



# wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 05:21 PM GMT

PDB ID : 4F2S  
Title : DNA Polymerase I Large Fragment complex 4  
Authors : Wang, W.; Beese, L.S.  
Deposited on : 2012-05-08  
Resolution : 1.65 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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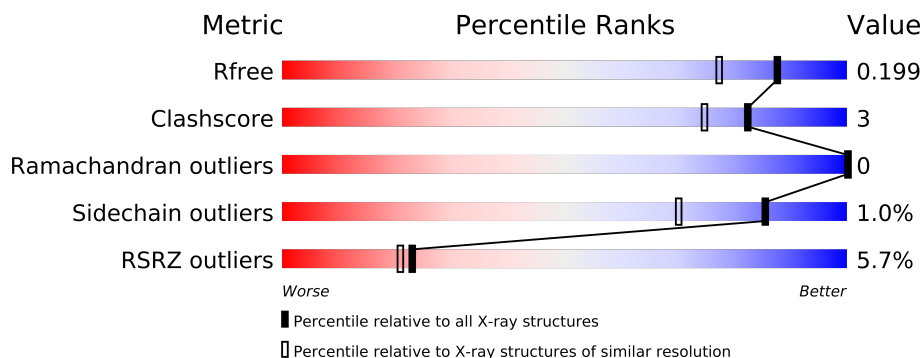
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.65 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	1404 (1.68-1.64)
Clashscore	79885	1001 (1.66-1.66)
Ramachandran outliers	78287	1581 (1.68-1.64)
Sidechain outliers	78261	1580 (1.68-1.64)
RSRZ outliers	66119	1404 (1.68-1.64)

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	A	592	
1	D	592	
2	B	9	
2	E	9	
3	C	13	
3	F	13	

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	SUC	A	902	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 21716 atoms, of which 10082 are hydrogens 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 protein called DNA polymerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	578	Total	C	H	N	O	S	0	5	0
			9402	2966	4743	805	869	19			
1	D	583	Total	C	H	N	O	S	0	9	0
			9524	3004	4814	813	876	17			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	598	ALA	ASP	ENGINEERED MUTATION	UNP Q5KWC1
A	710	TYR	PHE	ENGINEERED MUTATION	UNP Q5KWC1
A	823	HIS	ARG	SEE REMARK 999	UNP Q5KWC1
D	598	ALA	ASP	ENGINEERED MUTATION	UNP Q5KWC1
D	710	TYR	PHE	ENGINEERED MUTATION	UNP Q5KWC1
D	823	HIS	ARG	SEE REMARK 999	UNP Q5KWC1

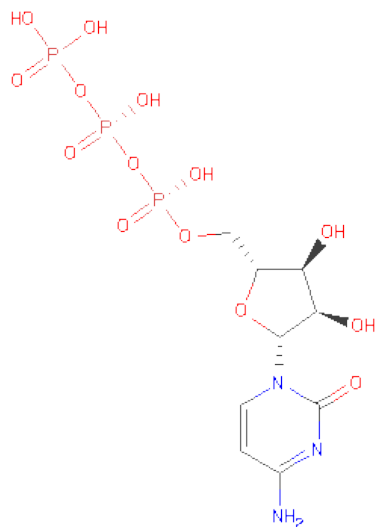
- Molecule 2 is a DNA chain called DNA (5'-D(\*CP\*CP\*TP\*GP\*AP\*CP\*TP\*CP\*(DOC))-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	9	Total	C	H	N	O	P	0	0	0
			274	85	100	29	52	8			
2	E	9	Total	C	H	N	O	P	0	0	0
			274	85	100	29	52	8			

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

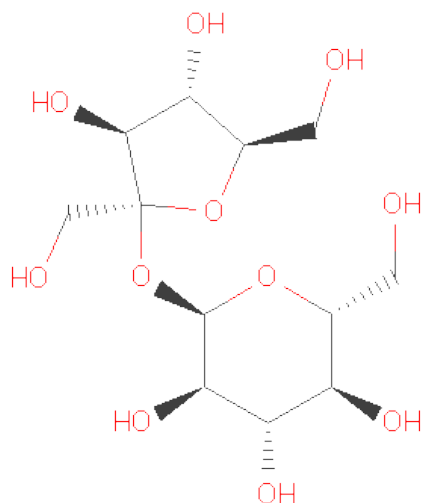
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	11	Total	C	H	N	O	P	0	0	0
			356	109	123	47	66	11			
3	F	12	Total	C	H	N	O	P	0	0	0
			385	119	134	52	69	11			

- Molecule 4 is CYTIDINE-5'-TRIPHOSPHATE (three-letter code: CTP) (formula:  $C_9H_{16}N_3O_{14}P_3$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	P		
4	A	1	41	9	12	3	14	3	0	0
4	D	1	41	9	12	3	14	3	0	0

- Molecule 5 is SUGAR (SUCROSE) (three-letter code: SUC) (formula:  $C_{12}H_{22}O_{11}$ ).

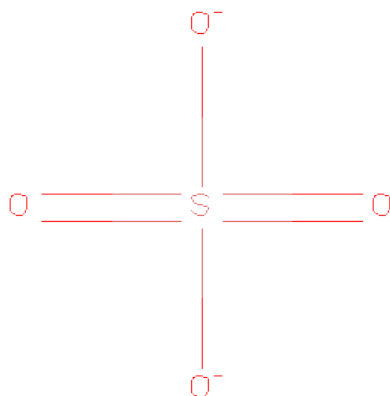


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			45	12	22	11		
5	D	1	Total	C	H	O	0	0
			45	12	22	11		

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	1	Total	Mn	0	0
			1	1		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is water.

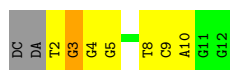
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	453	Total	O	0	0
			453	453		
8	C	44	Total	O	0	0
			44	44		
8	D	692	Total	O	0	0
			692	692		

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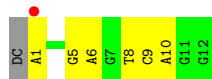
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	27	Total 27	O 27	0	0
8	E	39	Total 39	O 39	0	0
8	F	68	Total 68	O 68	0	0





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

Chain F: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.18Å 108.59Å 150.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.19 – 1.65 70.71 – 1.65	Depositor EDS
% Data completeness (in resolution range)	95.8 (34.19-1.65) 95.8 (70.71-1.65)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.90 (at 1.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1026)	Depositor
R, $R_{free}$	0.174 , 0.199 0.174 , 0.199	Depositor DCC
$R_{free}$ test set	7732 reflections (4.40%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.6	Xtriage
Anisotropy	0.211	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.43 , 43.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 175757 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	21716	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities 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: DOC, MN, SUC, SO4, CTP

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	0.46	0/4758	0.59	1/6429 (0.0%)
1	D	0.59	1/4827 (0.0%)	0.72	8/6525 (0.1%)
2	B	0.99	1/173 (0.6%)	1.76	6/264 (2.3%)
2	E	1.00	0/173	1.87	3/264 (1.1%)
3	C	0.98	0/262	1.62	5/404 (1.2%)
3	F	1.15	0/283	1.65	4/437 (0.9%)
All	All	0.59	2/10476 (0.0%)	0.82	27/14323 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	831	GLU	CB-CG	-5.84	1.41	1.52
2	B	25	DA	C3'-O3'	-5.30	1.37	1.44

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	23	DT	O4'-C1'-N1	-12.13	99.51	108.00
3	C	3	DG	O5'-P-OP1	-9.04	97.56	105.70
1	D	578	ARG	NE-CZ-NH2	-8.19	116.20	120.30
1	D	843	ARG	NE-CZ-NH2	-8.03	116.29	120.30
3	F	8	DT	O4'-C1'-N1	-8.01	102.40	108.00

There are no chirality outliers.

There are no planarity outliers.

## 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	A	4659	4743	0	29	0
1	D	4710	4814	0	30	0
2	B	174	100	0	1	0
2	E	174	100	0	1	0
3	C	233	123	0	3	0
3	F	251	134	0	2	0
4	A	29	12	0	2	0
4	D	29	12	0	2	0
5	A	23	22	0	2	0
5	D	23	22	0	1	0
6	D	1	0	0	0	0
7	D	5	0	0	0	0
8	A	453	0	0	12	0
8	B	27	0	0	0	0
8	C	44	0	0	0	0
8	D	692	0	0	15	0
8	E	39	0	0	0	0
8	F	68	0	0	1	0
All	All	11634	10082	0	64	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 3.

The worst 5 of 64 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:472:ARG:NH2	8:D:1607:HOH:O	1.89	1.02
1:A:599:THR:O	8:A:1446:HOH:O	1.92	0.86
1:A:812:ASN:HB3	8:A:1242:HOH:O	1.78	0.81
1:D:340:GLU:OE2	8:D:1453:HOH:O	2.03	0.75
1:D:632:GLU:OE1	8:D:1652:HOH:O	2.05	0.75

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	
1	A	581/592 (98%)	568 (98%)	13 (2%)	0	100	100
1	D	590/592 (100%)	577 (98%)	13 (2%)	0	100	100
All	All	1171/1184 (99%)	1145 (98%)	26 (2%)	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	
1	A	499/507 (98%)	495 (99%)	4 (1%)	89	78
1	D	506/507 (100%)	500 (99%)	6 (1%)	82	63
All	All	1005/1014 (99%)	995 (99%)	10 (1%)	85	70

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	356	GLN
1	D	505	LYS
1	D	561	LEU
1	A	786	PHE
1	D	517	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	502	GLN

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Mol	Chain	Res	Type
1	D	573	ASN
1	D	755	GLN
1	D	418	GLN
1	D	724	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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	$\# Z  > 2$
2	DOC	B	29	3,2	17,19,20	0.92	1 (5%)	20,26,29	1.54	5 (25%)
2	DOC	E	29	3,2	17,19,20	1.10	1 (5%)	20,26,29	1.30	1 (5%)

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
2	DOC	B	29	3,2	-	0/5/18/19	0/2/2/2
2	DOC	E	29	3,2	-	0/5/18/19	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	29	DOC	P-OP1	3.15	1.50	1.46
2	B	29	DOC	P-OP1	2.04	1.49	1.46

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	29	DOC	C2-N3-C4	4.52	122.11	115.57
2	B	29	DOC	C6-C5-C4	4.27	119.24	117.47
2	B	29	DOC	C4'-O4'-C1'	2.49	111.09	110.05
2	B	29	DOC	C6-N1-C2	2.11	121.94	117.73
2	B	29	DOC	C2-N3-C4	2.02	118.50	115.57

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 1 is 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	$\# Z  > 2$
4	CTP	A	901	-	30,30,30	1.94	7 (23%)	44,47,47	2.24	10 (22%)
5	SUC	A	902	-	24,24,24	0.34	0	36,36,36	1.36	4 (11%)
4	CTP	D	901	6	30,30,30	1.67	3 (10%)	44,47,47	2.25	13 (29%)
7	SO4	D	903	-	4,4,4	0.38	0	6,6,6	0.52	0
5	SUC	D	904	-	24,24,24	0.40	0	36,36,36	0.74	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	CTP	A	901	-	-	0/20/38/38	0/2/2/2
5	SUC	A	902	-	-	0/12/51/51	0/2/2/2
4	CTP	D	901	6	-	0/20/38/38	0/2/2/2
7	SO4	D	903	-	-	0/0/0/0	0/0/0/0
5	SUC	D	904	-	-	0/12/51/51	0/2/2/2

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	CTP	O2-C2	6.70	1.37	1.23
4	D	901	CTP	O2-C2	6.02	1.36	1.23
4	D	901	CTP	C2'-C1'	-4.01	1.47	1.53
4	A	901	CTP	C2'-C1'	-3.38	1.48	1.53
4	A	901	CTP	C2-N3	3.04	1.43	1.35

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	901	CTP	O4'-C1'-N1	7.71	124.31	108.06
4	D	901	CTP	C4'-O4'-C1'	-7.27	101.85	109.75
4	D	901	CTP	O4'-C1'-N1	6.07	120.87	108.06
4	A	901	CTP	C4'-O4'-C1'	-5.33	103.96	109.75
4	A	901	CTP	C6-C5-C4	4.90	119.51	117.47

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	A	578/592 (97%)	0.39	42 (7%) 15 13	16, 36, 55, 71	0
1	D	583/592 (98%)	0.21	26 (4%) 32 31	9, 23, 43, 61	0
2	B	9/9 (100%)	-0.63	0 100 100	21, 27, 42, 49	0
2	E	9/9 (100%)	-0.40	0 100 100	16, 22, 39, 49	0
3	C	11/13 (84%)	-0.44	0 100 100	18, 25, 43, 59	0
3	F	12/13 (92%)	0.05	1 (8%) 11 9	13, 25, 49, 60	0
All	All	1202/1228 (97%)	0.28	69 (5%) 23 21	9, 30, 51, 71	0

The worst 5 of 69 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	442	VAL	6.8
1	D	509	GLU	6.6
1	D	433	ALA	5.7
1	D	692	VAL	5.5
1	A	692	VAL	4.4

### 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(Å <sup>2</sup> )	Q<0.9
2	DOC	E	29	18/19	0.09	-0.39	14,18,23,24	0
2	DOC	B	29	18/19	0.07	-0.58	19,26,34,36	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(Å <sup>2</sup> )	Q<0.9
5	SUC	A	902	23/23	0.17	4.45	25,37,46,48	0
4	CTP	D	901	29/29	0.12	0.64	19,27,37,38	0
4	CTP	A	901	29/29	0.15	0.32	27,41,51,57	41
7	SO4	D	903	5/5	0.08	0.32	29,36,43,49	0
5	SUC	D	904	23/23	0.10	-0.25	16,24,31,33	0
6	MN	D	902	1/1	0.06	-1.30	29,29,29,29	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.