

wwPDB X-ray Structure Validation Summary Report (i)

Nov 2, 2023 – 07:20 AM EDT

PDB ID	:	3LBM
Title	:	D-sialic acid aldolase
Authors	:	Ko, TP.; Chou, CY.; Wang, A.HJ.
Deposited on	:	2010-01-08
Resolution	:	1.48 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

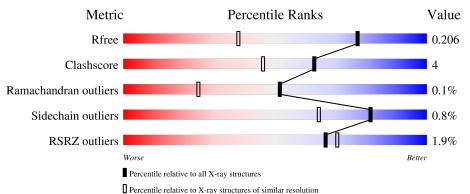
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.48 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	$\begin{array}{c} \textbf{Whole archive} \\ \textbf{(\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	4690 (1.50-1.46)
Clashscore	141614	4955 (1.50-1.46)
Ramachandran outliers	138981	4846 (1.50-1.46)
Sidechain outliers	138945	4844 (1.50-1.46)
RSRZ outliers	127900	4614 (1.50-1.46)

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	А	319	^{2%} 85%	6% • 8%
1	В	319	2% 84%	8% • 8%
1	С	319	2% 81%	10% • 8%
1	D	319	83%	9% • 8%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10679 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A 005		Total	С	Ν	0	\mathbf{S}	73	0	0
	А	295	2279	1452	386	431	10	10	0	0
1	В	295	Total	С	Ν	0	S	74	0	0
	D	295	2279	1452	386	431	10	74	0	U
1	С	294	Total	С	Ν	0	S	70	0	0
	U	294	2274	1449	385	430	10	10	0	0
1	Л	205	Total	С	Ν	0	S	54	0	0
	I D	295	2279	1452	386	431	10	04	U	U

• Molecule 1 is a protein called N-acetylneuraminate lyase.

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	-21	MET	-	expression tag	UNP P0A6L4
А	-20	GLY	-	expression tag	UNP P0A6L4
А	-19	HIS	-	expression tag	UNP P0A6L4
А	-18	HIS	-	expression tag	UNP P0A6L4
А	-17	HIS	-	expression tag	UNP P0A6L4
А	-16	HIS	-	expression tag	UNP P0A6L4
А	-15	HIS	-	expression tag	UNP P0A6L4
А	-14	HIS	-	expression tag	UNP P0A6L4
А	-13	HIS	-	expression tag	UNP P0A6L4
А	-12	HIS	-	expression tag	UNP P0A6L4
А	-11	HIS	-	expression tag	UNP P0A6L4
А	-10	HIS	-	expression tag	UNP P0A6L4
А	-9	SER	-	expression tag	UNP P0A6L4
А	-8	SER	-	expression tag	UNP P0A6L4
А	-7	GLY	-	expression tag	UNP P0A6L4
А	-6	HIS	-	expression tag	UNP P0A6L4
А	-5	ILE	-	expression tag	UNP P0A6L4
А	-4	GLU	-	expression tag	UNP P0A6L4
А	-3	GLY	-	expression tag	UNP P0A6L4
А	-2	ARG	-	expression tag	UNP P0A6L4
А	-1	HIS	-	expression tag	UNP P0A6L4

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Chain	Residue	Modelled	Actual	Comment	Reference
А	0	MET	-	expression tag	UNP P0A6L4
В	-21	MET	_	expression tag	UNP P0A6L4
В	-20	GLY	-	expression tag	UNP P0A6L4
В	-19	HIS	-	expression tag	UNP P0A6L4
В	-18	HIS	-	expression tag	UNP P0A6L4
В	-17	HIS	-	expression tag	UNP P0A6L4
В	-16	HIS	-	expression tag	UNP P0A6L4
В	-15	HIS	-	expression tag	UNP P0A6L4
В	-14	HIS	-	expression tag	UNP P0A6L4
В	-13	HIS	-	expression tag	UNP P0A6L4
В	-12	HIS	-	expression tag	UNP P0A6L4
В	-11	HIS	-	expression tag	UNP P0A6L4
В	-10	HIS	-	expression tag	UNP P0A6L4
В	-9	SER	-	expression tag	UNP P0A6L4
В	-8	SER	-	expression tag	UNP P0A6L4
В	-7	GLY	-	expression tag	UNP P0A6L4
В	-6	HIS	-	expression tag	UNP P0A6L4
В	-5	ILE	-	expression tag	UNP P0A6L4
В	-4	GLU	-	expression tag	UNP P0A6L4
В	-3	GLY	-	expression tag	UNP P0A6L4
В	-2	ARG	-	expression tag	UNP P0A6L4
В	-1	HIS	-	expression tag	UNP P0A6L4
В	0	MET	-	expression tag	UNP P0A6L4
С	-21	MET	-	expression tag	UNP P0A6L4
С	-20	GLY	-	expression tag	UNP P0A6L4
С	-19	HIS	-	expression tag	UNP P0A6L4
С	-18	HIS	-	expression tag	UNP P0A6L4
С	-17	HIS	-	expression tag	UNP P0A6L4
С	-16	HIS	-	expression tag	UNP P0A6L4
C	-15	HIS	-	expression tag	UNP P0A6L4
С	-14	HIS	-	expression tag	UNP P0A6L4
С	-13	HIS	-	expression tag	UNP P0A6L4
С	-12	HIS	-	expression tag	UNP P0A6L4
С	-11	HIS	-	expression tag	UNP P0A6L4
С	-10	HIS	-	expression tag	UNP P0A6L4
С	-9	SER	-	expression tag	UNP P0A6L4
С	-8	SER	-	expression tag	UNP P0A6L4
С	-7	GLY	-	expression tag	UNP P0A6L4
С	-6	HIS	-	expression tag	UNP P0A6L4
С	-5	ILE	-	expression tag	UNP P0A6L4
С	-4	GLU	-	expression tag	UNP P0A6L4
С	-3	GLY	-	expression tag	UNP P0A6L4

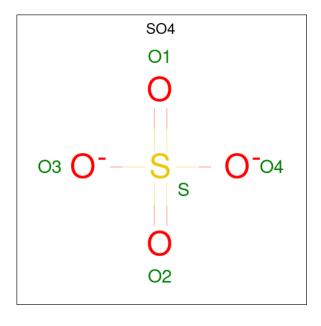
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Chain	Residue	Modelled	Actual	Comment	Reference
С	-2	ARG	-	expression tag	UNP P0A6L4
С	-1	HIS	-	expression tag	UNP P0A6L4
С	0	MET	-	expression tag	UNP P0A6L4
D	-21	MET	-	expression tag	UNP P0A6L4
D	-20	GLY	-	expression tag	UNP P0A6L4
D	-19	HIS	-	expression tag	UNP P0A6L4
D	-18	HIS	-	expression tag	UNP P0A6L4
D	-17	HIS	-	expression tag	UNP P0A6L4
D	-16	HIS	-	expression tag	UNP P0A6L4
D	-15	HIS	-	expression tag	UNP P0A6L4
D	-14	HIS	-	expression tag	UNP P0A6L4
D	-13	HIS	-	expression tag	UNP P0A6L4
D	-12	HIS	-	expression tag	UNP P0A6L4
D	-11	HIS	-	expression tag	UNP P0A6L4
D	-10	HIS	-	expression tag	UNP P0A6L4
D	-9	SER	-	expression tag	UNP P0A6L4
D	-8	SER	-	expression tag	UNP P0A6L4
D	-7	GLY	-	expression tag	UNP P0A6L4
D	-6	HIS	-	expression tag	UNP P0A6L4
D	-5	ILE	-	expression tag	UNP P0A6L4
D	-4	GLU	-	expression tag	UNP P0A6L4
D	-3	GLY	-	expression tag	UNP P0A6L4
D	-2	ARG	-	expression tag	UNP P0A6L4
D	-1	HIS	-	expression tag	UNP P0A6L4
D	0	MET	_	expression tag	UNP P0A6L4

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

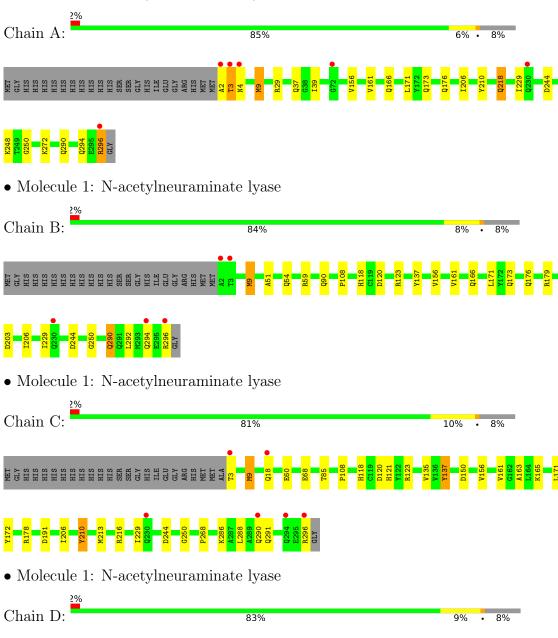
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	389	Total O 389 389	0	0
3	В	409	Total O 409 409	0	0
3	С	375	Total O 375 375	0	0
3	D	375	Total O 375 375	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: N-acetylneuraminate lyase









4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	121.01Å 121.01Å 197.57Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 - 1.48	Depositor
Resolution (A)	29.90 - 1.48	EDS
% Data completeness	91.0 (30.00-1.48)	Depositor
(in resolution range)	96.0 (29.90-1.48)	EDS
R _{merge}	0.06	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.56 (at 1.48 \text{\AA})$	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.186 , 0.203	Depositor
$10, 10_{free}$	0.186 , 0.206	DCC
R_{free} test set	13174 reflections (4.96%)	wwPDB-VP
Wilson B-factor $(Å^2)$	18.7	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.39, 50.2	EDS
L-test for twinning ²	$< L > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10679	wwPDB-VP
Average B, all atoms $(Å^2)$	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.69% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: SO4

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 B		nd lengths	Bond angles		
MOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.87	2/2319~(0.1%)	0.98	5/3139~(0.2%)	
1	В	0.86	0/2319	0.98	6/3139~(0.2%)	
1	С	0.87	1/2314~(0.0%)	1.00	7/3132~(0.2%)	
1	D	0.90	1/2319~(0.0%)	1.01	7/3139~(0.2%)	
All	All	0.87	4/9271~(0.0%)	0.99	25/12549~(0.2%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	В	0	1
1	С	0	2
1	D	0	1
All	All	0	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	9	MET	CB-CG	7.60	1.75	1.51
1	А	9	MET	CG-SD	-6.65	1.63	1.81
1	D	9	MET	CB-CG	5.88	1.70	1.51
1	С	9	MET	SD-CE	-5.70	1.46	1.77

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	9	MET	CG-SD-CE	-9.60	84.85	100.20
1	D	97	ARG	NE-CZ-NH2	-8.76	115.92	120.30

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$Ideal(^{o})$
1	D	97	ARG	NE-CZ-NH1	7.84	124.22	120.30
1	С	191	ASP	CB-CG-OD1	7.21	124.79	118.30
1	А	244	ASP	CB-CG-OD2	-6.93	112.06	118.30

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There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	137	TYR	Sidechain
1	С	137	TYR	Sidechain
1	С	210	TYR	Sidechain
1	D	137	TYR	Sidechain

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	А	2279	0	2300	19	0
1	В	2279	0	2300	16	0
1	С	2274	0	2295	23	0
1	D	2279	0	2300	24	0
2	А	5	0	0	0	0
2	В	5	0	0	0	0
2	С	5	0	0	0	0
2	D	5	0	0	0	0
3	А	389	0	0	4	0
3	В	409	0	0	3	0
3	С	375	0	0	7	0
3	D	375	0	0	7	0
All	All	10679	0	9195	76	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 76 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:9:MET:CB	1:A:9:MET:CG	1.75	1.55
1:C:150:ASP:HB3	3:C:1317:HOH:O	1.48	1.14
1:C:296:ARG:HG2	1:C:296:ARG:HH11	1.19	1.05
1:A:9:MET:CB	1:A:9:MET:SD	2.62	0.87
1:D:2:ALA:N	3:D:970:HOH:O	2.08	0.86

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	Perce	ntiles
1	А	293/319~(92%)	287~(98%)	5 (2%)	1 (0%)	41	18
1	В	293/319~(92%)	290~(99%)	3 (1%)	0	100	100
1	С	292/319~(92%)	289~(99%)	3 (1%)	0	100	100
1	D	293/319~(92%)	289~(99%)	4 (1%)	0	100	100
All	All	1171/1276~(92%)	1155~(99%)	15 (1%)	1 (0%)	51	25

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	3	THR

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed, and the total number of residues.



Mol	Chain	Analysed	Rotameric	Outliers	Percei	ntiles
1	А	243/263~(92%)	240~(99%)	3~(1%)	71	46
1	В	243/263~(92%)	241 (99%)	2(1%)	81	64
1	С	243/263~(92%)	241~(99%)	2(1%)	81	64
1	D	243/263~(92%)	242 (100%)	1 (0%)	91	81
All	All	972/1052~(92%)	964~(99%)	8 (1%)	81	64

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	D	294	GLN
1	С	268	PRO
1	В	290	GLN
1	В	166	GLN
1	С	18	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	С	18	GLN
1	С	138	ASN
1	D	291	GLN
1	С	121	HIS
1	С	166	GLN

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)

4 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	SO4	В	2004	-	4,4,4	0.63	0	$6,\!6,\!6$	0.48	0
2	SO4	С	2006	-	4,4,4	0.44	0	$6,\!6,\!6$	0.28	0
2	SO4	А	2002	-	4,4,4	0.34	0	$6,\!6,\!6$	0.26	0
2	SO4	D	2008	-	4,4,4	0.73	0	$6,\!6,\!6$	0.39	0

There are no bond length outliers.

There are no bond angle outliers.

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 (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^{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	А	295/319~(92%)	-0.34	6 (2%) 65 69	14, 19, 29, 49	17 (5%)
1	В	295/319~(92%)	-0.34	5 (1%) 70 73	15, 19, 31, 48	17 (5%)
1	С	294/319~(92%)	-0.28	6 (2%) 65 69	16, 20, 33, 49	17 (5%)
1	D	295/319~(92%)	-0.38	5 (1%) 70 73	14, 18, 29, 46	13 (4%)
All	All	1179/1276~(92%)	-0.34	22 (1%) 66 70	14, 19, 32, 49	64 (5%)

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	3	THR	10.4
1	С	3	THR	10.2
1	А	2	ALA	10.1
1	А	296	ARG	6.2
1	В	2	ALA	5.6

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^{th} 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
2	SO4	С	2006	5/5	0.99	0.04	19,19,21,21	0
2	SO4	D	2008	5/5	0.99	0.05	17,18,20,20	0
2	SO4	А	2002	5/5	1.00	0.03	17,19,19,20	0
2	SO4	В	2004	5/5	1.00	0.04	17,17,20,21	0

6.5 Other polymers (i)

There are no such residues in this entry.

