



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:26 AM GMT

PDB ID : 3LTF
Title : Crystal Structure of the Drosophila Epidermal Growth Factor Receptor ectodomain in complex with Spitz
Authors : Alvarado, D.; Klein, D.E.; Lemmon, M.A.
Deposited on : 2010-02-15
Resolution : 3.20 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
A user guide is available at
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

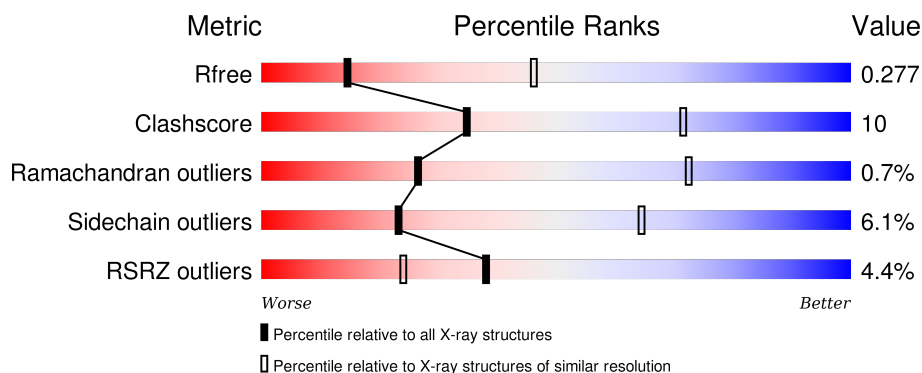
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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 ≥ 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.

Mol	Chain	Length	Quality of chain
1	A	601	<div> <div>4%</div> <div>66%</div> <div>19%</div> <div>•</div> <div>13%</div> </div>
1	C	601	<div> <div>3%</div> <div>65%</div> <div>21%</div> <div>•</div> <div>12%</div> </div>
2	B	58	<div> <div>10%</div> <div>84%</div> <div>12%</div> <div>• •</div> </div>
2	D	58	<div> <div>83%</div> <div>12%</div> <div>• •</div> </div>

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
3	MAN	A	4702	X	-	-	-
3	MAN	A	4703	X	-	-	-
3	MAN	A	4704	X	-	-	-
3	MAN	A	4705	X	-	-	-
4	NAG	C	596	X	-	-	-
6	MAN	C	4702	X	-	-	-
6	MAN	C	4703	X	-	-	-
7	MLI	A	596	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9221 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	522	Total	C	N	O	S	0	0	0
			4007	2495	707	757	48			
1	C	531	Total	C	N	O	S	0	1	0
			4109	2559	732	768	50			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	EXPRESSION TAG	UNP P04412
A	-4	HIS	-	EXPRESSION TAG	UNP P04412
A	-3	HIS	-	EXPRESSION TAG	UNP P04412
A	-2	HIS	-	EXPRESSION TAG	UNP P04412
A	-1	HIS	-	EXPRESSION TAG	UNP P04412
A	0	HIS	-	EXPRESSION TAG	UNP P04412
A	38	GLU	LYS	CONFLICT	UNP P04412
A	230	GLY	ALA	CONFLICT	UNP P04412
A	232	CYS	SER	CONFLICT	UNP P04412
A	359	LEU	ARG	CONFLICT	UNP P04412
A	493	ASN	THR	CONFLICT	UNP P04412
A	590	HIS	-	EXPRESSION TAG	UNP P04412
A	591	HIS	-	EXPRESSION TAG	UNP P04412
A	592	HIS	-	EXPRESSION TAG	UNP P04412
A	593	HIS	-	EXPRESSION TAG	UNP P04412
A	594	HIS	-	EXPRESSION TAG	UNP P04412
A	595	HIS	-	EXPRESSION TAG	UNP P04412
C	-5	HIS	-	EXPRESSION TAG	UNP P04412
C	-4	HIS	-	EXPRESSION TAG	UNP P04412
C	-3	HIS	-	EXPRESSION TAG	UNP P04412
C	-2	HIS	-	EXPRESSION TAG	UNP P04412
C	-1	HIS	-	EXPRESSION TAG	UNP P04412
C	0	HIS	-	EXPRESSION TAG	UNP P04412
C	38	GLU	LYS	CONFLICT	UNP P04412
C	230	GLY	ALA	CONFLICT	UNP P04412

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Chain	Residue	Modelled	Actual	Comment	Reference
C	232	CYS	SER	CONFLICT	UNP P04412
C	359	LEU	ARG	CONFLICT	UNP P04412
C	493	ASN	THR	CONFLICT	UNP P04412
C	590	HIS	-	EXPRESSION TAG	UNP P04412
C	591	HIS	-	EXPRESSION TAG	UNP P04412
C	592	HIS	-	EXPRESSION TAG	UNP P04412
C	593	HIS	-	EXPRESSION TAG	UNP P04412
C	594	HIS	-	EXPRESSION TAG	UNP P04412
C	595	HIS	-	EXPRESSION TAG	UNP P04412

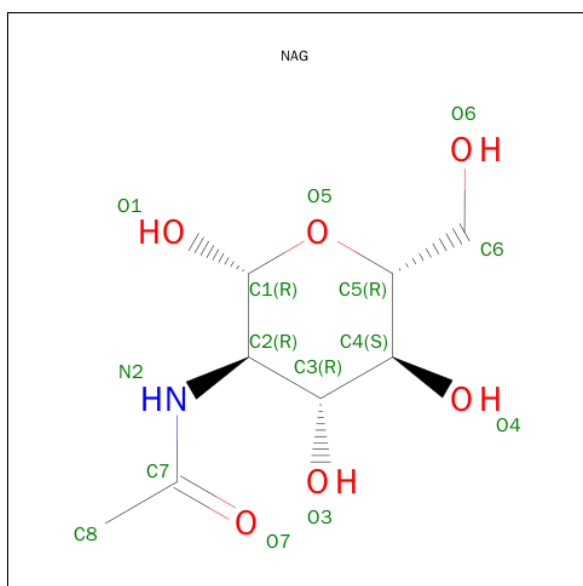
- Molecule 2 is a protein called Protein spitz.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	57	Total	C	N	O	S	0	0	0
			450	290	70	83	7			
2	B	57	Total	C	N	O	S	0	0	0
			456	296	70	83	7			

- Molecule 3 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

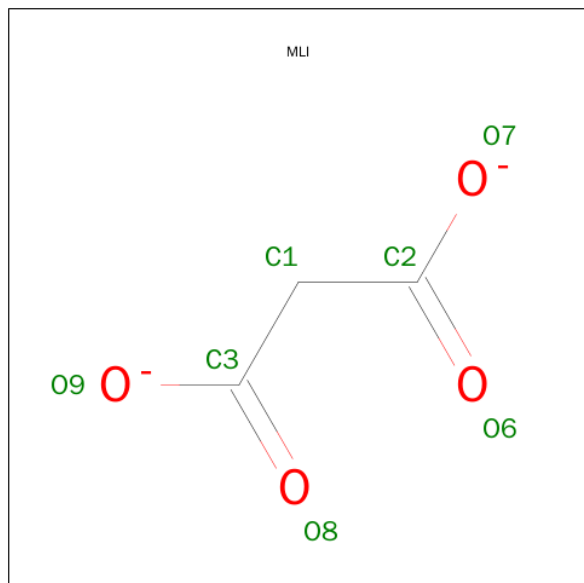
- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

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

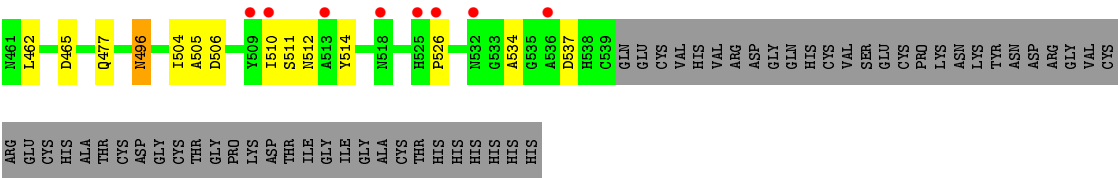
- Molecule 6 is a polymer of unknown type called SUGAR (4-MER).

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

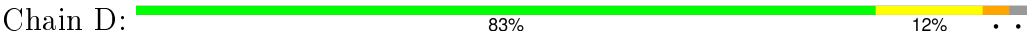
- Molecule 7 is MALONATE ION (three-letter code: MLI) (formula: $C_3H_2O_4$).



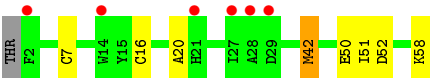
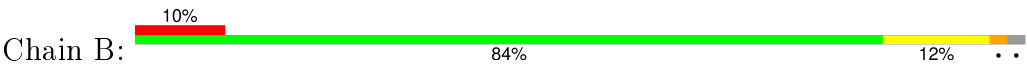
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			7	3	4		



• Molecule 2: Protein spitz



• Molecule 2: Protein spitz



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	118.21Å 124.24Å 186.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.20 36.05 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.00-3.20) 99.8 (36.05-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.237 , 0.275 0.238 , 0.277	Depositor DCC
R_{free} test set	4589 reflections (11.11%)	DCC
Wilson B-factor (Å ²)	82.8	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.0	EDS
Estimated twinning fraction	0.000 for k,h,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 45879 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	9221	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MLI, NAG, 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	0.37	1/4097 (0.0%)	0.55	0/5558
1	C	0.36	0/4205	0.55	0/5699
2	B	0.40	0/471	0.48	0/640
2	D	0.40	0/464	0.57	1/631 (0.2%)
All	All	0.37	1/9237 (0.0%)	0.55	1/12528 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	A	4	0
6	C	2	0
All	All	6	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3	CYS	CB-SG	-5.65	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	16	CYS	CA-CB-SG	-5.23	104.58	114.00

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	4702	MAN	C1

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Mol	Chain	Res	Type	Atom
3	A	4703	MAN	C1
3	A	4704	MAN	C1
3	A	4705	MAN	C1
6	C	4702	MAN	C1

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	4007	0	3741	83	0
1	C	4109	0	3884	93	0
2	B	456	0	413	5	0
2	D	450	0	406	10	0
3	A	72	0	61	3	0
4	A	14	0	13	0	0
4	C	28	0	26	0	0
5	C	28	0	25	0	0
6	C	50	0	43	0	0
7	A	7	0	2	0	0
All	All	9221	0	8614	176	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 10.

The worst 5 of 176 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:24:ARG:HH11	1:A:24:ARG:HG2	1.35	0.91
1:C:373:ASN:HB2	1:C:399:MET:HE3	1.58	0.85
1:A:194:ARG:HD3	1:A:210:GLY:O	1.77	0.83
1:C:333:GLN:NE2	2:D:47:GLU:HB2	1.92	0.83
1:A:194:ARG:O	1:A:204:CYS:HB2	1.77	0.83

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	514/601 (86%)	473 (92%)	38 (7%)	3 (1%)	30	75
1	C	528/601 (88%)	492 (93%)	31 (6%)	5 (1%)	21	67
2	B	55/58 (95%)	51 (93%)	4 (7%)	0	100	100
2	D	55/58 (95%)	52 (94%)	3 (6%)	0	100	100
All	All	1152/1318 (87%)	1068 (93%)	76 (7%)	8 (1%)	26	72

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	CYS
1	C	511	SER
1	A	0	HIS
1	A	476	ASP
1	C	212	CYS

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	438/531 (82%)	419 (96%)	19 (4%)	35	75
1	C	452/531 (85%)	417 (92%)	35 (8%)	16	54
2	B	48/51 (94%)	45 (94%)	3 (6%)	22	63
2	D	47/51 (92%)	44 (94%)	3 (6%)	22	62
All	All	985/1164 (85%)	925 (94%)	60 (6%)	23	64

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	102	SER
1	C	137	SER
2	D	27	ILE
1	C	125	ASN
1	C	185	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	54	ASN
1	C	177	ASN
1	C	498	ASN
1	C	66	HIS
1	C	205	HIS

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 ⓘ

12 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	4700	1,3	14,14,15	0.61	0	15,19,21	1.70	2 (13%)
3	NAG	A	4701	3	14,14,15	0.60	0	15,19,21	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MAN	A	4702	3	11,11,12	0.68	0	14,15,17	1.70	4 (28%)
3	MAN	A	4703	3	11,11,12	0.85	0	14,15,17	2.66	8 (57%)
3	MAN	A	4704	3	11,11,12	0.67	0	14,15,17	0.62	0
3	MAN	A	4705	3	11,11,12	0.66	0	14,15,17	1.29	2 (14%)
5	NAG	C	3830	1,5	14,14,15	0.60	0	15,19,21	1.07	1 (6%)
5	NAG	C	3831	5	14,14,15	0.46	0	15,19,21	1.18	2 (13%)
6	NAG	C	4700	1,6	14,14,15	0.48	0	15,19,21	1.31	2 (13%)
6	NAG	C	4701	6	14,14,15	0.45	0	15,19,21	1.02	1 (6%)
6	MAN	C	4702	6	11,11,12	0.70	0	14,15,17	1.34	1 (7%)
6	MAN	C	4703	6	11,11,12	0.69	0	14,15,17	1.59	3 (21%)

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	4700	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	4701	3	-	0/6/23/26	0/1/1/1
3	MAN	A	4702	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	A	4703	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	A	4704	3	1/1/4/5	0/2/19/22	0/1/1/1
3	MAN	A	4705	3	1/1/4/5	0/2/19/22	0/1/1/1
5	NAG	C	3830	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	3831	5	-	0/6/23/26	0/1/1/1
6	NAG	C	4700	1,6	-	0/6/23/26	0/1/1/1
6	NAG	C	4701	6	-	0/6/23/26	0/1/1/1
6	MAN	C	4702	6	1/1/4/5	0/2/19/22	0/1/1/1
6	MAN	C	4703	6	1/1/4/5	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	4703	MAN	C1-O5-C5	-5.99	104.64	112.25
6	C	4703	MAN	C1-O5-C5	-3.10	108.31	112.25
3	A	4703	MAN	O4-C4-C5	-2.82	101.76	109.24
3	A	4702	MAN	O3-C3-C2	-2.81	104.93	110.00
3	A	4703	MAN	O5-C1-C2	-2.78	106.35	110.86

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	4705	MAN	C1
3	A	4704	MAN	C1
3	A	4703	MAN	C1
6	C	4703	MAN	C1
3	A	4702	MAN	C1

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	4703	MAN	2	0
3	A	4705	MAN	1	0

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		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	A	3830	1	14,14,15	0.46	0	15,19,21	0.98	1 (6%)
7	MLI	A	596	-	0,6,6	0.00	-	0,7,7	0.00	-
4	NAG	C	3440	1	14,14,15	0.64	0	15,19,21	1.01	1 (6%)
4	NAG	C	596	1	14,14,15	0.63	0	15,19,21	0.79	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
4	NAG	A	3830	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MLI	A	596	-	-	0/0/4/4	0/0/0/0
4	NAG	C	3440	1	-	0/6/23/26	0/1/1/1
4	NAG	C	596	1	1/1/5/7	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	C	3440	NAG	C1-O5-C5	2.14	114.97	112.25
4	A	3830	NAG	C1-O5-C5	3.26	116.39	112.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	596	NAG	C1

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 [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	522/601 (86%)	0.13	26 (4%) 32 19	58, 81, 119, 169	0
1	C	531/601 (88%)	0.18	19 (3%) 46 31	52, 74, 121, 166	0
2	B	57/58 (98%)	0.27	6 (10%) 8 5	70, 103, 136, 144	0
2	D	57/58 (98%)	-0.09	0 100 100	58, 72, 95, 112	0
All	All	1167/1318 (88%)	0.15	51 (4%) 38 24	52, 78, 124, 169	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	507	CYS	6.5
1	C	299	PRO	5.0
1	A	506	ASP	4.9
1	A	508	GLY	4.0
1	A	518	ASN	3.8

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
6	NAG	C	4700	14/15	0.97	0.28	1.47	59,61,63,64	0
3	NAG	A	4700	14/15	0.94	0.23	-0.27	66,69,71,71	0
5	NAG	C	3830	14/15	0.90	0.18	-1.02	73,78,80,83	0
3	NAG	A	4701	14/15	0.95	0.23	-	73,74,76,79	0
6	NAG	C	4701	14/15	0.96	0.28	-	65,66,67,68	0
3	MAN	A	4705	11/12	0.73	0.40	-	94,95,95,96	0
3	MAN	A	4703	11/12	0.82	0.31	-	88,90,91,91	0
6	MAN	C	4703	11/12	0.84	0.25	-	70,72,73,73	0
5	NAG	C	3831	14/15	0.92	0.21	-	85,87,87,88	0
3	MAN	A	4702	11/12	0.87	0.28	-	82,85,89,92	0
3	MAN	A	4704	11/12	0.88	0.30	-	90,91,91,91	0
6	MAN	C	4702	11/12	0.90	0.24	-	69,70,71,71	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
7	MLI	A	596	7/7	0.76	0.41	4.88	69,70,70,71	0
4	NAG	A	3830	14/15	0.88	0.21	-0.61	76,79,80,80	0
4	NAG	C	3440	14/15	0.81	0.30	-	87,90,92,93	0
4	NAG	C	596	14/15	0.88	0.40	-	81,84,85,85	0

6.5 Other polymers [i](#)

There are no such residues in this entry.