



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 05:46 AM GMT

PDB ID : 2PYJ  
Title : Phi29 DNA polymerase complexed with primer-template DNA and incoming nucleotide substrates (ternary complex)  
Authors : Berman, A.J.; Kamtekar, S.; Goodman, J.L.; Lazaro, J.M.; de Vega, M.; Blanco, L.; Salas, M.; Steitz, T.A.  
Deposited on : 2007-05-16  
Resolution : 2.03 Å(reported)

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

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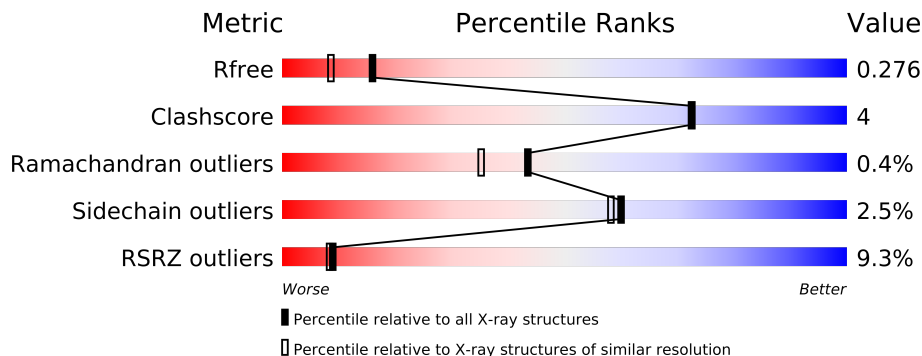
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.03 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))
$R_{free}$	66092	6003 (2.04-2.00)
Clashscore	79885	7467 (2.04-2.00)
Ramachandran outliers	78287	7370 (2.04-2.00)
Sidechain outliers	78261	7368 (2.04-2.00)
RSRZ outliers	66119	6006 (2.04-2.00)

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  $\geq 3$ , 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	J	10	
1	Q	10	
1	X	10	
2	K	14	
2	R	14	
2	Y	14	
3	A	575	
3	B	575	

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

Mol	Type	Chain	Res	Geometry	Electron density
7	EDO	A	2770	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
7	EDO	A	2771	-	X
7	EDO	A	2773	-	X
7	EDO	A	2784	-	X
7	EDO	A	2786	-	X
7	EDO	A	2790	-	X
7	EDO	A	2792	-	X
7	EDO	A	2793	-	X
7	EDO	A	2794	-	X
7	EDO	A	2801	-	X
7	EDO	B	2763	-	X
7	EDO	B	2777	-	X
7	EDO	B	2778	-	X
7	EDO	B	2779	-	X
7	EDO	B	2787	-	X
7	EDO	B	2789	-	X
7	EDO	B	2791	-	X
7	EDO	B	2795	-	X
7	EDO	B	2802	-	X
7	EDO	K	2765	-	X
7	EDO	K	2767	-	X
7	EDO	X	2782	-	X
7	EDO	X	2798	-	X
7	EDO	Y	2772	-	X
7	EDO	Y	2788	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11997 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(GACTGCTTA(DOC))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	10	Total	C	N	O	P	0	0	0
			199	97	35	58	9			
1	Q	10	Total	C	N	O	P	0	0	0
			199	97	35	58	9			
1	J	10	Total	C	N	O	P	0	0	0
			199	97	35	58	9			

- Molecule 2 is a DNA chain called 5'-d(ACACGTAAGCAGTC)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Y	14	Total	C	N	O	P	0	0	0
			284	136	56	79	13			
2	R	13	Total	C	N	O	P	0	0	0
			266	126	51	76	13			
2	K	14	Total	C	N	O	P	0	0	0
			284	136	56	79	13			

- Molecule 3 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	567	Total	C	N	O	S	0	4	0
			4660	3041	751	847	21			
3	B	572	Total	C	N	O	S	0	5	0
			4707	3071	758	856	22			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	ALA	ASP	ENGINEERED	UNP P03680
A	66	ALA	ASP	ENGINEERED	UNP P03680
B	12	ALA	ASP	ENGINEERED	UNP P03680
B	66	ALA	ASP	ENGINEERED	UNP P03680

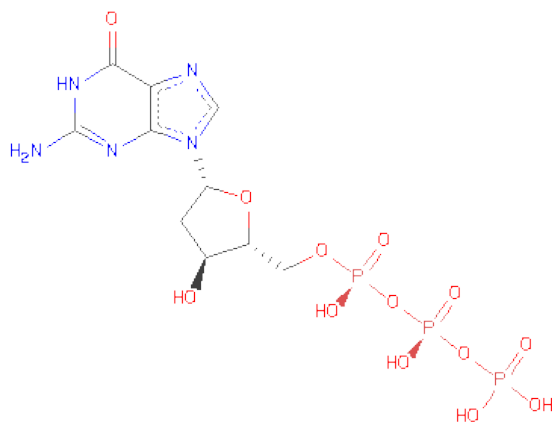
- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mn	0	0
			1	1		
4	A	1	Total	Mn	0	0
			1	1		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

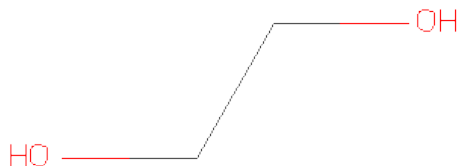
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mg	0	0
			1	1		
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (three-letter code: DGT) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total 31	C 10	N 5	O 13	P 3	0	0
6	B	1	Total 31	C 10	N 5	O 13	P 3	0	0

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	K	1	Total	C	O	0	0
			4	2	2		
7	K	1	Total	C	O	0	0
			4	2	2		
7	K	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	Y	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	X	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	Q	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	Y	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		
7	R	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	X	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	463	Total O 463 463	0	0
8	B	343	Total O 343 343	0	0
8	J	5	Total O 5 5	0	0
8	K	28	Total O 28 28	0	0
8	Q	15	Total O 15 15	0	0
8	R	26	Total O 26 26	0	0
8	X	44	Total O 44 44	0	0
8	Y	45	Total O 45 45	0	0

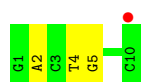


### 3 Residue-property plots

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(GACTGCTTA(DOC))-3'

Chain X: 



- Molecule 1: 5'-d(GACTGCTTA(DOC))-3'

Chain Q: 



- Molecule 1: 5'-d(GACTGCTTA(DOC))-3'

Chain J: 



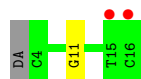
- Molecule 2: 5'-d(ACACGTAAGCAGTC)-3'

Chain Y: 



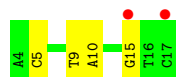
- Molecule 2: 5'-d(ACACGTAAGCAGTC)-3'

Chain R: 



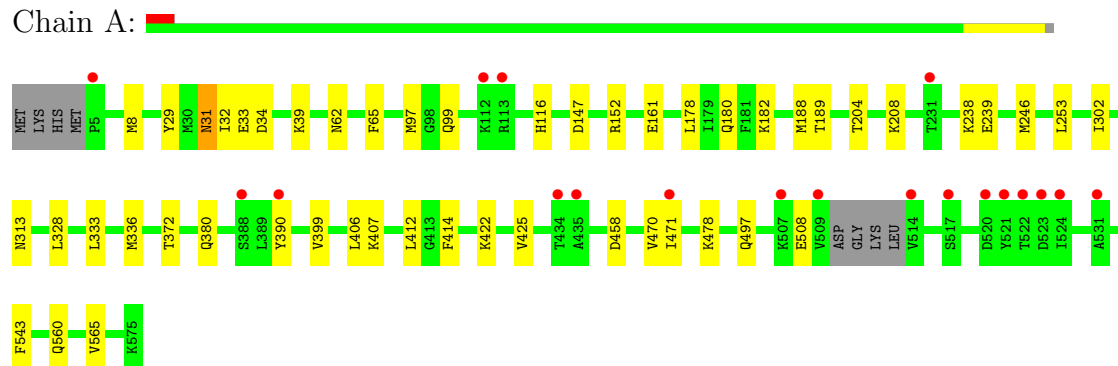
- Molecule 2: 5'-d(ACACGTAAGCAGTC)-3'

Chain K: 



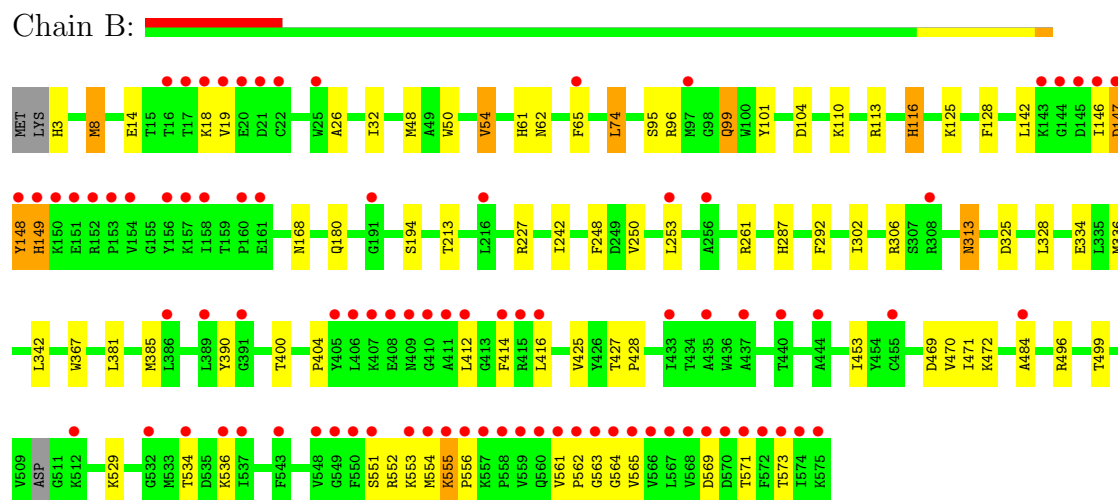
- Molecule 3: DNA polymerase

Chain A:



- Molecule 3: DNA polymerase

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	72.83Å 114.67Å 104.76Å 90.00° 94.07° 90.00°	Depositor
Resolution (Å)	41.07 – 2.03 41.06 – 2.03	Depositor EDS
% Data completeness (in resolution range)	97.7 (41.07-2.03) 97.7 (41.06-2.03)	Depositor EDS
$R_{merge}$	0.00	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.38 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.189 , 0.234 0.241 , 0.276	Depositor DCC
$R_{free}$ test set	5359 reflections (4.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.8	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 21.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 107419 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	11997	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.88% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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: DOC, MG, MN, EDO, DGT

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	J	1.23	2/202 (1.0%)	1.38	4/310 (1.3%)
1	Q	1.29	2/202 (1.0%)	1.24	2/310 (0.6%)
1	X	1.20	0/202	1.59	2/310 (0.6%)
2	K	0.89	0/319	1.26	2/490 (0.4%)
2	R	0.91	0/298	1.24	1/457 (0.2%)
2	Y	1.14	0/319	1.41	4/490 (0.8%)
3	A	0.54	0/4791	0.53	0/6463
3	B	0.56	0/4843	0.54	0/6532
All	All	0.65	4/11176 (0.0%)	0.72	15/15362 (0.1%)

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	B	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	9	DA	C3'-O3'	-6.10	1.36	1.44
1	Q	9	DA	N7-C5	-6.09	1.35	1.39
1	Q	9	DA	C8-N7	-5.27	1.27	1.31
1	J	9	DA	N9-C8	-5.13	1.33	1.37

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	5	DG	O4'-C1'-N9	11.76	116.23	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	2	DA	O4'-C1'-N9	8.06	113.64	108.00
2	Y	10	DA	O4'-C1'-N9	8.05	113.63	108.00
1	J	6	DC	O4'-C1'-N1	6.93	112.85	108.00
1	J	4	DT	P-O3'-C3'	6.90	127.98	119.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	552	ARG	Peptide
3	B	555	LYS	Peptide

## 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	J	199	0	115	1	0
1	Q	199	0	115	2	0
1	X	199	0	115	1	0
2	K	284	0	158	1	0
2	R	266	0	146	0	0
2	Y	284	0	158	1	0
3	A	4660	0	4685	28	0
3	B	4707	0	4722	59	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	31	0	12	0	0
6	B	31	0	12	0	0
7	A	68	0	102	1	0
7	B	60	0	90	2	0
7	K	12	0	18	0	0
7	Q	4	0	6	1	0
7	R	4	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	X	8	0	12	4	0
7	Y	8	0	12	1	0
8	A	463	0	0	3	0
8	B	343	0	0	4	0
8	J	5	0	0	0	0
8	K	28	0	0	0	0
8	Q	15	0	0	0	0
8	R	26	0	0	0	0
8	X	44	0	0	0	0
8	Y	45	0	0	0	0
All	All	11997	0	10484	93	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 4.

The worst 5 of 93 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:302:ILE:HD11	3:B:336:MET:HE2	1.61	0.83
3:B:554:MET:HB2	3:B:569:ASP:HB3	1.60	0.83
3:B:328:LEU:HD13	3:B:336:MET:HE3	1.64	0.77
3:B:65:PHE:HA	3:B:565:VAL:HG21	1.72	0.70
3:B:536:LYS:HB2	3:B:555:LYS:HD2	1.75	0.68

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	
3	A	567/575 (99%)	547 (96%)	18 (3%)	2 (0%)	43	35
3	B	573/575 (100%)	551 (96%)	20 (4%)	2 (0%)	50	43
All	All	1140/1150 (99%)	1098 (96%)	38 (3%)	4 (0%)	43	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	62	ASN
3	B	62	ASN
3	A	425	VAL
3	B	425	VAL

### 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	
3	A	503/506 (99%)	492 (98%)	11 (2%)	64	64
3	B	508/506 (100%)	494 (97%)	14 (3%)	56	53
All	All	1011/1012 (100%)	986 (98%)	25 (2%)	60	58

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	8	MET
3	B	54	VAL
3	B	390	TYR
3	B	18	LYS
3	B	74	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	99	GLN
3	B	116	HIS
3	B	183	GLN
3	B	61	HIS
3	B	171	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

3 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	DOC	J	10	1,2	17,19,20	1.12	1 (5%)	20,26,29	2.32	5 (25%)
1	DOC	Q	10	1,2	17,19,20	1.31	3 (17%)	20,26,29	1.88	4 (20%)
1	DOC	X	10	1,2	17,19,20	1.24	2 (11%)	20,26,29	1.65	3 (15%)

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	DOC	J	10	1,2	-	0/5/18/19	0/2/2/2
1	DOC	Q	10	1,2	-	0/5/18/19	0/2/2/2
1	DOC	X	10	1,2	-	0/5/18/19	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	10	DOC	P-OP1	-3.51	1.42	1.46
1	X	10	DOC	P-OP1	3.46	1.50	1.46
1	X	10	DOC	C2-N1	3.03	1.41	1.38
1	J	10	DOC	P-OP1	2.55	1.49	1.46
1	Q	10	DOC	C6-N1	-2.11	1.32	1.35

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	10	DOC	C6-C5-C4	6.24	120.06	117.47
1	J	10	DOC	C4'-O4'-C1'	-5.90	107.59	110.05
1	J	10	DOC	C6-C5-C4	5.71	119.84	117.47
1	X	10	DOC	C2-N3-C4	3.96	121.30	115.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	10	DOC	C6-C5-C4	3.46	118.91	117.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates i

There are no carbohydrates in this entry.

## 5.6 Ligand geometry i

Of 47 ligands modelled in this entry, 4 are monoatomic - leaving 43 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	$\# Z  > 2$
6	DGT	A	1588	5,4	33,33,33	1.55	5 (15%)	49,52,52	2.93	10 (20%)
7	EDO	A	2770	-	3,3,3	0.54	0	2,2,2	0.31	0
7	EDO	A	2771	-	3,3,3	0.55	0	2,2,2	0.15	0
7	EDO	A	2773	-	3,3,3	0.66	0	2,2,2	0.08	0
7	EDO	A	2774	-	3,3,3	0.50	0	2,2,2	0.38	0
7	EDO	A	2780	-	3,3,3	0.52	0	2,2,2	0.32	0
7	EDO	A	2781	-	3,3,3	0.62	0	2,2,2	0.24	0
7	EDO	A	2784	-	3,3,3	0.44	0	2,2,2	0.22	0
7	EDO	A	2786	-	3,3,3	0.54	0	2,2,2	0.32	0
7	EDO	A	2790	-	3,3,3	0.53	0	2,2,2	0.36	0
7	EDO	A	2792	-	3,3,3	0.58	0	2,2,2	0.24	0
7	EDO	A	2793	-	3,3,3	0.65	0	2,2,2	0.23	0
7	EDO	A	2794	-	3,3,3	0.62	0	2,2,2	0.26	0
7	EDO	A	2797	-	3,3,3	0.53	0	2,2,2	0.38	0
7	EDO	A	2800	-	3,3,3	0.67	0	2,2,2	0.22	0
7	EDO	A	2801	-	3,3,3	0.56	0	2,2,2	0.34	0
7	EDO	A	2803	-	3,3,3	0.35	0	2,2,2	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	EDO	A	2804	-	3,3,3	0.74	0	2,2,2	0.08	0
6	DGT	B	1589	5,4	33,33,33	1.46	6 (18%)	49,52,52	2.07	8 (16%)
7	EDO	B	2762	-	3,3,3	0.60	0	2,2,2	0.19	0
7	EDO	B	2763	-	3,3,3	0.54	0	2,2,2	0.30	0
7	EDO	B	2764	-	3,3,3	0.51	0	2,2,2	0.33	0
7	EDO	B	2769	-	3,3,3	0.39	0	2,2,2	0.41	0
7	EDO	B	2775	-	3,3,3	0.72	0	2,2,2	0.06	0
7	EDO	B	2776	-	3,3,3	0.60	0	2,2,2	0.18	0
7	EDO	B	2777	-	3,3,3	0.52	0	2,2,2	0.29	0
7	EDO	B	2778	-	3,3,3	0.73	0	2,2,2	0.17	0
7	EDO	B	2779	-	3,3,3	0.63	0	2,2,2	0.21	0
7	EDO	B	2787	-	3,3,3	0.65	0	2,2,2	0.09	0
7	EDO	B	2789	-	3,3,3	0.51	0	2,2,2	0.48	0
7	EDO	B	2791	-	3,3,3	0.62	0	2,2,2	0.26	0
7	EDO	B	2795	-	3,3,3	0.59	0	2,2,2	0.25	0
7	EDO	B	2802	-	3,3,3	0.49	0	2,2,2	0.21	0
7	EDO	B	2805	-	3,3,3	0.50	0	2,2,2	0.26	0
7	EDO	K	2765	-	3,3,3	0.60	0	2,2,2	0.20	0
7	EDO	K	2766	-	3,3,3	0.53	0	2,2,2	0.28	0
7	EDO	K	2767	-	3,3,3	0.68	0	2,2,2	0.06	0
7	EDO	Q	2785	-	3,3,3	0.37	0	2,2,2	0.43	0
7	EDO	R	2796	-	3,3,3	0.67	0	2,2,2	0.27	0
7	EDO	X	2782	-	3,3,3	0.56	0	2,2,2	0.43	0
7	EDO	X	2798	-	3,3,3	0.36	0	2,2,2	0.21	0
7	EDO	Y	2772	-	3,3,3	0.60	0	2,2,2	0.15	0
7	EDO	Y	2788	-	3,3,3	0.63	0	2,2,2	0.21	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
6	DGT	A	1588	5,4	-	0/20/34/34	0/1/3/3
7	EDO	A	2770	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2771	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2773	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2774	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2780	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2781	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2784	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2786	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	A	2790	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2792	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2793	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2794	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2797	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2800	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2801	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2803	-	-	0/1/1/1	0/0/0/0
7	EDO	A	2804	-	-	0/1/1/1	0/0/0/0
6	DGT	B	1589	5,4	-	0/20/34/34	0/1/3/3
7	EDO	B	2762	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2763	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2764	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2769	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2775	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2776	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2777	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2778	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2779	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2787	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2789	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2791	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2795	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2802	-	-	0/1/1/1	0/0/0/0
7	EDO	B	2805	-	-	0/1/1/1	0/0/0/0
7	EDO	K	2765	-	-	0/1/1/1	0/0/0/0
7	EDO	K	2766	-	-	0/1/1/1	0/0/0/0
7	EDO	K	2767	-	-	0/1/1/1	0/0/0/0
7	EDO	Q	2785	-	-	0/1/1/1	0/0/0/0
7	EDO	R	2796	-	-	0/1/1/1	0/0/0/0
7	EDO	X	2782	-	-	0/1/1/1	0/0/0/0
7	EDO	X	2798	-	-	0/1/1/1	0/0/0/0
7	EDO	Y	2772	-	-	0/1/1/1	0/0/0/0
7	EDO	Y	2788	-	-	0/1/1/1	0/0/0/0

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1588	DGT	C4-N9	-4.29	1.31	1.37
6	A	1588	DGT	C6-C5	4.02	1.47	1.41
6	B	1589	DGT	C4-N9	-3.88	1.32	1.37
6	B	1589	DGT	C6-C5	3.43	1.46	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1588	DGT	C2-N3	3.24	1.37	1.33

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1588	DGT	C6-C5-N7	17.09	136.44	134.14
6	B	1589	DGT	C6-C5-N7	9.97	135.48	134.14
6	A	1588	DGT	N3-C4-N9	4.19	133.05	126.91
6	B	1589	DGT	N3-C4-N9	4.17	133.03	126.91
6	B	1589	DGT	C2'-C1'-N9	-3.88	104.01	114.08

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	J	10/10 (100%)	1.50	3 (30%) 1 1	14, 17, 20, 20	0
1	Q	10/10 (100%)	1.18	0 100 100	12, 16, 23, 24	0
1	X	10/10 (100%)	0.51	1 (10%) 8 7	11, 15, 17, 18	0
2	K	14/14 (100%)	0.68	2 (14%) 3 3	12, 15, 20, 21	0
2	R	13/14 (92%)	0.81	2 (15%) 3 3	12, 15, 23, 24	0
2	Y	14/14 (100%)	0.68	1 (7%) 16 15	11, 14, 26, 48	0
3	A	567/575 (98%)	0.29	19 (3%) 43 43	7, 14, 24, 38	0
3	B	572/575 (99%)	0.92	86 (15%) 3 3	3, 14, 26, 43	0
All	All	1210/1222 (99%)	0.62	114 (9%) 9 8	3, 14, 25, 48	0

The worst 5 of 114 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	562	PRO	8.8
3	B	565	VAL	8.5
3	B	561	VAL	7.8
3	B	566	VAL	7.8
3	B	568	VAL	7.4

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

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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
1	DOC	X	10	18/19	0.21	0.69	10,14,15,16	0
1	DOC	Q	10	18/19	0.17	-0.12	10,12,14,15	0
1	DOC	J	10	18/19	0.14	-0.21	5,16,35,35	0

### 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
7	EDO	K	2767	4/4	0.47	10.35	27,27,28,29	0
7	EDO	A	2793	4/4	0.22	9.56	40,41,42,42	0
7	EDO	A	2790	4/4	0.25	9.06	35,35,36,36	0
7	EDO	X	2782	4/4	0.25	8.56	15,18,19,19	0
7	EDO	A	2771	4/4	0.30	7.87	15,17,18,19	0
7	EDO	B	2779	4/4	0.38	7.76	34,36,38,39	0
7	EDO	B	2789	4/4	0.29	7.52	15,16,16,17	0
7	EDO	B	2778	4/4	0.34	7.13	29,29,29,30	0
7	EDO	A	2792	4/4	0.37	6.99	38,38,39,39	0
7	EDO	B	2763	4/4	0.20	6.33	48,48,48,49	0
7	EDO	X	2798	4/4	0.30	5.97	16,17,18,19	0
7	EDO	A	2786	4/4	0.31	5.86	24,26,27,27	0
7	EDO	A	2773	4/4	0.30	5.40	39,39,39,39	0
7	EDO	K	2765	4/4	0.33	5.01	36,37,38,39	0
7	EDO	B	2791	4/4	0.27	4.75	44,45,45,46	0
7	EDO	B	2787	4/4	0.26	4.30	38,38,38,39	0
7	EDO	A	2794	4/4	0.29	4.27	31,32,32,32	0
7	EDO	Y	2788	4/4	0.19	4.00	31,31,32,32	0
7	EDO	A	2801	4/4	0.27	3.97	35,35,36,38	0
7	EDO	A	2770	4/4	0.23	3.76	31,31,31,31	0
7	EDO	B	2777	4/4	0.23	2.89	24,26,27,30	0
7	EDO	Y	2772	4/4	0.33	2.75	20,21,21,22	0
7	EDO	A	2784	4/4	0.15	2.61	17,20,21,22	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
7	EDO	B	2795	4/4	0.17	2.47	35,35,35,35	0
7	EDO	B	2802	4/4	0.21	2.42	24,24,25,25	0
7	EDO	B	2776	4/4	0.21	1.55	23,24,24,24	0
7	EDO	B	2805	4/4	0.20	1.52	18,20,21,24	0
7	EDO	A	2781	4/4	0.22	1.40	32,32,32,33	0
7	EDO	A	2774	4/4	0.18	0.95	31,31,32,33	0
7	EDO	A	2803	4/4	0.15	0.63	7,8,9,9	0
7	EDO	A	2804	4/4	0.16	0.41	4,11,14,14	0
7	EDO	B	2764	4/4	0.14	0.39	37,37,38,39	0
7	EDO	B	2762	4/4	0.18	0.12	25,26,26,27	0
7	EDO	K	2766	4/4	0.18	0.07	27,27,28,30	0
7	EDO	B	2769	4/4	0.16	-0.11	10,11,11,14	0
7	EDO	B	2775	4/4	0.15	-0.26	3,8,8,11	0
7	EDO	R	2796	4/4	0.15	-0.32	32,33,33,34	0
7	EDO	A	2797	4/4	0.13	-0.87	3,3,3,4	0
6	DGT	A	1588	31/31	0.12	-1.32	2,2,6,8	0
7	EDO	A	2780	4/4	0.13	-1.48	15,18,19,20	0
5	MG	A	9004	1/1	0.10	-1.63	16,16,16,16	0
7	EDO	Q	2785	4/4	0.12	-2.06	10,11,11,13	0
7	EDO	A	2800	4/4	0.14	-2.14	13,14,14,15	0
6	DGT	B	1589	31/31	0.11	-3.70	2,2,2,2	0
4	MN	A	9003	1/1	0.02	-4.11	5,5,5,5	0
4	MN	B	9001	1/1	0.04	-7.34	2,2,2,2	0
5	MG	B	9002	1/1	0.09	-8.18	6,6,6,6	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.