



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 12:44 PM UTC

PDB ID : 4JSN / pdb_00004jsn
Title : structure of mTORdeltaN-mLST8 complex
Authors : Pavletich, N.P.
Deposited on : 2013-03-22
Resolution : 3.20 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
Xtrriage (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

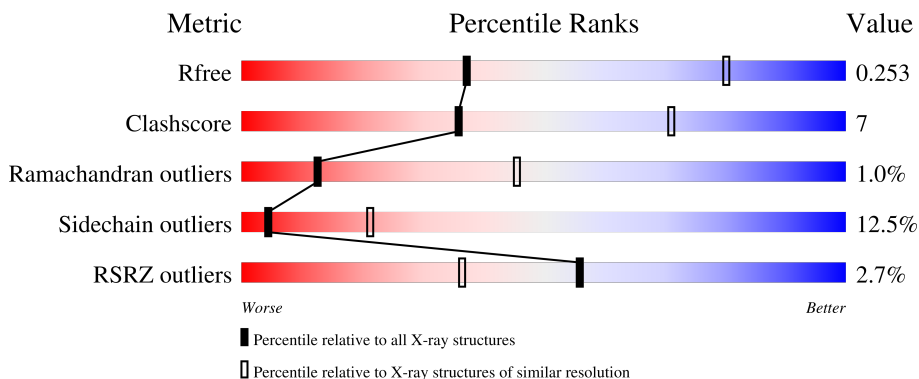
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	1174	 4% 67% 20% 10%
1	B	1174	 % 68% 19% 10%
2	C	326	 2% 65% 27% 5%
2	D	326	 2% 66% 27% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 22097 atoms, of which 0 are hydrogens and 0 are deuteriums.

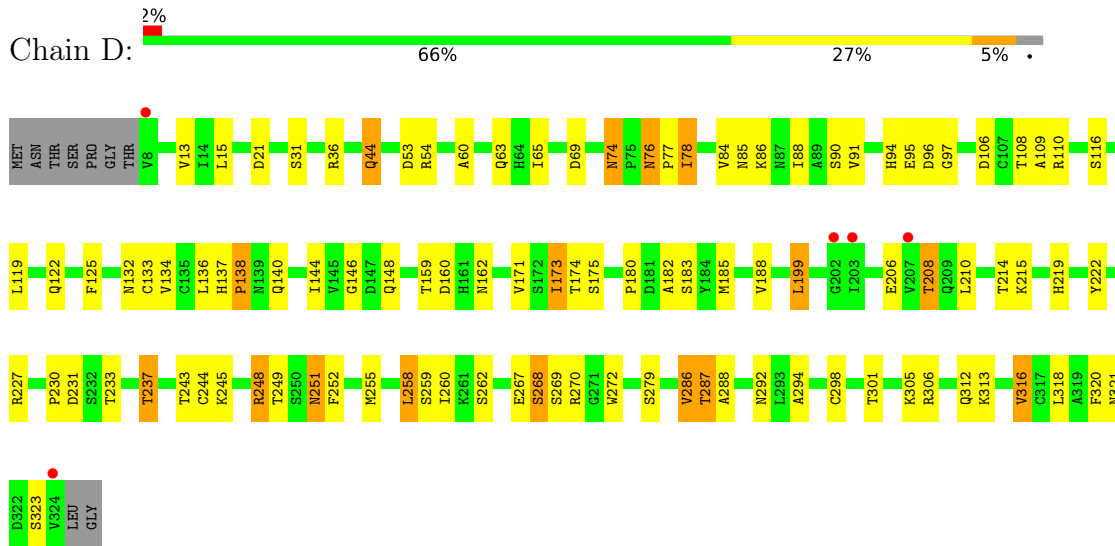
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Serine/threonine-protein kinase mTOR.

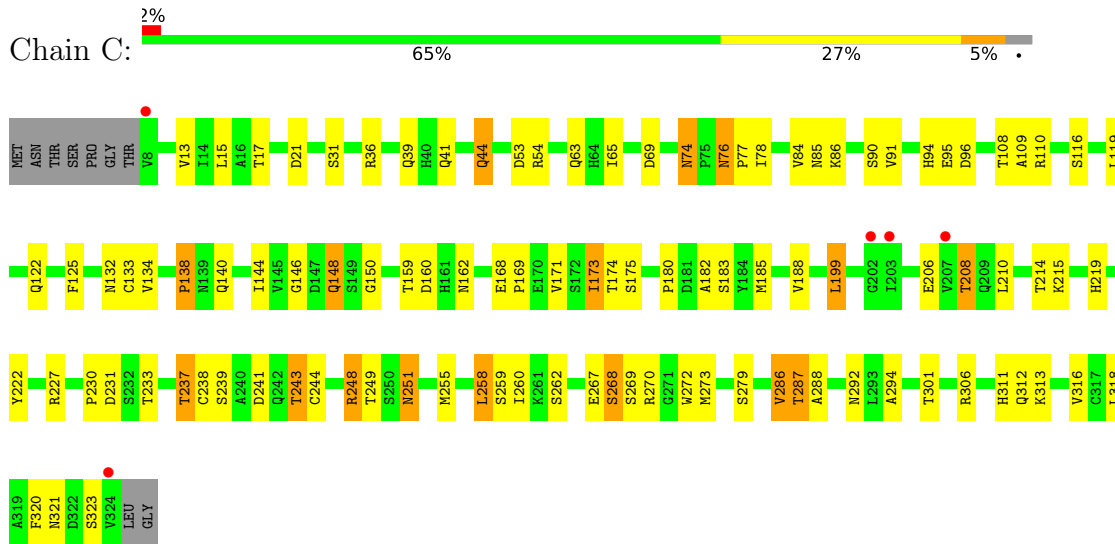
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	1058	8608	5472	1521	1552	63	0	0	0
1	A	1054	8577	5451	1517	1546	63	0	0	0

- Molecule 2 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	317	2456	1526	436	476	18	0	0	0
2	C	317	2456	1526	436	476	18	0	0	0



• Molecule 2: Target of rapamycin complex subunit LST8



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	139.40Å 163.20Å 207.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.86 – 3.20 29.86 – 3.20	Depositor EDS
% Data completeness (in resolution range)	86.6 (29.86-3.20) 86.7 (29.86-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 3.18Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.215 , 0.256 0.219 , 0.253	Depositor DCC
R_{free} test set	1857 reflections (2.35%)	wwPDB-VP
Wilson B-factor (Å ²)	56.0	Xtrriage
Anisotropy	0.333	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 54.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	22097	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.98 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6294e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.70	2/8772 (0.0%)	1.26	8/11872 (0.1%)
1	B	0.70	1/8805 (0.0%)	1.25	8/11920 (0.1%)
2	C	0.69	0/2514	1.11	6/3426 (0.2%)
2	D	0.72	0/2514	1.13	7/3426 (0.2%)
All	All	0.70	3/22605 (0.0%)	1.22	29/30644 (0.1%)

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
1	B	0	2
2	C	0	1
2	D	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1939	ILE	CA-CB	5.58	1.56	1.54
1	B	1939	ILE	CA-CB	5.52	1.56	1.54
1	A	1882	VAL	CA-CB	5.35	1.56	1.54

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1938	VAL	CB-CA-C	9.15	119.76	110.70
1	B	1445	ILE	N-CA-C	-8.00	97.05	108.58
1	A	1445	ILE	N-CA-C	-7.60	97.64	108.58
2	D	321	ASN	N-CA-C	7.10	120.05	108.26
2	C	321	ASN	N-CA-C	6.79	119.53	108.26

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1444	GLU	Peptide
1	A	1680	ASP	Peptide
1	B	1444	GLU	Peptide
1	B	1680	ASP	Peptide
2	D	267	GLU	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	8577	0	8559	124	1
1	B	8608	0	8593	120	0
2	C	2456	0	2341	44	0
2	D	2456	0	2341	45	0
All	All	22097	0	21834	321	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 7.

The worst 5 of 321 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:2380:THR:HG22	1:A:2383:LEU:HG	1.53	0.91
1:B:2380:THR:HG22	1:B:2383:LEU:HG	1.52	0.89
1:B:1930:ILE:HD11	1:B:1934:THR:HG21	1.57	0.87
1:A:1691:THR:HG23	1:A:1724:MET:HE1	1.58	0.86
1:A:1930:ILE:HD11	1:A:1934:THR:HG21	1.58	0.84

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:1612:ARG:NH2	1:A:1612:ARG:NH2[2_554]	1.96	0.24

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	1046/1174 (89%)	967 (92%)	72 (7%)	7 (1%)	18	52
1	B	1052/1174 (90%)	967 (92%)	77 (7%)	8 (1%)	16	50
2	C	315/326 (97%)	285 (90%)	24 (8%)	6 (2%)	6	33
2	D	315/326 (97%)	284 (90%)	24 (8%)	7 (2%)	5	29
All	All	2728/3000 (91%)	2503 (92%)	197 (7%)	28 (1%)	12	45

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1630	VAL
1	B	1692	VAL
1	B	1937	GLN
2	D	74	ASN
1	A	1692	VAL

5.3.2 Protein sidechains [i](#)

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	927/1024 (90%)	819 (88%)	108 (12%)	5	23
1	B	931/1024 (91%)	821 (88%)	110 (12%)	5	23
2	C	269/276 (98%)	228 (85%)	41 (15%)	3	14
2	D	269/276 (98%)	228 (85%)	41 (15%)	3	14
All	All	2396/2600 (92%)	2096 (88%)	300 (12%)	4	21

5 of 300 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2260	LEU
2	C	227	ARG
1	A	2345	MET
2	C	44	GLN
1	B	2390	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2082	GLN
2	C	22	HIS
1	A	2161	GLN
1	A	2343	ASN
2	C	94	HIS

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

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	1054/1174 (89%)	0.19	48 (4%) 37 23	38, 86, 178, 243	0
1	B	1058/1174 (90%)	-0.16	15 (1%) 73 54	28, 72, 150, 238	0
2	C	317/326 (97%)	-0.10	5 (1%) 70 51	40, 77, 147, 222	0
2	D	317/326 (97%)	-0.40	5 (1%) 70 51	27, 52, 116, 192	0
All	All	2746/3000 (91%)	-0.05	73 (2%) 56 36	27, 74, 170, 243	0

The worst 5 of 73 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1619	TRP	4.8
1	B	1582	SER	4.5
1	A	1599	LEU	4.2
1	A	1559	LEU	4.1
1	A	1582	SER	4.0

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](#)

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.