



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:35 PM UTC

PDB ID : 5UAJ / pdb_00005uaj
Title : Escherichia coli RNA polymerase RpoB S531L mutant
Authors : Molodtsov, V.; Scharf, N.T.; Stefan, M.A.; Garcia, G.A.; Murakami, K.S.
Deposited on : 2016-12-19
Resolution : 3.92 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

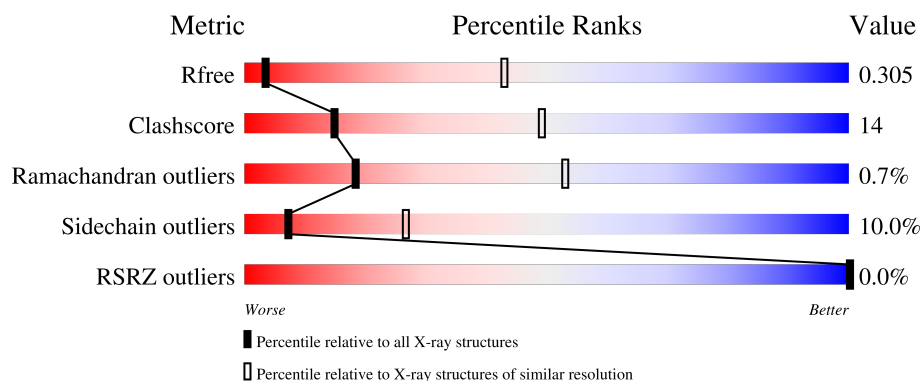
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.92 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	1033 (4.10-3.74)
Clashscore	190562	1070 (4.10-3.74)
Ramachandran outliers	187476	1017 (4.10-3.74)
Sidechain outliers	187428	1010 (4.10-3.74)
RSRZ outliers	180081	1033 (4.10-3.74)

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	329	
1	B	329	
1	G	329	
1	H	329	
2	C	1342	

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Mol	Chain	Length	Quality of chain
2	I	1342	
3	D	1407	
3	J	1407	
4	E	91	
4	K	91	
5	F	613	
5	L	613	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 54994 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	227	Total	C	N	O	S	0	0	0
			1753	1091	311	345	6			
1	B	214	Total	C	N	O	S	0	0	0
			1649	1029	290	324	6			
1	G	224	Total	C	N	O	S	0	0	0
			1730	1076	308	340	6			
1	H	215	Total	C	N	O	S	0	0	0
			1659	1037	291	325	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1342	Total	C	N	O	S	0	0	0
			10587	6644	1843	2056	44			
2	I	1340	Total	C	N	O	S	0	0	0
			10568	6632	1840	2053	43			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	531	LEU	SER	engineered mutation	UNP P0A8V2
I	531	LEU	SER	engineered mutation	UNP P0A8V2

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1166	Total	C	N	O	S	0	0	0
			9089	5714	1627	1702	46			
3	J	1155	Total	C	N	O	S	0	0	0
			9001	5659	1612	1684	46			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	89	Total	C	N	O	S	0	0	0
			691	421	129	140	1			
4	K	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	468	Total	C	N	O	S	0	0	0
			3813	2389	678	723	23			
5	L	469	Total	C	N	O	S	0	0	0
			3821	2393	679	726	23			

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	1	Total	Mg	0	0
			1	1		
6	J	1	Total	Mg	0	0
			1	1		

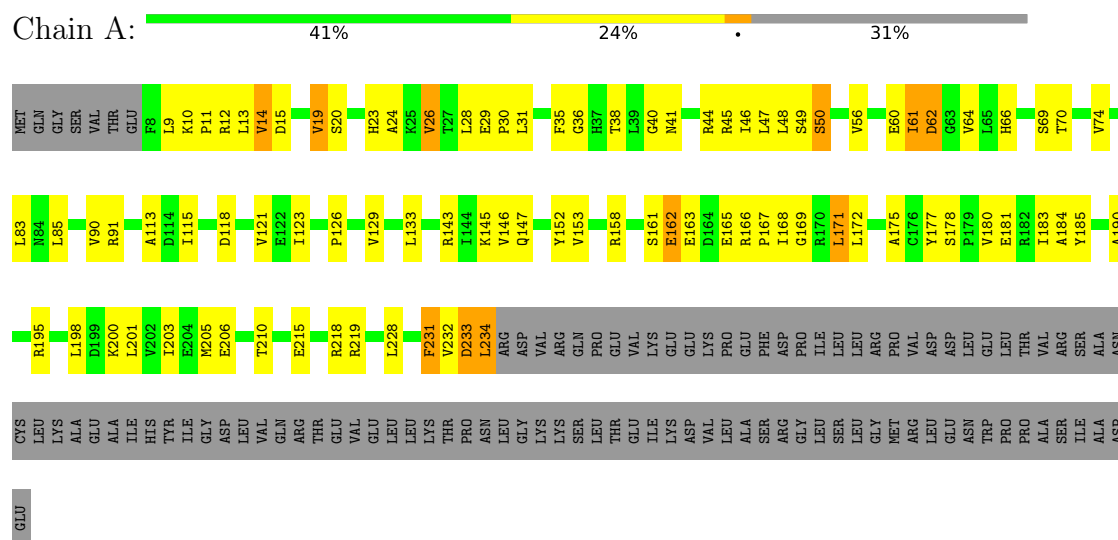
- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	2	Total	Zn	0	0
			2	2		
7	J	2	Total	Zn	0	0
			2	2		

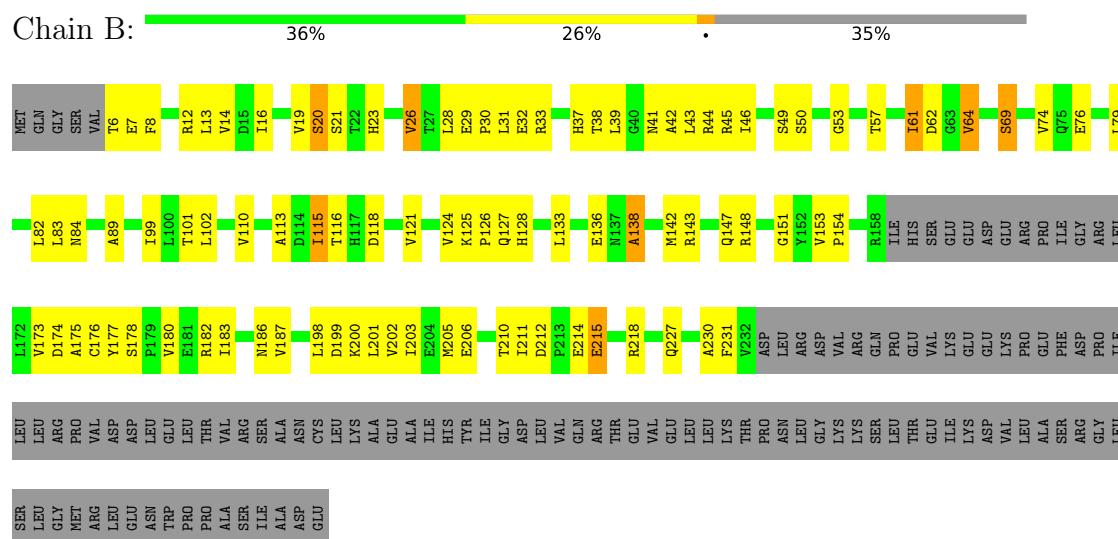
3 Residue-property plots

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

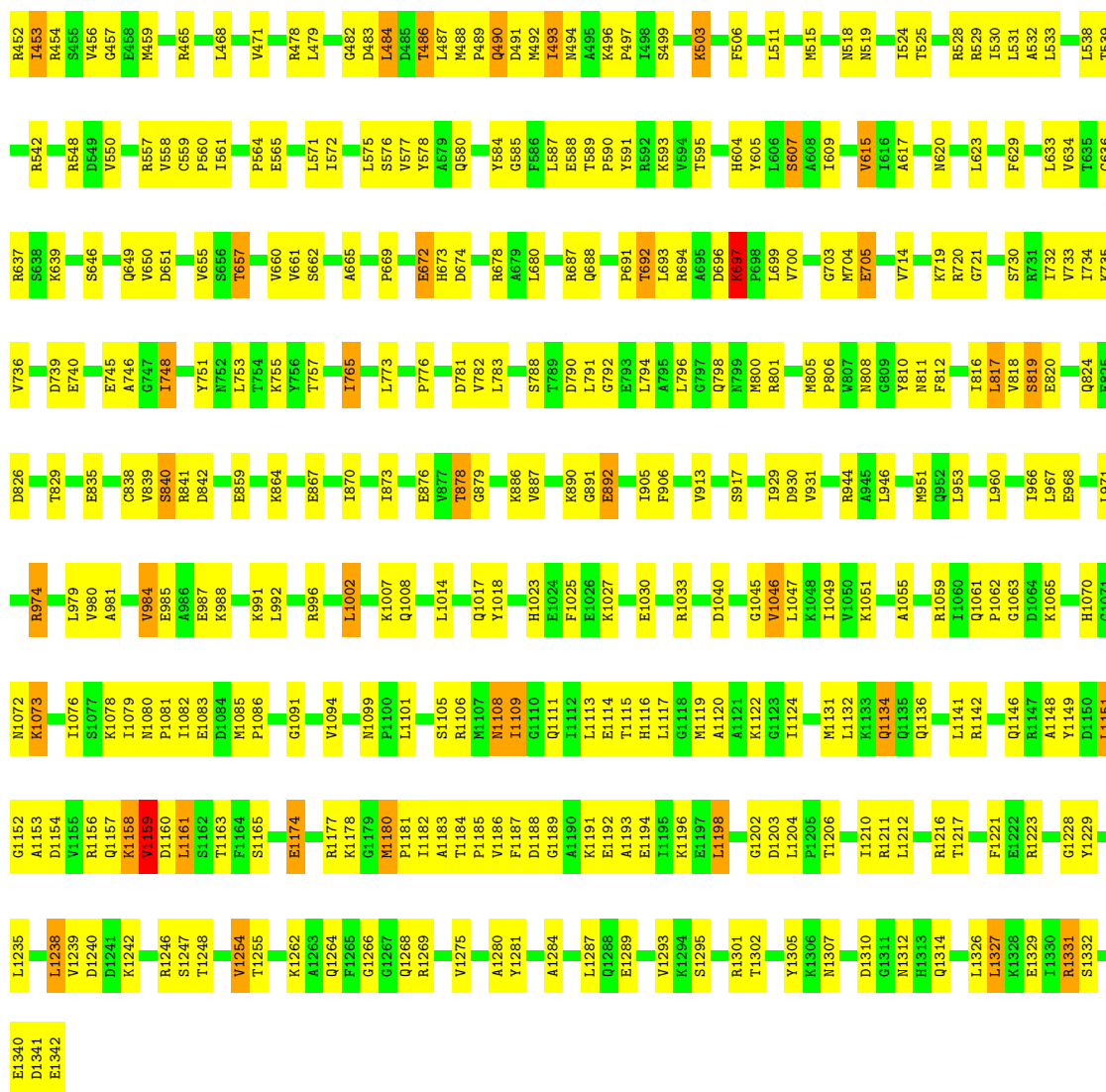


• Molecule 1: DNA-directed RNA polymerase subunit alpha

ILE	GLN	ASP	GLY	ASP	ILE	E215	L83	MET
ASP	LEU	GLY	GLN	GLY	R218	R91	V90	GLN
VAL	VAL	R219	THR	THR	T222	T223	A113	THR
GLN	ARG	T224	GLU	GLU	A225	L228	D114	FLU
ARG	THR	L228	VAL	LEU	LEU	LEU	I107	GLU
LEU	LEU	F231	LEU	LEU	VAL	VAL	A113	L9
THR	THR	ASP	ASP	ASN	ASP	ASP	D115	P11
PRO	PRO	LEU	LEU	LEU	ARG	ARG	V121	R12
ASN	LEU	LEU	GLY	GLY	ASP	ASP	P126	D15
LEU	LEU	LEU	LYS	LYS	VAL	VAL	V129	V19
LYS	LYS	ARG	ARG	GLN	GLN	GLN	L133	S20
SER	LEU	PRO	PRO	LEU	PRO	PRO	E136	H23
LEU	LEU	GLU	GLU	GLU	GLU	GLU	N137	V26
THR	THR	ILE	ILE	LYS	LYS	LYS	K145	T27
GLU	GLU	LYS	LYS	GLU	GLU	GLU	R158	L28
LYS	LYS	ASP	ASP	GLY	GLY	GLY	S161	E29
VAL	VAL	VAL	VAL	LEU	LEU	LEU	E162	P30
LEU	LEU	ALA	ALA	PRO	PRO	PRO	E163	L31
ALA	ALA	SER	SER	PHE	PHE	PHE	R166	F35
SER	SER	ARG	ARG	ASP	ASP	ASP	I167	G36
GLY	GLY	PRO	PRO	PRO	PRO	PRO	L168	H37
LEU	LEU	ILE	ILE	ILE	ILE	ILE	G169	T38
SER	SER	LEU	LEU	LEU	LEU	LEU	R170	R44
LEU	LEU	GLY	GLY	ARG	ARG	ARG	L171	R45
GLY	GLY	MET	MET	PRO	PRO	PRO	L172	I46
MET	MET	ARG	ARG	VAL	VAL	VAL	V180	L47
LEU	LEU	LEU	LEU	ASP	ASP	ASP	E181	L48
GLU	GLU	GLU	GLU	ASP	ASP	ASP	L182	S49
ASN	ASN	TRP	TRP	GLY	GLY	GLY	I183	S50
PRO	PRO	PRO	PRO	LEU	LEU	LEU	A184	E60
PRO	PRO	THR	THR	VAL	VAL	VAL	V187	D62
ALA	ALA	SER	SER	VAL	VAL	VAL	E188	G63
SER	SER	ILE	ILE	SER	SER	SER	A189	V64
ILE	ILE	ASP	ASP	ALA	ALA	ALA	A190	L65
ASP	ASP	GLU	GLU	ASN	ASN	ASN	R195	H66
GLU	GLU	LEU	LEU	LEU	LEU	LEU	D199	S69
		LYS	LYS	LYS	LYS	LYS	K200	T70
		ALA	ALA	ALA	ALA	ALA	T203	K71
		ALA	ALA	ILE	ILE	ILE	E204	V74
		HTS	HTS	HTS	HTS	HTS	K205	Q75
		TYR	TYR	TYR	TYR	TYR	F206	D77
								I78
								L79

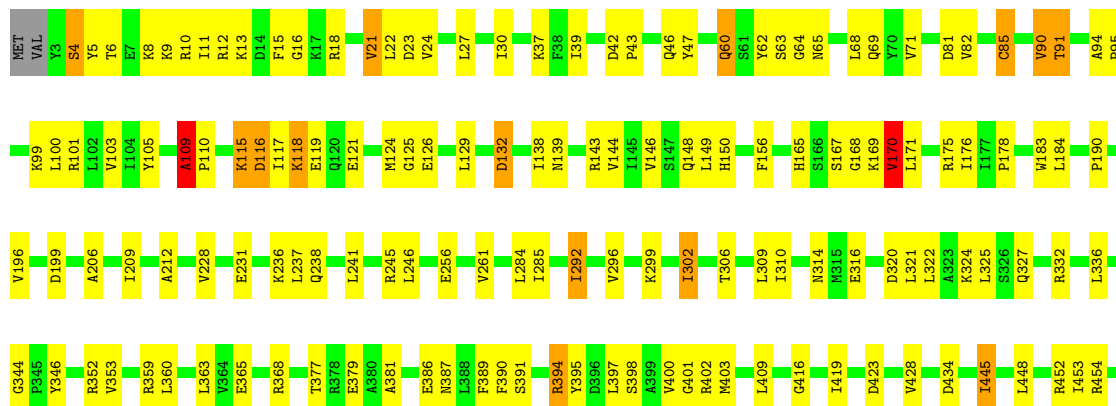
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|-----|-----|-----|-----|------|------|------|-----|
| GLU | ILE | GLY | VAL | PRO | ILE | GLN | MET |
| LYS | ASP | GLU | LYS | ILE | ARG | GLY | GLN |
| VAL | LEU | PRO | GLU | L171 | L172 | L82 | L79 |
| LEU | ALA | GLU | PHE | V173 | V174 | L83 | L84 |
| SER | ARG | ASP | GLY | A175 | A176 | R91 | V90 |
| GLY | LEU | ILE | LEU | Y177 | Y178 | D96 | F8 |
| SER | LEU | LEU | LEU | V180 | V181 | T101 | L13 |
| LEU | ARG | ARG | PRO | R182 | R183 | I107 | V14 |
| MET | GLY | VAL | ASP | A184 | A185 | A113 | D15 |
| ARG | LEU | ASP | ASP | Y186 | Y187 | D114 | I16 |
| LEU | GLU | ASN | TRP | V187 | V188 | T116 | H23 |
| GLU | TRP | GLU | LEU | PRO | THR | H117 | A24 |
| PRO | PRO | PRO | VAL | A190 | A191 | D118 | K25 |
| ALA | ALA | VAL | ARG | V192 | V193 | E122 | V26 |
| SER | ILE | SER | ALA | R195 | R196 | I123 | L31 |
| ASP | ASP | ASN | ASN | L198 | L199 | P126 | E32 |
| GLU | LEU | LEU | LYS | K200 | K201 | V129 | G34 |
| | ALA | ALA | ALA | V202 | V203 | L133 | R37 |
| | ILE | ILE | ILE | E204 | E205 | T134 | T38 |
| | THR | THR | THR | M206 | M207 | D135 | N41 |
| | ILE | GLY | GLY | T210 | T211 | E136 | R44 |
| | ASP | LEU | LEU | R218 | R219 | A138 | R45 |
| | VAL | VAL | GLN | A220 | A221 | S141 | I46 |
| | ARG | THR | THR | E222 | E223 | V146 | L47 |
| | GLU | GLU | LEU | Q227 | Q228 | G147 | L48 |
| | LEU | LEU | LEU | L228 | L229 | R148 | S49 |
| | LEU | LEU | LEU | A230 | A231 | G149 | S50 |
| | THR | THR | THR | F231 | F232 | R150 | M51 |
| | PRO | PRO | ASN | ASP | ASP | A55 | P52 |
| | LEU | LEU | LEU | ARG | ARG | G151 | G53 |
| | GLY | GLY | GLY | ASP | ASP | Y152 | C54 |
| | LYS | LYS | LYS | LEU | LEU | V153 | A55 |
| | SER | SER | SER | LEU | LEU | T156 | V56 |
| | THR | THR | THR | LEU | LEU | G63 | T57 |
| | LEU | LEU | LEU | LEU | LEU | V64 | T61 |
| | LEU | LEU | LEU | LEU | LEU | E67 | D62 |
| | LEU | LEU | LEU | LEU | LEU | S69 | L63 |
| | LEU | LEU | LEU | LEU | LEU | GLU | R68 |
| | LEU | LEU | LEU | LEU | LEU | ASP | V74 |
| | LEU | LEU | LEU | LEU | LEU | GLU | O75 |
| | LEU | LEU | LEU | LEU | LEU | GLU | S76 |

- | | | | |
|------|------|------|-----|
| D320 | P190 | V98 | H1 |
| L321 | K191 | G1 | V2 |
| L322 | D192 | R101 | Y3 |
| A323 | | L102 | S4 |
| K324 | R197 | | Y6 |
| L325 | I198 | Y105 | E7 |
| S326 | D199 | E106 | |
| Q327 | R200 | | |
| | R201 | A109 | R10 |
| G344 | R202 | P110 | I11 |
| P345 | | | R12 |
| Y346 | A206 | V114 | K13 |
| I347 | T207 | K115 | D14 |
| S348 | T208 | D116 | F15 |
| | T209 | I117 | G16 |
| R352 | L210 | E118 | K17 |
| V353 | R211 | E119 | |
| | | Q120 | V21 |
| T356 | L221 | E121 | L22 |
| N357 | | V122 | D23 |
| | F225 | Y123 | V24 |
| L360 | | M124 | |
| A361 | E231 | G125 | L27 |
| K362 | | E126 | L28 |
| L363 | K236 | | S29 |
| V364 | L237 | L129 | I30 |
| E365 | Q238 | | |
| | M239 | D132 | S34 |
| M370 | F240 | | |
| | L241 | I138 | I39 |
| T377 | V242 | M139 | E40 |
| R378 | P243 | | |
| E379 | E244 | V144 | S55 |
| A380 | R245 | I145 | V56 |
| A381 | L246 | V146 | |
| | | | Q60 |
| L384 | T289 | L149 | S61 |
| | | H150 | V62 |
| L388 | H273 | R151 | S63 |
| F399 | | | G64 |
| | E278 | D158 | N65 |
| R394 | | S159 | |
| | L284 | K163 | Q69 |
| V400 | T285 | T164 | Y73 |
| G401 | | H165 | R74 |
| R402 | I292 | S166 | L75 |
| | K299 | S167 | |
| L409 | | G168 | D81 |
| | T302 | K169 | V82 |
| I419 | | V170 | |
| D423 | T306 | L171 | C85 |
| | | | |
| D434 | L309 | R175 | V90 |
| | I310 | | T91 |
| I445 | N314 | R180 | Y92 |
| L446 | | V183 | S93 |
| | S318 | L184 | A94 |
| D451 | T319 | | S97 |



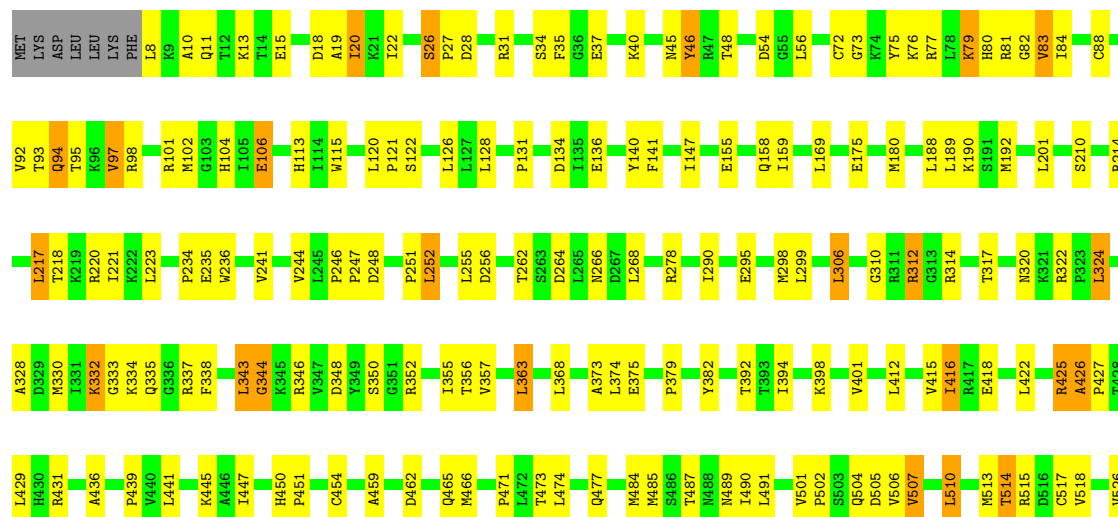
• Molecule 2: DNA-directed RNA polymerase subunit beta

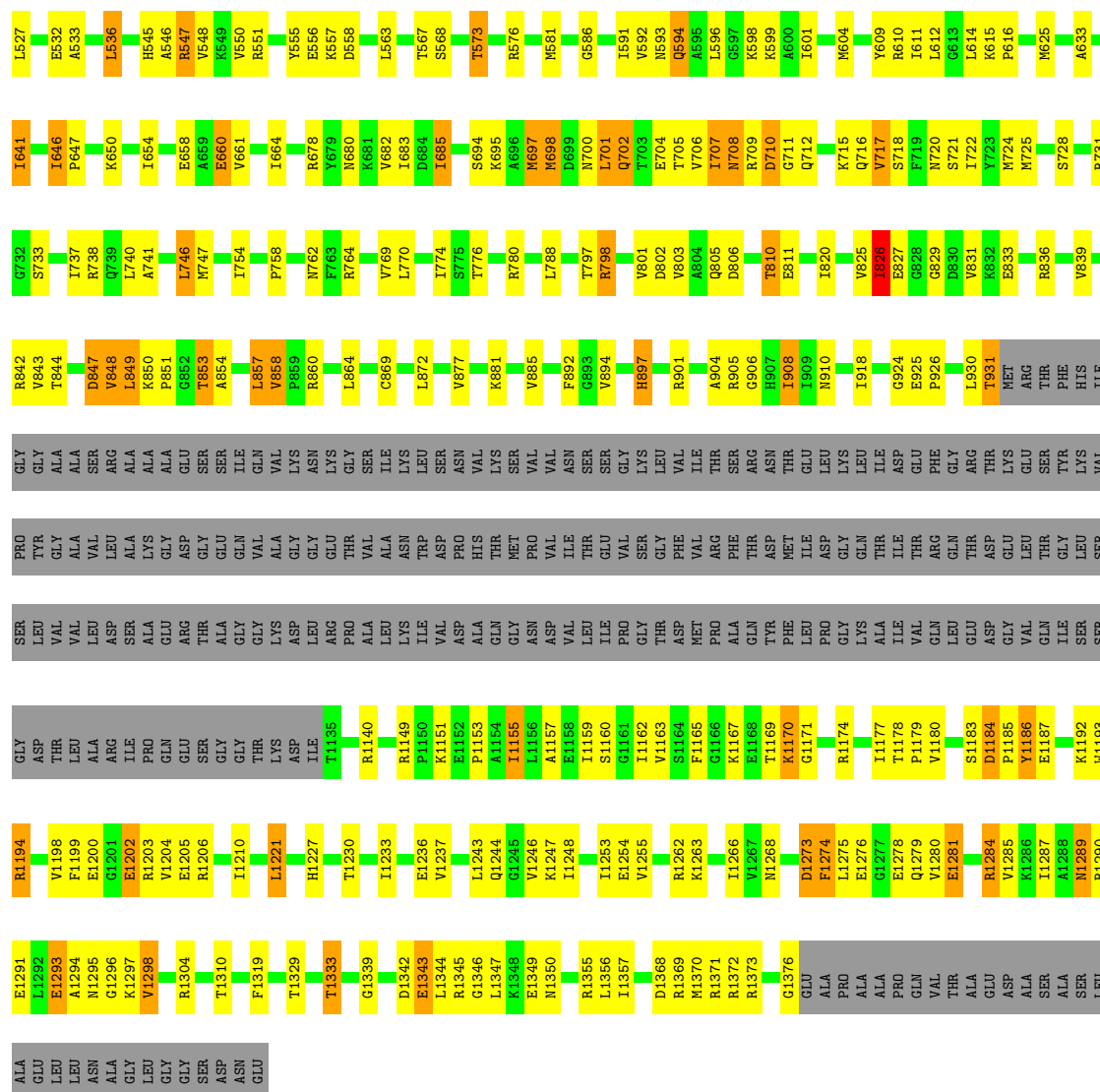
Chain I: 66% 31% •





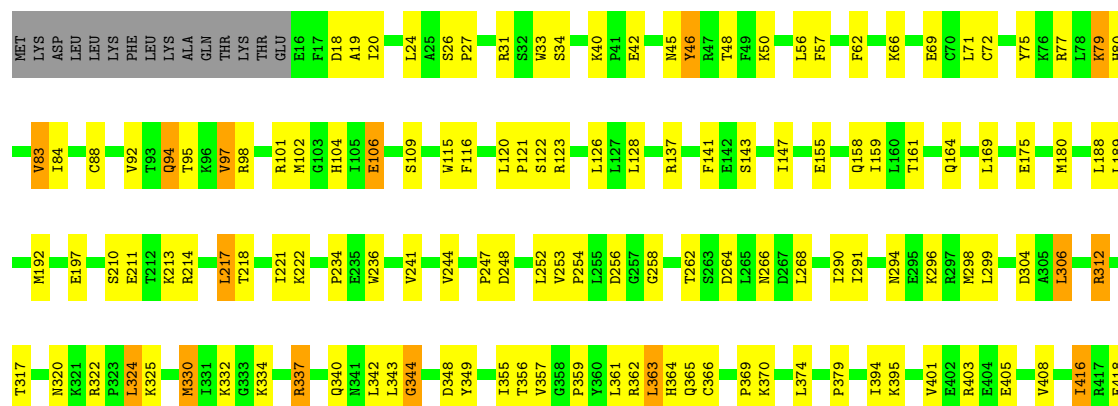
Chain D: 53% 25% 5% 17%

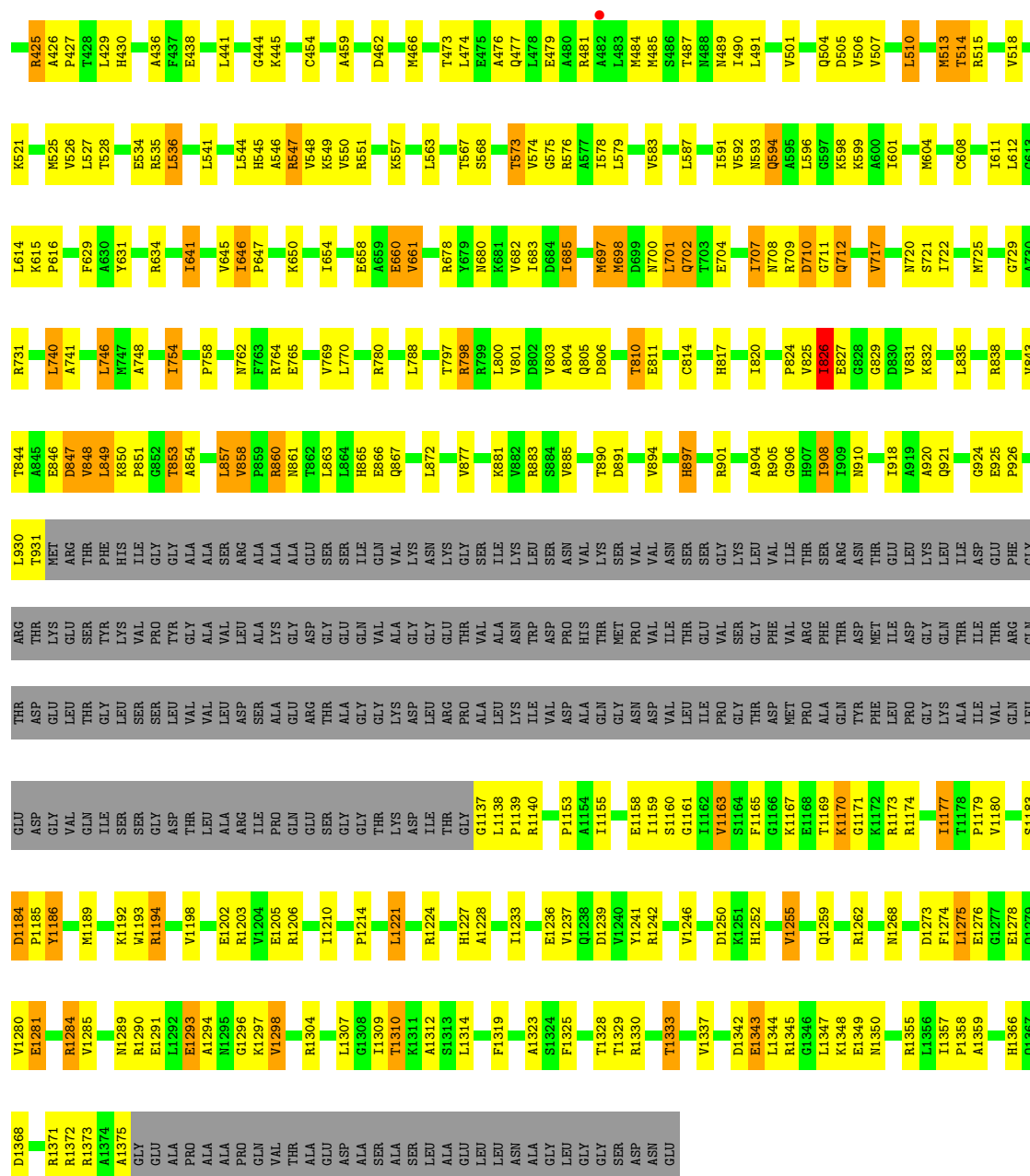




• Molecule 3: DNA-directed RNA polymerase subunit beta'

Chain J: 52% 26% 5% 18%





- Molecule 4: DNA-directed RNA polymerase subunit omega

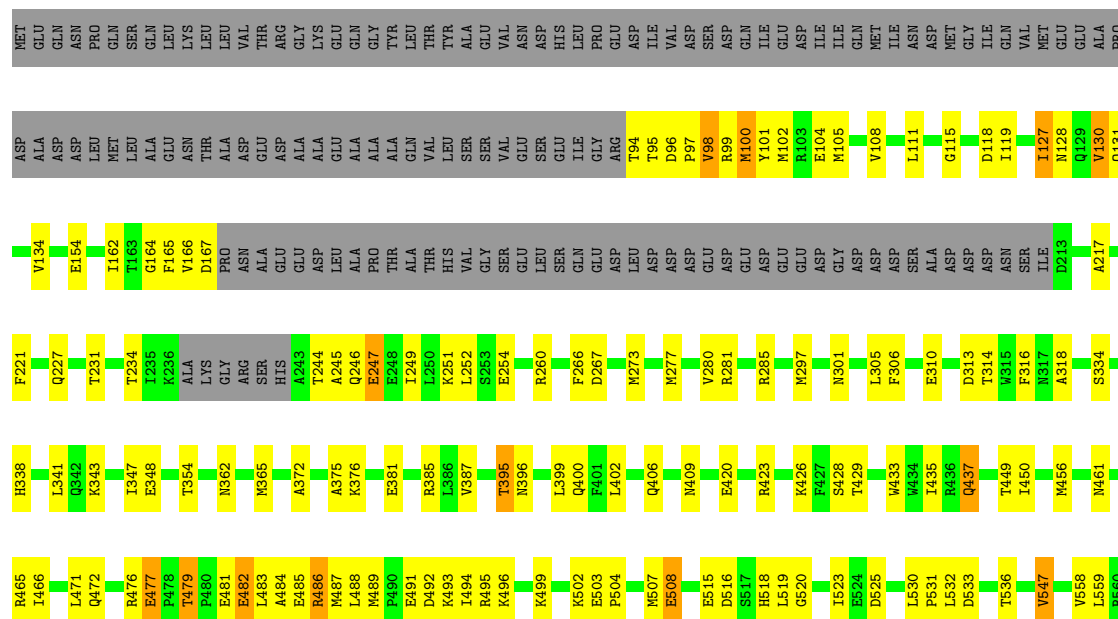
Chain E: 75% 20%

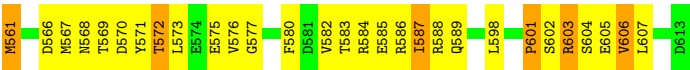


- Molecule 4: DNA-directed RNA polymerase subunit omega

Chain K: 55% 30% 13%







4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	187.22Å 204.43Å 310.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.96 – 3.92 29.96 – 3.92	Depositor EDS
% Data completeness (in resolution range)	79.1 (29.96-3.92) 78.9 (29.96-3.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 3.86Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.260 , 0.307 0.263 , 0.305	Depositor DCC
R_{free} test set	2000 reflections (1.86%)	wwPDB-VP
Wilson B-factor (Å ²)	167.5	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 136.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	54994	wwPDB-VP
Average B, all atoms (Å ²)	195.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.30	1/1774 (0.1%)	0.57	0/2405
1	B	0.25	0/1668	0.81	2/2260 (0.1%)
1	G	0.24	1/1751 (0.1%)	0.57	0/2373
1	H	0.22	0/1678	0.72	0/2274
2	C	0.22	0/10756	0.62	2/14512 (0.0%)
2	I	0.18	0/10737	0.60	2/14487 (0.0%)
3	D	0.24	1/9229 (0.0%)	0.62	2/12459 (0.0%)
3	J	0.20	0/9140	0.59	0/12341
4	E	0.17	0/693	0.53	0/935
4	K	0.16	0/629	0.53	0/847
5	F	0.17	0/3864	0.59	1/5194 (0.0%)
5	L	0.17	0/3872	0.55	1/5205 (0.0%)
All	All	0.21	3/55791 (0.0%)	0.61	10/75292 (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
2	C	0	3
2	I	0	2
3	D	0	2
3	J	0	2
5	F	0	1
5	L	0	1
All	All	0	11

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	29	GLU	C-N	9.19	1.55	1.33
3	D	426	ALA	C-N	7.74	1.51	1.33
1	G	29	GLU	C-N	6.45	1.49	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	109	ALA	CA-C-N	18.31	139.52	119.93
2	I	109	ALA	C-N-CA	18.31	139.52	119.93
2	C	109	ALA	CA-C-N	14.92	135.90	119.93
2	C	109	ALA	C-N-CA	14.92	135.90	119.93
5	F	602	SER	N-CA-C	-6.32	97.35	110.80

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	109	ALA	Peptide
2	C	2	VAL	Peptide
2	C	236	LYS	Peptide
3	D	1184	ASP	Peptide
3	D	1296	GLY	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	1753	0	1780	71	0
1	B	1649	0	1674	73	0
1	G	1730	0	1756	62	0
1	H	1659	0	1692	74	0
2	C	10587	0	10609	330	0
2	I	10568	0	10582	276	0
3	D	9089	0	9263	279	0
3	J	9001	0	9167	289	0
4	E	691	0	695	12	0
4	K	627	0	634	21	0
5	F	3813	0	3880	100	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	L	3821	0	3884	101	0
6	D	1	0	0	0	0
6	J	1	0	0	0	0
7	D	2	0	0	0	0
7	J	2	0	0	0	0
All	All	54994	0	55616	1526	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 14.

The worst 5 of 1526 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)
2:I:1272:GLU:H	3:J:343:LEU:HD12	1.37	0.90
1:H:32:GLU:HA	1:H:198:LEU:HD22	1.51	0.89
1:B:32:GLU:HA	1:B:198:LEU:HD22	1.54	0.89
3:D:660:GLU:HB3	3:D:685:ILE:HD12	1.55	0.88
2:I:1105:SER:HB2	3:J:731:ARG:HG2	1.57	0.87

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	225/329 (68%)	193 (86%)	28 (12%)	4 (2%)	6	34
1	B	210/329 (64%)	182 (87%)	23 (11%)	5 (2%)	4	29
1	G	222/329 (68%)	191 (86%)	27 (12%)	4 (2%)	6	34
1	H	211/329 (64%)	183 (87%)	22 (10%)	6 (3%)	4	27
2	C	1340/1342 (100%)	1230 (92%)	102 (8%)	8 (1%)	21	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	I	1338/1342 (100%)	1234 (92%)	98 (7%)	6 (0%)	30	65
3	D	1162/1407 (83%)	1069 (92%)	86 (7%)	7 (1%)	21	56
3	J	1151/1407 (82%)	1058 (92%)	84 (7%)	9 (1%)	16	50
4	E	87/91 (96%)	81 (93%)	6 (7%)	0	100	100
4	K	77/91 (85%)	74 (96%)	3 (4%)	0	100	100
5	F	462/613 (75%)	425 (92%)	36 (8%)	1 (0%)	43	75
5	L	463/613 (76%)	423 (91%)	39 (8%)	1 (0%)	43	75
All	All	6948/8222 (84%)	6343 (91%)	554 (8%)	51 (1%)	18	53

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	13	LEU
2	C	1159	VAL
3	D	332	LYS
1	H	20	SER
2	I	1159	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	194/286 (68%)	178 (92%)	16 (8%)	10	34
1	B	182/286 (64%)	170 (93%)	12 (7%)	15	41
1	G	191/286 (67%)	176 (92%)	15 (8%)	11	35
1	H	184/286 (64%)	177 (96%)	7 (4%)	29	51
2	C	1157/1157 (100%)	1043 (90%)	114 (10%)	7	27
2	I	1154/1157 (100%)	1040 (90%)	114 (10%)	7	27
3	D	970/1168 (83%)	857 (88%)	113 (12%)	5	21
3	J	960/1168 (82%)	850 (88%)	110 (12%)	5	22
4	E	72/75 (96%)	64 (89%)	8 (11%)	6	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	K	67/75 (89%)	62 (92%)	5 (8%)	12	37
5	F	417/540 (77%)	375 (90%)	42 (10%)	7	26
5	L	418/540 (77%)	377 (90%)	41 (10%)	7	27
All	All	5966/7024 (85%)	5369 (90%)	597 (10%)	7	27

5 of 597 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	J	324	LEU
5	L	437	GLN
3	J	507	VAL
3	J	312	ARG
3	J	857	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 106 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	186	ASN
2	I	766	ASN
5	L	258	GLN
2	I	69	GLN
2	I	573	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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(Å²)	Q<0.9
1	A	227/329 (68%)	-0.55	0	100	100	133, 170, 230, 390	0
1	B	214/329 (65%)	-0.52	0	100	100	146, 213, 308, 463	0
1	G	224/329 (68%)	-0.66	0	100	100	171, 216, 299, 368	0
1	H	215/329 (65%)	-0.53	0	100	100	173, 222, 293, 418	0
2	C	1342/1342 (100%)	-0.50	0	100	100	107, 161, 300, 496	0
2	I	1340/1342 (99%)	-0.56	0	100	100	146, 194, 325, 509	0
3	D	1166/1407 (82%)	-0.52	0	100	100	108, 149, 239, 419	0
3	J	1155/1407 (82%)	-0.51	1 (0%)	92	87	127, 170, 264, 409	0
4	E	89/91 (97%)	-0.58	0	100	100	186, 210, 243, 257	0
4	K	79/91 (86%)	-0.50	0	100	100	242, 288, 354, 398	0
5	F	468/613 (76%)	-0.57	0	100	100	151, 209, 338, 459	0
5	L	469/613 (76%)	-0.63	0	100	100	162, 215, 360, 527	0
All	All	6988/8222 (84%)	-0.54	1 (0%)	100	100	107, 184, 306, 527	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	J	482	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 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
6	MG	J	1501	1/1	0.71	0.10	130,130,130,130	0
6	MG	D	1501	1/1	0.90	0.08	104,104,104,104	0
7	ZN	D	1502	1/1	0.98	0.04	177,177,177,177	0
7	ZN	J	1502	1/1	0.98	0.03	213,213,213,213	0
7	ZN	J	1503	1/1	0.99	0.04	135,135,135,135	0
7	ZN	D	1503	1/1	1.00	0.02	117,117,117,117	0

6.5 Other polymers [i](#)

There are no such residues in this entry.