



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2021 – 10:38 PM EDT

PDB ID : 3ISM  
Title : Crystal structure of the EndoG/EndoGI complex: Mechanism of EndoG inhibition  
Authors : Loll, B.; Gebhardt, M.; Wahle, E.; Meinhart, A.  
Deposited on : 2009-08-26  
Resolution : 2.20 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
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) : 2.23.2

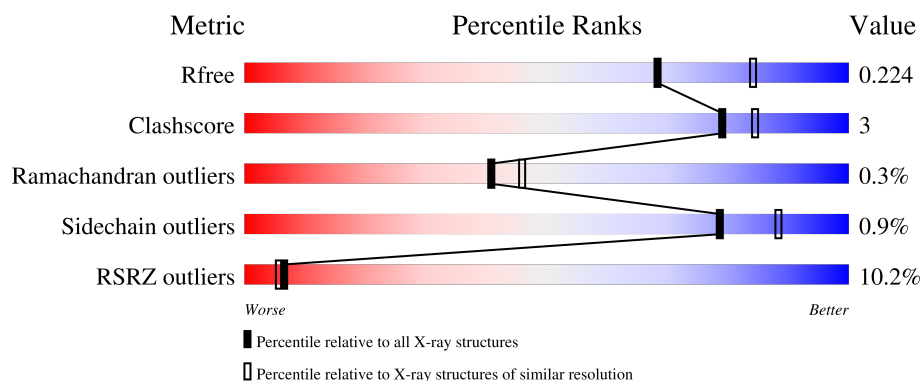
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	267	<div> <div>2%</div> <div>87%</div> <div>8%</div> </div>
1	B	267	<div> <div>5%</div> <div>86%</div> <div>6%</div> <div>7%</div> </div>
2	C	359	<div> <div>17%</div> <div>72%</div> <div>8%</div> <div>20%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6757 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 CG8862.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	245	Total	C	N	O	S	0	3	0
			1998	1255	366	369	8			
1	B	247	Total	C	N	O	S	0	13	0
			2051	1294	366	383	8			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	55	MET	-	initiating methionine	UNP Q7JXB9
A	311	ALA	-	expression tag	UNP Q7JXB9
A	312	ALA	-	expression tag	UNP Q7JXB9
A	313	ALA	-	expression tag	UNP Q7JXB9
A	314	LEU	-	expression tag	UNP Q7JXB9
A	315	GLU	-	expression tag	UNP Q7JXB9
A	316	HIS	-	expression tag	UNP Q7JXB9
A	317	HIS	-	expression tag	UNP Q7JXB9
A	318	HIS	-	expression tag	UNP Q7JXB9
A	319	HIS	-	expression tag	UNP Q7JXB9
A	320	HIS	-	expression tag	UNP Q7JXB9
A	321	HIS	-	expression tag	UNP Q7JXB9
B	55	MET	-	initiating methionine	UNP Q7JXB9
B	311	ALA	-	expression tag	UNP Q7JXB9
B	312	ALA	-	expression tag	UNP Q7JXB9
B	313	ALA	-	expression tag	UNP Q7JXB9
B	314	LEU	-	expression tag	UNP Q7JXB9
B	315	GLU	-	expression tag	UNP Q7JXB9
B	316	HIS	-	expression tag	UNP Q7JXB9
B	317	HIS	-	expression tag	UNP Q7JXB9
B	318	HIS	-	expression tag	UNP Q7JXB9
B	319	HIS	-	expression tag	UNP Q7JXB9
B	320	HIS	-	expression tag	UNP Q7JXB9
B	321	HIS	-	expression tag	UNP Q7JXB9

- Molecule 2 is a protein called CG4930.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	286	Total	C	N	O	S	0	7	0
			2370	1515	384	462	9			

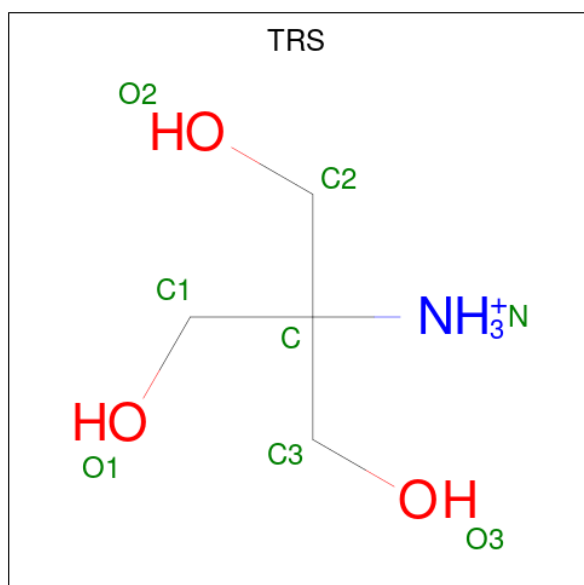
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	2	ALA	SER	engineered mutation	UNP Q9V3V9

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula:  $C_4H_{12}NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		

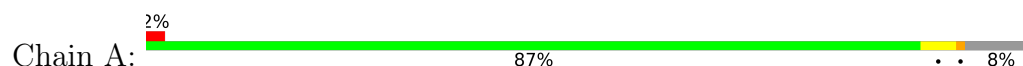
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	148	Total 148	O 148	0	0
5	B	114	Total 114	O 114	0	0
5	C	66	Total 66	O 66	0	0

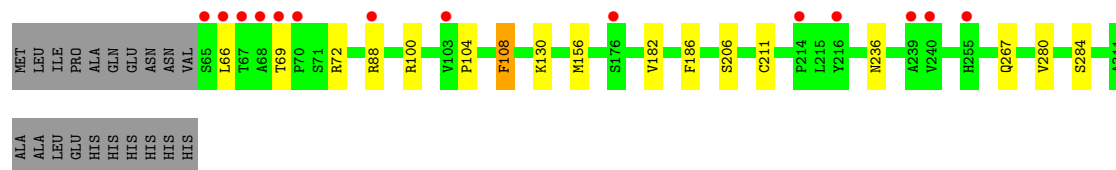
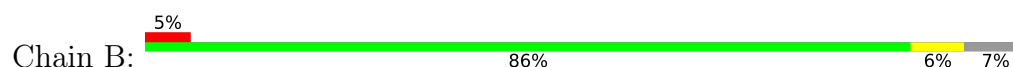
### 3 Residue-property plots [i](#)

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.

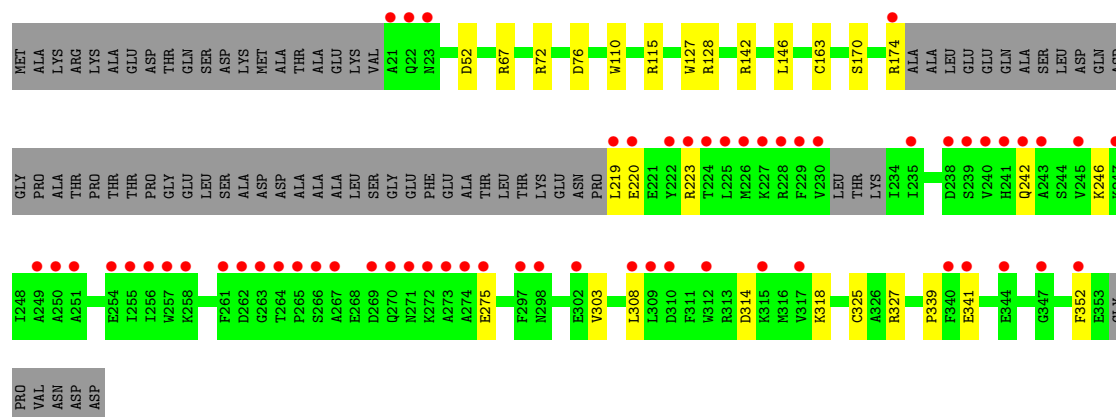
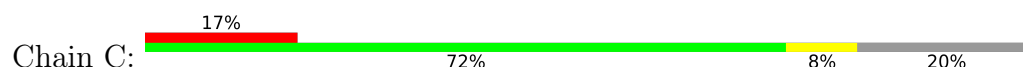
#### • Molecule 1: CG8862



#### • Molecule 1: CG8862



#### • Molecule 2: CG4930



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.79Å 109.15Å 121.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.23 – 2.20 43.22 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.23-2.20) 99.8 (43.22-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.18	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.44 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.184 , 0.223 0.187 , 0.224	Depositor DCC
$R_{free}$ test set	2412 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.8	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 47.5	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	6757	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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

### 5.1 Standard geometry

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

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	0.58	0/2060	0.62	0/2790
1	B	0.49	0/2143	0.56	0/2905
2	C	0.48	0/2446	0.54	0/3314
All	All	0.52	0/6649	0.58	0/9009

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

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	1998	0	1930	10	0
1	B	2051	0	2007	13	0
2	C	2370	0	2287	18	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	8	0	12	2	0
5	A	148	0	0	2	0
5	B	114	0	0	4	0
5	C	66	0	0	0	0
All	All	6757	0	6236	36	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.

All (36) 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:B:206[B]:SER:OG	5:B:365:HOH:O	1.73	1.05
1:B:206[A]:SER:HB2	5:B:365:HOH:O	1.93	0.69
2:C:170:SER:O	2:C:174:ARG:HG2	2.01	0.60
1:B:88[A]:ARG:NH2	5:B:417:HOH:O	2.36	0.59
1:B:280[A]:VAL:HG12	1:B:284:SER:OG	2.04	0.57
2:C:325[B]:CYS:SG	2:C:339:PRO:HD3	2.45	0.57
1:A:100[A]:ARG:HH22	1:B:100:ARG:HH22	1.53	0.56
2:C:219:LEU:HD22	2:C:275:GLU:HG2	1.88	0.55
1:B:69[B]:THR:HG22	1:B:72:ARG:H	1.72	0.54
2:C:67:ARG:HD2	2:C:110:TRP:CG	2.42	0.54
1:A:130:LYS:NZ	5:A:425:HOH:O	2.42	0.52
2:C:314:ASP:O	2:C:318:LYS:HE2	2.11	0.51
1:A:100[A]:ARG:NH2	5:A:406:HOH:O	2.45	0.50
4:A:6989:TRS:H12	2:C:146[A]:LEU:CD2	2.41	0.50
1:A:100[A]:ARG:NH2	1:B:100:ARG:NH2	2.59	0.50
1:B:104:PRO:HG2	1:B:156:MET:HG3	1.96	0.48
2:C:242:GLN:O	2:C:246:LYS:HG2	2.15	0.47
2:C:220:GLU:HA	2:C:223:ARG:HB2	1.96	0.47
1:A:287[B]:ARG:HH22	1:B:236:ASN:HA	1.79	0.47
2:C:72:ARG:O	2:C:76:ASP:HB2	2.14	0.47
2:C:128:ARG:HG2	2:C:163:CYS:SG	2.54	0.46
1:A:167:LYS:NZ	1:A:171:GLU:OE2	2.48	0.46
1:B:206[A]:SER:OG	5:B:399:HOH:O	2.17	0.46
2:C:115:ARG:HG3	2:C:127:TRP:CZ3	2.52	0.45
1:A:184:GLN:OE1	2:C:142[A]:ARG:HD3	2.17	0.44
1:B:108:PHE:CE1	1:B:211:CYS:HB2	2.53	0.43
4:A:6989:TRS:H12	2:C:146[A]:LEU:HD23	1.99	0.43
1:A:131:GLN:HG2	2:C:52[A]:ASP:OD2	2.19	0.43
2:C:67:ARG:HD2	2:C:110:TRP:CD2	2.53	0.43
2:C:341:GLU:CD	2:C:341:GLU:H	2.22	0.42
1:A:88:ARG:NH1	1:A:134:SER:OG	2.52	0.42
2:C:303:VAL:HG13	2:C:308:LEU:HB2	2.03	0.41
1:B:182:VAL:HG21	1:B:267:GLN:HA	2.02	0.41
2:C:327:ARG:CZ	2:C:352:PHE:HB3	2.51	0.40
1:A:108:PHE:CE2	1:A:211:CYS:HB2	2.56	0.40
1:B:66:LEU:HD12	1:B:66:LEU:HA	1.93	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	246/267 (92%)	239 (97%)	6 (2%)	1 (0%)	34	37
1	B	258/267 (97%)	250 (97%)	7 (3%)	1 (0%)	34	37
2	C	287/359 (80%)	279 (97%)	8 (3%)	0	100	100
All	All	791/893 (89%)	768 (97%)	21 (3%)	2 (0%)	41	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	ASP
1	B	186	PHE

### 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	219/235 (93%)	215 (98%)	4 (2%)	59	72
1	B	231/235 (98%)	229 (99%)	2 (1%)	78	88
2	C	257/306 (84%)	257 (100%)	0	100	100
All	All	707/776 (91%)	701 (99%)	6 (1%)	78	90

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	ARG

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Mol	Chain	Res	Type
1	A	108	PHE
1	A	252	SER
1	A	254	ASP
1	B	108	PHE
1	B	130	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are 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	$\# Z  > 2$
4	TRS	A	6989	-	7,7,7	0.31	0	9,9,9	0.44	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	TRS	A	6989	-	-	3/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	6989	TRS	C2-C-C1-O1
4	A	6989	TRS	C3-C-C1-O1
4	A	6989	TRS	N-C-C1-O1

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	6989	TRS	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

### 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	245/267 (91%)	0.19	5 (2%) 65 63	25, 29, 40, 46	0
1	B	247/267 (92%)	0.29	14 (5%) 23 22	24, 30, 41, 48	0
2	C	286/359 (79%)	0.83	60 (20%) 1 1	25, 31, 43, 53	0
All	All	778/893 (87%)	0.46	79 (10%) 6 6	24, 30, 41, 53	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	265	PRO	9.3
2	C	21	ALA	6.8
2	C	340	PHE	6.2
2	C	228	ARG	5.9
2	C	238	ASP	5.1
2	C	222	TYR	4.8
2	C	229	PHE	4.8
2	C	270	GLN	4.8
2	C	239	SER	4.6
2	C	274	ALA	4.6
2	C	273	ALA	4.5
2	C	235	ILE	4.3
1	B	65	SER	4.0
1	A	67	THR	4.0
2	C	302	GLU	3.9
2	C	220	GLU	3.8
1	B	255	HIS	3.8
2	C	262	ASP	3.8
1	B	69[A]	THR	3.7
2	C	266	SER	3.7
1	A	311	ALA	3.7
1	A	310	VAL	3.6
2	C	227	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
2	C	271	ASN	3.6
2	C	254	GLU	3.6
2	C	23	ASN	3.6
2	C	341	GLU	3.5
2	C	225	LEU	3.5
2	C	245	VAL	3.4
2	C	267	ALA	3.4
1	B	66	LEU	3.3
2	C	263	GLY	3.3
2	C	256	ILE	3.2
2	C	261	PHE	3.2
2	C	22	GLN	3.2
2	C	312	TRP	3.2
2	C	243	ALA	3.1
2	C	230	VAL	3.1
2	C	258	LYS	3.0
2	C	264	THR	3.0
1	B	70	PRO	2.9
2	C	226	MET	2.9
2	C	219	LEU	2.8
2	C	310	ASP	2.8
2	C	344	GLU	2.8
2	C	224	THR	2.7
2	C	240	VAL	2.7
2	C	247	LYS	2.7
2	C	249	ALA	2.6
2	C	315	LYS	2.6
2	C	352	PHE	2.6
2	C	250	ALA	2.6
2	C	257	TRP	2.5
2	C	174	ARG	2.5
2	C	297	PHE	2.5
2	C	251	ALA	2.5
2	C	308	LEU	2.5
2	C	223	ARG	2.5
1	B	216	TYR	2.4
1	B	68	ALA	2.4
1	B	88[A]	ARG	2.4
1	B	239	ALA	2.3
2	C	272	LYS	2.3
1	B	214	PRO	2.3
2	C	347	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	240	VAL	2.3
2	C	298	ASN	2.3
1	B	67	THR	2.2
2	C	242	GLN	2.2
2	C	317	VAL	2.2
1	B	176	SER	2.2
1	B	103	VAL	2.1
1	A	120[A]	ASP	2.1
1	A	100[A]	ARG	2.1
2	C	255	ILE	2.0
2	C	269	ASP	2.0
2	C	241	HIS	2.0
2	C	275	GLU	2.0
2	C	309	LEU	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 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, 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	B-factors( $\text{\AA}^2$ )	Q<0.9
4	TRS	A	6989	8/8	0.87	0.14	41,44,45,45	0
3	MG	B	1	1/1	0.90	0.05	25,25,25,25	0
3	MG	A	1	1/1	0.92	0.04	18,18,18,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.