



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:16 PM UTC

PDB ID : 5T5O / pdb_00005t5o
Title : LECTIN FROM BAUHINIA FORFICATA IN COMPLEX WITH TN-PEPTIDE
Authors : Lubkowski, J.; Wlodawer, A.
Deposited on : 2016-08-31
Resolution : 2.75 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:

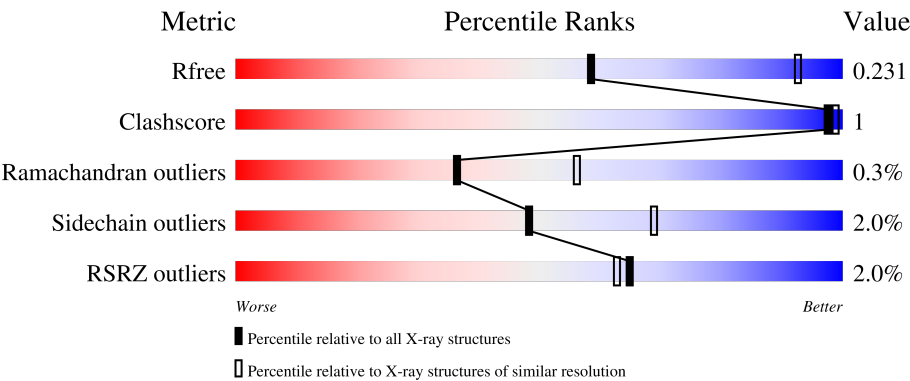
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	242	% 84%10%5%
1	B	242	% 84%10%5%
1	C	242	% 89%5%5%
1	D	242	% 88%6%5%
1	E	242	92%. 5%

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Mol	Chain	Length	Quality of chain
1	F	242	% 86% 8% 5%
1	G	242	2% 91% • • 5%
1	H	242	4% 89% 6% 5%
1	I	242	% 91% • 5%
1	J	242	2% 89% 5% 5%
2	a	6	67% 33%
2	b	6	17% 67% 33%
2	c	6	17% 67% 17% 17%
2	d	6	17% 83% 17%
2	e	6	17% 67% 33%
2	f	6	17% 50% 33% 17%
2	g	6	17% 50% 50%
2	h	6	17% 100%
2	i	6	17% 67% 33%
2	j	6	17% 67% 33%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 18803 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 Lectin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	229	Total	C	N	O	0	0	0
			1811	1156	305	350			
1	B	229	Total	C	N	O	0	0	0
			1811	1156	305	350			
1	C	229	Total	C	N	O	0	0	0
			1811	1156	305	350			
1	D	229	Total	C	N	O	0	0	0
			1811	1156	305	350			
1	E	229	Total	C	N	O	0	0	0
			1811	1156	305	350			
1	F	229	Total	C	N	O	0	0	0
			1811	1156	305	350			
1	G	229	Total	C	N	O	0	0	0
			1811	1156	305	350			
1	H	229	Total	C	N	O	0	0	0
			1811	1156	305	350			
1	I	229	Total	C	N	O	0	0	0
			1811	1156	305	350			
1	J	229	Total	C	N	O	0	0	0
			1811	1156	305	350			

There are 90 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	234	GLY	-	expression tag	UNP P86993
A	235	ALA	-	expression tag	UNP P86993
A	236	ARG	-	expression tag	UNP P86993
A	237	HIS	-	expression tag	UNP P86993
A	238	HIS	-	expression tag	UNP P86993
A	239	HIS	-	expression tag	UNP P86993
A	240	HIS	-	expression tag	UNP P86993
A	241	HIS	-	expression tag	UNP P86993
A	242	HIS	-	expression tag	UNP P86993

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Chain	Residue	Modelled	Actual	Comment	Reference
B	234	GLY	-	expression tag	UNP P86993
B	235	ALA	-	expression tag	UNP P86993
B	236	ARG	-	expression tag	UNP P86993
B	237	HIS	-	expression tag	UNP P86993
B	238	HIS	-	expression tag	UNP P86993
B	239	HIS	-	expression tag	UNP P86993
B	240	HIS	-	expression tag	UNP P86993
B	241	HIS	-	expression tag	UNP P86993
B	242	HIS	-	expression tag	UNP P86993
C	234	GLY	-	expression tag	UNP P86993
C	235	ALA	-	expression tag	UNP P86993
C	236	ARG	-	expression tag	UNP P86993
C	237	HIS	-	expression tag	UNP P86993
C	238	HIS	-	expression tag	UNP P86993
C	239	HIS	-	expression tag	UNP P86993
C	240	HIS	-	expression tag	UNP P86993
C	241	HIS	-	expression tag	UNP P86993
C	242	HIS	-	expression tag	UNP P86993
D	234	GLY	-	expression tag	UNP P86993
D	235	ALA	-	expression tag	UNP P86993
D	236	ARG	-	expression tag	UNP P86993
D	237	HIS	-	expression tag	UNP P86993
D	238	HIS	-	expression tag	UNP P86993
D	239	HIS	-	expression tag	UNP P86993
D	240	HIS	-	expression tag	UNP P86993
D	241	HIS	-	expression tag	UNP P86993
D	242	HIS	-	expression tag	UNP P86993
E	234	GLY	-	expression tag	UNP P86993
E	235	ALA	-	expression tag	UNP P86993
E	236	ARG	-	expression tag	UNP P86993
E	237	HIS	-	expression tag	UNP P86993
E	238	HIS	-	expression tag	UNP P86993
E	239	HIS	-	expression tag	UNP P86993
E	240	HIS	-	expression tag	UNP P86993
E	241	HIS	-	expression tag	UNP P86993
E	242	HIS	-	expression tag	UNP P86993
F	234	GLY	-	expression tag	UNP P86993
F	235	ALA	-	expression tag	UNP P86993
F	236	ARG	-	expression tag	UNP P86993
F	237	HIS	-	expression tag	UNP P86993
F	238	HIS	-	expression tag	UNP P86993
F	239	HIS	-	expression tag	UNP P86993

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Chain	Residue	Modelled	Actual	Comment	Reference
F	240	HIS	-	expression tag	UNP P86993
F	241	HIS	-	expression tag	UNP P86993
F	242	HIS	-	expression tag	UNP P86993
G	234	GLY	-	expression tag	UNP P86993
G	235	ALA	-	expression tag	UNP P86993
G	236	ARG	-	expression tag	UNP P86993
G	237	HIS	-	expression tag	UNP P86993
G	238	HIS	-	expression tag	UNP P86993
G	239	HIS	-	expression tag	UNP P86993
G	240	HIS	-	expression tag	UNP P86993
G	241	HIS	-	expression tag	UNP P86993
G	242	HIS	-	expression tag	UNP P86993
H	234	GLY	-	expression tag	UNP P86993
H	235	ALA	-	expression tag	UNP P86993
H	236	ARG	-	expression tag	UNP P86993
H	237	HIS	-	expression tag	UNP P86993
H	238	HIS	-	expression tag	UNP P86993
H	239	HIS	-	expression tag	UNP P86993
H	240	HIS	-	expression tag	UNP P86993
H	241	HIS	-	expression tag	UNP P86993
H	242	HIS	-	expression tag	UNP P86993
I	234	GLY	-	expression tag	UNP P86993
I	235	ALA	-	expression tag	UNP P86993
I	236	ARG	-	expression tag	UNP P86993
I	237	HIS	-	expression tag	UNP P86993
I	238	HIS	-	expression tag	UNP P86993
I	239	HIS	-	expression tag	UNP P86993
I	240	HIS	-	expression tag	UNP P86993
I	241	HIS	-	expression tag	UNP P86993
I	242	HIS	-	expression tag	UNP P86993
J	234	GLY	-	expression tag	UNP P86993
J	235	ALA	-	expression tag	UNP P86993
J	236	ARG	-	expression tag	UNP P86993
J	237	HIS	-	expression tag	UNP P86993
J	238	HIS	-	expression tag	UNP P86993
J	239	HIS	-	expression tag	UNP P86993
J	240	HIS	-	expression tag	UNP P86993
J	241	HIS	-	expression tag	UNP P86993
J	242	HIS	-	expression tag	UNP P86993

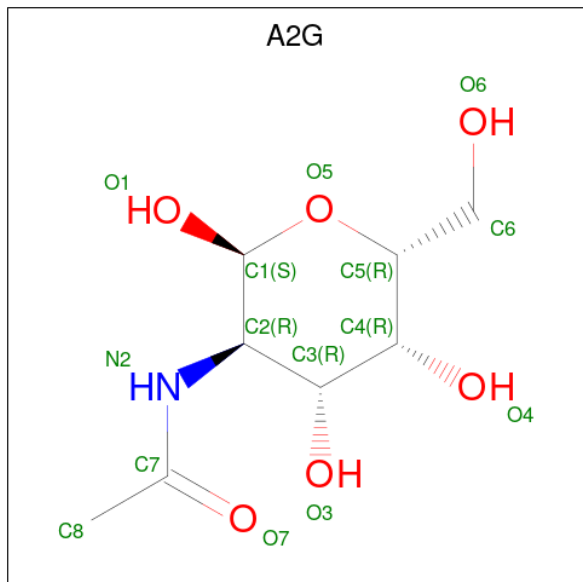
- Molecule 2 is a protein called TN-peptide ACE-GLY-VAL-THR-SER-ALA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	a	6	Total	C	N	O	0	0	0
			32	19	5	8			
2	b	6	Total	C	N	O	0	0	0
			32	19	5	8			
2	c	6	Total	C	N	O	0	0	0
			32	19	5	8			
2	d	6	Total	C	N	O	0	0	0
			32	19	5	8			
2	e	6	Total	C	N	O	0	0	0
			32	19	5	8			
2	f	6	Total	C	N	O	0	0	0
			32	19	5	8			
2	g	6	Total	C	N	O	0	0	0
			32	19	5	8			
2	h	6	Total	C	N	O	0	0	0
			32	19	5	8			
2	i	6	Total	C	N	O	0	0	0
			32	19	5	8			
2	j	6	Total	C	N	O	0	0	0
			32	19	5	8			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Ca	0	0
			2	2		
3	B	2	Total	Ca	0	0
			2	2		
3	C	2	Total	Ca	0	0
			2	2		
3	D	2	Total	Ca	0	0
			2	2		
3	E	2	Total	Ca	0	0
			2	2		
3	F	2	Total	Ca	0	0
			2	2		
3	G	2	Total	Ca	0	0
			2	2		
3	H	2	Total	Ca	0	0
			2	2		
3	I	2	Total	Ca	0	0
			2	2		
3	J	2	Total	Ca	0	0
			2	2		

- Molecule 4 is 2-acetamido-2-deoxy- α -D-galactopyranose (CCD ID: A2G) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	a	1	Total	C	N	O	0	0
			14	8	1	5		
4	b	1	Total	C	N	O	0	0
			14	8	1	5		
4	c	1	Total	C	N	O	0	0
			14	8	1	5		
4	d	1	Total	C	N	O	0	0
			14	8	1	5		
4	e	1	Total	C	N	O	0	0
			14	8	1	5		
4	f	1	Total	C	N	O	0	0
			14	8	1	5		
4	g	1	Total	C	N	O	0	0
			14	8	1	5		
4	h	1	Total	C	N	O	0	0
			14	8	1	5		
4	i	1	Total	C	N	O	0	0
			14	8	1	5		
4	j	1	Total	C	N	O	0	0
			14	8	1	5		

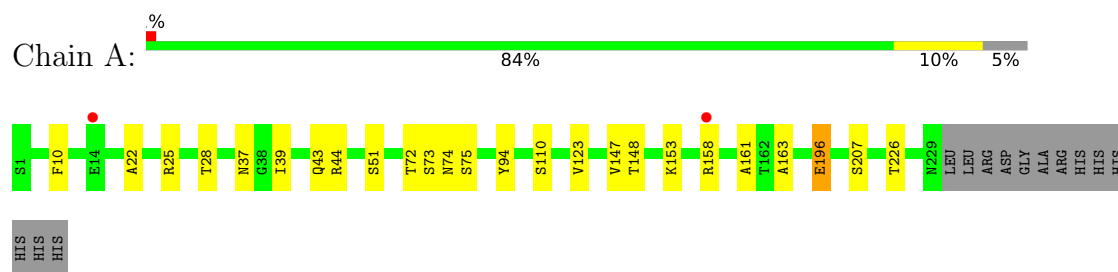
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	27	Total 27	O 27	0	0
5	a	1	Total 1	O 1	0	0
5	B	30	Total 30	O 30	0	0
5	b	1	Total 1	O 1	0	0
5	C	18	Total 18	O 18	0	0
5	D	29	Total 29	O 29	0	0
5	E	16	Total 16	O 16	0	0
5	F	26	Total 26	O 26	0	0
5	f	3	Total 3	O 3	0	0
5	G	16	Total 16	O 16	0	0
5	H	18	Total 18	O 18	0	0
5	h	1	Total 1	O 1	0	0
5	I	13	Total 13	O 13	0	0
5	i	1	Total 1	O 1	0	0
5	J	13	Total 13	O 13	0	0

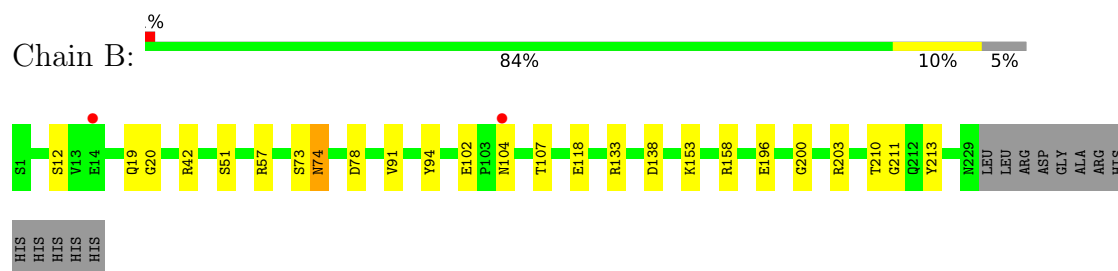
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

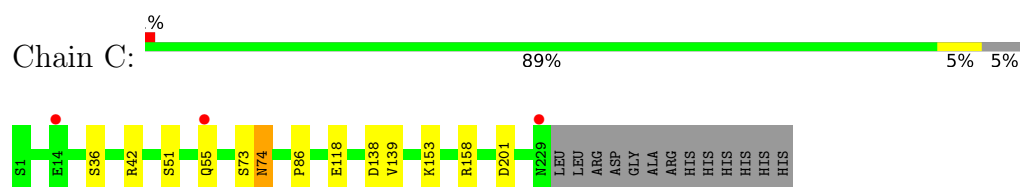
- Molecule 1: Lectin



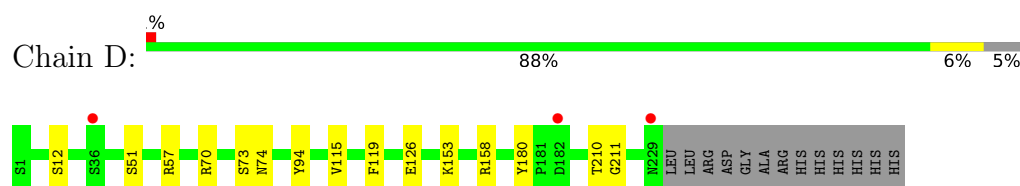
- Molecule 1: Lectin



- Molecule 1: Lectin



- Molecule 1: Lectin

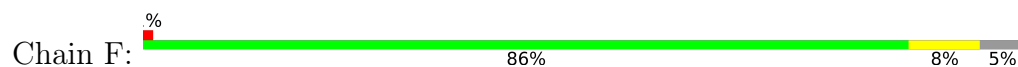


- Molecule 1: Lectin

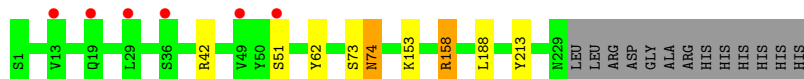




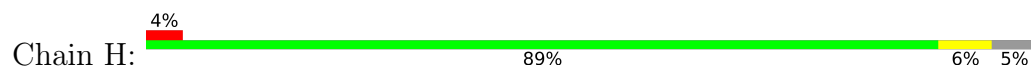
- Molecule 1: Lectin



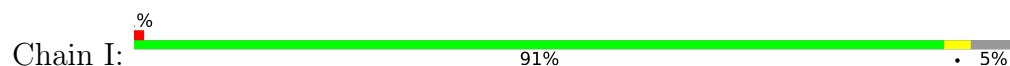
- Molecule 1: Lectin



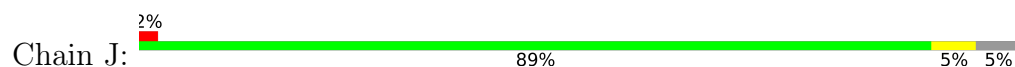
- Molecule 1: Lectin



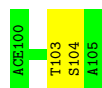
- Molecule 1: Lectin



- Molecule 1: Lectin

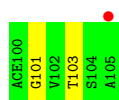


- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA

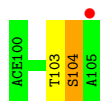


- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA

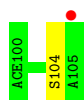
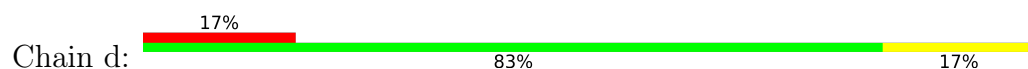




- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA



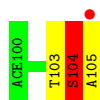
- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA



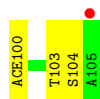
- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA



- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA



- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA

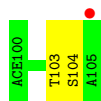


- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA

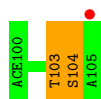




- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA



- Molecule 2: TN-peptide ACE-GLY-VAL-THR-SER-ALA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.08Å 187.29Å 258.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.38 – 2.75 49.38 – 2.75	Depositor EDS
% Data completeness (in resolution range)	79.7 (49.38-2.75) 83.6 (49.38-2.75)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.96 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.201 , 0.230 0.203 , 0.231	Depositor DCC
R_{free} test set	3493 reflections (3.99%)	wwPDB-VP
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.406	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.8	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	0.93	EDS
Total number of atoms	18803	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% 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: ACE, CA, A2G

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	1.56	19/1864 (1.0%)	1.22	5/2547 (0.2%)
1	B	1.52	12/1864 (0.6%)	1.21	2/2547 (0.1%)
1	C	1.15	3/1864 (0.2%)	1.03	2/2547 (0.1%)
1	D	1.32	5/1864 (0.3%)	1.14	2/2547 (0.1%)
1	E	1.11	1/1864 (0.1%)	1.02	2/2547 (0.1%)
1	F	1.27	7/1864 (0.4%)	1.13	6/2547 (0.2%)
1	G	1.05	0/1864	1.02	4/2547 (0.2%)
1	H	1.22	5/1864 (0.3%)	1.09	5/2547 (0.2%)
1	I	1.06	0/1864	1.01	2/2547 (0.1%)
1	J	1.04	0/1864	1.00	3/2547 (0.1%)
2	a	2.10	1/29 (3.4%)	1.82	0/39
2	b	2.31	1/29 (3.4%)	1.85	0/39
2	c	1.79	0/29	1.27	0/39
2	d	2.22	0/29	1.83	0/39
2	e	2.22	2/29 (6.9%)	1.87	0/39
2	f	2.64	2/29 (6.9%)	1.79	1/39 (2.6%)
2	g	1.89	0/29	1.23	0/39
2	h	1.84	0/29	1.37	0/39
2	i	2.24	1/29 (3.4%)	1.43	0/39
2	j	2.38	3/29 (10.3%)	1.48	1/39 (2.6%)
All	All	1.26	62/18930 (0.3%)	1.10	35/25860 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	c	0	1
2	d	0	1
2	f	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	j	0	1
All	All	0	4

All (62) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	f	104	SER	CA-C	10.06	1.64	1.52
1	B	91	VAL	C-O	-8.12	1.16	1.24
1	A	44	ARG	NE-CZ	7.91	1.41	1.33
1	A	44	ARG	CZ-NH1	7.63	1.43	1.32
1	A	74	ASN	C-O	-7.05	1.15	1.24
1	B	73	SER	C-O	-6.88	1.17	1.24
1	F	71	THR	C-O	-6.84	1.15	1.24
1	A	161	ALA	C-O	-6.79	1.15	1.23
1	B	104	ASN	CB-CG	-6.78	1.35	1.52
1	F	180	TYR	CA-C	6.70	1.59	1.52
1	F	210	THR	CA-C	6.69	1.60	1.52
1	A	73	SER	C-O	-6.65	1.17	1.24
1	H	86	PRO	CA-C	6.64	1.58	1.52
1	A	207	SER	C-O	-6.55	1.16	1.24
1	H	113	LYS	C-O	6.52	1.31	1.23
1	B	107	THR	C-O	-6.44	1.15	1.24
2	j	103	THR	CA-C	6.43	1.60	1.52
1	B	200	GLY	C-O	-6.42	1.15	1.23
1	C	139	VAL	CA-C	-6.36	1.47	1.53
1	D	73	SER	C-O	-6.30	1.18	1.24
1	A	25	ARG	C-O	-6.29	1.16	1.24
1	A	123	VAL	C-O	-6.28	1.17	1.23
1	A	163	ALA	C-O	-6.27	1.16	1.24
2	a	103	THR	C-O	-6.17	1.16	1.24
1	C	86	PRO	CA-C	6.11	1.57	1.52
1	B	102	GLU	CG-CD	6.10	1.67	1.52
1	D	115	VAL	C-O	-6.09	1.18	1.24
1	A	28	THR	C-O	-6.07	1.16	1.23
2	j	104	SER	N-CA	6.01	1.53	1.46
2	j	104	SER	CA-C	6.01	1.60	1.52
1	A	75	SER	CA-C	-6.01	1.45	1.52
1	F	191	VAL	C-O	-5.92	1.18	1.24
1	D	180	TYR	CA-C	5.88	1.58	1.52
1	A	72	THR	C-O	-5.85	1.15	1.24
1	B	19	GLN	CD-NE2	5.82	1.45	1.33
1	A	22	ALA	C-O	-5.81	1.16	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	114	VAL	C-O	-5.80	1.17	1.24
2	e	105	ALA	N-CA	5.79	1.57	1.46
1	D	74	ASN	CB-CG	-5.78	1.37	1.52
1	C	73	SER	C-O	-5.77	1.18	1.24
1	F	7	TYR	CA-C	5.77	1.58	1.52
2	e	104	SER	CA-C	5.71	1.59	1.53
2	f	105	ALA	N-CA	5.69	1.57	1.46
1	A	147	VAL	C-O	-5.66	1.17	1.23
1	B	203	ARG	CA-C	-5.63	1.45	1.52
1	A	39	ILE	CA-C	5.61	1.57	1.53
2	i	104	SER	CA-C	5.52	1.59	1.52
1	B	102	GLU	C-O	-5.51	1.17	1.24
1	B	133	ARG	C-O	-5.39	1.17	1.23
1	H	69	ILE	C-O	5.34	1.30	1.24
1	A	10	PHE	C-O	-5.33	1.17	1.24
1	A	196	GLU	C-O	-5.33	1.17	1.24
1	B	20	GLY	C-O	-5.29	1.17	1.24
1	F	141	SER	CA-C	-5.24	1.45	1.52
1	F	53	PRO	C-O	-5.24	1.17	1.23
1	D	126	GLU	C-O	-5.22	1.17	1.24
1	B	57	ARG	CZ-NH1	5.20	1.40	1.32
1	A	74	ASN	CG-OD1	-5.16	1.13	1.23
1	A	110	SER	C-O	-5.16	1.17	1.24
1	E	40	PRO	C-O	-5.08	1.17	1.23
1	H	63	THR	C-O	-5.06	1.17	1.23
2	b	101	GLY	N-CA	5.00	1.53	1.45

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	74	ASN	CB-CA-C	-9.37	95.82	110.81
1	H	74	ASN	CB-CA-C	-9.22	95.43	110.74
1	F	74	ASN	CB-CA-C	-8.73	93.05	110.42
1	J	74	ASN	CB-CA-C	-8.52	96.61	110.74
1	G	74	ASN	N-CA-C	8.39	121.18	111.11
1	B	74	ASN	CB-CA-C	-8.14	94.21	110.42
1	C	74	ASN	CB-CA-C	-7.61	98.10	110.74
1	H	74	ASN	N-CA-C	7.44	123.64	111.37
1	D	74	ASN	CB-CA-C	-7.36	95.77	110.42
1	I	74	ASN	CB-CA-C	-7.30	98.63	110.74
1	F	104	ASN	N-CA-C	7.24	120.09	111.33
1	A	74	ASN	CB-CA-C	-7.19	96.12	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	73	SER	N-CA-C	6.79	116.83	107.73
1	E	74	ASN	CB-CA-C	-6.61	97.27	110.42
1	D	73	SER	N-CA-C	6.60	116.58	107.73
1	H	106	ALA	N-CA-C	6.43	120.38	112.54
1	C	74	ASN	N-CA-C	6.27	121.71	111.37
1	A	44	ARG	NE-CZ-NH1	6.17	127.67	121.50
1	J	74	ASN	N-CA-C	6.17	121.55	111.37
1	G	73	SER	CA-C-N	6.09	128.76	120.54
1	G	73	SER	C-N-CA	6.09	128.76	120.54
2	j	104	SER	N-CA-C	5.86	123.27	110.80
1	A	43	GLN	N-CA-C	5.53	119.02	111.39
1	H	73	SER	N-CA-C	5.51	115.11	107.73
1	A	73	SER	N-CA-C	5.48	115.47	108.24
1	E	74	ASN	N-CA-C	5.47	122.46	110.80
1	J	73	SER	N-CA-C	5.31	114.85	107.73
1	I	74	ASN	N-CA-C	5.25	120.04	111.37
1	F	85	ALA	N-CA-C	5.25	112.74	108.07
1	F	83	PHE	N-CA-C	5.25	117.16	109.24
1	F	44	ARG	CG-CD-NE	-5.20	100.56	112.00
2	f	104	SER	N-CA-C	5.20	116.19	108.60
1	H	86	PRO	N-CA-C	5.18	117.02	110.70
1	A	37	ASN	N-CA-C	5.11	118.55	112.72
1	B	104	ASN	N-CA-C	5.04	121.53	110.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	c	104	SER	Peptide
2	d	104	SER	Peptide
2	f	104	SER	Peptide
2	j	104	SER	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1811	0	1718	0	0
1	B	1811	0	1718	6	0
1	C	1811	0	1718	4	2
1	D	1811	0	1718	4	0
1	E	1811	0	1718	1	0
1	F	1811	0	1718	5	0
1	G	1811	0	1718	5	0
1	H	1811	0	1718	1	0
1	I	1811	0	1718	4	0
1	J	1811	0	1718	7	0
2	a	32	0	31	0	0
2	b	32	0	31	1	0
2	c	32	0	31	1	0
2	d	32	0	31	0	0
2	e	32	0	31	0	0
2	f	32	0	31	1	0
2	g	32	0	31	2	0
2	h	32	0	31	0	0
2	i	32	0	31	1	0
2	j	32	0	31	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
3	G	2	0	0	0	0
3	H	2	0	0	0	0
3	I	2	0	0	0	0
3	J	2	0	0	0	0
4	a	14	0	12	0	0
4	b	14	0	12	1	0
4	c	14	0	12	0	0
4	d	14	0	12	0	0
4	e	14	0	12	0	0
4	f	14	0	12	0	0
4	g	14	0	12	0	0
4	h	14	0	12	0	0
4	i	14	0	12	0	0
4	j	14	0	12	0	0
5	A	27	0	0	0	0
5	B	30	0	0	0	0
5	C	18	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	29	0	0	1	0
5	E	16	0	0	0	0
5	F	26	0	0	0	0
5	G	16	0	0	1	0
5	H	18	0	0	0	0
5	I	13	0	0	1	0
5	J	13	0	0	1	0
5	a	1	0	0	0	0
5	b	1	0	0	0	0
5	f	3	0	0	0	0
5	h	1	0	0	0	0
5	i	1	0	0	0	0
All	All	18803	0	17610	30	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 1.

All (30) 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:G:74:ASN:HB3	2:j:103:THR:HB	1.70	0.72
1:J:144:SER:OG	5:J:401:HOH:O	2.11	0.68
1:B:74:ASN:HB3	2:f:103:THR:HB	1.75	0.67
1:C:74:ASN:HB3	2:i:103:THR:HB	1.75	0.66
2:c:103:THR:HB	1:I:74:ASN:HB3	1.78	0.65
1:B:78:ASP:OD1	4:b:201:A2G:O4	2.15	0.64
1:G:42:ARG:NH1	1:J:213:TYR:OH	2.34	0.60
2:g:100:ACE:H3	1:J:122:TRP:HA	1.89	0.54
2:g:103:THR:HB	1:J:74:ASN:HB3	1.90	0.53
1:D:57:ARG:HH22	1:F:55:GLN:HE22	1.56	0.53
1:C:55:GLN:NE2	1:C:201:ASP:OD1	2.41	0.53
1:G:62:TYR:HB2	1:H:187:VAL:CG2	2.40	0.51
1:C:42:ARG:NH1	1:I:213:TYR:OH	2.44	0.51
1:F:9:ASN:OD1	1:F:9:ASN:C	2.56	0.47
2:b:103:THR:HB	1:F:74:ASN:HB3	1.97	0.46
1:B:213:TYR:OH	1:F:42:ARG:NH1	2.49	0.45
1:D:210:THR:HB	1:D:211:GLY:C	2.42	0.45
1:I:73:SER:HB2	5:I:411:HOH:O	2.17	0.44
1:C:118:GLU:OE1	1:C:138:ASP:OD2	2.36	0.43
1:G:158:ARG:NH1	5:G:402:HOH:O	2.51	0.43
1:D:70:ARG:NH2	5:D:401:HOH:O	2.29	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:119:PHE:CD1	1:D:119:PHE:N	2.87	0.42
1:J:77:ALA:HA	1:J:78:ASP:HA	1.84	0.41
1:E:77:ALA:HA	1:E:78:ASP:HA	1.90	0.41
1:I:77:ALA:HA	1:I:78:ASP:HA	1.90	0.41
1:B:42:ARG:NH1	1:F:213:TYR:OH	2.54	0.41
1:B:210:THR:HB	1:B:211:GLY:C	2.45	0.41
1:B:118:GLU:OE1	1:B:138:ASP:OD2	2.38	0.40
1:G:213:TYR:OH	1:J:42:ARG:NH1	2.54	0.40
1:J:25:ARG:O	1:J:26:ASN:C	2.63	0.40

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:C:36:SER:CA	1:C:55:GLN:OE1[4_555]	1.90	0.30
1:C:36:SER:CB	1:C:55:GLN:OE1[4_555]	2.04	0.16

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	227/242 (94%)	215 (95%)	11 (5%)	1 (0%)	30	50
1	B	227/242 (94%)	214 (94%)	12 (5%)	1 (0%)	30	50
1	C	227/242 (94%)	215 (95%)	12 (5%)	0	100	100
1	D	227/242 (94%)	215 (95%)	11 (5%)	1 (0%)	30	50
1	E	227/242 (94%)	218 (96%)	9 (4%)	0	100	100
1	F	227/242 (94%)	217 (96%)	9 (4%)	1 (0%)	30	50
1	G	227/242 (94%)	216 (95%)	11 (5%)	0	100	100
1	H	227/242 (94%)	217 (96%)	9 (4%)	1 (0%)	30	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	227/242 (94%)	217 (96%)	10 (4%)	0	100	100
1	J	227/242 (94%)	216 (95%)	10 (4%)	1 (0%)	30	50
2	a	4/6 (67%)	3 (75%)	1 (25%)	0	100	100
2	b	4/6 (67%)	4 (100%)	0	0	100	100
2	c	4/6 (67%)	4 (100%)	0	0	100	100
2	d	4/6 (67%)	4 (100%)	0	0	100	100
2	e	4/6 (67%)	2 (50%)	2 (50%)	0	100	100
2	f	4/6 (67%)	4 (100%)	0	0	100	100
2	g	4/6 (67%)	3 (75%)	0	1 (25%)	0	0
2	h	4/6 (67%)	4 (100%)	0	0	100	100
2	i	4/6 (67%)	2 (50%)	2 (50%)	0	100	100
2	j	4/6 (67%)	3 (75%)	1 (25%)	0	100	100
All	All	2310/2480 (93%)	2193 (95%)	110 (5%)	7 (0%)	36	56

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	94	TYR
1	B	94	TYR
1	D	94	TYR
1	H	94	TYR
2	g	104	SER
1	F	94	TYR
1	J	94	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	198/209 (95%)	192 (97%)	6 (3%)	36	60
1	B	198/209 (95%)	193 (98%)	5 (2%)	42	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	198/209 (95%)	195 (98%)	3 (2%)	57	74
1	D	198/209 (95%)	194 (98%)	4 (2%)	48	69
1	E	198/209 (95%)	195 (98%)	3 (2%)	57	74
1	F	198/209 (95%)	195 (98%)	3 (2%)	57	74
1	G	198/209 (95%)	194 (98%)	4 (2%)	48	69
1	H	198/209 (95%)	194 (98%)	4 (2%)	48	69
1	I	198/209 (95%)	195 (98%)	3 (2%)	57	74
1	J	198/209 (95%)	195 (98%)	3 (2%)	57	74
2	a	3/3 (100%)	2 (67%)	1 (33%)	0	0
2	b	3/3 (100%)	3 (100%)	0	100	100
2	c	3/3 (100%)	2 (67%)	1 (33%)	0	0
2	d	3/3 (100%)	3 (100%)	0	100	100
2	e	3/3 (100%)	3 (100%)	0	100	100
2	f	3/3 (100%)	2 (67%)	1 (33%)	0	0
2	g	3/3 (100%)	3 (100%)	0	100	100
2	h	3/3 (100%)	3 (100%)	0	100	100
2	i	3/3 (100%)	3 (100%)	0	100	100
2	j	3/3 (100%)	3 (100%)	0	100	100
All	All	2010/2120 (95%)	1969 (98%)	41 (2%)	48	69

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	SER
1	A	148	THR
1	A	153	LYS
1	A	158	ARG
1	A	196	GLU
1	A	226	THR
2	a	104	SER
1	B	12	SER
1	B	51	SER
1	B	153	LYS
1	B	158	ARG
1	B	196	GLU
1	C	51	SER

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Mol	Chain	Res	Type
1	C	153	LYS
1	C	158	ARG
2	c	104	SER
1	D	12	SER
1	D	51	SER
1	D	153	LYS
1	D	158	ARG
1	E	51	SER
1	E	153	LYS
1	E	158	ARG
1	F	51	SER
1	F	153	LYS
1	F	158	ARG
2	f	104	SER
1	G	51	SER
1	G	153	LYS
1	G	158	ARG
1	G	188	LEU
1	H	51	SER
1	H	153	LYS
1	H	158	ARG
1	H	196	GLU
1	I	51	SER
1	I	153	LYS
1	I	158	ARG
1	J	51	SER
1	J	153	LYS
1	J	158	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	30	GLN
1	A	151	GLN
1	A	185	ASN
1	A	219	HIS
1	B	19	GLN
1	B	55	GLN
1	B	185	ASN
1	B	219	HIS
1	C	11	GLN

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Mol	Chain	Res	Type
1	C	30	GLN
1	C	185	ASN
1	C	219	HIS
1	D	11	GLN
1	D	30	GLN
1	D	151	GLN
1	D	185	ASN
1	E	11	GLN
1	E	30	GLN
1	E	55	GLN
1	E	151	GLN
1	E	185	ASN
1	E	219	HIS
1	F	26	ASN
1	F	43	GLN
1	F	55	GLN
1	F	185	ASN
1	G	11	GLN
1	G	185	ASN
1	G	219	HIS
1	H	11	GLN
1	H	30	GLN
1	H	55	GLN
1	H	185	ASN
1	H	219	HIS
1	I	11	GLN
1	I	30	GLN
1	I	55	GLN
1	I	151	GLN
1	I	185	ASN
1	I	219	HIS
1	J	11	GLN
1	J	55	GLN
1	J	151	GLN
1	J	185	ASN
1	J	219	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 20 are monoatomic - leaving 10 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	$\# Z > 2$
4	A2G	g	201	2	14,14,15	0.74	0	17,19,21	1.52	3 (17%)
4	A2G	e	201	2	14,14,15	0.72	0	17,19,21	2.16	5 (29%)
4	A2G	i	201	2	14,14,15	1.40	2 (14%)	17,19,21	1.69	5 (29%)
4	A2G	h	201	2	14,14,15	0.88	0	17,19,21	2.14	6 (35%)
4	A2G	j	201	2	14,14,15	0.67	0	17,19,21	2.29	4 (23%)
4	A2G	d	201	2	14,14,15	1.43	4 (28%)	17,19,21	2.04	5 (29%)
4	A2G	f	201	2	14,14,15	0.97	0	17,19,21	1.93	5 (29%)
4	A2G	b	201	2	14,14,15	1.23	1 (7%)	17,19,21	1.94	5 (29%)
4	A2G	c	201	2	14,14,15	0.74	0	17,19,21	1.58	3 (17%)
4	A2G	a	201	2	14,14,15	1.01	1 (7%)	17,19,21	3.24	8 (47%)

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
4	A2G	g	201	2	-	1/6/23/26	0/1/1/1
4	A2G	e	201	2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A2G	i	201	2	-	0/6/23/26	0/1/1/1
4	A2G	h	201	2	-	0/6/23/26	0/1/1/1
4	A2G	j	201	2	-	0/6/23/26	0/1/1/1
4	A2G	d	201	2	-	0/6/23/26	0/1/1/1
4	A2G	f	201	2	-	0/6/23/26	0/1/1/1
4	A2G	b	201	2	-	0/6/23/26	0/1/1/1
4	A2G	c	201	2	-	0/6/23/26	0/1/1/1
4	A2G	a	201	2	-	0/6/23/26	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	i	201	A2G	C1-C2	-3.55	1.47	1.52
4	a	201	A2G	C1-C2	-2.85	1.48	1.52
4	b	201	A2G	C3-C2	-2.82	1.46	1.52
4	d	201	A2G	C1-C2	-2.63	1.48	1.52
4	d	201	A2G	O5-C1	-2.59	1.39	1.43
4	d	201	A2G	C2-N2	-2.44	1.42	1.46
4	d	201	A2G	O5-C5	-2.16	1.39	1.43
4	i	201	A2G	C2-N2	-2.02	1.42	1.46

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	a	201	A2G	C1-O5-C5	9.59	125.04	112.19
4	j	201	A2G	C1-O5-C5	6.53	120.93	112.19
4	h	201	A2G	C1-O5-C5	5.34	119.35	112.19
4	e	201	A2G	C1-O5-C5	5.25	119.23	112.19
4	e	201	A2G	O5-C5-C4	-4.49	99.90	110.83
4	j	201	A2G	O5-C1-C2	4.31	117.97	111.29
4	a	201	A2G	C1-C2-N2	-4.11	103.96	110.43
4	a	201	A2G	O7-C7-C8	4.07	129.29	122.05
4	g	201	A2G	C1-C2-N2	-4.06	104.03	110.43
4	d	201	A2G	C3-C4-C5	-3.76	103.41	110.23
4	a	201	A2G	C4-C3-C2	-3.73	105.55	111.02
4	f	201	A2G	O3-C3-C4	3.64	118.96	110.38
4	d	201	A2G	C8-C7-N2	-3.57	110.20	116.12
4	h	201	A2G	C4-C3-C2	-3.56	105.80	111.02
4	f	201	A2G	C1-O5-C5	3.53	116.92	112.19
4	b	201	A2G	O5-C5-C6	3.51	114.49	107.66
4	b	201	A2G	O6-C6-C5	-3.41	99.73	111.33
4	b	201	A2G	O5-C1-C2	-3.34	106.12	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	a	201	A2G	C8-C7-N2	-3.25	110.73	116.12
4	h	201	A2G	O3-C3-C4	3.13	117.75	110.38
4	d	201	A2G	O3-C3-C2	-3.10	102.96	109.40
4	j	201	A2G	O7-C7-C8	-3.10	116.54	122.05
4	f	201	A2G	C3-C4-C5	-3.08	104.64	110.23
4	c	201	A2G	O5-C1-C2	-3.06	106.56	111.29
4	d	201	A2G	O7-C7-N2	3.04	127.35	121.98
4	b	201	A2G	C3-C4-C5	-3.01	104.78	110.23
4	i	201	A2G	O5-C5-C6	3.01	113.52	107.66
4	i	201	A2G	C1-O5-C5	2.95	116.15	112.19
4	c	201	A2G	C3-C4-C5	-2.83	105.10	110.23
4	h	201	A2G	C3-C4-C5	-2.78	105.19	110.23
4	e	201	A2G	O5-C5-C6	2.78	113.07	107.66
4	a	201	A2G	O4-C4-C3	2.54	116.36	110.38
4	h	201	A2G	C6-C5-C4	2.49	119.12	113.02
4	i	201	A2G	O5-C5-C4	-2.38	105.03	110.83
4	a	201	A2G	O6-C6-C5	-2.35	103.34	111.33
4	g	201	A2G	C3-C4-C5	-2.31	106.05	110.23
4	b	201	A2G	C1-C2-N2	-2.29	106.82	110.43
4	g	201	A2G	O5-C5-C6	2.29	112.12	107.66
4	j	201	A2G	O7-C7-N2	2.26	125.98	121.98
4	a	201	A2G	O4-C4-C5	-2.24	103.81	109.32
4	f	201	A2G	O5-C1-C2	-2.19	107.90	111.29
4	f	201	A2G	C4-C3-C2	-2.15	107.87	111.02
4	c	201	A2G	O5-C5-C4	-2.14	105.61	110.83
4	i	201	A2G	C4-C3-C2	-2.12	107.92	111.02
4	e	201	A2G	C1-C2-N2	2.11	113.76	110.43
4	e	201	A2G	O3-C3-C2	-2.06	105.12	109.40
4	d	201	A2G	C1-O5-C5	2.05	114.93	112.19
4	h	201	A2G	O5-C5-C4	-2.02	105.91	110.83
4	i	201	A2G	C3-C4-C5	-2.01	106.58	110.23

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	e	201	A2G	C4-C5-C6-O6
4	e	201	A2G	O5-C5-C6-O6
4	g	201	A2G	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	b	201	A2G	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 ⓘ

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	229/242 (94%)	-0.37	2 (0%) 81 81	30, 41, 56, 76	0
1	B	229/242 (94%)	-0.38	2 (0%) 81 81	30, 41, 56, 73	0
1	C	229/242 (94%)	0.10	3 (1%) 75 75	42, 58, 76, 89	0
1	D	229/242 (94%)	-0.31	3 (1%) 75 75	31, 43, 61, 78	0
1	E	229/242 (94%)	0.22	0 100 100	46, 65, 84, 96	0
1	F	229/242 (94%)	-0.16	3 (1%) 75 75	34, 48, 68, 82	0
1	G	229/242 (94%)	0.61	6 (2%) 57 55	54, 72, 95, 108	0
1	H	229/242 (94%)	0.51	9 (3%) 43 40	45, 61, 90, 101	0
1	I	229/242 (94%)	0.34	3 (1%) 75 75	54, 72, 96, 110	0
1	J	229/242 (94%)	0.61	6 (2%) 57 55	61, 76, 98, 110	0
2	a	5/6 (83%)	-0.03	0 100 100	41, 41, 44, 49	0
2	b	5/6 (83%)	0.89	1 (20%) 3 2	46, 47, 49, 56	0
2	c	5/6 (83%)	0.59	1 (20%) 3 2	62, 66, 70, 75	0
2	d	5/6 (83%)	0.50	1 (20%) 3 2	39, 39, 41, 46	0
2	e	5/6 (83%)	1.96	1 (20%) 3 2	67, 72, 77, 84	0
2	f	5/6 (83%)	0.48	1 (20%) 3 2	43, 43, 46, 50	0
2	g	5/6 (83%)	1.05	1 (20%) 3 2	67, 68, 70, 72	0
2	h	5/6 (83%)	0.90	1 (20%) 3 2	57, 58, 60, 61	0
2	i	5/6 (83%)	0.86	1 (20%) 3 2	60, 61, 62, 62	0
2	j	5/6 (83%)	1.22	1 (20%) 3 2	65, 66, 69, 69	0
All	All	2340/2480 (94%)	0.13	46 (1%) 65 63	30, 58, 89, 110	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	e	105	ALA	6.9
1	H	70	ARG	4.7
2	j	105	ALA	4.5
2	b	105	ALA	3.8
2	f	105	ALA	3.5
1	B	104	ASN	3.4
2	h	105	ALA	3.4
2	g	105	ALA	3.3
1	C	55	GLN	3.2
1	J	39	ILE	3.2
2	i	105	ALA	3.1
1	H	57	ARG	3.1
1	H	158	ARG	3.0
1	H	69	ILE	2.9
2	c	105	ALA	2.8
1	J	36	SER	2.8
1	D	229	ASN	2.8
2	d	105	ALA	2.8
1	D	36	SER	2.7
1	G	36	SER	2.7
1	H	214	GLU	2.7
1	J	73	SER	2.7
1	H	74	ASN	2.6
1	G	19	GLN	2.5
1	G	49	VAL	2.5
1	J	81	ALA	2.5
1	B	14	GLU	2.4
1	H	10	PHE	2.4
1	I	151	GLN	2.4
1	H	68	VAL	2.4
1	G	51	SER	2.3
1	F	14	GLU	2.3
1	D	182	ASP	2.3
1	I	209	ALA	2.2
1	A	14	GLU	2.2
1	C	14	GLU	2.2
1	F	229	ASN	2.2
1	F	158	ARG	2.1
1	G	29	LEU	2.1
1	H	229	ASN	2.1
1	C	229	ASN	2.1
1	A	158	ARG	2.1
1	I	153	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	13	VAL	2.0
1	J	91	VAL	2.0
1	J	213	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	A2G	e	201	14/15	0.92	0.10	63,67,68,68	0
4	A2G	b	201	14/15	0.93	0.10	38,40,42,44	0
4	A2G	c	201	14/15	0.94	0.08	56,59,61,62	0
4	A2G	a	201	14/15	0.94	0.09	35,37,38,38	0
4	A2G	g	201	14/15	0.94	0.08	63,65,66,67	0
4	A2G	i	201	14/15	0.94	0.09	58,60,63,65	0
4	A2G	j	201	14/15	0.94	0.08	63,65,67,68	0
4	A2G	h	201	14/15	0.95	0.07	52,55,60,61	0
4	A2G	d	201	14/15	0.97	0.07	32,34,35,36	0
4	A2G	f	201	14/15	0.98	0.06	37,39,40,41	0
3	CA	G	302	1/1	0.99	0.02	59,59,59,59	0
3	CA	H	301	1/1	0.99	0.02	49,49,49,49	0
3	CA	H	302	1/1	0.99	0.03	52,52,52,52	0
3	CA	I	301	1/1	0.99	0.03	52,52,52,52	0
3	CA	J	301	1/1	0.99	0.03	59,59,59,59	0
3	CA	A	302	1/1	0.99	0.04	36,36,36,36	0
3	CA	B	301	1/1	0.99	0.02	33,33,33,33	0
3	CA	B	302	1/1	0.99	0.02	36,36,36,36	0
3	CA	C	301	1/1	0.99	0.02	47,47,47,47	0
3	CA	C	302	1/1	0.99	0.05	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CA	E	301	1/1	0.99	0.05	54,54,54,54	0
3	CA	E	302	1/1	0.99	0.05	62,62,62,62	0
3	CA	F	301	1/1	0.99	0.02	36,36,36,36	0
3	CA	F	302	1/1	0.99	0.01	35,35,35,35	0
3	CA	G	301	1/1	0.99	0.03	60,60,60,60	0
3	CA	D	301	1/1	1.00	0.01	30,30,30,30	0
3	CA	D	302	1/1	1.00	0.02	31,31,31,31	0
3	CA	I	302	1/1	1.00	0.04	55,55,55,55	0
3	CA	A	301	1/1	1.00	0.02	32,32,32,32	0
3	CA	J	302	1/1	1.00	0.04	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.