



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:33 PM UTC

PDB ID : 3F98 / pdb_00003f98
Title : Crystal structure of human plasma platelet activating factor acetylhydrolase covalently inhibited by tabun
Authors : Samanta, U.; Bahnson, B.J.
Deposited on : 2008-11-13
Resolution : 1.70 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

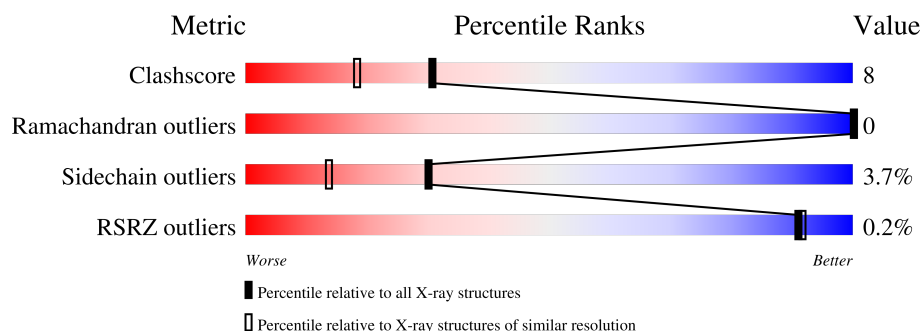
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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))
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	383	
1	B	383	
1	C	383	

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
3	FMT	A	513	-	-	X	-
3	FMT	A	554	-	-	X	-
3	FMT	A	555	-	-	X	-
3	FMT	A	556	-	-	X	-
3	FMT	B	514	-	-	X	-
3	FMT	B	530	-	-	X	-
3	FMT	B	542	-	-	X	-
3	FMT	B	550	-	-	X	-
3	FMT	B	586	-	-	X	-
3	FMT	C	578	-	-	X	-
3	FMT	C	579	-	-	X	-
3	FMT	C	584	-	-	X	-
3	FMT	C	585	-	-	X	-

2 Entry composition [i](#)

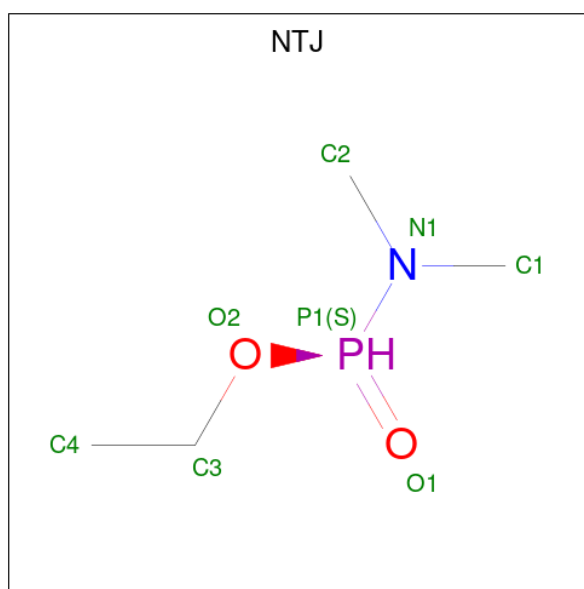
There are 4 unique types of molecules in this entry. The entry contains 10717 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Platelet-activating factor acetylhydrolase.

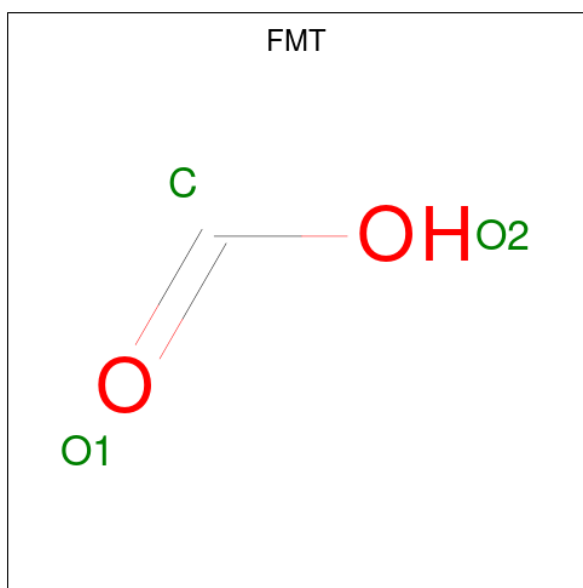
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	22	0
			3112	1996	530	572	14			
1	B	377	Total	C	N	O	S	0	24	0
			3125	2004	533	574	14			
1	C	377	Total	C	N	O	S	0	22	0
			3114	1996	532	572	14			

- Molecule 2 is R-ETHYL N,N-DIMETHYLPHOSPHONAMIDATE (CCD ID: NTJ) (formula: $C_4H_{12}NO_2P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			8	4	1	2	1		
2	B	1	Total	C	N	O	P	0	0
			8	4	1	2	1		
2	C	1	Total	C	N	O	P	0	0
			8	4	1	2	1		

- Molecule 3 is FORMIC ACID (CCD ID: FMT) (formula: CH_2O_2).



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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

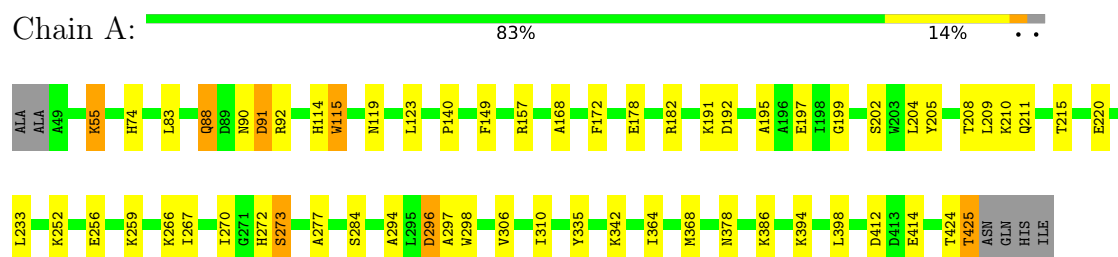
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	369	Total O 369 369	0	0
4	B	377	Total O 377 377	0	0
4	C	338	Total O 338 338	0	0

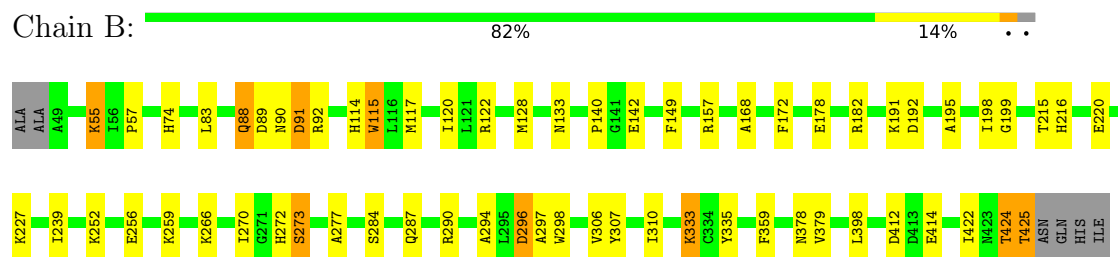
3 Residue-property plots

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.

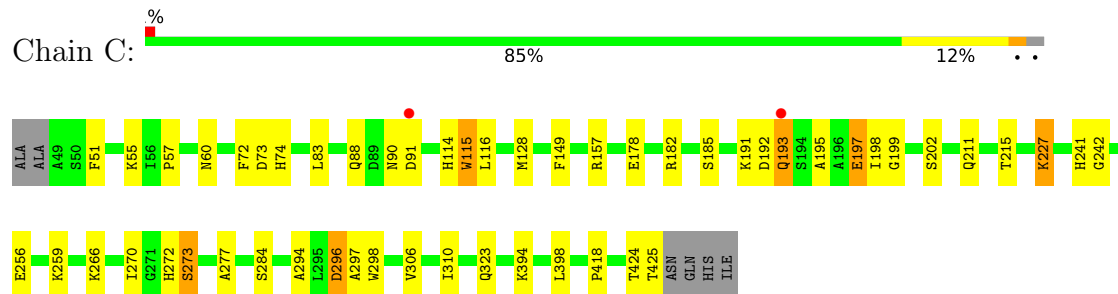
• Molecule 1: Platelet-activating factor acetylhydrolase



• Molecule 1: Platelet-activating factor acetylhydrolase



• Molecule 1: Platelet-activating factor acetylhydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	76.98Å 133.32Å 253.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.70 50.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-1.70) 98.3 (50.00-1.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.45 (at 1.70Å)	Xtriage
Refinement program	REFMAC OF CCP4I FOR REFINEMENT	Depositor
R, R_{free}	0.179 , 0.202 (Not available) , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	15.7	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.488 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.488 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10717	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% 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: FMT, NTJ

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	0.77	3/3276 (0.1%)	0.81	3/4426 (0.1%)
1	B	0.78	3/3289 (0.1%)	0.82	3/4442 (0.1%)
1	C	0.79	3/3279 (0.1%)	0.82	3/4430 (0.1%)
All	All	0.78	9/9844 (0.1%)	0.81	9/13298 (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	1
1	B	0	1
1	C	0	1
All	All	0	3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	272	HIS	C-N	20.79	1.62	1.33
1	B	272	HIS	C-N	20.78	1.62	1.33
1	C	272	HIS	C-N	20.24	1.62	1.33
1	B	273	SER	C-O	14.50	1.42	1.24
1	A	273	SER	C-O	14.47	1.42	1.24
1	C	273	SER	C-O	14.31	1.42	1.24
1	C	273	SER	C-N	11.44	1.48	1.33
1	B	273	SER	C-N	7.82	1.44	1.33
1	A	273	SER	C-N	7.62	1.44	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	273	SER	O-C-N	-12.56	105.89	122.59
1	B	273	SER	O-C-N	-10.94	108.04	122.59
1	A	273	SER	O-C-N	-10.93	108.06	122.59
1	B	273	SER	CA-C-N	5.39	127.51	120.28
1	B	273	SER	C-N-CA	5.39	127.51	120.28
1	C	273	SER	CA-C-N	5.07	127.32	120.38
1	C	273	SER	C-N-CA	5.07	127.32	120.38
1	A	273	SER	CA-C-N	5.01	127.49	120.28
1	A	273	SER	C-N-CA	5.01	127.49	120.28

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	91	ASP	Peptide
1	B	91	ASP	Peptide
1	C	91	ASP	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	3112	0	3066	48	0
1	B	3125	0	3083	59	0
1	C	3114	0	3062	45	0
2	A	8	0	11	3	0
2	B	8	0	11	1	0
2	C	8	0	11	1	0
3	A	93	0	31	15	0
3	B	81	0	27	22	0
3	C	84	0	28	19	0
4	A	369	0	0	10	0
4	B	377	0	0	8	0
4	C	338	0	0	11	0
All	All	10717	0	9330	158	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 (158) 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:259[A]:LYS:HG3	3:C:578:FMT:H	1.21	1.13
1:B:256[A]:GLU:O	1:B:259[A]:LYS:HG3	1.63	0.99
3:A:554:FMT:H	4:A:1050:HOH:O	1.63	0.97
1:B:259[A]:LYS:HG2	3:B:550:FMT:H	1.47	0.95
1:C:259[A]:LYS:HG3	3:C:578:FMT:C	1.97	0.95
1:A:55[A]:LYS:HE2	3:A:556:FMT:C	1.98	0.93
1:C:259[A]:LYS:CG	3:C:578:FMT:H	2.03	0.89
1:B:259[A]:LYS:HG2	3:B:550:FMT:C	2.01	0.89
1:C:323:GLN:HG3	3:C:585:FMT:H	1.58	0.85
2:B:473:NTJ:H4C1	4:B:1183:HOH:O	1.82	0.79
2:C:473:NTJ:H4C1	4:C:1842:HOH:O	1.83	0.78
1:B:256[A]:GLU:HG2	1:B:259[A]:LYS:HE3	1.65	0.77
1:C:323:GLN:CG	3:C:585:FMT:H	2.17	0.74
2:A:473:NTJ:H4C1	4:A:1210:HOH:O	1.87	0.73
1:A:414[A]:GLU:HB2	1:B:414[A]:GLU:HB2	1.70	0.72
1:C:182:ARG:HA	3:C:575:FMT:C	2.21	0.71
1:C:323:GLN:CB	3:C:585:FMT:H	2.20	0.71
1:A:378:ASN:HD21	3:A:555:FMT:H	1.54	0.70
1:C:55[A]:LYS:HE3	4:C:1446:HOH:O	1.89	0.70
1:A:182:ARG:HA	3:A:533:FMT:C	2.23	0.68
1:B:195:ALA:O	1:B:199:GLY:N	2.24	0.68
1:A:119:ASN:O	1:A:123:LEU:HG	1.93	0.67
1:A:209:LEU:H	3:A:554:FMT:C	2.07	0.67
1:A:91:ASP:N	4:A:1738:HOH:O	2.26	0.67
1:B:182:ARG:HA	3:B:535:FMT:C	2.27	0.65
1:A:342:LYS:HA	3:A:506:FMT:H	1.80	0.64
1:C:323:GLN:HB2	3:C:585:FMT:H	1.79	0.63
1:B:55[A]:LYS:NZ	4:B:1054:HOH:O	2.31	0.62
1:A:88:GLN:NE2	1:A:140:PRO:HD2	2.14	0.62
1:C:57:PRO:HG3	3:C:579:FMT:H	1.82	0.61
3:C:579:FMT:O1	4:C:1817:HOH:O	2.16	0.61
1:B:191:LYS:HA	4:B:1744:HOH:O	2.01	0.60
1:C:193:GLN:O	1:C:197:GLU:HG2	2.01	0.60
1:A:204:LEU:HD12	3:A:513:FMT:O1	2.02	0.60
1:B:422[A]:ILE:HD13	3:B:586:FMT:H	1.84	0.59
1:B:266:LYS:HD3	1:B:398:LEU:HD23	1.84	0.59
1:B:256[B]:GLU:HA	3:B:550:FMT:O2	2.03	0.59
1:A:195:ALA:O	1:A:199:GLY:N	2.30	0.59
1:C:55[A]:LYS:HD3	3:C:584:FMT:H	1.84	0.58
1:A:284:SER:CB	1:A:306[A]:VAL:HG13	2.34	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:582:FMT:H	4:C:1889:HOH:O	2.03	0.57
3:A:554:FMT:C	4:A:1050:HOH:O	2.38	0.56
1:C:273:SER:HA	1:C:296:ASP:O	2.06	0.56
1:A:92[A]:ARG:NH2	4:A:1269:HOH:O	2.38	0.56
1:B:287:GLN:NE2	4:B:1468:HOH:O	2.19	0.55
1:A:378:ASN:HD21	3:A:555:FMT:C	2.19	0.55
1:C:256:GLU:HA	3:C:578:FMT:O1	2.06	0.55
1:B:55[A]:LYS:HE2	4:B:1576:HOH:O	2.07	0.55
1:C:284:SER:CB	1:C:306[A]:VAL:HG13	2.37	0.55
1:B:239:ILE:O	3:B:550:FMT:H	2.07	0.54
1:A:266:LYS:HD3	1:A:398:LEU:HD23	1.88	0.54
1:A:88:GLN:HE22	1:A:140:PRO:HD2	1.72	0.53
1:B:273:SER:HA	1:B:296:ASP:O	2.09	0.53
1:C:114:HIS:CE1	1:C:115:TRP:HE3	2.27	0.53
1:B:117:MET:HE3	1:B:120:ILE:HB	1.91	0.53
1:B:55[B]:LYS:NZ	4:B:1602:HOH:O	2.42	0.53
1:A:284:SER:HB3	1:A:306[A]:VAL:HG13	1.91	0.53
1:B:239:ILE:O	3:B:550:FMT:C	2.57	0.53
1:C:418:PRO:HD3	4:C:1758:HOH:O	2.09	0.52
1:C:55[A]:LYS:CE	4:C:1446:HOH:O	2.51	0.52
1:C:57:PRO:CG	3:C:579:FMT:H	2.39	0.52
1:A:191:LYS:HE3	1:A:202:SER:OG	2.09	0.52
1:A:273:SER:HA	1:A:296:ASP:O	2.10	0.52
1:B:89:ASP:O	1:B:133:ASN:ND2	2.43	0.52
1:A:205:TYR:H	3:A:513:FMT:C	2.24	0.51
3:A:518:FMT:C	1:B:412:ASP:OD1	2.59	0.51
1:B:290:ARG:HG3	3:B:557:FMT:H	1.93	0.51
1:C:294:ALA:HB1	1:C:297:ALA:HB2	1.94	0.50
1:B:157:ARG:HB3	1:B:178:GLU:HB2	1.93	0.49
1:C:195:ALA:O	1:C:199:GLY:N	2.45	0.49
1:B:114:HIS:CE1	1:B:115:TRP:HE3	2.31	0.49
1:B:284:SER:CB	1:B:306[A]:VAL:HG13	2.42	0.49
3:A:551:FMT:C	4:A:1490:HOH:O	2.61	0.49
1:C:394:LYS:HE3	4:C:1763:HOH:O	2.13	0.49
1:A:55[A]:LYS:HE2	3:A:556:FMT:O2	2.11	0.48
1:A:425:THR:HG21	1:B:335:TYR:HB3	1.94	0.48
1:C:74:HIS:NE2	1:C:192:ASP:HA	2.29	0.48
1:C:323:GLN:HB2	3:C:585:FMT:C	2.42	0.48
1:B:90:ASN:OD1	1:B:90:ASN:O	2.32	0.48
1:B:378:ASN:HD21	3:B:530:FMT:C	2.26	0.48
1:B:379:VAL:HG13	3:B:517:FMT:H	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:259[A]:LYS:CG	3:C:578:FMT:C	2.77	0.48
1:C:90:ASN:O	1:C:90:ASN:OD1	2.31	0.48
1:C:266:LYS:HD3	1:C:398:LEU:HD23	1.95	0.47
1:A:364:ILE:O	1:A:368:MET:HG3	2.14	0.47
1:A:412:ASP:OD1	3:B:515:FMT:C	2.62	0.47
1:B:306[A]:VAL:HG12	1:B:310:ILE:HD11	1.95	0.47
1:A:386:LYS:NZ	4:A:1712:HOH:O	2.48	0.47
1:C:306[A]:VAL:HG12	1:C:310:ILE:HD11	1.96	0.47
1:C:115:TRP:CZ3	1:C:116:LEU:HG	2.50	0.47
1:A:294:ALA:HB1	1:A:297:ALA:HB2	1.96	0.47
1:B:424:THR:O	1:B:424:THR:OG1	2.29	0.47
1:B:307:TYR:CD2	1:B:333:LYS:HG2	2.50	0.46
1:B:294:ALA:HB1	1:B:297:ALA:HB2	1.96	0.46
1:B:277:ALA:HB2	1:B:298:TRP:O	2.16	0.46
1:B:114:HIS:CE1	1:B:115:TRP:CE3	3.04	0.46
1:B:422[B]:ILE:HG12	3:B:586:FMT:H	1.96	0.46
1:B:122:ARG:NH2	3:B:529:FMT:O2	2.49	0.46
1:A:74:HIS:NE2	1:A:192:ASP:HA	2.31	0.46
2:A:473:NTJ:H2C1	1:C:51:PHE:CZ	2.51	0.45
2:A:473:NTJ:C4	4:A:1392:HOH:O	2.64	0.45
3:C:584:FMT:O1	4:C:2032:HOH:O	2.20	0.45
1:A:114:HIS:CE1	1:A:115:TRP:CE3	3.05	0.45
1:A:210:LYS:HD3	4:C:1698:HOH:O	2.17	0.45
1:A:157:ARG:HB3	1:A:178:GLU:HB2	1.98	0.45
1:A:378:ASN:ND2	3:A:555:FMT:H	2.27	0.45
1:B:259[A]:LYS:HE2	3:B:550:FMT:C	2.46	0.45
1:A:114:HIS:CE1	1:A:115:TRP:HE3	2.35	0.45
1:B:128[A]:MET:HE3	1:B:128[A]:MET:HB2	1.91	0.45
1:B:256[A]:GLU:HG2	1:B:259[A]:LYS:CE	2.41	0.45
1:C:277:ALA:HB2	1:C:298:TRP:O	2.17	0.45
1:B:149:PHE:HA	1:B:270:ILE:O	2.17	0.44
1:C:128[A]:MET:HE3	1:C:128[A]:MET:HB2	1.93	0.44
1:A:211:GLN:HE21	1:C:60:ASN:ND2	2.14	0.44
1:A:277:ALA:HB2	1:A:298:TRP:O	2.18	0.44
1:B:422[A]:ILE:HD13	3:B:586:FMT:C	2.47	0.44
1:B:55[A]:LYS:HE3	3:B:514:FMT:O2	2.16	0.44
1:C:242:GLY:HA2	3:C:578:FMT:O2	2.17	0.44
1:B:266:LYS:HD3	1:B:398:LEU:CD2	2.46	0.44
1:C:284:SER:HB3	1:C:306[A]:VAL:HG13	1.99	0.44
1:A:149:PHE:HA	1:A:270:ILE:O	2.18	0.44
1:B:74:HIS:NE2	1:B:192:ASP:HA	2.33	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:LEU:HD11	1:A:267:ILE:HD13	1.99	0.44
1:A:220:GLU:OE1	4:A:1702:HOH:O	2.21	0.43
1:A:306[A]:VAL:HG12	1:A:310:ILE:HD11	2.00	0.43
1:A:266:LYS:HD3	1:A:398:LEU:CD2	2.49	0.43
1:B:57:PRO:HG3	3:B:542:FMT:H	2.00	0.43
1:B:284:SER:HB3	1:B:306[A]:VAL:HG13	2.00	0.43
1:C:149:PHE:HA	1:C:270:ILE:O	2.19	0.43
1:B:359:PHE:O	3:B:514:FMT:O2	2.37	0.43
1:C:157:ARG:HB3	1:C:178:GLU:HB2	2.01	0.42
1:B:90:ASN:O	1:B:91:ASP:C	2.62	0.42
1:A:90:ASN:O	1:A:90:ASN:OD1	2.37	0.42
1:A:335:TYR:HB3	1:B:425:THR:HG21	2.01	0.42
1:C:323:GLN:HG3	3:C:585:FMT:C	2.38	0.41
1:B:92[A]:ARG:NH2	4:B:1273:HOH:O	2.53	0.41
1:C:227:LYS:NZ	4:C:1978:HOH:O	2.53	0.41
1:B:378:ASN:HD21	3:B:530:FMT:H	1.84	0.41
1:B:57:PRO:CG	3:B:542:FMT:H	2.50	0.41
1:B:88:GLN:NE2	1:B:140:PRO:HD2	2.35	0.41
1:B:256[A]:GLU:HA	3:B:550:FMT:O2	2.19	0.41
1:B:259[A]:LYS:HE2	3:B:550:FMT:O1	2.19	0.41
1:A:256:GLU:HG2	1:A:259[A]:LYS:HE3	2.02	0.41
1:A:208:THR:HA	3:A:554:FMT:C	2.50	0.41
1:C:394:LYS:CE	4:C:1763:HOH:O	2.67	0.41
1:B:290:ARG:HG2	4:B:1119:HOH:O	2.20	0.41
1:A:168:ALA:HA	1:A:172:PHE:O	2.21	0.40
1:A:394:LYS:CE	4:A:1036:HOH:O	2.68	0.40
1:B:168:ALA:HA	1:B:172:PHE:O	2.21	0.40
1:B:216[A]:HIS:CD2	1:B:220:GLU:OE2	2.74	0.40
1:C:72:PHE:HA	1:C:73:ASP:HA	1.93	0.40
1:C:191:LYS:HE2	1:C:202:SER:OG	2.22	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	397/383 (104%)	386 (97%)	11 (3%)	0	100	100
1	B	399/383 (104%)	386 (97%)	13 (3%)	0	100	100
1	C	397/383 (104%)	386 (97%)	11 (3%)	0	100	100
All	All	1193/1149 (104%)	1158 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	347/329 (106%)	335 (96%)	12 (4%)	32	15
1	B	348/329 (106%)	332 (95%)	16 (5%)	24	9
1	C	347/329 (106%)	332 (96%)	15 (4%)	26	10
All	All	1042/987 (106%)	999 (96%)	43 (4%)	30	11

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55[A]	LYS
1	A	55[B]	LYS
1	A	83	LEU
1	A	88	GLN
1	A	115	TRP
1	A	197	GLU
1	A	215[A]	THR
1	A	215[B]	THR
1	A	252	LYS
1	A	296	ASP
1	A	424	THR
1	A	425	THR
1	B	55[A]	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	55[B]	LYS
1	B	83	LEU
1	B	88	GLN
1	B	115	TRP
1	B	142[A]	GLU
1	B	142[B]	GLU
1	B	198	ILE
1	B	215[A]	THR
1	B	215[B]	THR
1	B	227	LYS
1	B	252	LYS
1	B	296	ASP
1	B	333	LYS
1	B	424	THR
1	B	425	THR
1	C	83	LEU
1	C	88	GLN
1	C	115	TRP
1	C	185[A]	SER
1	C	185[B]	SER
1	C	193	GLN
1	C	197	GLU
1	C	198	ILE
1	C	211	GLN
1	C	215[A]	THR
1	C	215[B]	THR
1	C	227	LYS
1	C	296	ASP
1	C	424	THR
1	C	425	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	88	GLN
1	A	119	ASN
1	A	135	ASN
1	A	378	ASN
1	A	399	HIS
1	B	60	ASN
1	B	88	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	114	HIS
1	B	135	ASN
1	B	352	GLN
1	B	378	ASN
1	C	60	ASN
1	C	88	GLN
1	C	135	ASN
1	C	211	GLN
1	C	352	GLN
1	C	399	HIS
1	C	415	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 [i](#)

89 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	$\# Z > 2$
3	FMT	C	571	-	2,2,2	0.74	0	1,1,1	0.25	0
3	FMT	A	541	-	2,2,2	0.61	0	1,1,1	0.36	0
3	FMT	C	578	-	2,2,2	0.78	0	1,1,1	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FMT	B	502	-	2,2,2	0.53	0	1,1,1	0.32	0
3	FMT	C	575	-	2,2,2	1.10	0	1,1,1	0.91	0
3	FMT	B	501	-	2,2,2	0.66	0	1,1,1	0.13	0
3	FMT	B	530	-	2,2,2	0.66	0	1,1,1	0.22	0
3	FMT	B	537	-	2,2,2	0.76	0	1,1,1	0.27	0
3	FMT	A	558	-	2,2,2	0.73	0	1,1,1	0.29	0
3	FMT	B	542	-	2,2,2	0.87	0	1,1,1	0.32	0
3	FMT	A	503	-	2,2,2	0.72	0	1,1,1	0.04	0
3	FMT	B	520	-	2,2,2	0.61	0	1,1,1	0.01	0
3	FMT	C	564	-	2,2,2	0.71	0	1,1,1	0.24	0
3	FMT	C	577	-	2,2,2	0.68	0	1,1,1	0.17	0
3	FMT	B	549	-	2,2,2	0.63	0	1,1,1	0.20	0
3	FMT	C	519	-	2,2,2	0.77	0	1,1,1	0.08	0
3	FMT	C	579	-	2,2,2	0.98	0	1,1,1	0.33	0
3	FMT	B	545	-	2,2,2	0.73	0	1,1,1	0.16	0
3	FMT	B	515	-	2,2,2	0.88	0	1,1,1	0.36	0
3	FMT	B	532	-	2,2,2	0.74	0	1,1,1	0.27	0
3	FMT	B	512	-	2,2,2	0.59	0	1,1,1	0.08	0
3	FMT	C	560	-	2,2,2	0.62	0	1,1,1	0.19	0
3	FMT	A	551	-	2,2,2	0.82	0	1,1,1	0.46	0
3	FMT	B	514	-	2,2,2	0.71	0	1,1,1	0.17	0
3	FMT	C	574	-	2,2,2	0.97	0	1,1,1	0.26	0
3	FMT	A	553	-	2,2,2	0.74	0	1,1,1	0.21	0
3	FMT	A	527	-	2,2,2	0.73	0	1,1,1	0.22	0
3	FMT	B	523	-	2,2,2	0.80	0	1,1,1	0.29	0
3	FMT	B	550	-	2,2,2	0.81	0	1,1,1	0.22	0
3	FMT	C	568	-	2,2,2	0.75	0	1,1,1	0.17	0
3	FMT	A	547	-	2,2,2	0.70	0	1,1,1	0.22	0
3	FMT	C	559	-	2,2,2	0.77	0	1,1,1	0.33	0
3	FMT	B	517	-	2,2,2	0.62	0	1,1,1	0.08	0
3	FMT	B	557	-	2,2,2	0.76	0	1,1,1	0.30	0
3	FMT	B	505	-	2,2,2	0.64	0	1,1,1	0.06	0
3	FMT	A	510	-	2,2,2	0.70	0	1,1,1	0.19	0
3	FMT	A	556	-	2,2,2	0.78	0	1,1,1	0.24	0
3	FMT	B	526	-	2,2,2	0.74	0	1,1,1	0.25	0
3	FMT	A	508	-	2,2,2	0.71	0	1,1,1	0.20	0
3	FMT	B	504	-	2,2,2	0.74	0	1,1,1	0.26	0
3	FMT	C	565	-	2,2,2	0.84	0	1,1,1	0.23	0
3	FMT	C	563	-	2,2,2	0.56	0	1,1,1	0.11	0
3	FMT	A	536	-	2,2,2	0.74	0	1,1,1	0.30	0
3	FMT	C	562	-	2,2,2	0.76	0	1,1,1	0.10	0
3	FMT	C	583	-	2,2,2	0.76	0	1,1,1	0.25	0
3	FMT	A	518	-	2,2,2	0.83	0	1,1,1	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FMT	A	538	-	2,2,2	0.51	0	1,1,1	0.02	0
3	FMT	A	534	-	2,2,2	0.53	0	1,1,1	0.32	0
3	FMT	B	507	-	2,2,2	0.75	0	1,1,1	0.24	0
3	FMT	C	582	-	2,2,2	0.77	0	1,1,1	0.31	0
3	FMT	C	584	-	2,2,2	0.66	0	1,1,1	0.68	0
3	FMT	A	544	-	2,2,2	0.73	0	1,1,1	0.19	0
3	FMT	A	552	-	2,2,2	0.79	0	1,1,1	0.28	0
3	FMT	A	554	-	2,2,2	0.81	0	1,1,1	0.37	0
3	FMT	A	522	-	2,2,2	0.73	0	1,1,1	0.19	0
3	FMT	C	567	-	2,2,2	0.63	0	1,1,1	0.12	0
3	FMT	A	531	-	2,2,2	0.73	0	1,1,1	0.29	0
3	FMT	B	529	-	2,2,2	0.71	0	1,1,1	0.19	0
3	FMT	C	573	-	2,2,2	0.71	0	1,1,1	0.18	0
3	FMT	A	540	-	2,2,2	0.76	0	1,1,1	0.23	0
3	FMT	A	533	-	2,2,2	1.05	0	1,1,1	0.93	0
3	FMT	C	580	-	2,2,2	0.55	0	1,1,1	0.40	0
3	FMT	A	509	-	2,2,2	0.66	0	1,1,1	0.12	0
3	FMT	A	511	-	2,2,2	0.68	0	1,1,1	0.39	0
3	FMT	A	546	-	2,2,2	0.78	0	1,1,1	0.16	0
3	FMT	C	572	-	2,2,2	0.80	0	1,1,1	0.27	0
3	FMT	B	586	-	2,2,2	0.71	0	1,1,1	0.92	0
3	FMT	B	535	-	2,2,2	0.87	0	1,1,1	0.79	0
3	FMT	A	506	-	2,2,2	0.82	0	1,1,1	0.14	0
3	FMT	A	521	-	2,2,2	0.73	0	1,1,1	0.30	0
3	FMT	C	570	-	2,2,2	0.71	0	1,1,1	0.22	0
3	FMT	B	525	-	2,2,2	0.71	0	1,1,1	0.21	0
2	NTJ	C	473	1	4,7,7	0.38	0	4,8,8	2.80	1 (25%)
3	FMT	A	524	-	2,2,2	0.66	0	1,1,1	0.21	0
3	FMT	C	566	-	2,2,2	0.67	0	1,1,1	0.17	0
3	FMT	A	513	-	2,2,2	0.92	0	1,1,1	0.41	0
3	FMT	C	576	-	2,2,2	0.70	0	1,1,1	0.29	0
3	FMT	B	516	-	2,2,2	0.78	0	1,1,1	0.30	0
3	FMT	A	528	-	2,2,2	0.72	0	1,1,1	0.21	0
3	FMT	C	569	-	2,2,2	0.72	0	1,1,1	0.20	0
3	FMT	C	581	-	2,2,2	0.63	0	1,1,1	0.66	0
3	FMT	C	561	-	2,2,2	0.73	0	1,1,1	0.17	0
2	NTJ	A	473	1	4,7,7	0.31	0	4,8,8	2.48	1 (25%)
3	FMT	A	539	-	2,2,2	0.73	0	1,1,1	0.23	0
3	FMT	B	548	-	2,2,2	0.72	0	1,1,1	0.21	0
3	FMT	C	585	-	2,2,2	0.70	0	1,1,1	0.80	0
3	FMT	B	543	-	2,2,2	0.69	0	1,1,1	0.18	0
3	FMT	A	555	-	2,2,2	0.83	0	1,1,1	0.29	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NTJ	B	473	1	4,7,7	0.31	0	4,8,8	2.40	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
2	NTJ	B	473	1	-	0/1/7/7	-
2	NTJ	C	473	1	-	0/1/7/7	-
2	NTJ	A	473	1	-	0/1/7/7	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	473	NTJ	C1-N1-C2	5.49	122.32	113.60
2	A	473	NTJ	C1-N1-C2	4.87	121.33	113.60
2	B	473	NTJ	C1-N1-C2	4.68	121.03	113.60

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

27 monomers are involved in 61 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	578	FMT	6	0
3	C	575	FMT	1	0
3	B	530	FMT	2	0
3	B	542	FMT	2	0
3	C	579	FMT	3	0
3	B	515	FMT	1	0
3	A	551	FMT	1	0
3	B	514	FMT	2	0
3	B	550	FMT	8	0
3	B	517	FMT	1	0
3	B	557	FMT	1	0
3	A	556	FMT	2	0
3	A	518	FMT	1	0
3	C	582	FMT	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	584	FMT	2	0
3	A	554	FMT	4	0
3	B	529	FMT	1	0
3	A	533	FMT	1	0
3	B	586	FMT	3	0
3	B	535	FMT	1	0
3	A	506	FMT	1	0
2	C	473	NTJ	1	0
3	A	513	FMT	2	0
2	A	473	NTJ	3	0
3	C	585	FMT	6	0
3	A	555	FMT	3	0
2	B	473	NTJ	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	B	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	272:HIS	C	273:SER	N	1.62
1	B	272:HIS	C	273:SER	N	1.62
1	C	272:HIS	C	273:SER	N	1.62

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	377/383 (98%)	-1.18	0	100 100	8, 15, 33, 45	22 (5%)
1	B	377/383 (98%)	-1.17	0	100 100	8, 14, 33, 44	24 (6%)
1	C	377/383 (98%)	-1.16	2 (0%)	87 89	8, 14, 33, 45	22 (5%)
All	All	1131/1149 (98%)	-1.17	2 (0%)	91 92	8, 15, 33, 45	68 (6%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	193	GLN	2.2
1	C	91	ASP	2.1

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
3	FMT	C	571	3/3	0.93	0.07	72,72,72,72	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	FMT	B	549	3/3	0.94	0.09	41,41,42,43	0
3	FMT	B	543	3/3	0.96	0.11	29,29,30,31	0
3	FMT	A	528	3/3	0.97	0.09	46,46,46,46	0
3	FMT	A	531	3/3	0.97	0.10	43,43,43,43	0
3	FMT	A	539	3/3	0.97	0.08	59,59,60,60	0
3	FMT	A	547	3/3	0.97	0.07	54,54,54,54	0
3	FMT	A	552	3/3	0.97	0.11	44,44,44,44	0
3	FMT	B	516	3/3	0.97	0.09	41,41,41,41	0
3	FMT	B	523	3/3	0.97	0.10	50,50,50,50	0
3	FMT	B	525	3/3	0.97	0.08	60,60,60,60	0
3	FMT	A	518	3/3	0.97	0.28	40,40,40,41	0
3	FMT	A	521	3/3	0.97	0.08	50,50,50,50	0
3	FMT	B	550	3/3	0.97	0.07	54,54,54,55	0
3	FMT	B	557	3/3	0.97	0.06	46,46,47,47	0
3	FMT	C	566	3/3	0.97	0.07	53,53,53,54	0
3	FMT	C	569	3/3	0.97	0.06	59,59,59,59	0
3	FMT	A	522	3/3	0.97	0.09	41,41,41,41	0
3	FMT	C	576	3/3	0.97	0.09	38,38,38,38	0
3	FMT	C	577	3/3	0.97	0.06	52,52,52,52	0
3	FMT	C	582	3/3	0.97	0.20	43,43,43,44	0
3	FMT	B	514	3/3	0.98	0.18	40,40,41,41	0
3	FMT	B	515	3/3	0.98	0.26	41,41,41,41	0
3	FMT	A	510	3/3	0.98	0.09	42,42,42,42	0
3	FMT	B	517	3/3	0.98	0.08	28,28,31,32	0
3	FMT	A	506	3/3	0.98	0.08	26,26,29,29	0
3	FMT	A	536	3/3	0.98	0.04	38,38,38,39	0
3	FMT	B	526	3/3	0.98	0.07	56,56,56,56	0
3	FMT	B	537	3/3	0.98	0.06	61,61,61,61	0
3	FMT	B	542	3/3	0.98	0.13	33,33,34,35	0
3	FMT	A	538	3/3	0.98	0.10	33,33,34,34	0
3	FMT	B	545	3/3	0.98	0.06	42,42,42,43	0
3	FMT	B	548	3/3	0.98	0.07	68,68,68,68	0
3	FMT	A	508	3/3	0.98	0.05	56,56,56,56	0
3	FMT	A	509	3/3	0.98	0.09	29,29,30,31	0
3	FMT	A	551	3/3	0.98	0.12	40,40,40,41	0
3	FMT	C	559	3/3	0.98	0.05	39,39,39,40	0
3	FMT	C	561	3/3	0.98	0.10	44,44,45,45	0
3	FMT	C	564	3/3	0.98	0.08	40,40,41,41	0
3	FMT	C	565	3/3	0.98	0.21	38,38,39,41	0
3	FMT	A	524	3/3	0.98	0.07	65,65,65,65	0
3	FMT	C	567	3/3	0.98	0.04	40,40,41,41	0
3	FMT	A	553	3/3	0.98	0.07	36,36,37,37	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	FMT	C	570	3/3	0.98	0.06	58,58,59,59	0
3	FMT	A	558	3/3	0.98	0.05	51,51,51,51	0
3	FMT	C	572	3/3	0.98	0.08	38,38,38,38	0
3	FMT	C	573	3/3	0.98	0.05	43,43,43,44	0
3	FMT	B	501	3/3	0.98	0.10	26,26,28,29	0
3	FMT	B	504	3/3	0.98	0.05	61,61,61,61	0
3	FMT	C	578	3/3	0.98	0.09	50,50,50,50	0
3	FMT	C	580	3/3	0.98	0.06	60,60,60,60	0
3	FMT	C	581	3/3	0.98	0.08	51,51,51,51	0
3	FMT	B	505	3/3	0.98	0.04	33,33,35,35	0
3	FMT	C	583	3/3	0.98	0.06	65,65,65,65	0
3	FMT	C	584	3/3	0.98	0.12	43,43,44,44	0
3	FMT	B	507	3/3	0.99	0.07	41,41,41,41	0
3	FMT	B	586	3/3	0.99	0.05	15,15,15,18	0
3	FMT	B	512	3/3	0.99	0.04	29,29,32,33	0
3	FMT	C	560	3/3	0.99	0.06	27,27,29,29	0
3	FMT	A	541	3/3	0.99	0.04	23,23,24,25	0
3	FMT	C	562	3/3	0.99	0.05	27,27,30,32	0
3	FMT	C	563	3/3	0.99	0.09	22,22,27,29	0
3	FMT	A	544	3/3	0.99	0.06	53,53,53,53	0
3	FMT	A	546	3/3	0.99	0.04	21,21,24,24	0
2	NTJ	B	473	8/8	0.99	0.04	14,16,19,22	0
3	FMT	B	520	3/3	0.99	0.03	32,32,34,35	0
3	FMT	C	568	3/3	0.99	0.07	54,54,54,54	0
3	FMT	A	503	3/3	0.99	0.05	34,34,37,38	0
3	FMT	A	533	3/3	0.99	0.06	14,14,16,18	0
3	FMT	A	534	3/3	0.99	0.05	20,20,23,26	0
3	FMT	B	529	3/3	0.99	0.04	30,30,32,34	0
3	FMT	B	530	3/3	0.99	0.05	25,25,28,31	0
3	FMT	C	574	3/3	0.99	0.07	20,20,23,27	0
3	FMT	C	575	3/3	0.99	0.04	13,13,15,18	0
3	FMT	B	535	3/3	0.99	0.06	14,14,16,18	0
3	FMT	A	554	3/3	0.99	0.09	30,30,31,34	0
3	FMT	A	555	3/3	0.99	0.09	25,25,28,31	0
3	FMT	C	579	3/3	0.99	0.09	32,32,33,34	0
3	FMT	A	556	3/3	0.99	0.11	43,43,43,44	0
3	FMT	A	511	3/3	0.99	0.04	21,21,23,24	0
3	FMT	A	513	3/3	0.99	0.10	39,39,39,40	0
3	FMT	A	527	3/3	0.99	0.05	56,56,57,57	0
3	FMT	A	540	3/3	0.99	0.06	48,48,48,48	0
3	FMT	B	532	3/3	1.00	0.03	14,14,15,16	0
3	FMT	B	502	3/3	1.00	0.05	19,19,22,25	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NTJ	A	473	8/8	1.00	0.03	13,16,19,22	0
3	FMT	C	519	3/3	1.00	0.03	14,14,16,16	0
2	NTJ	C	473	8/8	1.00	0.03	13,15,19,22	0
3	FMT	C	585	3/3	1.00	0.04	15,15,16,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.