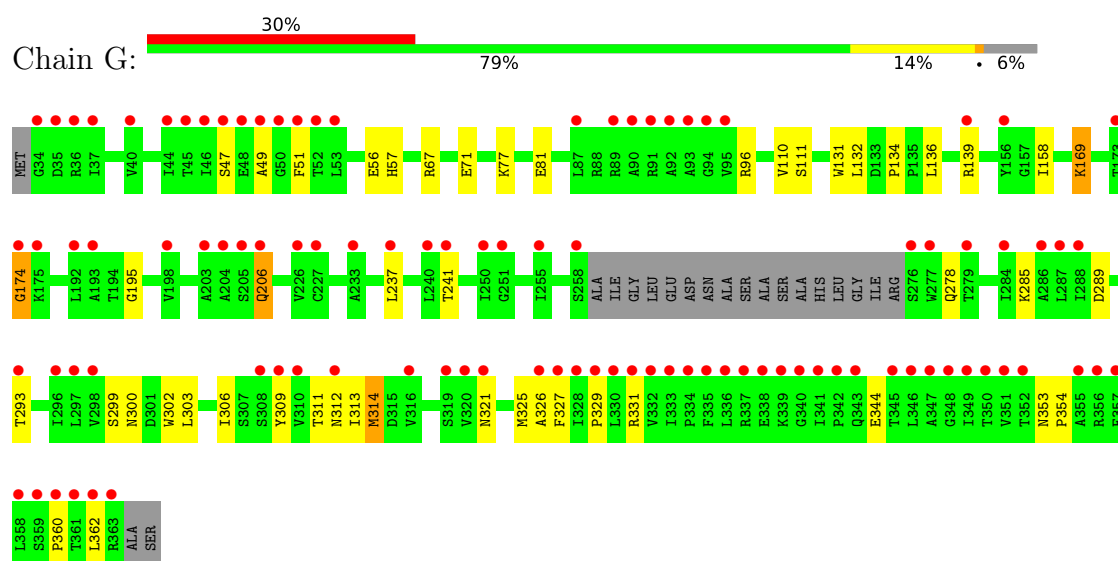
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, 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	85.51Å 85.89Å 88.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.25 – 1.46 39.25 – 1.46	Depositor EDS
% Data completeness (in resolution range)	99.4 (39.25-1.46) 99.4 (39.25-1.46)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 1.46Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.208 , 0.234 0.210 , 0.237	Depositor DCC
R_{free} test set	5683 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	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	0.95	EDS
Total number of atoms	5103	wwPDB-VP
Average B, all atoms (Å ²)	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.*

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: KCX, ZN, CAC, MPD

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	0.40	0/2448	0.60	0/3324
1	G	0.26	0/2443	0.49	0/3318
All	All	0.34	0/4891	0.55	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	21	1
1	G	2412	0	2436	31	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	56	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 6.

All (56) 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
1:G:314:MET:HA	1:G:314:MET:HE3	1.70	0.74
3:A:2403:MPD:O4	3:A:2403:MPD:O2	2.05	0.73
3:A:2404:MPD:O4	3:A:2404:MPD:O2	2.10	0.60
1:G:71[B]:GLU:H	1:G:71[B]:GLU:CD	2.10	0.60
1:G:77:LYS:NZ	1:G:81:GLU:OE2	2.34	0.60
1:G:174:GLY:HA2	1:G:206:GLN:HG2	1.83	0.60
1:A:314:MET:HE3	1:A:314:MET:HA	1.84	0.58
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: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:A:131:TRP:CG	1:A:132:LEU:H	2.27	0.53
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:131:TRP:CG	1:G:132:LEU:H	2.28	0.51
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:A:344:GLU:CD	1:A:344:GLU:H	2.18	0.50
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:G:56:GLU:HB3	1:G:325:MET:HE2	1.93	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:G:326:ALA:C	1:G:329:PRO:HD2	2.37	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
1:G:169:KCX:OQ2	4:G:2404:CAC:O2	2.35	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:H53	3:A:2403:MPD:HM1	2.01	0.42
1:G:51:PHE:HD1	1:G:51:PHE:C	2.26	0.42
1:G:51:PHE:C	1:G:51:PHE:CD1	2.97	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:A:51:PHE:C	1:A:51:PHE:CD1	2.98	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%)	36 16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	311/333 (93%)	300 (96%)	9 (3%)	2 (1%)	21	6
All	All	622/666 (93%)	603 (97%)	16 (3%)	3 (0%)	24	7

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	176	VAL
1	G	362	LEU
1	G	174	GLY

5.3.2 Protein sidechains [i](#)

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%)	250 (98%)	5 (2%)	48	16
1	G	254/265 (96%)	250 (98%)	4 (2%)	55	23
All	All	509/530 (96%)	500 (98%)	9 (2%)	51	19

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	ILE
1	A	152	ARG
1	A	276	SER
1	A	299	SER
1	A	338	GLU
1	G	47	SER
1	G	206	GLN
1	G	299	SER
1	G	314	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	148	GLN
1	G	206	GLN

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	2,1	10,11,12	0.87	0	6,12,14	1.35	1 (16%)
1	KCX	A	169	2,1	10,11,12	1.55	1 (10%)	6,12,14	1.64	2 (33%)

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	2,1	-	1/9/10/12	-
1	KCX	A	169	2,1	-	1/9/10/12	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	169	KCX	CE-NZ	4.33	1.55	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	169	KCX	OQ1-CX-NZ	-2.90	120.52	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	KCX	OQ1-CX-NZ	-2.80	120.67	124.92
1	A	169	KCX	CE-NZ-CX	2.57	126.34	121.98

There are no chirality outliers.

All (2) 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

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	A	2403	-	7,7,7	0.68	0	9,10,10	0.37	0
4	CAC	A	2405	2	2,4,4	1.90	1 (50%)	4,6,6	1.61	1 (25%)
3	MPD	G	2403	-	7,7,7	0.66	0	9,10,10	0.29	0
3	MPD	A	2404	-	7,7,7	0.64	0	9,10,10	0.50	0
4	CAC	G	2404	2	2,4,4	3.44	2 (100%)	4,6,6	8.16	4 (100%)

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	-	-	3/5/5/5	-
3	MPD	A	2404	-	-	3/5/5/5	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	2404	CAC	AS-C2	3.73	1.99	1.90
4	G	2404	CAC	AS-C1	3.13	1.97	1.90
4	A	2405	CAC	AS-C1	2.03	1.95	1.90

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	2404	CAC	O1-AS-C2	-9.55	99.63	111.50
4	G	2404	CAC	O1-AS-C1	-8.31	101.17	111.50
4	G	2404	CAC	O2-AS-C2	8.15	125.58	105.84
4	G	2404	CAC	O2-AS-C1	6.32	121.16	105.84
4	A	2405	CAC	O2-AS-C1	3.17	113.52	105.84

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2403	MPD	C2-C3-C4-C5
3	A	2404	MPD	C2-C3-C4-O4
3	A	2403	MPD	CM-C2-C3-C4
3	G	2403	MPD	C1-C2-C3-C4
3	G	2403	MPD	CM-C2-C3-C4
3	A	2404	MPD	O2-C2-C3-C4
3	G	2403	MPD	O2-C2-C3-C4
3	A	2403	MPD	C1-C2-C3-C4
3	A	2404	MPD	C1-C2-C3-C4

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2403	MPD	3	0
4	A	2405	CAC	1	0
3	G	2403	MPD	1	0
3	A	2404	MPD	1	0
4	G	2404	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, 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	310/333 (93%)	0.39	8 (2%) 57 59	10, 22, 37, 62	6 (1%)
1	G	312/333 (93%)	1.47	99 (31%) 1 1	11, 38, 57, 74	3 (0%)
All	All	622/666 (93%)	0.93	107 (17%) 4 4	10, 29, 54, 74	9 (1%)

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	362	LEU	8.8
1	G	34	GLY	5.4
1	G	320	VAL	5.1
1	G	46	ILE	5.0
1	G	174	GLY	4.7
1	A	362	LEU	4.4
1	G	37	ILE	4.0
1	G	330	LEU	4.0
1	G	341	ILE	3.9
1	G	51	PHE	3.9
1	G	310	VAL	3.8
1	G	327	PHE	3.7
1	G	319	SER	3.7
1	G	258	SER	3.6
1	G	351	VAL	3.6
1	G	346	LEU	3.6
1	G	360	PRO	3.6
1	G	363	ARG	3.6
1	G	349	ILE	3.5
1	G	49	ALA	3.4
1	G	286	ALA	3.4
1	G	328	ILE	3.4
1	G	173	THR	3.4
1	G	337	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
1	G	316	VAL	3.4
1	G	92	ALA	3.3
1	G	277	TRP	3.3
1	G	326	ALA	3.2
1	G	358	LEU	3.1
1	G	361	THR	3.1
1	G	94	GLY	3.1
1	G	335	PHE	3.1
1	G	44	ILE	3.1
1	G	333	ILE	3.1
1	G	204	ALA	3.1
1	G	334	PRO	3.0
1	G	350	THR	3.0
1	A	363	ARG	2.9
1	A	258	SER	2.9
1	G	332	VAL	2.9
1	G	336	LEU	2.9
1	G	347	ALA	2.9
1	G	255	ILE	2.9
1	G	309	TYR	2.9
1	G	139	ARG	2.9
1	G	355	ALA	2.8
1	A	46	ILE	2.8
1	G	279	THR	2.8
1	G	298	VAL	2.8
1	G	93	ALA	2.8
1	G	329	PRO	2.8
1	G	296	ILE	2.8
1	G	91	ARG	2.8
1	G	206	GLN	2.7
1	G	203	ALA	2.7
1	G	345	THR	2.7
1	G	233	ALA	2.7
1	G	50	GLY	2.7
1	G	45	THR	2.7
1	G	47	SER	2.7
1	G	338	GLU	2.6
1	G	308	SER	2.6
1	G	342	PRO	2.6
1	G	205	SER	2.6
1	G	241	THR	2.6
1	G	293	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	87	LEU	2.5
1	G	156	TYR	2.5
1	G	40	VAL	2.5
1	G	89	ARG	2.5
1	G	348	GLY	2.5
1	G	36	ARG	2.5
1	G	250	ILE	2.4
1	G	352	THR	2.4
1	A	174	GLY	2.4
1	G	276	SER	2.4
1	G	343	GLN	2.3
1	A	205	SER	2.3
1	G	284	ILE	2.3
1	G	288	ILE	2.3
1	G	297	LEU	2.3
1	G	357	PHE	2.3
1	G	52	THR	2.3
1	G	287	LEU	2.3
1	G	226	VAL	2.3
1	G	237	LEU	2.2
1	G	359	SER	2.2
1	G	331	ARG	2.2
1	G	35	ASP	2.2
1	G	53	LEU	2.2
1	A	173	THR	2.2
1	G	192	LEU	2.1
1	G	227	CYS	2.1
1	G	175	LYS	2.1
1	A	309	TYR	2.1
1	G	251	GLY	2.1
1	G	321	ASN	2.1
1	G	90	ALA	2.1
1	G	339	LYS	2.1
1	G	312	ASN	2.1
1	G	340	GLY	2.1
1	G	193	ALA	2.0
1	G	48	GLU	2.0
1	G	356	ARG	2.0
1	G	95	VAL	2.0
1	G	198	VAL	2.0
1	G	240	LEU	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	A	169	12/13	0.94	0.08	12,13,14,15	0
1	KCX	G	169	12/13	0.94	0.10	25,27,29,32	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	G	2403	8/8	0.52	0.31	43,44,46,47	8
3	MPD	A	2403	8/8	0.69	0.23	43,44,46,46	8
3	MPD	A	2404	8/8	0.75	0.18	40,44,45,45	0
4	CAC	G	2404	5/5	0.92	0.23	33,37,40,40	11
2	ZN	G	2401	1/1	0.98	0.04	30,30,30,30	0
4	CAC	A	2405	5/5	0.99	0.08	14,15,18,20	5
2	ZN	G	2402	1/1	0.99	0.03	31,31,31,31	0
2	ZN	A	2402	1/1	1.00	0.05	16,16,16,16	0
2	ZN	A	2401	1/1	1.00	0.02	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.