



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:41 PM UTC

PDB ID : 4IQZ / pdb_00004iqz
Title : The crystal structure of a large insert in RNA polymerase (RpoC) subunit from E. coli
Authors : Bhandari, V.; Sugiman-Marangos, S.N.; Naushad, H.S.; Gupta, R.S.; Junop, M.S.
Deposited on : 2013-01-14
Resolution : 2.10 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

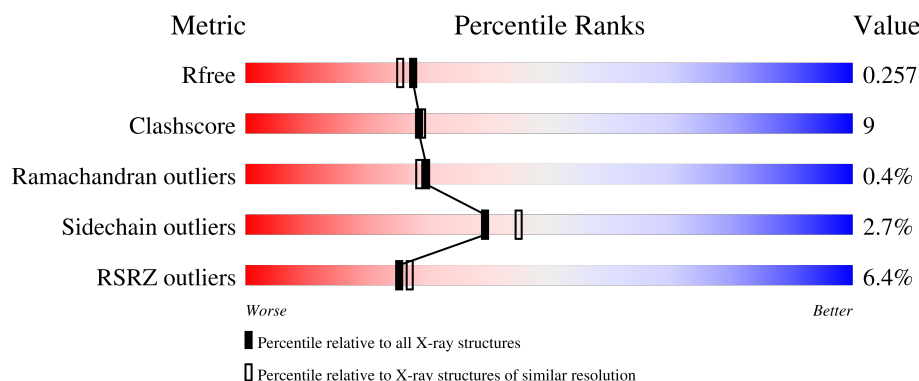
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

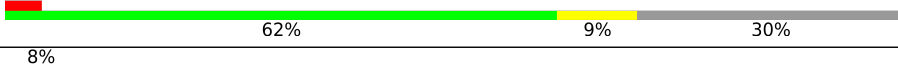
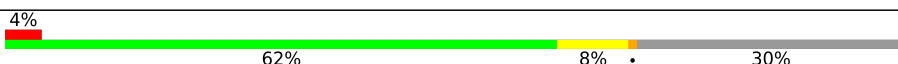
The reported resolution of this entry is 2.10 Å.

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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	250	
1	B	250	
1	C	250	
1	D	250	
1	E	250	

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
2	IOD	A	310	-	-	X	-
2	IOD	B	304	-	-	X	-
2	IOD	B	307	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6371 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 beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	168	Total	C	N	O	Se	0	0	1
			1178	743	197	235	3			
1	B	176	Total	C	N	O	Se	0	0	0
			1226	769	206	248	3			
1	C	176	Total	C	N	O	Se	0	0	0
			1193	756	196	238	3			
1	D	146	Total	C	N	O	Se	0	0	0
			1019	645	169	202	3			
1	E	175	Total	C	N	O	Se	0	0	0
			1164	737	194	230	3			

There are 89 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP P0A8T7
A	2	GLY	-	expression tag	UNP P0A8T7
A	3	SER	-	expression tag	UNP P0A8T7
A	4	SER	-	expression tag	UNP P0A8T7
A	5	HIS	-	expression tag	UNP P0A8T7
A	6	HIS	-	expression tag	UNP P0A8T7
A	7	HIS	-	expression tag	UNP P0A8T7
A	8	HIS	-	expression tag	UNP P0A8T7
A	9	HIS	-	expression tag	UNP P0A8T7
A	10	HIS	-	expression tag	UNP P0A8T7
A	11	SER	-	expression tag	UNP P0A8T7
A	12	SER	-	expression tag	UNP P0A8T7
A	13	GLY	-	expression tag	UNP P0A8T7
A	14	LEU	-	expression tag	UNP P0A8T7
A	15	VAL	-	expression tag	UNP P0A8T7
A	16	PRO	-	expression tag	UNP P0A8T7
A	17	ARG	-	expression tag	UNP P0A8T7
A	18	GLY	-	expression tag	UNP P0A8T7
A	19	SER	-	expression tag	UNP P0A8T7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	20	HIS	-	expression tag	UNP P0A8T7
A	230	MSE	VAL	engineered mutation	UNP P0A8T7
A	231	ASP	-	expression tag	UNP P0A8T7
A	232	PRO	-	expression tag	UNP P0A8T7
A	233	ALA	-	expression tag	UNP P0A8T7
A	234	ALA	-	expression tag	UNP P0A8T7
A	235	ASN	-	expression tag	UNP P0A8T7
A	236	LYS	-	expression tag	UNP P0A8T7
A	237	ALA	-	expression tag	UNP P0A8T7
A	238	ARG	-	expression tag	UNP P0A8T7
A	239	LYS	-	expression tag	UNP P0A8T7
A	240	GLU	-	expression tag	UNP P0A8T7
A	241	ALA	-	expression tag	UNP P0A8T7
A	242	GLU	-	expression tag	UNP P0A8T7
A	243	LEU	-	expression tag	UNP P0A8T7
A	244	ALA	-	expression tag	UNP P0A8T7
A	245	ALA	-	expression tag	UNP P0A8T7
A	246	ALA	-	expression tag	UNP P0A8T7
A	247	THR	-	expression tag	UNP P0A8T7
A	248	ALA	-	expression tag	UNP P0A8T7
A	249	GLU	-	expression tag	UNP P0A8T7
A	250	GLN	-	expression tag	UNP P0A8T7
B	1	MSE	-	expression tag	UNP P0A8T7
B	2	GLY	-	expression tag	UNP P0A8T7
B	3	SER	-	expression tag	UNP P0A8T7
B	4	SER	-	expression tag	UNP P0A8T7
B	5	HIS	-	expression tag	UNP P0A8T7
B	6	HIS	-	expression tag	UNP P0A8T7
B	7	HIS	-	expression tag	UNP P0A8T7
B	8	HIS	-	expression tag	UNP P0A8T7
B	9	HIS	-	expression tag	UNP P0A8T7
B	10	HIS	-	expression tag	UNP P0A8T7
B	11	SER	-	expression tag	UNP P0A8T7
B	12	SER	-	expression tag	UNP P0A8T7
B	13	GLY	-	expression tag	UNP P0A8T7
B	14	LEU	-	expression tag	UNP P0A8T7
B	15	VAL	-	expression tag	UNP P0A8T7
B	16	PRO	-	expression tag	UNP P0A8T7
B	17	ARG	-	expression tag	UNP P0A8T7
B	18	GLY	-	expression tag	UNP P0A8T7
B	19	SER	-	expression tag	UNP P0A8T7
B	20	HIS	-	expression tag	UNP P0A8T7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	230	MSE	VAL	engineered mutation	UNP P0A8T7
B	231	ASP	-	expression tag	UNP P0A8T7
B	232	PRO	-	expression tag	UNP P0A8T7
B	233	ALA	-	expression tag	UNP P0A8T7
B	234	ALA	-	expression tag	UNP P0A8T7
B	235	ASN	-	expression tag	UNP P0A8T7
B	236	LYS	-	expression tag	UNP P0A8T7
B	237	ALA	-	expression tag	UNP P0A8T7
B	238	ARG	-	expression tag	UNP P0A8T7
B	239	LYS	-	expression tag	UNP P0A8T7
B	240	GLU	-	expression tag	UNP P0A8T7
B	241	ALA	-	expression tag	UNP P0A8T7
B	242	GLU	-	expression tag	UNP P0A8T7
B	243	LEU	-	expression tag	UNP P0A8T7
B	244	ALA	-	expression tag	UNP P0A8T7
B	245	ALA	-	expression tag	UNP P0A8T7
B	246	ALA	-	expression tag	UNP P0A8T7
B	247	THR	-	expression tag	UNP P0A8T7
B	248	ALA	-	expression tag	UNP P0A8T7
B	249	GLU	-	expression tag	UNP P0A8T7
B	250	GLN	-	expression tag	UNP P0A8T7
C	1	MSE	-	expression tag	UNP P0A8T7
C	2	GLY	-	expression tag	UNP P0A8T7
C	3	SER	-	expression tag	UNP P0A8T7
C	4	SER	-	expression tag	UNP P0A8T7
C	5	HIS	-	expression tag	UNP P0A8T7
C	6	HIS	-	expression tag	UNP P0A8T7
C	ALA	HIS	-	?	UNP P0A8T7

- Molecule 2 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	15	Total I 15 15	0	0
2	B	13	Total I 13 13	0	0
2	C	11	Total I 11 11	0	0
2	D	13	Total I 13 13	0	0
2	E	4	Total I 4 4	0	0

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Na 2	0	0
3	B	1	Total 1	Na 1	0	0
3	C	2	Total 2	Na 2	0	0
3	D	1	Total 1	Na 1	0	0
3	E	1	Total 1	Na 1	0	0

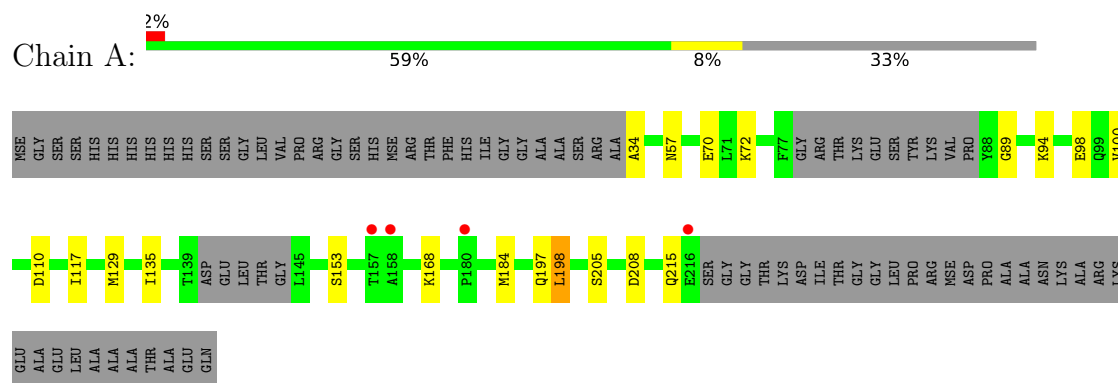
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	147	Total 147	O 147	0	0
4	B	121	Total 121	O 121	0	0
4	C	82	Total 82	O 82	0	0
4	D	93	Total 93	O 93	0	0
4	E	85	Total 85	O 85	0	0

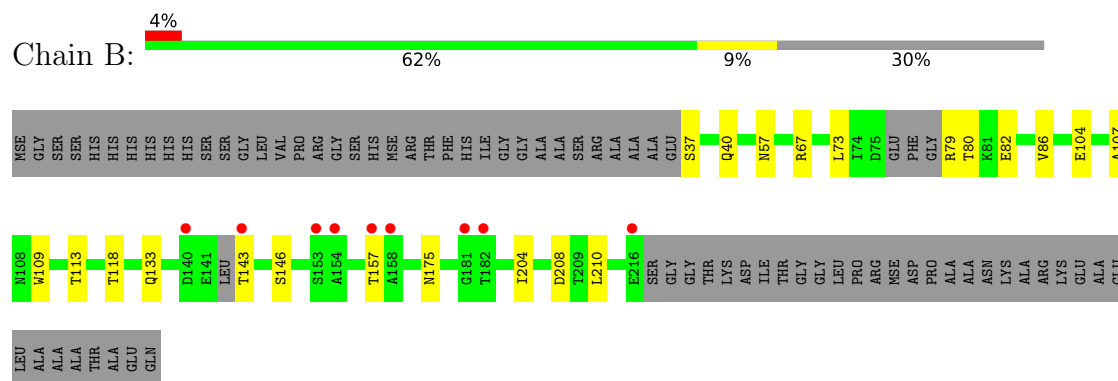
3 Residue-property plots [i](#)

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.

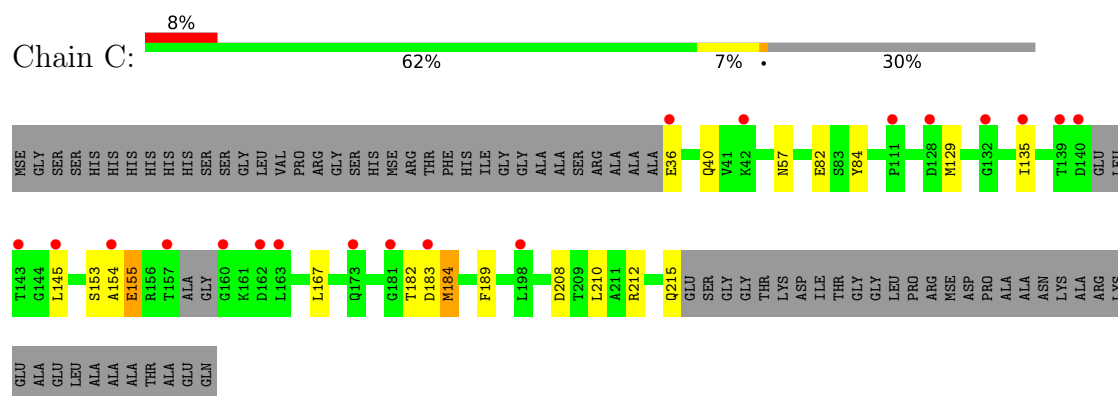
- Molecule 1: DNA-directed RNA polymerase subunit beta'



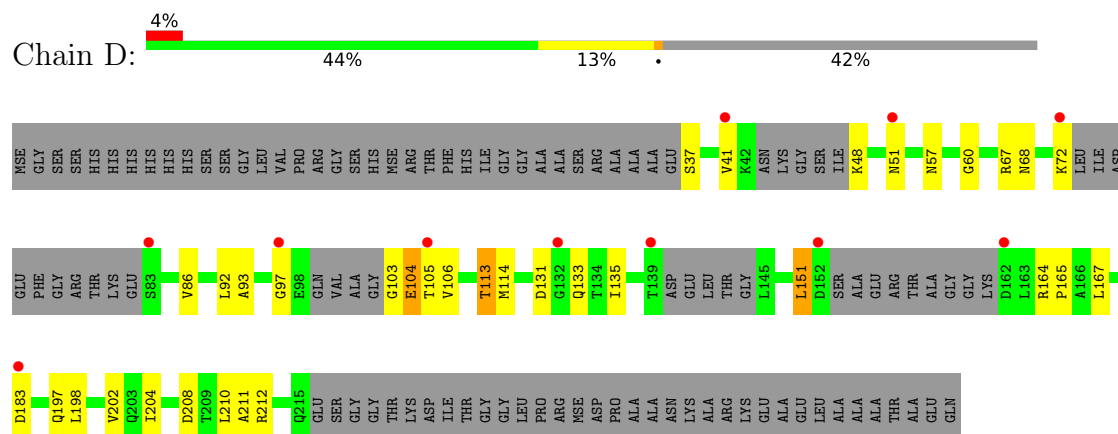
- Molecule 1: DNA-directed RNA polymerase subunit beta'



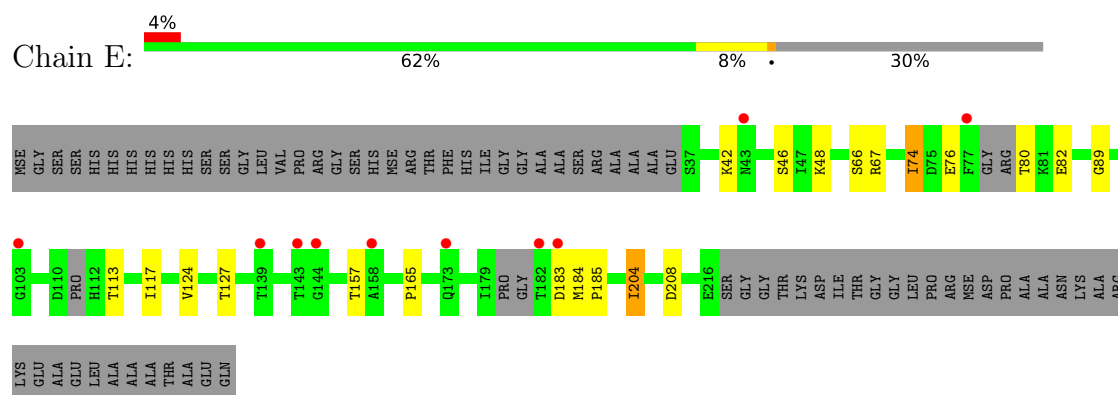
- Molecule 1: DNA-directed RNA polymerase subunit beta'



• Molecule 1: DNA-directed RNA polymerase subunit beta'



• Molecule 1: DNA-directed RNA polymerase subunit beta'



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	198.06Å 65.63Å 81.29Å 90.00° 108.92° 90.00°	Depositor
Resolution (Å)	35.99 – 2.10 35.99 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.8 (35.99-2.10) 98.6 (35.99-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.08Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.203 , 0.240 (Not available) , 0.257	Depositor DCC
R_{free} test set	2951 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	29.9	Xtriage
Anisotropy	0.169	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 70.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6371	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.94% 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: IOD, NA

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	0.49	0/1200	0.85	0/1629
1	B	0.57	0/1236	0.83	0/1682
1	C	0.53	0/1205	0.82	0/1643
1	D	0.61	0/1027	0.86	1/1396 (0.1%)
1	E	0.71	3/1171 (0.3%)	0.87	2/1597 (0.1%)
All	All	0.58	3/5839 (0.1%)	0.85	3/7947 (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	D	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	185	PRO	N-CD	5.40	1.55	1.47
1	E	74	ILE	C-O	-5.16	1.18	1.24
1	E	184	MSE	CA-C	-5.01	1.45	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	184	MSE	CA-C-N	-7.20	112.58	119.85
1	E	184	MSE	C-N-CA	-7.20	112.58	119.85
1	D	97	GLY	N-CA-C	-6.53	97.70	113.18

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	51	ASN	Peptide

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	1178	0	1154	17	0
1	B	1226	0	1161	17	0
1	C	1193	0	1089	19	0
1	D	1019	0	943	33	0
1	E	1164	0	1054	12	0
2	A	15	0	0	5	0
2	B	13	0	0	8	0
2	C	11	0	0	1	0
2	D	13	0	0	3	0
2	E	4	0	0	1	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
4	A	147	0	0	5	0
4	B	121	0	0	13	0
4	C	82	0	0	5	0
4	D	93	0	0	12	0
4	E	85	0	0	7	0
All	All	6371	0	5401	100	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 9.

All (100) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:GLU:CG	2:A:304:IOD:I	2.70	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:308:IOD:I	4:B:431:HOH:O	2.42	1.05
1:D:48:LYS:N	4:D:404:HOH:O	2.06	0.88
1:B:80:THR:OG1	4:B:485:HOH:O	1.93	0.87
1:A:34:ALA:N	4:A:501:HOH:O	2.07	0.86
2:E:304:IOD:I	4:E:482:HOH:O	2.64	0.85
2:B:309:IOD:I	4:B:416:HOH:O	2.65	0.84
1:E:208:ASP:OD1	4:E:470:HOH:O	1.93	0.84
1:C:212:ARG:NH1	4:C:478:HOH:O	2.08	0.81
1:D:212:ARG:NH2	4:D:468:HOH:O	2.12	0.79
1:E:67:ARG:NE	4:E:452:HOH:O	2.16	0.79
1:B:143:THR:N	4:B:515:HOH:O	2.15	0.78
1:B:40:GLN:OE1	4:B:457:HOH:O	2.00	0.78
1:A:215:GLN:NE2	2:A:310:IOD:I	2.87	0.76
2:B:307:IOD:I	4:B:466:HOH:O	2.76	0.74
1:A:110:ASP:OD2	4:A:523:HOH:O	2.06	0.74
1:D:113:THR:HG21	1:D:212:ARG:HD3	1.70	0.74
2:D:302:IOD:I	4:D:431:HOH:O	2.74	0.74
1:D:67:ARG:NH2	4:D:413:HOH:O	2.12	0.73
1:E:157:THR:O	4:E:432:HOH:O	2.06	0.72
1:C:36:GLU:O	4:C:438:HOH:O	2.07	0.71
1:B:79:ARG:N	4:B:521:HOH:O	2.24	0.70
1:A:57:ASN:HB2	1:A:208:ASP:OD1	1.93	0.69
2:B:311:IOD:I	4:B:430:HOH:O	2.83	0.66
1:D:37:SER:N	4:D:465:HOH:O	2.29	0.65
1:D:113:THR:HG22	1:D:212:ARG:HH11	1.61	0.65
1:D:183:ASP:OD2	4:D:446:HOH:O	2.15	0.65
1:D:103:GLY:O	1:D:104:GLU:HB2	1.96	0.65
1:D:103:GLY:HA3	4:D:487:HOH:O	1.98	0.64
1:C:40:GLN:O	4:C:418:HOH:O	2.15	0.63
1:A:168:LYS:NZ	2:A:307:IOD:I	3.02	0.62
1:D:37:SER:OG	4:D:448:HOH:O	2.15	0.60
1:E:80:THR:N	4:E:453:HOH:O	2.35	0.60
1:B:175:ASN:ND2	4:B:450:HOH:O	2.29	0.60
1:C:153:SER:C	1:C:155:GLU:H	2.09	0.60
1:D:72:LYS:O	4:D:463:HOH:O	2.15	0.60
1:E:89:GLY:HA2	1:E:117:ILE:HD11	1.84	0.59
1:D:183:ASP:OD2	4:D:462:HOH:O	2.17	0.57
1:C:57:ASN:HB2	1:C:208:ASP:OD1	2.04	0.57
1:B:37:SER:HB3	1:B:109:TRP:CE2	2.39	0.57
1:D:41:VAL:O	1:D:103:GLY:N	2.38	0.57
1:C:129:MSE:HE2	1:C:135:ILE:HG21	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:GLN:O	1:D:68:ASN:HB2	2.04	0.56
1:E:124:VAL:HG23	1:E:204:ILE:HD12	1.86	0.56
1:C:212:ARG:HG2	2:C:306:IOD:I	2.77	0.55
1:D:113:THR:HG23	1:D:212:ARG:HB3	1.89	0.54
1:B:118:THR:HB	1:B:210:LEU:HD11	1.90	0.54
1:C:82:GLU:OE1	1:C:84:TYR:OH	2.17	0.54
1:C:215:GLN:HB2	2:D:311:IOD:I	2.79	0.52
2:A:310:IOD:I	4:B:452:HOH:O	2.88	0.52
1:D:113:THR:CG2	1:D:212:ARG:HH11	2.22	0.52
1:D:113:THR:CG2	1:D:212:ARG:HD3	2.40	0.51
1:E:42:LYS:O	4:E:437:HOH:O	2.19	0.51
1:C:184:MSE:HE2	1:D:93:ALA:HB2	1.93	0.50
1:B:133:GLN:OE1	1:B:157:THR:OG1	2.29	0.50
2:B:304:IOD:I	4:B:413:HOH:O	2.90	0.50
1:E:46:SER:OG	1:E:76:GLU:O	2.23	0.50
1:E:48:LYS:CB	1:E:74:ILE:CD1	2.90	0.49
1:C:153:SER:O	1:C:155:GLU:N	2.45	0.49
1:C:129:MSE:HB3	1:C:135:ILE:HD13	1.94	0.48
1:C:212:ARG:NH2	4:C:454:HOH:O	1.99	0.48
1:D:92:LEU:O	4:D:407:HOH:O	2.20	0.48
1:B:73:LEU:HB3	1:B:82:GLU:HB2	1.95	0.48
1:B:67:ARG:HG3	2:B:307:IOD:I	2.84	0.47
1:B:104:GLU:HG2	4:B:484:HOH:O	2.12	0.47
1:D:197:GLN:HG2	1:D:211:ALA:HA	1.95	0.47
1:D:202:VAL:HG23	2:D:301:IOD:I	2.84	0.47
1:B:79:ARG:N	4:B:496:HOH:O	2.48	0.47
1:B:57:ASN:HB2	1:B:208:ASP:OD1	2.15	0.46
1:A:198:LEU:N	4:A:545:HOH:O	2.48	0.46
1:A:205:SER:HB2	1:D:114:MSE:HE1	1.98	0.46
1:C:167:LEU:HD12	1:C:210:LEU:HB3	1.98	0.46
1:C:184:MSE:HE2	1:D:105:THR:O	2.16	0.45
1:A:184:MSE:HE1	1:B:107:ALA:HA	1.98	0.45
1:B:146:SER:HB2	2:B:313:IOD:I	2.87	0.45
1:A:94:LYS:HG3	1:A:100:VAL:HG12	1.99	0.45
1:C:183:ASP:HB3	1:D:105:THR:CB	2.47	0.45
1:C:189:PHE:O	1:D:60:GLY:HA2	2.17	0.44
1:E:82:GLU:CG	4:E:425:HOH:O	2.64	0.44
1:D:113:THR:CG2	1:D:212:ARG:HB3	2.46	0.44
1:E:74:ILE:HG22	1:E:76:GLU:H	1.82	0.44
1:C:145:LEU:N	4:C:452:HOH:O	2.38	0.44
1:D:103:GLY:CA	4:D:487:HOH:O	2.62	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:133:GLN:C	1:D:151:LEU:HD23	2.43	0.43
1:D:106:VAL:O	1:D:106:VAL:HG22	2.18	0.43
1:D:167:LEU:HD12	1:D:210:LEU:HB3	2.02	0.42
1:A:89:GLY:HA2	1:A:117:ILE:HD11	2.02	0.42
1:B:113:THR:OG1	2:B:304:IOD:I	3.08	0.41
1:A:197:GLN:HB2	4:A:545:HOH:O	2.20	0.41
1:A:70:GLU:OE2	1:A:72:LYS:HD3	2.20	0.41
1:A:129:MSE:CE	1:A:135:ILE:HG21	2.50	0.41
1:C:153:SER:C	1:C:155:GLU:N	2.74	0.41
1:D:131:ASP:HA	1:D:135:ILE:HG13	2.02	0.41
1:D:57:ASN:HB2	1:D:208:ASP:OD1	2.21	0.41
1:D:164:ARG:HA	1:D:165:PRO:HD2	1.86	0.40
1:E:127:THR:O	1:E:165:PRO:HA	2.21	0.40
1:A:34:ALA:N	4:A:542:HOH:O	2.54	0.40
1:B:37:SER:HB3	1:B:109:TRP:NE1	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	164/250 (66%)	163 (99%)	1 (1%)	0	100	100
1	B	170/250 (68%)	165 (97%)	5 (3%)	0	100	100
1	C	170/250 (68%)	163 (96%)	5 (3%)	2 (1%)	10	7
1	D	134/250 (54%)	131 (98%)	2 (2%)	1 (1%)	18	15
1	E	167/250 (67%)	163 (98%)	4 (2%)	0	100	100
All	All	805/1250 (64%)	785 (98%)	17 (2%)	3 (0%)	30	28

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	154	ALA
1	C	155	GLU
1	D	104	GLU

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	119/193 (62%)	117 (98%)	2 (2%)	53	62
1	B	122/193 (63%)	120 (98%)	2 (2%)	55	64
1	C	110/193 (57%)	108 (98%)	2 (2%)	51	60
1	D	100/193 (52%)	95 (95%)	5 (5%)	22	22
1	E	102/193 (53%)	98 (96%)	4 (4%)	28	31
All	All	553/965 (57%)	538 (97%)	15 (3%)	39	45

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	SER
1	A	198	LEU
1	B	86	VAL
1	B	204	ILE
1	C	182	THR
1	C	184	MSE
1	D	86	VAL
1	D	113	THR
1	D	151	LEU
1	D	198	LEU
1	D	204	ILE
1	E	66	SER
1	E	113	THR
1	E	183	ASP
1	E	204	ILE

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

Mol	Chain	Res	Type
1	A	43	ASN
1	B	108	ASN
1	B	133	GLN

5.3.3 RNA [i](#)

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 63 ligands modelled in this entry, 63 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

6.1 Protein, DNA and RNA chains

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	163/250 (65%)	-0.03	4 (2%) 58 61	13, 25, 56, 69	0
1	B	173/250 (69%)	0.46	9 (5%) 33 35	17, 37, 60, 85	0
1	C	173/250 (69%)	0.59	19 (10%) 10 11	20, 37, 77, 101	0
1	D	143/250 (57%)	0.37	11 (7%) 19 21	18, 32, 66, 75	0
1	E	172/250 (68%)	0.50	10 (5%) 29 30	20, 37, 61, 83	0
All	All	824/1250 (65%)	0.38	53 (6%) 25 27	13, 33, 64, 101	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	181	GLY	4.9
1	C	139	THR	4.5
1	B	158	ALA	4.0
1	C	162	ASP	4.0
1	D	139	THR	3.8
1	C	157	THR	3.5
1	E	77	PHE	3.5
1	E	139	THR	3.5
1	D	51	ASN	3.4
1	B	181	GLY	3.2
1	D	83	SER	3.1
1	C	173	GLN	3.1
1	C	143	THR	3.1
1	A	158	ALA	3.0
1	B	153	SER	3.0
1	E	143	THR	3.0
1	C	154	ALA	2.9
1	A	157	THR	2.8
1	D	105	THR	2.8
1	D	97	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	162	ASP	2.7
1	D	41	VAL	2.5
1	C	135	ILE	2.5
1	E	144	GLY	2.5
1	A	216	GLU	2.5
1	C	42	LYS	2.5
1	D	183	ASP	2.4
1	D	152	ASP	2.4
1	C	163	LEU	2.4
1	C	160	GLY	2.4
1	C	140	ASP	2.4
1	C	183	ASP	2.4
1	E	158	ALA	2.4
1	E	103	GLY	2.3
1	B	182	THR	2.3
1	D	132	GLY	2.3
1	E	43	ASN	2.3
1	C	132	GLY	2.2
1	D	72	LYS	2.2
1	E	182	THR	2.2
1	C	36	GLU	2.2
1	B	157	THR	2.2
1	C	145	LEU	2.1
1	B	140	ASP	2.1
1	B	216	GLU	2.1
1	E	183	ASP	2.1
1	C	198	LEU	2.1
1	B	143	THR	2.1
1	C	111	PRO	2.1
1	B	154	ALA	2.1
1	E	173	GLN	2.0
1	C	128	ASP	2.0
1	A	180	PRO	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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(Å ²)	Q<0.9
2	IOD	B	307	1/1	0.87	0.11	47,47,47,47	1
2	IOD	D	311	1/1	0.90	0.09	51,51,51,51	1
3	NA	E	305	1/1	0.90	0.08	55,55,55,55	0
2	IOD	B	308	1/1	0.92	0.22	131,131,131,131	0
2	IOD	E	301	1/1	0.93	0.08	47,47,47,47	1
2	IOD	E	303	1/1	0.93	0.13	115,115,115,115	0
2	IOD	A	312	1/1	0.93	0.23	101,101,101,101	0
2	IOD	C	311	1/1	0.94	0.28	117,117,117,117	0
2	IOD	D	307	1/1	0.95	0.06	43,43,43,43	1
2	IOD	A	315	1/1	0.95	0.14	120,120,120,120	0
2	IOD	B	305	1/1	0.95	0.06	43,43,43,43	1
2	IOD	B	306	1/1	0.95	0.07	39,39,39,39	1
3	NA	C	312	1/1	0.95	0.06	35,35,35,35	0
3	NA	D	314	1/1	0.95	0.06	30,30,30,30	0
2	IOD	D	306	1/1	0.95	0.09	50,50,50,50	1
2	IOD	A	303	1/1	0.96	0.05	39,39,39,39	1
2	IOD	A	305	1/1	0.96	0.06	31,31,31,31	1
2	IOD	B	309	1/1	0.96	0.17	114,114,114,114	0
2	IOD	E	302	1/1	0.96	0.06	47,47,47,47	1
2	IOD	A	306	1/1	0.96	0.05	45,45,45,45	1
2	IOD	E	304	1/1	0.96	0.05	39,39,39,39	1
2	IOD	D	304	1/1	0.96	0.05	40,40,40,40	1
2	IOD	D	305	1/1	0.96	0.05	32,32,32,32	1
2	IOD	A	310	1/1	0.96	0.06	42,42,42,42	1
2	IOD	C	307	1/1	0.97	0.05	59,59,59,59	1
2	IOD	A	304	1/1	0.97	0.04	27,27,27,27	1
2	IOD	D	301	1/1	0.97	0.05	39,39,39,39	1
2	IOD	D	303	1/1	0.97	0.04	39,39,39,39	1
3	NA	C	313	1/1	0.97	0.07	26,26,26,26	0
2	IOD	D	312	1/1	0.97	0.21	102,102,102,102	0
2	IOD	A	307	1/1	0.97	0.04	31,31,31,31	1
2	IOD	B	311	1/1	0.98	0.15	94,94,94,94	0
2	IOD	D	313	1/1	0.98	0.04	30,30,30,30	1
2	IOD	D	302	1/1	0.98	0.07	58,58,58,58	0
2	IOD	B	313	1/1	0.98	0.03	34,34,34,34	1
2	IOD	C	304	1/1	0.98	0.04	40,40,40,40	1
2	IOD	C	305	1/1	0.98	0.07	25,25,25,25	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NA	A	316	1/1	0.98	0.06	21,21,21,21	0
3	NA	A	317	1/1	0.98	0.05	22,22,22,22	0
3	NA	B	314	1/1	0.98	0.03	24,24,24,24	0
2	IOD	A	309	1/1	0.98	0.03	24,24,24,24	1
2	IOD	C	308	1/1	0.98	0.10	97,97,97,97	0
2	IOD	D	308	1/1	0.98	0.21	87,87,87,87	0
2	IOD	B	310	1/1	0.98	0.20	80,80,80,80	0
2	IOD	C	303	1/1	0.99	0.03	34,34,34,34	1
2	IOD	D	310	1/1	0.99	0.02	26,26,26,26	0
2	IOD	B	304	1/1	0.99	0.03	42,42,42,42	1
2	IOD	A	301	1/1	0.99	0.02	28,28,28,28	1
2	IOD	C	306	1/1	0.99	0.03	47,47,47,47	1
2	IOD	A	311	1/1	0.99	0.04	42,42,42,42	1
2	IOD	A	308	1/1	0.99	0.04	30,30,30,30	1
2	IOD	C	310	1/1	0.99	0.02	24,24,24,24	0
2	IOD	A	313	1/1	0.99	0.02	30,30,30,30	0
2	IOD	A	302	1/1	0.99	0.02	29,29,29,29	1
2	IOD	B	301	1/1	0.99	0.03	34,34,34,34	1
2	IOD	B	302	1/1	0.99	0.03	31,31,31,31	1
2	IOD	B	312	1/1	0.99	0.04	37,37,37,37	0
2	IOD	B	303	1/1	0.99	0.03	39,39,39,39	1
2	IOD	C	301	1/1	0.99	0.03	30,30,30,30	0
2	IOD	C	302	1/1	0.99	0.02	31,31,31,31	1
2	IOD	A	314	1/1	1.00	0.02	37,37,37,37	1
2	IOD	C	309	1/1	1.00	0.05	36,36,36,36	0
2	IOD	D	309	1/1	1.00	0.02	27,27,27,27	1

6.5 Other polymers [i](#)

There are no such residues in this entry.