



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:45 AM UTC

PDB ID : 6G5Z / pdb_00006g5z
Title : Choline sulfatase from Ensifer (Sinorhizobium) meliloti
Authors : Martinez-Rodriguez, S.; Camara-Artigas, A.
Deposited on : 2018-03-30
Resolution : 1.98 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

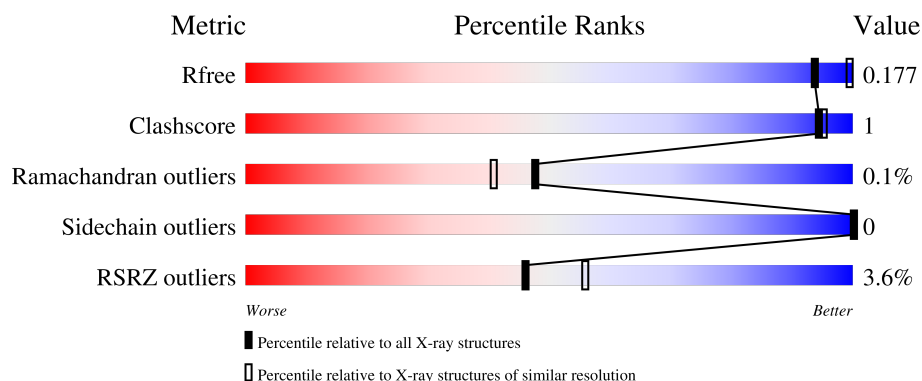
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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	508	% 97% .
1	B	508	6% 95% ..
1	C	508	2% 95% .
1	D	508	5% 97% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 32093 atoms, of which 15115 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 Choline-sulfatase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	508	Total	C	H	N	O	S	0	0	0
			7882	2559	3834	711	758	20			
1	B	503	Total	C	H	N	O	S	0	5	0
			7758	2534	3761	702	742	19			
1	C	506	Total	C	H	N	O	S	0	0	0
			7826	2545	3802	707	752	20			
1	D	505	Total	C	H	N	O	S	0	2	0
			7692	2515	3718	698	741	20			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		
2	D	1	Total	Mg	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	243	Total 243	O 243	0	0
4	B	270	Total 270	O 270	0	0
4	C	209	Total 209	O 209	0	0
4	D	139	Total 139	O 139	0	0

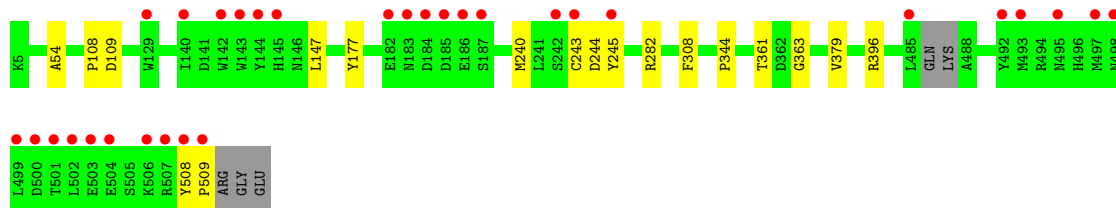
3 Residue-property plots [i](#)

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: Choline-sulfatase



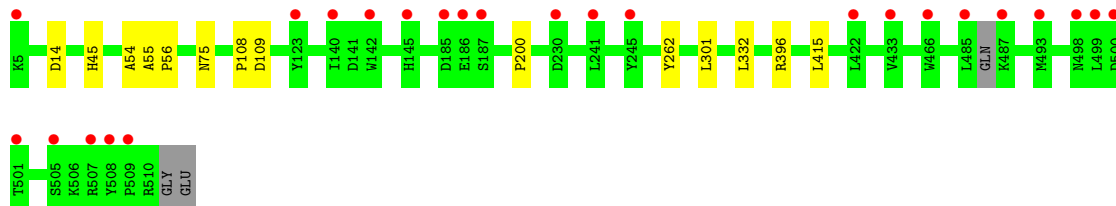
- Molecule 1: Choline-sulfatase



- Molecule 1: Choline-sulfatase



- Molecule 1: Choline-sulfatase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	128.20Å 206.45Å 116.67Å 90.00° 110.28° 90.00°	Depositor
Resolution (Å)	19.98 – 1.98 19.98 – 1.98	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.98-1.98) 99.9 (19.98-1.98)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 1.98Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.171 , 0.200 0.176 , 0.177	Depositor DCC
R_{free} test set	9884 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	32093	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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: DDZ, SO4, MG

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	0.24	0/4154	0.47	0/5659
1	B	0.28	0/4122	0.47	0/5622
1	C	0.25	0/4130	0.46	1/5630 (0.0%)
1	D	0.20	0/4083	0.40	0/5572
All	All	0.24	0/16489	0.45	1/22483 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	367	VAL	O-C-N	5.34	123.84	120.42

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	4048	3834	3833	7	0
1	B	3997	3761	3739	17	0
1	C	4024	3802	3800	10	0
1	D	3974	3718	3714	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	25	0	0	0	0
3	B	30	0	0	0	0
3	C	10	0	0	0	0
3	D	5	0	0	0	0
4	A	243	0	0	0	0
4	B	270	0	0	0	0
4	C	209	0	0	0	0
4	D	139	0	0	0	0
All	All	16978	15115	15086	39	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 1.

All (39) 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:243:CYS:HB2	1:B:245[B]:TYR:CE1	2.16	0.81
1:B:243:CYS:HB2	1:B:245[B]:TYR:CD1	2.28	0.68
1:B:361:THR:HG22	1:B:363:GLY:H	1.65	0.61
1:B:108:PRO:HG3	1:D:109:ASP:HB2	1.91	0.53
1:B:240:MET:O	1:B:245[B]:TYR:CD1	2.61	0.53
1:B:240:MET:HA	1:B:245[B]:TYR:CE1	2.45	0.51
1:B:240:MET:HA	1:B:245[B]:TYR:CD1	2.46	0.50
1:D:396:ARG:CZ	1:D:415:LEU:HD12	2.42	0.49
1:C:378:PRO:HG3	1:C:444:MET:HE1	1.96	0.48
1:A:108:PRO:HG3	1:C:109:ASP:HB2	1.95	0.47
1:B:243:CYS:HB2	1:B:245[B]:TYR:HE1	1.75	0.47
1:C:466:TRP:HA	1:C:466:TRP:CE3	2.52	0.45
1:B:177:TYR:OH	1:B:282:ARG:NH2	2.45	0.45
1:B:109:ASP:HB2	1:D:108:PRO:HG3	1.98	0.45
1:B:108:PRO:HG2	1:D:108:PRO:HG2	1.99	0.45
1:D:262:TYR:CE2	1:D:301:LEU:HD11	2.51	0.45
1:C:396:ARG:CZ	1:C:415:LEU:HD12	2.48	0.44
1:A:292:LEU:HG	1:A:323:ILE:HG12	2.00	0.44
1:D:55:ALA:HB3	1:D:75:ASN:HA	2.00	0.43
1:B:243:CYS:SG	1:B:245[B]:TYR:HE1	2.42	0.43
1:A:379:VAL:HB	1:A:396:ARG:HB3	2.01	0.43
1:A:55:ALA:HB3	1:A:56:PRO:HD3	2.01	0.42
1:D:45:HIS:HB2	1:D:332:LEU:HD11	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:PRO:HD3	1:B:361:THR:HG21	2.00	0.42
1:C:252:GLU:O	1:C:256:ARG:HG3	2.20	0.42
1:B:147:LEU:HD11	1:B:245[B]:TYR:CG	2.55	0.42
1:C:303:GLU:HG2	1:C:304:ARG:HG3	2.02	0.42
1:C:365:SER:OG	1:C:367:VAL:HG23	2.20	0.42
1:C:508:TYR:HA	1:C:509:PRO:C	2.44	0.42
1:B:508:TYR:HA	1:B:509:PRO:C	2.45	0.41
1:C:15:GLN:HG2	1:C:299:ASP:HB2	2.02	0.41
1:D:55:ALA:HB3	1:D:56:PRO:HD3	2.01	0.41
1:B:379:VAL:HB	1:B:396:ARG:HB3	2.01	0.41
1:A:201:HIS:ND1	1:A:202:ASP:O	2.54	0.41
1:A:262:TYR:CE1	1:A:301:LEU:HD11	2.56	0.41
1:C:55:ALA:HB3	1:C:75:ASN:HA	2.03	0.41
1:D:14:ASP:O	1:D:200:PRO:HD2	2.22	0.40
1:A:202:ASP:HA	1:A:203:PRO:C	2.47	0.40

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	505/508 (99%)	492 (97%)	13 (3%)	0	100	100
1	B	503/508 (99%)	486 (97%)	16 (3%)	1 (0%)	43	35
1	C	503/508 (99%)	491 (98%)	10 (2%)	2 (0%)	30	20
1	D	502/508 (99%)	486 (97%)	16 (3%)	0	100	100
All	All	2013/2032 (99%)	1955 (97%)	55 (3%)	3 (0%)	48	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	23	ASP
1	B	308	PHE
1	C	308	PHE

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	419/432 (97%)	419 (100%)	0	100	100
1	B	408/432 (94%)	408 (100%)	0	100	100
1	C	415/432 (96%)	415 (100%)	0	100	100
1	D	403/432 (93%)	403 (100%)	0	100	100
All	All	1645/1728 (95%)	1645 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	A	219	HIS
1	A	411	GLN
1	B	30	HIS
1	B	178	GLN
1	B	219	HIS
1	B	411	GLN
1	B	483	GLN
1	C	46	ASN
1	C	178	GLN
1	D	183	ASN
1	D	247	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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
1	DDZ	D	54	1,2	4,6,7	0.70	0	3,7,9	2.11	1 (33%)
1	DDZ	B	54	1,2	4,6,7	0.74	0	3,7,9	2.51	1 (33%)
1	DDZ	A	54	1,2	4,6,7	0.74	0	3,7,9	2.60	1 (33%)
1	DDZ	C	54	1,2	4,6,7	0.72	0	3,7,9	2.67	1 (33%)

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
1	DDZ	D	54	1,2	-	0/2/6/8	-
1	DDZ	B	54	1,2	-	0/2/6/8	-
1	DDZ	A	54	1,2	-	0/2/6/8	-
1	DDZ	C	54	1,2	-	0/2/6/8	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	54	DDZ	OG2-CB-OG1	-4.53	103.44	111.26
1	A	54	DDZ	OG2-CB-OG1	-4.49	103.52	111.26
1	B	54	DDZ	OG2-CB-OG1	-4.29	103.86	111.26
1	D	54	DDZ	OG2-CB-OG1	-3.64	104.98	111.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 4 are monoatomic - leaving 14 for Mogul analysis.

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	$\# Z > 2$
3	SO4	B	1002	-	4,4,4	0.24	0	6,6,6	0.10	0
3	SO4	B	1006	-	4,4,4	0.26	0	6,6,6	0.07	0
3	SO4	B	1007	-	4,4,4	0.25	0	6,6,6	0.14	0
3	SO4	C	1002	-	4,4,4	0.28	0	6,6,6	0.09	0
3	SO4	B	1003	-	4,4,4	0.25	0	6,6,6	0.23	0
3	SO4	A	1006	-	4,4,4	0.23	0	6,6,6	0.13	0
3	SO4	A	1003	-	4,4,4	0.28	0	6,6,6	0.11	0
3	SO4	A	1002	-	4,4,4	0.25	0	6,6,6	0.09	0
3	SO4	A	1005	-	4,4,4	0.25	0	6,6,6	0.08	0
3	SO4	B	1004	-	4,4,4	0.24	0	6,6,6	0.15	0
3	SO4	C	1003	-	4,4,4	0.20	0	6,6,6	0.17	0
3	SO4	D	1002	-	4,4,4	0.20	0	6,6,6	0.12	0
3	SO4	B	1005	-	4,4,4	0.22	0	6,6,6	0.21	0
3	SO4	A	1004	-	4,4,4	0.27	0	6,6,6	0.18	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 ⓘ

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, 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	507/508 (99%)	-0.43	7 (1%) 73 81	26, 38, 66, 92	0
1	B	502/508 (98%)	-0.25	31 (6%) 26 35	15, 36, 78, 189	2 (0%)
1	C	505/508 (99%)	-0.34	9 (1%) 67 76	28, 42, 68, 104	0
1	D	504/508 (99%)	0.15	25 (4%) 34 44	32, 51, 85, 152	1 (0%)
All	All	2018/2032 (99%)	-0.22	72 (3%) 46 56	15, 42, 76, 189	3 (0%)

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	499	LEU	7.3
1	B	497	MET	6.4
1	B	498	ASN	6.4
1	B	245[A]	TYR	6.2
1	D	485	LEU	6.1
1	B	183	ASN	5.9
1	B	501	THR	5.6
1	D	499	LEU	5.4
1	B	485	LEU	5.3
1	B	508	TYR	5.3
1	B	500	ASP	5.2
1	D	500	ASP	5.1
1	B	504	GLU	5.0
1	B	144	TYR	4.4
1	D	498	ASN	4.3
1	D	487	LYS	4.0
1	B	509	PRO	4.0
1	C	498	ASN	4.0
1	D	187	SER	4.0
1	D	501	THR	3.9
1	D	185	ASP	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	507	ARG	3.8
1	B	502	LEU	3.6
1	D	140	ILE	3.6
1	B	143	TRP	3.4
1	A	498	ASN	3.4
1	B	145	HIS	3.2
1	D	123	TYR	3.1
1	C	485	LEU	3.1
1	C	499	LEU	3.1
1	D	508	TYR	3.1
1	D	230	ASP	3.1
1	D	493	MET	3.1
1	B	185	ASP	3.0
1	B	492	TYR	3.0
1	B	493	MET	3.0
1	A	500	ASP	2.9
1	C	500	ASP	2.9
1	B	186	GLU	2.9
1	B	242	SER	2.8
1	B	243	CYS	2.8
1	D	433	VAL	2.8
1	D	241	LEU	2.8
1	A	511	GLY	2.7
1	B	129	TRP	2.7
1	B	503	GLU	2.7
1	D	5	LYS	2.6
1	A	486	GLN	2.6
1	C	486	GLN	2.6
1	D	186	GLU	2.6
1	D	245[A]	TYR	2.5
1	D	142	TRP	2.5
1	C	188	ARG	2.5
1	D	145	HIS	2.5
1	B	182	GLU	2.4
1	B	140	ILE	2.4
1	A	485	LEU	2.3
1	D	466	TRP	2.3
1	C	493	MET	2.3
1	D	505	SER	2.3
1	B	507	ARG	2.3
1	B	187	SER	2.2
1	C	216	ASP	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	495	ASN	2.1
1	A	499	LEU	2.1
1	C	508	TYR	2.1
1	B	184	ASP	2.1
1	B	142	TRP	2.1
1	D	422	LEU	2.1
1	D	509	PRO	2.1
1	A	466	TRP	2.1
1	B	506	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	DDZ	A	54	7/8	0.94	0.06	24,29,39,43	0
1	DDZ	C	54	7/8	0.94	0.06	27,37,48,48	0
1	DDZ	D	54	7/8	0.94	0.07	34,47,56,66	0
1	DDZ	B	54	7/8	0.95	0.07	22,30,42,45	0

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(Å ²)	Q<0.9
3	SO4	B	1004	5/5	0.77	0.13	37,61,73,75	0
3	SO4	C	1002	5/5	0.77	0.10	55,70,76,76	0
3	SO4	A	1004	5/5	0.85	0.14	48,56,69,70	0
3	SO4	A	1005	5/5	0.85	0.09	69,69,69,70	0
2	MG	C	1001	1/1	0.90	0.14	54,54,54,54	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	C	1003	5/5	0.90	0.16	46,50,56,60	5
3	SO4	B	1002	5/5	0.91	0.10	47,49,59,64	0
2	MG	B	1001	1/1	0.91	0.14	45,45,45,45	0
3	SO4	A	1002	5/5	0.92	0.07	58,67,67,69	0
3	SO4	A	1003	5/5	0.92	0.08	61,64,70,71	0
3	SO4	B	1006	5/5	0.92	0.07	56,67,75,76	0
2	MG	A	1001	1/1	0.92	0.07	51,51,51,51	0
2	MG	D	1001	1/1	0.92	0.10	51,51,51,51	0
3	SO4	D	1002	5/5	0.92	0.12	38,44,52,53	5
3	SO4	B	1003	5/5	0.93	0.17	44,53,67,69	0
3	SO4	B	1007	5/5	0.95	0.09	38,43,48,53	5
3	SO4	A	1006	5/5	0.95	0.10	45,49,59,59	5
3	SO4	B	1005	5/5	1.00	0.03	28,31,34,40	5

6.5 Other polymers [i](#)

There are no such residues in this entry.