



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 19, 2017 – 11:14 AM EDT

PDB ID : 5XFQ
Title : Ternary complex of PHF1, a DNA duplex and a histone peptide
Authors : Wang, Z.; Li, H.
Deposited on : unknown
Resolution : 2.40 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

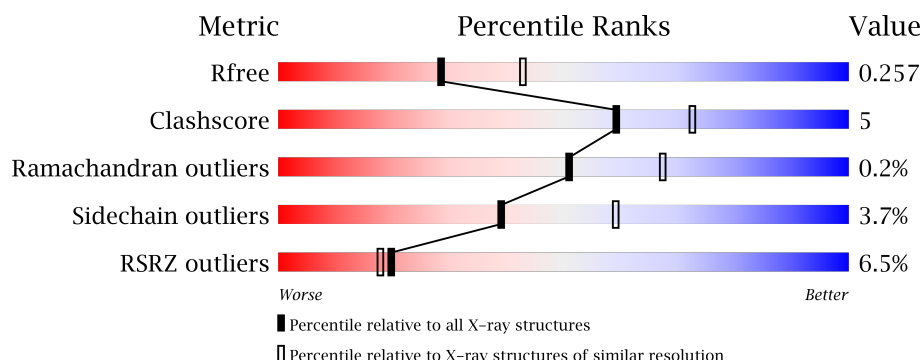
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


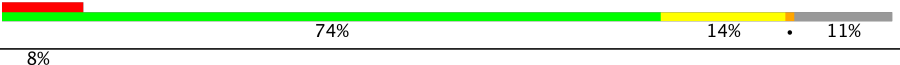

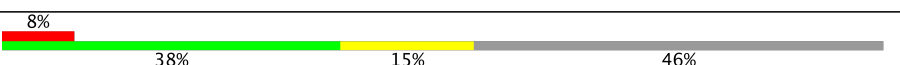

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	336	
1	B	336	
2	C	13	
2	D	13	
3	E	13	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	F	13	

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
4	ZN	A	401	-	-	-	X
4	ZN	A	403	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5601 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 PHD finger protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	S	0	0	0
			2484	1575	448	437	24			
1	B	300	Total	C	N	O	S	0	0	0
			2411	1531	433	423	24			

- Molecule 2 is a DNA chain called DNA (5'-D(*GP*GP*GP*CP*GP*GP*CP*CP*GP*CP*CP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	13	Total	C	N	O	P	0	0	0
			263	124	50	77	12			
2	D	12	Total	C	N	O	P	0	0	0
			243	114	48	70	11			

- Molecule 3 is a protein called Peptide from Histone H3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	7	Total	C	N	O	0	0	0
			68	46	14	8			
3	F	7	Total	C	N	O	0	0	0
			68	46	14	8			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	4	Total	Zn	0	0
			4	4		
4	A	4	Total	Zn	0	0
			4	4		

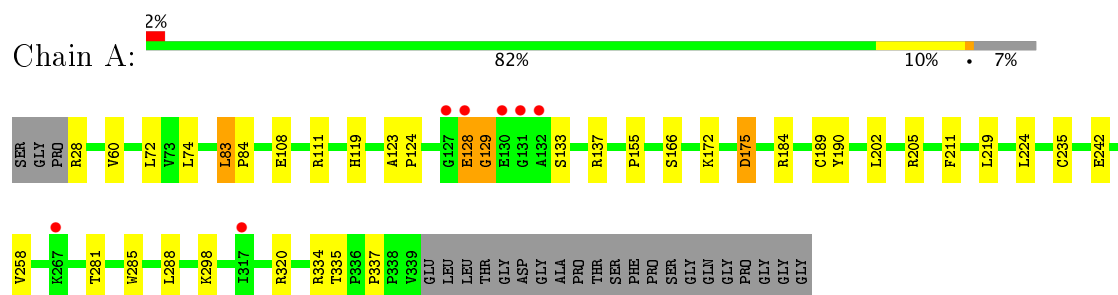
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	28	Total 28	O 28	0	0
5	B	26	Total 26	O 26	0	0
5	C	1	Total 1	O 1	0	0
5	E	1	Total 1	O 1	0	0

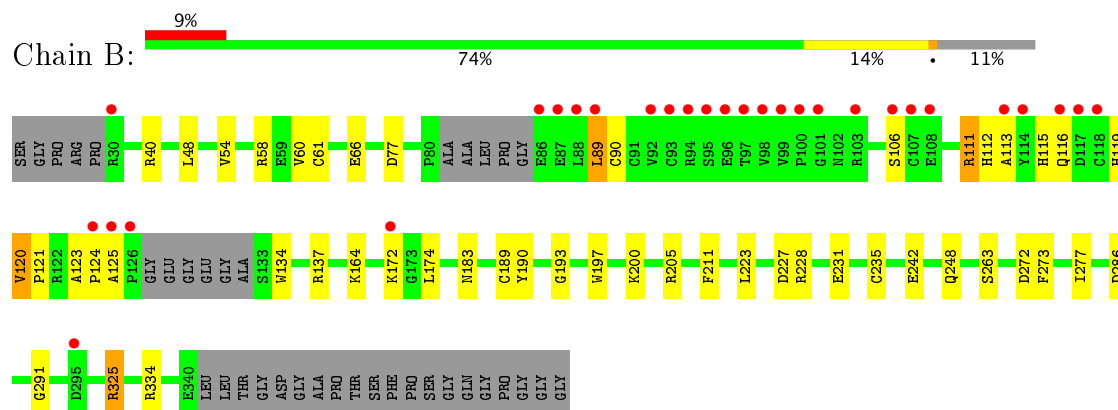
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

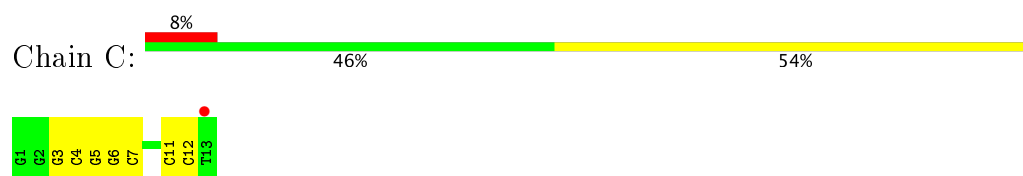
- Molecule 1: PHD finger protein 1



- Molecule 1: PHD finger protein 1



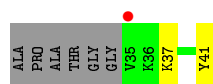
- Molecule 2: DNA (5'-D(*GP*GP*GP*CP*GP*GP*CP*CP*GP*CP*CP*CP*T)-3')



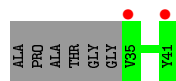
- Molecule 2: DNA (5'-D(*GP*GP*GP*CP*GP*GP*CP*CP*GP*CP*CP*CP*T)-3')



- Molecule 3: Peptide from Histone H3



- Molecule 3: Peptide from Histone H3



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	141.24Å 62.55Å 97.34Å 90.00° 103.04° 90.00°	Depositor
Resolution (Å)	47.41 – 2.40 47.41 – 2.39	Depositor EDS
% Data completeness (in resolution range)	98.6 (47.41-2.40) 98.8 (47.41-2.39)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.222 , 0.258 0.222 , 0.257	Depositor DCC
R_{free} test set	1643 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.589	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5601	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% 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: ZN, M3L

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	0.29	0/2548	0.42	1/3443 (0.0%)
1	B	0.32	0/2471	0.45	3/3335 (0.1%)
2	C	0.53	0/294	0.83	0/452
2	D	0.65	0/272	0.78	0/418
3	E	0.21	0/58	0.35	0/77
3	F	0.18	0/58	0.39	0/77
All	All	0.34	0/5701	0.49	4/7802 (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

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	123	ALA	C-N-CD	5.76	140.49	128.40
1	B	125	ALA	C-N-CD	5.72	140.42	128.40
1	A	335	THR	C-N-CD	5.59	140.14	128.40
1	B	120	VAL	C-N-CD	5.29	139.50	128.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	129	GLY	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	2484	0	2452	29	0
1	B	2411	0	2380	24	0
2	C	263	0	146	4	0
2	D	243	0	134	4	0
3	E	68	0	76	1	0
3	F	68	0	76	0	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
5	A	28	0	0	5	0
5	B	26	0	0	2	0
5	C	1	0	0	0	0
5	E	1	0	0	1	0
All	All	5601	0	5264	57	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 5.

All (57) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:GLU:OE1	1:A:129:GLY:N	1.97	0.96
1:B:89:LEU:O	1:B:113:ALA:HB3	1.82	0.79
1:A:337:PRO:O	5:A:501:HOH:O	1.99	0.79
2:D:9:DG:H2''	2:D:10:DC:C6	2.18	0.79
1:A:83:LEU:N	5:A:502:HOH:O	2.03	0.78
1:A:172:LYS:HB2	1:B:48:LEU:HD21	1.69	0.73
1:B:66:GLU:OE2	5:B:501:HOH:O	2.07	0.73
1:B:119:HIS:HE1	1:B:137:ARG:H	1.41	0.69
1:A:83:LEU:O	1:A:111:ARG:NH1	2.26	0.68
2:D:9:DG:H2''	2:D:10:DC:C5	2.30	0.67
1:B:272:ASP:OD2	1:B:325:ARG:NH1	2.29	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:HIS:CE1	1:A:137:ARG:H	2.16	0.64
2:C:3:DG:H2"	2:C:4:DC:H5"	1.80	0.62
1:A:155:PRO:HD2	5:A:524:HOH:O	2.02	0.60
2:C:6:DG:H2"	2:C:7:DC:H5'	1.86	0.58
1:A:83:LEU:HD13	1:A:84:PRO:HD2	1.84	0.58
3:E:41:TYR:O	5:E:101:HOH:O	2.17	0.57
1:A:285:TRP:HA	1:A:288:LEU:HD12	1.86	0.57
1:A:184:ARG:HD2	1:B:111:ARG:NH2	2.21	0.56
1:A:60:VAL:HG22	1:A:74:LEU:HD23	1.88	0.56
1:B:263:SER:O	1:B:334:ARG:NH2	2.38	0.56
1:A:184:ARG:HD2	1:B:111:ARG:HH22	1.69	0.56
1:A:128:GLU:CD	1:A:129:GLY:H	2.05	0.54
1:A:320:ARG:NH2	2:D:6:DG:OP2	2.35	0.54
1:A:189:CYS:SG	1:A:190:TYR:N	2.80	0.54
1:A:166:SER:OG	5:A:503:HOH:O	2.17	0.54
1:B:40:ARG:HD2	1:B:193:GLY:HA3	1.89	0.54
1:A:205:ARG:NH1	5:A:507:HOH:O	2.42	0.52
1:A:202:LEU:HD11	1:A:219:LEU:HD21	1.92	0.52
1:B:174:LEU:HD13	1:B:183:ASN:HD21	1.76	0.51
2:C:4:DC:H2"	2:C:5:DG:C8	2.46	0.50
1:B:200:LYS:NZ	1:B:223:LEU:O	2.37	0.50
1:B:106:SER:HA	1:B:112:HIS:O	2.12	0.50
1:A:60:VAL:HG11	1:A:72:LEU:HB3	1.96	0.47
1:A:189:CYS:HA	1:A:211:PHE:CD2	2.49	0.47
1:A:224:LEU:HD11	1:A:288:LEU:HD23	1.95	0.47
1:B:205:ARG:HD2	1:B:231:GLU:HG2	1.96	0.47
1:A:119:HIS:HE1	1:A:137:ARG:H	1.60	0.47
1:B:248:GLN:HE22	1:B:291:GLY:HA3	1.80	0.46
1:B:227:ASP:OD2	5:B:502:HOH:O	2.20	0.46
1:B:124:PRO:HD2	1:B:134:TRP:CD1	2.50	0.46
2:D:2:DG:H1'	2:D:3:DG:C8	2.51	0.46
1:B:40:ARG:NH1	1:B:77:ASP:OD1	2.50	0.45
1:A:235:CYS:SG	1:A:242:GLU:HG3	2.57	0.44
1:B:235:CYS:SG	1:B:242:GLU:HG3	2.59	0.43
1:B:197:TRP:HZ3	1:B:228:ARG:HD2	1.84	0.42
1:A:123:ALA:HA	1:A:124:PRO:HD3	1.88	0.42
1:A:83:LEU:HA	1:A:83:LEU:HD22	1.85	0.42
1:A:137:ARG:NH2	1:A:166:SER:O	2.53	0.42
1:B:90:CYS:HA	1:B:113:ALA:O	2.20	0.42
1:A:258:VAL:HG21	1:A:281:THR:HG22	2.02	0.42
2:C:11:DC:H2'	2:C:12:DC:C6	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:LYS:HE3	1:B:190:TYR:CE2	2.55	0.42
1:A:175:ASP:OD2	1:B:111:ARG:NH2	2.52	0.42
1:A:334:ARG:HH11	1:A:334:ARG:HG2	1.85	0.41
1:B:189:CYS:HA	1:B:211:PHE:CD1	2.55	0.41
1:B:273:PHE:HA	1:B:277:ILE:HB	2.03	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	310/336 (92%)	300 (97%)	10 (3%)	0	100	100
1	B	294/336 (88%)	284 (97%)	9 (3%)	1 (0%)	44	60
3	E	4/13 (31%)	4 (100%)	0	0	100	100
3	F	4/13 (31%)	4 (100%)	0	0	100	100
All	All	612/698 (88%)	592 (97%)	19 (3%)	1 (0%)	51	67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	121	PRO

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	269/284 (95%)	262 (97%)	7 (3%)	51	72
1	B	264/284 (93%)	252 (96%)	12 (4%)	32	50
3	E	6/8 (75%)	5 (83%)	1 (17%)	2	3
3	F	6/8 (75%)	6 (100%)	0	100	100
All	All	545/584 (93%)	525 (96%)	20 (4%)	39	59

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ARG
1	A	83	LEU
1	A	108	GLU
1	A	128	GLU
1	A	133	SER
1	A	175	ASP
1	A	298	LYS
1	B	54	VAL
1	B	58	ARG
1	B	60	VAL
1	B	61	CYS
1	B	89	LEU
1	B	111	ARG
1	B	115	HIS
1	B	116	GLN
1	B	120	VAL
1	B	172	LYS
1	B	286	ASP
1	B	325	ARG
3	E	37	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	HIS
1	A	186	GLN
1	A	304	GLN
1	A	312	HIS
1	B	119	HIS
1	B	183	ASN
1	B	248	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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$
3	M3L	E	36	3	11,11,12	0.84	1 (9%)	11,14,16	0.89	1 (9%)
3	M3L	F	36	3	11,11,12	0.76	1 (9%)	11,14,16	0.97	1 (9%)

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
3	M3L	E	36	3	-	0/8/10/12	0/0/0/0
3	M3L	F	36	3	-	0/8/10/12	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	36	M3L	CA-C	2.12	1.53	1.50
3	E	36	M3L	CA-C	2.40	1.53	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	36	M3L	CB-CA-C	-2.81	107.02	111.65
3	E	36	M3L	CB-CA-C	-2.45	107.61	111.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	312/336 (92%)	0.25	7 (2%) 62 59	37, 53, 74, 112	0
1	B	300/336 (89%)	0.51	29 (9%) 8 8	37, 54, 107, 129	0
2	C	13/13 (100%)	0.02	1 (7%) 14 12	64, 67, 82, 96	0
2	D	12/13 (92%)	0.27	2 (16%) 2 2	58, 64, 99, 106	0
3	E	6/13 (46%)	0.57	1 (16%) 2 2	57, 59, 68, 78	0
3	F	6/13 (46%)	0.94	2 (33%) 0 0	54, 61, 68, 81	0
All	All	649/724 (89%)	0.38	42 (6%) 20 18	37, 55, 91, 129	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	98	VAL	8.3
1	B	97	THR	6.0
1	A	127	GLY	6.0
1	B	100	PRO	5.4
1	B	99	VAL	5.4
1	B	95	SER	5.1
1	B	101	GLY	5.0
1	A	130	GLU	5.0
1	B	118	CYS	4.9
1	B	94	ARG	4.7
1	A	131	GLY	4.7
1	A	132	ALA	4.5
1	B	103	ARG	4.4
1	B	86	GLU	4.1
1	B	106	SER	3.7
1	B	117	ASP	3.7
1	B	89	LEU	3.6
1	B	113	ALA	3.5
3	E	35	VAL	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	93	CYS	3.3
1	B	87	GLU	3.1
3	F	41	TYR	2.9
1	A	317	ILE	2.8
2	D	11	DC	2.8
1	A	128	GLU	2.8
1	B	125	ALA	2.7
1	B	92	VAL	2.6
2	C	13	DT	2.6
1	B	116	GLN	2.5
1	B	96	GLU	2.5
1	B	295	ASP	2.2
2	D	12	DC	2.2
1	B	172	LYS	2.2
3	F	35	VAL	2.1
1	B	124	PRO	2.1
1	B	114	TYR	2.1
1	B	126	PRO	2.1
1	B	107	CYS	2.1
1	B	88	LEU	2.1
1	B	108	GLU	2.0
1	A	267	LYS	2.0
1	B	30	ARG	2.0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	M3L	F	36	12/13	0.94	0.21	-	47,57,61,64	0
3	M3L	E	36	12/13	0.90	0.20	-	54,64,76,80	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	ZN	A	401	1/1	0.99	0.20	2.12	48,48,48,48	0
4	ZN	A	403	1/1	0.99	0.19	2.04	40,40,40,40	0
4	ZN	B	401	1/1	0.99	0.19	0.88	42,42,42,42	0
4	ZN	A	404	1/1	1.00	0.16	0.74	44,44,44,44	0
4	ZN	A	402	1/1	0.99	0.17	0.31	41,41,41,41	0
4	ZN	B	402	1/1	0.97	0.15	-0.07	58,58,58,58	0
4	ZN	B	404	1/1	0.87	0.11	-1.35	68,68,68,68	0
4	ZN	B	403	1/1	0.85	0.11	-2.38	131,131,131,131	0

6.5 Other polymers [i](#)

There are no such residues in this entry.