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wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 11, 2023 – 11:21 PM EDT

PDB ID	:	4L4T
Title	:	Structure of human MAIT TCR in complex with human MR1-6-FP
Authors	:	Patel, O.; Kjer-Nielsen, L.; Le Nours, J.; Eckle, S.B.G.; Birkinshaw, R.W.; Beddoe, T.; Corbett, A.J.; Liu, L.; Miles, J.J.; Meehan, B.; Reantragoon, R.; Sandoval-Romero, M.L.; Sullivan, L.C.; Brooks, A.G.; Chen, Z.; Fairlie, D.P.; McCluskey, J.; Rossjohn, J.
Deposited on	:	2013-06-09
Resolution	:	2.00 Å(reported)

The following versions of software and data (see references ⓘ) were used in the production of this report:

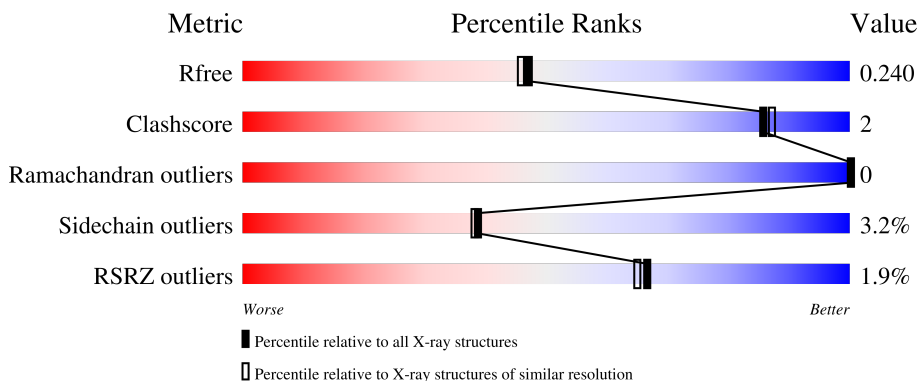|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.00 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.
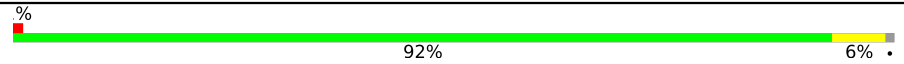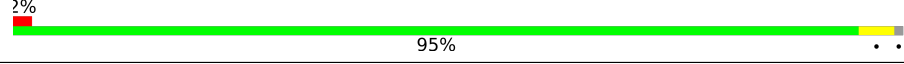
Metric	Percentile Ranks	Value
Rfree		0.240
Clashscore		2
Ramachandran outliers		0
Sidechain outliers		3.2%
RSRZ outliers		1.9%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	271	% 86% 11% •
1	C	271	88% • 8%
2	B	99	91% 6% •
2	F	99	9% 94% • •

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Mol	Chain	Length	Quality of chain
3	D	203	% 92% 6% ·
3	G	203	3% 83% 11% · 5%
4	E	245	2% 95% · ·
4	H	245	2% 87% 11% ··

2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 14034 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 Major histocompatibility complex class I-related gene protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	2	0
			2176	1397	376	392	11			
1	C	250	Total	C	N	O	S	0	1	0
			2066	1322	357	376	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q95460
A	261	SER	CYS	engineered mutation	UNP Q95460
C	0	MET	-	expression tag	UNP Q95460
C	261	SER	CYS	engineered mutation	UNP Q95460

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	96	Total	C	N	O	S	0	0	0
			789	504	131	152	2			
2	F	97	Total	C	N	O	S	0	0	0
			800	511	135	152	2			

- Molecule 3 is a protein called MAIT T-cell receptor alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	200	Total	C	N	O	S	0	0	0
			1555	981	250	315	9			
3	G	193	Total	C	N	O	S	0	1	0
			1496	949	241	297	9			

- Molecule 4 is a protein called MAIT T-cell receptor beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	243	Total 1926	C 1212	N 336	O 369	S 9	0	1	0
4	H	242	Total 1907	C 1200	N 331	O 367	S 9	0	0	0

- Molecule 5 is 2-amino-4-oxo-3,4-dihydropteridine-6-carbaldehyde (three-letter code: 6FP) (formula: $C_7H_5N_5O_2$).
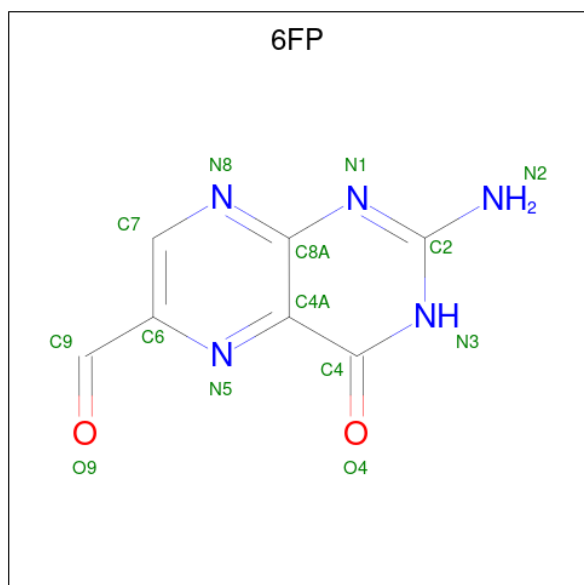
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total 13	C 7	N 5	O 1	0	0
5	C	1	Total 13	C 7	N 5	O 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	225	Total 225	O 225	0	0
6	B	99	Total 99	O 99	0	0
6	C	202	Total 202	O 202	0	0
6	D	171	Total 171	O 171	0	0
6	E	251	Total 251	O 251	0	0

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| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	59	Total 59	O 59	0	0
6	G	131	Total 131	O 131	0	0
6	H	155	Total 155	O 155	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.
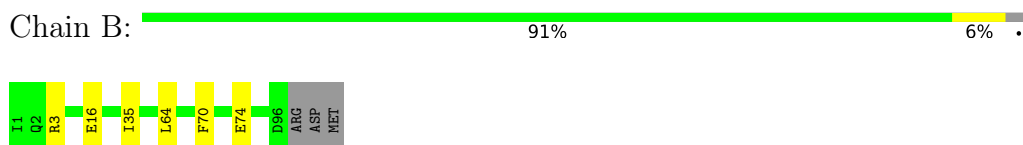
• Molecule 1: Major histocompatibility complex class I-related gene protein
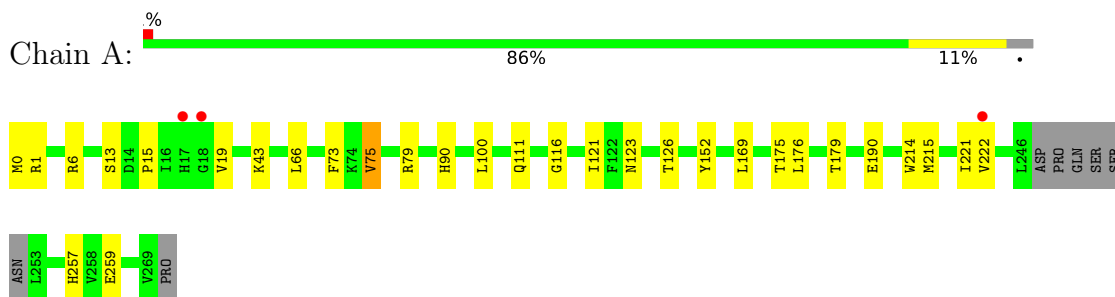
Chain A:

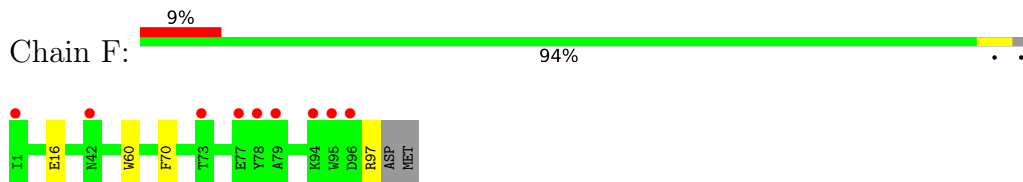• Molecule 1: Major histocompatibility complex class I-related gene protein

Chain C:

• Molecule 2: Beta-2-microglobulin
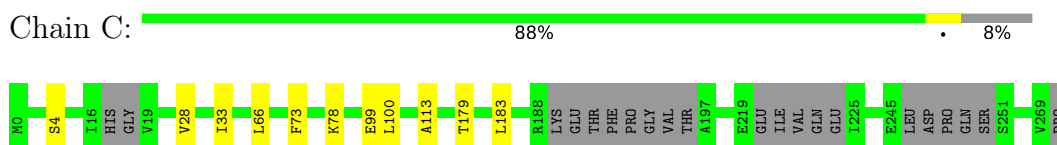
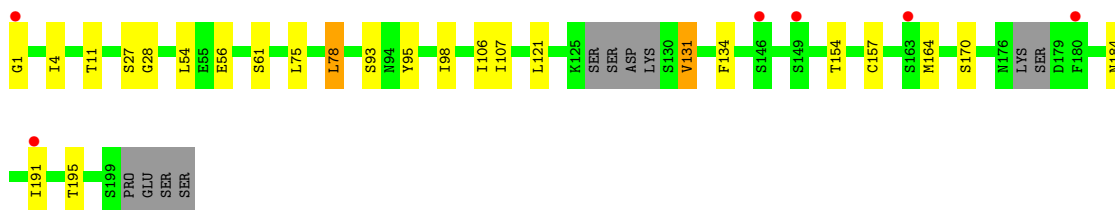Chain B:

• Molecule 2: Beta-2-microglobulin
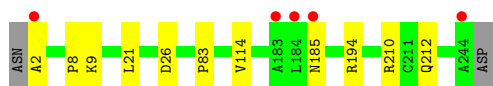
Chain F:

• Molecule 3: MAIT T-cell receptor alpha chain
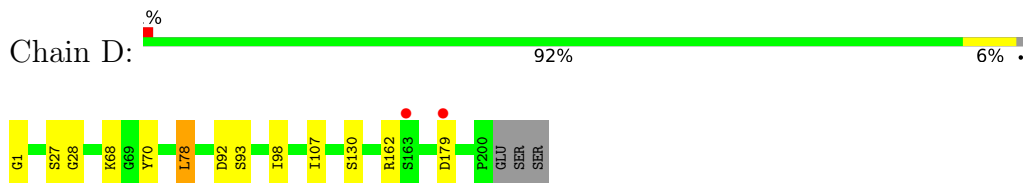
Chain D:

• Molecule 3: MAIT T-cell receptor alpha chain

Chain G:

• Molecule 4: MAIT T-cell receptor beta chain

Chain E:

• Molecule 4: MAIT T-cell receptor beta chain

Chain H:
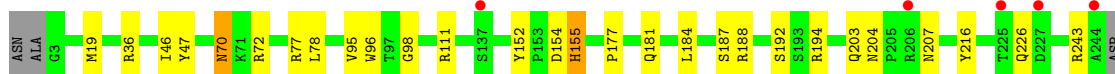
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	217.23Å 69.56Å 142.89Å 90.00° 104.42° 90.00°	Depositor
Resolution (Å)	49.38 – 2.00 49.38 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.38-2.00) 99.8 (49.38-2.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.97 (at 2.00Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.184 , 0.225 0.195 , 0.240	Depositor DCC
R_{free} test set	7014 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	23.9	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 53.4	EDS
L-test for twinning[2]	$< |L| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	14034	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 6FP

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	0.54	0/2248	0.65	0/3056
1	C	0.53	0/2129	0.65	0/2889
2	B	0.47	0/812	0.65	0/1105
2	F	0.46	0/823	0.62	0/1118
3	D	0.53	0/1590	0.68	0/2157
3	G	0.49	0/1531	0.68	0/2075
4	E	0.53	0/1981	0.65	0/2694
4	H	0.48	0/1958	0.67	0/2664
All	All	0.51	0/13072	0.66	0/17758

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 (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	2176	0	2069	14	0
1	C	2066	0	1947	4	0
2	B	789	0	735	1	0
2	F	800	0	753	1	0
3	D	1555	0	1463	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	1496	0	1408	12	0
4	E	1926	0	1826	7	0
4	H	1907	0	1799	13	0
5	A	13	0	4	0	0
5	C	13	0	4	0	0
6	A	225	0	0	2	0
6	B	99	0	0	0	0
6	C	202	0	0	1	0
6	D	171	0	0	0	0
6	E	251	0	0	0	0
6	F	59	0	0	0	0
6	G	131	0	0	0	0
6	H	155	0	0	0	0
All	All	14034	0	12008	54	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 2.

The worst 5 of 54 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)
4:E:210:ARG:HE	4:E:212:GLN:HE21	1.25	0.85
3:D:1:GLY:HA2	3:D:27:SER:H	1.40	0.84
3:G:1:GLY:HA2	3:G:27:SER:H	1.56	0.70
1:A:0:MET:HE2	1:A:169:LEU:HD13	1.77	0.66
1:A:215:MET:HG3	1:A:257:HIS:CD2	2.31	0.66

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	262/271 (97%)	256 (98%)	6 (2%)	0	100	100
1	C	241/271 (89%)	237 (98%)	4 (2%)	0	100	100
2	B	94/99 (95%)	94 (100%)	0	0	100	100
2	F	95/99 (96%)	94 (99%)	1 (1%)	0	100	100
3	D	198/203 (98%)	195 (98%)	3 (2%)	0	100	100
3	G	188/203 (93%)	182 (97%)	6 (3%)	0	100	100
4	E	242/245 (99%)	240 (99%)	2 (1%)	0	100	100
4	H	240/245 (98%)	239 (100%)	1 (0%)	0	100	100
All	All	1560/1636 (95%)	1537 (98%)	23 (2%)	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	230/241 (95%)	221 (96%)	9 (4%)	32	30
1	C	219/241 (91%)	214 (98%)	5 (2%)	50	53
2	B	88/94 (94%)	83 (94%)	5 (6%)	20	16
2	F	89/94 (95%)	86 (97%)	3 (3%)	37	36
3	D	173/180 (96%)	169 (98%)	4 (2%)	50	53
3	G	164/180 (91%)	158 (96%)	6 (4%)	34	32
4	E	209/211 (99%)	206 (99%)	3 (1%)	67	72
4	H	206/211 (98%)	197 (96%)	9 (4%)	28	25
All	All	1378/1452 (95%)	1334 (97%)	44 (3%)	39	38

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	97	ARG
4	H	19	MET

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Mol	Chain	Res	Type
3	G	75	LEU
3	G	157	CYS
4	H	77	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	120	GLN
4	H	70	ASN
3	D	184	ASN
4	H	155	HIS
4	E	212	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 ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 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
5	6FP	A	600	1	14,14,15	1.79	3 (21%)	16,20,21	1.92	6 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
5	6FP	C	600	1	14,14,15	1.90	4 (28%)	16,20,21	1.92	5 (31%)

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
5	6FP	A	600	1	-	-	0/2/2/2
5	6FP	C	600	1	-	-	0/2/2/2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	600	6FP	C9-C6	-4.54	1.39	1.50
5	A	600	6FP	C9-C6	-4.11	1.40	1.50
5	A	600	6FP	C4A-C4	-3.62	1.40	1.47
5	C	600	6FP	C4A-C4	-3.06	1.41	1.47
5	A	600	6FP	C7-N8	2.77	1.40	1.34

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	600	6FP	C4A-N5-C6	3.29	121.24	118.52
5	A	600	6FP	C4A-C4-N3	3.16	119.54	113.95
5	A	600	6FP	C2-N3-C4	-2.98	119.61	125.10
5	C	600	6FP	C2-N3-C4	-2.94	119.69	125.10
5	A	600	6FP	C4A-N5-C6	2.91	120.92	118.52

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 ⓘ

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(Å²)	Q<0.9
1	A	264/271 (97%)	-0.36	3 (1%)	80	79	13, 23, 44, 62	0
1	C	250/271 (92%)	-0.43	0	100	100	14, 25, 47, 75	0
2	B	96/99 (96%)	-0.37	0	100	100	16, 28, 49, 58	0
2	F	97/99 (97%)	0.44	9 (9%)	8	8	21, 39, 64, 82	0
3	D	200/203 (98%)	-0.46	2 (1%)	82	81	13, 22, 49, 59	0
3	G	193/203 (95%)	0.04	6 (3%)	49	48	16, 31, 66, 86	0
4	E	243/245 (99%)	-0.30	5 (2%)	63	62	14, 22, 39, 66	0
4	H	242/245 (98%)	-0.27	5 (2%)	63	62	17, 32, 53, 80	0
All	All	1585/1636 (96%)	-0.26	30 (1%)	66	65	13, 26, 56, 86	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	149	SER	5.3
4	E	244	ALA	3.7
1	A	17	HIS	3.5
3	G	1	GLY	3.3
3	D	179	ASP	3.1

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

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6.4 Ligands ⓘ

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	6FP	C	600	13/14	0.94	0.09	18,21,21,22	0
5	6FP	A	600	13/14	0.97	0.09	18,21,27,27	0

6.5 Other polymers ⓘ

There are no such residues in this entry.