



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:54 PM GMT

PDB ID : 3VD2  
Title : structure of p73 DNA binding domain tetramer modulates p73 transactivation  
Authors : Ethayathulla, A.S.; Tse, P.W.; Nguyen, S.; Viadiu, H.  
Deposited on : 2012-01-04  
Resolution : 4.00 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

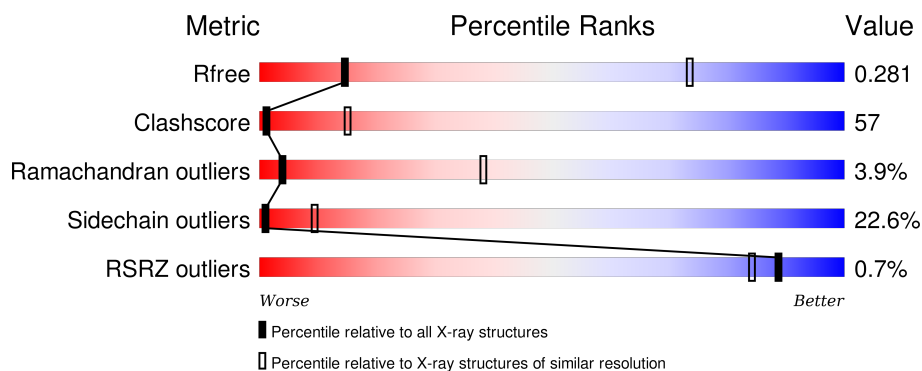
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 4.00 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1010 (4.42-3.56)
Clashscore	102246	1052 (4.40-3.60)
Ramachandran outliers	100387	1005 (4.40-3.60)
Sidechain outliers	100360	1013 (4.42-3.58)
RSRZ outliers	91569	1013 (4.42-3.56)

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. 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	210	 29% 51% 15% . .
1	B	210	 21% 56% 18% . 5%
1	C	210	 32% 50% 13% .
1	D	210	 31% 50% 14% 5%
1	I	210	 20% 56% 19% . .

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Mol	Chain	Length	Quality of chain
1	J	210	<div><div></div><div>29%47%20%••</div></div>
2	E	14	<div><div>14%</div><div>29%71%</div></div>
2	F	14	<div><div>14%</div><div>79%7%</div></div>
2	G	14	<div><div>7%</div><div>86%7%</div></div>
2	H	14	<div><div>21%</div><div>79%</div></div>
2	K	14	<div><div>7%</div><div>64%21%7%</div></div>
2	L	14	<div><div>7%</div><div>21%50%21%7%</div></div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 11152 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 Tumor protein p73.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	203	Total	C	N	O	S	0	0	0
			1590	994	289	296	11			
1	B	200	Total	C	N	O	S	0	0	0
			1569	981	283	294	11			
1	C	203	Total	C	N	O	S	0	0	0
			1596	997	291	297	11			
1	D	199	Total	C	N	O	S	0	0	0
			1563	981	282	289	11			
1	I	202	Total	C	N	O	S	0	0	0
			1576	985	284	296	11			
1	J	202	Total	C	N	O	S	0	0	0
			1586	993	284	298	11			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	MET	-	INITIATING METHIONINE	UNP O15350
A	104	GLY	-	EXPRESSION TAG	UNP O15350
A	105	HIS	-	EXPRESSION TAG	UNP O15350
A	106	HIS	-	EXPRESSION TAG	UNP O15350
A	107	HIS	-	EXPRESSION TAG	UNP O15350
A	108	HIS	-	EXPRESSION TAG	UNP O15350
A	109	HIS	-	EXPRESSION TAG	UNP O15350
A	110	HIS	-	EXPRESSION TAG	UNP O15350
A	111	HIS	-	EXPRESSION TAG	UNP O15350
A	112	HIS	-	EXPRESSION TAG	UNP O15350
A	113	GLU	-	EXPRESSION TAG	UNP O15350
A	114	PHE	-	EXPRESSION TAG	UNP O15350
B	103	MET	-	INITIATING METHIONINE	UNP O15350
B	104	GLY	-	EXPRESSION TAG	UNP O15350
B	105	HIS	-	EXPRESSION TAG	UNP O15350
B	106	HIS	-	EXPRESSION TAG	UNP O15350
B	107	HIS	-	EXPRESSION TAG	UNP O15350

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Chain	Residue	Modelled	Actual	Comment	Reference
B	108	HIS	-	EXPRESSION TAG	UNP 015350
B	109	HIS	-	EXPRESSION TAG	UNP 015350
B	110	HIS	-	EXPRESSION TAG	UNP 015350
B	111	HIS	-	EXPRESSION TAG	UNP 015350
B	112	HIS	-	EXPRESSION TAG	UNP 015350
B	113	GLU	-	EXPRESSION TAG	UNP 015350
B	114	PHE	-	EXPRESSION TAG	UNP 015350
C	103	MET	-	INITIATING METHIONINE	UNP 015350
C	104	GLY	-	EXPRESSION TAG	UNP 015350
C	105	HIS	-	EXPRESSION TAG	UNP 015350
C	106	HIS	-	EXPRESSION TAG	UNP 015350
C	107	HIS	-	EXPRESSION TAG	UNP 015350
C	108	HIS	-	EXPRESSION TAG	UNP 015350
C	109	HIS	-	EXPRESSION TAG	UNP 015350
C	110	HIS	-	EXPRESSION TAG	UNP 015350
C	111	HIS	-	EXPRESSION TAG	UNP 015350
C	112	HIS	-	EXPRESSION TAG	UNP 015350
C	113	GLU	-	EXPRESSION TAG	UNP 015350
C	114	PHE	-	EXPRESSION TAG	UNP 015350
D	103	MET	-	INITIATING METHIONINE	UNP 015350
D	104	GLY	-	EXPRESSION TAG	UNP 015350
D	105	HIS	-	EXPRESSION TAG	UNP 015350
D	106	HIS	-	EXPRESSION TAG	UNP 015350
D	107	HIS	-	EXPRESSION TAG	UNP 015350
D	108	HIS	-	EXPRESSION TAG	UNP 015350
D	109	HIS	-	EXPRESSION TAG	UNP 015350
D	110	HIS	-	EXPRESSION TAG	UNP 015350
D	111	HIS	-	EXPRESSION TAG	UNP 015350
D	112	HIS	-	EXPRESSION TAG	UNP 015350
D	113	GLU	-	EXPRESSION TAG	UNP 015350
D	114	PHE	-	EXPRESSION TAG	UNP 015350
I	103	MET	-	INITIATING METHIONINE	UNP 015350
I	104	GLY	-	EXPRESSION TAG	UNP 015350
I	105	HIS	-	EXPRESSION TAG	UNP 015350
I	106	HIS	-	EXPRESSION TAG	UNP 015350
I	107	HIS	-	EXPRESSION TAG	UNP 015350
I	108	HIS	-	EXPRESSION TAG	UNP 015350
I	109	HIS	-	EXPRESSION TAG	UNP 015350
I	110	HIS	-	EXPRESSION TAG	UNP 015350
I	111	HIS	-	EXPRESSION TAG	UNP 015350
I	112	HIS	-	EXPRESSION TAG	UNP 015350
I	113	GLU	-	EXPRESSION TAG	UNP 015350

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Chain	Residue	Modelled	Actual	Comment	Reference
I	114	PHE	-	EXPRESSION TAG	UNP O15350
J	103	MET	-	INITIATING METHIONINE	UNP O15350
J	104	GLY	-	EXPRESSION TAG	UNP O15350
J	105	HIS	-	EXPRESSION TAG	UNP O15350
J	106	HIS	-	EXPRESSION TAG	UNP O15350
J	107	HIS	-	EXPRESSION TAG	UNP O15350
J	108	HIS	-	EXPRESSION TAG	UNP O15350
J	109	HIS	-	EXPRESSION TAG	UNP O15350
J	110	HIS	-	EXPRESSION TAG	UNP O15350
J	111	HIS	-	EXPRESSION TAG	UNP O15350
J	112	HIS	-	EXPRESSION TAG	UNP O15350
J	113	GLU	-	EXPRESSION TAG	UNP O15350
J	114	PHE	-	EXPRESSION TAG	UNP O15350

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	14	Total	C	N	O	P	0	0	0
			284	137	52	82	13			
2	F	14	Total	C	N	O	P	0	0	0
			284	137	52	82	13			
2	G	14	Total	C	N	O	P	0	0	0
			284	137	52	82	13			
2	H	14	Total	C	N	O	P	0	0	0
			284	137	52	82	13			
2	L	13	Total	C	N	O	P	0	0	0
			266	127	47	79	13			
2	K	13	Total	C	N	O	P	0	0	0
			264	127	50	75	12			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		
3	I	1	Total	Zn	0	0
			1	1		

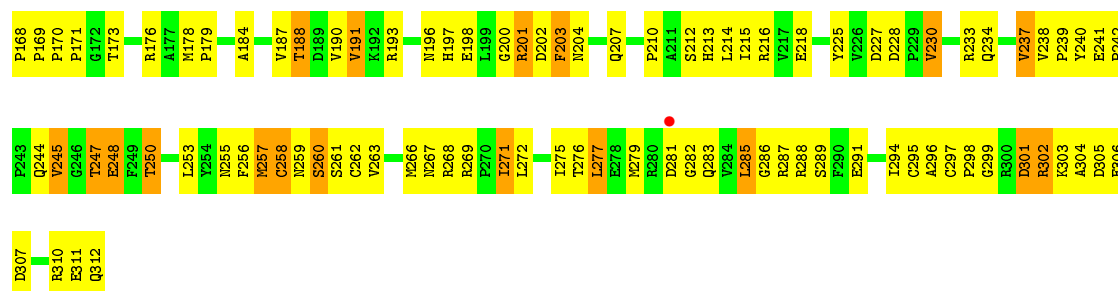
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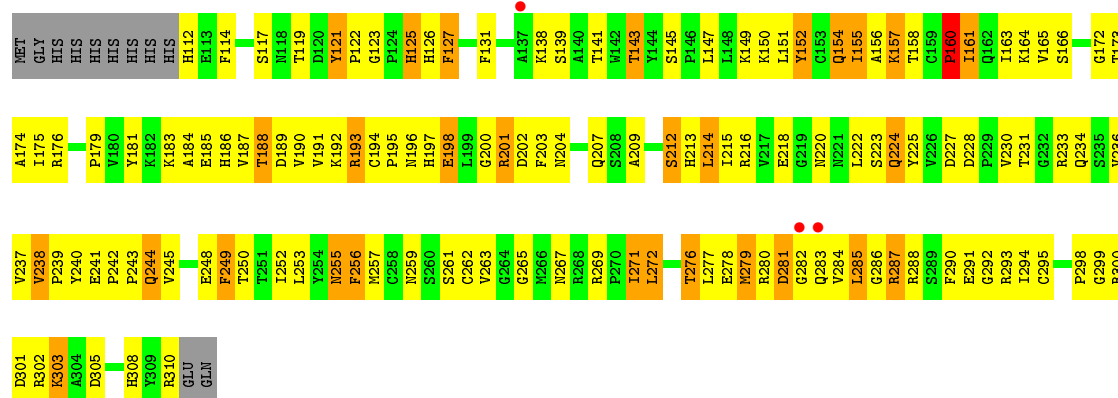
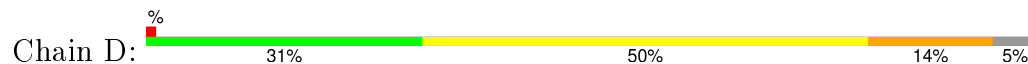
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total 1	Zn 1	0	0
3	A	1	Total 1	Zn 1	0	0



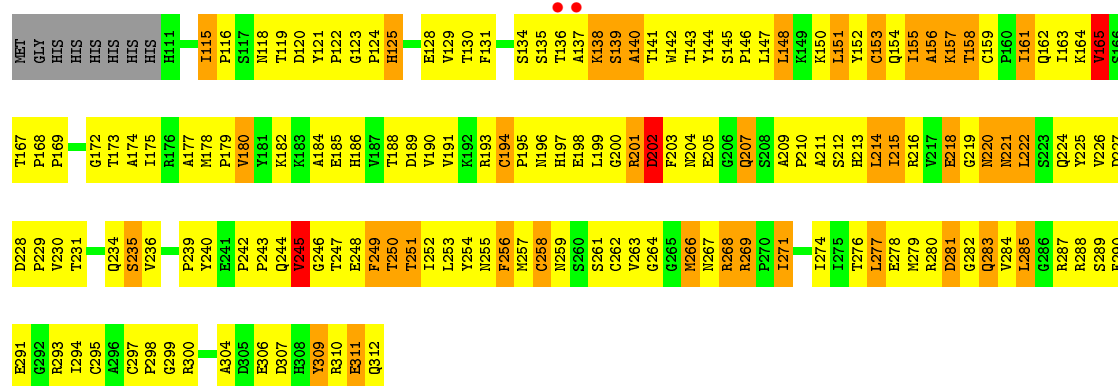




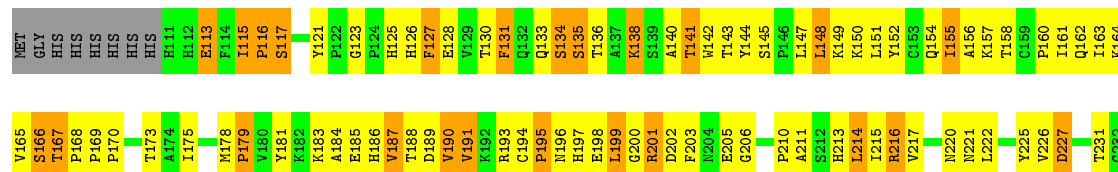
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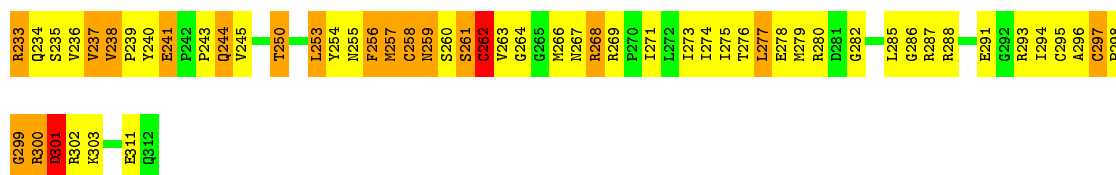


• Molecule 1: Tumor protein p73

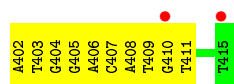


• Molecule 1: Tumor protein p73





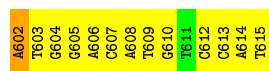
- Molecule 2: DNA (5'-D(\*AP\*TP\*GP\*GP\*AP\*CP\*AP\*TP\*GP\*TP\*CP\*CP\*AP\*T)-3')



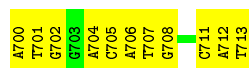
- Molecule 2: DNA (5'-D(\*AP\*TP\*GP\*GP\*AP\*CP\*AP\*TP\*GP\*TP\*CP\*CP\*AP\*T)-3')



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



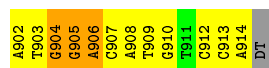
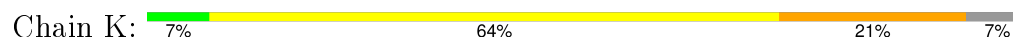
- Molecule 2: DNA (5'-D(\*AP\*TP\*GP\*GP\*AP\*CP\*AP\*TP\*GP\*TP\*CP\*CP\*AP\*T)-3')



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



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	158.40Å 91.13Å 137.47Å 90.00° 90.20° 90.00°	Depositor
Resolution (Å)	45.69 – 4.00 45.69 – 4.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (45.69-4.00) 98.1 (45.69-4.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.59 (at 4.00Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.248 , 0.284 0.246 , 0.281	Depositor DCC
$R_{free}$ test set	350 reflections (2.10%)	DCC
Wilson B-factor (Å <sup>2</sup> )	91.2	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.21 , -0.1	EDS
Estimated twinning fraction	0.019 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.018 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.429 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.429 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.020 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 16649 reflections	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	11152	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% 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, 0.375 respectively for untwinned datasets, and 0.333, 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

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	0.53	0/1631	0.87	3/2218 (0.1%)
1	B	0.46	0/1609	0.93	2/2187 (0.1%)
1	C	0.49	0/1638	0.83	2/2226 (0.1%)
1	D	0.49	0/1604	0.81	0/2181
1	I	0.51	0/1615	0.86	5/2195 (0.2%)
1	J	0.49	0/1626	0.83	2/2209 (0.1%)
2	E	0.59	0/318	0.92	0/489
2	F	0.71	0/318	0.98	1/489 (0.2%)
2	G	0.71	0/318	1.01	2/489 (0.4%)
2	H	0.63	0/318	0.96	0/489
2	K	1.03	1/296 (0.3%)	1.29	2/455 (0.4%)
2	L	1.10	0/297	1.40	7/456 (1.5%)
All	All	0.56	1/11588 (0.0%)	0.91	26/16083 (0.2%)

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
2	F	0	1
2	K	0	1
2	L	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	905	DG	C2'-C1'	-5.78	1.46	1.52

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	242	PRO	C-N-CD	-12.21	93.73	120.60
1	J	115	ILE	C-N-CD	-10.49	97.52	120.60
2	L	810	DC	O5'-P-OP2	8.05	120.36	110.70
2	L	810	DC	OP2-P-O3'	7.14	120.90	105.20
2	G	602	DA	O3'-P-O5'	-6.97	90.77	104.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	F	506	DA	Sidechain
2	K	904	DG	Sidechain
2	L	809	DT	Sidechain

## 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	1590	0	1549	192	0
1	B	1569	0	1535	233	0
1	C	1596	0	1554	152	0
1	D	1563	0	1533	194	0
1	I	1576	0	1537	202	0
1	J	1586	0	1548	175	0
2	E	284	0	160	12	0
2	F	284	0	160	18	0
2	G	284	0	160	19	0
2	H	284	0	160	16	0
2	K	264	0	148	14	0
2	L	266	0	148	16	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
All	All	11152	0	10192	1211	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 57.

The worst 5 of 1211 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:176:ARG:HG3	1:B:237:VAL:HG22	1.32	1.10
1:B:163:ILE:O	1:B:249:PHE:HB2	1.56	1.06
1:I:243:PRO:HB2	1:I:246:GLY:HA2	1.36	1.04
1:I:215:ILE:HD13	1:I:215:ILE:H	1.17	1.03
1:J:214:LEU:HD23	1:J:215:ILE:HG13	1.39	1.03

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	201/210 (96%)	162 (81%)	31 (15%)	8 (4%)	4	37
1	B	198/210 (94%)	150 (76%)	35 (18%)	13 (7%)	1	25
1	C	201/210 (96%)	158 (79%)	40 (20%)	3 (2%)	13	58
1	D	197/210 (94%)	152 (77%)	38 (19%)	7 (4%)	4	41
1	I	200/210 (95%)	159 (80%)	33 (16%)	8 (4%)	4	37
1	J	200/210 (95%)	161 (80%)	31 (16%)	8 (4%)	4	37
All	All	1197/1260 (95%)	942 (79%)	208 (17%)	47 (4%)	4	38

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	THR
1	B	170	PRO
1	B	243	PRO

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Mol	Chain	Res	Type
1	B	245	VAL
1	B	248	GLU

### 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	177/186 (95%)	140 (79%)	37 (21%)	1	11
1	B	176/186 (95%)	137 (78%)	39 (22%)	1	10
1	C	178/186 (96%)	145 (82%)	33 (18%)	2	15
1	D	175/186 (94%)	139 (79%)	36 (21%)	1	12
1	I	175/186 (94%)	128 (73%)	47 (27%)	0	5
1	J	177/186 (95%)	130 (73%)	47 (27%)	0	5
All	All	1058/1116 (95%)	819 (77%)	239 (23%)	1	9

5 of 239 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	312	GLN
1	D	255	ASN
1	J	238	VAL
1	D	127	PHE
1	D	183	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	126	HIS
1	C	259	ASN
1	J	213	HIS
1	C	154	GLN
1	C	186	HIS

### 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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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, 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	203/210 (96%)	-0.36	0 100 100	45, 74, 104, 125	3 (1%)
1	B	200/210 (95%)	-0.29	0 100 100	67, 88, 112, 123	1 (0%)
1	C	203/210 (96%)	-0.30	1 (0%) 91 88	50, 77, 103, 123	2 (0%)
1	D	199/210 (94%)	-0.17	3 (1%) 76 66	60, 87, 118, 127	2 (1%)
1	I	202/210 (96%)	-0.30	2 (0%) 84 77	57, 84, 111, 125	2 (0%)
1	J	202/210 (96%)	-0.32	0 100 100	54, 78, 108, 132	2 (0%)
2	E	14/14 (100%)	0.58	2 (14%) 4 4	76, 98, 132, 142	0
2	F	14/14 (100%)	0.00	0 100 100	76, 104, 126, 137	0
2	G	14/14 (100%)	-0.07	0 100 100	74, 102, 142, 159	0
2	H	14/14 (100%)	0.08	0 100 100	76, 100, 140, 151	0
2	K	13/14 (92%)	0.43	0 100 100	81, 103, 122, 137	0
2	L	13/14 (92%)	0.41	1 (7%) 16 11	90, 109, 135, 148	0
All	All	1291/1344 (96%)	-0.26	9 (0%) 89 84	45, 83, 117, 159	12 (0%)

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	136	THR	4.9
1	C	281	ASP	3.4
1	I	137	ALA	3.2
1	D	283	GLN	3.0
1	D	137	ALA	2.8

### 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 [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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	ZN	J	401	1/1	1.00	0.15	-0.48	56,56,56,56	0
3	ZN	B	401	1/1	0.98	0.14	-0.89	89,89,89,89	0
3	ZN	I	401	1/1	0.98	0.07	-1.49	76,76,76,76	0
3	ZN	D	401	1/1	0.97	0.05	-2.08	84,84,84,84	0
3	ZN	C	401	1/1	0.98	0.09	-2.11	58,58,58,58	0
3	ZN	A	401	1/1	0.98	0.08	-	73,73,73,73	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.