



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:23 PM UTC

PDB ID : 7A0A / pdb_00007a0a
Title : Crystal structure of mouse CSAD in apo form
Authors : Mahootchi, E.; Raasakka, A.; Haavik, J.; Kursula, P.
Deposited on : 2020-08-07
Resolution : 2.80 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

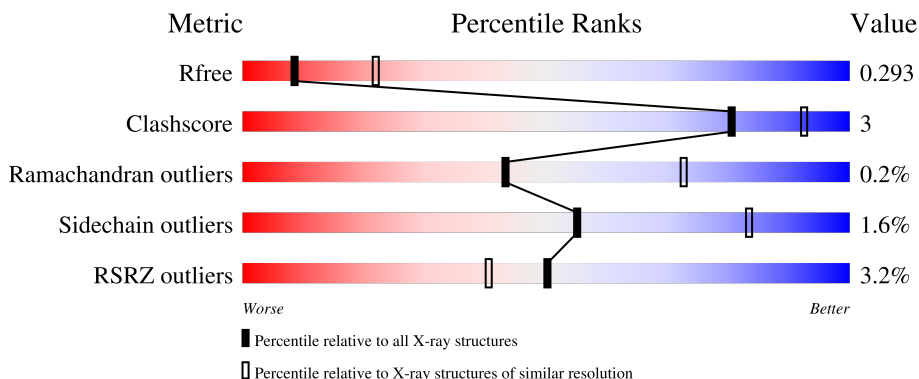
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	521	2% 85% 5% 9%
1	B	521	4% 82% 8% 10%
1	C	521	2% 85% 7% 8%
1	D	521	4% 83% 7% 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 29915 atoms, of which 14975 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 Cysteine sulfinic acid decarboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	474	Total	C	H	N	O	S	0	0	0
			7486	2375	3750	656	684	21			
1	B	470	Total	C	H	N	O	S	0	0	0
			7415	2355	3716	647	676	21			
1	C	478	Total	C	H	N	O	S	0	0	0
			7524	2386	3768	660	689	21			
1	D	473	Total	C	H	N	O	S	0	0	0
			7462	2367	3741	653	680	21			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	initiating methionine	UNP Q9DBE0
A	-26	GLY	-	expression tag	UNP Q9DBE0
A	-25	PRO	-	expression tag	UNP Q9DBE0
A	-24	HIS	-	expression tag	UNP Q9DBE0
A	-23	HIS	-	expression tag	UNP Q9DBE0
A	-22	HIS	-	expression tag	UNP Q9DBE0
A	-21	HIS	-	expression tag	UNP Q9DBE0
A	-20	HIS	-	expression tag	UNP Q9DBE0
A	-19	HIS	-	expression tag	UNP Q9DBE0
A	-18	LEU	-	expression tag	UNP Q9DBE0
A	-17	GLU	-	expression tag	UNP Q9DBE0
A	-16	SER	-	expression tag	UNP Q9DBE0
A	-15	THR	-	expression tag	UNP Q9DBE0
A	-14	SER	-	expression tag	UNP Q9DBE0
A	-13	LEU	-	expression tag	UNP Q9DBE0
A	-12	TYR	-	expression tag	UNP Q9DBE0
A	-11	LYS	-	expression tag	UNP Q9DBE0
A	-10	LYS	-	expression tag	UNP Q9DBE0
A	-9	ALA	-	expression tag	UNP Q9DBE0
A	-8	GLY	-	expression tag	UNP Q9DBE0
A	-7	SER	-	expression tag	UNP Q9DBE0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLU	-	expression tag	UNP Q9DBE0
A	-5	ASN	-	expression tag	UNP Q9DBE0
A	-4	LEU	-	expression tag	UNP Q9DBE0
A	-3	TYR	-	expression tag	UNP Q9DBE0
A	-2	PHE	-	expression tag	UNP Q9DBE0
A	-1	GLN	-	expression tag	UNP Q9DBE0
A	0	GLY	-	expression tag	UNP Q9DBE0
B	-27	MET	-	initiating methionine	UNP Q9DBE0
B	-26	GLY	-	expression tag	UNP Q9DBE0
B	-25	PRO	-	expression tag	UNP Q9DBE0
B	-24	HIS	-	expression tag	UNP Q9DBE0
B	-23	HIS	-	expression tag	UNP Q9DBE0
B	-22	HIS	-	expression tag	UNP Q9DBE0
B	-21	HIS	-	expression tag	UNP Q9DBE0
B	-20	HIS	-	expression tag	UNP Q9DBE0
B	-19	HIS	-	expression tag	UNP Q9DBE0
B	-18	LEU	-	expression tag	UNP Q9DBE0
B	-17	GLU	-	expression tag	UNP Q9DBE0
B	-16	SER	-	expression tag	UNP Q9DBE0
B	-15	THR	-	expression tag	UNP Q9DBE0
B	-14	SER	-	expression tag	UNP Q9DBE0
B	-13	LEU	-	expression tag	UNP Q9DBE0
B	-12	TYR	-	expression tag	UNP Q9DBE0
B	-11	LYS	-	expression tag	UNP Q9DBE0
B	-10	LYS	-	expression tag	UNP Q9DBE0
B	-9	ALA	-	expression tag	UNP Q9DBE0
B	-8	GLY	-	expression tag	UNP Q9DBE0
B	-7	SER	-	expression tag	UNP Q9DBE0
B	-6	GLU	-	expression tag	UNP Q9DBE0
B	-5	ASN	-	expression tag	UNP Q9DBE0
B	-4	LEU	-	expression tag	UNP Q9DBE0
B	-3	TYR	-	expression tag	UNP Q9DBE0
B	-2	PHE	-	expression tag	UNP Q9DBE0
B	-1	GLN	-	expression tag	UNP Q9DBE0
B	0	GLY	-	expression tag	UNP Q9DBE0
C	-27	MET	-	initiating methionine	UNP Q9DBE0
C	-26	GLY	-	expression tag	UNP Q9DBE0
C	-25	PRO	-	expression tag	UNP Q9DBE0
C	-24	HIS	-	expression tag	UNP Q9DBE0
C	-23	HIS	-	expression tag	UNP Q9DBE0
C	-22	HIS	-	expression tag	UNP Q9DBE0
C	-21	HIS	-	expression tag	UNP Q9DBE0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	HIS	-	expression tag	UNP Q9DBE0
C	-19	HIS	-	expression tag	UNP Q9DBE0
C	-18	LEU	-	expression tag	UNP Q9DBE0
C	-17	GLU	-	expression tag	UNP Q9DBE0
C	-16	SER	-	expression tag	UNP Q9DBE0
C	-15	THR	-	expression tag	UNP Q9DBE0
C	-14	SER	-	expression tag	UNP Q9DBE0
C	-13	LEU	-	expression tag	UNP Q9DBE0
C	-12	TYR	-	expression tag	UNP Q9DBE0
C	-11	LYS	-	expression tag	UNP Q9DBE0
C	-10	LYS	-	expression tag	UNP Q9DBE0
C	-9	ALA	-	expression tag	UNP Q9DBE0
C	-8	GLY	-	expression tag	UNP Q9DBE0
C	-7	SER	-	expression tag	UNP Q9DBE0
C	-6	GLU	-	expression tag	UNP Q9DBE0
C	-5	ASN	-	expression tag	UNP Q9DBE0
C	-4	LEU	-	expression tag	UNP Q9DBE0
C	-3	TYR	-	expression tag	UNP Q9DBE0
C	-2	PHE	-	expression tag	UNP Q9DBE0
C	-1	GLN	-	expression tag	UNP Q9DBE0
C	0	GLY	-	expression tag	UNP Q9DBE0
D	-27	MET	-	initiating methionine	UNP Q9DBE0
D	-26	GLY	-	expression tag	UNP Q9DBE0
D	-25	PRO	-	expression tag	UNP Q9DBE0
D	-24	HIS	-	expression tag	UNP Q9DBE0
D	-23	HIS	-	expression tag	UNP Q9DBE0
D	-22	HIS	-	expression tag	UNP Q9DBE0
D	-21	HIS	-	expression tag	UNP Q9DBE0
D	-20	HIS	-	expression tag	UNP Q9DBE0
D	-19	HIS	-	expression tag	UNP Q9DBE0
D	-18	LEU	-	expression tag	UNP Q9DBE0
D	-17	GLU	-	expression tag	UNP Q9DBE0
D	-16	SER	-	expression tag	UNP Q9DBE0
D	-15	THR	-	expression tag	UNP Q9DBE0
D	-14	SER	-	expression tag	UNP Q9DBE0
D	-13	LEU	-	expression tag	UNP Q9DBE0
D	-12	TYR	-	expression tag	UNP Q9DBE0
D	-11	LYS	-	expression tag	UNP Q9DBE0
D	-10	LYS	-	expression tag	UNP Q9DBE0
D	-9	ALA	-	expression tag	UNP Q9DBE0
D	-8	GLY	-	expression tag	UNP Q9DBE0
D	-7	SER	-	expression tag	UNP Q9DBE0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	GLU	-	expression tag	UNP Q9DBE0
D	-5	ASN	-	expression tag	UNP Q9DBE0
D	-4	LEU	-	expression tag	UNP Q9DBE0
D	-3	TYR	-	expression tag	UNP Q9DBE0
D	-2	PHE	-	expression tag	UNP Q9DBE0
D	-1	GLN	-	expression tag	UNP Q9DBE0
D	0	GLY	-	expression tag	UNP Q9DBE0

- 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		

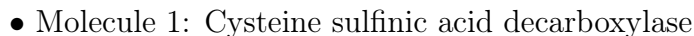
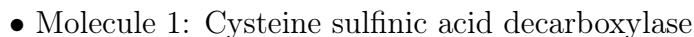
- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

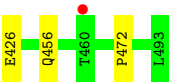
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		
3	C	1	Total	Na	0	0
			1	1		
3	D	1	Total	Na	0	0
			1	1		

- Molecule 4 is water.

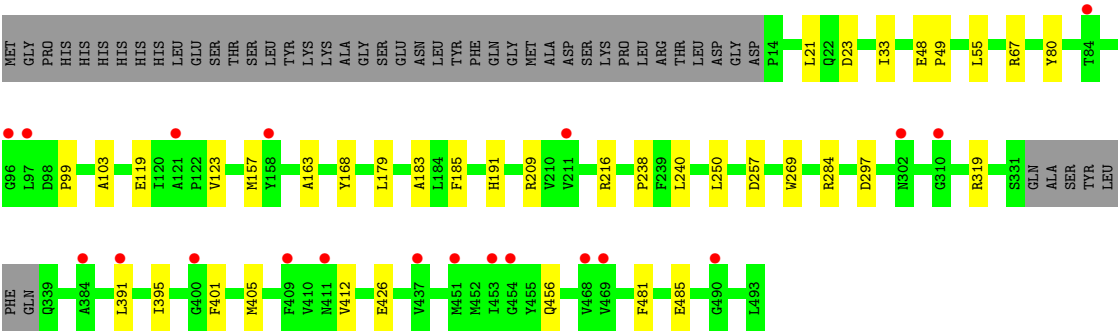
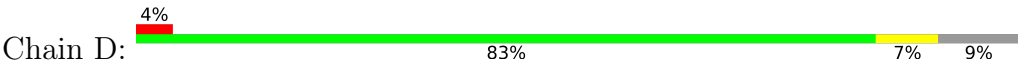
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total 5	O 5	0	0
4	B	4	Total 4	O 4	0	0
4	C	9	Total 9	O 9	0	0
4	D	2	Total 2	O 2	0	0

- Molecule 1: Cysteine sulfinic acid decarboxylase





● Molecule 1: Cysteine sulfinic acid decarboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.06Å 114.88Å 113.76Å 90.00° 95.80° 90.00°	Depositor
Resolution (Å)	47.02 – 2.80 47.02 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.4 (47.02-2.80) 79.0 (47.02-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.43	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.42 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.18rc7_3834	Depositor
R, R_{free}	0.243 , 0.292 0.244 , 0.293	Depositor DCC
R_{free} test set	2000 reflections (4.40%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.781	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	29915	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.74% 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, NA

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	0.16	0/3811	0.37	0/5149
1	B	0.17	0/3774	0.38	0/5100
1	C	0.17	0/3832	0.36	0/5179
1	D	0.16	0/3797	0.36	0/5131
All	All	0.16	0/15214	0.37	0/20559

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	311	LEU	Peptide

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	3736	3750	3748	19	0
1	B	3699	3716	3715	26	0
1	C	3756	3768	3767	24	0
1	D	3721	3741	3740	26	0
2	A	5	0	0	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	5	0	0	0	0
4	B	4	0	0	0	0
4	C	9	0	0	0	0
4	D	2	0	0	0	0
All	All	14940	14975	14970	79	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 3.

The worst 5 of 79 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:297:ASP:OD1	1:D:319:ARG:NH2	2.05	0.88
1:B:88:ARG:HD3	1:B:450:THR:O	1.79	0.82
1:C:225:GLU:OE1	1:C:266:HIS:NE2	2.13	0.82
1:B:39:ALA:O	1:B:88:ARG:NH2	2.20	0.74
1:B:21:LEU:HD13	1:D:33:ILE:HD13	1.76	0.67

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	468/521 (90%)	448 (96%)	20 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	464/521 (89%)	444 (96%)	17 (4%)	3 (1%)	21	51
1	C	474/521 (91%)	453 (96%)	21 (4%)	0	100	100
1	D	469/521 (90%)	448 (96%)	21 (4%)	0	100	100
All	All	1875/2084 (90%)	1793 (96%)	79 (4%)	3 (0%)	43	72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	311	LEU
1	B	312	GLN
1	B	463	ASN

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	401/440 (91%)	395 (98%)	6 (2%)	57	84
1	B	397/440 (90%)	389 (98%)	8 (2%)	48	80
1	C	402/440 (91%)	396 (98%)	6 (2%)	57	84
1	D	399/440 (91%)	394 (99%)	5 (1%)	61	86
All	All	1599/1760 (91%)	1574 (98%)	25 (2%)	55	83

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	191	HIS
1	C	332	GLN
1	D	456	GLN
1	C	284	ARG
1	C	426	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	383	GLN
1	B	411	ASN
1	D	92	GLN
1	C	286	HIS
1	D	22	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	A	501	-	4,4,4	0.24	0	6,6,6	0.12	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	474/521 (90%)	0.63	9 (1%) 66 57	40, 59, 80, 106	0
1	B	470/521 (90%)	0.82	20 (4%) 40 31	47, 70, 90, 104	0
1	C	478/521 (91%)	0.69	11 (2%) 61 51	43, 60, 83, 98	0
1	D	473/521 (90%)	0.86	20 (4%) 40 32	48, 70, 90, 108	0
All	All	1895/2084 (90%)	0.75	60 (3%) 50 40	40, 65, 86, 108	0

The worst 5 of 60 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	469	VAL	4.0
1	A	469	VAL	4.0
1	D	451	MET	3.0
1	B	97	LEU	2.8
1	B	207	SER	2.8

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
3	NA	C	501	1/1	0.74	0.21	50,50,50,50	0
3	NA	D	501	1/1	0.77	0.32	55,55,55,55	0
2	SO4	A	501	5/5	0.79	0.13	65,75,88,99	0
3	NA	A	502	1/1	0.88	0.08	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.