



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2024 – 02:28 AM EDT

PDB ID : 2ULL
Title : MULTIPLE CONFORMATION STRUCTURE OF ALPHA-LYTIC PROTEASE AT 120 K
Authors : Rader, S.D.; Agard, D.A.
Deposited on : 1996-11-26
Resolution : 1.50 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

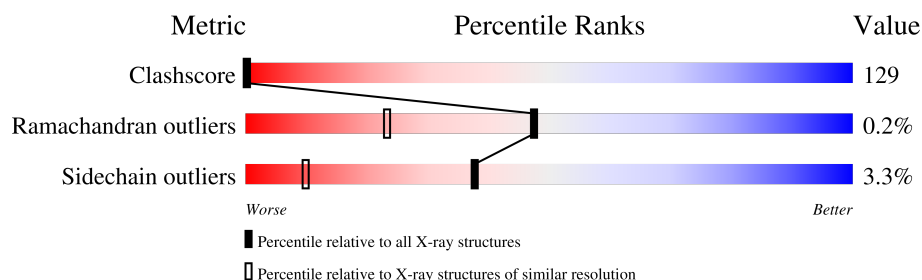
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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))
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	1-A	198	97% .
1	10-A	198	97% .
1	11-A	198	98% .
1	12-A	198	97% .
1	13-A	198	97% .
1	14-A	198	97% .
1	15-A	198	97% .
1	16-A	198	97% .

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Mol	Chain	Length	Quality of chain
1	2-A	198	 98%
1	3-A	198	 98%
1	4-A	198	 97%
1	5-A	198	 96%
1	6-A	198	 97%
1	7-A	198	 97%
1	8-A	198	 97%
1	9-A	198	 97%

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	1-A	4	-	X	-	-
2	SO4	10-A	4	-	X	-	-
2	SO4	11-A	4	-	X	-	-
2	SO4	12-A	4	-	X	-	-
2	SO4	13-A	4	-	X	-	-
2	SO4	14-A	4	-	X	-	-
2	SO4	15-A	4	-	X	-	-
2	SO4	16-A	4	-	X	-	-
2	SO4	2-A	4	-	X	-	-
2	SO4	3-A	4	-	X	-	-
2	SO4	4-A	4	-	X	-	-
2	SO4	5-A	4	-	X	-	-
2	SO4	6-A	4	-	X	-	-
2	SO4	7-A	4	-	X	-	-
2	SO4	8-A	4	-	X	-	-
2	SO4	9-A	4	-	X	-	-
3	TAM	1-A	1	-	X	-	-
3	TAM	10-A	1	-	X	-	-
3	TAM	11-A	1	-	X	-	-
3	TAM	12-A	1	-	X	-	-
3	TAM	13-A	1	-	X	-	-
3	TAM	14-A	1	-	X	-	-
3	TAM	15-A	1	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	TAM	16-A	1	-	X	-	-
3	TAM	2-A	1	-	X	-	-
3	TAM	3-A	1	-	X	-	-
3	TAM	4-A	1	-	X	-	-
3	TAM	5-A	1	-	X	-	-
3	TAM	6-A	1	-	X	-	-
3	TAM	7-A	1	-	X	-	-
3	TAM	8-A	1	-	X	-	-
3	TAM	9-A	1	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 27440 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 ALPHA-LYTIC PROTEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	2-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	3-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	4-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	5-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	6-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	7-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	8-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	9-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	10-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	11-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	12-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	13-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	14-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	15-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			
1	16-A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	1-A	1	Total	O	S	0	0
			5	4	1		
2	2-A	1	Total	O	S	0	0
			5	4	1		
2	3-A	1	Total	O	S	0	0
			5	4	1		
2	4-A	1	Total	O	S	0	0
			5	4	1		
2	5-A	1	Total	O	S	0	0
			5	4	1		
2	6-A	1	Total	O	S	0	0
			5	4	1		
2	7-A	1	Total	O	S	0	0
			5	4	1		
2	8-A	1	Total	O	S	0	0
			5	4	1		
2	9-A	1	Total	O	S	0	0
			5	4	1		
2	10-A	1	Total	O	S	0	0
			5	4	1		
2	11-A	1	Total	O	S	0	0
			5	4	1		
2	12-A	1	Total	O	S	0	0
			5	4	1		
2	13-A	1	Total	O	S	0	0
			5	4	1		

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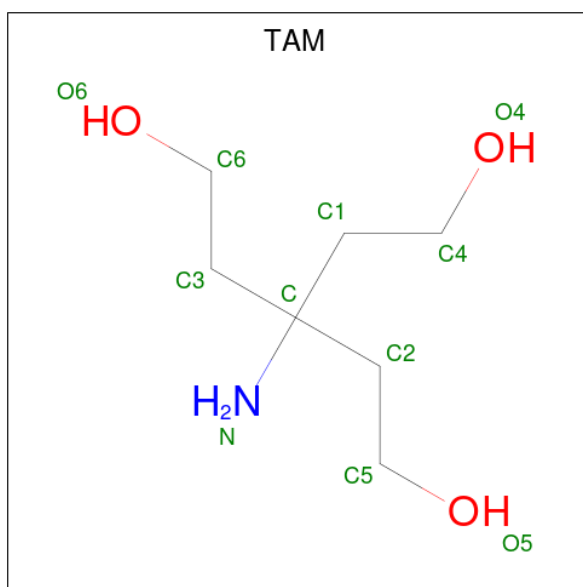
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	14-A	1	Total	O	S	0	0
			5	4	1		
2	15-A	1	Total	O	S	0	0
			5	4	1		
2	16-A	1	Total	O	S	0	0
			5	4	1		
2	1-A	1	Total	O	S	0	0
			5	4	1		
2	2-A	1	Total	O	S	0	0
			5	4	1		
2	3-A	1	Total	O	S	0	0
			5	4	1		
2	4-A	1	Total	O	S	0	0
			5	4	1		
2	5-A	1	Total	O	S	0	0
			5	4	1		
2	6-A	1	Total	O	S	0	0
			5	4	1		
2	7-A	1	Total	O	S	0	0
			5	4	1		
2	8-A	1	Total	O	S	0	0
			5	4	1		
2	9-A	1	Total	O	S	0	0
			5	4	1		
2	10-A	1	Total	O	S	0	0
			5	4	1		
2	11-A	1	Total	O	S	0	0
			5	4	1		
2	12-A	1	Total	O	S	0	0
			5	4	1		
2	13-A	1	Total	O	S	0	0
			5	4	1		
2	14-A	1	Total	O	S	0	0
			5	4	1		
2	15-A	1	Total	O	S	0	0
			5	4	1		
2	16-A	1	Total	O	S	0	0
			5	4	1		
2	1-A	1	Total	O	S	0	0
			5	4	1		
2	2-A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	3-A	1	Total	O	S	0	0
			5	4	1		
2	4-A	1	Total	O	S	0	0
			5	4	1		
2	5-A	1	Total	O	S	0	0
			5	4	1		
2	6-A	1	Total	O	S	0	0
			5	4	1		
2	7-A	1	Total	O	S	0	0
			5	4	1		
2	8-A	1	Total	O	S	0	0
			5	4	1		
2	9-A	1	Total	O	S	0	0
			5	4	1		
2	10-A	1	Total	O	S	0	0
			5	4	1		
2	11-A	1	Total	O	S	0	0
			5	4	1		
2	12-A	1	Total	O	S	0	0
			5	4	1		
2	13-A	1	Total	O	S	0	0
			5	4	1		
2	14-A	1	Total	O	S	0	0
			5	4	1		
2	15-A	1	Total	O	S	0	0
			5	4	1		
2	16-A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is TRIS(HYDROXYETHYL)AMINOMETHANE (three-letter code: TAM) (formula: C₇H₁₇NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	1-A	1	Total	C	N	0	0
			8	7	1		
3	2-A	1	Total	C	N	0	0
			8	7	1		
3	3-A	1	Total	C	N	0	0
			8	7	1		
3	4-A	1	Total	C	N	0	0
			8	7	1		
3	5-A	1	Total	C	N	0	0
			8	7	1		
3	6-A	1	Total	C	N	0	0
			8	7	1		
3	7-A	1	Total	C	N	0	0
			8	7	1		
3	8-A	1	Total	C	N	0	0
			8	7	1		
3	9-A	1	Total	C	N	0	0
			8	7	1		
3	10-A	1	Total	C	N	0	0
			8	7	1		
3	11-A	1	Total	C	N	0	0
			8	7	1		
3	12-A	1	Total	C	N	0	0
			8	7	1		
3	13-A	1	Total	C	N	0	0
			8	7	1		
3	14-A	1	Total	C	N	0	0
			8	7	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	15-A	1	Total	C	N	0	0
			8	7	1		
3	16-A	1	Total	C	N	0	0
			8	7	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	1-A	301	Total	O	2	0
			301	301		
4	2-A	301	Total	O	2	0
			301	301		
4	3-A	301	Total	O	2	0
			301	301		
4	4-A	301	Total	O	2	0
			301	301		
4	5-A	301	Total	O	2	0
			301	301		
4	6-A	301	Total	O	2	0
			301	301		
4	7-A	301	Total	O	2	0
			301	301		
4	8-A	301	Total	O	2	0
			301	301		
4	9-A	301	Total	O	2	0
			301	301		
4	10-A	301	Total	O	2	0
			301	301		
4	11-A	301	Total	O	2	0
			301	301		
4	12-A	301	Total	O	2	0
			301	301		
4	13-A	301	Total	O	2	0
			301	301		
4	14-A	301	Total	O	2	0
			301	301		
4	15-A	301	Total	O	2	0
			301	301		
4	16-A	301	Total	O	2	0
			301	301		

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. 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. 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: ALPHA-LYTIC PROTEASE

Chain 1-A:  97% .



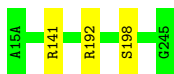
- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 2-A:  98% .



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 3-A:  98% .



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 4-A:  97% .



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 5-A:  96% .



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 6-A:  97% .



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 7-A:  97%



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 8-A:  97%



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 9-A:  97%



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 10-A:  97%



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 11-A:  98%



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 12-A:  97%



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 13-A:  97%



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 14-A:  97% .



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 15-A:  97% .



- Molecule 1: ALPHA-LYTIC PROTEASE

Chain 16-A:  97% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	65.80Å 65.80Å 79.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 1.50 13.57 – 1.48	Depositor EDS
% Data completeness (in resolution range)	99.0 (6.00-1.50) 98.5 (13.57-1.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.50 (at 1.48Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.165 , 0.192 0.500 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	5.5	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.38 , 8.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
F_o, F_c correlation	0.48	EDS
Total number of atoms	27440	wwPDB-VP
Average B, all atoms (Å ²)	6.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.20% 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, TAM

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	1-A	0.34	0/1409	0.69	0/1909
1	2-A	0.34	0/1409	0.69	0/1909
1	3-A	0.34	0/1409	0.68	0/1909
1	4-A	0.34	0/1409	0.70	0/1909
1	5-A	0.34	0/1409	0.70	1/1909 (0.1%)
1	6-A	0.36	0/1409	0.80	2/1909 (0.1%)
1	7-A	0.36	0/1409	0.69	0/1909
1	8-A	0.34	0/1409	0.69	0/1909
1	9-A	0.34	0/1409	0.69	0/1909
1	10-A	0.34	0/1409	0.69	0/1909
1	11-A	0.34	0/1409	0.69	0/1909
1	12-A	0.34	0/1409	0.67	0/1909
1	13-A	0.37	1/1409 (0.1%)	0.74	2/1909 (0.1%)
1	14-A	0.35	0/1409	0.70	0/1909
1	15-A	0.34	0/1409	0.71	1/1909 (0.1%)
1	16-A	0.34	0/1409	0.70	0/1909
All	All	0.35	1/22544 (0.0%)	0.70	6/30544 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	13-A	48(A)	ARG	CZ-NH2	-5.97	1.25	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	6-A	122	ARG	NE-CZ-NH2	-14.31	113.14	120.30
1	13-A	48(A)	ARG	NE-CZ-NH1	9.44	125.02	120.30
1	6-A	122	ARG	NH1-CZ-NH2	6.68	126.75	119.40
1	13-A	48(A)	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	15-A	120(A)	ARG	NE-CZ-NH2	-5.44	117.58	120.30

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	1-A	1391	0	1363	0	0
1	2-A	1391	0	1361	0	0
1	3-A	1391	0	1363	0	0
1	4-A	1391	0	1361	0	0
1	5-A	1391	0	1363	0	0
1	6-A	1391	0	1363	0	0
1	7-A	1391	0	1365	0	0
1	8-A	1391	0	1361	0	0
1	9-A	1391	0	1363	0	0
1	10-A	1391	0	1363	0	0
1	11-A	1391	0	1361	0	0
1	12-A	1391	0	1361	0	0
1	13-A	1391	0	1363	0	0
1	14-A	1391	0	1361	0	0
1	15-A	1391	0	1361	0	0
1	16-A	1391	0	1363	0	0
2	1-A	15	0	0	0	0
2	2-A	15	0	0	0	0
2	3-A	15	0	0	0	0
2	4-A	15	0	0	0	0
2	5-A	15	0	0	0	0
2	6-A	15	0	0	0	0
2	7-A	15	0	0	0	0
2	8-A	15	0	0	0	0
2	9-A	15	0	0	0	0
2	10-A	15	0	0	0	0
2	11-A	15	0	0	0	0
2	12-A	15	0	0	0	0
2	13-A	15	0	0	0	0
2	14-A	15	0	0	0	0
2	15-A	15	0	0	0	0
2	16-A	15	0	0	0	0
3	1-A	8	0	8	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	2-A	8	0	8	4	0
3	3-A	8	0	8	4	0
3	4-A	8	0	8	4	0
3	5-A	8	0	8	4	0
3	6-A	8	0	8	4	0
3	7-A	8	0	8	4	0
3	8-A	8	0	8	4	0
3	9-A	8	0	8	4	0
3	10-A	8	0	8	4	0
3	11-A	8	0	8	4	0
3	12-A	8	0	8	4	0
3	13-A	8	0	8	4	0
3	14-A	8	0	8	4	0
3	15-A	8	0	8	4	0
3	16-A	8	0	8	4	0
4	1-A	301	0	0	4	0
4	2-A	301	0	0	4	0
4	3-A	301	0	0	4	0
4	4-A	301	0	0	4	0
4	5-A	301	0	0	4	0
4	6-A	301	0	0	4	0
4	7-A	301	0	0	4	0
4	8-A	301	0	0	4	0
4	9-A	301	0	0	4	0
4	10-A	301	0	0	4	0
4	11-A	301	0	0	4	0
4	12-A	301	0	0	4	0
4	13-A	301	0	0	4	0
4	14-A	301	0	0	4	0
4	15-A	301	0	0	4	0
4	16-A	301	0	0	4	0
All	All	27440	0	21924	64	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 129.

The worst 5 of 64 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)
3:A:1:TAM:C4	4:A:339:HOH:O	2.36	0.74
3:A:1:TAM:C4	4:A:339:HOH:O	2.36	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1:TAM:C4	4:A:339:HOH:O	2.36	0.74
3:A:1:TAM:C4	4:A:339:HOH:O	2.36	0.74
3:A:1:TAM:C4	4:A:339:HOH:O	2.36	0.74

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	1-A	196/198 (99%)	183 (93%)	12 (6%)	1 (0%)	29	9
1	2-A	196/198 (99%)	184 (94%)	12 (6%)	0	100	100
1	3-A	196/198 (99%)	184 (94%)	11 (6%)	1 (0%)	29	9
1	4-A	196/198 (99%)	182 (93%)	13 (7%)	1 (0%)	29	9
1	5-A	196/198 (99%)	185 (94%)	10 (5%)	1 (0%)	29	9
1	6-A	196/198 (99%)	185 (94%)	11 (6%)	0	100	100
1	7-A	196/198 (99%)	180 (92%)	16 (8%)	0	100	100
1	8-A	196/198 (99%)	186 (95%)	10 (5%)	0	100	100
1	9-A	196/198 (99%)	186 (95%)	10 (5%)	0	100	100
1	10-A	196/198 (99%)	187 (95%)	9 (5%)	0	100	100
1	11-A	196/198 (99%)	187 (95%)	9 (5%)	0	100	100
1	12-A	196/198 (99%)	184 (94%)	12 (6%)	0	100	100
1	13-A	196/198 (99%)	188 (96%)	8 (4%)	0	100	100
1	14-A	196/198 (99%)	184 (94%)	12 (6%)	0	100	100
1	15-A	196/198 (99%)	184 (94%)	11 (6%)	1 (0%)	29	9
1	16-A	196/198 (99%)	183 (93%)	13 (7%)	0	100	100
All	All	3136/3168 (99%)	2952 (94%)	179 (6%)	5 (0%)	47	23

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	5-A	110	SER
1	15-A	67	GLY
1	4-A	110	SER
1	3-A	192	ARG
1	1-A	59(B)	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	1-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
1	2-A	142/142 (100%)	138 (97%)	4 (3%)	43	14
1	3-A	142/142 (100%)	140 (99%)	2 (1%)	67	42
1	4-A	142/142 (100%)	138 (97%)	4 (3%)	43	14
1	5-A	142/142 (100%)	136 (96%)	6 (4%)	30	6
1	6-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
1	7-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
1	8-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
1	9-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
1	10-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
1	11-A	142/142 (100%)	138 (97%)	4 (3%)	43	14
1	12-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
1	13-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
1	14-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
1	15-A	142/142 (100%)	138 (97%)	4 (3%)	43	14
1	16-A	142/142 (100%)	137 (96%)	5 (4%)	36	9
All	All	2272/2272 (100%)	2198 (97%)	74 (3%)	38	10

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	13-A	141	ARG
1	16-A	189	CYS
1	13-A	223	GLN
1	15-A	87	THR
1	6-A	190	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	11-A	166	ASN
1	13-A	182	GLN
1	12-A	60	ASN
1	13-A	101	ASN
1	14-A	60	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

64 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
3	TAM	4-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
3	TAM	3-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	9-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	5-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	2-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	4-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	3-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	11-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
3	TAM	7-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	13-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	7-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	8-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	2-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	3-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	15-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	1-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	14-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	2-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
3	TAM	16-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	15-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	8-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	7-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	5-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	10-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	16-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	1-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	10-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	12-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
3	TAM	2-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	11-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
3	TAM	14-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
3	TAM	15-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	8-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	6-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	14-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	1-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	11-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
3	TAM	9-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	5-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	12-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
3	TAM	1-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	13-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	6-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	7-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	14-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	4-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	6-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	12-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
3	TAM	8-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	4-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	10-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
3	TAM	11-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	16-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
2	SO4	3-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
3	TAM	12-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	16-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	9-A	4	-	4,4,4	1.51	1 (25%)	6,6,6	5.55	5 (83%)
2	SO4	9-A	3	-	4,4,4	1.55	1 (25%)	6,6,6	0.95	0
3	TAM	13-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
3	TAM	6-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
3	TAM	10-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)
2	SO4	13-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
2	SO4	15-A	2	-	4,4,4	0.99	0	6,6,6	2.48	2 (33%)
3	TAM	5-A	1	-	7,7,10	2.12	4 (57%)	6,9,12	5.88	4 (66%)

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	TAM	4-A	1	-	-	3/9/9/12	-
3	TAM	3-A	1	-	-	3/9/9/12	-
3	TAM	11-A	1	-	-	3/9/9/12	-
3	TAM	1-A	1	-	-	3/9/9/12	-
3	TAM	16-A	1	-	-	3/9/9/12	-
3	TAM	12-A	1	-	-	3/9/9/12	-
3	TAM	7-A	1	-	-	3/9/9/12	-
3	TAM	13-A	1	-	-	3/9/9/12	-
3	TAM	14-A	1	-	-	3/9/9/12	-
3	TAM	2-A	1	-	-	3/9/9/12	-
3	TAM	6-A	1	-	-	3/9/9/12	-
3	TAM	10-A	1	-	-	3/9/9/12	-
3	TAM	15-A	1	-	-	3/9/9/12	-
3	TAM	8-A	1	-	-	3/9/9/12	-
3	TAM	5-A	1	-	-	3/9/9/12	-
3	TAM	9-A	1	-	-	3/9/9/12	-

The worst 5 of 96 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	1-A	1	TAM	C5-C2	-2.88	1.40	1.51
3	2-A	1	TAM	C5-C2	-2.88	1.40	1.51
3	3-A	1	TAM	C5-C2	-2.88	1.40	1.51
3	4-A	1	TAM	C5-C2	-2.88	1.40	1.51
3	5-A	1	TAM	C5-C2	-2.88	1.40	1.51

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1-A	1	TAM	C3-C-C1	12.62	134.15	110.67
3	2-A	1	TAM	C3-C-C1	12.62	134.15	110.67
3	3-A	1	TAM	C3-C-C1	12.62	134.15	110.67
3	4-A	1	TAM	C3-C-C1	12.62	134.15	110.67
3	5-A	1	TAM	C3-C-C1	12.62	134.15	110.67

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	1-A	1	TAM	C2-C-C1-C4
3	1-A	1	TAM	C3-C-C1-C4
3	1-A	1	TAM	N-C-C1-C4
3	2-A	1	TAM	C2-C-C1-C4
3	2-A	1	TAM	C3-C-C1-C4

There are no ring outliers.

16 monomers are involved in 64 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	4-A	1	TAM	4	0
3	3-A	1	TAM	4	0
3	7-A	1	TAM	4	0
3	16-A	1	TAM	4	0
3	2-A	1	TAM	4	0
3	14-A	1	TAM	4	0
3	15-A	1	TAM	4	0
3	9-A	1	TAM	4	0
3	1-A	1	TAM	4	0
3	8-A	1	TAM	4	0
3	11-A	1	TAM	4	0
3	12-A	1	TAM	4	0
3	13-A	1	TAM	4	0
3	6-A	1	TAM	4	0
3	10-A	1	TAM	4	0
3	5-A	1	TAM	4	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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.