



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 12:23 AM GMT

PDB ID : 2GWS
Title : Crystal Structure of human DNA Polymerase lambda with a G/G mismatch in the primer terminus
Authors : Garcia-Diaz, M.; Picher, A.J.; Bebenek, K.; Pedersen, L.C.; Kunkel, T.A.; Blanco, L.
Deposited on : 2006-05-05
Resolution : 2.40 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

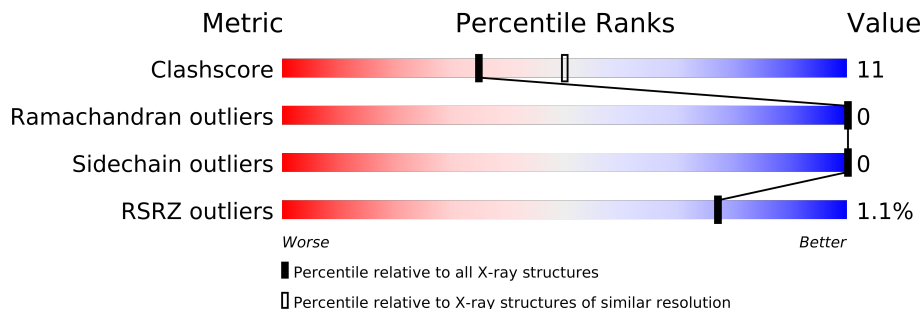
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.40 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))
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	F	11	
1	J	11	
1	N	11	
1	T	11	
2	G	6	
2	K	6	
2	P	6	
2	R	6	
3	D	4	
3	H	4	
3	L	4	
3	Q	4	
4	A	335	
4	E	335	
4	I	335	
4	M	335	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
5	NA	M	947	-	X
6	MG	F	946	-	X
7	CAC	D	949	X	-
7	CAC	H	950	X	-
7	CAC	J	951	X	-
9	EDO	E	2802	-	X
9	EDO	N	2801	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 12600 atoms, of which 0 are hydrogen and 0 are deuterium.

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(*CP*GP*GP*CP*AP*GP*CP*GP*CP*AP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	11	Total	C	N	O	P	0	0	0
			222	105	45	62	10			
1	F	11	Total	C	N	O	P	0	0	0
			222	105	45	62	10			
1	J	11	Total	C	N	O	P	0	0	0
			222	105	45	62	10			
1	N	11	Total	C	N	O	P	0	0	0
			222	105	45	62	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	6	Total	C	N	O	P	0	0	0
			124	59	25	35	5			
2	G	6	Total	C	N	O	P	0	0	0
			124	59	25	35	5			
2	K	6	Total	C	N	O	P	0	0	0
			124	59	25	35	5			
2	R	6	Total	C	N	O	P	0	0	0
			124	59	25	35	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			
3	H	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			
3	L	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			
3	Q	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			

- Molecule 4 is a protein called DNA polymerase lambda.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	327	Total	C	N	O	S	0	2	0
			2562	1607	466	477	12			
4	E	326	Total	C	N	O	S	0	0	0
			2446	1538	441	455	12			
4	I	326	Total	C	N	O	S	0	1	0
			2514	1576	459	467	12			
4	M	326	Total	C	N	O	S	0	0	0
			2530	1588	460	470	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	MET	-	CLONING ARTIFACT	UNP Q9UGP5
E	241	MET	-	CLONING ARTIFACT	UNP Q9UGP5
I	241	MET	-	CLONING ARTIFACT	UNP Q9UGP5
M	241	MET	-	CLONING ARTIFACT	UNP Q9UGP5

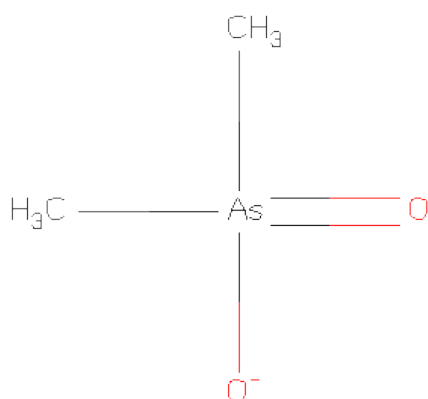
- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	P	1	Total	Na	0	0
			1	1		
5	Q	1	Total	Na	0	0
			1	1		
5	E	1	Total	Na	0	0
			1	1		
5	I	1	Total	Na	0	0
			1	1		
5	A	1	Total	Na	0	0
			1	1		
5	T	1	Total	Na	0	0
			1	1		
5	M	2	Total	Na	0	0
			2	2		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 7 is CACODYLATE ION (three-letter code: CAC) (formula: $\text{C}_2\text{H}_6\text{AsO}_2$).

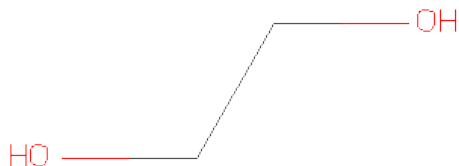


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	D	1	Total	As	C	O	0	0
			5	1	2	2		
7	H	1	Total	As	C	O	0	0
			5	1	2	2		
7	J	1	Total	As	C	O	0	0
			5	1	2	2		

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Cl	0	0
			1	1		

- Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\text{C}_2\text{H}_6\text{O}_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	N	1	Total	C	O	0	0
			4	2	2		
9	E	1	Total	C	O	0	0
			4	2	2		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	206	Total	O	0	0
			206	206		
10	D	7	Total	O	0	0
			7	7		
10	E	77	Total	O	0	0
			77	77		
10	F	17	Total	O	0	0
			17	17		
10	G	7	Total	O	0	0
			7	7		
10	H	4	Total	O	0	0
			4	4		
10	I	89	Total	O	0	0
			89	89		
10	J	18	Total	O	0	0
			18	18		
10	K	10	Total	O	0	0
			10	10		
10	L	4	Total	O	0	0
			4	4		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	M	243	Total 243	O 243	0	0
10	N	35	Total 35	O 35	0	0
10	P	17	Total 17	O 17	0	0
10	Q	6	Total 6	O 6	0	0
10	R	16	Total 16	O 16	0	0
10	T	43	Total 43	O 43	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

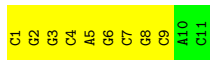
- Molecule 1: 5'-D(*CP*GP*GP*CP*AP*GP*CP*GP*CP*AP*C)-3'

Chain T: 



- Molecule 1: 5'-D(*CP*GP*GP*CP*AP*GP*CP*GP*CP*AP*C)-3'

Chain F: 



- Molecule 1: 5'-D(*CP*GP*GP*CP*AP*GP*CP*GP*CP*AP*C)-3'

Chain J: 



- Molecule 1: 5'-D(*CP*GP*GP*CP*AP*GP*CP*GP*CP*AP*C)-3'

Chain N: 



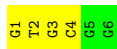
- Molecule 2: 5'-D(*GP*TP*GP*CP*GP*G)-3'

Chain P: 



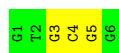
- Molecule 2: 5'-D(*GP*TP*GP*CP*GP*G)-3'

Chain G: 



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

Chain K: 



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

Chain R:



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

Chain D:



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

Chain H:



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

Chain L:



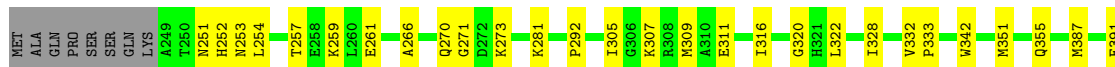
- Molecule 3: 5'-D(P*GP*CP*CP*G)-3'

Chain Q:



- Molecule 4: DNA polymerase lambda

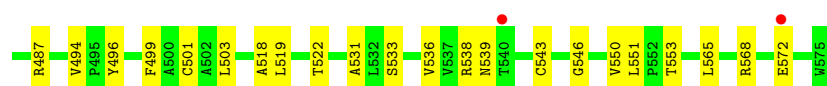
Chain A:



- Molecule 4: DNA polymerase lambda

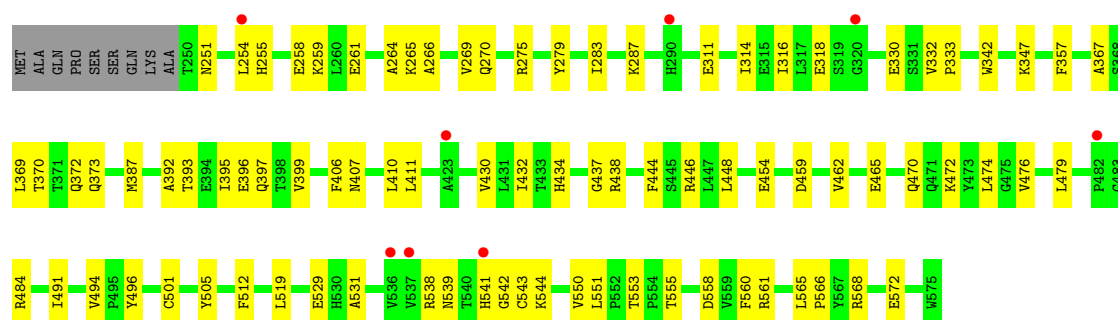
Chain E:





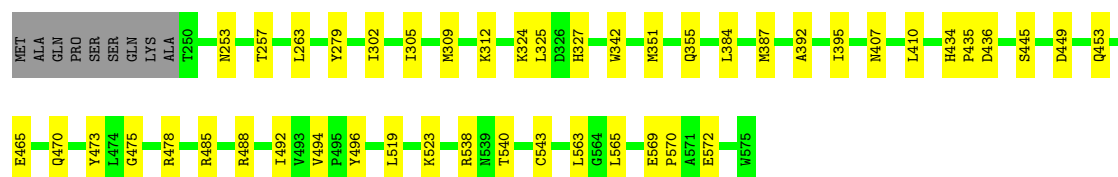
• Molecule 4: DNA polymerase lambda

Chain I:



• Molecule 4: DNA polymerase lambda

Chain M:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	192.37Å 98.27Å 104.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 28.50 – 2.41	Depositor EDS
% Data completeness (in resolution range)	92.2 (50.00-2.40) 93.0 (28.50-2.41)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.42Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.209 , 0.253 0.211 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 31.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 76713 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12600	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CAC, NA, MG, EDO, CL

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	F	0.32	0/249	0.68	0/382
1	J	0.30	0/249	0.69	0/382
1	N	0.38	0/249	0.77	0/382
1	T	0.45	0/249	0.79	0/382
2	G	0.31	0/139	0.60	0/214
2	K	0.32	0/139	0.63	0/214
2	P	0.40	0/139	0.68	0/214
2	R	0.50	0/139	0.70	0/214
3	D	0.96	1/92 (1.1%)	0.76	0/138
3	H	0.96	1/92 (1.1%)	0.78	0/138
3	L	0.93	1/92 (1.1%)	0.74	0/138
3	Q	0.96	1/92 (1.1%)	0.74	0/138
4	A	0.37	0/2614	0.59	0/3531
4	E	0.34	0/2495	0.54	0/3385
4	I	0.35	1/2566 (0.0%)	0.52	0/3474
4	M	0.38	0/2583	0.62	0/3493
All	All	0.39	5/12178 (0.0%)	0.60	0/16819

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	L	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1	DG	OP3-P	-7.26	1.52	1.61
3	Q	1	DG	OP3-P	-7.19	1.52	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	1	DG	OP3-P	-6.93	1.52	1.61
3	H	1	DG	OP3-P	-6.92	1.52	1.61
4	I	265	LYS	CD-CE	5.50	1.65	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	L	1	DG	Sidechain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	222	0	123	9	0
1	J	222	0	123	8	0
1	N	222	0	123	7	0
1	T	222	0	123	6	0
2	G	124	0	69	5	0
2	K	124	0	69	4	0
2	P	124	0	69	1	0
2	R	124	0	69	5	0
3	D	83	0	45	1	0
3	H	83	0	45	2	0
3	L	83	0	45	0	0
3	Q	83	0	45	2	0
4	A	2562	0	2527	34	0
4	E	2446	0	2358	67	0
4	I	2514	0	2441	66	0
4	M	2530	0	2484	37	0
5	A	1	0	0	0	0
5	E	1	0	0	0	0
5	I	1	0	0	0	0
5	M	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	P	1	0	0	0	0
5	Q	1	0	0	0	0
5	T	1	0	0	0	0
6	F	1	0	0	0	0
7	D	5	0	0	0	0
7	H	5	0	0	0	0
7	J	5	0	0	0	0
8	A	1	0	0	0	0
9	E	4	0	6	0	0
9	N	4	0	6	0	0
10	A	206	0	0	1	0
10	D	7	0	0	0	0
10	E	77	0	0	0	0
10	F	17	0	0	1	0
10	G	7	0	0	0	0
10	H	4	0	0	0	0
10	I	89	0	0	1	0
10	J	18	0	0	0	0
10	K	10	0	0	0	0
10	L	4	0	0	0	0
10	M	243	0	0	4	0
10	N	35	0	0	0	0
10	P	17	0	0	0	0
10	Q	6	0	0	0	0
10	R	16	0	0	0	0
10	T	43	0	0	1	0
All	All	12600	0	10770	241	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 11.

The worst 5 of 241 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:3:DG:H2''	1:F:4:DC:H5'	1.55	0.87
1:N:9:DC:H5'	4:M:465:GLU:HG3	1.58	0.85
4:I:251:ASN:HD22	4:I:287:LYS:HA	1.45	0.81
4:I:251:ASN:ND2	4:I:287:LYS:HA	1.95	0.81
4:M:519:LEU:HD22	4:M:565:LEU:HD11	1.64	0.80

There are no symmetry-related clashes.

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	
4	A	327/335 (98%)	313 (96%)	14 (4%)	0	100	100
4	E	324/335 (97%)	314 (97%)	10 (3%)	0	100	100
4	I	325/335 (97%)	312 (96%)	13 (4%)	0	100	100
4	M	324/335 (97%)	316 (98%)	8 (2%)	0	100	100
All	All	1300/1340 (97%)	1255 (96%)	45 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
4	A	269/281 (96%)	269 (100%)	0	100	100
4	E	247/281 (88%)	247 (100%)	0	100	100
4	I	259/281 (92%)	259 (100%)	0	100	100
4	M	265/281 (94%)	265 (100%)	0	100	100
All	All	1040/1124 (92%)	1040 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
4	E	397	GLN
4	I	297	GLN
4	M	397	GLN

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Mol	Chain	Res	Type
4	E	350	GLN
4	I	486	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 15 ligands modelled in this entry, 10 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$
7	CAC	D	949	-	4,4,4	5.37	3 (75%)	6,6,6	11.12	3 (50%)
9	EDO	E	2802	-	3,3,3	0.62	0	2,2,2	0.59	0
7	CAC	H	950	-	4,4,4	5.37	3 (75%)	6,6,6	10.96	3 (50%)
7	CAC	J	951	-	4,4,4	5.36	3 (75%)	6,6,6	10.71	3 (50%)
9	EDO	N	2801	-	3,3,3	0.82	0	2,2,2	0.71	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
7	CAC	D	949	-	-	0/0/0/0	0/0/0/0
9	EDO	E	2802	-	-	0/1/1/1	0/0/0/0
7	CAC	H	950	-	-	0/0/0/0	0/0/0/0
7	CAC	J	951	-	-	0/0/0/0	0/0/0/0
9	EDO	N	2801	-	-	0/1/1/1	0/0/0/0

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	J	951	CAC	AS-C2	-8.59	1.76	1.90
7	D	949	CAC	AS-C2	-8.41	1.77	1.90
7	H	950	CAC	AS-C2	-8.29	1.77	1.90
7	H	950	CAC	O2-AS	-6.06	1.61	1.68
7	D	949	CAC	O2-AS	-5.86	1.61	1.68

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	949	CAC	O2-AS-O1	-26.76	106.77	112.54
7	H	950	CAC	O2-AS-O1	-26.34	106.86	112.54
7	J	951	CAC	O2-AS-O1	-25.69	107.00	112.54
7	J	951	CAC	O2-AS-C2	-4.41	105.54	109.15
7	H	950	CAC	O2-AS-C2	-4.29	105.64	109.15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	F	11/11 (100%)	-0.31	0 100 100	46, 51, 58, 58	0
1	J	11/11 (100%)	-0.26	0 100 100	40, 45, 58, 63	0
1	N	11/11 (100%)	-0.56	0 100 100	22, 26, 43, 47	0
1	T	11/11 (100%)	-0.77	0 100 100	22, 28, 38, 39	0
2	G	6/6 (100%)	-0.37	0 100 100	43, 49, 65, 66	0
2	K	6/6 (100%)	0.00	0 100 100	39, 47, 58, 61	0
2	P	6/6 (100%)	-0.49	0 100 100	21, 26, 39, 44	0
2	R	6/6 (100%)	-0.56	0 100 100	18, 24, 35, 36	0
3	D	4/4 (100%)	-0.95	0 100 100	32, 33, 38, 43	0
3	H	4/4 (100%)	0.14	0 100 100	52, 58, 58, 61	0
3	L	4/4 (100%)	-0.46	0 100 100	55, 57, 59, 61	0
3	Q	4/4 (100%)	-0.61	0 100 100	32, 33, 36, 37	0
4	A	327/335 (97%)	-0.30	0 100 100	17, 32, 62, 76	0
4	E	326/335 (97%)	0.08	7 (2%) 60 58	36, 57, 84, 99	0
4	I	326/335 (97%)	0.01	8 (2%) 54 52	37, 54, 80, 91	0
4	M	326/335 (97%)	-0.38	0 100 100	16, 29, 55, 72	0
All	All	1389/1424 (97%)	-0.16	15 (1%) 77 77	16, 44, 75, 99	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	E	483	GLY	4.0
4	I	320	GLY	2.9
4	I	537	VAL	2.9
4	E	482	PRO	2.9
4	E	321	HIS	2.7

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	NA	M	947	1/1	0.32	18.27	43,43,43,43	0
9	EDO	N	2801	4/4	0.40	10.74	38,42,42,44	0
9	EDO	E	2802	4/4	0.31	5.52	64,66,67,67	0
6	MG	F	946	1/1	0.17	2.29	56,56,56,56	0
5	NA	A	940	1/1	0.15	1.80	25,25,25,25	0
5	NA	Q	948	1/1	0.12	1.79	53,53,53,53	0
7	CAC	J	951	5/5	0.19	1.13	171,171,172,172	0
7	CAC	D	949	5/5	0.13	0.29	142,143,143,143	0
7	CAC	H	950	5/5	0.17	0.17	160,160,160,160	0
8	CL	A	952	1/1	0.13	0.12	41,41,41,41	0
5	NA	M	943	1/1	0.10	-0.76	25,25,25,25	0
5	NA	E	941	1/1	0.08	-1.93	44,44,44,44	0
5	NA	I	942	1/1	0.07	-3.19	41,41,41,41	0
5	NA	P	945	1/1	0.04	-3.79	39,39,39,39	0
5	NA	T	944	1/1	0.06	-4.00	43,43,43,43	0

6.5 Other polymers ⓘ

There are no such residues in this entry.