



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 08:53 PM UTC

PDB ID : 1UVJ / pdb_00001uvj
Title : The structural basis for RNA specificity and Ca²⁺ inhibition of an RNA-dependent RNA polymerase phi6p2 with 7nt RNA
Authors : Salgado, P.S.; Makeyev, E.V.; Butcher, S.; Bamford, D.; Stuart, D.I.; Grimes, J.M.
Deposited on : 2004-01-21
Resolution : 1.90 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:

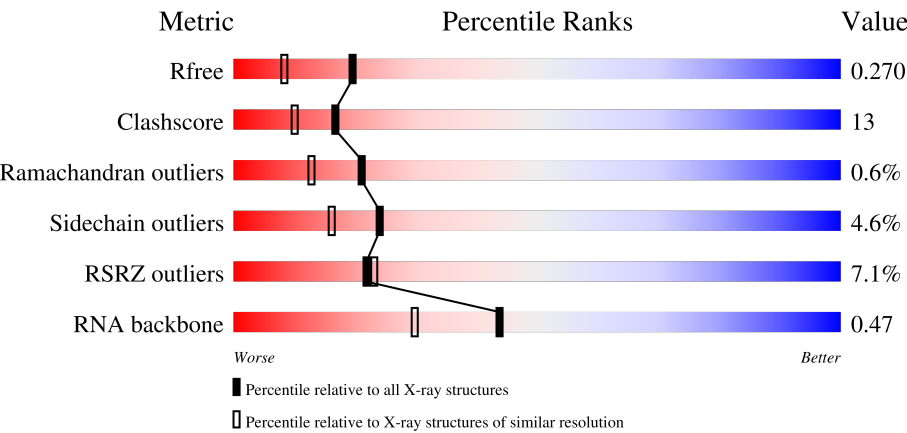
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)
RNA backbone	3983	1098 (2.30-1.50)

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	664	6% 76% 21% .
1	B	664	6% 75% 21% .
1	C	664	8% 74% 23% .
2	D	7	57% 43% 14% 43%

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Mol	Chain	Length	Quality of chain		
2	E	7	57%		
			43%	14%	43%
2	F	7	57%		
			43%	14%	43%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16633 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 RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	664	Total	C	N	O	S	0	0	0
			5265	3342	914	977	32			
1	B	664	Total	C	N	O	S	0	0	0
			5265	3342	914	977	32			
1	C	664	Total	C	N	O	S	0	0	0
			5265	3342	914	977	32			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	456	MET	ILE	conflict	UNP P11124
B	456	MET	ILE	conflict	UNP P11124
C	456	MET	ILE	conflict	UNP P11124

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	4	Total	C	N	O	P	0	0	0
			77	36	10	28	3			
2	E	4	Total	C	N	O	P	0	0	0
			77	36	10	28	3			
2	F	4	Total	C	N	O	P	0	0	0
			77	36	10	28	3			

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total 1	Mn 1	0	0

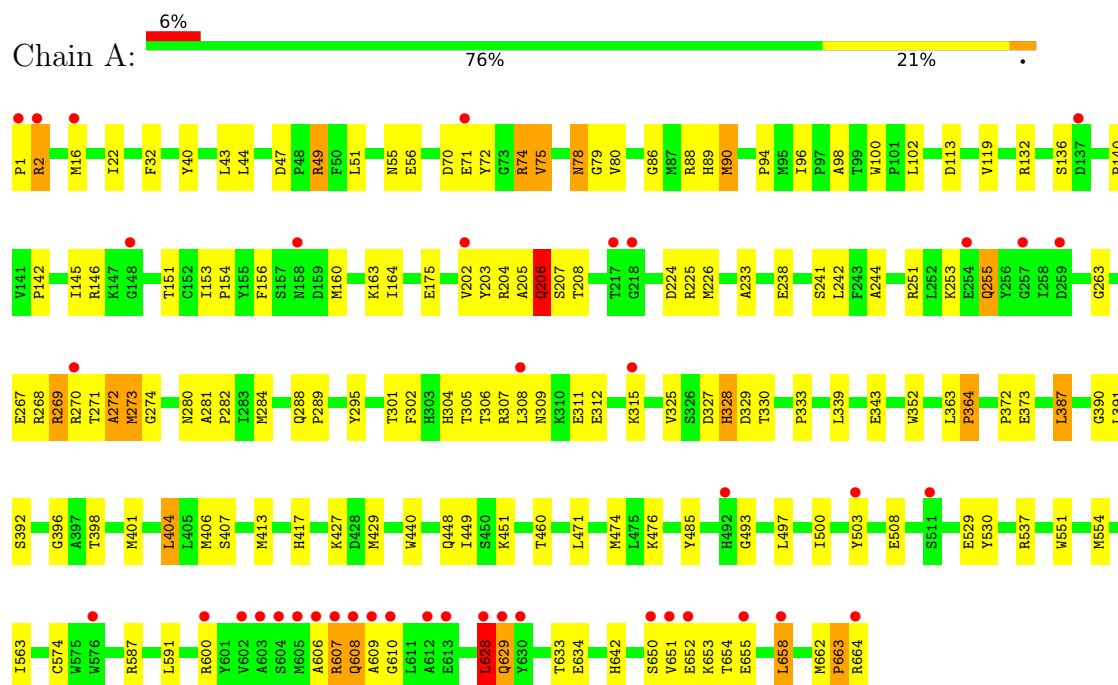
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	179	Total 179	O 179	0	0
4	B	271	Total 271	O 271	0	0
4	C	151	Total 151	O 151	0	0
4	D	1	Total 1	O 1	0	0
4	E	1	Total 1	O 1	0	0
4	F	1	Total 1	O 1	0	0

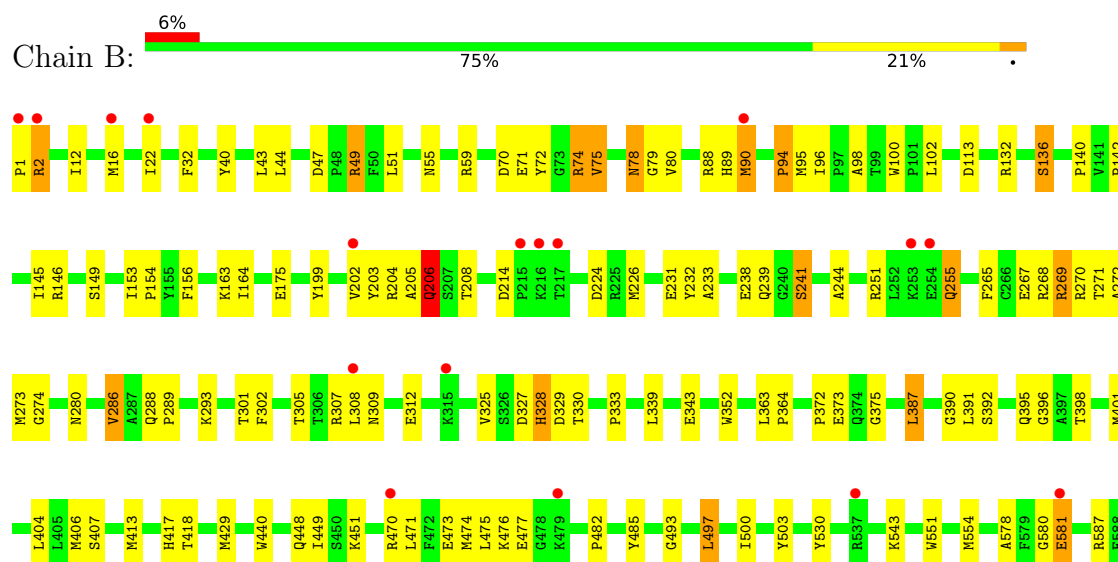
3 Residue-property plots [i](#)

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: RNA-directed RNA polymerase

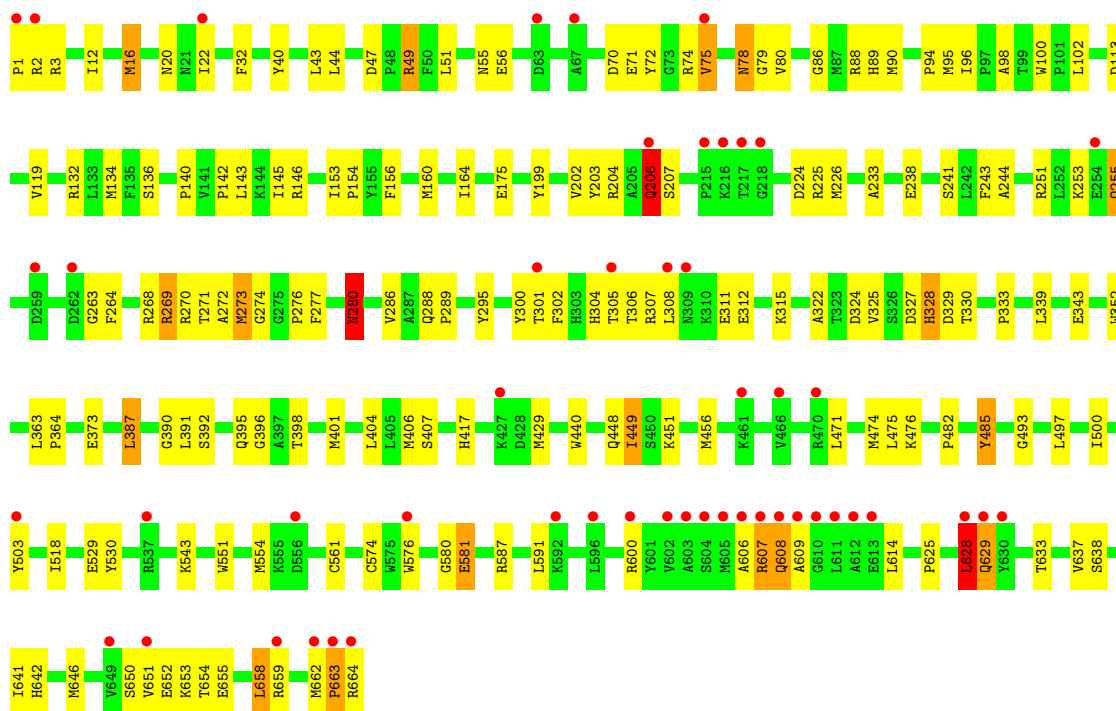
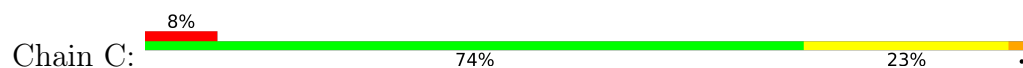


• Molecule 1: RNA-directed RNA polymerase

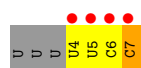




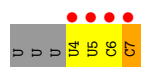
- Molecule 1: RNA-directed RNA polymerase



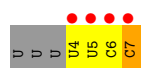
- Molecule 2: 5'-R(*UP*UP*CP*CP)-3'



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.06Å 93.51Å 140.71Å 90.00° 101.19° 90.00°	Depositor
Resolution (Å)	18.74 – 1.90 18.74 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (18.74-1.90) 99.7 (18.74-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.90Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.242 , 0.271 0.241 , 0.270	Depositor DCC
R_{free} test set	10430 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	26.6	Xtriage
Anisotropy	0.559	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 36.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16633	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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

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	0.66	1/5396 (0.0%)	1.04	27/7297 (0.4%)
1	B	0.69	1/5396 (0.0%)	1.04	32/7297 (0.4%)
1	C	0.65	0/5396	1.03	29/7297 (0.4%)
2	D	0.37	0/84	0.72	0/128
2	E	0.40	0/84	0.74	0/128
2	F	0.35	0/84	0.72	0/128
All	All	0.66	2/16440 (0.0%)	1.03	88/22275 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	413	MET	SD-CE	-6.76	1.62	1.79
1	A	413	MET	SD-CE	-5.80	1.65	1.79

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	136	SER	N-CA-C	10.15	124.34	111.24
1	B	136	SER	N-CA-C	10.03	124.18	111.24
1	B	100	TRP	N-CA-C	-9.21	98.46	110.07
1	C	206	GLN	N-CA-C	-9.17	88.89	107.41
1	B	206	GLN	N-CA-C	-8.41	90.43	107.41
1	C	302	PHE	N-CA-C	7.96	124.16	113.97
1	A	206	GLN	N-CA-C	-7.86	91.53	107.41
1	C	333	PRO	N-CA-C	7.59	122.92	110.55
1	A	302	PHE	N-CA-C	7.52	123.13	113.88
1	A	100	TRP	N-CA-C	-7.52	100.33	109.72
1	A	363	LEU	N-CA-C	7.51	120.44	110.08
1	B	98	ALA	N-CA-C	-7.41	100.97	110.53
1	C	136	SER	N-CA-C	7.38	122.48	111.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	363	LEU	N-CA-C	7.21	118.99	109.83
1	C	100	TRP	N-CA-C	-7.18	101.02	110.07
1	B	22	ILE	N-CA-C	7.17	117.94	110.62
1	B	333	PRO	N-CA-C	7.10	122.12	110.55
1	B	302	PHE	N-CA-C	7.01	122.94	113.97
1	A	98	ALA	N-CA-C	-6.91	100.57	110.59
1	A	255	GLN	N-CA-C	6.89	120.17	111.69
1	C	255	GLN	N-CA-C	6.68	119.91	111.69
1	C	95	MET	N-CA-C	-6.64	101.77	110.53
1	A	333	PRO	N-CA-C	6.59	121.29	110.55
1	C	396	GLY	N-CA-C	6.55	121.67	114.40
1	C	98	ALA	N-CA-C	-6.55	102.09	110.53
1	C	207	SER	N-CA-C	6.45	120.25	112.38
1	A	272	ALA	N-CA-C	-6.44	99.52	109.24
1	C	485	TYR	N-CA-C	6.40	121.12	113.12
1	B	396	GLY	N-CA-C	6.38	121.48	114.40
1	B	241	SER	N-CA-C	6.35	119.07	109.23
1	A	328	HIS	N-CA-C	6.30	118.67	111.11
1	C	449	ILE	N-CA-C	-6.29	99.06	108.12
1	B	485	TYR	N-CA-C	6.28	120.97	113.12
1	A	485	TYR	N-CA-C	6.23	121.11	112.45
1	B	95	MET	N-CA-C	-6.19	101.93	110.35
1	B	199	TYR	N-CA-C	-6.18	100.49	110.32
1	B	214	ASP	CA-C-N	6.05	125.54	119.24
1	B	214	ASP	C-N-CA	6.05	125.54	119.24
1	C	363	LEU	N-CA-C	6.02	118.39	110.08
1	B	136	SER	CA-C-N	-6.01	114.73	122.79
1	B	136	SER	C-N-CA	-6.01	114.73	122.79
1	C	136	SER	CA-C-N	-5.98	114.78	122.79
1	C	136	SER	C-N-CA	-5.98	114.78	122.79
1	B	94	PRO	N-CA-C	5.96	120.63	111.57
1	C	328	HIS	N-CA-C	5.95	118.25	111.11
1	C	22	ILE	N-CA-C	5.94	117.39	110.62
1	C	280	ASN	N-CA-C	5.78	117.66	111.36
1	A	449	ILE	N-CA-C	-5.75	99.84	108.12
1	B	418	THR	CA-C-N	-5.71	116.26	122.59
1	B	418	THR	C-N-CA	-5.71	116.26	122.59
1	A	396	GLY	N-CA-C	5.69	120.71	114.40
1	A	207	SER	N-CA-C	5.67	119.30	112.38
1	B	267	GLU	N-CA-C	5.66	118.86	110.48
1	A	136	SER	CA-C-N	-5.62	115.26	122.79
1	A	136	SER	C-N-CA	-5.62	115.26	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	265	PHE	N-CA-C	5.59	117.91	109.41
1	A	563	ILE	N-CA-C	5.55	116.85	111.91
1	C	199	TYR	N-CA-C	-5.52	101.55	110.32
1	C	390	GLY	N-CA-C	-5.52	104.67	111.45
1	A	241	SER	N-CA-C	5.47	117.50	109.24
1	B	390	GLY	N-CA-C	-5.46	104.73	111.45
1	C	395	GLN	N-CA-C	-5.46	102.19	110.28
1	A	22	ILE	N-CA-C	5.39	116.12	110.62
1	C	253	LYS	N-CA-C	-5.37	105.07	111.03
1	A	628	LEU	N-CA-C	-5.37	106.68	113.18
1	A	267	GLU	N-CA-C	5.33	118.37	110.48
1	A	253	LYS	N-CA-C	-5.32	105.12	111.03
1	C	277	PHE	N-CA-C	5.31	118.55	111.75
1	C	3	ARG	N-CA-C	-5.30	102.64	110.48
1	B	286	VAL	N-CA-C	-5.25	107.29	111.81
1	C	153	ILE	N-CA-C	5.25	114.68	108.96
1	B	628	LEU	N-CA-C	-5.25	106.88	113.28
1	C	628	LEU	N-CA-C	-5.22	106.91	113.28
1	B	153	ILE	N-CA-C	5.21	114.64	108.96
1	C	134	MET	N-CA-C	5.20	117.02	111.36
1	B	662	MET	N-CA-C	5.19	117.67	110.20
1	B	255	GLN	N-CA-C	5.15	118.02	111.69
1	B	375	GLY	N-CA-C	5.14	116.75	111.56
1	C	241	SER	N-CA-C	5.13	116.99	109.24
1	B	328	HIS	N-CA-C	5.13	117.27	111.11
1	A	390	GLY	N-CA-C	-5.13	105.14	111.45
1	A	242	LEU	N-CA-C	-5.13	100.05	108.41
1	A	460	THR	N-CA-C	-5.10	102.47	110.17
1	B	578	ALA	N-CA-C	5.05	117.90	111.69
1	C	276	PRO	N-CA-C	-5.04	102.09	112.47
1	B	449	ILE	N-CA-C	-5.03	100.88	108.12
1	A	508	GLU	CA-C-N	5.01	124.61	119.05
1	A	508	GLU	C-N-CA	5.01	124.61	119.05

There are no chirality outliers.

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	5265	0	5165	137	0
1	B	5265	0	5165	129	0
1	C	5265	0	5165	144	0
2	D	77	0	44	17	0
2	E	77	0	44	18	0
2	F	77	0	44	20	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	179	0	0	5	0
4	B	271	0	0	10	0
4	C	151	0	0	3	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
All	All	16633	0	15627	406	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 (406) 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:269:ARG:HH11	1:A:269:ARG:HG2	1.15	1.09
1:B:606:ALA:HB3	1:B:609:ALA:HB2	1.45	0.98
1:C:251:ARG:HH11	1:C:255:GLN:HE22	1.11	0.97
1:A:142:PRO:HG3	1:A:651:VAL:HG22	1.46	0.96
1:B:142:PRO:HG3	1:B:651:VAL:HG22	1.48	0.95
1:C:142:PRO:HG3	1:C:651:VAL:HG22	1.46	0.94
1:C:606:ALA:HB3	1:C:609:ALA:HB2	1.50	0.94
1:B:2:ARG:NH1	4:B:2003:HOH:O	2.00	0.93
1:C:269:ARG:HG2	1:C:269:ARG:HH11	1.32	0.93
1:A:47:ASP:OD1	1:A:49:ARG:HD3	1.71	0.90
1:A:269:ARG:HG2	1:A:269:ARG:NH1	1.82	0.87
1:B:451:LYS:HE2	2:E:7:C:N4	1.90	0.87
1:A:606:ALA:HB3	1:A:609:ALA:HB2	1.57	0.85
1:A:251:ARG:HH11	1:A:255:GLN:HE22	1.22	0.83
1:B:51:LEU:HD13	1:B:90:MET:HE1	1.60	0.83
1:C:325:VAL:HG21	1:C:406:MET:HE2	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:451:LYS:HE2	2:F:7:C:N4	1.95	0.81
1:C:47:ASP:OD1	1:C:49:ARG:HD3	1.81	0.81
1:A:451:LYS:HE2	2:D:7:C:N4	1.97	0.80
1:C:301:THR:HG23	1:C:440:TRP:O	1.82	0.80
1:B:269:ARG:HD2	4:B:2146:HOH:O	1.82	0.79
1:B:269:ARG:HG2	1:B:269:ARG:HH11	1.48	0.79
1:A:608:GLN:HE22	1:B:593:ARG:CZ	1.96	0.78
1:C:629:GLN:HG2	2:F:6:C:C4	2.17	0.78
1:B:251:ARG:HH11	1:B:255:GLN:HE22	1.32	0.77
1:A:608:GLN:HE22	1:B:593:ARG:NH1	1.83	0.77
1:C:269:ARG:HG2	1:C:269:ARG:NH1	1.94	0.76
1:B:47:ASP:OD1	1:B:49:ARG:HD3	1.85	0.76
1:A:51:LEU:CD1	1:A:90:MET:HE1	2.16	0.75
1:B:12:ILE:O	1:B:16:MET:HG2	1.88	0.74
1:C:251:ARG:HH11	1:C:255:GLN:NE2	1.85	0.74
1:A:364:PRO:HA	1:A:387:LEU:HD22	1.69	0.74
1:B:658:LEU:HD21	4:B:2149:HOH:O	1.88	0.73
1:A:629:GLN:HG2	2:D:6:C:C4	2.24	0.73
1:B:51:LEU:CD1	1:B:90:MET:HE1	2.18	0.73
1:C:75:VAL:HG21	1:C:500:ILE:HG21	1.69	0.72
1:A:301:THR:HG23	1:A:440:TRP:O	1.90	0.72
1:C:90:MET:HE3	1:C:264:PHE:HB3	1.72	0.72
1:A:203:TYR:HB3	1:A:269:ARG:HD3	1.72	0.72
1:A:51:LEU:HD11	1:A:90:MET:HE1	1.71	0.71
1:B:451:LYS:HE2	2:E:7:C:H41	1.55	0.71
1:A:75:VAL:HG21	1:A:500:ILE:HG21	1.73	0.70
1:A:607:ARG:O	1:A:608:GLN:HG3	1.91	0.70
1:B:607:ARG:O	1:B:608:GLN:HG3	1.92	0.70
1:B:75:VAL:HG21	1:B:500:ILE:HG21	1.74	0.70
1:B:301:THR:HG23	1:B:440:TRP:O	1.91	0.70
1:C:140:PRO:HB3	1:C:658:LEU:HD23	1.72	0.70
1:C:301:THR:HG22	4:C:2114:HOH:O	1.92	0.70
1:C:269:ARG:HD2	4:C:2082:HOH:O	1.91	0.70
1:B:269:ARG:HG2	1:B:269:ARG:NH1	2.05	0.70
1:B:55:ASN:OD1	1:B:88:ARG:NH2	2.23	0.69
1:C:364:PRO:HA	1:C:387:LEU:HD22	1.73	0.69
1:C:633:THR:HA	2:F:7:C:H2'	1.73	0.69
1:B:301:THR:HG22	4:B:2202:HOH:O	1.94	0.68
1:C:132:ARG:NH1	1:C:343:GLU:OE2	2.25	0.68
1:C:600:ARG:NH1	1:C:600:ARG:HB2	2.09	0.68
1:A:55:ASN:OD1	1:A:88:ARG:NH2	2.25	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:SER:O	1:A:398:THR:HG21	1.93	0.68
1:B:2:ARG:O	1:B:2:ARG:HD3	1.94	0.67
1:A:140:PRO:HB3	1:A:658:LEU:HD23	1.77	0.67
1:A:651:VAL:O	1:A:655:GLU:HB2	1.95	0.67
1:B:364:PRO:HA	1:B:387:LEU:HD22	1.75	0.66
1:C:607:ARG:O	1:C:608:GLN:HG3	1.95	0.66
1:C:600:ARG:HB2	1:C:600:ARG:HH11	1.60	0.66
1:B:59:ARG:HD3	4:B:2044:HOH:O	1.95	0.66
1:A:72:TYR:CE1	1:A:476:LYS:HD3	2.30	0.66
1:B:140:PRO:HB3	1:B:658:LEU:HD23	1.76	0.66
1:C:451:LYS:CE	2:F:7:C:N4	2.58	0.66
1:B:75:VAL:HG21	1:B:500:ILE:CG2	2.26	0.66
1:A:308:LEU:O	1:A:312:GLU:HG3	1.96	0.66
1:B:132:ARG:NH1	1:B:343:GLU:OE2	2.29	0.65
1:C:203:TYR:HB3	1:C:269:ARG:HD3	1.78	0.65
1:A:251:ARG:HH11	1:A:255:GLN:NE2	1.92	0.65
1:A:156:PHE:HD1	2:D:4:U:H5	1.45	0.65
1:B:629:GLN:HG2	2:E:6:C:C4	2.32	0.65
1:C:75:VAL:HG21	1:C:500:ILE:CG2	2.26	0.65
1:A:274:GLY:HA2	2:D:5:U:H1'	1.78	0.65
1:A:600:ARG:HH11	1:A:600:ARG:HB2	1.62	0.65
1:C:202:VAL:HG11	2:F:4:U:C4'	2.27	0.65
1:A:1:PRO:HD2	1:A:238:GLU:OE1	1.97	0.64
1:C:392:SER:O	1:C:398:THR:HG21	1.98	0.64
1:C:72:TYR:CE1	1:C:476:LYS:HD3	2.32	0.64
1:C:78:ASN:HD22	1:C:79:GLY:N	1.96	0.64
1:C:308:LEU:O	1:C:312:GLU:HG3	1.98	0.63
1:A:451:LYS:HE2	2:D:7:C:H41	1.63	0.63
1:B:471:LEU:HD12	1:B:474:MET:HE3	1.81	0.63
1:C:132:ARG:HD2	1:C:429:MET:HE2	1.80	0.63
1:C:206:GLN:HE21	1:C:268:ARG:HH11	1.46	0.63
1:A:537:ARG:HD3	4:A:2143:HOH:O	1.98	0.63
1:B:392:SER:O	1:B:398:THR:HG21	1.98	0.63
1:C:251:ARG:NH1	1:C:255:GLN:HE22	1.92	0.63
1:A:658:LEU:HB3	1:A:662:MET:CE	2.28	0.63
1:C:55:ASN:OD1	1:C:88:ARG:NH2	2.27	0.62
1:B:606:ALA:CB	1:B:609:ALA:HB2	2.24	0.62
1:B:650:SER:OG	1:B:653:LYS:HG3	2.00	0.62
1:C:224:ASP:HB3	1:C:226:MET:HE1	1.81	0.62
1:B:224:ASP:HB3	1:B:226:MET:HE1	1.81	0.62
1:A:90:MET:HA	1:A:90:MET:HE2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:SER:O	1:A:398:THR:CG2	2.48	0.61
1:B:651:VAL:O	1:B:655:GLU:HB2	1.99	0.61
1:A:451:LYS:CE	2:D:7:C:N4	2.63	0.61
1:A:650:SER:OG	1:A:653:LYS:HG3	2.00	0.61
1:B:606:ALA:C	1:B:608:GLN:H	2.08	0.61
1:B:72:TYR:CE1	1:B:476:LYS:HD3	2.36	0.61
1:C:206:GLN:HG3	1:C:270:ARG:HD2	1.82	0.61
1:C:651:VAL:O	1:C:655:GLU:HB2	2.00	0.61
1:B:224:ASP:HB3	1:B:226:MET:CE	2.31	0.61
1:A:606:ALA:C	1:A:608:GLN:H	2.08	0.60
1:B:658:LEU:HB3	1:B:662:MET:CE	2.31	0.60
1:B:606:ALA:HB3	1:B:609:ALA:CB	2.27	0.60
1:A:600:ARG:HB2	1:A:600:ARG:NH1	2.16	0.60
1:A:629:GLN:NE2	2:D:7:C:H5''	2.15	0.60
1:A:417:HIS:CE1	1:A:474:MET:HE1	2.37	0.60
1:A:327:ASP:CG	1:A:330:THR:OG1	2.44	0.60
1:C:600:ARG:HH11	1:C:600:ARG:CB	2.15	0.60
1:A:2:ARG:O	1:A:2:ARG:HD3	2.01	0.59
1:A:280:ASN:ND2	4:A:2082:HOH:O	2.35	0.59
1:B:471:LEU:CD1	1:B:474:MET:HE3	2.32	0.59
1:C:269:ARG:HH11	1:C:269:ARG:CG	2.10	0.59
1:C:325:VAL:CG2	1:C:406:MET:HE2	2.31	0.59
1:A:51:LEU:CD2	1:A:90:MET:HE1	2.33	0.59
1:B:308:LEU:O	1:B:312:GLU:HG3	2.01	0.59
1:A:224:ASP:HB3	1:A:226:MET:HE1	1.83	0.59
1:A:202:VAL:HG11	2:D:4:U:H4'	1.83	0.59
1:B:633:THR:HA	2:E:7:C:H2'	1.83	0.59
1:B:629:GLN:NE2	2:E:7:C:H5''	2.17	0.58
1:C:606:ALA:C	1:C:608:GLN:H	2.11	0.58
1:B:202:VAL:HG23	1:B:272:ALA:HB3	1.86	0.58
1:B:206:GLN:HE21	1:B:268:ARG:HH11	1.51	0.58
1:C:543:LYS:NZ	2:F:5:U:OP2	2.36	0.58
1:B:1:PRO:HD2	1:B:238:GLU:OE1	2.03	0.58
1:A:119:VAL:HG23	1:C:20:ASN:OD1	2.04	0.58
1:A:269:ARG:NH1	1:A:269:ARG:CG	2.61	0.58
1:A:295:TYR:HH	2:D:7:C:H5	1.52	0.57
1:B:600:ARG:HB2	1:B:600:ARG:NH1	2.19	0.57
1:A:132:ARG:NH1	1:A:343:GLU:OE2	2.35	0.57
1:B:51:LEU:HD13	1:B:90:MET:CE	2.33	0.57
1:A:203:TYR:HE1	1:A:271:THR:HG22	1.67	0.57
1:A:301:THR:HG22	4:A:2117:HOH:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:628:LEU:O	2:E:7:C:H3'	2.04	0.57
1:C:12:ILE:O	1:C:16:MET:HG3	2.04	0.57
1:C:51:LEU:HD13	1:C:90:MET:HE1	1.86	0.57
1:A:633:THR:HA	2:D:7:C:H2'	1.85	0.57
1:A:325:VAL:HG21	1:A:406:MET:HE2	1.86	0.57
1:A:202:VAL:HG11	2:D:4:U:C4'	2.35	0.57
1:C:202:VAL:HG11	2:F:4:U:H4'	1.87	0.57
1:B:145:ILE:HD12	1:B:164:ILE:HD13	1.86	0.56
1:C:417:HIS:CE1	1:C:474:MET:HE1	2.39	0.56
1:B:132:ARG:HD2	1:B:429:MET:HE2	1.87	0.56
1:B:274:GLY:HA2	2:E:5:U:H1'	1.86	0.56
1:B:205:ALA:HB2	1:B:269:ARG:HH12	1.70	0.56
1:C:32:PHE:CZ	1:C:96:ILE:HD11	2.40	0.56
1:A:78:ASN:ND2	1:A:80:VAL:H	2.02	0.56
1:C:1:PRO:O	1:C:2:ARG:HB3	2.06	0.56
1:A:606:ALA:O	1:A:608:GLN:N	2.39	0.56
1:B:451:LYS:CE	2:E:7:C:N4	2.66	0.56
1:C:145:ILE:HD12	1:C:164:ILE:HD13	1.88	0.56
1:C:328:HIS:HD2	1:C:329:ASP:OD1	1.89	0.56
1:A:251:ARG:NH1	1:A:255:GLN:HE22	1.99	0.55
1:A:156:PHE:HD1	2:D:4:U:C5	2.24	0.55
1:B:417:HIS:CE1	1:B:474:MET:HE1	2.41	0.55
1:C:1:PRO:HD2	1:C:238:GLU:OE1	2.06	0.55
1:C:339:LEU:C	1:C:339:LEU:HD23	2.31	0.55
1:A:75:VAL:HG21	1:A:500:ILE:CG2	2.35	0.55
1:A:288:GLN:HB3	1:A:289:PRO:HD3	1.88	0.55
1:B:40:TYR:OH	1:B:587:ARG:NH2	2.39	0.55
1:B:600:ARG:HB2	1:B:600:ARG:HH11	1.70	0.55
1:C:156:PHE:HD1	2:F:4:U:H5	1.54	0.54
1:C:576:TRP:CD1	4:C:2143:HOH:O	2.60	0.54
1:C:652:GLU:H	1:C:652:GLU:CD	2.16	0.54
1:A:132:ARG:HD2	1:A:429:MET:HE2	1.87	0.54
1:C:78:ASN:HD22	1:C:78:ASN:C	2.14	0.54
1:C:175:GLU:HA	1:C:352:TRP:CE3	2.43	0.54
1:A:78:ASN:HD22	1:A:79:GLY:N	2.05	0.54
1:B:328:HIS:HD2	1:B:329:ASP:OD1	1.90	0.54
1:C:392:SER:O	1:C:398:THR:CG2	2.54	0.54
1:C:295:TYR:HH	2:F:7:C:H5	1.54	0.54
1:A:78:ASN:HD22	1:A:78:ASN:C	2.15	0.54
1:A:206:GLN:HG3	1:A:270:ARG:HD2	1.90	0.54
1:A:339:LEU:C	1:A:339:LEU:HD23	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:451:LYS:CE	2:F:7:C:H41	2.21	0.54
1:B:600:ARG:HH11	1:B:600:ARG:CB	2.20	0.54
1:C:327:ASP:CG	1:C:330:THR:OG1	2.51	0.54
1:C:606:ALA:HB3	1:C:609:ALA:CB	2.31	0.54
1:A:269:ARG:HH11	1:A:269:ARG:CG	1.99	0.53
1:A:628:LEU:O	2:D:7:C:O2	2.26	0.53
1:C:606:ALA:CB	1:C:609:ALA:HB2	2.30	0.53
1:A:608:GLN:NE2	1:B:593:ARG:NH1	2.53	0.53
1:B:94:PRO:HB2	1:B:269:ARG:HG3	1.90	0.53
1:B:580:GLY:C	1:B:581:GLU:HG2	2.33	0.53
1:C:401:MET:HE2	1:C:401:MET:HA	1.89	0.53
1:A:51:LEU:HD21	1:A:90:MET:HE1	1.91	0.53
1:A:471:LEU:CD1	1:A:474:MET:HE3	2.39	0.53
1:B:606:ALA:O	1:B:608:GLN:N	2.42	0.53
1:C:94:PRO:HB2	1:C:269:ARG:HG3	1.91	0.53
1:C:663:PRO:O	1:C:664:ARG:CZ	2.57	0.53
1:A:451:LYS:CE	2:D:7:C:H41	2.22	0.52
1:C:274:GLY:HA2	2:F:5:U:H1'	1.90	0.52
1:C:580:GLY:C	1:C:581:GLU:HG2	2.33	0.52
1:A:75:VAL:HG12	1:A:493:GLY:HA2	1.91	0.52
1:A:94:PRO:HB2	1:A:269:ARG:HG3	1.91	0.52
1:B:392:SER:O	1:B:398:THR:CG2	2.58	0.52
1:A:74:ARG:HB3	1:A:503:TYR:CD2	2.44	0.52
1:A:226:MET:N	1:A:226:MET:HE2	2.25	0.52
1:C:301:THR:HG21	1:C:440:TRP:HA	1.92	0.52
1:B:156:PHE:HD1	2:E:4:U:H5	1.57	0.51
1:B:32:PHE:CZ	1:B:96:ILE:HD11	2.45	0.51
1:B:325:VAL:HG21	1:B:406:MET:HE2	1.93	0.51
1:C:204:ARG:HD2	1:C:530:TYR:OH	2.10	0.51
1:A:407:SER:HA	1:A:448:GLN:HE22	1.76	0.51
1:A:203:TYR:CE1	1:A:271:THR:HG22	2.46	0.51
1:B:652:GLU:CD	1:B:652:GLU:H	2.18	0.51
1:C:471:LEU:HD12	1:C:474:MET:HE3	1.93	0.51
1:C:658:LEU:HB3	1:C:662:MET:CE	2.40	0.51
1:A:663:PRO:O	1:A:664:ARG:CZ	2.58	0.51
1:A:70:ASP:OD2	1:A:74:ARG:HD3	2.11	0.51
1:B:628:LEU:O	2:E:7:C:O2	2.29	0.51
1:A:86:GLY:O	1:A:89:HIS:HD2	1.94	0.50
1:A:327:ASP:CG	1:A:330:THR:HG1	2.19	0.50
1:A:204:ARG:HD2	1:A:530:TYR:OH	2.11	0.50
1:C:226:MET:HE2	1:C:226:MET:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:175:GLU:HA	1:C:352:TRP:CD2	2.46	0.50
1:C:417:HIS:ND1	1:C:474:MET:HE1	2.26	0.50
1:B:70:ASP:OD2	1:B:74:ARG:HD3	2.12	0.50
1:B:226:MET:HE1	1:B:244:ALA:HB2	1.93	0.50
1:B:417:HIS:ND1	1:B:474:MET:HE1	2.27	0.50
1:B:75:VAL:HG12	1:B:493:GLY:HA2	1.93	0.50
1:A:427:LYS:HE3	1:C:12:ILE:HG21	1.93	0.50
1:A:224:ASP:HB3	1:A:226:MET:CE	2.40	0.50
1:B:327:ASP:CG	1:B:330:THR:OG1	2.55	0.50
1:B:286:VAL:C	1:B:289:PRO:HD2	2.37	0.50
1:C:1:PRO:HD2	1:C:238:GLU:CD	2.37	0.50
1:B:251:ARG:HH11	1:B:255:GLN:NE2	2.07	0.49
1:C:311:GLU:O	1:C:315:LYS:HG2	2.12	0.49
1:A:206:GLN:HE21	1:A:268:ARG:HH11	1.61	0.49
1:C:75:VAL:HG12	1:C:493:GLY:HA2	1.95	0.49
1:B:203:TYR:HB3	1:B:269:ARG:HD3	1.93	0.49
1:C:203:TYR:HE1	1:C:271:THR:HG22	1.78	0.49
1:A:40:TYR:OH	1:A:587:ARG:NH2	2.46	0.49
1:B:74:ARG:HB3	1:B:503:TYR:CD2	2.48	0.49
1:C:451:LYS:HE2	2:F:7:C:H41	1.73	0.49
1:B:301:THR:HG21	1:B:440:TRP:HA	1.94	0.49
1:B:606:ALA:C	1:B:608:GLN:N	2.70	0.49
1:B:1:PRO:HD2	1:B:238:GLU:CD	2.38	0.48
1:C:88:ARG:HD3	1:C:263:GLY:O	2.13	0.48
1:C:78:ASN:ND2	1:C:80:VAL:H	2.10	0.48
1:C:471:LEU:CD1	1:C:474:MET:HE3	2.43	0.48
1:C:650:SER:O	1:C:654:THR:HG23	2.14	0.48
1:A:471:LEU:HD12	1:A:474:MET:HE3	1.96	0.48
1:C:224:ASP:HB3	1:C:226:MET:CE	2.43	0.48
1:B:78:ASN:C	1:B:78:ASN:HD22	2.20	0.48
1:B:395:GLN:O	1:B:398:THR:HG23	2.13	0.48
1:A:226:MET:HE1	1:A:244:ALA:HB2	1.95	0.48
1:A:311:GLU:O	1:A:315:LYS:HG2	2.13	0.48
1:A:600:ARG:HH11	1:A:600:ARG:CB	2.25	0.48
1:B:633:THR:HG22	1:B:636:ASP:OD2	2.14	0.48
1:B:451:LYS:CE	2:E:7:C:H41	2.25	0.48
1:B:475:LEU:HD21	1:B:482:PRO:HG3	1.96	0.48
1:C:40:TYR:OH	1:C:587:ARG:NH2	2.47	0.47
1:A:401:MET:HE2	1:A:401:MET:HA	1.96	0.47
1:C:90:MET:HE3	1:C:264:PHE:CB	2.41	0.47
1:A:273:MET:HE3	1:A:392:SER:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:MET:HE1	1:C:244:ALA:HB2	1.96	0.47
1:C:606:ALA:C	1:C:608:GLN:N	2.72	0.47
1:A:1:PRO:HD2	1:A:238:GLU:CD	2.39	0.47
1:C:650:SER:OG	1:C:653:LYS:HG3	2.14	0.47
1:B:78:ASN:ND2	1:B:80:VAL:H	2.12	0.47
1:B:663:PRO:O	1:B:664:ARG:CZ	2.63	0.47
1:C:119:VAL:HG22	1:C:485:TYR:OH	2.15	0.47
2:F:7:C:H3'	2:F:7:C:O2	2.14	0.47
1:A:32:PHE:CD2	1:A:372:PRO:HG3	2.50	0.47
1:A:88:ARG:HD3	1:A:263:GLY:O	2.15	0.47
1:B:231:GLU:HG2	4:B:2122:HOH:O	2.15	0.47
1:C:629:GLN:NE2	2:F:7:C:H5''	2.30	0.47
1:A:160:MET:O	1:A:164:ILE:HG12	2.14	0.47
1:B:202:VAL:HG11	2:E:4:U:H4'	1.96	0.47
1:B:650:SER:O	1:B:654:THR:HG23	2.15	0.47
1:C:628:LEU:O	2:F:7:C:O2	2.33	0.47
1:A:610:GLY:HA3	4:A:2169:HOH:O	2.14	0.47
1:A:654:THR:O	1:A:658:LEU:HD22	2.15	0.47
1:B:280:ASN:ND2	4:B:2148:HOH:O	2.47	0.47
1:A:175:GLU:HA	1:A:352:TRP:CE3	2.51	0.47
1:C:86:GLY:O	1:C:89:HIS:HD2	1.97	0.47
1:C:295:TYR:OH	2:F:7:C:H5	1.97	0.46
1:C:518:ILE:HB	1:C:561:CYS:SG	2.55	0.46
2:E:7:C:H3'	2:E:7:C:O2	2.15	0.46
1:C:74:ARG:HB3	1:C:503:TYR:CD2	2.50	0.46
1:B:206:GLN:HG3	1:B:270:ARG:HD2	1.96	0.46
1:C:70:ASP:OD2	1:C:74:ARG:HD3	2.15	0.46
1:C:56:GLU:HG2	1:C:574:CYS:SG	2.56	0.46
1:B:204:ARG:NE	2:E:5:U:O4	2.48	0.46
1:A:225:ARG:C	1:A:226:MET:HE2	2.40	0.46
1:A:273:MET:HE3	1:A:392:SER:CB	2.46	0.46
1:C:225:ARG:C	1:C:226:MET:HE2	2.41	0.46
1:A:274:GLY:HA2	2:D:5:U:C1'	2.43	0.46
1:A:102:LEU:HD12	1:A:233:ALA:HA	1.97	0.46
1:A:175:GLU:HA	1:A:352:TRP:CD2	2.51	0.46
1:A:205:ALA:HB2	1:A:269:ARG:HH12	1.81	0.45
1:A:51:LEU:HD21	1:A:90:MET:CE	2.46	0.45
1:B:175:GLU:HA	1:B:352:TRP:CD2	2.51	0.45
1:C:102:LEU:HD12	1:C:233:ALA:HA	1.98	0.45
1:A:32:PHE:CZ	1:A:96:ILE:HD11	2.51	0.45
1:A:56:GLU:HG2	1:A:574:CYS:SG	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:PRO:CB	1:C:658:LEU:HD23	2.43	0.45
1:A:145:ILE:HD12	1:A:164:ILE:HD13	1.98	0.45
1:B:175:GLU:HA	1:B:352:TRP:CE3	2.51	0.45
1:C:606:ALA:O	1:C:608:GLN:N	2.49	0.45
1:A:417:HIS:ND1	1:A:474:MET:HE1	2.32	0.45
1:C:551:TRP:CH2	1:C:554:MET:HE1	2.52	0.45
1:C:625:PRO:O	1:C:628:LEU:HB2	2.17	0.45
1:B:203:TYR:HE1	1:B:271:THR:HG22	1.81	0.44
1:C:407:SER:HA	1:C:448:GLN:HE22	1.83	0.44
1:C:614:LEU:HD21	1:C:641:ILE:HD11	2.00	0.44
1:B:239:GLN:NE2	4:B:2128:HOH:O	2.51	0.44
1:C:288:GLN:HB3	1:C:289:PRO:HD3	1.99	0.44
1:A:325:VAL:CG2	1:A:406:MET:HE2	2.48	0.44
1:A:652:GLU:CD	1:A:652:GLU:H	2.26	0.44
1:A:94:PRO:CB	1:A:269:ARG:HG3	2.48	0.44
1:B:205:ALA:CB	1:B:269:ARG:HH12	2.30	0.44
1:A:364:PRO:HA	1:A:387:LEU:CD2	2.44	0.44
1:A:305:THR:H	1:A:309:ASN:ND2	2.16	0.43
1:B:32:PHE:CD2	1:B:372:PRO:HG3	2.52	0.43
1:C:202:VAL:HG23	1:C:272:ALA:HB3	2.00	0.43
1:C:659:ARG:NH1	1:C:659:ARG:HB2	2.33	0.43
1:B:78:ASN:HD22	1:B:79:GLY:N	2.15	0.43
1:B:497:LEU:HD12	1:B:497:LEU:HA	1.76	0.43
1:B:202:VAL:HG11	2:E:4:U:C4'	2.47	0.43
1:B:305:THR:H	1:B:309:ASN:ND2	2.15	0.43
1:C:650:SER:HB2	1:C:652:GLU:OE1	2.19	0.43
1:B:286:VAL:O	1:B:289:PRO:HD2	2.19	0.43
1:C:628:LEU:O	2:F:7:C:H3'	2.18	0.43
1:A:301:THR:HG21	1:A:440:TRP:HA	2.00	0.43
1:B:274:GLY:HA2	2:E:5:U:C1'	2.48	0.43
1:B:650:SER:HB2	1:B:652:GLU:OE1	2.19	0.43
1:C:529:GLU:O	1:C:529:GLU:HG2	2.18	0.43
1:A:151:THR:CG2	1:A:163:LYS:HG2	2.49	0.43
1:C:12:ILE:O	1:C:16:MET:CG	2.65	0.43
1:C:475:LEU:HD21	1:C:482:PRO:HG3	2.00	0.43
1:C:642:HIS:CE1	1:C:646:MET:HG3	2.54	0.43
1:B:149:SER:OG	1:B:163:LYS:HE3	2.19	0.43
1:B:204:ARG:CZ	2:E:5:U:O4	2.67	0.43
1:C:322:ALA:HB2	1:C:456:MET:HE2	1.99	0.43
1:A:634:GLU:HB2	1:A:642:HIS:NE2	2.34	0.43
1:B:401:MET:HA	1:B:401:MET:HE2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:ASN:HD22	1:A:280:ASN:HA	1.62	0.42
1:A:328:HIS:HD2	1:A:329:ASP:OD1	2.02	0.42
1:B:204:ARG:HD3	2:E:5:U:O4	2.19	0.42
1:C:304:HIS:CE1	1:C:449:ILE:HB	2.54	0.42
1:A:206:GLN:OE1	1:A:208:THR:O	2.37	0.42
1:B:140:PRO:CB	1:B:658:LEU:HD23	2.46	0.42
1:B:175:GLU:HG3	1:B:352:TRP:CD1	2.55	0.42
1:C:203:TYR:CE1	1:C:271:THR:HG22	2.55	0.42
1:B:407:SER:HA	1:B:448:GLN:HE22	1.85	0.42
1:C:664:ARG:NH1	1:C:664:ARG:HG2	2.34	0.42
1:B:470:ARG:HD2	4:B:2212:HOH:O	2.19	0.42
2:D:7:C:O2	2:D:7:C:H3'	2.19	0.42
1:A:610:GLY:CA	4:A:2169:HOH:O	2.67	0.42
1:B:339:LEU:HD23	1:B:339:LEU:C	2.45	0.42
1:C:273:MET:HE3	1:C:392:SER:HB3	2.01	0.42
1:B:51:LEU:CD1	1:B:90:MET:CE	2.94	0.42
1:A:427:LYS:HE3	1:C:12:ILE:CG2	2.50	0.42
1:C:274:GLY:HA2	2:F:5:U:C1'	2.50	0.42
1:C:286:VAL:C	1:C:289:PRO:HD2	2.45	0.42
1:C:280:ASN:HD22	1:C:280:ASN:HA	1.64	0.42
1:A:153:ILE:HA	1:A:154:PRO:HA	1.78	0.41
1:C:300:TYR:CD1	1:C:300:TYR:C	2.98	0.41
1:A:119:VAL:CG2	1:C:20:ASN:OD1	2.67	0.41
1:B:204:ARG:HD2	1:B:530:TYR:OH	2.20	0.41
1:B:551:TRP:CH2	1:B:554:MET:HE1	2.55	0.41
1:C:86:GLY:O	1:C:89:HIS:CD2	2.73	0.41
1:C:160:MET:O	1:C:164:ILE:HG12	2.20	0.41
1:C:637:VAL:O	1:C:638:SER:C	2.63	0.41
1:A:404:LEU:HD12	1:A:404:LEU:C	2.45	0.41
1:A:529:GLU:O	1:A:529:GLU:HG2	2.19	0.41
1:B:288:GLN:HB3	1:B:289:PRO:HD3	2.02	0.41
1:B:543:LYS:O	1:B:625:PRO:HD2	2.19	0.41
1:C:51:LEU:CD1	1:C:90:MET:HE1	2.51	0.41
1:C:156:PHE:HD1	2:F:4:U:C5	2.37	0.41
1:B:206:GLN:OE1	1:B:208:THR:O	2.38	0.41
1:C:94:PRO:CB	1:C:269:ARG:HG3	2.50	0.41
1:A:304:HIS:HA	1:A:309:ASN:HD21	1.86	0.41
1:C:273:MET:O	2:F:5:U:H1'	2.21	0.41
1:A:51:LEU:CD2	1:A:90:MET:CE	2.97	0.41
1:A:284:MET:HE3	2:D:7:C:OP1	2.21	0.41
1:A:404:LEU:C	1:A:404:LEU:CD1	2.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:606:ALA:C	1:A:608:GLN:N	2.70	0.41
1:B:89:HIS:HE1	4:B:2133:HOH:O	2.04	0.41
1:C:305:THR:OG1	1:C:306:THR:N	2.54	0.41
1:A:202:VAL:HG23	1:A:272:ALA:HB3	2.03	0.41
1:C:143:LEU:HD23	1:C:143:LEU:C	2.46	0.41
1:C:225:ARG:HD3	1:C:225:ARG:HA	1.84	0.41
1:A:305:THR:OG1	1:A:306:THR:N	2.53	0.40
1:B:232:TYR:HA	1:B:239:GLN:O	2.20	0.40
1:C:16:MET:HE2	1:C:16:MET:HB3	1.96	0.40
1:A:551:TRP:CH2	1:A:554:MET:HE1	2.55	0.40
1:B:473:GLU:O	1:B:477:GLU:HG3	2.21	0.40
1:B:647:HIS:ND1	1:B:648:GLY:N	2.68	0.40
1:C:628:LEU:HD12	1:C:628:LEU:HA	1.96	0.40
1:A:175:GLU:HG3	1:A:352:TRP:CD1	2.57	0.40
1:A:281:ALA:HB3	1:A:282:PRO:CD	2.52	0.40
1:B:102:LEU:HD12	1:B:233:ALA:HA	2.03	0.40
1:C:70:ASP:OD2	1:C:74:ARG:CD	2.70	0.40
1:B:658:LEU:HB3	1:B:662:MET:HE1	2.02	0.40
1:B:136:SER:OG	1:B:293:LYS:NZ	2.55	0.40
1:C:1:PRO:HD2	1:C:238:GLU:OE2	2.21	0.40
1:C:243:PHE:CD1	1:C:243:PHE:N	2.89	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	662/664 (100%)	638 (96%)	20 (3%)	4 (1%)	21	13
1	B	662/664 (100%)	635 (96%)	23 (4%)	4 (1%)	21	13
1	C	662/664 (100%)	634 (96%)	25 (4%)	3 (0%)	24	16
All	All	1986/1992 (100%)	1907 (96%)	68 (3%)	11 (1%)	21	13

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	607	ARG
1	A	608	GLN
1	B	607	ARG
1	B	608	GLN
1	C	607	ARG
1	C	608	GLN
1	A	2	ARG
1	B	2	ARG
1	A	663	PRO
1	B	663	PRO
1	C	663	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	557/557 (100%)	532 (96%)	25 (4%)	24	17
1	B	557/557 (100%)	531 (95%)	26 (5%)	23	15
1	C	557/557 (100%)	531 (95%)	26 (5%)	23	15
All	All	1671/1671 (100%)	1594 (95%)	77 (5%)	24	16

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	MET
1	A	43	LEU
1	A	44	LEU
1	A	49	ARG
1	A	71	GLU
1	A	74	ARG
1	A	75	VAL
1	A	78	ASN
1	A	90	MET
1	A	113	ASP

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Mol	Chain	Res	Type
1	A	146	ARG
1	A	206	GLN
1	A	269	ARG
1	A	273	MET
1	A	307	ARG
1	A	364	PRO
1	A	373	GLU
1	A	387	LEU
1	A	391	LEU
1	A	404	LEU
1	A	497	LEU
1	A	591	LEU
1	A	628	LEU
1	A	629	GLN
1	A	658	LEU
1	B	43	LEU
1	B	44	LEU
1	B	49	ARG
1	B	71	GLU
1	B	74	ARG
1	B	75	VAL
1	B	78	ASN
1	B	90	MET
1	B	113	ASP
1	B	146	ARG
1	B	154	PRO
1	B	206	GLN
1	B	241	SER
1	B	269	ARG
1	B	273	MET
1	B	307	ARG
1	B	373	GLU
1	B	387	LEU
1	B	391	LEU
1	B	404	LEU
1	B	497	LEU
1	B	581	GLU
1	B	591	LEU
1	B	628	LEU
1	B	629	GLN
1	B	658	LEU
1	C	16	MET

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Mol	Chain	Res	Type
1	C	43	LEU
1	C	44	LEU
1	C	49	ARG
1	C	71	GLU
1	C	75	VAL
1	C	78	ASN
1	C	113	ASP
1	C	146	ARG
1	C	154	PRO
1	C	206	GLN
1	C	269	ARG
1	C	273	MET
1	C	280	ASN
1	C	307	ARG
1	C	324	ASP
1	C	373	GLU
1	C	387	LEU
1	C	391	LEU
1	C	404	LEU
1	C	497	LEU
1	C	581	GLU
1	C	591	LEU
1	C	628	LEU
1	C	629	GLN
1	C	658	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	78	ASN
1	A	89	HIS
1	A	91	ASN
1	A	183	GLN
1	A	191	GLN
1	A	206	GLN
1	A	255	GLN
1	A	280	ASN
1	A	309	ASN
1	A	328	HIS
1	A	448	GLN
1	A	519	ASN

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Mol	Chain	Res	Type
1	A	525	GLN
1	A	608	GLN
1	A	626	ASN
1	A	629	GLN
1	B	26	GLN
1	B	64	HIS
1	B	78	ASN
1	B	89	HIS
1	B	91	ASN
1	B	191	GLN
1	B	194	GLN
1	B	206	GLN
1	B	239	GLN
1	B	255	GLN
1	B	280	ASN
1	B	309	ASN
1	B	328	HIS
1	B	448	GLN
1	B	525	GLN
1	B	626	ASN
1	B	629	GLN
1	C	15	GLN
1	C	26	GLN
1	C	78	ASN
1	C	89	HIS
1	C	91	ASN
1	C	183	GLN
1	C	191	GLN
1	C	206	GLN
1	C	255	GLN
1	C	280	ASN
1	C	309	ASN
1	C	328	HIS
1	C	448	GLN
1	C	519	ASN
1	C	525	GLN
1	C	626	ASN
1	C	629	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	D	3/7 (42%)	1 (33%)	0
2	E	3/7 (42%)	1 (33%)	0
2	F	3/7 (42%)	1 (33%)	0
All	All	9/21 (42%)	3 (33%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	D	7	C
2	E	7	C
2	F	7	C

There are no RNA pucker outliers to report.

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 3 ligands modelled in this entry, 3 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

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	664/664 (100%)	0.35	41 (6%)	26	28	18, 30, 50, 101	0
1	B	664/664 (100%)	0.31	40 (6%)	27	29	19, 28, 50, 101	0
1	C	664/664 (100%)	0.57	50 (7%)	20	21	19, 32, 52, 102	0
2	D	4/7 (57%)	5.44	4 (100%)	0	0	119, 122, 123, 127	0
2	E	4/7 (57%)	5.23	4 (100%)	0	0	119, 122, 124, 127	0
2	F	4/7 (57%)	5.07	4 (100%)	0	0	119, 122, 123, 127	0
All	All	2004/2013 (99%)	0.44	143 (7%)	22	23	18, 30, 52, 127	0

All (143) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	609	ALA	11.3
1	A	606	ALA	10.0
1	B	609	ALA	9.9
1	C	606	ALA	9.6
1	C	603	ALA	8.1
1	B	606	ALA	8.0
1	B	1	PRO	7.3
1	B	607	ARG	7.2
1	B	603	ALA	6.7
1	C	610	GLY	6.6
1	A	1	PRO	6.3
2	D	4	U	6.2
2	F	4	U	5.7
1	C	576	TRP	5.7
1	A	609	ALA	5.6
2	E	7	C	5.5
1	A	603	ALA	5.5
1	C	470	ARG	5.5
1	C	1	PRO	5.5

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Mol	Chain	Res	Type	RSRZ
2	E	6	C	5.4
1	A	576	TRP	5.3
2	E	5	U	5.3
2	D	7	C	5.3
2	D	5	U	5.2
1	B	2	ARG	5.2
1	C	607	ARG	5.0
1	C	608	GLN	5.0
1	C	605	MET	5.0
2	D	6	C	5.0
2	F	6	C	5.0
2	F	7	C	4.9
1	B	608	GLN	4.9
1	C	2	ARG	4.9
1	C	612	ALA	4.8
1	C	664	ARG	4.7
1	B	610	GLY	4.7
2	F	5	U	4.7
2	E	4	U	4.6
1	B	664	ARG	4.5
1	B	604	SER	4.3
1	B	651	VAL	4.3
1	C	651	VAL	4.3
1	A	604	SER	4.1
1	A	610	GLY	4.1
1	A	664	ARG	4.1
1	C	63	ASP	4.1
1	A	607	ARG	3.9
1	C	602	VAL	3.9
1	B	605	MET	3.9
1	B	537	ARG	3.9
1	B	22	ILE	3.9
1	C	254	GLU	3.9
1	B	611	LEU	3.8
1	B	600	ARG	3.8
1	C	611	LEU	3.7
1	A	257	GLY	3.7
1	A	608	GLN	3.7
1	C	596	LEU	3.6
1	A	254	GLU	3.5
1	B	612	ALA	3.5
1	B	216	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	602	VAL	3.4
1	A	651	VAL	3.4
1	B	581	GLU	3.3
1	C	22	ILE	3.3
1	C	216	LYS	3.3
1	C	604	SER	3.3
1	A	2	ARG	3.3
1	C	659	ARG	3.3
1	A	605	MET	3.2
1	C	556	ASP	3.2
1	C	215	PRO	3.2
1	A	202	VAL	3.1
1	C	308	LEU	3.1
1	C	630	TYR	3.0
1	C	613	GLU	3.0
1	B	215	PRO	3.0
1	A	613	GLU	3.0
1	B	16	MET	3.0
1	B	662	MET	3.0
1	B	217	THR	2.9
1	C	537	ARG	2.8
1	B	613	GLU	2.8
1	B	602	VAL	2.8
1	C	461	LYS	2.7
1	A	630	TYR	2.7
1	B	470	ARG	2.7
1	B	202	VAL	2.7
1	A	652	GLU	2.6
1	A	315	LYS	2.6
1	B	630	TYR	2.6
1	B	308	LEU	2.6
1	A	628	LEU	2.5
1	A	158	ASN	2.5
1	B	254	GLU	2.5
1	C	663	PRO	2.5
1	A	629	GLN	2.4
1	B	90	MET	2.4
1	A	217	THR	2.4
1	A	16	MET	2.4
1	A	308	LEU	2.4
1	C	259	ASP	2.4
1	C	217	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	67	ALA	2.4
1	C	262	ASP	2.3
1	A	492	HIS	2.3
1	C	309	ASN	2.3
1	C	592	LYS	2.3
1	A	71	GLU	2.3
1	C	503	TYR	2.3
1	B	253	LYS	2.3
1	A	612	ALA	2.3
1	A	218	GLY	2.2
1	A	137	ASP	2.2
1	A	658	LEU	2.2
1	B	658	LEU	2.2
1	A	148	GLY	2.2
1	A	600	ARG	2.2
1	C	75	VAL	2.2
1	C	629	GLN	2.2
1	B	479	LYS	2.2
1	C	427	LYS	2.2
1	A	259	ASP	2.1
1	A	650	SER	2.1
1	C	305	THR	2.1
1	C	649	VAL	2.1
1	C	662	MET	2.1
1	B	589	ASP	2.1
1	A	270	ARG	2.1
1	C	466	VAL	2.1
1	C	206	GLN	2.1
1	C	628	LEU	2.1
1	B	635	ALA	2.1
1	A	655	GLU	2.0
1	C	301	THR	2.0
1	C	218	GLY	2.0
1	B	663	PRO	2.0
1	B	659	ARG	2.0
1	B	315	LYS	2.0
1	A	511	SER	2.0
1	A	503	TYR	2.0
1	B	656	ARG	2.0
1	C	600	ARG	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](#)

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($\text{\AA}^2$)	Q<0.9
3	MN	A	1665	1/1	0.99	0.02	27,27,27,27	0
3	MN	B	1665	1/1	0.99	0.02	25,25,25,25	0
3	MN	C	1665	1/1	0.99	0.02	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.