



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 02:11 PM UTC

PDB ID : 4GUA / pdb_00004gua
Title : Alphavirus P23pro-zbd
Authors : Shin, G.; Yost, S.; Miller, M.; Marcotrigiano, J.
Deposited on : 2012-08-29
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

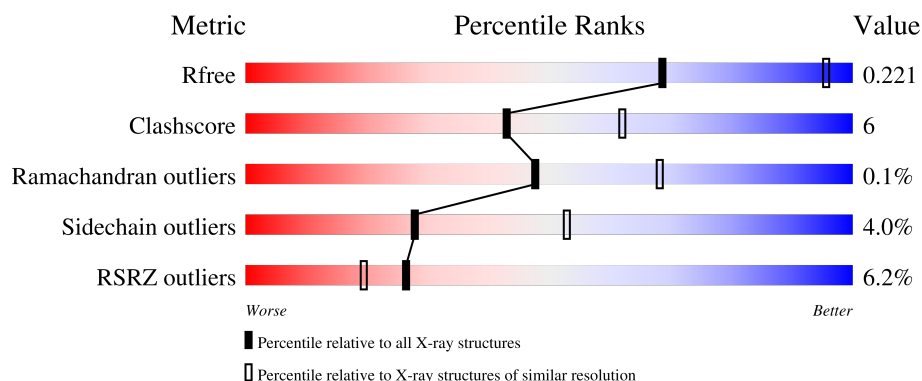
1 Overall quality at a glance

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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	670	 5% 85% 12% ..
1	B	670	 7% 85% 13% ..
1	C	670	 6% 83% 14% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15707 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 Non-structural polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	662	Total	C	N	O	S	0	0	0
			5118	3238	895	957	28			
1	B	662	Total	C	N	O	S	0	0	0
			5110	3228	895	959	28			
1	C	662	Total	C	N	O	S	0	0	0
			5190	3282	921	959	28			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1006	GLY	-	expression tag	UNP P03317
A	1007	PRO	-	expression tag	UNP P03317
A	1008	LEU	-	expression tag	UNP P03317
A	1009	GLY	-	expression tag	UNP P03317
A	1010	SER	-	expression tag	UNP P03317
B	1006	GLY	-	expression tag	UNP P03317
B	1007	PRO	-	expression tag	UNP P03317
B	1008	LEU	-	expression tag	UNP P03317
B	1009	GLY	-	expression tag	UNP P03317
B	1010	SER	-	expression tag	UNP P03317
C	1006	GLY	-	expression tag	UNP P03317
C	1007	PRO	-	expression tag	UNP P03317
C	1008	LEU	-	expression tag	UNP P03317
C	1009	GLY	-	expression tag	UNP P03317
C	1010	SER	-	expression tag	UNP P03317

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

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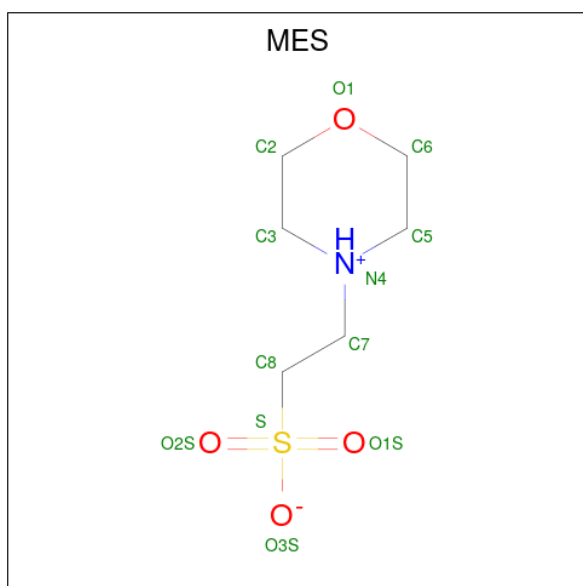
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total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

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

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

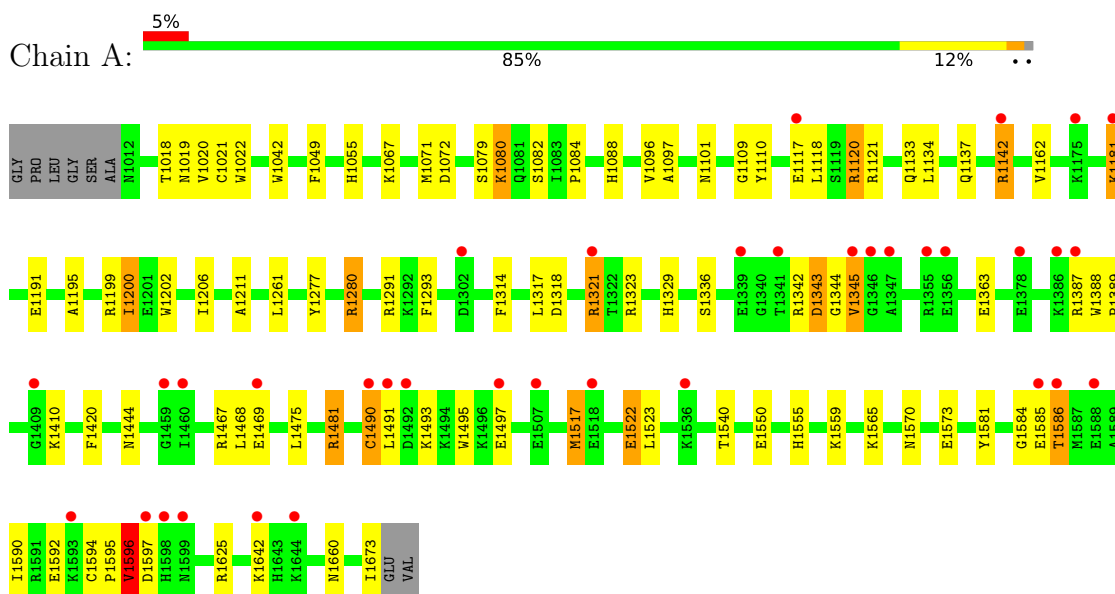
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Zn 1	0	0
4	B	1	Total 1	Zn 1	0	0
4	C	1	Total 1	Zn 1	0	0

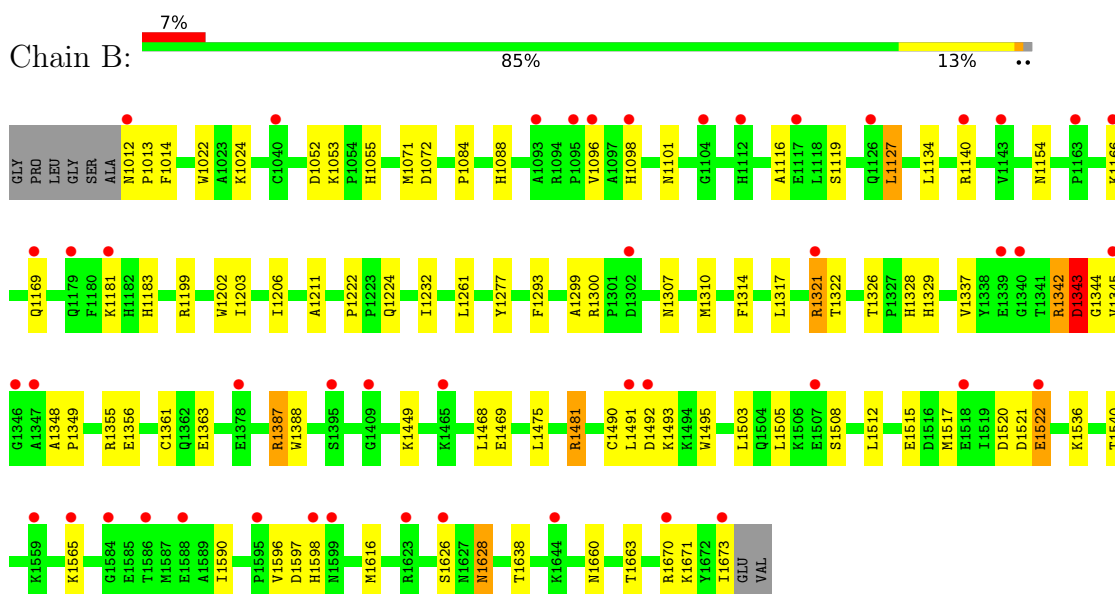
3 Residue-property plots [i](#)

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.

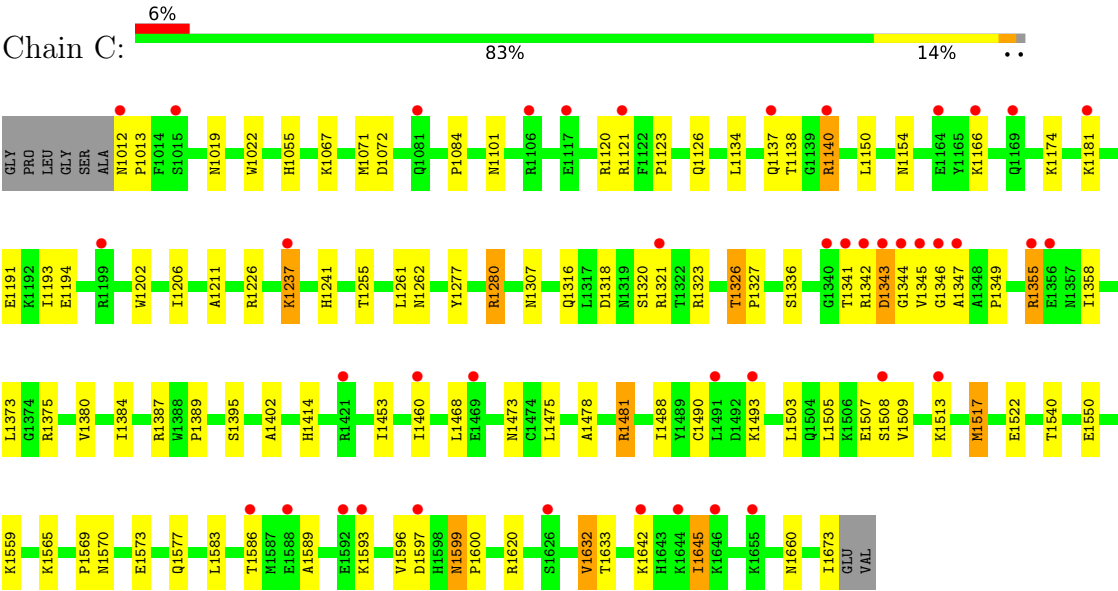
• Molecule 1: Non-structural polypeptide



• Molecule 1: Non-structural polypeptide



• Molecule 1: Non-structural polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	147.18Å 147.18Å 360.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.18 – 2.85 48.18 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.18-2.85) 95.8 (48.18-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.86Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1066)	Depositor
R, R_{free}	0.186 , 0.217 0.192 , 0.221	Depositor DCC
R_{free} test set	5285 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	60.8	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 65.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15707	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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: ZN, MES, 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	0.43	0/5242	0.82	9/7139 (0.1%)
1	B	0.41	0/5234	0.82	5/7134 (0.1%)
1	C	0.46	0/5314	0.86	8/7218 (0.1%)
All	All	0.43	0/15790	0.84	22/21491 (0.1%)

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	2
1	C	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1599	ASN	CA-C-N	9.06	128.70	119.82
1	C	1599	ASN	C-N-CA	9.06	128.70	119.82
1	A	1660	ASN	CA-C-N	6.80	126.43	119.56
1	A	1660	ASN	C-N-CA	6.80	126.43	119.56
1	C	1326	THR	CA-C-N	6.66	127.51	120.12

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1490	CYS	Peptide
1	B	1343	ASP	Peptide
1	B	1490	CYS	Peptide
1	C	1320	SER	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	5118	0	4999	65	0
1	B	5110	0	4959	57	0
1	C	5190	0	5157	72	0
2	A	75	0	0	1	0
2	B	25	0	0	0	0
2	C	90	0	0	4	0
3	A	36	0	37	0	0
3	B	24	0	26	0	0
3	C	36	0	39	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
All	All	15707	0	15217	191	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 6.

The worst 5 of 191 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:C:1280:ARG:NH2	1:C:1550:GLU:OE2	2.06	0.87
1:A:1343:ASP:HB2	1:A:1344:GLY:HA2	1.61	0.82
1:A:1342:ARG:NH2	1:A:1444:ASN:O	2.14	0.80
1:B:1492:ASP:OD1	1:B:1493:LYS:N	2.18	0.76
1:A:1321:ARG:HD3	1:A:1321:ARG:H	1.52	0.75

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	660/670 (98%)	641 (97%)	18 (3%)	1 (0%)	43	62
1	B	660/670 (98%)	643 (97%)	17 (3%)	0	100	100
1	C	660/670 (98%)	645 (98%)	15 (2%)	0	100	100
All	All	1980/2010 (98%)	1929 (97%)	50 (2%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1586	THR

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	551/574 (96%)	530 (96%)	21 (4%)	29	54
1	B	548/574 (96%)	524 (96%)	24 (4%)	25	49
1	C	566/574 (99%)	544 (96%)	22 (4%)	28	54
All	All	1665/1722 (97%)	1598 (96%)	67 (4%)	28	53

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1481	ARG
1	C	1505	LEU

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Mol	Chain	Res	Type
1	C	1642	LYS
1	B	1140	ARG
1	B	1134	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1224	GLN
1	C	1414	HIS
1	B	1446	HIS
1	C	1446	HIS
1	C	1214	ASN

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 49 ligands modelled in this entry, 3 are monoatomic - leaving 46 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	1706	-	4,4,4	0.24	0	6,6,6	0.12	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	C	1702	-	4,4,4	0.26	0	6,6,6	0.24	0
3	MES	C	1720	-	12,12,12	2.23	1 (8%)	15,16,16	1.59	3 (20%)
2	SO4	C	1711	-	4,4,4	0.28	0	6,6,6	0.19	0
2	SO4	A	1705	-	4,4,4	0.24	0	6,6,6	0.12	0
2	SO4	C	1704	-	4,4,4	0.24	0	6,6,6	0.16	0
2	SO4	A	1701	-	4,4,4	0.23	0	6,6,6	0.29	0
2	SO4	B	1704	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	C	1713	-	4,4,4	0.21	0	6,6,6	0.20	0
2	SO4	C	1703	-	4,4,4	0.24	0	6,6,6	0.10	0
2	SO4	C	1701	-	4,4,4	0.25	0	6,6,6	0.14	0
2	SO4	B	1701	-	4,4,4	0.28	0	6,6,6	0.08	0
2	SO4	A	1710	-	4,4,4	0.27	0	6,6,6	0.10	0
2	SO4	C	1710	-	4,4,4	0.27	0	6,6,6	0.13	0
2	SO4	A	1707	-	4,4,4	0.25	0	6,6,6	0.13	0
3	MES	B	1707	-	12,12,12	2.15	1 (8%)	15,16,16	1.64	3 (20%)
2	SO4	C	1718	-	4,4,4	0.28	0	6,6,6	0.22	0
2	SO4	C	1717	-	4,4,4	0.26	0	6,6,6	0.28	0
2	SO4	A	1714	-	4,4,4	0.26	0	6,6,6	0.26	0
3	MES	C	1719	-	12,12,12	2.23	1 (8%)	15,16,16	1.51	3 (20%)
2	SO4	A	1715	-	4,4,4	0.23	0	6,6,6	0.16	0
3	MES	A	1717	-	12,12,12	2.25	1 (8%)	15,16,16	2.06	4 (26%)
2	SO4	A	1708	-	4,4,4	0.23	0	6,6,6	0.20	0
2	SO4	C	1706	-	4,4,4	0.24	0	6,6,6	0.25	0
2	SO4	A	1713	-	4,4,4	0.24	0	6,6,6	0.17	0
2	SO4	A	1709	-	4,4,4	0.25	0	6,6,6	0.17	0
2	SO4	A	1702	-	4,4,4	0.25	0	6,6,6	0.10	0
2	SO4	C	1705	-	4,4,4	0.28	0	6,6,6	0.10	0
2	SO4	C	1707	-	4,4,4	0.25	0	6,6,6	0.10	0
2	SO4	A	1712	-	4,4,4	0.22	0	6,6,6	0.07	0
2	SO4	B	1703	-	4,4,4	0.25	0	6,6,6	0.11	0
3	MES	B	1706	-	12,12,12	2.21	1 (8%)	15,16,16	1.48	4 (26%)
2	SO4	B	1705	-	4,4,4	0.21	0	6,6,6	0.22	0
2	SO4	C	1714	-	4,4,4	0.26	0	6,6,6	0.11	0
3	MES	A	1716	-	12,12,12	2.23	1 (8%)	15,16,16	2.03	5 (33%)
2	SO4	C	1715	-	4,4,4	0.30	0	6,6,6	0.08	0
2	SO4	A	1711	-	4,4,4	0.29	0	6,6,6	0.19	0
2	SO4	C	1708	-	4,4,4	0.24	0	6,6,6	0.20	0
2	SO4	B	1702	-	4,4,4	0.23	0	6,6,6	0.20	0
2	SO4	C	1709	-	4,4,4	0.25	0	6,6,6	0.17	0
2	SO4	C	1716	-	4,4,4	0.26	0	6,6,6	0.21	0
2	SO4	C	1712	-	4,4,4	0.28	0	6,6,6	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MES	C	1721	-	12,12,12	2.19	1 (8%)	15,16,16	1.47	2 (13%)
2	SO4	A	1703	-	4,4,4	0.23	0	6,6,6	0.16	0
2	SO4	A	1704	-	4,4,4	0.24	0	6,6,6	0.09	0
3	MES	A	1718	-	12,12,12	2.21	1 (8%)	15,16,16	1.37	2 (13%)

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	MES	A	1717	-	-	4/6/14/14	0/1/1/1
3	MES	A	1716	-	-	3/6/14/14	0/1/1/1
3	MES	C	1720	-	-	2/6/14/14	0/1/1/1
3	MES	C	1719	-	-	1/6/14/14	0/1/1/1
3	MES	B	1707	-	-	0/6/14/14	0/1/1/1
3	MES	C	1721	-	-	4/6/14/14	0/1/1/1
3	MES	B	1706	-	-	0/6/14/14	0/1/1/1
3	MES	A	1718	-	-	2/6/14/14	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1719	MES	C8-S	-7.51	1.67	1.77
3	A	1717	MES	C8-S	-7.48	1.67	1.77
3	A	1716	MES	C8-S	-7.40	1.67	1.77
3	C	1720	MES	C8-S	-7.37	1.67	1.77
3	B	1706	MES	C8-S	-7.34	1.67	1.77

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1717	MES	C6-C5-N4	-5.20	102.21	110.12
3	A	1716	MES	O1S-S-C8	4.18	113.04	106.73
3	C	1719	MES	O1S-S-C8	3.64	112.23	106.73
3	B	1707	MES	C6-C5-N4	-3.46	104.86	110.12
3	A	1716	MES	C2-C3-N4	-3.29	105.12	110.12

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1717	MES	C8-C7-N4-C5
3	A	1718	MES	C8-C7-N4-C3
3	C	1720	MES	C8-C7-N4-C3
3	C	1720	MES	C8-C7-N4-C5
3	C	1721	MES	C8-C7-N4-C3

There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1720	MES	1	0
2	C	1701	SO4	1	0
2	A	1707	SO4	1	0
2	C	1717	SO4	1	0
2	C	1706	SO4	1	0
2	C	1714	SO4	1	0
3	C	1721	MES	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	662/670 (98%)	0.13	36 (5%)	31	23	45, 68, 103, 154	0
1	B	662/670 (98%)	0.19	46 (6%)	23	17	43, 71, 107, 158	0
1	C	662/670 (98%)	-0.07	42 (6%)	26	19	37, 55, 87, 134	0
All	All	1986/2010 (98%)	0.09	124 (6%)	26	19	37, 65, 102, 158	0

The worst 5 of 124 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1460	ILE	8.8
1	B	1347	ALA	7.0
1	B	1598	HIS	6.7
1	C	1237	LYS	6.7
1	C	1346	GLY	6.4

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	1711	5/5	0.63	0.17	113,131,134,135	0
2	SO4	A	1713	5/5	0.64	0.14	128,129,132,136	0
2	SO4	A	1714	5/5	0.68	0.21	124,125,130,133	0
2	SO4	C	1712	5/5	0.73	0.17	127,128,131,131	0
2	SO4	B	1704	5/5	0.74	0.15	141,142,145,146	0
2	SO4	C	1713	5/5	0.76	0.21	114,118,130,135	0
2	SO4	A	1710	5/5	0.77	0.31	106,116,120,126	0
2	SO4	A	1715	5/5	0.79	0.12	120,125,128,133	0
2	SO4	C	1711	5/5	0.79	0.20	113,116,130,130	0
2	SO4	C	1718	5/5	0.79	0.27	99,102,114,115	0
2	SO4	A	1708	5/5	0.80	0.14	117,121,126,132	0
2	SO4	A	1705	5/5	0.81	0.11	119,121,126,128	0
2	SO4	C	1707	5/5	0.81	0.11	134,141,142,143	0
2	SO4	A	1707	5/5	0.81	0.15	119,120,122,124	0
2	SO4	B	1705	5/5	0.82	0.18	116,122,128,134	0
2	SO4	C	1714	5/5	0.82	0.26	105,109,114,118	0
2	SO4	A	1712	5/5	0.82	0.13	154,156,157,157	0
2	SO4	B	1702	5/5	0.83	0.20	118,125,128,134	0
2	SO4	B	1703	5/5	0.83	0.12	123,125,127,133	0
2	SO4	C	1704	5/5	0.83	0.10	123,125,130,131	0
2	SO4	C	1716	5/5	0.84	0.24	108,112,119,123	0
2	SO4	C	1717	5/5	0.84	0.19	99,105,107,109	0
2	SO4	A	1702	5/5	0.84	0.15	105,109,114,120	0
2	SO4	C	1705	5/5	0.85	0.25	104,109,117,131	0
2	SO4	A	1706	5/5	0.85	0.24	119,121,124,126	0
2	SO4	A	1704	5/5	0.85	0.12	140,140,142,144	0
2	SO4	C	1709	5/5	0.86	0.19	124,128,139,143	0
2	SO4	C	1703	5/5	0.86	0.19	106,108,118,121	0
2	SO4	C	1706	5/5	0.86	0.26	116,118,122,125	0
2	SO4	A	1701	5/5	0.86	0.20	102,103,109,113	0
2	SO4	C	1701	5/5	0.87	0.15	95,100,105,110	0
3	MES	A	1718	12/12	0.87	0.23	107,116,124,129	0
3	MES	C	1721	12/12	0.87	0.19	82,96,116,116	0
2	SO4	C	1715	5/5	0.88	0.22	90,95,98,100	0
2	SO4	A	1709	5/5	0.89	0.18	121,124,126,129	0
2	SO4	C	1702	5/5	0.89	0.20	112,114,122,128	0
2	SO4	C	1708	5/5	0.90	0.21	99,109,111,116	0
2	SO4	B	1701	5/5	0.90	0.14	112,117,122,125	0
3	MES	B	1706	12/12	0.91	0.17	63,81,92,94	0
3	MES	C	1720	12/12	0.91	0.20	76,93,103,104	0
3	MES	A	1717	12/12	0.91	0.14	62,77,80,85	0
2	SO4	A	1703	5/5	0.92	0.32	114,115,117,119	0
2	SO4	C	1710	5/5	0.94	0.28	101,104,109,112	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MES	A	1716	12/12	0.95	0.14	67,91,97,98	0
3	MES	B	1707	12/12	0.96	0.12	49,67,77,77	0
3	MES	C	1719	12/12	0.98	0.06	36,47,54,64	0
4	ZN	A	1719	1/1	0.99	0.09	91,91,91,91	0
4	ZN	B	1708	1/1	0.99	0.09	96,96,96,96	0
4	ZN	C	1722	1/1	0.99	0.10	70,70,70,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.