



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2026 – 09:19 AM UTC

PDB ID : 4H5U / pdb_00004h5u
Title : Structural insights into yeast Nit2: wild-type yeast Nit2
Authors : Liu, H.; Qiu, X.; Zhang, M.; Gao, Y.; Niu, L.; Teng, M.
Deposited on : 2012-09-18
Resolution : 1.92 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

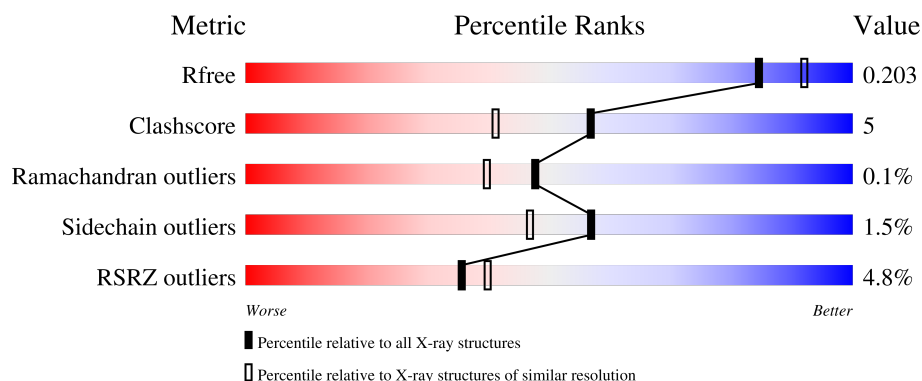
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.92 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	1188 (1.92-1.92)
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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	341	4% 82% 6% 11%
1	B	341	4% 82% 7% 11%
1	C	341	2% 77% 9% 13%
1	D	341	7% 79% 9% 11%

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
1	CAF	C	169	-	-	X	-
2	GOL	D	403	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10365 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 Probable hydrolase NIT2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	303	Total	As	C	N	O	S	0	4	0
			2410	1	1533	420	443	13			
1	B	303	Total	As	C	N	O	S	0	1	0
			2396	1	1520	417	447	11			
1	C	296	Total	As	C	N	O	S	0	3	0
			2353	1	1493	409	439	11			
1	D	302	Total	As	C	N	O	S	0	3	0
			2339	1	1492	396	438	12			

There are 136 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MET	-	expression tag	UNP P47016
A	-32	GLY	-	expression tag	UNP P47016
A	-31	SER	-	expression tag	UNP P47016
A	-30	SER	-	expression tag	UNP P47016
A	-29	HIS	-	expression tag	UNP P47016
A	-28	HIS	-	expression tag	UNP P47016
A	-27	HIS	-	expression tag	UNP P47016
A	-26	HIS	-	expression tag	UNP P47016
A	-25	HIS	-	expression tag	UNP P47016
A	-24	HIS	-	expression tag	UNP P47016
A	-23	SER	-	expression tag	UNP P47016
A	-22	SER	-	expression tag	UNP P47016
A	-21	GLY	-	expression tag	UNP P47016
A	-20	LEU	-	expression tag	UNP P47016
A	-19	VAL	-	expression tag	UNP P47016
A	-18	PRO	-	expression tag	UNP P47016
A	-17	ARG	-	expression tag	UNP P47016
A	-16	GLY	-	expression tag	UNP P47016
A	-15	SER	-	expression tag	UNP P47016
A	-14	HIS	-	expression tag	UNP P47016
A	-13	MET	-	expression tag	UNP P47016

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	ALA	-	expression tag	UNP P47016
A	-11	SER	-	expression tag	UNP P47016
A	-10	MET	-	expression tag	UNP P47016
A	-9	THR	-	expression tag	UNP P47016
A	-8	GLY	-	expression tag	UNP P47016
A	-7	GLY	-	expression tag	UNP P47016
A	-6	GLN	-	expression tag	UNP P47016
A	-5	GLN	-	expression tag	UNP P47016
A	-4	MET	-	expression tag	UNP P47016
A	-3	GLY	-	expression tag	UNP P47016
A	-2	ARG	-	expression tag	UNP P47016
A	-1	GLY	-	expression tag	UNP P47016
A	0	SER	-	expression tag	UNP P47016
B	-33	MET	-	expression tag	UNP P47016
B	-32	GLY	-	expression tag	UNP P47016
B	-31	SER	-	expression tag	UNP P47016
B	-30	SER	-	expression tag	UNP P47016
B	-29	HIS	-	expression tag	UNP P47016
B	-28	HIS	-	expression tag	UNP P47016
B	-27	HIS	-	expression tag	UNP P47016
B	-26	HIS	-	expression tag	UNP P47016
B	-25	HIS	-	expression tag	UNP P47016
B	-24	HIS	-	expression tag	UNP P47016
B	-23	SER	-	expression tag	UNP P47016
B	-22	SER	-	expression tag	UNP P47016
B	-21	GLY	-	expression tag	UNP P47016
B	-20	LEU	-	expression tag	UNP P47016
B	-19	VAL	-	expression tag	UNP P47016
B	-18	PRO	-	expression tag	UNP P47016
B	-17	ARG	-	expression tag	UNP P47016
B	-16	GLY	-	expression tag	UNP P47016
B	-15	SER	-	expression tag	UNP P47016
B	-14	HIS	-	expression tag	UNP P47016
B	-13	MET	-	expression tag	UNP P47016
B	-12	ALA	-	expression tag	UNP P47016
B	-11	SER	-	expression tag	UNP P47016
B	-10	MET	-	expression tag	UNP P47016
B	-9	THR	-	expression tag	UNP P47016
B	-8	GLY	-	expression tag	UNP P47016
B	-7	GLY	-	expression tag	UNP P47016
B	-6	GLN	-	expression tag	UNP P47016
B	-5	GLN	-	expression tag	UNP P47016

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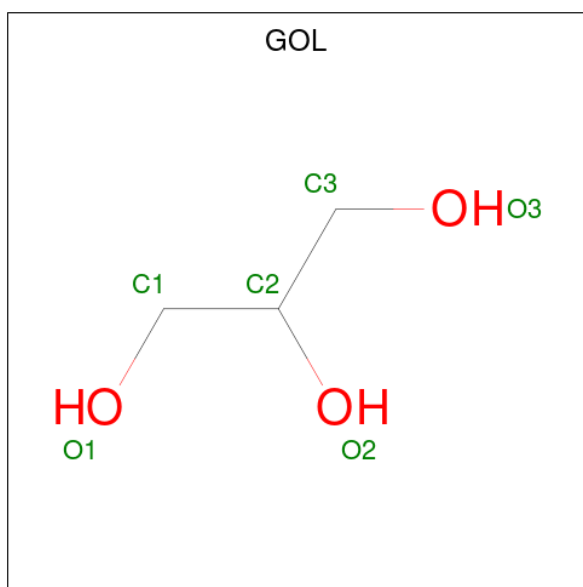
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B	-4	MET	-	expression tag	UNP P47016
B	-3	GLY	-	expression tag	UNP P47016
B	-2	ARG	-	expression tag	UNP P47016
B	-1	GLY	-	expression tag	UNP P47016
B	0	SER	-	expression tag	UNP P47016
C	-33	MET	-	expression tag	UNP P47016
C	-32	GLY	-	expression tag	UNP P47016
C	-31	SER	-	expression tag	UNP P47016
C	-30	SER	-	expression tag	UNP P47016
C	-29	HIS	-	expression tag	UNP P47016
C	-28	HIS	-	expression tag	UNP P47016
C	-27	HIS	-	expression tag	UNP P47016
C	-26	HIS	-	expression tag	UNP P47016
C	-25	HIS	-	expression tag	UNP P47016
C	-24	HIS	-	expression tag	UNP P47016
C	-23	SER	-	expression tag	UNP P47016
C	-22	SER	-	expression tag	UNP P47016
C	-21	GLY	-	expression tag	UNP P47016
C	-20	LEU	-	expression tag	UNP P47016
C	-19	VAL	-	expression tag	UNP P47016
C	-18	PRO	-	expression tag	UNP P47016
C	-17	ARG	-	expression tag	UNP P47016
C	-16	GLY	-	expression tag	UNP P47016
C	-15	SER	-	expression tag	UNP P47016
C	-14	HIS	-	expression tag	UNP P47016
C	-13	MET	-	expression tag	UNP P47016
C	-12	ALA	-	expression tag	UNP P47016
C	-11	SER	-	expression tag	UNP P47016
C	-10	MET	-	expression tag	UNP P47016
C	-9	THR	-	expression tag	UNP P47016
C	-8	GLY	-	expression tag	UNP P47016
C	-7	GLY	-	expression tag	UNP P47016
C	-6	GLN	-	expression tag	UNP P47016
C	-5	GLN	-	expression tag	UNP P47016
C	-4	MET	-	expression tag	UNP P47016
C	-3	GLY	-	expression tag	UNP P47016
C	-2	ARG	-	expression tag	UNP P47016
C	-1	GLY	-	expression tag	UNP P47016
C	0	SER	-	expression tag	UNP P47016
D	-33	MET	-	expression tag	UNP P47016
D	-32	GLY	-	expression tag	UNP P47016
D	-31	SER	-	expression tag	UNP P47016

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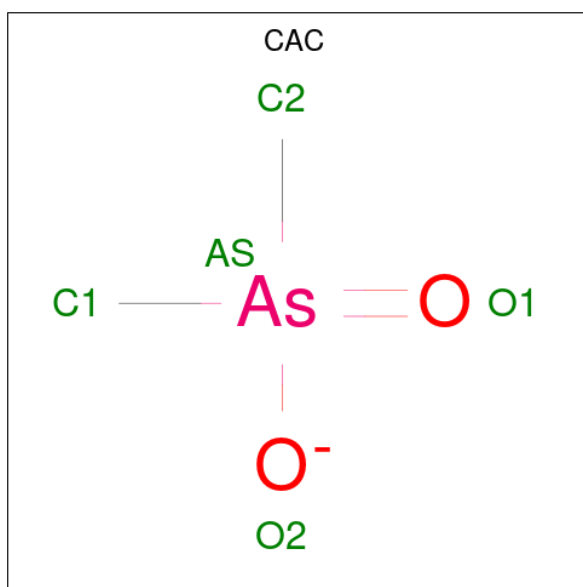
Chain	Residue	Modelled	Actual	Comment	Reference
D	-30	SER	-	expression tag	UNP P47016
D	-29	HIS	-	expression tag	UNP P47016
D	-28	HIS	-	expression tag	UNP P47016
D	-27	HIS	-	expression tag	UNP P47016
D	-26	HIS	-	expression tag	UNP P47016
D	-25	HIS	-	expression tag	UNP P47016
D	-24	HIS	-	expression tag	UNP P47016
D	-23	SER	-	expression tag	UNP P47016
D	-22	SER	-	expression tag	UNP P47016
D	-21	GLY	-	expression tag	UNP P47016
D	-20	LEU	-	expression tag	UNP P47016
D	-19	VAL	-	expression tag	UNP P47016
D	-18	PRO	-	expression tag	UNP P47016
D	-17	ARG	-	expression tag	UNP P47016
D	-16	GLY	-	expression tag	UNP P47016
D	-15	SER	-	expression tag	UNP P47016
D	-14	HIS	-	expression tag	UNP P47016
D	-13	MET	-	expression tag	UNP P47016
D	-12	ALA	-	expression tag	UNP P47016
D	-11	SER	-	expression tag	UNP P47016
D	-10	MET	-	expression tag	UNP P47016
D	-9	THR	-	expression tag	UNP P47016
D	-8	GLY	-	expression tag	UNP P47016
D	-7	GLY	-	expression tag	UNP P47016
D	-6	GLN	-	expression tag	UNP P47016
D	-5	GLN	-	expression tag	UNP P47016
D	-4	MET	-	expression tag	UNP P47016
D	-3	GLY	-	expression tag	UNP P47016
D	-2	ARG	-	expression tag	UNP P47016
D	-1	GLY	-	expression tag	UNP P47016
D	0	SER	-	expression tag	UNP P47016

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is CACODYLATE ION (CCD ID: CAC') (formula: $C_2H_6AsO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	As	C	O	0	0
			5	1	2	2		

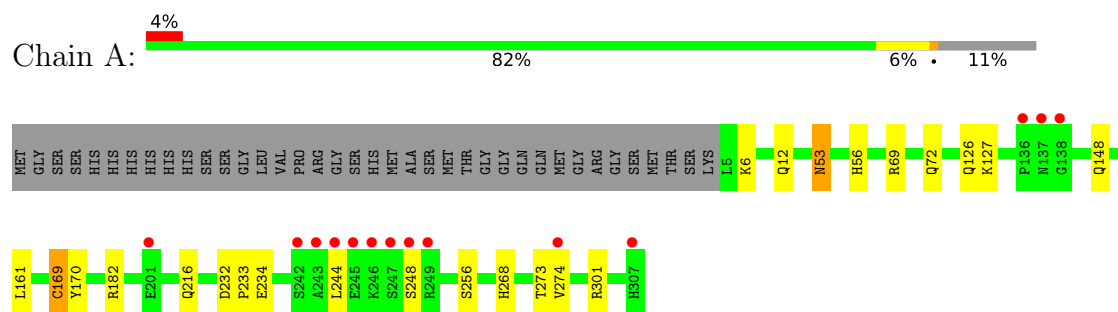
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	222	Total	O	0	0
			222	222		
4	B	211	Total	O	0	0
			211	211		
4	C	202	Total	O	0	0
			202	202		
4	D	149	Total	O	0	0
			149	149		

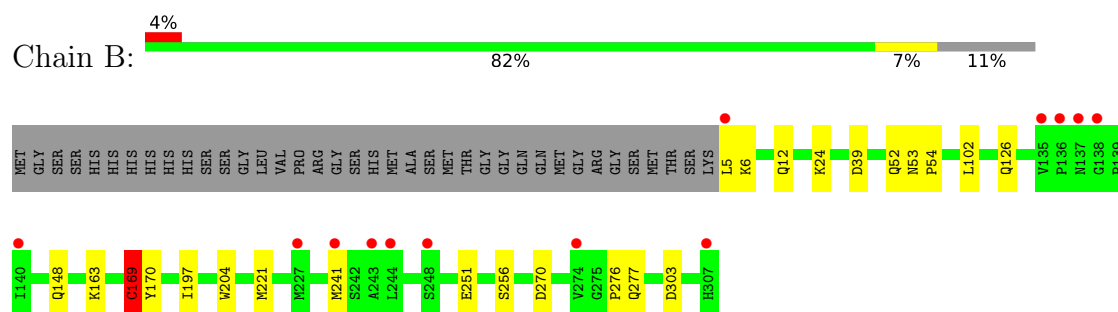
3 Residue-property plots [i](#)

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.

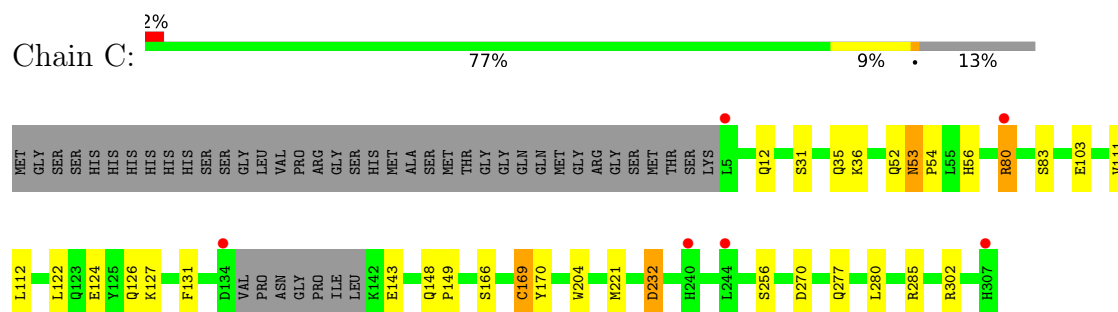
- Molecule 1: Probable hydrolase NIT2



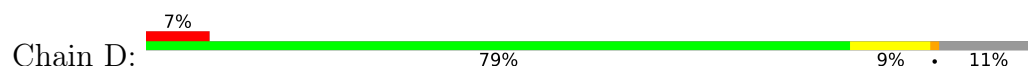
- Molecule 1: Probable hydrolase NIT2

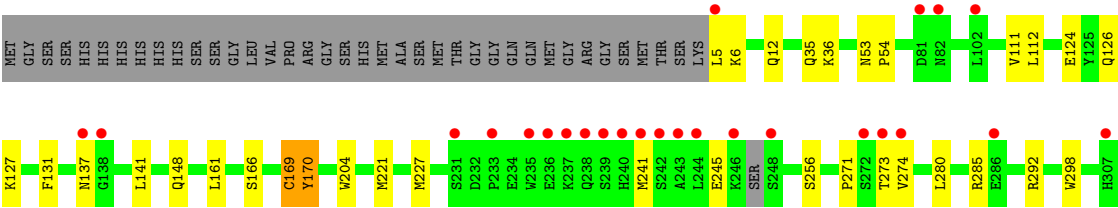


- Molecule 1: Probable hydrolase NIT2



- Molecule 1: Probable hydrolase NIT2





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.26Å 125.67Å 77.67Å 90.00° 95.23° 90.00°	Depositor
Resolution (Å)	48.00 – 1.92 48.00 – 1.92	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.00-1.92) 99.9 (48.00-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.64 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.171 , 0.202 0.172 , 0.203	Depositor DCC
R_{free} test set	4778 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	15.1	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10365	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CAC, CAF

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	0.63	4/2461 (0.2%)	0.76	0/3329
1	B	0.58	2/2438 (0.1%)	0.78	0/3301
1	C	0.65	4/2399 (0.2%)	0.77	0/3248
1	D	0.54	0/2386	0.79	0/3237
All	All	0.60	10/9684 (0.1%)	0.77	0/13115

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	B	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	6	LYS	C-O	-6.60	1.15	1.24
1	C	103	GLU	C-O	-6.34	1.15	1.24
1	A	232	ASP	C-O	-6.33	1.17	1.24
1	A	234	GLU	C-O	-6.32	1.16	1.24
1	C	302	ARG	C-O	-6.24	1.15	1.23
1	B	303	ASP	C-O	-5.93	1.16	1.24
1	A	233	PRO	C-O	-5.92	1.16	1.24
1	A	301	ARG	C-O	-5.80	1.16	1.23
1	C	143	GLU	C-O	-5.46	1.17	1.24
1	C	232	ASP	C-O	-5.12	1.17	1.24

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	169	CAF	Mainchain

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	2410	0	2429	16	0
1	B	2396	0	2401	15	0
1	C	2353	0	2329	28	0
1	D	2339	0	2272	29	0
2	A	24	0	32	0	0
2	B	24	0	31	0	0
2	C	12	0	16	0	0
2	D	18	0	24	6	0
3	B	5	0	0	0	0
4	A	222	0	0	1	0
4	B	211	0	0	0	0
4	C	202	0	0	0	0
4	D	149	0	0	2	0
All	All	10365	0	9534	87	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (87) 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:80:ARG:HG3	1:C:80:ARG:HH11	1.11	1.14
1:C:80:ARG:HG3	1:C:80:ARG:NH1	1.74	0.96
1:C:80:ARG:HH11	1:C:80:ARG:CG	1.81	0.92
1:C:111:VAL:HG11	1:C:124[A]:GLU:HG3	1.57	0.85
1:B:270:ASP:H	1:B:277:GLN:HE22	1.30	0.80
1:A:169:CAF:CE2	1:A:170:TYR:H	1.97	0.78
1:D:5:LEU:HD13	4:D:645:HOH:O	1.83	0.78
1:C:52:GLN:H	1:C:56:HIS:HD2	1.32	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:169:CAF:CE2	1:D:170:TYR:HB2	2.19	0.71
1:A:182:ARG:HH12	1:A:216:GLN:HE21	1.37	0.71
1:C:270:ASP:H	1:C:277:GLN:HE22	1.37	0.69
1:D:36:LYS:HD3	1:D:280:LEU:HD11	1.74	0.68
1:D:298:TRP:H	2:D:403:GOL:H31	1.60	0.67
1:C:127:LYS:NZ	1:C:169:CAF:CE2	2.57	0.67
1:C:31:SER:O	1:C:35[B]:GLN:HG2	1.97	0.64
1:B:169:CAF:CE1	1:B:170:TYR:HB2	2.27	0.64
1:D:111:VAL:HG11	1:D:124:GLU:HG3	1.79	0.63
1:C:53:ASN:ND2	1:C:56:HIS:H	1.96	0.63
1:A:169:CAF:CE2	1:A:170:TYR:HB2	2.30	0.62
1:D:53:ASN:HB2	1:D:54:PRO:HD2	1.82	0.60
1:B:5:LEU:HB3	1:B:39:ASP:OD2	2.01	0.60
1:C:52:GLN:H	1:C:56:HIS:CD2	2.16	0.59
1:C:127:LYS:HZ3	1:C:169:CAF:CE2	2.15	0.59
1:C:53:ASN:C	1:C:53:ASN:HD22	2.11	0.58
1:C:112:LEU:HD23	1:C:166:SER:HB3	1.86	0.58
1:C:169:CAF:CE2	1:C:170:TYR:H	2.18	0.57
1:D:298:TRP:N	2:D:403:GOL:H31	2.20	0.57
1:A:12:GLN:HE22	1:A:256:SER:H	1.53	0.56
1:C:169:CAF:CE2	1:C:170:TYR:HB2	2.35	0.56
1:D:127:LYS:NZ	1:D:169:CAF:CE2	2.69	0.55
1:D:127:LYS:HZ3	1:D:169:CAF:CE2	2.20	0.55
1:A:53:ASN:HD22	1:A:53:ASN:C	2.15	0.55
1:A:12:GLN:NE2	1:A:256:SER:H	2.05	0.55
1:D:298:TRP:HB2	2:D:403:GOL:H32	1.89	0.55
1:A:274:VAL:HG12	1:A:274:VAL:O	2.07	0.55
1:B:12:GLN:HE22	1:B:256:SER:H	1.54	0.55
1:A:53:ASN:ND2	1:A:56:HIS:H	2.05	0.54
1:D:12:GLN:NE2	1:D:256:SER:H	2.06	0.54
1:B:12:GLN:NE2	1:B:256:SER:H	2.06	0.53
1:B:52:GLN:HE22	1:B:241:MET:HE1	1.74	0.52
1:C:12:GLN:NE2	1:C:256:SER:H	2.08	0.52
1:C:126:GLN:HE22	1:C:148:GLN:HE21	1.58	0.51
1:D:169:CAF:CE2	1:D:170:TYR:H	2.24	0.51
1:C:36:LYS:HB3	1:C:280:LEU:HD11	1.92	0.51
1:A:127:LYS:NZ	1:A:169:CAF:CE2	2.74	0.51
1:A:126:GLN:HE22	1:A:148:GLN:HE21	1.57	0.50
1:D:112:LEU:HD23	1:D:166:SER:HB3	1.94	0.50
1:C:12:GLN:HE22	1:C:256:SER:H	1.59	0.50
1:B:197:ILE:HD11	1:B:251:GLU:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:CAF:CE1	1:B:170:TYR:H	2.23	0.50
1:D:5:LEU:HD22	1:D:285:ARG:H	1.76	0.50
1:D:298:TRP:H	2:D:403:GOL:C3	2.25	0.49
1:D:131:PHE:HB2	1:D:169:CAF:CE2	2.43	0.49
1:D:5:LEU:CD2	1:D:285:ARG:H	2.26	0.48
1:D:12:GLN:HE22	1:D:256:SER:H	1.60	0.48
1:B:270:ASP:H	1:B:277:GLN:NE2	2.05	0.47
1:C:53:ASN:HB2	1:C:54:PRO:HD2	1.97	0.47
1:A:126:GLN:HE22	1:A:148:GLN:NE2	2.13	0.47
1:B:53:ASN:HB2	1:B:54:PRO:HD2	1.98	0.46
1:C:127:LYS:HZ1	1:C:169:CAF:CE2	2.25	0.46
1:C:131:PHE:HB2	1:C:169:CAF:CE2	2.45	0.45
1:C:56:HIS:HE1	1:C:232:ASP:OD2	1.98	0.45
1:D:204:TRP:CZ2	1:D:221[B]:MET:HB3	2.51	0.45
1:D:241:MET:HG2	1:D:245:GLU:HB2	1.99	0.45
1:B:52:GLN:NE2	1:B:241:MET:HE1	2.31	0.44
1:C:53:ASN:HB2	1:C:54:PRO:CD	2.47	0.44
1:A:244:LEU:HD12	1:C:149:PRO:HG2	1.98	0.44
1:C:53:ASN:HD22	1:C:56:HIS:H	1.66	0.44
1:D:227[B]:MET:HE3	1:D:227[B]:MET:HB3	1.86	0.44
1:D:6:LYS:HB3	1:D:161:LEU:HD23	2.00	0.44
1:D:204:TRP:CZ2	1:D:221[A]:MET:HB3	2.53	0.44
1:D:298:TRP:HB2	2:D:403:GOL:C3	2.47	0.44
1:B:12:GLN:O	1:B:276:PRO:HA	2.17	0.43
1:B:53:ASN:HB2	1:B:54:PRO:CD	2.49	0.43
1:D:131:PHE:HE2	1:D:141:LEU:HD12	1.84	0.43
1:A:69:ARG:HA	1:A:72:GLN:HE21	1.83	0.43
1:A:127:LYS:HZ3	1:A:169:CAF:CE2	2.31	0.42
1:B:204:TRP:CZ2	1:B:221[A]:MET:HB3	2.54	0.42
1:D:292:ARG:O	2:D:403:GOL:O2	2.37	0.42
1:C:111:VAL:CG1	1:C:124[A]:GLU:HG3	2.40	0.42
1:D:53:ASN:HB2	1:D:54:PRO:CD	2.49	0.42
1:D:126:GLN:HE22	1:D:148:GLN:HE21	1.65	0.42
1:B:126:GLN:HE22	1:B:148:GLN:HE21	1.68	0.41
1:D:271:PRO:HG3	4:D:646:HOH:O	2.20	0.41
1:A:6:LYS:HD3	1:A:161:LEU:HA	2.03	0.41
1:A:268:HIS:HE1	4:A:589:HOH:O	2.04	0.41
1:C:204:TRP:CZ2	1:C:221[A]:MET:HB3	2.56	0.40

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	304/341 (89%)	302 (99%)	2 (1%)	0	100	100
1	B	301/341 (88%)	299 (99%)	2 (1%)	0	100	100
1	C	294/341 (86%)	288 (98%)	6 (2%)	0	100	100
1	D	300/341 (88%)	296 (99%)	3 (1%)	1 (0%)	36	26
All	All	1199/1364 (88%)	1185 (99%)	13 (1%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	170	TYR

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	266/299 (89%)	263 (99%)	3 (1%)	65	60
1	B	264/299 (88%)	261 (99%)	3 (1%)	65	60
1	C	255/299 (85%)	250 (98%)	5 (2%)	48	35
1	D	246/299 (82%)	242 (98%)	4 (2%)	55	44
All	All	1031/1196 (86%)	1016 (98%)	15 (2%)	57	47

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	248	SER
1	A	273	THR
1	B	24	LYS
1	B	102	LEU
1	B	163	LYS
1	C	53	ASN
1	C	80	ARG
1	C	83	SER
1	C	122	LEU
1	C	285	ARG
1	D	35	GLN
1	D	137	ASN
1	D	273	THR
1	D	274	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	52	GLN
1	A	53	ASN
1	A	72	GLN
1	A	148	GLN
1	A	216	GLN
1	A	268	HIS
1	B	12	GLN
1	B	52	GLN
1	B	70	GLN
1	B	72	GLN
1	B	148	GLN
1	B	277	GLN
1	C	12	GLN
1	C	53	ASN
1	C	56	HIS
1	C	148	GLN
1	C	238	GLN
1	C	240	HIS
1	C	277	GLN
1	D	12	GLN
1	D	35	GLN
1	D	52	GLN
1	D	148	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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$
1	CAF	A	169	1	5,9,10	2.53	2 (40%)	4,12,14	0.78	0
1	CAF	B	169	1	5,9,10	2.48	2 (40%)	4,12,14	2.94	3 (75%)
1	CAF	D	169	1	5,9,10	1.76	1 (20%)	4,12,14	3.09	2 (50%)
1	CAF	C	169	1	5,9,10	0.74	0	4,12,14	1.91	1 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CAF	A	169	1	-	0/0/8/10	-
1	CAF	B	169	1	-	0/0/8/10	-
1	CAF	D	169	1	-	0/0/8/10	-
1	CAF	C	169	1	-	0/0/8/10	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	169	CAF	AS-CE1	-4.14	1.58	1.89
1	A	169	CAF	AS-CE2	-3.85	1.60	1.89
1	D	169	CAF	CA-N	-3.78	1.37	1.48
1	B	169	CAF	AS-CE2	-3.54	1.63	1.89
1	A	169	CAF	AS-CE1	-3.50	1.63	1.89

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	169	CAF	CA-CB-SG	5.60	125.33	112.49
1	B	169	CAF	CA-CB-SG	4.81	123.52	112.49
1	C	169	CAF	O1-AS-CE2	-3.08	94.73	109.44
1	B	169	CAF	CB-CA-C	-2.51	103.98	110.80
1	B	169	CAF	O1-AS-CE2	2.24	120.13	109.44
1	D	169	CAF	O1-AS-CE2	-2.08	99.52	109.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	169	CAF	4	0
1	B	169	CAF	2	0
1	D	169	CAF	5	0
1	C	169	CAF	6	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 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	GOL	A	404	-	5,5,5	0.44	0	5,5,5	0.33	0
2	GOL	D	401	-	5,5,5	0.36	0	5,5,5	0.33	0
2	GOL	A	401	-	5,5,5	0.34	0	5,5,5	0.26	0
2	GOL	D	403	-	5,5,5	0.52	0	5,5,5	0.59	0
2	GOL	A	403	-	5,5,5	0.36	0	5,5,5	0.26	0
2	GOL	B	402	-	5,5,5	0.38	0	5,5,5	0.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	A	402	-	5,5,5	0.38	0	5,5,5	0.21	0
2	GOL	B	401	-	5,5,5	0.35	0	5,5,5	0.42	0
2	GOL	C	402	-	5,5,5	0.36	0	5,5,5	0.22	0
3	CAC	B	405	-	2,4,4	2.49	2 (100%)	4,6,6	0.90	0
2	GOL	B	404	-	5,5,5	1.42	1 (20%)	5,5,5	0.90	0
2	GOL	C	401	-	5,5,5	0.38	0	5,5,5	0.37	0
2	GOL	D	402	-	5,5,5	0.44	0	5,5,5	0.36	0
2	GOL	B	403	-	5,5,5	0.33	0	5,5,5	0.30	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
2	GOL	A	404	-	-	2/4/4/4	-
2	GOL	D	401	-	-	0/4/4/4	-
2	GOL	A	401	-	-	2/4/4/4	-
2	GOL	D	403	-	-	4/4/4/4	-
2	GOL	A	403	-	-	2/4/4/4	-
2	GOL	B	402	-	-	2/4/4/4	-
2	GOL	A	402	-	-	0/4/4/4	-
2	GOL	B	401	-	-	0/4/4/4	-
2	GOL	C	402	-	-	2/4/4/4	-
2	GOL	B	404	-	-	2/4/4/4	-
2	GOL	C	401	-	-	0/4/4/4	-
2	GOL	D	402	-	-	4/4/4/4	-
2	GOL	B	403	-	-	2/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	405	CAC	AS-C2	2.79	1.96	1.90
2	B	404	GOL	O3-C3	-2.37	1.32	1.42
3	B	405	CAC	AS-C1	2.14	1.95	1.90

There are no bond angle outliers.

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	403	GOL	O1-C1-C2-C3
2	A	404	GOL	O1-C1-C2-C3
2	D	402	GOL	C1-C2-C3-O3
2	D	403	GOL	O1-C1-C2-C3
2	D	403	GOL	C1-C2-C3-O3
2	D	403	GOL	O1-C1-C2-O2
2	D	403	GOL	O2-C2-C3-O3
2	A	401	GOL	O1-C1-C2-C3
2	B	402	GOL	C1-C2-C3-O3
2	B	403	GOL	O1-C1-C2-C3
2	B	404	GOL	C1-C2-C3-O3
2	C	402	GOL	C1-C2-C3-O3
2	D	402	GOL	O1-C1-C2-C3
2	A	401	GOL	O1-C1-C2-O2
2	A	404	GOL	O1-C1-C2-O2
2	D	402	GOL	O2-C2-C3-O3
2	A	403	GOL	O1-C1-C2-O2
2	B	403	GOL	O1-C1-C2-O2
2	B	404	GOL	O2-C2-C3-O3
2	C	402	GOL	O2-C2-C3-O3
2	D	402	GOL	O1-C1-C2-O2
2	B	402	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	403	GOL	6	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

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	302/341 (88%)	-0.19	14 (4%) 37 42	4, 10, 24, 35	4 (1%)
1	B	302/341 (88%)	-0.13	13 (4%) 40 44	5, 12, 26, 35	1 (0%)
1	C	295/341 (86%)	-0.15	6 (2%) 65 71	5, 12, 25, 37	3 (1%)
1	D	301/341 (88%)	0.38	25 (8%) 17 21	8, 21, 35, 52	3 (0%)
All	All	1200/1364 (87%)	-0.02	58 (4%) 35 40	4, 13, 29, 52	11 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	137	ASN	4.4
1	B	138	GLY	4.3
1	B	136	PRO	4.2
1	D	244	LEU	4.2
1	A	274	VAL	4.1
1	B	243	ALA	4.1
1	B	5	LEU	3.8
1	A	248	SER	3.8
1	D	243	ALA	3.7
1	D	235	TRP	3.4
1	A	137	ASN	3.2
1	D	274	VAL	3.2
1	D	5	LEU	3.1
1	D	272	SER	3.0
1	D	241	MET	2.9
1	C	307	HIS	2.9
1	C	5	LEU	2.9
1	B	140	ILE	2.8
1	D	137	ASN	2.7
1	D	240	HIS	2.7
1	A	249	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	135	VAL	2.7
1	D	238	GLN	2.6
1	C	244	LEU	2.6
1	D	102	LEU	2.6
1	D	233	PRO	2.5
1	A	246	LYS	2.5
1	D	248	SER	2.5
1	D	273	THR	2.5
1	D	237	LYS	2.5
1	D	307	HIS	2.5
1	C	134	ASP	2.5
1	A	138	GLY	2.4
1	C	80	ARG	2.4
1	B	244	LEU	2.4
1	A	136	PRO	2.4
1	A	242	SER	2.4
1	C	240	HIS	2.4
1	A	201	GLU	2.3
1	A	243	ALA	2.3
1	D	242	SER	2.3
1	D	246	LYS	2.3
1	D	239	SER	2.3
1	A	307	HIS	2.3
1	B	248	SER	2.3
1	A	245	GLU	2.3
1	B	307	HIS	2.3
1	D	82	ASN	2.3
1	A	244	LEU	2.3
1	D	286	GLU	2.2
1	D	81	ASP	2.2
1	D	236	GLU	2.2
1	D	138	GLY	2.2
1	B	274	VAL	2.1
1	B	241	MET	2.1
1	A	247	SER	2.1
1	D	231	SER	2.1
1	B	227	MET	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	CAF	C	169	10/11	0.91	0.14	20,20,20,20	4
1	CAF	D	169	10/11	0.95	0.10	20,20,20,20	4
1	CAF	A	169	10/11	0.96	0.11	20,20,20,20	4
1	CAF	B	169	10/11	0.96	0.10	20,20,20,20	4

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GOL	B	403	6/6	0.78	0.19	39,39,39,39	0
2	GOL	D	403	6/6	0.78	0.18	23,26,28,30	0
2	GOL	A	404	6/6	0.80	0.16	29,30,31,32	0
2	GOL	B	402	6/6	0.80	0.15	30,32,33,34	0
2	GOL	D	402	6/6	0.85	0.14	24,28,28,29	0
2	GOL	A	403	6/6	0.85	0.13	25,28,28,28	0
2	GOL	C	401	6/6	0.86	0.10	24,25,25,26	0
2	GOL	D	401	6/6	0.86	0.11	30,30,31,32	0
3	CAC	B	405	5/5	0.86	0.22	30,31,32,35	5
2	GOL	B	404	6/6	0.89	0.14	20,20,20,20	0
2	GOL	C	402	6/6	0.92	0.11	19,23,24,24	0
2	GOL	A	401	6/6	0.93	0.09	19,20,21,21	0
2	GOL	B	401	6/6	0.97	0.05	12,13,13,14	0
2	GOL	A	402	6/6	0.97	0.05	13,13,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.