



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 10, 2021 – 01:45 PM EDT

PDB ID : 3DWK
Title : Identification of Dynamic Structural Motifs Involved in Peptidoglycan Glycosyltransfer
Authors : Lovering, A.L.; De Castro, L.; Strynadka, N.C.J.
Deposited on : 2008-07-22
Resolution : 3.10 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

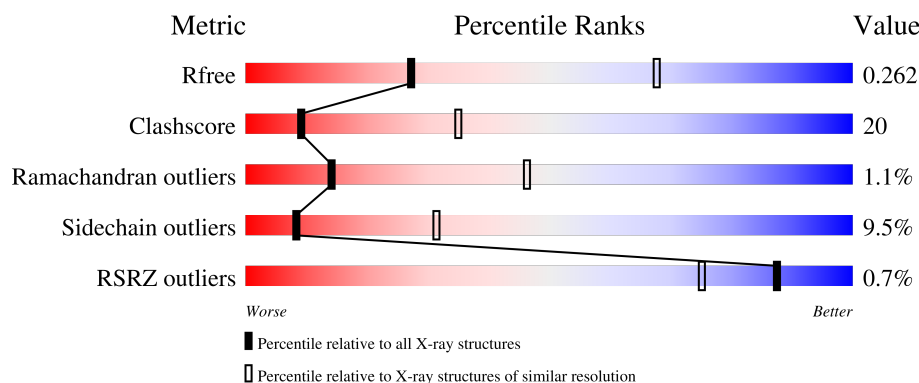
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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	625	<div> <div>%</div> <div> <div></div> <div>57%</div> <div>34%</div> <div>• •</div> </div> </div>
1	B	625	<div> <div>%</div> <div> <div></div> <div>62%</div> <div>32%</div> <div>• •</div> </div> </div>
1	C	625	<div> <div>61%</div> <div>34%</div> <div>5%</div> </div>
1	D	625	<div> <div>60%</div> <div>32%</div> <div>• •</div> </div>

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	A	11	-	-	X	-
2	SO4	A	15	-	-	X	-
2	SO4	A	17	-	-	X	-
2	SO4	A	41	-	-	X	-
2	SO4	B	38	-	-	X	-
2	SO4	C	31	-	-	X	-
2	SO4	D	39	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19474 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 Penicillin-binding protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	598	Total	C	N	O	S	0	0	0
			4712	2953	809	938	12			
1	B	621	Total	C	N	O	S	0	0	0
			4874	3051	839	972	12			
1	C	623	Total	C	N	O	S	0	0	0
			4891	3060	843	976	12			
1	D	602	Total	C	N	O	S	0	0	0
			4751	2977	817	945	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	68	MET	LYS	engineered mutation	UNP Q5HFX3
B	68	MET	LYS	engineered mutation	UNP Q5HFX3
C	68	MET	LYS	engineered mutation	UNP Q5HFX3
D	68	MET	LYS	engineered mutation	UNP Q5HFX3

- Molecule 2 is SULFATE ION (three-letter code: 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		

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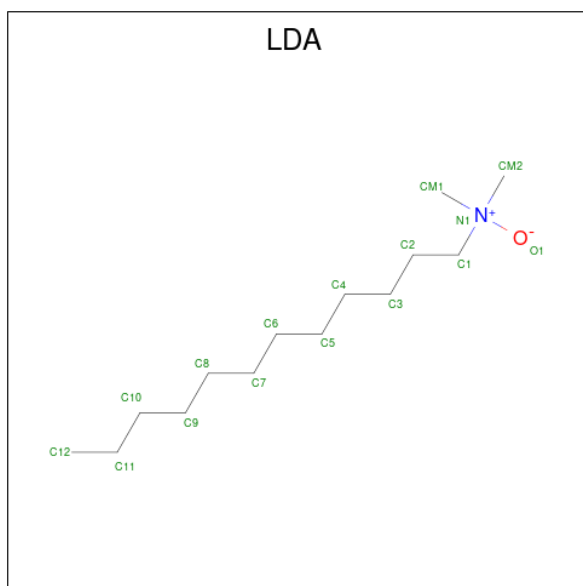
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total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

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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	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).

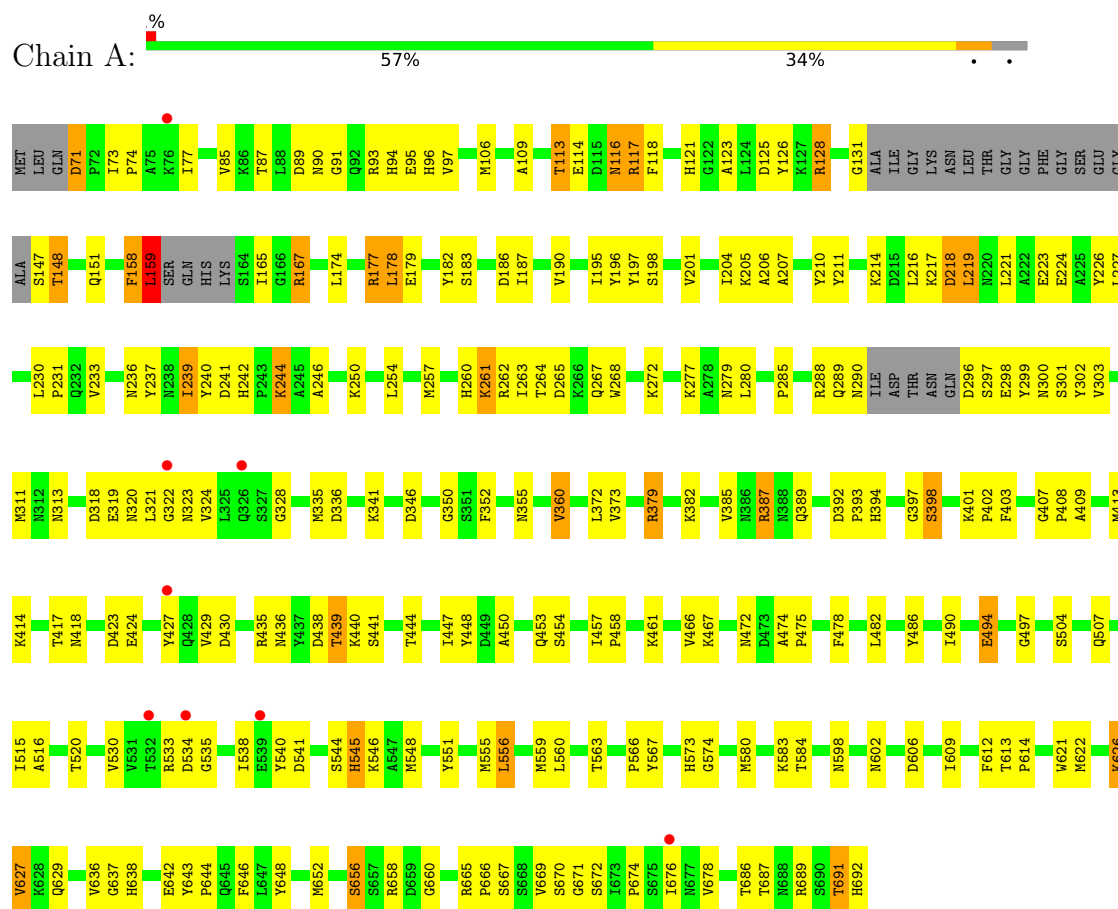


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			16	14	1	1		

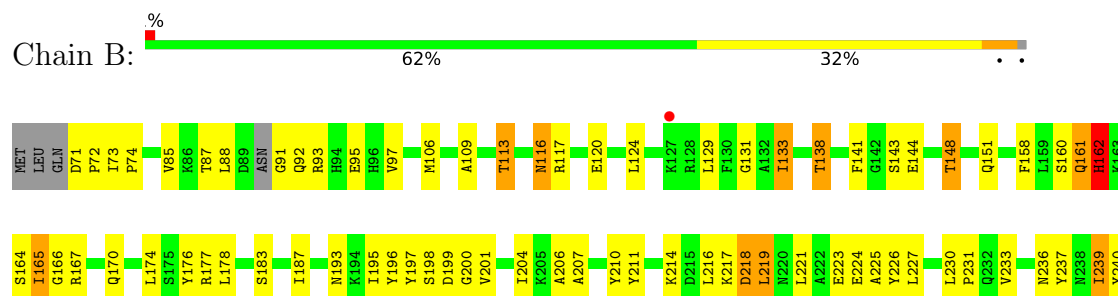
3 Residue-property plots

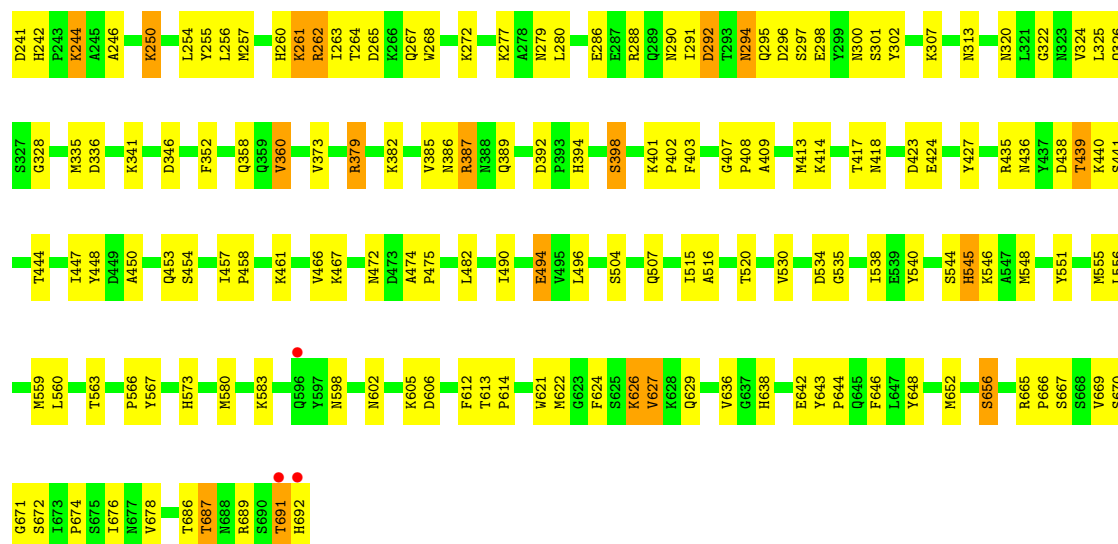
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Penicillin-binding protein 2



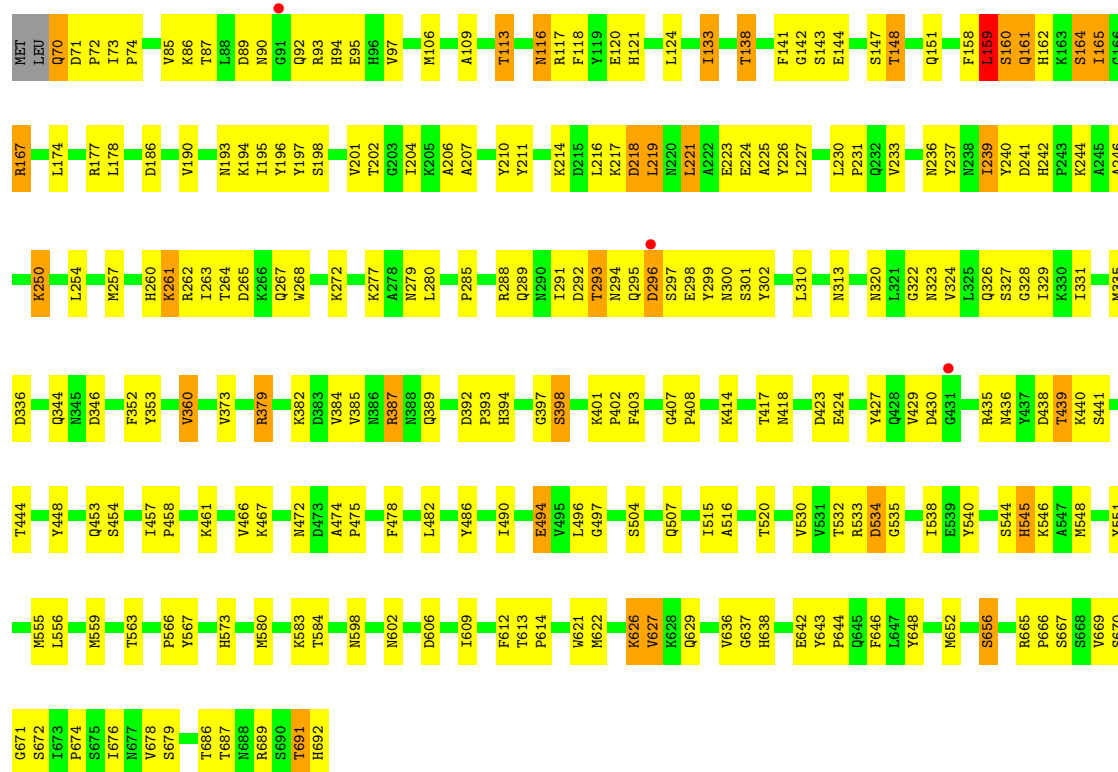
• Molecule 1: Penicillin-binding protein 2





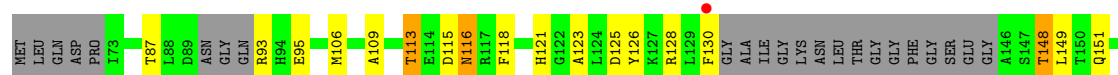
• Molecule 1: Penicillin-binding protein 2

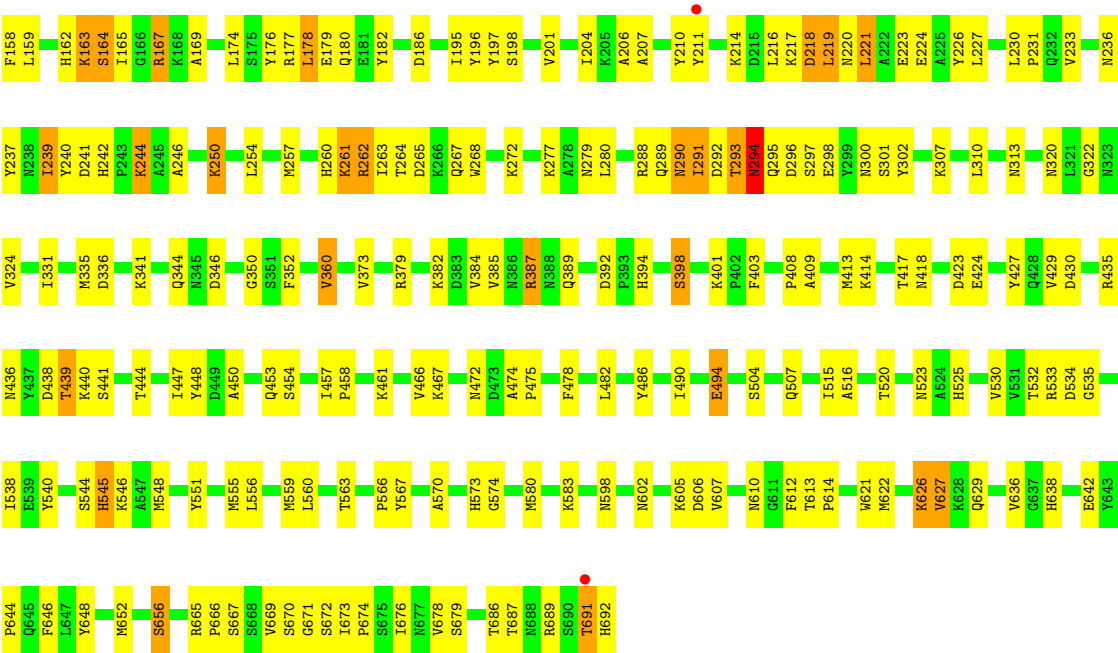
Chain C: 61% 34% 5%



• Molecule 1: Penicillin-binding protein 2

Chain D: 60% 32% 8%





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.35Å 217.47Å 95.73Å 90.00° 90.30° 90.00°	Depositor
Resolution (Å)	41.88 – 3.10 41.88 – 3.10	Depositor EDS
% Data completeness (in resolution range)	95.8 (41.88-3.10) 94.4 (41.88-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 3.12Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.218 , 0.264 0.217 , 0.262	Depositor DCC
R_{free} test set	3052 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	63.1	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 36.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.125 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	19474	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% 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: SO4, LDA

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	0.36	0/4813	0.53	2/6504 (0.0%)
1	B	0.35	0/4979	0.51	0/6729
1	C	0.38	0/4997	0.54	1/6755 (0.0%)
1	D	0.37	0/4853	0.53	0/6559
All	All	0.37	0/19642	0.53	3/26547 (0.0%)

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	C	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	159	LEU	CA-CB-CG	-7.58	97.86	115.30
1	A	131	GLY	N-CA-C	-6.72	96.29	113.10
1	A	159	LEU	N-CA-C	5.02	124.56	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	158	PHE	Peptide

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Mol	Chain	Res	Type	Group
1	C	159	LEU	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	4712	0	4518	190	0
1	B	4874	0	4676	191	0
1	C	4891	0	4691	208	0
1	D	4751	0	4562	185	0
2	A	75	0	0	14	0
2	B	65	0	0	8	0
2	C	45	0	0	6	0
2	D	45	0	0	5	0
3	D	16	0	31	7	0
All	All	19474	0	18478	759	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 20.

The worst 5 of 759 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:B:162:HIS:CE1	1:B:164:SER:HB2	1.78	1.18
1:C:160:SER:HB2	1:C:167:ARG:NH1	1.61	1.15
1:C:160:SER:CB	1:C:167:ARG:HH11	1.59	1.14
1:C:159:LEU:HD22	1:C:532:THR:HB	1.23	1.11
1:D:118:PHE:HA	1:D:121:HIS:CE1	1.95	1.01

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	590/625 (94%)	534 (90%)	50 (8%)	6 (1%)	15	49
1	B	617/625 (99%)	565 (92%)	46 (8%)	6 (1%)	15	49
1	C	621/625 (99%)	563 (91%)	50 (8%)	8 (1%)	12	42
1	D	596/625 (95%)	545 (91%)	45 (8%)	6 (1%)	15	49
All	All	2424/2500 (97%)	2207 (91%)	191 (8%)	26 (1%)	14	46

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	143	SER
1	B	162	HIS
1	B	292	ASP
1	C	143	SER
1	C	160	SER

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	506/526 (96%)	457 (90%)	49 (10%)	8	30
1	B	522/526 (99%)	472 (90%)	50 (10%)	8	31
1	C	524/526 (100%)	474 (90%)	50 (10%)	8	31
1	D	511/526 (97%)	464 (91%)	47 (9%)	9	33
All	All	2063/2104 (98%)	1867 (90%)	196 (10%)	8	31

5 of 196 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	218	ASP
1	C	667	SER
1	C	244	LYS
1	C	398	SER
1	D	113	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	121	HIS
1	D	692	HIS
1	C	389	GLN
1	D	598	ASN
1	D	389	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

47 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	17	-	4,4,4	0.15	0	6,6,6	0.26	0
2	SO4	A	16	-	4,4,4	0.13	0	6,6,6	0.20	0
2	SO4	B	25	-	4,4,4	0.13	0	6,6,6	0.21	0
2	SO4	C	1	-	4,4,4	0.12	0	6,6,6	0.23	0
2	SO4	D	7	-	4,4,4	0.13	0	6,6,6	0.22	0
2	SO4	A	29	-	4,4,4	0.16	0	6,6,6	0.14	0
2	SO4	D	14	-	4,4,4	0.12	0	6,6,6	0.25	0
2	SO4	B	20	-	4,4,4	0.14	0	6,6,6	0.14	0
2	SO4	B	34	-	4,4,4	0.14	0	6,6,6	0.15	0
2	SO4	A	24	-	4,4,4	0.17	0	6,6,6	0.26	0
2	SO4	C	6	-	4,4,4	0.14	0	6,6,6	0.23	0
2	SO4	C	19	-	4,4,4	0.18	0	6,6,6	0.41	0
2	SO4	D	10	-	4,4,4	0.16	0	6,6,6	0.26	0
2	SO4	A	11	-	4,4,4	0.11	0	6,6,6	0.43	0
2	SO4	A	43	-	4,4,4	0.15	0	6,6,6	0.24	0
2	SO4	A	46	-	4,4,4	0.13	0	6,6,6	0.11	0
2	SO4	A	41	-	4,4,4	0.15	0	6,6,6	0.34	0
2	SO4	B	36	-	4,4,4	0.14	0	6,6,6	0.34	0
2	SO4	B	42	-	4,4,4	0.13	0	6,6,6	0.20	0
2	SO4	A	26	-	4,4,4	0.15	0	6,6,6	0.12	0
2	SO4	B	8	-	4,4,4	0.16	0	6,6,6	0.26	0
2	SO4	A	12	-	4,4,4	0.11	0	6,6,6	0.18	0
2	SO4	D	13	-	4,4,4	0.12	0	6,6,6	0.21	0
2	SO4	C	18	-	4,4,4	0.17	0	6,6,6	0.25	0
2	SO4	D	9	-	4,4,4	0.17	0	6,6,6	0.39	0
2	SO4	C	33	-	4,4,4	0.14	0	6,6,6	0.27	0
2	SO4	B	21	-	4,4,4	0.21	0	6,6,6	0.25	0
2	SO4	A	15	-	4,4,4	0.16	0	6,6,6	0.41	0
2	SO4	B	38	-	4,4,4	0.19	0	6,6,6	0.28	0
2	SO4	B	44	-	4,4,4	0.15	0	6,6,6	0.15	0
2	SO4	D	30	-	4,4,4	0.15	0	6,6,6	0.07	0
2	SO4	B	23	-	4,4,4	0.15	0	6,6,6	0.26	0
2	SO4	B	35	-	4,4,4	0.14	0	6,6,6	0.15	0
2	SO4	A	3	-	4,4,4	0.14	0	6,6,6	0.36	0
2	SO4	A	27	-	4,4,4	0.20	0	6,6,6	0.22	0
2	SO4	D	5	-	4,4,4	0.14	0	6,6,6	0.29	0
2	SO4	C	2	-	4,4,4	0.14	0	6,6,6	0.18	0
2	SO4	C	31	-	4,4,4	0.15	0	6,6,6	0.44	0
2	SO4	B	32	-	4,4,4	0.16	0	6,6,6	0.26	0
2	SO4	A	45	-	4,4,4	0.15	0	6,6,6	0.08	0
2	SO4	C	4	-	4,4,4	0.13	0	6,6,6	0.39	0
2	SO4	B	37	-	4,4,4	0.13	0	6,6,6	0.13	0
3	LDA	D	1	-	12,15,15	2.06	1 (8%)	14,17,17	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	D	40	-	4,4,4	0.13	0	6,6,6	0.26	0
2	SO4	C	28	-	4,4,4	0.11	0	6,6,6	0.23	0
2	SO4	D	39	-	4,4,4	0.10	0	6,6,6	0.13	0
2	SO4	A	22	-	4,4,4	0.19	0	6,6,6	0.23	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	LDA	D	1	-	-	8/13/13/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1	LDA	O1-N1	-7.10	1.25	1.42

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1	LDA	C2-C1-N1-O1
3	D	1	LDA	C2-C1-N1-CM1
3	D	1	LDA	C7-C8-C9-C10
3	D	1	LDA	C3-C4-C5-C6
3	D	1	LDA	C9-C10-C11-C12

There are no ring outliers.

18 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	17	SO4	4	0
2	B	25	SO4	1	0
2	D	7	SO4	1	0
2	C	19	SO4	1	0
2	A	11	SO4	2	0
2	A	41	SO4	5	0
2	C	18	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	9	SO4	1	0
2	A	15	SO4	2	0
2	B	38	SO4	5	0
2	B	23	SO4	1	0
2	B	35	SO4	1	0
2	A	3	SO4	1	0
2	D	5	SO4	1	0
2	C	31	SO4	3	0
2	C	4	SO4	1	0
3	D	1	LDA	7	0
2	D	39	SO4	2	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	598/625 (95%)	0.19	8 (1%) 77 59	30, 74, 136, 217	0
1	B	621/625 (99%)	0.09	4 (0%) 89 78	24, 68, 118, 219	0
1	C	623/625 (99%)	0.03	3 (0%) 91 81	14, 60, 112, 317	0
1	D	602/625 (96%)	0.07	3 (0%) 91 81	24, 64, 129, 183	0
All	All	2444/2500 (97%)	0.09	18 (0%) 87 75	14, 66, 125, 317	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	91	GLY	4.2
1	B	691	THR	3.3
1	B	692	HIS	3.2
1	D	130	PHE	3.0
1	A	326	GLN	2.9

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 monosaccharides 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(\AA^2)	Q<0.9
2	SO4	A	43	5/5	0.83	0.18	129,129,129,129	0
2	SO4	B	37	5/5	0.86	0.17	123,123,123,123	0
2	SO4	A	27	5/5	0.88	0.30	101,101,101,101	0
2	SO4	C	2	5/5	0.88	0.18	106,106,106,106	0
2	SO4	D	39	5/5	0.88	0.12	123,123,123,123	0
2	SO4	C	28	5/5	0.89	0.17	120,120,120,120	0
2	SO4	A	16	5/5	0.90	0.14	108,108,108,108	0
2	SO4	A	46	5/5	0.90	0.21	151,151,151,151	0
2	SO4	D	40	5/5	0.91	0.16	104,104,104,104	0
2	SO4	B	32	5/5	0.92	0.17	104,104,104,104	0
2	SO4	A	12	5/5	0.92	0.20	108,108,108,108	0
2	SO4	C	4	5/5	0.93	0.20	79,79,79,79	0
2	SO4	B	36	5/5	0.93	0.18	94,94,94,94	0
2	SO4	C	31	5/5	0.93	0.16	81,81,81,81	0
2	SO4	C	33	5/5	0.93	0.16	101,101,101,101	0
2	SO4	D	13	5/5	0.93	0.16	102,102,102,102	0
2	SO4	D	14	5/5	0.93	0.22	105,105,105,105	0
2	SO4	B	20	5/5	0.93	0.12	119,119,119,119	0
2	SO4	A	41	5/5	0.93	0.19	91,91,91,91	0
2	SO4	A	22	5/5	0.94	0.14	77,77,77,77	0
2	SO4	A	24	5/5	0.94	0.18	79,79,79,79	0
2	SO4	A	11	5/5	0.94	0.12	90,90,90,90	0
2	SO4	D	9	5/5	0.94	0.18	75,75,75,75	0
2	SO4	B	42	5/5	0.95	0.15	94,94,94,94	0
2	SO4	B	44	5/5	0.95	0.12	118,118,118,118	0
2	SO4	B	25	5/5	0.95	0.12	100,100,100,100	0
2	SO4	B	38	5/5	0.96	0.12	91,91,91,91	0
2	SO4	A	45	5/5	0.96	0.15	115,115,115,115	0
2	SO4	D	30	5/5	0.96	0.16	112,112,112,112	0
2	SO4	D	5	5/5	0.96	0.15	85,85,85,85	0
2	SO4	B	21	5/5	0.96	0.12	87,87,87,87	0
2	SO4	A	26	5/5	0.97	0.17	101,101,101,101	0
2	SO4	B	23	5/5	0.97	0.11	95,95,95,95	0
2	SO4	A	3	5/5	0.97	0.17	79,79,79,79	0
2	SO4	A	29	5/5	0.97	0.08	112,112,112,112	0
2	SO4	C	1	5/5	0.97	0.18	82,82,82,82	0
2	SO4	B	34	5/5	0.97	0.19	69,69,69,69	0
2	SO4	B	35	5/5	0.97	0.12	102,102,102,102	0
2	SO4	C	19	5/5	0.97	0.16	58,58,58,58	0
2	SO4	A	17	5/5	0.97	0.15	88,88,88,88	0
3	LDA	D	1	16/16	0.97	0.42	49,49,49,49	0
2	SO4	C	18	5/5	0.98	0.12	75,75,75,75	0
2	SO4	B	8	5/5	0.98	0.16	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	A	15	5/5	0.98	0.21	50,50,50,50	0
2	SO4	D	10	5/5	0.98	0.18	53,53,53,53	0
2	SO4	C	6	5/5	0.98	0.14	77,77,77,77	0
2	SO4	D	7	5/5	0.99	0.14	81,81,81,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.