



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:05 AM UTC

PDB ID : 6KQN / pdb_00006kqn
Title : Thermus thermophilus initial transcription complex comprising sigma A and 5'-triphosphate RNA of 6 nt
Authors : Zhang, Y.; Li, L.; Ebright, R.H.
Deposited on : 2019-08-18
Resolution : 3.49 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

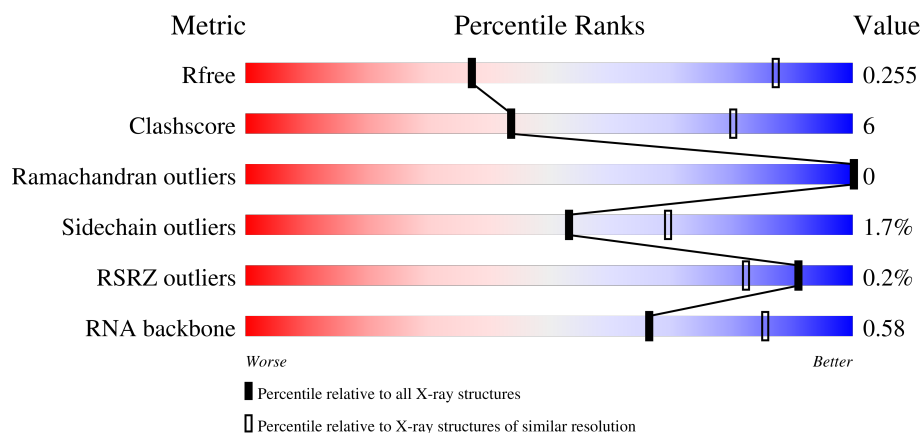
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.49 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



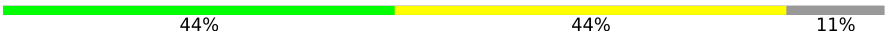
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1083 (3.52-3.44)
Clashscore	190562	1139 (3.52-3.44)
Ramachandran outliers	187476	1111 (3.52-3.44)
Sidechain outliers	187428	1112 (3.52-3.44)
RSRZ outliers	180081	1082 (3.52-3.44)
RNA backbone	3983	1001 (3.94-3.02)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	315	
1	B	315	
2	C	1119	
3	D	1524	

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Mol	Chain	Length	Quality of chain
4	E	99	 80% 15% 5%
5	F	443	 68% 8% 24%
6	G	21	 38% 48% 14%
7	H	27	 44% 44% 11%
8	I	6	 67% 33%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 28637 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	231	Total	C	N	O	S	0	1	0
			1814	1158	316	338	2			
1	B	223	Total	C	N	O	S	0	0	0
			1755	1123	304	326	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1112	Total	C	N	O	S	0	3	0
			8785	5556	1570	1635	24			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1486	Total	C	N	O	S	0	3	0
			11753	7455	2067	2195	36			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	94	Total	C	N	O	S	0	0	0
			761	486	132	139	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	337	Total	C	N	O	S	0	0	0
			2737	1726	499	508	4			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-19	MET	-	initiating methionine	UNP Q5SKW1
F	-18	GLY	-	expression tag	UNP Q5SKW1
F	-17	SER	-	expression tag	UNP Q5SKW1
F	-16	SER	-	expression tag	UNP Q5SKW1
F	-15	HIS	-	expression tag	UNP Q5SKW1
F	-14	HIS	-	expression tag	UNP Q5SKW1
F	-13	HIS	-	expression tag	UNP Q5SKW1
F	-12	HIS	-	expression tag	UNP Q5SKW1
F	-11	HIS	-	expression tag	UNP Q5SKW1
F	-10	HIS	-	expression tag	UNP Q5SKW1
F	-9	SER	-	expression tag	UNP Q5SKW1
F	-8	SER	-	expression tag	UNP Q5SKW1
F	-7	GLY	-	expression tag	UNP Q5SKW1
F	-6	LEU	-	expression tag	UNP Q5SKW1
F	-5	VAL	-	expression tag	UNP Q5SKW1
F	-4	PRO	-	expression tag	UNP Q5SKW1
F	-3	ARG	-	expression tag	UNP Q5SKW1
F	-2	GLY	-	expression tag	UNP Q5SKW1
F	-1	SER	-	expression tag	UNP Q5SKW1
F	0	HIS	-	expression tag	UNP Q5SKW1

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	18	Total	C	N	O	P	0	0	0
			372	176	73	106	17			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	24	Total	C	N	O	P	0	0	0
			495	236	94	142	23			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	6	Total	C	N	O	P	0	0	0
			134	56	21	49	8			

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total Mg 1 1	0	0
9	D	2	Total Mg 2 2	0	0
9	F	1	Total Mg 1 1	0	0

- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

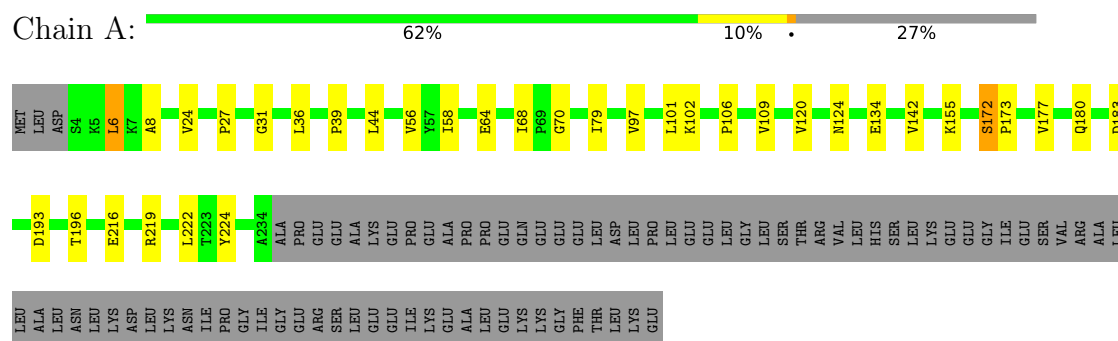
- Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	B	2	Total O 2 2	0	0
11	C	7	Total O 7 7	0	0
11	D	14	Total O 14 14	0	0
11	G	1	Total O 1 1	0	0
11	H	1	Total O 1 1	0	0

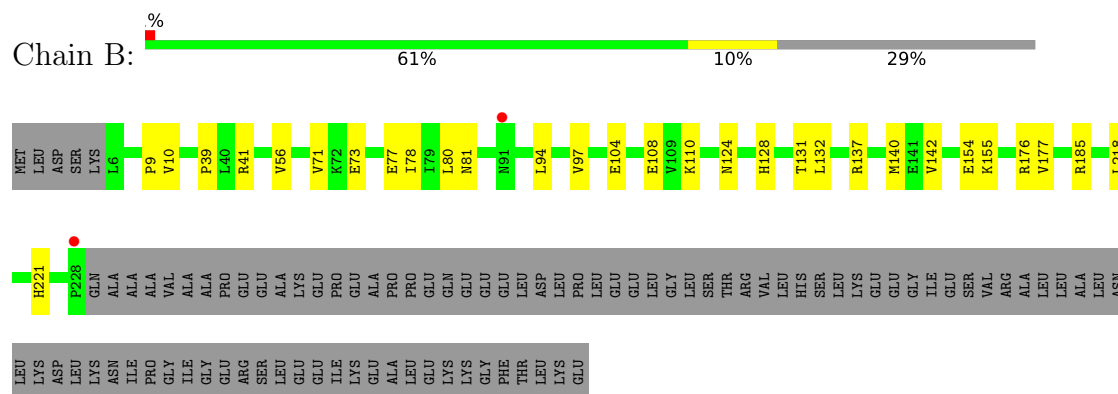
3 Residue-property plots

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.

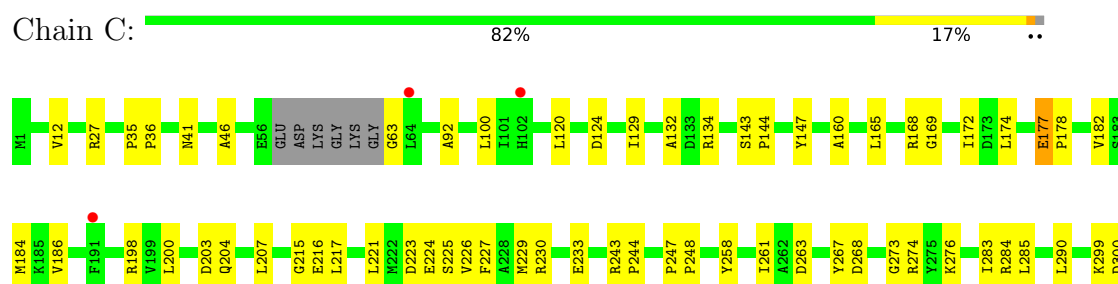
- Molecule 1: DNA-directed RNA polymerase subunit alpha

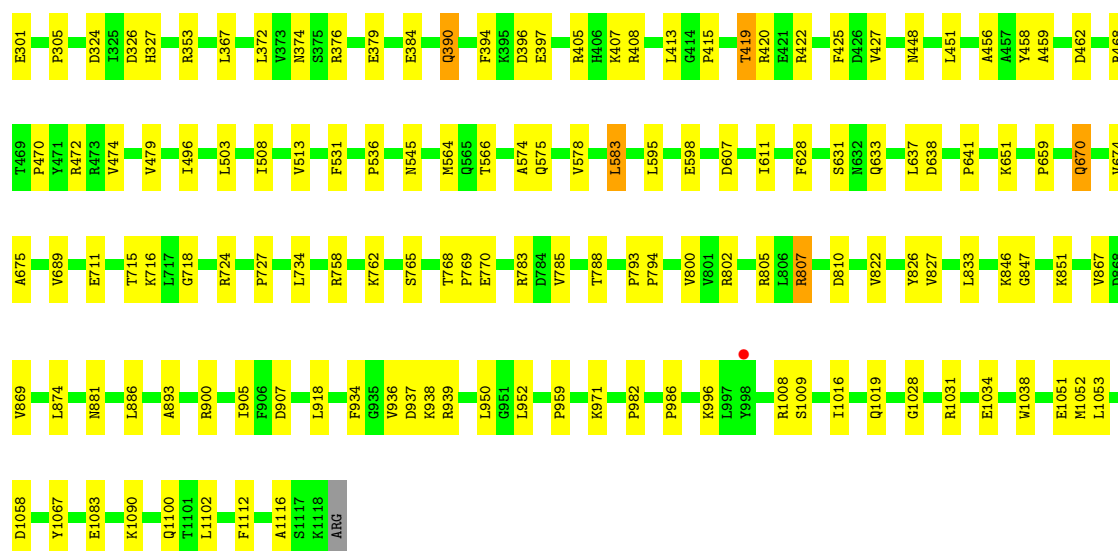


- Molecule 1: DNA-directed RNA polymerase subunit alpha



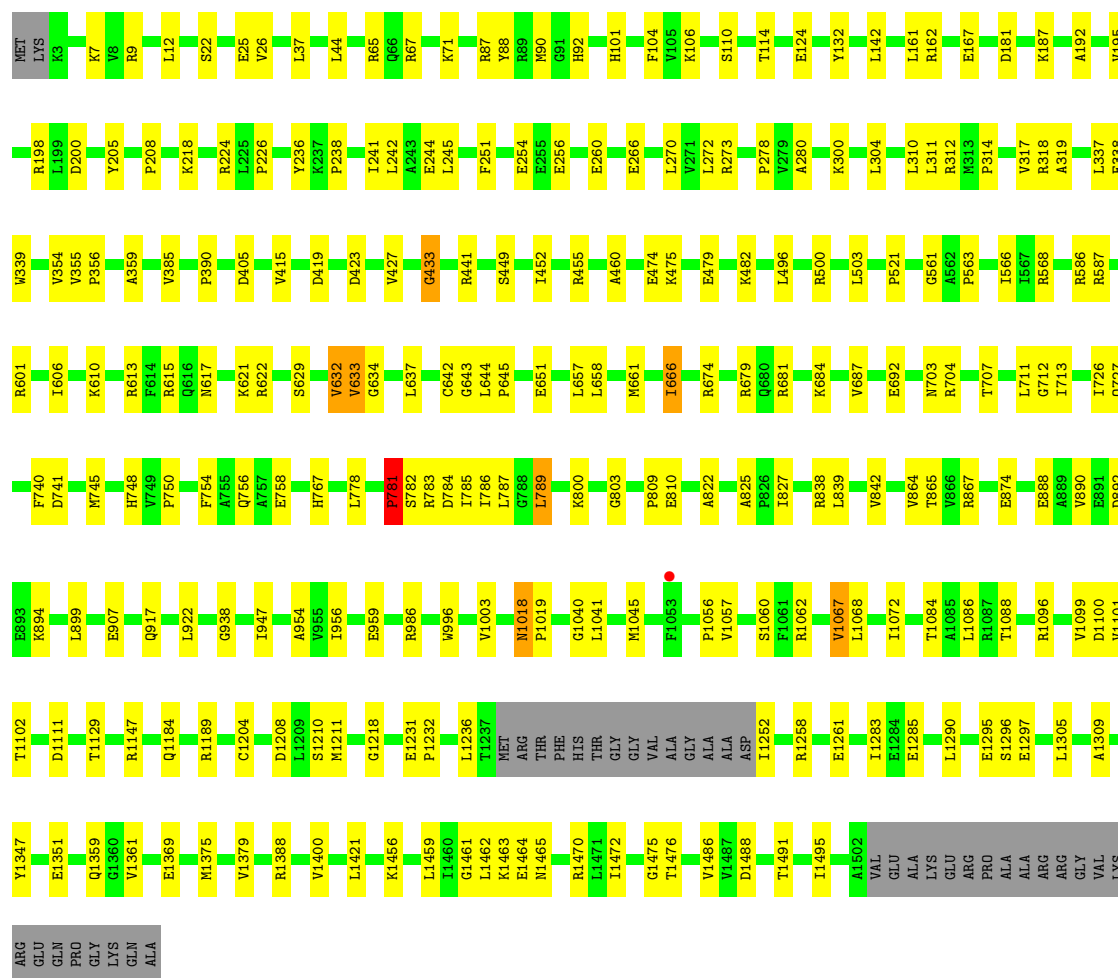
- Molecule 2: DNA-directed RNA polymerase subunit beta





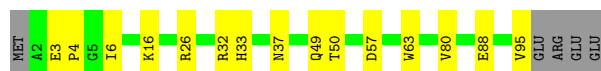
• Molecule 3: DNA-directed RNA polymerase subunit beta'

Chain D: 81% 16%



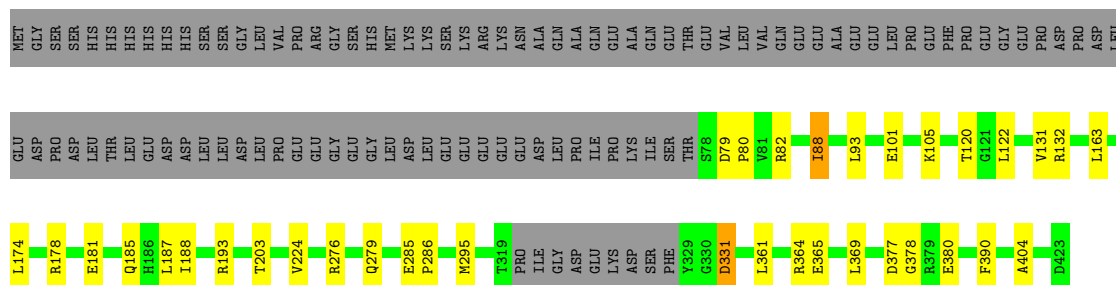
• Molecule 4: DNA-directed RNA polymerase subunit omega

Chain E:  80% 15% 5%

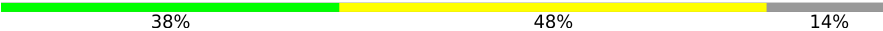


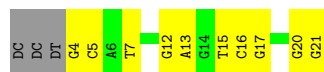
- Molecule 5: RNA polymerase sigma factor SigA

Chain F:  68% 8% 24%

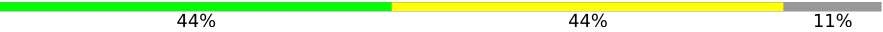


- Molecule 6: DNA (5'-D(*CP*CP*TP*GP*CP*AP*TP*CP*CP*GP*TP*GP*AP*GP*TP*CP*GP*AP*GP*GP*G)-3')

Chain G:  38% 48% 14%



- Molecule 7: DNA (5'-D(*TP*AP*TP*AP*AP*TP*GP*GP*GP*AP*GP*CP*TP*GP*TP*CP*AP*CP*GP*GP*AP*TP*GP*CP*AP*GP*G*G)-3')

Chain H:  44% 44% 11%



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

Chain I:  67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	184.62Å 101.92Å 296.11Å 90.00° 98.83° 90.00°	Depositor
Resolution (Å)	48.79 – 3.49 48.79 – 3.49	Depositor EDS
% Data completeness (in resolution range)	93.2 (48.79-3.49) 93.4 (48.79-3.49)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.213 , 0.258 0.212 , 0.255	Depositor DCC
R_{free} test set	3249 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	99.9	Xtriage
Anisotropy	0.677	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 59.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	28637	wwPDB-VP
Average B, all atoms (Å ²)	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, 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	A	0.27	0/1849	0.77	4/2515 (0.2%)
1	B	0.27	0/1787	0.78	0/2431
2	C	0.28	0/8961	0.74	2/12118 (0.0%)
3	D	0.30	1/11969 (0.0%)	0.75	8/16182 (0.0%)
4	E	0.27	0/775	0.69	0/1045
5	F	0.27	0/2779	0.71	0/3737
6	G	0.21	0/418	0.50	0/645
7	H	0.15	0/556	0.54	0/858
8	I	0.08	0/116	0.16	0/178
All	All	0.28	1/29210 (0.0%)	0.74	14/39709 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	781	PRO	C-O	-6.07	1.16	1.23

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	634	GLY	CA-C-N	6.66	126.11	118.85
3	D	634	GLY	C-N-CA	6.66	126.11	118.85
1	A	172	SER	CA-C-N	6.61	126.23	119.56
1	A	172	SER	C-N-CA	6.61	126.23	119.56
3	D	1231	GLU	CA-C-N	-6.55	115.03	121.65
3	D	1231	GLU	C-N-CA	-6.55	115.03	121.65
2	C	169	GLY	CA-C-N	6.26	126.22	120.03
2	C	169	GLY	C-N-CA	6.26	126.22	120.03
3	D	433	GLY	N-CA-C	5.65	118.20	110.69
3	D	1018	ASN	CA-C-N	5.58	125.68	119.32
3	D	1018	ASN	C-N-CA	5.58	125.68	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	783	ARG	CB-CA-C	-5.25	110.55	116.63
1	A	8	ALA	CA-C-N	5.06	125.27	120.31
1	A	8	ALA	C-N-CA	5.06	125.27	120.31

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	1814	0	1869	25	0
1	B	1755	0	1804	20	0
2	C	8785	0	8895	123	0
3	D	11753	0	11992	157	0
4	E	761	0	778	11	0
5	F	2737	0	2819	24	0
6	G	372	0	203	21	0
7	H	495	0	272	16	0
8	I	134	0	65	1	0
9	B	1	0	0	0	0
9	D	2	0	0	0	0
9	F	1	0	0	0	0
10	D	2	0	0	0	0
11	B	2	0	0	0	0
11	C	7	0	0	0	0
11	D	14	0	0	0	0
11	G	1	0	0	0	0
11	H	1	0	0	0	0
All	All	28637	0	28697	344	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 (344) 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)
3:D:782:SER:HA	3:D:786:ILE:HD12	1.49	0.95
2:C:874:LEU:HD22	3:D:784:ASP:OD1	1.75	0.87
3:D:782:SER:HA	3:D:786:ILE:CD1	2.05	0.85
2:C:768:THR:CG2	2:C:769:PRO:HD2	2.06	0.85
2:C:768:THR:HG23	2:C:769:PRO:HD2	1.59	0.85
6:G:12:DG:N2	7:H:16:DC:N3	2.27	0.80
2:C:168:ARG:HD3	2:C:268:ASP:HB3	1.64	0.78
2:C:628:PHE:H	2:C:638:ASP:HB3	1.48	0.77
7:H:17:DA:C2	7:H:18:DC:C2	2.74	0.76
6:G:16:DC:H2'	6:G:17:DG:H8	1.50	0.74
6:G:20:DG:H1	8:I:2:CTP:HN41	1.35	0.74
6:G:12:DG:N2	7:H:16:DC:C2	2.56	0.72
2:C:165:LEU:HB2	2:C:168:ARG:HG3	1.70	0.71
7:H:17:DA:N3	7:H:18:DC:C2	2.61	0.69
4:E:32:ARG:O	4:E:95:VAL:HG13	1.93	0.69
3:D:787:LEU:HD21	3:D:947:ILE:HG21	1.76	0.67
2:C:758:ARG:HH21	2:C:788:THR:HB	1.59	0.67
3:D:405:ASP:HB3	3:D:423:ASP:HA	1.77	0.67
2:C:63:GLY:HA3	2:C:100:LEU:HD21	1.77	0.66
3:D:954:ALA:O	3:D:1062:ARG:NH2	2.28	0.65
6:G:12:DG:H1	7:H:16:DC:H42	1.44	0.65
3:D:65:ARG:NH1	5:F:378:GLY:O	2.29	0.65
6:G:16:DC:H2'	6:G:17:DG:C8	2.32	0.65
2:C:768:THR:HG22	2:C:770:GLU:OE1	1.98	0.64
2:C:1019:GLN:HG2	2:C:1058:ASP:HB3	1.80	0.63
2:C:12:VAL:HG21	2:C:472:ARG:HD3	1.79	0.63
2:C:800:VAL:HG22	2:C:827:VAL:HG22	1.79	0.63
3:D:124:GLU:OE2	3:D:587:ARG:NH2	2.32	0.62
1:B:56:VAL:HG22	1:B:142:VAL:HG12	1.80	0.62
2:C:420:ARG:NH2	2:C:448:ASN:OD1	2.30	0.62
3:D:711:LEU:HD22	3:D:778:LEU:HD23	1.82	0.62
6:G:21:DG:OP2	6:G:21:DG:H8	1.82	0.62
1:A:24:VAL:HG22	1:A:196:THR:HG23	1.82	0.61
3:D:356:PRO:HG2	3:D:359:ALA:HB2	1.83	0.61
3:D:132:TYR:OH	3:D:568:ARG:NH1	2.34	0.61
2:C:575:GLN:HG3	2:C:670:GLN:HE21	1.66	0.61
2:C:1083:GLU:OE2	3:D:87:ARG:NH2	2.34	0.60
3:D:1495:ILE:HG12	4:E:88:GLU:HG3	1.83	0.60
3:D:455:ARG:HB2	3:D:460:ALA:HB2	1.82	0.60
3:D:899:LEU:HD22	3:D:917:GLN:HB3	1.84	0.59
3:D:803:GLY:HA2	3:D:827:ILE:HA	1.83	0.59
1:A:6:LEU:HD11	1:A:27:PRO:HG2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:874:LEU:HD11	3:D:787:LEU:HD22	1.84	0.59
6:G:20:DG:C2'	6:G:21:DG:O4'	2.50	0.59
6:G:20:DG:H2''	6:G:21:DG:O4'	2.03	0.59
3:D:657:LEU:HG	3:D:661:MET:HE2	1.84	0.58
3:D:1258:ARG:NH1	3:D:1261:GLU:OE2	2.36	0.58
7:H:17:DA:C2	7:H:18:DC:O2	2.56	0.58
2:C:768:THR:HG22	2:C:769:PRO:HD2	1.84	0.58
3:D:236:TYR:HB2	3:D:319:ALA:HB3	1.83	0.58
2:C:1034:GLU:OE2	3:D:1096:ARG:NH2	2.37	0.58
2:C:711:GLU:HG2	2:C:822:VAL:HG22	1.85	0.58
3:D:956:ILE:HD11	3:D:1062:ARG:HG2	1.86	0.58
3:D:106:LYS:O	3:D:586:ARG:NH1	2.37	0.57
1:A:106:PRO:HG3	1:A:134:GLU:HG2	1.85	0.57
5:F:365:GLU:HB2	5:F:404:ALA:HB2	1.86	0.57
7:H:15:DT:H1'	7:H:16:DC:H5'	1.86	0.57
2:C:768:THR:CG2	2:C:769:PRO:CD	2.80	0.57
5:F:331:ASP:OD2	5:F:331:ASP:N	2.36	0.57
6:G:15:DT:H2'	6:G:16:DC:C6	2.39	0.57
3:D:192:ALA:HB3	3:D:195:VAL:HB	1.87	0.57
3:D:260:GLU:OE1	3:D:273:ARG:NH1	2.34	0.57
3:D:1465:ASN:OD1	3:D:1470:ARG:NH1	2.38	0.57
2:C:326:ASP:OD1	7:H:14:DG:N2	2.32	0.56
5:F:193:ARG:NH1	7:H:7:DG:N7	2.54	0.56
2:C:223:ASP:OD1	2:C:225:SER:OG	2.21	0.56
2:C:229:MET:HB2	2:C:233:GLU:HB2	1.88	0.56
1:A:196:THR:HG21	2:C:934:PHE:HE2	1.70	0.55
2:C:715:THR:OG1	2:C:718:GLY:O	2.24	0.55
3:D:355:VAL:HG11	3:D:385:VAL:HG21	1.87	0.55
4:E:33:HIS:HA	4:E:95:VAL:HG22	1.88	0.55
3:D:241:ILE:HA	3:D:312:ARG:HG2	1.89	0.55
3:D:644:LEU:HD12	3:D:645:PRO:HD2	1.88	0.55
3:D:22:SER:HB2	3:D:92:HIS:HB3	1.89	0.55
2:C:637:LEU:HG	2:C:659:PRO:HG3	1.89	0.55
2:C:674:VAL:HG12	2:C:869:VAL:HB	1.89	0.55
2:C:1016:ILE:O	3:D:87:ARG:NH1	2.39	0.55
3:D:266:GLU:HG3	3:D:314:PRO:HB3	1.88	0.55
2:C:92:ALA:HB2	2:C:120:LEU:HD11	1.88	0.54
2:C:244:PRO:O	5:F:82:ARG:NH1	2.40	0.54
3:D:9:ARG:HB2	3:D:1456:LYS:HG2	1.89	0.54
3:D:1375:MET:HE2	3:D:1421:LEU:HD11	1.89	0.54
2:C:1031:ARG:HA	3:D:622:ARG:HA	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:207:LEU:HD13	2:C:221:LEU:HD21	1.89	0.54
2:C:611:ILE:HD11	2:C:641:PRO:HB3	1.89	0.54
3:D:242:LEU:HB3	3:D:311:LEU:HD12	1.90	0.54
3:D:167:GLU:OE2	3:D:198:ARG:NH1	2.41	0.54
3:D:789:LEU:HD23	3:D:938:GLY:HA2	1.89	0.54
5:F:120:THR:HG22	5:F:122:LEU:HD13	1.90	0.54
3:D:822:ALA:HB3	3:D:825:ALA:HB2	1.90	0.54
3:D:317:VAL:HG23	3:D:339:TRP:HB3	1.89	0.53
2:C:160:ALA:HB3	2:C:174:LEU:HB2	1.89	0.53
3:D:800:LYS:HB3	3:D:822:ALA:HB2	1.90	0.53
2:C:456:ALA:HB3	2:C:459:ALA:HB2	1.91	0.53
2:C:462:ASP:HB3	2:C:468:ARG:HD2	1.91	0.53
1:A:36:LEU:HD11	1:B:221:HIS:HB3	1.90	0.53
3:D:643:GLY:HA3	3:D:727:GLN:HB2	1.90	0.53
2:C:939:ARG:HG2	2:C:982:PRO:HD3	1.91	0.53
3:D:273:ARG:HB3	3:D:278:PRO:HA	1.90	0.53
3:D:637:LEU:HD13	3:D:642:CYS:HA	1.90	0.53
3:D:142:LEU:HB2	3:D:161:LEU:HD21	1.91	0.52
3:D:781:PRO:O	3:D:786:ILE:HD11	2.09	0.52
3:D:224:ARG:NE	3:D:254:GLU:OE2	2.34	0.52
1:A:216:GLU:OE2	1:A:219:ARG:NH2	2.42	0.52
2:C:408:ARG:NH1	2:C:456:ALA:O	2.42	0.52
2:C:172:ILE:HD13	2:C:184:MET:HE3	1.91	0.52
3:D:415:VAL:HG13	3:D:419:ASP:HB2	1.92	0.52
1:B:104:GLU:OE2	1:B:137:ARG:NH1	2.43	0.52
3:D:1111:ASP:OD1	3:D:1189:ARG:NH2	2.42	0.52
2:C:1100:GLN:HG3	3:D:9:ARG:HH21	1.74	0.51
3:D:218:LYS:HG2	3:D:338:GLU:HG2	1.90	0.51
3:D:226:PRO:HG2	3:D:245:LEU:HD11	1.92	0.51
3:D:1236:LEU:HA	3:D:1359:GLN:HG3	1.93	0.51
3:D:890:VAL:HB	3:D:922:LEU:HD13	1.91	0.51
6:G:12:DG:H2'	6:G:13:DA:C8	2.45	0.51
6:G:12:DG:H1	7:H:16:DC:N4	2.09	0.51
5:F:279:GLN:HB3	5:F:286:PRO:HD3	1.91	0.51
3:D:256:GLU:HG3	3:D:300:LYS:HG3	1.92	0.51
6:G:20:DG:H2'	6:G:21:DG:C1'	2.41	0.51
4:E:32:ARG:O	4:E:95:VAL:CG1	2.58	0.51
3:D:707:THR:HG23	3:D:712:GLY:HA3	1.93	0.50
1:B:80:LEU:HD21	3:D:842:VAL:HG12	1.93	0.50
2:C:41:ASN:O	2:C:46:ALA:HB2	2.11	0.50
1:A:222:LEU:HD21	1:B:218:LEU:HD23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:807[A]:ARG:NH1	2:C:810:ASP:OD2	2.44	0.50
3:D:110:SER:O	3:D:114:THR:OG1	2.21	0.50
3:D:1100:ASP:OD2	3:D:1463:LYS:NZ	2.36	0.50
2:C:367:LEU:HD13	2:C:372:LEU:HD21	1.92	0.50
5:F:193:ARG:HB2	7:H:6:DT:H1'	1.92	0.50
3:D:474:GLU:HG3	3:D:496:LEU:HD11	1.92	0.50
3:D:704:ARG:HB2	3:D:745:MET:HG2	1.93	0.50
6:G:4:DG:H2''	6:G:5:DC:C6	2.46	0.50
1:A:101:LEU:HD21	1:A:109:VAL:HG11	1.92	0.50
4:E:57:ASP:HB3	4:E:63:TRP:HE1	1.77	0.50
1:A:64:GLU:HG3	1:A:79:ILE:HD12	1.94	0.50
6:G:20:DG:C2'	6:G:21:DG:C1'	2.89	0.50
3:D:238:PRO:HD3	3:D:318:ARG:HG3	1.93	0.50
4:E:37:ASN:OD1	4:E:37:ASN:N	2.42	0.50
2:C:243:ARG:NH1	7:H:9:DG:O6	2.45	0.49
2:C:1052:MET:HE1	3:D:748:HIS:HB3	1.93	0.49
2:C:129:ILE:HB	2:C:134:ARG:HD2	1.94	0.49
2:C:419:THR:HG23	2:C:422:ARG:HB2	1.94	0.49
2:C:1053:LEU:HA	3:D:621:LYS:HD2	1.94	0.49
3:D:208:PRO:HA	3:D:390:PRO:HA	1.94	0.49
2:C:144:PRO:HB2	2:C:273:GLY:HA3	1.95	0.49
2:C:390:GLN:HB3	2:C:415:PRO:HD3	1.94	0.49
3:D:563:PRO:HD2	3:D:566:ILE:HD12	1.93	0.49
3:D:1040:GLY:O	3:D:1060:SER:HB3	2.12	0.49
1:A:31:GLY:N	1:A:193:ASP:OD1	2.43	0.49
3:D:758:GLU:HG2	3:D:1476:THR:HG21	1.95	0.49
3:D:1461:GLY:O	3:D:1465:ASN:ND2	2.45	0.49
2:C:324:ASP:HB3	2:C:327:HIS:HB2	1.93	0.49
3:D:272:LEU:HB2	3:D:280:ALA:HB3	1.95	0.49
6:G:20:DG:H2'	6:G:21:DG:C8	2.48	0.49
1:B:78:ILE:HG21	1:B:140:MET:HE1	1.93	0.49
2:C:675:ALA:HB2	2:C:867:VAL:HG11	1.95	0.49
1:B:81:ASN:OD1	3:D:867:ARG:NH2	2.41	0.49
2:C:168:ARG:HE	2:C:168:ARG:HA	1.78	0.49
3:D:1045[B]:MET:HE1	3:D:1057:VAL:HG23	1.94	0.49
3:D:1211:MET:HE1	4:E:16:LYS:HD2	1.95	0.49
3:D:842:VAL:HG22	3:D:865:THR:HB	1.95	0.48
3:D:433:GLY:HA2	3:D:449:SER:H	1.78	0.48
2:C:226:VAL:HA	2:C:229:MET:HE2	1.94	0.48
2:C:224:GLU:CD	2:C:224:GLU:H	2.21	0.48
2:C:1116:ALA:HB2	3:D:88:TYR:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:959:GLU:N	3:D:959:GLU:OE1	2.44	0.48
2:C:937:ASP:OD1	2:C:938:LYS:N	2.46	0.48
3:D:1486:VAL:HG11	4:E:26:ARG:HB2	1.95	0.48
3:D:789:LEU:HD23	3:D:789:LEU:N	2.29	0.48
2:C:802:ARG:HB2	2:C:826:TYR:HB2	1.96	0.48
3:D:12:LEU:HD21	3:D:104:PHE:CZ	2.49	0.48
2:C:132:ALA:HB1	2:C:394:PHE:HE1	1.79	0.47
3:D:187:LYS:N	3:D:200:ASP:OD1	2.39	0.47
2:C:177:GLU:HG3	2:C:178:PRO:HD2	1.96	0.47
3:D:101:HIS:HB3	3:D:104:PHE:HD2	1.78	0.47
3:D:162:ARG:HH11	3:D:452:ILE:H	1.61	0.47
2:C:405:ARG:HD3	2:C:566:THR:HG21	1.95	0.47
2:C:503:LEU:HD23	2:C:508:ILE:HA	1.97	0.47
2:C:768:THR:CG2	2:C:770:GLU:OE1	2.62	0.47
1:B:71:VAL:HG22	1:B:132:LEU:HG	1.96	0.47
3:D:1045[B]:MET:HE3	3:D:1045[B]:MET:HB2	1.82	0.47
3:D:1495:ILE:HD13	4:E:80:VAL:HG21	1.96	0.47
2:C:727:PRO:HB3	2:C:783:ARG:HD3	1.96	0.47
1:B:176:ARG:NH2	3:D:888:GLU:OE1	2.44	0.47
3:D:314:PRO:HB2	3:D:317:VAL:HG12	1.96	0.47
3:D:356:PRO:HB3	3:D:441:ARG:HA	1.96	0.47
3:D:1459:LEU:HD22	3:D:1464:GLU:HB3	1.97	0.47
1:A:97:VAL:HG11	1:A:120:VAL:HG21	1.96	0.46
2:C:168:ARG:O	2:C:267:TYR:HA	2.15	0.46
2:C:458:TYR:HB3	2:C:470:PRO:HG3	1.97	0.46
3:D:26:VAL:HG11	3:D:44:LEU:HD23	1.96	0.46
3:D:890:VAL:HG23	3:D:892:ASP:H	1.80	0.46
2:C:768:THR:HG22	2:C:769:PRO:CD	2.46	0.46
2:C:545:ASN:HB3	2:C:583:LEU:HD22	1.98	0.46
2:C:574:ALA:HA	2:C:670:GLN:HE22	1.81	0.46
2:C:578:VAL:HA	2:C:900:ARG:HG2	1.98	0.46
3:D:1068:LEU:O	3:D:1072:ILE:HG12	2.16	0.46
2:C:689:VAL:HG13	2:C:851:LYS:HB3	1.96	0.46
5:F:131:VAL:HG13	5:F:178:ARG:HD3	1.97	0.46
1:A:180:GLN:HB3	1:A:196:THR:HB	1.97	0.46
1:B:108:GLU:HG2	1:B:131:THR:HG22	1.97	0.46
3:D:629:SER:HB3	3:D:726:ILE:HG13	1.97	0.46
3:D:561:GLY:HA3	5:F:132:ARG:HD3	1.97	0.45
2:C:1009:SER:HB3	3:D:651:GLU:O	2.15	0.45
2:C:300:ASP:OD1	2:C:301:GLU:N	2.49	0.45
3:D:658:LEU:HA	3:D:661:MET:HE3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:789:LEU:CD2	3:D:938:GLY:HA2	2.46	0.45
1:A:124:ASN:OD1	1:A:124:ASN:N	2.49	0.45
2:C:283:ILE:HD13	2:C:305:PRO:HG2	1.96	0.45
3:D:703:ASN:HB2	3:D:713:ILE:HG12	1.98	0.45
3:D:319:ALA:HA	3:D:337:LEU:HD23	1.98	0.45
3:D:679:ARG:HH22	3:D:681:ARG:HD2	1.81	0.45
3:D:1463:LYS:HE2	3:D:1463:LYS:HB3	1.75	0.45
2:C:203:ASP:OD2	2:C:204:GLN:N	2.50	0.45
2:C:847:GLY:HA2	3:D:741:ASP:HA	1.98	0.45
2:C:893:ALA:HB2	2:C:918:LEU:HD23	1.97	0.45
2:C:172:ILE:HG12	2:C:186:VAL:HG22	1.99	0.45
3:D:479:GLU:HA	3:D:482:LYS:HE2	1.99	0.45
2:C:833:LEU:HD13	2:C:996:LYS:HE2	1.98	0.45
3:D:1379:VAL:HG21	3:D:1400:VAL:HG11	1.97	0.45
1:B:41:ARG:HA	1:B:177:VAL:HG11	1.98	0.44
3:D:1101:VAL:HG13	3:D:1102:THR:HG23	1.98	0.44
5:F:187:LEU:HD23	5:F:224:VAL:HG13	1.99	0.44
1:A:56:VAL:HG22	1:A:142:VAL:HG12	1.98	0.44
2:C:950:LEU:HB3	2:C:952:LEU:HD13	1.98	0.44
3:D:633:VAL:HB	3:D:740:PHE:CZ	2.52	0.44
3:D:1003:VAL:HG21	3:D:1041:LEU:HG	1.98	0.44
3:D:1296:SER:OG	3:D:1297:GLU:N	2.50	0.44
1:B:185:ARG:HH21	3:D:692:GLU:HG3	1.83	0.44
3:D:65:ARG:HD3	3:D:65:ARG:HA	1.81	0.44
1:B:155:LYS:HD3	1:B:155:LYS:HA	1.83	0.44
6:G:12:DG:H5"	6:G:12:DG:H8	1.83	0.44
3:D:750:PRO:HG2	3:D:756:GLN:NE2	2.33	0.44
7:H:10:DA:H2"	7:H:11:DG:C8	2.52	0.44
5:F:361:LEU:HB3	5:F:365:GLU:HG3	1.99	0.44
2:C:564:MET:SD	2:C:846:LYS:HD3	2.57	0.44
2:C:536:PRO:HB3	3:D:1067:VAL:HG11	1.99	0.44
3:D:632:VAL:O	3:D:727:GLN:HA	2.18	0.44
3:D:661:MET:HG2	3:D:666:ILE:HD12	2.00	0.44
7:H:10:DA:H2"	7:H:11:DG:H5"	1.99	0.44
1:A:70:GLY:H	2:C:607:ASP:CG	2.26	0.43
1:A:172:SER:HA	1:A:173:PRO:HD2	1.85	0.43
2:C:881:ASN:OD1	2:C:881:ASN:N	2.51	0.43
3:D:864:VAL:HG22	3:D:865:THR:H	1.83	0.43
3:D:1290:LEU:HD22	3:D:1305:LEU:HD11	2.00	0.43
5:F:101:GLU:HG2	5:F:105:LYS:HE2	2.00	0.43
5:F:285:GLU:HA	5:F:286:PRO:HD3	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1008:ARG:HH11	2:C:1028:GLY:HA2	1.82	0.43
3:D:601:ARG:NH1	3:D:606:ILE:HG12	2.33	0.43
6:G:20:DG:H2''	6:G:21:DG:C1'	2.48	0.43
2:C:724:ARG:NH2	2:C:734:LEU:O	2.51	0.43
3:D:606:ILE:O	3:D:613:ARG:N	2.47	0.43
3:D:1283:ILE:H	3:D:1283:ILE:HG13	1.71	0.43
5:F:93:LEU:HD21	5:F:193:ARG:HD2	2.00	0.43
2:C:496:ILE:HG12	2:C:531:PHE:HB2	2.00	0.43
3:D:1462:LEU:HD22	3:D:1472:ILE:HB	1.99	0.43
3:D:1488:ASP:OD1	3:D:1488:ASP:N	2.48	0.43
6:G:7:DT:H3	7:H:21:DA:H61	1.66	0.43
2:C:425:PHE:CE1	3:D:1086:LEU:HD12	2.53	0.43
3:D:90:MET:SD	3:D:521:PRO:HD3	2.58	0.43
7:H:18:DC:H2'	7:H:19:DG:C8	2.54	0.43
2:C:397:GLU:HB2	2:C:631:SER:HB2	2.00	0.43
3:D:25:GLU:HB2	3:D:92:HIS:CE1	2.54	0.43
3:D:1189:ARG:HB3	3:D:1204:CYS:HA	2.01	0.43
3:D:500:ARG:NH1	3:D:1388:ARG:O	2.48	0.43
5:F:364:ARG:HG3	5:F:390:PHE:CE2	2.53	0.43
2:C:143:SER:O	2:C:147:TYR:OH	2.27	0.42
2:C:1038:TRP:CE2	3:D:1099:VAL:HG11	2.54	0.42
3:D:684:LYS:O	3:D:687:VAL:HG22	2.19	0.42
6:G:20:DG:H2'	6:G:21:DG:N9	2.33	0.42
1:A:70:GLY:N	2:C:607:ASP:OD1	2.51	0.42
1:B:124:ASN:OD1	1:B:124:ASN:N	2.52	0.42
2:C:247:PRO:HA	2:C:248:PRO:HD3	1.74	0.42
3:D:244:GLU:HG3	3:D:310:LEU:HG	2.02	0.42
3:D:1347:TYR:CZ	3:D:1351:GLU:HG3	2.55	0.42
1:A:183:ASP:HA	2:C:938:LYS:HE3	2.01	0.42
3:D:12:LEU:HD23	3:D:12:LEU:HA	1.83	0.42
3:D:996:TRP:CD2	3:D:1056:PRO:HG3	2.55	0.42
2:C:716:LYS:HE3	3:D:37:LEU:HG	2.00	0.42
2:C:267:TYR:CE2	2:C:290:LEU:HG	2.54	0.42
2:C:1067:TYR:OH	3:D:674[B]:ARG:NH1	2.53	0.42
2:C:1090:LYS:HE2	2:C:1112:PHE:CZ	2.55	0.42
3:D:181:ASP:HB2	3:D:205:TYR:CD1	2.54	0.42
3:D:1305:LEU:HD13	3:D:1309:ALA:HB3	2.00	0.42
5:F:181:GLU:O	5:F:185:GLN:HG2	2.19	0.42
2:C:198:ARG:HE	2:C:227:PHE:HA	1.84	0.42
2:C:474:VAL:HG22	2:C:479:VAL:HG22	2.02	0.42
2:C:1102:LEU:HB2	3:D:7:LYS:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1018:ASN:HA	3:D:1019:PRO:HD3	1.83	0.42
3:D:1147:ARG:NH2	3:D:1369:GLU:OE1	2.53	0.42
2:C:215:GLY:C	2:C:216:GLU:HG2	2.45	0.42
1:A:58:ILE:HG21	1:A:68:ILE:HD11	2.01	0.42
5:F:79:ASP:HA	5:F:80:PRO:HD3	1.93	0.42
2:C:805:ARG:HG2	2:C:807[A]:ARG:HE	1.84	0.42
2:C:376:ARG:NH1	2:C:379:GLU:OE1	2.53	0.41
3:D:67:ARG:HB3	5:F:377:ASP:O	2.19	0.41
3:D:610:LYS:HA	3:D:615:ARG:HD3	2.02	0.41
3:D:106:LYS:NZ	3:D:587:ARG:HG3	2.34	0.41
2:C:1031:ARG:HB2	3:D:622:ARG:HG2	2.02	0.41
3:D:500:ARG:HA	3:D:503:LEU:HB2	2.02	0.41
3:D:767:HIS:CE1	4:E:6:ILE:HG12	2.56	0.41
2:C:374:ASN:OD1	5:F:276:ARG:HD2	2.20	0.41
1:A:196:THR:HG21	2:C:934:PHE:CE2	2.53	0.41
2:C:258:TYR:O	2:C:263:ASP:N	2.53	0.41
2:C:971:LYS:HB3	2:C:986:PRO:HB2	2.02	0.41
3:D:613:ARG:NH1	3:D:617:ASN:OD1	2.53	0.41
3:D:1491:THR:O	3:D:1495:ILE:HG13	2.21	0.41
6:G:15:DT:C4	6:G:16:DC:N4	2.88	0.41
1:A:155:LYS:HA	1:A:155:LYS:HD2	1.86	0.41
3:D:1218:GLY:O	3:D:1475:GLY:N	2.43	0.41
2:C:598:GLU:O	2:C:651:LYS:NZ	2.43	0.41
3:D:475:LYS:O	3:D:479:GLU:HG2	2.20	0.41
3:D:1084:THR:O	3:D:1088:THR:HG23	2.21	0.41
1:B:73:GLU:HB3	1:B:77:GLU:HB3	2.02	0.41
1:B:185:ARG:NH2	3:D:692:GLU:HG3	2.35	0.41
5:F:88:ILE:HG23	5:F:193:ARG:HG2	2.03	0.41
1:A:44:LEU:HB3	1:A:177:VAL:HG21	2.03	0.41
1:A:224:TYR:HB3	1:B:9:PRO:HG2	2.03	0.41
1:B:94:LEU:HD11	1:B:97:VAL:HG22	2.02	0.41
1:B:110:LYS:HD3	1:B:128:HIS:HA	2.03	0.41
2:C:230:ARG:HG3	2:C:233:GLU:HG3	2.03	0.41
2:C:762:LYS:HE3	2:C:785:VAL:O	2.20	0.41
2:C:793:PRO:HA	2:C:794:PRO:HD3	1.96	0.41
2:C:1008:ARG:NH1	2:C:1028:GLY:HA2	2.36	0.41
3:D:1208:ASP:OD1	3:D:1210:SER:OG	2.34	0.41
2:C:124:ASP:OD2	2:C:407:LYS:NZ	2.41	0.41
3:D:838:ARG:HD3	3:D:874:GLU:CD	2.45	0.41
3:D:1285:GLU:HG3	3:D:1290:LEU:HG	2.03	0.41
5:F:163:LEU:HD13	5:F:174:LEU:HD13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:LYS:HE3	1:A:102:LYS:HB2	1.91	0.40
2:C:905:ILE:C	2:C:907:ASP:H	2.29	0.40
1:A:39:PRO:HG3	1:B:39:PRO:HG3	2.03	0.40
2:C:35:PRO:HA	2:C:36:PRO:HD3	1.86	0.40
2:C:396:ASP:HA	2:C:633:GLN:NE2	2.36	0.40
2:C:413:LEU:HD21	2:C:451:LEU:HD13	2.02	0.40
3:D:809:PRO:HB3	3:D:839:LEU:HD13	2.02	0.40
3:D:1232:PRO:HG3	3:D:1361:VAL:HG11	2.03	0.40
5:F:188:ILE:HG12	5:F:224:VAL:HG21	2.04	0.40
2:C:353:ARG:NH2	5:F:203:THR:OG1	2.55	0.40
2:C:936:VAL:HG11	2:C:959:PRO:HB2	2.02	0.40
3:D:251:PHE:HE2	3:D:304:LEU:HD12	1.86	0.40
4:E:3:GLU:HA	4:E:4:PRO:HD3	1.97	0.40
2:C:886:LEU:HD23	2:C:886:LEU:HA	1.92	0.40
2:C:274:ARG:NH2	2:C:285:LEU:O	2.54	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	230/315 (73%)	225 (98%)	5 (2%)	0	100	100
1	B	221/315 (70%)	215 (97%)	6 (3%)	0	100	100
2	C	1111/1119 (99%)	1082 (97%)	29 (3%)	0	100	100
3	D	1485/1524 (97%)	1449 (98%)	36 (2%)	0	100	100
4	E	92/99 (93%)	91 (99%)	1 (1%)	0	100	100
5	F	333/443 (75%)	330 (99%)	3 (1%)	0	100	100
All	All	3472/3815 (91%)	3392 (98%)	80 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	201/273 (74%)	200 (100%)	1 (0%)	81	80
1	B	195/273 (71%)	193 (99%)	2 (1%)	68	75
2	C	938/941 (100%)	917 (98%)	21 (2%)	45	65
3	D	1255/1279 (98%)	1235 (98%)	20 (2%)	55	70
4	E	83/88 (94%)	81 (98%)	2 (2%)	43	64
5	F	293/388 (76%)	288 (98%)	5 (2%)	53	69
All	All	2965/3242 (92%)	2914 (98%)	51 (2%)	53	69

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	B	10	VAL
1	B	154	GLU
2	C	27	ARG
2	C	177	GLU
2	C	182	VAL
2	C	200	LEU
2	C	217	LEU
2	C	261	ILE
2	C	276	LYS
2	C	284	ARG
2	C	299	LYS
2	C	384	GLU
2	C	390	GLN
2	C	419	THR
2	C	427	VAL
2	C	513	VAL
2	C	583	LEU
2	C	595	LEU
2	C	670	GLN
2	C	765	SER
2	C	807[A]	ARG

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Mol	Chain	Res	Type
2	C	807[B]	ARG
2	C	1051	GLU
3	D	71	LYS
3	D	270	LEU
3	D	354	VAL
3	D	427	VAL
3	D	632	VAL
3	D	633	VAL
3	D	666	ILE
3	D	754	PHE
3	D	781	PRO
3	D	785	ILE
3	D	789	LEU
3	D	810	GLU
3	D	894	LYS
3	D	907	GLU
3	D	986	ARG
3	D	1067	VAL
3	D	1129	THR
3	D	1184	GLN
3	D	1252	ILE
3	D	1295	GLU
4	E	49	GLN
4	E	50	THR
5	F	88	ILE
5	F	295	MET
5	F	331	ASP
5	F	369	LEU
5	F	380	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	188	GLN
2	C	99	GLN
2	C	117	HIS
2	C	187	ASN
2	C	390	GLN
2	C	498	GLN
2	C	538	GLN
2	C	834	GLN
2	C	860	HIS

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Mol	Chain	Res	Type
2	C	991	GLN
3	D	442	ASN
3	D	709	HIS
3	D	714	GLN
3	D	724	GLN
3	D	976	GLN
3	D	994	GLN
3	D	1014	ASN
3	D	1025	GLN
3	D	1037	GLN
3	D	1124	GLN
3	D	1184	GLN
5	F	86	HIS
5	F	218	GLN
5	F	280	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	I	4/6 (66%)	1 (25%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	I	7	A

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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, 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	231/315 (73%)	-0.50	0 100 100	86, 128, 153, 181	1 (0%)
1	B	223/315 (70%)	-0.55	2 (0%) 81 58	89, 124, 155, 169	0
2	C	1112/1119 (99%)	-0.47	4 (0%) 88 73	66, 122, 175, 217	3 (0%)
3	D	1486/1524 (97%)	-0.51	1 (0%) 92 87	72, 118, 178, 205	4 (0%)
4	E	94/99 (94%)	-0.49	0 100 100	89, 128, 169, 184	0
5	F	337/443 (76%)	-0.39	0 100 100	95, 140, 219, 231	0
6	G	18/21 (85%)	-0.53	0 100 100	87, 119, 213, 213	0
7	H	24/27 (88%)	-0.57	0 100 100	117, 137, 195, 221	0
8	I	5/6 (83%)	-1.39	0 100 100	92, 92, 94, 110	0
All	All	3530/3869 (91%)	-0.49	7 (0%) 91 82	66, 124, 182, 231	8 (0%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	228	PRO	2.9
2	C	64	LEU	2.7
2	C	102[A]	HIS	2.5
3	D	1053[A]	PHE	2.4
2	C	191	PHE	2.3
1	B	91	ASN	2.1
2	C	998	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	MG	B	2001	1/1	0.62	0.16	132,132,132,132	0
9	MG	D	2004	1/1	0.95	0.16	67,67,67,67	0
9	MG	F	2001	1/1	0.95	0.03	137,137,137,137	0
9	MG	D	2003	1/1	0.99	0.03	84,84,84,84	0
10	ZN	D	2002	1/1	0.99	0.06	169,169,169,169	0
10	ZN	D	2001	1/1	1.00	0.06	105,105,105,105	0

6.5 Other polymers [i](#)

There are no such residues in this entry.