



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 05:33 AM UTC

PDB ID : 6QJ4 / pdb_00006qj4
Title : Crystal structure of the C. thermophilum condensin Ycs4-Brn1 subcomplex bound to the Smc4 ATPase head in complex with the C-terminal domain of Brn1
Authors : Hassler, M.; Haering, C.H.; Kschonsak, M.
Deposited on : 2019-01-22
Resolution : 5.80 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

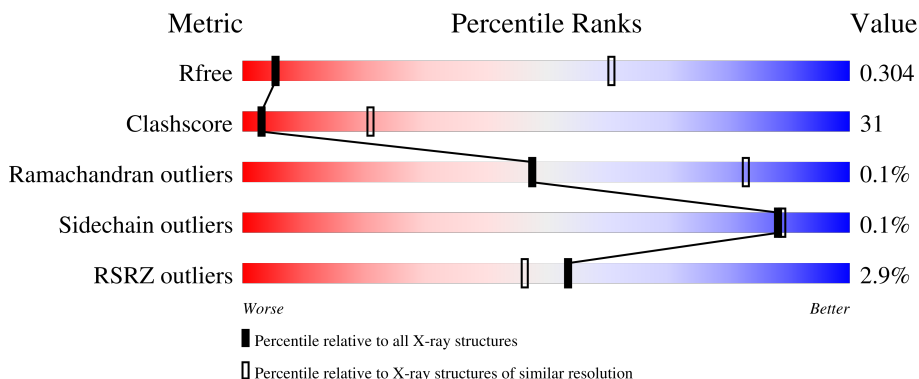
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.80 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	1125 (7.60-4.00)
Clashscore	190562	1190 (7.60-4.00)
Ramachandran outliers	187476	1019 (7.60-4.00)
Sidechain outliers	187428	1009 (7.60-3.98)
RSRZ outliers	180081	1118 (7.60-4.00)

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	1155	2% 41% 42% 17%
2	B	197	2% 12% 13% 75%
3	C	403	% 30% 46% 24%
4	D	23	87% 9% .
5	E	135	% 27% 26% 47%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10778 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 Condensin complex subunit 1, Condensin complex subunit 1, Condensin complex subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	963	Total	C	N	O	S	0	0	0
			7240	4571	1260	1361	48			

There are 121 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	initiating methionine	UNP G0SB82
A	?	-	CYS	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	ILE	deletion	UNP G0SB82
A	?	-	PHE	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	HIS	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	LEU	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	PHE	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	TYR	deletion	UNP G0SB82
A	?	-	GLY	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	GLU	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82
A	?	-	GLY	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	LEU	deletion	UNP G0SB82
A	?	-	LEU	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	CYS	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	THR	deletion	UNP G0SB82
A	?	-	HIS	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	THR	deletion	UNP G0SB82
A	?	-	LYS	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82
A	?	-	LYS	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82
A	?	-	ILE	deletion	UNP G0SB82
A	?	-	HIS	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	ARG	deletion	UNP G0SB82
A	?	-	LEU	deletion	UNP G0SB82
A	?	-	ARG	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	GLU	deletion	UNP G0SB82
A	?	-	LEU	deletion	UNP G0SB82
A	?	-	VAL	deletion	UNP G0SB82
A	?	-	LYS	deletion	UNP G0SB82
A	?	-	LYS	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	ARG	deletion	UNP G0SB82
A	?	-	GLN	deletion	UNP G0SB82
A	?	-	GLN	deletion	UNP G0SB82
A	?	-	GLU	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	ARG	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	ARG	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82
A	?	-	GLU	deletion	UNP G0SB82
A	?	-	MET	deletion	UNP G0SB82

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP G0SB82
A	?	-	ILE	deletion	UNP G0SB82
A	?	-	GLU	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	GLN	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	THR	deletion	UNP G0SB82
A	?	-	LEU	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82
A	?	-	GLY	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	THR	deletion	UNP G0SB82
A	?	-	VAL	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	GLN	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	PRO	deletion	UNP G0SB82
A	?	-	THR	deletion	UNP G0SB82
A	?	-	LYS	deletion	UNP G0SB82
A	?	-	ARG	deletion	UNP G0SB82
A	?	-	GLN	deletion	UNP G0SB82
A	?	-	ASN	deletion	UNP G0SB82
A	?	-	LYS	deletion	UNP G0SB82
A	?	-	ASP	deletion	UNP G0SB82
A	?	-	ARG	deletion	UNP G0SB82
A	?	-	HIS	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	LEU	deletion	UNP G0SB82
A	?	-	GLY	deletion	UNP G0SB82
A	?	-	ALA	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	THR	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	ARG	deletion	UNP G0SB82

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	deletion	UNP G0SB82
A	?	-	GLY	deletion	UNP G0SB82
A	?	-	GLY	deletion	UNP G0SB82
A	?	-	GLY	deletion	UNP G0SB82
A	?	-	GLN	deletion	UNP G0SB82
A	?	-	ASN	deletion	UNP G0SB82
A	?	-	LYS	deletion	UNP G0SB82
A	?	-	SER	deletion	UNP G0SB82
A	?	-	LYS	deletion	UNP G0SB82
A	?	-	GLN	deletion	UNP G0SB82
A	?	-	GLN	deletion	UNP G0SB82

- Molecule 2 is a protein called Condensin complex subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	50	Total	C	N	O	S	0	0	0
			392	256	62	73	1			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	222	GLY	-	expression tag	UNP G0SBJ6
B	223	HIS	-	expression tag	UNP G0SBJ6
B	224	MET	-	expression tag	UNP G0SBJ6

- Molecule 3 is a protein called Uncharacterized protein,Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	306	Total	C	N	O	S	0	0	0
			2443	1563	419	450	11			

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	261	MET	-	initiating methionine	UNP G0S2G2
C	262	ALA	-	expression tag	UNP G0S2G2
C	1360	SER	-	linker	UNP G0S2G2
C	1361	GLY	-	linker	UNP G0S2G2
C	1362	GLY	-	linker	UNP G0S2G2
C	1363	SER	-	linker	UNP G0S2G2
C	1364	GLY	-	linker	UNP G0S2G2
C	1365	GLY	-	linker	UNP G0S2G2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1366	SER	ALA	conflict	UNP G0S2G2
C	1543	GLY	-	expression tag	UNP G0S2G2
C	1544	ILE	-	expression tag	UNP G0S2G2
C	1545	SER	-	expression tag	UNP G0S2G2
C	1546	SER	-	expression tag	UNP G0S2G2
C	1547	ALA	-	expression tag	UNP G0S2G2
C	1548	SER	-	expression tag	UNP G0S2G2
C	1549	HIS	-	expression tag	UNP G0S2G2
C	1550	HIS	-	expression tag	UNP G0S2G2
C	1551	HIS	-	expression tag	UNP G0S2G2
C	1552	HIS	-	expression tag	UNP G0S2G2
C	1553	HIS	-	expression tag	UNP G0S2G2
C	1554	HIS	-	expression tag	UNP G0S2G2
C	1555	HIS	-	expression tag	UNP G0S2G2
C	1556	HIS	-	expression tag	UNP G0S2G2

- Molecule 4 is a protein called Brn1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	22	Total	C	N	O	0	0	0
			110	66	22	22			

- Molecule 5 is a protein called Condensin complex subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	71	Total	C	N	O	S	0	0	0
			593	379	100	110	4			

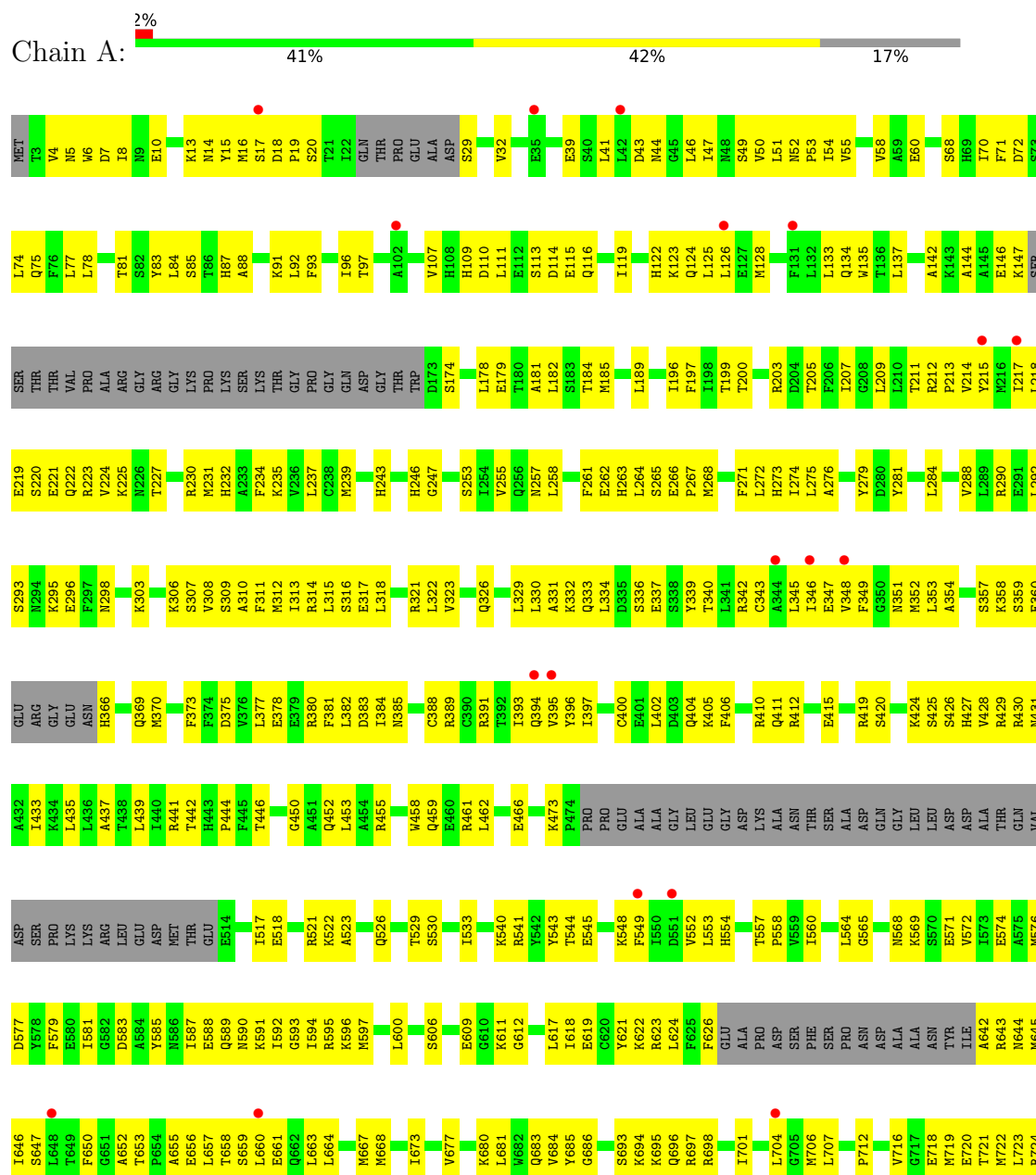
There is a discrepancy between the modelled and reference sequences:

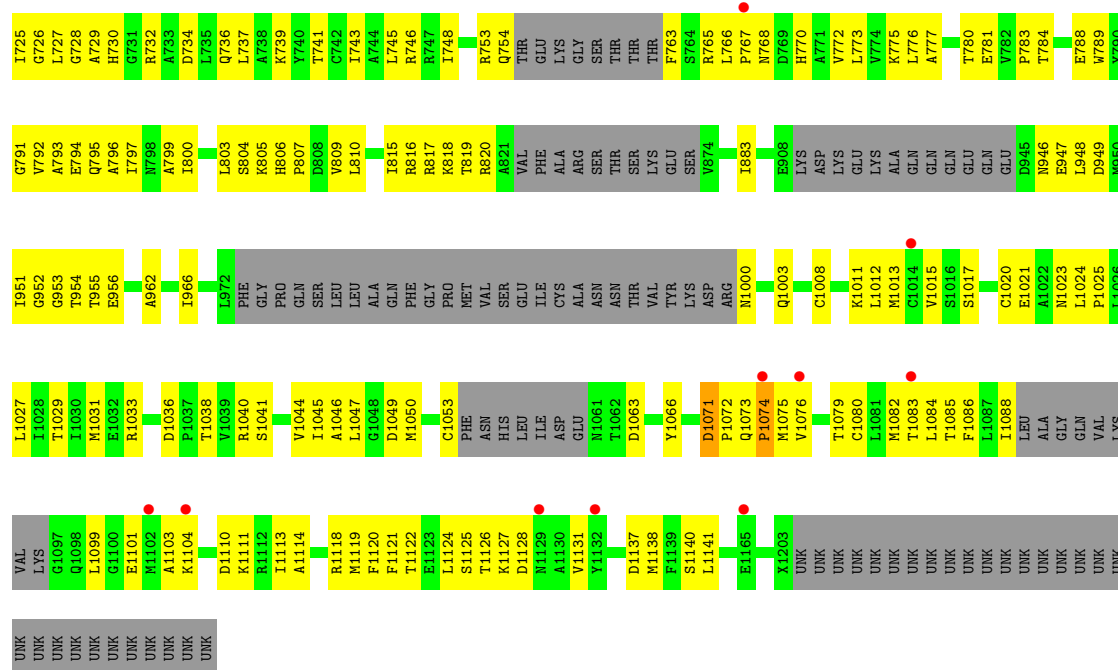
Chain	Residue	Modelled	Actual	Comment	Reference
E	764	MET	VAL	conflict	UNP G0SBJ6

3 Residue-property plots

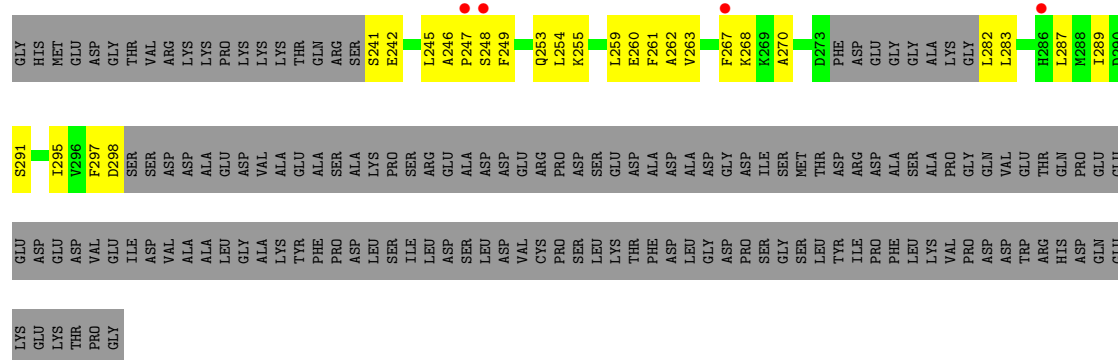
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Condensin complex subunit 1, Condensin complex subunit 1, Condensin complex subunit 1

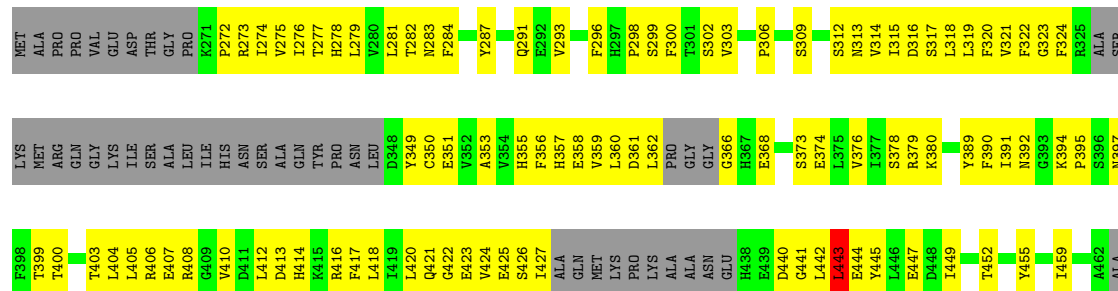




• Molecule 2: Condensin complex subunit 2



• Molecule 3: Uncharacterized protein, Uncharacterized protein

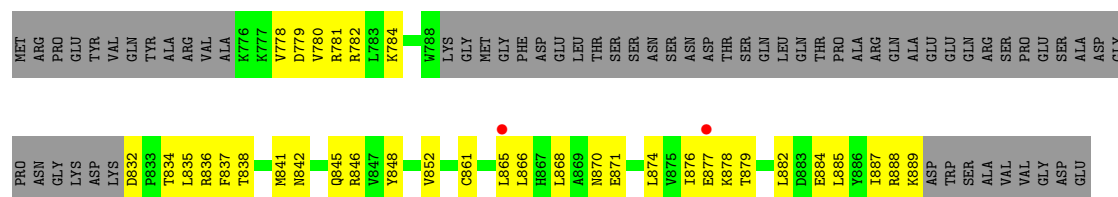




Chain D: 87% 9% .



Chain E: 27% 26% 47%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.41Å 82.38Å 177.83Å 90.00° 98.77° 90.00°	Depositor
Resolution (Å)	47.74 – 5.80 47.74 – 5.80	Depositor EDS
% Data completeness (in resolution range)	96.5 (47.74-5.80) 96.3 (47.74-5.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 5.73Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.292 , 0.301 0.293 , 0.304	Depositor DCC
R_{free} test set	347 reflections (4.30%)	wwPDB-VP
Wilson B-factor (Å ²)	327.9	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 321.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	10778	wwPDB-VP
Average B, all atoms (Å ²)	210.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.74% 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](#)

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	0.24	0/7199	0.44	2/9737 (0.0%)
2	B	0.21	0/398	0.61	0/534
3	C	0.21	0/2489	0.45	2/3352 (0.1%)
5	E	0.19	0/601	0.37	0/808
All	All	0.23	0/10687	0.45	4/14431 (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	A	0	2
3	C	0	1
All	All	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	443	LEU	CA-C-N	7.54	135.27	121.70
3	C	443	LEU	C-N-CA	7.54	135.27	121.70
1	A	1127	LYS	CA-C-N	6.25	132.96	121.70
1	A	1127	LYS	C-N-CA	6.25	132.96	121.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1071	ASP	Peptide
1	A	243	HIS	Peptide
3	C	443	LEU	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	7240	0	6987	453	1
2	B	392	0	398	34	0
3	C	2443	0	2454	173	0
4	D	110	0	31	1	0
5	E	593	0	610	31	0
All	All	10778	0	10480	665	1

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 31.

The worst 5 of 665 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:C:356:PHE:O	3:C:374:GLU:HA	1.71	0.90
3:C:1494:GLU:HA	3:C:1497:ARG:HH22	1.43	0.83
1:A:265:SER:HB3	1:A:311:PHE:HB2	1.61	0.83
1:A:723:LEU:HA	1:A:727:LEU:HB2	1.59	0.82
1:A:266:GLU:OE1	1:A:314:ARG:HB2	1.78	0.82

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:ARG:NH1	1:A:446:THR:O[2_745]	2.15	0.05

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	911/1155 (79%)	819 (90%)	91 (10%)	1 (0%)	48	83
2	B	46/197 (23%)	36 (78%)	10 (22%)	0	100	100
3	C	294/403 (73%)	266 (90%)	28 (10%)	0	100	100
5	E	67/135 (50%)	58 (87%)	9 (13%)	0	100	100
All	All	1318/1890 (70%)	1179 (90%)	138 (10%)	1 (0%)	48	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1074	PRO

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	728/953 (76%)	728 (100%)	0	100	100
2	B	43/166 (26%)	43 (100%)	0	100	100
3	C	274/345 (79%)	273 (100%)	1 (0%)	84	84
5	E	69/122 (57%)	69 (100%)	0	100	100
All	All	1114/1586 (70%)	1113 (100%)	1 (0%)	88	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	1473	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1073	GLN
3	C	1484	ASN

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Mol	Chain	Res	Type
3	C	1463	HIS
3	C	1490	ASN
1	A	394	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2
4	D	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1180:UNK	C	1188:UNK	N	12.75
1	D	15:UNK	C	17:UNK	N	11.71
1	A	1165:GLU	C	1169:UNK	N	5.63

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	8:UNK	C	10:UNK	N	3.08

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	935/1155 (80%)	0.21	28 (2%) 52 46	128, 199, 242, 282	0
2	B	50/197 (25%)	0.52	4 (8%) 18 24	147, 213, 247, 260	0
3	C	306/403 (75%)	0.16	5 (1%) 70 59	186, 230, 288, 330	0
4	D	0/23	-	-	-	-
5	E	71/135 (52%)	0.26	2 (2%) 55 47	188, 234, 264, 272	0
All	All	1362/1913 (71%)	0.21	39 (2%) 53 46	128, 210, 258, 330	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	1406	GLN	4.8
1	A	217	ILE	4.2
1	A	549	PHE	3.9
5	E	877	GLU	3.9
2	B	248	SER	3.4

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.