



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:06 PM UTC

PDB ID : 6JYJ / pdb_00006jyj
Title : Crystal structure of FAM46B (TENT5B)
Authors : Zhang, H.; Hu, J.L.; Gao, S.
Deposited on : 2019-04-26
Resolution : 2.69 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

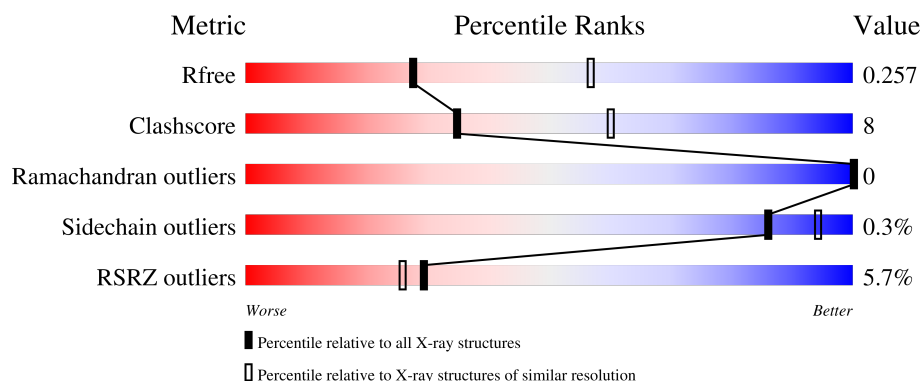
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	402	5% 69% 12% 18%
1	B	402	4% 72% 10% 18%
1	C	402	4% 66% 16% 18%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FLC	C	401	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8067 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 Terminal nucleotidyltransferase 5B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	329	Total	C	N	O	S	0	0	0
			2652	1677	473	480	22			
1	B	330	Total	C	N	O	S	0	0	0
			2664	1685	474	483	22			
1	C	330	Total	C	N	O	S	0	0	0
			2672	1690	477	483	22			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP F7E7M3
A	-5	PRO	-	expression tag	UNP F7E7M3
A	-4	HIS	-	expression tag	UNP F7E7M3
A	-3	MET	-	expression tag	UNP F7E7M3
A	-2	GLY	-	expression tag	UNP F7E7M3
A	-1	GLY	-	expression tag	UNP F7E7M3
A	0	SER	-	expression tag	UNP F7E7M3
B	-6	GLY	-	expression tag	UNP F7E7M3
B	-5	PRO	-	expression tag	UNP F7E7M3
B	-4	HIS	-	expression tag	UNP F7E7M3
B	-3	MET	-	expression tag	UNP F7E7M3
B	-2	GLY	-	expression tag	UNP F7E7M3
B	-1	GLY	-	expression tag	UNP F7E7M3
B	0	SER	-	expression tag	UNP F7E7M3
C	-6	GLY	-	expression tag	UNP F7E7M3
C	-5	PRO	-	expression tag	UNP F7E7M3
C	-4	HIS	-	expression tag	UNP F7E7M3
C	-3	MET	-	expression tag	UNP F7E7M3
C	-2	GLY	-	expression tag	UNP F7E7M3
C	-1	GLY	-	expression tag	UNP F7E7M3
C	0	SER	-	expression tag	UNP F7E7M3

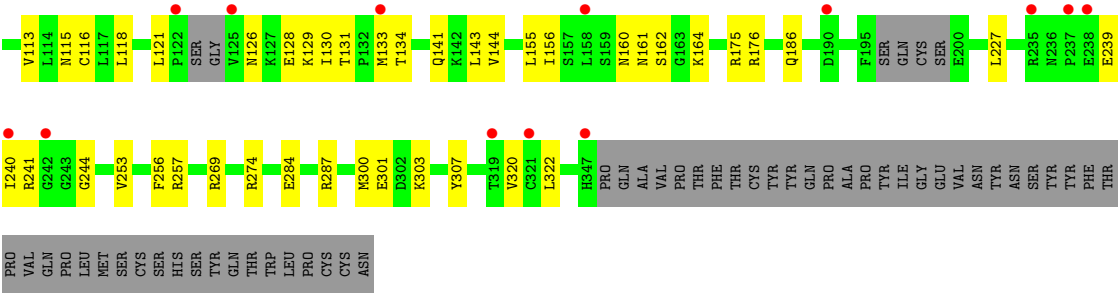
- Molecule 2 is CITRATE ANION (CCD ID: FLC) (formula: C₆H₅O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		
2	C	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total	O	0	0
			13	13		
3	B	11	Total	O	0	0
			11	11		
3	C	16	Total	O	0	0
			16	16		



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.60Å 76.12Å 135.07Å 90.00° 96.51° 90.00°	Depositor
Resolution (Å)	47.13 – 2.69 47.13 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.13-2.69) 99.3 (47.13-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.204 , 0.252 0.209 , 0.257	Depositor DCC
R_{free} test set	1684 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	49.8	Xtriage
Anisotropy	0.499	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 53.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8067	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FLC

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	0.12	0/2703	0.34	0/3641
1	B	0.11	0/2716	0.33	1/3659 (0.0%)
1	C	0.13	0/2724	0.33	0/3669
All	All	0.12	0/8143	0.34	1/10969 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	129	LYS	N-CA-C	-5.53	107.11	112.97

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2652	0	2664	36	0
1	B	2664	0	2677	30	0
1	C	2672	0	2681	57	0
2	A	13	0	5	1	0
2	B	13	0	5	0	0
2	C	13	0	5	4	0
3	A	13	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	11	0	0	0	0
3	C	16	0	0	0	0
All	All	8067	0	8037	121	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 8.

All (121) 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:25:ARG:HH12	2:C:401:FLC:HA1	1.09	1.06
1:C:241:ARG:HH12	1:C:274:ARG:HH11	1.04	0.98
1:C:25:ARG:NH1	2:C:401:FLC:HA1	1.91	0.85
1:A:37:HIS:HB2	1:A:161:ASN:HB3	1.65	0.78
1:A:160:ASN:HB2	1:A:164:LYS:HB2	1.69	0.74
1:C:241:ARG:NH1	1:C:274:ARG:HH11	1.83	0.71
1:B:37:HIS:HB2	1:B:161:ASN:HB3	1.74	0.69
1:C:45:LEU:HD21	1:C:121:LEU:HD23	1.75	0.68
1:A:148:THR:HG23	1:A:151:ASP:H	1.59	0.68
1:C:162:SER:HB3	1:C:164:LYS:NZ	2.08	0.67
1:A:34:VAL:HG21	1:A:166:MET:HE1	1.76	0.67
1:C:31:CYS:SG	1:C:50:ARG:NH1	2.70	0.65
1:C:144:VAL:HG22	1:C:155:LEU:HB3	1.80	0.64
1:C:241:ARG:HH12	1:C:274:ARG:NH1	1.88	0.64
1:C:301:GLU:N	1:C:301:GLU:OE2	2.29	0.64
1:B:225:ASP:OD1	1:B:229:ASN:ND2	2.31	0.64
1:A:147:CYS:SG	1:A:152:ARG:NH1	2.71	0.64
1:C:269:ARG:NH1	1:C:320:VAL:HG11	2.13	0.63
1:C:25:ARG:HH22	2:C:401:FLC:HG1	1.61	0.63
1:C:35:PRO:O	1:C:160:ASN:ND2	2.29	0.63
1:C:118:LEU:HD12	1:C:121:LEU:HD12	1.81	0.62
1:A:73:ASN:CG	1:A:74:GLY:H	2.08	0.61
1:A:45:LEU:HD21	1:A:121:LEU:HD23	1.83	0.61
1:C:25:ARG:HH12	2:C:401:FLC:CA	2.00	0.61
1:C:284:GLU:CD	1:C:287:ARG:HH12	2.09	0.60
1:C:110:LYS:NZ	1:C:133:MET:HE1	2.17	0.60
1:B:73:ASN:CG	1:B:74:GLY:H	2.09	0.60
1:C:73:ASN:CG	1:C:74:GLY:H	2.10	0.60
1:A:97:MET:HA	1:A:97:MET:HE2	1.82	0.59
1:A:319:THR:HG21	1:A:327:ARG:HB2	1.84	0.59
1:B:160:ASN:HB2	1:B:164:LYS:HB2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:28:ALA:O	1:C:32:GLU:HG2	2.03	0.58
1:C:37:HIS:HB2	1:C:161:ASN:HB3	1.85	0.58
1:A:35:PRO:O	1:A:160:ASN:ND2	2.31	0.58
1:C:37:HIS:HB2	1:C:161:ASN:HD22	1.68	0.57
1:C:160:ASN:HB2	1:C:164:LYS:HB2	1.87	0.56
1:C:39:ARG:HH22	1:C:141:GLN:HG3	1.70	0.55
1:C:269:ARG:HH11	1:C:320:VAL:HG11	1.71	0.54
1:C:256:PHE:O	1:C:257:ARG:NH1	2.38	0.54
1:C:176:ARG:NH1	1:C:239:GLU:HB2	2.23	0.54
1:C:57:ARG:HG3	1:C:67:VAL:HG11	1.90	0.54
1:C:162:SER:HB3	1:C:164:LYS:HZ2	1.71	0.53
1:B:57:ARG:HG3	1:B:67:VAL:HG11	1.92	0.52
1:A:25:ARG:HH22	2:A:401:FLC:HG2	1.75	0.52
1:A:36:ILE:HB	1:A:45:LEU:HB2	1.90	0.52
1:A:241:ARG:HH21	1:A:274:ARG:HH11	1.57	0.52
1:C:126:ASN:HB3	1:C:128:GLU:HG2	1.91	0.52
1:A:284:GLU:OE1	1:A:287:ARG:NH2	2.38	0.52
1:C:253:VAL:HG11	1:C:307:TYR:HA	1.90	0.52
1:A:118:LEU:HD12	1:A:121:LEU:HD12	1.92	0.52
1:B:82:HIS:CE1	1:B:228:ARG:HG2	2.45	0.51
1:B:241:ARG:HH21	1:B:274:ARG:HH21	1.58	0.51
1:A:240:ILE:O	1:A:274:ARG:HG2	2.10	0.51
1:B:35:PRO:O	1:B:160:ASN:ND2	2.36	0.51
1:C:128:GLU:HG3	1:C:129:LYS:HG2	1.92	0.50
1:C:128:GLU:O	1:C:130:ILE:HG13	2.11	0.50
1:C:131:THR:O	1:C:134:THR:HG22	2.11	0.50
1:C:31:CYS:SG	1:C:50:ARG:NE	2.84	0.50
1:C:59:ARG:HD3	1:C:116:CYS:SG	2.52	0.50
1:A:57:ARG:HG3	1:A:67:VAL:HG11	1.94	0.50
1:A:67:VAL:HG22	1:A:98:VAL:HG12	1.94	0.50
1:A:28:ALA:O	1:A:32:GLU:HG2	2.12	0.49
1:A:95:ILE:HG22	1:A:97:MET:HE3	1.94	0.49
1:A:59:ARG:NH2	1:A:115:ASN:HB3	2.28	0.48
1:B:36:ILE:HB	1:B:45:LEU:HB2	1.96	0.48
1:A:176:ARG:HH11	1:A:239:GLU:HB2	1.79	0.48
1:A:248:TYR:CG	1:A:271:MET:HE1	2.49	0.48
1:C:85:SER:C	1:C:87:LEU:H	2.22	0.47
1:A:217:TYR:CE1	1:A:235:ARG:HG3	2.49	0.47
1:C:27:ASP:OD1	1:C:50:ARG:NH1	2.44	0.47
1:C:31:CYS:SG	1:C:50:ARG:CZ	3.03	0.47
1:A:186:GLN:CD	1:A:216:MET:HE3	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:85:SER:HB2	1:C:227:LEU:HD11	1.97	0.47
1:C:162:SER:HB3	1:C:164:LYS:HZ3	1.80	0.46
1:C:176:ARG:HH11	1:C:239:GLU:HB2	1.80	0.46
1:B:155:LEU:HD11	1:B:167:GLU:HB3	1.96	0.46
1:B:261:GLU:HG2	1:B:265:LYS:HZ1	1.81	0.46
1:C:284:GLU:OE1	1:C:287:ARG:NH1	2.40	0.46
1:C:241:ARG:HA	1:C:241:ARG:HD2	1.69	0.46
1:A:73:ASN:HD22	1:A:186:GLN:CG	2.29	0.46
1:B:261:GLU:HG2	1:B:265:LYS:NZ	2.31	0.46
1:A:241:ARG:HD2	1:A:274:ARG:NH1	2.31	0.45
1:C:48:ARG:CZ	1:C:50:ARG:HD2	2.46	0.45
1:C:143:LEU:HD23	1:C:156:ILE:HG12	1.99	0.45
1:A:240:ILE:O	1:A:274:ARG:NH2	2.50	0.44
1:C:36:ILE:HB	1:C:45:LEU:HB2	2.00	0.44
1:C:110:LYS:HZ1	1:C:133:MET:HE1	1.83	0.44
1:B:73:ASN:HD22	1:B:186:GLN:HG2	1.82	0.44
1:B:326:GLU:OE2	1:B:326:GLU:N	2.46	0.44
1:C:110:LYS:HZ3	1:C:133:MET:HE1	1.83	0.44
1:C:300:MET:HE3	1:C:303:LYS:HG3	2.00	0.44
1:A:148:THR:CG2	1:A:151:ASP:H	2.28	0.44
1:A:14:ARG:HG3	1:A:15:PHE:CD1	2.53	0.44
1:B:237:PRO:HG2	1:B:270:TYR:CD2	2.53	0.44
1:B:39:ARG:HG3	1:B:39:ARG:NH1	2.33	0.43
1:C:175:ARG:NH2	1:C:239:GLU:OE2	2.51	0.43
1:A:147:CYS:HG	1:A:152:ARG:NH1	2.15	0.43
1:B:39:ARG:HH22	1:B:141:GLN:HB3	1.83	0.43
1:B:241:ARG:HH21	1:B:274:ARG:NH2	2.16	0.42
1:A:73:ASN:CG	1:A:74:GLY:N	2.76	0.42
1:B:148:THR:HG22	1:B:149:GLU:N	2.34	0.42
1:C:59:ARG:HH22	1:C:115:ASN:HB3	1.84	0.42
1:B:9:SER:HA	1:B:10:PRO:HD3	1.88	0.42
1:B:137:GLU:OE2	1:C:24:ARG:NH2	2.51	0.42
1:A:39:ARG:HD2	1:A:137:GLU:O	2.20	0.42
1:B:71:ARG:HD3	1:B:186:GLN:OE1	2.20	0.42
1:C:73:ASN:HD22	1:C:186:GLN:HG2	1.83	0.42
1:A:148:THR:HG22	1:A:151:ASP:O	2.20	0.42
1:B:204:SER:O	1:B:208:HIS:HB3	2.20	0.42
1:C:240:ILE:CG2	1:C:244:GLY:HA3	2.50	0.42
1:B:90:LYS:O	1:B:164:LYS:HB3	2.19	0.41
1:C:92:LEU:HD23	1:C:92:LEU:HA	1.95	0.41
1:B:241:ARG:NH2	1:B:274:ARG:HH21	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:ARG:HG3	1:B:39:ARG:HH11	1.86	0.41
1:B:73:ASN:HD22	1:B:186:GLN:CG	2.34	0.41
1:B:118:LEU:HD12	1:B:121:LEU:HD12	2.01	0.41
1:A:339:VAL:HG11	1:B:12:ALA:HB2	2.03	0.41
1:B:298:VAL:O	1:B:301:GLU:OE2	2.39	0.41
1:C:131:THR:HG22	1:C:133:MET:H	1.85	0.40
1:C:113:VAL:HG11	1:C:156:ILE:HD12	2.03	0.40
1:A:106:PHE:HB3	1:A:145:LYS:HE2	2.04	0.40

There are no symmetry-related clashes.

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	323/402 (80%)	314 (97%)	9 (3%)	0	100	100
1	B	324/402 (81%)	310 (96%)	14 (4%)	0	100	100
1	C	324/402 (81%)	313 (97%)	11 (3%)	0	100	100
All	All	971/1206 (80%)	937 (96%)	34 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	300/365 (82%)	298 (99%)	2 (1%)	76	90
1	B	302/365 (83%)	302 (100%)	0	100	100
1	C	302/365 (83%)	301 (100%)	1 (0%)	86	94
All	All	904/1095 (83%)	901 (100%)	3 (0%)	86	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	MET
1	A	320	VAL
1	C	322	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	ASN
1	A	296	HIS
1	A	316	ASN
1	B	68	HIS
1	B	268	GLN
1	B	296	HIS
1	B	316	ASN
1	C	296	HIS
1	C	316	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

3 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	FLC	A	401	-	12,12,12	1.09	0	17,17,17	1.39	1 (5%)
2	FLC	C	401	-	12,12,12	1.09	0	17,17,17	1.32	1 (5%)
2	FLC	B	401	-	12,12,12	1.08	0	17,17,17	1.34	1 (5%)

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	FLC	A	401	-	-	6/16/16/16	-
2	FLC	C	401	-	-	0/16/16/16	-
2	FLC	B	401	-	-	12/16/16/16	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	FLC	OB2-CBC-CB	3.60	120.05	113.14
2	B	401	FLC	OB2-CBC-CB	3.55	119.95	113.14
2	C	401	FLC	OB2-CBC-CB	3.54	119.92	113.14

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	FLC	CAC-CA-CB-CG
2	B	401	FLC	CAC-CA-CB-OHB
2	B	401	FLC	CG-CB-CBC-OB2

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Mol	Chain	Res	Type	Atoms
2	B	401	FLC	OHB-CB-CBC-OB1
2	B	401	FLC	OHB-CB-CBC-OB2
2	B	401	FLC	OHB-CB-CG-CGC
2	B	401	FLC	CAC-CA-CB-CBC
2	B	401	FLC	CA-CB-CG-CGC
2	B	401	FLC	CG-CB-CBC-OB1
2	B	401	FLC	CBC-CB-CG-CGC
2	A	401	FLC	CB-CA-CAC-OA1
2	A	401	FLC	CB-CA-CAC-OA2
2	B	401	FLC	CA-CB-CBC-OB1
2	A	401	FLC	CA-CB-CBC-OB1
2	A	401	FLC	CA-CB-CBC-OB2
2	A	401	FLC	CG-CB-CBC-OB1
2	A	401	FLC	CG-CB-CBC-OB2
2	B	401	FLC	CA-CB-CBC-OB2

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	FLC	1	0
2	C	401	FLC	4	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	329/402 (81%)	0.29	21 (6%)	25 22	30, 56, 109, 137	0
1	B	330/402 (82%)	0.31	18 (5%)	30 27	30, 57, 104, 137	0
1	C	330/402 (82%)	0.41	17 (5%)	33 29	29, 61, 116, 146	0
All	All	989/1206 (82%)	0.33	56 (5%)	29 26	29, 58, 112, 146	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	10	PRO	4.3
1	A	129	LYS	3.8
1	C	240	ILE	3.8
1	A	125	VAL	3.6
1	C	347	HIS	3.5
1	A	133	MET	3.4
1	C	237	PRO	3.4
1	A	122	PRO	3.3
1	B	11	THR	3.3
1	A	12	ALA	3.1
1	B	321	CYS	3.1
1	C	122	PRO	3.0
1	A	345	GLN	2.9
1	A	298	VAL	2.9
1	B	240	ILE	2.8
1	B	103	PRO	2.8
1	B	89	TYR	2.8
1	B	235	ARG	2.8
1	B	133	MET	2.8
1	C	319	THR	2.7
1	C	133	MET	2.7
1	A	299	GLY	2.7
1	A	130	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	197	GLN	2.6
1	A	321	CYS	2.6
1	C	12	ALA	2.6
1	B	345	GLN	2.6
1	A	41	ASN	2.5
1	C	50	ARG	2.5
1	C	321	CYS	2.4
1	C	125	VAL	2.4
1	B	202	PRO	2.4
1	C	242	GLY	2.4
1	B	259	LYS	2.3
1	A	88	GLY	2.3
1	B	92	LEU	2.3
1	B	123	SER	2.3
1	B	243	GLY	2.3
1	A	160	ASN	2.3
1	B	201	ASN	2.3
1	B	236	ASN	2.3
1	C	235	ARG	2.3
1	A	201	ASN	2.3
1	C	190	ASP	2.2
1	B	50	ARG	2.2
1	A	89	TYR	2.2
1	C	103	PRO	2.2
1	C	104	ASP	2.2
1	A	195	PHE	2.2
1	A	161	ASN	2.1
1	C	238	GLU	2.1
1	A	196	SER	2.1
1	A	259	LYS	2.1
1	C	158	LEU	2.1
1	A	104	ASP	2.1
1	B	241	ARG	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($\text{\AA}^2$)	Q<0.9
2	FLC	B	401	13/13	0.62	0.18	92,110,118,119	0
2	FLC	C	401	13/13	0.69	0.16	81,100,107,109	0
2	FLC	A	401	13/13	0.79	0.13	83,93,98,100	0

6.5 Other polymers [i](#)

There are no such residues in this entry.