



# wwPDB X-ray Structure Validation Summary Report

Sep 2, 2023 – 09:49 PM EDT

PDB ID : 3Q06  
Title : An induced fit mechanism regulates p53 DNA binding kinetics to confer sequence specificity  
Authors : Petty, T.J.; Halazonetis, T.D.  
Deposited on : 2010-12-15  
Resolution : 3.20 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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

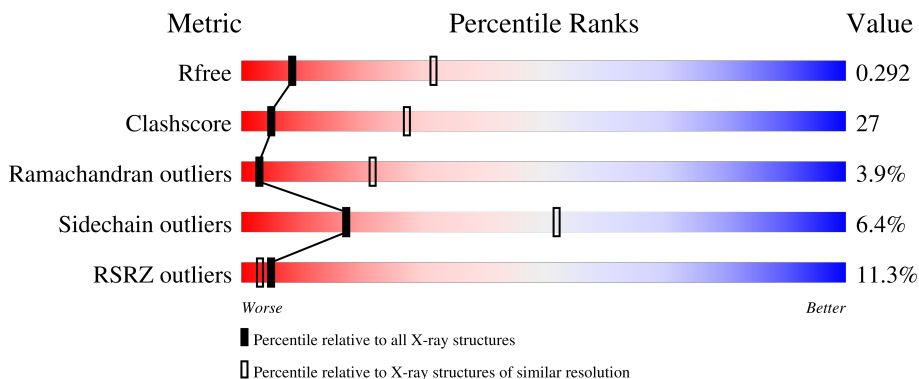
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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  $\geq 3$ , 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	231	
1	B	231	
1	C	231	
1	D	231	
2	K	26	

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Mol	Chain	Length	Quality of chain
3	L	26	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '8%', a green segment in the middle labeled '42%', and a yellow segment on the right labeled '58%'. The segments are stacked horizontally, with the red segment starting from the left edge of the bar.</p>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8456 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 Cellular tumor antigen p53.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	231	1848	1150	337	348	13	0	0	0
1	C	231	1848	1150	337	348	13	0	0	0
1	D	231	1848	1150	337	348	13	0	0	0
1	B	231	1848	1150	337	348	13	0	0	0

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	135	VAL	CYS	engineered mutation	UNP P04637
A	141	VAL	CYS	engineered mutation	UNP P04637
A	146	TYR	TRP	engineered mutation	UNP P04637
A	182	SER	CYS	engineered mutation	UNP P04637
A	203	ALA	VAL	engineered mutation	UNP P04637
A	209	PRO	ARG	engineered mutation	UNP P04637
A	229	TYR	CYS	engineered mutation	UNP P04637
A	233	TYR	HIS	engineered mutation	UNP P04637
A	234	PHE	TYR	engineered mutation	UNP P04637
A	235	LYS	ASN	engineered mutation	UNP P04637
A	236	PHE	TYR	engineered mutation	UNP P04637
A	253	VAL	THR	engineered mutation	UNP P04637
A	268	ASP	ASN	engineered mutation	UNP P04637
A	322	THR	PRO	engineered mutation	UNP P04637
A	323	MET	LEU	engineered mutation	UNP P04637
A	340	GLN	MET	engineered mutation	UNP P04637
A	344	ARG	LEU	engineered mutation	UNP P04637
C	135	VAL	CYS	engineered mutation	UNP P04637
C	141	VAL	CYS	engineered mutation	UNP P04637
C	146	TYR	TRP	engineered mutation	UNP P04637
C	182	SER	CYS	engineered mutation	UNP P04637

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Chain	Residue	Modelled	Actual	Comment	Reference
C	203	ALA	VAL	engineered mutation	UNP P04637
C	209	PRO	ARG	engineered mutation	UNP P04637
C	229	TYR	CYS	engineered mutation	UNP P04637
C	233	TYR	HIS	engineered mutation	UNP P04637
C	234	PHE	TYR	engineered mutation	UNP P04637
C	235	LYS	ASN	engineered mutation	UNP P04637
C	236	PHE	TYR	engineered mutation	UNP P04637
C	253	VAL	THR	engineered mutation	UNP P04637
C	268	ASP	ASN	engineered mutation	UNP P04637
C	322	THR	PRO	engineered mutation	UNP P04637
C	323	MET	LEU	engineered mutation	UNP P04637
C	340	GLN	MET	engineered mutation	UNP P04637
C	344	ARG	LEU	engineered mutation	UNP P04637
D	135	VAL	CYS	engineered mutation	UNP P04637
D	141	VAL	CYS	engineered mutation	UNP P04637
D	146	TYR	TRP	engineered mutation	UNP P04637
D	182	SER	CYS	engineered mutation	UNP P04637
D	203	ALA	VAL	engineered mutation	UNP P04637
D	209	PRO	ARG	engineered mutation	UNP P04637
D	229	TYR	CYS	engineered mutation	UNP P04637
D	233	TYR	HIS	engineered mutation	UNP P04637
D	234	PHE	TYR	engineered mutation	UNP P04637
D	235	LYS	ASN	engineered mutation	UNP P04637
D	236	PHE	TYR	engineered mutation	UNP P04637
D	253	VAL	THR	engineered mutation	UNP P04637
D	268	ASP	ASN	engineered mutation	UNP P04637
D	322	THR	PRO	engineered mutation	UNP P04637
D	323	MET	LEU	engineered mutation	UNP P04637
D	340	GLN	MET	engineered mutation	UNP P04637
D	344	ARG	LEU	engineered mutation	UNP P04637
B	135	VAL	CYS	engineered mutation	UNP P04637
B	141	VAL	CYS	engineered mutation	UNP P04637
B	146	TYR	TRP	engineered mutation	UNP P04637
B	182	SER	CYS	engineered mutation	UNP P04637
B	203	ALA	VAL	engineered mutation	UNP P04637
B	209	PRO	ARG	engineered mutation	UNP P04637
B	229	TYR	CYS	engineered mutation	UNP P04637
B	233	TYR	HIS	engineered mutation	UNP P04637
B	234	PHE	TYR	engineered mutation	UNP P04637
B	235	LYS	ASN	engineered mutation	UNP P04637
B	236	PHE	TYR	engineered mutation	UNP P04637
B	253	VAL	THR	engineered mutation	UNP P04637

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Chain	Residue	Modelled	Actual	Comment	Reference
B	268	ASP	ASN	engineered mutation	UNP P04637
B	322	THR	PRO	engineered mutation	UNP P04637
B	323	MET	LEU	engineered mutation	UNP P04637
B	340	GLN	MET	engineered mutation	UNP P04637
B	344	ARG	LEU	engineered mutation	UNP P04637

- Molecule 2 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	K	26	Total	C	N	O	P	0	0	0
			527	252	96	154	25			

- Molecule 3 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	26	Total	C	N	O	P	0	0	0
			533	254	100	154	25			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	C	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		

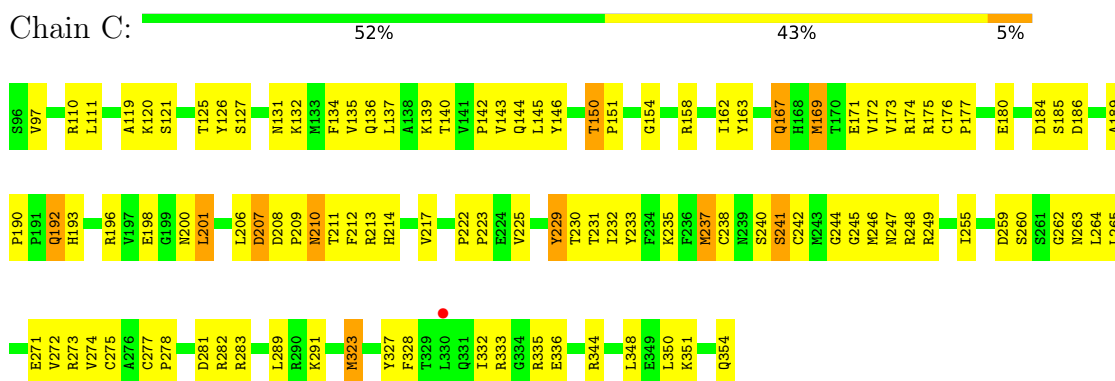
### 3 Residue-property plots [i](#)

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.

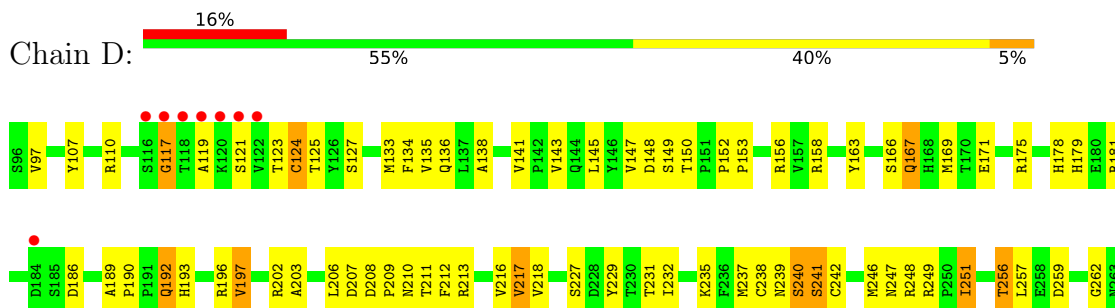
- Molecule 1: Cellular tumor antigen p53

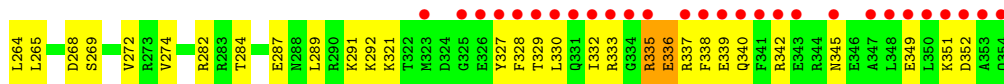


- Molecule 1: Cellular tumor antigen p53

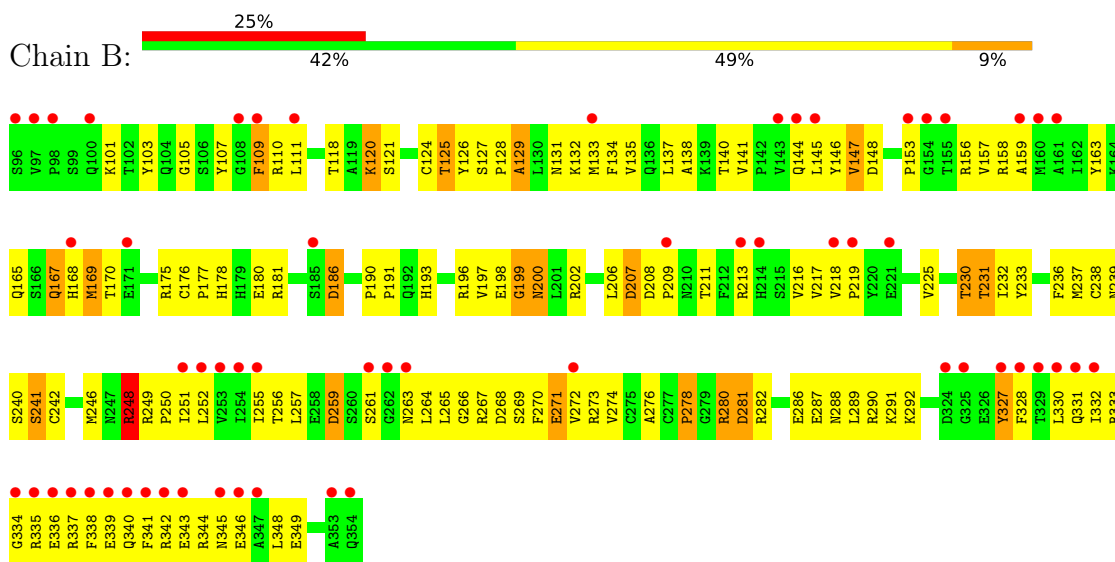


- Molecule 1: Cellular tumor antigen p53

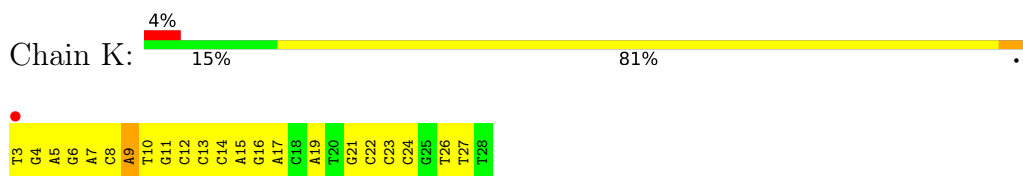




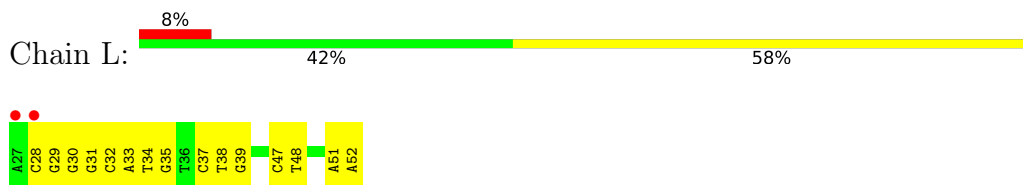
● Molecule 1: Cellular tumor antigen p53



● Molecule 2: DNA (26-MER)



● Molecule 3: DNA (26-MER)





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	164.59Å 169.36Å 55.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.20 46.32 – 3.21	Depositor EDS
% Data completeness (in resolution range)	90.1 (50.00-3.20) 99.2 (46.32-3.21)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.18	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.39 (at 3.19Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.258 , 0.314 0.243 , 0.292	Depositor DCC
$R_{free}$ test set	1296 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	58.0	Xtrriage
Anisotropy	0.579	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 56.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.029 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	8456	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.45% 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:  
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	0.36	0/1888	0.60	0/2549
1	B	0.34	0/1888	0.58	0/2549
1	C	0.46	0/1888	0.71	0/2549
1	D	0.39	0/1888	0.60	0/2549
2	K	0.45	0/590	0.80	2/908 (0.2%)
3	L	0.45	0/598	0.74	0/922
All	All	0.40	0/8740	0.65	2/12026 (0.0%)

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	K	0	2
3	L	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	10	DT	C3'-C2'-C1'	-5.20	96.26	102.50
2	K	10	DT	C1'-O4'-C4'	-5.09	105.00	110.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	K	13	DC	Sidechain
2	K	9	DA	Sidechain
3	L	37	DC	Sidechain

## 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	1848	0	1813	76	0
1	B	1848	0	1815	166	0
1	C	1848	0	1813	92	0
1	D	1848	0	1813	93	0
2	K	527	0	294	24	0
3	L	533	0	294	16	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	8456	0	7842	440	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 27.

The worst 5 of 440 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)
2:K:23:DC:H2''	2:K:24:DC:H5''	1.25	1.13
1:D:330:LEU:HD13	1:B:342:ARG:HG3	1.40	1.03
1:B:131:ASN:HD21	1:B:270:PHE:HA	1.30	0.96
2:K:21:DG:H2''	2:K:22:DC:H5''	1.46	0.93
1:B:147:VAL:HG22	1:B:148:ASP:H	1.34	0.92

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	229/231 (99%)	193 (84%)	30 (13%)	6 (3%)	5 31
1	B	229/231 (99%)	164 (72%)	48 (21%)	17 (7%)	1 7
1	C	229/231 (99%)	187 (82%)	35 (15%)	7 (3%)	4 26
1	D	229/231 (99%)	193 (84%)	30 (13%)	6 (3%)	5 31
All	All	916/924 (99%)	737 (80%)	143 (16%)	36 (4%)	3 22

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	CYS
1	A	241	SER
1	D	124	CYS
1	D	241	SER
1	B	109	PHE

### 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	206/206 (100%)	189 (92%)	17 (8%)	11 40
1	B	206/206 (100%)	197 (96%)	9 (4%)	28 64
1	C	206/206 (100%)	195 (95%)	11 (5%)	22 58
1	D	206/206 (100%)	190 (92%)	16 (8%)	12 43
All	All	824/824 (100%)	771 (94%)	53 (6%)	17 52

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	110	ARG
1	D	202	ARG
1	B	231	THR
1	D	149	SER
1	D	186	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	214	HIS
1	B	144	GLN
1	B	340	GLN
1	B	131	ASN
1	B	167	GLN

### 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](#)

Of 4 ligands modelled in this entry, 4 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

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	231/231 (100%)	0.26	12 (5%) 27 15	7, 33, 117, 126	0
1	B	231/231 (100%)	1.23	58 (25%) 0 0	42, 90, 128, 134	0
1	C	231/231 (100%)	-0.35	1 (0%) 92 89	5, 17, 73, 112	0
1	D	231/231 (100%)	0.56	36 (15%) 2 1	6, 31, 118, 127	0
2	K	26/26 (100%)	0.14	1 (3%) 40 26	10, 46, 102, 114	0
3	L	26/26 (100%)	0.33	2 (7%) 13 7	12, 49, 113, 120	0
All	All	976/976 (100%)	0.42	110 (11%) 5 3	5, 38, 120, 134	0

The worst 5 of 110 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	116	SER	14.3
1	A	121	SER	11.9
1	A	118	THR	11.4
1	A	117	GLY	11.1
1	D	117	GLY	10.5

### 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
4	ZN	B	1	1/1	0.96	0.15	64,64,64,64	0
4	ZN	A	1	1/1	0.97	0.10	17,17,17,17	0
4	ZN	C	1	1/1	0.99	0.18	18,18,18,18	0
4	ZN	D	1	1/1	1.00	0.13	12,12,12,12	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.