



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:38 PM UTC

PDB ID : 6A7H / pdb_00006a7h
Title : Bacterial protein toxins
Authors : Kim, M.H.; Hwang, J.; Jang, S.Y.
Deposited on : 2018-07-03
Resolution : 2.30 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

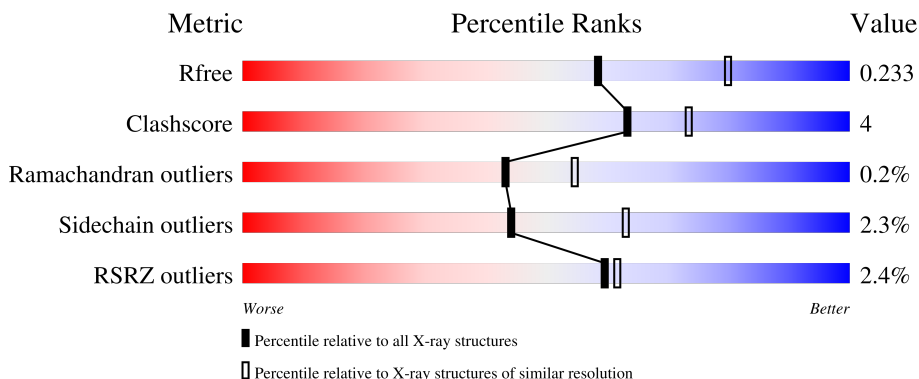
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

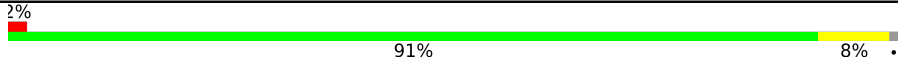
The reported resolution of this entry is 2.30 Å.

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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 $\leq 5\%$. 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	481	
1	B	481	
1	C	481	
1	D	481	

2 Entry composition [i](#)

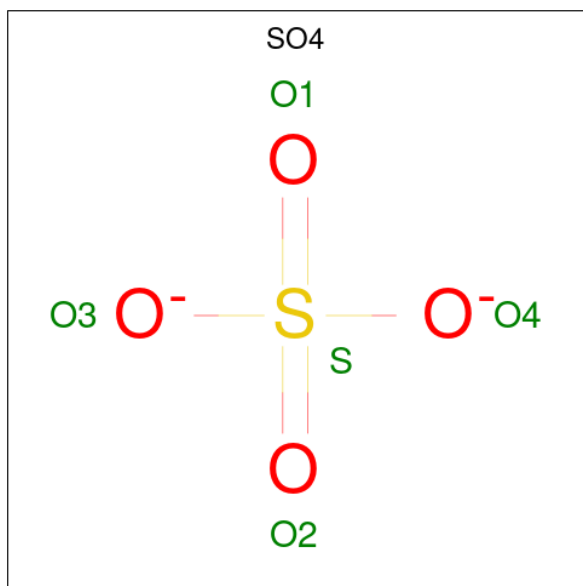
There are 3 unique types of molecules in this entry. The entry contains 15720 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 RTX toxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total	C	N	O	S	0	0	0
			3690	2313	640	724	13			
1	B	471	Total	C	N	O	S	0	0	0
			3635	2281	629	712	13			
1	C	469	Total	C	N	O	S	0	0	0
			3632	2279	630	710	13			
1	D	468	Total	C	N	O	S	0	0	0
			3619	2272	626	708	13			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

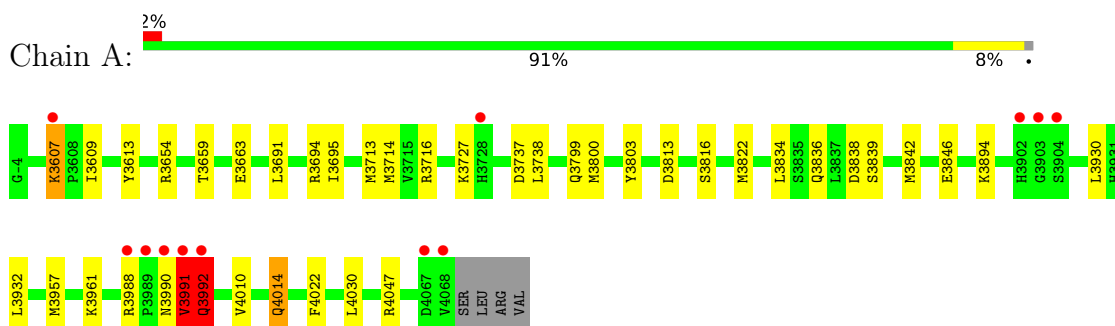
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	252	Total	O	0	0
			252	252		
3	B	292	Total	O	0	0
			292	292		
3	C	268	Total	O	0	0
			268	268		
3	D	287	Total	O	0	0
			287	287		

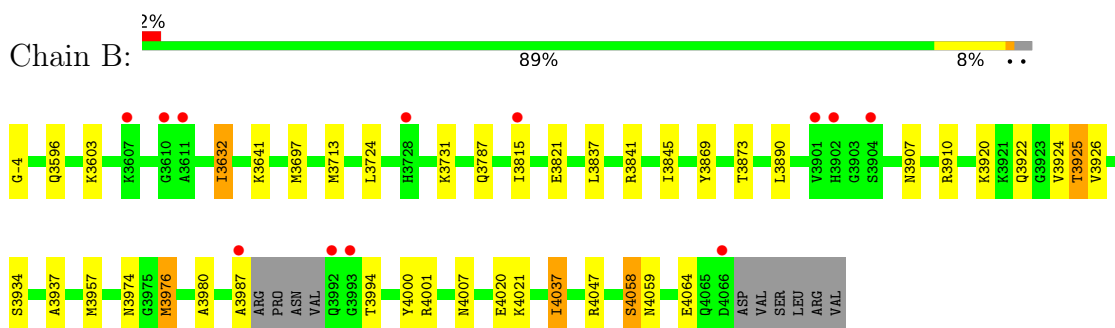
3 Residue-property plots

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.

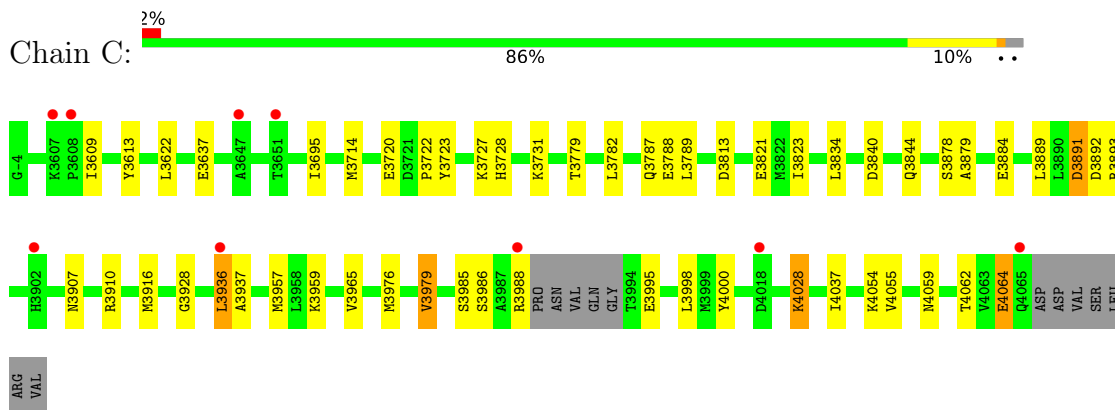
- Molecule 1: RTX toxin



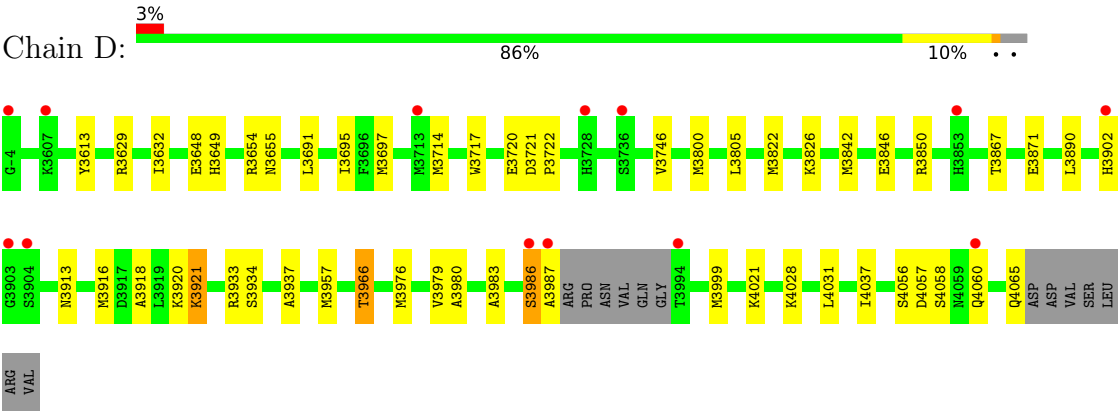
- Molecule 1: RTX toxin



- Molecule 1: RTX toxin



- Molecule 1: RTX toxin



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	178.54Å 198.28Å 164.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.88 – 2.30 34.88 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (34.88-2.30) 99.7 (34.88-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.178 , 0.230 0.182 , 0.233	Depositor DCC
R_{free} test set	6423 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15720	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.30 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.8573e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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.

5 Model quality

5.1 Standard geometry

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	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.50	0/3751	0.77	0/5066
1	B	0.51	0/3694	0.78	0/4986
1	C	0.51	0/3691	0.78	0/4981
1	D	0.51	0/3678	0.80	3/4964 (0.1%)
All	All	0.51	0/14814	0.78	3/19997 (0.0%)

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	A	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	D	3655	ASN	N-CA-C	5.17	116.91	111.28
1	D	3721	ASP	CA-C-N	5.10	125.38	119.47
1	D	3721	ASP	C-N-CA	5.10	125.38	119.47

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3991	VAL	Peptide

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	3690	0	3650	26	0
1	B	3635	0	3593	30	0
1	C	3632	0	3599	29	0
1	D	3619	0	3581	34	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
2	C	15	0	0	0	0
2	D	10	0	0	0	0
3	A	252	0	0	4	1
3	B	292	0	0	8	5
3	C	268	0	0	2	0
3	D	287	0	0	2	4
All	All	15720	0	14423	116	5

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 116 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:D:3632:ILE:HG13	1:D:3697:MET:HE1	1.54	0.89
1:D:3695:ILE:HG12	1:D:3714:MET:HE2	1.64	0.80
1:D:3937:ALA:HB2	1:D:3957:MET:HE1	1.67	0.75
1:A:3988:ARG:HD3	1:A:3991:VAL:HA	1.71	0.72
1:C:3907:ASN:OD1	1:C:3910:ARG:NH1	2.24	0.70

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:4386:HOH:O	3:D:4423:HOH:O[7_454]	1.98	0.22
3:B:4416:HOH:O	3:D:4447:HOH:O[7_454]	2.10	0.10
3:A:4399:HOH:O	3:B:4436:HOH:O[6_455]	2.14	0.06
3:B:4386:HOH:O	3:D:4440:HOH:O[7_454]	2.16	0.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:4479:HOH:O	3:D:4423:HOH:O[7_454]	2.16	0.04

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	475/481 (99%)	461 (97%)	13 (3%)	1 (0%)	43	55
1	B	467/481 (97%)	461 (99%)	6 (1%)	0	100	100
1	C	465/481 (97%)	454 (98%)	10 (2%)	1 (0%)	43	55
1	D	464/481 (96%)	453 (98%)	10 (2%)	1 (0%)	43	55
All	All	1871/1924 (97%)	1829 (98%)	39 (2%)	3 (0%)	43	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3992	GLN
1	C	3878	SER
1	D	3986	SER

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	389/393 (99%)	380 (98%)	9 (2%)	44	63
1	B	381/393 (97%)	372 (98%)	9 (2%)	43	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	382/393 (97%)	371 (97%)	11 (3%)	37	55
1	D	380/393 (97%)	373 (98%)	7 (2%)	51	70
All	All	1532/1572 (98%)	1496 (98%)	36 (2%)	44	63

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

Mol	Chain	Res	Type
1	C	4064	GLU
1	D	4065	GLN
1	D	3902	HIS
1	D	3979	VAL
1	B	3815	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	3922	GLN
1	D	3996	HIS
1	B	3596	GLN
1	B	3649	HIS
1	B	3704	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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	B	4102	-	4,4,4	0.27	0	6,6,6	0.13	0
2	SO4	A	4102	-	4,4,4	0.23	0	6,6,6	0.11	0
2	SO4	C	4101	-	4,4,4	0.23	0	6,6,6	0.21	0
2	SO4	D	4101	-	4,4,4	0.25	0	6,6,6	0.21	0
2	SO4	A	4101	-	4,4,4	0.23	0	6,6,6	0.41	0
2	SO4	C	4102	-	4,4,4	0.26	0	6,6,6	0.18	0
2	SO4	C	4103	-	4,4,4	0.22	0	6,6,6	0.16	0
2	SO4	D	4102	-	4,4,4	0.22	0	6,6,6	0.07	0
2	SO4	B	4101	-	4,4,4	0.28	0	6,6,6	0.23	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, 95th 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	477/481 (99%)	-0.14	12 (2%) 58 60	25, 41, 81, 128	0
1	B	471/481 (97%)	-0.15	12 (2%) 58 60	24, 41, 75, 113	0
1	C	469/481 (97%)	-0.20	9 (1%) 66 68	24, 40, 70, 102	0
1	D	468/481 (97%)	-0.22	13 (2%) 55 57	22, 40, 75, 131	0
All	All	1885/1924 (97%)	-0.18	46 (2%) 59 62	22, 40, 75, 131	0

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	4068	VAL	8.1
1	D	3987	ALA	7.2
1	A	3989	PRO	5.9
1	C	3607	LYS	4.9
1	B	4066	ASP	4.7

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 oligosaccharides 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, 95th 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
2	SO4	B	4102	5/5	0.54	0.17	115,120,120,122	0
2	SO4	A	4102	5/5	0.83	0.14	86,89,104,104	0
2	SO4	A	4101	5/5	0.86	0.14	53,64,74,82	0
2	SO4	C	4103	5/5	0.88	0.15	86,89,93,94	0
2	SO4	B	4101	5/5	0.90	0.14	63,70,84,90	0
2	SO4	D	4101	5/5	0.91	0.17	52,72,82,83	0
2	SO4	C	4102	5/5	0.92	0.13	59,64,71,77	0
2	SO4	D	4102	5/5	0.93	0.12	63,75,78,84	0
2	SO4	C	4101	5/5	0.95	0.12	64,65,72,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.