



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 04:07 PM UTC

PDB ID : 6N60 / pdb_00006n60
Title : Escherichia coli RNA polymerase sigma70-holoenzyme bound to upstream fork promoter DNA and Microcin J25 (MccJ25)
Authors : Braffman, N.; Hauver, J.; Campbell, E.A.; Darst, S.A.
Deposited on : 2018-11-23
Resolution : 3.68 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 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
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

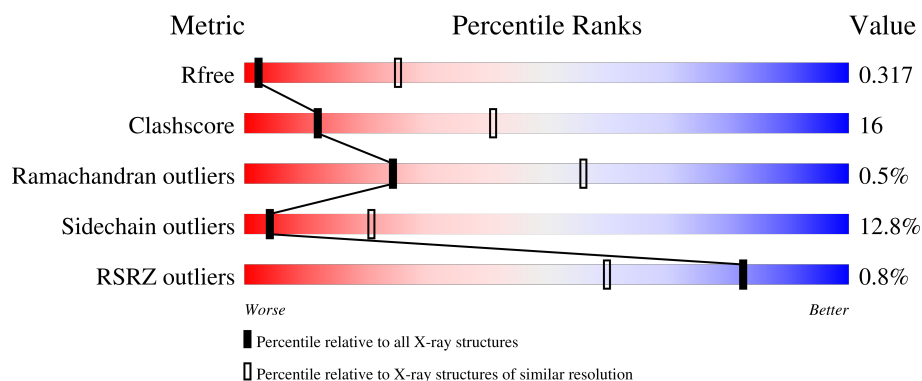
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.68 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	1263 (3.80-3.56)
Clashscore	190562	1305 (3.80-3.56)
Ramachandran outliers	187476	1259 (3.80-3.56)
Sidechain outliers	187428	1256 (3.80-3.56)
RSRZ outliers	180081	1262 (3.80-3.56)

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	239	2% 65% 29% • •
1	B	239	% 50% 35% 6% 9%
2	C	1342	% 60% 33% 6% •
3	D	1409	% 54% 29% 5% 12%
4	E	91	54% 26% 7% 13%

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Mol	Chain	Length	Quality of chain
5	F	612	 34% 15% • 48%
6	M	21	 24% 62% 10% 5%
7	N	29	 59% 41%
8	T	24	 4% 50% 50%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 27705 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	0	0
			1759	1094	312	347	6			
1	B	218	Total	C	N	O	S	0	0	0
			1638	1023	284	325	6			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	GLU	-	expression tag	UNP P0A7Z4
A	236	VAL	-	expression tag	UNP P0A7Z4
A	237	LEU	-	expression tag	UNP P0A7Z4
A	238	PHE	-	expression tag	UNP P0A7Z4
A	239	GLN	-	expression tag	UNP P0A7Z4
B	235	GLU	-	expression tag	UNP P0A7Z4
B	236	VAL	-	expression tag	UNP P0A7Z4
B	237	LEU	-	expression tag	UNP P0A7Z4
B	238	PHE	-	expression tag	UNP P0A7Z4
B	239	GLN	-	expression tag	UNP P0A7Z4

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1335	Total	C	N	O	S	0	0	0
			10470	6569	1822	2036	43			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1236	Total	C	N	O	S	0	0	0
			9578	6015	1711	1806	46			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	VAL	-	expression tag	UNP P0A8T7
D	1408	LEU	-	expression tag	UNP P0A8T7
D	1409	GLU	-	expression tag	UNP P0A8T7

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	79	Total	C	N	O	S	0	0	0
			627	382	118	126	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	318	Total	C	N	O	S	0	0	0
			2399	1499	442	446	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	149	ASN	ASP	conflict	UNP Q0P6L9
F	?	-	LEU	deletion	UNP Q0P6L9

- Molecule 6 is a protein called Microcin J25.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	M	21	Total	C	N	O	0	0	0
			144	95	23	26			

- Molecule 7 is a DNA chain called non-template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	N	29	Total	C	N	O	P	0	0	0
			595	284	106	176	29			

- Molecule 8 is a DNA chain called template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	T	24	Total	C	N	O	P	0	0	0
			492	233	94	141	24			

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

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

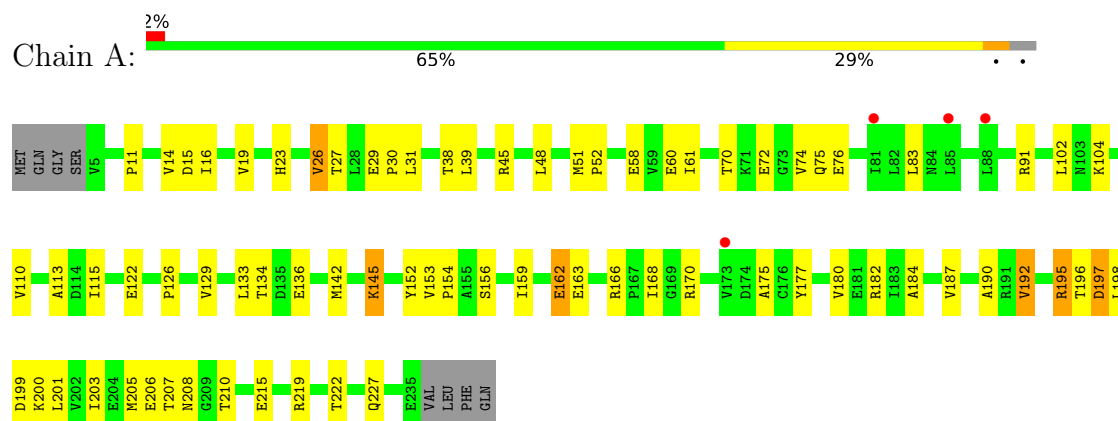
- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

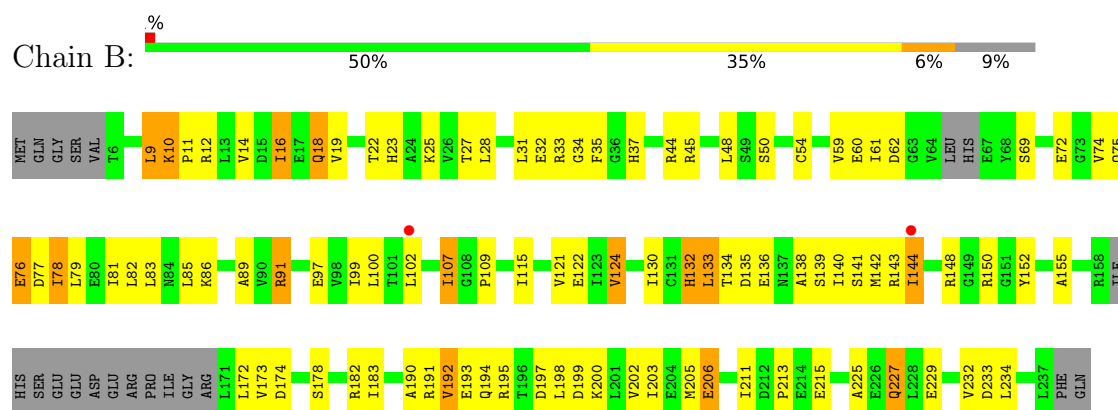
3 Residue-property plots

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.

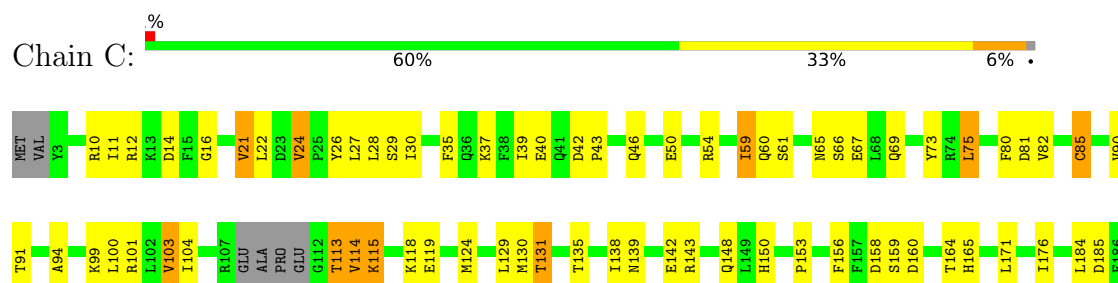
• Molecule 1: DNA-directed RNA polymerase subunit alpha

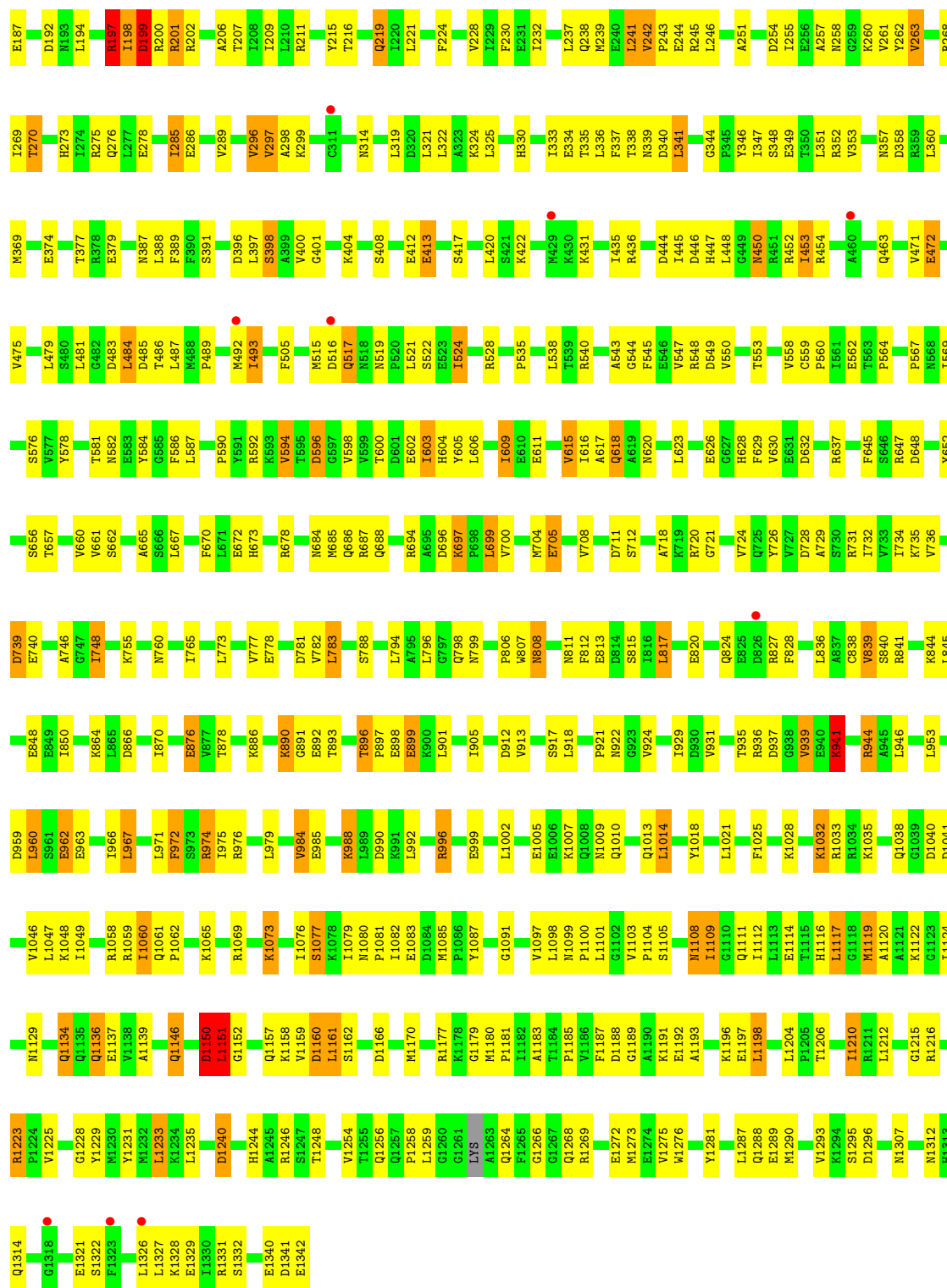


• Molecule 1: DNA-directed RNA polymerase subunit alpha

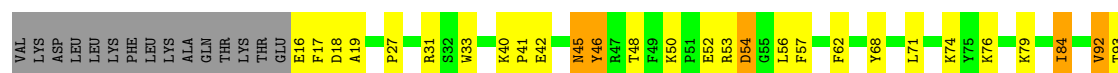


• Molecule 2: DNA-directed RNA polymerase subunit beta

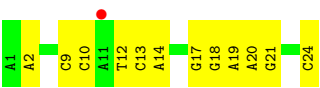




● Molecule 3: DNA-directed RNA polymerase subunit beta'







4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	172.91Å 172.91Å 387.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.55 – 3.68 49.55 – 3.68	Depositor EDS
% Data completeness (in resolution range)	98.3 (49.55-3.68) 98.3 (49.55-3.68)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.10 (at 3.67Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.263 , 0.306 0.275 , 0.317	Depositor DCC
R_{free} test set	1971 reflections (3.05%)	wwPDB-VP
Wilson B-factor (Å ²)	175.9	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 122.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	27705	wwPDB-VP
Average B, all atoms (Å ²)	182.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.63% 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

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	0.14	0/1780	0.41	0/2415
1	B	0.17	0/1655	0.46	2/2247 (0.1%)
2	C	0.18	0/10634	0.42	2/14353 (0.0%)
3	D	0.15	0/9724	0.41	0/13134
4	E	0.12	0/629	0.35	0/847
5	F	0.17	0/2428	0.51	4/3280 (0.1%)
6	M	0.43	0/149	0.98	2/202 (1.0%)
7	N	0.28	0/666	0.44	0/1026
8	T	0.25	0/552	0.41	0/849
All	All	0.17	0/28217	0.43	10/38353 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
2	C	0	5
3	D	0	3
5	F	0	1
6	M	0	1
All	All	0	11

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	517	GLN	N-CA-C	10.33	125.04	110.68
5	F	583	THR	CA-C-N	7.20	135.30	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	583	THR	C-N-CA	7.20	135.30	121.54
1	B	9	LEU	CA-C-N	5.65	131.87	121.70
1	B	9	LEU	C-N-CA	5.65	131.87	121.70

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	14	VAL	Peptide
2	C	197	ARG	Peptide
2	C	198	ILE	Peptide
2	C	939	VAL	Peptide
2	C	941	LYS	Peptide

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	1759	0	1759	48	0
1	B	1638	0	1629	73	0
2	C	10470	0	10445	347	0
3	D	9578	0	9710	340	0
4	E	627	0	634	21	0
5	F	2399	0	2324	77	0
6	M	144	0	131	16	0
7	N	595	0	329	14	0
8	T	492	0	269	10	0
9	D	1	0	0	0	0
10	D	2	0	0	0	0
All	All	27705	0	27230	853	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 16.

The worst 5 of 853 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:1006:GLY:N	3:D:1009:GLU:OE2	1.92	1.01
5:F:414:LYS:HB2	5:F:434:TRP:HE1	1.30	0.94
5:F:600:HIS:HE2	5:F:602:SER:HG	1.05	0.94
3:D:208:THR:O	3:D:214:ARG:NH1	2.01	0.92
1:B:76:GLU:OE2	1:B:132:HIS:ND1	2.05	0.88

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	229/239 (96%)	204 (89%)	23 (10%)	2 (1%)	14	45
1	B	212/239 (89%)	189 (89%)	23 (11%)	0	100	100
2	C	1329/1342 (99%)	1243 (94%)	77 (6%)	9 (1%)	18	50
3	D	1230/1409 (87%)	1166 (95%)	62 (5%)	2 (0%)	43	71
4	E	77/91 (85%)	73 (95%)	3 (4%)	1 (1%)	9	38
5	F	312/612 (51%)	293 (94%)	18 (6%)	1 (0%)	36	65
6	M	19/21 (90%)	13 (68%)	4 (21%)	2 (10%)	0	5
All	All	3408/3953 (86%)	3181 (93%)	210 (6%)	17 (0%)	24	56

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	199	ASP
2	C	200	ARG
2	C	1151	LEU
1	A	177	TYR
2	C	340	ASP

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	190/206 (92%)	174 (92%)	16 (8%)	10	34
1	B	176/206 (85%)	150 (85%)	26 (15%)	3	16
2	C	1138/1157 (98%)	983 (86%)	155 (14%)	3	19
3	D	1022/1170 (87%)	896 (88%)	126 (12%)	4	21
4	E	67/75 (89%)	59 (88%)	8 (12%)	5	23
5	F	232/539 (43%)	202 (87%)	30 (13%)	4	20
6	M	13/14 (93%)	10 (77%)	3 (23%)	1	6
All	All	2838/3367 (84%)	2474 (87%)	364 (13%)	4	21

5 of 364 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	416	ILE
3	D	972	LYS
3	D	518	VAL
3	D	746	LEU
3	D	1209	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	1288	GLN
3	D	435	GLN
3	D	1268	ASN
2	C	1313	HIS
3	D	200	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 3 ligands modelled in this entry, 3 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	231/239 (96%)	-0.30	4 (1%) 69 43	138, 193, 227, 277	0
1	B	218/239 (91%)	-0.45	2 (0%) 81 57	133, 191, 230, 261	0
2	C	1335/1342 (99%)	-0.42	9 (0%) 84 63	93, 170, 229, 271	0
3	D	1236/1409 (87%)	-0.43	10 (0%) 82 60	99, 176, 247, 304	0
4	E	79/91 (86%)	-0.61	0 100 100	144, 183, 238, 268	0
5	F	318/612 (51%)	-0.49	1 (0%) 90 76	128, 190, 250, 265	0
6	M	21/21 (100%)	-0.49	0 100 100	151, 194, 226, 256	0
7	N	29/29 (100%)	-0.41	0 100 100	139, 222, 253, 255	0
8	T	24/24 (100%)	-0.32	1 (4%) 40 25	125, 223, 249, 259	0
All	All	3491/4006 (87%)	-0.43	27 (0%) 82 60	93, 179, 240, 304	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	85	LEU	3.2
2	C	516	ASP	3.1
2	C	826	ASP	2.7
3	D	675	ALA	2.7
3	D	1320	ILE	2.6

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	D	1501	1/1	0.97	0.06	83,83,83,83	0
10	ZN	D	1502	1/1	1.00	0.02	162,162,162,162	0
10	ZN	D	1503	1/1	1.00	0.04	185,185,185,185	0

6.5 Other polymers [i](#)

There are no such residues in this entry.