



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:15 PM UTC

PDB ID : 5A97 / pdb_00005a97
Title : Hazara virus nucleocapsid protein
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Deposited on : 2015-07-17
Resolution : 2.70 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

<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

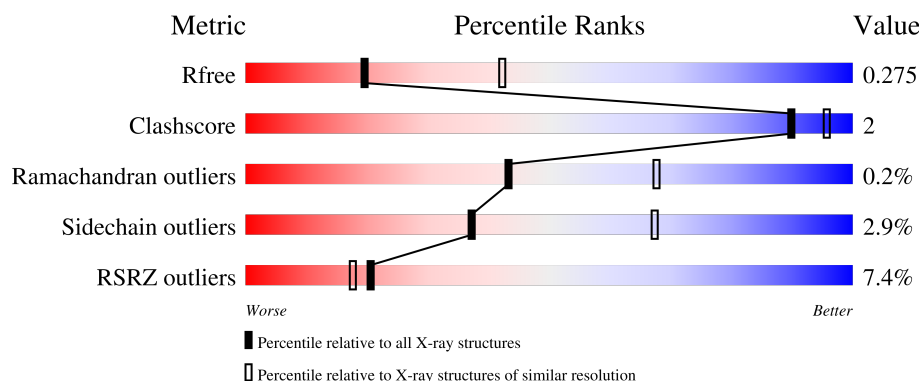
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	489	21% 92% 5% .
1	B	489	2% 92% 6% .
1	C	489	4% 92% 6% .
1	D	489	2% 92% 5% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15226 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 NUCLEOCAPSID PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	473	Total	C	N	O	S	0	3	0
			3760	2393	641	708	18			
1	B	477	Total	C	N	O	S	0	6	0
			3800	2416	648	718	18			
1	C	479	Total	C	N	O	S	0	5	0
			3808	2421	653	716	18			
1	D	477	Total	C	N	O	S	0	4	0
			3788	2408	648	714	18			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	PRO	-	expression tag	UNP M4PWE6
A	-2	LEU	-	expression tag	UNP M4PWE6
A	-1	GLY	-	expression tag	UNP M4PWE6
A	0	SER	-	expression tag	UNP M4PWE6
B	-3	PRO	-	expression tag	UNP M4PWE6
B	-2	LEU	-	expression tag	UNP M4PWE6
B	-1	GLY	-	expression tag	UNP M4PWE6
B	0	SER	-	expression tag	UNP M4PWE6
C	-3	PRO	-	expression tag	UNP M4PWE6
C	-2	LEU	-	expression tag	UNP M4PWE6
C	-1	GLY	-	expression tag	UNP M4PWE6
C	0	SER	-	expression tag	UNP M4PWE6
D	-3	PRO	-	expression tag	UNP M4PWE6
D	-2	LEU	-	expression tag	UNP M4PWE6
D	-1	GLY	-	expression tag	UNP M4PWE6
D	0	SER	-	expression tag	UNP M4PWE6

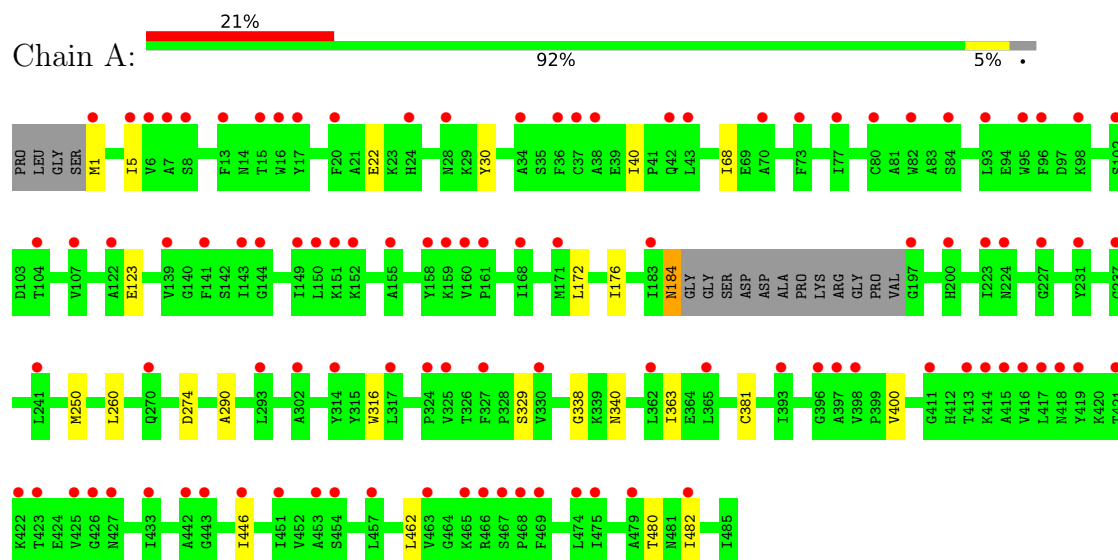
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	6	Total 6	O 6	0	0
2	B	26	Total 26	O 26	0	0
2	C	24	Total 24	O 24	0	0
2	D	14	Total 14	O 14	0	0

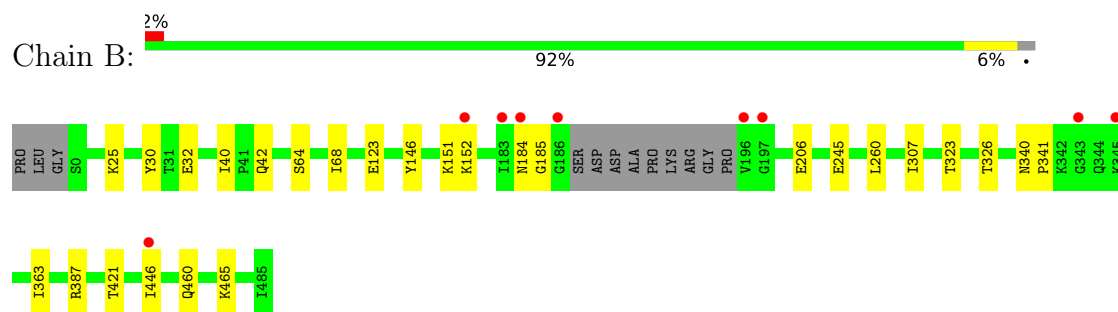
3 Residue-property plots [i](#)

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.

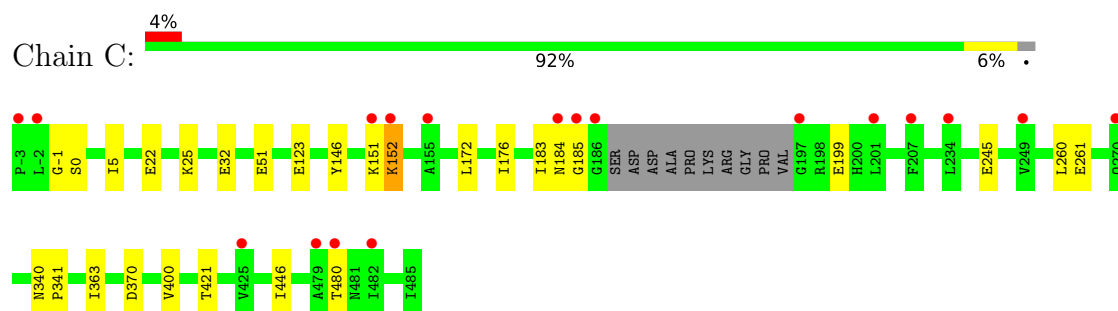
• Molecule 1: NUCLEOCAPSID PROTEIN



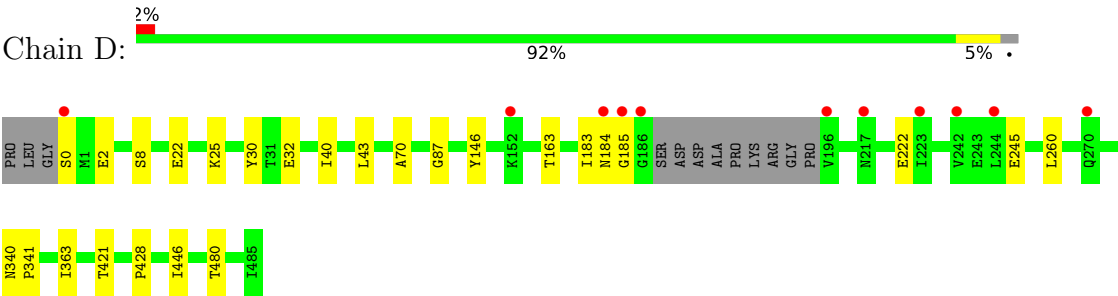
• Molecule 1: NUCLEOCAPSID PROTEIN



• Molecule 1: NUCLEOCAPSID PROTEIN



● Molecule 1: NUCLEOCAPSID PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.99Å 76.10Å 449.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	224.64 – 2.70 224.64 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (224.64-2.70) 98.5 (224.64-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0124	Depositor
R, R_{free}	0.242 , 0.282 (Not available) , 0.275	Depositor DCC
R_{free} test set	3135 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	63.2	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15226	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% 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](#)

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	0.58	0/3842	0.83	0/5185
1	B	0.55	0/3885	0.83	0/5242
1	C	0.57	0/3891	0.86	1/5249 (0.0%)
1	D	0.57	0/3867	0.85	0/5218
All	All	0.57	0/15485	0.84	1/20894 (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
1	C	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	0	SER	N-CA-C	-5.23	102.74	110.48

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	-1	GLY	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	3760	0	3760	8	0
1	B	3800	0	3796	21	0
1	C	3808	0	3809	13	0
1	D	3788	0	3784	13	0
2	A	6	0	0	0	0
2	B	26	0	0	0	0
2	C	24	0	0	0	0
2	D	14	0	0	0	0
All	All	15226	0	15149	55	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 2.

All (55) 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:184[B]:ASN:CB	1:B:185[B]:GLY:HA3	1.27	1.47
1:C:184[B]:ASN:CB	1:C:185[B]:GLY:HA3	1.31	1.42
1:D:184[B]:ASN:CB	1:D:185[B]:GLY:HA3	1.21	1.42
1:D:184[B]:ASN:CB	1:D:185[B]:GLY:CA	2.11	1.29
1:D:184[B]:ASN:HB2	1:D:185[B]:GLY:CA	1.66	1.21
1:B:184[B]:ASN:CB	1:B:185[B]:GLY:CA	2.17	1.20
1:C:184[B]:ASN:HB3	1:C:185[B]:GLY:CA	1.73	1.19
1:C:184[B]:ASN:CB	1:C:185[B]:GLY:CA	2.21	1.17
1:D:184[B]:ASN:HB3	1:D:185[B]:GLY:HA3	1.21	1.16
1:C:184[B]:ASN:HB2	1:C:185[B]:GLY:HA3	1.26	1.10
1:B:184[B]:ASN:HB3	1:B:185[B]:GLY:HA3	1.09	1.09
1:B:184[B]:ASN:HB2	1:B:185[B]:GLY:CA	1.80	1.05
1:B:184[B]:ASN:HB2	1:B:185[B]:GLY:HA3	1.03	1.01
1:C:184[B]:ASN:HB3	1:C:185[B]:GLY:HA3	0.92	0.91
1:D:184[B]:ASN:HB3	1:D:185[B]:GLY:CA	1.90	0.89
1:B:184[B]:ASN:HB3	1:B:185[B]:GLY:CA	1.89	0.89
1:C:151[B]:LYS:O	1:C:152[B]:LYS:HB2	1.70	0.89
1:D:184[B]:ASN:HB2	1:D:185[B]:GLY:HA3	0.82	0.81
1:C:151[B]:LYS:O	1:C:152[B]:LYS:CB	2.29	0.79
1:B:206[B]:GLU:HA	1:B:206[B]:GLU:OE1	1.84	0.78
1:B:151[B]:LYS:O	1:B:152[B]:LYS:CB	2.40	0.69
1:C:184[B]:ASN:HB2	1:C:185[B]:GLY:CA	2.05	0.67
1:B:151[B]:LYS:O	1:B:152[B]:LYS:HB2	1.93	0.66
1:B:151[B]:LYS:H	1:B:152[B]:LYS:HE3	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151[B]:LYS:C	1:B:152[B]:LYS:HG3	2.25	0.61
1:B:151[B]:LYS:C	1:B:152[B]:LYS:CG	2.76	0.57
1:D:43:LEU:HD11	1:D:70:ALA:HB2	1.88	0.55
1:A:5:ILE:HD12	1:A:400:VAL:HG12	1.89	0.55
1:B:30:TYR:CD1	1:B:40:ILE:HD11	2.45	0.52
1:B:307:ILE:HD11	1:B:387:ARG:NE	2.28	0.49
1:B:206[B]:GLU:OE1	1:B:206[B]:GLU:CA	2.58	0.48
1:D:183:ILE:O	1:D:184[A]:ASN:HB2	2.13	0.48
1:D:8:SER:HA	1:D:87:GLY:HA3	1.95	0.48
1:B:64:SER:O	1:B:68:ILE:HG12	2.15	0.47
1:A:316:TRP:NE1	1:A:381:CYS:O	2.46	0.46
1:C:5:ILE:HD12	1:C:400:VAL:HG12	1.98	0.45
1:B:323:THR:H	1:B:326:THR:HG1	1.64	0.45
1:D:32:GLU:HG3	1:D:146:TYR:OH	2.17	0.44
1:D:30:TYR:CD1	1:D:40:ILE:HD11	2.52	0.44
1:A:172:LEU:O	1:A:176:ILE:HG12	2.18	0.44
1:B:460:GLN:HE21	1:B:465:LYS:HE2	1.82	0.43
1:C:151[B]:LYS:O	1:C:152[B]:LYS:CG	2.65	0.43
1:D:40:ILE:HD12	1:D:428:PRO:HB3	2.01	0.43
1:A:30:TYR:CD1	1:A:40:ILE:HD11	2.54	0.43
1:D:184[A]:ASN:HA	1:D:185[A]:GLY:HA2	1.59	0.42
1:A:462:LEU:HD22	1:A:482:ILE:HG21	2.02	0.41
1:C:183:ILE:O	1:C:184[A]:ASN:HB2	2.20	0.41
1:B:32:GLU:HG3	1:B:146:TYR:OH	2.20	0.41
1:C:32:GLU:HG3	1:C:146:TYR:CZ	2.56	0.41
1:A:184:ASN:C	1:A:184:ASN:HD22	2.27	0.41
1:A:250:MET:HE1	1:A:290:ALA:HB3	2.03	0.41
1:B:151[B]:LYS:O	1:B:152[B]:LYS:CG	2.69	0.41
1:C:172:LEU:O	1:C:176:ILE:HG12	2.21	0.40
1:B:32:GLU:HG3	1:B:146:TYR:CZ	2.55	0.40
1:A:68:ILE:HD12	1:A:338:GLY:O	2.22	0.40

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	472/489 (96%)	464 (98%)	8 (2%)	0	100	100
1	B	479/489 (98%)	462 (96%)	16 (3%)	1 (0%)	43	68
1	C	480/489 (98%)	468 (98%)	9 (2%)	3 (1%)	21	44
1	D	477/489 (98%)	464 (97%)	12 (2%)	1 (0%)	43	68
All	All	1908/1956 (98%)	1858 (97%)	45 (2%)	5 (0%)	43	60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	152[A]	LYS
1	C	152[B]	LYS
1	C	341	PRO
1	B	341	PRO
1	D	341	PRO

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	401/409 (98%)	389 (97%)	12 (3%)	36	66
1	B	405/409 (99%)	395 (98%)	10 (2%)	42	71
1	C	405/409 (99%)	391 (96%)	14 (4%)	32	61
1	D	403/409 (98%)	390 (97%)	13 (3%)	34	64
All	All	1614/1636 (99%)	1565 (97%)	49 (3%)	37	66

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	22	GLU
1	A	123	GLU

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Mol	Chain	Res	Type
1	A	184	ASN
1	A	260	LEU
1	A	274[A]	ASP
1	A	274[B]	ASP
1	A	329	SER
1	A	340	ASN
1	A	363	ILE
1	A	446	ILE
1	A	480	THR
1	B	25	LYS
1	B	42	GLN
1	B	123[A]	GLU
1	B	123[B]	GLU
1	B	245	GLU
1	B	260	LEU
1	B	340	ASN
1	B	363	ILE
1	B	421	THR
1	B	446	ILE
1	C	22	GLU
1	C	25	LYS
1	C	51	GLU
1	C	123	GLU
1	C	199	GLU
1	C	245	GLU
1	C	260	LEU
1	C	261	GLU
1	C	340	ASN
1	C	363	ILE
1	C	370	ASP
1	C	421	THR
1	C	446	ILE
1	C	480	THR
1	D	0	SER
1	D	2	GLU
1	D	22	GLU
1	D	25	LYS
1	D	163	THR
1	D	222	GLU
1	D	245	GLU
1	D	260	LEU
1	D	340	ASN

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Mol	Chain	Res	Type
1	D	363	ILE
1	D	421	THR
1	D	446	ILE
1	D	480	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	166	ASN
1	A	184	ASN
1	A	200	HIS
1	A	344	GLN
1	A	348	GLN
1	A	460	GLN
1	A	471	ASN
1	B	42	GLN
1	B	57	ASN
1	B	111	ASN
1	B	166	ASN
1	B	259	GLN
1	B	348	GLN
1	B	412	HIS
1	B	460	GLN
1	C	57	ASN
1	C	270	GLN
1	C	344	GLN
1	C	348	GLN
1	C	369	ASN
1	D	57	ASN
1	D	129	GLN
1	D	166	ASN
1	D	200	HIS
1	D	340	ASN
1	D	344	GLN
1	D	348	GLN
1	D	460	GLN

5.3.3 RNA ⓘ

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](#)

There are no ligands in this entry.

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	473/489 (96%)	1.32	103 (21%) 2 2	52, 135, 191, 246	3 (0%)
1	B	477/489 (97%)	0.03	9 (1%) 66 63	32, 61, 86, 144	6 (1%)
1	C	479/489 (97%)	0.17	18 (3%) 44 40	25, 62, 110, 140	5 (1%)
1	D	477/489 (97%)	0.24	11 (2%) 61 58	35, 70, 120, 147	4 (0%)
All	All	1906/1956 (97%)	0.44	141 (7%) 20 18	25, 72, 162, 246	18 (0%)

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	416	VAL	6.4
1	C	152[A]	LYS	6.2
1	B	186	GLY	4.9
1	C	186	GLY	4.7
1	A	419	TYR	4.7
1	A	415	ALA	4.6
1	A	398	VAL	4.5
1	D	186	GLY	4.3
1	A	417	LEU	4.0
1	B	196	VAL	3.9
1	C	-2	LEU	3.9
1	A	152[A]	LYS	3.8
1	A	397	ALA	3.7
1	B	152[A]	LYS	3.7
1	A	327	PHE	3.6
1	A	453	ALA	3.6
1	A	479	ALA	3.5
1	D	152[A]	LYS	3.5
1	A	200	HIS	3.5
1	A	197	GLY	3.5
1	D	196	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	414	LYS	3.4
1	A	422	LYS	3.4
1	A	158	TYR	3.3
1	A	36	PHE	3.3
1	A	330	VAL	3.3
1	C	-3	PRO	3.2
1	C	185[A]	GLY	3.2
1	C	184[A]	ASN	3.1
1	A	5	ILE	3.1
1	D	217	ASN	3.1
1	A	151[A]	LYS	3.0
1	A	96	PHE	3.0
1	A	141	PHE	3.0
1	C	480	THR	3.0
1	A	442	ALA	3.0
1	A	418	ASN	2.9
1	A	150	LEU	2.9
1	A	159	LYS	2.9
1	C	270	GLN	2.8
1	A	425	VAL	2.8
1	A	107	VAL	2.8
1	A	423	THR	2.8
1	C	155	ALA	2.7
1	C	479	ALA	2.7
1	D	244	LEU	2.7
1	D	223	ILE	2.7
1	A	171	MET	2.7
1	A	17	TYR	2.7
1	A	139	VAL	2.7
1	A	227	GLY	2.6
1	A	270	GLN	2.6
1	A	482	ILE	2.6
1	C	482	ILE	2.6
1	A	160	VAL	2.6
1	A	95	TRP	2.6
1	D	0	SER	2.6
1	A	454	SER	2.5
1	A	43	LEU	2.5
1	A	15	THR	2.5
1	B	446	ILE	2.5
1	A	474	LEU	2.5
1	A	82	TRP	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	393	ILE	2.5
1	A	93	LEU	2.5
1	B	343	GLY	2.5
1	A	20	PHE	2.5
1	A	122	ALA	2.5
1	A	16	TRP	2.4
1	A	80	CYS	2.4
1	C	207	PHE	2.4
1	A	37	CYS	2.4
1	A	144	GLY	2.4
1	A	325	VAL	2.4
1	A	7	ALA	2.4
1	C	151[A]	LYS	2.4
1	A	468	PRO	2.4
1	A	314	TYR	2.3
1	A	362	LEU	2.3
1	A	77	ILE	2.3
1	A	324	PRO	2.3
1	A	426	GLY	2.3
1	C	425	VAL	2.3
1	A	84	SER	2.3
1	A	34	ALA	2.3
1	A	302	ALA	2.3
1	A	98	LYS	2.3
1	A	8	SER	2.3
1	B	197	GLY	2.3
1	A	463	VAL	2.3
1	D	242	VAL	2.3
1	A	293	LEU	2.3
1	A	155	ALA	2.3
1	A	413	THR	2.3
1	A	6	VAL	2.3
1	A	475	ILE	2.2
1	A	143	ILE	2.2
1	A	446	ILE	2.2
1	A	465	LYS	2.2
1	A	421	THR	2.2
1	A	161	PRO	2.2
1	A	42	GLN	2.2
1	D	270	GLN	2.2
1	A	443	GLY	2.2
1	A	467	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	317	LEU	2.2
1	C	197	GLY	2.2
1	A	168	ILE	2.2
1	A	451	ILE	2.2
1	A	411	GLY	2.2
1	D	185[A]	GLY	2.2
1	A	102	SER	2.2
1	A	13	PHE	2.2
1	A	38	ALA	2.1
1	A	104	THR	2.1
1	A	466	ARG	2.1
1	B	184[A]	ASN	2.1
1	A	457	LEU	2.1
1	A	237	GLY	2.1
1	A	73	PHE	2.1
1	A	469	PHE	2.1
1	A	70	ALA	2.1
1	B	345	LYS	2.1
1	A	1	MET	2.1
1	A	224	ASN	2.1
1	D	184[A]	ASN	2.1
1	A	433	ILE	2.1
1	C	249	VAL	2.1
1	A	231	TYR	2.1
1	A	241	LEU	2.0
1	C	201	LEU	2.0
1	A	28	ASN	2.0
1	A	427	ASN	2.0
1	A	365	LEU	2.0
1	C	234	LEU	2.0
1	A	24	HIS	2.0
1	A	149	ILE	2.0
1	A	183	ILE	2.0
1	A	223	ILE	2.0
1	A	396	GLY	2.0
1	B	183	ILE	2.0

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.