



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 12, 2017 – 07:59 AM EDT

PDB ID : 5BTL  
Title : Crystal structure of a topoisomerase II complex  
Authors : Blower, T.R.; Williamson, B.H.; Kerns, R.J.; Berger, J.M.  
Deposited on : unknown  
Resolution : 2.50 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20029824

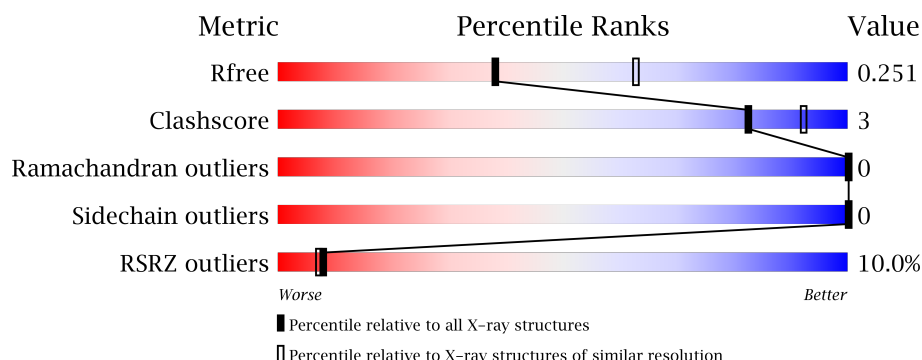
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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.



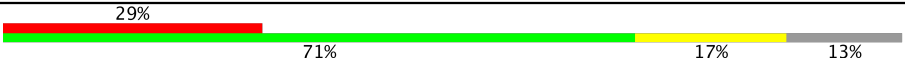


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	503	<div> <div>8%</div> <div>93%</div> <div>• •</div> </div>
1	C	503	<div> <div>11%</div> <div>93%</div> <div>• •</div> </div>
2	B	253	<div> <div>8%</div> <div>92%</div> <div>• •</div> </div>
2	D	253	<div> <div>6%</div> <div>91%</div> <div>7% •</div> </div>
3	E	24	<div> <div>21%</div> <div>71%</div> <div>17% 13%</div> </div>

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Mol	Chain	Length	Quality of chain
3	H	24	
4	F	24	
4	G	24	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	PTR	A	129	-	-	X	-
1	PTR	C	129	-	-	X	-

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 25993 atoms, of which 12526 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 DNA gyrase subunit A.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	487	Total	C	H	N	O	P	S	0	1	0
			7691	2388	3853	704	732	1	13			
1	C	487	Total	C	H	N	O	P	S	0	1	0
			7689	2388	3851	704	732	1	13			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	501	ILE	-	expression tag	UNP P9WG47
A	502	GLY	-	expression tag	UNP P9WG47
A	503	SER	-	expression tag	UNP P9WG47
A	504	GLY	-	expression tag	UNP P9WG47
C	501	ILE	-	expression tag	UNP P9WG47
C	502	GLY	-	expression tag	UNP P9WG47
C	503	SER	-	expression tag	UNP P9WG47
C	504	GLY	-	expression tag	UNP P9WG47

- Molecule 2 is a protein called DNA gyrase subunit B.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	245	Total	C	H	N	O	S	0	0	0
			3906	1217	1974	348	360	7			
2	D	247	Total	C	H	N	O	S	0	0	0
			3930	1224	1984	351	364	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	423	SER	-	expression tag	UNP P9WG44
B	424	ASN	-	expression tag	UNP P9WG44
B	425	ALA	-	expression tag	UNP P9WG44
D	423	SER	-	expression tag	UNP P9WG44

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Chain	Residue	Modelled	Actual	Comment	Reference
D	424	ASN	-	expression tag	UNP P9WG44
D	425	ALA	-	expression tag	UNP P9WG44

- Molecule 3 is a DNA chain called DNA substrate 24-mer GGTCATGAATGACTATGCAC GTAA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	E	21	Total	C	H	N	O	P	0	21	0
			620	196	210	74	120	20			
3	H	21	Total	C	H	N	O	P	0	21	0
			615	196	205	74	120	20			

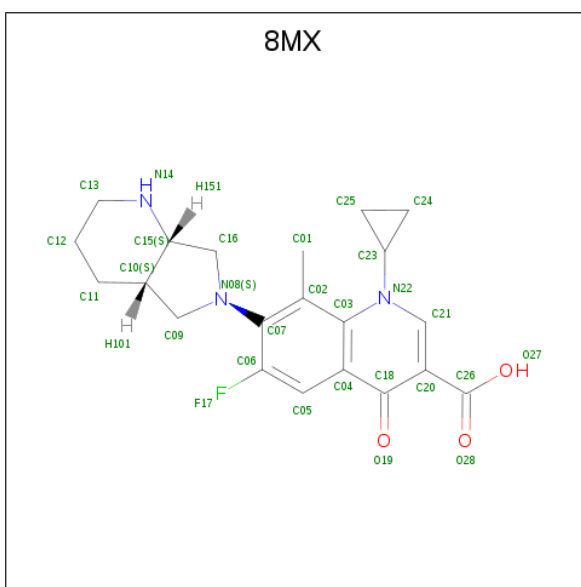
- Molecule 4 is a DNA chain called DNA substrate 24-mer TTACGTGCATAGTCATTTCAT GACC.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	F	21	Total	C	H	N	O	P	0	21	0
			612	196	202	74	120	20			
4	G	21	Total	C	H	N	O	P	0	21	0
			611	196	201	74	120	20			

- 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	D	1	Total	Mg	0	0
			1	1		
5	F	1	Total	Mg	0	0
			1	1		
5	E	1	Total	Mg	0	0
			1	1		

- Molecule 6 is 1-cyclopropyl-6-fluoro-8-methyl-7-[(4aS,7aS)-octahydro-6H-pyrrolo[3,4-b]pyridin-6-yl]-4-oxo-1,4-dihydroquinoline-3-carboxylic acid (three-letter code: 8MX) (formula: C<sub>21</sub>H<sub>24</sub>FN<sub>3</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	E	1	Total	C	F	H	N	O	0	0
			51	21	1	23	3	3		
6	H	1	Total	C	F	H	N	O	0	0
			51	21	1	23	3	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	95	Total	O	0	0
			95	95		
7	B	32	Total	O	0	0
			32	32		
7	C	38	Total	O	0	0
			38	38		
7	D	28	Total	O	0	0
			28	28		
7	E	7	Total	O	0	0
			7	7		
7	F	6	Total	O	0	0
			6	6		
7	G	1	Total	O	0	0
			1	1		
7	H	6	Total	O	0	0
			6	6		

These plots are drawn for all protein, RNA and DNA 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 ( $\text{RSRZ} > 2$ ). 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.

Chain A:

93%

8%

THR ASP THR THR LEU PRO PRO ASP ASP SER LEU ASP ARG I15 Y31 L48 V51 H52 P66 S91 I92 F123 A126 Y129 T130 R248 V259 E260 E261 D262 S263 R264 G265 R266 P275 V278 T287 Q290 V291 R292 K295 I302 E312

V323 A324 K325 R387 V395 L401 V404 R408 R409 A410 S411 E412 T413 V414 L421 L424 L425 D426 L427 D428 E429 I430 Q431 A434 T435 L436 D437 H438 R441 R442 L443 L446 L452 A470 I501 GLY SER GLY

Chain C: 

Amino Acid	Category
L440	Red
R441	Red
R442	Red
R450	Red
I451	Red
I452	Red
A463	Red
A470	Red
I501	Red
GLY	Grey
SER	Grey
GLY	Grey
T387	Green
V291	Yellow
R292	Red
D293	Red
G294	Red
K295	Red
L296	Red
A297	Red
G298	Red
T302	Green
V315	Red
T316	Red
E317	Red
T318	Red
A322	Red
V323	Red
A324	Red
K325	Red
V326	Red
L331	Red
T335	Red
V344	Yellow
R387	Red
A388	Yellow
H389	Green
L394	Red
V404	Red
L407	Red
E412	Red
T413	Red
V414	Red
D415	Red
T416	Red
A419	Red
E423	Red
D428	Red
E429	Red
I430	Red
Q431	Red
L436	Red
D437	Red
V438	Red
V439	Red
T440	Red
T441	Red
L442	Red
L443	Red
L444	Red
L445	Red
L446	Red
L447	Red
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L451	Red
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L464	Red
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L529	Red
L530	Red
L531	Red
L532	Red
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L539	Red
L540	Red
L541	Red
L542	Red
L543	Red
L544	Red
L545	Red
L546	Red
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L548	Red
L549	Red
L550	Red
L551	Red
L552	Red
L553	Red
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L557	Red
L558	Red
L559	Red
L560	Red
L561	Red
L562	Red
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L567	Red
L568	Red
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L572	Red
L573	Red
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L583	Red
L584	Red
L585	Red
L586	Red
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L589	Red
L590	Red
L591	Red
L592	Red
L593	Red
L594	Red
L595	Red
L596	Red
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L601	Red
L602	Red
L603	Red
L604	Red
L605	Red
L606	

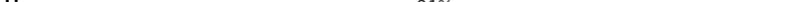
Chain B:

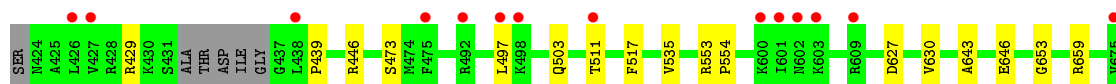
8%

92%

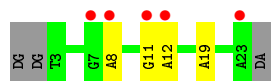
SER ASN L426 Y427 R428 R429 R430 SER ALA THR ASP ILE GLY G437 L438 P439 R446 P450 S462 A467 S473 R474 F475 L481 R492 L497 R498 L506 T507 A508 D515 R523 V535 R553 P554 I601 H602 I603 R609 G612 R634

D674 V675

Chain D:  6% 91% 7%



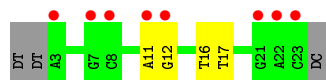
- Molecule 3: DNA substrate 24-mer GGTCATGAATGACTATGCACGTAA



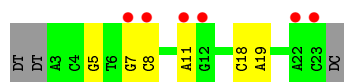
- Molecule 3: DNA substrate 24-mer GGTCATGAATGACTATGCACGTAA



- Molecule 4: DNA substrate 24-mer TTACGTGCATAGTCATTCATGACC



- Molecule 4: DNA substrate 24-mer TTACGTGCATAGTCATTCATGACC



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.94Å 83.05Å 128.74Å 90.00° 108.88° 90.00°	Depositor
Resolution (Å)	49.60 – 2.50 49.11 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.3 (49.60-2.50) 94.5 (49.11-2.50)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.10 (at 2.51Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.230 , 0.256 0.225 , 0.251	Depositor DCC
$R_{free}$ test set	3547 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	50.4	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 41.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	25993	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 8MX, PTR

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	0.21	0/3881	0.39	0/5253
1	C	0.21	0/3881	0.38	0/5253
2	B	0.23	0/1960	0.39	0/2634
2	D	0.22	0/1974	0.39	0/2653
3	E	0.53	0/458	0.95	0/704
3	H	0.54	0/458	0.96	0/704
4	F	0.53	0/458	0.94	0/704
4	G	0.50	0/458	0.94	0/704
All	All	0.28	0/13528	0.51	0/18609

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	3838	3853	3853	18	0
1	C	3838	3851	3853	20	0
2	B	1932	1974	1973	8	0
2	D	1946	1984	1984	14	0
3	E	410	210	210	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	410	205	205	6	0
4	F	410	202	202	5	0
4	G	410	201	201	8	0
5	B	1	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
6	E	28	23	0	1	0
6	H	28	23	0	2	0
7	A	95	0	0	1	0
7	B	32	0	0	1	0
7	C	38	0	0	1	0
7	D	28	0	0	0	0
7	E	7	0	0	0	0
7	F	6	0	0	0	0
7	G	1	0	0	0	0
7	H	6	0	0	0	0
All	All	13467	12526	12481	61	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 3.

The worst 5 of 61 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:129:PTR:O2P	4:G:11[B]:DA:C5'	2.03	1.06
1:A:129:PTR:O3P	3:H:11[B]:DG:C5'	2.17	0.93
1:C:129:PTR:O2P	3:E:11[A]:DG:H4'	1.74	0.86
1:A:129:PTR:O3P	3:H:11[B]:DG:H4'	1.78	0.83
2:D:653:GLY:O	2:D:659:ARG:NH2	2.11	0.83

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	485/503 (96%)	469 (97%)	16 (3%)	0	100	100
1	C	485/503 (96%)	468 (96%)	17 (4%)	0	100	100
2	B	241/253 (95%)	233 (97%)	8 (3%)	0	100	100
2	D	243/253 (96%)	235 (97%)	8 (3%)	0	100	100
All	All	1454/1512 (96%)	1405 (97%)	49 (3%)	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	407/420 (97%)	407 (100%)	0	100	100
1	C	407/420 (97%)	407 (100%)	0	100	100
2	B	205/211 (97%)	205 (100%)	0	100	100
2	D	207/211 (98%)	207 (100%)	0	100	100
All	All	1226/1262 (97%)	1226 (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. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules 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$
1	PTR	A	129	1	15,16,17	1.28	1 (6%)	19,22,24	0.98	1 (5%)
1	PTR	C	129	1	15,16,17	1.04	1 (6%)	19,22,24	1.06	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
1	PTR	A	129	1	-	0/9/11/13	0/1/1/1
1	PTR	C	129	1	-	0/9/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	129	PTR	CA-C	-3.03	1.46	1.50
1	C	129	PTR	CA-C	-2.64	1.46	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	129	PTR	CB-CA-C	-2.84	105.94	111.41
1	A	129	PTR	CB-CA-C	-2.54	106.52	111.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	129	PTR	6	0
1	C	129	PTR	6	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	8MX	E	101	5	24,32,32	5.82	12 (50%)	24,49,49	2.14	9 (37%)
6	8MX	H	101	5	24,32,32	5.82	10 (41%)	24,49,49	3.00	14 (58%)

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	8MX	E	101	5	-	0/8/33/33	1/4/5/5
6	8MX	H	101	5	-	0/8/33/33	0/4/5/5

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	H	101	8MX	C16-C15	-19.29	1.19	1.52
6	E	101	8MX	C16-C15	-16.89	1.23	1.52
6	H	101	8MX	C09-C10	-15.74	1.29	1.53
6	E	101	8MX	C09-C10	-15.06	1.30	1.53
6	H	101	8MX	C04-C03	-3.54	1.38	1.41

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	101	8MX	C13-N14-C15	-8.88	105.97	111.62
6	H	101	8MX	C09-N08-C07	-3.90	115.62	123.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	101	8MX	C05-C04-C18	-3.29	116.32	121.69
6	H	101	8MX	C05-C04-C18	-3.28	116.34	121.69
6	E	101	8MX	C21-C20-C18	-3.13	118.53	119.99

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	E	101	8MX	C10-C11-C12-C13-C15-N14

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	101	8MX	1	0
6	H	101	8MX	2	0

## 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, 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	486/503 (96%)	0.82	41 (8%) 12 11	33, 56, 105, 163	0
1	C	486/503 (96%)	0.91	55 (11%) 6 5	37, 58, 105, 149	0
2	B	245/253 (96%)	0.85	19 (7%) 14 14	42, 64, 97, 130	0
2	D	247/253 (97%)	0.64	14 (5%) 24 25	44, 61, 95, 150	0
3	E	21/24 (87%)	1.90	5 (23%) 1 0	64, 105, 173, 203	21 (100%)
3	H	21/24 (87%)	1.50	7 (33%) 0 0	26, 57, 128, 179	21 (100%)
4	F	21/24 (87%)	1.83	8 (38%) 0 0	59, 98, 176, 209	21 (100%)
4	G	21/24 (87%)	1.89	6 (28%) 1 0	32, 56, 157, 183	21 (100%)
All	All	1548/1608 (96%)	0.88	155 (10%) 8 7	26, 61, 112, 209	84 (5%)

The worst 5 of 155 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	23[A]	DA	10.6
4	G	23[B]	DC	9.9
1	C	292	ARG	8.4
1	A	264	ARG	8.1
2	B	426	LEU	6.3

### 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. 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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	PTR	A	129	16/17	0.95	0.24	-	45,50,70,72	0
1	PTR	C	129	16/17	0.94	0.31	-	48,52,67,78	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	MG	F	101	1/1	0.98	0.33	1.47	47,47,47,47	0
5	MG	E	102	1/1	0.95	0.33	1.03	65,65,65,65	0
6	8MX	E	101	28/28	0.83	0.29	0.60	41,50,65,66	0
6	8MX	H	101	28/28	0.89	0.25	-0.10	39,47,56,56	0
5	MG	D	701	1/1	0.97	0.18	-1.27	40,40,40,40	0
5	MG	B	701	1/1	0.94	0.20	-1.76	48,48,48,48	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.