



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 10:06 PM UTC

PDB ID : 2C0B / pdb_00002c0b
Title : Catalytic domain of E. coli RNase E in complex with 13-mer RNA
Authors : Marcaida, M.J.; Callaghan, A.J.; Scott, W.G.; Luisi, B.F.
Deposited on : 2005-08-30
Resolution : 3.18 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

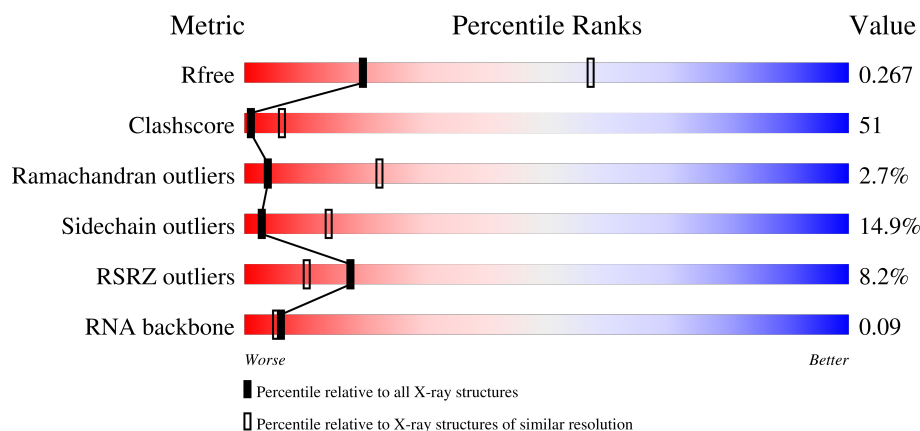
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.18 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	2001 (3.20-3.16)
Clashscore	190562	2119 (3.20-3.16)
Ramachandran outliers	187476	2070 (3.20-3.16)
Sidechain outliers	187428	2069 (3.20-3.16)
RSRZ outliers	180081	2001 (3.20-3.16)
RNA backbone	3983	1138 (3.46-2.90)

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	517	
2	R	13	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3821 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 RIBONUCLEASE E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	488	Total	C	N	O	S	0	0	0
			3555	2221	656	668	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	11	Total	C	N	O	P	0	0	0
			214	94	33	76	11			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	2	Total	Mg	0	0
			2	2		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	1	Total	Zn	0	0
			1	1		

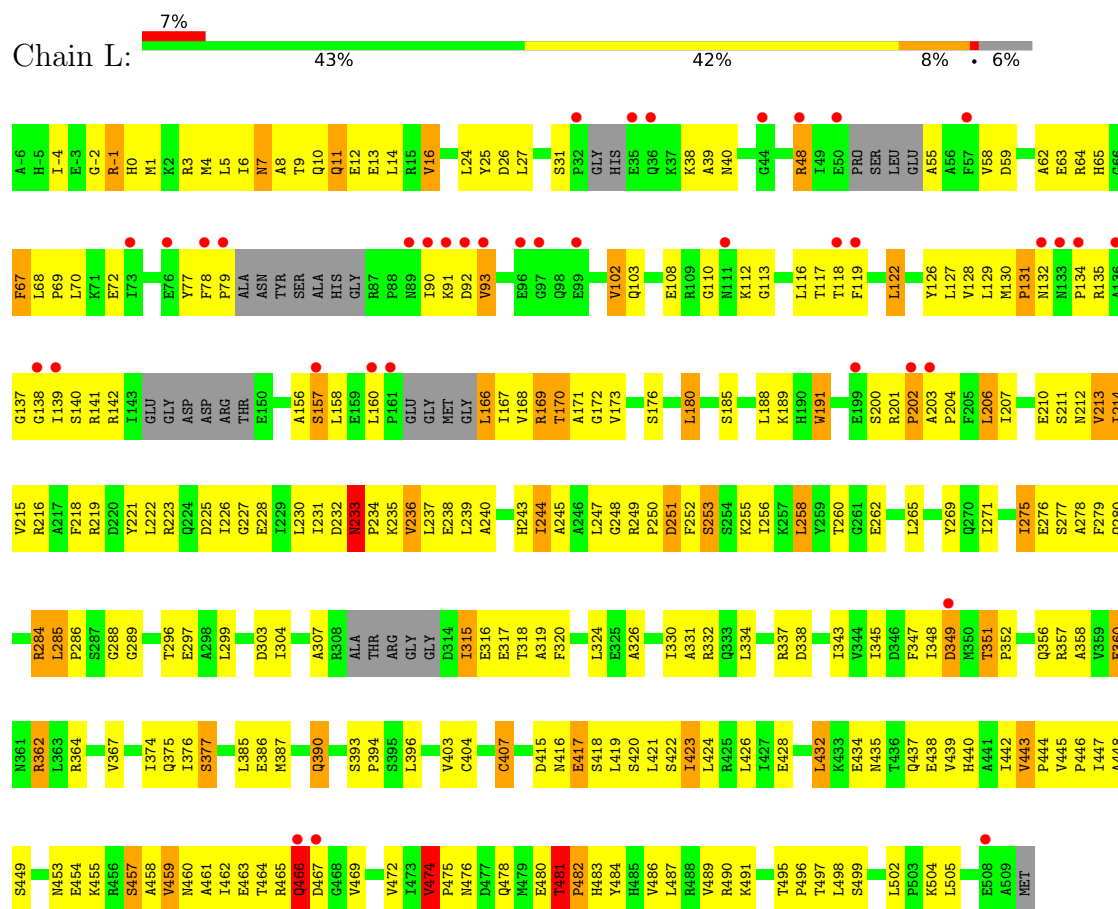
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	46	Total	O	0	0
			46	46		
5	R	3	Total	O	0	0
			3	3		

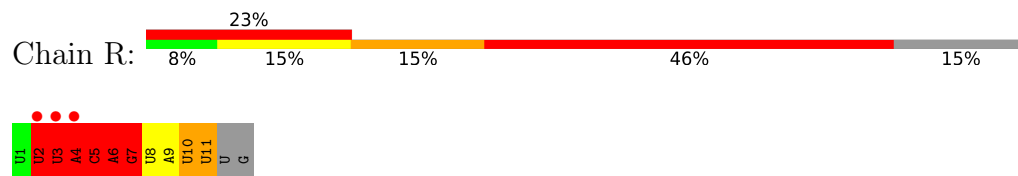
3 Residue-property plots

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: RIBONUCLEASE H



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α , β , γ	196.05Å 196.05Å 142.66Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	12.00 – 3.18 12.00 – 3.18	Depositor EDS
% Data completeness (in resolution range)	99.3 (12.00-3.18) 97.0 (12.00-3.18)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.87 (at 3.17Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.252 , 0.282 0.232 , 0.267	Depositor DCC
R_{free} test set	1376 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	72.6	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 34.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3821	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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: MG, 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	L	0.77	0/3604	1.09	15/4893 (0.3%)
2	R	1.92	3/237 (1.3%)	2.15	16/365 (4.4%)
All	All	0.89	3/3841 (0.1%)	1.19	31/5258 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	10	U	O3'-P	24.28	1.97	1.61
2	R	11	U	P-O5'	9.55	1.78	1.59
2	R	5	C	C4-N4	-5.30	1.23	1.33

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	10	U	OP1-P-O3'	12.29	144.85	108.00
2	R	2	U	O4'-C1'-C2'	-10.33	97.27	107.60
2	R	10	U	OP2-P-O3'	-10.30	77.08	108.00
2	R	2	U	C3'-C2'-C1'	-10.17	91.13	101.30
1	L	233	ASN	CA-C-N	9.47	131.68	119.84
1	L	233	ASN	C-N-CA	9.47	131.68	119.84
2	R	10	U	O3'-P-O5'	-9.40	89.91	104.00
2	R	7	G	P-O5'-C5'	-8.86	107.61	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	7	G	C5'-C4'-C3'	-7.93	104.10	116.00
1	L	407	CYS	N-CA-C	-7.47	100.47	110.55
2	R	6	A	N9-C1'-C2'	-6.97	101.54	112.00
2	R	5	C	O4'-C1'-C2'	-6.89	100.71	107.60
2	R	7	G	N9-C1'-C2'	-6.43	102.35	112.00
1	L	474	VAL	N-CA-C	6.30	115.49	108.05
2	R	3	U	C3'-C2'-C1'	-6.10	95.40	101.50
2	R	6	A	C3'-C2'-O2'	6.07	119.80	110.70
2	R	7	G	C4'-C3'-C2'	5.79	108.39	102.60
2	R	2	U	C1'-O4'-C4'	-5.68	104.22	109.90
1	L	93	VAL	N-CA-C	5.64	116.41	110.72
1	L	285	LEU	CA-C-N	5.51	126.72	119.84
1	L	285	LEU	C-N-CA	5.51	126.72	119.84
1	L	48	ARG	N-CA-C	5.42	116.77	107.28
2	R	7	G	O4'-C1'-N9	5.41	116.61	108.50
1	L	102	VAL	N-CA-C	5.40	116.05	108.17
2	R	4	A	C3'-C2'-O2'	5.25	118.57	110.70
1	L	481	THR	CA-C-N	5.22	126.37	119.84
1	L	481	THR	C-N-CA	5.22	126.37	119.84
1	L	351	THR	CA-C-N	5.21	126.36	119.84
1	L	351	THR	C-N-CA	5.21	126.36	119.84
1	L	262	GLU	N-CA-C	-5.04	105.70	111.14
1	L	416	ASN	N-CA-C	5.03	116.45	110.97

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	466	GLN	Peptide
1	L	481	THR	Mainchain,Peptide

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	L	3555	0	3347	328	0
2	R	214	0	102	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	2	0	0	0	0
4	L	1	0	0	0	0
5	L	46	0	0	2	0
5	R	3	0	0	0	0
All	All	3821	0	3449	366	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 51.

All (366) 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:L:1:MET:CE	1:L:227:GLY:HA3	1.37	1.50
1:L:67:PHE:CD1	2:R:10:U:C5	2.00	1.49
1:L:55:ALA:HB1	1:L:68:LEU:O	1.17	1.27
1:L:67:PHE:HD1	2:R:10:U:C6	1.53	1.25
2:R:10:U:O3'	2:R:11:U:P	1.97	1.22
1:L:67:PHE:CD1	2:R:10:U:C6	2.26	1.22
1:L:1:MET:HE3	1:L:227:GLY:HA3	1.22	1.15
2:R:6:A:C8	2:R:6:A:H5''	1.84	1.12
2:R:4:A:H8	2:R:4:A:H5''	1.11	1.12
1:L:1:MET:CE	1:L:227:GLY:CA	2.26	1.12
1:L:166:LEU:HD23	1:L:166:LEU:O	1.50	1.10
1:L:206:LEU:HD12	1:L:207:ILE:N	1.62	1.10
1:L:1:MET:HE2	1:L:227:GLY:HA3	1.34	1.10
1:L:284:ARG:HG2	1:L:284:ARG:HH11	0.98	1.09
2:R:2:U:C6	2:R:2:U:C5'	2.36	1.08
1:L:166:LEU:HD23	1:L:166:LEU:C	1.79	1.07
1:L:6:ILE:HD13	1:L:214:ILE:HD13	1.32	1.07
1:L:284:ARG:HH11	1:L:284:ARG:CG	1.65	1.07
1:L:258:LEU:HD21	1:L:260:THR:HG23	1.37	1.04
1:L:376:ILE:HG22	1:L:377:SER:H	1.19	1.04
1:L:417:GLU:OE2	1:L:417:GLU:N	1.89	1.04
1:L:180:LEU:H	1:L:180:LEU:HD23	1.24	1.02
1:L:432:LEU:CD1	1:L:466:GLN:HG3	1.89	1.01
1:L:258:LEU:HD21	1:L:260:THR:CG2	1.90	1.00
2:R:2:U:H6	2:R:2:U:O5'	1.42	1.00
2:R:4:A:H8	2:R:4:A:C5'	1.73	1.00
2:R:2:U:C6	2:R:2:U:O5'	2.14	1.00
2:R:4:A:H5''	2:R:4:A:C8	2.00	0.97
1:L:180:LEU:HD23	1:L:180:LEU:N	1.80	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:6:A:H5''	2:R:6:A:H8	1.14	0.97
1:L:55:ALA:HB2	1:L:70:LEU:N	1.79	0.97
2:R:3:U:H4'	2:R:4:A:OP1	1.65	0.96
1:L:55:ALA:CB	1:L:69:PRO:HA	1.96	0.96
1:L:258:LEU:CD2	1:L:260:THR:HG23	1.95	0.96
1:L:284:ARG:HG2	1:L:284:ARG:NH1	1.76	0.94
1:L:67:PHE:CE1	2:R:10:U:C5	2.54	0.94
2:R:2:U:H3'	2:R:2:U:C2	2.02	0.93
1:L:55:ALA:CB	1:L:68:LEU:O	2.14	0.92
1:L:68:LEU:HD23	1:L:69:PRO:HD2	1.54	0.90
1:L:55:ALA:HB2	1:L:69:PRO:HA	1.54	0.89
1:L:69:PRO:HG2	1:L:72:GLU:CB	2.03	0.88
1:L:108:GLU:HG2	1:L:113:GLY:O	1.75	0.87
2:R:2:U:C6	2:R:2:U:H5''	2.08	0.87
1:L:356:GLN:O	1:L:360:GLU:HG3	1.76	0.86
1:L:376:ILE:HG22	1:L:377:SER:N	1.90	0.85
1:L:55:ALA:HB2	1:L:70:LEU:H	1.38	0.85
1:L:139:ILE:O	2:R:2:U:O4'	1.93	0.85
1:L:7:ASN:HD22	1:L:7:ASN:C	1.83	0.84
1:L:222:LEU:HA	1:L:226:ILE:HD12	1.57	0.84
1:L:249:ARG:N	1:L:250:PRO:CD	2.42	0.82
1:L:244:ILE:HD12	1:L:256:ILE:HD11	1.61	0.82
1:L:6:ILE:HD13	1:L:214:ILE:CD1	2.09	0.82
1:L:180:LEU:N	1:L:180:LEU:CD2	2.43	0.82
1:L:233:ASN:ND2	1:L:236:VAL:HG23	1.95	0.81
2:R:4:A:C5'	2:R:4:A:C8	2.61	0.81
1:L:244:ILE:HG22	1:L:245:ALA:N	1.94	0.81
1:L:243:HIS:O	1:L:247:LEU:HB2	1.81	0.81
1:L:67:PHE:CE1	2:R:10:U:H5	1.99	0.81
1:L:6:ILE:CD1	1:L:214:ILE:HD13	2.11	0.81
1:L:7:ASN:C	1:L:7:ASN:ND2	2.39	0.80
1:L:237:LEU:C	1:L:237:LEU:HD23	2.07	0.80
1:L:67:PHE:C	1:L:67:PHE:CD2	2.60	0.78
1:L:465:ARG:C	1:L:467:ASP:H	1.92	0.78
1:L:223:ARG:HB2	1:L:225:ASP:OD2	1.84	0.78
1:L:233:ASN:C	1:L:233:ASN:OD1	2.27	0.78
1:L:455:LYS:O	1:L:459:VAL:HG23	1.84	0.78
1:L:476:ASN:OD1	1:L:476:ASN:C	2.27	0.78
1:L:1:MET:HE3	1:L:227:GLY:CA	2.01	0.78
1:L:376:ILE:CG2	1:L:377:SER:H	1.97	0.77
1:L:233:ASN:CG	1:L:236:VAL:HG23	2.10	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:6:A:C8	2:R:6:A:C5'	2.67	0.76
1:L:131:PRO:HB3	1:L:191:TRP:NE1	1.99	0.76
1:L:206:LEU:HD12	1:L:206:LEU:C	2.10	0.75
1:L:55:ALA:HB1	1:L:68:LEU:C	2.10	0.75
1:L:206:LEU:HD12	1:L:207:ILE:H	1.52	0.74
1:L:222:LEU:HD23	1:L:226:ILE:HD13	1.67	0.74
1:L:27:LEU:CD2	1:L:275:ILE:HG23	2.17	0.74
1:L:67:PHE:C	1:L:67:PHE:HD2	1.95	0.74
1:L:315:ILE:HG22	1:L:316:GLU:N	2.02	0.74
1:L:55:ALA:HB2	1:L:69:PRO:CA	2.16	0.74
1:L:108:GLU:CG	1:L:113:GLY:O	2.36	0.74
1:L:249:ARG:N	1:L:250:PRO:HD2	2.02	0.74
1:L:166:LEU:C	1:L:166:LEU:CD2	2.55	0.73
1:L:1:MET:HE1	1:L:227:GLY:HA3	1.61	0.73
1:L:1:MET:HE1	1:L:227:GLY:C	2.14	0.72
1:L:140:SER:C	1:L:142:ARG:H	1.97	0.72
1:L:244:ILE:HD12	1:L:256:ILE:CD1	2.19	0.72
1:L:419:LEU:O	1:L:422:SER:HB3	1.89	0.72
1:L:364:ARG:HH21	1:L:364:ARG:HG3	1.55	0.72
1:L:67:PHE:CD1	2:R:10:U:H5	1.95	0.72
1:L:55:ALA:HB2	1:L:69:PRO:C	2.15	0.71
1:L:55:ALA:CB	1:L:69:PRO:CA	2.68	0.71
1:L:27:LEU:HD22	1:L:275:ILE:HD13	1.72	0.71
1:L:222:LEU:HD23	1:L:226:ILE:CD1	2.21	0.71
1:L:466:GLN:HA	1:L:466:GLN:NE2	2.05	0.71
1:L:1:MET:HE1	1:L:228:GLU:N	2.06	0.70
1:L:7:ASN:HD22	1:L:8:ALA:N	1.89	0.69
1:L:432:LEU:HD12	1:L:466:GLN:HG3	1.72	0.69
1:L:351:THR:OG1	1:L:352:PRO:HD3	1.91	0.69
1:L:356:GLN:O	1:L:360:GLU:CG	2.41	0.69
1:L:237:LEU:HD12	1:L:258:LEU:HB2	1.75	0.68
1:L:233:ASN:ND2	1:L:236:VAL:CG2	2.56	0.67
1:L:221:TYR:O	1:L:226:ILE:HD11	1.93	0.67
1:L:482:PRO:HD2	1:L:483:HIS:H	1.58	0.67
1:L:58:VAL:O	1:L:65:HIS:CB	2.42	0.67
1:L:248:GLY:C	1:L:250:PRO:HD2	2.19	0.67
1:L:385:LEU:C	1:L:385:LEU:HD23	2.19	0.67
1:L:385:LEU:HD23	1:L:386:GLU:N	2.10	0.67
1:L:167:ILE:HD13	2:R:2:U:C6	2.30	0.66
1:L:1:MET:HE1	1:L:227:GLY:CA	2.19	0.66
1:L:130:MET:N	1:L:131:PRO:CD	2.59	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:497:THR:HG22	1:L:498:LEU:N	2.10	0.65
1:L:237:LEU:O	1:L:240:ALA:HB3	1.96	0.65
1:L:167:ILE:HG22	1:L:168:VAL:N	2.12	0.65
1:L:223:ARG:HG3	1:L:223:ARG:HH11	1.60	0.65
1:L:68:LEU:HD23	1:L:69:PRO:CD	2.27	0.64
1:L:138:GLY:O	1:L:167:ILE:HG23	1.97	0.64
1:L:140:SER:O	1:L:142:ARG:N	2.31	0.64
2:R:7:G:C5'	2:R:7:G:N3	2.60	0.64
1:L:129:LEU:C	1:L:131:PRO:HD2	2.23	0.64
1:L:303:ASP:OD2	5:L:2024:HOH:O	2.15	0.64
1:L:476:ASN:OD1	1:L:478:GLN:N	2.29	0.64
1:L:129:LEU:C	1:L:131:PRO:CD	2.72	0.63
1:L:284:ARG:CG	1:L:284:ARG:NH1	2.38	0.63
1:L:486:VAL:C	1:L:487:LEU:HD12	2.23	0.63
1:L:5:LEU:N	1:L:5:LEU:HD23	2.14	0.63
2:R:7:G:N3	2:R:7:G:H5''	2.14	0.63
1:L:167:ILE:CG2	1:L:168:VAL:N	2.63	0.62
1:L:6:ILE:HG12	1:L:16:VAL:HG13	1.81	0.62
1:L:38:LYS:O	1:L:39:ALA:HB3	1.99	0.62
1:L:112:LYS:HA	2:R:10:U:O2	1.98	0.62
1:L:251:ASP:N	1:L:251:ASP:OD2	2.32	0.62
1:L:90:ILE:C	1:L:92:ASP:H	2.07	0.61
1:L:222:LEU:HA	1:L:226:ILE:CD1	2.30	0.61
1:L:442:ILE:C	1:L:443:VAL:CG1	2.73	0.61
1:L:390:GLN:HB2	2:R:6:A:H4'	1.82	0.61
1:L:432:LEU:CD1	1:L:466:GLN:CG	2.75	0.61
2:R:9:A:O2'	2:R:10:U:H5'	1.99	0.61
1:L:237:LEU:CD1	1:L:258:LEU:HB2	2.31	0.61
1:L:484:TYR:CD1	1:L:484:TYR:C	2.78	0.61
1:L:237:LEU:C	1:L:237:LEU:CD2	2.73	0.61
1:L:67:PHE:CE1	2:R:10:U:C6	2.84	0.61
1:L:466:GLN:NE2	1:L:466:GLN:CA	2.63	0.61
1:L:252:PHE:O	1:L:255:LYS:HB2	2.01	0.61
1:L:465:ARG:C	1:L:467:ASP:N	2.59	0.61
1:L:67:PHE:CG	2:R:10:U:C5	2.85	0.60
1:L:252:PHE:O	1:L:255:LYS:N	2.29	0.60
1:L:466:GLN:HA	1:L:466:GLN:HE21	1.65	0.60
1:L:176:SER:O	1:L:180:LEU:CD2	2.48	0.60
1:L:237:LEU:O	1:L:240:ALA:N	2.35	0.60
1:L:3:ARG:HH21	1:L:3:ARG:HG3	1.66	0.60
1:L:289:GLY:N	1:L:307:ALA:HB2	2.17	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:10:U:O3'	2:R:11:U:OP2	2.20	0.60
1:L:170:THR:O	1:L:170:THR:HG22	2.02	0.60
2:R:2:U:C6	2:R:2:U:C4'	2.85	0.59
1:L:230:LEU:N	1:L:230:LEU:HD23	2.15	0.59
1:L:285:LEU:HB3	1:L:286:PRO:HD2	1.84	0.59
1:L:167:ILE:CD1	2:R:2:U:C6	2.85	0.59
1:L:393:SER:HB2	1:L:394:PRO:CD	2.33	0.59
1:L:27:LEU:HD22	1:L:275:ILE:HG23	1.84	0.58
1:L:79:PRO:HD2	1:L:93:VAL:O	2.02	0.58
2:R:4:A:H5'	2:R:5:C:OP2	2.03	0.58
1:L:212:ASN:C	1:L:212:ASN:OD1	2.45	0.58
1:L:90:ILE:C	1:L:92:ASP:N	2.61	0.58
1:L:244:ILE:CG2	1:L:245:ALA:N	2.61	0.58
1:L:288:GLY:C	1:L:307:ALA:HB2	2.30	0.57
1:L:231:ILE:HG22	1:L:233:ASN:H	1.68	0.57
1:L:258:LEU:O	1:L:258:LEU:HD23	2.04	0.57
1:L:396:LEU:HD12	5:L:2018:HOH:O	2.04	0.57
1:L:8:ALA:HB2	1:L:14:LEU:CD1	2.34	0.56
2:R:9:A:O2'	2:R:10:U:C5'	2.53	0.56
1:L:131:PRO:HB3	1:L:191:TRP:CD1	2.39	0.56
2:R:2:U:H5''	2:R:2:U:C5	2.40	0.56
1:L:258:LEU:HD23	1:L:260:THR:HG23	1.84	0.56
1:L:78:PHE:O	1:L:79:PRO:C	2.48	0.56
1:L:1:MET:HE1	1:L:228:GLU:HG3	1.88	0.56
2:R:2:U:C2	2:R:2:U:C3'	2.70	0.56
1:L:211:SER:HB3	1:L:215:VAL:HB	1.87	0.56
1:L:330:ILE:HD13	1:L:345:ILE:HD13	1.88	0.56
1:L:103:GLN:O	1:L:116:LEU:HA	2.06	0.56
1:L:131:PRO:HB3	1:L:191:TRP:CE2	2.42	0.55
1:L:497:THR:CG2	1:L:498:LEU:N	2.68	0.55
1:L:364:ARG:HG3	1:L:364:ARG:NH2	2.20	0.55
2:R:6:A:C3'	2:R:7:G:H5''	2.36	0.55
1:L:-4:ILE:HD12	1:L:-1:ARG:NH1	2.21	0.55
1:L:176:SER:O	1:L:180:LEU:HD21	2.07	0.55
1:L:223:ARG:HG3	1:L:223:ARG:NH1	2.19	0.55
1:L:167:ILE:HD11	2:R:2:U:C4	2.42	0.55
1:L:27:LEU:CD2	1:L:275:ILE:HD13	2.36	0.55
1:L:385:LEU:C	1:L:385:LEU:CD2	2.79	0.55
1:L:240:ALA:O	1:L:243:HIS:HB2	2.07	0.54
2:R:6:A:H5'	2:R:7:G:OP2	2.07	0.54
1:L:482:PRO:CD	1:L:483:HIS:H	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:428:GLU:OE1	1:L:465:ARG:NH1	2.39	0.54
2:R:6:A:H3'	2:R:7:G:H5''	1.89	0.54
1:L:138:GLY:C	2:R:2:U:H1'	2.32	0.54
1:L:324:LEU:HD22	1:L:362:ARG:HG2	1.90	0.54
1:L:357:ARG:HG2	1:L:357:ARG:HH11	1.73	0.54
1:L:443:VAL:HG23	1:L:444:PRO:O	2.08	0.54
1:L:67:PHE:CD2	1:L:68:LEU:N	2.76	0.53
1:L:277:SER:HA	1:L:280:GLN:OE1	2.08	0.53
1:L:203:ALA:N	1:L:204:PRO:CD	2.70	0.53
1:L:24:LEU:HD22	1:L:275:ILE:HG12	1.91	0.53
1:L:269:TYR:O	1:L:271:ILE:HG23	2.09	0.53
2:R:5:C:O5'	2:R:5:C:H6	1.92	0.53
1:L:118:THR:O	1:L:132:ASN:ND2	2.42	0.53
1:L:167:ILE:CD1	2:R:2:U:C5	2.91	0.53
1:L:11:GLN:CD	1:L:11:GLN:H	2.16	0.53
1:L:482:PRO:HD2	1:L:483:HIS:N	2.23	0.53
1:L:417:GLU:O	1:L:418:SER:C	2.52	0.53
1:L:188:LEU:O	1:L:189:LYS:C	2.51	0.52
1:L:495:THR:HB	1:L:496:PRO:HD2	1.92	0.52
1:L:258:LEU:HD23	1:L:258:LEU:C	2.34	0.52
1:L:432:LEU:HD13	1:L:466:GLN:HG3	1.85	0.52
1:L:167:ILE:HD11	2:R:2:U:C5	2.45	0.52
2:R:5:C:H6	2:R:5:C:C5'	2.23	0.52
1:L:244:ILE:CD1	1:L:256:ILE:HD11	2.38	0.52
2:R:6:A:H2'	2:R:6:A:N3	2.24	0.51
1:L:357:ARG:HG2	1:L:357:ARG:NH1	2.26	0.51
1:L:495:THR:HB	1:L:496:PRO:CD	2.40	0.51
1:L:505:LEU:HD12	1:L:505:LEU:O	2.10	0.51
1:L:348:ILE:HG22	1:L:349:ASP:N	2.24	0.51
1:L:330:ILE:O	1:L:334:LEU:HG	2.11	0.51
2:R:5:C:H3'	2:R:5:C:C6	2.45	0.51
1:L:237:LEU:HD23	1:L:237:LEU:O	2.10	0.50
2:R:7:G:N3	2:R:7:G:H5'	2.26	0.50
1:L:437:GLN:HB2	1:L:491:LYS:HA	1.94	0.50
1:L:25:TYR:O	1:L:26:ASP:HB2	2.12	0.50
1:L:58:VAL:CG1	1:L:59:ASP:N	2.74	0.50
1:L:424:LEU:HD21	1:L:458:ALA:HB1	1.94	0.50
1:L:169:ARG:C	1:L:171:ALA:H	2.20	0.50
1:L:404:CYS:O	1:L:407:CYS:O	2.29	0.50
1:L:129:LEU:CB	1:L:131:PRO:HD3	2.42	0.49
1:L:236:VAL:O	1:L:237:LEU:C	2.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:460:ASN:O	1:L:463:GLU:N	2.46	0.49
1:L:474:VAL:O	1:L:474:VAL:HG22	2.13	0.49
1:L:299:LEU:C	1:L:299:LEU:HD12	2.38	0.49
1:L:278:ALA:O	1:L:396:LEU:HD12	2.11	0.49
1:L:348:ILE:CG2	1:L:349:ASP:N	2.76	0.49
1:L:444:PRO:HB2	1:L:447:ILE:HG12	1.95	0.49
1:L:487:LEU:N	1:L:487:LEU:CD1	2.76	0.49
1:L:69:PRO:CG	1:L:72:GLU:CB	2.86	0.49
1:L:213:VAL:HG23	1:L:216:ARG:NH2	2.28	0.49
1:L:218:PHE:HA	1:L:222:LEU:CD1	2.43	0.49
1:L:466:GLN:N	1:L:466:GLN:CD	2.70	0.48
1:L:222:LEU:HB2	1:L:249:ARG:NH1	2.27	0.48
1:L:482:PRO:CD	1:L:483:HIS:N	2.74	0.48
2:R:4:A:C8	2:R:4:A:C4'	2.96	0.48
1:L:440:HIS:CE1	1:L:489:VAL:HG21	2.48	0.48
1:L:8:ALA:HB2	1:L:14:LEU:HD11	1.94	0.48
1:L:374:ILE:CG2	1:L:375:GLN:N	2.75	0.48
1:L:156:ALA:O	1:L:158:LEU:N	2.46	0.48
2:R:5:C:C6	2:R:5:C:C3'	2.97	0.48
1:L:357:ARG:O	1:L:358:ALA:C	2.56	0.48
1:L:130:MET:O	1:L:131:PRO:C	2.55	0.48
1:L:140:SER:C	1:L:142:ARG:N	2.60	0.48
1:L:453:ASN:O	1:L:454:GLU:C	2.56	0.48
1:L:126:TYR:O	1:L:127:LEU:HD12	2.14	0.47
1:L:417:GLU:H	1:L:417:GLU:CD	1.98	0.47
1:L:3:ARG:HG3	1:L:3:ARG:NH2	2.27	0.47
1:L:203:ALA:H	1:L:204:PRO:CD	2.26	0.47
1:L:403:VAL:O	1:L:404:CYS:C	2.57	0.47
1:L:-2:GLY:O	1:L:-1:ARG:C	2.57	0.47
1:L:221:TYR:O	1:L:226:ILE:CD1	2.62	0.47
1:L:417:GLU:O	1:L:420:SER:N	2.48	0.47
1:L:276:GLU:O	1:L:277:SER:C	2.57	0.47
1:L:337:ARG:HA	1:L:396:LEU:HG	1.97	0.47
1:L:38:LYS:O	1:L:39:ALA:CB	2.63	0.46
1:L:465:ARG:O	1:L:467:ASP:N	2.44	0.46
1:L:137:GLY:HA2	1:L:167:ILE:HG12	1.98	0.46
1:L:48:ARG:O	1:L:48:ARG:CG	2.63	0.46
1:L:40:ASN:OD1	1:L:210:GLU:N	2.39	0.46
1:L:445:VAL:N	1:L:446:PRO:HD2	2.30	0.46
1:L:504:LYS:O	1:L:505:LEU:C	2.56	0.46
1:L:67:PHE:CD1	2:R:10:U:C4	2.91	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:463:GLU:O	1:L:467:ASP:O	2.34	0.46
1:L:303:ASP:C	1:L:304:ILE:CG1	2.89	0.46
1:L:119:PHE:HA	1:L:132:ASN:HD22	1.80	0.46
1:L:-1:ARG:HG2	1:L:0:HIS:ND1	2.31	0.46
1:L:376:ILE:CG2	1:L:377:SER:N	2.61	0.46
1:L:236:VAL:O	1:L:240:ALA:N	2.47	0.46
1:L:296:THR:O	1:L:297:GLU:C	2.58	0.46
1:L:432:LEU:HD11	1:L:466:GLN:HG3	1.89	0.46
1:L:58:VAL:HG12	1:L:59:ASP:N	2.30	0.45
2:R:6:A:N6	2:R:7:G:C6	2.85	0.45
1:L:343:ILE:HB	1:L:387:MET:HG2	1.98	0.45
1:L:437:GLN:HA	1:L:437:GLN:NE2	2.32	0.45
1:L:443:VAL:HG23	1:L:447:ILE:HB	1.98	0.45
2:R:6:A:C8	2:R:6:A:C4'	2.99	0.45
1:L:4:MET:C	1:L:5:LEU:HD23	2.42	0.45
1:L:487:LEU:HD12	1:L:487:LEU:N	2.32	0.45
1:L:277:SER:C	1:L:279:PHE:H	2.25	0.45
1:L:432:LEU:HD11	1:L:466:GLN:CG	2.47	0.45
1:L:237:LEU:O	1:L:240:ALA:CB	2.64	0.45
1:L:156:ALA:C	1:L:158:LEU:H	2.25	0.45
1:L:318:THR:O	1:L:319:ALA:C	2.56	0.44
1:L:-1:ARG:HG2	1:L:0:HIS:CE1	2.52	0.44
1:L:434:GLU:O	1:L:435:ASN:HB3	2.16	0.44
1:L:364:ARG:HH21	1:L:364:ARG:CG	2.25	0.44
1:L:304:ILE:HD13	1:L:326:ALA:HB1	1.99	0.44
1:L:448:ALA:O	1:L:449:SER:C	2.57	0.44
1:L:222:LEU:HD23	1:L:226:ILE:HD12	1.99	0.44
1:L:122:LEU:O	1:L:128:VAL:HA	2.18	0.44
1:L:200:SER:O	1:L:201:ARG:CB	2.66	0.44
1:L:252:PHE:O	1:L:253:SER:C	2.61	0.44
1:L:129:LEU:C	1:L:131:PRO:HD3	2.43	0.44
1:L:364:ARG:NH2	1:L:364:ARG:CG	2.81	0.44
2:R:10:U:H2'	2:R:10:U:O5'	2.18	0.44
1:L:191:TRP:HE3	1:L:191:TRP:HA	1.83	0.44
1:L:423:ILE:HD11	1:L:484:TYR:CD2	2.53	0.44
1:L:62:ALA:C	1:L:64:ARG:N	2.76	0.43
1:L:77:TYR:O	1:L:79:PRO:HD3	2.18	0.43
1:L:442:ILE:C	1:L:443:VAL:HG13	2.43	0.43
1:L:191:TRP:HA	1:L:191:TRP:CE3	2.54	0.43
1:L:250:PRO:O	1:L:253:SER:HB2	2.19	0.43
1:L:9:THR:HG23	1:L:232:ASP:CG	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:131:PRO:CB	1:L:191:TRP:CE2	3.01	0.43
1:L:201:ARG:C	1:L:202:PRO:O	2.61	0.43
1:L:6:ILE:HG21	1:L:214:ILE:HD11	2.01	0.43
1:L:331:ALA:HB1	1:L:367:VAL:HG12	2.01	0.42
1:L:442:ILE:C	1:L:443:VAL:HG12	2.43	0.42
1:L:315:ILE:O	1:L:316:GLU:C	2.60	0.42
1:L:129:LEU:O	1:L:131:PRO:HD2	2.19	0.42
1:L:245:ALA:C	1:L:247:LEU:N	2.74	0.42
1:L:474:VAL:HG23	1:L:475:PRO:O	2.20	0.42
1:L:498:LEU:O	1:L:499:SER:C	2.61	0.42
1:L:234:PRO:O	1:L:235:LYS:C	2.61	0.42
1:L:445:VAL:HG12	1:L:446:PRO:N	2.35	0.42
1:L:472:VAL:HG11	1:L:502:LEU:HD12	2.01	0.42
1:L:276:GLU:C	1:L:278:ALA:N	2.76	0.42
1:L:304:ILE:HD12	1:L:347:PHE:HA	2.02	0.42
1:L:317:GLU:O	1:L:320:PHE:N	2.53	0.42
1:L:210:GLU:HG3	1:L:211:SER:N	2.33	0.42
1:L:233:ASN:OD1	1:L:235:LYS:N	2.53	0.42
1:L:457:SER:O	1:L:460:ASN:HB2	2.20	0.42
2:R:3:U:C4'	2:R:4:A:OP1	2.52	0.42
1:L:334:LEU:HD23	1:L:334:LEU:HA	1.81	0.41
1:L:134:PRO:CD	1:L:135:ARG:H	2.32	0.41
1:L:210:GLU:OE2	1:L:219:ARG:NH2	2.45	0.41
1:L:231:ILE:HG22	1:L:232:ASP:N	2.34	0.41
1:L:421:LEU:HD23	1:L:421:LEU:HA	1.77	0.41
1:L:185:SER:O	1:L:188:LEU:N	2.53	0.41
1:L:385:LEU:HD23	1:L:386:GLU:O	2.21	0.41
1:L:108:GLU:HG3	1:L:113:GLY:O	2.17	0.41
1:L:134:PRO:HD2	1:L:135:ARG:H	1.84	0.41
1:L:390:GLN:HG3	2:R:7:G:OP1	2.20	0.41
1:L:461:ALA:O	1:L:462:ILE:C	2.63	0.41
1:L:502:LEU:HD23	1:L:502:LEU:HA	1.83	0.41
1:L:113:GLY:N	2:R:10:U:O2	2.49	0.41
1:L:374:ILE:HG22	1:L:375:GLN:N	2.34	0.41
1:L:172:GLY:O	1:L:173:VAL:C	2.63	0.41
1:L:237:LEU:O	1:L:238:GLU:C	2.63	0.41
1:L:276:GLU:O	1:L:278:ALA:N	2.53	0.41
1:L:460:ASN:O	1:L:461:ALA:C	2.64	0.41
1:L:222:LEU:HA	1:L:222:LEU:HD23	1.85	0.41
1:L:225:ASP:OD2	1:L:225:ASP:N	2.52	0.41
1:L:463:GLU:HG2	1:L:469:VAL:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:10:U:C3'	2:R:11:U:P	3.02	0.41
1:L:239:LEU:HD23	1:L:239:LEU:HA	1.77	0.40
1:L:62:ALA:O	1:L:64:ARG:N	2.54	0.40
1:L:317:GLU:O	1:L:318:THR:C	2.64	0.40
1:L:169:ARG:C	1:L:171:ALA:N	2.78	0.40
1:L:238:GLU:O	1:L:239:LEU:C	2.62	0.40
1:L:244:ILE:O	1:L:247:LEU:N	2.49	0.40
1:L:490:ARG:O	1:L:491:LYS:C	2.65	0.40
1:L:245:ALA:C	1:L:247:LEU:H	2.30	0.40

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	L	474/517 (92%)	382 (81%)	79 (17%)	13 (3%)	4 22

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	202	PRO
1	L	482	PRO
1	L	141	ARG
1	L	157	SER
1	L	415	ASP
1	L	63	GLU
1	L	91	LYS
1	L	170	THR
1	L	131	PRO
1	L	160	LEU
1	L	265	LEU
1	L	481	THR

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Mol	Chain	Res	Type
1	L	110	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	L	336/439 (76%)	286 (85%)	50 (15%)	3 14

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	-1	ARG
1	L	7	ASN
1	L	10	GLN
1	L	11	GLN
1	L	12	GLU
1	L	13	GLU
1	L	16	VAL
1	L	31	SER
1	L	67	PHE
1	L	102	VAL
1	L	117	THR
1	L	122	LEU
1	L	157	SER
1	L	166	LEU
1	L	169	ARG
1	L	180	LEU
1	L	191	TRP
1	L	206	LEU
1	L	213	VAL
1	L	214	ILE
1	L	233	ASN
1	L	236	VAL
1	L	244	ILE
1	L	251	ASP
1	L	253	SER

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Mol	Chain	Res	Type
1	L	258	LEU
1	L	275	ILE
1	L	284	ARG
1	L	315	ILE
1	L	332	ARG
1	L	338	ASP
1	L	349	ASP
1	L	360	GLU
1	L	362	ARG
1	L	377	SER
1	L	390	GLN
1	L	417	GLU
1	L	423	ILE
1	L	426	LEU
1	L	432	LEU
1	L	438	GLU
1	L	439	VAL
1	L	443	VAL
1	L	457	SER
1	L	459	VAL
1	L	464	THR
1	L	466	GLN
1	L	474	VAL
1	L	480	GLU
1	L	481	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	7	ASN
1	L	132	ASN
1	L	242	GLN
1	L	321	ASN
1	L	378	HIS
1	L	416	ASN
1	L	437	GLN
1	L	466	GLN
1	L	485	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	R	9/13 (69%)	7 (77%)	4 (44%)

All (7) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	R	2	U
2	R	3	U
2	R	4	A
2	R	5	C
2	R	6	A
2	R	7	G
2	R	8	U

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	R	3	U
2	R	5	C
2	R	6	A
2	R	7	G

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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	10:U	O3'	11:U	P	1.97

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	488/517 (94%)	-0.02	38 (7%) 19 11	15, 40, 100, 100	0
2	R	11/13 (84%)	1.13	3 (27%) 1 1	40, 62, 99, 100	0
All	All	499/530 (94%)	0.00	41 (8%) 17 10	15, 40, 100, 100	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	R	4	A	6.1
1	L	133	ASN	5.5
2	R	3	U	5.5
1	L	203	ALA	5.5
1	L	93	VAL	5.2
1	L	92	ASP	5.1
1	L	57	PHE	4.5
1	L	73	ILE	4.1
1	L	35	GLU	3.7
1	L	91	LYS	3.7
1	L	96	GLU	3.6
1	L	50	GLU	3.3
1	L	97	GLY	3.3
1	L	79	PRO	3.2
1	L	132	ASN	3.1
1	L	36	GLN	3.1
1	L	160	LEU	3.1
1	L	467	ASP	3.1
1	L	136	ALA	3.0
1	L	78	PHE	2.9
1	L	161	PRO	2.9
1	L	76	GLU	2.8
1	L	99	GLU	2.8
1	L	111	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	L	32	PRO	2.6
1	L	134	PRO	2.6
1	L	508	GLU	2.6
1	L	139	ILE	2.6
1	L	466	GLN	2.5
2	R	2	U	2.4
1	L	90	ILE	2.4
1	L	157	SER	2.4
1	L	118	THR	2.3
1	L	89	ASN	2.2
1	L	44	GLY	2.2
1	L	138	GLY	2.2
1	L	119	PHE	2.1
1	L	199	GLU	2.1
1	L	202	PRO	2.1
1	L	349	ASP	2.0
1	L	48	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	MG	L	1512	1/1	0.84	0.36	30,30,30,30	1
3	MG	L	1510	1/1	1.00	0.07	21,21,21,21	0
4	ZN	L	1511	1/1	1.00	0.01	18,18,18,18	1

6.5 Other polymers [i](#)

There are no such residues in this entry.