



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 11:11 AM UTC

PDB ID : 4MZR / pdb_00004mzr
Title : Crystal structure of a polypeptide p53 mutant bound to DNA
Authors : Emamzadah, S.T.; Tropia, L.; Vincenti, I.; Falquet, B.; Halazonetis, T.D.
Deposited on : 2013-09-30
Resolution : 2.90 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

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>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

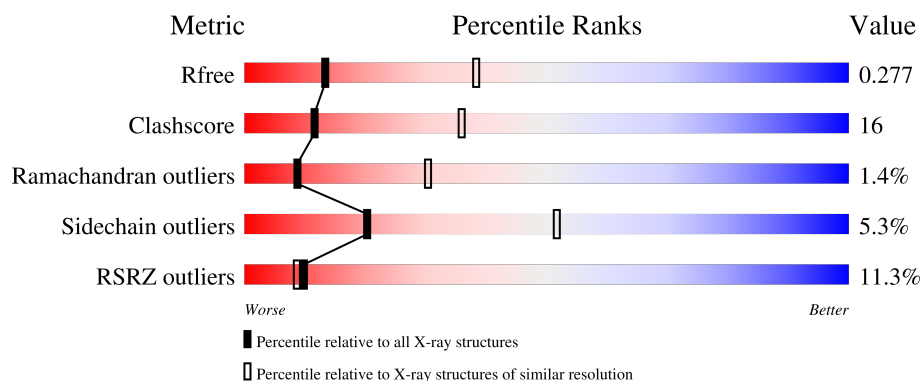
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 $\leq 5\%$. 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	237	
1	B	237	
1	C	237	
1	D	237	
2	K	26	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	L	26	4% 62% 38%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8593 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
1	A	234	Total	C	N	O	S	0	0	0
			1865	1160	339	353	13			
1	B	234	Total	C	N	O	S	0	0	0
			1865	1160	339	353	13			
1	C	234	Total	C	N	O	S	0	0	0
			1865	1160	339	353	13			
1	D	234	Total	C	N	O	S	0	0	0
			1865	1160	339	353	13			

There are 200 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	93	MET	-	initiating methionine	UNP P04637
A	121	PHE	SER	engineered mutation	UNP P04637
A	122	GLY	VAL	engineered mutation	UNP P04637
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	?	-	LYS	deletion	UNP P04637
A	?	-	GLY	deletion	UNP P04637
A	?	-	GLU	deletion	UNP P04637
A	?	-	PRO	deletion	UNP P04637
A	?	-	HIS	deletion	UNP P04637

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	HIS	deletion	UNP P04637
A	?	-	GLU	deletion	UNP P04637
A	?	-	LEU	deletion	UNP P04637
A	?	-	PRO	deletion	UNP P04637
A	?	-	PRO	deletion	UNP P04637
A	?	-	GLY	deletion	UNP P04637
A	?	-	SER	deletion	UNP P04637
A	?	-	THR	deletion	UNP P04637
A	?	-	LYS	deletion	UNP P04637
A	?	-	ARG	deletion	UNP P04637
A	?	-	ALA	deletion	UNP P04637
A	?	-	LEU	deletion	UNP P04637
A	?	-	PRO	deletion	UNP P04637
A	?	-	ASN	deletion	UNP P04637
A	?	-	ASN	deletion	UNP P04637
A	?	-	SER	deletion	UNP P04637
A	?	-	SER	deletion	UNP P04637
A	?	-	SER	deletion	UNP P04637
A	?	-	PRO	deletion	UNP P04637
A	?	-	GLN	deletion	UNP P04637
A	?	-	PRO	deletion	UNP P04637
A	?	-	LYS	deletion	UNP P04637
A	?	-	LYS	deletion	UNP P04637
A	322	THR	PRO	conflict	UNP P04637
A	323	MET	LEU	variant	UNP P04637
A	340	GLN	MET	conflict	UNP P04637
A	344	ARG	LEU	variant	UNP P04637
A	356	THR	GLY	conflict	UNP P04637
A	357	GLU	LYS	conflict	UNP P04637
B	93	MET	-	initiating methionine	UNP P04637
B	121	PHE	SER	engineered mutation	UNP P04637
B	122	GLY	VAL	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

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	236	PHE	TYR	engineered mutation	UNP P04637
B	253	VAL	THR	engineered mutation	UNP P04637
B	268	ASP	ASN	engineered mutation	UNP P04637
B	?	-	GLY	deletion	UNP P04637
B	?	-	GLU	deletion	UNP P04637
B	?	-	PRO	deletion	UNP P04637
B	?	-	HIS	deletion	UNP P04637
B	?	-	HIS	deletion	UNP P04637
B	?	-	GLU	deletion	UNP P04637
B	?	-	LEU	deletion	UNP P04637
B	?	-	PRO	deletion	UNP P04637
B	?	-	PRO	deletion	UNP P04637
B	?	-	GLY	deletion	UNP P04637
B	?	-	SER	deletion	UNP P04637
B	?	-	THR	deletion	UNP P04637
B	?	-	LYS	deletion	UNP P04637
B	?	-	ARG	deletion	UNP P04637
B	?	-	ALA	deletion	UNP P04637
B	?	-	LEU	deletion	UNP P04637
B	?	-	PRO	deletion	UNP P04637
B	?	-	ASN	deletion	UNP P04637
B	?	-	ASN	deletion	UNP P04637
B	?	-	SER	deletion	UNP P04637
B	?	-	SER	deletion	UNP P04637
B	?	-	SER	deletion	UNP P04637
B	?	-	PRO	deletion	UNP P04637
B	?	-	GLN	deletion	UNP P04637
B	?	-	PRO	deletion	UNP P04637
B	?	-	LYS	deletion	UNP P04637
B	?	-	LYS	deletion	UNP P04637
B	?	-	LYS	deletion	UNP P04637
B	?	-	PRO	deletion	UNP P04637
B	323	MET	LEU	variant	UNP P04637
B	340	GLN	MET	conflict	UNP P04637
B	344	ARG	LEU	variant	UNP P04637
B	356	THR	GLY	conflict	UNP P04637
B	357	GLU	LYS	conflict	UNP P04637
C	93	MET	-	initiating methionine	UNP P04637
C	121	PHE	SER	engineered mutation	UNP P04637
C	122	GLY	VAL	engineered mutation	UNP P04637
C	135	VAL	CYS	engineered mutation	UNP P04637
C	141	VAL	CYS	engineered mutation	UNP P04637

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	146	TYR	TRP	engineered mutation	UNP P04637
C	182	SER	CYS	engineered mutation	UNP P04637
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	conflict	UNP P04637
C	268	ASP	ASN	conflict	UNP P04637
C	?	-	GLY	deletion	UNP P04637
C	?	-	GLU	deletion	UNP P04637
C	?	-	PRO	deletion	UNP P04637
C	?	-	HIS	deletion	UNP P04637
C	?	-	HIS	deletion	UNP P04637
C	?	-	GLU	deletion	UNP P04637
C	?	-	LEU	deletion	UNP P04637
C	?	-	PRO	deletion	UNP P04637
C	?	-	PRO	deletion	UNP P04637
C	?	-	GLY	deletion	UNP P04637
C	?	-	SER	deletion	UNP P04637
C	?	-	THR	deletion	UNP P04637
C	?	-	LYS	deletion	UNP P04637
C	?	-	ARG	deletion	UNP P04637
C	?	-	ALA	deletion	UNP P04637
C	?	-	LEU	deletion	UNP P04637
C	?	-	PRO	deletion	UNP P04637
C	?	-	ASN	deletion	UNP P04637
C	?	-	ASN	deletion	UNP P04637
C	?	-	SER	deletion	UNP P04637
C	?	-	SER	deletion	UNP P04637
C	?	-	SER	deletion	UNP P04637
C	?	-	PRO	deletion	UNP P04637
C	?	-	GLN	deletion	UNP P04637
C	?	-	PRO	deletion	UNP P04637
C	?	-	LYS	deletion	UNP P04637
C	?	-	LYS	deletion	UNP P04637
C	?	-	LYS	deletion	UNP P04637
C	?	-	PRO	deletion	UNP P04637
C	323	MET	LEU	variant	UNP P04637
C	340	GLN	MET	conflict	UNP P04637

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	344	ARG	LEU	variant	UNP P04637
C	356	THR	GLY	conflict	UNP P04637
C	357	GLU	LYS	conflict	UNP P04637
D	93	MET	-	initiating methionine	UNP P04637
D	121	PHE	SER	engineered mutation	UNP P04637
D	122	GLY	VAL	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	?	-	GLY	deletion	UNP P04637
D	?	-	GLU	deletion	UNP P04637
D	?	-	PRO	deletion	UNP P04637
D	?	-	HIS	deletion	UNP P04637
D	?	-	HIS	deletion	UNP P04637
D	?	-	GLU	deletion	UNP P04637
D	?	-	LEU	deletion	UNP P04637
D	?	-	PRO	deletion	UNP P04637
D	?	-	PRO	deletion	UNP P04637
D	?	-	GLY	deletion	UNP P04637
D	?	-	SER	deletion	UNP P04637
D	?	-	THR	deletion	UNP P04637
D	?	-	LYS	deletion	UNP P04637
D	?	-	ARG	deletion	UNP P04637
D	?	-	ALA	deletion	UNP P04637
D	?	-	LEU	deletion	UNP P04637
D	?	-	PRO	deletion	UNP P04637
D	?	-	ASN	deletion	UNP P04637
D	?	-	ASN	deletion	UNP P04637
D	?	-	SER	deletion	UNP P04637
D	?	-	SER	deletion	UNP P04637
D	?	-	SER	deletion	UNP P04637
D	?	-	PRO	deletion	UNP P04637

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	GLN	deletion	UNP P04637
D	?	-	PRO	deletion	UNP P04637
D	?	-	LYS	deletion	UNP P04637
D	?	-	LYS	deletion	UNP P04637
D	?	-	LYS	deletion	UNP P04637
D	?	-	PRO	deletion	UNP P04637
D	323	MET	LEU	variant	UNP P04637
D	340	GLN	MET	conflict	UNP P04637
D	344	ARG	LEU	variant	UNP P04637
D	356	THR	GLY	conflict	UNP P04637
D	357	GLU	LYS	conflict	UNP P04637

- Molecule 2 is a DNA chain called consensus DNA sense strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	K	26	Total	C	N	O	P	0	0	0
			525	252	90	158	25			

- Molecule 3 is a DNA chain called consensus DNA anti-sense strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	26	Total	C	N	O	P	0	0	0
			535	254	106	150	25			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	15	Total	O	0	0
			15	15		

Continued on next page...

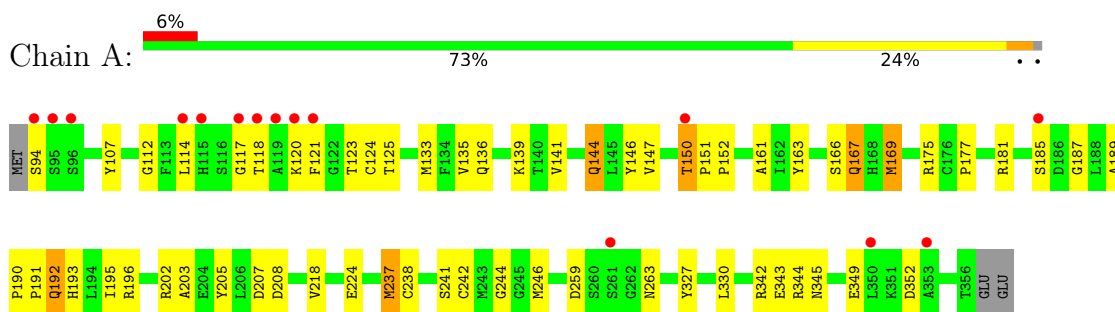
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total 1	O 1	0	0
5	C	31	Total 31	O 31	0	0
5	D	21	Total 21	O 21	0	0
5	L	1	Total 1	O 1	0	0

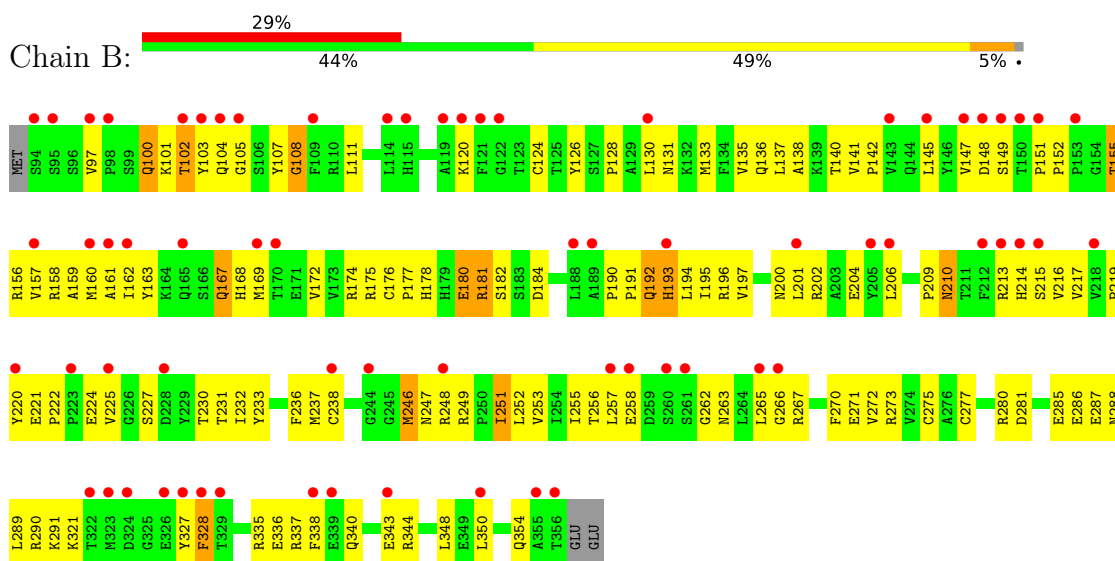
3 Residue-property plots [i](#)

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.

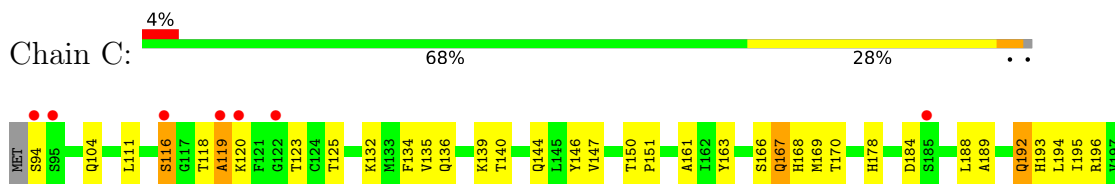
• Molecule 1: Cellular tumor antigen p53

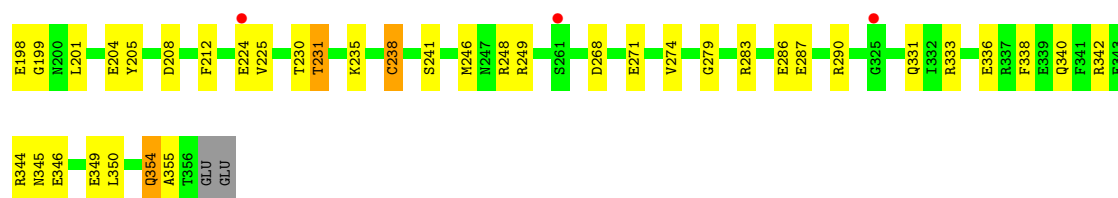


• Molecule 1: Cellular tumor antigen p53

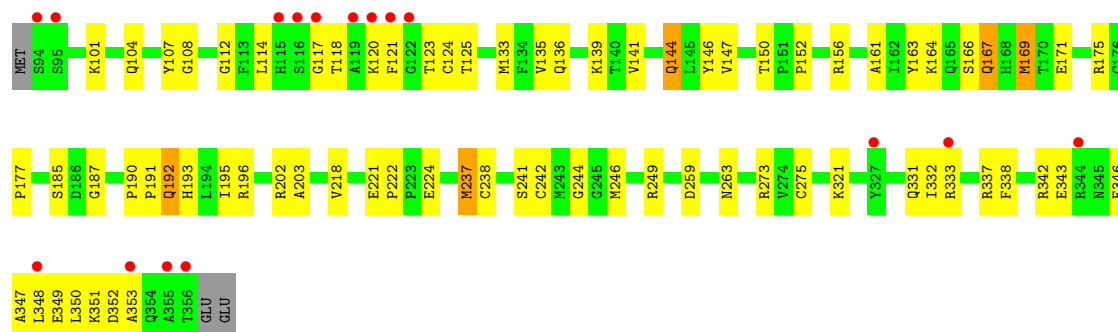


• Molecule 1: Cellular tumor antigen p53

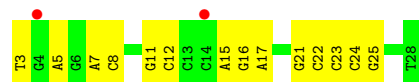




● Molecule 1: Cellular tumor antigen p53



● Molecule 2: consensus DNA sense strand



● Molecule 3: consensus DNA anti-sense strand



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	163.30Å 169.76Å 55.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.00 – 2.90 80.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (80.00-2.90) 92.2 (80.00-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 2.91Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.234 , 0.281 0.233 , 0.277	Depositor DCC
R_{free} test set	1618 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	61.2	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 53.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.022 for k,h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8593	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.72% 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 [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	0.39	0/1906	0.88	4/2574 (0.2%)
1	B	0.37	0/1906	0.79	0/2574
1	C	0.48	0/1906	0.88	1/2574 (0.0%)
1	D	0.40	0/1906	0.86	4/2574 (0.2%)
2	K	0.31	0/586	0.76	0/902
3	L	0.30	0/602	0.69	0/928
All	All	0.40	0/8812	0.84	9/12126 (0.1%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	150	THR	CA-C-N	8.16	125.54	119.66
1	A	150	THR	C-N-CA	8.16	125.54	119.66
1	D	237	MET	N-CA-C	5.84	119.16	112.97
1	A	237	MET	N-CA-C	5.77	119.09	112.97
1	A	244	GLY	N-CA-C	-5.71	108.29	115.08

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	1865	0	1820	46	0
1	B	1865	0	1821	117	0
1	C	1865	0	1820	47	0
1	D	1865	0	1820	53	0
2	K	525	0	296	11	0
3	L	535	0	292	14	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
5	A	15	0	0	0	0
5	B	1	0	0	0	0
5	C	31	0	0	0	0
5	D	21	0	0	1	0
5	L	1	0	0	0	0
All	All	8593	0	7869	262	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 16.

The worst 5 of 262 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:D:192:GLN:H	1:D:192:GLN:HE21	1.08	0.99
1:B:327:TYR:HB3	1:D:331:GLN:HB3	1.43	0.99
3:L:27:DA:H4'	3:L:28:DC:H5'	1.44	0.98
3:L:33:DA:H2''	3:L:34:DA:H5''	1.47	0.97
1:A:192:GLN:H	1:A:192:GLN:HE21	1.08	0.94

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	232/237 (98%)	219 (94%)	13 (6%)	0	100	100
1	B	232/237 (98%)	184 (79%)	38 (16%)	10 (4%)	2	8
1	C	232/237 (98%)	210 (90%)	20 (9%)	2 (1%)	14	41
1	D	232/237 (98%)	212 (91%)	19 (8%)	1 (0%)	30	59
All	All	928/948 (98%)	825 (89%)	90 (10%)	13 (1%)	9	30

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	148	ASP
1	C	355	ALA
1	B	102	THR
1	B	182	SER
1	B	263	ASN

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	207/210 (99%)	197 (95%)	10 (5%)	23	55
1	B	207/210 (99%)	195 (94%)	12 (6%)	18	49
1	C	207/210 (99%)	194 (94%)	13 (6%)	16	45
1	D	207/210 (99%)	198 (96%)	9 (4%)	26	60
All	All	828/840 (99%)	784 (95%)	44 (5%)	20	52

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

Mol	Chain	Res	Type
1	C	201	LEU
1	D	125	THR
1	C	204	GLU
1	C	331	GLN
1	D	167	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	136	GLN
1	D	144	GLN
1	B	168	HIS
1	B	167	GLN
1	D	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 oligosaccharides 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 [i](#)

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, 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	234/237 (98%)	0.36	15 (6%) 25 20	27, 49, 95, 95	0
1	B	234/237 (98%)	1.60	68 (29%) 1 1	63, 95, 95, 95	0
1	C	234/237 (98%)	0.05	10 (4%) 40 31	20, 39, 90, 95	0
1	D	234/237 (98%)	0.53	16 (6%) 23 18	30, 48, 95, 95	0
2	K	26/26 (100%)	0.65	2 (7%) 19 16	36, 59, 87, 93	0
3	L	26/26 (100%)	0.65	1 (3%) 44 36	44, 64, 86, 90	0
All	All	988/1000 (98%)	0.64	112 (11%) 10 9	20, 55, 95, 95	0

The worst 5 of 112 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	213	ARG	5.6
1	C	120	LYS	5.3
1	B	119	ALA	5.1
1	D	121	PHE	4.5
1	B	329	THR	4.5

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 oligosaccharides 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, 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
4	ZN	B	401	1/1	0.97	0.09	82,82,82,82	0
4	ZN	A	401	1/1	0.99	0.08	49,49,49,49	0
4	ZN	C	401	1/1	0.99	0.06	35,35,35,35	0
4	ZN	D	401	1/1	0.99	0.09	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.