



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 08:42 PM UTC

PDB ID : 4OY4 / pdb_00004oy4
Title : calcium-free CaMPARI v0.2
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Deposited on : 2014-02-10
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 ⓘ 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

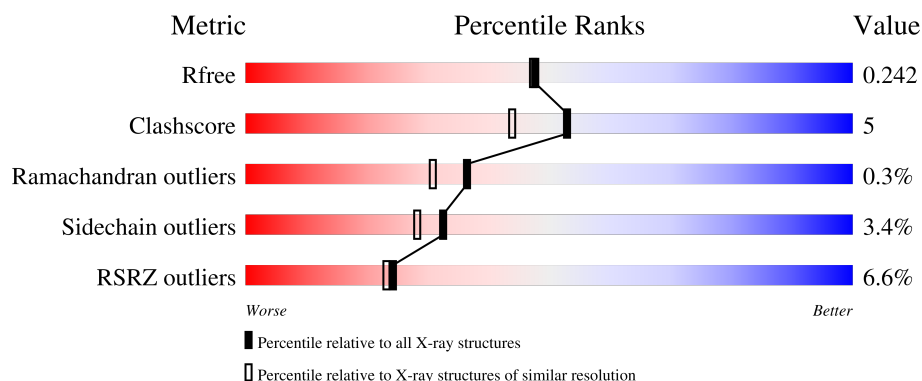
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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 $\leq 5\%$. 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	413	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2870 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 Chimera protein of Calmodulin, GPF-like protein EosFP, and Myosin light chain kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	2	3	0
			2744	1742	461	519	22			

There are 46 discrepancies between the modelled and reference sequences:

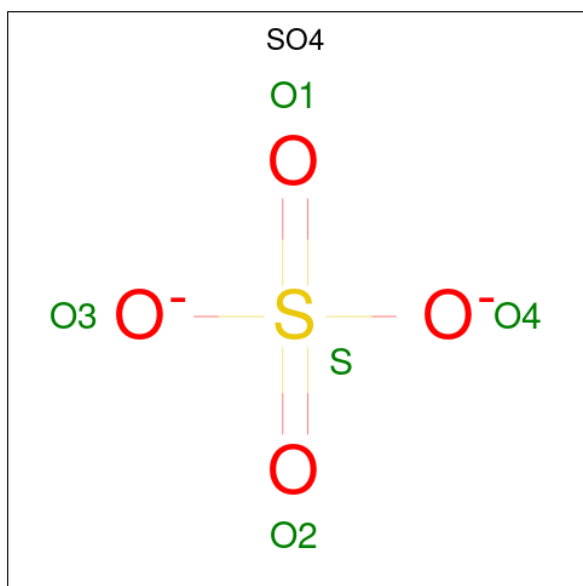
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	expression tag	UNP P62161
A	-7	HIS	-	expression tag	UNP P62161
A	-6	HIS	-	expression tag	UNP P62161
A	-5	HIS	-	expression tag	UNP P62161
A	-4	HIS	-	expression tag	UNP P62161
A	-3	HIS	-	expression tag	UNP P62161
A	-2	HIS	-	expression tag	UNP P62161
A	-1	GLY	-	expression tag	UNP P62161
A	0	SER	-	expression tag	UNP P62161
A	59	ASP	ASN	engineered mutation	UNP P62161
A	146	ALA	-	linker	UNP P62161
A	147	LYS	-	linker	UNP P62161
A	148	LEU	-	linker	UNP P62161
A	149	GLU	-	linker	UNP P62161
A	150	CYS	-	linker	UNP P62161
A	165	HIS	THR	engineered mutation	UNP Q5S6Z9
A	232	ARG	-	linker	UNP Q5S6Z9
A	233	ARG	-	linker	UNP Q5S6Z9
A	234	GLY	-	linker	UNP Q5S6Z9
A	235	GLY	-	linker	UNP Q5S6Z9
A	236	THR	-	linker	UNP Q5S6Z9
A	237	GLY	-	linker	UNP Q5S6Z9
A	238	GLY	-	linker	UNP Q5S6Z9
A	239	SER	-	linker	UNP Q5S6Z9
A	240	MET	-	linker	UNP Q5S6Z9
A	241	VAL	-	linker	UNP Q5S6Z9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	251	LYS	ASN	engineered mutation	UNP Q5S6Z9
A	274	TYR	PHE	engineered mutation	UNP Q5S6Z9
A	279	THR	SER	engineered mutation	UNP Q5S6Z9
A	303	CR8	HIS	chromophore	UNP Q5S6Z9
A	303	CR8	TYR	chromophore	UNP Q5S6Z9
A	303	CR8	GLY	chromophore	UNP Q5S6Z9
A	309	VAL	ALA	engineered mutation	UNP Q5S6Z9
A	310	LYS	GLU	engineered mutation	UNP Q5S6Z9
A	314	ASN	HIS	engineered mutation	UNP Q5S6Z9
A	333	MET	LEU	engineered mutation	UNP Q5S6Z9
A	342	TYR	ILE	engineered mutation	UNP Q5S6Z9
A	361	TYR	HIS	engineered mutation	UNP Q5S6Z9
A	363	THR	VAL	engineered mutation	UNP Q5S6Z9
A	380	MET	GLU	engineered mutation	UNP Q5S6Z9
A	383	TRP	-	linker	UNP Q5S6Z9
A	384	THR	-	linker	UNP Q5S6Z9
A	385	ARG	-	linker	UNP Q5S6Z9
A	386	SER	-	linker	UNP Q5S6Z9
A	387	SER	-	linker	UNP Q5S6Z9
A	392	ASN	GLN	engineered mutation	UNP Q6LDG3

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



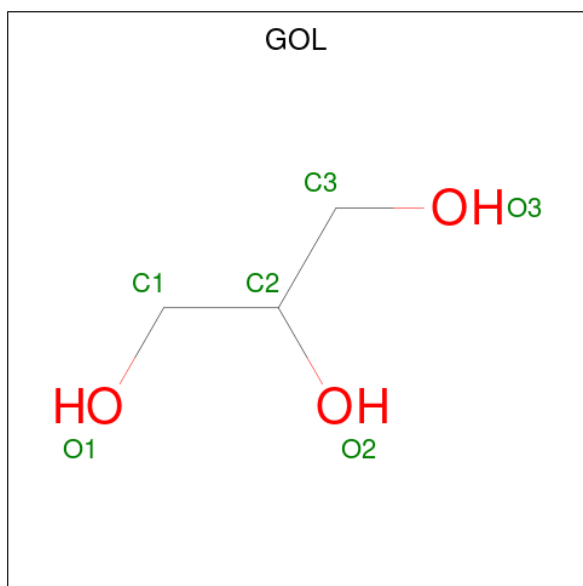
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		

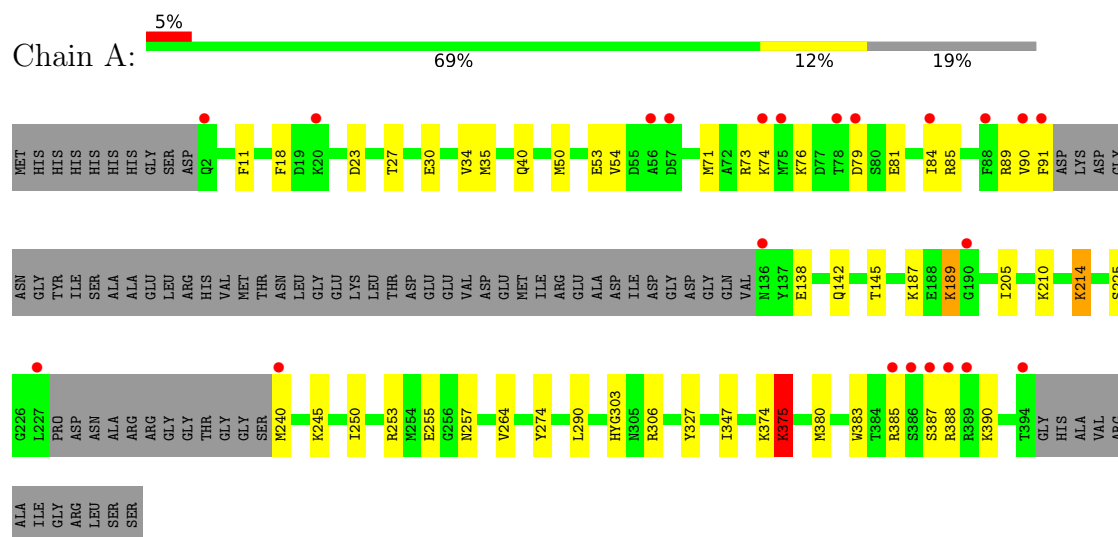
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	104	Total	O	0	0
			104	104		

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: Chimera protein of Calmodulin, GPF-like protein EosFP, and Myosin light chain kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	68.67Å 68.67Å 172.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.75 – 2.03 53.75 – 2.03	Depositor EDS
% Data completeness (in resolution range)	99.9 (53.75-2.03) 99.9 (53.75-2.03)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.33 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.196 , 0.235 0.205 , 0.242	Depositor DCC
R_{free} test set	1389 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	26.5	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 33.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2870	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CR8, 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	1.30	5/2788 (0.2%)	1.16	8/3744 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	214	LYS	CD-CE	-23.11	0.83	1.52
1	A	205	ILE	C-O	-6.94	1.16	1.24
1	A	290	LEU	CA-C	-5.98	1.47	1.53
1	A	257	ASN	N-CA	-5.80	1.39	1.46
1	A	264	VAL	C-O	5.09	1.29	1.24

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	214	LYS	CG-CD-CE	11.30	137.28	111.30
1	A	23	ASP	N-CA-CB	-6.70	100.80	110.65
1	A	189	LYS	N-CA-C	6.52	118.93	111.11
1	A	214	LYS	CD-CE-NZ	-5.32	94.88	111.90
1	A	375	LYS	CB-CA-C	-5.19	102.38	110.94

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	2744	0	2640	27	0
2	A	10	0	0	0	0
3	A	12	0	16	0	0
4	A	104	0	0	2	0
All	All	2870	0	2656	27	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 5.

The worst 5 of 27 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:A:35[A]:MET:HE1	1:A:50:MET:HE1	1.61	0.81
1:A:50:MET:HE2	1:A:74:LYS:HE3	1.68	0.76
1:A:73:ARG:NH2	1:A:225:SER:O	2.28	0.66
1:A:253[A]:ARG:NH1	1:A:255:GLU:OE2	2.26	0.63
1:A:50:MET:HE2	1:A:74:LYS:CE	2.28	0.62

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	329/413 (80%)	324 (98%)	4 (1%)	1 (0%)	36 31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	90	VAL

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	294/351 (84%)	284 (97%)	10 (3%)	32	28

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	385	ARG
1	A	387	SER
1	A	388	ARG
1	A	210	LYS
1	A	214	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	CR8	A	303	1	25,27,28	1.89	6 (24%)	24,37,39	1.95	10 (41%)

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	CR8	A	303	1	-	4/12/25/26	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	303	CR8	C4-C11	-4.30	1.35	1.46
1	A	303	CR8	O13-C11	4.13	1.37	1.24
1	A	303	CR8	CA3-N3	-3.96	1.39	1.47
1	A	303	CR8	O3-C3	3.34	1.39	1.20
1	A	303	CR8	C12-C11	-2.15	1.40	1.46

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	303	CR8	C8-CA2-C2	-3.54	122.09	129.19
1	A	303	CR8	C23-C21-N22	3.43	109.70	105.65
1	A	303	CR8	C4-C5-C7	-3.20	119.07	122.10
1	A	303	CR8	N3-C1-N2	-3.04	109.09	111.48
1	A	303	CR8	CA1-C1-N2	2.71	128.86	123.57

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	303	CR8	CA1-C20-C21-N22
1	A	303	CR8	CA1-C20-C21-C23
1	A	303	CR8	C5-C7-C8-CA2
1	A	303	CR8	C6-C7-C8-CA2

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](#)

4 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	A	501	-	4,4,4	0.54	0	6,6,6	0.50	0
3	GOL	A	503	-	5,5,5	0.90	0	5,5,5	2.34	2 (40%)
3	GOL	A	504	-	5,5,5	0.27	0	5,5,5	0.60	0
2	SO4	A	502	-	4,4,4	0.45	0	6,6,6	0.42	0

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
3	GOL	A	503	-	-	1/4/4/4	-
3	GOL	A	504	-	-	0/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	GOL	O1-C1-C2	3.95	128.17	110.38
3	A	503	GOL	C3-C2-C1	-2.86	101.32	111.80

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	GOL	O1-C1-C2-O2

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	334/413 (80%)	0.23	22 (6%) 24 23	14, 27, 60, 84	4 (1%)

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	56	ALA	5.6
1	A	91	PHE	4.6
1	A	386	SER	4.2
1	A	388	ARG	3.8
1	A	90	VAL	3.5

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	CR8	A	303	25/26	0.97	0.05	15,17,20,20	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
2	SO4	A	502	5/5	0.85	0.08	67,70,74,75	0
2	SO4	A	501	5/5	0.87	0.10	56,67,72,73	0
3	GOL	A	504	6/6	0.88	0.12	43,44,44,44	0
3	GOL	A	503	6/6	0.90	0.12	29,43,49,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.