



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 08:05 am BST

PDB ID : 4WLE
Title : Crystal structure of citrate bound MDH2
Authors : Eo, Y.M.; Han, B.G.; Ahn, H.C.
Deposited on : 2014-10-07
Resolution : 1.90 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 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 : 2.11
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) : 2.11

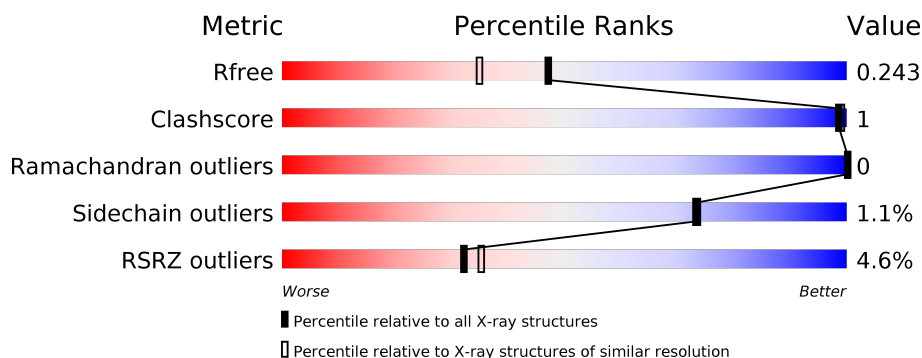
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 on 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	340	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>
1	B	340	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>8%</div> </div> </div>
1	C	340	<div> <div>6%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>
1	D	340	<div> <div>6%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9417 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 Malate dehydrogenase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2312	1472	390	437	13			
1	B	314	Total	C	N	O	S	0	2	0
			2319	1477	390	439	13			
1	C	314	Total	C	N	O	S	0	1	0
			2315	1474	390	438	13			
1	D	314	Total	C	N	O	S	0	0	0
			2312	1472	390	437	13			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P40926
A	0	GLY	-	expression tag	UNP P40926
A	1	SER	-	expression tag	UNP P40926
A	2	SER	-	expression tag	UNP P40926
A	3	HIS	-	expression tag	UNP P40926
A	4	HIS	-	expression tag	UNP P40926
A	5	HIS	-	expression tag	UNP P40926
A	6	HIS	-	expression tag	UNP P40926
A	7	HIS	-	expression tag	UNP P40926
A	8	HIS	-	expression tag	UNP P40926
A	9	SER	-	expression tag	UNP P40926
A	10	SER	-	expression tag	UNP P40926
A	11	GLY	-	expression tag	UNP P40926
A	12	LEU	-	expression tag	UNP P40926
A	13	VAL	-	expression tag	UNP P40926
A	14	PRO	-	expression tag	UNP P40926
A	15	ARG	-	expression tag	UNP P40926
A	16	GLY	-	expression tag	UNP P40926
A	17	SER	-	expression tag	UNP P40926
A	18	HIS	-	expression tag	UNP P40926
A	19	MET	-	expression tag	UNP P40926

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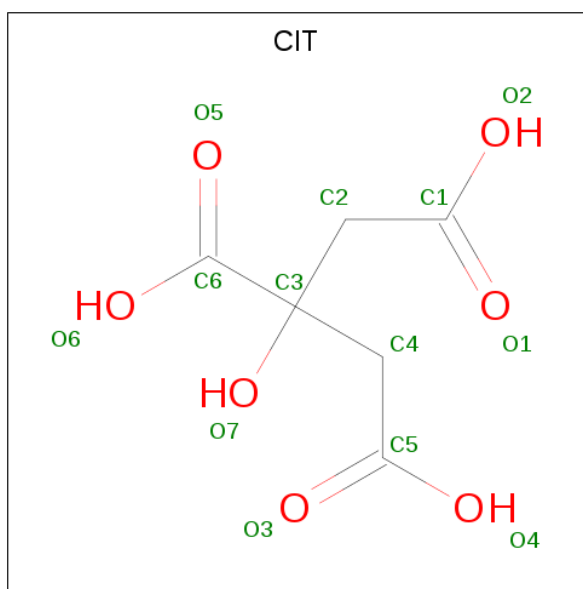
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	MET	-	expression tag	UNP P40926
B	0	GLY	-	expression tag	UNP P40926
B	1	SER	-	expression tag	UNP P40926
B	2	SER	-	expression tag	UNP P40926
B	3	HIS	-	expression tag	UNP P40926
B	4	HIS	-	expression tag	UNP P40926
B	5	HIS	-	expression tag	UNP P40926
B	6	HIS	-	expression tag	UNP P40926
B	7	HIS	-	expression tag	UNP P40926
B	8	HIS	-	expression tag	UNP P40926
B	9	SER	-	expression tag	UNP P40926
B	10	SER	-	expression tag	UNP P40926
B	11	GLY	-	expression tag	UNP P40926
B	12	LEU	-	expression tag	UNP P40926
B	13	VAL	-	expression tag	UNP P40926
B	14	PRO	-	expression tag	UNP P40926
B	15	ARG	-	expression tag	UNP P40926
B	16	GLY	-	expression tag	UNP P40926
B	17	SER	-	expression tag	UNP P40926
B	18	HIS	-	expression tag	UNP P40926
B	19	MET	-	expression tag	UNP P40926
C	-1	MET	-	expression tag	UNP P40926
C	0	GLY	-	expression tag	UNP P40926
C	1	SER	-	expression tag	UNP P40926
C	2	SER	-	expression tag	UNP P40926
C	3	HIS	-	expression tag	UNP P40926
C	4	HIS	-	expression tag	UNP P40926
C	5	HIS	-	expression tag	UNP P40926
C	6	HIS	-	expression tag	UNP P40926
C	7	HIS	-	expression tag	UNP P40926
C	8	HIS	-	expression tag	UNP P40926
C	9	SER	-	expression tag	UNP P40926
C	10	SER	-	expression tag	UNP P40926
C	11	GLY	-	expression tag	UNP P40926
C	12	LEU	-	expression tag	UNP P40926
C	13	VAL	-	expression tag	UNP P40926
C	14	PRO	-	expression tag	UNP P40926
C	15	ARG	-	expression tag	UNP P40926
C	16	GLY	-	expression tag	UNP P40926
C	17	SER	-	expression tag	UNP P40926
C	18	HIS	-	expression tag	UNP P40926
C	19	MET	-	expression tag	UNP P40926

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	MET	-	expression tag	UNP P40926
D	0	GLY	-	expression tag	UNP P40926
D	1	SER	-	expression tag	UNP P40926
D	2	SER	-	expression tag	UNP P40926
D	3	HIS	-	expression tag	UNP P40926
D	4	HIS	-	expression tag	UNP P40926
D	5	HIS	-	expression tag	UNP P40926
D	6	HIS	-	expression tag	UNP P40926
D	7	HIS	-	expression tag	UNP P40926
D	8	HIS	-	expression tag	UNP P40926
D	9	SER	-	expression tag	UNP P40926
D	10	SER	-	expression tag	UNP P40926
D	11	GLY	-	expression tag	UNP P40926
D	12	LEU	-	expression tag	UNP P40926
D	13	VAL	-	expression tag	UNP P40926
D	14	PRO	-	expression tag	UNP P40926
D	15	ARG	-	expression tag	UNP P40926
D	16	GLY	-	expression tag	UNP P40926
D	17	SER	-	expression tag	UNP P40926
D	18	HIS	-	expression tag	UNP P40926
D	19	MET	-	expression tag	UNP P40926

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		

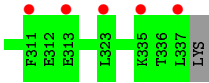
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			13	6	7		
2	C	1	Total	C	O	0	0
			13	6	7		
2	D	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	46	Total	O	0	0
			46	46		
3	B	32	Total	O	0	0
			32	32		
3	C	17	Total	O	0	0
			17	17		
3	D	12	Total	O	0	0
			12	12		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.70 Å 151.22 Å 154.65 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.10 – 1.90 45.10 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.10-1.90) 99.5 (45.10-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.28 (at 1.91 Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.218 , 0.238 0.224 , 0.243	Depositor DCC
R_{free} test set	5506 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.5	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.014 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9417	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.27	0/2351	0.46	0/3192
1	B	0.27	0/2365	0.46	0/3212
1	C	0.26	0/2358	0.44	0/3202
1	D	0.26	0/2351	0.43	0/3192
All	All	0.27	0/9425	0.45	0/12798

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 [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	2312	0	2400	0	0
1	B	2319	0	2410	7	0
1	C	2315	0	2403	4	0
1	D	2312	0	2400	2	0
2	A	13	0	5	0	0
2	B	13	0	5	0	0
2	C	13	0	5	0	0
2	D	13	0	5	1	0
3	A	46	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	32	0	0	0	0
3	C	17	0	0	0	0
3	D	12	0	0	0	0
All	All	9417	0	9633	10	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 1.

All (10) 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:116:THR:HG23	1:C:106:PRO:O	2.10	0.52
1:D:142:ASN:ND2	2:D:401:CIT:O7	2.46	0.49
1:D:136:MET:CE	1:D:262:LEU:HD11	2.46	0.46
1:B:217:ASP:N	1:B:217:ASP:OD1	2.50	0.45
1:C:24:ASN:HA	1:C:51:SER:HB3	1.99	0.45
1:B:97:VAL:HG21	1:B:259:VAL:HG21	1.98	0.44
1:B:102:VAL:HG21	1:B:116:THR:HG21	2.00	0.43
1:B:286[B]:THR:HG23	1:B:287:TYR:CD1	2.56	0.40
1:B:116:THR:OG1	1:C:108:MET:CG	2.69	0.40
1:B:116:THR:OG1	1:C:108:MET:HG3	2.22	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	Percentiles	
1	A	312/340 (92%)	305 (98%)	7 (2%)	0	100	100
1	B	314/340 (92%)	306 (98%)	8 (2%)	0	100	100
1	C	313/340 (92%)	306 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	312/340 (92%)	305 (98%)	7 (2%)	0	100	100
All	All	1251/1360 (92%)	1222 (98%)	29 (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	253/275 (92%)	247 (98%)	6 (2%)	49	43
1	B	255/275 (93%)	254 (100%)	1 (0%)	91	91
1	C	254/275 (92%)	252 (99%)	2 (1%)	81	82
1	D	253/275 (92%)	251 (99%)	2 (1%)	81	82
All	All	1015/1100 (92%)	1004 (99%)	11 (1%)	73	73

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

Mol	Chain	Res	Type
1	A	61	THR
1	A	78	LYS
1	A	91	LYS
1	A	157	LYS
1	A	262	LEU
1	A	335	LYS
1	B	61	THR
1	C	61	THR
1	C	203	LYS
1	D	61	THR
1	D	307	LYS

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

Mol	Chain	Res	Type
1	A	24	ASN
1	A	130	GLN
1	A	164	ASN
1	A	267	ASN
1	B	24	ASN
1	B	164	ASN
1	B	267	ASN
1	C	24	ASN
1	C	164	ASN
1	C	267	ASN
1	D	24	ASN
1	D	267	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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	$\# Z > 2$
2	CIT	D	401	-	3,12,12	0.83	0	3,17,17	1.33	0
2	CIT	C	401	-	3,12,12	0.79	0	3,17,17	1.17	0
2	CIT	B	401	-	3,12,12	0.70	0	3,17,17	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CIT	A	401	-	3,12,12	0.75	0	3,17,17	1.67	1 (33%)

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
2	CIT	D	401	-	-	1/6/16/16	-
2	CIT	C	401	-	-	3/6/16/16	-
2	CIT	B	401	-	-	1/6/16/16	-
2	CIT	A	401	-	-	3/6/16/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	401	CIT	C3-C4-C5	-2.67	110.72	114.98

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	CIT	C6-C3-C4-C5
2	C	401	CIT	C2-C3-C4-C5
2	A	401	CIT	C2-C3-C4-C5
2	A	401	CIT	O7-C3-C4-C5
2	C	401	CIT	C6-C3-C4-C5
2	D	401	CIT	C2-C3-C4-C5
2	C	401	CIT	O7-C3-C4-C5
2	B	401	CIT	C2-C3-C4-C5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	CIT	1	0

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	314/340 (92%)	0.21	7 (2%) 62 64	21, 28, 40, 58	0
1	B	314/340 (92%)	0.37	12 (3%) 40 43	21, 32, 46, 54	0
1	C	314/340 (92%)	0.55	20 (6%) 19 22	26, 36, 50, 67	0
1	D	314/340 (92%)	0.67	19 (6%) 21 24	27, 39, 55, 63	0
All	All	1256/1360 (92%)	0.45	58 (4%) 32 35	21, 34, 50, 67	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	220	GLN	4.4
1	D	191	ARG	4.2
1	C	24	ASN	4.0
1	B	193	ASN	3.9
1	D	297	LYS	3.7
1	D	281	GLN	3.5
1	C	221	ASP	3.4
1	C	215	LYS	3.3
1	D	296	LYS	3.3
1	C	91	LYS	3.2
1	D	313	GLU	3.2
1	C	217	ASP	3.0
1	D	91	LYS	3.0
1	A	307	LYS	3.0
1	C	297	LYS	2.9
1	D	161	TYR	2.8
1	C	337	LEU	2.7
1	D	270	GLU	2.7
1	C	134	GLU	2.7
1	B	84	GLU	2.6
1	D	307	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	217	ASP	2.6
1	A	336	THR	2.6
1	D	335	LYS	2.6
1	B	311	PHE	2.5
1	B	191	ARG	2.5
1	B	91	LYS	2.5
1	C	296	LYS	2.5
1	D	284	GLU	2.4
1	B	217	ASP	2.4
1	B	318	ASP	2.4
1	B	215	LYS	2.4
1	B	310	SER	2.3
1	B	314	LYS	2.3
1	C	218	PHE	2.3
1	D	311	PHE	2.3
1	C	74	LYS	2.3
1	D	323	LEU	2.3
1	D	282	GLU	2.3
1	C	267	ASN	2.2
1	A	311	PHE	2.2
1	A	193	ASN	2.2
1	B	220	GLN	2.2
1	C	111	ASP	2.2
1	C	157	LYS	2.2
1	C	323	LEU	2.2
1	A	335	LYS	2.2
1	D	186	GLY	2.1
1	C	160	VAL	2.1
1	C	313	GLU	2.1
1	C	281	GLN	2.1
1	B	284	GLU	2.1
1	C	311	PHE	2.1
1	D	26	LYS	2.1
1	A	84	GLU	2.1
1	A	313	GLU	2.0
1	D	337	LEU	2.0
1	D	268	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates 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(\AA^2)	Q<0.9
2	CIT	D	401	13/13	0.85	0.18	35,38,45,46	0
2	CIT	C	401	13/13	0.87	0.17	35,37,45,46	0
2	CIT	B	401	13/13	0.88	0.13	34,36,43,44	0
2	CIT	A	401	13/13	0.90	0.17	27,29,36,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.