



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1A3A / pdb_00001a3a
Title : CRYSTAL STRUCTURE OF IIA MANNITOL FROM ESCHERICHIA COLI
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Deposited on : 1998-01-19
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

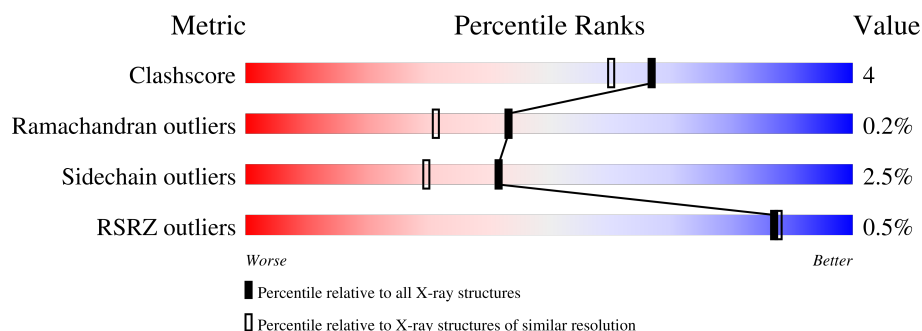
1 Overall quality at a glance

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))
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	148	88% 9% ••
1	B	148	81% 13% • 5%
1	C	148	88% 11% •
1	D	148	82% 16% •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5041 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 MANNITOL-SPECIFIC EII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	145	Total	C	N	O	S	0	0	0
			1128	711	194	221	2			
1	B	141	Total	C	N	O	S	0	0	0
			1095	691	186	216	2			
1	C	146	Total	C	N	O	S	0	0	0
			1132	712	195	223	2			
1	D	144	Total	C	N	O	S	0	0	0
			1118	705	192	219	2			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	182	Total	O	0	0
			182	182		
2	B	119	Total	O	0	0
			119	119		
2	C	164	Total	O	0	0
			164	164		
2	D	103	Total	O	0	0
			103	103		

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: MANNITOL-SPECIFIC EII

Chain A: 



- Molecule 1: MANNITOL-SPECIFIC EII

Chain B: 



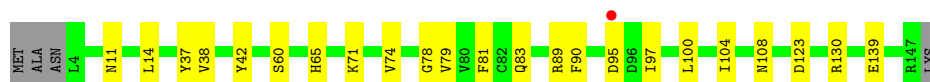
- Molecule 1: MANNITOL-SPECIFIC EII

Chain C: 



- Molecule 1: MANNITOL-SPECIFIC EII

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.57Å 66.01Å 73.86Å 90.00° 99.76° 90.00°	Depositor
Resolution (Å)	5.00 – 1.80 5.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (5.00-1.80) 91.3 (5.00-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 1.80Å)	Xtriage
Refinement program	REFMAC, X-PLOR	Depositor
R, R_{free}	0.190 , 0.242 0.189 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.146	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.29 , 111.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5041	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.66 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2600e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.54	0/1143	1.22	2/1543 (0.1%)
1	B	0.48	0/1110	1.22	3/1502 (0.2%)
1	C	0.54	0/1147	1.31	5/1550 (0.3%)
1	D	0.46	0/1133	1.28	4/1532 (0.3%)
All	All	0.51	0/4533	1.26	14/6127 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	11	ASN	CA-CB-CG	9.64	122.24	112.60
1	C	107	ARG	CD-NE-CZ	7.70	135.18	124.40
1	A	133	HIS	CA-CB-CG	-7.40	106.40	113.80
1	B	11	ASN	CA-CB-CG	7.37	119.97	112.60
1	A	5	PHE	CA-CB-CG	6.73	120.53	113.80
1	C	96	ASP	CA-CB-CG	6.11	118.71	112.60
1	D	123	ASP	CA-CB-CG	5.62	118.22	112.60
1	C	16	ARG	CD-NE-CZ	5.52	132.12	124.40
1	B	58	GLY	N-CA-C	-5.45	105.73	112.33
1	B	66	GLY	CA-C-O	5.38	127.57	121.92
1	D	108	ASN	N-CA-CB	-5.37	104.14	112.30
1	C	87	GLY	CA-C-O	5.31	127.33	122.39
1	D	95	ASP	CA-CB-CG	5.22	117.82	112.60
1	C	133	HIS	CA-CB-CG	-5.22	108.58	113.80

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	1128	0	1135	8	0
1	B	1095	0	1095	10	0
1	C	1132	0	1130	6	0
1	D	1118	0	1122	11	0
2	A	182	0	0	2	0
2	B	119	0	0	3	0
2	C	164	0	0	4	0
2	D	103	0	0	1	0
All	All	5041	0	4482	33	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 4.

All (33) 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:C:122:LEU:HD21	1:C:144:LEU:HD21	1.59	0.83
1:D:79:VAL:HG12	1:D:104:ILE:HG22	1.78	0.65
1:B:74:VAL:HB	1:B:107:ARG:HG2	1.84	0.59
1:A:56:TYR:HB2	1:A:90:PHE:HB3	1.85	0.58
1:C:10:GLU:HG2	2:C:190:HOH:O	2.03	0.57
1:B:30:GLU:HG3	2:B:259:HOH:O	2.04	0.56
1:B:102:ILE:HD13	1:B:118:LEU:HD22	1.87	0.55
1:D:89:ARG:HA	1:D:97:ILE:HD13	1.90	0.54
1:A:97:ILE:HD11	2:A:307:HOH:O	2.08	0.53
1:C:120:ASN:ND2	2:C:217:HOH:O	2.42	0.52
1:B:92:GLU:HG2	1:D:71:LYS:NZ	2.24	0.52
1:A:68:VAL:HG12	2:C:192:HOH:O	2.10	0.51
1:A:74:VAL:HB	1:A:107:ARG:HG3	1.95	0.49
1:D:37:TYR:CD1	1:D:78:GLY:HA3	2.48	0.48
1:D:74:VAL:HG21	2:D:213:HOH:O	2.12	0.48
1:A:91:GLY:HA3	1:A:96:ASP:HB3	1.97	0.47
1:B:43:VAL:HG11	2:B:259:HOH:O	2.14	0.47
1:B:22:GLU:O	1:B:26:ARG:HG3	2.16	0.46
1:C:3:ASN:HB3	2:C:178:HOH:O	2.16	0.45
1:B:122:LEU:HD21	1:B:144:LEU:HD21	1.98	0.45
1:C:37:TYR:CD1	1:C:78:GLY:HA3	2.52	0.45
1:A:56:TYR:CZ	1:A:58:GLY:HA2	2.52	0.45
1:B:92:GLU:HG2	1:D:71:LYS:HZ2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:SER:HB3	2:B:242:HOH:O	2.19	0.43
1:C:38:VAL:HG11	1:C:42:TYR:CD2	2.54	0.42
1:B:56:TYR:HB2	1:B:90:PHE:HB3	2.00	0.42
1:D:65:HIS:HB3	1:D:104:ILE:HG13	2.02	0.42
1:D:81:PHE:CZ	1:D:100:LEU:HD22	2.55	0.42
1:D:130:ARG:NH2	1:D:139:GLU:OE2	2.52	0.42
1:D:14:LEU:HA	1:D:83:GLN:HB3	2.02	0.41
1:D:38:VAL:HG11	1:D:42:TYR:CD2	2.55	0.41
1:A:60:SER:HA	1:A:97:ILE:O	2.21	0.40
1:A:99:ARG:HD3	2:A:324:HOH:O	2.21	0.40

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	143/148 (97%)	142 (99%)	1 (1%)	0	100	100
1	B	139/148 (94%)	137 (99%)	1 (1%)	1 (1%)	18	8
1	C	144/148 (97%)	142 (99%)	2 (1%)	0	100	100
1	D	142/148 (96%)	140 (99%)	2 (1%)	0	100	100
All	All	568/592 (96%)	561 (99%)	6 (1%)	1 (0%)	43	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	53	THR

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	119/121 (98%)	116 (98%)	3 (2%)	42	30
1	B	116/121 (96%)	111 (96%)	5 (4%)	26	13
1	C	119/121 (98%)	117 (98%)	2 (2%)	53	45
1	D	118/121 (98%)	116 (98%)	2 (2%)	53	45
All	All	472/484 (98%)	460 (98%)	12 (2%)	42	30

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	LYS
1	A	107	ARG
1	A	119	THR
1	B	92	GLU
1	B	94	GLU
1	B	123	ASP
1	B	125	GLU
1	B	126	SER
1	C	6	LYS
1	C	60	SER
1	D	60	SER
1	D	90	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	HIS
1	A	113	GLN
1	A	120	ASN
1	B	113	GLN
1	B	133	HIS
1	C	120	ASN
1	D	44	GLN

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Mol	Chain	Res	Type
1	D	65	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 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 [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	145/148 (97%)	-0.76	1 (0%) 84 85	8, 15, 23, 38	0
1	B	141/148 (95%)	-0.40	1 (0%) 84 85	10, 21, 39, 47	0
1	C	146/148 (98%)	-0.78	0 100 100	8, 16, 25, 38	0
1	D	144/148 (97%)	-0.36	1 (0%) 84 85	13, 23, 36, 41	0
All	All	576/592 (97%)	-0.57	3 (0%) 87 88	8, 18, 34, 47	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	4	LEU	3.0
1	B	123	ASP	2.7
1	D	95	ASP	2.1

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.