wwPDB X-ray Structure Validation Summary Report (i)

Aug 28, 2023 – 10:41 AM EDT

PDB ID	:	3KNT
Title	:	Crystal structure of Methanocaldococcus jannaschii 8-oxoguanine glycosylase/lyase in complex with 15mer DNA containing 8-oxoguanine
Authors	:	Faucher, F.; Doublie, S.
Deposited on	:	2009-11-12
Resolution	:	2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

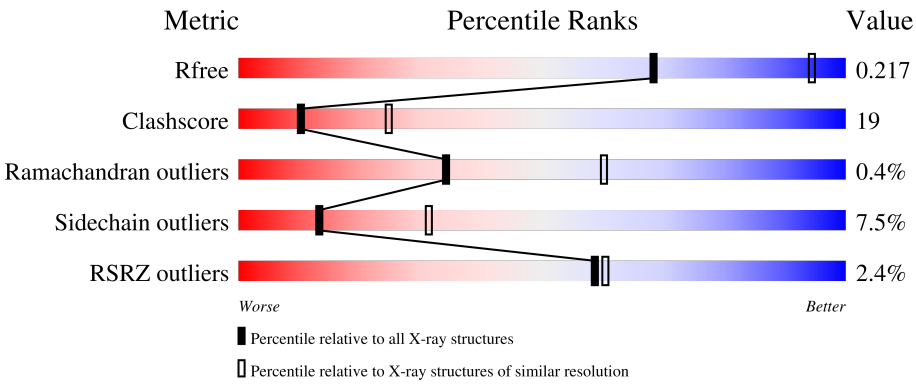
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 <=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	207	2%, 62%, 35%, •
1	B	207	3%, 56%, 38%, 6%
1	C	207	53%, 40%, 7%, •
1	D	207	4%, 53%, 42%, •
2	E	15	47%, 47%, 7%

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Mol	Chain	Length	Quality of chain
2	G	15	13% 47% 33% 7% 13%
2	I	15	27% 60% 7% 7%
2	K	15	40% 53% 7%
3	F	15	67% 33%
3	H	15	20% 67% 13%
3	J	15	27% 60% 13%
3	L	15	13% 87%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9326 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 N-glycosylase/DNA lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	207	1753	1126	304	319	4	0	0	0
1	B	207	1753	1126	304	319	4	0	0	0
1	C	205	1737	1116	302	317	2	0	0	0
1	D	206	1745	1121	303	318	3	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	129	GLN	LYS	engineered mutation	UNP Q58134
B	129	GLN	LYS	engineered mutation	UNP Q58134
C	129	GLN	LYS	engineered mutation	UNP Q58134
D	129	GLN	LYS	engineered mutation	UNP Q58134

- Molecule 2 is a DNA chain called 5'-D(*AP*CP*GP*TP*CP*CP*AP*(8OG)P*GP*TP*CP*TP*AP*CP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	E	15	301	144	54	89	14	0	0	0
2	G	13	263	126	48	77	12	0	0	0
2	I	14	282	135	51	83	13	0	0	0
2	K	15	301	144	54	89	14	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	F	15	309	147	60	88	14	0	0	0
			Total	C	N	O	P			
3	H	13	267	127	53	75	12	0	0	0
			Total	C	N	O	P			
3	J	13	267	127	53	75	12	0	0	0
			Total	C	N	O	P			
3	L	15	309	147	60	88	14	0	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
4	A	1	1	1	0	0
			Total	Na		
4	B	1	1	1	0	0
			Total	Na		
4	C	1	1	1	0	0
			Total	Na		
4	D	1	1	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	7	7	7	0	0
			Total	O		
5	B	7	7	7	0	0
			Total	O		
5	C	7	7	7	0	0
			Total	O		
5	D	1	1	1	0	0
			Total	O		
5	E	1	1	1	0	0
			Total	O		
5	F	1	1	1	0	0
			Total	O		
5	H	1	1	1	0	0
			Total	O		
5	I	2	2	2	0	0
			Total	O		
5	J	3	3	3	0	0
			Total	O		
5	K	3	3	3	0	0

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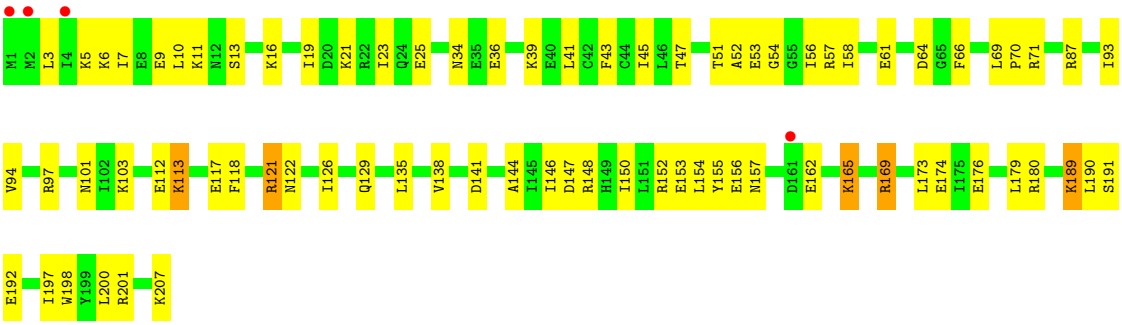
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	L	2	2	2	0	0

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.

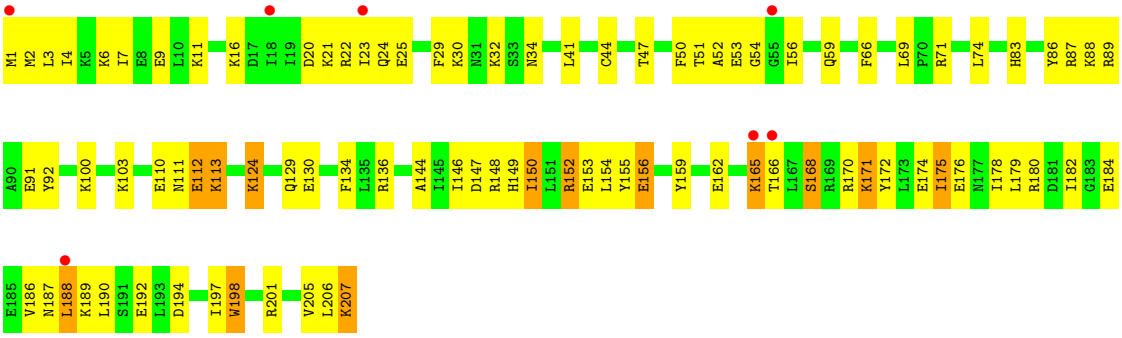
• Molecule 1: N-glycosylase/DNA lyase

Chain A: 2% 62% 35%



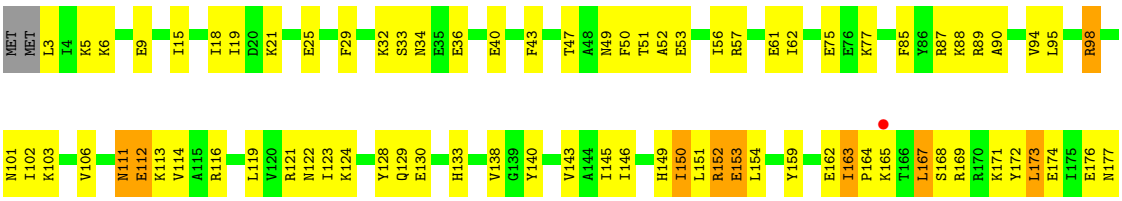
• Molecule 1: N-glycosylase/DNA lyase

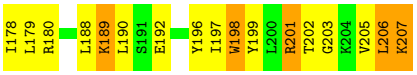
Chain B: 3% 56% 38% 6%



• Molecule 1: N-glycosylase/DNA lyase

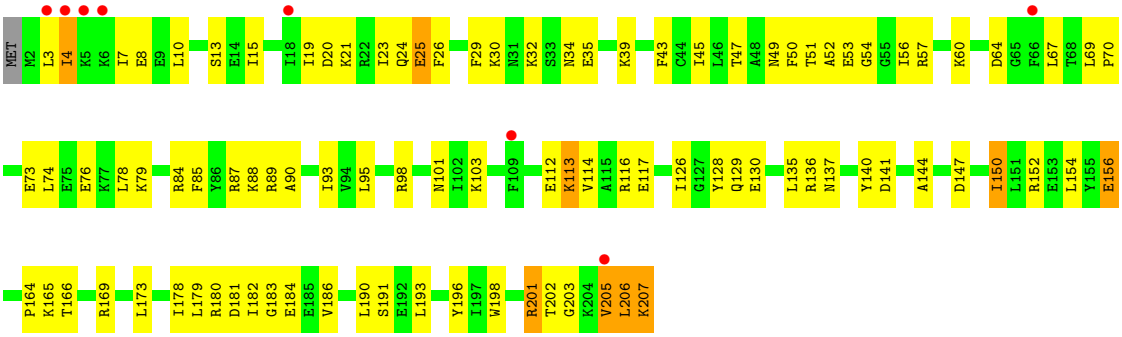
Chain C: 53% 40% 7%





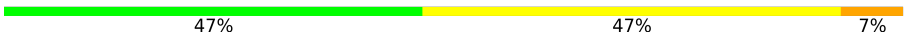
• Molecule 1: N-glycosylase/DNA lyase

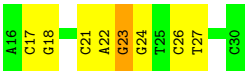
Chain D:



• Molecule 2: 5'-D(*AP*CP*GP*TP*CP*CP*AP*(8OG)P*GP*TP*CP*TP*AP*CP*C)-3'

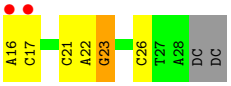
Chain E:





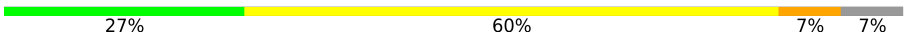
• Molecule 2: 5'-D(*AP*CP*GP*TP*CP*CP*AP*(8OG)P*GP*TP*CP*TP*AP*CP*C)-3'

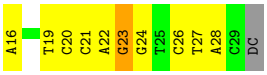
Chain G:



• Molecule 2: 5'-D(*AP*CP*GP*TP*CP*CP*AP*(8OG)P*GP*TP*CP*TP*AP*CP*C)-3'

Chain I:



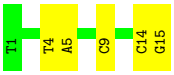


• Molecule 2: 5'-D(*AP*CP*GP*TP*CP*CP*AP*(8OG)P*GP*TP*CP*TP*AP*CP*C)-3'

Chain K:

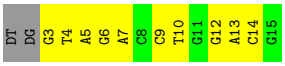
• Molecule 3: 5'-D(*TP*GP*GP*TP*AP*GP*AP*CP*CP*TP*GP*GP*AP*CP*G)-3'

Chain F: 67% 33%



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

Chain H: 20% 67% 13%

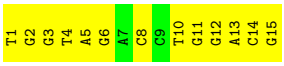


• Molecule 3: 5'-D(*TP*GP*GP*TP*AP*GP*AP*CP*CP*TP*GP*GP*AP*CP*G)-3'

Chain J: 27% 60% 13%

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

Chain L: 13% 87%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	54.80Å 150.03Å 90.27Å 90.00° 107.53° 90.00°	Depositor
Resolution (Å)	19.80 – 2.70 19.84 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (19.80-2.70) 98.6 (19.84-2.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.17 (at 2.71Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.188 , 0.225 0.187 , 0.217	Depositor DCC
R_{free} test set	1893 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	63.6	Xtriage
Anisotropy	0.593	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 47.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.296 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	9326	wwPDB-VP
Average B, all atoms (Å^2)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.31% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: NA, 8OG

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	0.23	0/1781	0.38	0/2381
1	B	0.30	0/1781	0.46	0/2381
1	C	0.32	0/1765	0.47	0/2361
1	D	0.31	0/1773	0.48	0/2371
2	E	0.45	0/309	1.07	0/471
2	G	0.52	0/267	1.01	0/407
2	I	0.47	0/288	1.03	0/439
2	K	0.47	0/309	1.01	0/471
3	F	0.46	0/347	1.04	0/535
3	H	0.47	0/300	1.00	0/462
3	J	0.47	0/300	0.99	0/462
3	L	0.44	0/347	1.03	0/535
All	All	0.35	0/9567	0.67	0/13276

There are no bond length outliers.

There are no bond angle outliers.

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	1753	0	1800	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1753	0	1800	71	0
1	C	1737	0	1779	85	0
1	D	1745	0	1788	74	0
2	E	301	0	170	12	0
2	G	263	0	148	6	0
2	I	282	0	159	13	0
2	K	301	0	170	14	0
3	F	309	0	170	5	0
3	H	267	0	147	7	0
3	J	267	0	147	8	0
3	L	309	0	170	13	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	7	0	0	0	0
5	B	7	0	0	0	0
5	C	7	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	H	1	0	0	0	0
5	I	2	0	0	0	0
5	J	3	0	0	0	0
5	K	3	0	0	0	0
5	L	2	0	0	0	0
All	All	9326	0	8448	334	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 19.

The worst 5 of 334 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:C:167:LEU:HD23	1:C:171:LYS:HB3	1.23	1.11
1:C:168:SER:OG	1:C:171:LYS:HD3	1.49	1.10
1:B:165:LYS:HD2	1:B:165:LYS:N	1.67	1.09
1:B:165:LYS:HD2	1:B:165:LYS:H	0.84	0.99
1:B:165:LYS:H	1:B:165:LYS:CD	1.75	0.97

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	
1	A	205/207 (99%)	190 (93%)	15 (7%)	0	100	100
1	B	205/207 (99%)	188 (92%)	17 (8%)	0	100	100
1	C	203/207 (98%)	189 (93%)	13 (6%)	1 (0%)	29	54
1	D	204/207 (99%)	184 (90%)	18 (9%)	2 (1%)	15	37
All	All	817/828 (99%)	751 (92%)	63 (8%)	3 (0%)	34	60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	206	LEU
1	C	163	ILE
1	D	205	VAL

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	
1	A	190/190 (100%)	181 (95%)	9 (5%)	26	54
1	B	190/190 (100%)	171 (90%)	19 (10%)	7	18
1	C	188/190 (99%)	171 (91%)	17 (9%)	9	22
1	D	189/190 (100%)	177 (94%)	12 (6%)	18	40
All	All	757/760 (100%)	700 (92%)	57 (8%)	13	31

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	47	THR
1	D	201	ARG
1	C	152	ARG
1	D	156	GLU
1	D	87	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	157	ASN
1	C	157	ASN
1	C	111	ASN
1	C	24	GLN
1	C	122	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 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	8OG	I	23	2	22,25,26	3.27	3 (13%)	30,37,40	2.74	11 (36%)
2	8OG	K	23	2	22,25,26	3.28	3 (13%)	30,37,40	2.71	11 (36%)
2	8OG	G	23	2	22,25,26	3.27	3 (13%)	30,37,40	2.71	10 (33%)
2	8OG	E	23	2	22,25,26	3.26	3 (13%)	30,37,40	2.75	12 (40%)

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	8OG	I	23	2	-	2/7/21/22	0/3/3/3
2	8OG	K	23	2	-	2/7/21/22	0/3/3/3
2	8OG	G	23	2	-	0/7/21/22	0/3/3/3
2	8OG	E	23	2	-	0/7/21/22	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	23	8OG	O8-C8	13.87	1.48	1.23
2	E	23	8OG	O8-C8	13.77	1.48	1.23
2	I	23	8OG	O8-C8	13.77	1.48	1.23
2	G	23	8OG	O8-C8	13.75	1.48	1.23
2	G	23	8OG	C8-N9	-4.29	1.33	1.40

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	23	8OG	C5-C4-N3	-7.78	119.77	127.80
2	G	23	8OG	C5-C4-N3	-7.74	119.80	127.80
2	I	23	8OG	C5-C4-N3	-7.73	119.82	127.80
2	K	23	8OG	C5-C4-N3	-7.71	119.83	127.80
2	G	23	8OG	N7-C8-N9	7.00	114.88	106.58

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	I	23	8OG	O4'-C4'-C5'-O5'
2	K	23	8OG	O4'-C4'-C5'-O5'
2	I	23	8OG	C3'-C4'-C5'-O5'
2	K	23	8OG	C3'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	23	8OG	1	0
2	K	23	8OG	3	0
2	G	23	8OG	2	0
2	E	23	8OG	4	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	207/207 (100%)	0.19	4 (1%)	66	69	42, 60, 76, 82	25 (12%)
1	B	207/207 (100%)	0.24	7 (3%)	45	45	48, 61, 79, 95	21 (10%)
1	C	205/207 (99%)	0.12	1 (0%)	91	92	45, 60, 75, 90	20 (9%)
1	D	206/207 (99%)	0.23	8 (3%)	39	38	44, 63, 79, 87	30 (14%)
2	E	14/15 (93%)	-0.19	0	100	100	47, 69, 82, 84	0
2	G	12/15 (80%)	0.31	2 (16%)	1	1	62, 88, 109, 110	0
2	I	13/15 (86%)	-0.48	0	100	100	53, 71, 91, 96	0
2	K	14/15 (93%)	-0.35	0	100	100	45, 68, 77, 79	0
3	F	15/15 (100%)	-0.59	0	100	100	53, 71, 92, 93	0
3	H	13/15 (86%)	-0.06	0	100	100	70, 93, 104, 105	0
3	J	13/15 (86%)	-0.61	0	100	100	60, 73, 98, 99	0
3	L	15/15 (100%)	-0.34	0	100	100	58, 74, 80, 82	0
All	All	934/948 (98%)	0.14	22 (2%)	59	60	42, 62, 82, 110	96 (10%)

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	5	LYS	3.8
1	B	166	THR	3.8
1	B	1	MET	3.1
1	D	3	LEU	3.1
2	G	16	DA	2.9

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
2	8OG	G	23	23/24	0.94	0.16	57,62,65,67	0
2	8OG	E	23	23/24	0.95	0.15	52,54,59,65	0
2	8OG	I	23	23/24	0.95	0.16	52,58,61,65	0
2	8OG	K	23	23/24	0.96	0.17	54,59,65,70	0

6.3 Carbohydrates (i)

There are no monosaccharides 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	NA	D	208	1/1	0.66	0.14	47,47,47,47	0
4	NA	C	208	1/1	0.77	0.11	57,57,57,57	0
4	NA	A	208	1/1	0.83	0.12	58,58,58,58	0
4	NA	B	208	1/1	0.87	0.12	51,51,51,51	0

6.5 Other polymers (i)

There are no such residues in this entry.