



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:23 PM UTC

PDB ID : 3R3L / pdb_00003r3l
Title : Structure of NP protein from Lassa AV strain
Authors : Perbandt, M.; Brunotte, L.; Gunther, S.; Betzel, C.
Deposited on : 2011-03-16
Resolution : 2.45 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

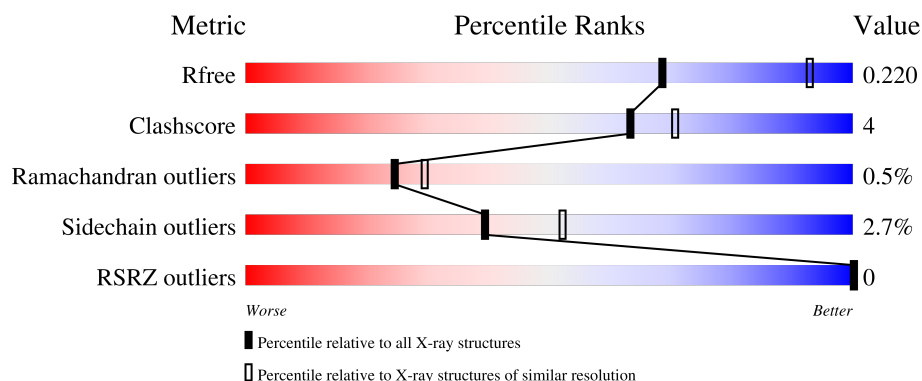
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	2340 (2.46-2.42)
Clashscore	190562	2400 (2.46-2.42)
Ramachandran outliers	187476	2379 (2.46-2.42)
Sidechain outliers	187428	2379 (2.46-2.42)
RSRZ outliers	180081	2340 (2.46-2.42)

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	582	
1	B	582	
1	C	582	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12140 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 Nucleoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	513	Total	C	N	O	S	0	0	0
			4009	2522	698	763	26			
1	B	514	Total	C	N	O	S	0	0	0
			4018	2528	700	764	26			
1	C	510	Total	C	N	O	S	0	0	0
			3986	2508	694	758	26			

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	570	ASP	-	expression tag	UNP Q9DQX7
A	571	TYR	-	expression tag	UNP Q9DQX7
A	572	LYS	-	expression tag	UNP Q9DQX7
A	573	ASP	-	expression tag	UNP Q9DQX7
A	574	HIS	-	expression tag	UNP Q9DQX7
A	575	ASP	-	expression tag	UNP Q9DQX7
A	576	GLY	-	expression tag	UNP Q9DQX7
A	577	HIS	-	expression tag	UNP Q9DQX7
A	578	HIS	-	expression tag	UNP Q9DQX7
A	579	HIS	-	expression tag	UNP Q9DQX7
A	580	HIS	-	expression tag	UNP Q9DQX7
A	581	HIS	-	expression tag	UNP Q9DQX7
A	582	HIS	-	expression tag	UNP Q9DQX7
B	570	ASP	-	expression tag	UNP Q9DQX7
B	571	TYR	-	expression tag	UNP Q9DQX7
B	572	LYS	-	expression tag	UNP Q9DQX7
B	573	ASP	-	expression tag	UNP Q9DQX7
B	574	HIS	-	expression tag	UNP Q9DQX7
B	575	ASP	-	expression tag	UNP Q9DQX7
B	576	GLY	-	expression tag	UNP Q9DQX7
B	577	HIS	-	expression tag	UNP Q9DQX7
B	578	HIS	-	expression tag	UNP Q9DQX7
B	579	HIS	-	expression tag	UNP Q9DQX7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	580	HIS	-	expression tag	UNP Q9DQX7
B	581	HIS	-	expression tag	UNP Q9DQX7
B	582	HIS	-	expression tag	UNP Q9DQX7
C	570	ASP	-	expression tag	UNP Q9DQX7
C	571	TYR	-	expression tag	UNP Q9DQX7
C	572	LYS	-	expression tag	UNP Q9DQX7
C	573	ASP	-	expression tag	UNP Q9DQX7
C	574	HIS	-	expression tag	UNP Q9DQX7
C	575	ASP	-	expression tag	UNP Q9DQX7
C	576	GLY	-	expression tag	UNP Q9DQX7
C	577	HIS	-	expression tag	UNP Q9DQX7
C	578	HIS	-	expression tag	UNP Q9DQX7
C	579	HIS	-	expression tag	UNP Q9DQX7
C	580	HIS	-	expression tag	UNP Q9DQX7
C	581	HIS	-	expression tag	UNP Q9DQX7
C	582	HIS	-	expression tag	UNP Q9DQX7

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mn 2 2	0	0
2	B	2	Total Mn 2 2	0	0
2	C	1	Total Mn 1 1	0	0

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	41	Total O 41 41	0	0

Continued on next page...

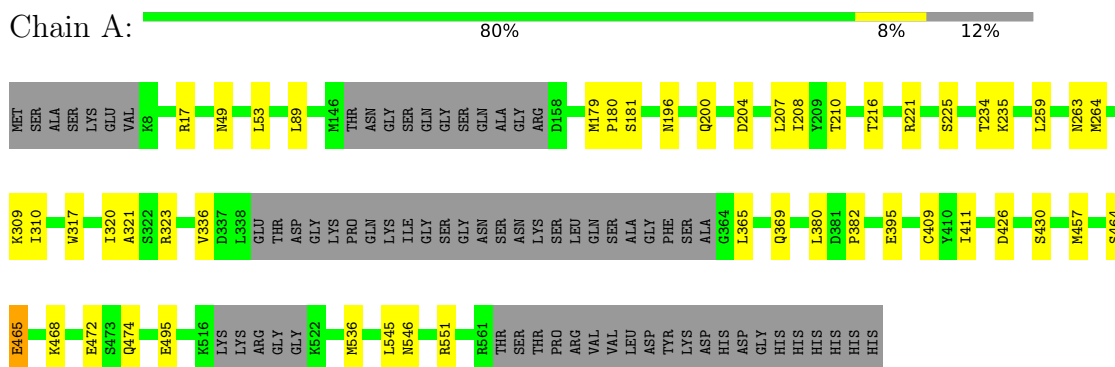
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	48	Total 48	O 48	0	0
4	C	30	Total 30	O 30	0	0

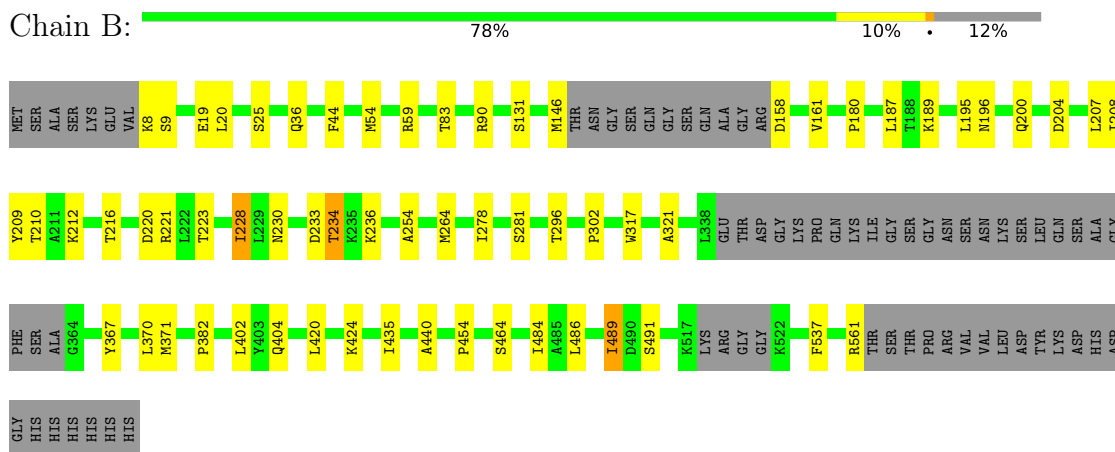
3 Residue-property plots [i](#)

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.

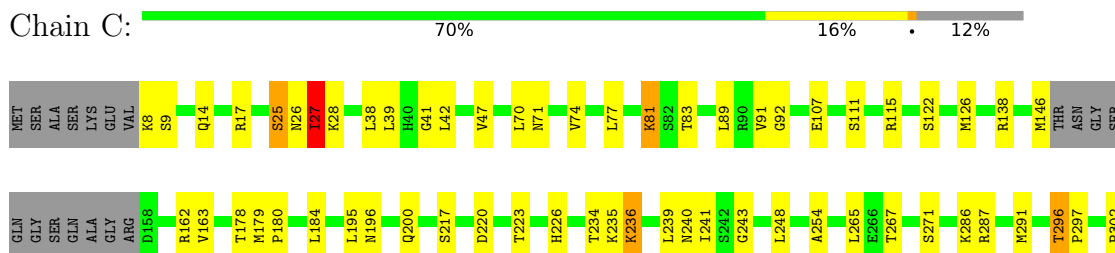
• Molecule 1: Nucleoprotein



• Molecule 1: Nucleoprotein



• Molecule 1: Nucleoprotein





4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	176.32Å 176.32Å 56.58Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.45 30.00 – 2.45	Depositor EDS
% Data completeness (in resolution range)	51.4 (30.00-2.45) 51.4 (30.00-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.184 , 0.219 0.182 , 0.220	Depositor DCC
R_{free} test set	1878 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.2	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	0.315 for -h,-k,l 0.499 for h,-h-k,-l 0.354 for -k,-h,-l	Xtriage
Reported twinning fraction	0.332 for H, K, L 0.163 for -H, H+K, -L 0.163 for -h,-k,l 0.342 for -H-K, K, -L	Depositor
Outliers	0 of 37572 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12140	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.72% 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: MN, 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	0.41	0/4066	0.82	0/5489
1	B	0.41	0/4075	0.81	2/5500 (0.0%)
1	C	0.44	0/4042	0.83	5/5454 (0.1%)
All	All	0.42	0/12183	0.82	7/16443 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	404	GLN	CA-C-N	6.45	126.02	119.19
1	B	404	GLN	C-N-CA	6.45	126.02	119.19
1	C	179	MET	CA-C-N	5.57	125.03	119.24
1	C	179	MET	C-N-CA	5.57	125.03	119.24
1	C	550	LEU	N-CA-C	5.34	118.21	110.42
1	C	28	LYS	N-CA-C	-5.07	107.07	114.12
1	C	320	ILE	N-CA-C	5.07	117.09	112.43

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	4009	0	4089	24	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	4018	0	4102	31	0
1	C	3986	0	4064	47	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	41	0	0	0	0
4	B	48	0	0	0	0
4	C	30	0	0	0	0
All	All	12140	0	12255	98	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 4.

All (98) 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:A:216:THR:HA	1:A:234:THR:HG21	1.73	0.70
1:C:455:ARG:O	1:C:456:ASN:HB2	1.94	0.67
1:C:146:MET:HE3	1:C:163:VAL:HG23	1.78	0.66
1:B:196:ASN:O	1:B:200:GLN:HG2	1.99	0.63
1:B:420:LEU:HD13	1:B:435:ILE:HD12	1.85	0.58
1:C:81:LYS:HA	1:C:322:SER:H	1.68	0.58
1:A:89:LEU:HD12	1:A:336:VAL:HG22	1.87	0.56
1:C:416:GLU:HG3	1:C:438:LEU:O	2.05	0.56
1:C:47:VAL:HG22	1:C:70:LEU:HD21	1.87	0.55
1:C:373:LEU:O	1:C:377:MET:HG2	2.07	0.55
1:B:187:LEU:HB3	1:B:228:ILE:HD11	1.88	0.55
1:A:49:ASN:O	1:A:53:LEU:HG	2.07	0.54
1:A:17:ARG:HG2	1:A:263:ASN:O	2.08	0.54
1:A:221:ARG:HE	1:B:207:LEU:HD21	1.73	0.53
1:B:233:ASP:HB3	1:B:236:LYS:HG3	1.90	0.53
1:C:464:SER:O	1:C:466:ASP:N	2.42	0.53
1:B:223:THR:HG23	1:B:230:ASN:OD1	2.08	0.53
1:C:122:SER:HA	1:C:551:ARG:HD3	1.90	0.53
1:A:382:PRO:HA	1:A:457:MET:HE3	1.90	0.53
1:B:382:PRO:HB3	1:B:454:PRO:HB3	1.91	0.53
1:C:239:LEU:C	1:C:241:ILE:H	2.18	0.52
1:B:146:MET:HE1	1:B:161:VAL:HG12	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:PRO:HB3	1:B:254:ALA:HA	1.91	0.52
1:C:388:MET:HG3	1:C:402:LEU:HG	1.92	0.52
1:C:41:GLY:O	1:C:77:LEU:HD11	2.10	0.51
1:C:196:ASN:O	1:C:200:GLN:HG2	2.11	0.51
1:B:420:LEU:O	1:B:424:LYS:HG2	2.10	0.51
1:C:382:PRO:HB3	1:C:454:PRO:CB	2.41	0.50
1:C:17:ARG:HG2	1:C:265:LEU:HG	1.94	0.50
1:C:126:MET:HE2	1:C:138:ARG:HG3	1.94	0.49
1:B:484:ILE:HG22	1:B:486:LEU:HG	1.94	0.49
1:A:196:ASN:O	1:A:200:GLN:HG2	2.11	0.49
1:C:27:ILE:HD11	1:C:267:THR:HG22	1.95	0.49
1:C:502:TYR:O	1:C:532:MET:HE1	2.13	0.49
1:C:468:LYS:O	1:C:472:GLU:HB2	2.11	0.49
1:C:14:GLN:HA	1:C:17:ARG:HD2	1.95	0.48
1:C:9:SER:O	1:C:302:PRO:HG2	2.13	0.48
1:C:234:THR:HA	1:C:248:LEU:HD13	1.95	0.48
1:B:204:ASP:O	1:B:208:ILE:HG12	2.14	0.48
1:A:409:CYS:HA	1:A:551:ARG:O	2.14	0.48
1:C:396:ASP:HA	1:C:415:ARG:HH12	1.79	0.47
1:A:317:TRP:HB2	1:A:321:ALA:HB2	1.96	0.47
1:C:71:ASN:HB3	1:C:324:THR:HB	1.96	0.47
1:B:440:ALA:O	1:B:561:ARG:HG2	2.14	0.47
1:B:491:SER:HB2	1:B:537:PHE:CE1	2.50	0.47
1:C:502:TYR:CE1	1:C:550:LEU:HD13	2.49	0.47
1:A:365:LEU:HD23	1:A:369:GLN:HB3	1.97	0.47
1:B:216:THR:HA	1:B:234:THR:HG21	1.96	0.47
1:B:367:TYR:O	1:B:371:MET:HG3	2.15	0.47
1:B:489:ILE:H	1:B:489:ILE:HG13	1.54	0.47
1:C:38:LEU:HD22	1:C:42:LEU:HD22	1.95	0.47
1:B:36:GLN:HE21	1:B:195:LEU:CD2	2.28	0.46
1:C:387:TRP:HA	1:C:460:THR:O	2.16	0.46
1:A:204:ASP:O	1:A:208:ILE:HG12	2.15	0.46
1:B:220:ASP:O	1:B:223:THR:HB	2.16	0.46
1:C:286:LYS:HA	1:C:291:MET:HB2	1.98	0.45
1:B:317:TRP:HB2	1:B:321:ALA:HB2	1.99	0.45
1:C:180:PRO:HB3	1:C:254:ALA:HA	1.98	0.45
1:A:180:PRO:HG2	1:A:320:ILE:HG22	1.99	0.44
1:C:408:GLY:O	1:C:550:LEU:HA	2.17	0.44
1:A:464:SER:O	1:A:465:GLU:C	2.59	0.44
1:C:25:SER:HB2	1:C:26:ASN:H	1.69	0.43
1:C:217:SER:HA	1:C:220:ASP:HB2	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:LEU:HD11	1:B:221:ARG:HB2	2.00	0.43
1:A:468:LYS:O	1:A:472:GLU:HB2	2.17	0.43
1:C:420:LEU:HD11	1:C:424:LYS:HE2	2.00	0.43
1:A:207:LEU:HD21	1:B:221:ARG:HE	1.84	0.43
1:B:20:LEU:HD22	1:B:278:ILE:HG23	1.99	0.43
1:C:236:LYS:N	1:C:236:LYS:HD3	2.34	0.43
1:B:9:SER:O	1:B:302:PRO:HG2	2.19	0.43
1:C:223:THR:HA	1:C:226:HIS:O	2.18	0.43
1:C:382:PRO:HB3	1:C:454:PRO:HB2	2.01	0.42
1:C:491:SER:HB2	1:C:537:PHE:CE1	2.54	0.42
1:B:54:MET:O	1:B:59:ARG:NH2	2.51	0.42
1:C:178:THR:HG22	1:C:243:GLY:HA2	2.01	0.42
1:C:380:LEU:HD11	1:C:411:ILE:HD11	2.02	0.42
1:B:210:THR:HG23	1:B:264:MET:HE2	2.01	0.42
1:C:316:GLY:O	1:C:318:PRO:HD3	2.19	0.42
1:C:455:ARG:O	1:C:456:ASN:CB	2.66	0.42
1:A:426:ASP:O	1:A:430:SER:N	2.50	0.42
1:A:495:GLU:HG3	1:A:536:MET:HE1	2.02	0.42
1:C:296:THR:HA	1:C:297:PRO:HD3	1.89	0.42
1:B:44:PHE:CG	1:B:189:LYS:HG2	2.55	0.42
1:C:146:MET:HE1	1:C:162:ARG:HA	2.02	0.42
1:A:472:GLU:C	1:A:474:GLN:H	2.28	0.41
1:C:437:ASP:HB3	1:C:508:MET:SD	2.61	0.41
1:A:309:LYS:HE3	1:A:323:ARG:HH12	1.86	0.41
1:C:39:LEU:HD11	1:C:195:LEU:HD13	2.01	0.41
1:A:210:THR:HG22	1:A:264:MET:CE	2.50	0.41
1:B:209:TYR:HA	1:B:212:LYS:O	2.21	0.41
1:B:420:LEU:HG	1:B:424:LYS:HE2	2.03	0.41
1:A:179:MET:HE3	1:A:181:SER:OG	2.21	0.41
1:B:19:GLU:HG3	1:B:281:SER:HB3	2.03	0.40
1:C:111:SER:O	1:C:115:ARG:HG3	2.22	0.40
1:A:380:LEU:HD11	1:A:411:ILE:HD11	2.03	0.40
1:A:225:SER:HB3	1:B:200:GLN:HB3	2.04	0.40
1:C:38:LEU:HD21	1:C:74:VAL:HG13	2.04	0.40
1:C:401:ALA:HA	1:C:411:ILE:O	2.21	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	505/582 (87%)	486 (96%)	19 (4%)	0	100	100
1	B	506/582 (87%)	490 (97%)	16 (3%)	0	100	100
1	C	500/582 (86%)	465 (93%)	28 (6%)	7 (1%)	9	8
All	All	1511/1746 (86%)	1441 (95%)	63 (4%)	7 (0%)	24	29

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	91	VAL
1	C	464	SER
1	C	465	GLU
1	C	27	ILE
1	C	240	ASN
1	C	456	ASN
1	C	92	GLY

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	450/505 (89%)	443 (98%)	7 (2%)	55	68
1	B	451/505 (89%)	438 (97%)	13 (3%)	37	49
1	C	447/505 (88%)	430 (96%)	17 (4%)	29	41
All	All	1348/1515 (89%)	1311 (97%)	37 (3%)	39	52

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	235	LYS
1	A	259	LEU
1	A	310	ILE
1	A	395	GLU
1	A	465	GLU
1	A	545	LEU
1	A	546	ASN
1	B	8	LYS
1	B	25	SER
1	B	83	THR
1	B	90	ARG
1	B	131	SER
1	B	158	ASP
1	B	228	ILE
1	B	234	THR
1	B	296	THR
1	B	370	LEU
1	B	402	LEU
1	B	464	SER
1	B	489	ILE
1	C	8	LYS
1	C	25	SER
1	C	27	ILE
1	C	81	LYS
1	C	83	THR
1	C	89	LEU
1	C	107	GLU
1	C	184	LEU
1	C	235	LYS
1	C	236	LYS
1	C	271	SER
1	C	287	ARG
1	C	296	THR
1	C	327	VAL
1	C	465	GLU
1	C	549	VAL
1	C	556	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	ASN
1	A	200	GLN
1	A	383	ASN
1	B	36	GLN
1	B	215	ASN
1	B	224	GLN
1	B	404	GLN
1	B	425	GLN
1	B	546	ASN
1	C	76	ASN
1	C	230	ASN
1	C	245	ASN
1	C	263	ASN
1	C	379	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 8 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 [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	513/582 (88%)	-1.42	0 100 100	13, 20, 20, 26	1 (0%)
1	B	514/582 (88%)	-1.40	0 100 100	20, 20, 20, 20	0
1	C	510/582 (87%)	-1.41	0 100 100	20, 20, 20, 30	0
All	All	1537/1746 (88%)	-1.41	0 100 100	13, 20, 20, 30	1 (0%)

There are no RSRZ outliers to report.

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
2	MN	B	584	1/1	0.99	0.04	30,30,30,30	0
2	MN	A	584	1/1	1.00	0.01	30,30,30,30	0
2	MN	B	583	1/1	1.00	0.01	30,30,30,30	0
2	MN	A	583	1/1	1.00	0.03	30,30,30,30	0
2	MN	C	583	1/1	1.00	0.02	30,30,30,30	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ZN	A	585	1/1	1.00	0.02	20,20,20,20	0
3	ZN	B	585	1/1	1.00	0.01	20,20,20,20	0
3	ZN	C	584	1/1	1.00	0.01	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.