



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:59 AM UTC

PDB ID : 2VON / pdb_00002von
Title : Crystal structure of N-terminal domains of Human La protein complexed with RNA oligomer AUAAUUU
Authors : Kotik-Kogan, O.; Valentine, E.R.; Sanfelice, D.; Conte, M.R.; Curry, S.
Deposited on : 2008-02-19
Resolution : 2.10 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

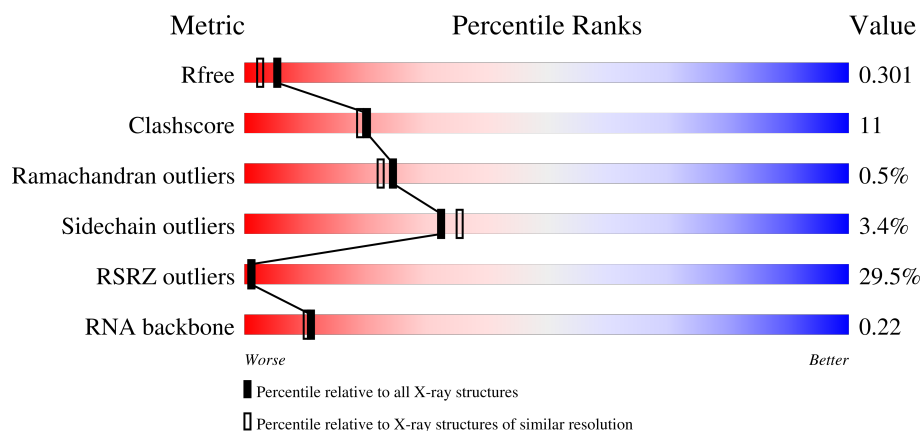
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)
RNA backbone	3983	1006 (2.42-1.78)

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	A	193	23% 76% 19% ..
1	B	193	33% 70% 24% ...
2	C	7	29% 14% 57% 29%
2	D	7	57% 29% 43% 29%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3520 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 LUPUS LA PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	187	Total	C	N	O	S	0	0	0
			1523	981	251	286	5			
1	B	186	Total	C	N	O	S	0	0	0
			1505	972	245	283	5			

- Molecule 2 is a RNA chain called 5'-R(*AP*UP*AP*AP*UP*UP*UP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	P	0	0	0
			143	66	23	48	6			
2	D	7	Total	C	N	O	P	0	0	0
			143	66	23	48	6			

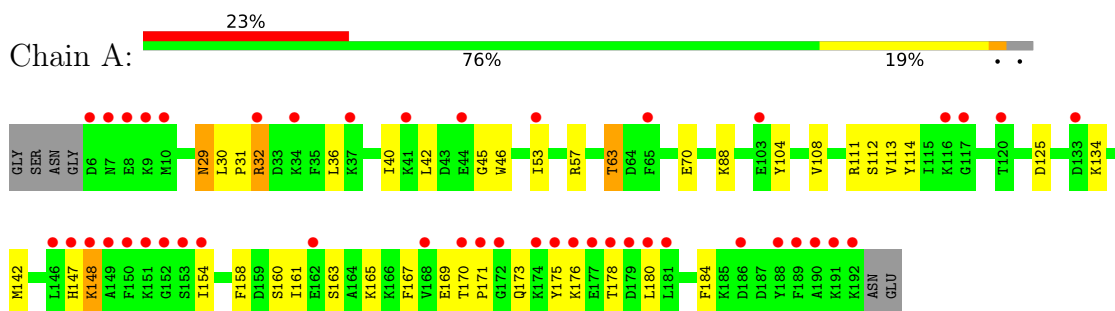
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	89	Total	O	0	0
			89	89		
3	B	89	Total	O	0	0
			89	89		
3	C	15	Total	O	0	0
			15	15		
3	D	13	Total	O	0	0
			13	13		

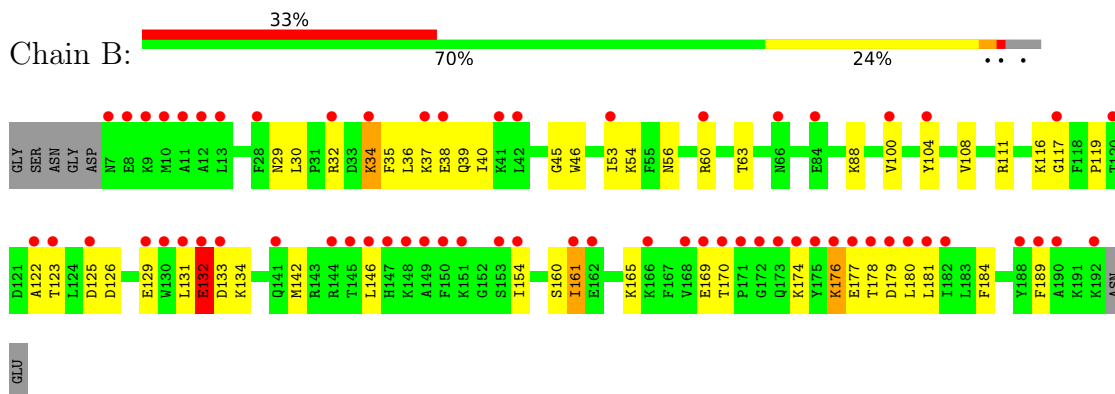
3 Residue-property plots

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.

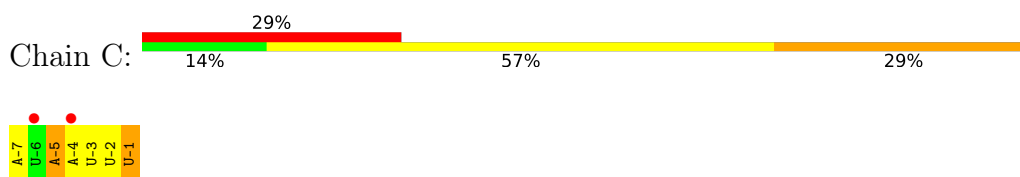
• Molecule 1: LUPUS LA PROTEIN



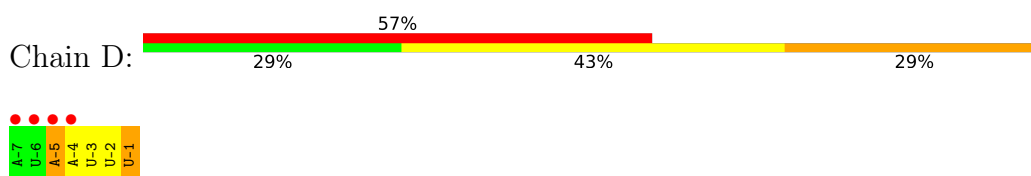
• Molecule 1: LUPUS LA PROTEIN



• Molecule 2: 5'-R(*AP*UP*AP*AP*UP*UP*UP)-3'



• Molecule 2: 5'-R(*AP*UP*AP*AP*UP*UP*UP)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	140.03Å 44.47Å 91.28Å 90.00° 114.35° 90.00°	Depositor
Resolution (Å)	43.00 – 2.10 43.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.7 (43.00-2.10) 97.8 (43.00-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.81 (at 2.08Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.230 , 0.260 0.276 , 0.301	Depositor DCC
R_{free} test set	1352 reflections (4.49%)	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	3520	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.16% 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	A	0.37	0/1553	0.89	3/2090 (0.1%)
1	B	0.38	0/1534	0.90	4/2067 (0.2%)
2	C	0.37	0/159	1.37	3/245 (1.2%)
2	D	0.38	0/159	1.35	3/245 (1.2%)
All	All	0.38	0/3405	0.95	13/4647 (0.3%)

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	C	1	0
2	D	1	0
All	All	2	0

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	-5	A	C2'-C3'-O3'	13.15	129.23	109.50
2	D	-5	A	C2'-C3'-O3'	12.96	128.94	109.50
2	D	-5	A	C4'-C3'-O3'	9.40	123.50	109.40
2	C	-5	A	C4'-C3'-O3'	9.24	123.26	109.40
1	A	29	ASN	N-CA-C	7.58	119.33	111.14
1	A	42	LEU	N-CA-C	6.86	118.55	111.14
1	B	170	THR	CA-C-N	6.65	126.10	118.85
1	B	170	THR	C-N-CA	6.65	126.10	118.85
1	B	29	ASN	N-CA-C	6.55	118.22	111.14
2	C	-1	U	C2'-C3'-O3'	5.90	118.35	109.50
2	D	-1	U	C2'-C3'-O3'	5.86	118.29	109.50
1	B	184	PHE	N-CA-C	-5.81	101.02	110.20
1	A	184	PHE	N-CA-C	-5.79	101.70	110.28

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	-5	A	C3'
2	D	-5	A	C3'

There are no planarity outliers.

5.2 Too-close contacts

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	1523	0	1517	23	0
1	B	1505	0	1492	46	0
2	C	143	0	75	3	0
2	D	143	0	75	1	0
3	A	89	0	0	2	0
3	B	89	0	0	3	0
3	C	15	0	0	2	0
3	D	13	0	0	0	0
All	All	3520	0	3159	73	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 11.

All (73) 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:34:LYS:HD3	1:B:34:LYS:H	1.05	1.11
1:B:116:LYS:HB3	1:B:181:LEU:HD21	1.37	1.03
1:B:34:LYS:H	1:B:34:LYS:CD	1.87	0.88
2:C:-7:A:H2'	3:C:2013:HOH:O	1.74	0.87
1:B:34:LYS:HD3	1:B:34:LYS:N	1.90	0.86
1:A:165:LYS:O	1:A:169:GLU:HG2	1.78	0.83
1:B:174:LYS:HG3	1:B:178:THR:O	1.85	0.77
2:C:-7:A:C2'	3:C:2013:HOH:O	2.32	0.76
1:B:174:LYS:HG3	1:B:178:THR:C	2.14	0.73
1:B:189:PHE:O	3:B:2090:HOH:O	2.11	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:GLY:HA3	1:B:180:LEU:HD23	1.76	0.67
1:B:165:LYS:O	1:B:169:GLU:HG3	1.97	0.64
1:B:181:LEU:HD23	1:B:181:LEU:H	1.63	0.63
1:B:123:THR:HG22	1:B:126:ASP:CG	2.23	0.63
1:B:116:LYS:HB3	1:B:181:LEU:CD2	2.21	0.62
1:B:146:LEU:O	1:B:146:LEU:HD23	2.01	0.60
1:A:148:LYS:NZ	1:A:148:LYS:HB3	2.17	0.59
1:A:46:TRP:HB3	1:A:88:LYS:HD2	1.84	0.58
1:B:123:THR:HG22	1:B:126:ASP:OD2	2.04	0.57
1:B:176:LYS:O	1:B:177:GLU:HB3	2.04	0.57
1:B:53:ILE:C	1:B:53:ILE:HD12	2.31	0.56
1:B:123:THR:HG23	1:B:126:ASP:H	1.70	0.56
1:A:111:ARG:HG2	1:A:160:SER:C	2.31	0.54
1:B:142:MET:HA	1:B:154:ILE:HG22	1.90	0.54
1:A:134:LYS:HG2	1:A:167:PHE:HE1	1.72	0.53
1:B:123:THR:CG2	1:B:126:ASP:H	2.22	0.53
1:B:34:LYS:O	1:B:38:GLU:HG2	2.09	0.53
1:B:119:PRO:HG2	1:B:122:ALA:HB2	1.91	0.53
1:B:111:ARG:HG3	1:B:161:ILE:HD12	1.90	0.53
1:B:111:ARG:HD3	1:B:160:SER:HA	1.91	0.52
1:B:129:GLU:O	1:B:132:GLU:HB3	2.10	0.52
1:B:46:TRP:HB3	1:B:88:LYS:HD2	1.92	0.51
1:B:56:ASN:O	1:B:60:ARG:HG3	2.10	0.51
1:A:148:LYS:HB3	1:A:148:LYS:HZ2	1.75	0.49
1:A:175:TYR:O	1:A:176:LYS:C	2.56	0.48
1:B:35:PHE:O	1:B:39:GLN:HG2	2.13	0.48
1:B:40:ILE:HG23	1:B:45:GLY:HA2	1.96	0.48
1:B:111:ARG:CG	1:B:161:ILE:HD12	2.44	0.47
1:A:111:ARG:HG2	1:A:161:ILE:N	2.29	0.47
1:B:32:ARG:HD2	1:B:32:ARG:C	2.39	0.47
1:A:113:VAL:HG12	1:A:114:TYR:N	2.30	0.46
1:B:123:THR:HG23	1:B:125:ASP:N	2.31	0.46
1:B:132:GLU:OE1	1:B:134:LYS:HG3	2.14	0.46
1:A:70:GLU:HG2	3:A:2036:HOH:O	2.15	0.46
1:A:158:PHE:HB3	1:A:163:SER:OG	2.15	0.46
1:B:116:LYS:CB	1:B:181:LEU:HD21	2.26	0.46
1:B:174:LYS:HD2	1:B:177:GLU:C	2.40	0.46
1:A:40:ILE:HG23	1:A:45:GLY:HA2	1.97	0.46
1:A:170:THR:HB	1:A:173:GLN:NE2	2.31	0.46
2:C:-3:U:H1'	2:C:-1:U:O5'	2.16	0.46
1:A:142:MET:HA	1:A:154:ILE:HG22	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:LEU:O	1:B:37:LYS:HD2	2.14	0.46
1:B:32:ARG:NE	3:B:2014:HOH:O	2.49	0.46
1:B:132:GLU:HG2	1:B:133:ASP:N	2.31	0.45
2:D:-3:U:H1'	2:D:-1:U:O5'	2.17	0.45
1:B:176:LYS:O	1:B:176:LYS:HG3	2.17	0.45
1:A:176:LYS:O	1:A:178:THR:HG23	2.17	0.45
1:A:29:ASN:O	1:A:32:ARG:HG3	2.17	0.45
1:A:169:GLU:O	1:A:171:PRO:HD3	2.17	0.44
1:B:104:TYR:O	1:B:108:VAL:HG23	2.17	0.44
1:B:132:GLU:CG	1:B:133:ASP:N	2.81	0.43
1:B:174:LYS:HD3	1:B:179:ASP:OD1	2.19	0.43
1:B:132:GLU:CG	1:B:133:ASP:H	2.31	0.42
1:B:131:LEU:O	1:B:132:GLU:C	2.62	0.42
1:A:104:TYR:O	1:A:108:VAL:HG23	2.19	0.42
1:A:57:ARG:HH22	1:A:125:ASP:CG	2.27	0.42
1:B:53:ILE:HD12	1:B:54:LYS:N	2.35	0.41
1:A:63:THR:O	1:A:63:THR:CG2	2.68	0.41
1:B:100:VAL:HB	3:B:2054:HOH:O	2.20	0.41
1:A:30:LEU:HB3	1:A:31:PRO:HD3	2.03	0.41
1:A:112:SER:OG	3:A:2067:HOH:O	2.05	0.41
1:A:175:TYR:HB2	1:A:180:LEU:HD11	2.02	0.41
1:B:181:LEU:O	1:B:181:LEU:HG	2.21	0.41

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	185/193 (96%)	183 (99%)	2 (1%)	0	100	100
1	B	184/193 (95%)	177 (96%)	5 (3%)	2 (1%)	11	8
All	All	369/386 (96%)	360 (98%)	7 (2%)	2 (0%)	24	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	132	GLU
1	B	176	LYS

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	165/176 (94%)	159 (96%)	6 (4%)	31	34
1	B	161/176 (92%)	156 (97%)	5 (3%)	35	39
All	All	326/352 (93%)	315 (97%)	11 (3%)	32	35

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	ARG
1	A	36	LEU
1	A	53	ILE
1	A	63	THR
1	A	147	HIS
1	A	148	LYS
1	B	34	LYS
1	B	36	LEU
1	B	63	THR
1	B	132	GLU
1	B	161	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	ASN
1	A	110	ASN
1	A	173	GLN
1	B	19	HIS

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Mol	Chain	Res	Type
1	B	56	ASN
1	B	139	ASN
1	B	173	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	6/7 (85%)	2 (33%)	1 (16%)
2	D	6/7 (85%)	2 (33%)	1 (16%)
All	All	12/14 (85%)	4 (33%)	2 (16%)

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	-4	A
2	C	-2	U
2	D	-4	A
2	D	-2	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	C	-5	A
2	D	-5	A

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

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

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	187/193 (96%)	1.46	45 (24%) 2 2	6, 21, 46, 70	0
1	B	186/193 (96%)	1.76	63 (33%) 1 1	6, 21, 47, 64	0
2	C	7/7 (100%)	1.14	2 (28%) 1 1	13, 17, 26, 28	0
2	D	7/7 (100%)	1.45	4 (57%) 0 0	12, 18, 27, 29	0
All	All	387/400 (96%)	1.60	114 (29%) 1 1	6, 21, 47, 70	0

All (114) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	172	GLY	6.6
1	A	172	GLY	6.2
1	B	9	LYS	5.1
1	A	190	ALA	5.1
1	B	146	LEU	5.1
1	A	175	TYR	4.9
1	B	161	ILE	4.8
1	A	189	PHE	4.8
1	B	189	PHE	4.7
1	B	181	LEU	4.6
1	A	147	HIS	4.6
1	B	133	ASP	4.4
1	A	8	GLU	4.4
1	B	34	LYS	4.3
1	B	10	MET	4.2
1	B	8	GLU	4.1
1	A	6	ASP	4.1
1	A	133	ASP	4.0
1	A	178	THR	4.0
1	B	178	THR	4.0
1	B	7	ASN	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	123	THR	3.9
1	B	179	ASP	3.8
1	B	42	LEU	3.7
1	A	7	ASN	3.7
1	B	177	GLU	3.7
1	B	175	TYR	3.6
1	B	84	GLU	3.6
1	A	34	LYS	3.5
1	B	190	ALA	3.5
1	B	132	GLU	3.5
1	B	170	THR	3.5
1	A	179	ASP	3.4
1	A	9	LYS	3.3
1	B	32	ARG	3.3
1	B	176	LYS	3.2
1	B	11	ALA	3.2
1	B	149	ALA	3.2
1	B	147	HIS	3.2
1	A	171	PRO	3.2
1	B	174	LYS	3.2
1	B	12	ALA	3.1
1	A	177	GLU	3.1
1	A	176	LYS	3.1
1	A	146	LEU	3.0
1	A	53	ILE	3.0
1	B	13	LEU	3.0
1	B	169	GLU	3.0
1	B	120	THR	3.0
1	B	41	LYS	3.0
1	B	130	TRP	3.0
1	A	168	VAL	2.9
1	B	37	LYS	2.9
1	A	170	THR	2.9
2	D	-5	A	2.8
1	B	180	LEU	2.7
1	A	192	LYS	2.7
1	B	192	LYS	2.7
1	A	149	ALA	2.7
1	B	117	GLY	2.7
1	B	38	GLU	2.6
1	B	153	SER	2.6
1	A	180	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	53	ILE	2.6
1	A	181	LEU	2.6
1	B	129	GLU	2.6
1	A	10	MET	2.6
2	D	-7	A	2.6
1	B	171	PRO	2.6
1	A	186	ASP	2.5
1	B	150	PHE	2.5
2	D	-4	A	2.5
1	B	28	PHE	2.5
1	B	168	VAL	2.4
1	A	32	ARG	2.4
1	A	154	ILE	2.4
1	B	173	GLN	2.4
1	B	100	VAL	2.4
1	A	174	LYS	2.4
1	B	145	THR	2.4
1	A	103	GLU	2.3
1	B	122	ALA	2.3
1	A	117	GLY	2.3
1	A	153	SER	2.3
1	A	152	GLY	2.3
1	A	37	LYS	2.3
1	B	148	LYS	2.3
1	B	154	ILE	2.3
1	B	182	ILE	2.3
1	A	120	THR	2.3
1	B	66	ASN	2.3
1	B	125	ASP	2.3
1	B	166	LYS	2.3
1	A	188	TYR	2.2
2	C	-4	A	2.2
1	A	148	LYS	2.2
1	B	151	LYS	2.2
1	B	188	TYR	2.2
1	A	150	PHE	2.1
1	B	60	ARG	2.1
1	B	131	LEU	2.1
1	A	65	PHE	2.1
1	A	116	LYS	2.1
1	A	151	LYS	2.1
1	B	162	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
2	C	-6	U	2.1
1	B	144	ARG	2.1
1	A	191	LYS	2.1
1	A	162	GLU	2.0
1	B	141	GLN	2.0
1	B	104	TYR	2.0
1	A	44	GLU	2.0
1	A	41	LYS	2.0
2	D	-6	U	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.