

# Full wwPDB X-ray Structure Validation Report (i)

#### Oct 11, 2021 - 04:31 AM EDT

PDB ID : 2RLB

Title: Crystal Structure cation-dependent mannose 6-phosphate receptor at pH 6.5

bound to M6P in absence of Mn

Authors: Olson, L.J.; Hindsgaul, O.; Dahms, N.M.; Kim, J.-J.P.

Deposited on : 2007-10-18

Resolution : 1.75 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 (i) symbol.

The following versions of software and data (see references (1)) 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 : 2.23.2buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

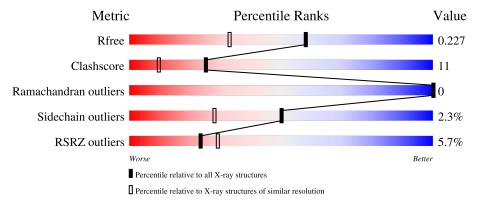
Validation Pipeline (wwPDB-VP) : 2.23.2

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$ 

The reported resolution of this entry is 1.75 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
$R_{free}$	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 <=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	154	77%	18%		-		
1	В	154	81%	18%				



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2726 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 Cation-dependent mannose-6-phosphate receptor.

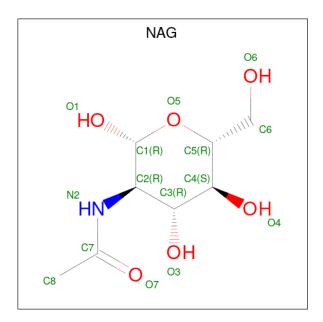
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	148	Total	С	N	О	S	0	0	0
1	A	140	1177	730	207	230	10	0	0	0
1	В	152	Total	С	N	О	S	0	0	0
1	Ъ	152	1203	745	212	236	10	U	0	U

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	GLN	ASN	engineered mutation	UNP P11456
A	57	GLN	ASN	engineered mutation	UNP P11456
A	68	GLN	ASN	engineered mutation	UNP P11456
A	87	GLN	ASN	engineered mutation	UNP P11456
В	31	GLN	ASN	engineered mutation	UNP P11456
В	57	GLN	ASN	engineered mutation	UNP P11456
В	68	GLN	ASN	engineered mutation	UNP P11456
В	87	GLN	ASN	engineered mutation	UNP P11456

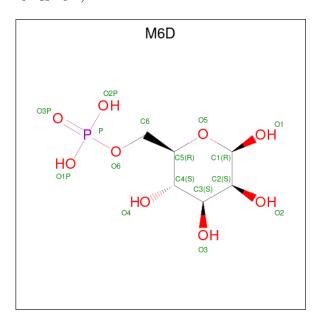
• Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 14				0	0
2	В	1	Total 14	C 8	N 1	O 5	0	0

• Molecule 3 is 6-O-phosphono-beta-D-mannopyranose (three-letter code: M6D) (formula:  $C_6H_{13}O_9P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 16	C 6	O 9	P 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total C O P 16 6 9 1	0	0

#### • Molecule 4 is water.

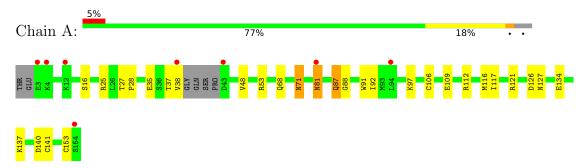
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	141	Total O 141 141	0	0
4	В	145	Total O 145 145	0	0



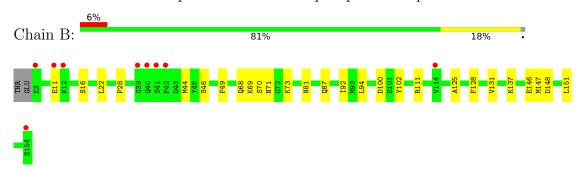
# 3 Residue-property plots (i)

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: Cation-dependent mannose-6-phosphate receptor



• Molecule 1: Cation-dependent mannose-6-phosphate receptor





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	91.39Å 91.39Å 84.82Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 - 1.75	Depositor
rtesolution (A)	29.43 - 1.75	EDS
% Data completeness	95.2 (30.00-1.75)	Depositor
(in resolution range)	95.2 (29.43-1.75)	EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.66 (at 1.75Å)	Xtriage
Refinement program	CNS	Depositor
P. P.	0.203 , $0.229$	Depositor
$R, R_{free}$	0.200 , $0.227$	DCC
$R_{free}$ test set	3475 reflections $(9.91%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.3	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36, 45.8	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2726	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.55% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: NAG, M6D

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		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.31	0/1195	0.59	0/1598	
1	В	0.31	0/1223	0.60	0/1638	
All	All	0.31	0/2418	0.60	0/3236	

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	1177	0	1132	29	0
1	В	1203	0	1156	23	0
2	A	14	0	13	2	0
2	В	14	0	13	2	0
3	A	16	0	11	0	0
3	В	16	0	11	1	0
4	A	141	0	0	3	0
4	В	145	0	0	3	0
All	All	2726	0	2336	51	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 11.



All (51) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A	A	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:128:PHE:HB2	1:B:147:MET:HE2	1.61	0.80
1:A:91:TRP:HB2	1:A:116:MET:HE1	1.65	0.78
1:B:46:SER:HB2	1:B:69:LYS:HE3	1.65	0.77
1:A:91:TRP:HB2	1:A:116:MET:CE	2.16	0.74
1:A:37:THR:O	1:A:38:VAL:HG23	1.91	0.70
1:B:71:ASN:HD21	1:B:73:LYS:HB2	1.63	0.61
1:B:71:ASN:ND2	1:B:73:LYS:HB2	2.14	0.60
1:A:112:ARG:NH1	1:A:140:ASP:HA	2.17	0.60
1:B:68:GLN:HE21	1:B:70:SER:H	1.49	0.59
1:A:106:CYS:O	1:A:109:GLU:HG2	2.02	0.59
1:A:116:MET:HE3	1:A:117:ILE:N	2.18	0.59
1:A:121:ARG:NH1	1:A:153:CYS:HB3	2.18	0.58
1:A:27:THR:N	1:A:28:PRO:HD2	2.20	0.57
1:A:121:ARG:HG2	4:A:3103:HOH:O	2.06	0.55
1:B:28:PRO:HG2	1:B:151:LEU:HD11	1.88	0.55
1:B:87:GLN:HB3	1:B:92:ILE:HG12	1.89	0.54
1:A:25:ARG:HH22	1:A:87:GLN:HE22	1.55	0.54
1:A:81:ASN:OD1	2:A:3001:NAG:C7	2.56	0.54
1:A:37:THR:HG22	4:A:3025:HOH:O	2.08	0.53
1:A:112:ARG:HH12	1:A:140:ASP:HA	1.75	0.51
1:A:81:ASN:OD1	2:A:3001:NAG:N2	2.44	0.50
1:A:116:MET:HE3	1:A:117:ILE:H	1.75	0.50
1:A:88:GLY:HA3	1:A:91:TRP:CE2	2.47	0.50
1:A:126:ASP:CG	1:A:127:ASN:H	2.15	0.50
1:B:100:ASP:O	1:B:111:ARG:HG3	2.13	0.49
1:B:94:LEU:C	1:B:94:LEU:HD23	2.33	0.49
1:A:25:ARG:HH22	1:A:87:GLN:NE2	2.10	0.48
1:B:131:VAL:HG21	1:B:146:GLU:HG3	1.94	0.48
1:B:128:PHE:HD1	1:B:147:MET:HE3	1.79	0.47
1:A:81:ASN:HB3	4:A:3010:HOH:O	2.14	0.47
1:A:137:LYS:CG	1:B:16:SER:HB2	2.44	0.46
1:A:137:LYS:HG3	1:B:16:SER:HB2	1.97	0.46
1:B:102:TYR:CE1	1:B:111:ARG:NH1	2.84	0.46
1:B:44:MET:HE3	1:B:69:LYS:HG3	1.98	0.46
1:A:16:SER:HB2	1:B:137:LYS:HG2	1.98	0.46
1:A:92:ILE:O	1:A:116:MET:HE3	2.16	0.45
1:B:111:ARG:HH12	3:B:501:M6D:H4	1.82	0.45
1:A:97:LYS:HG2	1:A:112:ARG:HD3	1.99	0.44
1:B:11:GLU:HG3	4:B:4142:HOH:O	2.17	0.44
1:B:128:PHE:CD1	1:B:147:MET:HE3	2.53	0.43

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance} \; ({ m \AA})$	overlap (Å)
1:A:91:TRP:HB2	1:A:116:MET:HE2	2.00	0.43
1:A:134:GLU:O	1:A:141:CYS:HB3	2.18	0.42
2:B:4001:NAG:H5	4:B:4145:HOH:O	2.18	0.42
1:A:126:ASP:CG	1:A:127:ASN:N	2.72	0.42
1:A:68:GLN:HB3	1:A:71:ASN:HD21	1.84	0.42
1:B:49:PHE:HD2	1:B:147:MET:HE1	1.84	0.42
2:B:4001:NAG:H62	4:B:4112:HOH:O	2.19	0.42
1:B:49:PHE:CD2	1:B:147:MET:HE1	2.55	0.41
1:B:128:PHE:HB2	1:B:147:MET:CE	2.41	0.41
1:B:125:ALA:HA	1:B:148:ASP:O	2.21	0.40
1:A:35:GLU:HG3	1:A:48:VAL:HG22	2.03	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	Perce	$\mathbf{ntiles}$
1	A	$144/154 \ (94\%)$	138 (96%)	6 (4%)	0	100	100
1	В	150/154~(97%)	146 (97%)	4 (3%)	0	100	100
All	All	294/308~(96%)	284 (97%)	10 (3%)	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	${f ed}$ Rotameric Outliers		Percentiles		
1	A	130/135 (96%)	126 (97%)	4 (3%)	40 17		
1	В	133/135 (98%)	131 (98%)	2 (2%)	65 49		
All	All	263/270 (97%)	257 (98%)	6 (2%)	50 28		

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	ARG
1	A	71	ASN
1	A	81	ASN
1	A	87	GLN
1	В	22	LEU
1	В	81	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	66	GLN
1	A	68	GLN
1	A	71	ASN
1	A	87	GLN
1	В	40	GLN
1	В	66	GLN
1	В	68	GLN
1	В	87	GLN

#### 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)

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			
IVIOI	Type		nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	В	4001	1	14,14,15	0.50	0	17,19,21	0.75	1 (5%)
2	NAG	A	3001	1	14,14,15	0.61	0	17,19,21	0.73	1 (5%)
3	M6D	В	501	-	16,16,16	1.12	1 (6%)	24,24,24	0.85	0
3	M6D	A	500	-	16,16,16	1.13	1 (6%)	24,24,24	0.84	0

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	NAG	В	4001	1	-	2/6/23/26	0/1/1/1
2	NAG	A	3001	1	-	2/6/23/26	0/1/1/1
3	M6D	В	501	-	-	0/6/26/26	0/1/1/1
3	M6D	A	500	-	-	0/6/26/26	0/1/1/1

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
3	A	500	M6D	O5-C1	2.09	1.48	1.42
3	В	501	M6D	O5-C1	2.07	1.48	1.42

#### All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
2	В	4001	NAG	C2-N2-C7	-2.23	119.73	122.90
2	A	3001	NAG	C2-N2-C7	-2.14	119.86	122.90

There are no chirality outliers.



All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	4001	NAG	C4-C5-C6-O6
2	В	4001	NAG	O5-C5-C6-O6
2	A	3001	NAG	C4-C5-C6-O6
2	A	3001	NAG	O5-C5-C6-O6

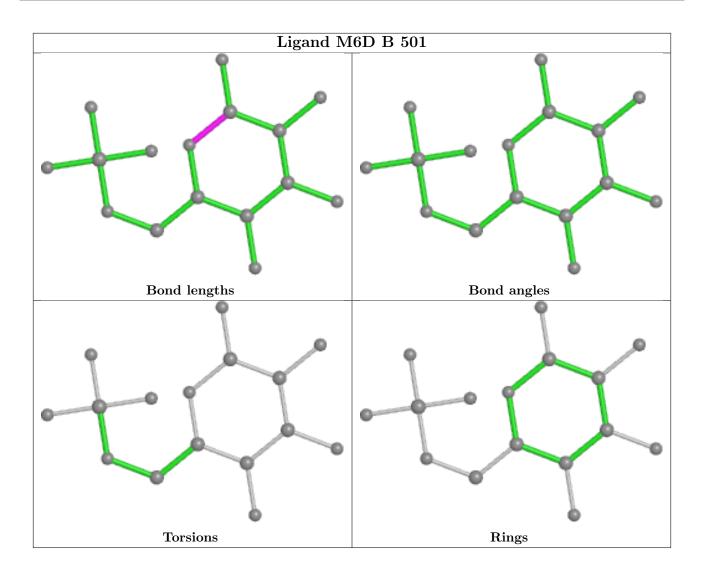
There are no ring outliers.

3 monomers are involved in 5 short contacts:

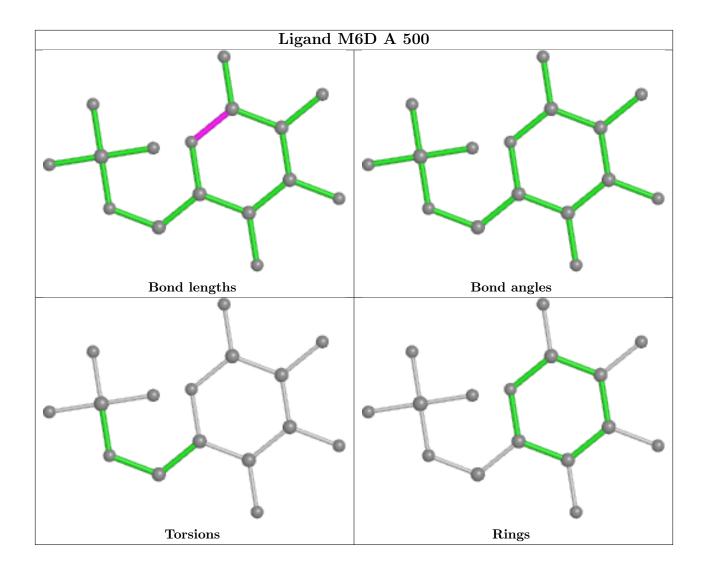
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	4001	NAG	2	0
2	A	3001	NAG	2	0
3	В	501	M6D	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









# 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,  $95^{th}$  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	$\langle { m RSRZ} \rangle$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	148/154 (96%)	0.29	8 (5%) 25 32	9, 16, 28, 49	0
1	В	152/154 (98%)	0.34	9 (5%) 22 27	9, 16, 35, 44	0
All	All	300/308 (97%)	0.32	17 (5%) 23 29	9, 16, 34, 49	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	38	VAL	7.9
1	A	3	GLU	5.1
1	A	154	SER	3.8
1	В	154	SER	3.5
1	В	40	GLN	3.4
1	В	12	LYS	3.3
1	В	41	SER	3.2
1	В	3	GLU	2.9
1	A	4	LYS	2.8
1	A	12	LYS	2.8
1	В	11	GLU	2.8
1	A	43	ASP	2.7
1	В	39	GLY	2.6
1	В	42	PRO	2.2
1	A	81	ASN	2.0
1	В	114	VAL	2.0
1	A	94	LEU	2.0

## 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)

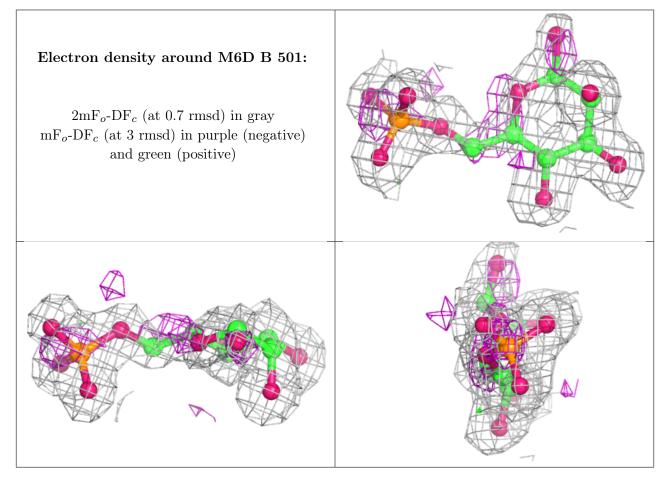
There are no monosaccharides in this entry.

## 6.4 Ligands (i)

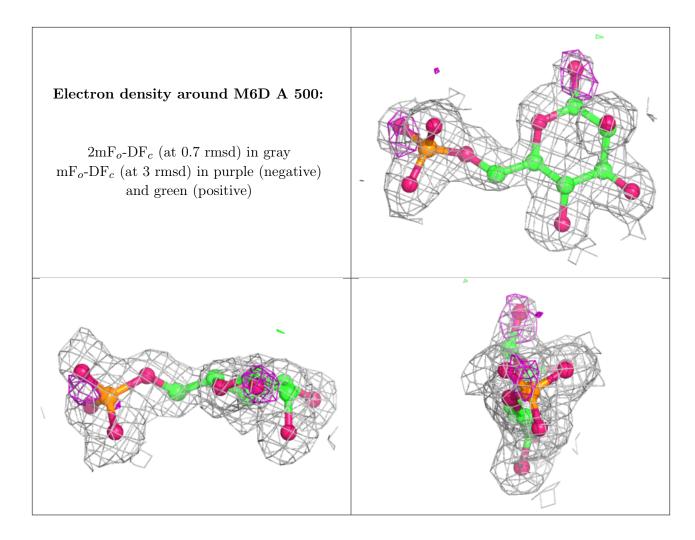
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q<0.9
2	NAG	В	4001	14/15	0.54	0.29	40,43,44,46	0
2	NAG	A	3001	14/15	0.69	0.21	34,35,37,37	0
3	M6D	В	501	16/16	0.85	0.17	17,23,27,28	0
3	M6D	A	500	16/16	0.91	0.14	12,19,24,26	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.







# 6.5 Other polymers (i)

There are no such residues in this entry.

