



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 10:32 pm GMT

PDB ID : 2JZO  
Title : Solution NMR structure of the non-productive complex between IIMannose and IIBMannose of the mannose transporter of the E. coli phosphotransferase system  
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Deposited on : 2008-01-10

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : trunk28760  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

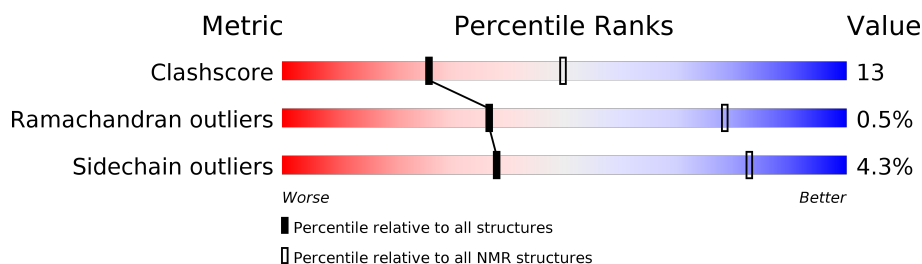
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*




The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	133	 84%8%5%.
1	B	133	 84%11%..
2	D	165	 71%27%..

## 2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6587 atoms, of which 3328 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PTS system mannose-specific EIIAB component.

Mol	Chain	Residues	Atoms						Trace
1	A	129	Total	C	H	N	O	S	0
			1979	632	991	160	193	3	
1	B	129	Total	C	H	N	O	S	0
			1979	632	991	160	193	3	


- Molecule 2 is a protein called PTS system mannose-specific EIIAB component.

Mol	Chain	Residues	Atoms						Trace
2	D	165	Total	C	H	N	O	S	0
			2629	805	1346	230	242	6	

## 4 Residue-property plots [i](#)


These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: PTS system mannose-specific EIIAB component

Chain A: 



- Molecule 1: PTS system mannose-specific EIIAB component

Chain B: 



- Molecule 2: PTS system mannose-specific EIIAB component

Chain D: 



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *conjoined rigid body/torsion angle simulated annealing*.

Of the 120 calculated structures, 1 were deposited, based on the following criterion: *restrained regularized mean*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR NIH	structure solution	2.18.1
X-PLOR NIH	refinement	2.18.1

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 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 (average) 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	0.91	3/1005 (0.3%)	1.02	4/1367 (0.3%)
1	B	0.85	2/1005 (0.2%)	0.99	6/1367 (0.4%)
2	D	1.19	2/1297 (0.2%)	1.17	1/1751 (0.1%)
All	All	1.01	7/3307 (0.2%)	1.07	11/4485 (0.2%)

All bond outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	323	LYS	C-O	15.54	1.52	1.23
2	D	323	LYS	C-OXT	13.51	1.49	1.23
1	A	105	ARG	CD-NE	11.65	1.66	1.46
1	A	130	LYS	C-O	10.71	1.43	1.23
1	B	130	LYS	C-O	10.71	1.43	1.23
1	B	105	ARG	CD-NE	7.70	1.59	1.46
1	A	105	ARG	NE-CZ	-5.35	1.26	1.33

All angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	184	LYS	CD-CE-NZ	-30.70	41.09	111.70
1	A	105	ARG	NE-CZ-NH2	-12.23	114.19	120.30
1	A	130	LYS	CA-C-O	12.21	145.74	120.10
1	B	130	LYS	CA-C-O	12.17	145.66	120.10
1	A	105	ARG	NE-CZ-NH1	9.98	125.29	120.30
1	A	105	ARG	CD-NE-CZ	-7.94	112.49	123.60
1	B	105	ARG	NE-CZ-NH2	-7.82	116.39	120.30
1	B	123	ARG	NE-CZ-NH2	7.03	123.81	120.30
1	B	123	ARG	NE-CZ-NH1	-6.46	117.07	120.30
1	B	105	ARG	CD-NE-CZ	-5.83	115.44	123.60
1	B	105	ARG	NE-CZ-NH1	5.14	122.87	120.30

There are no chirality outliers.

There are no planarity outliers.

## 6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	988	991	986	15
1	B	988	991	986	15
2	D	1283	1346	1339	54
All	All	3259	3328	3311	84

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 13.

All clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:B:22:GLU:OE2	1:B:27:GLU:HG2	1.26	1.24
2:D:323:LYS:HA	2:D:323:LYS:NZ	1.17	1.54
1:B:22:GLU:OE2	1:B:27:GLU:CG	1.07	2.02
1:B:22:GLU:HG3	1:B:27:GLU:HA	0.92	1.37
1:A:22:GLU:C	1:A:22:GLU:OE1	0.88	2.12
2:D:323:LYS:HZ3	2:D:323:LYS:HA	0.87	1.20
1:A:22:GLU:O	1:A:22:GLU:OE1	0.85	1.93
2:D:168:ARG:NH1	2:D:178:VAL:HG12	0.77	1.94
1:A:100:GLU:OE1	1:A:100:GLU:CA	0.76	2.33
2:D:224:ALA:O	2:D:227:ILE:HG22	0.74	1.82
1:B:22:GLU:CG	1:B:27:GLU:HA	0.73	2.12
2:D:323:LYS:CE	2:D:323:LYS:HA	0.72	2.14
1:A:78:SER:O	1:A:82:VAL:HG13	0.72	1.84
2:D:173:LEU:HD12	2:D:173:LEU:N	0.71	2.00
1:A:100:GLU:OE1	1:A:100:GLU:N	0.71	2.23
1:B:22:GLU:HG3	1:B:27:GLU:CA	0.71	2.15
2:D:159:ASN:ND2	2:D:259:LYS:NZ	0.70	2.39
1:B:78:SER:O	1:B:82:VAL:HG13	0.69	1.87
2:D:172:ARG:NH2	2:D:175:HIS:CE1	0.68	2.61
2:D:172:ARG:NH2	2:D:175:HIS:NE2	0.67	2.41
1:A:100:GLU:OE1	1:A:100:GLU:HA	0.64	1.93
2:D:222:ASP:OD1	2:D:225:LYS:N	0.64	2.23
2:D:183:THR:HG21	2:D:216:VAL:HG21	0.63	1.71
2:D:323:LYS:CA	2:D:323:LYS:NZ	0.62	2.49
2:D:303:VAL:CG2	2:D:314:MET:SD	0.61	2.88
1:A:10:HIS:ND1	1:A:67:ASP:OD2	0.60	2.34

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
2:D:173:LEU:CD1	2:D:173:LEU:N	0.59	2.65
2:D:323:LYS:HA	2:D:323:LYS:HZ2	0.58	1.54
1:A:19:LYS:O	1:A:22:GLU:HG3	0.58	1.99
1:B:100:GLU:CA	1:B:100:GLU:OE1	0.57	2.52
2:D:159:ASN:HD21	2:D:259:LYS:NZ	0.56	1.96
1:B:100:GLU:HA	1:B:100:GLU:OE1	0.56	2.01
1:B:22:GLU:CD	1:B:27:GLU:CG	0.56	2.72
2:D:162:MET:SD	2:D:240:VAL:CG2	0.55	2.94
2:D:172:ARG:CZ	2:D:175:HIS:CE1	0.55	2.90
1:A:67:ASP:OD1	1:A:67:ASP:N	0.55	2.39
1:B:9:THR:HG21	1:B:13:ALA:HB3	0.55	1.78
2:D:162:MET:SD	2:D:240:VAL:HG21	0.54	2.42
2:D:270:PHE:CD1	2:D:271:ARG:N	0.54	2.76
1:B:67:ASP:OD1	1:B:67:ASP:N	0.54	2.40
2:D:270:PHE:CG	2:D:271:ARG:N	0.53	2.75
1:A:3:ILE:O	1:A:105:ARG:HD2	0.52	2.04
1:A:22:GLU:C	1:A:22:GLU:CD	0.51	2.68
1:B:3:ILE:O	1:B:105:ARG:HD2	0.51	2.05
1:A:9:THR:HG21	1:A:13:ALA:HB3	0.51	1.83
2:D:284:ASP:OD1	2:D:287:ASP:N	0.50	2.32
2:D:295:ASN:OD1	2:D:295:ASN:O	0.50	2.30
2:D:181:ARG:NH1	2:D:308:THR:HG21	0.49	2.22
2:D:182:TRP:O	2:D:186:THR:HG23	0.49	2.08
2:D:319:SER:O	2:D:323:LYS:C	0.48	2.52
2:D:175:HIS:O	2:D:175:HIS:CG	0.48	2.66
2:D:295:ASN:C	2:D:295:ASN:OD1	0.48	2.52
2:D:222:ASP:OD1	2:D:225:LYS:CB	0.47	2.61
1:B:79:ARG:O	1:B:82:VAL:HG22	0.47	2.10
2:D:182:TRP:CH2	2:D:264:ASN:ND2	0.47	2.82
2:D:159:ASN:HD21	2:D:259:LYS:HZ3	0.47	1.53
1:A:22:GLU:OE1	1:A:23:MET:N	0.47	2.47
2:D:278:ASN:OD1	2:D:279:ASN:N	0.47	2.44
2:D:181:ARG:HH12	2:D:308:THR:HG21	0.47	1.69
2:D:254:VAL:CG2	2:D:260:ILE:HD12	0.46	2.40
2:D:177:GLN:O	2:D:178:VAL:C	0.46	2.53
2:D:159:ASN:ND2	2:D:259:LYS:HZ3	0.46	2.07
2:D:159:ASN:ND2	2:D:259:LYS:HZ2	0.45	2.06
2:D:322:ASP:O	2:D:323:LYS:C	0.45	2.54
2:D:246:ASN:OD1	2:D:246:ASN:O	0.44	2.34
2:D:182:TRP:O	2:D:186:THR:OG1	0.44	2.34
2:D:295:ASN:HD22	2:D:315:MET:HG3	0.43	1.73
1:B:22:GLU:OE2	1:B:27:GLU:HA	0.43	2.13

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
2:D:178:VAL:O	2:D:182:TRP:CD1	0.43	2.72
1:A:36:PHE:C	1:A:36:PHE:CD1	0.43	2.92
2:D:179:ALA:O	2:D:183:THR:OG1	0.43	2.30
2:D:323:LYS:HZ3	2:D:323:LYS:CA	0.42	2.08
2:D:181:ARG:NH1	2:D:308:THR:CG2	0.42	2.80
2:D:205:LYS:O	2:D:209:THR:HG23	0.42	2.15
1:A:82:VAL:HG23	1:A:83:ASP:OD1	0.42	2.14
2:D:230:TYR:CD1	2:D:230:TYR:C	0.41	2.94
2:D:305:LYS:H	2:D:305:LYS:CD	0.41	2.28
2:D:168:ARG:NH1	2:D:178:VAL:CG1	0.41	2.76
2:D:168:ARG:HH12	2:D:178:VAL:HG12	0.41	1.69
1:B:36:PHE:C	1:B:36:PHE:CD1	0.41	2.92
2:D:235:TYR:O	2:D:238:GLU:HB2	0.41	2.16
2:D:270:PHE:CD1	2:D:270:PHE:C	0.41	2.94
2:D:277:VAL:HG22	2:D:281:VAL:O	0.41	2.16
2:D:181:ARG:NH2	2:D:308:THR:CG2	0.40	2.85

## 6.3 Torsion angles

### 6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	127/133 (95%)	126 (99%)	0 (0%)	1 (1%)	27	73
1	B	127/133 (95%)	126 (99%)	0 (0%)	1 (1%)	27	73
2	D	163/165 (99%)	155 (95%)	8 (5%)	0 (0%)	100	100
All	All	417/431 (97%)	407 (98%)	8 (2%)	2 (0%)	37	78

All 2 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	82	VAL
1	B	82	VAL

### 6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	104/107 (97%)	98 (94%)	6 (6%)	28	74
1	B	104/107 (97%)	100 (96%)	4 (4%)	42	86
2	D	143/143 (100%)	138 (97%)	5 (3%)	45	87
All	All	351/357 (98%)	336 (96%)	15 (4%)	38	83

All 15 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	84	LYS
1	B	23	MET
1	B	83	ASP
1	A	83	ASP
2	D	323	LYS
1	A	22	GLU
2	D	305	LYS
1	A	79	ARG
1	B	84	LYS
1	A	100	GLU
1	A	23	MET
2	D	228	ARG
1	B	100	GLU
2	D	162	MET
2	D	319	SER

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided