



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:55 PM GMT

PDB ID : 1MOX  
Title : Crystal Structure of Human Epidermal Growth Factor Receptor (residues 1-501) in complex with TGF-alpha  
Authors : Garrett, T.P.J.; McKern, N.M.; Lou, M.; Elleman, T.C.; Adams, T.E.; Lovrecz, G.O.; Zhu, H.-J.; Walker, F.; Frenkel, M.J.; Hoyne, P.A.; Jorissen, R.N.; Nice, E.C.; Burgess, A.W.; Ward, C.W.  
Deposited on : 2002-09-10  
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/XrayValidationReportHelp>

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:

MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	<b>NOT EXECUTED</b>
EDS	:	<b>NOT EXECUTED</b>
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

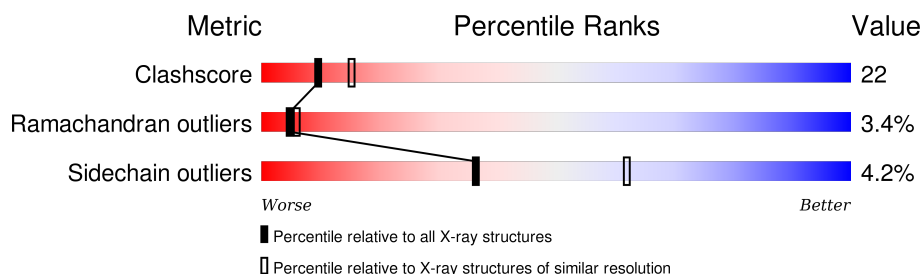
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	501	 63% 32% .
1	B	501	 66% 30% .
2	C	50	 62% 32% . .
2	D	50	 52% 34% 8% . .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	CL	A	737	-	-	X	-
10	CL	A	739	-	-	X	-
3	NAG	A	600	-	-	X	-
8	PT	B	702	-	-	X	-

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 8686 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 Epidermal Growth Factor Receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total	C	N	O	S	0	0	0
			3820	2369	674	735	42			
1	B	501	Total	C	N	O	S	0	0	0
			3844	2381	682	739	42			

- Molecule 2 is a protein called Transforming Growth Factor alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	49	Total	C	N	O	S	0	0	0
			377	232	69	70	6			
2	D	48	Total	C	N	O	S	0	0	0
			365	225	66	68	6			

- Molecule 3 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 4 is a polymer of unknown type called SUGAR (4-MER).

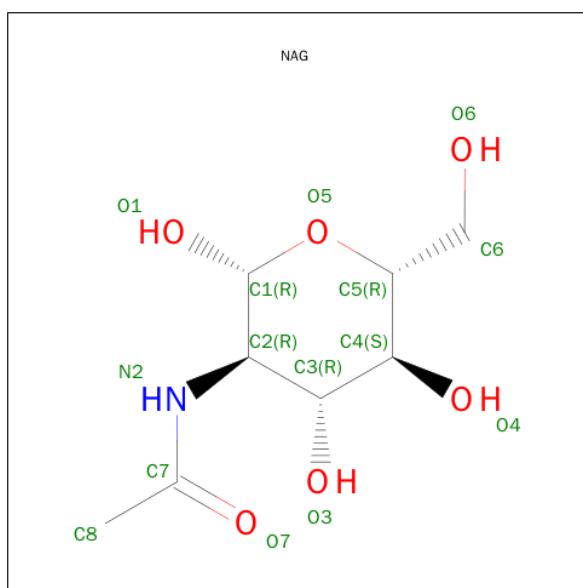
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 5 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:

C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 8 is PLATINUM (II) ION (three-letter code: PT) (formula: Pt).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	4	Total	Pt	0	0
			4	4		
8	A	3	Total	Pt	0	0
			3	3		

- Molecule 9 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	5	Total	Cd	0	0
			5	5		
9	A	4	Total	Cd	0	0
			4	4		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	1	Total 1	Cd 1	0	0
9	C	1	Total 1	Cd 1	0	0

- Molecule 10 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	1	Total 1	Cl 1	0	0
10	A	3	Total 3	Cl 3	0	0

- Molecule 11 is water.

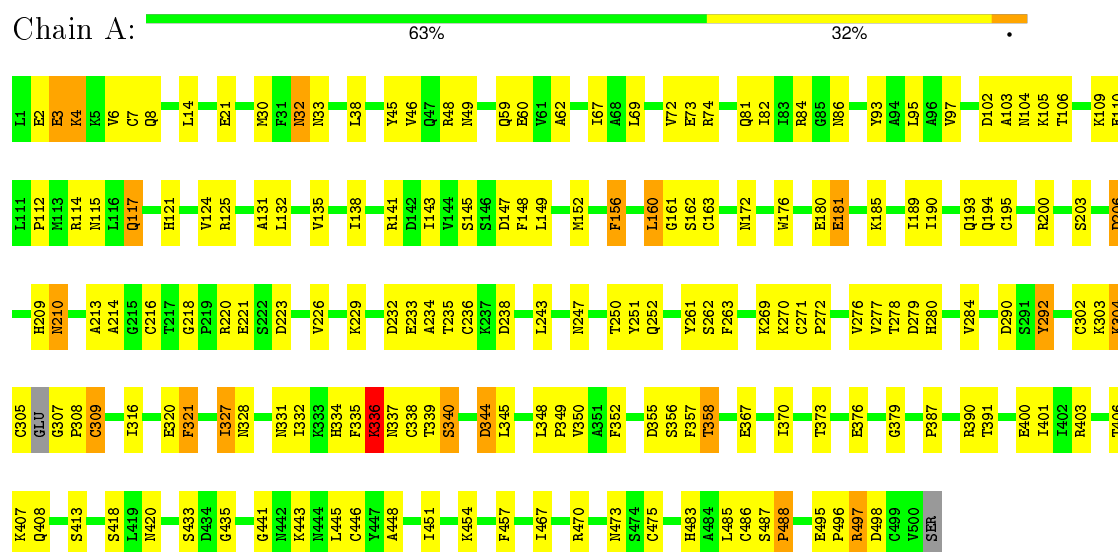
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	29	Total 29	O 29	0	0
11	B	39	Total 39	O 39	0	0
11	C	6	Total 6	O 6	0	0
11	D	5	Total 5	O 5	0	0

### 3 Residue-property plots

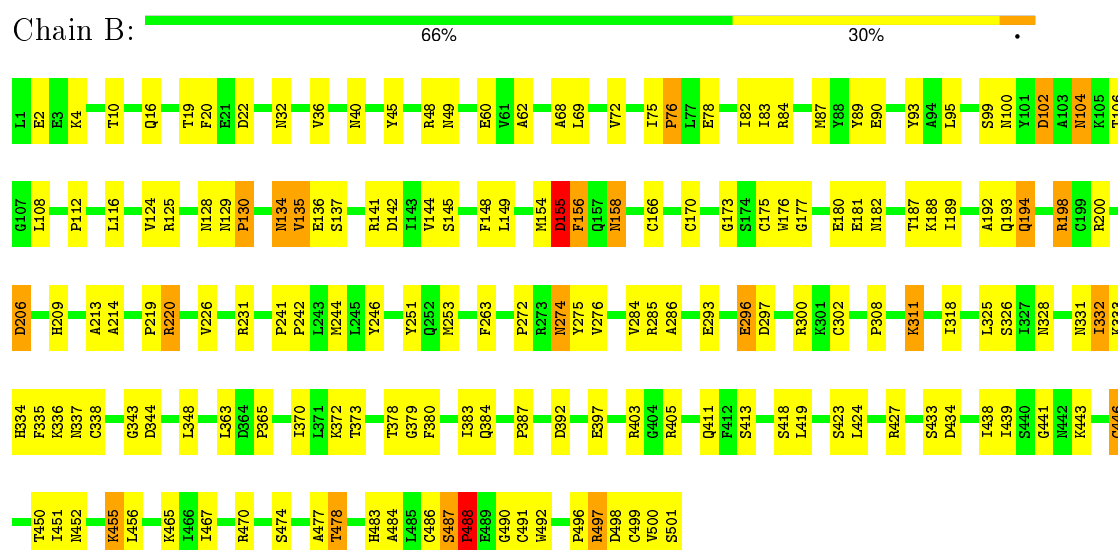
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

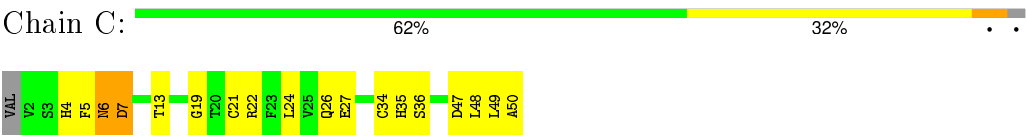
#### • Molecule 1: Epidermal Growth Factor Receptor



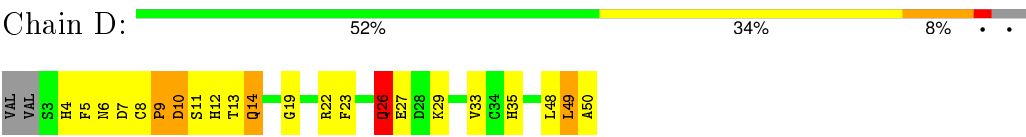
#### • Molecule 1: Epidermal Growth Factor Receptor



● Molecule 2: Transforming Growth Factor alpha



● Molecule 2: Transforming Growth Factor alpha





## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.59Å 198.71Å 78.90Å 90.00° 102.03° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.50)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.237 , 0.289	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8686	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

## 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: BMA, NAG, PT, CL, CD, FUC, MAN

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	0.39	1/3889 (0.0%)	0.69	2/5259 (0.0%)
1	B	0.39	1/3914 (0.0%)	0.70	2/5291 (0.0%)
2	C	0.44	0/388	0.77	0/524
2	D	0.41	0/375	0.69	0/506
All	All	0.39	2/8566 (0.0%)	0.70	4/11580 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	296	GLU	CB-CG	-5.29	1.42	1.52
1	A	2	GLU	CB-CG	-5.25	1.42	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	308	PRO	N-CA-CB	5.87	110.35	103.30
1	A	308	PRO	N-CA-CB	5.38	109.76	103.30
1	A	327	ILE	N-CA-C	-5.14	97.11	111.00
1	B	446	CYS	N-CA-C	5.08	124.72	111.00

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	3820	0	3676	176	5
1	B	3844	0	3705	161	4
2	C	377	0	323	21	0
2	D	365	0	311	14	0
3	A	38	0	34	8	0
4	A	50	0	43	4	0
5	B	49	0	43	1	0
6	B	14	0	13	0	0
7	B	28	0	25	4	0
8	A	3	0	0	0	0
8	B	4	0	0	2	0
9	A	4	0	0	0	1
9	B	5	0	0	0	0
9	C	1	0	0	0	0
9	D	1	0	0	0	0
10	A	3	0	0	4	0
10	B	1	0	0	0	0
11	A	29	0	0	6	0
11	B	39	0	0	0	0
11	C	6	0	0	0	0
11	D	5	0	0	0	0
All	All	8686	0	8173	372	5

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 22.

The worst 5 of 372 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:141:ARG:HH21	1:A:189:ILE:HD11	1.16	1.05
3:A:600:NAG:H62	3:A:601:FUC:H3	1.53	0.90
1:A:496:PRO:HD2	1:A:497:ARG:NH2	1.87	0.88
1:B:158:ASN:HD22	1:B:158:ASN:H	1.21	0.88
4:A:652:BMA:H3	4:A:653:MAN:H3	1.56	0.87

All (5) 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:180:GLU:OE1	9:A:730:CD:CD[1_554]	1.40	0.80
1:A:21:GLU:CD	1:B:474:SER:OG[2_546]	1.55	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:GLU:OE1	1:B:474:SER:OG[2_546]	1.75	0.45
1:A:49:ASN:O	1:B:477:ALA:O[2_546]	2.03	0.17
1:A:21:GLU:OE2	1:B:474:SER:OG[2_546]	2.10	0.10

## 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	495/501 (99%)	417 (84%)	66 (13%)	12 (2%)	7	11
1	B	499/501 (100%)	420 (84%)	62 (12%)	17 (3%)	5	6
2	C	47/50 (94%)	38 (81%)	8 (17%)	1 (2%)	9	14
2	D	46/50 (92%)	32 (70%)	7 (15%)	7 (15%)	0	0
All	All	1087/1102 (99%)	907 (83%)	143 (13%)	37 (3%)	5	6

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	GLU
1	A	4	LYS
1	A	104	ASN
1	A	488	PRO
1	B	166	CYS

### 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	426/440 (97%)	409 (96%)	17 (4%)	38	64
1	B	429/440 (98%)	414 (96%)	15 (4%)	43	70
2	C	40/43 (93%)	38 (95%)	2 (5%)	30	53
2	D	38/43 (88%)	33 (87%)	5 (13%)	5	9
All	All	933/966 (97%)	894 (96%)	39 (4%)	36	62

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	87	MET
1	B	156	PHE
2	D	22	ARG
1	B	104	ASN
1	B	154	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	483	HIS
1	B	104	ASN
2	C	6	ASN
1	B	49	ASN
1	B	117	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 ⓘ

13 carbohydrates 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$
3	NAG	A	600	1,3	14,14,15	0.66	0	15,19,21	0.89	1 (6%)
3	FUC	A	601	3	10,10,11	0.52	0	14,14,16	0.80	1 (7%)
3	NAG	A	602	3	14,14,15	0.46	0	15,19,21	0.72	1 (6%)
4	NAG	A	650	1,4	14,14,15	0.52	0	15,19,21	0.69	1 (6%)
4	NAG	A	651	4	14,14,15	0.58	0	15,19,21	0.71	1 (6%)
4	BMA	A	652	4	11,11,12	0.68	0	14,15,17	0.49	0
4	MAN	A	653	4	11,11,12	0.54	0	14,15,17	0.94	1 (7%)
5	NAG	B	600	1,5	14,14,15	0.51	0	15,19,21	0.91	1 (6%)
5	FUC	B	601	5	10,10,11	0.46	0	14,14,16	0.58	0
5	NAG	B	602	5	14,14,15	0.61	0	15,19,21	0.70	0
5	BMA	B	603	5	11,11,12	0.49	0	14,15,17	0.26	0
7	NAG	B	650	1,7	14,14,15	0.66	0	15,19,21	0.63	0
7	NAG	B	651	7	14,14,15	0.48	0	15,19,21	0.79	1 (6%)

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
3	NAG	A	600	1,3	-	0/6/23/26	0/1/1/1
3	FUC	A	601	3	-	0/0/17/20	0/1/1/1
3	NAG	A	602	3	-	1/6/23/26	0/1/1/1
4	NAG	A	650	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	651	4	-	0/6/23/26	0/1/1/1
4	BMA	A	652	4	-	0/2/19/22	0/1/1/1
4	MAN	A	653	4	-	0/2/19/22	0/1/1/1
5	NAG	B	600	1,5	-	0/6/23/26	0/1/1/1
5	FUC	B	601	5	-	0/0/17/20	0/1/1/1
5	NAG	B	602	5	-	0/6/23/26	0/1/1/1
5	BMA	B	603	5	-	0/2/19/22	0/1/1/1
7	NAG	B	650	1,7	-	0/6/23/26	0/1/1/1
7	NAG	B	651	7	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	600	NAG	C2-N2-C7	-2.77	119.47	123.04
7	B	651	NAG	C2-N2-C7	-2.58	119.73	123.04
3	A	602	NAG	C2-N2-C7	-2.25	120.15	123.04
3	A	600	NAG	C2-N2-C7	-2.22	120.19	123.04
4	A	651	NAG	C2-N2-C7	-2.14	120.30	123.04

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	NAG	O7-C7-N2-C2

There are no ring outliers.

7 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	600	NAG	8	0
3	A	601	FUC	5	0
4	A	650	NAG	1	0
4	A	652	BMA	3	0
4	A	653	MAN	3	0
5	B	602	NAG	1	0
7	B	650	NAG	4	0

## 5.6 Ligand geometry ⓘ

Of 23 ligands modelled in this entry, 22 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z  > 2$
6	NAG	B	630	1	14,14,15	0.51	0	15,19,21	0.71	1 (6%)

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
6	NAG	B	630	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
6	B	630	NAG	C2-N2-C7	-2.24	120.16	123.04

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 [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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.