



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2020 – 10:01 AM BST

PDB ID : 3OC3  
Title : Crystal structure of the Mot1 N-terminal domain in complex with TBP  
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Deposited on : 2010-08-09  
Resolution : 3.10 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](mailto: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.

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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	:	2.13.1
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)	:	2.13.1

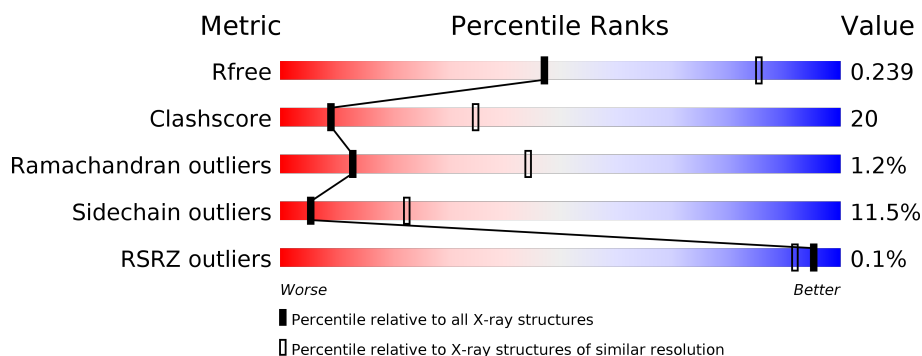
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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))
$R_{free}$	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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  $\geq 3$ , 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	800	
1	B	800	
2	C	218	
2	D	218	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15037 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 HELICASE MOT1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	752	Total	C	N	O	S	104	0	0
			6086	3926	984	1153	23			
1	B	749	Total	C	N	O	S	72	0	0
			6064	3911	981	1149	23			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	EXPRESSION TAG	UNP Q8SVZ5
A	-20	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
A	-19	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-18	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-17	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-16	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-15	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-14	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-13	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-12	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-11	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-10	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
A	-9	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
A	-8	GLY	-	EXPRESSION TAG	UNP Q8SVZ5
A	-7	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
A	-6	GLY	-	EXPRESSION TAG	UNP Q8SVZ5
A	-5	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
A	-4	ARG	-	EXPRESSION TAG	UNP Q8SVZ5
A	-3	ASN	-	EXPRESSION TAG	UNP Q8SVZ5
A	-2	MET	-	EXPRESSION TAG	UNP Q8SVZ5
A	-1	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
A	0	SER	-	EXPRESSION TAG	UNP Q8SVZ5
B	-21	MET	-	EXPRESSION TAG	UNP Q8SVZ5
B	-20	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
B	-19	HIS	-	EXPRESSION TAG	UNP Q8SVZ5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
B	-17	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
B	-16	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
B	-15	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
B	-14	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
B	-13	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
B	-12	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
B	-11	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
B	-10	HIS	-	EXPRESSION TAG	UNP Q8SVZ5
B	-9	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
B	-8	GLY	-	EXPRESSION TAG	UNP Q8SVZ5
B	-7	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
B	-6	GLY	-	EXPRESSION TAG	UNP Q8SVZ5
B	-5	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
B	-4	ARG	-	EXPRESSION TAG	UNP Q8SVZ5
B	-3	ASN	-	EXPRESSION TAG	UNP Q8SVZ5
B	-2	MET	-	EXPRESSION TAG	UNP Q8SVZ5
B	-1	ALA	-	EXPRESSION TAG	UNP Q8SVZ5
B	0	SER	-	EXPRESSION TAG	UNP Q8SVZ5

- Molecule 2 is a protein called TRANSCRIPTION INITIATION FACTOR TFIIID (TFIID-1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	178	Total	C	N	O	S	8	1	0
			1417	919	247	244	7			
2	D	178	Total	C	N	O	S	6	1	0
			1417	919	247	244	7			

There are 40 discrepancies between the modelled and reference sequences:

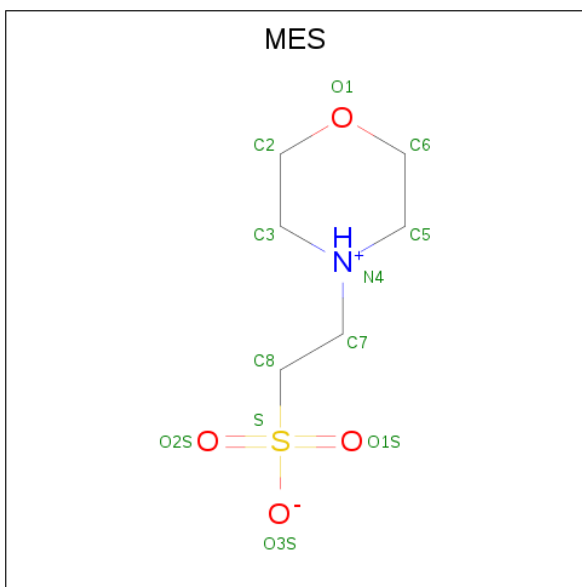
Chain	Residue	Modelled	Actual	Comment	Reference
C	-19	MET	-	EXPRESSION TAG	UNP Q8ST28
C	-18	GLY	-	EXPRESSION TAG	UNP Q8ST28
C	-17	SER	-	EXPRESSION TAG	UNP Q8ST28
C	-16	SER	-	EXPRESSION TAG	UNP Q8ST28
C	-15	HIS	-	EXPRESSION TAG	UNP Q8ST28
C	-14	HIS	-	EXPRESSION TAG	UNP Q8ST28
C	-13	HIS	-	EXPRESSION TAG	UNP Q8ST28
C	-12	HIS	-	EXPRESSION TAG	UNP Q8ST28
C	-11	HIS	-	EXPRESSION TAG	UNP Q8ST28
C	-10	HIS	-	EXPRESSION TAG	UNP Q8ST28
C	-9	SER	-	EXPRESSION TAG	UNP Q8ST28

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	SER	-	EXPRESSION TAG	UNP Q8ST28
C	-7	GLY	-	EXPRESSION TAG	UNP Q8ST28
C	-6	LEU	-	EXPRESSION TAG	UNP Q8ST28
C	-5	VAL	-	EXPRESSION TAG	UNP Q8ST28
C	-4	PRO	-	EXPRESSION TAG	UNP Q8ST28
C	-3	ARG	-	EXPRESSION TAG	UNP Q8ST28
C	-2	GLY	-	EXPRESSION TAG	UNP Q8ST28
C	-1	SER	-	EXPRESSION TAG	UNP Q8ST28
C	0	HIS	-	EXPRESSION TAG	UNP Q8ST28
D	-19	MET	-	EXPRESSION TAG	UNP Q8ST28
D	-18	GLY	-	EXPRESSION TAG	UNP Q8ST28
D	-17	SER	-	EXPRESSION TAG	UNP Q8ST28
D	-16	SER	-	EXPRESSION TAG	UNP Q8ST28
D	-15	HIS	-	EXPRESSION TAG	UNP Q8ST28
D	-14	HIS	-	EXPRESSION TAG	UNP Q8ST28
D	-13	HIS	-	EXPRESSION TAG	UNP Q8ST28
D	-12	HIS	-	EXPRESSION TAG	UNP Q8ST28
D	-11	HIS	-	EXPRESSION TAG	UNP Q8ST28
D	-10	HIS	-	EXPRESSION TAG	UNP Q8ST28
D	-9	SER	-	EXPRESSION TAG	UNP Q8ST28
D	-8	SER	-	EXPRESSION TAG	UNP Q8ST28
D	-7	GLY	-	EXPRESSION TAG	UNP Q8ST28
D	-6	LEU	-	EXPRESSION TAG	UNP Q8ST28
D	-5	VAL	-	EXPRESSION TAG	UNP Q8ST28
D	-4	PRO	-	EXPRESSION TAG	UNP Q8ST28
D	-3	ARG	-	EXPRESSION TAG	UNP Q8ST28
D	-2	GLY	-	EXPRESSION TAG	UNP Q8ST28
D	-1	SER	-	EXPRESSION TAG	UNP Q8ST28
D	0	HIS	-	EXPRESSION TAG	UNP Q8ST28

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula:  $C_6H_{13}NO_4S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

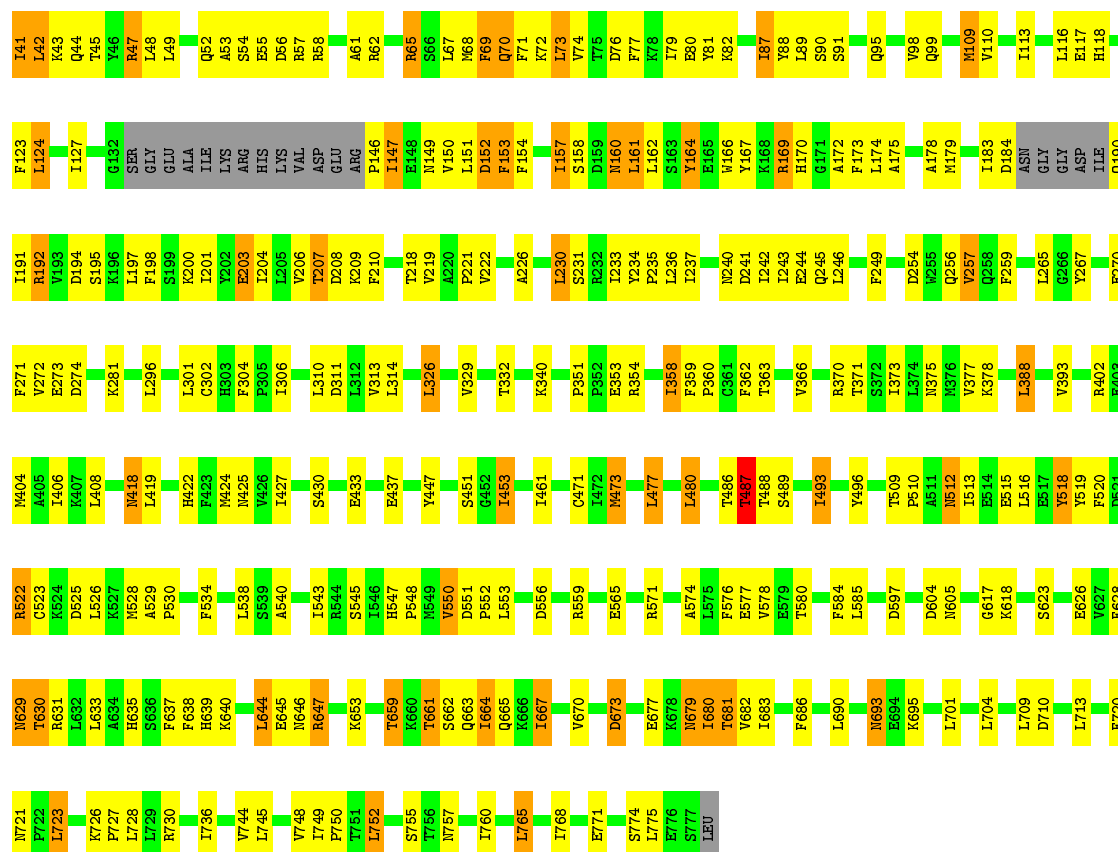
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	12	Total	O	0	0
			12	12		
4	B	11	Total	O	0	0
			11	11		
4	C	4	Total	O	0	0
			4	4		
4	D	2	Total	O	0	0
			2	2		

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.

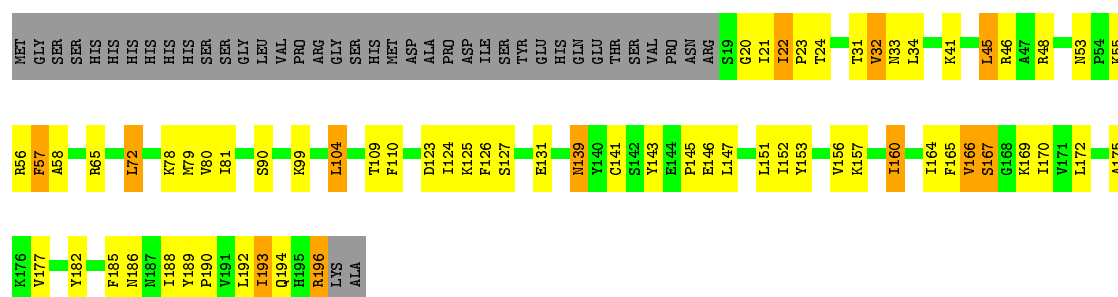
Chain A:  56% 32% 6% 6%

Chain B:



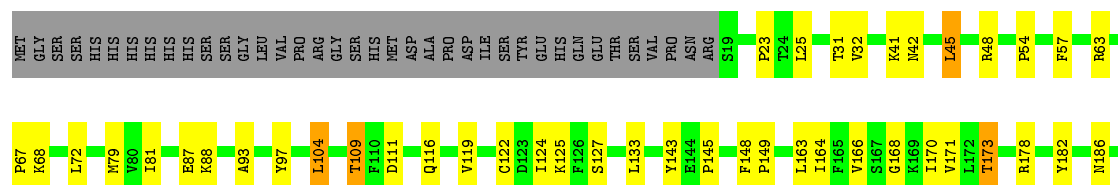
• Molecule 2: TRANSCRIPTION INITIATION FACTOR TFIIID (TFIIID-1)

Chain C: 51% 25% 6% 18%



• Molecule 2: TRANSCRIPTION INITIATION FACTOR TFIIID (TFIIID-1)

Chain D: 60% 20% 18%



P190
V191
L192
I193
Q194
H195
R196
LYS
ALA

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.26 Å 147.82 Å 103.44 Å 90.00° 94.52° 90.00°	Depositor
Resolution (Å)	47.28 – 3.10 47.28 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.28-3.10) 99.7 (47.28-3.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.66 (at 3.12 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, $R_{free}$	0.187 , 0.242 0.181 , 0.239	Depositor DCC
$R_{free}$ test set	2700 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	76.1	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 69.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.020 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	15037	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.27	0/6203	0.46	0/8365
1	B	0.29	0/6181	0.47	0/8335
2	C	0.28	0/1447	0.46	0/1952
2	D	0.30	0/1447	0.46	0/1952
All	All	0.28	0/15278	0.46	0/20604

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	40	TYR	Peptide

### 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	6086	0	6157	263	0
1	B	6064	0	6130	274	0
2	C	1417	0	1491	46	0
2	D	1417	0	1491	27	0
3	C	12	0	12	1	0
3	D	12	0	12	2	0
4	A	12	0	0	1	0
4	B	11	0	0	0	0
4	C	4	0	0	0	0
4	D	2	0	0	0	0
All	All	15037	0	15293	598	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 20.

The worst 5 of 598 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:B:79:ILE:HD11	1:B:237:ILE:HD11	1.21	1.14
2:D:42:ASN:HD21	3:D:199:MES:H72	1.17	1.09
1:B:19:LEU:HA	1:B:31:ILE:HD11	1.35	1.09
1:A:33:GLU:HG2	1:A:62:ARG:HH22	1.22	1.02
1:A:149:ASN:HD22	1:A:149:ASN:H	1.09	1.00

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	746/800 (93%)	659 (88%)	76 (10%)	11 (2%)	10	39
1	B	743/800 (93%)	655 (88%)	78 (10%)	10 (1%)	12	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	177/218 (81%)	164 (93%)	12 (7%)	1 (1%)	25	59
2	D	177/218 (81%)	167 (94%)	9 (5%)	1 (1%)	25	59
All	All	1843/2036 (90%)	1645 (89%)	175 (10%)	23 (1%)	13	44

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	183	ILE
1	A	629	ASN
1	B	70	GLN
1	B	487	THR
1	A	24	THR

### 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	690/727 (95%)	616 (89%)	74 (11%)	6	26
1	B	687/727 (94%)	600 (87%)	87 (13%)	4	18
2	C	154/188 (82%)	134 (87%)	20 (13%)	4	18
2	D	154/188 (82%)	142 (92%)	12 (8%)	12	40
All	All	1685/1830 (92%)	1492 (88%)	193 (12%)	5	22

5 of 193 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	69	PHE
1	B	296	LEU
2	C	186	ASN
1	B	87	ILE
1	B	161	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	454	ASN
1	B	679	ASN
2	D	53	ASN
1	B	635	HIS
1	B	684	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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$
3	MES	C	199	-	12,12,12	2.26	1 (8%)	14,16,16	2.60	8 (57%)
3	MES	D	199	-	12,12,12	2.25	1 (8%)	14,16,16	2.61	7 (50%)

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	MES	C	199	-	-	4/6/14/14	0/1/1/1
3	MES	D	199	-	-	1/6/14/14	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	199	MES	C8-S	-7.54	1.66	1.77
3	D	199	MES	C8-S	-7.49	1.66	1.77

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	199	MES	C5-N4-C3	4.72	119.46	108.83
3	D	199	MES	C5-N4-C3	4.61	119.21	108.83
3	C	199	MES	C6-C5-N4	-3.88	104.21	110.10
3	D	199	MES	C6-C5-N4	-3.75	104.42	110.10
3	D	199	MES	C7-N4-C3	3.69	120.66	111.23

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	199	MES	C8-C7-N4-C3
3	C	199	MES	C7-C8-S-O1S
3	C	199	MES	C7-C8-S-O3S
3	D	199	MES	C8-C7-N4-C5
3	C	199	MES	C7-C8-S-O2S

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	199	MES	1	0
3	D	199	MES	2	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	752/800 (94%)	-0.51	1 (0%) 95 92	38, 82, 150, 206	36 (4%)
1	B	749/800 (93%)	-0.58	0 100 100	26, 72, 137, 208	23 (3%)
2	C	178/218 (81%)	-0.57	0 100 100	44, 68, 108, 160	2 (1%)
2	D	178/218 (81%)	-0.59	0 100 100	37, 58, 91, 123	3 (1%)
All	All	1857/2036 (91%)	-0.55	1 (0%) 95 92	26, 73, 138, 208	64 (3%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	76	ASP	2.4

### 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 monosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	MES	C	199	12/12	0.95	0.19	89,103,123,129	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MES	D	199	12/12	0.95	0.37	96,115,130,133	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.