



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:40 PM GMT

PDB ID : 4U16  
Title : M3-mT4L receptor bound to NMS  
Authors : Thorsen, T.S.; Matt, R.; Weis, W.I.; Kobilka, B.  
Deposited on : 2014-07-15  
Resolution : 3.70 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](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.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

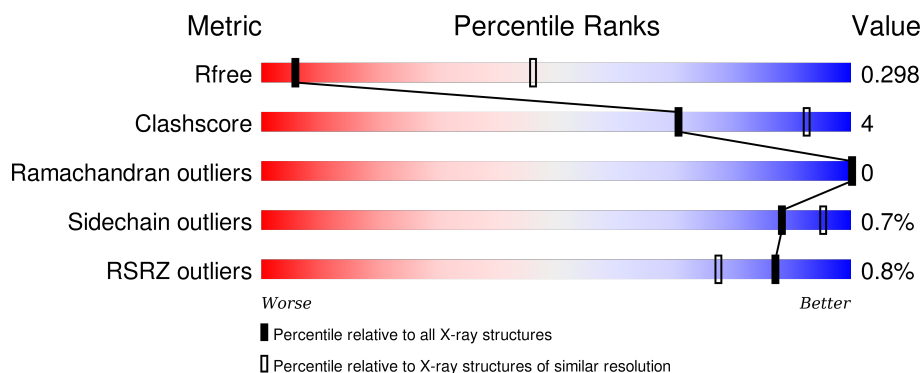
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.70 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))
$R_{free}$	91344	1101 (3.90-3.50)
Clashscore	102246	1224 (3.90-3.50)
Ramachandran outliers	100387	1172 (3.90-3.50)
Sidechain outliers	100360	1170 (3.90-3.50)
RSRZ outliers	91569	1108 (3.90-3.50)

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	418	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%; text-align: center;">%</div> <div style="position: absolute; top: 10px; left: 0; width: 100%; text-align: center;">80% 11% 9%</div> </div> </div>
1	B	418	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: 10px; left: 0; width: 100%; text-align: center;">87% 7% 6%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5860 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 Muscarinic acetylcholine receptor M3, Lysozyme, Muscarinic acetylcholine receptor M3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	381	Total	C	N	O	S	0	0	0
			2820	1847	449	506	18			
1	B	392	Total	C	N	O	S	0	0	0
			2964	1940	480	525	19			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	56	GLY	-	expression tag	UNP P08483
A	1000	MET	-	linker	UNP P08483
A	1001	ASN	-	linker	UNP P08483
A	1002	ILE	-	linker	UNP P08483
A	1003	PHE	-	linker	UNP P08483
A	1004	GLU	-	linker	UNP P08483
A	1005	MET	-	linker	UNP P08483
A	1006	LEU	-	linker	UNP P08483
A	1007	ARG	-	linker	UNP P08483
A	1008	ILE	-	linker	UNP P08483
A	1009	ASP	-	linker	UNP P08483
A	1010	GLU	-	linker	UNP P08483
A	1011	GLY	-	linker	UNP P08483
A	1012	GLY	-	linker	UNP P08483
A	1013	GLY	-	linker	UNP P08483
A	1014	SER	-	linker	UNP P08483
A	1015	GLY	-	linker	UNP P08483
A	1016	GLY	-	linker	UNP P08483
A	1053	ALA	CYS	conflict	UNP D9IEF7
A	564	LYS	-	expression tag	UNP P08483
A	565	ARG	-	expression tag	UNP P08483
A	566	LYS	-	expression tag	UNP P08483
A	567	ARG	-	expression tag	UNP P08483
A	568	ARG	-	expression tag	UNP P08483

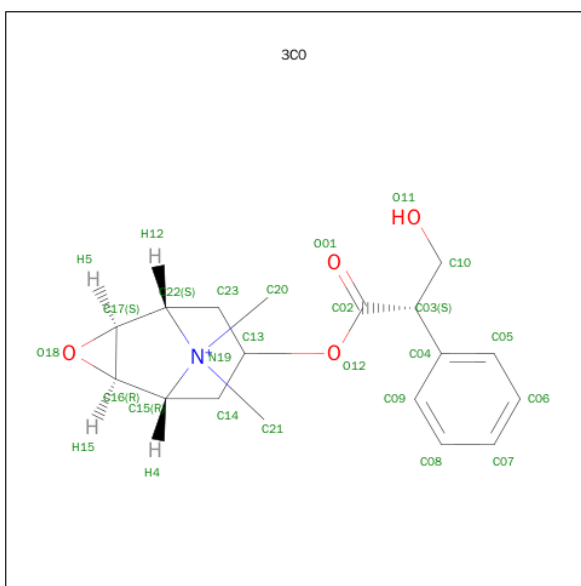
*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	569	LYS	-	expression tag	UNP P08483
A	570	HIS	-	expression tag	UNP P08483
A	571	HIS	-	expression tag	UNP P08483
A	572	HIS	-	expression tag	UNP P08483
A	573	HIS	-	expression tag	UNP P08483
A	574	HIS	-	expression tag	UNP P08483
A	575	HIS	-	expression tag	UNP P08483
A	576	HIS	-	expression tag	UNP P08483
A	577	HIS	-	expression tag	UNP P08483
B	56	GLY	-	expression tag	UNP P08483
B	1000	MET	-	linker	UNP P08483
B	1001	ASN	-	linker	UNP P08483
B	1002	ILE	-	linker	UNP P08483
B	1003	PHE	-	linker	UNP P08483
B	1004	GLU	-	linker	UNP P08483
B	1005	MET	-	linker	UNP P08483
B	1006	LEU	-	linker	UNP P08483
B	1007	ARG	-	linker	UNP P08483
B	1008	ILE	-	linker	UNP P08483
B	1009	ASP	-	linker	UNP P08483
B	1010	GLU	-	linker	UNP P08483
B	1011	GLY	-	linker	UNP P08483
B	1012	GLY	-	linker	UNP P08483
B	1013	GLY	-	linker	UNP P08483
B	1014	SER	-	linker	UNP P08483
B	1015	GLY	-	linker	UNP P08483
B	1016	GLY	-	linker	UNP P08483
B	1053	ALA	CYS	conflict	UNP D9IEF7
B	564	LYS	-	expression tag	UNP P08483
B	565	ARG	-	expression tag	UNP P08483
B	566	LYS	-	expression tag	UNP P08483
B	567	ARG	-	expression tag	UNP P08483
B	568	ARG	-	expression tag	UNP P08483
B	569	LYS	-	expression tag	UNP P08483
B	570	HIS	-	expression tag	UNP P08483
B	571	HIS	-	expression tag	UNP P08483
B	572	HIS	-	expression tag	UNP P08483
B	573	HIS	-	expression tag	UNP P08483
B	574	HIS	-	expression tag	UNP P08483
B	575	HIS	-	expression tag	UNP P08483
B	576	HIS	-	expression tag	UNP P08483
B	577	HIS	-	expression tag	UNP P08483

- 
- Chemical structure of Tartronic acid (2,3-dihydroxybutanedioic acid) with stereochemistry. The structure shows a central C2-C3 bond. C2 is bonded to a carboxyl group (C1=O, O1) and a hydroxyl group (OH, O11). C3 is bonded to a hydroxyl group (OH, O2) and a carboxyl group (C4=O, O4). The stereochemistry at C2 and C3 is (S) and (S) respectively, indicated by wedged bonds to the hydroxyl groups. The labels O1, O11, O2, O4, C1, C2(S), C3(S), C4, and HO are in green, while the OH groups are in red.

- Molecule 3 is N-methyl scopolamine (three-letter code: 3C0) (formula:  $C_{18}H_{24}NO_4$ ).

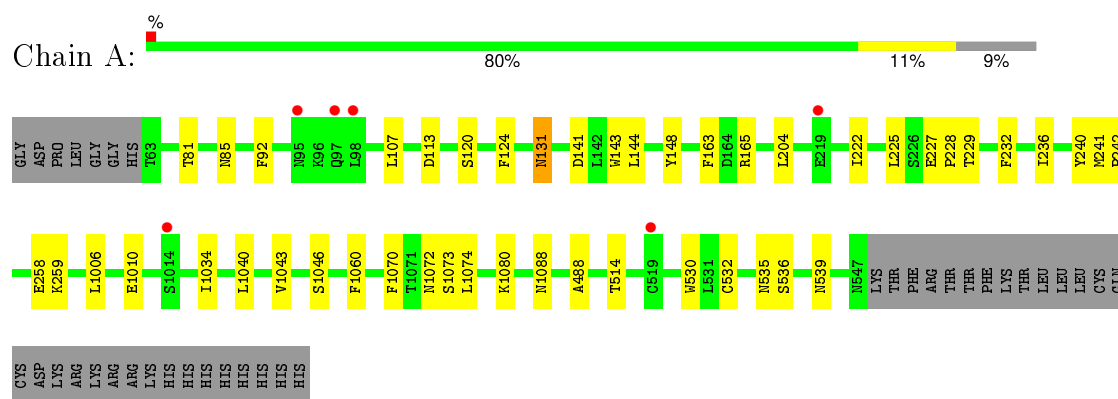


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			23	18	1	4		
3	B	1	Total	C	N	O	0	0
			23	18	1	4		

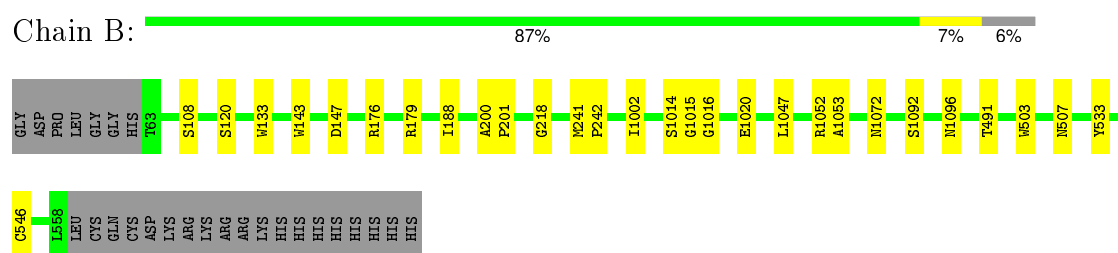
### 3 Residue-property plots

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: Muscarinic acetylcholine receptor M3, Lysozyme, Muscarinic acetylcholine receptor M3



- Molecule 1: Muscarinic acetylcholine receptor M3, Lysozyme, Muscarinic acetylcholine receptor M3



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	153.39Å 187.18Å 53.55Å 90.00° 99.78° 90.00°	Depositor
Resolution (Å)	33.67 – 3.70 33.67 – 3.50	Depositor EDS
% Data completeness (in resolution range)	92.9 (33.67-3.70) 91.0 (33.67-3.50)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.58 (at 3.47Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, $R_{free}$	0.239 , 0.285 0.254 , 0.298	Depositor DCC
$R_{free}$ test set	750 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	117.6	Xtriage
Anisotropy	0.559	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 86.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 17038 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5860	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	147.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 3C0, TAR

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	0/2891	0.36	0/3974
1	B	0.21	0/3035	0.36	0/4161
All	All	0.21	0/5926	0.36	0/8135

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	2820	0	2625	27	0
1	B	2964	0	2854	17	0
2	A	10	0	4	1	0
2	B	20	0	8	1	0
3	A	23	0	24	5	0
3	B	23	0	24	4	0
All	All	5860	0	5539	50	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 4.

The worst 5 of 50 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:535:ASN:O	1:A:539:ASN:ND2	2.33	0.61
1:A:81:THR:O	1:A:85:ASN:ND2	2.31	0.61
1:A:120:SER:HA	1:A:143:TRP:HE1	1.66	0.60
1:A:148:TYR:CD2	3:A:1202:3C0:H21	2.38	0.59
3:B:1203:3C0:O01	3:B:1203:3C0:O11	2.24	0.56

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	379/418 (91%)	362 (96%)	17 (4%)	0	100	100
1	B	390/418 (93%)	369 (95%)	21 (5%)	0	100	100
All	All	769/836 (92%)	731 (95%)	38 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	268/360 (74%)	264 (98%)	4 (2%)	72	90
1	B	294/360 (82%)	294 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	562/720 (78%)	558 (99%)	4 (1%)	88	95

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	A	163	PHE
1	A	1060	PHE
1	A	530	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	157	ASN
1	A	1025	GLN
1	B	1096	ASN
1	B	535	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](#)

5 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	$\# Z  > 2$
2	TAR	A	1201	-	3,9,9	0.34	0	6,12,12	1.14	0
3	3C0	A	1202	-	26,26,26	2.28	4 (15%)	35,40,40	2.92	11 (31%)
2	TAR	B	1201	-	3,9,9	0.32	0	6,12,12	1.22	1 (16%)
2	TAR	B	1202	-	3,9,9	0.41	0	6,12,12	1.17	0
3	3C0	B	1203	-	26,26,26	2.14	4 (15%)	35,40,40	2.79	12 (34%)

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	TAR	A	1201	-	-	0/4/12/12	0/0/0/0
3	3C0	A	1202	-	-	0/14/47/47	0/1/4/4
2	TAR	B	1201	-	-	0/4/12/12	0/0/0/0
2	TAR	B	1202	-	-	0/4/12/12	0/0/0/0
3	3C0	B	1203	-	-	0/14/47/47	0/1/4/4

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1202	3C0	C04-C03	-9.46	1.38	1.52
3	B	1203	3C0	C04-C03	-8.85	1.39	1.52
3	A	1202	3C0	C22-N19	-2.99	1.47	1.53
3	B	1203	3C0	C22-N19	-2.94	1.47	1.53
3	A	1202	3C0	C15-N19	-2.82	1.47	1.53

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1202	3C0	C15-C16-C17	-7.37	103.19	107.53
3	B	1203	3C0	C15-C16-C17	-6.97	103.43	107.53
3	A	1202	3C0	C22-C17-C16	-6.42	103.75	107.53
3	B	1203	3C0	C22-C17-C16	-6.08	103.95	107.53
3	B	1203	3C0	C13-O12-C02	-5.69	109.14	117.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	TAR	1	0
3	A	1202	3C0	5	0
2	B	1201	TAR	1	0
3	B	1203	3C0	4	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	381/418 (91%)	-0.34	6 (1%) 74 60	112, 149, 190, 223	0
1	B	392/418 (93%)	-0.49	0 100 100	109, 142, 180, 223	0
All	All	773/836 (92%)	-0.42	6 (0%) 87 77	109, 145, 186, 223	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	98	LEU	5.0
1	A	97	GLN	4.5
1	A	95	ASN	3.4
1	A	519	CYS	2.3
1	A	1014	SER	2.2

### 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( $\text{\AA}^2$ )	Q<0.9
2	TAR	B	1201	10/10	0.89	0.27	1.71	151,186,210,211	0
2	TAR	A	1201	10/10	0.89	0.23	1.44	127,177,190,200	0
3	3C0	B	1203	23/23	0.95	0.28	1.16	118,126,139,156	0
2	TAR	B	1202	10/10	0.91	0.21	1.02	122,174,195,207	0
3	3C0	A	1202	23/23	0.95	0.25	0.33	118,129,159,176	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.