



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:32 AM UTC

PDB ID : 4JNG / pdb_00004jng
Title : Schmallenberg virus nucleoprotein-RNA complex
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Deposited on : 2013-03-15
Resolution : 2.12 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

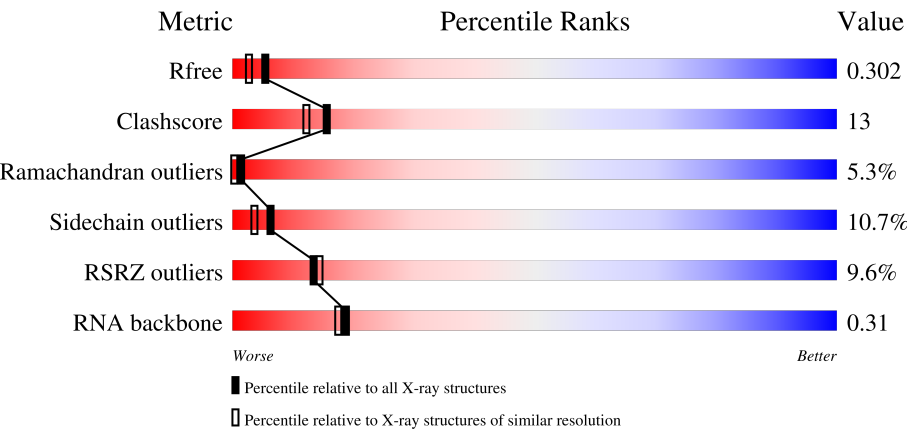
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)
RNA backbone	3983	1037 (2.46-1.78)

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	L	42	48%33%17%.
2	A	233	9% 75%19%. .
2	B	233	7% 67%20%. . 8%
2	C	233	15% 64%24%8%. .

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Mol	Chain	Length	Quality of chain
2	D	233	7% 62% 24% 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8038 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 RNA chain called RNA (42-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	42	Total	C	N	O	P	0	0	0
			840	378	84	336	42			

- Molecule 2 is a protein called Nucleocapsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	226	Total	C	N	O	S	0	0	0
			1796	1168	301	315	12			
2	B	214	Total	C	N	O	S	0	0	0
			1689	1097	284	296	12			
2	C	224	Total	C	N	O	S	0	0	0
			1781	1160	298	311	12			
2	D	223	Total	C	N	O	S	0	0	0
			1769	1146	298	313	12			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	33	Total	O	0	0
			33	33		
3	A	97	Total	O	0	0
			97	97		
3	B	17	Total	O	0	0
			17	17		
3	C	16	Total	O	0	0
			16	16		

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.

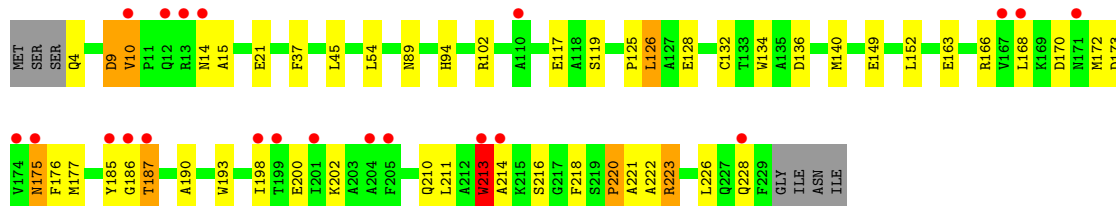
- Molecule 1: RNA (42-MER)

Chain L: 



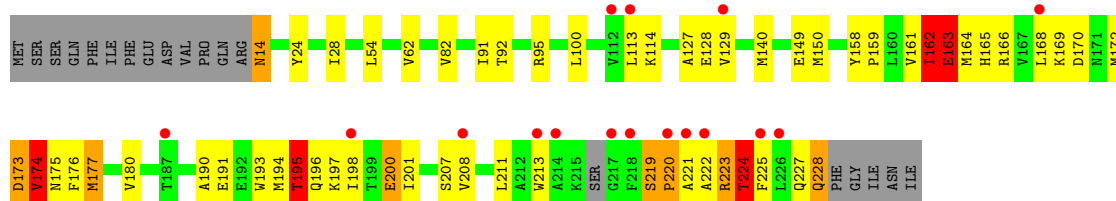
- Molecule 2: Nucleocapsid protein

Chain A: 



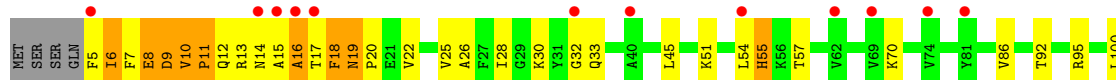
- Molecule 2: Nucleocapsid protein

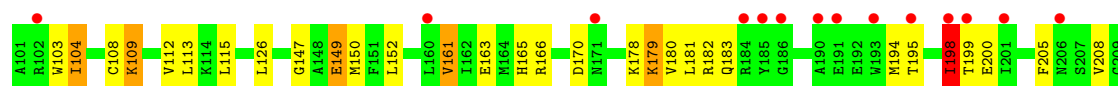
Chain B: 



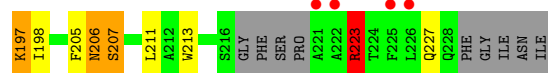
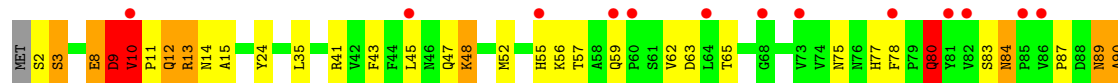
- Molecule 2: Nucleocapsid protein

Chain C: 





● Molecule 2: Nucleocapsid protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	76.35Å 85.96Å 77.33Å 90.00° 102.02° 90.00°	Depositor
Resolution (Å)	37.40 – 2.12 37.40 – 2.12	Depositor EDS
% Data completeness (in resolution range)	97.7 (37.40-2.12) 97.7 (37.40-2.12)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.12Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.264 , 0.283 0.281 , 0.302	Depositor DCC
R_{free} test set	2821 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	36.6	Xtriage
Anisotropy	0.653	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 29.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.023 for l,-k,h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8038	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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

5.1 Standard geometry

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	L	0.39	0/923	0.80	1/1424 (0.1%)
2	A	0.50	0/1844	0.87	5/2497 (0.2%)
2	B	0.51	0/1732	0.86	1/2344 (0.0%)
2	C	0.47	0/1828	0.83	0/2474
2	D	0.49	0/1813	0.96	10/2453 (0.4%)
All	All	0.48	0/8140	0.87	17/11192 (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	B	0	1

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	206	ASN	N-CA-C	13.99	126.60	111.36
2	D	206	ASN	CA-C-N	7.26	134.77	121.70
2	D	206	ASN	C-N-CA	7.26	134.77	121.70
2	D	9	ASP	CA-C-N	6.31	133.05	121.70
2	D	9	ASP	C-N-CA	6.31	133.05	121.70
2	A	220	PRO	CA-C-N	6.30	133.04	121.70
2	A	220	PRO	C-N-CA	6.30	133.04	121.70
2	D	99	TYR	N-CA-C	-6.27	101.66	110.50
2	A	9	ASP	CA-C-N	5.59	131.76	121.70
2	A	9	ASP	C-N-CA	5.59	131.76	121.70
2	B	162	ILE	N-CA-C	-5.48	102.45	109.30
2	D	12	GLN	CA-C-N	5.43	131.48	121.70
2	D	12	GLN	C-N-CA	5.43	131.48	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	40	U	C2'-C3'-O3'	5.16	117.24	109.50
2	D	10	VAL	C-N-CD	-5.11	109.36	120.60
2	A	216	SER	N-CA-C	5.09	116.26	108.42
2	D	170	ASP	N-CA-C	-5.01	102.60	110.36

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	224	THR	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	L	840	0	421	29	0
2	A	1796	0	1781	36	0
2	B	1689	0	1682	54	0
2	C	1781	0	1767	53	0
2	D	1769	0	1757	64	0
3	A	97	0	0	3	0
3	B	17	0	0	0	0
3	C	16	0	0	0	0
3	L	33	0	0	0	0
All	All	8038	0	7408	205	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 13.

All (205) 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:B:220:PRO:HB2	2:B:221:ALA:HA	1.28	1.15
2:C:12:GLN:HB3	2:C:13:ARG:HA	1.11	1.10
2:A:9:ASP:HA	2:A:10:VAL:HG22	1.36	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:12:U:H6	1:L:12:U:H5'	1.24	1.03
2:B:162:ILE:O	2:B:163:GLU:HB2	1.55	1.01
2:C:12:GLN:CB	2:C:13:ARG:HA	1.92	0.99
2:C:12:GLN:HB3	2:C:13:ARG:CA	1.95	0.96
2:D:8:GLU:HB2	2:D:9:ASP:HB2	1.47	0.95
2:D:9:ASP:N	2:D:10:VAL:HB	1.83	0.94
2:D:161:VAL:HG21	2:D:205:PHE:HA	1.48	0.93
2:B:194:MET:HB2	2:C:223:ARG:HD3	1.50	0.91
2:D:12:GLN:HA	2:D:13:ARG:CG	2.01	0.90
1:L:12:U:H5'	1:L:12:U:C6	2.07	0.88
1:L:12:U:H6	1:L:12:U:C5'	1.86	0.88
2:D:12:GLN:HA	2:D:13:ARG:CB	2.05	0.86
2:C:220:PRO:HA	2:C:221:ALA:C	2.04	0.82
1:L:27:U:O2	2:A:172:MET:HE1	1.80	0.82
2:C:220:PRO:HA	2:C:222:ALA:N	1.95	0.81
2:B:24:TYR:CZ	2:B:28:ILE:HD11	2.17	0.79
2:B:223:ARG:HH11	2:B:223:ARG:HG3	1.49	0.78
2:D:12:GLN:HA	2:D:13:ARG:HB2	1.67	0.77
2:D:188:MET:HG2	2:D:192:GLU:HB2	1.68	0.76
2:A:220:PRO:HA	2:A:222:ALA:H	1.50	0.76
2:B:220:PRO:HB2	2:B:221:ALA:CA	2.14	0.75
1:L:23:U:H5''	1:L:23:U:H6	1.51	0.75
2:C:7:PHE:HA	2:C:8:GLU:HB2	1.68	0.74
2:D:8:GLU:CB	2:D:9:ASP:HB2	2.17	0.74
2:B:164:MET:HG2	2:B:177:MET:HE1	1.70	0.74
2:D:99:TYR:O	2:D:100:LEU:HB2	1.89	0.73
2:D:96:MET:O	2:D:99:TYR:O	2.06	0.72
2:C:20:PRO:HB3	2:C:150:MET:HG2	1.70	0.71
1:L:23:U:H6	1:L:23:U:C5'	2.03	0.71
2:A:9:ASP:HA	2:A:10:VAL:CG2	2.18	0.70
1:L:27:U:O2	2:A:172:MET:CE	2.40	0.68
2:B:194:MET:HB2	2:C:223:ARG:CD	2.23	0.68
3:A:301:HOH:O	2:B:92:THR:HG21	1.92	0.68
1:L:23:U:C5'	1:L:23:U:C6	2.78	0.66
2:B:219:SER:HB3	2:B:220:PRO:HD3	1.78	0.66
2:B:113:LEU:O	2:B:114:LYS:HB2	1.95	0.66
2:D:133:THR:HG22	2:D:135:ALA:H	1.62	0.65
2:A:220:PRO:HA	2:A:222:ALA:N	2.12	0.65
2:B:220:PRO:CB	2:B:221:ALA:HA	2.14	0.65
2:C:8:GLU:O	2:C:9:ASP:HB2	1.96	0.65
2:D:12:GLN:HA	2:D:13:ARG:HG2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:59:GLN:HG2	2:D:62:VAL:HG22	1.79	0.65
2:A:213:TRP:CD1	2:A:214:ALA:HA	2.33	0.64
1:L:2:U:H2'	1:L:3:U:C6	2.33	0.64
1:L:30:U:H5'	2:A:125:PRO:HB3	1.81	0.63
2:A:223:ARG:HG3	2:D:194:MET:HG2	1.81	0.63
1:L:31:U:O2	2:D:13:ARG:HB3	1.99	0.62
1:L:31:U:O2	2:D:13:ARG:CB	2.47	0.62
2:C:20:PRO:HB3	2:C:150:MET:CG	2.30	0.61
2:D:9:ASP:CA	2:D:10:VAL:HB	2.30	0.61
2:C:7:PHE:HB2	2:D:65:THR:O	2.00	0.60
2:C:13:ARG:HD2	2:D:123:VAL:HG21	1.83	0.60
2:B:172:MET:HE2	2:B:176:PHE:CB	2.32	0.60
2:D:75:ASN:HD21	2:D:77:HIS:HB2	1.67	0.60
1:L:12:U:C6	1:L:12:U:C5'	2.75	0.60
2:C:100:LEU:O	2:C:103:TRP:O	2.19	0.60
2:D:89:ASN:O	2:D:90:ALA:CB	2.48	0.59
2:D:165:HIS:O	2:D:169:LYS:HG2	2.02	0.59
2:D:92:THR:O	2:D:93:LEU:HB2	2.03	0.59
1:L:31:U:C2	2:D:13:ARG:HB3	2.37	0.58
2:C:103:TRP:O	2:C:104:ILE:HB	2.03	0.58
2:D:161:VAL:CG2	2:D:205:PHE:HA	2.30	0.58
2:C:7:PHE:CA	2:C:8:GLU:HB2	2.34	0.58
2:A:21:GLU:OE1	2:A:102:ARG:NH2	2.36	0.57
2:B:166:ARG:NH1	2:B:172:MET:SD	2.77	0.57
2:B:95:ARG:HG2	2:B:150:MET:HE1	1.86	0.57
2:B:54:LEU:CD2	2:B:62:VAL:HG21	2.35	0.57
2:B:172:MET:HE2	2:B:176:PHE:HB2	1.86	0.57
2:A:223:ARG:HH21	2:D:160:LEU:HD21	1.70	0.56
1:L:10:U:O4'	2:B:14:ASN:HB3	2.06	0.55
2:D:12:GLN:CA	2:D:13:ARG:HG2	2.36	0.54
2:C:112:VAL:HG12	2:C:113:LEU:H	1.72	0.54
2:A:128:GLU:OE1	2:A:128:GLU:HA	2.06	0.54
2:C:54:LEU:O	2:C:55:HIS:HB2	2.06	0.54
2:C:161:VAL:HG11	2:C:205:PHE:HA	1.90	0.54
2:D:99:TYR:O	2:D:100:LEU:CB	2.57	0.53
2:A:226:LEU:HD23	2:D:198:ILE:HD11	1.90	0.53
1:L:3:U:O4	2:C:179:LYS:NZ	2.41	0.53
2:A:223:ARG:NH2	2:D:160:LEU:HD21	2.23	0.53
2:B:173:ASP:O	2:B:174:VAL:HG12	2.09	0.53
2:B:201:ILE:HG21	2:C:223:ARG:HH12	1.74	0.53
2:D:48:LYS:O	2:D:52:MET:HG2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:190:ALA:HA	2:A:193:TRP:NE1	2.24	0.52
2:B:128:GLU:O	2:B:129:VAL:HB	2.09	0.52
2:B:158:TYR:O	2:B:162:ILE:HG12	2.09	0.52
2:B:92:THR:HG22	2:B:95:ARG:HG3	1.90	0.52
2:D:163:GLU:HG2	2:D:172:MET:HE1	1.92	0.52
2:B:225:PHE:CD1	2:B:228:GLN:O	2.64	0.51
1:L:40:U:H1'	2:D:125:PRO:HB2	1.92	0.51
2:D:83:SER:O	2:D:84:ASN:HB2	2.11	0.51
2:B:54:LEU:HD21	2:B:62:VAL:HG21	1.93	0.50
2:B:162:ILE:CG2	2:B:208:VAL:HG21	2.41	0.50
2:D:55:HIS:HD2	2:D:56:LYS:HG2	1.76	0.50
2:A:89:ASN:ND2	3:A:331:HOH:O	2.44	0.50
2:B:223:ARG:HG3	2:B:224:THR:N	2.26	0.50
2:C:108:CYS:O	2:C:109:LYS:HB3	2.11	0.50
2:A:175:ASN:O	2:A:176:PHE:HB2	2.10	0.50
1:L:31:U:O2	2:D:13:ARG:HB2	2.12	0.50
2:D:140:MET:CE	2:D:211:LEU:HD22	2.42	0.50
3:A:334:HOH:O	2:B:14:ASN:ND2	2.43	0.49
2:B:168:LEU:HD11	2:C:228:GLN:HB2	1.94	0.49
2:C:15:ALA:O	2:C:16:ALA:HB2	2.12	0.49
2:A:213:TRP:CB	2:A:214:ALA:HA	2.42	0.49
2:C:5:PHE:CD2	2:C:6:ILE:HD13	2.48	0.49
2:C:161:VAL:CG1	2:C:205:PHE:HA	2.43	0.49
2:C:165:HIS:CE1	2:C:208:VAL:HG23	2.46	0.49
2:C:180:VAL:HA	2:C:183:GLN:HG2	1.94	0.49
2:C:194:MET:O	2:C:194:MET:HG3	2.12	0.49
2:D:103:TRP:O	2:D:107:THR:HG23	2.13	0.49
2:A:140:MET:CE	2:A:211:LEU:HD22	2.42	0.49
2:D:12:GLN:H	2:D:13:ARG:HG2	1.77	0.49
1:L:19:U:H2'	1:L:20:U:O4'	2.13	0.48
2:A:94:HIS:HE1	2:A:149:GLU:OE2	1.96	0.48
2:B:162:ILE:O	2:B:163:GLU:CB	2.40	0.48
2:C:165:HIS:CE1	2:C:208:VAL:CG2	2.97	0.48
2:D:47:GLN:O	2:D:48:LYS:CB	2.61	0.48
2:D:169:LYS:HE2	2:D:213:TRP:CD2	2.49	0.48
2:C:22:VAL:O	2:C:25:VAL:HG12	2.14	0.47
2:D:153:ASP:HA	2:D:185:TYR:CE1	2.49	0.47
2:D:190:ALA:HA	2:D:193:TRP:NE1	2.29	0.47
1:L:23:U:C6	1:L:23:U:H5'	2.50	0.47
2:C:178:LYS:O	2:C:182:ARG:HG3	2.14	0.47
2:A:213:TRP:HD1	2:A:214:ALA:HA	1.76	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:190:ALA:O	2:B:191:GLU:C	2.55	0.47
2:C:112:VAL:HG12	2:C:113:LEU:N	2.30	0.47
2:C:112:VAL:O	2:C:113:LEU:HB2	2.15	0.47
2:A:220:PRO:HB3	2:A:223:ARG:N	2.30	0.46
2:A:166:ARG:NH1	2:A:172:MET:HE1	2.31	0.46
2:C:103:TRP:O	2:C:104:ILE:CB	2.63	0.46
2:A:168:LEU:HD21	2:B:227:GLN:HB3	1.98	0.46
2:C:161:VAL:HG12	2:C:208:VAL:HG21	1.98	0.46
2:C:8:GLU:O	2:C:9:ASP:CB	2.61	0.46
2:A:173:ASP:OD2	2:A:175:ASN:HB2	2.16	0.46
2:B:162:ILE:HG22	2:B:208:VAL:HG21	1.97	0.46
2:C:10:VAL:HG11	2:D:41:ARG:HE	1.79	0.46
2:B:92:THR:HG23	2:B:95:ARG:H	1.81	0.46
2:C:10:VAL:HG23	2:C:11:PRO:N	2.30	0.46
2:C:213:TRP:O	2:C:214:ALA:HB2	2.16	0.46
2:A:132:CYS:O	2:A:136:ASP:OD2	2.34	0.45
2:C:147:GLY:N	2:C:149:GLU:OE2	2.46	0.45
2:D:89:ASN:O	2:D:90:ALA:HB3	2.16	0.45
2:D:164:MET:HG2	2:D:177:MET:HE1	1.97	0.45
2:A:175:ASN:C	2:A:177:MET:H	2.25	0.45
2:C:20:PRO:CB	2:C:150:MET:HG2	2.43	0.45
2:C:166:ARG:O	2:C:170:ASP:O	2.33	0.45
2:D:132:CYS:HB2	2:D:211:LEU:HD21	1.99	0.45
1:L:30:U:C5'	2:A:125:PRO:HB3	2.47	0.45
2:B:220:PRO:HA	2:B:222:ALA:H	1.82	0.45
2:B:127:ALA:C	2:B:128:GLU:O	2.59	0.45
2:C:10:VAL:CG1	2:D:41:ARG:HE	2.30	0.45
2:B:169:LYS:HD2	2:B:213:TRP:HE3	1.82	0.45
2:B:219:SER:CB	2:B:220:PRO:HD3	2.47	0.45
2:B:223:ARG:HG3	2:B:223:ARG:NH1	2.27	0.44
2:C:26:ALA:O	2:C:30:LYS:HG2	2.17	0.44
2:D:12:GLN:N	2:D:13:ARG:HG2	2.31	0.44
2:B:191:GLU:O	2:B:195:THR:OG1	2.35	0.44
1:L:28:U:C2	2:A:166:ARG:NH1	2.86	0.44
1:L:41:U:O2'	2:D:128:GLU:HB3	2.18	0.44
2:B:223:ARG:HH11	2:B:223:ARG:CG	2.24	0.44
2:C:212:ALA:HB1	2:C:215:LYS:HD3	1.99	0.44
2:B:173:ASP:O	2:B:173:ASP:CG	2.61	0.44
2:B:190:ALA:HA	2:B:193:TRP:NE1	2.33	0.44
2:C:219:SER:HA	2:C:221:ALA:HB3	2.00	0.44
2:D:2:SER:O	2:D:3:SER:CB	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:9:ASP:HB3	2:D:10:VAL:HG23	1.99	0.44
2:C:7:PHE:HA	2:C:8:GLU:CB	2.34	0.44
2:D:140:MET:HE1	2:D:211:LEU:HD22	2.00	0.44
2:B:174:VAL:HG13	2:B:175:ASN:N	2.33	0.43
2:D:206:ASN:N	2:D:207:SER:HB3	2.33	0.43
2:B:113:LEU:O	2:B:114:LYS:CB	2.66	0.43
2:C:103:TRP:CE3	2:C:104:ILE:HG13	2.53	0.43
2:D:223:ARG:HG2	2:D:223:ARG:O	2.19	0.43
2:B:140:MET:HE1	2:B:211:LEU:HD21	2.01	0.42
1:L:30:U:C4	2:A:45:LEU:HD22	2.55	0.42
2:C:227:GLN:HB3	2:C:228:GLN:HG3	2.00	0.42
2:C:51:LYS:O	2:C:54:LEU:O	2.37	0.42
2:C:198:ILE:HG13	2:C:199:THR:H	1.84	0.42
2:A:172:MET:O	2:A:173:ASP:C	2.62	0.42
2:D:188:MET:HE1	2:D:197:LYS:CE	2.50	0.42
1:L:28:U:O2	2:A:166:ARG:NH1	2.53	0.42
2:B:173:ASP:C	2:B:174:VAL:O	2.61	0.42
2:D:43:PHE:HE2	2:D:96:MET:HE3	1.84	0.42
1:L:34:U:OP1	2:D:179:LYS:NZ	2.46	0.42
2:A:37:PHE:HE2	2:A:117:GLU:HG3	1.85	0.41
2:A:132:CYS:HA	2:A:211:LEU:HD11	2.02	0.41
2:B:149:GLU:HB2	2:B:180:VAL:HG23	2.02	0.41
2:B:159:PRO:O	2:B:162:ILE:O	2.37	0.41
2:A:119:SER:HA	2:A:134:TRP:CE2	2.55	0.41
2:C:92:THR:HG22	2:C:95:ARG:HG3	2.02	0.41
2:D:9:ASP:H	2:D:10:VAL:HB	1.77	0.41
2:B:174:VAL:O	2:B:176:PHE:N	2.47	0.41
2:A:185:TYR:O	2:A:187:THR:N	2.53	0.41
2:B:24:TYR:CE2	2:B:28:ILE:HD11	2.53	0.41
1:L:34:U:OP2	2:D:182:ARG:HD2	2.21	0.41
2:B:197:LYS:HD2	2:B:200:GLU:CG	2.51	0.41
2:D:78:PHE:O	2:D:80:GLN:N	2.42	0.41
2:D:24:TYR:CZ	2:D:102:ARG:HG3	2.56	0.41
2:D:87:PRO:HB2	2:D:89:ASN:O	2.21	0.41
2:D:89:ASN:OD1	2:D:89:ASN:N	2.54	0.40
1:L:9:U:O2	2:B:14:ASN:ND2	2.54	0.40
2:B:165:HIS:CE1	2:B:208:VAL:HG13	2.55	0.40
1:L:12:U:C6	1:L:12:U:C4'	3.04	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	
2	A	224/233 (96%)	198 (88%)	19 (8%)	7 (3%)	3	1
2	B	210/233 (90%)	181 (86%)	21 (10%)	8 (4%)	2	0
2	C	220/233 (94%)	184 (84%)	19 (9%)	17 (8%)	1	0
2	D	219/233 (94%)	190 (87%)	15 (7%)	14 (6%)	1	0
All	All	873/932 (94%)	753 (86%)	74 (8%)	46 (5%)	1	0

All (46) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	126	LEU
2	A	213	TRP
2	A	221	ALA
2	B	163	GLU
2	B	174	VAL
2	B	207	SER
2	B	219	SER
2	C	9	ASP
2	C	11	PRO
2	C	16	ALA
2	C	17	THR
2	C	18	PHE
2	C	33	GLN
2	C	55	HIS
2	C	214	ALA
2	C	220	PRO
2	C	221	ALA
2	D	3	SER
2	D	10	VAL
2	D	11	PRO
2	D	13	ARG
2	D	48	LYS

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Mol	Chain	Res	Type
2	D	90	ALA
2	D	207	SER
2	D	223	ARG
2	A	186	GLY
2	B	224	THR
2	C	228	GLN
2	D	9	ASP
2	D	84	ASN
2	D	93	LEU
2	D	100	LEU
2	A	15	ALA
2	A	175	ASN
2	B	173	ASP
2	B	195	THR
2	C	8	GLU
2	C	195	THR
2	D	15	ALA
2	B	220	PRO
2	C	19	ASN
2	C	104	ILE
2	D	80	GLN
2	A	10	VAL
2	C	32	GLY
2	C	198	ILE

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	
2	A	187/193 (97%)	171 (91%)	16 (9%)	10	7
2	B	175/193 (91%)	158 (90%)	17 (10%)	8	5
2	C	185/193 (96%)	160 (86%)	25 (14%)	4	2
2	D	185/193 (96%)	165 (89%)	20 (11%)	6	3
All	All	732/772 (95%)	654 (89%)	78 (11%)	6	3

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	4	GLN
2	A	14	ASN
2	A	54	LEU
2	A	126	LEU
2	A	152	LEU
2	A	163	GLU
2	A	170	ASP
2	A	187	THR
2	A	198	ILE
2	A	200	GLU
2	A	202	LYS
2	A	210	GLN
2	A	213	TRP
2	A	218	PHE
2	A	223	ARG
2	A	228	GLN
2	B	14	ASN
2	B	82	VAL
2	B	91	ILE
2	B	100	LEU
2	B	161	VAL
2	B	162	ILE
2	B	163	GLU
2	B	170	ASP
2	B	174	VAL
2	B	177	MET
2	B	195	THR
2	B	196	GLN
2	B	198	ILE
2	B	200	GLU
2	B	223	ARG
2	B	224	THR
2	B	228	GLN
2	C	6	ILE
2	C	10	VAL
2	C	14	ASN
2	C	18	PHE
2	C	19	ASN
2	C	28	ILE
2	C	45	LEU
2	C	57	THR
2	C	70	LYS

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Mol	Chain	Res	Type
2	C	86	VAL
2	C	109	LYS
2	C	115	LEU
2	C	126	LEU
2	C	149	GLU
2	C	152	LEU
2	C	161	VAL
2	C	163	GLU
2	C	179	LYS
2	C	181	LEU
2	C	198	ILE
2	C	200	GLU
2	C	210	GLN
2	C	226	LEU
2	C	227	GLN
2	C	228	GLN
2	D	8	GLU
2	D	10	VAL
2	D	14	ASN
2	D	35	LEU
2	D	45	LEU
2	D	57	THR
2	D	63	ASP
2	D	80	GLN
2	D	89	ASN
2	D	115	LEU
2	D	152	LEU
2	D	153	ASP
2	D	161	VAL
2	D	163	GLU
2	D	170	ASP
2	D	172	MET
2	D	191	GLU
2	D	197	LYS
2	D	223	ARG
2	D	227	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	34	GLN
2	A	89	ASN

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Mol	Chain	Res	Type
2	A	94	HIS
2	A	121	GLN
2	A	210	GLN
2	A	227	GLN
2	B	14	ASN
2	B	76	ASN
2	B	94	HIS
2	B	183	GLN
2	B	196	GLN
2	B	206	ASN
2	C	33	GLN
2	C	34	GLN
2	C	47	GLN
2	C	121	GLN
2	C	165	HIS
2	C	210	GLN
2	D	47	GLN
2	D	55	HIS
2	D	75	ASN
2	D	76	ASN
2	D	121	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L	41/42 (97%)	14 (34%)	6 (14%)

All (14) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L	6	U
1	L	11	U
1	L	12	U
1	L	13	U
1	L	19	U
1	L	22	U
1	L	23	U
1	L	24	U
1	L	27	U
1	L	30	U
1	L	33	U

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Mol	Chain	Res	Type
1	L	34	U
1	L	41	U
1	L	42	U

All (6) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L	11	U
1	L	12	U
1	L	22	U
1	L	23	U
1	L	33	U
1	L	40	U

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	L	42/42 (100%)	-0.61	0 100 100	5, 18, 32, 54	0
2	A	226/233 (96%)	0.67	21 (9%) 14 15	5, 10, 40, 49	0
2	B	214/233 (91%)	0.58	16 (7%) 20 22	5, 13, 42, 67	0
2	C	224/233 (96%)	1.12	35 (15%) 5 5	10, 28, 49, 78	0
2	D	223/233 (95%)	0.65	17 (7%) 20 21	5, 16, 41, 52	0
All	All	929/974 (95%)	0.70	89 (9%) 13 14	5, 17, 43, 78	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	221	ALA	6.6
2	B	213	TRP	5.2
2	A	167	VAL	5.1
2	D	78	PHE	4.4
2	D	226	LEU	4.2
2	C	218	PHE	4.0
2	C	217	GLY	4.0
2	B	222	ALA	3.9
2	C	17	THR	3.9
2	A	199	THR	3.7
2	C	40	ALA	3.7
2	C	15	ALA	3.6
2	B	220	PRO	3.6
2	D	60	PRO	3.5
2	A	213	TRP	3.5
2	D	68	GLY	3.5
2	C	198	ILE	3.4
2	A	201	ILE	3.3
2	B	218	PHE	3.3
2	B	198	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
2	A	174	VAL	3.3
2	C	225	PHE	3.2
2	A	186	GLY	3.0
2	B	217	GLY	3.0
2	A	204	ALA	3.0
2	D	73	VAL	3.0
2	C	199	THR	3.0
2	B	208	VAL	3.0
2	C	220	PRO	3.0
2	C	191	GLU	3.0
2	B	168	LEU	2.9
2	A	10	VAL	2.9
2	D	10	VAL	2.9
2	D	64	LEU	2.9
2	A	110	ALA	2.9
2	C	193	TRP	2.8
2	D	82	VAL	2.8
2	D	86	VAL	2.8
2	C	5	PHE	2.8
2	C	190	ALA	2.8
2	C	16	ALA	2.7
2	C	206	ASN	2.7
2	D	81	TYR	2.7
2	C	215	LYS	2.7
2	A	14	ASN	2.7
2	C	201	ILE	2.7
2	D	225	PHE	2.6
2	C	69	VAL	2.6
2	B	129	VAL	2.6
2	C	81	TYR	2.6
2	A	214	ALA	2.6
2	A	168	LEU	2.6
2	C	74	VAL	2.5
2	B	112	VAL	2.5
2	C	32	GLY	2.5
2	C	186	GLY	2.5
2	A	198	ILE	2.5
2	A	12	GLN	2.4
2	A	171	ASN	2.4
2	B	214	ALA	2.3
2	A	187	THR	2.3
2	A	185	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
2	C	214	ALA	2.3
2	B	113	LEU	2.3
2	C	184	ARG	2.3
2	C	62	VAL	2.3
2	C	195	THR	2.3
2	D	221	ALA	2.3
2	D	85	PRO	2.2
2	C	224	THR	2.2
2	C	185	TYR	2.2
2	C	54	LEU	2.2
2	C	160	LEU	2.2
2	A	13	ARG	2.2
2	B	187	THR	2.2
2	C	226	LEU	2.1
2	C	171	ASN	2.1
2	C	213	TRP	2.1
2	D	55	HIS	2.1
2	A	205	PHE	2.1
2	B	226	LEU	2.1
2	D	45	LEU	2.1
2	A	175	ASN	2.1
2	B	225	PHE	2.1
2	C	14	ASN	2.0
2	A	228	GLN	2.0
2	D	59	GLN	2.0
2	C	102	ARG	2.0
2	D	222	ALA	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.