



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 27, 2022 – 10:05 AM EST

PDB ID : 7MLJ
Title : Crystal structure of Thermus thermophilus reiterative transcription complex with 4nt oligo-G RNA
Authors : Liu, Y.; Ebright, R.H.
Deposited on : 2021-04-28
Resolution : 3.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.26
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)	:	2.26

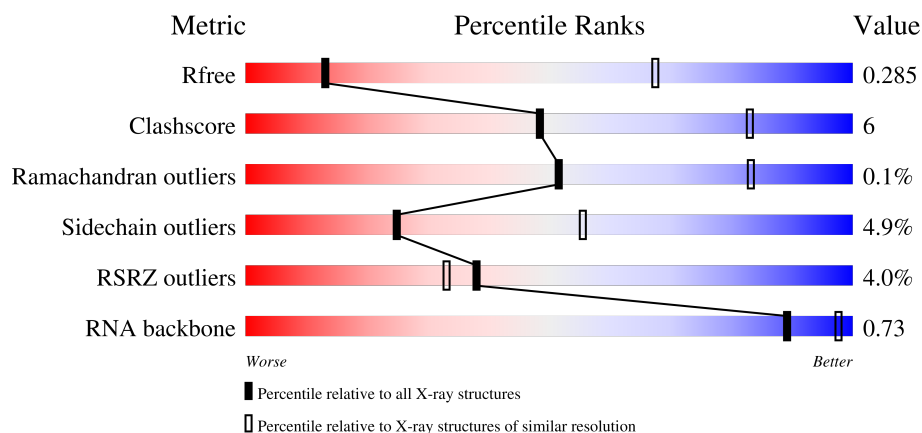
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.75 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	1039 (3.94-3.58)
Clashscore	141614	1051 (3.92-3.60)
Ramachandran outliers	138981	1015 (3.92-3.60)
Sidechain outliers	138945	1011 (3.92-3.60)
RSRZ outliers	127900	1050 (3.96-3.56)
RNA backbone	3102	1035 (4.52-3.00)

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	<div> <div>2%</div> <div>59% 13% 28%</div> </div>
1	B	315	<div> <div>57% 12% 30%</div> </div>
2	C	1119	<div> <div>4%</div> <div>81% 17% ..</div> </div>
3	D	1524	<div> <div>5%</div> <div>78% 18% ..</div> </div>

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Mol	Chain	Length	Quality of chain
4	E	99	 80% 15% 5%
5	F	443	 5% 64% 14% 22%
6	G	20	 5% 15% 60% 25%
7	I	4	 50% 50%
8	H	27	 41% 44% 15%

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
9	MG	B	2002	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 28489 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	226	Total	C	N	O	S	0	0	0
			1782	1138	310	332	2			
1	B	222	Total	C	N	O	S	0	0	0
			1750	1118	304	326	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1111	Total	C	N	O	S	0	0	0
			8770	5548	1564	1634	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	0	0
			11738	7441	2067	2195	35			

- 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	346	Total	C	N	O	S	0	0	0
			2807	1770	509	524	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(P*CP*AP*TP*CP*CP*GP*TP*GP*CP*CP*CP*TP*GP*AP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	15	Total	C	N	O	P	0	0	0
			304	144	54	91	15			

- Molecule 7 is a RNA chain called RNA (5'-R(P*GP*GP*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	I	4	Total	C	N	O	P	0	0	0
			92	40	20	28	4			

- Molecule 8 is a DNA chain called DNA (5'-D(*TP*AP*TP*AP*AP*TP*GP*GP*GP*AP*GP*CP*TP*GP*GP*CP*AP*CP*GP*GP*AP*TP*G)-3').

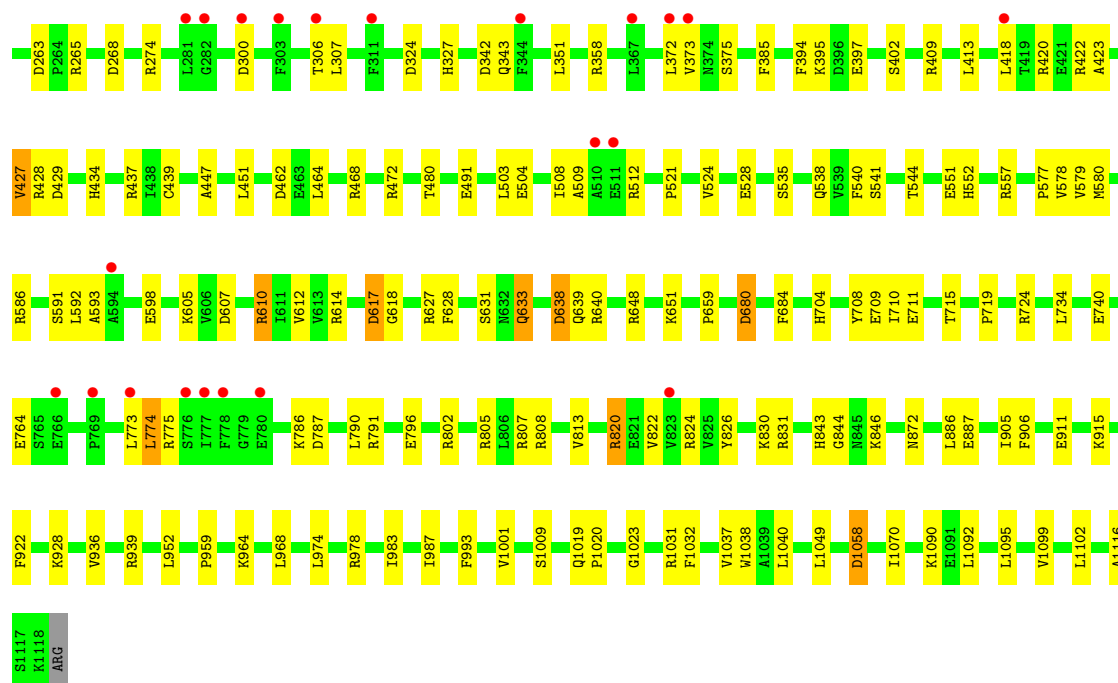
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	23	Total	C	N	O	P	0	0	0
			478	227	94	135	22			

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

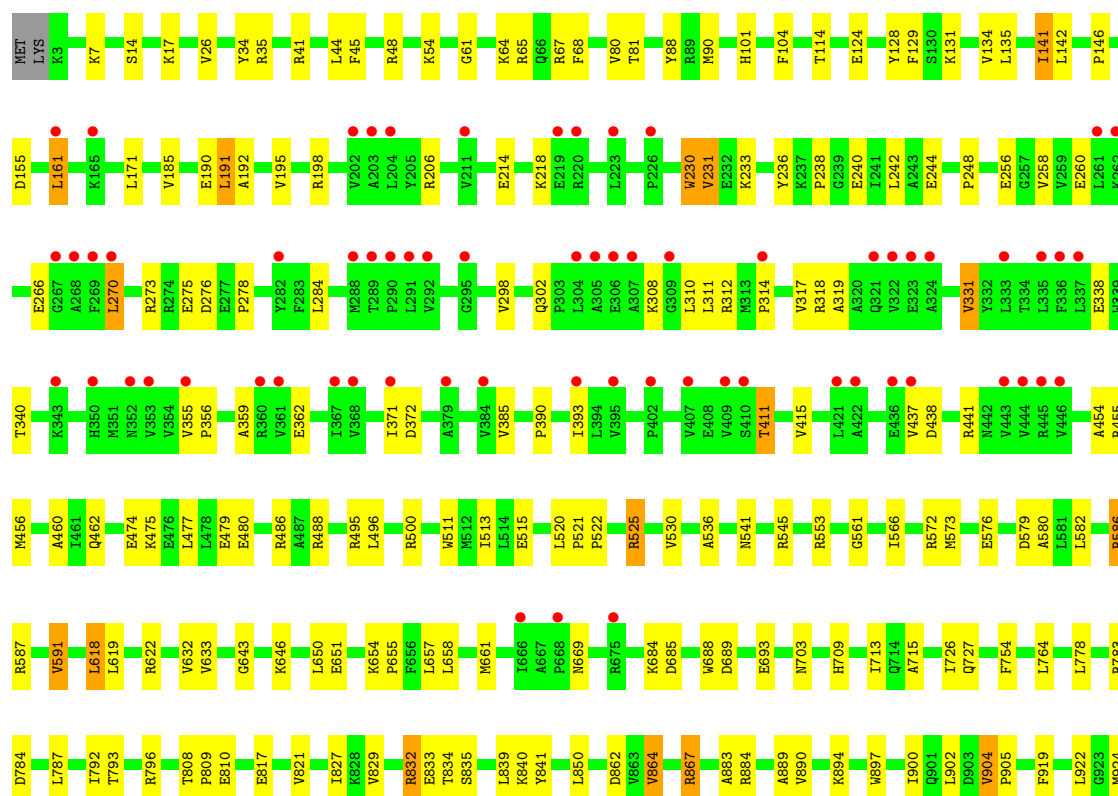
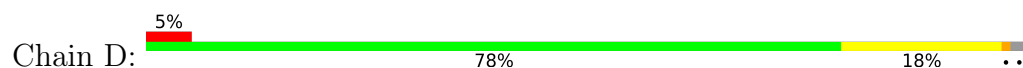
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	2	Total 2	Mg 2	0	0
9	D	2	Total 2	Mg 2	0	0
9	F	1	Total 1	Mg 1	0	0

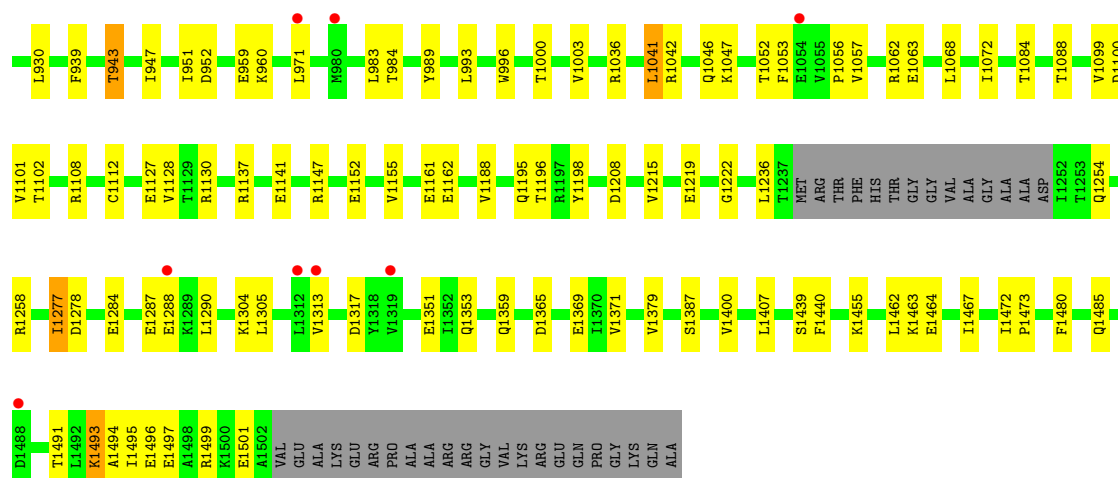
- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

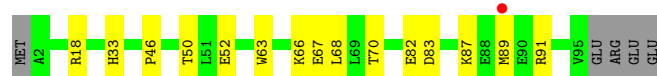
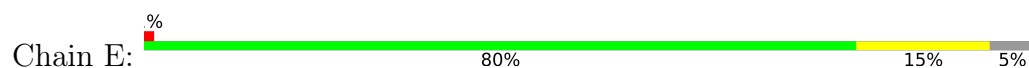


• Molecule 3: DNA-directed RNA polymerase subunit beta'

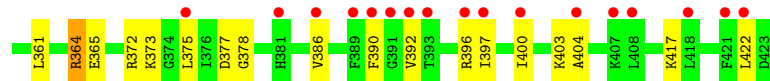
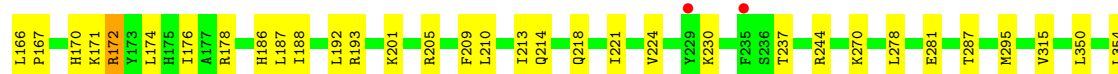
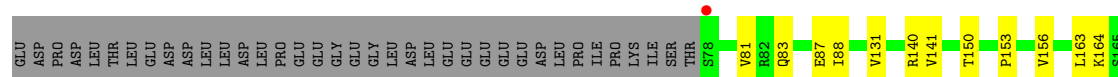
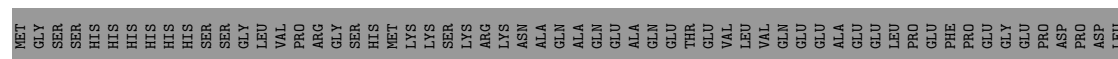




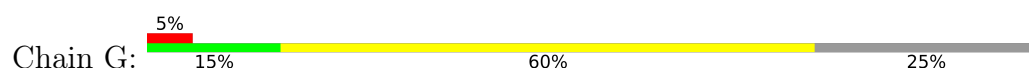
- Molecule 4: DNA-directed RNA polymerase subunit omega



- Molecule 5: RNA polymerase sigma factor SigA



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

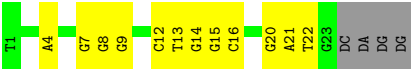


- Molecule 7: RNA (5'-R(P*GP*GP*GP*G)-3')





● Molecule 8: DNA (5'-D(*TP*AP*TP*AP*AP*TP*GP*GP*GP*AP*GP*CP*TP*GP*GP*CP*AP*CP*GP*GP*AP*TP*G)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	186.31Å 104.66Å 298.41Å 90.00° 98.12° 90.00°	Depositor
Resolution (Å)	46.21 – 3.75 49.32 – 3.75	Depositor EDS
% Data completeness (in resolution range)	97.1 (46.21-3.75) 97.5 (49.32-3.75)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 3.77Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.265 , 0.283 0.265 , 0.285	Depositor DCC
R_{free} test set	2009 reflections (3.51%)	wwPDB-VP
Wilson B-factor (Å ²)	106.3	Xtriage
Anisotropy	0.807	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 80.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	28489	wwPDB-VP
Average B, all atoms (Å ²)	152.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% 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, 0.333 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: 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	0.25	0/1814	0.51	0/2466
1	B	0.25	0/1782	0.52	0/2424
2	C	0.25	0/8937	0.52	0/12087
3	D	0.25	0/11944	0.50	0/16149
4	E	0.24	0/775	0.47	0/1045
5	F	0.24	0/2852	0.49	0/3837
6	G	0.58	0/339	0.93	0/520
7	I	0.36	0/103	1.04	0/160
8	H	0.53	0/538	0.90	0/831
All	All	0.26	0/29084	0.53	0/39519

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

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	1782	0	1834	23	0
1	B	1750	0	1797	24	0
2	C	8770	0	8874	113	0
3	D	11738	0	11971	154	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	761	0	778	12	0
5	F	2807	0	2882	40	0
6	G	304	0	169	9	0
7	I	92	0	44	2	0
8	H	478	0	260	18	0
9	B	2	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
All	All	28489	0	28609	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.

The worst 5 of 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:1491:THR:HG21	4:E:89:MET:HG2	1.63	0.79
2:C:773:LEU:HB2	5:F:375:LEU:HD11	1.67	0.77
1:B:206:THR:HG22	1:B:209:GLU:H	1.52	0.74
2:C:462:ASP:HB3	2:C:468:ARG:HD2	1.69	0.74
2:C:422:ARG:HA	8:H:16:DC:H5'	1.68	0.74

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	224/315 (71%)	219 (98%)	5 (2%)	0	100	100
1	B	220/315 (70%)	215 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	1107/1119 (99%)	1082 (98%)	23 (2%)	2 (0%)	47	78
3	D	1482/1524 (97%)	1449 (98%)	31 (2%)	2 (0%)	51	83
4	E	92/99 (93%)	91 (99%)	1 (1%)	0	100	100
5	F	344/443 (78%)	338 (98%)	6 (2%)	0	100	100
All	All	3469/3815 (91%)	3394 (98%)	71 (2%)	4 (0%)	51	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	592	LEU
3	D	1440	PHE
2	C	215	GLY
3	D	530	VAL

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	199/273 (73%)	192 (96%)	7 (4%)	36	63
1	B	195/273 (71%)	190 (97%)	5 (3%)	46	70
2	C	936/941 (100%)	885 (95%)	51 (5%)	22	54
3	D	1253/1279 (98%)	1185 (95%)	68 (5%)	22	54
4	E	83/88 (94%)	82 (99%)	1 (1%)	71	84
5	F	301/388 (78%)	289 (96%)	12 (4%)	31	60
All	All	2967/3242 (92%)	2823 (95%)	144 (5%)	25	55

5 of 144 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	1188	VAL
5	F	422	LEU
3	D	1284	GLU

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Mol	Chain	Res	Type
3	D	1501	GLU
2	C	774	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	350	HIS
3	D	1172	HIS
3	D	1195	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	I	3/4 (75%)	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 7 ligands modelled in this entry, 7 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	226/315 (71%)	-0.07	5 (2%) 62 56	113, 141, 165, 179	0
1	B	222/315 (70%)	-0.18	0 100 100	105, 148, 179, 195	0
2	C	1111/1119 (99%)	0.23	40 (3%) 42 37	83, 151, 200, 219	0
3	D	1486/1524 (97%)	0.26	74 (4%) 28 26	90, 142, 197, 245	1 (0%)
4	E	94/99 (94%)	-0.04	1 (1%) 80 77	123, 166, 198, 211	0
5	F	346/443 (78%)	0.26	20 (5%) 23 19	112, 160, 213, 223	0
6	G	15/20 (75%)	-0.27	1 (6%) 17 14	130, 168, 224, 224	0
7	I	4/4 (100%)	1.32	0 100 100	155, 174, 199, 203	0
8	H	23/27 (85%)	0.10	0 100 100	168, 198, 281, 298	0
All	All	3527/3866 (91%)	0.19	141 (3%) 38 33	83, 149, 201, 298	1 (0%)

The worst 5 of 141 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	367	ILE	7.7
3	D	289	THR	6.9
3	D	305	ALA	6.8
3	D	322	VAL	6.5
3	D	355	VAL	6.5

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, 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(\AA^2)	Q<0.9
9	MG	B	2002	1/1	0.74	0.48	92,92,92,92	0
9	MG	B	2001	1/1	0.83	0.38	139,139,139,139	0
10	ZN	D	2002	1/1	0.90	0.06	197,197,197,197	0
9	MG	F	2001	1/1	0.91	0.08	147,147,147,147	0
9	MG	D	2004	1/1	0.91	0.27	149,149,149,149	0
10	ZN	D	2001	1/1	0.95	0.22	123,123,123,123	0
9	MG	D	2003	1/1	0.98	0.40	98,98,98,98	0

6.5 Other polymers [i](#)

There are no such residues in this entry.