wwPDB X-ray Structure Validation Summary Report (i)

Mar 10, 2021 – 02:03 am GMT

PDB ID	:	6ZNJ
Title	:	MaeB full-length enzyme apoprotein form
Authors	:	Lovering, A.L.; Harding, C.J.
Deposited on	:	2020-07-06
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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

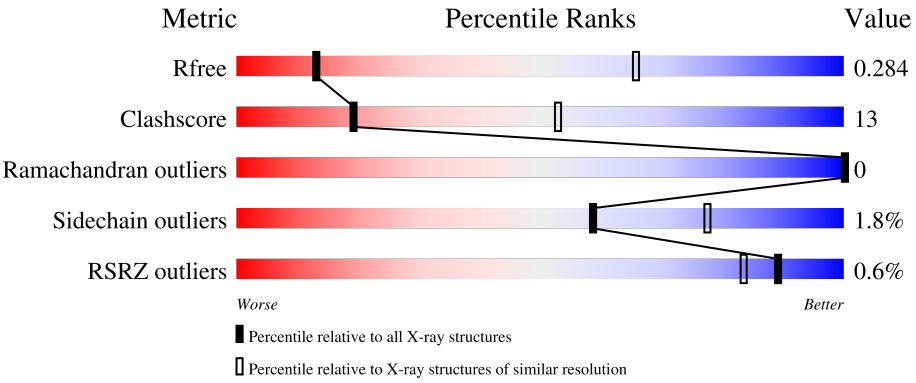
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.17.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.17.1

1 Overall quality at a glance (i)

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}	130704	1049 (3.88-3.52)
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (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 of the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	791	66% 29%
1	B	791	67% 29%
1	C	791	69% 27%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 17400 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 NADP-dependent malate dehydrogenase,Malate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	761	Total	C	N	O	S	0	2	0
			5800	3684	992	1096	28			
1	C	761	Total	C	N	O	S	0	2	0
			5800	3684	992	1096	28			
1	A	761	Total	C	N	O	S	0	2	0
			5800	3684	992	1096	28			

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	MET	-	initiating methionine	UNP Q6MM14
B	-9	GLY	-	expression tag	UNP Q6MM14
B	-8	SER	-	expression tag	UNP Q6MM14
B	-7	SER	-	expression tag	UNP Q6MM14
B	-6	HIS	-	expression tag	UNP Q6MM14
B	-5	HIS	-	expression tag	UNP Q6MM14
B	-4	HIS	-	expression tag	UNP Q6MM14
B	-3	HIS	-	expression tag	UNP Q6MM14
B	-2	HIS	-	expression tag	UNP Q6MM14
B	-1	HIS	-	expression tag	UNP Q6MM14
B	0	SER	-	expression tag	UNP Q6MM14
B	121	ASP	-	linker	UNP Q6MM14
B	122	ILE	-	linker	UNP Q6MM14
B	123	GLU	-	linker	UNP Q6MM14
B	124	VAL	-	linker	UNP Q6MM14
C	-10	MET	-	initiating methionine	UNP Q6MM14
C	-9	GLY	-	expression tag	UNP Q6MM14
C	-8	SER	-	expression tag	UNP Q6MM14
C	-7	SER	-	expression tag	UNP Q6MM14
C	-6	HIS	-	expression tag	UNP Q6MM14
C	-5	HIS	-	expression tag	UNP Q6MM14
C	-4	HIS	-	expression tag	UNP Q6MM14

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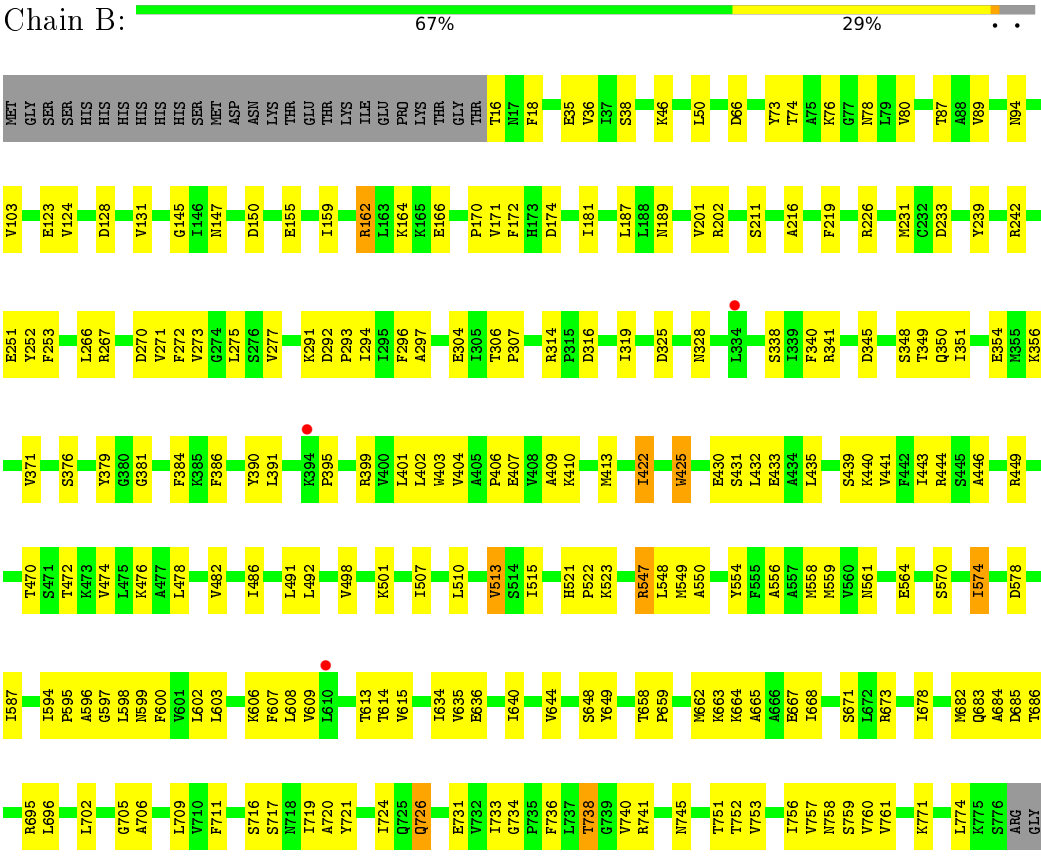
Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	HIS	-	expression tag	UNP Q6MM14
C	-2	HIS	-	expression tag	UNP Q6MM14
C	-1	HIS	-	expression tag	UNP Q6MM14
C	0	SER	-	expression tag	UNP Q6MM14
C	121	ASP	-	linker	UNP Q6MM14
C	122	ILE	-	linker	UNP Q6MM14
C	123	GLU	-	linker	UNP Q6MM14
C	124	VAL	-	linker	UNP Q6MM14
A	-10	MET	-	initiating methionine	UNP Q6MM14
A	-9	GLY	-	expression tag	UNP Q6MM14
A	-8	SER	-	expression tag	UNP Q6MM14
A	-7	SER	-	expression tag	UNP Q6MM14
A	-6	HIS	-	expression tag	UNP Q6MM14
A	-5	HIS	-	expression tag	UNP Q6MM14
A	-4	HIS	-	expression tag	UNP Q6MM14
A	-3	HIS	-	expression tag	UNP Q6MM14
A	-2	HIS	-	expression tag	UNP Q6MM14
A	-1	HIS	-	expression tag	UNP Q6MM14
A	0	SER	-	expression tag	UNP Q6MM14
A	121	ASP	-	linker	UNP Q6MM14
A	122	ILE	-	linker	UNP Q6MM14
A	123	GLU	-	linker	UNP Q6MM14
A	124	VAL	-	linker	UNP Q6MM14

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.

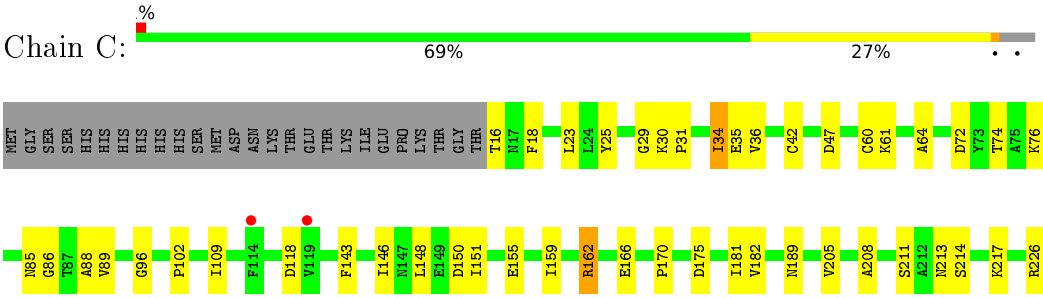
- Molecule 1: NADP-dependent malate dehydrogenase,Malate dehydrogenase

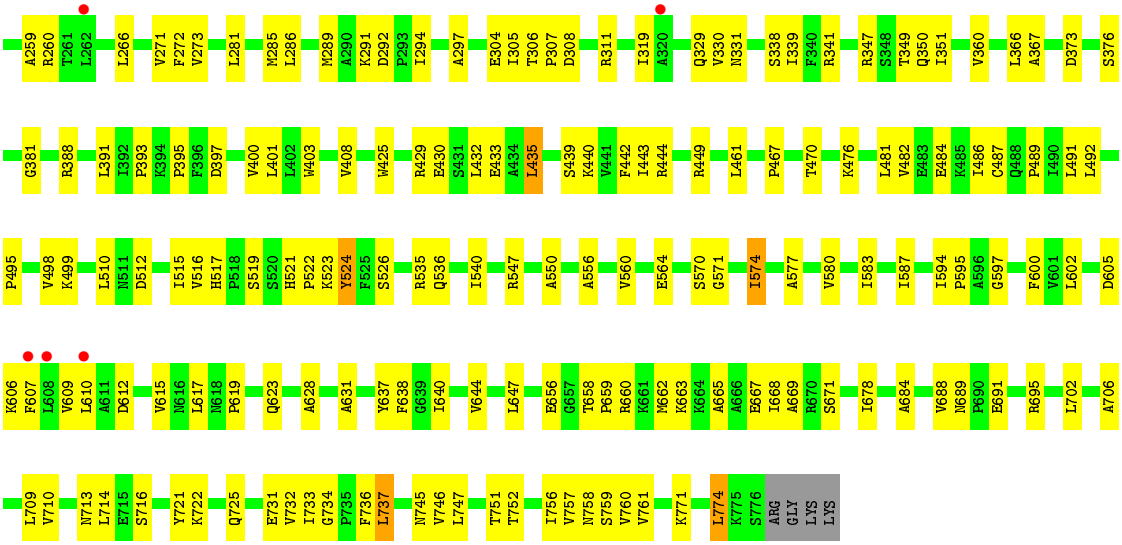
Chain B:



- Molecule 1: NADP-dependent malate dehydrogenase,Malate dehydrogenase

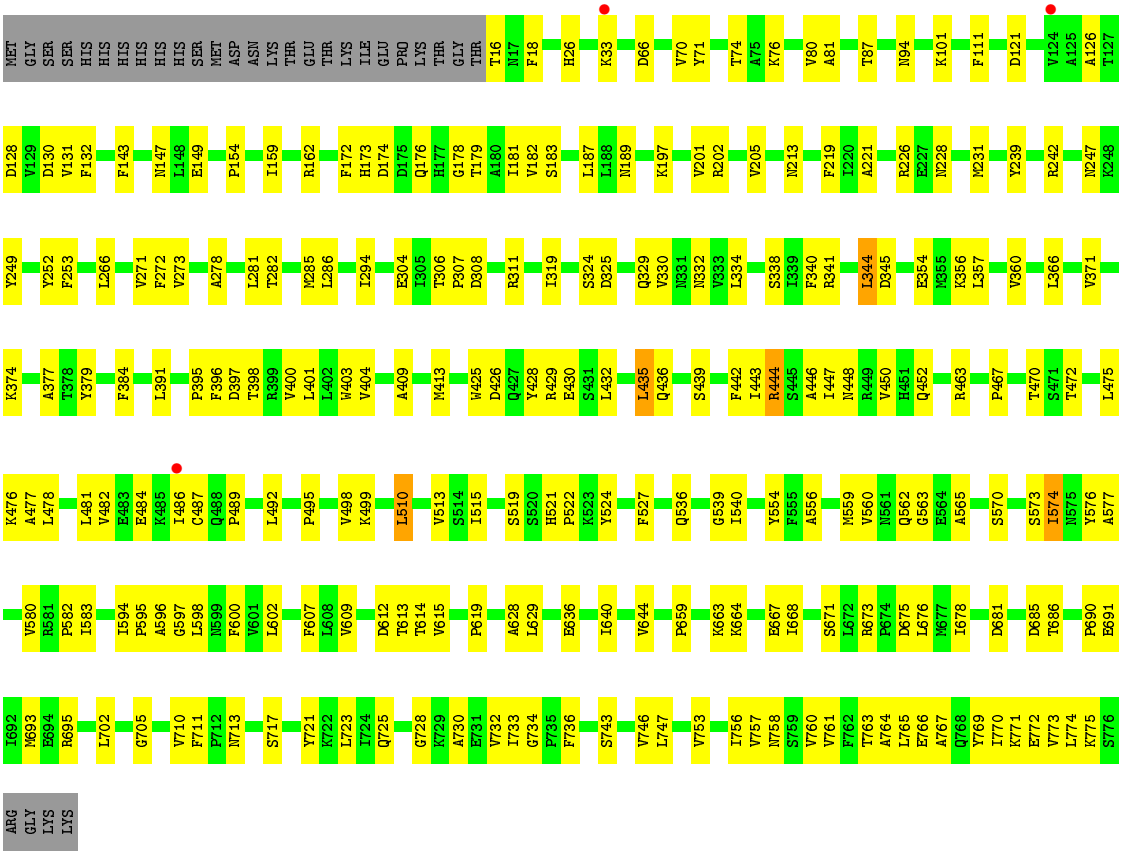
Chain C:





• Molecule 1: NADP-dependent malate dehydrogenase,Malate dehydrogenase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	81.70Å 273.58Å 308.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.77 – 3.70 154.12 – 3.70	Depositor EDS
% Data completeness (in resolution range)	96.5 (66.77-3.70) 96.7 (154.12-3.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.08 (at 3.68Å)	Xtriage
Refinement program	PHENIX v1.0	Depositor
R, R_{free}	0.210 , 0.270 0.220 , 0.284	Depositor DCC
R_{free} test set	1791 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å^2)	101.5	Xtriage
Anisotropy	0.946	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 34.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.41$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	17400	wwPDB-VP
Average B, all atoms (Å^2)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	0.67	0/5909	0.85	4/8004 (0.0%)
1	B	0.65	0/5909	0.81	0/8004
1	C	0.62	0/5909	0.77	1/8004 (0.0%)
All	All	0.65	0/17727	0.81	5/24012 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	436	GLN	CB-CA-C	9.80	130.00	110.40
1	A	436	GLN	N-CA-C	-7.31	91.26	111.00
1	A	510	LEU	CA-CB-CG	-5.72	102.15	115.30
1	A	344	LEU	CB-CG-CD2	-5.54	101.58	111.00
1	C	737	LEU	CA-CB-CG	-5.39	102.89	115.30

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	5800	0	5906	153	0
1	B	5800	0	5906	165	0
1	C	5800	0	5906	155	0
All	All	17400	0	17718	454	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.

The worst 5 of 454 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:607:PHE:HE2	1:B:640:ILE:HD12	1.32	0.94
1:C:443:ILE:HD11	1:C:758:ASN:HB3	1.49	0.94
1:C:607:PHE:HE2	1:C:640:ILE:HD12	1.34	0.91
1:A:226:ARG:HH21	1:A:253:PHE:HD1	1.20	0.88
1:A:307:PRO:HA	1:A:319:ILE:HD13	1.55	0.87

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	761/791 (96%)	731 (96%)	30 (4%)	0	100	100
1	B	761/791 (96%)	731 (96%)	30 (4%)	0	100	100
1	C	761/791 (96%)	738 (97%)	23 (3%)	0	100	100
All	All	2283/2373 (96%)	2200 (96%)	83 (4%)	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	617/642 (96%)	607 (98%)	10 (2%)	62	80
1	B	617/642 (96%)	601 (97%)	16 (3%)	46	69
1	C	617/642 (96%)	607 (98%)	10 (2%)	62	80
All	All	1851/1926 (96%)	1815 (98%)	36 (2%)	59	76

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	ASP
1	A	721	TYR
1	A	162	ARG
1	A	435	LEU
1	B	721	TYR

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

Mol	Chain	Res	Type
1	C	20	GLN
1	C	329	GLN
1	C	511	ASN
1	A	758	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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^2)	Q<0.9
1	A	761/791 (96%)	-0.16	3 (0%)	92	88	68, 92, 121, 142	0
1	B	761/791 (96%)	-0.13	3 (0%)	92	88	67, 100, 132, 164	0
1	C	761/791 (96%)	-0.09	7 (0%)	84	76	68, 109, 143, 163	0
All	All	2283/2373 (96%)	-0.13	13 (0%)	89	83	67, 101, 136, 164	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	262	LEU	3.8
1	B	334	LEU	2.6
1	C	119	VAL	2.5
1	C	610	LEU	2.2
1	C	320	ALA	2.2

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.