



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 12:41 PM EDT

PDB ID : 8DT6 / pdb_00008dt6
Title : Crystal Structure of DNA Polymerase III beta subunit from Elizabethkingia anophelis
Authors : Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2022-07-25
Resolution : 2.35 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
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

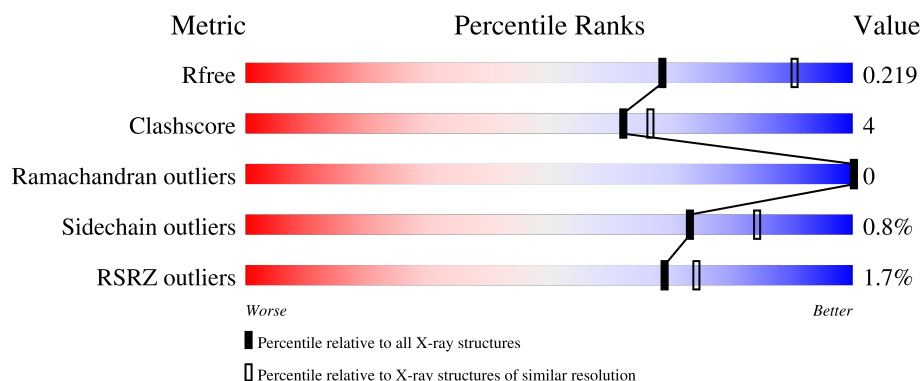
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	384	 3% 87% 10% •
1	B	384	 % 86% 10% •
1	C	384	 % 91% 8% •
1	D	384	 2% 84% 13% •

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11930 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 Beta sliding clamp.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	371	Total	C	N	O	S	0	1	0
			2801	1775	457	554	15			
1	B	371	Total	C	N	O	S	0	1	0
			2861	1813	471	562	15			
1	C	381	Total	C	N	O	S	0	0	0
			2901	1834	480	572	15			
1	D	371	Total	C	N	O	S	0	1	0
			2841	1796	463	567	15			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	377	ALA	-	expression tag	UNP A0A077EHW1
A	378	GLY	-	expression tag	UNP A0A077EHW1
A	379	HIS	-	expression tag	UNP A0A077EHW1
A	380	HIS	-	expression tag	UNP A0A077EHW1
A	381	HIS	-	expression tag	UNP A0A077EHW1
A	382	HIS	-	expression tag	UNP A0A077EHW1
A	383	HIS	-	expression tag	UNP A0A077EHW1
A	384	HIS	-	expression tag	UNP A0A077EHW1
B	377	ALA	-	expression tag	UNP A0A077EHW1
B	378	GLY	-	expression tag	UNP A0A077EHW1
B	379	HIS	-	expression tag	UNP A0A077EHW1
B	380	HIS	-	expression tag	UNP A0A077EHW1
B	381	HIS	-	expression tag	UNP A0A077EHW1
B	382	HIS	-	expression tag	UNP A0A077EHW1
B	383	HIS	-	expression tag	UNP A0A077EHW1
B	384	HIS	-	expression tag	UNP A0A077EHW1
C	377	ALA	-	expression tag	UNP A0A077EHW1
C	378	GLY	-	expression tag	UNP A0A077EHW1
C	379	HIS	-	expression tag	UNP A0A077EHW1
C	380	HIS	-	expression tag	UNP A0A077EHW1
C	381	HIS	-	expression tag	UNP A0A077EHW1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	382	HIS	-	expression tag	UNP A0A077EHW1
C	383	HIS	-	expression tag	UNP A0A077EHW1
C	384	HIS	-	expression tag	UNP A0A077EHW1
D	377	ALA	-	expression tag	UNP A0A077EHW1
D	378	GLY	-	expression tag	UNP A0A077EHW1
D	379	HIS	-	expression tag	UNP A0A077EHW1
D	380	HIS	-	expression tag	UNP A0A077EHW1
D	381	HIS	-	expression tag	UNP A0A077EHW1
D	382	HIS	-	expression tag	UNP A0A077EHW1
D	383	HIS	-	expression tag	UNP A0A077EHW1
D	384	HIS	-	expression tag	UNP A0A077EHW1

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Cl 1 1	0	0
3	C	1	Total Cl 1 1	0	0

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Na 1 1	0	0
4	D	1	Total Na 1 1	0	0

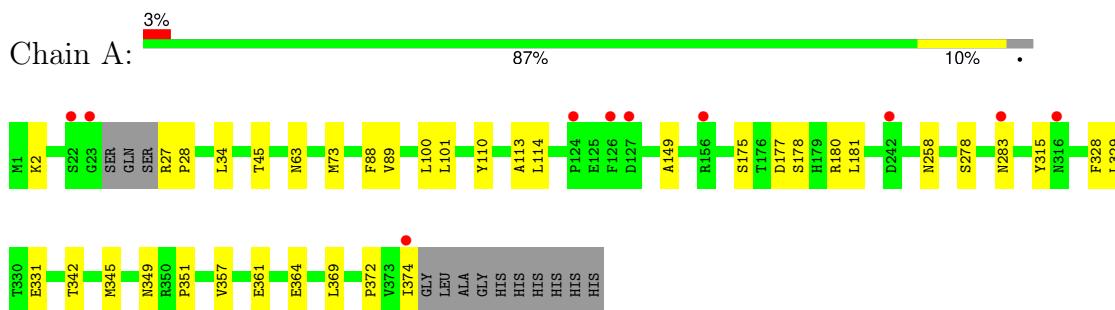
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	67	Total 67	O 67	0	0
5	B	146	Total 146	O 146	0	0
5	C	171	Total 171	O 171	0	0
5	D	129	Total 129	O 129	0	0

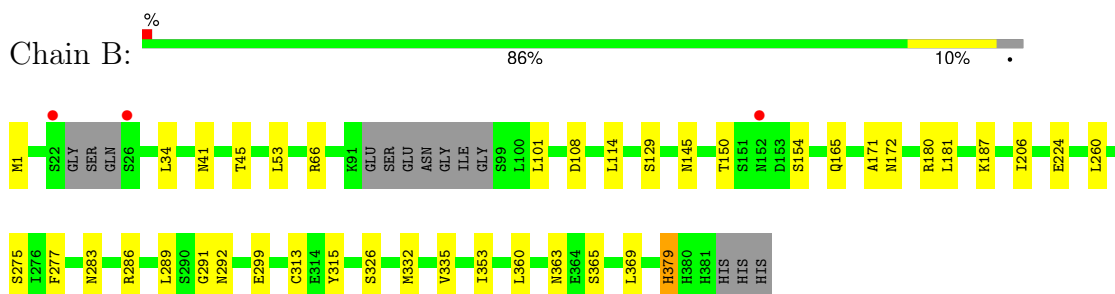
3 Residue-property plots [i](#)

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.

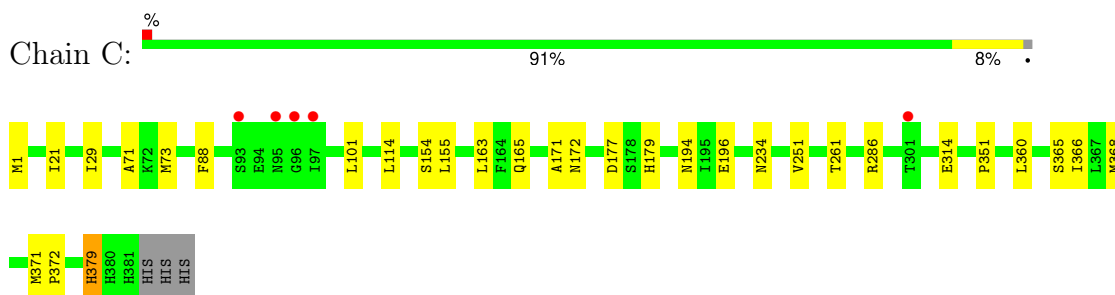
- Molecule 1: Beta sliding clamp



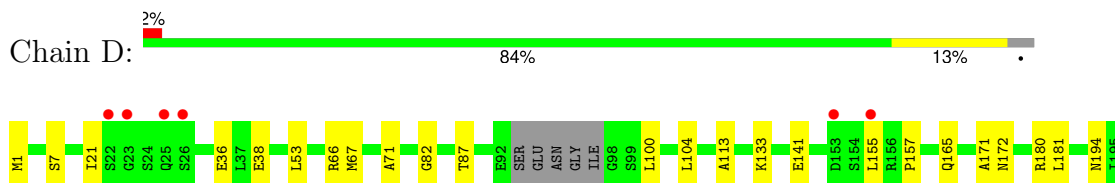
- Molecule 1: Beta sliding clamp

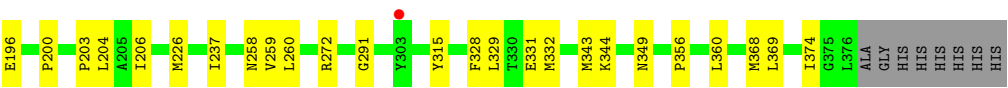


- Molecule 1: Beta sliding clamp



- Molecule 1: Beta sliding clamp





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.41Å 88.01Å 100.24Å 90.00° 95.75° 90.00°	Depositor
Resolution (Å)	40.26 – 2.35 40.26 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.26-2.35) 99.8 (40.26-2.35)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.20.1-4487	Depositor
R, R_{free}	0.176 , 0.218 0.176 , 0.219	Depositor DCC
R_{free} test set	2024 reflections (3.03%)	wwPDB-VP
Wilson B-factor (Å ²)	44.2	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11930	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.61% 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: NA, CA, CL

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	0/2851	0.51	0/3879
1	B	0.35	0/2914	0.55	0/3959
1	C	0.38	0/2951	0.58	0/4010
1	D	0.35	0/2888	0.55	0/3925
All	All	0.35	0/11604	0.55	0/15773

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 [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	2801	0	2685	21	0
1	B	2861	0	2778	25	0
1	C	2901	0	2814	20	0
1	D	2841	0	2749	30	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1	0	0	0	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	A	67	0	0	1	0
5	B	146	0	0	5	0
5	C	171	0	0	4	0
5	D	129	0	0	4	0
All	All	11930	0	11026	93	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 4.

All (93) 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:C:179:HIS:ND1	5:C:503:HOH:O	2.27	0.68
1:D:141:GLU:OE2	5:D:501:HOH:O	2.12	0.68
1:A:180:ARG:NH1	1:A:331:GLU:OE1	2.26	0.67
1:B:108:ASP:OD2	5:B:501:HOH:O	2.14	0.64
1:B:360:LEU:HD13	1:B:365:SER:HA	1.82	0.61
1:D:180:ARG:NH1	1:D:331:GLU:OE1	2.31	0.60
1:B:53:LEU:HD11	1:B:206:ILE:HG21	1.83	0.60
1:B:275:SER:HB2	1:B:283:ASN:OD1	2.04	0.58
1:C:21:ILE:HD13	1:C:71:ALA:CB	2.34	0.58
1:B:353:ILE:HG12	1:B:369:LEU:CD2	2.34	0.57
1:A:349:ASN:HA	1:A:374:ILE:HD11	1.87	0.56
1:D:53:LEU:HD11	1:D:206:ILE:HG21	1.88	0.56
1:B:379:HIS:HE1	5:C:560:HOH:O	1.89	0.55
1:B:292:ASN:HB3	1:B:313:CYS:O	2.07	0.55
1:C:1:MET:N	5:C:504:HOH:O	2.31	0.55
1:B:34:LEU:HD21	1:B:66:ARG:NH2	2.23	0.54
1:B:41:ASN:ND2	5:B:513:HOH:O	2.40	0.53
1:B:1:MET:N	5:B:504:HOH:O	2.26	0.53
1:B:180:ARG:HG2	1:B:332:MET:HE2	1.91	0.53
1:C:155:LEU:HD11	1:C:177:ASP:HA	1.90	0.52
1:D:36:GLU:HG2	1:D:66:ARG:HG3	1.92	0.52
1:B:291:GLY:O	1:B:315:TYR:HB3	2.10	0.52
1:A:351:PRO:HA	1:A:372:PRO:HD3	1.92	0.52
1:A:100:LEU:HD23	1:A:113:ALA:HA	1.92	0.50
1:A:180:ARG:HD3	1:A:328:PHE:HB3	1.94	0.50
1:C:366:ILE:HD11	1:C:368:MET:HE3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:194:ASN:HD22	1:D:194:ASN:N	2.11	0.49
1:C:261:THR:HB	1:C:314:GLU:HB3	1.95	0.49
1:D:226:MET:HE3	1:D:237:ILE:HG22	1.95	0.49
1:D:181:LEU:HB3	1:D:369:LEU:HB3	1.95	0.48
1:D:260:LEU:HD23	1:D:343:MET:HE3	1.96	0.48
1:D:349:ASN:HA	1:D:374:ILE:HD11	1.94	0.48
1:A:177:ASP:O	1:A:178:SER:OG	2.29	0.48
1:B:224:GLU:O	5:B:502:HOH:O	2.20	0.47
1:B:154:SER:O	1:C:286:ARG:NH1	2.48	0.47
1:A:2:LYS:HG3	1:A:89:VAL:HG22	1.97	0.46
1:A:329:LEU:HD12	1:A:329:LEU:HA	1.69	0.46
1:D:7:SER:OG	1:D:82:GLY:O	2.29	0.46
1:A:278:SER:OG	1:A:283:ASN:OD1	2.29	0.46
1:D:133:LYS:NZ	5:D:505:HOH:O	2.35	0.46
1:C:163:LEU:HD11	1:C:196:GLU:HG3	1.97	0.46
1:D:165:GLN:HG2	1:D:196:GLU:HG3	1.97	0.46
1:A:101:LEU:HB2	1:A:114:LEU:HD21	1.97	0.46
1:D:66:ARG:NH1	5:D:504:HOH:O	2.34	0.46
1:D:258:ASN:HB3	1:D:315:TYR:OH	2.16	0.46
1:D:1:MET:HE2	1:D:67:MET:HE2	1.98	0.45
1:C:88:PHE:HB3	1:C:101:LEU:HD11	1.99	0.45
1:D:291:GLY:O	1:D:315:TYR:HB3	2.17	0.45
1:B:181:LEU:HB3	1:B:369:LEU:HB2	1.99	0.45
1:D:356:PRO:HG2	1:D:360:LEU:HD11	2.00	0.45
1:A:27:ARG:HA	1:A:28:PRO:HD3	1.87	0.44
1:D:87:THR:HB	1:D:104:LEU:HB2	1.99	0.44
1:B:187:LYS:HB2	1:B:363:ASN:HB3	2.00	0.44
1:D:155:LEU:O	1:D:157:PRO:HD3	2.18	0.44
1:D:165:GLN:HB2	1:D:172:ASN:HB3	1.99	0.44
1:B:101:LEU:HB2	1:B:114:LEU:HD21	1.99	0.44
1:C:351:PRO:HA	1:C:372:PRO:HD3	1.99	0.44
1:D:21:ILE:HD13	1:D:71:ALA:CB	2.48	0.44
1:A:149:ALA:HB3	1:A:175:SER:OG	2.19	0.43
1:B:145:ASN:HA	1:B:335:VAL:HG11	2.01	0.43
1:C:101:LEU:HB2	1:C:114:LEU:HD21	2.00	0.43
1:C:371:MET:HE3	1:C:372:PRO:HD2	2.00	0.43
1:D:259:VAL:HG22	1:D:344:LYS:HG2	1.98	0.43
1:B:260:LEU:HD13	1:B:289:LEU:HD21	2.01	0.42
1:D:200:PRO:HG2	1:D:203:PRO:CG	2.48	0.42
1:C:165:GLN:O	1:C:171:ALA:HA	2.19	0.42
1:B:34:LEU:HB3	1:B:45:THR:HB	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:514:HOH:O	1:C:379:HIS:HE1	2.03	0.42
1:D:272:ARG:NH1	5:D:502:HOH:O	2.28	0.42
1:A:63:ASN:N	5:A:503:HOH:O	2.51	0.42
1:D:165:GLN:O	1:D:171:ALA:HA	2.19	0.42
1:C:360:LEU:HD13	1:C:365:SER:HA	2.02	0.41
1:A:88:PHE:HB3	1:A:101:LEU:HD11	2.02	0.41
1:C:165:GLN:HB2	1:C:172:ASN:HB2	2.02	0.41
1:D:329:LEU:HD12	1:D:329:LEU:HA	1.80	0.41
1:B:165:GLN:O	1:B:171:ALA:HA	2.20	0.41
1:C:29:ILE:HD12	1:C:29:ILE:HA	1.92	0.41
1:D:100:LEU:HD23	1:D:113:ALA:HA	2.01	0.41
1:B:353:ILE:HG12	1:B:369:LEU:HD21	2.00	0.41
1:D:180:ARG:HD3	1:D:328:PHE:HB3	2.03	0.41
1:D:204:LEU:HD23	1:D:204:LEU:HA	1.88	0.41
1:A:361:GLU:HG3	1:A:364:GLU:OE1	2.21	0.41
1:A:345:MET:HE3	1:A:345:MET:HB2	1.98	0.40
1:B:286:ARG:NH1	1:C:154:SER:O	2.51	0.40
1:D:332:MET:HG3	1:D:368:MET:SD	2.61	0.40
1:A:110:TYR:HB3	1:B:277:PHE:CE2	2.56	0.40
1:C:234:ASN:HB3	5:C:568:HOH:O	2.21	0.40
1:A:34:LEU:HB3	1:A:45:THR:HB	2.03	0.40
1:A:181:LEU:HB3	1:A:369:LEU:HB3	2.03	0.40
1:A:258:ASN:HB3	1:A:315:TYR:OH	2.21	0.40
1:A:342:THR:HG23	1:A:357:VAL:HG22	2.03	0.40
1:B:165:GLN:HB2	1:B:172:ASN:HB2	2.02	0.40
1:C:194:ASN:N	1:C:194:ASN:HD22	2.18	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	368/384 (96%)	361 (98%)	7 (2%)	0	100	100
1	B	366/384 (95%)	360 (98%)	6 (2%)	0	100	100
1	C	379/384 (99%)	373 (98%)	6 (2%)	0	100	100
1	D	368/384 (96%)	360 (98%)	8 (2%)	0	100	100
All	All	1481/1536 (96%)	1454 (98%)	27 (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	305/345 (88%)	304 (100%)	1 (0%)	86	92
1	B	319/345 (92%)	314 (98%)	5 (2%)	55	70
1	C	321/345 (93%)	318 (99%)	3 (1%)	70	82
1	D	317/345 (92%)	316 (100%)	1 (0%)	86	92
All	All	1262/1380 (91%)	1252 (99%)	10 (1%)	73	84

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	MET
1	B	129	SER
1	B	150	THR
1	B	299	GLU
1	B	326	SER
1	B	379	HIS
1	C	73	MET
1	C	251	VAL
1	C	379	HIS
1	D	38	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	GLN
1	A	165	GLN
1	A	169	ASN
1	A	179	HIS
1	A	225	ASN
1	B	380	HIS
1	C	213	ASN
1	D	11	GLN
1	D	109	ASN
1	D	234	ASN

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 13 ligands modelled in this entry, 13 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 ⓘ

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	371/384 (96%)	0.14	10 (2%) 56 63	35, 63, 97, 116	1 (0%)
1	B	371/384 (96%)	-0.20	3 (0%) 82 86	25, 49, 74, 115	1 (0%)
1	C	381/384 (99%)	-0.25	5 (1%) 75 79	32, 44, 76, 102	0
1	D	371/384 (96%)	-0.16	7 (1%) 66 71	22, 50, 78, 123	1 (0%)
All	All	1494/1536 (97%)	-0.12	25 (1%) 69 74	22, 51, 86, 123	3 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	23	GLY	4.9
1	C	95	ASN	3.6
1	A	316	ASN	3.4
1	A	127	ASP	3.2
1	C	96	GLY	3.2
1	A	374	ILE	3.0
1	A	126	PHE	2.7
1	A	283	ASN	2.7
1	A	242	ASP	2.6
1	C	97	ILE	2.6
1	D	303	TYR	2.6
1	B	22	SER	2.5
1	B	152	ASN	2.5
1	C	93	SER	2.4
1	D	22	SER	2.4
1	A	124	PRO	2.3
1	D	153	ASP	2.3
1	D	23	GLY	2.3
1	B	26	SER	2.3
1	C	301	THR	2.3
1	A	22	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	25	GLN	2.2
1	D	155	LEU	2.2
1	A	156	ARG	2.1
1	D	26	SER	2.1

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
2	CA	D	401	1/1	0.85	0.12	88,88,88,88	0
2	CA	B	402	1/1	0.86	0.13	92,92,92,92	0
4	NA	D	404	1/1	0.89	0.12	43,43,43,43	0
2	CA	A	401	1/1	0.92	0.09	93,93,93,93	0
2	CA	C	403	1/1	0.95	0.04	80,80,80,80	0
2	CA	D	402	1/1	0.96	0.09	74,74,74,74	0
2	CA	B	403	1/1	0.97	0.07	64,64,64,64	0
4	NA	B	404	1/1	0.97	0.07	44,44,44,44	0
2	CA	C	402	1/1	0.97	0.04	53,53,53,53	0
2	CA	D	403	1/1	0.98	0.04	55,55,55,55	0
2	CA	C	404	1/1	0.99	0.03	36,36,36,36	0
3	CL	B	401	1/1	0.99	0.04	39,39,39,39	0
3	CL	C	401	1/1	1.00	0.04	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.