



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 02:36 AM UTC

PDB ID : 6DKN / pdb_00006dkn
Title : CRYSTAL STRUCTURE OF ARABIDOPSIS THALIANA DECAPPING
NUCLEASE DXO1
Authors : Tong, L.; Wang, V.Y.F.
Deposited on : 2018-05-30
Resolution : 1.80 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

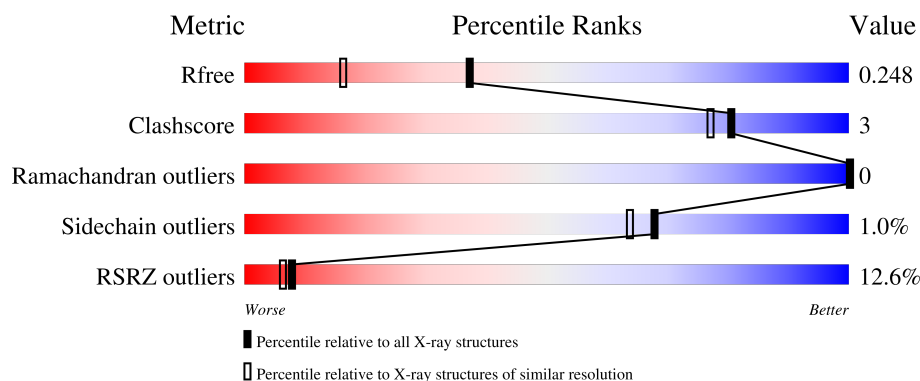
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	349	6% 90% 7% .
1	B	349	19% 89% 7% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5941 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 Decapping nuclease DXO homolog, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	0	0
			2756	1738	496	507	15			
1	B	334	Total	C	N	O	S	0	0	0
			2718	1716	486	501	15			

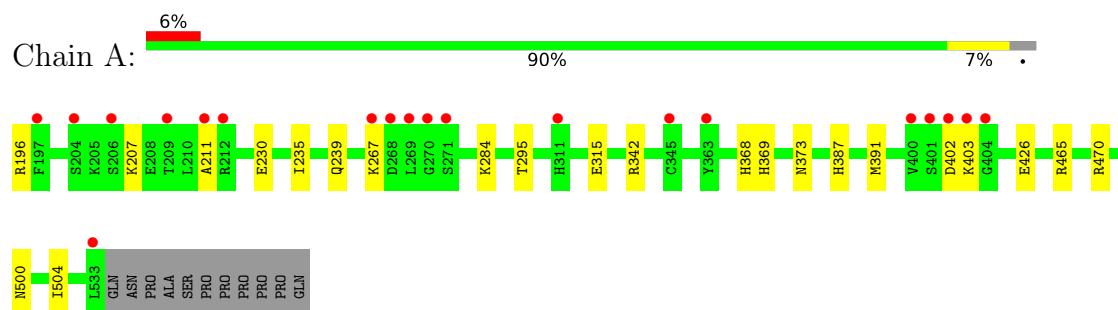
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	260	Total	O	0	0
			260	260		
2	B	207	Total	O	0	0
			207	207		

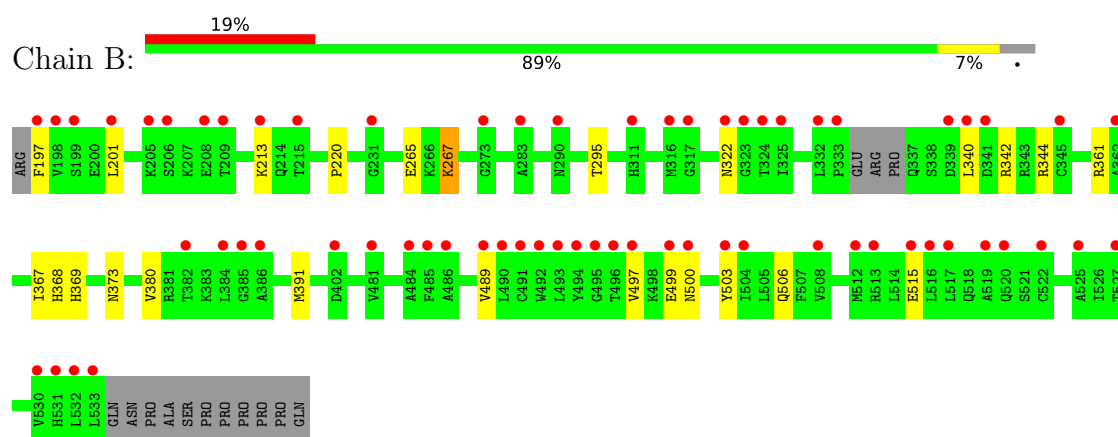
3 Residue-property plots [i](#)

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: Decapping nuclease DXO homolog, chloroplastic



- Molecule 1: Decapping nuclease DXO homolog, chloroplastic



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.08Å 80.88Å 125.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.52 – 1.80 48.52 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.8 (48.52-1.80) 98.7 (48.52-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.201 , 0.242 0.209 , 0.248	Depositor DCC
R_{free} test set	3312 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	24.6	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 34.8	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	0.95	EDS
Total number of atoms	5941	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% 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	0.75	0/2815	0.84	0/3794
1	B	0.76	0/2775	0.86	0/3739
All	All	0.76	0/5590	0.85	0/7533

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

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	2756	0	2695	13	0
1	B	2718	0	2655	15	0
2	A	260	0	0	5	0
2	B	207	0	0	1	0
All	All	5941	0	5350	28	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 3.

All (28) 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:B:267:LYS:H	1:B:373:ASN:HD21	1.13	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:361:ARG:HD3	1:B:367:ILE:HD13	1.64	0.80
1:A:426:GLU:OE1	1:A:470:ARG:NH1	2.19	0.72
1:B:361:ARG:CD	1:B:367:ILE:HD13	2.23	0.67
1:A:368:HIS:ND1	1:A:369:HIS:HD2	1.92	0.67
1:B:197:PHE:N	2:B:603:HOH:O	2.31	0.62
1:A:465:ARG:NH2	2:A:602:HOH:O	2.32	0.61
1:A:267:LYS:H	1:A:373:ASN:HD21	1.49	0.59
1:A:387:HIS:HD2	2:A:611:HOH:O	1.86	0.57
1:A:284:LYS:NZ	2:A:604:HOH:O	2.39	0.56
1:A:295:THR:O	1:A:391:MET:HA	2.08	0.53
1:B:361:ARG:CD	1:B:367:ILE:CD1	2.89	0.51
1:A:342:ARG:NH2	2:A:606:HOH:O	2.43	0.51
1:B:340:LEU:HD11	1:B:344:ARG:NH1	2.26	0.50
1:B:497:VAL:HG13	1:B:503:TYR:CE2	2.48	0.49
1:B:295:THR:O	1:B:391:MET:HA	2.13	0.48
1:B:265:GLU:CD	1:B:342:ARG:HE	2.21	0.48
1:A:402:ASP:OD1	1:A:403:LYS:N	2.46	0.48
1:A:315:GLU:HG3	1:A:504:ILE:CG2	2.43	0.48
1:A:207:LYS:O	1:A:211:ALA:N	2.42	0.47
1:B:265:GLU:OE2	1:B:342:ARG:NE	2.42	0.46
1:B:506:GLN:NE2	1:B:515:GLU:OE1	2.48	0.45
1:B:322:ASN:N	1:B:499:GLU:OE2	2.51	0.43
1:A:504:ILE:HD13	2:A:804:HOH:O	2.19	0.43
1:B:220:PRO:HB3	1:B:380:VAL:CG1	2.49	0.42
1:B:201:LEU:HD23	1:B:489:VAL:HG22	2.03	0.41
1:B:368:HIS:ND1	1:B:369:HIS:HD2	2.18	0.41
1:A:235:ILE:HG21	1:A:239:GLN:NE2	2.36	0.41

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	336/349 (96%)	331 (98%)	5 (2%)	0	100	100
1	B	330/349 (95%)	324 (98%)	6 (2%)	0	100	100
All	All	666/698 (95%)	655 (98%)	11 (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	295/305 (97%)	292 (99%)	3 (1%)	68	64
1	B	291/305 (95%)	288 (99%)	3 (1%)	68	64
All	All	586/610 (96%)	580 (99%)	6 (1%)	68	64

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	196	ARG
1	A	230	GLU
1	A	500	ASN
1	B	213	LYS
1	B	267	LYS
1	B	500	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	216	ASN
1	A	285	ASN
1	A	369	HIS
1	A	373	ASN
1	A	387	HIS
1	A	500	ASN
1	B	290	ASN

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Mol	Chain	Res	Type
1	B	311	HIS
1	B	369	HIS
1	B	373	ASN
1	B	478	GLN
1	B	500	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

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	338/349 (96%)	0.29	20 (5%) 28 27	14, 24, 48, 68	0
1	B	334/349 (95%)	0.98	65 (19%) 3 2	14, 30, 53, 71	0
All	All	672/698 (96%)	0.64	85 (12%) 8 6	14, 27, 51, 71	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	197	PHE	4.9
1	B	491	CYS	4.6
1	A	197	PHE	4.5
1	B	495	GLY	4.5
1	B	533	LEU	4.3
1	A	211	ALA	4.1
1	B	496	THR	4.1
1	B	532	LEU	4.1
1	B	504	ILE	4.0
1	B	324	THR	3.9
1	A	401	SER	3.9
1	B	323	GLY	3.6
1	B	489	VAL	3.5
1	B	402	ASP	3.5
1	A	269	LEU	3.4
1	B	213	LYS	3.3
1	B	333	PRO	3.3
1	A	206	SER	3.2
1	A	363	TYR	3.2
1	B	513	ARG	3.2
1	B	519	ALA	3.2
1	B	499	GLU	3.2
1	B	484	ALA	3.1
1	B	317	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	517	LEU	3.0
1	B	512	MET	3.0
1	A	204	SER	3.0
1	A	404	GLY	2.9
1	A	402	ASP	2.9
1	B	332	LEU	2.9
1	B	493	LEU	2.9
1	B	508	VAL	2.8
1	B	339	ASP	2.8
1	A	209	THR	2.8
1	B	531	HIS	2.8
1	B	198	VAL	2.8
1	A	271	SER	2.7
1	B	492	TRP	2.7
1	B	385	GLY	2.7
1	A	400	VAL	2.7
1	A	270	GLY	2.6
1	B	522	CYS	2.6
1	B	490	LEU	2.6
1	B	516	LEU	2.6
1	B	316	MET	2.6
1	B	486	ALA	2.6
1	B	206	SER	2.6
1	A	268	ASP	2.5
1	B	340	LEU	2.5
1	B	386	ALA	2.5
1	B	500	ASN	2.5
1	B	362	ALA	2.5
1	B	209	THR	2.5
1	B	503	TYR	2.4
1	B	384	LEU	2.4
1	B	199	SER	2.4
1	B	481	VAL	2.4
1	B	497	VAL	2.4
1	B	485	PHE	2.4
1	A	212	ARG	2.4
1	A	267	LYS	2.4
1	B	201	LEU	2.3
1	A	403	LYS	2.3
1	B	515	GLU	2.3
1	B	231	GLY	2.3
1	B	530	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	382	THR	2.3
1	B	283	ALA	2.2
1	B	494	TYR	2.2
1	B	525	ALA	2.2
1	B	527	THR	2.2
1	B	520	GLN	2.2
1	B	290	ASN	2.2
1	B	311	HIS	2.2
1	A	311	HIS	2.2
1	B	205	LYS	2.2
1	B	322	ASN	2.1
1	B	273	GLY	2.1
1	A	533	LEU	2.1
1	B	341	ASP	2.1
1	B	208	GLU	2.1
1	B	325	ILE	2.1
1	A	345	CYS	2.1
1	B	345	CYS	2.1
1	B	215	THR	2.0

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 [i](#)

There are no such residues in this entry.