



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7B1A
Title : Myosin-II-AA mutant motor domain
Authors : Ewert, W.; Preller, M.
Deposited on : 2020-11-24
Resolution : 2.60 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	:	2.16
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)	:	2.16

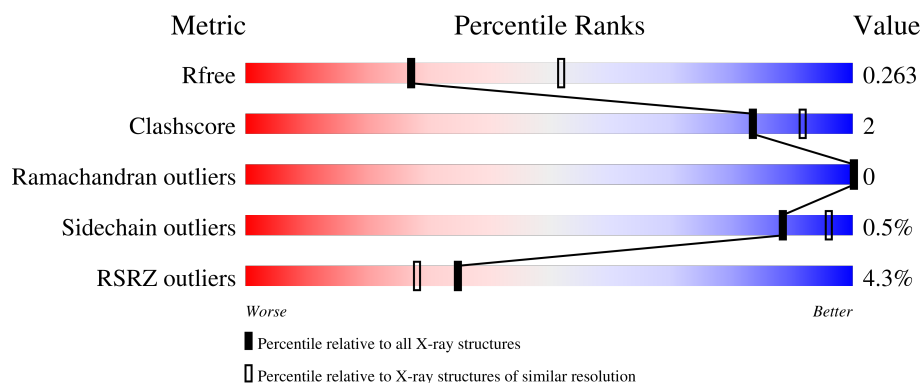
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	788	<div> <div>4%</div> <div> <div></div> <div>89%</div> <div>• 8%</div> </div> </div>
2	D	2	<div> <div>100%</div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11696 atoms, of which 5738 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 Myosin-2 heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	728	Total	C	H	N	O	S	0	0	0
			11471	3679	5683	994	1099	16			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	initiating methionine	UNP P08799
A	-9	HIS	-	expression tag	UNP P08799
A	-8	HIS	-	expression tag	UNP P08799
A	-7	HIS	-	expression tag	UNP P08799
A	-6	HIS	-	expression tag	UNP P08799
A	-5	HIS	-	expression tag	UNP P08799
A	-4	HIS	-	expression tag	UNP P08799
A	-3	HIS	-	expression tag	UNP P08799
A	-2	ASP	-	expression tag	UNP P08799
A	-1	GLY	-	expression tag	UNP P08799
A	0	THR	-	expression tag	UNP P08799
A	1	GLU	-	expression tag	UNP P08799
A	647	ALA	THR	engineered mutation	UNP P08799
A	648	ALA	THR	engineered mutation	UNP P08799
A	762	LEU	-	expression tag	UNP P08799
A	763	GLU	-	expression tag	UNP P08799
A	764	SER	-	expression tag	UNP P08799
A	765	ASN	-	expression tag	UNP P08799
A	766	GLU	-	expression tag	UNP P08799
A	767	PRO	-	expression tag	UNP P08799
A	768	PRO	-	expression tag	UNP P08799
A	769	MET	-	expression tag	UNP P08799
A	770	ASP	-	expression tag	UNP P08799
A	771	PHE	-	expression tag	UNP P08799
A	772	ASP	-	expression tag	UNP P08799
A	773	ASP	-	expression tag	UNP P08799
A	774	ASP	-	expression tag	UNP P08799

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Chain	Residue	Modelled	Actual	Comment	Reference
A	775	ILE	-	expression tag	UNP P08799
A	776	PRO	-	expression tag	UNP P08799
A	777	PHE	-	expression tag	UNP P08799

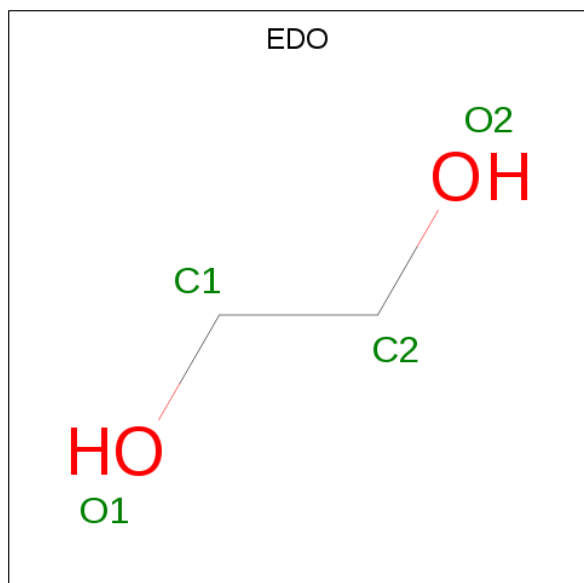
- Molecule 2 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	2	Total	C	H	O	0	0	0
			44	12	21	11			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

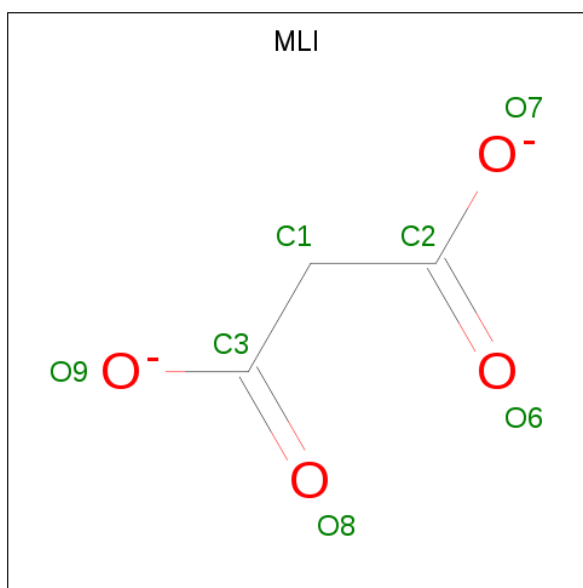
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



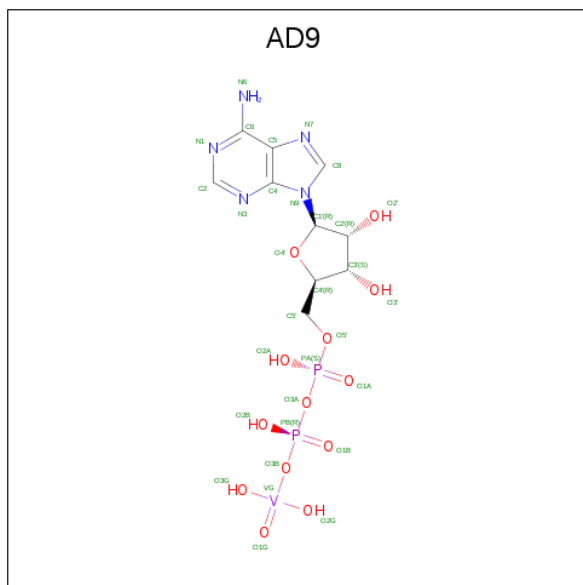
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is MALONATE ION (three-letter code: MLI) (formula: $C_3H_2O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			9	3	2	4		

- Molecule 6 is ADP METAVANADATE (three-letter code: AD9) (formula: $C_{10}H_{16}N_5O_{13}P_2V$).

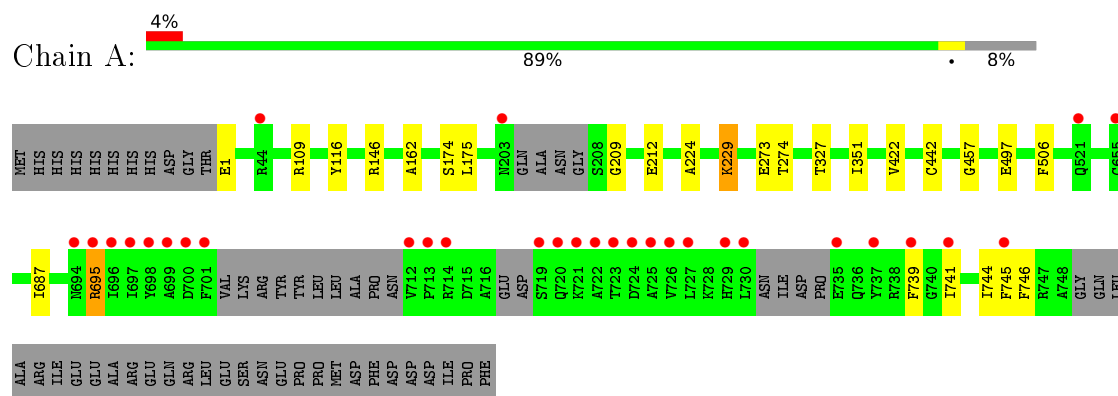


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	96	Total	O	0	0
			96	96		

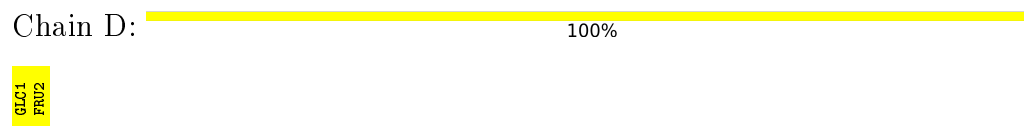
3 Residue-property plots [i](#)

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: Myosin-2 heavy chain



- Molecule 2: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	89.76Å 146.47Å 154.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.11 – 2.60 43.11 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (43.11-2.60) 99.8 (43.11-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.209 , 0.263 0.209 , 0.263	Depositor DCC
R_{free} test set	1439 reflections (4.55%)	wwPDB-VP
Wilson B-factor (Å ²)	52.9	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.021 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11696	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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: MG, MLI, GLC, EDO, AD9, FRU

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	0.42	0/5898	0.48	0/7960

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	5788	5683	5690	27	2
2	D	23	21	21	1	0
3	A	1	0	0	0	0
4	A	12	18	18	0	0
5	A	7	2	2	0	0
6	A	31	14	13	1	0
7	A	96	0	0	1	0
All	All	5958	5738	5744	28	2

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 (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:A:695:ARG:HB3	1:A:745:PHE:CD1	2.08	0.89
1:A:695:ARG:HB3	1:A:745:PHE:CE1	2.23	0.74
1:A:224:ALA:HB2	1:A:327:THR:HG21	1.74	0.69
1:A:229:LYS:HE2	1:A:274:THR:O	1.92	0.68
1:A:695:ARG:HD2	1:A:745:PHE:CE1	2.31	0.66
1:A:273:GLU:O	1:A:274:THR:OG1	2.15	0.62
1:A:739:PHE:CD1	1:A:744:ILE:HD13	2.35	0.60
1:A:497:GLU:HA	1:A:497:GLU:OE1	2.02	0.59
1:A:695:ARG:HD2	1:A:745:PHE:HE1	1.67	0.59
1:A:695:ARG:CD	1:A:745:PHE:HE1	2.23	0.52
1:A:695:ARG:CB	1:A:745:PHE:CE1	2.94	0.50
1:A:174:SER:C	1:A:175:LEU:HD12	2.33	0.48
2:D:1:GLC:O2	2:D:2:FRU:H61	2.15	0.47
1:A:1:GLU:HG2	1:A:146:ARG:HH22	1.80	0.47
1:A:695:ARG:CD	1:A:745:PHE:CE1	2.97	0.47
1:A:739:PHE:HA	1:A:744:ILE:HD12	1.98	0.46
1:A:744:ILE:HG23	1:A:744:ILE:O	2.15	0.46
1:A:506:PHE:CE2	1:A:687:ILE:HD13	2.49	0.46
1:A:209:GLY:CA	1:A:212:GLU:OE1	2.63	0.46
1:A:506:PHE:CZ	1:A:687:ILE:HD13	2.50	0.46
1:A:695:ARG:HD3	1:A:695:ARG:N	2.31	0.46
1:A:162:ALA:CB	1:A:175:LEU:HD11	2.46	0.46
1:A:741:ILE:O	1:A:741:ILE:HG23	2.15	0.45
1:A:109:ARG:NH1	7:A:917:HOH:O	2.50	0.44
1:A:695:ARG:CG	1:A:745:PHE:CE1	3.01	0.43
1:A:457:GLY:N	6:A:806:AD9:O2G	2.52	0.42
1:A:351:ILE:HG23	1:A:422:VAL:HG13	2.02	0.41
1:A:109:ARG:NH2	1:A:116:TYR:O	2.54	0.41

All (2) 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:442:CYS:SG	1:A:442:CYS:SG[3_655]	0.94	1.26
1:A:442:CYS:SG	1:A:442:CYS:HG[3_655]	0.70	0.90

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	718/788 (91%)	707 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	622/689 (90%)	619 (100%)	3 (0%)	88	96

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	229	LYS
1	A	695	ARG
1	A	746	PHE

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	171	GLN
1	A	633	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

2 monosaccharides are modelled in this entry.

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.

No monomer is involved in short contacts.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

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 ⓘ

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	728/788 (92%)	0.13	31 (4%) 35 28	35, 58, 113, 215	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	696	ILE	6.9
1	A	729	HIS	6.6
1	A	720	GLN	4.7
1	A	697	ILE	4.6
1	A	698	TYR	4.1
1	A	726	VAL	4.0
1	A	739	PHE	4.0
1	A	735	GLU	3.8
1	A	737	TYR	3.7
1	A	727	LEU	3.6
1	A	713	PRO	3.6
1	A	725	ALA	3.5
1	A	699	ALA	3.4
1	A	723	THR	3.3
1	A	695	ARG	3.2
1	A	719	SER	3.2
1	A	521	GLN	3.1
1	A	722	ALA	3.0
1	A	694	ASN	3.0
1	A	700	ASP	2.9
1	A	730	LEU	2.9
1	A	701	PHE	2.9
1	A	44	ARG	2.9
1	A	745	PHE	2.8
1	A	724	ASP	2.7
1	A	721	LYS	2.5
1	A	203	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	655	CYS	2.5
1	A	712	VAL	2.5
1	A	714	ARG	2.2
1	A	741	ILE	2.2

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](#)

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	FRU	D	2	12/12	0.72	0.16	71,105,121,126	0
2	GLC	D	1	11/12	0.72	0.16	74,105,127,132	0

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
5	MLI	A	805	7/7	0.80	0.36	73,85,110,110	0
4	EDO	A	802	4/4	0.82	0.17	58,70,85,85	0
4	EDO	A	804	4/4	0.86	0.23	54,73,88,89	0
4	EDO	A	803	4/4	0.86	0.34	42,61,74,78	0
6	AD9	A	806	31/31	0.95	0.26	36,48,56,63	0
3	MG	A	801	1/1	0.97	0.32	40,40,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.