

Full wwPDB X-ray Structure Validation Report (i)

Feb 28, 2024 – 12:13 pm GMT

PDB ID : 8Q66

Title: Crystal Structure of the C. elegans MUT-7 MUT-8 CTD complex

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Deposited on : 2023-08-11

Resolution : 2.03 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 (i) 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS: 2.36

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

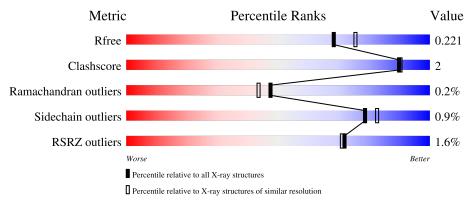
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 2.03 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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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 <=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	272	94%	6%
2	В	251	92%	



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8632 atoms, of which 4201 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 Exonuclease mut-7.

Mol	Chain	Residues			Atom	ıs			ZeroOcc	AltConf	Trace
1	A	271	Total 4424	C 1416	H 2199	N 392	O 403	S 14	0	1	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	628	GLY	-	expression tag	UNP P34607
A	629	PRO	-	expression tag	
A	630	ASP	-	expression tag	UNP P34607
A	631	SER	-	expression tag	UNP P34607
A	632	MET	-	expression tag	UNP P34607

• Molecule 2 is a protein called SH2 domain-containing protein.

Mol	Chain	Residues			Atoms	S			ZeroOcc	AltConf	Trace
2	В	242	Total 3927	C 1238	H 1984	N 338	O 359	S 8	0	1	0

There are 5 discrepancies between the modelled and reference sequences:

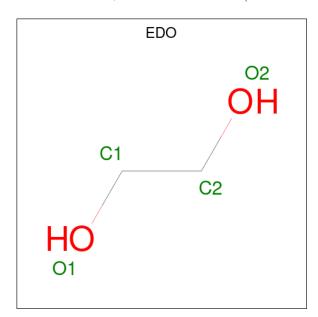
Chain	Residue	Modelled	Actual	Comment	Reference
В	317	GLY	-	expression tag	UNP Q19672
В	318	PRO	-	expression tag	UNP Q19672
В	319	ASP	-	expression tag	UNP Q19672
В	320	SER	-	expression tag	UNP Q19672
В	321	MET	-	expression tag	UNP Q19672

• Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Zn 1 1	0	0

 \bullet Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\mathrm{C_2H_6O_2}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C H O 10 2 6 2	0	0
4	A	1	Total C H O 10 2 6 2	0	0
4	A	1	Total C H O 10 2 6 2	0	0

 \bullet Molecule 5 is water.

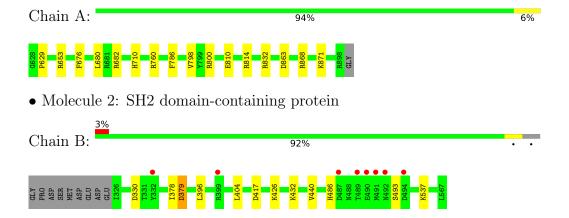
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	154	Total O 154 154	0	0
5	В	96	Total O 96 96	0	0



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: Exonuclease mut-7





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	145.09Å 59.05Å 88.16Å	Donositor
a, b, c, α , β , γ	90.00° 119.80° 90.00°	Depositor
Resolution (Å)	67.91 - 2.03	Depositor
Resolution (A)	67.91 - 2.03	EDS
% Data completeness	99.6 (67.91-2.03)	Depositor
(in resolution range)	99.6 (67.91-2.03)	EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.31 (at 2.03Å)	Xtriage
Refinement program	PHENIX 1.12.1-4487, PDB-REDO	Depositor
D D	0.191 , 0.225	Depositor
R, R_{free}	0.188 , 0.221	DCC
R_{free} test set	2113 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	39.1	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39, 42.8	EDS
L-test for twinning ²	$< L > = 0.50, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8632	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 4.89% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: ZN, EDO

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.25	0/2287	0.53	0/3106	
2	В	0.26	0/1985	0.51	0/2683	
All	All	0.25	0/4272	0.52	0/5789	

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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	760	ARG	Sidechain

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	2225	2199	2199	10	0
2	В	1943	1984	1984	7	0
3	A	1	0	0	0	0
4	A	12	18	18	0	0
5	A	154	0	0	2	0
5	В	96	0	0	1	0
All	All	4431	4201	4201	15	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 2.

All (15) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
	1100111 _	${ m distance}({ m \AA})$	overlap(A)
1:A:810:GLU:OE2	1:A:814:ARG:NH2	2.12	0.82
1:A:871:LYS:HD2	1:A:871:LYS:N	2.09	0.67
1:A:863[B]:ASP:OD1	2:B:537:LYS:NZ	2.42	0.52
2:B:417:ASP:O	2:B:440:VAL:HG22	2.11	0.51
1:A:653:ARG:NH2	5:A:1005:HOH:O	2.44	0.50
2:B:396:LEU:HD21	2:B:404:LEU:HD11	1.95	0.48
1:A:868:ARG:HB3	1:A:871:LYS:HD3	1.96	0.47
1:A:871:LYS:HD2	1:A:871:LYS:H	1.80	0.47
1:A:832:ARG:NH1	5:A:1007:HOH:O	2.45	0.46
2:B:486:HIS:HE1	2:B:493:SER:O	1.97	0.46
2:B:378:ILE:O	2:B:379:ASP:C	2.55	0.45
1:A:710:HIS:NE2	2:B:426:LYS:HD2	2.34	0.43
1:A:676:PHE:CE2	1:A:680:LEU:HD11	2.56	0.41
2:B:432:LYS:NZ	5:B:606:HOH:O	2.53	0.41
1:A:798:VAL:HG22	1:A:800:ARG:CZ	2.51	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	Perce	ntiles
1	A	270/272~(99%)	267 (99%)	3 (1%)	0	100	100
2	В	241/251 (96%)	233 (97%)	7 (3%)	1 (0%)	34	28
All	All	511/523 (98%)	500 (98%)	10 (2%)	1 (0%)	47	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	379	ASP

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	Rotameric Outliers		Percentiles		
1	A	253/252 (100%)	250 (99%)	3 (1%)	71	75		
2	В	219/226 (97%)	218 (100%)	1 (0%)	88	91		
All	All	472/478 (99%)	468 (99%)	4 (1%)	78	85		

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	629	PRO
1	A	682	ARG
1	A	786	PHE
2	В	330	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	В	486	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol Type Chain Res		Link Bond lengths			В	ond ang	gles			
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	903	-	3,3,3	0.48	0	2,2,2	0.27	0
4	EDO	A	904	-	3,3,3	0.49	0	2,2,2	0.21	0
4	EDO	A	902	-	3,3,3	0.46	0	2,2,2	0.30	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	903	-	-	1/1/1/1	-
4	EDO	A	904	-	-	1/1/1/1	-
4	EDO	A	902	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
4	A	903	EDO	O1-C1-C2-O2
4	A	904	EDO	O1-C1-C2-O2

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 (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, 95^{th} 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	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	271/272 (99%)	-0.07	0 100 100	29, 44, 64, 93	0
2	В	$242/251 \ (96\%)$	0.11	8 (3%) 46 46	33, 48, 97, 151	0
All	All	513/523 (98%)	0.01	8 (1%) 72 71	29, 45, 75, 151	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	491	MET	5.0
2	В	490	GLU	4.8
2	В	487	ASP	4.5
2	В	489	THR	3.7
2	В	492	ASN	3.6
2	В	332	TYR	3.4
2	В	494	ASP	2.5
2	В	399	ARG	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 monosaccharides 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,

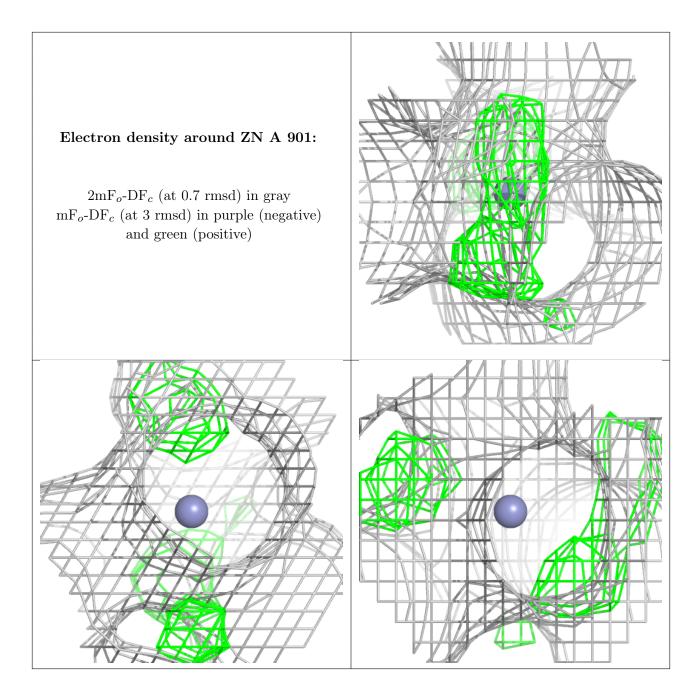


median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	EDO	A	904	4/4	0.66	0.26	54,75,155,155	0
4	EDO	A	903	4/4	0.89	0.18	50,60,65,76	0
4	EDO	A	902	4/4	0.96	0.19	48,57,66,68	0
3	ZN	A	901	1/1	1.00	0.18	30,30,30,30	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers (i)

There are no such residues in this entry.

