



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 31, 2016 – 04:26 AM EDT

PDB ID : 5K95  
Title : Crystal Structure of GTP Cyclohydrolase-IB with 8-oxo-GTP  
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Deposited on : 2016-05-31  
Resolution : 2.77 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027939  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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-20027939

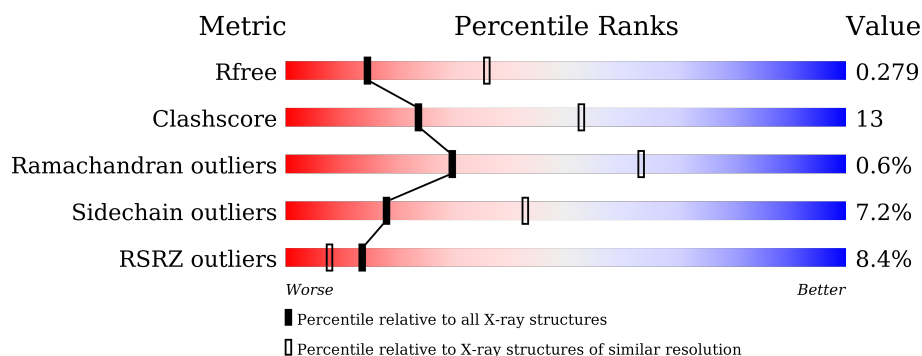
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.77 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))
$R_{free}$	91344	3004 (2.80-2.76)
Clashscore	102246	3480 (2.80-2.76)
Ramachandran outliers	100387	3423 (2.80-2.76)
Sidechain outliers	100360	3425 (2.80-2.76)
RSRZ outliers	91569	3016 (2.80-2.76)

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	257	<div> <div>15%</div> <div>67%</div> <div>26%</div> <div>• 5%</div> </div>
1	B	257	<div> <div>%</div> <div>71%</div> <div>22%</div> <div>• 5%</div> </div>

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
2	8GT	B	301	-	-	-	X

## 2 Entry composition [i](#)

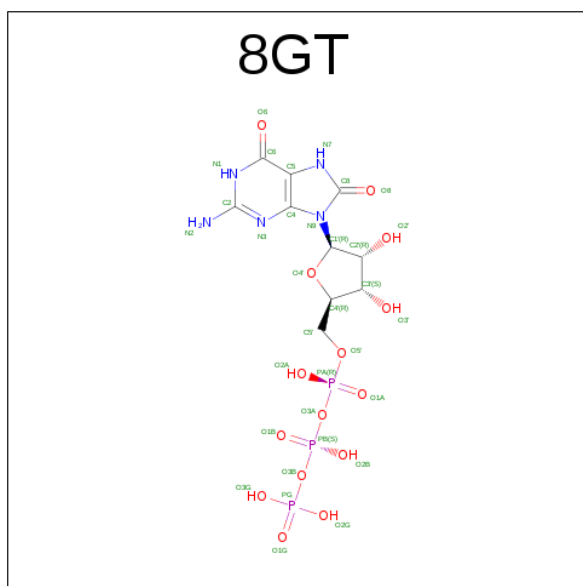
There are 4 unique types of molecules in this entry. The entry contains 4067 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GTP cyclohydrolase FolE2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	245	Total	C	N	O	S	0	1	0
			1940	1226	331	372	11			
1	B	245	Total	C	N	O	S	0	6	0
			1982	1250	340	379	13			

- Molecule 2 is 8-OXO-GUANOSINE-5'-TRIPHOSPHATE (three-letter code: 8GT) (formula:  $C_{10}H_{16}N_5O_{15}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			33	10	5	15	3		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula:  $Zn$ ).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		

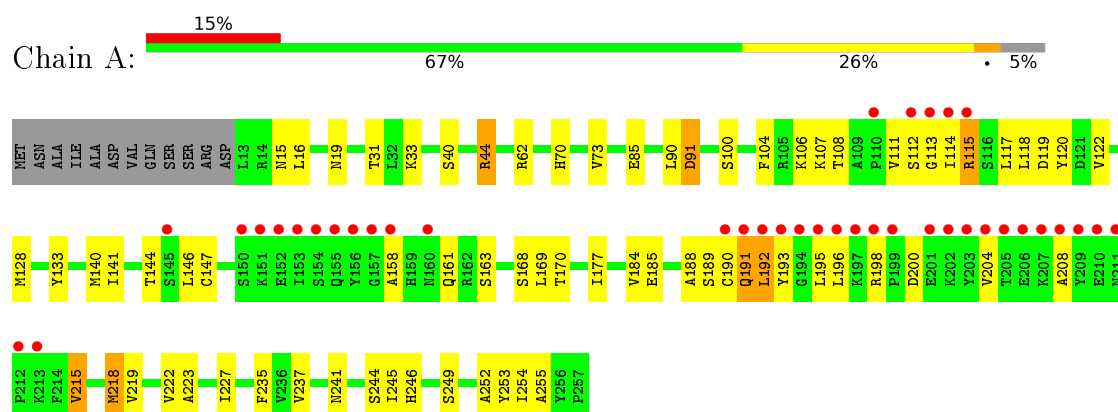
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	40	Total 40	O 40	0	0
4	B	71	Total 71	O 71	0	0

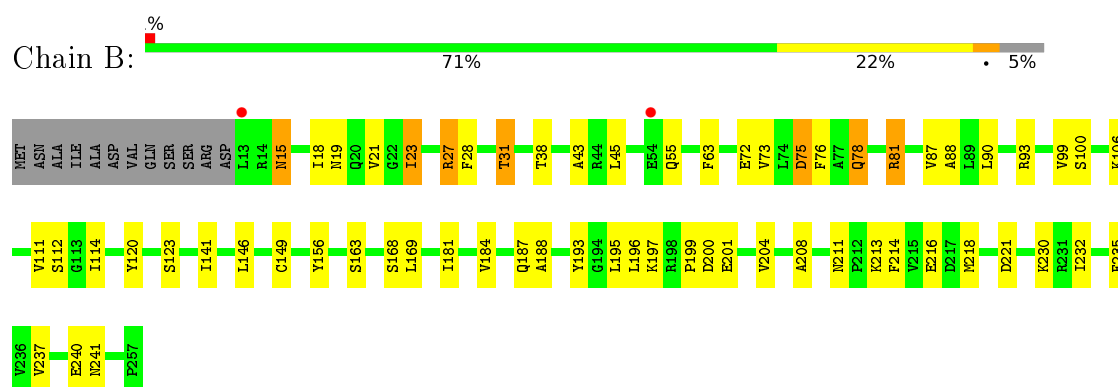
### 3 Residue-property plots [i](#)

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: GTP cyclohydrolase FolE2



#### • Molecule 1: GTP cyclohydrolase FolE2



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.88Å 100.56Å 115.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.07 – 2.77 46.07 – 2.77	Depositor EDS
% Data completeness (in resolution range)	98.1 (46.07-2.77) 98.2 (46.07-2.77)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.175 , 0.277 0.180 , 0.279	Depositor DCC
$R_{free}$ test set	684 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	65.4	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 42.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4067	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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: ZN, 8GT, SNC

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	0.56	0/1969	0.72	1/2662 (0.0%)
1	B	0.59	0/2013	0.72	1/2719 (0.0%)
All	All	0.57	0/3982	0.72	2/5381 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	ARG	NE-CZ-NH2	-7.35	116.63	120.30
1	B	27	ARG	NE-CZ-NH2	-5.34	117.63	120.30

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	1940	0	1935	60	0
1	B	1982	0	1980	50	0
2	B	33	0	12	1	0
3	B	1	0	0	0	0
4	A	40	0	0	7	0
4	B	71	0	0	3	0
All	All	4067	0	3927	104	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 13.

All (104) 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:A:128:MET:SD	4:A:427:HOH:O	2.25	0.94
1:B:31:THR:HG22	1:B:73:VAL:HG23	1.48	0.93
1:B:81[A]:ARG:HH11	1:B:81[A]:ARG:HG3	1.34	0.90
1:B:31:THR:CG2	1:B:73:VAL:HG23	2.10	0.81
1:A:163:SER:HB3	1:A:241:ASN:HD22	1.48	0.79
1:B:81[A]:ARG:NH1	1:B:81[A]:ARG:HG3	1.93	0.78
1:A:254:ILE:HA	1:B:19:ASN:HD22	1.49	0.77
1:B:15:ASN:N	1:B:15:ASN:HD22	1.83	0.77
1:A:33:LYS:HB2	1:A:73:VAL:HG11	1.69	0.73
1:A:252:ALA:HB2	1:B:21:VAL:HG23	1.71	0.70
1:B:188:ALA:HA	1:B:218[A]:MET:HE1	1.74	0.67
1:B:163:SER:HB2	1:B:241:ASN:ND2	2.10	0.67
1:A:144:THR:HG23	1:A:192:LEU:CD2	2.25	0.66
1:A:188:ALA:HB3	1:A:191:GLN:NE2	2.12	0.64
1:A:254:ILE:HA	1:B:19:ASN:ND2	2.13	0.64
1:A:141:ILE:HD13	1:A:184:VAL:HG21	1.79	0.63
1:A:215:VAL:HG23	1:A:241:ASN:HB2	1.80	0.63
1:B:163:SER:HB2	1:B:241:ASN:HD22	1.64	0.62
1:A:118:LEU:HD12	1:A:119:ASP:H	1.64	0.62
1:A:112:SER:O	1:A:114:ILE:N	2.33	0.61
1:B:23:ILE:H	1:B:23:ILE:HD13	1.65	0.61
1:A:140:MET:HE3	4:A:426:HOH:O	2.01	0.60
1:B:81[A]:ARG:HH11	1:B:81[A]:ARG:CG	2.05	0.60
1:A:104:PHE:CE1	1:A:119:ASP:HB3	2.37	0.60
1:B:15:ASN:H	1:B:15:ASN:HD22	1.47	0.60
1:B:114:ILE:HG21	1:B:195:LEU:HD13	1.82	0.59
1:A:196:LEU:HD22	1:A:200:ASP:OD2	2.02	0.59
1:A:169:LEU:HD12	1:A:169:LEU:O	2.03	0.59
1:B:45:LEU:HD23	1:B:99:VAL:HG22	1.85	0.58
1:A:146:LEU:HD21	1:A:158:ALA:HB3	1.85	0.58
1:A:169:LEU:C	1:A:169:LEU:HD12	2.24	0.58
1:A:62:ARG:HB2	1:A:90:LEU:HD21	1.86	0.57
1:A:144:THR:CG2	1:A:192:LEU:HD22	2.36	0.55
1:A:144:THR:HG23	1:A:192:LEU:HD22	1.88	0.54
1:B:45:LEU:CD2	1:B:99:VAL:HG22	2.38	0.54
1:B:55:GLN:N	4:B:403:HOH:O	2.40	0.54
1:A:223:ALA:O	1:A:227:ILE:HD12	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:ILE:HG23	1:A:246:HIS:CD2	2.44	0.53
1:A:170:THR:CG2	4:A:428:HOH:O	2.57	0.52
1:A:106:LYS:HZ2	1:A:115:ARG:HB2	1.74	0.52
1:A:128:MET:CE	4:A:427:HOH:O	2.52	0.52
1:A:146:LEU:HD23	1:A:147:CYS:N	2.25	0.51
1:B:146:LEU:HD13	1:B:208:ALA:C	2.30	0.51
1:A:31:THR:HG22	1:A:40:SER:OG	2.11	0.51
1:A:128:MET:HE2	4:A:427:HOH:O	2.11	0.50
1:B:78:GLN:HA	1:B:78:GLN:HE21	1.75	0.50
1:B:211[B]:ASN:ND2	4:B:406:HOH:O	2.45	0.49
1:B:111:VAL:HG11	1:B:199:PRO:HB2	1.93	0.49
1:A:133:TYR:HA	4:A:427:HOH:O	2.11	0.49
1:A:245:ILE:HG23	1:A:246:HIS:NE2	2.28	0.49
1:B:169:LEU:HD22	1:B:232:ILE:HG12	1.94	0.48
1:A:163:SER:HB3	1:A:241:ASN:ND2	2.23	0.48
1:A:255:ALA:H	1:B:19:ASN:ND2	2.11	0.48
1:A:219:VAL:HG21	1:B:18:ILE:HD13	1.95	0.48
1:B:235:PHE:CD1	1:B:237:VAL:HG23	2.50	0.47
1:A:62:ARG:HD2	1:A:90:LEU:HD23	1.97	0.47
1:B:193:TYR:HB2	1:B:196:LEU:HD21	1.97	0.47
1:A:111:VAL:HG12	1:A:112:SER:H	1.80	0.47
1:A:19:ASN:HD22	1:A:19:ASN:H	1.62	0.47
1:A:31:THR:HG23	4:A:434:HOH:O	2.14	0.47
1:A:215:VAL:HG13	1:A:252:ALA:HB3	1.95	0.47
1:A:235:PHE:CE1	1:A:237:VAL:HG23	2.50	0.47
1:B:218[B]:MET:HE1	1:B:241:ASN:HD21	1.81	0.46
1:A:33:LYS:HB2	1:A:73:VAL:CG1	2.41	0.46
1:A:70:HIS:NE2	1:A:85:GLU:OE1	2.49	0.46
1:B:72:GLU:N	1:B:72:GLU:OE2	2.50	0.45
1:B:43:ALA:HA	1:B:100:SER:O	2.17	0.45
1:B:149:SNC:SG	2:B:301:8GT:O2'	2.60	0.45
1:A:161:GLN:NE2	1:A:241:ASN:HD21	2.15	0.44
1:B:15:ASN:ND2	1:B:15:ASN:N	2.55	0.44
1:B:187:GLN:NE2	4:B:402:HOH:O	2.29	0.44
1:B:214:PHE:HB3	1:B:216:GLU:OE1	2.17	0.44
1:A:237:VAL:O	1:A:253:TYR:HA	2.17	0.44
1:A:190:CYS:SG	1:A:204:VAL:HG13	2.57	0.44
1:B:169:LEU:HD12	1:B:169:LEU:C	2.38	0.44
1:A:118:LEU:HD12	1:A:119:ASP:N	2.30	0.44
1:A:118:LEU:HD23	1:A:120:TYR:OH	2.18	0.44
1:A:218:MET:O	1:A:222:VAL:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:31:THR:HG22	1:B:73:VAL:CG2	2.34	0.44
1:A:200:ASP:O	1:A:204:VAL:HG23	2.17	0.43
1:A:108:THR:HA	1:A:115:ARG:HB3	2.01	0.43
1:A:185:GLU:O	1:A:188:ALA:HB3	2.19	0.43
1:B:197:LYS:O	1:B:200:ASP:N	2.51	0.43
1:A:106:LYS:NZ	1:A:115:ARG:O	2.51	0.43
1:A:16:LEU:HD12	1:A:16:LEU:N	2.33	0.43
1:B:111:VAL:HG12	1:B:112:SER:N	2.34	0.43
1:A:122:VAL:HG21	1:A:177:ILE:HG21	2.01	0.42
1:A:188:ALA:HB3	1:A:191:GLN:HE21	1.82	0.42
1:B:240:GLU:C	1:B:241:ASN:HD22	2.23	0.42
1:B:120:TYR:CE2	1:B:181:ILE:HD13	2.54	0.42
1:A:144:THR:CG2	1:A:192:LEU:CD2	2.92	0.42
1:A:146:LEU:HD13	1:A:208:ALA:C	2.40	0.42
1:B:213:LYS:NZ	1:B:221:ASP:OD2	2.42	0.42
1:A:219:VAL:CG2	1:B:18:ILE:HD13	2.51	0.41
1:B:23:ILE:HD12	1:B:63:PHE:CG	2.55	0.41
1:B:23:ILE:HD12	1:B:63:PHE:CB	2.51	0.41
1:B:75:ASP:O	1:B:76:PHE:C	2.57	0.41
1:A:107:LYS:HE2	1:A:118:LEU:HB3	2.01	0.41
1:B:28:PHE:HB3	1:B:45:LEU:HD12	2.02	0.41
1:B:169:LEU:HD12	1:B:169:LEU:O	2.21	0.40
1:A:91:ASP:N	1:A:91:ASP:OD1	2.54	0.40
1:B:63:PHE:CZ	1:B:90:LEU:HD22	2.55	0.40
1:B:141:ILE:HD13	1:B:184:VAL:HG21	2.04	0.40
1:B:201:GLU:HA	1:B:204:VAL:HG22	2.04	0.40

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	243/257 (95%)	226 (93%)	15 (6%)	2 (1%)	24	56
1	B	248/257 (96%)	231 (93%)	16 (6%)	1 (0%)	39	73
All	All	491/514 (96%)	457 (93%)	31 (6%)	3 (1%)	30	63

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	113	GLY
1	A	198	ARG
1	B	88	ALA

### 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	215/224 (96%)	199 (93%)	16 (7%)	17	41
1	B	220/224 (98%)	203 (92%)	17 (8%)	16	39
All	All	435/448 (97%)	402 (92%)	33 (8%)	18	40

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	44	ARG
1	A	91	ASP
1	A	100	SER
1	A	115	ARG
1	A	117	LEU
1	A	168	SER
1	A	189	SER
1	A	191	GLN
1	A	192	LEU
1	A	193	TYR
1	A	195	LEU
1	A	215	VAL

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Mol	Chain	Res	Type
1	A	218	MET
1	A	244	SER
1	A	249	SER
1	B	15	ASN
1	B	23	ILE
1	B	27	ARG
1	B	31	THR
1	B	38	THR
1	B	75	ASP
1	B	78	GLN
1	B	81[A]	ARG
1	B	81[B]	ARG
1	B	87	VAL
1	B	93[A]	ARG
1	B	93[B]	ARG
1	B	106	LYS
1	B	123	SER
1	B	156	TYR
1	B	168	SER
1	B	230	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	19	ASN
1	A	191	GLN
1	A	241	ASN
1	B	15	ASN
1	B	19	ASN
1	B	78	GLN
1	B	241	ASN

### 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	SNC	A	149	1	2,7,8	0.72	0	1,7,9	2.02	1 (100%)
1	SNC	B	149	1	2,7,8	0.44	0	1,7,9	2.04	1 (100%)

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	SNC	A	149	1	-	0/0/6/8	0/0/0/0
1	SNC	B	149	1	-	0/0/6/8	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	149	SNC	O-C-CA	-2.04	120.25	125.72
1	A	149	SNC	O-C-CA	-2.02	120.30	125.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	149	SNC	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z  > 2$
2	8GT	B	301	3	26,35,35	1.18	2 (7%)	28,56,56	1.84	5 (17%)

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	8GT	B	301	3	-	0/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	8GT	C5-C4	3.41	1.48	1.40
2	B	301	8GT	C6-C5	3.54	1.48	1.41

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	8GT	C6-C5-C4	-3.89	116.41	120.86
2	B	301	8GT	N3-C2-N1	-3.78	122.41	127.56
2	B	301	8GT	C5-C6-N1	-3.45	119.01	123.52
2	B	301	8GT	O4'-C1'-N9	3.39	112.24	108.30
2	B	301	8GT	C6-N1-C2	5.33	122.13	115.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	8GT	1	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

### 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	244/257 (94%)	0.80	39 (15%) <b>3</b> <b>1</b>	34, 64, 192, 228	0
1	B	244/257 (94%)	-0.39	2 (0%) <b>87</b> <b>83</b>	33, 54, 84, 143	0
All	All	488/514 (94%)	0.20	41 (8%) <b>14</b> <b>8</b>	33, 58, 178, 228	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	205	THR	16.5
1	A	206	GLU	16.1
1	A	193	TYR	15.0
1	A	203	TYR	15.0
1	A	194	GLY	14.6
1	A	199	PRO	12.1
1	A	204	VAL	10.2
1	A	150	SER	10.1
1	A	156	TYR	9.2
1	A	192	LEU	8.9
1	A	152	GLU	8.4
1	A	153	ILE	7.5
1	A	198	ARG	7.4
1	A	201	GLU	6.6
1	A	196	LEU	6.5
1	A	191	GLN	6.3
1	A	113	GLY	6.3
1	A	114	ILE	6.2
1	A	197	LYS	6.0
1	A	190	CYS	5.5
1	A	155	GLN	5.2
1	A	195	LEU	5.1
1	A	210	GLU	4.7
1	A	151	LYS	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	110	PRO	4.1
1	A	112	SER	3.9
1	A	207	LYS	3.8
1	A	202	LYS	3.6
1	A	157	GLY	3.6
1	A	158	ALA	3.5
1	A	211	ASN	3.1
1	A	154	SER	3.1
1	A	115	ARG	3.0
1	A	209	TYR	2.8
1	A	212	PRO	2.7
1	B	13	LEU	2.5
1	B	54[A]	GLU	2.5
1	A	208	ALA	2.4
1	A	213	LYS	2.3
1	A	160	ASN	2.1
1	A	145	SER	2.0

## 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(Å <sup>2</sup> )	Q<0.9
1	SNC	A	149	8/9	0.32	0.80	-	131,168,187,188	0
1	SNC	B	149	8/9	0.91	0.14	-	59,70,81,85	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
2	8GT	B	301	33/33	0.92	0.28	2.78	56,84,114,118	8
3	ZN	B	302	1/1	1.00	0.04	-2.24	55,55,55,55	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.