



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:46 AM UTC

PDB ID : 3TSW / pdb_00003tsw
Title : crystal structure of the PDZ3-SH3-GUK core module of Human ZO-1
Authors : Nomme, J.; Lavie, A.
Deposited on : 2011-09-13
Resolution : 2.85 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

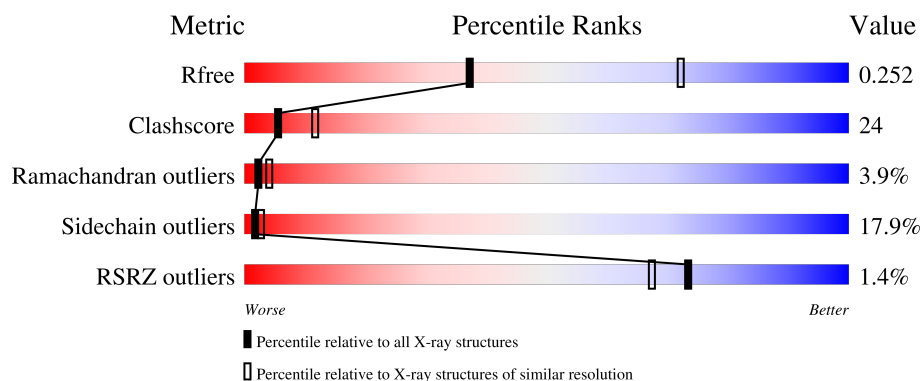
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	391	% 42% 35% 8% 15%
1	B	391	19% 24% 5% 50%
1	C	391	2% 42% 38% 6% 14%
1	D	391	% 23% 23% 5% 49%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8637 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.

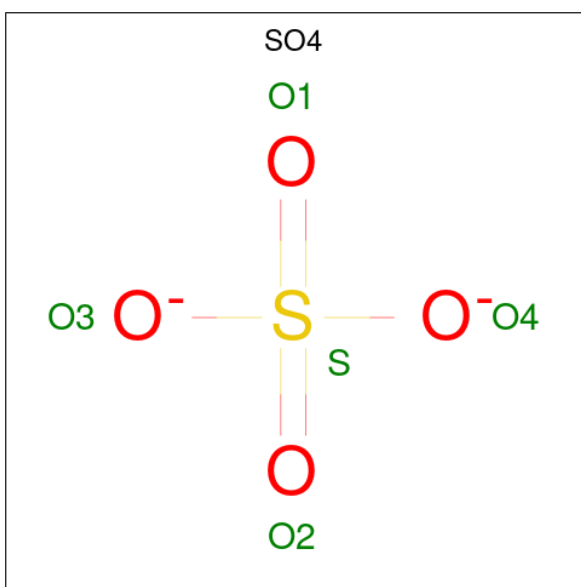
- Molecule 1 is a protein called Tight junction protein ZO-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	0	0
			2687	1709	481	491	6			
1	B	194	Total	C	N	O	S	0	0	0
			1552	991	270	290	1			
1	C	337	Total	C	N	O	S	0	0	0
			2703	1714	488	495	6			
1	D	199	Total	C	N	O	S	0	0	0
			1590	1011	281	297	1			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	413	GLY	-	expression tag	UNP Q07157
A	414	SER	-	expression tag	UNP Q07157
A	415	HIS	-	expression tag	UNP Q07157
A	416	MET	-	expression tag	UNP Q07157
B	413	GLY	-	expression tag	UNP Q07157
B	414	SER	-	expression tag	UNP Q07157
B	415	HIS	-	expression tag	UNP Q07157
B	416	MET	-	expression tag	UNP Q07157
C	413	GLY	-	expression tag	UNP Q07157
C	414	SER	-	expression tag	UNP Q07157
C	415	HIS	-	expression tag	UNP Q07157
C	416	MET	-	expression tag	UNP Q07157
D	413	GLY	-	expression tag	UNP Q07157
D	414	SER	-	expression tag	UNP Q07157
D	415	HIS	-	expression tag	UNP Q07157
D	416	MET	-	expression tag	UNP Q07157

- 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		
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	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

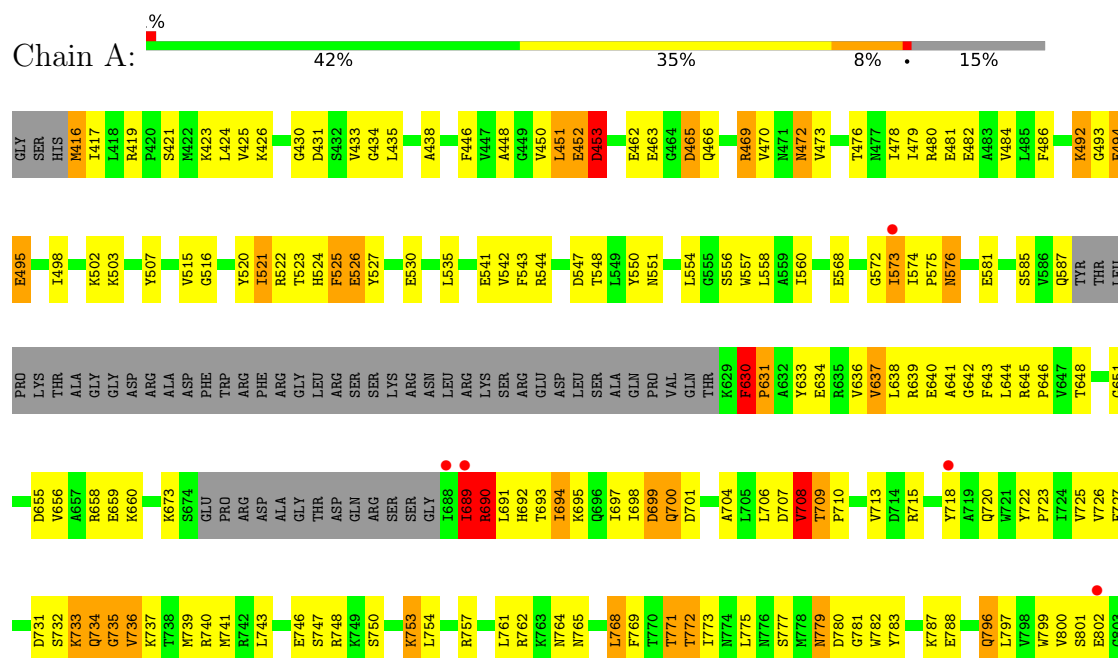
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	20	Total	O	0	0
			20	20		
3	B	13	Total	O	0	0
			13	13		
3	C	22	Total	O	0	0
			22	22		
3	D	15	Total	O	0	0
			15	15		

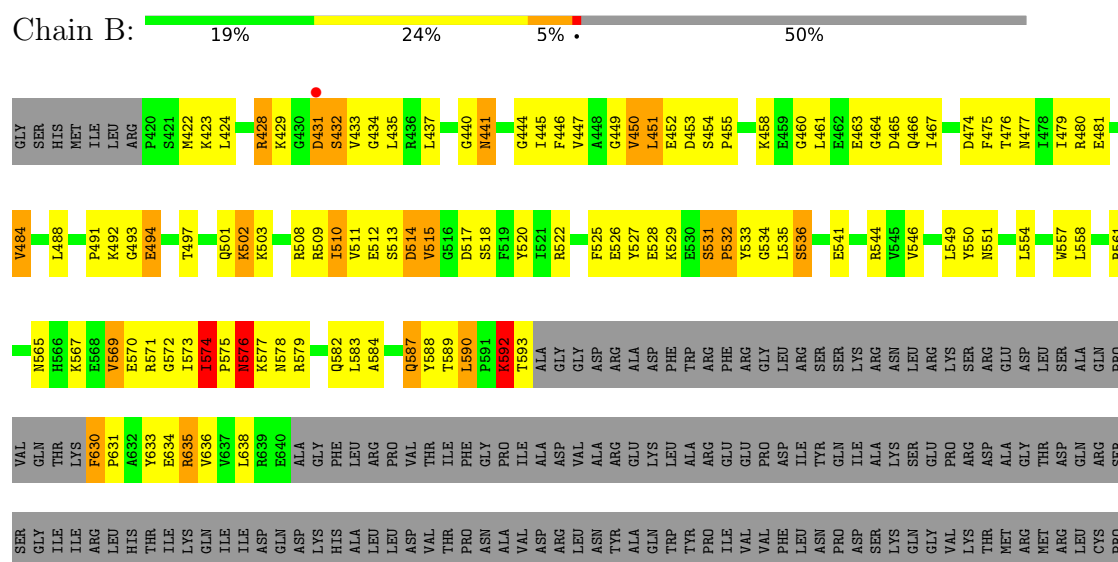
3 Residue-property plots

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: Tight junction protein ZO-1



• Molecule 1: Tight junction protein ZO-1



Chain C:

42%

38%

6%

14%

Chain D:

Amino Acid	Percentage
GLY	49%
SER	23%
HIS	23%
MET	5%
ILE	49%
LEU	23%
ASP	23%
THR	23%
VAL	23%
PRO	23%
ASN	23%
GLN	23%
ARG	23%
ALA	23%
TYR	23%
GLU	23%
LYS	23%
PHE	23%
LEU	23%
THR	23%
VAL	23%
PRO	23%
ASN	23%
GLN	23%
ARG	23%
ALA	23%
TYR	23%
GLU	23%
LYS	23%
PHE	23%
LEU	23%
THR	23%
VAL	23%
PRO	23%
ASN	23%
GLN	23%
ARG	23%
ALA	23%
TYR	23%
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ALA	23%
TYR	23%
GLU	23%
LYS	23%
PHE	23%
LEU	23%
THR	23%
VAL	23%
PRO	23%
ASN	23%
GLN	23

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	100.63Å 100.63Å 182.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	87.17 – 2.85 87.15 – 2.85	Depositor EDS
% Data completeness (in resolution range)	96.2 (87.17-2.85) 97.5 (87.15-2.85)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 2.85Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.211 , 0.290 0.190 , 0.252	Depositor DCC
R_{free} test set	4762 reflections (9.83%)	wwPDB-VP
Wilson B-factor (Å ²)	75.9	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l 0.002 for h,-h-k,-l 0.139 for -k,-h,-l	Xtriage
Reported twinning fraction	0.508 for 1.000H, 1.000K, L 0.492 for -1.000H, 1.000H+1.000K, -L	Depositor
Outliers	0 of 47162 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8637	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [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	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.72	0/2736	1.03	6/3688 (0.2%)
1	B	0.76	0/1578	1.09	9/2124 (0.4%)
1	C	0.69	0/2753	1.01	1/3712 (0.0%)
1	D	0.83	0/1615	1.09	2/2175 (0.1%)
All	All	0.74	0/8682	1.04	18/11699 (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	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	651	GLY	CA-C-N	8.42	128.07	119.82
1	A	651	GLY	C-N-CA	8.42	128.07	119.82
1	B	502	LYS	N-CA-C	7.70	119.31	111.07
1	B	574	ILE	CA-C-N	-6.86	112.58	119.92
1	B	574	ILE	C-N-CA	-6.86	112.58	119.92

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	482	GLU	Peptide
1	B	795	ASN	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	2687	0	2722	123	0
1	B	1552	0	1564	93	0
1	C	2703	0	2722	111	0
1	D	1590	0	1605	100	0
2	A	10	0	0	1	0
2	B	10	0	0	2	0
2	C	5	0	0	0	0
2	D	10	0	0	0	0
3	A	20	0	0	4	0
3	B	13	0	0	0	0
3	C	22	0	0	6	0
3	D	15	0	0	3	0
All	All	8637	0	8613	406	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 24.

The worst 5 of 406 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:450:VAL:HG12	1:D:451:LEU:H	1.19	1.08
1:A:558:LEU:HD12	1:A:573:ILE:HG22	1.28	1.05
1:B:582:GLN:NE2	1:D:478:ILE:HD12	1.77	0.99
1:B:518:SER:OG	2:B:7:SO4:O4	1.88	0.92
1:B:431:ASP:H	1:B:492:LYS:HG2	1.33	0.92

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	328/391 (84%)	266 (81%)	48 (15%)	14 (4%)	2	3
1	B	188/391 (48%)	153 (81%)	29 (15%)	6 (3%)	3	6
1	C	331/391 (85%)	265 (80%)	53 (16%)	13 (4%)	2	4
1	D	193/391 (49%)	150 (78%)	35 (18%)	8 (4%)	2	3
All	All	1040/1564 (66%)	834 (80%)	165 (16%)	41 (4%)	2	4

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	515	VAL
1	A	631	PRO
1	A	689	ILE
1	C	454	SER
1	C	676	PRO

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	289/338 (86%)	237 (82%)	52 (18%)	2	3
1	B	167/338 (49%)	128 (77%)	39 (23%)	1	0
1	C	289/338 (86%)	242 (84%)	47 (16%)	2	4
1	D	171/338 (51%)	145 (85%)	26 (15%)	3	5
All	All	916/1352 (68%)	752 (82%)	164 (18%)	2	3

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	576	ASN
1	D	459	GLU
1	C	665	GLU
1	C	761	LEU
1	D	530	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	794	GLN
1	C	538	ASN
1	D	576	ASN
1	C	501	GLN
1	C	566	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

7 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	C	3	-	4,4,4	0.27	0	6,6,6	0.33	0
2	SO4	D	2	-	4,4,4	0.40	0	6,6,6	0.46	0
2	SO4	A	6	-	4,4,4	0.30	0	6,6,6	0.15	0
2	SO4	B	1	-	4,4,4	0.38	0	6,6,6	0.24	0
2	SO4	B	7	-	4,4,4	0.38	0	6,6,6	0.44	0
2	SO4	D	4	-	4,4,4	0.24	0	6,6,6	0.33	0
2	SO4	A	5	-	4,4,4	0.25	0	6,6,6	0.24	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.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	SO4	1	0
2	B	7	SO4	1	0
2	A	5	SO4	1	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, 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	334/391 (85%)	0.08	5 (1%) 72 65	53, 74, 86, 89	0
1	B	194/391 (49%)	-0.01	1 (0%) 87 85	52, 65, 82, 85	0
1	C	337/391 (86%)	0.14	7 (2%) 63 55	52, 76, 92, 100	0
1	D	199/391 (50%)	-0.10	2 (1%) 79 75	47, 62, 85, 91	0
All	All	1064/1564 (68%)	0.05	15 (1%) 73 67	47, 71, 89, 100	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	433	VAL	3.0
1	C	689	ILE	2.9
1	A	688	ILE	2.8
1	C	451	LEU	2.6
1	B	431	ASP	2.5

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	A	6	5/5	0.90	0.07	109,110,111,111	0
2	SO4	A	5	5/5	0.91	0.06	97,97,98,98	0
2	SO4	C	3	5/5	0.95	0.11	67,67,69,70	0
2	SO4	B	7	5/5	0.96	0.14	70,70,71,71	0
2	SO4	D	2	5/5	0.96	0.08	55,57,60,61	0
2	SO4	B	1	5/5	0.97	0.05	64,65,66,67	0
2	SO4	D	4	5/5	0.98	0.06	72,73,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.