



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 09:14 PM UTC

PDB ID : 9L5Z / pdb_00009l5z
Title : Crystal structure of a parallel-stranded PNA duplex
Authors : Shibata, M.; Aiba, Y.; Sugimoto, H.; Shoji, O.
Deposited on : 2024-12-23
Resolution : 1.70 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
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

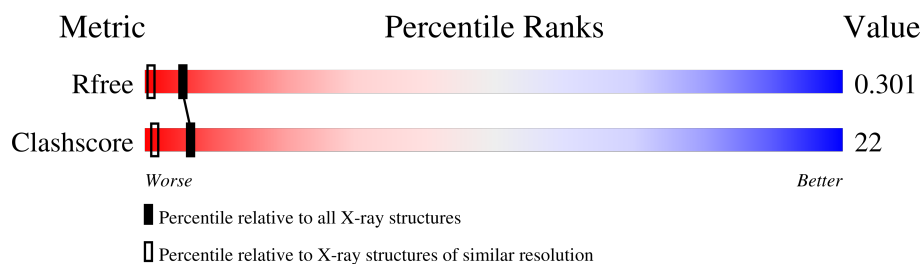
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

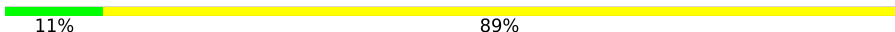
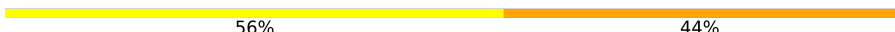
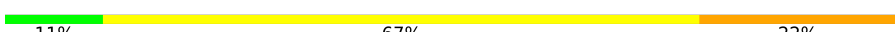
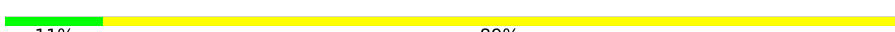
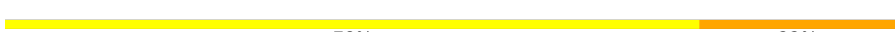
The reported resolution of this entry is 1.70 Å.

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))
R _{free}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (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	9	 11% 89%
1	C	9	 56% 44%
1	E	9	 67% 33%
1	G	9	 11% 67% 22%
2	B	9	 11% 89%
2	D	9	 78% 22%
2	F	9	 44% 56%
2	H	9	 44% 56%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1868 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 (TPN)(GPN)(APN)(APN)(CPN)(TPN)(GPN)(CPN)(LYN).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	9	Total	C	N	O	0	0	0
			166	92	49	25			
1	C	9	Total	C	N	O	0	0	0
			166	92	49	25			
1	E	9	Total	C	N	O	0	0	0
			166	92	49	25			
1	G	9	Total	C	N	O	0	9	0
			324	179	96	49			

- Molecule 2 is a protein called (APN)(CPN)(TPN)(TPN)(GPN)(APN)(CPN)(GPN)(LYN).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	9	Total	C	N	O	0	0	1
			158	87	47	24			
2	D	9	Total	C	N	O	0	0	0
			166	92	49	25			
2	F	9	Total	C	N	O	0	0	0
			166	92	49	25			
2	H	9	Total	C	N	O	0	9	0
			324	179	96	49			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	32	Total	O	0	0
			32	32		
3	B	28	Total	O	0	0
			28	28		
3	C	27	Total	O	0	1
			28	28		
3	D	39	Total	O	0	0
			39	39		

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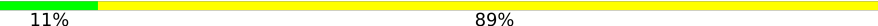
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	22	Total 22	O 22	0	0
3	F	29	Total 29	O 29	0	0
3	G	18	Total 18	O 18	0	0
3	H	35	Total 36	O 36	0	4

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: (TPN)(GPN)(APN)(APN)(CPN)(TPN)(GPN)(CPN)(LYN)

Chain A: 



- Molecule 1: (TPN)(GPN)(APN)(APN)(CPN)(TPN)(GPN)(CPN)(LYN)

Chain C: 



- Molecule 1: (TPN)(GPN)(APN)(APN)(CPN)(TPN)(GPN)(CPN)(LYN)

Chain E: 



- Molecule 1: (TPN)(GPN)(APN)(APN)(CPN)(TPN)(GPN)(CPN)(LYN)

Chain G: 

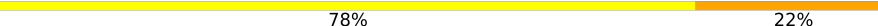


- Molecule 2: (APN)(CPN)(TPN)(TPN)(GPN)(APN)(CPN)(GPN)(LYN)

Chain B: 



- Molecule 2: (APN)(CPN)(TPN)(TPN)(GPN)(APN)(CPN)(GPN)(LYN)

Chain D: 

APN1
CPN2
TPN3
TPN4
GPN5
APN6
CPN7
GPN8
K9

- Molecule 2: (APN)(CPN)(TPN)(TPN)(GPN)(APN)(CPN)(GPN)(LYN)

Chain F:  44% 56%

APN1
CPN2
TPN3
TPN4
GPN5
APN6
CPN7
GPN8
K9

- Molecule 2: (APN)(CPN)(TPN)(TPN)(GPN)(APN)(CPN)(GPN)(LYN)

Chain H:  44% 56%

APN1
CPN2
TPN3
TPN4
GPN5
APN6
CPN7
GPN8
K9

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	38.06Å 52.87Å 53.34Å 90.00° 94.89° 90.00°	Depositor
Resolution (Å)	10.00 – 1.70 10.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.8 (10.00-1.70) 97.8 (10.00-1.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0430	Depositor
R, R_{free}	0.249 , 0.290 0.259 , 0.301	Depositor DCC
R_{free} test set	1176 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	26.7	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.61$, $\langle L^2 \rangle = 0.46$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	1868	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.41 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3148e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GPN, CPN, LYN, APN, TPN

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	166	0	80	0	0
1	C	166	0	79	12	0
1	E	166	0	79	10	0
1	G	324	0	146	1	0
2	B	158	0	66	0	0
2	D	166	0	79	10	0
2	F	166	0	79	12	0
2	H	324	0	146	7	0
3	A	32	0	0	0	0
3	B	28	0	0	0	0
3	C	28	0	0	1	0
3	D	39	0	0	1	0
3	E	22	0	0	0	0
3	F	29	0	0	1	0
3	G	18	0	0	1	0
3	H	36	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	1868	0	754	52	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 22.

The worst 5 of 52 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)
3:C:115:HOH:O	2:D:4:TPN:HM52	1.33	1.24
2:D:9:LYN:HZ3	2:D:9:LYN:HZ2	1.40	1.03
1:C:9:LYN:HZ3	1:C:9:LYN:HZ2	1.40	1.03
2:D:9:LYN:HZ2	2:D:9:LYN:HZ1	1.40	1.02
1:E:9:LYN:HZ3	1:E:9:LYN:HZ1	1.40	1.02

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

90 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	CPN	F	7	2	18,18,19	0.97	1 (5%)	21,23,25	1.60	5 (23%)
1	GPN	C	2	1	22,22,23	1.00	1 (4%)	29,30,32	1.45	5 (17%)
1	APN	A	3	1	21,21,22	0.98	1 (4%)	27,28,30	1.80	6 (22%)
1	APN	A	4	1	21,21,22	1.14	1 (4%)	27,28,30	1.28	2 (7%)
2	APN	F	6	2	21,21,22	0.84	0	27,28,30	1.24	2 (7%)
1	APN	E	3	1	21,21,22	1.03	1 (4%)	27,28,30	1.58	5 (18%)
2	APN	B	6	2	21,21,22	0.77	0	27,28,30	2.04	5 (18%)
2	TPN	H	3[A]	2	19,19,20	0.52	0	24,25,27	1.07	1 (4%)
1	CPN	A	5	1	18,18,19	1.13	2 (11%)	21,23,25	1.28	2 (9%)
1	TPN	A	6	1	19,19,20	0.82	1 (5%)	24,25,27	1.17	2 (8%)
2	GPN	H	8[A]	2	22,22,23	0.81	1 (4%)	29,30,32	0.90	0
1	CPN	C	8	1	18,18,19	0.90	0	21,23,25	1.82	5 (23%)
1	TPN	E	6	1	19,19,20	1.03	1 (5%)	24,25,27	1.26	2 (8%)
1	CPN	C	5	1	18,18,19	1.27	2 (11%)	21,23,25	1.73	4 (19%)
2	CPN	H	7[B]	2	18,18,19	0.77	1 (5%)	21,23,25	1.62	6 (28%)
1	APN	G	3[B]	1	21,21,22	0.84	0	27,28,30	1.07	2 (7%)
2	CPN	H	7[A]	2	18,18,19	0.75	0	21,23,25	0.92	2 (9%)
1	APN	G	3[A]	1	21,21,22	0.89	1 (4%)	27,28,30	0.62	0
2	GPN	D	8	2	22,22,23	1.04	1 (4%)	29,30,32	1.42	5 (17%)
1	GPN	E	2	1	22,22,23	1.10	2 (9%)	29,30,32	1.26	3 (10%)
1	APN	C	3	1	21,21,22	1.48	2 (9%)	27,28,30	1.41	4 (14%)
2	TPN	B	3	2	19,19,20	0.91	2 (10%)	24,25,27	1.46	4 (16%)
2	LYN	D	9	2	9,9,9	0.44	0	9,10,10	0.48	0
1	LYN	C	9	1	9,9,9	0.42	0	9,10,10	0.32	0
1	TPN	C	6	1	19,19,20	0.89	1 (5%)	24,25,27	1.31	4 (16%)
1	GPN	E	7	1	22,22,23	0.75	0	29,30,32	1.36	2 (6%)
1	TPN	C	1	1	19,19,20	1.02	1 (5%)	24,25,27	2.25	8 (33%)
2	LYN	H	9[B]	2	9,9,9	0.50	0	9,10,10	0.24	0
1	GPN	A	7	1	22,22,23	0.81	0	29,30,32	0.82	1 (3%)
2	CPN	F	2	2	18,18,19	1.69	4 (22%)	21,23,25	1.98	8 (38%)
2	TPN	F	3	2	19,19,20	1.03	1 (5%)	24,25,27	1.33	3 (12%)
1	LYN	E	9	1	9,9,9	0.43	0	9,10,10	0.45	0
1	GPN	G	2[B]	1	22,22,23	0.78	1 (4%)	29,30,32	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	GPN	G	2[A]	1	22,22,23	0.73	1 (4%)	29,30,32	1.15	2 (6%)
2	CPN	B	2	2	18,18,19	1.39	4 (22%)	21,23,25	1.65	5 (23%)
1	APN	C	4	1	21,21,22	1.36	2 (9%)	27,28,30	2.72	7 (25%)
1	APN	G	4[B]	1	21,21,22	1.20	2 (9%)	27,28,30	1.53	2 (7%)
2	CPN	D	2	2	18,18,19	1.00	2 (11%)	21,23,25	1.65	6 (28%)
2	CPN	H	2[B]	2	18,18,19	0.80	0	21,23,25	1.06	1 (4%)
2	LYN	B	9	2	1,1,9	0.38	0	-		
1	APN	G	4[A]	1	21,21,22	1.01	1 (4%)	27,28,30	1.09	1 (3%)
2	CPN	H	2[A]	2	18,18,19	0.75	1 (5%)	21,23,25	1.10	1 (4%)
2	TPN	H	4[B]	2	19,19,20	0.91	0	24,25,27	1.57	4 (16%)
1	APN	E	4	1	21,21,22	1.10	1 (4%)	27,28,30	1.51	5 (18%)
1	CPN	E	5	1	18,18,19	1.04	2 (11%)	21,23,25	1.17	1 (4%)
2	GPN	B	5	2	22,22,23	1.12	3 (13%)	29,30,32	1.73	5 (17%)
1	TPN	G	1[B]	1	19,19,20	0.78	0	24,25,27	1.30	3 (12%)
1	TPN	G	1[A]	1	19,19,20	0.68	0	24,25,27	1.83	8 (33%)
1	CPN	G	5[B]	1	18,18,19	0.77	0	21,23,25	1.05	1 (4%)
2	CPN	B	7	2	18,18,19	0.95	1 (5%)	21,23,25	1.24	1 (4%)
2	TPN	D	3	2	19,19,20	0.90	1 (5%)	24,25,27	2.00	8 (33%)
1	GPN	G	7[B]	1	22,22,23	0.88	0	29,30,32	1.48	3 (10%)
2	TPN	D	4	2	19,19,20	1.09	1 (5%)	24,25,27	1.23	2 (8%)
1	GPN	G	7[A]	1	22,22,23	0.87	1 (4%)	29,30,32	0.82	0
1	TPN	A	1	1	19,19,20	0.86	1 (5%)	24,25,27	1.35	4 (16%)
2	APN	D	6	2	21,21,22	1.32	2 (9%)	27,28,30	1.38	5 (18%)
1	LYN	G	9[B]	1	1,1,9	0.28	0	-		
1	GPN	C	7	1	22,22,23	1.08	3 (13%)	29,30,32	1.23	3 (10%)
1	TPN	G	6[B]	1	19,19,20	0.74	0	24,25,27	0.91	1 (4%)
1	LYN	G	9[A]	1	9,9,9	0.49	0	9,10,10	0.40	0
2	GPN	D	5	2	22,22,23	0.97	1 (4%)	29,30,32	1.29	3 (10%)
2	LYN	H	9[A]	2	1,1,9	0.37	0	-		
2	CPN	D	7	2	18,18,19	1.13	2 (11%)	21,23,25	1.67	5 (23%)
2	TPN	F	4	2	19,19,20	0.97	1 (5%)	24,25,27	2.04	6 (25%)
1	GPN	A	2	1	22,22,23	1.02	1 (4%)	29,30,32	1.83	5 (17%)
1	TPN	E	1	1	19,19,20	0.90	1 (5%)	24,25,27	0.90	0
1	LYN	A	9	1	9,9,9	0.32	0	9,10,10	0.22	0
2	APN	D	1	2	21,21,22	1.22	2 (9%)	27,28,30	1.44	6 (22%)
1	CPN	A	8	1	18,18,19	1.35	3 (16%)	21,23,25	1.34	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	APN	H	1[B]	2	21,21,22	0.86	1 (4%)	27,28,30	1.12	1 (3%)
2	TPN	H	4[A]	2	19,19,20	0.80	1 (5%)	24,25,27	1.52	4 (16%)
2	APN	H	1[A]	2	21,21,22	0.72	0	27,28,30	1.08	2 (7%)
2	GPN	F	5	2	22,22,23	1.16	4 (18%)	29,30,32	1.46	3 (10%)
2	TPN	B	4	2	19,19,20	0.71	0	24,25,27	1.45	6 (25%)
2	GPN	F	8	2	22,22,23	1.16	1 (4%)	29,30,32	1.03	2 (6%)
2	APN	F	1	2	21,21,22	1.18	1 (4%)	27,28,30	1.29	4 (14%)
2	GPN	B	8	2	22,22,23	1.10	2 (9%)	29,30,32	1.02	2 (6%)
2	TPN	H	3[B]	2	19,19,20	0.80	0	24,25,27	1.21	3 (12%)
1	CPN	G	8[B]	1	18,18,19	0.88	0	21,23,25	1.24	2 (9%)
1	CPN	G	8[A]	1	18,18,19	0.80	0	21,23,25	1.43	2 (9%)
1	CPN	G	5[A]	1	18,18,19	0.88	0	21,23,25	0.99	1 (4%)
2	GPN	H	8[B]	2	22,22,23	0.73	0	29,30,32	1.10	2 (6%)
2	GPN	H	5[B]	2	22,22,23	0.78	0	29,30,32	0.97	2 (6%)
2	GPN	H	5[A]	2	22,22,23	0.80	1 (4%)	29,30,32	0.94	1 (3%)
2	APN	H	6[B]	2	21,21,22	0.84	1 (4%)	27,28,30	1.22	4 (14%)
1	TPN	G	6[A]	1	19,19,20	0.76	0	24,25,27	1.34	3 (12%)
2	APN	H	6[A]	2	21,21,22	0.94	1 (4%)	27,28,30	1.29	4 (14%)
1	CPN	E	8	1	18,18,19	1.55	3 (16%)	21,23,25	1.50	4 (19%)
2	APN	B	1	2	21,21,22	1.20	2 (9%)	27,28,30	1.35	3 (11%)
2	LYN	F	9	2	9,9,9	0.51	0	9,10,10	0.53	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CPN	F	7	2	-	0/13/14/15	0/1/1/1
1	GPN	C	2	1	-	0/13/14/15	0/2/2/2
1	APN	A	3	1	-	1/13/14/15	0/2/2/2
1	APN	A	4	1	-	0/13/14/15	0/2/2/2
2	APN	F	6	2	-	0/13/14/15	0/2/2/2
1	APN	E	3	1	-	0/13/14/15	0/2/2/2
2	APN	B	6	2	-	0/13/14/15	0/2/2/2
2	TPN	H	3[A]	2	-	0/13/14/15	0/1/1/1
1	CPN	A	5	1	-	0/13/14/15	0/1/1/1
1	TPN	A	6	1	-	0/13/14/15	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GPN	H	8[A]	2	-	0/13/14/15	0/2/2/2
1	CPN	C	8	1	-	0/13/14/15	0/1/1/1
1	TPN	E	6	1	-	0/13/14/15	0/1/1/1
1	CPN	C	5	1	-	0/13/14/15	0/1/1/1
2	CPN	H	7[B]	2	-	0/13/14/15	0/1/1/1
1	APN	G	3[B]	1	-	0/13/14/15	0/2/2/2
2	CPN	H	7[A]	2	-	0/13/14/15	0/1/1/1
1	APN	G	3[A]	1	-	0/13/14/15	0/2/2/2
2	GPN	D	8	2	-	0/13/14/15	0/2/2/2
1	GPN	E	2	1	-	1/13/14/15	0/2/2/2
1	APN	C	3	1	-	0/13/14/15	0/2/2/2
2	TPN	B	3	2	-	0/13/14/15	0/1/1/1
2	LYN	D	9	2	-	4/9/9/9	-
1	LYN	C	9	1	-	5/9/9/9	-
1	TPN	C	6	1	-	0/13/14/15	0/1/1/1
1	GPN	E	7	1	-	0/13/14/15	0/2/2/2
1	TPN	C	1	1	-	1/13/14/15	0/1/1/1
2	LYN	H	9[B]	2	-	4/9/9/9	-
1	GPN	A	7	1	-	0/13/14/15	0/2/2/2
2	CPN	F	2	2	-	0/13/14/15	0/1/1/1
2	TPN	F	3	2	-	0/13/14/15	0/1/1/1
1	LYN	E	9	1	-	4/9/9/9	-
1	GPN	G	2[B]	1	-	0/13/14/15	0/2/2/2
1	GPN	G	2[A]	1	-	0/13/14/15	0/2/2/2
2	CPN	B	2	2	-	0/13/14/15	0/1/1/1
1	APN	C	4	1	-	1/13/14/15	0/2/2/2
1	APN	G	4[B]	1	-	0/13/14/15	0/2/2/2
2	CPN	D	2	2	-	0/13/14/15	0/1/1/1
2	CPN	H	2[B]	2	-	0/13/14/15	0/1/1/1
1	APN	G	4[A]	1	-	0/13/14/15	0/2/2/2
2	CPN	H	2[A]	2	-	1/13/14/15	0/1/1/1
2	TPN	H	4[B]	2	-	0/13/14/15	0/1/1/1
1	APN	E	4	1	-	0/13/14/15	0/2/2/2
1	CPN	E	5	1	-	0/13/14/15	0/1/1/1
2	GPN	B	5	2	-	0/13/14/15	0/2/2/2
1	TPN	G	1[B]	1	-	1/13/14/15	0/1/1/1
1	TPN	G	1[A]	1	-	0/13/14/15	0/1/1/1
1	CPN	G	5[B]	1	-	0/13/14/15	0/1/1/1
2	CPN	B	7	2	-	0/13/14/15	0/1/1/1
2	TPN	D	3	2	-	0/13/14/15	0/1/1/1
1	GPN	G	7[B]	1	-	0/13/14/15	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TPN	D	4	2	-	0/13/14/15	0/1/1/1
1	GPN	G	7[A]	1	-	0/13/14/15	0/2/2/2
1	TPN	A	1	1	-	1/13/14/15	0/1/1/1
2	APN	D	6	2	-	0/13/14/15	0/2/2/2
1	GPN	C	7	1	-	0/13/14/15	0/2/2/2
1	TPN	G	6[B]	1	-	0/13/14/15	0/1/1/1
1	LYN	G	9[A]	1	-	4/9/9/9	-
2	GPN	D	5	2	-	0/13/14/15	0/2/2/2
2	CPN	D	7	2	-	0/13/14/15	0/1/1/1
2	TPN	F	4	2	-	0/13/14/15	0/1/1/1
1	GPN	A	2	1	-	1/13/14/15	0/2/2/2
1	TPN	E	1	1	-	1/13/14/15	0/1/1/1
1	LYN	A	9	1	-	1/9/9/9	-
2	APN	D	1	2	-	0/13/14/15	0/2/2/2
1	CPN	A	8	1	-	2/13/14/15	0/1/1/1
2	APN	H	1[B]	2	-	2/13/14/15	0/2/2/2
2	TPN	H	4[A]	2	-	0/13/14/15	0/1/1/1
2	APN	H	1[A]	2	-	1/13/14/15	0/2/2/2
2	GPN	F	5	2	-	0/13/14/15	0/2/2/2
2	TPN	B	4	2	-	0/13/14/15	0/1/1/1
2	GPN	F	8	2	-	1/13/14/15	0/2/2/2
2	APN	F	1	2	-	2/13/14/15	0/2/2/2
2	GPN	B	8	2	-	0/13/14/15	0/2/2/2
2	TPN	H	3[B]	2	-	0/13/14/15	0/1/1/1
1	CPN	G	8[B]	1	-	0/13/14/15	0/1/1/1
1	CPN	G	8[A]	1	-	1/13/14/15	0/1/1/1
1	CPN	G	5[A]	1	-	0/13/14/15	0/1/1/1
2	GPN	H	8[B]	2	-	2/13/14/15	0/2/2/2
2	GPN	H	5[B]	2	-	0/13/14/15	0/2/2/2
2	GPN	H	5[A]	2	-	0/13/14/15	0/2/2/2
2	APN	H	6[B]	2	-	0/13/14/15	0/2/2/2
1	TPN	G	6[A]	1	-	0/13/14/15	0/1/1/1
2	APN	H	6[A]	2	-	0/13/14/15	0/2/2/2
1	CPN	E	8	1	-	1/13/14/15	0/1/1/1
2	APN	B	1	2	-	0/13/14/15	0/2/2/2
2	LYN	F	9	2	-	5/9/9/9	-

The worst 5 of 87 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	3	APN	C8'-N9	-4.66	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	8	GPN	C8'-N9	-4.53	1.40	1.46
1	E	8	CPN	C6-N1	-4.07	1.31	1.37
2	F	2	CPN	C5'-N4'	-3.73	1.41	1.47
2	D	6	APN	C4-N9	-3.62	1.33	1.37

The worst 5 of 262 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	4	APN	C2'-C3'-N4'	9.84	135.01	112.91
2	B	6	APN	C8'-N9-C8	7.09	134.29	127.27
1	G	4[B]	APN	C7'-C8'-N9	-6.10	102.84	110.81
1	A	2	GPN	C2'-C3'-N4'	5.57	125.41	112.91
2	D	7	CPN	O2-C2-N1	5.05	123.94	119.17

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	G	1[B]	TPN	N-C2'-C3'-N4'
1	A	8	CPN	C-C5'-N4'-C7'
1	E	8	CPN	C-C5'-N4'-C7'
1	C	9	LYN	O-C-CA-N
1	C	9	LYN	NT-C-CA-N

There are no ring outliers.

30 monomers are involved in 52 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	2	GPN	1	0
2	F	6	APN	1	0
2	H	8[A]	GPN	1	0
1	C	8	CPN	1	0
1	E	6	TPN	3	0
1	E	2	GPN	1	0
2	D	9	LYN	3	0
1	C	9	LYN	5	0
1	C	6	TPN	3	0
1	C	1	TPN	4	0
2	H	9[B]	LYN	1	0
2	F	2	CPN	1	0
2	F	3	TPN	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	9	LYN	3	0
2	H	2[A]	CPN	1	0
2	H	4[B]	TPN	1	0
2	D	3	TPN	3	0
2	D	4	TPN	4	0
1	G	7[A]	GPN	1	0
2	H	9[A]	LYN	1	0
2	F	4	TPN	4	0
1	E	1	TPN	4	0
2	H	1[B]	APN	1	0
2	H	4[A]	TPN	2	0
2	F	1	APN	1	0
2	H	8[B]	GPN	1	0
2	H	5[B]	GPN	1	0
2	H	5[A]	GPN	2	0
1	G	6[A]	TPN	1	0
2	F	9	LYN	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	0/9	-	-	-	-
1	C	0/9	-	-	-	-
1	E	0/9	-	-	-	-
1	G	0/9	-	-	-	-
2	B	0/9	-	-	-	-
2	D	0/9	-	-	-	-
2	F	0/9	-	-	-	-
2	H	0/9	-	-	-	-
All	All	0/72	-	-	-	-

There are no RSRZ outliers to report.

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	LYN	B	9	2/10	0.27	0.19	64,64,64,68	0
1	LYN	A	9	10/10	0.55	0.15	58,73,87,89	0
1	LYN	E	9	10/10	0.63	0.17	62,76,82,84	0
1	LYN	C	9	10/10	0.64	0.18	60,75,79,80	0
2	LYN	F	9	10/10	0.64	0.18	93,104,114,115	0
1	LYN	G	9[A]	10/10	0.67	0.22	52,66,72,75	10
1	LYN	G	9[B]	2/10	0.67	0.22	42,42,42,44	2
2	LYN	H	9[A]	2/10	0.68	0.18	47,47,47,50	2
2	LYN	H	9[B]	10/10	0.68	0.18	54,64,67,68	10
2	LYN	D	9	10/10	0.69	0.17	62,67,88,90	0
1	TPN	E	1	19/20	0.75	0.15	41,46,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	TPN	G	1[A]	19/20	0.78	0.13	32,37,54,55	19
1	TPN	G	1[B]	19/20	0.78	0.13	26,30,49,52	19
1	TPN	A	1	19/20	0.79	0.14	35,39,48,55	0
2	GPN	B	8	21/22	0.81	0.12	32,39,60,71	0
1	TPN	C	1	19/20	0.81	0.12	32,36,56,63	0
1	GPN	A	2	21/22	0.83	0.10	34,38,51,56	0
2	TPN	D	4	19/20	0.83	0.11	26,29,33,34	0
1	GPN	E	2	21/22	0.84	0.10	31,35,48,54	0
2	TPN	H	4[B]	19/20	0.85	0.09	24,26,31,32	19
2	APN	B	1	20/21	0.85	0.10	33,40,58,58	0
2	GPN	F	8	21/22	0.85	0.11	36,39,66,90	0
2	TPN	H	4[A]	19/20	0.85	0.09	20,23,29,31	19
2	GPN	B	5	21/22	0.86	0.09	22,26,32,40	0
1	TPN	G	6[A]	19/20	0.86	0.08	20,22,27,27	19
1	TPN	G	6[B]	19/20	0.86	0.08	24,26,28,30	19
2	CPN	B	2	18/19	0.86	0.10	26,32,52,54	0
2	APN	F	1	20/21	0.87	0.10	33,41,64,65	0
2	APN	H	1[A]	20/21	0.87	0.11	24,27,44,48	20
2	APN	H	1[B]	20/21	0.87	0.11	28,30,36,36	20
1	CPN	A	8	18/19	0.87	0.10	30,33,44,51	0
2	CPN	B	7	18/19	0.87	0.09	31,34,51,54	0
2	CPN	H	7[A]	18/19	0.87	0.10	28,31,40,44	18
2	CPN	H	7[B]	18/19	0.87	0.10	23,25,29,31	18
1	CPN	G	8[B]	18/19	0.88	0.09	33,37,44,46	18
1	CPN	G	8[A]	18/19	0.88	0.09	29,34,45,46	18
2	CPN	F	7	18/19	0.88	0.09	32,34,48,48	0
2	GPN	F	5	21/22	0.89	0.08	23,26,32,34	0
2	GPN	D	8	21/22	0.89	0.10	30,36,52,59	0
2	APN	B	6	20/21	0.89	0.08	27,30,38,43	0
2	APN	F	6	20/21	0.89	0.09	28,31,46,53	0
1	CPN	E	8	18/19	0.89	0.10	27,32,53,55	0
1	GPN	E	7	21/22	0.89	0.09	21,25,31,32	0
1	APN	E	4	20/21	0.89	0.08	22,27,44,45	0
2	APN	D	1	20/21	0.89	0.09	30,35,48,50	0
2	TPN	H	3[A]	19/20	0.90	0.08	21,23,28,28	19
2	TPN	H	3[B]	19/20	0.90	0.08	23,26,28,29	19
1	GPN	G	2[B]	21/22	0.90	0.08	22,26,38,39	21
1	GPN	C	2	21/22	0.90	0.08	28,31,41,46	0
1	CPN	G	5[A]	18/19	0.90	0.07	22,24,27,30	18
1	CPN	C	8	18/19	0.90	0.09	29,32,43,48	0
2	GPN	H	8[A]	21/22	0.90	0.09	35,38,48,54	21
2	GPN	H	8[B]	21/22	0.90	0.09	29,30,37,42	21

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	CPN	G	5[B]	18/19	0.90	0.07	21,24,29,29	18
1	GPN	G	2[A]	21/22	0.90	0.08	24,27,34,40	21
2	CPN	H	2[A]	18/19	0.90	0.07	22,24,31,32	18
2	CPN	H	2[B]	18/19	0.90	0.07	25,28,31,32	18
2	CPN	D	7	18/19	0.90	0.08	27,32,38,39	0
1	CPN	A	5	18/19	0.91	0.08	21,22,28,29	0
2	TPN	D	3	19/20	0.91	0.08	24,27,33,35	0
1	APN	E	3	20/21	0.91	0.07	28,30,45,45	0
1	APN	G	3[A]	20/21	0.91	0.07	20,22,25,26	20
1	APN	G	3[B]	20/21	0.91	0.07	23,25,35,36	20
2	TPN	F	4	19/20	0.91	0.07	21,23,27,28	0
1	APN	C	3	20/21	0.91	0.08	24,26,30,31	0
2	CPN	D	2	18/19	0.91	0.07	25,30,37,37	0
1	GPN	A	7	21/22	0.91	0.08	22,25,33,35	0
2	TPN	B	4	19/20	0.92	0.07	20,23,28,31	0
1	TPN	C	6	19/20	0.92	0.07	24,27,30,32	0
1	APN	G	4[A]	20/21	0.92	0.07	18,21,28,30	20
1	APN	G	4[B]	20/21	0.92	0.07	23,26,31,32	20
1	APN	A	4	20/21	0.92	0.07	24,28,30,31	0
2	CPN	F	2	18/19	0.92	0.07	28,31,45,46	0
1	CPN	C	5	18/19	0.92	0.08	25,28,34,36	0
1	CPN	E	5	18/19	0.92	0.07	22,26,30,31	0
2	TPN	B	3	19/20	0.92	0.07	24,25,34,34	0
1	APN	C	4	20/21	0.92	0.07	26,31,45,48	0
1	APN	A	3	20/21	0.92	0.07	27,33,44,47	0
1	TPN	A	6	19/20	0.92	0.07	21,23,27,28	0
1	TPN	E	6	19/20	0.93	0.07	20,23,26,27	0
2	TPN	F	3	19/20	0.93	0.07	21,24,26,27	0
1	GPN	G	7[A]	21/22	0.93	0.07	23,27,32,36	21
1	GPN	G	7[B]	21/22	0.93	0.07	25,29,37,41	21
1	GPN	C	7	21/22	0.93	0.07	23,26,32,36	0
2	GPN	D	5	21/22	0.93	0.08	23,26,31,33	0
2	APN	H	6[B]	20/21	0.94	0.06	21,22,27,27	20
2	GPN	H	5[A]	21/22	0.94	0.07	19,22,27,30	21
2	GPN	H	5[B]	21/22	0.94	0.07	21,22,26,27	21
2	APN	H	6[A]	20/21	0.94	0.06	21,25,28,29	20
2	APN	D	6	20/21	0.95	0.06	23,27,32,40	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.