



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:42 AM UTC

PDB ID : 5Y7G / pdb_00005y7g
Title : Crystal structure of paFAN1 bound to 1nt 5'flap DNA with gap
Authors : Cho, Y.; Jin, H.
Deposited on : 2017-08-17
Resolution : 3.40 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	:	4-5-2 with Phenix2.0
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

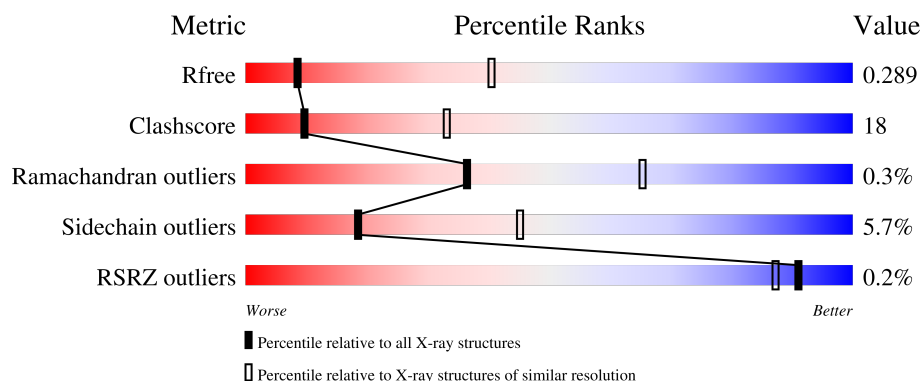
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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.



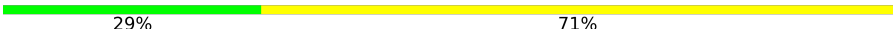
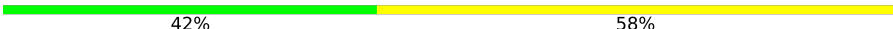
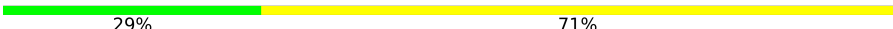
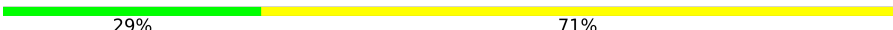
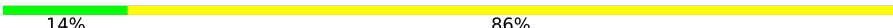
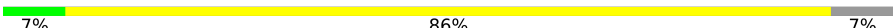
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	580	
1	B	580	
1	C	580	
2	D	10	
2	F	10	

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Mol	Chain	Length	Quality of chain
2	H	10	 10%90%
3	E	24	 29%71%
3	G	24	 42%58%
3	I	24	 29%71%
4	J	14	 29%71%
4	L	14	 14%86%
4	N	14	 7%86%7%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16164 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 Fanconi-associated nuclease 1 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	542	Total	C	N	O	S	0	0	0
			4406	2816	799	771	20			
1	B	543	Total	C	N	O	S	0	0	0
			4424	2827	800	777	20			
1	C	540	Total	C	N	O	S	0	0	0
			4401	2813	794	774	20			

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP Q9I2N0
A	-19	GLY	-	expression tag	UNP Q9I2N0
A	-18	SER	-	expression tag	UNP Q9I2N0
A	-17	SER	-	expression tag	UNP Q9I2N0
A	-16	HIS	-	expression tag	UNP Q9I2N0
A	-15	HIS	-	expression tag	UNP Q9I2N0
A	-14	HIS	-	expression tag	UNP Q9I2N0
A	-13	HIS	-	expression tag	UNP Q9I2N0
A	-12	HIS	-	expression tag	UNP Q9I2N0
A	-11	HIS	-	expression tag	UNP Q9I2N0
A	-10	SER	-	expression tag	UNP Q9I2N0
A	-9	SER	-	expression tag	UNP Q9I2N0
A	-8	GLY	-	expression tag	UNP Q9I2N0
A	-7	LEU	-	expression tag	UNP Q9I2N0
A	-6	VAL	-	expression tag	UNP Q9I2N0
A	-5	PRO	-	expression tag	UNP Q9I2N0
A	-4	ARG	-	expression tag	UNP Q9I2N0
A	-3	GLY	-	expression tag	UNP Q9I2N0
A	-2	SER	-	expression tag	UNP Q9I2N0
A	-1	HIS	-	expression tag	UNP Q9I2N0
A	0	MET	-	expression tag	UNP Q9I2N0
B	-20	MET	-	expression tag	UNP Q9I2N0
B	-19	GLY	-	expression tag	UNP Q9I2N0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	SER	-	expression tag	UNP Q9I2N0
B	-17	SER	-	expression tag	UNP Q9I2N0
B	-16	HIS	-	expression tag	UNP Q9I2N0
B	-15	HIS	-	expression tag	UNP Q9I2N0
B	-14	HIS	-	expression tag	UNP Q9I2N0
B	-13	HIS	-	expression tag	UNP Q9I2N0
B	-12	HIS	-	expression tag	UNP Q9I2N0
B	-11	HIS	-	expression tag	UNP Q9I2N0
B	-10	SER	-	expression tag	UNP Q9I2N0
B	-9	SER	-	expression tag	UNP Q9I2N0
B	-8	GLY	-	expression tag	UNP Q9I2N0
B	-7	LEU	-	expression tag	UNP Q9I2N0
B	-6	VAL	-	expression tag	UNP Q9I2N0
B	-5	PRO	-	expression tag	UNP Q9I2N0
B	-4	ARG	-	expression tag	UNP Q9I2N0
B	-3	GLY	-	expression tag	UNP Q9I2N0
B	-2	SER	-	expression tag	UNP Q9I2N0
B	-1	HIS	-	expression tag	UNP Q9I2N0
B	0	MET	-	expression tag	UNP Q9I2N0
C	-20	MET	-	expression tag	UNP Q9I2N0
C	-19	GLY	-	expression tag	UNP Q9I2N0
C	-18	SER	-	expression tag	UNP Q9I2N0
C	-17	SER	-	expression tag	UNP Q9I2N0
C	-16	HIS	-	expression tag	UNP Q9I2N0
C	-15	HIS	-	expression tag	UNP Q9I2N0
C	-14	HIS	-	expression tag	UNP Q9I2N0
C	-13	HIS	-	expression tag	UNP Q9I2N0
C	-12	HIS	-	expression tag	UNP Q9I2N0
C	-11	HIS	-	expression tag	UNP Q9I2N0
C	-10	SER	-	expression tag	UNP Q9I2N0
C	-9	SER	-	expression tag	UNP Q9I2N0
C	-8	GLY	-	expression tag	UNP Q9I2N0
C	-7	LEU	-	expression tag	UNP Q9I2N0
C	-6	VAL	-	expression tag	UNP Q9I2N0
C	-5	PRO	-	expression tag	UNP Q9I2N0
C	-4	ARG	-	expression tag	UNP Q9I2N0
C	-3	GLY	-	expression tag	UNP Q9I2N0
C	-2	SER	-	expression tag	UNP Q9I2N0
C	-1	HIS	-	expression tag	UNP Q9I2N0
C	0	MET	-	expression tag	UNP Q9I2N0

- Molecule 2 is a DNA chain called DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	10	Total	C	N	O	P	0	0	0
			211	100	38	63	10			
2	F	10	Total	C	N	O	P	0	0	0
			211	100	38	63	10			
2	H	10	Total	C	N	O	P	0	0	0
			211	100	38	63	10			

- Molecule 3 is a DNA chain called DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*TP*CP*CP*CP*AP*AP*CP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	24	Total	C	N	O	P	0	0	0
			488	234	84	146	24			
3	G	24	Total	C	N	O	P	0	0	0
			487	233	84	146	24			
3	I	24	Total	C	N	O	P	0	0	0
			488	234	84	146	24			

- Molecule 4 is a DNA chain called DNA (5'-D(P*TP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*CP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	J	14	Total	C	N	O	P	0	0	0
			284	136	53	81	14			
4	L	14	Total	C	N	O	P	0	0	0
			284	136	53	81	14			
4	N	13	Total	C	N	O	P	0	0	0
			264	126	51	74	13			

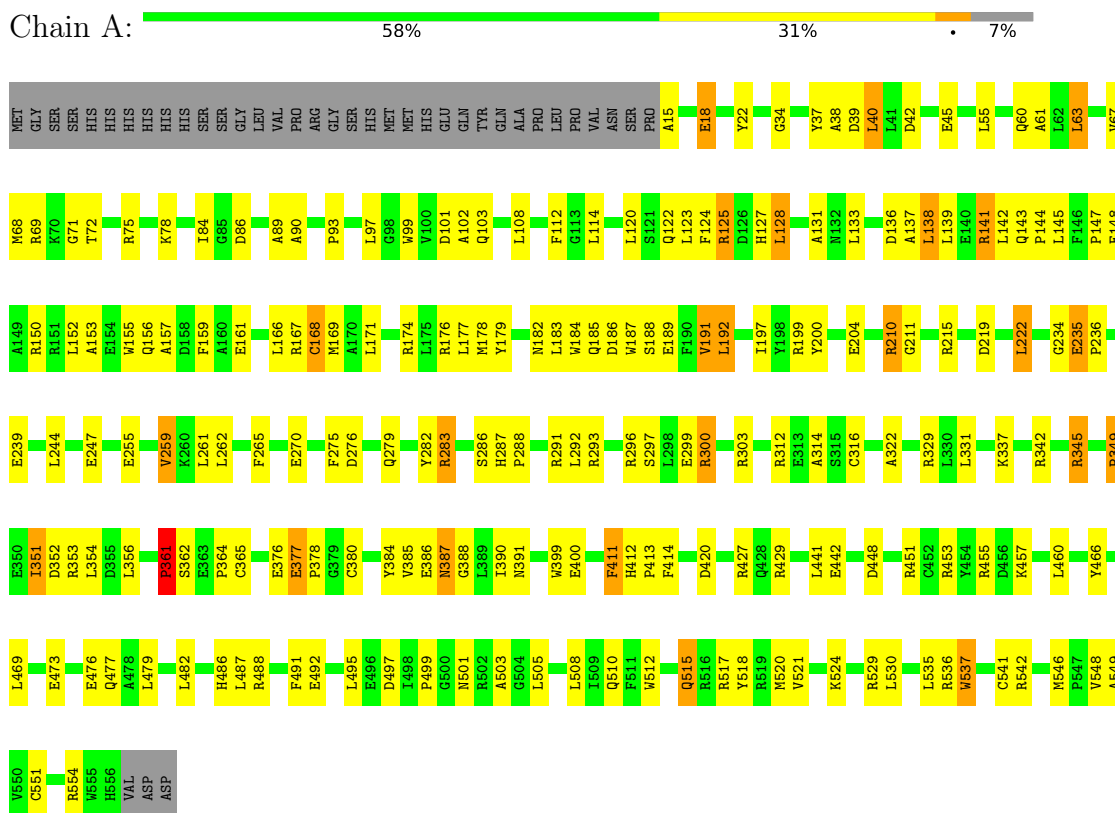
- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Ca	0	0
			2	2		
5	B	2	Total	Ca	0	0
			2	2		
5	C	1	Total	Ca	0	0
			1	1		

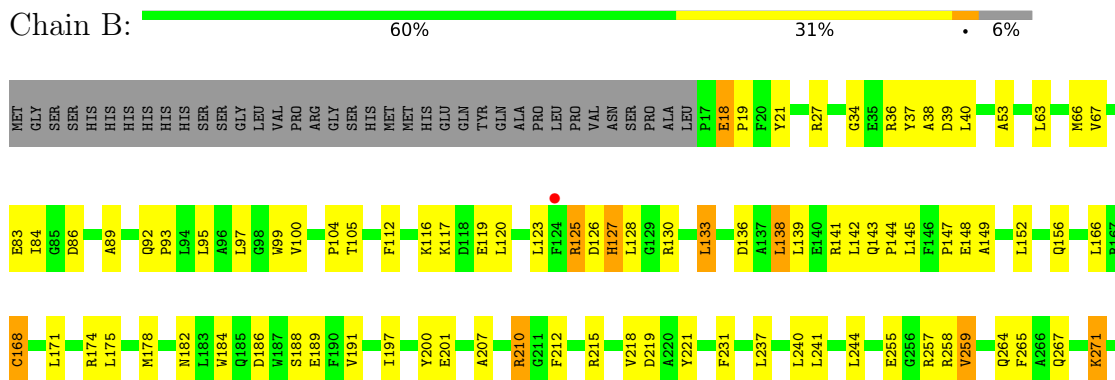
3 Residue-property plots

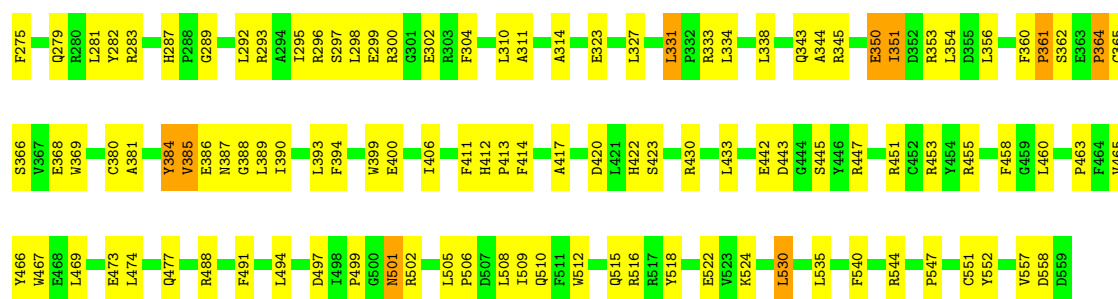
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: Fanconi-associated nuclease 1 homolog



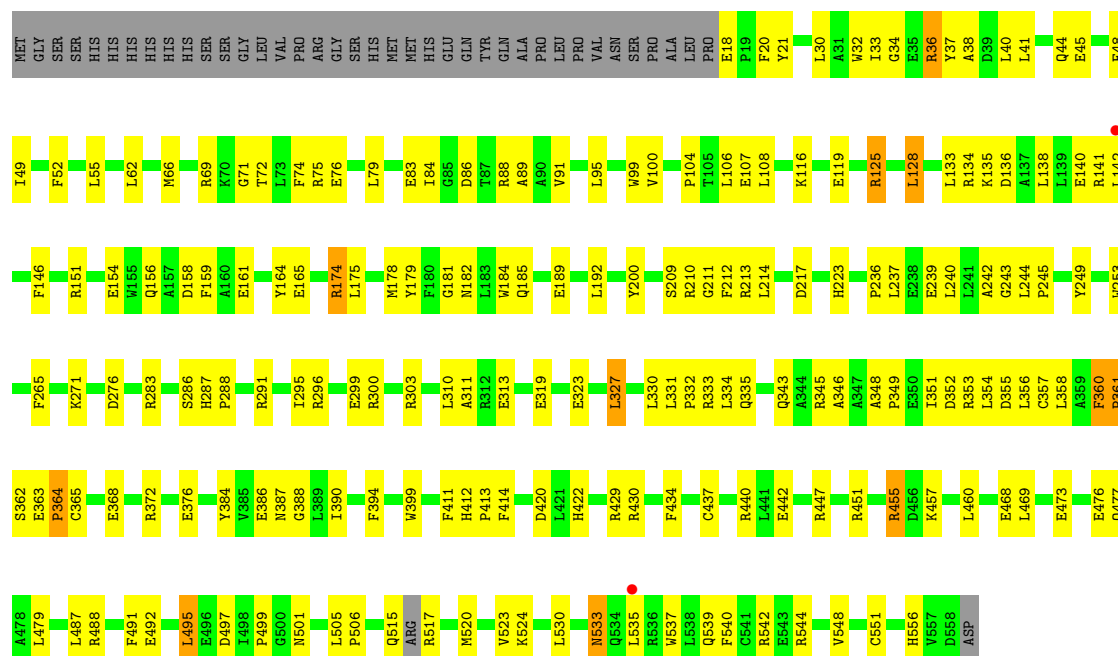
- Molecule 1: Fanconi-associated nuclease 1 homolog





- Molecule 1: Fanconi-associated nuclease 1 homolog

Chain C: 60% 31% 7%



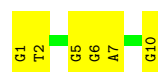
- Molecule 2: DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3')

Chain D: 20% 80%



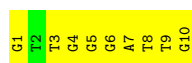
- Molecule 2: DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3')

Chain F: 40% 60%

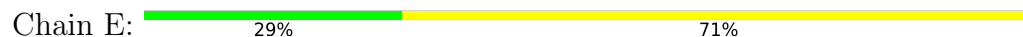


- Molecule 2: DNA (5'-D(P*GP*TP*TP*GP*GP*GP*AP*TP*TP*G)-3')

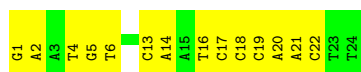
Chain H: 10% 90%



• Molecule 3: DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*T
P*CP*CP*CP*AP*AP*CP*TP*T)-3')



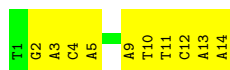
• Molecule 3: DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*T
P*CP*CP*CP*AP*AP*CP*TP*T)-3')



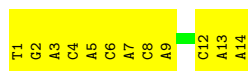
• Molecule 3: DNA (5'-D(P*GP*AP*AP*TP*GP*TP*GP*TP*GP*TP*CP*TP*CP*AP*AP*T
P*CP*CP*CP*AP*AP*CP*TP*T)-3')



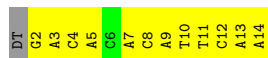
• Molecule 4: DNA (5'-D(P*TP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*CP*AP*A)-3'
)



• Molecule 4: DNA (5'-D(P*TP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*CP*AP*A)-3'
)



• Molecule 4: DNA (5'-D(P*TP*GP*AP*CP*AP*CP*AP*CP*AP*TP*TP*CP*AP*A)-3'
)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	140.29Å 143.26Å 172.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.58 – 3.40 33.58 – 3.40	Depositor EDS
% Data completeness (in resolution range)	95.6 (33.58-3.40) 95.6 (33.58-3.40)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.10.1-2155_1069: ???)	Depositor
R, R_{free}	0.221 , 0.280 0.227 , 0.289	Depositor DCC
R_{free} test set	2868 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	105.5	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 105.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.004 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16164	wwPDB-VP
Average B, all atoms (Å ²)	163.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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: CA

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	0.58	0/4522	0.92	12/6125 (0.2%)
1	B	0.51	1/4541 (0.0%)	0.85	6/6150 (0.1%)
1	C	0.43	0/4516	0.75	3/6115 (0.0%)
2	D	0.63	0/236	0.70	0/364
2	F	0.50	0/236	0.61	0/364
2	H	0.36	0/236	0.59	0/364
3	E	0.73	0/545	0.70	0/838
3	G	0.54	0/544	0.64	0/836
3	I	0.45	0/545	0.67	0/838
4	J	0.66	0/318	0.73	0/487
4	L	0.51	0/318	0.60	0/487
4	N	0.35	0/296	0.56	0/453
All	All	0.52	1/16853 (0.0%)	0.81	21/23421 (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
1	A	0	2
1	B	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	351	ILE	CA-CB	5.30	1.61	1.54

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	377	GLU	CA-C-N	7.80	145.72	127.00
1	A	377	GLU	C-N-CA	7.80	145.72	127.00
1	B	127	HIS	CA-C-N	-7.36	112.03	123.13
1	B	127	HIS	C-N-CA	-7.36	112.03	123.13
1	A	377	GLU	C-N-CD	-7.32	104.49	120.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	361	PRO	Peptide
1	A	71	GLY	Peptide
1	B	361	PRO	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	4406	0	4306	155	1
1	B	4424	0	4317	143	0
1	C	4401	0	4293	138	1
2	D	211	0	115	16	0
2	F	211	0	115	5	0
2	H	211	0	115	14	0
3	E	488	0	273	16	0
3	G	487	0	270	15	0
3	I	488	0	273	20	0
4	J	284	0	158	11	0
4	L	284	0	158	16	0
4	N	264	0	146	11	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	1	0	0	0	0
All	All	16164	0	14539	543	1

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 18.

The worst 5 of 543 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:A:342:ARG:NH1	4:J:14:DA:OP1	1.91	1.03
1:B:387:ASN:HB3	1:B:505:LEU:HB2	1.48	0.96
3:E:21:DA:H2''	3:E:22:DC:H5''	1.49	0.94
3:G:21:DA:H2''	3:G:22:DC:H5''	1.49	0.94
4:N:9:DA:H2''	4:N:10:DT:H5''	1.50	0.93

All (1) 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:A:376:GLU:O	1:C:447:ARG:NH2[3_545]	2.18	0.02

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	540/580 (93%)	520 (96%)	18 (3%)	2 (0%)	30	59
1	B	541/580 (93%)	523 (97%)	16 (3%)	2 (0%)	30	59
1	C	536/580 (92%)	511 (95%)	24 (4%)	1 (0%)	43	71
All	All	1617/1740 (93%)	1554 (96%)	58 (4%)	5 (0%)	36	65

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	361	PRO
1	A	18	GLU
1	B	344	ALA
1	B	19	PRO
1	A	235	GLU

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	441/478 (92%)	410 (93%)	31 (7%)	14	40
1	B	444/478 (93%)	422 (95%)	22 (5%)	22	49
1	C	442/478 (92%)	419 (95%)	23 (5%)	21	48
All	All	1327/1434 (92%)	1251 (94%)	76 (6%)	18	45

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	133	LEU
1	C	468	GLU
1	C	174	ARG
1	C	357	CYS
1	C	533	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	515	GLN
1	C	25	ASN
1	C	533	ASN
1	C	415	HIS
1	C	531	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	542/580 (93%)	-0.72	0 100 100	80, 130, 180, 258	0
1	B	543/580 (93%)	-0.86	1 (0%) 91 87	105, 148, 200, 248	0
1	C	540/580 (93%)	-0.73	2 (0%) 88 81	119, 185, 246, 291	0
2	D	10/10 (100%)	-0.66	0 100 100	135, 155, 227, 236	0
2	F	10/10 (100%)	-0.84	0 100 100	141, 160, 230, 255	0
2	H	10/10 (100%)	-0.81	0 100 100	190, 195, 246, 261	0
3	E	24/24 (100%)	-0.53	0 100 100	126, 159, 201, 221	0
3	G	24/24 (100%)	-0.88	0 100 100	154, 196, 248, 275	0
3	I	24/24 (100%)	-0.58	0 100 100	185, 205, 249, 272	0
4	J	14/14 (100%)	-0.34	0 100 100	120, 155, 194, 200	0
4	L	14/14 (100%)	-0.77	0 100 100	188, 211, 230, 240	0
4	N	13/14 (92%)	-0.89	0 100 100	174, 206, 249, 263	0
All	All	1768/1884 (93%)	-0.76	3 (0%) 91 87	80, 155, 230, 291	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	124	PHE	2.4
1	C	535	LEU	2.4
1	C	142	LEU	2.4

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 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
5	CA	A	602	1/1	0.94	0.06	142,142,142,142	0
5	CA	B	602	1/1	0.94	0.07	148,148,148,148	0
5	CA	C	601	1/1	0.97	0.04	189,189,189,189	0
5	CA	A	601	1/1	0.99	0.02	92,92,92,92	0
5	CA	B	601	1/1	0.99	0.02	142,142,142,142	0

6.5 Other polymers [i](#)

There are no such residues in this entry.