



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 02:05 am GMT

PDB ID : 1TFY
Title : How CCA is added to the 3' end of immature tRNA without the use of an oligonucleotide template
Authors : Xiong, Y.; Steitz, T.A.
Deposited on : 2004-05-27
Resolution : 3.20 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

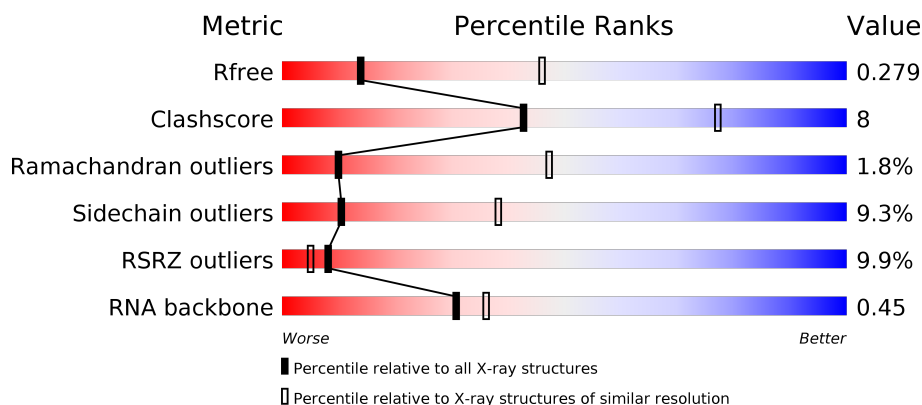
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	100719	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)
RNA backbone	2435	1045 (3.60-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	E	13	<div> <div>23%</div> <div> <div>62%</div> <div>31%</div> <div>8%</div> </div> </div>
1	F	13	<div> <div>46%</div> <div>46%</div> <div>54%</div> </div>
2	H	14	<div> <div>29%</div> <div>57%</div> <div>21%</div> <div>14%</div> <div>7%</div> </div>
2	I	14	<div> <div>14%</div> <div>36%</div> <div>64%</div> </div>

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Mol	Chain	Length	Quality of chain
3	G	11	<p>9% 27% 27% 36%</p>
4	J	8	<p>13% 50% 75% 13%</p>
5	A	437	<p>7% 79% 17%</p>
5	B	437	<p>14% 76% 21%</p>
5	C	437	<p>5% 72% 23%</p>
5	D	437	<p>9% 75% 22%</p>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16180 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 5'-R(*GP*CP*GP*GP*AP*UP*AP*UP*CP*CP*GP*CP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	13	Total	C	N	O	P	0	0	0
			276	124	51	89	12			
1	F	13	Total	C	N	O	P	0	0	0
			276	124	51	89	12			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	14	Total	C	N	O	P	0	0	0
			295	133	54	95	13			
2	I	14	Total	C	N	O	P	0	0	0
			295	133	54	95	13			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	11	Total	C	N	O	P	0	0	0
			230	104	42	74	10			

- Molecule 4 is a RNA chain called 5'-R(*CP*GP*CP*GP*GP*AP*UP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	J	8	Total	C	N	O	P	0	0	0
			168	76	31	54	7			

- Molecule 5 is a protein called tRNA nucleotidyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	A	437	Total	C	N	O	S	0	0	0
			3630	2333	632	652	13			

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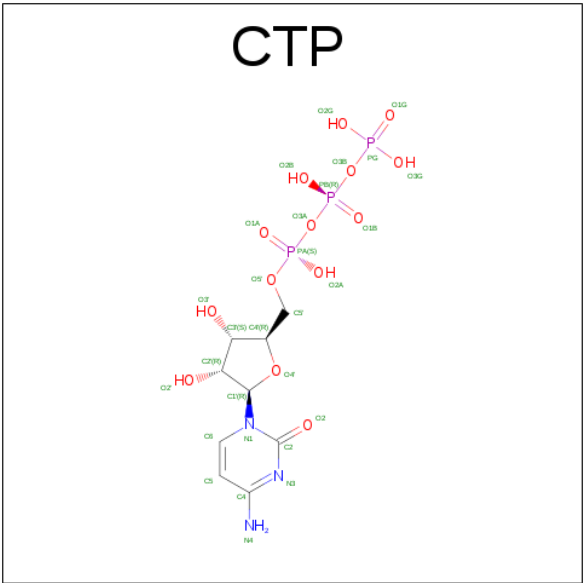
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	437	Total	C	N	O	S	0	0	0
			3630	2333	632	652	13			
5	C	437	Total	C	N	O	S	0	0	0
			3630	2333	632	652	13			
5	D	437	Total	C	N	O	S	0	0	0
			3630	2333	632	652	13			

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Mg	0	0
			1	1		
6	A	1	Total	Mg	0	0
			1	1		
6	D	1	Total	Mg	0	0
			1	1		
6	C	1	Total	Mg	0	0
			1	1		

- Molecule 7 is CYTIDINE-5'-TRIPHOSPHATE (three-letter code: CTP) (formula: C₉H₁₆N₃O₁₄P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			29	9	3	14	3		
7	B	1	Total	C	N	O	P	0	0
			29	9	3	14	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	C	1	Total	C	N	O	P	0	0
			29	9	3	14	3		
7	D	1	Total	C	N	O	P	0	0
			29	9	3	14	3		

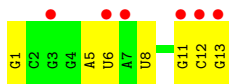
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

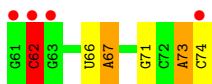
- Molecule 1: 5'-R(*GP*CP*GP*GP*AP*UP*AP*UP*CP*CP*GP*CP*G)-3'



- Molecule 1: 5'-R(*GP*CP*GP*GP*AP*UP*AP*UP*CP*CP*GP*CP*G)-3'



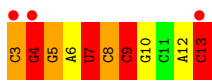
- Molecule 2: 5'-R(*GP*CP*GP*GP*AP*UP*AP*UP*CP*CP*GP*CP*AP*C)-3'



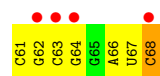
- Molecule 2: 5'-R(*GP*CP*GP*GP*AP*UP*AP*UP*CP*CP*GP*CP*AP*C)-3'



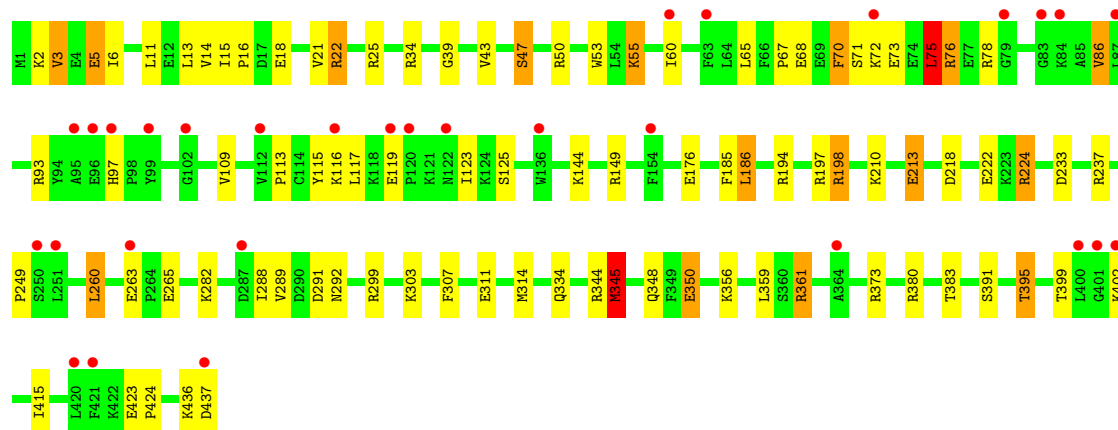
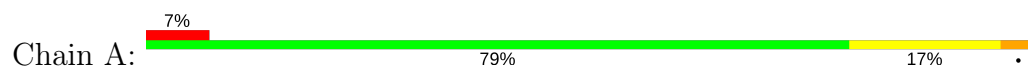
- Molecule 3: 5'-R(*CP*GP*GP*AP*UP*CP*CP*GP*CP*AP*C)-3'



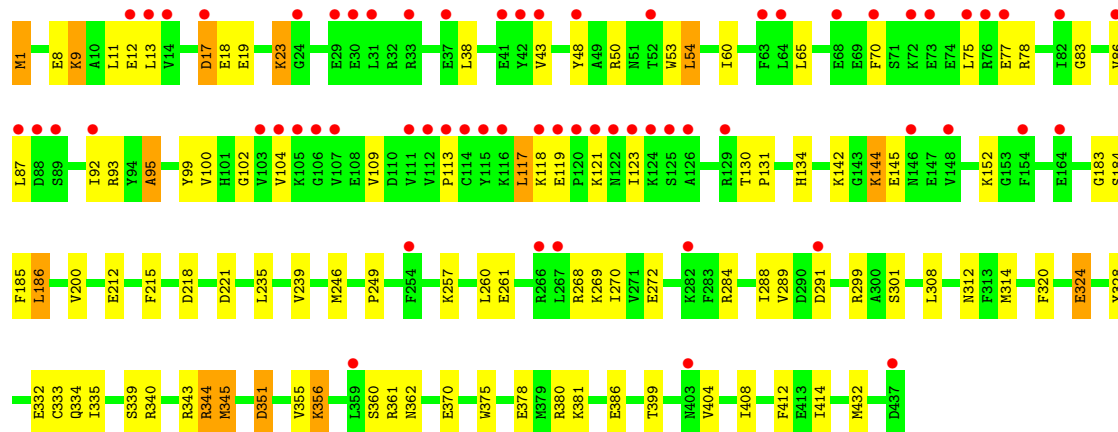
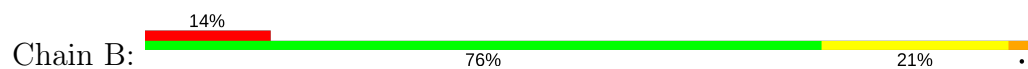
- Molecule 4: 5'-R(*CP*GP*CP*GP*GP*AP*UP*C)-3'



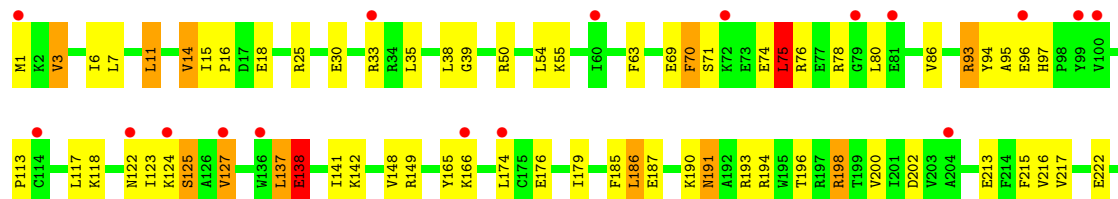
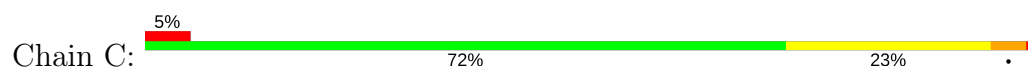
• Molecule 5: tRNA nucleotidyltransferase

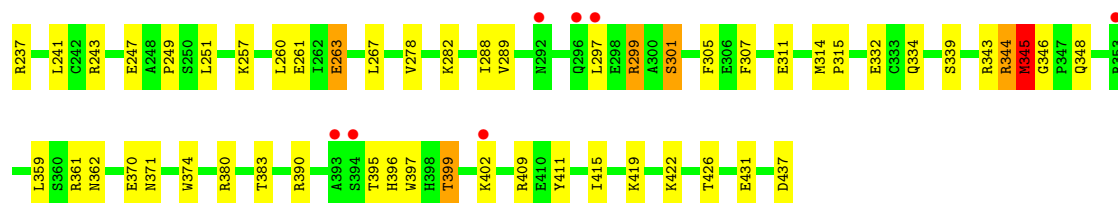


• Molecule 5: tRNA nucleotidyltransferase

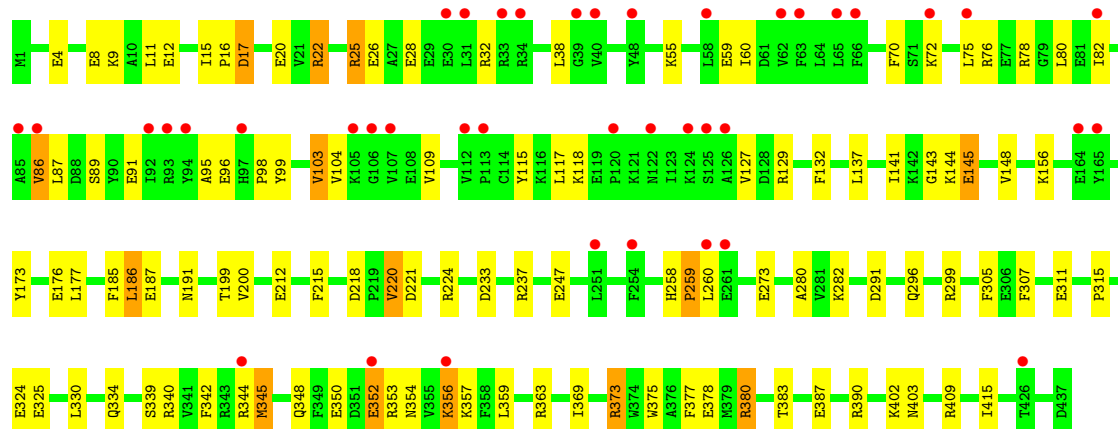
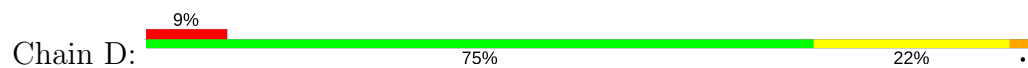


• Molecule 5: tRNA nucleotidyltransferase





• Molecule 5: tRNA nucleotidyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	114.09Å 84.02Å 134.56Å 90.00° 102.38° 90.00°	Depositor
Resolution (Å)	44.28 – 3.20 44.18 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.1 (44.28-3.20) 98.8 (44.18-3.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.235 , 0.290 0.226 , 0.279	Depositor DCC
R_{free} test set	2053 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	103.6	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 124.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16180	wwPDB-VP
Average B, all atoms (Å ²)	131.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% 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, CTP

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	E	0.67	0/308	1.26	2/479 (0.4%)
1	F	0.72	0/308	1.17	0/479
2	H	0.78	0/329	1.39	3/511 (0.6%)
2	I	0.77	0/329	1.40	3/511 (0.6%)
3	G	0.99	1/256 (0.4%)	1.95	12/397 (3.0%)
4	J	0.77	0/187	1.46	1/290 (0.3%)
5	A	0.35	0/3713	0.52	1/4987 (0.0%)
5	B	0.36	0/3713	0.51	0/4987
5	C	0.36	0/3713	0.53	1/4987 (0.0%)
5	D	0.38	0/3713	0.53	0/4987
All	All	0.43	1/16569 (0.0%)	0.70	23/22615 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	13	C	C1'-N1	5.26	1.56	1.48

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	5	G	P-O3'-C3'	-11.56	105.83	119.70
3	G	8	C	P-O3'-C3'	-9.96	107.75	119.70
3	G	6	A	P-O3'-C3'	-6.96	111.35	119.70
3	G	7	U	C5'-C4'-O4'	6.75	117.20	109.10
4	J	68	C	O4'-C1'-N1	6.46	113.37	108.20
1	E	12	C	O4'-C1'-N1	6.01	113.01	108.20
3	G	3	C	C2-N1-C1'	5.95	125.35	118.80
3	G	7	U	O4'-C4'-C3'	-5.93	98.07	104.00
1	E	10	C	O4'-C1'-N1	5.92	112.94	108.20
2	I	69	C	O4'-C1'-N1	5.83	112.87	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	75	LEU	CA-CB-CG	5.82	128.69	115.30
2	H	66	U	O4'-C1'-N1	5.79	112.83	108.20
3	G	8	C	O4'-C1'-N1	5.66	112.73	108.20
3	G	13	C	C6-N1-C2	-5.64	118.04	120.30
3	G	4	G	O4'-C1'-N9	5.54	112.64	108.20
2	H	73	A	C3'-C2'-C1'	5.51	105.91	101.50
3	G	3	C	N1-C2-O2	5.38	122.13	118.90
2	I	70	C	O4'-C1'-N1	5.37	112.50	108.20
3	G	13	C	O4'-C1'-N1	5.37	112.50	108.20
2	I	64	G	C4'-C3'-C2'	-5.32	97.28	102.60
2	H	62	C	O4'-C1'-N1	5.23	112.39	108.20
3	G	9	C	O4'-C1'-N1	5.16	112.33	108.20
5	C	75	LEU	CA-CB-CG	5.07	126.95	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	276	0	143	4	0
1	F	276	0	143	3	0
2	H	295	0	154	3	0
2	I	295	0	154	2	0
3	G	230	0	122	12	0
4	J	168	0	89	11	0
5	A	3630	0	3633	60	0
5	B	3630	0	3633	55	0
5	C	3630	0	3633	71	0
5	D	3630	0	3633	60	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	29	0	12	0	0
7	B	29	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	29	0	12	0	0
7	D	29	0	12	1	0
All	All	16180	0	15385	244	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 8.

All (244) 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)
5:A:198:ARG:HH11	5:A:198:ARG:HG2	1.02	1.11
5:A:198:ARG:NH1	5:A:198:ARG:HG2	1.78	0.89
5:C:395:THR:HG23	5:C:396:HIS:HD2	1.40	0.87
5:D:132:PHE:HB3	5:D:220:VAL:HG21	1.55	0.87
5:D:22:ARG:HE	5:D:25:ARG:HG2	1.39	0.87
5:C:14:VAL:HG13	5:C:149:ARG:HB3	1.64	0.79
3:G:7:U:H3	4:J:66:A:H61	1.31	0.79
5:C:186:LEU:O	5:C:190:LYS:HB2	1.83	0.78
5:A:16:PRO:HA	5:A:55:LYS:HG2	1.66	0.77
5:C:267:LEU:HD22	5:C:426:THR:HG23	1.66	0.76
5:C:299:ARG:NH1	5:C:399:THR:O	2.18	0.75
5:D:141:ILE:HD11	5:D:148:VAL:HG21	1.67	0.74
5:A:71:SER:C	5:A:73:GLU:H	1.88	0.74
5:D:344:ARG:O	5:D:345:MET:HB3	1.88	0.74
5:A:198:ARG:HH11	5:A:198:ARG:CG	1.93	0.73
5:A:391:SER:O	5:A:395:THR:HG22	1.88	0.73
5:B:268:ARG:HH21	5:B:269:LYS:HE2	1.55	0.71
5:C:380:ARG:HH12	5:D:334:GLN:NE2	1.89	0.70
5:A:299:ARG:NH1	5:A:399:THR:O	2.24	0.70
1:E:12:C:H2'	1:E:13:G:O4'	1.92	0.69
5:D:87:LEU:HD23	5:D:104:VAL:HG23	1.76	0.68
5:C:380:ARG:HH12	5:D:334:GLN:HE21	1.41	0.68
5:C:14:VAL:CG1	5:C:149:ARG:HB3	2.24	0.68
5:C:395:THR:HG23	5:C:396:HIS:CD2	2.24	0.68
5:B:83:GLY:HA3	5:B:100:VAL:HG21	1.76	0.67
5:B:95:ALA:HB3	5:B:99:TYR:HE2	1.60	0.66
5:A:380:ARG:HH22	5:B:334:GLN:HE22	1.42	0.66
5:A:43:VAL:HG22	5:A:65:LEU:HD11	1.77	0.66
5:C:124:LYS:O	5:C:125:SER:HB3	1.95	0.66
5:B:344:ARG:O	5:B:345:MET:HB3	1.96	0.65
5:C:16:PRO:HA	5:C:55:LYS:HG2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:50:ARG:HD3	5:C:137:LEU:HB3	1.77	0.65
5:B:185:PHE:O	5:B:186:LEU:CB	2.44	0.65
5:C:30:GLU:HA	5:C:33:ARG:NH1	2.12	0.65
4:J:62:G:N2	5:C:165:TYR:HE1	1.95	0.65
5:B:345:MET:HB2	5:B:375:TRP:CZ3	2.32	0.64
5:A:3:VAL:HG22	5:A:249:PRO:HG2	1.80	0.64
5:D:82:ILE:O	5:D:86:VAL:HB	1.98	0.63
5:D:280:ALA:HB2	5:D:330:LEU:HD23	1.81	0.63
5:D:173:TYR:HB2	7:D:504:CTP:H2'	1.80	0.63
5:C:185:PHE:O	5:C:186:LEU:CB	2.47	0.63
3:G:5:G:O2'	5:A:292:ASN:ND2	2.32	0.62
5:D:95:ALA:HB3	5:D:99:TYR:HE2	1.63	0.62
3:G:9:C:H6	3:G:9:C:OP2	1.82	0.62
5:B:19:GLU:O	5:B:23:LYS:HB2	2.01	0.61
3:G:7:U:H3	4:J:66:A:N6	1.98	0.61
5:C:344:ARG:O	5:C:345:MET:HB3	1.99	0.61
5:B:87:LEU:HD23	5:B:104:VAL:HG23	1.83	0.60
3:G:9:C:OP2	3:G:9:C:C6	2.54	0.60
5:B:339:SER:O	5:B:380:ARG:HD2	2.01	0.60
5:A:47:SER:HB3	5:A:53:TRP:HB3	1.83	0.60
3:G:12:A:H61	4:J:61:C:H42	1.49	0.60
5:C:185:PHE:O	5:C:186:LEU:HB3	2.02	0.60
5:C:63:PHE:CE2	5:C:127:VAL:HG12	2.37	0.59
4:J:62:G:N2	5:C:165:TYR:CE1	2.71	0.59
5:A:71:SER:O	5:A:73:GLU:N	2.35	0.59
5:C:282:LYS:HD2	5:C:415:ILE:HD11	1.85	0.59
5:A:22:ARG:HA	5:A:25:ARG:HB2	1.85	0.58
5:D:11:LEU:HB3	5:D:15:ILE:HD12	1.84	0.58
5:C:96:GLU:HG2	5:C:127:VAL:CG2	2.34	0.58
5:A:198:ARG:NH1	5:A:198:ARG:CG	2.61	0.57
5:A:68:GLU:HA	5:A:115:TYR:CD2	2.40	0.57
5:D:22:ARG:HA	5:D:25:ARG:HB3	1.87	0.57
4:J:63:C:H2'	4:J:64:G:C8	2.39	0.56
5:A:380:ARG:HH22	5:B:334:GLN:NE2	2.01	0.56
5:A:314:MET:HE3	5:B:312:ASN:HB3	1.87	0.56
5:C:371:ASN:N	5:D:233:ASP:OD1	2.39	0.56
5:D:129:ARG:NH1	5:D:224:ARG:HD3	2.21	0.56
5:B:17:ASP:OD2	5:B:19:GLU:HB3	2.06	0.56
2:H:73:A:O2'	5:B:291:ASP:OD2	2.25	0.55
5:A:71:SER:C	5:A:73:GLU:N	2.59	0.55
5:D:95:ALA:HB3	5:D:99:TYR:CE2	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:233:ASP:HB3	5:D:237:ARG:NH1	2.22	0.55
5:D:129:ARG:CZ	5:D:224:ARG:HD3	2.37	0.55
5:A:380:ARG:HH12	5:B:334:GLN:NE2	2.05	0.55
5:A:307:PHE:CE1	5:A:311:GLU:HG3	2.42	0.54
5:A:65:LEU:HD23	5:A:116:LYS:HG3	1.89	0.54
5:D:305:PHE:CE1	5:D:315:PRO:HB2	2.42	0.54
5:C:187:GLU:O	5:C:191:ASN:HB2	2.07	0.54
5:B:43:VAL:HG22	5:B:65:LEU:HD11	1.90	0.54
5:C:11:LEU:O	5:C:15:ILE:HG12	2.08	0.54
5:B:50:ARG:HE	5:B:134:HIS:HA	1.72	0.53
3:G:12:A:N6	4:J:61:C:H42	2.07	0.53
5:A:185:PHE:O	5:A:186:LEU:CB	2.56	0.53
5:A:34:ARG:HB3	5:A:86:VAL:HG22	1.91	0.53
5:A:348:GLN:NE2	5:C:39:GLY:O	2.42	0.53
5:C:196:THR:HG23	5:C:198:ARG:H	1.72	0.53
5:C:278:VAL:HG22	5:C:332:GLU:HG3	1.91	0.53
5:D:185:PHE:O	5:D:186:LEU:CB	2.57	0.52
5:D:185:PHE:O	5:D:186:LEU:HB3	2.10	0.52
5:D:354:ASN:HA	5:D:357:LYS:HG2	1.91	0.52
5:A:14:VAL:HG13	5:A:149:ARG:HB3	1.92	0.52
4:J:67:U:OP1	5:A:224:ARG:NH1	2.42	0.52
5:B:53:TRP:HD1	5:B:54:LEU:O	1.93	0.52
5:C:334:GLN:HG2	5:D:339:SER:OG	2.10	0.52
5:B:356:LYS:O	5:B:360:SER:HB3	2.10	0.51
5:C:200:VAL:HG22	5:C:215:PHE:HB3	1.92	0.51
5:D:89:SER:HB3	5:D:103:VAL:HG12	1.92	0.51
5:A:218:ASP:HB2	5:A:224:ARG:HG2	1.93	0.51
5:C:93:ARG:HD3	5:C:94:TYR:H	1.76	0.51
5:D:17:ASP:HB2	5:D:20:GLU:HB2	1.92	0.51
5:B:144:LYS:HZ1	5:B:183:GLY:HA2	1.76	0.50
5:D:22:ARG:NE	5:D:25:ARG:HG2	2.19	0.50
5:D:200:VAL:HG13	5:D:215:PHE:HB3	1.93	0.50
1:E:11:G:H1	2:H:62:C:H42	1.59	0.50
4:J:63:C:H2'	4:J:64:G:H8	1.76	0.50
5:B:314:MET:HE3	5:B:335:ILE:HD11	1.93	0.50
5:B:185:PHE:O	5:B:186:LEU:HB2	2.11	0.50
5:D:4:GLU:O	5:D:8:GLU:HG3	2.11	0.50
5:A:299:ARG:O	5:A:303:LYS:HG2	2.12	0.50
5:A:423:GLU:HB3	5:A:424:PRO:HD2	1.94	0.49
5:B:83:GLY:O	5:B:87:LEU:HD12	2.11	0.49
5:C:75:LEU:HD12	5:C:76:ARG:N	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:13:C:H2'	5:C:95:ALA:HA	1.94	0.49
5:A:380:ARG:HH12	5:B:334:GLN:HE21	1.59	0.49
5:C:307:PHE:CE1	5:C:311:GLU:HG3	2.47	0.49
3:G:3:C:H3'	3:G:4:G:C5'	2.42	0.49
5:A:75:LEU:HD22	5:A:113:PRO:HB2	1.95	0.49
5:A:314:MET:HB2	5:A:334:GLN:HB2	1.94	0.49
5:C:190:LYS:HG2	5:C:193:ARG:HH21	1.78	0.48
5:C:260:LEU:HD23	5:C:437:ASP:HB2	1.94	0.48
5:C:35:LEU:HD23	5:C:86:VAL:HG21	1.94	0.48
5:C:124:LYS:O	5:C:125:SER:CB	2.61	0.48
5:D:218:ASP:HB2	5:D:224:ARG:O	2.14	0.48
5:B:87:LEU:HD22	5:B:102:GLY:HA3	1.96	0.48
5:D:187:GLU:O	5:D:191:ASN:HB2	2.13	0.48
5:A:47:SER:HB3	5:A:53:TRP:CB	2.44	0.48
5:A:314:MET:CE	5:B:312:ASN:HB3	2.44	0.48
5:A:50:ARG:NH1	5:A:176:GLU:OE2	2.46	0.48
5:B:269:LYS:HA	5:B:272:GLU:HB3	1.94	0.48
5:D:9:LYS:O	5:D:12:GLU:HG2	2.13	0.48
2:I:73:A:O2'	5:D:291:ASP:OD2	2.27	0.48
5:A:345:MET:HG2	5:A:373:ARG:HD3	1.95	0.48
5:D:356:LYS:HA	5:D:359:LEU:HB2	1.96	0.48
5:D:387:GLU:HA	5:D:390:ARG:NH2	2.28	0.48
3:G:7:U:H5'	5:A:299:ARG:HD2	1.96	0.47
5:B:386:GLU:HB3	5:B:414:ILE:HG21	1.96	0.47
5:B:185:PHE:O	5:B:186:LEU:HB3	2.14	0.47
5:C:174:LEU:HD11	5:C:216:VAL:HG21	1.95	0.47
5:B:60:ILE:HB	5:B:109:VAL:HG22	1.96	0.47
5:C:148:VAL:HA	5:C:179:ILE:HG13	1.95	0.47
5:C:297:LEU:O	5:C:301:SER:HB2	2.14	0.47
5:C:305:PHE:CE1	5:C:315:PRO:HB2	2.50	0.47
5:C:237:ARG:HG3	5:D:369:ILE:HD12	1.97	0.47
5:B:235:LEU:O	5:B:239:VAL:HG23	2.14	0.47
5:B:144:LYS:NZ	5:B:183:GLY:HA2	2.31	0.46
5:D:296:GLN:HE22	5:D:403:ASN:H	1.64	0.46
5:C:63:PHE:HE2	5:C:127:VAL:HG12	1.77	0.46
5:C:243:ARG:NH2	5:D:350:GLU:O	2.32	0.46
5:C:30:GLU:HA	5:C:33:ARG:HH11	1.80	0.46
5:C:397:TRP:CE2	5:C:409:ARG:HD2	2.51	0.46
5:A:344:ARG:O	5:A:345:MET:CB	2.64	0.46
5:D:60:ILE:HB	5:D:109:VAL:HG22	1.98	0.46
5:A:197:ARG:O	5:A:213:GLU:HA	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:93:ARG:HD3	5:B:289:VAL:HG11	1.98	0.45
5:C:137:LEU:O	5:C:138:GLU:C	2.54	0.45
5:D:345:MET:HB2	5:D:375:TRP:CZ3	2.51	0.45
5:A:282:LYS:HD3	5:A:415:ILE:HD11	1.98	0.45
5:B:324:GLU:OE2	5:B:324:GLU:HA	2.16	0.45
5:C:141:ILE:HD11	5:C:148:VAL:HG21	1.99	0.45
5:B:340:ARG:O	5:B:380:ARG:HG3	2.17	0.45
5:B:54:LEU:HD11	5:B:152:LYS:HB2	1.99	0.45
5:A:350:GLU:HG3	5:C:38:LEU:C	2.36	0.45
5:A:76:ARG:HG2	5:A:97:HIS:HB3	1.98	0.45
5:B:344:ARG:HG3	5:B:378:GLU:OE2	2.16	0.44
5:B:351:ASP:O	5:B:355:VAL:HG23	2.17	0.44
5:C:75:LEU:HD13	5:C:113:PRO:HB2	1.99	0.44
5:C:346:GLY:N	5:C:374:TRP:O	2.45	0.44
5:A:263:GLU:C	5:A:265:GLU:H	2.21	0.44
5:C:334:GLN:HE21	5:D:380:ARG:HH12	1.63	0.44
5:D:15:ILE:HA	5:D:16:PRO:HD3	1.90	0.44
5:D:307:PHE:CE1	5:D:311:GLU:HG3	2.53	0.44
5:D:348:GLN:C	5:D:350:GLU:H	2.21	0.44
5:C:343:ARG:HH22	5:C:370:GLU:CD	2.21	0.44
5:D:258:HIS:HA	5:D:259:PRO:HD3	1.90	0.44
5:A:361:ARG:H	5:A:361:ARG:HG2	1.65	0.44
5:B:320:PHE:HA	5:B:328:TYR:O	2.18	0.44
5:C:339:SER:O	5:C:380:ARG:HD2	2.17	0.44
5:D:342:PHE:O	5:D:377:PHE:HA	2.18	0.44
1:F:8:U:H3	2:I:65:A:H61	1.66	0.43
5:C:3:VAL:HG22	5:C:249:PRO:HG2	1.99	0.43
5:D:369:ILE:HA	5:D:373:ARG:O	2.18	0.43
5:C:263:GLU:H	5:C:263:GLU:HG2	1.53	0.43
5:D:212:GLU:HA	5:D:212:GLU:OE1	2.18	0.43
5:B:48:TYR:HA	5:B:53:TRP:CE3	2.54	0.43
5:B:8:GLU:HA	5:B:11:LEU:HD12	2.00	0.43
5:B:332:GLU:HB2	5:B:432:MET:HE3	2.00	0.43
5:C:70:PHE:HB3	5:C:71:SER:H	1.60	0.43
5:A:18:GLU:O	5:A:21:VAL:HG12	2.17	0.43
5:A:233:ASP:O	5:A:237:ARG:HB2	2.19	0.43
5:B:1:MET:HG3	5:B:249:PRO:HD2	2.01	0.43
5:B:343:ARG:HH22	5:B:370:GLU:CD	2.22	0.43
5:B:332:GLU:HB2	5:B:432:MET:CE	2.49	0.43
5:D:143:GLY:N	5:D:145:GLU:OE1	2.51	0.43
5:A:14:VAL:CG1	5:A:149:ARG:HB3	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:142:LYS:HA	5:B:145:GLU:OE2	2.19	0.43
5:A:185:PHE:O	5:A:186:LEU:HB2	2.18	0.42
5:D:218:ASP:HB3	5:D:221:ASP:O	2.19	0.42
5:D:282:LYS:HD3	5:D:415:ILE:HD11	2.01	0.42
5:C:137:LEU:HD23	5:C:141:ILE:HB	2.01	0.42
5:C:397:TRP:CE2	5:C:409:ARG:CD	3.02	0.42
5:D:75:LEU:HD11	5:D:115:TYR:CE1	2.54	0.42
5:A:67:PRO:HG2	5:A:70:PHE:CE1	2.54	0.42
5:B:75:LEU:HD22	5:B:113:PRO:HB2	2.01	0.42
5:C:344:ARG:HA	5:C:344:ARG:HD2	1.88	0.42
1:F:1:G:H5'	5:D:402:LYS:HE3	2.01	0.42
5:B:408:ILE:HG23	5:B:412:PHE:HB3	2.00	0.42
4:J:62:G:H22	5:C:165:TYR:HE1	1.66	0.42
5:C:202:ASP:HA	5:C:217:VAL:HB	2.01	0.42
3:G:3:C:H3'	3:G:4:G:H5'	2.02	0.42
5:C:7:LEU:HD11	5:C:186:LEU:HD13	2.02	0.42
5:A:345:MET:SD	5:C:74:GLU:HG2	2.59	0.42
5:D:282:LYS:HD3	5:D:415:ILE:CD1	2.50	0.42
5:D:76:ARG:O	5:D:80:LEU:HB2	2.19	0.42
1:F:5:A:H2'	1:F:6:U:C6	2.54	0.42
5:A:260:LEU:HD23	5:A:437:ASP:OD2	2.20	0.41
5:A:39:GLY:O	5:C:348:GLN:NE2	2.53	0.41
5:B:130:THR:N	5:B:131:PRO:HD2	2.35	0.41
5:D:137:LEU:HD21	5:D:177:LEU:HD23	2.01	0.41
5:B:200:VAL:HA	5:B:215:PHE:O	2.20	0.41
5:D:80:LEU:HD11	5:D:98:PRO:HB2	2.02	0.41
3:G:12:A:H61	4:J:61:C:N4	2.15	0.41
1:E:6:U:H3	2:H:67:A:H61	1.69	0.41
5:C:75:LEU:HD12	5:C:75:LEU:C	2.41	0.41
5:D:137:LEU:HD13	5:D:176:GLU:OE1	2.20	0.41
5:A:11:LEU:HD22	5:A:15:ILE:HD11	2.03	0.41
5:B:53:TRP:CD1	5:B:54:LEU:O	2.72	0.41
5:C:137:LEU:HD21	5:C:176:GLU:HB3	2.02	0.41
5:A:60:ILE:HB	5:A:109:VAL:HG13	2.02	0.41
5:B:218:ASP:HB3	5:B:221:ASP:O	2.20	0.41
5:B:299:ARG:NH1	5:B:399:THR:O	2.54	0.41
5:A:75:LEU:HD13	5:A:76:ARG:N	2.36	0.41
5:C:247:GLU:O	5:C:249:PRO:HD3	2.20	0.41
5:C:76:ARG:HE	5:C:97:HIS:CE1	2.39	0.41
5:B:9:LYS:O	5:B:12:GLU:HG2	2.20	0.41
5:C:243:ARG:CZ	5:D:352:GLU:HG3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:5:GLU:HG3	5:A:6:ILE:N	2.34	0.41
5:A:345:MET:HE3	5:C:70:PHE:CE1	2.57	0.40
5:A:350:GLU:HG2	5:A:350:GLU:H	1.65	0.40
5:B:308:LEU:HD13	5:B:333:CYS:SG	2.61	0.40
5:D:28:GLU:OE2	5:D:32:ARG:NE	2.51	0.40
5:A:68:GLU:HA	5:A:115:TYR:HD2	1.83	0.40
5:D:363:ARG:NE	5:D:378:GLU:OE2	2.52	0.40
1:E:13:G:H5''	1:E:13:G:H8	1.87	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	
5	A	435/437 (100%)	404 (93%)	23 (5%)	8 (2%)	10	47
5	B	435/437 (100%)	395 (91%)	32 (7%)	8 (2%)	10	47
5	C	435/437 (100%)	403 (93%)	23 (5%)	9 (2%)	8	42
5	D	435/437 (100%)	390 (90%)	39 (9%)	6 (1%)	13	53
All	All	1740/1748 (100%)	1592 (92%)	117 (7%)	31 (2%)	10	47

All (31) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	A	72	LYS
5	A	186	LEU
5	B	186	LEU
5	C	70	PHE
5	C	117	LEU
5	C	125	SER
5	C	186	LEU

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Mol	Chain	Res	Type
5	D	186	LEU
5	A	117	LEU
5	B	184	SER
5	B	351	ASP
5	D	86	VAL
5	A	70	PHE
5	B	261	GLU
5	C	261	GLU
5	D	96	GLU
5	D	117	LEU
5	D	345	MET
5	A	125	SER
5	C	138	GLU
5	C	402	LYS
5	A	3	VAL
5	A	345	MET
5	B	95	ALA
5	B	345	MET
5	A	402	LYS
5	B	117	LEU
5	C	345	MET
5	C	3	VAL
5	D	259	PRO
5	B	123	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	
5	A	387/387 (100%)	355 (92%)	32 (8%)	13	46
5	B	387/387 (100%)	354 (92%)	33 (8%)	12	44
5	C	387/387 (100%)	341 (88%)	46 (12%)	6	26
5	D	387/387 (100%)	354 (92%)	33 (8%)	12	44
All	All	1548/1548 (100%)	1404 (91%)	144 (9%)	10	38

All (144) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	A	2	LYS
5	A	5	GLU
5	A	13	LEU
5	A	22	ARG
5	A	47	SER
5	A	55	LYS
5	A	75	LEU
5	A	76	ARG
5	A	78	ARG
5	A	86	VAL
5	A	93	ARG
5	A	119	GLU
5	A	123	ILE
5	A	144	LYS
5	A	194	ARG
5	A	198	ARG
5	A	210	LYS
5	A	213	GLU
5	A	222	GLU
5	A	224	ARG
5	A	260	LEU
5	A	288	ILE
5	A	289	VAL
5	A	291	ASP
5	A	345	MET
5	A	350	GLU
5	A	356	LYS
5	A	359	LEU
5	A	361	ARG
5	A	383	THR
5	A	395	THR
5	A	436	LYS
5	B	1	MET
5	B	9	LYS
5	B	13	LEU
5	B	17	ASP
5	B	18	GLU
5	B	23	LYS
5	B	38	LEU
5	B	54	LEU
5	B	70	PHE
5	B	77	GLU

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Mol	Chain	Res	Type
5	B	78	ARG
5	B	86	VAL
5	B	92	ILE
5	B	117	LEU
5	B	118	LYS
5	B	119	GLU
5	B	121	LYS
5	B	144	LYS
5	B	212	GLU
5	B	246	MET
5	B	257	LYS
5	B	260	LEU
5	B	270	ILE
5	B	284	ARG
5	B	288	ILE
5	B	301	SER
5	B	324	GLU
5	B	344	ARG
5	B	356	LYS
5	B	361	ARG
5	B	362	ASN
5	B	381	LYS
5	B	404	VAL
5	C	1	MET
5	C	6	ILE
5	C	11	LEU
5	C	14	VAL
5	C	18	GLU
5	C	25	ARG
5	C	54	LEU
5	C	69	GLU
5	C	75	LEU
5	C	78	ARG
5	C	80	LEU
5	C	93	ARG
5	C	118	LYS
5	C	122	ASN
5	C	123	ILE
5	C	127	VAL
5	C	137	LEU
5	C	138	GLU
5	C	142	LYS

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Mol	Chain	Res	Type
5	C	166	LYS
5	C	191	ASN
5	C	194	ARG
5	C	198	ARG
5	C	213	GLU
5	C	222	GLU
5	C	241	LEU
5	C	251	LEU
5	C	257	LYS
5	C	263	GLU
5	C	288	ILE
5	C	289	VAL
5	C	299	ARG
5	C	301	SER
5	C	314	MET
5	C	344	ARG
5	C	345	MET
5	C	359	LEU
5	C	361	ARG
5	C	362	ASN
5	C	383	THR
5	C	390	ARG
5	C	399	THR
5	C	411	TYR
5	C	419	LYS
5	C	422	LYS
5	C	431	GLU
5	D	17	ASP
5	D	22	ARG
5	D	25	ARG
5	D	26	GLU
5	D	38	LEU
5	D	55	LYS
5	D	59	GLU
5	D	70	PHE
5	D	72	LYS
5	D	78	ARG
5	D	91	GLU
5	D	103	VAL
5	D	118	LYS
5	D	127	VAL
5	D	144	LYS

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Mol	Chain	Res	Type
5	D	145	GLU
5	D	156	LYS
5	D	199	THR
5	D	220	VAL
5	D	247	GLU
5	D	260	LEU
5	D	273	GLU
5	D	299	ARG
5	D	324	GLU
5	D	325	GLU
5	D	340	ARG
5	D	352	GLU
5	D	353	ARG
5	D	356	LYS
5	D	373	ARG
5	D	380	ARG
5	D	383	THR
5	D	409	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
5	A	229	ASN
5	A	292	ASN
5	A	348	GLN
5	A	371	ASN
5	A	396	HIS
5	B	97	HIS
5	B	312	ASN
5	B	334	GLN
5	C	334	GLN
5	C	362	ASN
5	C	396	HIS
5	D	334	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	12/13 (92%)	1 (8%)	0
1	F	12/13 (92%)	3 (25%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	H	13/14 (92%)	4 (30%)	0
2	I	13/14 (92%)	4 (30%)	0
3	G	10/11 (90%)	6 (60%)	0
4	J	7/8 (87%)	1 (14%)	0
All	All	67/73 (91%)	19 (28%)	0

All (19) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	E	12	C
2	H	62	C
2	H	67	A
2	H	71	G
2	H	74	C
1	F	11	G
1	F	12	C
1	F	13	G
2	I	62	C
2	I	66	U
2	I	67	A
2	I	74	C
3	G	4	G
3	G	7	U
3	G	8	C
3	G	9	C
3	G	10	G
3	G	13	C
4	J	68	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 carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
7	CTP	A	501	6	24,30,30	0.89	0	24,47,47	0.82	1 (4%)
7	CTP	B	502	6	24,30,30	0.71	0	24,47,47	0.86	0
7	CTP	C	503	6	24,30,30	0.91	1 (4%)	24,47,47	1.25	3 (12%)
7	CTP	D	504	6	24,30,30	0.75	0	24,47,47	0.73	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	CTP	A	501	6	-	0/18/38/38	0/2/2/2
7	CTP	B	502	6	-	0/18/38/38	0/2/2/2
7	CTP	C	503	6	-	0/18/38/38	0/2/2/2
7	CTP	D	504	6	-	0/18/38/38	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C	503	CTP	C6-N1	2.09	1.38	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	503	CTP	C5-C4-N3	-2.04	119.25	121.68
7	C	503	CTP	N4-C4-N3	2.11	120.20	116.64
7	A	501	CTP	O4'-C1'-N1	2.32	112.73	108.08
7	C	503	CTP	O4'-C1'-N1	3.83	115.74	108.08

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	504	CTP	1	0

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	E	13/13 (100%)	1.19	3 (23%) 1 1	130, 131, 132, 132	0
1	F	13/13 (100%)	1.76	6 (46%) 0 0	130, 131, 131, 132	0
2	H	14/14 (100%)	1.36	4 (28%) 1 1	129, 131, 133, 134	0
2	I	14/14 (100%)	1.50	2 (14%) 3 2	130, 131, 133, 133	0
3	G	11/11 (100%)	1.58	3 (27%) 1 1	130, 131, 132, 132	0
4	J	8/8 (100%)	2.09	4 (50%) 0 0	129, 130, 131, 131	0
5	A	437/437 (100%)	0.38	30 (6%) 18 10	130, 131, 132, 133	0
5	B	437/437 (100%)	0.73	63 (14%) 3 2	130, 131, 132, 132	0
5	C	437/437 (100%)	0.37	24 (5%) 26 15	130, 131, 132, 133	0
5	D	437/437 (100%)	0.62	41 (9%) 9 5	130, 131, 132, 132	0
All	All	1821/1821 (100%)	0.57	180 (9%) 8 5	129, 131, 132, 134	0

All (180) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	61	G	8.3
5	D	92	ILE	7.3
5	C	72	LYS	7.0
5	B	107	VAL	6.9
5	D	94	TYR	6.8
5	A	96	GLU	6.3
5	B	68	GLU	6.1
5	B	113	PRO	6.0
5	D	122	ASN	6.0
5	B	122	ASN	5.8
5	B	73	GLU	5.3
5	B	437	ASP	5.1
5	A	250	SER	4.9

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Mol	Chain	Res	Type	RSRZ
5	B	72	LYS	4.9
5	A	84	LYS	4.8
3	G	4	G	4.8
5	D	125	SER	4.7
2	H	74	C	4.7
5	D	93	ARG	4.6
5	C	122	ASN	4.6
5	C	100	VAL	4.6
5	B	75	LEU	4.5
1	F	13	G	4.5
5	B	87	LEU	4.5
5	D	30	GLU	4.5
5	C	124	LYS	4.4
5	A	119	GLU	4.4
5	B	124	LYS	4.4
5	B	89	SER	4.4
5	B	63	PHE	4.3
5	D	85	ALA	4.3
5	B	120	PRO	4.2
5	B	126	ALA	4.2
5	D	124	LYS	4.1
5	A	122	ASN	4.1
5	D	126	ALA	4.1
2	H	63	G	4.1
5	D	58	LEU	4.0
5	B	267	LEU	4.0
5	C	1	MET	4.0
5	B	88	ASP	4.0
3	G	13	C	3.9
5	D	251	LEU	3.9
2	H	61	G	3.9
5	B	123	ILE	3.9
5	B	42	TYR	3.9
5	D	260	LEU	3.8
5	B	13	LEU	3.8
5	B	114	CYS	3.7
5	B	115	TYR	3.7
5	B	103	VAL	3.7
5	A	97	HIS	3.7
2	H	62	C	3.6
1	E	12	C	3.5
5	B	41	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
5	B	254	PHE	3.4
5	B	129	ARG	3.4
5	D	254	PHE	3.3
5	B	119	GLU	3.3
1	E	13	G	3.2
5	D	40	VAL	3.2
5	C	99	TYR	3.2
5	D	48	TYR	3.2
5	A	87	LEU	3.2
5	A	420	LEU	3.2
5	A	60	ILE	3.2
5	D	72	LYS	3.1
5	A	421	PHE	3.1
1	F	7	A	3.0
5	B	86	VAL	3.0
5	B	37	GLU	2.9
5	B	106	GLY	2.9
5	B	403	ASN	2.9
5	D	33	ARG	2.9
5	B	105	LYS	2.9
5	C	296	GLN	2.9
5	B	148	VAL	2.8
5	A	437	ASP	2.8
5	D	261	GLU	2.8
1	F	11	G	2.8
5	C	114	CYS	2.8
5	D	107	VAL	2.8
5	D	112	VAL	2.8
5	C	204	ALA	2.8
5	B	104	VAL	2.8
5	C	136	TRP	2.7
4	J	68	C	2.7
5	B	154	PHE	2.7
5	D	62	VAL	2.7
5	A	287	ASP	2.7
5	B	118	LYS	2.7
5	D	86	VAL	2.7
5	B	43	VAL	2.6
5	C	292	ASN	2.6
5	D	113	PRO	2.6
5	A	95	ALA	2.6
5	B	29	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
5	B	164	GLU	2.6
5	C	297	LEU	2.6
5	B	64	LEU	2.6
5	B	121	LYS	2.5
5	D	344	ARG	2.5
5	A	83	GLY	2.5
3	G	3	C	2.5
5	C	353	ARG	2.5
5	B	359	LEU	2.5
5	C	127	VAL	2.5
1	F	12	C	2.5
5	D	34	ARG	2.5
5	B	12	GLU	2.5
5	A	102	GLY	2.5
5	A	400	LEU	2.5
5	B	14	VAL	2.4
5	B	24	GLY	2.4
5	C	402	LYS	2.4
5	D	75	LEU	2.4
5	A	402	LYS	2.4
5	D	39	GLY	2.4
4	J	63	C	2.4
5	A	112	VAL	2.4
5	A	251	LEU	2.4
5	B	116	LYS	2.4
5	D	63	PHE	2.3
5	C	79	GLY	2.3
5	A	116	LYS	2.3
5	C	393	ALA	2.3
5	C	81	GLU	2.3
1	F	3	G	2.3
5	C	96	GLU	2.3
5	D	106	GLY	2.3
5	B	266	ARG	2.3
5	B	52	THR	2.3
5	C	33	ARG	2.3
5	D	82	ILE	2.3
5	B	77	GLU	2.3
5	C	394	SER	2.3
2	I	73	A	2.3
5	B	125	SER	2.2
5	D	66	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
5	C	174	LEU	2.2
5	A	79	GLY	2.2
5	B	30	GLU	2.2
1	F	6	U	2.2
5	B	92	ILE	2.2
5	D	97	HIS	2.2
5	C	60	ILE	2.2
5	C	166	LYS	2.2
5	B	146	ASN	2.2
5	B	48	TYR	2.2
5	A	136	TRP	2.2
5	A	401	GLY	2.2
5	B	31	LEU	2.1
5	B	33	ARG	2.1
5	B	112	VAL	2.1
5	A	364	ALA	2.1
5	A	72	LYS	2.1
5	B	76	ARG	2.1
5	D	31	LEU	2.1
5	B	111	VAL	2.1
5	D	356	LYS	2.1
5	B	70	PHE	2.1
5	B	282	LYS	2.1
5	D	120	PRO	2.1
4	J	62	G	2.1
5	A	154	PHE	2.1
5	A	99	TYR	2.1
5	A	63	PHE	2.1
4	J	64	G	2.1
5	D	65	LEU	2.1
5	D	105	LYS	2.1
5	D	164	GLU	2.0
5	B	17	ASP	2.0
5	D	352	GLU	2.0
5	D	426	THR	2.0
5	B	82	ILE	2.0
5	A	120	PRO	2.0
5	A	263	GLU	2.0
5	B	291	ASP	2.0
5	D	165	TYR	2.0
1	E	2	C	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
7	CTP	C	503	29/29	0.75	0.29	0.30	134,135,137,138	0
7	CTP	A	501	29/29	0.73	0.30	0.12	134,135,138,138	0
7	CTP	B	502	29/29	0.90	0.21	-0.73	132,132,133,133	0
7	CTP	D	504	29/29	0.91	0.24	-0.77	131,131,132,132	0
6	MG	C	603	1/1	0.87	0.16	-	109,109,109,109	0
6	MG	A	601	1/1	0.64	0.34	-	117,117,117,117	0
6	MG	B	602	1/1	0.83	0.22	-	95,95,95,95	0
6	MG	D	604	1/1	0.90	0.19	-	102,102,102,102	0

6.5 Other polymers [i](#)

There are no such residues in this entry.