wwPDB X-ray Structure Validation Summary Report (i)

Mar 8, 2026 – 04:53 PM UTC

PDB ID	:	8WBS / pdb_00008wbs
Title	:	Crystal structure of cis-Epoxysuccinate Hydrolases KlCESH[L]-D48N complexed with sulfate ions
Authors	:	Dong, S.; Xuan, J.S.; Feng, Y.G.; Cui, Q.
Deposited on	:	2023-09-10
Resolution	:	2.03 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 (i)) were used in the production of this report:

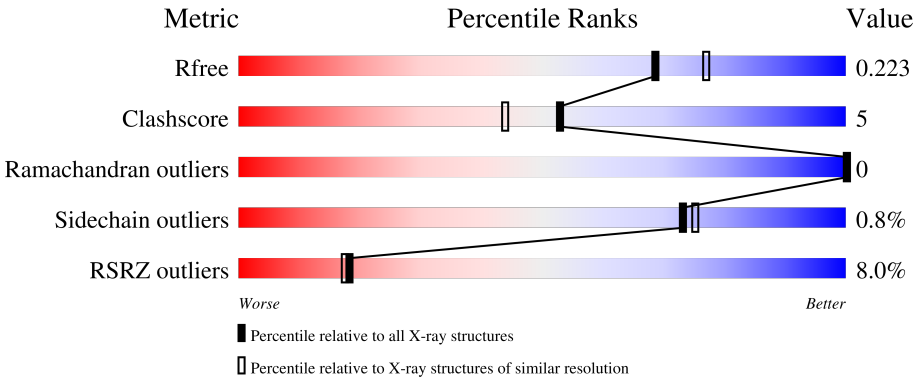
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)

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	243	2% 91% 6%
1	B	243	2% 91% 6%
1	C	243	12% 86% 11%
1	D	243	15% 73% 17% 9%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	D	301	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7748 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 (S)-2-haloacid dehalogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	236	Total	C	N	O	S	0	0	0
			1865	1193	321	345	6			
1	B	236	Total	C	N	O	S	0	0	0
			1865	1193	321	345	6			
1	C	237	Total	C	N	O	S	0	0	0
			1866	1194	321	346	5			
1	D	221	Total	C	N	O	S	0	0	0
			1753	1124	296	328	5			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	40	MET	-	initiating methionine	UNP W8PFD2
A	48	ASN	ASP	engineered mutation	UNP W8PFD2
A	275	LEU	-	expression tag	UNP W8PFD2
A	276	GLU	-	expression tag	UNP W8PFD2
A	277	HIS	-	expression tag	UNP W8PFD2
A	278	HIS	-	expression tag	UNP W8PFD2
A	279	HIS	-	expression tag	UNP W8PFD2
A	280	HIS	-	expression tag	UNP W8PFD2
A	281	HIS	-	expression tag	UNP W8PFD2
A	282	HIS	-	expression tag	UNP W8PFD2
B	40	MET	-	initiating methionine	UNP W8PFD2
B	48	ASN	ASP	engineered mutation	UNP W8PFD2
B	275	LEU	-	expression tag	UNP W8PFD2
B	276	GLU	-	expression tag	UNP W8PFD2
B	277	HIS	-	expression tag	UNP W8PFD2
B	278	HIS	-	expression tag	UNP W8PFD2
B	279	HIS	-	expression tag	UNP W8PFD2
B	280	HIS	-	expression tag	UNP W8PFD2
B	281	HIS	-	expression tag	UNP W8PFD2
B	282	HIS	-	expression tag	UNP W8PFD2
C	40	MET	-	initiating methionine	UNP W8PFD2

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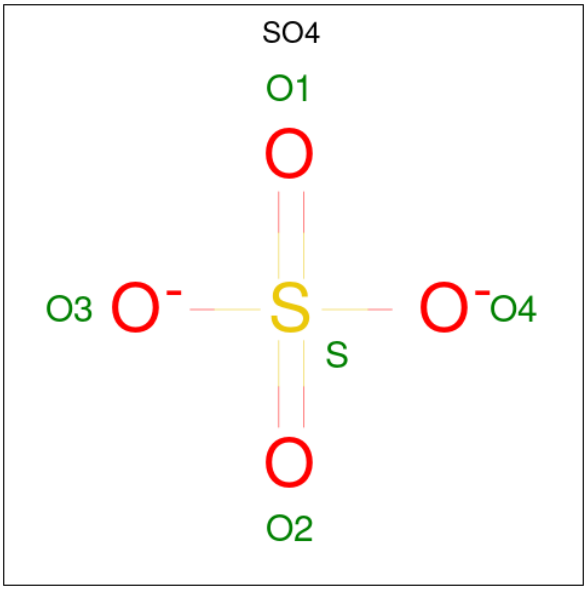
Chain	Residue	Modelled	Actual	Comment	Reference
C	48	ASN	ASP	engineered mutation	UNP W8PFD2
C	275	LEU	-	expression tag	UNP W8PFD2
C	276	GLU	-	expression tag	UNP W8PFD2
C	277	HIS	-	expression tag	UNP W8PFD2
C	278	HIS	-	expression tag	UNP W8PFD2
C	279	HIS	-	expression tag	UNP W8PFD2
C	280	HIS	-	expression tag	UNP W8PFD2
C	281	HIS	-	expression tag	UNP W8PFD2
C	282	HIS	-	expression tag	UNP W8PFD2
D	40	MET	-	initiating methionine	UNP W8PFD2
D	48	ASN	ASP	engineered mutation	UNP W8PFD2
D	275	LEU	-	expression tag	UNP W8PFD2
D	276	GLU	-	expression tag	UNP W8PFD2
D	277	HIS	-	expression tag	UNP W8PFD2
D	278	HIS	-	expression tag	UNP W8PFD2
D	279	HIS	-	expression tag	UNP W8PFD2
D	280	HIS	-	expression tag	UNP W8PFD2
D	281	HIS	-	expression tag	UNP W8PFD2
D	282	HIS	-	expression tag	UNP W8PFD2

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

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

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0
3	C	1	Total Ca 1 1	0	0

- Molecule 4 is water.

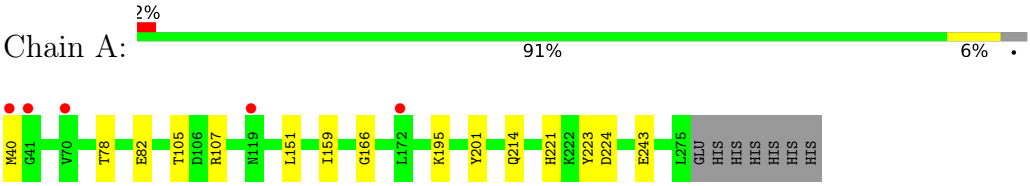
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	141	Total O 141 141	0	0
4	B	129	Total O 129 129	0	0
4	C	68	Total O 68 68	0	0
4	D	19	Total O 19 19	0	0

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.

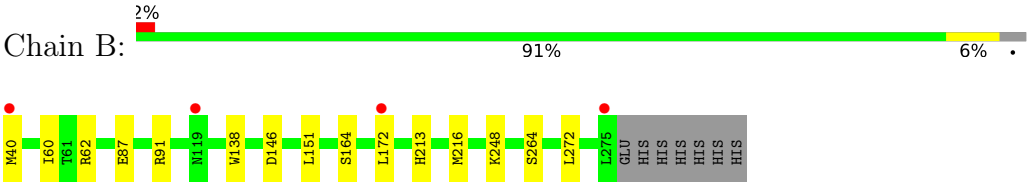
• Molecule 1: (S)-2-haloacid dehalogenase

Chain A:



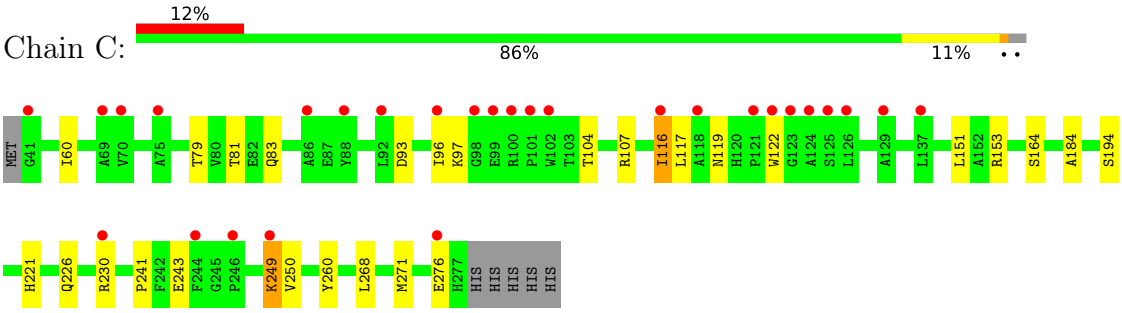
• Molecule 1: (S)-2-haloacid dehalogenase

Chain B:



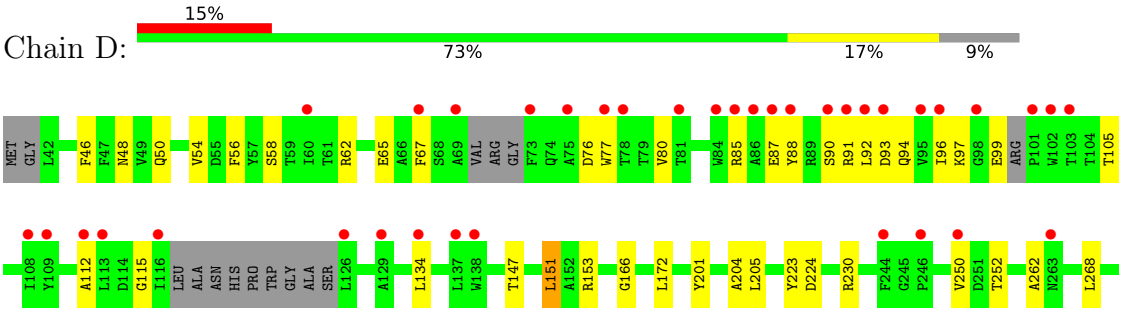
• Molecule 1: (S)-2-haloacid dehalogenase

Chain C:



• Molecule 1: (S)-2-haloacid dehalogenase

Chain D:



M271
L275
GLU
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	119.85Å 94.43Å 99.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.60 – 2.03 76.60 – 2.03	Depositor EDS
% Data completeness (in resolution range)	99.9 (76.60-2.03) 100.0 (76.60-2.03)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.14 (at 2.03Å)	Xtriage
Refinement program	PHENIX v1.21	Depositor
R, R_{free}	0.178 , 0.209 0.192 , 0.223	Depositor DCC
R_{free} test set	3813 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å^2)	36.6	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 59.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7748	wwPDB-VP
Average B, all atoms (Å^2)	54.0	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.*

[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

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, CA

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	0.39	0/1909	0.56	0/2589
1	B	0.35	0/1909	0.54	0/2589
1	C	0.43	0/1911	0.66	2/2594 (0.1%)
1	D	0.22	0/1790	0.46	1/2422 (0.0%)
All	All	0.36	0/7519	0.56	3/10194 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	116	ILE	N-CA-C	-14.21	100.21	113.71
1	C	119	ASN	N-CA-C	-10.41	98.75	114.16
1	D	92	LEU	N-CA-C	-5.38	105.49	111.36

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	1865	0	1851	8	0
1	B	1865	0	1851	10	0
1	C	1866	0	1840	20	0
1	D	1753	0	1740	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	10	0	0	0	0
2	B	10	0	0	1	0
2	C	10	0	0	1	0
2	D	10	0	0	6	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	141	0	0	0	1
4	B	129	0	0	0	0
4	C	68	0	0	1	1
4	D	19	0	0	1	0
All	All	7748	0	7282	74	1

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 5.

The worst 5 of 74 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:87:GLU:HA	1:D:90:SER:HB3	1.49	0.94
1:D:153:ARG:NH2	4:D:401:HOH:O	2.09	0.84
1:D:48:ASN:ND2	2:D:301:SO4:O3	2.25	0.69
1:D:93:ASP:HB3	1:D:97:LYS:HZ1	1.58	0.68
1:D:58:SER:O	1:D:62:ARG:HG2	1.93	0.67

All (1) 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)
4:A:470:HOH:O	4:C:461:HOH:O[3_555]	2.12	0.08

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	234/243 (96%)	232 (99%)	2 (1%)	0	100	100
1	B	234/243 (96%)	231 (99%)	3 (1%)	0	100	100
1	C	235/243 (97%)	232 (99%)	3 (1%)	0	100	100
1	D	213/243 (88%)	203 (95%)	10 (5%)	0	100	100
All	All	916/972 (94%)	898 (98%)	18 (2%)	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	195/202 (96%)	194 (100%)	1 (0%)	81	81
1	B	195/202 (96%)	194 (100%)	1 (0%)	81	81
1	C	194/202 (96%)	191 (98%)	3 (2%)	57	59
1	D	185/202 (92%)	184 (100%)	1 (0%)	81	81
All	All	769/808 (95%)	763 (99%)	6 (1%)	73	75

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	151	LEU
1	C	249	LYS
1	D	151	LEU
1	B	151	LEU
1	A	151	LEU

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	94	GLN
1	D	256	GLN
1	A	263	ASN

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Mol	Chain	Res	Type
1	C	83	GLN
1	C	120	HIS

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)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
2	SO4	C	301	-	4,4,4	0.28	0	6,6,6	0.24	0
2	SO4	B	302	-	4,4,4	0.27	0	6,6,6	0.29	0
2	SO4	C	302	-	4,4,4	0.25	0	6,6,6	0.21	0
2	SO4	A	301	-	4,4,4	0.43	0	6,6,6	0.48	0
2	SO4	D	301	-	4,4,4	0.25	0	6,6,6	0.09	0
2	SO4	D	302	-	4,4,4	0.28	0	6,6,6	0.14	0
2	SO4	B	301	-	4,4,4	0.36	0	6,6,6	0.97	0
2	SO4	A	302	-	4,4,4	0.30	0	6,6,6	0.14	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.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	SO4	1	0
2	D	301	SO4	5	0
2	D	302	SO4	1	0
2	B	301	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

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	236/243 (97%)	-0.09	5 (2%)	63	63	25, 35, 61, 76	0
1	B	236/243 (97%)	-0.10	4 (1%)	69	69	25, 37, 59, 73	0
1	C	237/243 (97%)	0.63	28 (11%)	9	8	28, 54, 103, 122	0
1	D	221/243 (90%)	1.16	37 (16%)	4	4	38, 72, 141, 156	0
All	All	930/972 (95%)	0.39	74 (7%)	18	17	25, 46, 116, 156	0

The worst 5 of 74 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	126	LEU	8.3
1	D	92	LEU	6.4
1	D	88	TYR	6.3
1	D	86	ALA	6.1
1	C	124	ALA	5.3

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 oligosaccharides in this entry.

6.4 Ligands

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	B-factors(Å^2)	Q<0.9
2	SO4	A	302	5/5	0.47	0.23	85,88,96,104	0
2	SO4	D	302	5/5	0.60	0.20	96,98,101,104	0
2	SO4	C	302	5/5	0.83	0.15	74,75,78,81	0
3	CA	C	303	1/1	0.84	0.20	70,70,70,70	0
2	SO4	B	301	5/5	0.90	0.14	48,55,57,60	0
2	SO4	D	301	5/5	0.90	0.12	76,79,81,85	0
2	SO4	C	301	5/5	0.93	0.11	47,54,61,67	0
3	CA	A	303	1/1	0.94	0.22	61,61,61,61	0
2	SO4	A	301	5/5	0.96	0.08	32,38,45,52	0
2	SO4	B	302	5/5	0.96	0.10	39,50,53,56	0

6.5 Other polymers (i)

There are no such residues in this entry.