



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 07:44 PM UTC

PDB ID : 2BCR / pdb_00002bcr
Title : DNA polymerase lambda in complex with a DNA duplex containing an unpaired Damp
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Deposited on : 2005-10-19
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

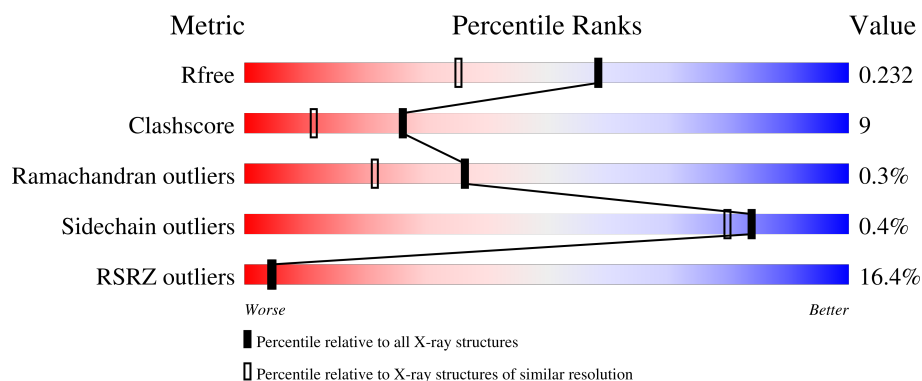
1 Overall quality at a glance

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	D	4	75% 25%
2	P	7	100%
3	T	12	92% 8%
4	A	335	17% 78% 19% .

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 3579 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 DNA chain called 5'-D(P*GP*CP*CP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			

- Molecule 2 is a DNA chain called 5'-D(*CP*AP*GP*TP*AP*CP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	7	Total	C	N	O	P	0	0	0
			141	68	28	39	6			

- Molecule 3 is a DNA chain called 5'-D(*CP*GP*GP*CP*CP*GP*AP*TP*AP*CP*TP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	12	Total	C	N	O	P	0	0	0
			243	116	46	70	11			

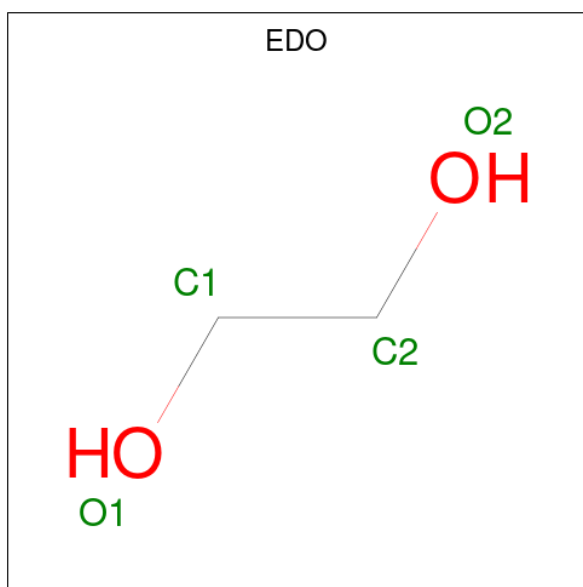
- Molecule 4 is a protein called DNA polymerase lambda.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	325	Total	C	N	O	S	0	6	0
			2555	1604	462	478	11			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	MET	-	initiating methionine	UNP Q9UGP5

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

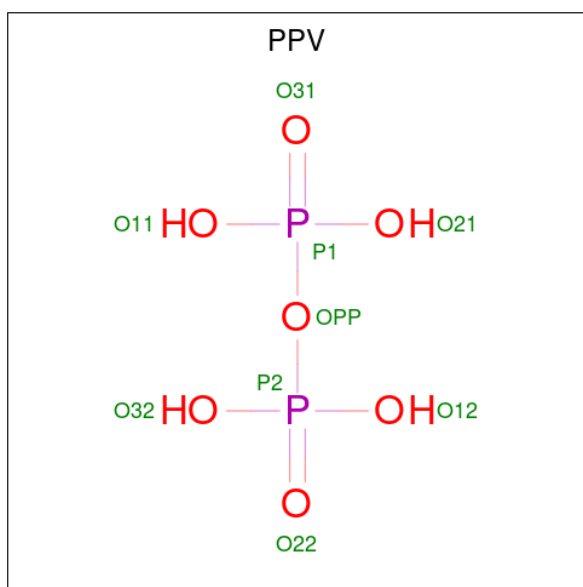
- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		

- Molecule 7 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	3	Total	Na	0	0
			3	3		

- Molecule 8 is PYROPHOSPHATE (CCD ID: PPV) (formula: H₄O₇P₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	P	0	0
			9	7	2		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	22	Total	O	0	0
			22	22		
9	P	43	Total	O	0	0
			43	43		
9	T	91	Total	O	0	0
			91	91		
9	A	368	Total	O	0	0
			368	368		

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: 5'-D(P*GP*CP*CP*G)-3'

Chain D: 



- Molecule 2: 5'-D(*CP*AP*GP*TP*AP*CP*G)-3'

Chain P: 

There are no outlier residues recorded for this chain.

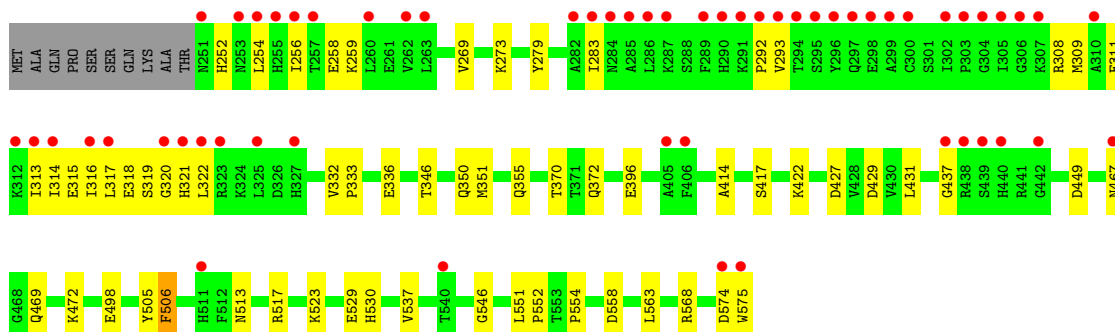
- Molecule 3: 5'-D(*CP*GP*GP*CP*CP*GP*AP*TP*AP*CP*TP*G)-3'

Chain T: 



- Molecule 4: DNA polymerase lambda

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.08Å 62.92Å 139.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.87 – 1.75 41.87 – 1.75	Depositor EDS
% Data completeness (in resolution range)	90.8 (41.87-1.75) 91.5 (41.87-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.54 (at 1.75Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.202 , 0.231 0.205 , 0.232	Depositor DCC
R_{free} test set	2384 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	20.1	Xtriage
Anisotropy	0.557	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 46.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3579	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 5.42% 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: MG, NA, EDO, PPV

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	D	0.50	0/92	0.57	0/138
2	P	0.27	0/158	0.60	0/242
3	T	0.27	0/272	0.64	0/418
4	A	0.37	0/2606	0.81	2/3521 (0.1%)
All	All	0.36	0/3128	0.78	2/4319 (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
3	T	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	273	LYS	N-CA-C	5.76	118.30	111.33
4	A	370	THR	N-CA-C	-5.70	103.17	110.53

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	T	11	DT	Sidechain

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	D	83	0	45	1	0
2	P	141	0	80	0	0
3	T	243	0	136	0	0
4	A	2555	0	2510	55	0
5	A	16	0	24	0	0
5	P	4	0	6	0	0
6	A	1	0	0	0	0
7	A	3	0	0	0	0
8	A	9	0	0	0	0
9	A	368	0	0	6	0
9	D	22	0	0	0	0
9	P	43	0	0	0	0
9	T	91	0	0	1	0
All	All	3579	0	2801	55	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 9.

All (55) 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)
4:A:417:SER:HB2	4:A:422[B]:LYS:HD3	1.40	1.01
4:A:269:VAL:HG11	4:A:336:GLU:HG2	1.54	0.88
4:A:314:ILE:HD12	4:A:315:GLU:N	1.92	0.84
4:A:311:GLU:O	4:A:314:ILE:HG13	1.83	0.78
4:A:417:SER:CB	4:A:422[B]:LYS:HD3	2.15	0.76
4:A:259:LYS:HE2	4:A:316:ILE:HG23	1.68	0.74
4:A:568:ARG:HH22	4:A:575:TRP:NE1	1.87	0.73
4:A:252:HIS:HB3	4:A:292:PRO:HG3	1.71	0.72
4:A:568:ARG:HH22	4:A:575:TRP:HE1	1.39	0.70
4:A:256:ILE:HD11	4:A:317:LEU:HD11	1.75	0.66
4:A:319:SER:C	4:A:321:HIS:H	2.04	0.64
4:A:346[A]:THR:O	4:A:350:GLN:HG3	2.02	0.59
4:A:346[B]:THR:O	4:A:350:GLN:HG3	2.03	0.58
4:A:568:ARG:NH2	4:A:575:TRP:HE1	1.99	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:321:HIS:CG	4:A:322:LEU:H	2.21	0.58
4:A:351:MET:O	4:A:355:GLN:HG3	2.04	0.57
4:A:346[B]:THR:HG23	9:A:833:HOH:O	2.03	0.57
4:A:537:VAL:HB	4:A:546:GLY:HA3	1.86	0.57
4:A:523:LYS:HE3	4:A:563:LEU:O	2.06	0.55
4:A:431:LEU:C	4:A:431:LEU:HD23	2.33	0.54
1:D:1:DG:OP2	4:A:308:ARG:HD3	2.09	0.53
4:A:568:ARG:HH12	4:A:575:TRP:HZ2	1.55	0.53
4:A:254:LEU:HD23	4:A:254:LEU:O	2.10	0.52
4:A:321:HIS:CG	4:A:322:LEU:N	2.77	0.52
4:A:467:ASN:OD1	4:A:469:GLN:HB2	2.10	0.52
4:A:314:ILE:HD12	4:A:314:ILE:C	2.34	0.52
4:A:256:ILE:HD11	4:A:317:LEU:CD1	2.41	0.51
4:A:319:SER:C	4:A:321:HIS:N	2.67	0.51
4:A:554:PRO:HG2	4:A:558:ASP:OD2	2.11	0.51
4:A:332:VAL:HB	4:A:333:PRO:HD3	1.92	0.50
4:A:396:GLU:HG3	4:A:414:ALA:HB2	1.95	0.49
4:A:498:GLU:HG2	4:A:530:HIS:O	2.13	0.48
4:A:318:GLU:HG2	9:A:1169:HOH:O	2.13	0.48
4:A:437:GLY:HA2	9:A:979:HOH:O	2.14	0.47
4:A:422[B]:LYS:CE	9:A:931:HOH:O	2.62	0.47
4:A:293:VAL:O	4:A:317:LEU:HD21	2.14	0.47
4:A:513:ASN:O	4:A:517:ARG:HG3	2.15	0.47
4:A:315:GLU:O	4:A:319:SER:HB3	2.15	0.46
9:T:15:HOH:O	4:A:372:GLN:HG3	2.17	0.45
4:A:332:VAL:O	4:A:336:GLU:HG3	2.17	0.45
4:A:449:ASP:HB3	9:A:1134:HOH:O	2.16	0.45
4:A:314:ILE:HD12	4:A:315:GLU:CA	2.47	0.44
4:A:472:LYS:HE2	9:A:981:HOH:O	2.17	0.44
4:A:427:ASP:C	4:A:427:ASP:OD1	2.61	0.43
4:A:568:ARG:NH2	4:A:575:TRP:NE1	2.60	0.43
4:A:279:TYR:O	4:A:283:ILE:HG13	2.19	0.43
4:A:551:LEU:HA	4:A:552:PRO:HD3	1.89	0.42
4:A:429:ASP:HB3	4:A:506:PHE:CE2	2.55	0.42
4:A:309:MET:O	4:A:313:ILE:HG13	2.19	0.42
4:A:422[A]:LYS:HD3	4:A:422[A]:LYS:HA	1.90	0.42
4:A:254:LEU:O	4:A:258:GLU:HG2	2.20	0.41
4:A:314:ILE:O	4:A:318:GLU:CB	2.69	0.41
4:A:259:LYS:HE2	4:A:316:ILE:CG2	2.44	0.41
4:A:505:TYR:CG	4:A:529:GLU:HB3	2.56	0.41
4:A:574:ASP:C	4:A:575:TRP:HD1	2.30	0.40

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
4	A	329/335 (98%)	321 (98%)	7 (2%)	1 (0%)	36 21

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	320	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
4	A	267/281 (95%)	266 (100%)	1 (0%)	84 80

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	506	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	270	GLN

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Mol	Chain	Res	Type
4	A	350	GLN
4	A	355	GLN
4	A	400	GLN
4	A	469	GLN
4	A	511	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

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	$\# Z > 2$
5	EDO	A	801	-	3,3,3	0.52	0	2,2,2	0.52	0
5	EDO	A	805	-	3,3,3	0.51	0	2,2,2	0.51	0
5	EDO	A	802	-	3,3,3	0.43	0	2,2,2	0.43	0
5	EDO	A	804	-	3,3,3	0.48	0	2,2,2	0.52	0
8	PPV	A	638	6	6,8,8	1.05	1 (16%)	12,13,13	1.31	1 (8%)
5	EDO	P	803	-	3,3,3	0.46	0	2,2,2	0.43	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
5	EDO	A	801	-	-	0/1/1/1	-
5	EDO	A	805	-	-	1/1/1/1	-
5	EDO	A	802	-	-	0/1/1/1	-
5	EDO	A	804	-	-	0/1/1/1	-
8	PPV	A	638	6	-	0/6/6/6	-
5	EDO	P	803	-	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	638	PPV	P2-O12	-2.42	1.45	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	638	PPV	O32-P2-OPP	-2.07	97.71	104.64

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	805	EDO	O1-C1-C2-O2
5	P	803	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	D	4/4 (100%)	0.17	0	100 100	25, 26, 27, 27	0
2	P	7/7 (100%)	-1.03	0	100 100	14, 15, 17, 18	0
3	T	12/12 (100%)	-0.62	0	100 100	15, 19, 26, 32	0
4	A	325/335 (97%)	0.90	57 (17%)	4 4	8, 27, 69, 80	6 (1%)
All	All	348/358 (97%)	0.80	57 (16%)	4 4	8, 26, 67, 80	6 (1%)

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	575	TRP	7.7
4	A	317	LEU	6.7
4	A	310	ALA	6.7
4	A	293	VAL	6.5
4	A	316	ILE	6.1
4	A	296	TYR	5.5
4	A	314	ILE	5.1
4	A	256	ILE	4.7
4	A	294	THR	4.7
4	A	286	LEU	4.6
4	A	313	ILE	4.6
4	A	322	LEU	4.4
4	A	290	HIS	4.4
4	A	254	LEU	4.2
4	A	574	ASP	4.2
4	A	289	PHE	4.1
4	A	299	ALA	3.9
4	A	292	PRO	3.8
4	A	321	HIS	3.8
4	A	295	SER	3.7
4	A	305	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
4	A	285	ALA	3.6
4	A	437	GLY	3.4
4	A	442	GLY	3.4
4	A	284	ASN	3.4
4	A	302	ILE	3.3
4	A	282	ALA	3.3
4	A	467	ASN	3.2
4	A	263	LEU	3.0
4	A	297	GLN	3.0
4	A	255	HIS	2.9
4	A	291	LYS	2.9
4	A	405	ALA	2.9
4	A	251	ASN	2.9
4	A	540	THR	2.8
4	A	325	LEU	2.8
4	A	440	HIS	2.8
4	A	260	LEU	2.7
4	A	312	LYS	2.6
4	A	257	THR	2.6
4	A	320	GLY	2.6
4	A	283	ILE	2.5
4	A	303	PRO	2.5
4	A	511	HIS	2.4
4	A	307	LYS	2.4
4	A	300	CYS	2.4
4	A	253	ASN	2.3
4	A	298	GLU	2.3
4	A	327	HIS	2.3
4	A	304	GLY	2.3
4	A	406	PHE	2.3
4	A	262	VAL	2.3
4	A	439	SER	2.2
4	A	287	LYS	2.2
4	A	438	ARG	2.1
4	A	323	ARG	2.1
4	A	306	GLY	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
5	EDO	P	803	4/4	0.85	0.18	41,42,42,42	0
5	EDO	A	801	4/4	0.85	0.14	32,36,37,39	0
5	EDO	A	802	4/4	0.85	0.18	42,43,43,45	0
5	EDO	A	805	4/4	0.87	0.15	41,42,44,45	0
7	NA	A	604	1/1	0.89	0.09	42,42,42,42	0
8	PPV	A	638	9/9	0.91	0.12	24,30,33,34	0
5	EDO	A	804	4/4	0.93	0.09	32,34,34,35	0
7	NA	A	602	1/1	0.97	0.05	25,25,25,25	0
6	MG	A	600	1/1	0.98	0.03	22,22,22,22	0
7	NA	A	603	1/1	0.99	0.04	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.