



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 08:17 PM UTC

PDB ID : 4XD6 / pdb_00004xd6
Title : Phosphotriesterase Variant E2a
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Deposited on : 2014-12-19
Resolution : 1.75 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

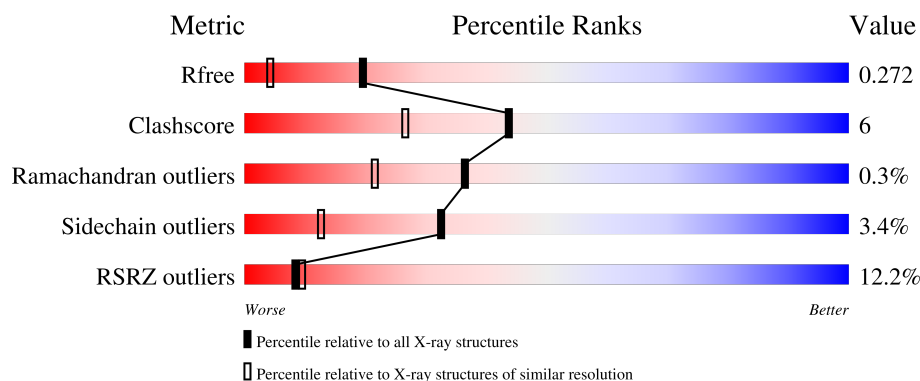
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	 7% 87% 10% ..
1	G	333	 17% 83% 15% ..

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	CAC	A	403	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5868 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

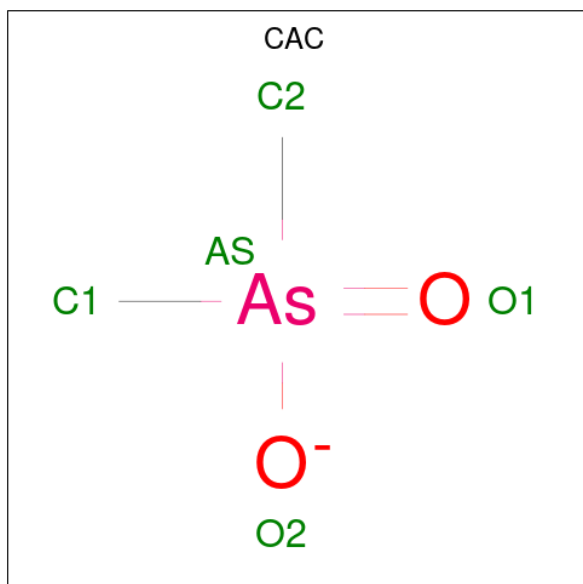
- Molecule 1 is a protein called Phosphotriesterase variant PTE-E2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	8	0
			2585	1630	465	482	8			
1	G	329	Total	C	N	O	S	0	5	0
			2547	1609	453	477	8			

- 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 CACODYLATE ION (CCD ID: CAC) (formula: C₂H₆AsO₂).



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

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



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

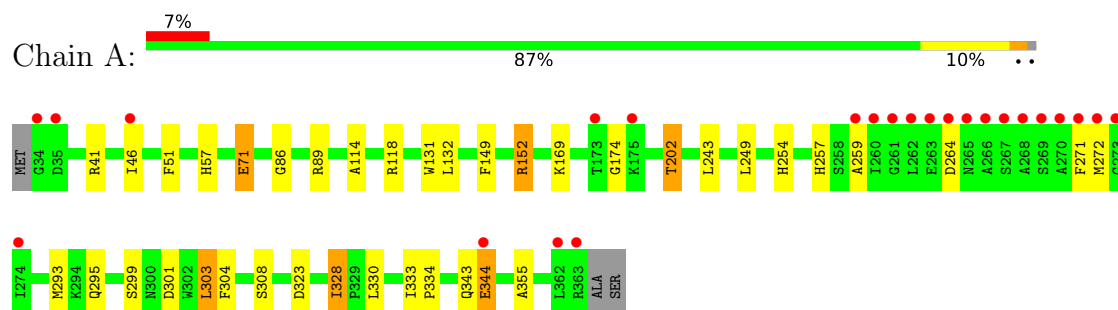
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	370	Total	O	0	0
			370	370		
5	G	320	Total	O	0	0
			320	320		

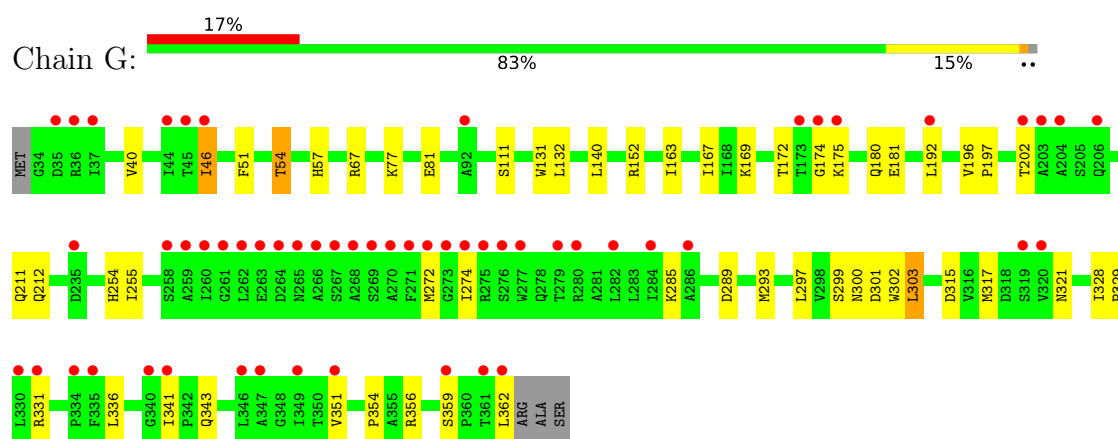
3 Residue-property plots

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 variant PTE-E2



• Molecule 1: Phosphotriesterase variant PTE-E2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	85.74Å 85.76Å 88.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.28 – 1.75 39.28 – 1.75	Depositor EDS
% Data completeness (in resolution range)	89.4 (39.28-1.75) 83.2 (39.28-1.75)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 1.75Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.9_1692)	Depositor
R, R_{free}	0.214 , 0.269 0.218 , 0.272	Depositor DCC
R_{free} test set	3157 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	12.9	Xtriage
Anisotropy	0.359	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.025 for -h,l,k 0.025 for -l,-k,-h 0.027 for k,h,-l 0.016 for k,l,h 0.016 for l,h,k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5868	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CAC, ZN, KCX, 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	0.54	0/2620	0.79	0/3554
1	G	0.45	0/2582	0.82	3/3505 (0.1%)
All	All	0.50	0/5202	0.80	3/7059 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	255	ILE	CA-C-N	-5.77	114.95	120.83
1	G	255	ILE	C-N-CA	-5.77	114.95	120.83
1	G	255	ILE	CB-CA-C	-5.54	108.44	113.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2585	0	2600	31	0
1	G	2547	0	2564	33	0
2	A	2	0	0	0	0
2	G	2	0	0	0	0
3	A	5	0	0	0	0
3	G	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	16	0	28	2	0
4	G	16	0	28	2	0
5	A	370	0	0	10	1
5	G	320	0	0	6	0
All	All	5868	0	5220	63	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 (63) 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:343:GLN:HE22	4:G:405:MPD:H12	1.39	0.85
1:G:301:ASP:OD2	5:G:815:HOH:O	1.98	0.82
1:A:301:ASP:OD2	5:A:859:HOH:O	1.99	0.81
1:A:118[B]:ARG:NH2	5:A:844:HOH:O	2.20	0.73
1:G:181:GLU:OE2	5:G:803:HOH:O	2.06	0.73
1:A:343:GLN:HE22	4:A:404:MPD:H12	1.54	0.71
1:A:118[A]:ARG:NH1	5:A:501:HOH:O	2.27	0.67
1:A:254:HIS:NE2	5:A:859:HOH:O	2.31	0.63
1:G:285:LYS:NZ	1:G:289:ASP:OD2	2.32	0.62
1:G:254:HIS:NE2	5:G:815:HOH:O	2.31	0.61
1:A:89[B]:ARG:HD3	5:A:695:HOH:O	2.01	0.60
1:A:89[B]:ARG:HG2	5:A:525:HOH:O	2.03	0.59
1:A:131:TRP:CG	1:A:132:LEU:H	2.24	0.56
1:G:131:TRP:CG	1:G:132:LEU:H	2.22	0.56
1:A:57:HIS:HB2	1:A:303:LEU:HB3	1.90	0.54
1:G:67:ARG:NH2	1:G:111[A]:SER:OG	2.40	0.54
1:A:257:HIS:HA	1:A:272:MET:HE2	1.90	0.53
1:A:344:GLU:CD	1:A:344:GLU:H	2.17	0.53
1:G:46[B]:ILE:HG21	1:G:359[B]:SER:OG	2.09	0.52
1:A:46:ILE:HD11	1:A:355:ALA:HB1	1.91	0.52
1:G:192:LEU:O	1:G:362:LEU:HD11	2.10	0.52
1:G:57:HIS:HB2	1:G:303:LEU:HB3	1.90	0.52
1:G:77:LYS:NZ	1:G:81:GLU:OE2	2.37	0.51
1:A:202:THR:HG21	5:A:631:HOH:O	2.10	0.51
4:A:405:MPD:O4	4:A:405:MPD:O2	2.28	0.51
1:A:71:GLU:H	1:A:71:GLU:CD	2.20	0.50
1:G:343:GLN:NE2	4:G:405:MPD:H12	2.17	0.50
1:A:259:ALA:HB2	1:A:272:MET:SD	2.51	0.50
1:G:272:MET:HE3	1:G:317:MET:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:300:ASN:OD1	1:G:328:ILE:HG12	2.12	0.49
1:A:41:ARG:NH2	5:A:502:HOH:O	2.29	0.49
1:G:54:THR:HG21	1:G:297:LEU:HB3	1.96	0.48
1:A:114:ALA:O	1:A:118[B]:ARG:HG2	2.14	0.47
1:G:167:ILE:HG13	1:G:197:PRO:HG2	1.96	0.47
1:A:149:PHE:O	1:A:152:ARG:HG3	2.15	0.47
1:G:172:THR:HG22	1:G:180:GLN:HB3	1.97	0.45
1:G:202:THR:HG22	1:G:212:GLN:NE2	2.31	0.45
1:A:86:GLY:HA3	1:A:304:PHE:CE1	2.52	0.45
1:A:71:GLU:OE1	1:G:152:ARG:NE	2.41	0.45
1:G:51:PHE:CE2	1:G:329:PRO:HB3	2.52	0.45
1:A:57:HIS:O	1:A:303:LEU:HA	2.18	0.44
1:G:302:TRP:CH2	1:G:321:ASN:HB3	2.53	0.44
1:G:40:VAL:HA	1:G:163:ILE:HG23	2.00	0.44
1:A:333:ILE:HB	1:A:334:PRO:HD3	2.00	0.43
1:G:336:LEU:HB3	1:G:341:ILE:HD12	2.00	0.43
1:A:323:ASP:O	5:A:695:HOH:O	2.22	0.43
1:G:300:ASN:CG	1:G:328:ILE:HG12	2.44	0.42
1:G:362:LEU:HD12	1:G:362:LEU:HA	1.79	0.42
1:A:131:TRP:CG	1:A:132:LEU:N	2.88	0.41
1:A:118[B]:ARG:HG3	5:A:602:HOH:O	2.19	0.41
1:A:249:LEU:HD13	1:A:295:GLN:HA	2.02	0.41
1:G:293:MET:HE2	1:G:293:MET:HB2	1.91	0.41
1:G:131:TRP:CG	1:G:132:LEU:N	2.89	0.41
1:A:308:SER:O	1:G:140:LEU:HD22	2.21	0.41
1:G:57:HIS:O	1:G:303:LEU:HA	2.19	0.41
1:A:243:LEU:HD23	1:A:243:LEU:HA	1.93	0.41
1:A:328:ILE:HD13	1:A:328:ILE:HA	1.88	0.41
1:G:175:LYS:HG3	5:G:748:HOH:O	2.21	0.41
1:G:356:ARG:HD2	5:G:561:HOH:O	2.20	0.41
1:G:315:ASP:OD1	5:G:693:HOH:O	2.21	0.40
1:A:51:PHE:C	1:A:51:PHE:CD1	2.99	0.40
1:A:330:LEU:O	1:A:334:PRO:HG2	2.21	0.40
1:G:351:VAL:C	1:G:354:PRO:HD2	2.45	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)
5:A:545:HOH:O	5:A:549:HOH:O[3_555]	2.15	0.05

5.3 Torsion angles

5.3.1 Protein backbone

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	335/333 (101%)	322 (96%)	12 (4%)	1 (0%)	36	21
1	G	331/333 (99%)	318 (96%)	12 (4%)	1 (0%)	36	21
All	All	666/666 (100%)	640 (96%)	24 (4%)	2 (0%)	36	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	174	GLY
1	A	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	271/266 (102%)	261 (96%)	10 (4%)	30	11
1	G	268/266 (101%)	259 (97%)	9 (3%)	32	13
All	All	539/532 (101%)	520 (96%)	19 (4%)	32	12

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	GLU
1	A	152	ARG
1	A	202	THR
1	A	264	ASP

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Mol	Chain	Res	Type
1	A	271	PHE
1	A	293	MET
1	A	299	SER
1	A	303	LEU
1	A	328	ILE
1	A	344	GLU
1	G	46[A]	ILE
1	G	46[B]	ILE
1	G	54	THR
1	G	196	VAL
1	G	211	GLN
1	G	274	ILE
1	G	299	SER
1	G	303	LEU
1	G	331	ARG

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	343	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	1.14	1 (10%)	6,12,14	2.06	2 (33%)

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	0.98	0	6,12,14	1.38	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	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	G	169	KCX	OQ1-CX	2.44	1.26	1.21

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	169	KCX	OQ1-CX-NZ	-3.68	119.33	124.92
1	G	169	KCX	CE-NZ-CX	-3.28	116.41	121.98
1	A	169	KCX	OQ1-CX-NZ	-2.72	120.79	124.92

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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	CAC	G	402	2	2,4,4	2.82	2 (100%)	4,6,6	1.04	0
4	MPD	G	405	-	7,7,7	0.29	0	9,10,10	0.74	0
3	CAC	A	403	2	2,4,4	2.89	2 (100%)	4,6,6	2.23	2 (50%)
4	MPD	A	405	-	7,7,7	0.34	0	9,10,10	0.20	0
4	MPD	A	404	-	7,7,7	0.27	0	9,10,10	0.73	0
4	MPD	G	404	-	7,7,7	0.28	0	9,10,10	0.28	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
4	MPD	A	404	-	-	4/5/5/5	-
4	MPD	G	405	-	-	3/5/5/5	-
4	MPD	G	404	-	-	1/5/5/5	-
4	MPD	A	405	-	-	2/5/5/5	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	402	CAC	AS-C2	2.91	1.97	1.90
3	A	403	CAC	AS-C1	2.89	1.97	1.90
3	A	403	CAC	AS-C2	2.88	1.97	1.90
3	G	402	CAC	AS-C1	2.73	1.96	1.90

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	403	CAC	O2-AS-C2	3.31	113.85	105.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	403	CAC	O1-AS-C2	-2.36	108.56	111.50

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	404	MPD	C1-C2-C3-C4
4	A	404	MPD	C2-C3-C4-C5
4	A	404	MPD	CM-C2-C3-C4
4	A	405	MPD	C1-C2-C3-C4
4	G	404	MPD	C2-C3-C4-C5
4	G	405	MPD	C2-C3-C4-C5
4	G	405	MPD	O2-C2-C3-C4
4	A	404	MPD	C2-C3-C4-O4
4	A	405	MPD	CM-C2-C3-C4
4	G	405	MPD	C1-C2-C3-C4

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	405	MPD	2	0
4	A	405	MPD	1	0
4	A	404	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	329/333 (98%)	0.51	24 (7%)	21 24	5, 13, 50, 138	8 (2%)
1	G	328/333 (98%)	1.11	56 (17%)	4 4	8, 22, 56, 95	5 (1%)
All	All	657/666 (98%)	0.81	80 (12%)	8 9	5, 18, 56, 138	13 (1%)

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	260	ILE	10.7
1	A	273	GLY	10.6
1	A	266	ALA	9.9
1	A	262	LEU	9.4
1	A	270	ALA	9.3
1	A	271	PHE	8.9
1	G	274	ILE	7.5
1	A	268	ALA	7.3
1	A	261	GLY	7.2
1	A	259	ALA	6.9
1	G	260	ILE	6.6
1	G	271	PHE	6.4
1	A	265	ASN	6.3
1	A	274	ILE	6.2
1	G	262	LEU	6.1
1	G	268	ALA	5.5
1	G	270	ALA	5.5
1	A	267	SER	5.3
1	A	263	GLU	5.2
1	A	269	SER	5.2
1	G	266	ALA	5.1
1	G	273	GLY	5.0
1	G	259	ALA	5.0
1	G	265	ASN	4.9

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Mol	Chain	Res	Type	RSRZ
1	G	362	LEU	4.9
1	G	261	GLY	4.6
1	G	263	GLU	4.5
1	A	34	GLY	4.4
1	A	264	ASP	4.4
1	G	37	ILE	3.9
1	A	272	MET	3.9
1	G	269	SER	3.7
1	G	267	SER	3.5
1	G	46[A]	ILE	3.5
1	G	335	PHE	3.5
1	G	264	ASP	3.4
1	A	362	LEU	3.3
1	G	258	SER	3.2
1	G	275	ARG	3.2
1	A	363	ARG	3.0
1	G	320	VAL	2.9
1	G	204	ALA	2.9
1	A	46	ILE	2.9
1	G	272	MET	2.8
1	G	330	LEU	2.8
1	G	276	SER	2.8
1	A	173	THR	2.7
1	G	206	GLN	2.6
1	G	203	ALA	2.6
1	G	286	ALA	2.6
1	G	361	THR	2.5
1	G	175	LYS	2.5
1	G	35	ASP	2.5
1	G	174	GLY	2.5
1	G	36[A]	ARG	2.4
1	G	173	THR	2.4
1	G	319	SER	2.4
1	G	282	LEU	2.4
1	G	340	GLY	2.3
1	A	35	ASP	2.3
1	G	92	ALA	2.3
1	G	347	ALA	2.3
1	A	175	LYS	2.3
1	G	277	TRP	2.2
1	G	45	THR	2.2
1	G	192	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	44	ILE	2.2
1	G	341	ILE	2.2
1	G	359[A]	SER	2.2
1	G	351	VAL	2.1
1	G	280	ARG	2.1
1	G	334	PRO	2.1
1	G	349	ILE	2.1
1	G	331	ARG	2.1
1	G	235	ASP	2.1
1	G	202	THR	2.1
1	A	344	GLU	2.0
1	G	346	LEU	2.0
1	G	279	THR	2.0
1	G	284	ILE	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	0.93	0.08	11,16,18,20	0
1	KCX	A	169	12/13	0.94	0.07	3,7,9,11	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
4	MPD	G	404	8/8	0.73	0.22	25,39,47,50	0
4	MPD	A	405	8/8	0.75	0.17	18,41,44,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MPD	A	404	8/8	0.79	0.15	23,33,42,50	0
4	MPD	G	405	8/8	0.79	0.20	34,46,49,49	0
3	CAC	A	403	5/5	0.82	0.20	15,33,56,79	0
3	CAC	G	402	5/5	0.82	0.19	19,28,63,72	0
2	ZN	G	401	1/1	0.98	0.03	22,22,22,22	0
2	ZN	A	402	1/1	0.99	0.02	12,12,12,12	0
2	ZN	A	401	1/1	0.99	0.01	8,8,8,8	0
2	ZN	G	403	1/1	0.99	0.02	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.