



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 3, 2024 – 10:24 PM EST

PDB ID : 1NCY
Title : TROPONIN-C, COMPLEX WITH MANGANESE
Authors : Sundaralingam, M.; Rao, S.T.
Deposited on : 1996-06-02
Resolution : 2.10 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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

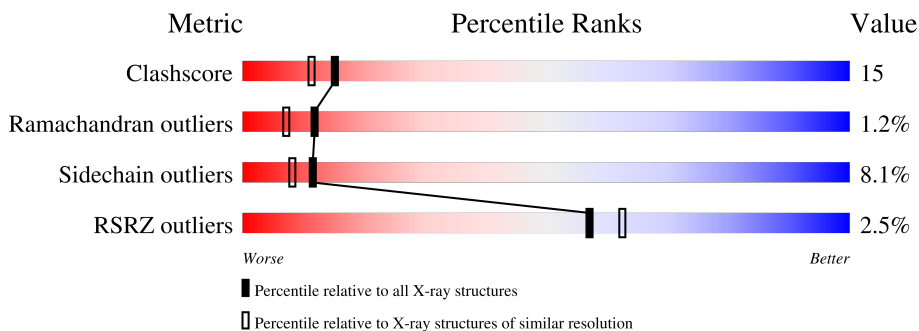
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	162	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1383 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 TROPONIN C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	162	1271	781	202	276	12	0	0	0

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mn	0	0
			2	2		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

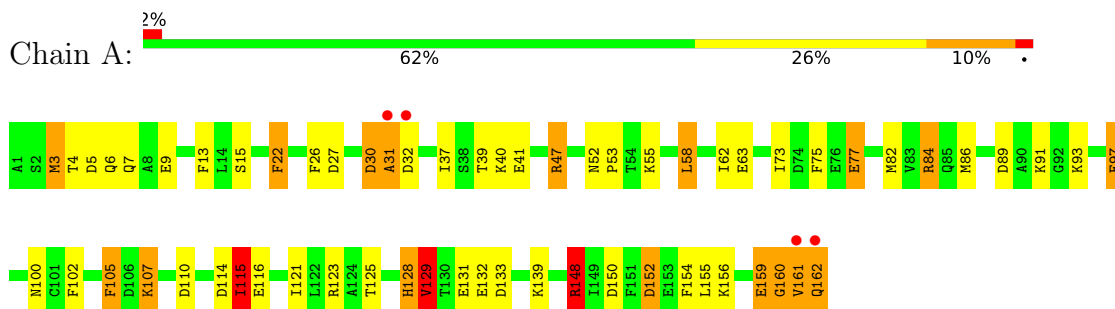
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	105	Total 105	O 105	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: TROPONIN C



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	66.70Å 66.70Å 60.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.10 7.96 – 2.12	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.10) 70.8 (7.96-2.12)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtrriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.130 , (Not available) 0.156 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	17.0	Xtrriage
Anisotropy	0.249	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 81.8	EDS
L-test for twinning ¹	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtrriage
Estimated twinning fraction	0.090 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1383	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, MN

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	1.61	6/1283 (0.5%)	2.06	47/1712 (2.7%)

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	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	132	GLU	CD-OE1	-6.58	1.18	1.25
1	A	150	ASP	C-O	6.42	1.35	1.23
1	A	15	SER	CB-OG	-5.99	1.34	1.42
1	A	13	PHE	CD1-CE1	5.28	1.49	1.39
1	A	63	GLU	CG-CD	-5.19	1.44	1.51
1	A	75	PHE	CE2-CZ	5.14	1.47	1.37

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	ASP	CB-CG-OD1	10.37	127.63	118.30
1	A	148	ARG	NE-CZ-NH1	-9.58	115.51	120.30
1	A	148	ARG	CD-NE-CZ	9.39	136.75	123.60
1	A	132	GLU	OE1-CD-OE2	9.07	134.18	123.30
1	A	84	ARG	NE-CZ-NH1	8.35	124.47	120.30
1	A	84	ARG	NE-CZ-NH2	-8.18	116.21	120.30
1	A	77	GLU	CG-CD-OE1	7.32	132.93	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	105	PHE	CA-CB-CG	7.18	131.12	113.90
1	A	123	ARG	CD-NE-CZ	6.89	133.25	123.60
1	A	105	PHE	CB-CG-CD1	6.79	125.55	120.80
1	A	159	GLU	CA-C-N	6.44	129.09	116.20
1	A	110	ASP	CB-CG-OD1	6.32	123.98	118.30
1	A	152	ASP	CB-CG-OD2	6.16	123.84	118.30
1	A	115	ILE	N-CA-CB	6.12	124.87	110.80
1	A	154	PHE	CB-CG-CD1	6.06	125.04	120.80
1	A	26	PHE	O-C-N	-6.04	113.03	122.70
1	A	47	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	A	27	ASP	CB-CG-OD1	5.92	123.63	118.30
1	A	116	GLU	CG-CD-OE1	5.82	129.93	118.30
1	A	154	PHE	CB-CG-CD2	-5.77	116.76	120.80
1	A	63	GLU	CA-CB-CG	-5.70	100.87	113.40
1	A	150	ASP	CB-CA-C	5.69	121.78	110.40
1	A	41	GLU	OE1-CD-OE2	5.63	130.06	123.30
1	A	115	ILE	CB-CA-C	-5.61	100.38	111.60
1	A	162	GLN	N-CA-C	-5.61	95.86	111.00
1	A	73	ILE	O-C-N	5.50	131.50	122.70
1	A	114	ASP	CB-CG-OD2	-5.49	113.36	118.30
1	A	148	ARG	NE-CZ-NH2	5.48	123.04	120.30
1	A	125	THR	CA-CB-CG2	5.38	119.93	112.40
1	A	89	ASP	OD1-CG-OD2	-5.38	113.09	123.30
1	A	13	PHE	CD1-CE1-CZ	-5.33	113.70	120.10
1	A	162	GLN	CA-C-O	-5.32	108.92	120.10
1	A	77	GLU	CG-CD-OE2	-5.31	107.69	118.30
1	A	131	GLU	OE1-CD-OE2	-5.27	116.97	123.30
1	A	37	ILE	CA-C-O	5.26	131.16	120.10
1	A	97	GLU	OE1-CD-OE2	-5.25	116.99	123.30
1	A	40	LYS	N-CA-CB	5.24	120.03	110.60
1	A	97	GLU	CG-CD-OE2	5.20	128.69	118.30
1	A	148	ARG	CG-CD-NE	-5.19	100.90	111.80
1	A	128	HIS	CA-CB-CG	-5.19	104.78	113.60
1	A	30	ASP	CB-CG-OD1	5.19	122.97	118.30
1	A	22	PHE	CZ-CE2-CD2	-5.14	113.93	120.10
1	A	13	PHE	CB-CG-CD2	-5.13	117.21	120.80
1	A	129	VAL	CB-CA-C	-5.09	101.74	111.40
1	A	102	PHE	CB-CG-CD1	-5.07	117.25	120.80
1	A	32	ASP	CA-CB-CG	-5.00	102.40	113.40
1	A	123	ARG	NE-CZ-NH2	-5.00	117.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	148	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	1271	0	1195	37	0
2	A	2	0	0	0	0
3	A	5	0	0	1	0
4	A	105	0	0	12	0
All	All	1383	0	1195	37	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 15.

All (37) 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:6:GLN:HE22	1:A:84:ARG:HH21	1.18	0.90
1:A:156:LYS:O	1:A:162:GLN:O	1.99	0.79
1:A:77:GLU:HG2	4:A:185:HOH:O	1.82	0.79
1:A:139:LYS:HG3	4:A:318:HOH:O	1.83	0.79
1:A:152:ASP:OD2	4:A:319:HOH:O	2.00	0.79
1:A:30:ASP:O	1:A:31:ALA:HB3	1.80	0.78
1:A:5:ASP:O	1:A:9:GLU:HG3	1.88	0.73
1:A:4:THR:O	4:A:331:HOH:O	2.06	0.72
1:A:22:PHE:HE2	1:A:86:MET:HE1	1.53	0.72
1:A:3:MET:SD	4:A:185:HOH:O	2.48	0.71
1:A:152:ASP:OD1	4:A:291:HOH:O	2.09	0.70
1:A:22:PHE:CE2	1:A:86:MET:HE1	2.28	0.69
1:A:39:THR:HB	1:A:62:ILE:HG12	1.74	0.68
1:A:30:ASP:OD2	4:A:339:HOH:O	2.13	0.67
1:A:97:GLU:HA	1:A:97:GLU:OE1	1.97	0.65
1:A:30:ASP:O	1:A:31:ALA:CB	2.46	0.64
1:A:156:LYS:NZ	4:A:319:HOH:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:MET:O	1:A:7:GLN:HG3	2.06	0.55
1:A:22:PHE:CE2	1:A:86:MET:CE	2.90	0.55
1:A:100:ASN:ND2	4:A:375:HOH:O	1.88	0.54
1:A:107:LYS:CE	1:A:121:ILE:HD11	2.40	0.52
1:A:52:ASN:O	1:A:52:ASN:ND2	2.43	0.51
1:A:129:VAL:HG12	1:A:133:ASP:HB2	1.94	0.49
1:A:129:VAL:HG12	1:A:133:ASP:CB	2.44	0.48
1:A:156:LYS:C	1:A:162:GLN:O	2.53	0.47
1:A:82:MET:HB3	1:A:86:MET:HE3	1.97	0.47
1:A:160:GLY:O	1:A:161:VAL:C	2.53	0.46
1:A:47:ARG:NH2	3:A:225:SO4:O1	2.45	0.46
1:A:6:GLN:NE2	4:A:199:HOH:O	2.38	0.45
1:A:22:PHE:CZ	1:A:86:MET:HE2	2.52	0.44
1:A:159:GLU:OE1	1:A:162:GLN:NE2	2.51	0.43
1:A:156:LYS:CA	1:A:162:GLN:O	2.66	0.43
1:A:156:LYS:HA	1:A:162:GLN:O	2.18	0.43
1:A:115:ILE:HG13	4:A:170:HOH:O	2.17	0.43
1:A:53:PRO:HG2	1:A:58:LEU:HD22	2.01	0.43
1:A:128:HIS:CD2	1:A:128:HIS:N	2.88	0.42
1:A:55:LYS:HD3	4:A:348:HOH:O	2.19	0.41

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	Percentiles
1	A	160/162 (99%)	156 (98%)	2 (1%)	2 (1%)	12 7

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	31	ALA

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Mol	Chain	Res	Type
1	A	160	GLY

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	136/136 (100%)	125 (92%)	11 (8%)	11 8

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	MET
1	A	58	LEU
1	A	91	LYS
1	A	93	LYS
1	A	105	PHE
1	A	107	LYS
1	A	115	ILE
1	A	129	VAL
1	A	148	ARG
1	A	155	LEU
1	A	161	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	128	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 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	225	-	4,4,4	0.66	0	6,6,6	0.37	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	225	SO4	1	0

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	162/162 (100%)	-0.44	4 (2%) 57 62	6, 18, 45, 62	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	32	ASP	3.7
1	A	161	VAL	3.5
1	A	31	ALA	3.1
1	A	162	GLN	2.9

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, 95th 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	B-factors(Å ²)	Q<0.9
2	MN	A	164	1/1	0.98	0.04	20,20,20,20	0
3	SO4	A	225	5/5	0.98	0.15	43,44,48,50	0
2	MN	A	163	1/1	1.00	0.04	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.