



# Full wwPDB X-ray Structure Validation Report i

Aug 20, 2020 – 08:49 PM BST

PDB ID : 6DVC  
Title : Crystal structure of Mycobacterium tuberculosis transcription initiation complex(ECF sigma factor L) containing 5nt RNA with 6nt spacer  
Authors : Lin, W.; Das, K.; Feng, Y.; Ebright, R.H.  
Deposited on : 2018-06-23  
Resolution : 3.30 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](mailto: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 i symbol.

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The following versions of software and data (see references ①) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

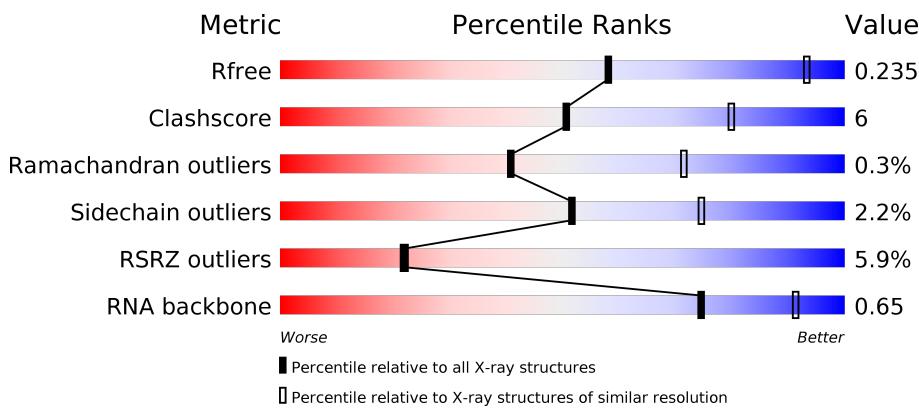
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## X-RAY DIFFRACTION

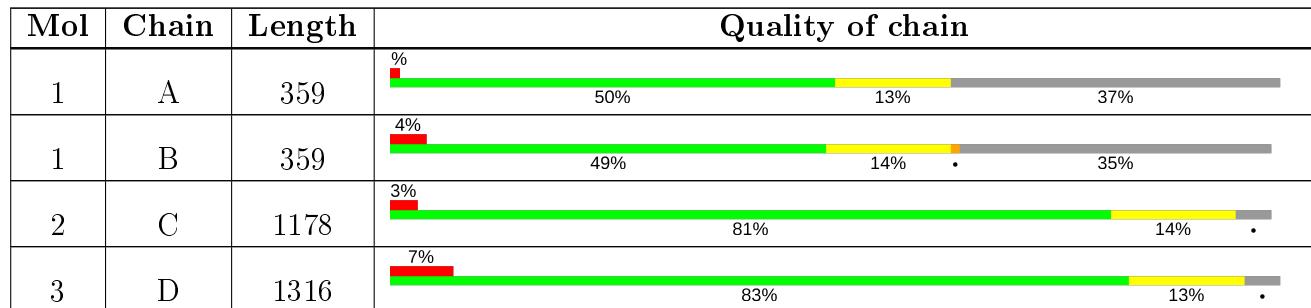
The reported resolution of this entry is 3.30 Å.

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.



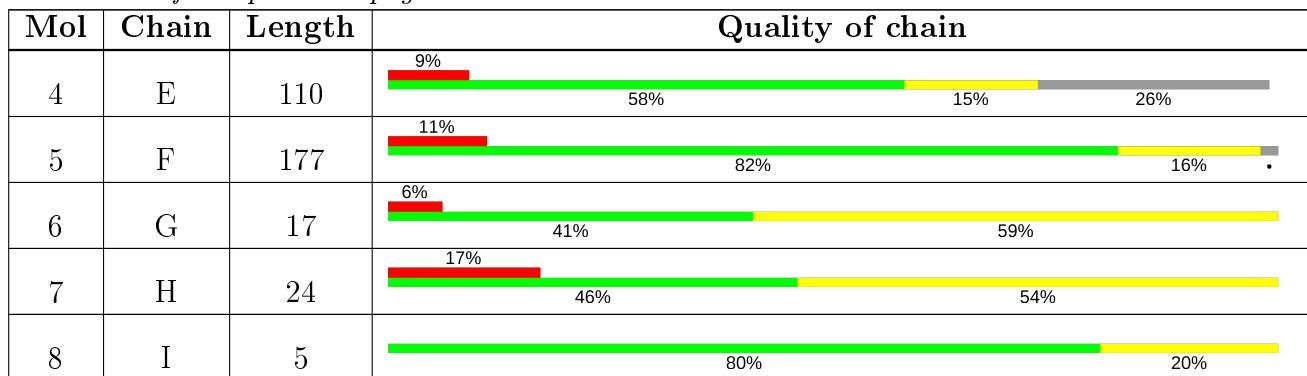
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)
RNA backbone	3102	1117 (3.70-2.90)

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 on 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.



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## 2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 24983 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 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C 1716	N 1080	O 296	S 338	2	0	0
1	B	232	Total	C 1732	N 1093	O 296	S 341	2	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP P9WGZ1
A	-10	GLY	-	expression tag	UNP P9WGZ1
A	-9	HIS	-	expression tag	UNP P9WGZ1
A	-8	HIS	-	expression tag	UNP P9WGZ1
A	-7	HIS	-	expression tag	UNP P9WGZ1
A	-6	HIS	-	expression tag	UNP P9WGZ1
A	-5	HIS	-	expression tag	UNP P9WGZ1
A	-4	HIS	-	expression tag	UNP P9WGZ1
A	-3	HIS	-	expression tag	UNP P9WGZ1
A	-2	HIS	-	expression tag	UNP P9WGZ1
A	-1	HIS	-	expression tag	UNP P9WGZ1
A	0	HIS	-	expression tag	UNP P9WGZ1
B	-11	MET	-	initiating methionine	UNP P9WGZ1
B	-10	GLY	-	expression tag	UNP P9WGZ1
B	-9	HIS	-	expression tag	UNP P9WGZ1
B	-8	HIS	-	expression tag	UNP P9WGZ1
B	-7	HIS	-	expression tag	UNP P9WGZ1
B	-6	HIS	-	expression tag	UNP P9WGZ1
B	-5	HIS	-	expression tag	UNP P9WGZ1
B	-4	HIS	-	expression tag	UNP P9WGZ1
B	-3	HIS	-	expression tag	UNP P9WGZ1
B	-2	HIS	-	expression tag	UNP P9WGZ1
B	-1	HIS	-	expression tag	UNP P9WGZ1
B	0	HIS	-	expression tag	UNP P9WGZ1

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	1126	8724	5459	1531	1695	39	0	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	1264	9884	6189	1790	1865	40	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O				
4	E	81	630	403	106	121		0	0	0

- Molecule 5 is a protein called ECF RNA polymerase sigma factor SigL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	F	174	1352	840	256	254	2	0	0	0

- Molecule 6 is a DNA chain called DNA (5'-D(\*GP\*CP\*AP\*TP\*CP\*CP\*GP\*TP\*GP\*AP\*GP\*TP\*CP\*GP\*AP\*GP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
6	G	17	350	166	68	100	16	0	0	0

- Molecule 7 is a DNA chain called DNA (5'-D(P\*CP\*GP\*TP\*GP\*TP\*CP\*AP\*GP\*TP\*AP\*GP\*TP\*GP\*TP\*CP\*AP\*CP\*GP\*GP\*AP\*TP\*GP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
7	H	24	491	234	90	144	23	0	0	0

- Molecule 8 is a RNA chain called RNA (5'-R(\*CP\*UP\*CP\*GP\*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
8	I	5	102	47	18	33	4	0	0	0

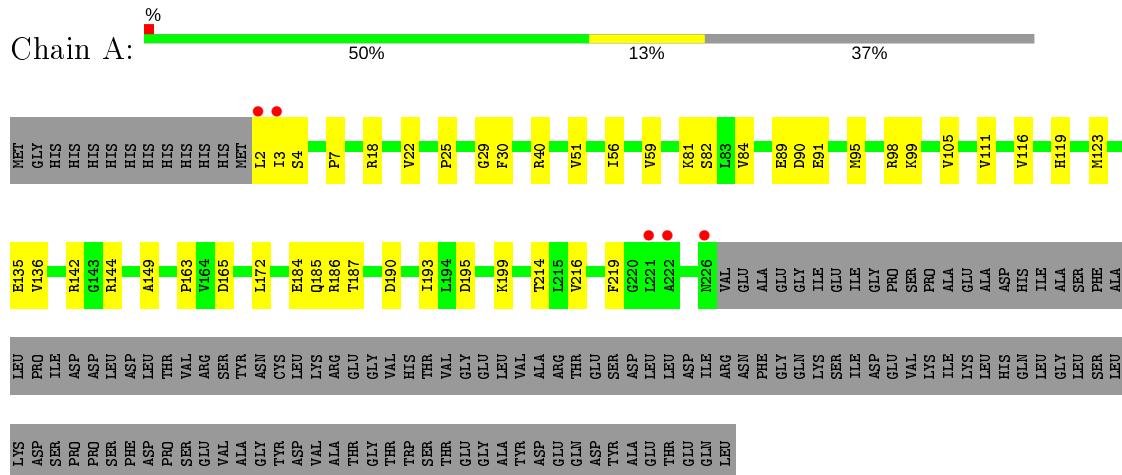
- Molecule 9 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	D	2	Total    Zn 2      2	0	0

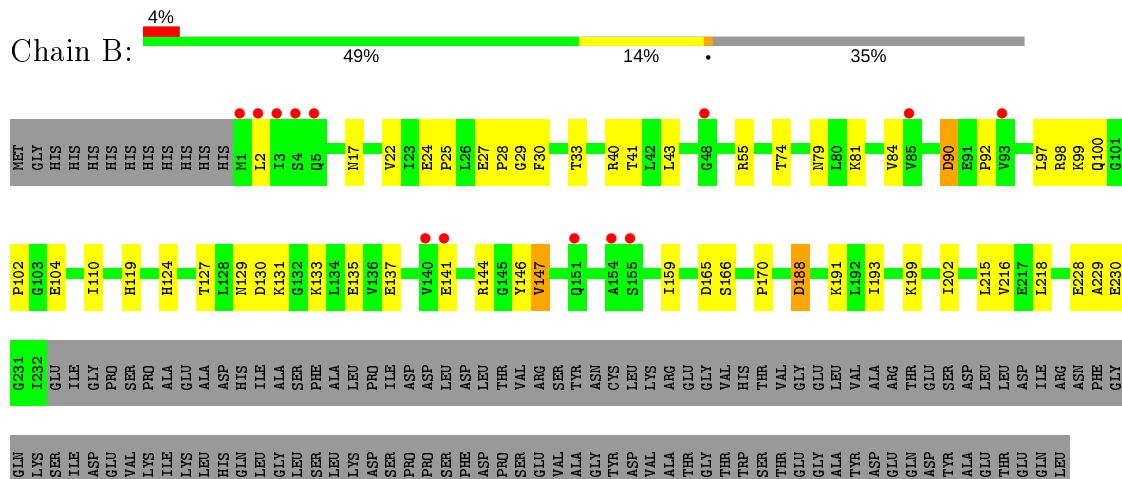
### 3 Residue-property plots ⓘ

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.

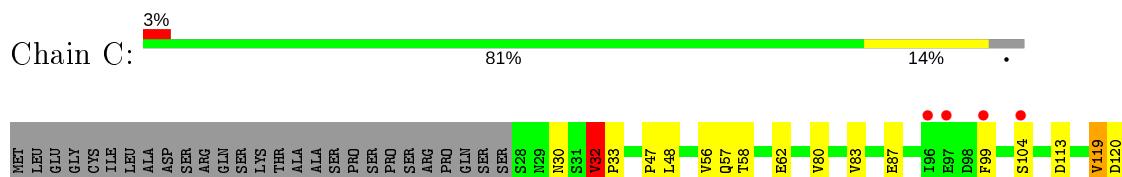
- Molecule 1: DNA-directed RNA polymerase subunit alpha



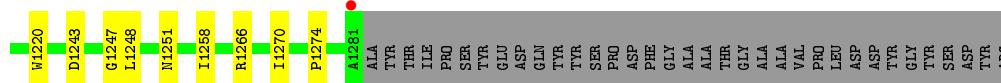
- Molecule 1: DNA-directed RNA polymerase subunit alpha



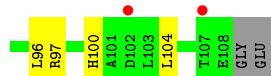
- Molecule 2: DNA-directed RNA polymerase subunit beta



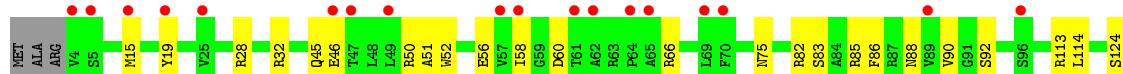
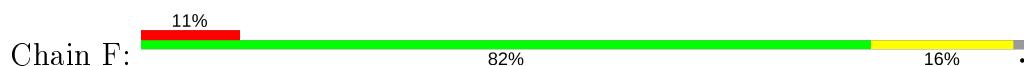




- Molecule 4: DNA-directed RNA polymerase subunit omega



- Molecule 5: ECF RNA polymerase sigma factor SigL



- Molecule 6: DNA (5'-D(\*GP\*CP\*AP\*TP\*CP\*CP\*GP\*TP\*GP\*AP\*GP\*TP\*CP\*GP\*AP\*GP\*G)-3')



- Molecule 7: DNA (5'-D(P\*CP\*GP\*TP\*GP\*TP\*CP\*AP\*GP\*TP\*AP\*GP\*TP\*GP\*TP\*CP\*A  
P\*CP\*GP\*GP\*AP\*TP\*GP\*C)-3')



- Molecule 8: RNA (5'-R(\*CP\*UP\*CP\*GP\*A)-3')



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	146.32Å    161.52Å    240.59Å 90.00°    90.00°    90.00°	Depositor
Resolution (Å)	92.92 – 3.30 92.92 – 3.30	Depositor EDS
% Data completeness (in resolution range)	98.9 (92.92-3.30) 99.4 (92.92-3.30)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) >$ <sup>1</sup>	1.86 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
$R$ , $R_{free}$	0.198 , 0.235 0.198 , 0.235	Depositor DCC
$R_{free}$ test set	4265 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	91.3	Xtriage
Anisotropy	0.439	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 67.0	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.48$ , $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	24983	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $< |L| >$ ,  $< L^2 >$  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: 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	A	0.23	0/1742	0.44	0/2370
1	B	0.24	0/1758	0.44	0/2397
2	C	0.24	0/8883	0.42	0/12043
3	D	0.23	0/10049	0.40	0/13583
4	E	0.23	0/643	0.39	0/877
5	F	0.22	0/1374	0.38	0/1869
6	G	0.51	0/393	0.88	0/606
7	H	0.56	0/550	0.97	0/848
8	I	0.14	0/113	0.70	0/174
All	All	0.25	0/25505	0.45	0/34767

There are no bond length outliers.

There are no bond angle outliers.

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	A	1716	0	1756	28	0
1	B	1732	0	1754	36	0
2	C	8724	0	8651	101	0
3	D	9884	0	9939	107	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	630	0	622	13	0
5	F	1352	0	1346	21	0
6	G	350	0	192	9	0
7	H	491	0	272	22	0
8	I	102	0	56	1	0
9	D	2	0	0	0	0
All	All	24983	0	24588	282	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 (282) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:ARG:HE	1:B:33:THR:HG22	1.32	0.93
2:C:467:ARG:HG3	7:H:16:DT:H5'	1.63	0.79
2:C:593:MET:HA	2:C:628:THR:HG21	1.68	0.74
1:A:4:SER:HB3	1:B:144:ARG:HH12	1.52	0.74
3:D:363:PRO:HG2	5:F:15:MET:HG3	1.70	0.74
5:F:124:SER:HG	5:F:127:HIS:HD1	1.31	0.73
3:D:832:ILE:HG22	3:D:834:ARG:H	1.54	0.73
2:C:1024:THR:H	3:D:730:THR:HG21	1.53	0.72
2:C:32:VAL:HG13	2:C:33:PRO:HD3	1.71	0.71
3:D:1090:LYS:HE2	3:D:1103:ASP:HA	1.71	0.71
5:F:50:ARG:NH1	7:H:4:DT:O4	2.25	0.70
2:C:558:ARG:HB3	2:C:570:TYR:HB3	1.74	0.70
3:D:1090:LYS:HB3	3:D:1092:GLU:HG2	1.74	0.69
3:D:454:PRO:HA	3:D:457:MET:HE2	1.74	0.69
2:C:467:ARG:NH1	7:H:14:DT:OP1	2.26	0.69
1:B:84:VAL:HG12	1:B:199:LYS:HD2	1.74	0.68
2:C:541:VAL:HG12	2:C:578:TYR:HB2	1.76	0.68
1:B:90:ASP:OD1	1:B:90:ASP:N	2.26	0.67
3:D:907:ASP:N	3:D:907:ASP:OD1	2.20	0.67
5:F:75:ASN:ND2	7:H:4:DT:O2	2.28	0.66
3:D:50:LYS:HE2	3:D:79:GLY:HA3	1.77	0.66
2:C:113:ASP:HB3	2:C:132:PRO:HG2	1.76	0.66
2:C:1087:GLU:HG3	2:C:1091:ILE:HD11	1.79	0.64
2:C:536:GLU:OE2	2:C:562:ARG:NH2	2.29	0.64
3:D:557:ILE:HG23	4:E:40:ILE:HD11	1.79	0.64
1:A:144:ARG:NH2	1:B:27:GLU:OE2	2.31	0.64
3:D:1055:LEU:H	3:D:1101:ASP:HB3	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:458:LEU:HD21	2:C:496:LEU:HD13	1.81	0.63
3:D:1248:LEU:HD22	3:D:1258:ILE:HB	1.81	0.61
3:D:291:ARG:NH2	7:H:24:DG:O6	2.33	0.61
3:D:1045:PRO:HG2	3:D:1111:LEU:HB2	1.83	0.61
1:A:186:ARG:HG3	1:A:187:THR:HG23	1.83	0.60
2:C:104:SER:HB3	2:C:140:ILE:HB	1.83	0.60
2:C:30:ASN:ND2	2:C:629:GLY:O	2.34	0.60
3:D:111:PRO:O	3:D:113:ARG:NH1	2.33	0.60
3:D:1173:THR:HG22	3:D:1193:VAL:HG21	1.82	0.60
3:D:500:ARG:HD2	3:D:534:ALA:HB2	1.84	0.59
2:C:181:ARG:NH1	7:H:15:DG:OP2	2.36	0.58
2:C:168:ILE:HG12	2:C:431:PHE:HB3	1.85	0.58
1:B:55:ARG:NH2	1:B:137:GLU:OE1	2.36	0.58
1:A:40:ARG:NE	1:B:33:THR:HG22	2.13	0.58
2:C:571:VAL:HG22	2:C:572:PRO:HD2	1.86	0.58
2:C:982:GLU:HG3	3:D:841:ARG:HH12	1.69	0.57
1:B:24:GLU:HB2	1:B:191:LYS:HG3	1.86	0.57
3:D:1051:GLY:HA2	3:D:1069:ASP:HB2	1.85	0.57
3:D:1085:ARG:HA	3:D:1112:MET:HA	1.87	0.57
3:D:356:ARG:NH2	5:F:46:GLU:OE2	2.37	0.57
3:D:826:ASN:HB3	3:D:832:ILE:HD11	1.87	0.56
6:G:11:DT:H2'	6:G:12:DG:C8	2.40	0.56
2:C:285:GLU:OE1	7:H:9:DG:N2	2.37	0.56
2:C:182:SER:HB2	2:C:377:ARG:HB2	1.86	0.56
2:C:628:THR:HG23	2:C:630:MET:H	1.70	0.56
3:D:611:VAL:HG22	3:D:634:LYS:HB2	1.86	0.56
3:D:827:PRO:HD3	3:D:854:HIS:HB3	1.88	0.56
5:F:140:SER:HB3	5:F:143:GLN:HG3	1.87	0.56
1:B:17:ASN:OD1	1:B:17:ASN:N	2.38	0.56
3:D:104:ILE:HD12	3:D:379:ASP:HB3	1.89	0.55
2:C:234:VAL:HG12	2:C:261:THR:HG21	1.87	0.55
2:C:83:VAL:HG13	2:C:87:GLU:HB2	1.89	0.55
1:A:7:PRO:HA	1:A:25:PRO:HD2	1.89	0.55
1:B:100:GLN:HG3	1:B:133:LYS:HB2	1.88	0.55
3:D:1164:ARG:NH2	3:D:1216:ALA:O	2.40	0.55
2:C:473:ARG:NH2	2:C:492:PRO:O	2.39	0.54
2:C:47:PRO:HG2	2:C:581:VAL:HG13	1.89	0.54
2:C:524:VAL:HG21	2:C:548:ILE:HD13	1.89	0.54
3:D:334:ARG:HD3	5:F:90:VAL:HG21	1.88	0.54
3:D:173:ARG:HH21	3:D:201:GLY:HA2	1.73	0.54
3:D:505:HIS:CD2	3:D:507:LEU:HB2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:34:ILE:HA	3:D:41:PRO:HA	1.88	0.54
2:C:377:ARG:NH2	2:C:383:GLU:OE1	2.38	0.54
3:D:1092:GLU:HG3	3:D:1094:GLY:H	1.72	0.53
3:D:1165:VAL:HG12	3:D:1205:PRO:HA	1.90	0.53
7:H:14:DT:H4'	7:H:15:DG:O5'	2.09	0.53
3:D:1247:GLY:O	3:D:1251:ASN:ND2	2.29	0.53
3:D:867:THR:HG22	3:D:1008:THR:HG23	1.90	0.53
1:B:84:VAL:HG23	1:B:119:HIS:HB2	1.90	0.53
1:B:92:PRO:HB3	1:B:141:GLU:HG2	1.91	0.52
1:B:81:LYS:HD3	1:B:165:ASP:HB2	1.91	0.52
2:C:228:ARG:HD3	7:H:14:DT:H73	1.90	0.52
3:D:1131:GLN:HE21	3:D:1162:LEU:HD12	1.74	0.52
2:C:467:ARG:HG2	7:H:15:DG:H2"	1.91	0.52
4:E:60:ARG:NH2	4:E:80:GLY:O	2.43	0.52
1:A:89:GLU:HB3	1:A:91:GLU:HG2	1.92	0.52
2:C:257:ILE:HD11	2:C:346:VAL:HG23	1.90	0.52
4:E:87:LEU:HG	4:E:88:GLN:HG3	1.91	0.51
3:D:122:PRO:HG2	7:H:23:DT:H3'	1.91	0.51
2:C:168:ILE:HB	2:C:173:ARG:HD2	1.93	0.51
1:A:56:ILE:HG12	1:A:136:VAL:HG22	1.93	0.51
1:B:228:GLU:HG2	1:B:229:ALA:H	1.75	0.51
3:D:1045:PRO:HB2	3:D:1111:LEU:HD12	1.93	0.51
3:D:128:ILE:HD11	3:D:234:LEU:HD11	1.92	0.51
2:C:217:ASP:OD2	2:C:231:ARG:NH2	2.44	0.51
3:D:1274:PRO:HB3	4:E:82:LEU:HD11	1.92	0.51
3:D:1270:ILE:HD13	4:E:56:TYR:HE2	1.75	0.51
3:D:369:ASN:ND2	5:F:45:GLN:OE1	2.39	0.50
2:C:853:PHE:HD2	2:C:868:LEU:HD23	1.76	0.50
3:D:1042:GLY:O	3:D:1083:ARG:NH2	2.43	0.50
2:C:140:ILE:HA	2:C:147:ILE:HG12	1.92	0.50
2:C:172:GLU:OE1	2:C:442:GLN:NE2	2.45	0.50
1:A:22:VAL:HG12	1:A:193:ILE:HG12	1.94	0.50
3:D:443:LEU:HD13	3:D:448:ALA:HB2	1.93	0.50
6:G:20:DG:H5"	6:G:20:DG:H8	1.77	0.50
1:B:102:PRO:HB3	1:B:130:ASP:HA	1.93	0.50
3:D:460:LEU:HD11	3:D:483:VAL:HG12	1.94	0.49
1:B:147:VAL:HG13	1:B:166:SER:HB2	1.92	0.49
3:D:778:TRP:CD2	3:D:835:PRO:HG3	2.47	0.49
1:B:74:THR:HG21	3:D:608:GLU:HB2	1.95	0.49
4:E:42:GLU:OE1	4:E:100:HIS:NE2	2.37	0.49
6:G:5:DC:H2"	6:G:6:DA:N7	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:33:PRO:HG2	2:C:632:LEU:HD21	1.94	0.49
1:A:56:ILE:HB	1:A:59:VAL:HG22	1.94	0.49
2:C:120:ASP:N	2:C:120:ASP:OD1	2.46	0.49
3:D:600:GLN:HB2	3:D:609:THR:HB	1.94	0.49
2:C:213:GLU:OE1	2:C:225:ARG:NH1	2.46	0.49
3:D:1166:THR:HB	3:D:1206:VAL:HG21	1.95	0.49
2:C:824:ILE:HG22	5:F:163:VAL:HG13	1.94	0.48
2:C:592:ALA:HA	2:C:976:VAL:HG21	1.95	0.48
3:D:565:ILE:HG23	3:D:575:ALA:HB3	1.95	0.48
1:A:3:ILE:HG13	1:A:4:SER:H	1.79	0.48
2:C:99:PHE:HB3	7:H:7:DC:H1'	1.95	0.48
3:D:789:LEU:HD22	3:D:793:TYR:HE2	1.79	0.48
6:G:19:DG:H1	8:I:3:C:H42	1.61	0.48
1:A:214:THR:OG1	1:B:230:GLU:HG3	2.13	0.48
1:A:30:PHE:HE1	1:B:41:THR:HA	1.79	0.48
2:C:742:VAL:HG13	2:C:878:LYS:HD3	1.96	0.48
3:D:63:GLY:HA2	3:D:66:LYS:HE2	1.96	0.48
3:D:1169:ASP:H	3:D:1202:ALA:HB3	1.77	0.48
2:C:298:ASN:HA	2:C:302:LYS:HB2	1.96	0.48
5:F:124:SER:OG	5:F:127:HIS:ND1	2.33	0.48
1:A:216:VAL:HG13	1:B:216:VAL:HG13	1.96	0.47
1:B:170:PRO:HB2	1:B:202:ILE:HD11	1.96	0.47
3:D:59:GLU:HG2	3:D:66:LYS:HD3	1.96	0.47
3:D:190:LYS:HE3	3:D:192:ASP:HB3	1.95	0.47
4:E:33:LEU:H	4:E:33:LEU:HD23	1.80	0.47
1:B:129:ASN:OD1	1:B:130:ASP:N	2.44	0.47
4:E:89:GLU:OE2	4:E:97:ARG:NH1	2.47	0.47
2:C:982:GLU:HG3	3:D:841:ARG:NH1	2.29	0.47
3:D:337:THR:O	5:F:92:SER:HA	2.14	0.47
2:C:190:THR:HG23	2:C:199:LEU:HB2	1.96	0.47
2:C:848:ILE:HD13	2:C:874:ALA:HB2	1.96	0.47
3:D:334:ARG:CD	5:F:90:VAL:HG21	2.45	0.46
2:C:754:GLU:HG3	2:C:872:TYR:HE2	1.80	0.46
1:A:98:ARG:HG3	1:A:135:GLU:HG3	1.97	0.46
6:G:14:DG:H8	6:G:14:DG:H5'	1.81	0.46
2:C:369:ASP:C	2:C:371:ASP:H	2.18	0.46
3:D:821:LYS:HB3	3:D:836:VAL:HB	1.96	0.46
3:D:556:ARG:HG3	4:E:35:ILE:HD11	1.97	0.46
2:C:1055:GLN:HG2	2:C:1094:ASP:HB3	1.98	0.46
2:C:189:GLU:HB2	2:C:367:THR:HG21	1.98	0.46
3:D:585:LEU:HD13	3:D:673:PHE:HE2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:398:ARG:HH12	5:F:32:ARG:HB2	1.80	0.46
2:C:1045:SER:HB3	3:D:450:GLU:O	2.16	0.46
2:C:218:LYS:NZ	6:G:7:DT:OP2	2.47	0.46
2:C:454:ARG:HH12	2:C:487:GLU:HG2	1.80	0.46
3:D:16:THR:HG22	3:D:18:GLU:H	1.81	0.46
1:B:98:ARG:HG2	1:B:135:GLU:HG2	1.98	0.46
2:C:442:GLN:HB2	2:C:679:ASN:HB2	1.97	0.46
2:C:751:HIS:CD2	2:C:877:ARG:HD2	2.51	0.46
3:D:895:ARG:HD2	3:D:1128:ARG:HH22	1.81	0.46
2:C:642:VAL:HB	2:C:703:ALA:HB3	1.97	0.46
1:A:144:ARG:HH12	1:B:2:LEU:HB2	1.81	0.45
3:D:463:LEU:HB2	3:D:465:HIS:HD2	1.81	0.45
3:D:677:LEU:H	3:D:677:LEU:HG	1.55	0.45
6:G:5:DC:H2"	6:G:6:DA:C8	2.51	0.45
7:H:7:DC:OP1	7:H:7:DC:H4'	2.15	0.45
1:B:124:HIS:HE1	1:B:127:THR:HG23	1.82	0.45
2:C:404:MET:HE3	2:C:404:MET:HB2	1.87	0.45
1:A:95:MET:HE2	1:A:95:MET:HB3	1.92	0.45
2:C:549:ASP:OD1	2:C:550:ALA:N	2.50	0.45
6:G:12:DG:H2'	6:G:13:DA:C8	2.52	0.45
7:H:9:DG:N3	7:H:9:DG:H2'	2.32	0.45
1:A:185:GLN:HG2	1:A:186:ARG:H	1.81	0.45
1:B:146:TYR:O	3:D:624:ARG:NE	2.50	0.45
2:C:1104:GLU:OE1	5:F:113:ARG:NH1	2.50	0.45
1:B:188:ASP:N	1:B:188:ASP:OD1	2.48	0.45
5:F:88:ASN:O	5:F:90:VAL:N	2.49	0.45
3:D:290:LEU:HD23	3:D:293:LEU:HD12	1.98	0.45
3:D:882:GLN:HG3	3:D:997:ILE:HD11	1.98	0.45
2:C:122:CYS:HA	2:C:127:MET:HG3	1.99	0.45
2:C:369:ASP:O	2:C:370:ILE:HG12	2.15	0.45
2:C:513:GLU:HB3	2:C:530:TYR:HB3	1.98	0.45
3:D:436:LEU:HD11	3:D:523:GLN:HB3	1.98	0.44
2:C:927:ASN:O	2:C:930:GLN:HG2	2.16	0.44
1:B:102:PRO:HD3	1:B:131:LYS:H	1.82	0.44
3:D:500:ARG:HB2	3:D:541:MET:HG2	1.98	0.44
3:D:732:SER:HB3	3:D:735:ASP:OD1	2.18	0.44
7:H:6:DT:H3'	7:H:7:DC:H5"	1.99	0.44
2:C:1043:ALA:HB2	3:D:447:MET:HG2	1.99	0.44
2:C:1108:LYS:HE3	5:F:114:LEU:HD22	1.99	0.44
2:C:686:GLN:HA	2:C:705:GLY:HA2	1.99	0.44
2:C:704:ASP:HB2	2:C:708:THR:HB	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:595:ASP:HB3	3:D:631:ALA:HB2	1.99	0.44
1:B:30:PHE:HA	1:B:33:THR:HG23	2.00	0.44
2:C:853:PHE:HB2	2:C:868:LEU:HB3	1.99	0.44
4:E:96:LEU:HD12	4:E:96:LEU:HA	1.85	0.44
1:A:29:GLY:N	1:A:190:ASP:OD2	2.44	0.44
1:B:99:LYS:NZ	1:B:104:GLU:O	2.46	0.44
3:D:823:LEU:HD23	3:D:835:PRO:HB3	2.00	0.44
7:H:14:DT:H2''	7:H:15:DG:H5''	1.99	0.44
1:B:28:PRO:HA	1:B:29:GLY:HA2	1.48	0.43
1:B:24:GLU:HA	1:B:25:PRO:HA	1.75	0.43
7:H:10:DT:H2'	7:H:11:DA:C8	2.53	0.43
1:A:81:LYS:NZ	1:A:165:ASP:HB2	2.34	0.43
2:C:1074:TRP:CE2	3:D:878:VAL:HG11	2.53	0.43
2:C:1079:TYR:CD2	3:D:559:MET:HG2	2.54	0.43
3:D:453:LYS:O	3:D:457:MET:HG3	2.18	0.43
2:C:236:VAL:HG13	2:C:273:ALA:HB1	2.00	0.43
3:D:1101:ASP:OD1	3:D:1101:ASP:N	2.52	0.43
1:A:172:LEU:HB2	1:A:199:LYS:HG2	2.00	0.43
2:C:56:VAL:HG21	2:C:500:LEU:HD22	2.01	0.43
2:C:899:LEU:HB2	2:C:904:MET:CE	2.48	0.43
3:D:1220:TRP:CD1	3:D:1243:ASP:HB2	2.54	0.43
3:D:435:GLN:OE1	3:D:435:GLN:N	2.39	0.43
3:D:991:ILE:HD12	3:D:1266:ARG:HH12	1.83	0.43
3:D:20:ILE:HG23	3:D:318:PRO:HB3	2.00	0.43
4:E:47:VAL:HG11	4:E:53:LEU:HB2	2.01	0.43
3:D:103:HIS:HB3	3:D:106:TYR:HD2	1.84	0.42
1:A:90:ASP:OD1	1:A:142:ARG:HD3	2.19	0.42
2:C:732:GLU:HB3	3:D:579:LEU:HD12	2.01	0.42
3:D:1152:LYS:O	3:D:1156:VAL:HG23	2.20	0.42
1:B:40:ARG:HD3	1:B:40:ARG:HA	1.88	0.42
2:C:228:ARG:O	2:C:228:ARG:HG3	2.18	0.42
2:C:486:ILE:HD11	3:D:849:TYR:HE2	1.84	0.42
3:D:290:LEU:HA	3:D:293:LEU:HD12	2.01	0.42
3:D:893:THR:HG21	3:D:969:ALA:HB3	2.02	0.42
5:F:51:ALA:HB1	5:F:58:ILE:HD11	2.02	0.42
2:C:543:GLN:HG3	3:D:847:LEU:HD13	2.00	0.42
3:D:1080:ILE:HG22	3:D:1082:LYS:H	1.83	0.42
3:D:921:TYR:HE1	3:D:946:ASP:HA	1.85	0.42
1:A:219:PHE:CD1	1:B:215:LEU:HD13	2.55	0.42
2:C:48:LEU:HB2	2:C:528:ILE:HD13	2.00	0.42
7:H:14:DT:H5'	7:H:15:DG:OP1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:111:PRO:HB3	7:H:22:DA:H5"	2.02	0.42
2:C:473:ARG:HB3	2:C:495:GLY:HA3	2.02	0.42
2:C:209:GLY:O	7:H:13:DC:N4	2.53	0.42
1:A:82:SER:C	1:A:123:MET:HE1	2.40	0.42
3:D:1154:ILE:O	3:D:1158:VAL:HG23	2.20	0.42
2:C:119:VAL:HG23	2:C:167:ILE:HD11	2.02	0.41
2:C:344:TYR:OH	2:C:364:PRO:O	2.27	0.41
2:C:516:TYR:HB3	2:C:578:TYR:HB3	2.02	0.41
1:A:84:VAL:HG13	1:A:119:HIS:HB2	2.02	0.41
2:C:202:VAL:HG21	2:C:345:LEU:HB2	2.03	0.41
2:C:214:PHE:CD1	2:C:224:VAL:HB	2.55	0.41
2:C:904:MET:HG2	2:C:913:VAL:O	2.21	0.41
1:B:97:LEU:HB2	1:B:110:ILE:HG13	2.02	0.41
2:C:451:HIS:HA	2:C:454:ARG:HG2	2.02	0.41
2:C:442:GLN:H	2:C:680:HIS:CD2	2.39	0.41
2:C:885:LEU:HG	2:C:895:ILE:HD11	2.03	0.41
3:D:369:ASN:O	3:D:373:MET:HG3	2.21	0.41
3:D:1274:PRO:HA	4:E:104:LEU:HD23	2.03	0.41
2:C:1060:LYS:N	6:G:18:DA:OP1	2.51	0.41
1:A:149:ALA:HB1	1:A:163:PRO:HB2	2.03	0.41
2:C:285:GLU:OE2	7:H:9:DG:N1	2.53	0.41
3:D:575:ALA:O	3:D:713:VAL:HG21	2.20	0.41
3:D:73:ILE:O	3:D:82:VAL:HG22	2.21	0.41
5:F:32:ARG:HD2	7:H:9:DG:O3'	2.20	0.41
2:C:32:VAL:H	2:C:33:PRO:CD	2.33	0.41
2:C:455:LEU:HD12	2:C:483:MET:HG3	2.03	0.41
3:D:409:LYS:HG2	3:D:414:ARG:CZ	2.51	0.41
3:D:579:LEU:HA	3:D:579:LEU:HD23	1.94	0.41
2:C:388:GLN:HG3	2:C:430:PHE:HB2	2.03	0.41
2:C:720:LEU:HD23	2:C:913:VAL:HA	2.03	0.41
3:D:294:LYS:HB2	3:D:294:LYS:HE3	1.79	0.41
3:D:789:LEU:HD22	3:D:793:TYR:CE2	2.55	0.41
3:D:363:PRO:HD3	5:F:52:TRP:CE2	2.56	0.41
3:D:447:MET:HE1	3:D:543:VAL:HG21	2.03	0.41
2:C:57:GLN:HG3	2:C:452:LYS:HB3	2.03	0.41
2:C:615:ALA:HB3	2:C:715:LEU:HD22	2.02	0.41
1:A:99:LYS:HG2	1:A:105:VAL:HG22	2.03	0.41
2:C:588:SER:OG	2:C:589:VAL:N	2.54	0.41
2:C:906:PHE:HA	2:C:912:PRO:HA	2.02	0.41
3:D:589:THR:HG21	3:D:688:MET:HG2	2.02	0.41
3:D:717:LYS:HB3	3:D:717:LYS:HE2	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:28:ARG:O	5:F:32:ARG:HG3	2.21	0.41
3:D:1089:PHE:HA	3:D:1095:SER:HA	2.03	0.40
3:D:350:ARG:HD2	3:D:377:SER:OG	2.21	0.40
2:C:58:THR:O	2:C:62:GLU:HG3	2.22	0.40
1:A:18:ARG:NH1	1:A:195:ASP:OD2	2.54	0.40
1:B:22:VAL:HG12	1:B:193:ILE:HG12	2.02	0.40
2:C:1020:PRO:HB2	2:C:1021:TYR:CD2	2.56	0.40
3:D:1270:ILE:HG21	4:E:56:TYR:CE2	2.56	0.40
5:F:82:ARG:HB3	5:F:83:SER:H	1.71	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	A	223/359 (62%)	217 (97%)	5 (2%)	1 (0%)	34 66
1	B	230/359 (64%)	213 (93%)	16 (7%)	1 (0%)	34 66
2	C	1124/1178 (95%)	1071 (95%)	48 (4%)	5 (0%)	34 66
3	D	1258/1316 (96%)	1205 (96%)	51 (4%)	2 (0%)	47 77
4	E	79/110 (72%)	76 (96%)	3 (4%)	0	100 100
5	F	172/177 (97%)	168 (98%)	4 (2%)	0	100 100
All	All	3086/3499 (88%)	2950 (96%)	127 (4%)	9 (0%)	41 71

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	159	ILE
2	C	370	ILE
2	C	732	GLU

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Mol	Chain	Res	Type
3	D	1089	PHE
2	C	32	VAL
3	D	607	PRO
1	A	184	GLU
2	C	520	VAL
2	C	922	VAL

### 5.3.2 Protein sidechains [\(i\)](#)

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	194/308 (63%)	190 (98%)	4 (2%)	53 75
1	B	191/308 (62%)	185 (97%)	6 (3%)	40 67
2	C	950/998 (95%)	932 (98%)	18 (2%)	57 77
3	D	1049/1095 (96%)	1026 (98%)	23 (2%)	52 74
4	E	66/90 (73%)	66 (100%)	0	100 100
5	F	134/136 (98%)	128 (96%)	6 (4%)	27 58
All	All	2584/2935 (88%)	2527 (98%)	57 (2%)	52 74

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	51	VAL
1	A	111	VAL
1	A	116	VAL
1	B	43	LEU
1	B	79	ASN
1	B	90	ASP
1	B	147	VAL
1	B	188	ASP
1	B	218	LEU
2	C	32	VAL
2	C	80	VAL

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Mol	Chain	Res	Type
2	C	119	VAL
2	C	126	ASP
2	C	208	ARG
2	C	246	GLU
2	C	363	VAL
2	C	370	ILE
2	C	373	PHE
2	C	514	THR
2	C	534	ASP
2	C	562	ARG
2	C	571	VAL
2	C	691	ASP
2	C	875	GLN
2	C	1057	LEU
2	C	1062	GLN
2	C	1137	VAL
3	D	82	VAL
3	D	101	VAL
3	D	256	MET
3	D	279	ASP
3	D	283	ASN
3	D	359	ASP
3	D	427	ARG
3	D	443	LEU
3	D	459	ARG
3	D	461	VAL
3	D	515	MET
3	D	535	ASP
3	D	539	ASP
3	D	578	ARG
3	D	588	LEU
3	D	595	ASP
3	D	650	LEU
3	D	677	LEU
3	D	738	VAL
3	D	804	ASP
3	D	907	ASP
3	D	910	LEU
3	D	1009	GLN
5	F	19	TYR
5	F	56	GLU
5	F	60	ASP

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Mol	Chain	Res	Type
5	F	66	ARG
5	F	85	ARG
5	F	86	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [\(i\)](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	I	4/5 (80%)	0	0

There are no RNA backbone outliers to report.

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 monosaccharides in this entry.

### 5.6 Ligand geometry [\(i\)](#)

Of 2 ligands modelled in this entry, 2 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 (i)

### 6.1 Protein, DNA and RNA chains (i)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	225/359 (62%)	0.19	5 (2%) 62 60	48, 74, 136, 172	0
1	B	232/359 (64%)	0.63	13 (5%) 24 23	62, 95, 148, 179	0
2	C	1126/1178 (95%)	0.29	41 (3%) 42 40	44, 85, 156, 184	0
3	D	1264/1316 (96%)	0.42	93 (7%) 14 14	42, 90, 176, 221	0
4	E	81/110 (73%)	0.69	10 (12%) 4 3	68, 97, 172, 188	0
5	F	174/177 (98%)	0.85	20 (11%) 4 4	60, 101, 168, 190	0
6	G	17/17 (100%)	0.42	1 (5%) 22 22	77, 88, 163, 163	0
7	H	24/24 (100%)	0.97	4 (16%) 1 1	100, 150, 211, 215	0
8	I	5/5 (100%)	1.34	0 100 100	74, 75, 90, 117	0
All	All	3148/3545 (88%)	0.41	187 (5%) 22 22	42, 89, 164, 221	0

All (187) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	ILE	7.1
3	D	1053	VAL	6.0
3	D	1099	LEU	6.0
3	D	1064	ILE	5.5
1	B	4	SER	5.5
3	D	1074	GLU	5.4
1	B	1	MET	5.2
3	D	1049	VAL	5.1
7	H	9	DG	4.9
3	D	1050	THR	4.8
5	F	177	ARG	4.8
4	E	78	TYR	4.7
2	C	252	PHE	4.6
3	D	1066	ILE	4.6
5	F	65	ALA	4.5

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Mol	Chain	Res	Type	RSRZ
3	D	1105	VAL	4.5
2	C	104	SER	4.3
2	C	261	THR	4.2
2	C	220	ASP	4.2
2	C	326	GLU	4.2
1	A	3	ILE	4.2
7	H	6	DT	4.2
3	D	1093	ASP	4.2
3	D	1055	LEU	4.1
4	E	74	GLY	4.1
3	D	1100	SER	4.1
1	A	2	LEU	4.1
3	D	1104	HIS	4.1
3	D	1102	GLY	4.0
3	D	1057	ASP	4.0
3	D	73	ILE	4.0
2	C	192	ASP	4.0
2	C	96	ILE	3.9
2	C	1150	GLY	3.9
6	G	20	DG	3.9
7	H	8	DA	3.9
3	D	1059	GLU	3.9
2	C	219	ARG	3.8
3	D	1091	HIS	3.8
3	D	1056	GLU	3.7
3	D	1101	ASP	3.7
3	D	1075	VAL	3.7
1	A	226	ASN	3.7
4	E	76	LEU	3.7
4	E	75	ILE	3.7
3	D	80	VAL	3.7
3	D	930	VAL	3.7
3	D	1062	TYR	3.6
3	D	1089	PHE	3.6
3	D	1054	ARG	3.5
3	D	1051	GLY	3.5
2	C	325	GLY	3.4
2	C	398	ARG	3.4
2	C	402	GLU	3.4
5	F	69	LEU	3.3
3	D	1061	PHE	3.3
1	B	2	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
4	E	71	LEU	3.3
5	F	62	ALA	3.3
5	F	58	ILE	3.2
3	D	1081	SER	3.2
3	D	1076	VAL	3.2
3	D	900	GLU	3.2
3	D	1069	ASP	3.1
2	C	524	VAL	3.1
1	B	5	GLN	3.1
3	D	1095	SER	3.1
3	D	58	TRP	3.1
3	D	1063	LYS	3.1
2	C	221	THR	3.0
5	F	57	VAL	3.0
2	C	559	VAL	3.0
3	D	71	LYS	2.9
5	F	19	TYR	2.9
2	C	299	LEU	2.9
3	D	1177	PRO	2.9
1	B	154	ALA	2.9
1	B	155	SER	2.9
2	C	404	MET	2.8
2	C	218	LYS	2.8
3	D	1201	ALA	2.8
5	F	15	MET	2.8
2	C	97	GLU	2.8
3	D	60	CYS	2.7
3	D	1080	ILE	2.7
2	C	560	LEU	2.7
2	C	956	ALA	2.7
3	D	1175	PHE	2.7
4	E	82	LEU	2.7
3	D	77	ARG	2.7
5	F	89	VAL	2.7
7	H	7	DC	2.7
3	D	1077	TYR	2.7
2	C	258	MET	2.7
2	C	257	ILE	2.7
3	D	927	THR	2.6
3	D	1103	ASP	2.6
2	C	401	ARG	2.6
1	A	222	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
3	D	935	ASN	2.6
3	D	191	ALA	2.6
3	D	287	GLN	2.6
3	D	1067	VAL	2.6
5	F	49	LEU	2.6
5	F	70	PHE	2.6
3	D	742	LYS	2.6
3	D	943	ASP	2.6
2	C	241	LEU	2.6
2	C	551	ASP	2.5
3	D	965	VAL	2.5
3	D	960	VAL	2.5
3	D	1068	PRO	2.5
2	C	295	LEU	2.5
2	C	1153	GLU	2.5
5	F	5	SER	2.5
5	F	61	THR	2.5
1	B	48	GLY	2.5
3	D	957	ILE	2.5
2	C	99	PHE	2.5
2	C	248	ILE	2.5
4	E	107	THR	2.5
4	E	56	TYR	2.5
2	C	580	ASP	2.5
3	D	1073	GLU	2.5
2	C	405	THR	2.4
2	C	652	GLU	2.4
3	D	1090	LYS	2.4
4	E	77	GLU	2.4
2	C	237	LEU	2.4
3	D	959	GLN	2.4
3	D	769	GLU	2.4
3	D	964	SER	2.4
3	D	1168	ILE	2.4
2	C	235	THR	2.4
3	D	82	VAL	2.4
3	D	1087	ARG	2.4
3	D	773	ALA	2.4
2	C	323	HIS	2.4
1	A	221	LEU	2.4
1	B	141	GLU	2.3
3	D	1111	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
3	D	1065	THR	2.3
3	D	937	ILE	2.3
3	D	1070	ASP	2.3
2	C	1152	ASP	2.3
5	F	172	GLU	2.3
3	D	285	LYS	2.3
3	D	958	THR	2.3
3	D	1078	ASP	2.3
3	D	1106	GLU	2.2
5	F	64	PRO	2.2
3	D	65	TYR	2.2
2	C	284	GLY	2.2
3	D	78	CYS	2.2
5	F	96	SER	2.2
2	C	659	THR	2.2
4	E	102	ASP	2.2
5	F	47	THR	2.2
3	D	69	ARG	2.2
5	F	25	VAL	2.2
3	D	926	GLY	2.2
3	D	59	GLU	2.2
3	D	61	TYR	2.1
3	D	357	LEU	2.1
3	D	944	LEU	2.1
1	B	93	VAL	2.1
3	D	356	ARG	2.1
3	D	1060	ARG	2.1
3	D	70	PHE	2.1
3	D	281	ILE	2.1
3	D	1200	PRO	2.1
5	F	4	VAL	2.1
1	B	85	VAL	2.1
2	C	324	VAL	2.1
3	D	1107	VAL	2.1
3	D	1026	GLY	2.1
1	B	151	GLN	2.1
3	D	942	GLN	2.1
3	D	1176	LEU	2.1
3	D	194	ARG	2.1
2	C	576	VAL	2.1
3	D	167	ASP	2.1
3	D	1072	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
5	F	46	GLU	2.0
1	B	140	VAL	2.0
3	D	190	LYS	2.0
3	D	1281	ALA	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 monosaccharides 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, 95<sup>th</sup> 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(Å <sup>2</sup> )	Q<0.9
9	ZN	D	2002	1/1	0.98	0.08	105,105,105,105	0
9	ZN	D	2001	1/1	0.99	0.10	100,100,100,100	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.