



wwPDB X-ray Structure Validation Summary Report ⓘ

May 7, 2026 – 09:14 AM EDT

PDB ID : 4N0A / pdb_00004n0a
Title : Crystal structure of Lsm2-3-Pat1C complex from *Saccharomyces cerevisiae*
Authors : Wu, D.H.
Deposited on : 2013-10-01
Resolution : 3.15 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

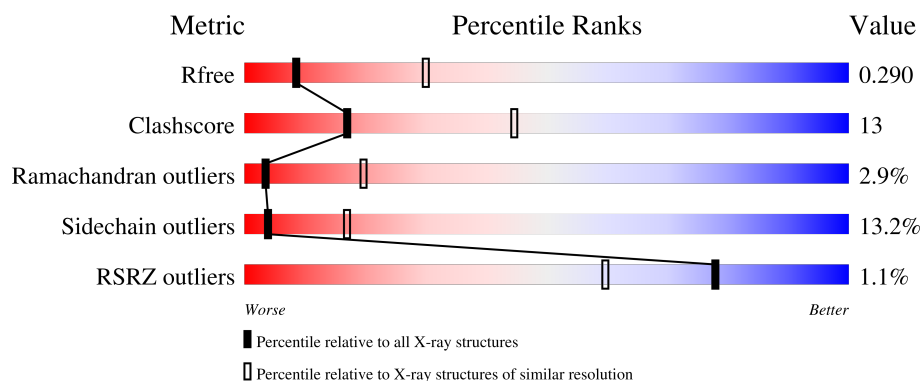
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	89	% 58% 27% • 10%
1	B	89	2% 43% 40% 6% • 10%
1	E	89	69% 8% 24%
1	F	89	58% 21% • 16%
2	C	109	% 49% 25% 6% 21%

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Mol	Chain	Length	Quality of chain
2	D	109	% 44%27%6%•23%
2	G	109	50%26%•21%
3	H	380	% 58%19%5%•16%
3	I	380	% 56%23%••17%
3	J	380	2% 61%18%••16%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12345 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 U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	80	Total	C	N	O	S	0	0	0
			633	395	108	126	4			
1	B	80	Total	C	N	O	S	0	0	0
			634	395	108	127	4			
1	E	68	Total	C	N	O	S	0	0	0
			534	334	93	103	4			
1	F	75	Total	C	N	O	S	0	0	0
			594	372	102	116	4			

- Molecule 2 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	86	Total	C	N	O	S	0	0	0
			704	446	117	137	4			
2	D	84	Total	C	N	O	S	0	0	0
			689	438	113	134	4			
2	G	86	Total	C	N	O	S	0	0	0
			704	446	117	137	4			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-13	MET	-	expression tag	UNP P38203
C	-12	GLY	-	expression tag	UNP P38203
C	-11	SER	-	expression tag	UNP P38203
C	-10	SER	-	expression tag	UNP P38203
C	-9	HIS	-	expression tag	UNP P38203
C	-8	HIS	-	expression tag	UNP P38203
C	-7	HIS	-	expression tag	UNP P38203
C	-6	HIS	-	expression tag	UNP P38203
C	-5	HIS	-	expression tag	UNP P38203
C	-4	HIS	-	expression tag	UNP P38203

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	SER	-	expression tag	UNP P38203
C	-2	GLN	-	expression tag	UNP P38203
C	-1	ASP	-	expression tag	UNP P38203
C	0	PRO	-	expression tag	UNP P38203
D	-13	MET	-	expression tag	UNP P38203
D	-12	GLY	-	expression tag	UNP P38203
D	-11	SER	-	expression tag	UNP P38203
D	-10	SER	-	expression tag	UNP P38203
D	-9	HIS	-	expression tag	UNP P38203
D	-8	HIS	-	expression tag	UNP P38203
D	-7	HIS	-	expression tag	UNP P38203
D	-6	HIS	-	expression tag	UNP P38203
D	-5	HIS	-	expression tag	UNP P38203
D	-4	HIS	-	expression tag	UNP P38203
D	-3	SER	-	expression tag	UNP P38203
D	-2	GLN	-	expression tag	UNP P38203
D	-1	ASP	-	expression tag	UNP P38203
D	0	PRO	-	expression tag	UNP P38203
G	-13	MET	-	expression tag	UNP P38203
G	-12	GLY	-	expression tag	UNP P38203
G	-11	SER	-	expression tag	UNP P38203
G	-10	SER	-	expression tag	UNP P38203
G	-9	HIS	-	expression tag	UNP P38203
G	-8	HIS	-	expression tag	UNP P38203
G	-7	HIS	-	expression tag	UNP P38203
G	-6	HIS	-	expression tag	UNP P38203
G	-5	HIS	-	expression tag	UNP P38203
G	-4	HIS	-	expression tag	UNP P38203
G	-3	SER	-	expression tag	UNP P38203
G	-2	GLN	-	expression tag	UNP P38203
G	-1	ASP	-	expression tag	UNP P38203
G	0	PRO	-	expression tag	UNP P38203

- Molecule 3 is a protein called DNA topoisomerase 2-associated protein PAT1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	318	Total	C	N	O	S	0	0	0
			2595	1676	423	488	8			
3	I	317	Total	C	N	O	S	0	0	0
			2586	1671	422	485	8			
3	J	318	Total	C	N	O	S	0	0	0
			2595	1676	423	488	8			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	417	GLY	-	expression tag	UNP P25644
H	418	PRO	-	expression tag	UNP P25644
H	419	LEU	-	expression tag	UNP P25644
H	420	GLY	-	expression tag	UNP P25644
H	421	SER	-	expression tag	UNP P25644
H	688	VAL	ASP	engineered mutation	UNP P25644
I	417	GLY	-	expression tag	UNP P25644
I	418	PRO	-	expression tag	UNP P25644
I	419	LEU	-	expression tag	UNP P25644
I	420	GLY	-	expression tag	UNP P25644
I	421	SER	-	expression tag	UNP P25644
I	688	VAL	ASP	engineered mutation	UNP P25644
J	417	GLY	-	expression tag	UNP P25644
J	418	PRO	-	expression tag	UNP P25644
J	419	LEU	-	expression tag	UNP P25644
J	420	GLY	-	expression tag	UNP P25644
J	421	SER	-	expression tag	UNP P25644
J	688	VAL	ASP	engineered mutation	UNP P25644

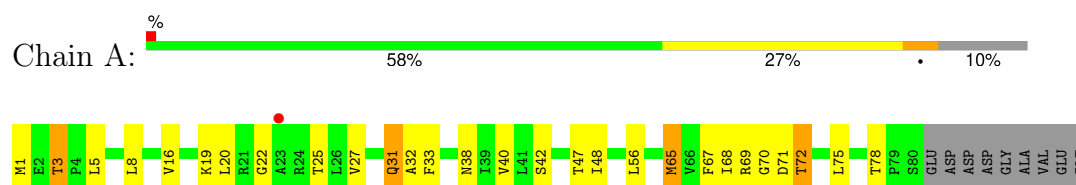
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	7	Total O 7 7	0	0
4	B	3	Total O 3 3	0	0
4	C	11	Total O 11 11	0	0
4	D	13	Total O 13 13	0	0
4	E	2	Total O 2 2	0	0
4	F	3	Total O 3 3	0	0
4	G	3	Total O 3 3	0	0
4	H	13	Total O 13 13	0	0
4	I	13	Total O 13 13	0	0
4	J	9	Total O 9 9	0	0

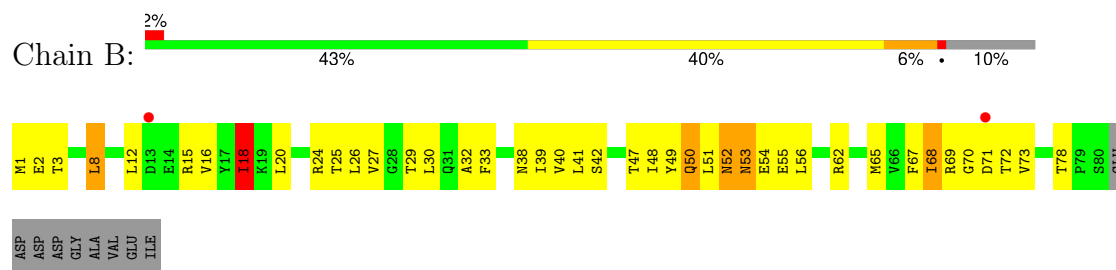
3 Residue-property plots [i](#)

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.

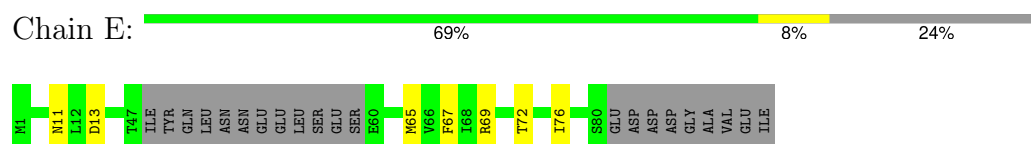
- Molecule 1: U6 snRNA-associated Sm-like protein LSm3



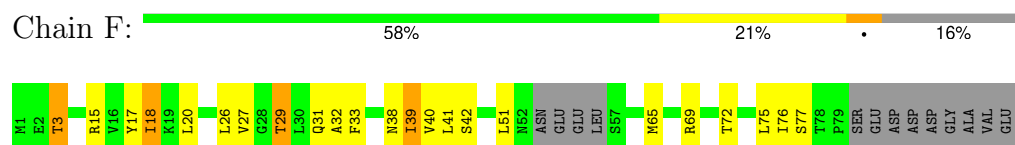
- Molecule 1: U6 snRNA-associated Sm-like protein LSm3



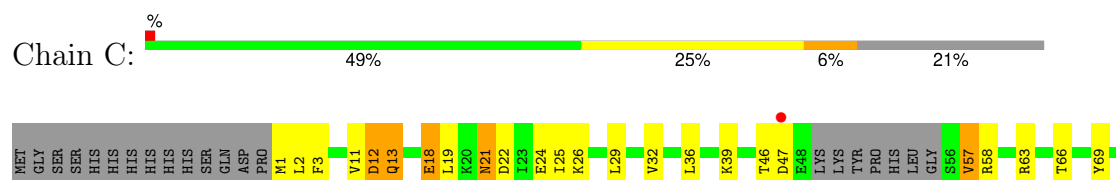
- Molecule 1: U6 snRNA-associated Sm-like protein LSm3

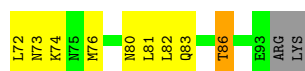


- Molecule 1: U6 snRNA-associated Sm-like protein LSm3

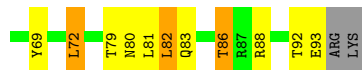
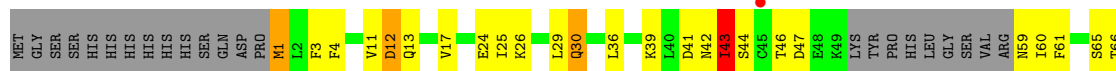
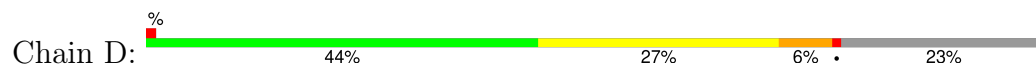


- Molecule 2: U6 snRNA-associated Sm-like protein LSm2

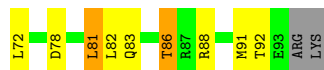




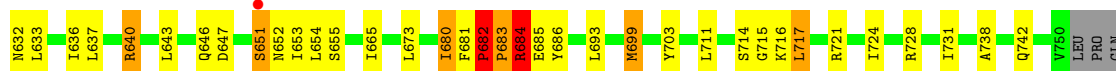
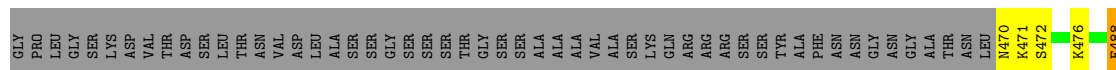
• Molecule 2: U6 snRNA-associated Sm-like protein LSm2



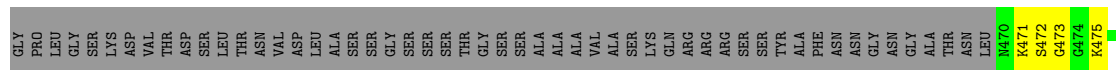
• Molecule 2: U6 snRNA-associated Sm-like protein LSm2

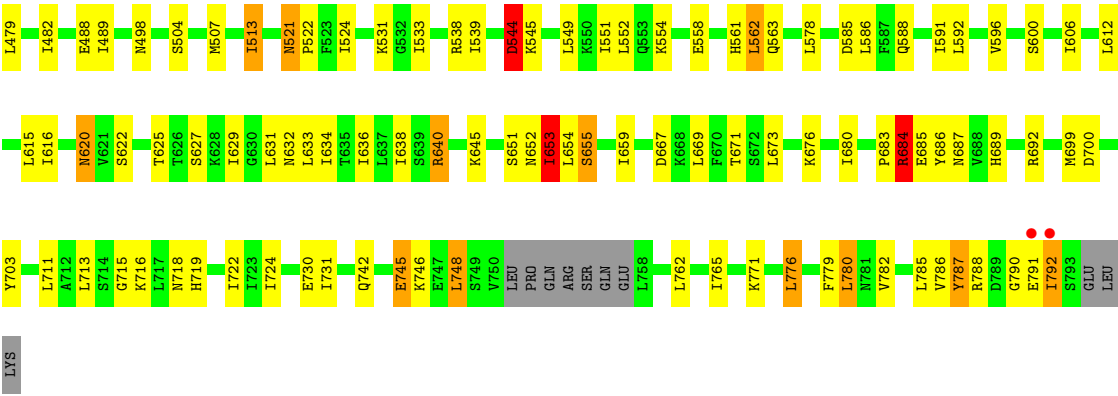


• Molecule 3: DNA topoisomerase 2-associated protein PAT1

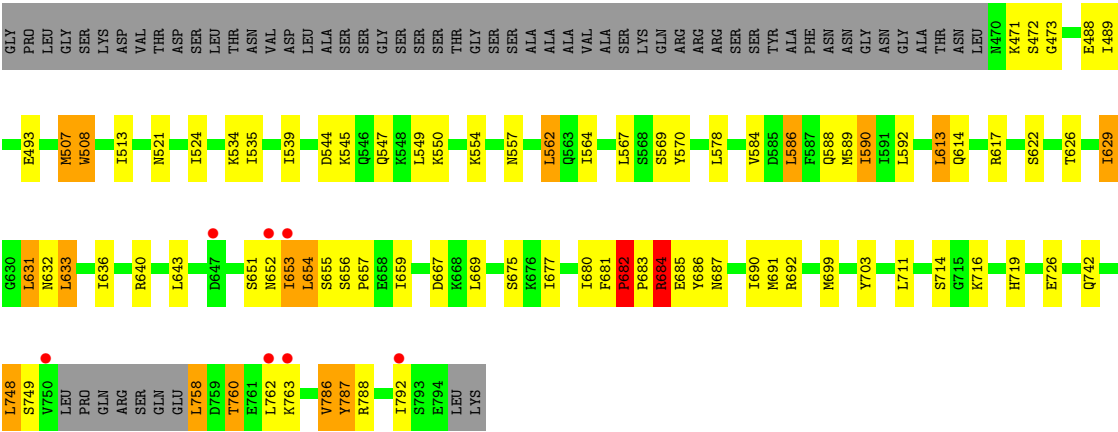


• Molecule 3: DNA topoisomerase 2-associated protein PAT1





● Molecule 3: DNA topoisomerase 2-associated protein PAT1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	138.45Å 251.51Å 120.31Å 90.00° 112.09° 90.00°	Depositor
Resolution (Å)	19.88 – 3.15 19.88 – 3.15	Depositor EDS
% Data completeness (in resolution range)	98.6 (19.88-3.15) 98.6 (19.88-3.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 3.15Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.272 , 0.300 0.260 , 0.290	Depositor DCC
R_{free} test set	3283 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	115.8	Xtriage
Anisotropy	0.427	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 28.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12345	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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

5.1 Standard geometry

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	0.53	0/639	0.84	2/865 (0.2%)
1	B	0.68	1/640 (0.2%)	0.86	0/866
1	E	0.48	0/538	0.75	0/726
1	F	0.42	0/599	0.74	0/809
2	C	0.57	0/710	0.79	0/955
2	D	0.50	0/695	0.82	0/934
2	G	0.48	0/710	0.80	0/955
3	H	0.51	0/2635	0.87	1/3552 (0.0%)
3	I	0.45	0/2626	0.89	2/3540 (0.1%)
3	J	0.43	0/2635	0.85	0/3552
All	All	0.49	1/12427 (0.0%)	0.85	5/16754 (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
3	H	0	1
3	J	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	18	ILE	CA-CB	5.34	1.61	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	682	PRO	N-CA-C	5.94	117.94	110.70
1	A	78	THR	CA-C-N	5.41	126.16	120.11
1	A	78	THR	C-N-CA	5.41	126.16	120.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	521	ASN	CA-C-N	5.23	126.38	119.84
3	I	521	ASN	C-N-CA	5.23	126.38	119.84

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	H	682	PRO	Peptide
3	J	682	PRO	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	633	0	643	20	1
1	B	634	0	643	32	1
1	E	534	0	552	3	0
1	F	594	0	608	15	0
2	C	704	0	713	30	0
2	D	689	0	699	28	0
2	G	704	0	713	20	0
3	H	2595	0	2683	77	0
3	I	2586	0	2677	59	0
3	J	2595	0	2683	53	0
4	A	7	0	0	1	0
4	B	3	0	0	1	0
4	C	11	0	0	3	0
4	D	13	0	0	2	0
4	E	2	0	0	0	0
4	F	3	0	0	0	0
4	G	3	0	0	1	0
4	H	13	0	0	6	0
4	I	13	0	0	2	0
4	J	9	0	0	6	0
All	All	12345	0	12614	316	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 13.

The worst 5 of 316 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:H:594:ILE:HG22	3:H:595:ILE:N	1.55	1.15
2:C:57:VAL:HB	2:C:58:ARG:HA	1.29	1.14
2:D:43:ILE:HB	2:D:44:SER:HA	1.23	1.09
1:B:78:THR:HB	4:B:103:HOH:O	1.51	1.06
3:J:471:LYS:HB2	3:J:472:SER:HB3	1.13	1.06

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:22:GLY:O	1:B:54:GLU:OE1[2_657]	2.01	0.19

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	78/89 (88%)	66 (85%)	10 (13%)	2 (3%)	4	21
1	B	78/89 (88%)	66 (85%)	10 (13%)	2 (3%)	4	21
1	E	64/89 (72%)	56 (88%)	8 (12%)	0	100	100
1	F	71/89 (80%)	67 (94%)	3 (4%)	1 (1%)	9	34
2	C	82/109 (75%)	71 (87%)	8 (10%)	3 (4%)	2	15
2	D	80/109 (73%)	70 (88%)	7 (9%)	3 (4%)	2	15
2	G	82/109 (75%)	74 (90%)	5 (6%)	3 (4%)	2	15
3	H	314/380 (83%)	279 (89%)	20 (6%)	15 (5%)	2	11
3	I	313/380 (82%)	285 (91%)	19 (6%)	9 (3%)	3	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	J	314/380 (83%)	287 (91%)	22 (7%)	5 (2%)	7	32
All	All	1476/1823 (81%)	1321 (90%)	112 (8%)	43 (3%)	3	20

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	THR
1	B	52	ASN
1	B	71	ASP
2	C	57	VAL
2	G	25	ILE

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	74/81 (91%)	63 (85%)	11 (15%)	3	13
1	B	74/81 (91%)	60 (81%)	14 (19%)	1	8
1	E	62/81 (76%)	59 (95%)	3 (5%)	23	52
1	F	69/81 (85%)	59 (86%)	10 (14%)	3	14
2	C	83/104 (80%)	68 (82%)	15 (18%)	2	8
2	D	81/104 (78%)	62 (76%)	19 (24%)	1	4
2	G	83/104 (80%)	73 (88%)	10 (12%)	5	20
3	H	299/348 (86%)	262 (88%)	37 (12%)	4	19
3	I	298/348 (86%)	265 (89%)	33 (11%)	6	22
3	J	299/348 (86%)	264 (88%)	35 (12%)	5	20
All	All	1422/1680 (85%)	1235 (87%)	187 (13%)	4	17

5 of 187 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	780	LEU

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Mol	Chain	Res	Type
3	I	711	LEU
3	I	498	ASN
3	I	586	LEU
3	I	780	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	632	ASN
3	J	495	ASN
3	I	678	GLN
3	I	736	ASN
3	J	620	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](#)

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](#)

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	80/89 (89%)	-0.23	1 (1%) 75 55	46, 62, 73, 77	0
1	B	80/89 (89%)	-0.06	2 (2%) 58 37	59, 72, 83, 86	0
1	E	68/89 (76%)	-0.05	0 100 100	108, 111, 117, 118	0
1	F	75/89 (84%)	-0.21	0 100 100	84, 90, 98, 98	0
2	C	86/109 (78%)	0.01	1 (1%) 76 57	51, 83, 96, 106	0
2	D	84/109 (77%)	-0.13	1 (1%) 76 57	47, 73, 87, 90	0
2	G	86/109 (78%)	-0.16	0 100 100	54, 94, 120, 126	0
3	H	318/380 (83%)	-0.17	2 (0%) 85 72	61, 90, 135, 151	0
3	I	317/380 (83%)	-0.19	2 (0%) 85 72	64, 87, 124, 143	0
3	J	318/380 (83%)	-0.09	7 (2%) 62 41	72, 101, 135, 143	0
All	All	1512/1823 (82%)	-0.14	16 (1%) 78 60	46, 91, 128, 151	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	J	762	LEU	4.1
3	J	652	ASN	3.5
3	J	750	VAL	3.4
2	C	47	ASP	3.4
3	H	651	SER	3.3

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.