



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 19, 2017 – 08:02 AM EST

PDB ID : 5H24  
Title : EED in complex with PRC2 allosteric inhibitor compound 8  
Authors : Zhao, K.; Zhao, M.; Luo, X.; Zhang, H.  
Deposited on : 2016-10-14  
Resolution : 2.50 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-20028442  
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-20028442

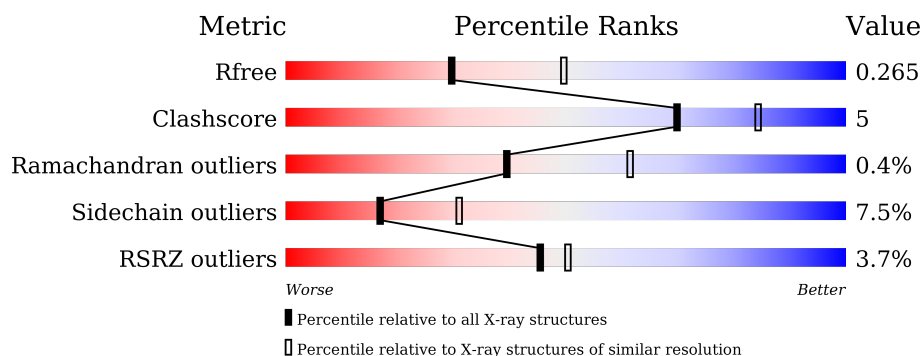
# 1 Overall quality at a glance

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))
$R_{free}$	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (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	367	 2% 85% 13% ..
1	B	367	 3% 80% 17% ..
2	C	29	 14% 79% 21%
2	D	29	 14% 79% 21%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6497 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 Polycomb protein EED.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	364	Total	C	N	O	S	0	0	0
			2948	1867	517	542	22			
1	B	359	Total	C	N	O	S	0	0	0
			2909	1844	509	534	22			

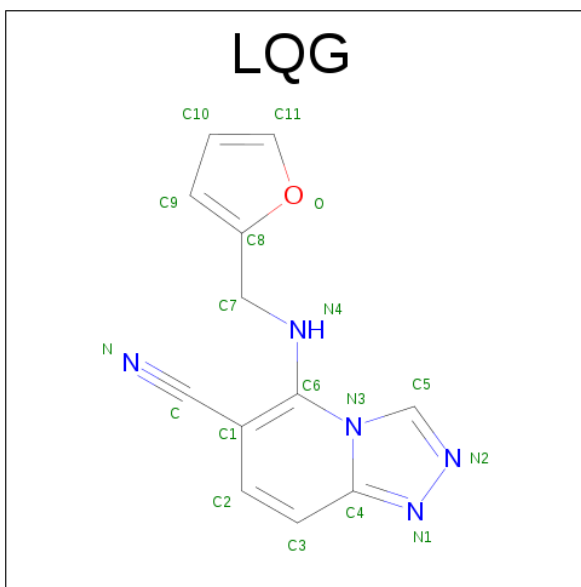
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	GLY	-	expression tag	UNP O75530
B	75	GLY	-	expression tag	UNP O75530

- Molecule 2 is a protein called Histone-lysine N-methyltransferase EZH2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	29	Total	C	N	O	S	0	0	0
			254	157	50	46	1			
2	D	29	Total	C	N	O	S	0	0	0
			254	157	50	46	1			

- Molecule 3 is 5-(furan-2-ylmethylamino)-[1,2,4]triazolo[4,3-a]pyridine-6-carbonitrile (three-letter code: LQG) (formula: C<sub>12</sub>H<sub>9</sub>N<sub>5</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			18	12	5	1		
3	B	1	Total	C	N	O	0	0
			18	12	5	1		

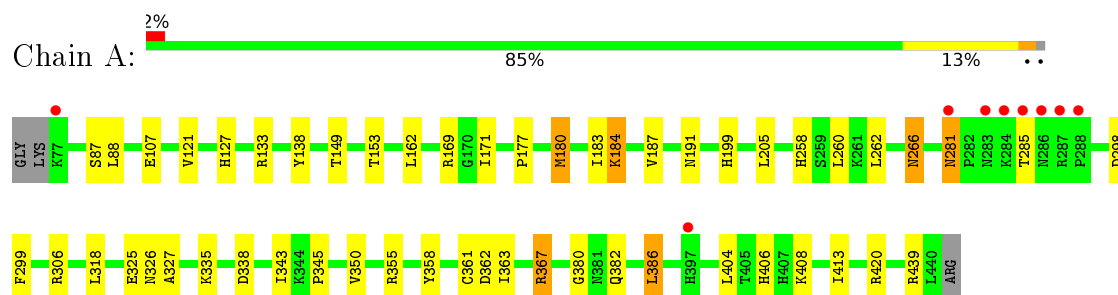
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	54	Total	O	0	0
			54	54		
4	B	35	Total	O	0	0
			35	35		
4	C	2	Total	O	0	0
			2	2		
4	D	5	Total	O	0	0
			5	5		

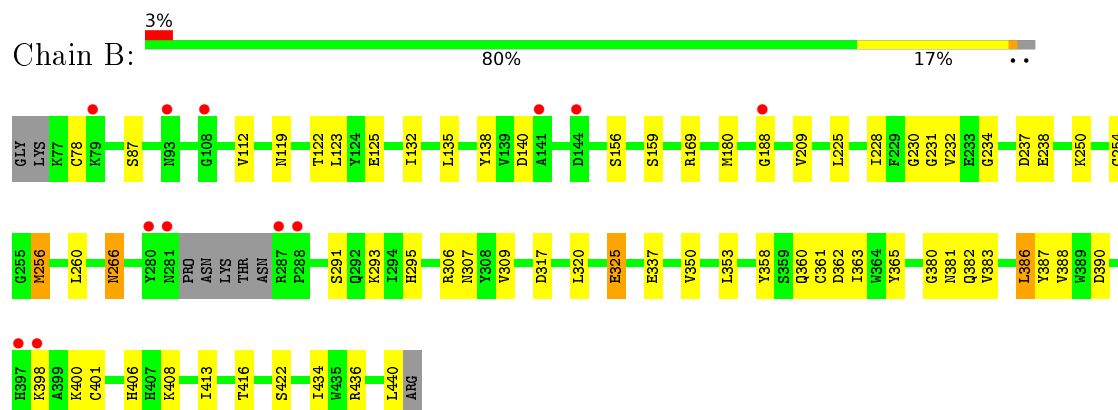
### 3 Residue-property plots

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.

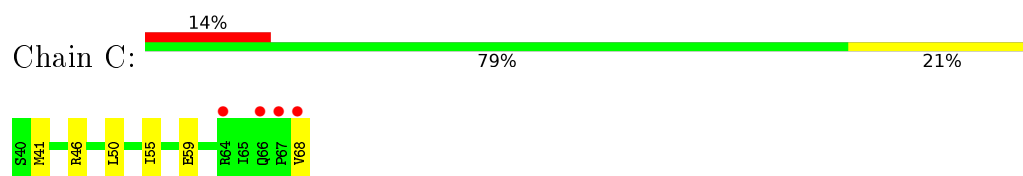
#### • Molecule 1: Polycomb protein EED



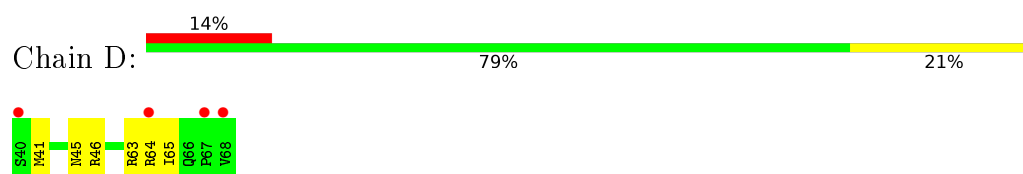
#### • Molecule 1: Polycomb protein EED



#### • Molecule 2: Histone-lysine N-methyltransferase EZH2



#### • Molecule 2: Histone-lysine N-methyltransferase EZH2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.09 Å   177.80 Å   50.69 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	29.68 – 2.50 29.68 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.68-2.50) 99.0 (29.68-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.16	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.83 (at 2.51 Å)	Xtriage
Refinement program	BUSTER	Depositor
R, $R_{free}$	0.187   ,   0.255 0.191   ,   0.265	Depositor DCC
$R_{free}$ test set	1501 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.5	Xtriage
Anisotropy	0.433	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 46.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6497	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.50% 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: LQG

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	0.50	0/3023	0.72	0/4093
1	B	0.50	0/2982	0.73	0/4035
2	C	0.52	0/257	0.70	0/341
2	D	0.51	0/257	0.67	0/341
All	All	0.50	0/6519	0.72	0/8810

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	2948	0	2866	24	0
1	B	2909	0	2826	31	0
2	C	254	0	260	2	0
2	D	254	0	260	3	0
3	A	18	0	0	0	0
3	B	18	0	0	0	0
4	A	54	0	0	0	0
4	B	35	0	0	0	0
4	C	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	5	0	0	0	0
All	All	6497	0	6212	57	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 5.

All (57) 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:138:TYR:HB2	1:A:180:MET:HG3	1.71	0.72
1:B:317:ASP:H	2:D:45:ASN:HD21	1.39	0.70
1:B:232:VAL:H	1:B:295:HIS:HD2	1.40	0.69
1:A:327:ALA:HB1	1:A:355:ARG:HG2	1.74	0.69
1:B:386:LEU:HD21	1:B:416:THR:HG21	1.75	0.67
1:A:127:HIS:CD2	1:A:133:ARG:HE	2.15	0.64
1:B:123:LEU:HD22	1:B:180:MET:HE1	1.80	0.64
1:B:360:GLN:O	1:B:381:ASN:HB2	2.01	0.60
1:A:171:ILE:HG12	1:A:187:VAL:HG22	1.86	0.57
1:B:238:GLU:HB2	1:B:256:MET:HG3	1.85	0.57
1:A:177:PRO:HB2	2:C:68:VAL:HG21	1.88	0.56
1:B:317:ASP:H	2:D:45:ASN:ND2	2.04	0.56
1:B:231:GLY:HA3	1:B:295:HIS:CD2	2.42	0.54
1:B:254:CYS:HB2	1:B:309:VAL:HB	1.88	0.54
1:B:266:ASN:H	1:B:266:ASN:HD22	1.54	0.53
2:D:63:ARG:HD2	2:D:65:ILE:HD11	1.91	0.52
1:B:406:HIS:CD2	1:B:408:LYS:H	2.29	0.51
1:A:298:ASP:O	1:A:345:PRO:HA	2.11	0.51
1:A:121:VAL:HB	1:A:138:TYR:HB3	1.92	0.51
1:B:228:ILE:HD12	1:B:293:LYS:HE3	1.93	0.50
1:B:225:LEU:O	1:B:291:SER:HB3	2.11	0.49
1:B:138:TYR:HB2	1:B:180:MET:HG3	1.95	0.49
1:A:326:ASN:HA	1:A:358:TYR:CE2	2.49	0.48
1:B:381:ASN:HD22	1:B:387:TYR:HE2	1.61	0.47
1:A:406:HIS:CE1	1:A:408:LYS:HB2	2.49	0.47
1:B:132:ILE:HD11	1:B:436:ARG:HB2	1.96	0.47
1:A:386:LEU:HB3	1:A:404:LEU:HB2	1.96	0.47
1:B:237:ASP:HB3	1:B:256:MET:HB2	1.96	0.46
1:B:387:TYR:HB3	1:B:400:LYS:HZ1	1.81	0.46
1:A:153:THR:HG23	1:A:162:LEU:HB2	1.97	0.46
1:A:262:LEU:HB3	1:A:299:PHE:HB3	1.98	0.46
1:B:406:HIS:HD2	1:B:408:LYS:H	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ILE:HG22	1:A:184:LYS:HG2	1.97	0.45
1:A:338:ASP:HB3	1:A:343:ILE:HD11	1.99	0.45
1:B:387:TYR:HD1	1:B:400:LYS:HZ1	1.66	0.45
1:B:87:SER:HA	1:B:434:ILE:O	2.17	0.44
1:B:358:TYR:CE1	1:B:361:CYS:HB3	2.53	0.44
1:A:149:THR:HB	1:A:367:ARG:HH22	1.81	0.44
1:B:380:GLY:HA3	1:B:413:ILE:HB	2.01	0.43
1:B:406:HIS:CD2	1:B:408:LYS:HB2	2.54	0.43
1:A:358:TYR:HE2	1:A:361:CYS:HB3	1.82	0.42
1:A:380:GLY:HA3	1:A:413:ILE:HB	2.01	0.42
1:B:232:VAL:H	1:B:295:HIS:CD2	2.29	0.42
1:B:78:CYS:SG	1:B:390:ASP:HB2	2.59	0.42
1:B:230:GLY:HA2	1:B:234:GLY:HA3	2.01	0.42
2:C:55:ILE:O	2:C:59:GLU:HG3	2.18	0.42
1:A:406:HIS:ND1	1:A:408:LYS:HB2	2.34	0.42
1:A:338:ASP:HB3	1:A:343:ILE:CD1	2.50	0.42
1:B:125:GLU:HB2	1:B:135:LEU:HD21	2.02	0.41
1:B:119:ASN:HB2	1:B:140:ASP:HB3	2.02	0.41
1:A:199:HIS:HB2	1:A:205:LEU:HB2	2.03	0.41
1:B:387:TYR:HB3	1:B:400:LYS:NZ	2.36	0.41
1:A:281:ASN:O	1:A:285:THR:HG22	2.20	0.41
1:B:112:VAL:HG22	1:B:125:GLU:HG3	2.03	0.41
1:A:358:TYR:CE2	1:A:361:CYS:HB3	2.55	0.41
1:A:363:ILE:HG12	1:A:382:GLN:OE1	2.21	0.41
1:A:266:ASN:H	1:A:266:ASN:HD22	1.68	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	362/367 (99%)	351 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	355/367 (97%)	338 (95%)	14 (4%)	3 (1%)	24	41
2	C	27/29 (93%)	26 (96%)	1 (4%)	0	100	100
2	D	27/29 (93%)	26 (96%)	1 (4%)	0	100	100
All	All	771/792 (97%)	741 (96%)	27 (4%)	3 (0%)	39	61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	325	GLU
1	B	365	TYR
1	B	188	GLY

### 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	327/329 (99%)	306 (94%)	21 (6%)	22	39
1	B	322/329 (98%)	296 (92%)	26 (8%)	15	27
2	C	29/29 (100%)	26 (90%)	3 (10%)	9	17
2	D	29/29 (100%)	26 (90%)	3 (10%)	9	17
All	All	707/716 (99%)	654 (92%)	53 (8%)	17	31

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	87	SER
1	A	88	LEU
1	A	107	GLU
1	A	169	ARG
1	A	180	MET
1	A	184	LYS
1	A	191	ASN
1	A	258	HIS

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Mol	Chain	Res	Type
1	A	260	LEU
1	A	266	ASN
1	A	281	ASN
1	A	306	ARG
1	A	318	LEU
1	A	325	GLU
1	A	335	LYS
1	A	350	VAL
1	A	362	ASP
1	A	367	ARG
1	A	386	LEU
1	A	420	ARG
1	A	439	ARG
1	B	122	THR
1	B	156	SER
1	B	159	SER
1	B	169	ARG
1	B	209	VAL
1	B	250	LYS
1	B	256	MET
1	B	260	LEU
1	B	266	ASN
1	B	306	ARG
1	B	307	ASN
1	B	320	LEU
1	B	325	GLU
1	B	337	GLU
1	B	350	VAL
1	B	353	LEU
1	B	362	ASP
1	B	363	ILE
1	B	382	GLN
1	B	383	VAL
1	B	386	LEU
1	B	388	VAL
1	B	398	LYS
1	B	401	CYS
1	B	422	SER
1	B	440	LEU
2	C	41	MET
2	C	46	ARG
2	C	50	LEU

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Mol	Chain	Res	Type
2	D	41	MET
2	D	46	ARG
2	D	64	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	GLN
1	A	266	ASN
1	B	119	ASN
1	B	213	HIS
1	B	258	HIS
1	B	266	ASN
1	B	295	HIS
1	B	406	HIS
2	D	45	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

2 ligands 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
3	LQG	A	501	-	14,20,20	2.05	6 (42%)	12,27,27	2.58	6 (50%)
3	LQG	B	501	-	14,20,20	1.99	6 (42%)	12,27,27	2.44	6 (50%)

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
3	LQG	A	501	-	-	0/4/7/7	0/2/3/3
3	LQG	B	501	-	-	0/4/7/7	0/2/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	LQG	C1-C	-3.58	1.39	1.44
3	B	501	LQG	C7-C8	-3.06	1.47	1.51
3	B	501	LQG	C9-C8	-2.59	1.34	1.39
3	B	501	LQG	C1-C	-2.28	1.41	1.44
3	A	501	LQG	C5-N2	2.13	1.35	1.31
3	A	501	LQG	C2-C1	2.37	1.43	1.40
3	A	501	LQG	C1-C6	2.41	1.44	1.42
3	B	501	LQG	C5-N2	2.44	1.36	1.31
3	A	501	LQG	C3-C4	2.67	1.44	1.40
3	B	501	LQG	C1-C6	2.92	1.45	1.42
3	B	501	LQG	C4-N1	3.14	1.37	1.33
3	A	501	LQG	C4-N1	4.15	1.38	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	LQG	C8-C7-N4	-3.56	105.12	112.72
3	A	501	LQG	C8-C7-N4	-3.29	105.70	112.72
3	A	501	LQG	C2-C3-C4	-2.99	116.04	119.70
3	A	501	LQG	C2-C1-C	-2.50	114.85	119.32
3	B	501	LQG	C2-C1-C	-2.30	115.20	119.32
3	B	501	LQG	C5-N3-C4	-2.08	104.39	108.43
3	A	501	LQG	C6-C1-C	2.18	122.24	119.46
3	B	501	LQG	C6-C1-C	2.20	122.26	119.46
3	B	501	LQG	C7-C8-C9	2.94	133.97	128.51
3	A	501	LQG	C7-C8-C9	3.55	135.08	128.51
3	A	501	LQG	C3-C2-C1	5.10	124.37	120.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	LQG	C3-C2-C1	5.22	124.46	120.54

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

### 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	364/367 (99%)	-0.13	9 (2%) 61 65	14, 30, 57, 90	0
1	B	359/367 (97%)	-0.11	12 (3%) 50 55	16, 31, 59, 90	0
2	C	29/29 (100%)	0.51	4 (13%) 4 4	26, 41, 77, 83	0
2	D	29/29 (100%)	0.54	4 (13%) 4 4	24, 41, 66, 76	0
All	All	781/792 (98%)	-0.07	29 (3%) 45 50	14, 32, 60, 90	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	68	VAL	6.0
2	C	67	PRO	4.0
1	A	284	LYS	3.8
2	C	68	VAL	3.6
1	A	286	ASN	3.5
1	A	397	HIS	3.4
1	A	283	ASN	3.4
2	D	67	PRO	3.4
1	B	141	ALA	3.3
1	B	287	ARG	3.2
1	A	287	ARG	3.1
1	B	188	GLY	3.0
2	C	66	GLN	2.9
1	B	288	PRO	2.9
1	B	144	ASP	2.7
2	C	64	ARG	2.6
1	A	285	THR	2.6
1	B	397	HIS	2.5
1	A	77	LYS	2.4
1	B	79	LYS	2.4
2	D	40	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	108	GLY	2.3
1	B	280	TYR	2.3
2	D	64	ARG	2.3
1	A	288	PRO	2.2
1	B	281	ASN	2.2
1	A	281	ASN	2.2
1	B	93	ASN	2.1
1	B	398	LYS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 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(Å <sup>2</sup> )	Q<0.9
3	LQG	B	501	18/18	0.94	0.15	-0.10	18,35,39,39	0
3	LQG	A	501	18/18	0.97	0.13	-0.54	14,21,28,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.