



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:37 PM GMT

PDB ID : 5C3E
Title : Crystal structure of a transcribing RNA Polymerase II complex reveals a complete transcription bubble
Authors : Barnes, C.O.; Calero, M.; Malik, I.; Spahr, H.; Zhang, Q.; Pullara, F.; Kaplan, C.D.; Calero, G.
Deposited on : 2015-06-17
Resolution : 3.70 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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : rb-20026982

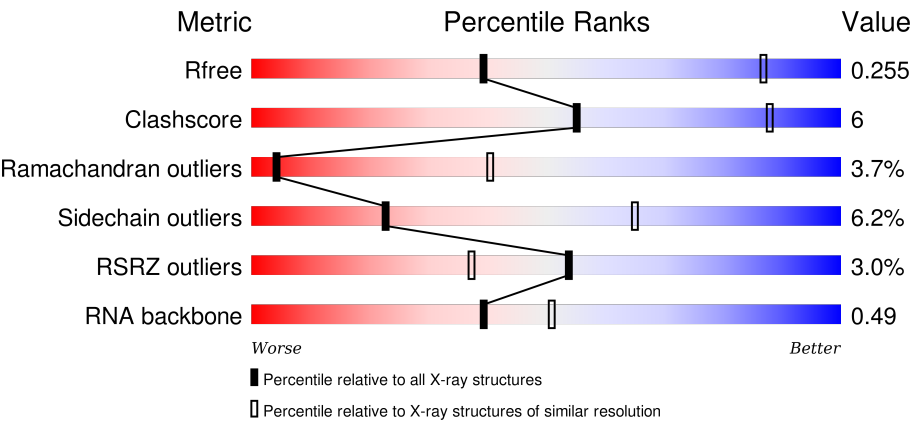
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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}	91344	1101 (3.90-3.50)
Clashscore	102246	1224 (3.90-3.50)
Ramachandran outliers	100387	1172 (3.90-3.50)
Sidechain outliers	100360	1170 (3.90-3.50)
RSRZ outliers	91569	1108 (3.90-3.50)
RNA backbone	2183	1067 (4.60-2.80)

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	A	1733	<div><div>%</div><div><div></div><div>62%</div><div>18%</div><div>•</div><div>17%</div></div></div>
2	B	1224	<div><div>4%</div><div><div></div><div>71%</div><div>22%</div><div>•</div><div>5%</div></div></div>
3	C	318	<div><div>%</div><div><div></div><div>64%</div><div>17%</div><div>•</div><div>17%</div></div></div>
4	D	221	<div><div>%</div><div><div></div><div>67%</div><div>13%</div><div></div><div>19%</div></div></div>

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Mol	Chain	Length	Quality of chain
5	E	215	
6	F	155	
7	G	179	
8	H	146	
9	I	122	
10	J	70	
11	K	120	
12	L	70	
13	R	9	
14	S	45	
15	U	45	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
16	ZN	C	401	-	-	-	X
17	MG	A	1804	-	-	-	X

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 32515 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 DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1430	Total	C	N	O	S	0	0	0
			11227	7069	1962	2134	62			

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1157	Total	C	N	O	S	0	0	0
			9130	5767	1599	1708	56			

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	265	Total	C	N	O	S	0	0	0
			2086	1312	347	414	13			

- Molecule 4 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	178	Total	C	N	O	S	0	0	0
			1417	875	254	286	2			

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	214	Total	C	N	O	S	0	0	0
			1752	1111	309	321	11			

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	87	Total	C	N	O	S	0	0	0
			705	451	119	132	3			

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	171	Total	C	N	O	S	0	0	0
			1339	861	222	248	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	172	LEU	-	expression tag	UNP P34087
G	173	GLU	-	expression tag	UNP P34087
G	174	HIS	-	expression tag	UNP P34087
G	175	HIS	-	expression tag	UNP P34087
G	176	HIS	-	expression tag	UNP P34087
G	177	HIS	-	expression tag	UNP P34087
G	178	HIS	-	expression tag	UNP P34087
G	179	HIS	-	expression tag	UNP P34087

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	135	Total	C	N	O	S	0	0	0
			1080	679	182	214	5			

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	114	Total	C	N	O	S	0	0	0
			927	571	168	178	10			

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	66	Total	C	N	O	S	0	0	0
			540	345	94	95	6			

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	115	Total	C	N	O	S	0	0	0
			924	593	157	172	2			

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	43	Total	C	N	O	S	0	0	0
			344	211	69	60	4			

- Molecule 13 is a RNA chain called Synthetic RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	R	9	Total	C	N	O	P	0	0	0
			197	88	40	60	9			

- Molecule 14 is a DNA chain called Synthetic DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	S	14	Total	C	N	O	P	0	0	0
			286	137	49	86	14			

- Molecule 15 is a DNA chain called Synthetic DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	U	27	Total	C	N	O	P	0	0	0
			550	262	101	160	27			

- Molecule 16 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	J	1	Total	Zn	0	0
			1	1		
16	B	1	Total	Zn	0	0
			1	1		
16	I	2	Total	Zn	0	0
			2	2		
16	C	2	Total	Zn	0	0
			2	2		
16	A	2	Total	Zn	0	0
			2	2		
16	L	1	Total	Zn	0	0
			1	1		

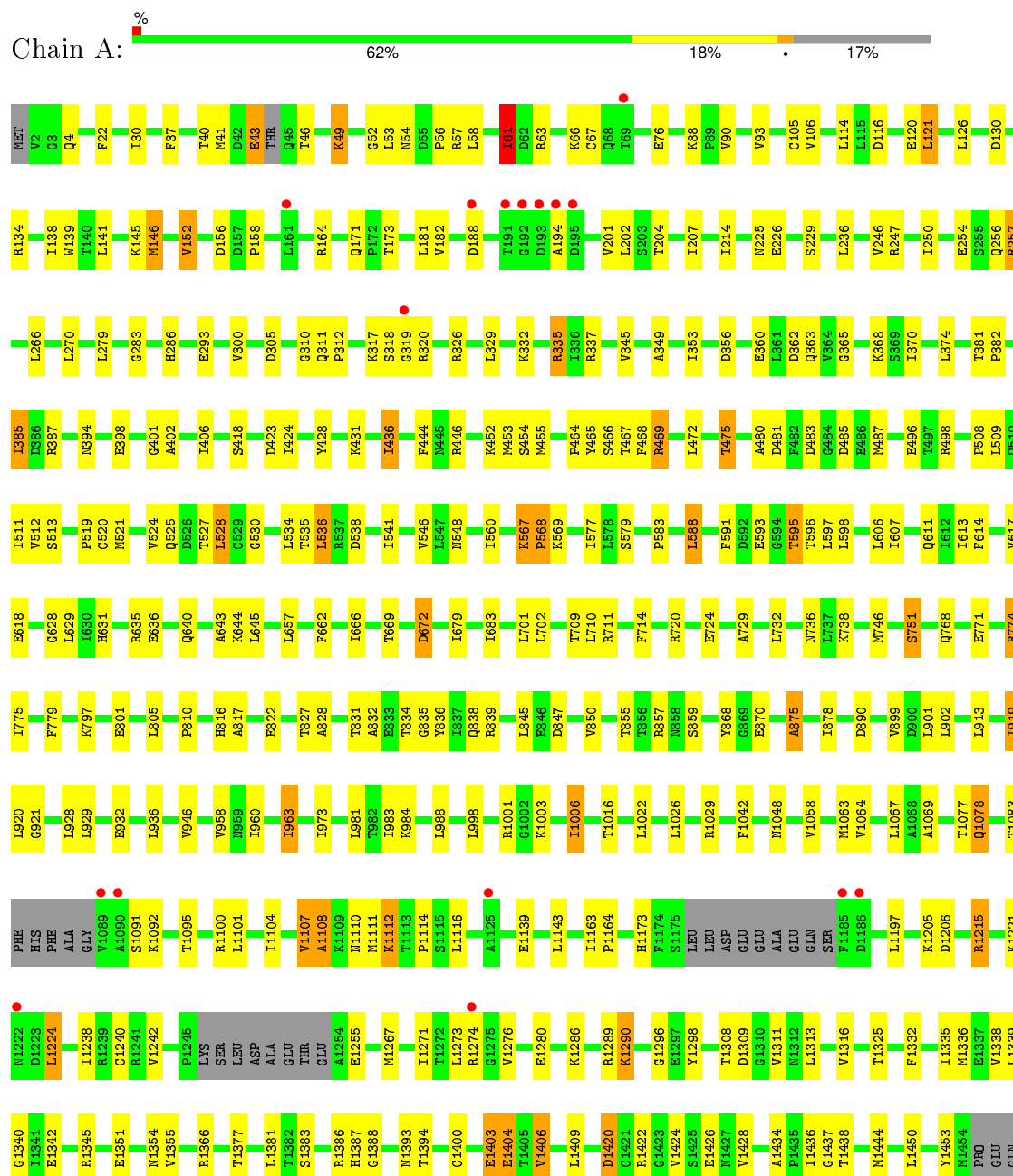
- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

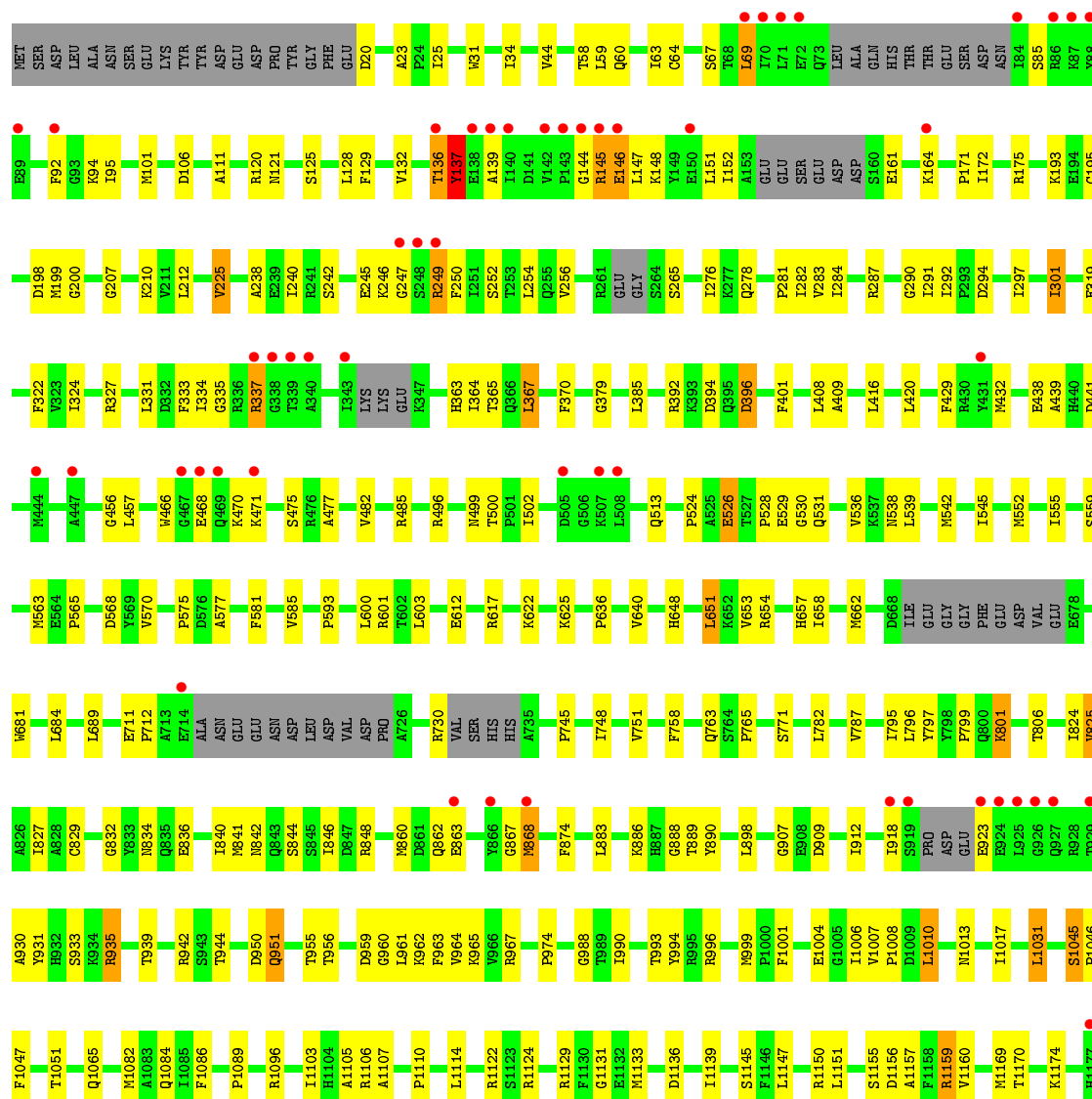
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	2	Total	Mg	0	0
			2	2		

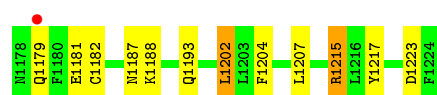
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

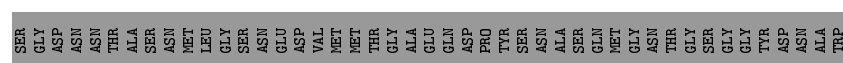
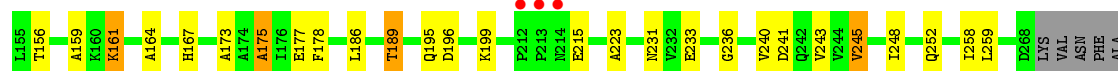
- Molecule 1: DNA-directed RNA polymerase II subunit RPB1



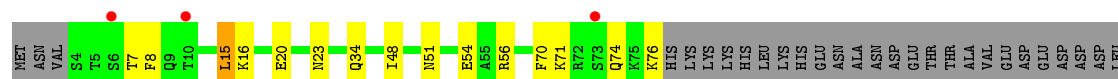




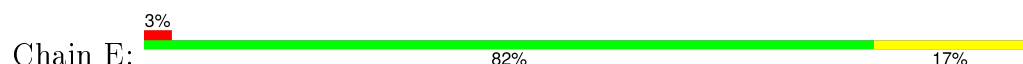
• Molecule 3: DNA-directed RNA polymerase II subunit RPB3



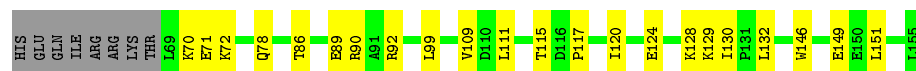
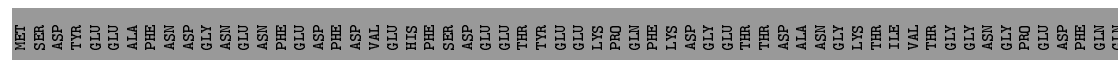
• Molecule 4: DNA-directed RNA polymerase II subunit RPB4



• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

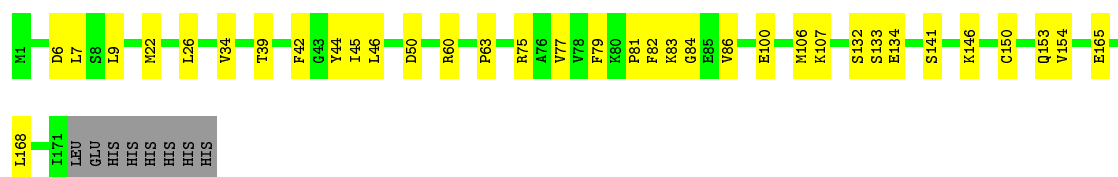


• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

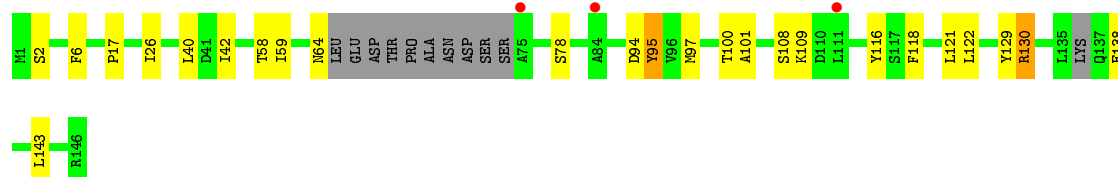


• Molecule 7: DNA-directed RNA polymerase II subunit RPB7

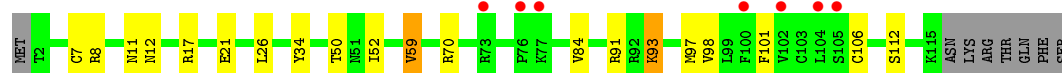
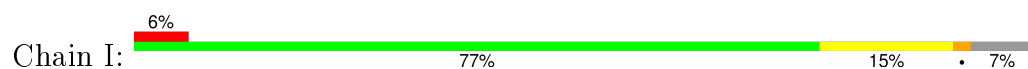




- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



- Molecule 9: DNA-directed RNA polymerase II subunit RPB9



- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



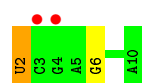
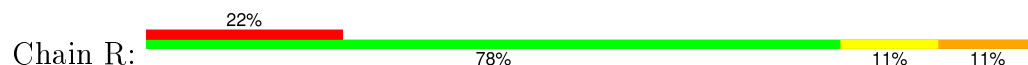
- Molecule 11: DNA-directed RNA polymerase II subunit RPB11



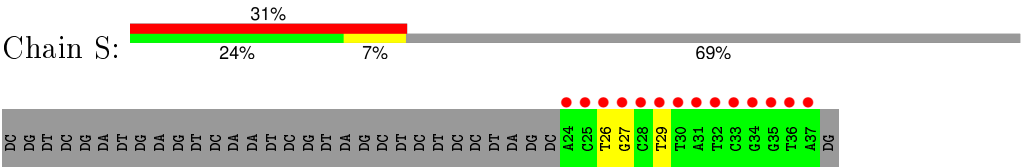
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



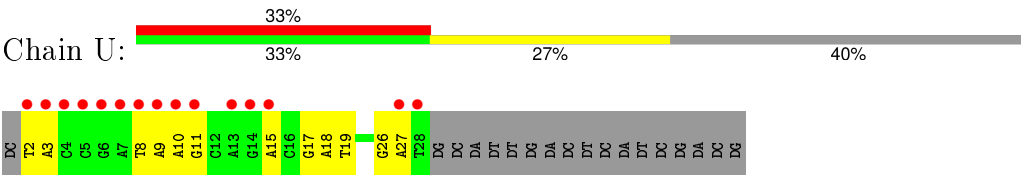
- Molecule 13: Synthetic RNA



● Molecule 14: Synthetic DNA



● Molecule 15: Synthetic DNA



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	219.05Å 390.94Å 278.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.70 39.98 – 3.70	Depositor EDS
% Data completeness (in resolution range)	96.4 (40.00-3.70) 96.4 (39.98-3.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.32	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 3.66Å)	Xtriage
Refinement program	BUSTER-TNT	Depositor
R, R_{free}	0.201 , 0.220 0.229 , 0.255	Depositor DCC
R_{free} test set	3687 reflections (3.02%)	DCC
Wilson B-factor (Å ²)	92.7	Xtriage
Anisotropy	0.383	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 100.9	EDS
Estimated twinning fraction	0.108 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.125 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.19$	Xtriage
Outliers	0 of 122114 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	32515	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 1.79% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, MG

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	0.40	0/11427	0.66	0/15457
2	B	0.39	0/9302	0.64	2/12542 (0.0%)
3	C	0.38	0/2124	0.62	0/2879
4	D	0.38	0/1427	0.62	0/1911
5	E	0.38	0/1788	0.58	0/2406
6	F	0.40	0/717	0.64	0/967
7	G	0.38	0/1367	0.65	0/1844
8	H	0.38	0/1097	0.61	0/1484
9	I	0.38	0/945	0.63	0/1273
10	J	0.39	0/549	0.65	0/738
11	K	0.37	0/942	0.58	0/1272
12	L	0.41	0/346	0.68	0/457
13	R	0.88	0/221	0.87	1/343 (0.3%)
14	S	1.04	0/319	0.97	0/490
15	U	1.19	2/616 (0.3%)	0.96	0/947
All	All	0.43	2/33187 (0.0%)	0.65	3/45010 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	U	15	DA	O3'-P	-6.68	1.53	1.61
15	U	15	DA	N9-C8	-5.06	1.33	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	136	THR	C-N-CA	5.30	134.95	121.70
2	B	145	ARG	C-N-CA	5.14	134.54	121.70
13	R	2	U	C1'-O4'-C4'	-5.07	105.85	109.90

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	11227	0	11270	167	0
2	B	9130	0	9099	143	0
3	C	2086	0	2045	34	0
4	D	1417	0	1428	7	0
5	E	1752	0	1776	21	0
6	F	705	0	731	10	0
7	G	1339	0	1357	16	0
8	H	1080	0	1049	14	0
9	I	927	0	883	11	0
10	J	540	0	554	16	0
11	K	924	0	934	17	0
12	L	344	0	365	7	0
13	R	197	0	96	1	0
14	S	286	0	160	3	0
15	U	550	0	304	11	0
16	A	2	0	0	0	0
16	B	1	0	0	0	0
16	C	2	0	0	0	0
16	I	2	0	0	0	0
16	J	1	0	0	0	0
16	L	1	0	0	0	0
17	A	2	0	0	0	0
All	All	32515	0	32051	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 6.

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)
10:J:36:LEU:HD21	10:J:50:ILE:HD11	1.38	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:446:ARG:HD2	1:A:480:ALA:HB2	1.49	0.91
1:A:1107:VAL:HA	1:A:1108:ALA:HB2	1.54	0.88
2:B:120:ARG:HG2	2:B:955:THR:HG21	1.61	0.83
2:B:145:ARG:HA	2:B:146:GLU:HB2	1.62	0.81
2:B:136:THR:HA	2:B:137:TYR:HB2	1.63	0.79
3:C:39:ALA:HA	3:C:164:ALA:HB3	1.67	0.77
1:A:374:LEU:HB2	1:A:436:ILE:HD11	1.68	0.75
1:A:535:THR:HG21	1:A:617:VAL:HG23	1.69	0.75
3:C:175:ALA:HB2	10:J:10:CYS:HB2	1.67	0.75
2:B:1181:GLU:HB3	2:B:1188:LYS:HG3	1.68	0.74
1:A:464:PRO:HD2	11:K:67:PHE:HD2	1.53	0.74
1:A:254:GLU:HB3	2:B:935:ARG:HH21	1.53	0.73
1:A:394:ASN:HB3	1:A:398:GLU:HB3	1.71	0.72
1:A:855:THR:HG21	1:A:857:ARG:HE	1.54	0.72
15:U:10:DA:H2"	15:U:11:DG:O5'	1.90	0.72
2:B:145:ARG:HA	2:B:146:GLU:CB	2.21	0.71
1:A:868:TYR:HD2	1:A:1058:VAL:HG21	1.56	0.70
1:A:567:LYS:HB3	1:A:568:PRO:HD3	1.74	0.70
10:J:36:LEU:CD2	10:J:50:ILE:HD11	2.18	0.70
1:A:1107:VAL:HA	1:A:1108:ALA:CB	2.22	0.70
1:A:528:LEU:HD12	1:A:751:SER:H	1.58	0.69
2:B:20:ASP:HB3	2:B:23:ALA:HB2	1.76	0.68
1:A:362:ASP:HB3	1:A:508:PRO:HD3	1.77	0.67
1:A:1083:THR:HG21	1:A:1095:THR:HA	1.78	0.66
4:D:51:ASN:OD1	4:D:54:GLU:HB2	1.96	0.66
1:A:464:PRO:HD2	11:K:67:PHE:CD2	2.31	0.66
1:A:1063:MET:HG3	2:B:1139:ILE:HG22	1.78	0.66
1:A:225:ASN:HB3	1:A:229:SER:H	1.62	0.65
1:A:508:PRO:HB3	1:A:643:ALA:HB2	1.77	0.65
1:A:1335:ILE:HG23	1:A:1339:LEU:HD12	1.79	0.65
2:B:559:SER:HA	2:B:563:MET:HB2	1.78	0.63
8:H:95:TYR:HE1	8:H:97:MET:HG3	1.63	0.63
1:A:768:GLN:HG2	1:A:816:HIS:HA	1.79	0.63
2:B:364:ILE:HG22	2:B:585:VAL:HG13	1.81	0.63
15:U:26:DG:H2"	15:U:27:DA:O5'	1.98	0.63
1:A:356:ASP:HB2	1:A:469:ARG:HD2	1.81	0.63
1:A:444:PHE:HE2	1:A:487:MET:SD	2.22	0.62
1:A:567:LYS:CB	1:A:568:PRO:HD3	2.29	0.62
1:A:49:LYS:HD2	1:A:61:ILE:HG12	1.81	0.62
12:L:57:LEU:HD23	12:L:59:ALA:H	1.63	0.62
1:A:1428:VAL:HG13	2:B:1151:LEU:HD13	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:898:LEU:HD21	2:B:964:VAL:HG11	1.81	0.61
5:E:80:VAL:HG12	5:E:109:ILE:HB	1.82	0.61
4:D:194:LEU:HD22	7:G:86:VAL:HG11	1.81	0.61
2:B:468:GLU:HB3	2:B:470:LYS:HG2	1.82	0.61
2:B:1006:ILE:HD11	10:J:43:ARG:HB3	1.81	0.61
3:C:55:THR:HB	3:C:152:GLU:H	1.65	0.60
2:B:364:ILE:HG13	2:B:365:THR:H	1.66	0.60
1:A:56:PRO:HD2	1:A:58:LEU:HG	1.83	0.60
1:A:1340:GLY:HA2	5:E:183:PRO:HD2	1.84	0.60
1:A:1116:LEU:HG	1:A:1308:THR:CG2	2.32	0.60
1:A:496:GLU:HB2	6:F:99:LEU:HD12	1.84	0.60
2:B:136:THR:HA	2:B:137:TYR:CB	2.32	0.60
2:B:485:ARG:HH21	2:B:782:LEU:HD11	1.67	0.60
2:B:292:ILE:HD11	2:B:327:ARG:HB2	1.83	0.60
14:S:29:DT:H3	15:U:10:DA:H61	1.50	0.59
2:B:825:VAL:HG23	2:B:1010:LEU:HD12	1.85	0.59
2:B:95:ILE:HD11	2:B:128:LEU:HB3	1.83	0.59
1:A:370:ILE:HD13	2:B:1105:ALA:HB2	1.84	0.59
2:B:290:GLY:HA2	2:B:327:ARG:HG3	1.83	0.59
7:G:34:VAL:HG13	7:G:45:ILE:HG21	1.84	0.59
1:A:1006:ILE:HD11	5:E:163:GLU:HG3	1.85	0.59
2:B:956:THR:HG22	2:B:960:GLY:HA2	1.85	0.58
1:A:1107:VAL:CA	1:A:1108:ALA:HB2	2.31	0.58
2:B:363:HIS:HD2	2:B:364:ILE:HG23	1.67	0.58
2:B:367:LEU:HB2	2:B:370:PHE:HE2	1.68	0.58
1:A:890:ASP:H	1:A:1296:GLY:HA3	1.68	0.58
3:C:6:PRO:HG2	11:K:101:LEU:HB2	1.85	0.58
1:A:960:ILE:HA	1:A:963:ILE:HG22	1.85	0.58
2:B:193:LYS:HE3	10:J:64:ASN:HB2	1.85	0.58
1:A:1453:TYR:HB3	6:F:129:LYS:HE2	1.85	0.58
1:A:1444:MET:HG3	7:G:60:ARG:HA	1.86	0.58
1:A:847:ASP:HB2	1:A:859:SER:H	1.69	0.58
1:A:182:VAL:HG12	1:A:201:VAL:HA	1.86	0.58
1:A:1100:ARG:HG3	1:A:1104:ILE:HD11	1.86	0.58
1:A:246:VAL:HA	2:B:1202:LEU:HD21	1.84	0.57
1:A:810:PRO:HB3	2:B:745:PRO:HB3	1.86	0.57
2:B:101:MET:HG2	2:B:111:ALA:HA	1.85	0.57
1:A:834:THR:HG21	1:A:1077:THR:HA	1.86	0.57
2:B:842:ASN:O	2:B:846:ILE:HG12	2.04	0.57
2:B:918:ILE:HB	2:B:935:ARG:HH12	1.69	0.57
1:A:374:LEU:HA	2:B:1107:ALA:HB2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:946:VAL:HG22	5:E:201:LYS:HD2	1.87	0.57
11:K:58:PHE:HB3	11:K:76:GLN:HB3	1.87	0.56
8:H:95:TYR:CE1	8:H:97:MET:HG3	2.40	0.56
1:A:1424:VAL:HG22	1:A:1436:ILE:HD11	1.86	0.56
2:B:930:ALA:HA	2:B:931:TYR:C	2.26	0.56
1:A:1434:ALA:HB1	1:A:1436:ILE:HD13	1.87	0.56
1:A:519:PRO:HD3	1:A:631:HIS:CD2	2.41	0.56
1:A:835:GLY:HA3	15:U:18:DA:H4'	1.88	0.56
1:A:1205:LYS:HB3	1:A:1274:ARG:HH21	1.70	0.56
1:A:560:ILE:HD12	8:H:78:SER:HB2	1.88	0.56
1:A:121:LEU:HD22	1:A:141:LEU:HD11	1.87	0.56
1:A:326:ARG:HG3	1:A:1406:VAL:HG21	1.88	0.56
1:A:567:LYS:CG	1:A:568:PRO:HD3	2.36	0.55
1:A:1215:ARG:HE	1:A:1273:LEU:HA	1.71	0.55
3:C:186:LEU:HD23	3:C:223:ALA:HB1	1.89	0.55
1:A:850:VAL:HG23	1:A:1064:VAL:HG21	1.88	0.55
8:H:6:PHE:HB3	8:H:59:ILE:HD12	1.89	0.55
2:B:1133:MET:HG3	15:U:19:DT:H4'	1.88	0.55
1:A:899:VAL:HB	1:A:1029:ARG:HG3	1.88	0.55
2:B:955:THR:HG22	2:B:956:THR:H	1.72	0.55
2:B:364:ILE:HG13	2:B:365:THR:N	2.21	0.55
1:A:828:ALA:HB2	2:B:530:GLY:HA2	1.87	0.55
3:C:50:GLU:HB2	3:C:156:THR:HB	1.89	0.55
1:A:568:PRO:HD2	1:A:569:LYS:H	1.72	0.54
1:A:683:ILE:HG21	1:A:801:GLU:HG3	1.88	0.54
1:A:662:PHE:HB3	2:B:829:CYS:SG	2.47	0.54
3:C:77:ILE:HG13	3:C:161:LYS:HE3	1.89	0.54
2:B:281:PRO:HD2	2:B:284:ILE:HD12	1.87	0.54
3:C:44:LEU:HB2	3:C:77:ILE:HD13	1.89	0.54
2:B:1001:PHE:HE2	3:C:178:PHE:HB3	1.73	0.54
2:B:225:VAL:H	2:B:396:ASP:HB2	1.73	0.54
11:K:7:PHE:HB2	11:K:11:LEU:HD12	1.88	0.54
2:B:1106:ARG:HE	2:B:1110:PRO:HD2	1.73	0.54
2:B:796:LEU:HB3	2:B:799:PRO:HG3	1.89	0.54
2:B:294:ASP:HB2	9:I:12:ASN:HA	1.90	0.54
2:B:860:MET:HB3	2:B:965:LYS:HG2	1.89	0.54
8:H:58:THR:HB	8:H:143:LEU:HB2	1.90	0.54
12:L:38:LEU:HD21	12:L:48:CYS:HA	1.89	0.53
1:A:311:GLN:HB2	1:A:312:PRO:HD3	1.91	0.53
1:A:444:PHE:CE2	1:A:487:MET:SD	3.01	0.53
1:A:899:VAL:HG11	1:A:929:LEU:HD22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:36:LEU:HD21	10:J:50:ILE:CD1	2.25	0.53
2:B:654:ARG:H	2:B:657:HIS:HD2	1.57	0.53
3:C:252:GLN:HB2	11:K:95:ILE:HG23	1.91	0.53
1:A:30:ILE:HG12	2:B:1170:THR:HG21	1.89	0.53
7:G:165:GLU:HB2	7:G:168:LEU:HD12	1.91	0.52
1:A:679:ILE:HG23	1:A:729:ALA:HB1	1.91	0.52
3:C:133:ILE:HG21	3:C:236:GLY:HA3	1.92	0.52
2:B:429:PHE:HA	2:B:432:MET:HB2	1.90	0.52
1:A:541:ILE:HD13	1:A:577:ILE:HD11	1.91	0.52
1:A:1110:ASN:HB2	14:S:26:DT:OP1	2.08	0.52
2:B:996:ARG:HH21	3:C:173:ALA:HB1	1.75	0.52
1:A:1114:PRO:HB2	1:A:1311:VAL:HB	1.92	0.52
7:G:83:LYS:HE2	7:G:150:CYS:H	1.74	0.52
1:A:37:PHE:HB2	1:A:52:GLY:HA3	1.91	0.52
2:B:144:GLY:HA2	2:B:146:GLU:HB2	1.92	0.52
1:A:1332:PHE:HA	1:A:1335:ILE:HD12	1.92	0.52
1:A:567:LYS:HE2	1:A:568:PRO:HD3	1.92	0.52
1:A:567:LYS:HG2	1:A:568:PRO:HD3	1.91	0.52
2:B:420:LEU:HD21	2:B:456:GLY:HA3	1.91	0.52
1:A:1313:LEU:HD23	1:A:1338:VAL:HG11	1.90	0.52
2:B:834:ASN:HB3	2:B:840:ILE:HG13	1.92	0.52
1:A:1006:ILE:HD12	5:E:167:ARG:HB2	1.92	0.51
2:B:1159:ARG:HD3	2:B:1193:GLN:HB2	1.93	0.51
2:B:416:LEU:HD23	2:B:457:LEU:HD23	1.92	0.51
9:I:101:PHE:HE1	9:I:112:SER:HB3	1.76	0.51
1:A:567:LYS:HB3	1:A:568:PRO:CD	2.39	0.51
1:A:365:GLY:HA3	1:A:469:ARG:HB3	1.93	0.51
15:U:2:DT:H2''	15:U:3:DA:N7	2.26	0.51
1:A:709:THR:HG22	1:A:711:ARG:H	1.75	0.51
1:A:832:ALA:HA	15:U:18:DA:H5'	1.91	0.51
1:A:382:PRO:HD3	1:A:428:TYR:HE2	1.75	0.51
5:E:78:LEU:HB3	5:E:107:THR:HB	1.93	0.51
5:E:86:PRO:HA	5:E:113:GLN:HB2	1.93	0.50
2:B:283:VAL:HG23	2:B:297:ILE:HG21	1.93	0.50
8:H:118:PHE:HB2	8:H:121:LEU:HB2	1.92	0.50
2:B:210:LYS:HE2	2:B:482:VAL:HG22	1.94	0.50
5:E:178:ILE:HB	5:E:212:ARG:HD3	1.93	0.50
1:A:368:LYS:HB2	11:K:2:ASN:HD21	1.76	0.50
1:A:1280:GLU:HB3	1:A:1309:ASP:HB3	1.93	0.50
1:A:106:VAL:HG11	1:A:214:ILE:HG12	1.94	0.50
2:B:245:GLU:N	2:B:246:LYS:HA	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:71:LYS:HD3	4:D:74:GLN:HG3	1.94	0.50
1:A:332:LYS:H	1:A:337:ARG:HD3	1.76	0.50
3:C:245:VAL:HA	3:C:248:ILE:HD12	1.93	0.50
5:E:12:LEU:HD11	5:E:55:ARG:HH21	1.76	0.50
2:B:1136:ASP:HA	2:B:1139:ILE:HD12	1.93	0.50
2:B:129:PHE:HB3	2:B:164:LYS:HB3	1.93	0.50
3:C:259:LEU:HD12	11:K:91:CYS:HB3	1.93	0.50
6:F:128:LYS:HD3	6:F:149:GLU:HA	1.94	0.50
2:B:581:PHE:HB2	2:B:625:LYS:HG2	1.93	0.50
4:D:23:ASN:HB3	7:G:82:PHE:HD1	1.76	0.50
2:B:526:GLU:HG3	2:B:771:SER:HB2	1.93	0.50
6:F:109:VAL:HG22	6:F:124:GLU:HG2	1.93	0.50
6:F:130:ILE:HG22	6:F:132:LEU:HB2	1.94	0.50
2:B:499:ASN:HA	2:B:536:VAL:HG22	1.93	0.49
2:B:408:LEU:HD13	2:B:545:ILE:HG21	1.93	0.49
1:A:381:THR:O	1:A:385:ILE:HG13	2.10	0.49
2:B:195:CYS:O	2:B:198:ASP:HB2	2.12	0.49
3:C:46:ILE:HA	3:C:159:ALA:HA	1.94	0.49
4:D:155:ARG:H	4:D:219:THR:HG21	1.77	0.49
1:A:596:THR:C	1:A:598:LEU:H	2.13	0.49
2:B:951:GLN:HG2	12:L:57:LEU:HD11	1.95	0.49
1:A:1267:MET:HA	1:A:1271:ILE:HD12	1.92	0.49
3:C:241:ASP:HB3	11:K:109:TRP:CE2	2.47	0.49
3:C:50:GLU:HB3	12:L:64:LEU:HD21	1.93	0.49
2:B:653:VAL:HG22	2:B:689:LEU:HB3	1.94	0.49
2:B:848:ARG:HA	3:C:69:LEU:HD21	1.94	0.49
2:B:565:PRO:HG2	2:B:568:ASP:HB2	1.94	0.49
11:K:75:ILE:HD13	11:K:83:PRO:HB2	1.94	0.49
2:B:883:LEU:H	2:B:935:ARG:H	1.61	0.49
1:A:512:VAL:HA	1:A:519:PRO:HA	1.95	0.49
2:B:824:ILE:HD13	2:B:1089:PRO:HB3	1.95	0.49
2:B:1007:VAL:HG22	2:B:1008:PRO:HD2	1.94	0.49
2:B:806:THR:HG23	2:B:1045:SER:HA	1.95	0.49
2:B:212:LEU:HD13	2:B:409:ALA:HA	1.95	0.49
2:B:485:ARG:HE	2:B:782:LEU:HD11	1.77	0.49
1:A:984:LYS:O	1:A:988:LEU:HB2	2.13	0.49
2:B:841:MET:SD	2:B:846:ILE:HD11	2.53	0.48
2:B:496:ARG:HB2	2:B:539:LEU:HB2	1.94	0.48
1:A:1336:MET:HG3	1:A:1381:LEU:HD13	1.95	0.48
7:G:6:ASP:HA	7:G:75:ARG:HA	1.95	0.48
5:E:23:VAL:HG12	5:E:28:TYR:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:1:MET:H1	10:J:57:ILE:H	1.60	0.48
1:A:329:LEU:HA	1:A:335:ARG:HB3	1.93	0.48
1:A:105:CYS:SG	1:A:139:TRP:HA	2.54	0.48
1:A:822:GLU:HB2	2:B:513:GLN:HE22	1.78	0.48
1:A:614:PHE:HB3	8:H:122:LEU:HD21	1.96	0.48
7:G:9:LEU:HD22	7:G:34:VAL:HG23	1.96	0.48
3:C:258:ILE:HG13	11:K:19:LEU:HD11	1.95	0.48
10:J:5:VAL:HA	10:J:14:VAL:O	2.13	0.48
7:G:46:LEU:HB2	7:G:77:VAL:HG23	1.94	0.48
7:G:39:THR:HG23	7:G:42:PHE:H	1.79	0.48
3:C:18:VAL:HG12	3:C:20:PHE:HD1	1.77	0.48
1:A:446:ARG:HB2	1:A:487:MET:SD	2.54	0.47
1:A:1342:GLU:HG3	5:E:198:ILE:HG21	1.95	0.47
2:B:1004:GLU:HG3	2:B:1006:ILE:HG13	1.96	0.47
1:A:963:ILE:HD11	1:A:1048:ASN:HB3	1.95	0.47
2:B:60:GLN:HE22	2:B:94:LYS:HA	1.78	0.47
1:A:1438:THR:HG23	6:F:92:ARG:HB2	1.97	0.47
1:A:1100:ARG:HH21	1:A:1351:GLU:HG2	1.80	0.47
15:U:18:DA:H2'	15:U:19:DT:C6	2.49	0.47
2:B:291:ILE:HG22	2:B:297:ILE:HG13	1.96	0.47
1:A:583:PRO:HD3	1:A:645:LEU:HD13	1.96	0.47
6:F:146:TRP:HB3	6:F:151:LEU:HD11	1.96	0.47
5:E:147:HIS:HB3	5:E:150:VAL:HG23	1.97	0.47
1:A:845:LEU:HD12	1:A:1069:ALA:HB2	1.96	0.47
1:A:855:THR:CG2	1:A:857:ARG:HE	2.25	0.47
1:A:1095:THR:HG21	1:A:1112:LYS:HB3	1.96	0.47
1:A:836:TYR:HB2	15:U:17:DG:H4'	1.97	0.47
1:A:1420:ASP:HB2	1:A:1422:ARG:HG2	1.97	0.47
3:C:43:THR:HG22	3:C:44:LEU:H	1.80	0.47
1:A:1290:LYS:HG2	1:A:1298:TYR:HB3	1.96	0.47
1:A:1224:LEU:HD21	1:A:1240:CYS:HB3	1.96	0.47
1:A:345:VAL:HG12	2:B:1155:SER:HB2	1.97	0.47
7:G:44:TYR:HB2	7:G:79:PHE:HB3	1.97	0.47
1:A:353:ILE:HG22	1:A:468:PHE:HB2	1.97	0.47
1:A:899:VAL:HG13	1:A:929:LEU:HB3	1.96	0.47
1:A:1386:ARG:HD3	1:A:1403:GLU:HG2	1.96	0.47
1:A:720:ARG:O	1:A:724:GLU:HB2	2.14	0.46
1:A:827:THR:O	1:A:831:THR:HB	2.16	0.46
1:A:483:ASP:HA	2:B:988:GLY:HA2	1.97	0.46
1:A:360:GLU:HB3	1:A:363:GLN:HB2	1.96	0.46
2:B:681:TRP:HA	2:B:684:LEU:HD12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:542:MET:HB3	2:B:636:PRO:HD2	1.97	0.46
3:C:11:ARG:HB2	3:C:19:ASP:HB3	1.97	0.46
2:B:622:LYS:HE2	9:I:59:VAL:HG22	1.95	0.46
2:B:955:THR:HG22	2:B:956:THR:N	2.30	0.46
2:B:287:ARG:HG2	2:B:292:ILE:HA	1.97	0.46
1:A:847:ASP:HB2	1:A:859:SER:N	2.29	0.46
1:A:567:LYS:HG3	8:H:94:ASP:O	2.16	0.46
11:K:33:ILE:HD11	11:K:75:ILE:HD11	1.97	0.46
2:B:136:THR:CA	2:B:137:TYR:HB2	2.39	0.46
2:B:1179:GLN:HA	2:B:1188:LYS:HE3	1.97	0.46
1:A:902:LEU:HD23	1:A:921:GLY:HA2	1.97	0.46
1:A:1383:SER:HB2	1:A:1388:GLY:HA3	1.97	0.46
1:A:672:ASP:HB2	1:A:736:ASN:ND2	2.31	0.46
1:A:88:LYS:HD3	1:A:293:GLU:HG3	1.97	0.46
3:C:69:LEU:O	10:J:6:ARG:HD2	2.16	0.46
1:A:114:LEU:HD21	1:A:145:LYS:O	2.15	0.45
1:A:90:VAL:HA	1:A:204:THR:HG21	1.96	0.45
2:B:1174:LYS:HD2	2:B:1179:GLN:HB2	1.98	0.45
2:B:238:ALA:HB3	2:B:256:VAL:HB	1.97	0.45
7:G:100:GLU:HB3	7:G:107:LYS:HG2	1.98	0.45
11:K:18:LYS:HE2	11:K:38:GLU:HG2	1.99	0.45
1:A:714:PHE:CD2	9:I:97:MET:HE3	2.51	0.45
2:B:640:VAL:HA	2:B:651:LEU:HA	1.97	0.45
2:B:125:SER:HA	2:B:171:PRO:HA	1.99	0.45
2:B:848:ARG:HD3	10:J:7:CYS:O	2.17	0.45
1:A:548:ASN:HD21	11:K:47:ARG:HE	1.65	0.45
2:B:64:CYS:HA	2:B:67:SER:HB2	1.98	0.45
4:D:56:ARG:HD2	4:D:149:THR:HA	1.97	0.45
2:B:246:LYS:HE3	2:B:249:ARG:HA	1.99	0.45
3:C:67:LEU:HA	3:C:70:ILE:HG12	1.99	0.45
2:B:319:GLU:HA	2:B:322:PHE:HB2	1.98	0.45
2:B:745:PRO:HB2	2:B:1047:PHE:CD2	2.52	0.45
3:C:45:ALA:HA	3:C:72:LEU:HD12	1.98	0.45
1:A:579:SER:HB3	1:A:611:GLN:HA	1.98	0.45
1:A:530:GLY:HA2	1:A:657:LEU:HD13	1.99	0.45
2:B:888:GLY:O	2:B:909:ASP:HA	2.16	0.45
2:B:276:ILE:HG22	2:B:278:GLN:H	1.82	0.45
2:B:85:SER:HB3	2:B:139:ALA:HB3	1.97	0.45
15:U:8:DT:H2"	15:U:9:DA:H8	1.82	0.45
8:H:100:THR:HG23	8:H:138:GLU:HB3	1.99	0.45
9:I:8:ARG:HG2	9:I:34:TYR:CE1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:466:SER:HB2	2:B:1103:ILE:HD13	1.98	0.45
2:B:827:ILE:HD13	2:B:1086:PHE:HD2	1.82	0.44
2:B:1204:PHE:HA	2:B:1207:LEU:HD12	1.99	0.44
1:A:134:ARG:O	1:A:138:ILE:HG12	2.17	0.44
1:A:567:LYS:HG3	8:H:95:TYR:HA	1.99	0.44
2:B:640:VAL:HG22	2:B:651:LEU:HB3	1.99	0.44
1:A:317:LYS:HA	1:A:318:SER:C	2.37	0.44
7:G:84:GLY:HA2	7:G:146:LYS:HE2	1.98	0.44
2:B:886:LYS:O	2:B:890:TYR:HE1	2.00	0.44
1:A:1022:LEU:HG	1:A:1026:LEU:HD12	2.00	0.44
1:A:467:THR:HG23	1:A:469:ARG:HH12	1.82	0.44
2:B:846:ILE:HD12	2:B:974:PRO:HG2	1.99	0.44
1:A:536:LEU:HD13	1:A:538:ASP:HB3	2.00	0.44
1:A:93:VAL:HG11	1:A:305:ASP:HB3	1.99	0.44
1:A:335:ARG:HH22	2:B:1114:LEU:HD21	1.83	0.44
2:B:44:VAL:HG11	2:B:200:GLY:HA2	2.00	0.44
1:A:998:LEU:HD23	1:A:1001:ARG:HD3	1.99	0.44
1:A:669:THR:HG23	1:A:805:LEU:HD13	1.99	0.44
3:C:196:ASP:HB3	3:C:199:LYS:HB2	1.99	0.44
1:A:817:ALA:HB1	2:B:524:PRO:HB2	1.99	0.44
1:A:1197:LEU:HD11	1:A:1238:ILE:HD11	1.99	0.44
1:A:1116:LEU:HG	1:A:1308:THR:HG22	1.99	0.44
2:B:193:LYS:HB3	2:B:787:VAL:HG11	2.00	0.44
5:E:178:ILE:HB	5:E:212:ARG:HB3	2.00	0.44
2:B:1082:MET:HA	3:C:189:THR:HA	1.99	0.44
1:A:202:LEU:HB3	1:A:207:ILE:HD11	1.99	0.44
2:B:758:PHE:HZ	2:B:1031:LEU:HD13	1.83	0.44
3:C:164:ALA:HA	3:C:167:HIS:O	2.18	0.44
3:C:38:ILE:HA	3:C:173:ALA:HB2	2.00	0.44
1:A:43:GLU:H	1:A:46:THR:H	1.66	0.44
2:B:92:PHE:HD1	2:B:132:VAL:HG22	1.83	0.43
2:B:867:GLY:HA3	2:B:868:MET:HB3	2.00	0.43
2:B:238:ALA:HB2	2:B:385:LEU:HB2	2.00	0.43
5:E:124:VAL:HG13	5:E:132:ILE:HG23	2.00	0.43
12:L:28:LYS:HB2	12:L:39:SER:HA	2.00	0.43
1:A:406:ILE:HB	1:A:431:LYS:HB2	2.00	0.43
9:I:50:THR:HB	9:I:52:ILE:HG13	2.00	0.43
1:A:1377:THR:HB	5:E:176:PRO:HB3	2.00	0.43
1:A:1107:VAL:CA	1:A:1108:ALA:CB	2.95	0.43
11:K:42:LEU:HD23	11:K:46:ILE:HD11	2.01	0.43
2:B:593:PRO:HG2	2:B:617:ARG:HH21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:62:PHE:O	3:C:66:ARG:HG3	2.19	0.43
2:B:528:PRO:HD2	2:B:536:VAL:O	2.18	0.43
2:B:31:TRP:HA	2:B:34:ILE:HD12	2.00	0.43
2:B:301:ILE:HD13	2:B:379:GLY:HA2	2.00	0.43
1:A:349:ALA:HB2	1:A:374:LEU:HD11	2.01	0.43
2:B:121:ASN:HA	2:B:207:GLY:HA3	2.01	0.43
10:J:14:VAL:HA	10:J:17:LYS:HD3	2.00	0.42
1:A:90:VAL:HG21	1:A:300:VAL:HG11	2.00	0.42
9:I:52:ILE:H	9:I:52:ILE:HG13	1.66	0.42
1:A:606:LEU:HD23	1:A:613:ILE:HG21	2.02	0.42
2:B:600:LEU:HA	2:B:603:LEU:HD12	2.01	0.42
6:F:117:PRO:HA	6:F:120:ILE:HD12	2.01	0.42
2:B:392:ARG:HE	9:I:52:ILE:HD13	1.84	0.42
3:C:177:GLU:HB2	3:C:231:ASN:H	1.83	0.42
1:A:709:THR:HG21	9:I:93:LYS:O	2.19	0.42
1:A:588:LEU:HD22	1:A:607:ILE:HD12	2.00	0.42
2:B:883:LEU:HG	2:B:931:TYR:HB3	2.00	0.42
4:D:56:ARG:HD3	4:D:152:SER:HB2	2.02	0.42
15:U:8:DT:H2"	15:U:9:DA:C8	2.55	0.42
1:A:472:LEU:O	1:A:475:THR:HB	2.19	0.42
14:S:26:DT:H2"	14:S:27:DG:OP2	2.20	0.42
1:A:774:ARG:HH21	1:A:797:LYS:HB2	1.85	0.42
2:B:1129:ARG:HE	2:B:1131:GLY:HA2	1.83	0.42
1:A:513:SER:HB2	1:A:520:CYS:HB3	2.02	0.42
1:A:981:LEU:HD11	1:A:1042:PHE:HB2	2.01	0.42
8:H:2:SER:HB2	8:H:64:ASN:HB2	2.02	0.41
8:H:40:LEU:HG	8:H:42:ILE:HG13	2.02	0.41
2:B:862:GLN:HB3	2:B:963:PHE:HD1	1.84	0.41
5:E:12:LEU:HD21	5:E:55:ARG:HE	1.85	0.41
2:B:867:GLY:HA3	2:B:868:MET:CB	2.50	0.41
2:B:801:LYS:HE3	10:J:52:THR:HA	2.02	0.41
2:B:394:ASP:HB3	9:I:91:ARG:HD3	2.03	0.41
1:A:353:ILE:CG2	1:A:487:MET:HB2	2.50	0.41
1:A:709:THR:HG22	1:A:710:LEU:N	2.35	0.41
1:A:1078:GLN:H	1:A:1078:GLN:HG2	1.74	0.41
11:K:29:ASN:HD21	11:K:79:GLU:HA	1.85	0.41
1:A:1163:ILE:HA	1:A:1164:PRO:HD3	1.99	0.41
7:G:22:MET:HG2	7:G:26:LEU:HD12	2.03	0.41
10:J:20:SER:HB2	10:J:39:LEU:HD21	2.01	0.41
2:B:863:GLU:HB2	2:B:962:LYS:HB2	2.02	0.41
5:E:3:GLN:HG3	5:E:5:ASN:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:148:ARG:HH12	10:J:64:ASN:HA	1.85	0.41
2:B:526:GLU:HB3	2:B:538:ASN:HB2	2.03	0.41
3:C:69:LEU:HD23	10:J:6:ARG:HD3	2.03	0.41
10:J:39:LEU:HB3	10:J:41:LEU:HD23	2.02	0.41
2:B:438:GLU:HG2	2:B:439:ALA:HA	2.02	0.41
1:A:1111:MET:HG3	1:A:1112:LYS:H	1.85	0.41
1:A:335:ARG:HH12	2:B:1202:LEU:HD13	1.86	0.41
2:B:477:ALA:HB3	13:R:6:G:H5'	2.03	0.41
2:B:950:ASP:O	2:B:967:ARG:HB3	2.21	0.41
9:I:70:ARG:HG2	9:I:84:VAL:HG23	2.01	0.41
11:K:12:LEU:HA	11:K:37:LYS:HG3	2.03	0.41
1:A:901:LEU:HD22	1:A:919:ILE:HG23	2.02	0.41
5:E:145:THR:HG22	5:E:184:VAL:HG12	2.02	0.41
2:B:59:LEU:O	2:B:63:ILE:HG12	2.21	0.41
7:G:81:PRO:HG3	7:G:106:MET:SD	2.61	0.41
12:L:31:CYS:HA	12:L:56:LEU:HA	2.02	0.40
8:H:101:ALA:HA	8:H:116:TYR:HA	2.03	0.40
1:A:1139:GLU:HB3	1:A:1274:ARG:HH12	1.86	0.40
1:A:1325:THR:HA	5:E:147:HIS:HA	2.04	0.40
2:B:912:ILE:HB	2:B:939:THR:HB	2.03	0.40
2:B:334:ILE:HG13	2:B:335:GLY:H	1.84	0.40
1:A:525:GLN:HG3	2:B:836:GLU:HG2	2.04	0.40
8:H:130:ARG:H	8:H:130:ARG:HG3	1.75	0.40
1:A:875:ALA:HA	1:A:878:ILE:HD13	2.02	0.40
3:C:17:ASN:HA	3:C:233:GLU:HA	2.03	0.40
2:B:1181:GLU:HA	2:B:1187:ASN:O	2.20	0.40
12:L:47:ARG:HA	12:L:54:ARG:HG2	2.02	0.40
2:B:994:TYR:HB2	2:B:999:MET:HG3	2.03	0.40
7:G:7:LEU:HD23	7:G:7:LEU:H	1.87	0.40
5:E:15:ALA:O	5:E:19:VAL:HG23	2.20	0.40
2:B:763:GLN:HG2	2:B:765:PRO:HD2	2.02	0.40
2:B:69:LEU:HD12	2:B:429:PHE:HD1	1.86	0.40
1:A:146:MET:O	1:A:171:GLN:HB3	2.21	0.40
1:A:387:ARG:HH12	6:F:115:THR:HB	1.86	0.40
6:F:86:THR:HG23	6:F:89:GLU:H	1.87	0.40
5:E:38:PRO:HD2	5:E:41:ASP:HB2	2.03	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	1420/1733 (82%)	1220 (86%)	141 (10%)	59 (4%)	3	36
2	B	1139/1224 (93%)	973 (85%)	123 (11%)	43 (4%)	4	39
3	C	263/318 (83%)	230 (88%)	26 (10%)	7 (3%)	6	48
4	D	174/221 (79%)	154 (88%)	11 (6%)	9 (5%)	2	30
5	E	212/215 (99%)	194 (92%)	14 (7%)	4 (2%)	10	55
6	F	85/155 (55%)	76 (89%)	6 (7%)	3 (4%)	4	43
7	G	169/179 (94%)	143 (85%)	19 (11%)	7 (4%)	3	37
8	H	129/146 (88%)	105 (81%)	20 (16%)	4 (3%)	5	45
9	I	112/122 (92%)	96 (86%)	13 (12%)	3 (3%)	6	48
10	J	64/70 (91%)	57 (89%)	5 (8%)	2 (3%)	5	45
11	K	113/120 (94%)	109 (96%)	4 (4%)	0	100	100
12	L	41/70 (59%)	31 (76%)	6 (15%)	4 (10%)	1	13
All	All	3921/4573 (86%)	3388 (86%)	388 (10%)	145 (4%)	4	40

All (145) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	LYS
1	A	66	LYS
1	A	67	CYS
1	A	76	GLU
1	A	158	PRO
1	A	310	GLY
1	A	385	ILE
1	A	401	GLY
1	A	567	LYS
1	A	595	THR
1	A	629	LEU
1	A	751	SER

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Mol	Chain	Res	Type
1	A	775	ILE
1	A	1016	THR
1	A	1092	LYS
1	A	1108	ALA
2	B	58	THR
2	B	137	TYR
2	B	146	GLU
2	B	148	LYS
2	B	151	LEU
2	B	152	ILE
2	B	575	PRO
2	B	907	GLY
2	B	933	SER
2	B	1156	ASP
2	B	1157	ALA
3	C	142	VAL
3	C	161	LYS
4	D	15	LEU
7	G	141	SER
7	G	153	GLN
9	I	98	VAL
9	I	106	CYS
1	A	146	MET
1	A	152	VAL
1	A	156	ASP
1	A	188	ASP
1	A	194	ALA
1	A	250	ILE
1	A	257	ARG
1	A	283	GLY
1	A	286	HIS
1	A	319	GLY
1	A	423	ASP
1	A	875	ALA
1	A	1091	SER
1	A	1437	GLY
2	B	247	GLY
2	B	252	SER
2	B	282	ILE
2	B	337	ARG
2	B	367	LEU
2	B	712	PRO

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Mol	Chain	Res	Type
2	B	751	VAL
2	B	889	THR
2	B	1046	PRO
3	C	175	ALA
3	C	215	GLU
4	D	20	GLU
4	D	118	THR
4	D	198	LEU
6	F	71	GLU
6	F	72	LYS
7	G	50	ASP
10	J	2	ILE
12	L	45	ALA
1	A	130	ASP
1	A	256	GLN
1	A	402	ALA
1	A	418	SER
1	A	452	LYS
1	A	568	PRO
1	A	593	GLU
1	A	640	GLN
1	A	779	PHE
1	A	1112	LYS
1	A	1404	GLU
2	B	249	ARG
2	B	250	PHE
2	B	265	SER
2	B	441	ASP
2	B	502	ILE
2	B	711	GLU
2	B	935	ARG
2	B	1223	ASP
3	C	40	GLU
3	C	90	ASP
5	E	3	GLN
5	E	91	LYS
5	E	104	ASN
6	F	78	GLN
7	G	63	PRO
8	H	109	LYS
12	L	59	ALA
1	A	4	GLN

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Mol	Chain	Res	Type
1	A	54	ASN
1	A	57	ARG
1	A	63	ARG
1	A	335	ARG
1	A	453	MET
1	A	465	TYR
1	A	1003	LYS
1	A	1221	LYS
2	B	475	SER
2	B	531	GLN
2	B	577	ALA
2	B	648	HIS
2	B	951	GLN
2	B	1045	SER
4	D	8	PHE
4	D	16	LYS
4	D	169	SER
4	D	199	ASN
7	G	132	SER
7	G	154	VAL
8	H	17	PRO
8	H	108	SER
9	I	11	ASN
10	J	6	ARG
1	A	424	ILE
1	A	958	VAL
1	A	1206	ASP
1	A	1403	GLU
2	B	147	LEU
2	B	161	GLU
2	B	199	MET
2	B	961	LEU
2	B	1215	ARG
4	D	119	ARG
8	H	129	TYR
12	L	60	ARG
1	A	591	PHE
1	A	628	GLY
1	A	870	GLU
2	B	1017	ILE
2	B	1169	MET
3	C	243	VAL

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Mol	Chain	Res	Type
5	E	45	LYS
7	G	133	SER
1	A	61	ILE
1	A	1107	VAL
12	L	55	ILE
2	B	301	ILE
2	B	832	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	A	1245/1520 (82%)	1150 (92%)	95 (8%)	16	57
2	B	986/1061 (93%)	924 (94%)	62 (6%)	22	64
3	C	233/274 (85%)	218 (94%)	15 (6%)	22	64
4	D	156/200 (78%)	146 (94%)	10 (6%)	22	64
5	E	196/197 (100%)	190 (97%)	6 (3%)	47	81
6	F	77/137 (56%)	74 (96%)	3 (4%)	39	76
7	G	152/160 (95%)	151 (99%)	1 (1%)	88	95
8	H	118/128 (92%)	115 (98%)	3 (2%)	55	84
9	I	108/116 (93%)	102 (94%)	6 (6%)	26	68
10	J	61/65 (94%)	55 (90%)	6 (10%)	10	45
11	K	99/102 (97%)	94 (95%)	5 (5%)	29	70
12	L	38/57 (67%)	34 (90%)	4 (10%)	8	42
All	All	3469/4017 (86%)	3253 (94%)	216 (6%)	23	65

All (216) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	PHE
1	A	40	THR
1	A	41	MET

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Mol	Chain	Res	Type
1	A	43	GLU
1	A	53	LEU
1	A	61	ILE
1	A	116	ASP
1	A	120	GLU
1	A	121	LEU
1	A	126	LEU
1	A	152	VAL
1	A	164	ARG
1	A	173	THR
1	A	181	LEU
1	A	226	GLU
1	A	236	LEU
1	A	247	ARG
1	A	257	ARG
1	A	266	LEU
1	A	270	LEU
1	A	279	LEU
1	A	320	ARG
1	A	436	ILE
1	A	454	SER
1	A	455	MET
1	A	469	ARG
1	A	475	THR
1	A	481	ASP
1	A	485	ASP
1	A	498	ARG
1	A	509	LEU
1	A	511	ILE
1	A	521	MET
1	A	524	VAL
1	A	527	THR
1	A	528	LEU
1	A	534	LEU
1	A	536	LEU
1	A	546	VAL
1	A	588	LEU
1	A	595	THR
1	A	597	LEU
1	A	618	GLU
1	A	635	ARG
1	A	636	GLU

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Mol	Chain	Res	Type
1	A	644	LYS
1	A	666	ILE
1	A	672	ASP
1	A	701	LEU
1	A	702	LEU
1	A	732	LEU
1	A	738	LYS
1	A	746	MET
1	A	771	GLU
1	A	774	ARG
1	A	838	GLN
1	A	839	ARG
1	A	913	LEU
1	A	919	ILE
1	A	920	LEU
1	A	928	LEU
1	A	932	GLU
1	A	936	LEU
1	A	963	ILE
1	A	973	ILE
1	A	983	ILE
1	A	1006	ILE
1	A	1067	LEU
1	A	1078	GLN
1	A	1101	LEU
1	A	1143	LEU
1	A	1173	HIS
1	A	1215	ARG
1	A	1224	LEU
1	A	1242	VAL
1	A	1255	GLU
1	A	1276	VAL
1	A	1286	LYS
1	A	1289	ARG
1	A	1290	LYS
1	A	1316	VAL
1	A	1345	ARG
1	A	1354	ASN
1	A	1355	VAL
1	A	1366	ARG
1	A	1387	HIS
1	A	1393	ASN

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Mol	Chain	Res	Type
1	A	1394	THR
1	A	1400	CYS
1	A	1404	GLU
1	A	1406	VAL
1	A	1409	LEU
1	A	1420	ASP
1	A	1426	GLU
1	A	1450	LEU
2	B	25	ILE
2	B	69	LEU
2	B	106	ASP
2	B	137	TYR
2	B	172	ILE
2	B	175	ARG
2	B	225	VAL
2	B	240	ILE
2	B	242	SER
2	B	254	LEU
2	B	324	ILE
2	B	331	LEU
2	B	333	PHE
2	B	337	ARG
2	B	396	ASP
2	B	401	PHE
2	B	466	TRP
2	B	471	LYS
2	B	500	THR
2	B	526	GLU
2	B	529	GLU
2	B	552	MET
2	B	555	ILE
2	B	570	VAL
2	B	601	ARG
2	B	612	GLU
2	B	651	LEU
2	B	658	ILE
2	B	662	MET
2	B	730	ARG
2	B	748	ILE
2	B	795	ILE
2	B	797	TYR
2	B	801	LYS

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Mol	Chain	Res	Type
2	B	825	VAL
2	B	844	SER
2	B	868	MET
2	B	874	PHE
2	B	923	GLU
2	B	942	ARG
2	B	944	THR
2	B	959	ASP
2	B	990	ILE
2	B	993	THR
2	B	1010	LEU
2	B	1013	ASN
2	B	1031	LEU
2	B	1051	THR
2	B	1065	GLN
2	B	1084	GLN
2	B	1096	ARG
2	B	1122	ARG
2	B	1124	ARG
2	B	1145	SER
2	B	1147	LEU
2	B	1150	ARG
2	B	1159	ARG
2	B	1160	VAL
2	B	1182	CYS
2	B	1202	LEU
2	B	1215	ARG
2	B	1217	TYR
3	C	19	ASP
3	C	33	LEU
3	C	44	LEU
3	C	80	LEU
3	C	91	HIS
3	C	92	CYS
3	C	102	GLN
3	C	118	LEU
3	C	133	ILE
3	C	148	ARG
3	C	154	LYS
3	C	189	THR
3	C	195	GLN
3	C	240	VAL

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Mol	Chain	Res	Type
3	C	245	VAL
4	D	7	THR
4	D	15	LEU
4	D	34	GLN
4	D	48	ILE
4	D	70	PHE
4	D	76	LYS
4	D	131	GLU
4	D	160	VAL
4	D	187	THR
4	D	214	LEU
5	E	12	LEU
5	E	37	LEU
5	E	121	MET
5	E	123	LEU
5	E	152	LYS
5	E	175	LEU
6	F	70	LYS
6	F	90	ARG
6	F	111	LEU
7	G	134	GLU
8	H	26	ILE
8	H	95	TYR
8	H	130	ARG
9	I	7	CYS
9	I	17	ARG
9	I	21	GLU
9	I	26	LEU
9	I	59	VAL
9	I	93	LYS
10	J	2	ILE
10	J	24	LEU
10	J	30	LEU
10	J	39	LEU
10	J	42	LYS
10	J	64	ASN
11	K	2	ASN
11	K	57	LEU
11	K	75	ILE
11	K	91	CYS
11	K	114	LEU
12	L	33	GLU

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Mol	Chain	Res	Type
12	L	40	LEU
12	L	57	LEU
12	L	58	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	451	HIS
1	A	458	HIS
1	A	490	HIS
1	A	548	ASN
1	A	717	ASN
1	A	1082	ASN
2	B	363	HIS
2	B	986	GLN
2	B	1013	ASN
2	B	1178	ASN
5	E	61	GLN
5	E	101	GLN
11	K	29	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	R	8/9 (88%)	0	1 (12%)

There are no RNA backbone outliers to report.

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
13	R	2	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 [i](#)

Of 11 ligands modelled in this entry, 11 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](#)

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	1430/1733 (82%)	-0.19	16 (1%) 82 70	47, 113, 205, 298	0
2	B	1157/1224 (94%)	0.02	53 (4%) 36 24	47, 128, 231, 294	0
3	C	265/318 (83%)	-0.20	3 (1%) 82 70	57, 113, 177, 299	0
4	D	178/221 (80%)	-0.16	3 (1%) 73 58	60, 118, 193, 250	0
5	E	214/215 (99%)	0.02	6 (2%) 56 41	63, 159, 239, 274	0
6	F	87/155 (56%)	-0.40	0 100 100	46, 78, 133, 162	0
7	G	171/179 (95%)	-0.28	0 100 100	59, 98, 151, 229	0
8	H	135/146 (92%)	0.13	3 (2%) 65 50	99, 162, 231, 247	0
9	I	114/122 (93%)	0.17	7 (6%) 25 15	70, 160, 237, 280	0
10	J	66/70 (94%)	-0.22	0 100 100	53, 103, 177, 216	0
11	K	115/120 (95%)	-0.23	0 100 100	56, 105, 158, 176	0
12	L	43/70 (61%)	-0.16	0 100 100	75, 141, 215, 234	0
13	R	9/9 (100%)	1.22	2 (22%) 1 1	143, 199, 257, 275	0
14	S	14/45 (31%)	3.46	14 (100%) 0 0	261, 296, 300, 300	0
15	U	27/45 (60%)	1.93	15 (55%) 0 1	136, 253, 300, 300	0
All	All	4025/4672 (86%)	-0.08	122 (3%) 54 37	46, 121, 222, 300	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1090	ALA	6.4
5	E	51	GLY	6.0
2	B	71	LEU	5.4
15	U	6	DG	5.3
1	A	69	THR	5.3
14	S	34	DG	4.8
2	B	340	ALA	4.7

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Mol	Chain	Res	Type	RSRZ
14	S	27	DG	4.4
2	B	248	SER	4.3
2	B	143	PRO	4.3
15	U	4	DC	4.2
2	B	924	GLU	4.2
2	B	919	SER	4.1
14	S	26	DT	4.1
15	U	9	DA	4.1
15	U	11	DG	4.0
14	S	33	DC	3.9
1	A	161	LEU	3.9
14	S	24	DA	3.8
13	R	3	C	3.8
1	A	1185	PHE	3.8
15	U	5	DC	3.8
2	B	86	ARG	3.8
15	U	2	DT	3.8
14	S	35	DG	3.6
1	A	192	GLY	3.5
5	E	50	MET	3.5
2	B	72	GLU	3.5
2	B	926	GLY	3.5
15	U	3	DA	3.5
2	B	927	GLN	3.4
2	B	136	THR	3.4
14	S	37	DA	3.4
2	B	1179	GLN	3.4
2	B	339	THR	3.3
2	B	247	GLY	3.3
15	U	10	DA	3.3
14	S	25	DC	3.3
2	B	144	GLY	3.3
14	S	29	DT	3.3
14	S	36	DT	3.3
2	B	150	GLU	3.2
2	B	925	LEU	3.2
2	B	88	TYR	3.2
2	B	866	TYR	3.2
9	I	76	PRO	3.2
14	S	30	DT	3.2
4	D	10	THR	3.2
1	A	1089	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	193	ASP	3.0
5	E	93	MET	3.0
2	B	863	GLU	2.9
9	I	104	LEU	2.9
2	B	1177	HIS	2.9
9	I	105	SER	2.9
2	B	87	LYS	2.9
8	H	84	ALA	2.9
2	B	929	THR	2.8
14	S	31	DA	2.8
15	U	7	DA	2.7
15	U	28	DT	2.7
2	B	505	ASP	2.7
9	I	77	LYS	2.7
15	U	8	DT	2.7
1	A	1186	ASP	2.7
1	A	191	THR	2.6
2	B	139	ALA	2.6
2	B	471	LYS	2.6
2	B	145	ARG	2.6
2	B	142	VAL	2.6
1	A	319	GLY	2.6
1	A	195	ASP	2.6
1	A	188	ASP	2.6
2	B	89	GLU	2.5
2	B	467	GLY	2.5
2	B	714	GLU	2.5
2	B	918	ILE	2.5
1	A	1222	ASN	2.5
2	B	70	ILE	2.4
5	E	110	PHE	2.4
2	B	92	PHE	2.4
3	C	213	PRO	2.4
2	B	468	GLU	2.4
1	A	194	ALA	2.4
2	B	469	GLN	2.4
15	U	14	DG	2.4
8	H	75	ALA	2.4
14	S	32	DT	2.4
3	C	214	ASN	2.4
15	U	15	DA	2.4
2	B	507	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	447	ALA	2.4
13	R	4	G	2.3
2	B	508	LEU	2.3
2	B	164	LYS	2.3
1	A	1274	ARG	2.3
5	E	102	GLU	2.3
8	H	111	LEU	2.3
2	B	140	ILE	2.3
9	I	100	PHE	2.3
5	E	123	LEU	2.2
2	B	343	ILE	2.2
2	B	138	GLU	2.2
14	S	28	DC	2.2
2	B	338	GLY	2.2
2	B	444	MET	2.2
15	U	27	DA	2.1
3	C	212	PRO	2.1
1	A	1125	ALA	2.1
2	B	249	ARG	2.1
2	B	337	ARG	2.1
9	I	102	VAL	2.1
2	B	868	MET	2.1
2	B	431	TYR	2.1
15	U	13	DA	2.1
4	D	73	SER	2.1
2	B	84	ILE	2.1
2	B	923	GLU	2.1
2	B	69	LEU	2.0
2	B	146	GLU	2.0
9	I	73	ARG	2.0
4	D	6	SER	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
17	MG	A	1804	1/1	0.50	0.59	12.67	63,63,63,63	0
16	ZN	C	401	1/1	0.69	0.72	3.74	193,193,193,193	0
16	ZN	A	1802	1/1	0.99	0.14	-0.98	67,67,67,67	0
16	ZN	B	1301	1/1	0.99	0.14	-1.06	72,72,72,72	0
16	ZN	C	402	1/1	0.99	0.08	-1.23	74,74,74,74	0
16	ZN	I	202	1/1	0.98	0.06	-1.60	183,183,183,183	0
16	ZN	I	201	1/1	0.99	0.07	-1.60	113,113,113,113	0
16	ZN	A	1801	1/1	0.98	0.07	-1.64	90,90,90,90	0
16	ZN	L	101	1/1	0.99	0.06	-1.64	93,93,93,93	0
16	ZN	J	101	1/1	0.99	0.18	-2.26	93,93,93,93	0
17	MG	A	1803	1/1	0.91	0.12	-	82,82,82,82	0

6.5 Other polymers [i](#)

There are no such residues in this entry.