



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 8, 2023 – 04:20 am GMT

PDB ID : 2J3Z
Title : Crystal structure of the enzymatic component C2-I of the C2-toxin from Clostridium botulinum at pH 6.1
Authors : Schleberger, C.; Hochmann, H.; Barth, H.; Aktories, K.; Schulz, G.E.
Deposited on : 2006-08-23
Resolution : 2.30 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 : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

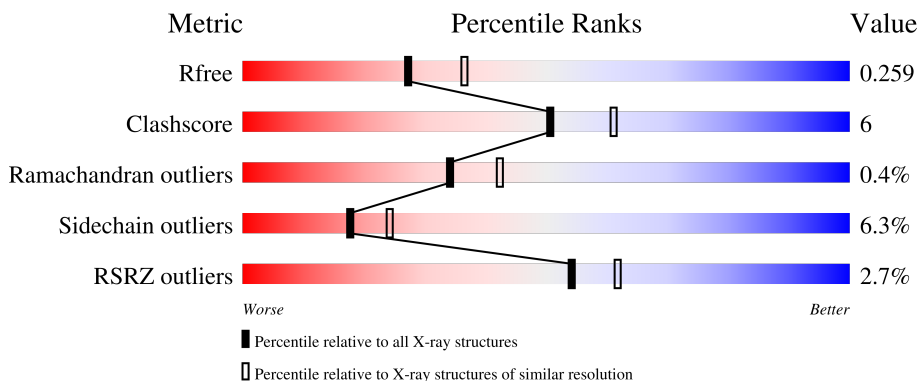
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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.



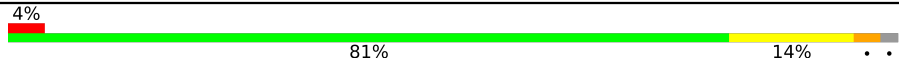
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	431	 3% 80% 18% .
1	B	431	 2% 82% 16% .
1	C	431	 2% 85% 13% ..
1	D	431	 2% 79% 16% ..
1	E	431	 3% 82% 14% ...

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Mol	Chain	Length	Quality of chain
1	F	431	 A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a small red segment on the left labeled '4%', a large green segment in the middle labeled '81%', and a small yellow segment on the right labeled '14%'. There are two small black dots at the far right end of the bar.

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
4	SO4	F	1430	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 21502 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 C2 TOXIN COMPONENT I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	430	Total 3476	C 2216	N 575	O 683	S 2	0	0	0
1	B	430	Total 3476	C 2216	N 575	O 683	S 2	0	0	0
1	C	428	Total 3459	C 2205	N 573	O 679	S 2	0	0	0
1	D	421	Total 3401	C 2167	N 562	O 670	S 2	0	0	0
1	E	423	Total 3418	C 2176	N 566	O 674	S 2	0	0	0
1	F	421	Total 3401	C 2167	N 562	O 670	S 2	0	0	0

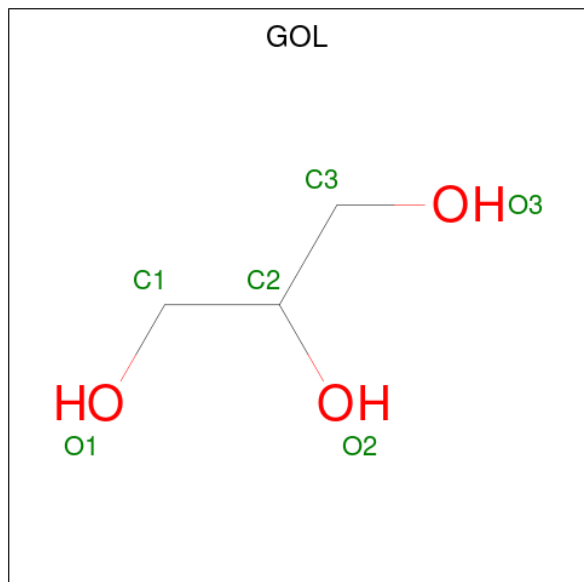
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ARG	HIS	engineered mutation	UNP O69275
B	77	ARG	HIS	engineered mutation	UNP O69275
C	77	ARG	HIS	engineered mutation	UNP O69275
D	77	ARG	HIS	engineered mutation	UNP O69275
E	77	ARG	HIS	engineered mutation	UNP O69275
F	77	ARG	HIS	engineered mutation	UNP O69275
A	121	ASP	ASN	conflict	UNP O69275
B	121	ASP	ASN	conflict	UNP O69275
C	121	ASP	ASN	conflict	UNP O69275
D	121	ASP	ASN	conflict	UNP O69275
E	121	ASP	ASN	conflict	UNP O69275
F	121	ASP	ASN	conflict	UNP O69275

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Co 1 1	0	0
2	B	2	Total Co 2 2	0	0
2	C	1	Total Co 1 1	0	0
2	D	1	Total Co 1 1	0	0
2	E	1	Total Co 1 1	0	0
2	F	1	Total Co 1 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



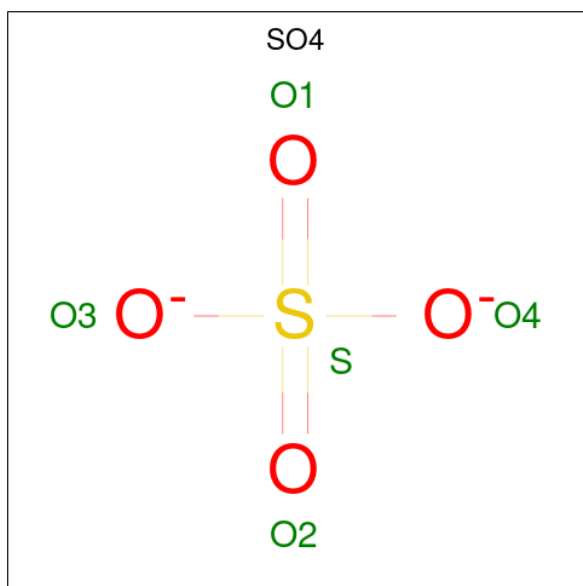
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0
3	F	1	Total C O 6 3 3	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	103	Total	O	0	0
			103	103		
5	B	97	Total	O	0	0
			97	97		
5	C	119	Total	O	0	0
			119	119		
5	D	86	Total	O	0	0
			86	86		
5	E	98	Total	O	0	0
			98	98		

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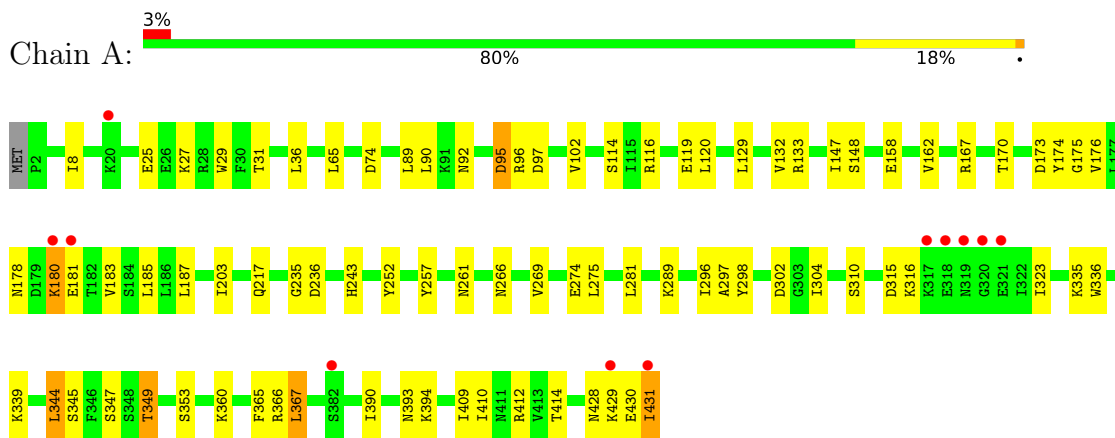
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	89	Total	O	0	0
			89	89		

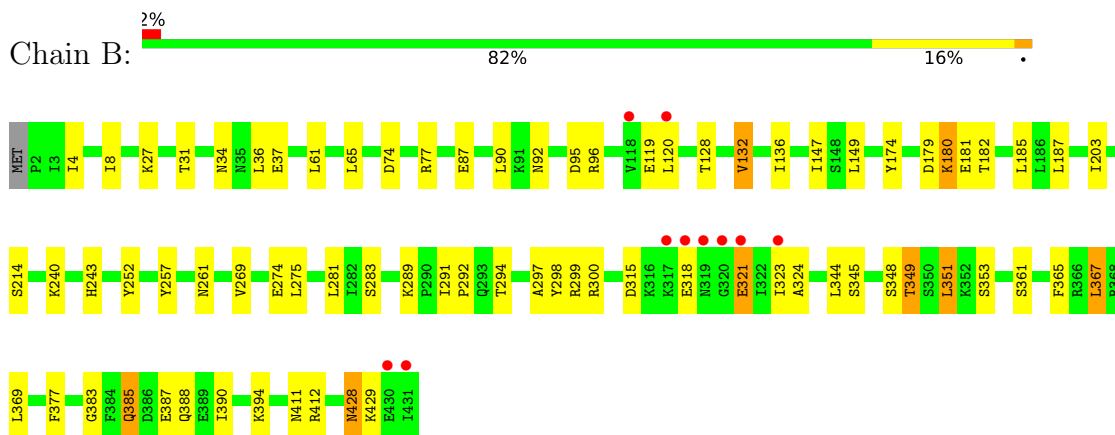
3 Residue-property plots [i](#)

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.

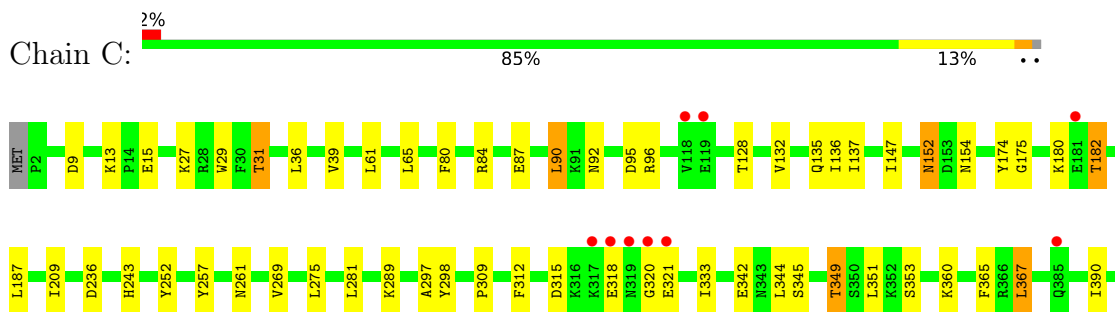
- Molecule 1: C2 TOXIN COMPONENT I

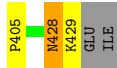


- Molecule 1: C2 TOXIN COMPONENT I



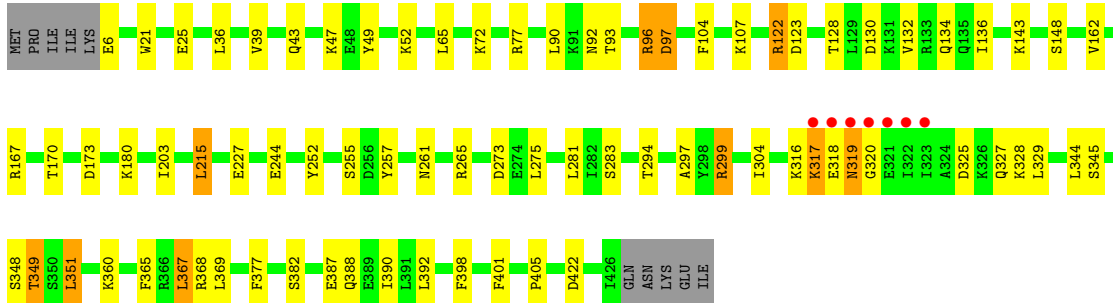
- Molecule 1: C2 TOXIN COMPONENT I





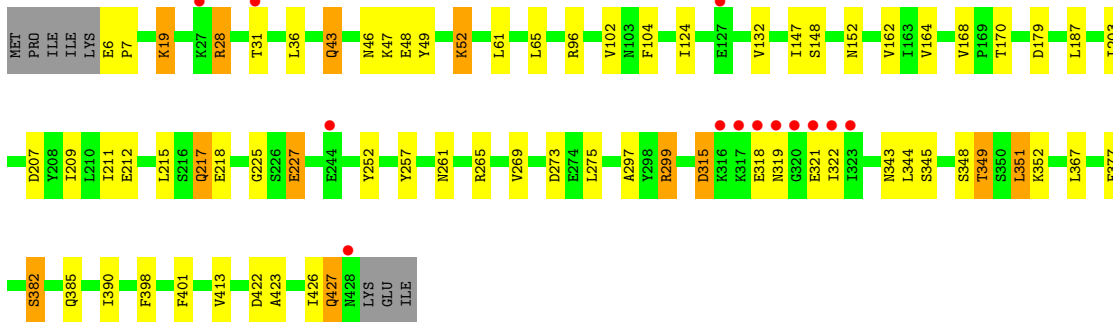
- Molecule 1: C2 TOXIN COMPONENT I

Chain D: 2% 79% 16% ..



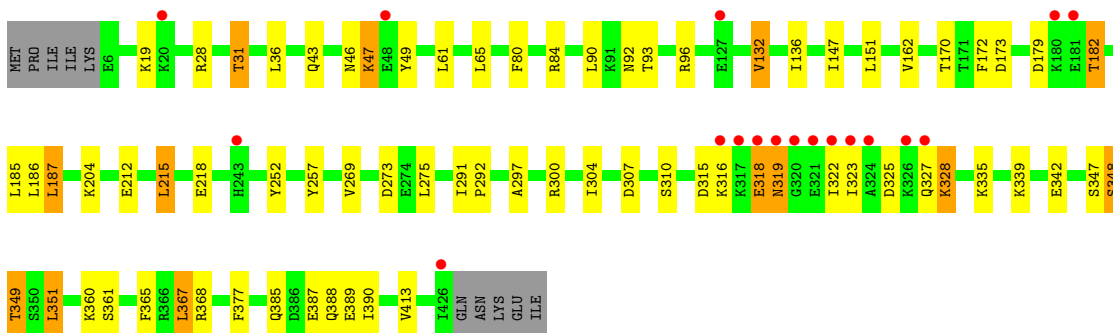
- Molecule 1: C2 TOXIN COMPONENT I

Chain E: 3% 82% 14% ..



- Molecule 1: C2 TOXIN COMPONENT I

Chain F: 4% 81% 14% ..



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	93.42Å 272.90Å 246.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.30 46.29 – 2.25	Depositor EDS
% Data completeness (in resolution range)	100.0 (40.00-2.30) 92.7 (46.29-2.25)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	22.11 (at 2.24Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.200 , 0.258 0.201 , 0.259	Depositor DCC
R_{free} test set	2756 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	27.3	Xtrriage
Anisotropy	0.443	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 35.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	21502	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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, CO, GOL

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	0.68	0/3537	0.75	0/4771
1	B	0.70	0/3537	0.77	0/4771
1	C	0.68	0/3520	0.78	1/4748 (0.0%)
1	D	0.75	2/3461 (0.1%)	0.79	5/4670 (0.1%)
1	E	0.66	0/3478	0.78	1/4693 (0.0%)
1	F	0.78	3/3461 (0.1%)	0.79	3/4670 (0.1%)
All	All	0.71	5/20994 (0.0%)	0.78	10/28323 (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	B	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	328	LYS	CE-NZ	19.60	1.98	1.49
1	D	317	LYS	CE-NZ	14.63	1.85	1.49
1	D	317	LYS	CD-CE	8.74	1.73	1.51
1	F	327	GLN	CD-NE2	7.13	1.50	1.32
1	F	318	GLU	CD-OE1	5.21	1.31	1.25

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	317	LYS	CD-CE-NZ	-8.07	93.15	111.70
1	D	299	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	F	328	LYS	CD-CE-NZ	-6.03	97.83	111.70
1	D	368	ARG	NE-CZ-NH1	-5.85	117.38	120.30
1	C	95	ASP	CB-CA-C	-5.66	99.08	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	428	ASN	Peptide
1	B	428	ASN	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	3476	0	3484	52	0
1	B	3476	0	3484	45	0
1	C	3459	0	3467	32	0
1	D	3401	0	3397	37	1
1	E	3418	0	3411	40	1
1	F	3401	0	3397	39	1
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	24	0	32	0	0
3	B	12	0	16	2	0
3	C	12	0	16	1	0
3	D	12	0	16	0	0
3	E	6	0	8	2	0
3	F	6	0	8	0	0
4	A	25	0	0	0	0
4	B	40	0	0	1	0
4	C	35	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	30	0	0	0	0
4	E	35	0	0	0	0
4	F	35	0	0	0	0
5	A	103	0	0	3	0
5	B	97	0	0	1	0
5	C	119	0	0	2	0
5	D	86	0	0	1	0
5	E	98	0	0	4	0
5	F	89	0	0	0	0
All	All	21502	0	20736	236	2

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 236 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:317:LYS:NZ	1:D:317:LYS:CE	1.85	1.39
1:F:328:LYS:NZ	1:F:328:LYS:CE	1.98	1.25
1:A:394:LYS:HZ3	1:A:431:ILE:HG21	1.22	1.02
1:E:299:ARG:HA	3:E:1430:GOL:H32	1.43	0.96
1:D:39:VAL:O	1:D:43:GLN:HG3	1.68	0.92

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:273:ASP:OD2	1:F:273:ASP:OD1[3_554]	1.71	0.49
1:D:273:ASP:OD1	1:D:273:ASP:OD2[3_554]	1.97	0.23

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	428/431 (99%)	410 (96%)	18 (4%)	0	100	100
1	B	428/431 (99%)	405 (95%)	20 (5%)	3 (1%)	22	26
1	C	426/431 (99%)	412 (97%)	13 (3%)	1 (0%)	47	58
1	D	419/431 (97%)	407 (97%)	9 (2%)	3 (1%)	22	26
1	E	421/431 (98%)	401 (95%)	19 (4%)	1 (0%)	47	58
1	F	419/431 (97%)	402 (96%)	15 (4%)	2 (0%)	29	35
All	All	2541/2586 (98%)	2437 (96%)	94 (4%)	10 (0%)	34	42

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	385	GLN
1	B	180	LYS
1	B	321	GLU
1	D	180	LYS
1	F	385	GLN

5.3.2 Protein sidechains [i](#)

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	393/394 (100%)	369 (94%)	24 (6%)	18	25
1	B	393/394 (100%)	369 (94%)	24 (6%)	18	25
1	C	391/394 (99%)	372 (95%)	19 (5%)	25	35
1	D	384/394 (98%)	358 (93%)	26 (7%)	16	21
1	E	386/394 (98%)	358 (93%)	28 (7%)	14	18
1	F	384/394 (98%)	357 (93%)	27 (7%)	15	19
All	All	2331/2364 (99%)	2183 (94%)	148 (6%)	18	24

5 of 148 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	349	THR

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Mol	Chain	Res	Type
1	F	348	SER
1	E	413	VAL
1	F	132	VAL
1	C	31	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	152	ASN
1	F	55	ASN
1	D	55	ASN
1	F	188	ASN
1	E	266	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](#)

Of 59 ligands modelled in this entry, 7 are monoatomic - leaving 52 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
3	GOL	C	1431	-	5,5,5	0.23	0	5,5,5	0.98	0
3	GOL	B	1434	-	5,5,5	0.41	0	5,5,5	0.58	0
4	SO4	F	1434	-	4,4,4	0.21	0	6,6,6	0.28	0
4	SO4	D	1430	-	4,4,4	0.12	0	6,6,6	0.38	0
4	SO4	D	1433	-	4,4,4	0.14	0	6,6,6	0.45	0
3	GOL	A	1435	-	5,5,5	0.33	0	5,5,5	0.67	0
3	GOL	D	1429	-	5,5,5	0.26	0	5,5,5	0.90	0
4	SO4	E	1434	-	4,4,4	0.19	0	6,6,6	0.27	0
4	SO4	B	1438	-	4,4,4	0.25	0	6,6,6	0.36	0
4	SO4	C	1434	-	4,4,4	0.21	0	6,6,6	0.21	0
3	GOL	D	1428	-	5,5,5	0.41	0	5,5,5	0.49	0
4	SO4	B	1443	-	4,4,4	0.29	0	6,6,6	0.24	0
4	SO4	E	1436	-	4,4,4	0.21	0	6,6,6	0.20	0
3	GOL	B	1435	-	5,5,5	0.63	0	5,5,5	0.86	0
3	GOL	E	1430	-	5,5,5	0.33	0	5,5,5	0.62	0
4	SO4	D	1431	-	4,4,4	0.19	0	6,6,6	0.49	0
4	SO4	A	1440	-	4,4,4	0.20	0	6,6,6	0.43	0
4	SO4	B	1441	-	4,4,4	0.27	0	6,6,6	0.23	0
4	SO4	E	1437	-	4,4,4	0.23	0	6,6,6	0.43	0
4	SO4	A	1441	-	4,4,4	0.22	0	6,6,6	0.12	0
4	SO4	C	1439	-	4,4,4	0.24	0	6,6,6	0.39	0
4	SO4	F	1432	-	4,4,4	0.18	0	6,6,6	0.38	0
3	GOL	A	1434	-	5,5,5	0.43	0	5,5,5	1.33	0
4	SO4	A	1437	-	4,4,4	0.23	0	6,6,6	0.44	0
4	SO4	F	1435	-	4,4,4	0.21	0	6,6,6	0.51	0
4	SO4	C	1433	-	4,4,4	0.19	0	6,6,6	0.32	0
3	GOL	F	1428	-	5,5,5	0.32	0	5,5,5	1.15	0
4	SO4	F	1429	-	4,4,4	0.24	0	6,6,6	0.43	0
4	SO4	E	1435	-	4,4,4	0.25	0	6,6,6	0.34	0
4	SO4	F	1433	-	4,4,4	0.13	0	6,6,6	0.46	0
4	SO4	F	1430	-	4,4,4	0.20	0	6,6,6	0.24	0
4	SO4	C	1435	-	4,4,4	0.18	0	6,6,6	0.20	0
4	SO4	B	1437	-	4,4,4	0.26	0	6,6,6	0.45	0
4	SO4	F	1431	-	4,4,4	0.24	0	6,6,6	0.25	0
4	SO4	D	1434	-	4,4,4	0.20	0	6,6,6	0.35	0
4	SO4	E	1431	-	4,4,4	0.16	0	6,6,6	0.42	0
4	SO4	A	1438	-	4,4,4	0.16	0	6,6,6	0.40	0
4	SO4	E	1433	-	4,4,4	0.17	0	6,6,6	0.34	0
4	SO4	C	1436	-	4,4,4	0.17	0	6,6,6	0.18	0
4	SO4	D	1435	-	4,4,4	0.23	0	6,6,6	0.30	0
4	SO4	B	1442	-	4,4,4	0.22	0	6,6,6	0.52	0
4	SO4	C	1437	-	4,4,4	0.23	0	6,6,6	0.51	0
4	SO4	B	1436	-	4,4,4	0.22	0	6,6,6	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	D	1432	-	4,4,4	0.17	0	6,6,6	0.24	0
4	SO4	B	1439	-	4,4,4	0.22	0	6,6,6	0.34	0
4	SO4	C	1438	-	4,4,4	0.24	0	6,6,6	0.15	0
3	GOL	A	1433	-	5,5,5	0.50	0	5,5,5	0.28	0
4	SO4	A	1439	-	4,4,4	0.13	0	6,6,6	0.18	0
3	GOL	C	1432	-	5,5,5	0.29	0	5,5,5	0.56	0
4	SO4	E	1432	-	4,4,4	0.34	0	6,6,6	0.49	0
4	SO4	B	1440	-	4,4,4	0.32	0	6,6,6	0.44	0
3	GOL	A	1436	-	5,5,5	0.35	0	5,5,5	0.43	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	F	1428	-	-	2/4/4/4	-
3	GOL	C	1431	-	-	2/4/4/4	-
3	GOL	B	1434	-	-	1/4/4/4	-
3	GOL	B	1435	-	-	2/4/4/4	-
3	GOL	E	1430	-	-	3/4/4/4	-
3	GOL	A	1435	-	-	3/4/4/4	-
3	GOL	D	1429	-	-	2/4/4/4	-
3	GOL	A	1434	-	-	4/4/4/4	-
3	GOL	A	1433	-	-	2/4/4/4	-
3	GOL	C	1432	-	-	4/4/4/4	-
3	GOL	D	1428	-	-	2/4/4/4	-
3	GOL	A	1436	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1434	GOL	O1-C1-C2-O2
3	A	1434	GOL	O1-C1-C2-C3
3	A	1436	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	B	1435	GOL	O1-C1-C2-O2
3	B	1435	GOL	O1-C1-C2-C3

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1434	GOL	1	0
3	B	1435	GOL	1	0
3	E	1430	GOL	2	0
4	B	1437	SO4	1	0
3	C	1432	GOL	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	430/431 (99%)	-0.05	11 (2%) 56 63	22, 33, 49, 78	1 (0%)
1	B	430/431 (99%)	-0.05	10 (2%) 60 67	22, 34, 54, 81	1 (0%)
1	C	428/431 (99%)	-0.07	9 (2%) 63 70	22, 32, 48, 80	1 (0%)
1	D	421/431 (97%)	-0.11	7 (1%) 70 76	22, 35, 57, 89	1 (0%)
1	E	423/431 (98%)	-0.01	13 (3%) 49 56	24, 35, 55, 73	1 (0%)
1	F	421/431 (97%)	0.07	18 (4%) 35 42	23, 37, 62, 117	1 (0%)
All	All	2553/2586 (98%)	-0.03	68 (2%) 54 62	22, 34, 55, 117	6 (0%)

The worst 5 of 68 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	431	ILE	11.7
1	F	319	ASN	6.7
1	B	320	GLY	6.6
1	F	317	LYS	6.6
1	B	319	ASN	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 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(Å ²)	Q<0.9
4	SO4	F	1430	5/5	0.41	0.46	110,110,111,111	0
3	GOL	B	1435	6/6	0.66	0.32	45,52,55,56	0
4	SO4	E	1432	5/5	0.72	0.20	75,75,77,77	0
4	SO4	B	1440	5/5	0.77	0.23	70,71,72,73	0
3	GOL	A	1435	6/6	0.80	0.23	60,61,61,62	0
3	GOL	D	1428	6/6	0.81	0.15	48,54,55,55	0
4	SO4	D	1434	5/5	0.82	0.24	92,92,93,93	0
3	GOL	A	1433	6/6	0.82	0.20	49,52,53,53	0
4	SO4	B	1442	5/5	0.82	0.18	76,77,78,78	0
4	SO4	E	1431	5/5	0.83	0.28	84,85,85,85	0
3	GOL	E	1430	6/6	0.84	0.20	48,56,57,58	0
3	GOL	F	1428	6/6	0.84	0.19	38,42,43,44	0
3	GOL	C	1432	6/6	0.84	0.15	56,57,58,59	0
3	GOL	B	1434	6/6	0.84	0.21	38,41,43,44	0
4	SO4	C	1433	5/5	0.85	0.15	70,71,72,73	0
4	SO4	F	1429	5/5	0.85	0.14	77,79,80,80	0
4	SO4	C	1436	5/5	0.85	0.22	78,79,79,80	0
4	SO4	F	1433	5/5	0.86	0.20	81,81,81,82	0
4	SO4	B	1437	5/5	0.87	0.22	64,65,66,68	0
4	SO4	B	1443	5/5	0.87	0.15	73,74,75,75	0
4	SO4	D	1430	5/5	0.87	0.21	77,77,78,79	0
4	SO4	A	1437	5/5	0.88	0.16	59,60,62,63	0
3	GOL	A	1434	6/6	0.88	0.19	39,40,43,43	0
4	SO4	B	1439	5/5	0.88	0.20	71,71,71,72	0
4	SO4	F	1435	5/5	0.88	0.15	63,63,63,63	0
4	SO4	A	1440	5/5	0.89	0.15	59,59,62,62	0
4	SO4	E	1437	5/5	0.89	0.31	74,75,75,76	0
4	SO4	D	1432	5/5	0.89	0.24	78,78,79,80	0
4	SO4	E	1435	5/5	0.90	0.14	62,64,64,65	0
4	SO4	B	1438	5/5	0.90	0.13	68,69,70,70	0
3	GOL	D	1429	6/6	0.90	0.15	37,43,44,45	0
4	SO4	A	1441	5/5	0.90	0.19	82,82,83,83	0
3	GOL	C	1431	6/6	0.90	0.19	39,39,40,42	0
4	SO4	E	1434	5/5	0.90	0.20	79,79,80,80	0
4	SO4	D	1431	5/5	0.91	0.36	75,75,75,76	0
4	SO4	C	1439	5/5	0.91	0.15	72,72,73,74	0
4	SO4	B	1436	5/5	0.91	0.14	71,72,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	F	1431	5/5	0.92	0.18	64,66,67,67	0
4	SO4	F	1432	5/5	0.92	0.11	64,66,66,66	0
4	SO4	D	1435	5/5	0.92	0.14	64,64,66,66	0
4	SO4	C	1435	5/5	0.92	0.18	79,79,79,80	0
4	SO4	E	1433	5/5	0.93	0.41	75,75,76,76	0
3	GOL	A	1436	6/6	0.93	0.19	56,58,58,58	0
4	SO4	F	1434	5/5	0.94	0.14	69,69,70,71	0
4	SO4	D	1433	5/5	0.94	0.20	74,76,76,76	0
4	SO4	A	1439	5/5	0.95	0.14	70,71,71,71	0
2	CO	A	1432	1/1	0.95	0.10	69,69,69,69	0
4	SO4	C	1434	5/5	0.95	0.14	73,73,73,74	0
4	SO4	B	1441	5/5	0.95	0.13	55,55,56,57	0
4	SO4	A	1438	5/5	0.95	0.10	75,75,76,76	0
4	SO4	C	1438	5/5	0.96	0.11	60,60,60,61	0
4	SO4	E	1436	5/5	0.96	0.10	62,63,63,64	0
2	CO	E	1429	1/1	0.96	0.09	57,57,57,57	0
2	CO	B	1433	1/1	0.96	0.14	64,64,64,64	0
4	SO4	C	1437	5/5	0.96	0.09	52,55,56,56	0
2	CO	C	1430	1/1	0.97	0.13	51,51,51,51	0
2	CO	D	1427	1/1	0.98	0.12	56,56,56,56	0
2	CO	B	1432	1/1	0.99	0.09	46,46,46,46	0
2	CO	F	1427	1/1	0.99	0.10	55,55,55,55	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.