



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:23 AM GMT

PDB ID : 3EE5
Title : Crystal structure of human M340H-Beta1,4-Galactosyltransferase-I (M340H-B4GAL-T1) in complex with GLCNAC-Beta1,3-Gal-Beta-Naphthalenemethanol
Authors : Ramakrishnan, B.; Qasba, P.K.
Deposited on : 2008-09-04
Resolution : 2.20 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

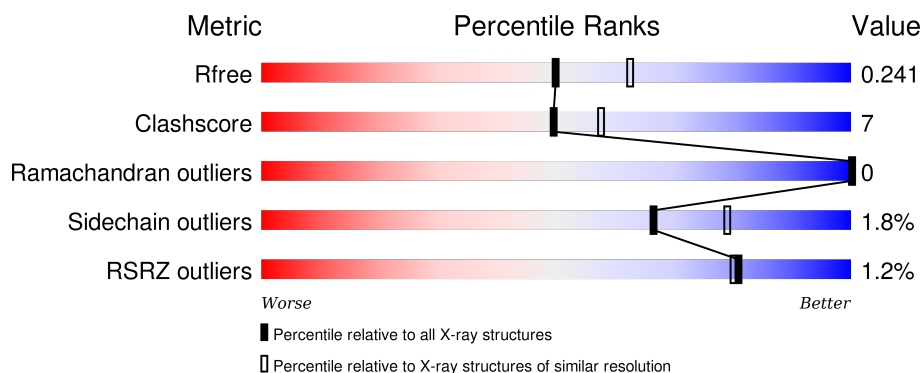
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	287	<div> <div> <div></div> <div>83%</div> <div>11%</div> <div>5%</div> </div> </div>
1	B	287	<div> <div> <div></div> <div>83%</div> <div>12%</div> <div>5%</div> </div> </div>
1	C	287	<div> <div> <div>2%</div> <div>73%</div> <div>22%</div> <div>5%</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
4	2NA	B	101	-	-	-	X
4	2NA	C	102	-	-	-	X
5	SO4	A	607	-	-	-	X
5	SO4	A	609	-	-	-	X
5	SO4	B	603	-	-	-	X
5	SO4	B	606	-	-	-	X
5	SO4	B	614	-	-	-	X
7	GOL	A	417	-	-	-	X
7	GOL	A	420	-	-	-	X
7	GOL	B	414	-	-	-	X
7	GOL	B	415	-	-	-	X
7	GOL	B	416	-	-	X	X
7	GOL	B	419	-	-	-	X
7	GOL	C	418	-	-	-	X
9	MES	C	436	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 7469 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 Beta-1,4-galactosyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	0	0
			2218	1420	386	401	11			
1	B	273	Total	C	N	O	S	0	0	0
			2218	1420	386	401	11			
1	C	273	Total	C	N	O	S	0	0	0
			2218	1420	386	401	11			

There are 51 discrepancies between the modelled and reference sequences:

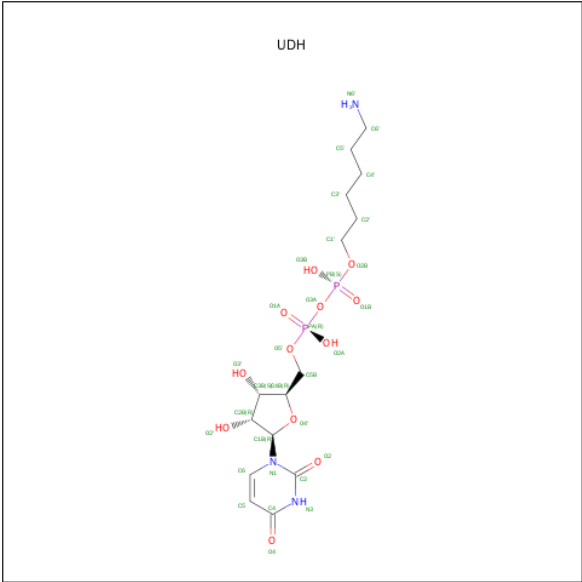
Chain	Residue	Modelled	Actual	Comment	Reference
A	112	ALA	-	EXPRESSION TAG	UNP P15291
A	113	SER	-	EXPRESSION TAG	UNP P15291
A	114	MET	-	EXPRESSION TAG	UNP P15291
A	115	THR	-	EXPRESSION TAG	UNP P15291
A	116	GLY	-	EXPRESSION TAG	UNP P15291
A	117	GLY	-	EXPRESSION TAG	UNP P15291
A	118	GLN	-	EXPRESSION TAG	UNP P15291
A	119	GLN	-	EXPRESSION TAG	UNP P15291
A	120	MET	-	EXPRESSION TAG	UNP P15291
A	121	GLY	-	EXPRESSION TAG	UNP P15291
A	122	ARG	-	EXPRESSION TAG	UNP P15291
A	123	GLY	-	EXPRESSION TAG	UNP P15291
A	124	SER	-	EXPRESSION TAG	UNP P15291
A	125	ALA	-	EXPRESSION TAG	UNP P15291
A	337	THR	ARG	ENGINEERED	UNP P15291
A	338	THR	CYS	ENGINEERED	UNP P15291
A	340	HIS	MET	ENGINEERED	UNP P15291
B	112	ALA	-	EXPRESSION TAG	UNP P15291
B	113	SER	-	EXPRESSION TAG	UNP P15291
B	114	MET	-	EXPRESSION TAG	UNP P15291
B	115	THR	-	EXPRESSION TAG	UNP P15291
B	116	GLY	-	EXPRESSION TAG	UNP P15291
B	117	GLY	-	EXPRESSION TAG	UNP P15291

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Chain	Residue	Modelled	Actual	Comment	Reference
B	118	GLN	-	EXPRESSION TAG	UNP P15291
B	119	GLN	-	EXPRESSION TAG	UNP P15291
B	120	MET	-	EXPRESSION TAG	UNP P15291
B	121	GLY	-	EXPRESSION TAG	UNP P15291
B	122	ARG	-	EXPRESSION TAG	UNP P15291
B	123	GLY	-	EXPRESSION TAG	UNP P15291
B	124	SER	-	EXPRESSION TAG	UNP P15291
B	125	ALA	-	EXPRESSION TAG	UNP P15291
B	337	THR	ARG	ENGINEERED	UNP P15291
B	338	THR	CYS	ENGINEERED	UNP P15291
B	340	HIS	MET	ENGINEERED	UNP P15291
C	112	ALA	-	EXPRESSION TAG	UNP P15291
C	113	SER	-	EXPRESSION TAG	UNP P15291
C	114	MET	-	EXPRESSION TAG	UNP P15291
C	115	THR	-	EXPRESSION TAG	UNP P15291
C	116	GLY	-	EXPRESSION TAG	UNP P15291
C	117	GLY	-	EXPRESSION TAG	UNP P15291
C	118	GLN	-	EXPRESSION TAG	UNP P15291
C	119	GLN	-	EXPRESSION TAG	UNP P15291
C	120	MET	-	EXPRESSION TAG	UNP P15291
C	121	GLY	-	EXPRESSION TAG	UNP P15291
C	122	ARG	-	EXPRESSION TAG	UNP P15291
C	123	GLY	-	EXPRESSION TAG	UNP P15291
C	124	SER	-	EXPRESSION TAG	UNP P15291
C	125	ALA	-	EXPRESSION TAG	UNP P15291
C	337	THR	ARG	ENGINEERED	UNP P15291
C	338	THR	CYS	ENGINEERED	UNP P15291
C	340	HIS	MET	ENGINEERED	UNP P15291

- Molecule 2 is 6-AMINOHEXYL-URIDINE-C1,5'-DIPHOSPHATE (three-letter code: UDH) (formula: C₁₅H₂₇N₃O₁₂P₂).

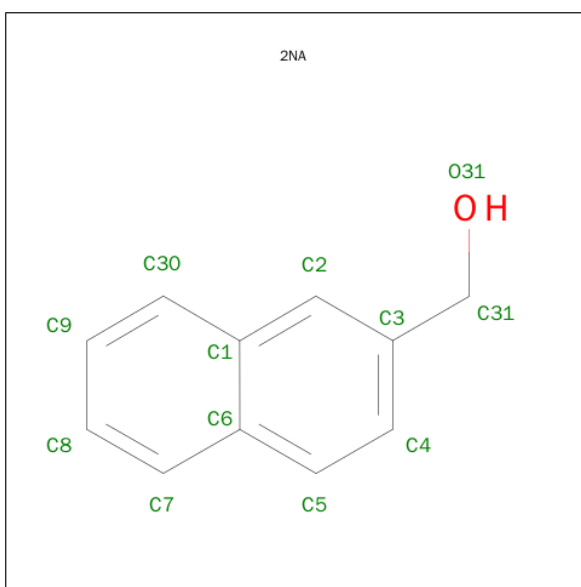


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			32	15	3	12	2		
2	B	1	Total	C	N	O	P	0	0
			32	15	3	12	2		
2	C	1	Total	C	N	O	P	0	0
			32	15	3	12	2		

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

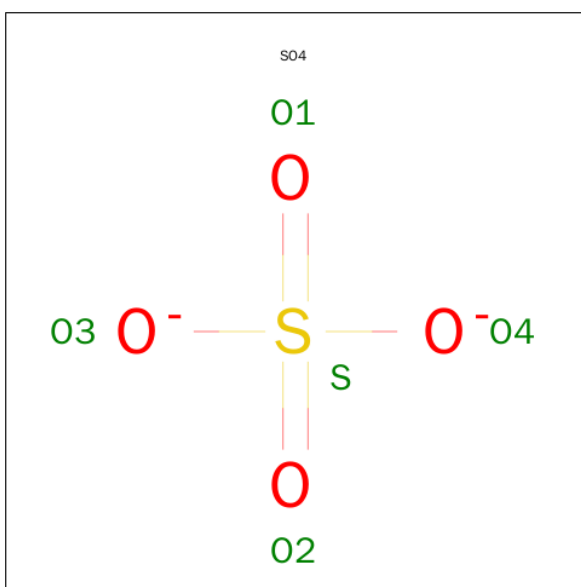
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			25	14	1	10		
3	B	2	Total	C	N	O	0	0
			25	14	1	10		
3	C	2	Total	C	N	O	0	0
			25	14	1	10		

- Molecule 4 is NAPHTHALEN-2-YLMETHANOL (three-letter code: 2NA) (formula: C₁₁H₁₀O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	11	1		
4	B	1	Total	C	O	0	0
			12	11	1		
4	C	1	Total	C	O	0	0
			12	11	1		

- Molecule 5 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

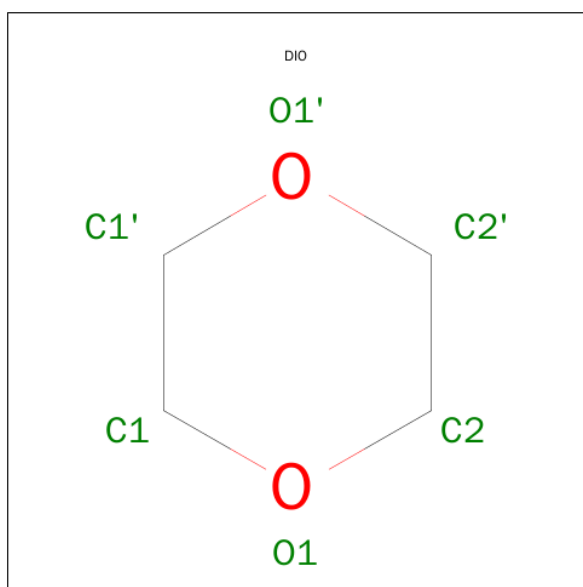
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Mn	0	0
			1	1		
6	A	1	Total	Mn	0	0
			1	1		
6	C	1	Total	Mn	0	0
			1	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



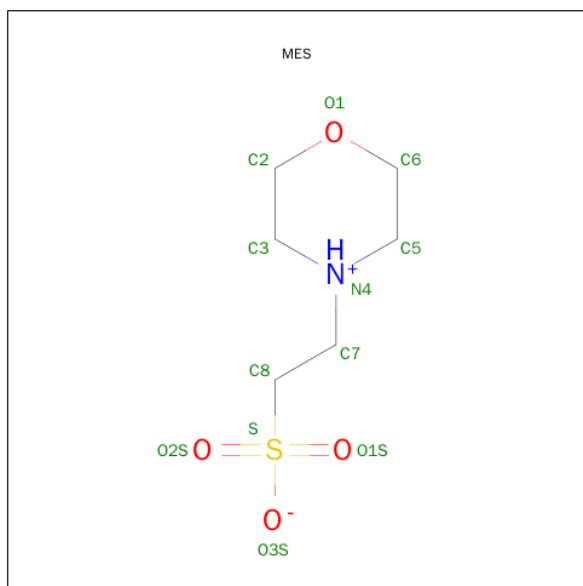
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: C₄H₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			6	4	2		

- Molecule 9 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

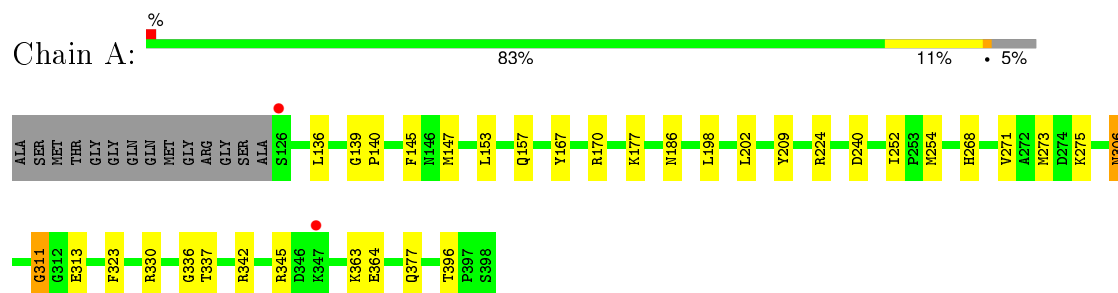
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	152	Total 152	O 152	0	0
10	B	192	Total 192	O 192	0	0
10	C	131	Total 131	O 131	0	0

3 Residue-property plots [i](#)

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.

• Molecule 1: Beta-1,4-galactosyltransferase 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	107.13Å 195.74Å 143.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.33 – 2.20 46.33 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.4 (46.33-2.20) 98.4 (46.33-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.99 (at 2.20Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.206 , 0.240 0.207 , 0.241	Depositor DCC
R_{free} test set	7621 reflections (10.09%)	DCC
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.659	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.6	EDS
Estimated twinning fraction	0.000 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.009 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 75619 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7469	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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: GOL, DIO, NAG, 2NA, MN, GAL, SO4, MES, UDH

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	0.61	0/2280	0.78	1/3097 (0.0%)
1	B	0.66	0/2280	0.77	0/3097
1	C	0.55	0/2280	0.73	2/3097 (0.1%)
All	All	0.61	0/6840	0.76	3/9291 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	208	ASP	N-CA-C	-5.25	96.82	111.00
1	A	311	GLY	N-CA-C	5.13	125.92	113.10
1	C	312	GLY	N-CA-C	5.12	125.89	113.10

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	2218	0	2162	31	0
1	B	2218	0	2162	34	0
1	C	2218	0	2162	39	0
2	A	32	0	25	0	0
2	B	32	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	32	0	25	0	0
3	A	25	0	22	0	0
3	B	25	0	22	0	0
3	C	25	0	22	0	0
4	A	12	0	9	0	0
4	B	12	0	9	0	0
4	C	12	0	9	0	0
5	A	25	0	0	0	0
5	B	35	0	0	1	0
5	C	10	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
7	A	12	0	16	4	0
7	B	24	0	31	10	0
7	C	6	0	8	1	0
8	C	6	0	8	1	0
9	C	12	0	13	2	0
10	A	152	0	0	0	0
10	B	192	0	0	1	0
10	C	131	0	0	0	0
All	All	7469	0	6730	97	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 7.

The worst 5 of 97 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:B:186:ASN:HD21	7:B:416:GOL:H11	1.29	0.96
1:B:313:GLU:OE1	7:B:414:GOL:H31	1.71	0.90
1:A:170:ARG:HD2	1:C:342:ARG:HE	1.42	0.84
1:B:186:ASN:ND2	7:B:416:GOL:H11	1.92	0.84
1:B:313:GLU:OE2	7:B:414:GOL:H11	1.81	0.81

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	271/287 (94%)	263 (97%)	8 (3%)	0	100	100
1	B	271/287 (94%)	267 (98%)	4 (2%)	0	100	100
1	C	271/287 (94%)	255 (94%)	16 (6%)	0	100	100
All	All	813/861 (94%)	785 (97%)	28 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	244/252 (97%)	240 (98%)	4 (2%)	70	82
1	B	244/252 (97%)	241 (99%)	3 (1%)	78	88
1	C	244/252 (97%)	238 (98%)	6 (2%)	55	67
All	All	732/756 (97%)	719 (98%)	13 (2%)	66	79

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	153	LEU
1	B	306	ASN
1	C	257	HIS
1	B	147	MET
1	C	233	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	186	ASN
1	B	257	HIS
1	C	206	GLN
1	A	377	GLN
1	B	306	ASN

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 ⓘ

6 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	400	3	14,14,15	0.97	1 (7%)	15,19,21	0.91	0
3	GAL	A	401	3,4	11,11,12	1.47	2 (18%)	14,15,17	1.29	2 (14%)
3	NAG	B	1400	3	14,14,15	1.04	1 (7%)	15,19,21	0.90	1 (6%)
3	GAL	B	1401	3,4	11,11,12	1.19	1 (9%)	14,15,17	1.02	1 (7%)
3	NAG	C	2400	3	14,14,15	1.07	1 (7%)	15,19,21	1.04	2 (13%)
3	GAL	C	2401	3,4	11,11,12	1.03	0	14,15,17	0.83	1 (7%)

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	400	3	-	0/6/23/26	0/1/1/1
3	GAL	A	401	3,4	-	0/2/19/22	0/1/1/1
3	NAG	B	1400	3	-	0/6/23/26	0/1/1/1
3	GAL	B	1401	3,4	-	0/2/19/22	0/1/1/1
3	NAG	C	2400	3	-	0/6/23/26	0/1/1/1
3	GAL	C	2401	3,4	-	0/2/19/22	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	400	NAG	C4-C5	2.04	1.57	1.53
3	B	1401	GAL	C4-C5	2.20	1.57	1.53
3	B	1400	NAG	C4-C5	2.43	1.58	1.53
3	A	401	GAL	C2-C3	2.50	1.55	1.52
3	C	2400	NAG	C4-C5	2.53	1.58	1.53

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	GAL	C1-C2-C3	-2.56	106.52	109.54
3	C	2400	NAG	C8-C7-N2	-2.09	112.10	116.11
3	B	1400	NAG	C1-O5-C5	2.10	114.92	112.25
3	C	2400	NAG	C1-O5-C5	2.30	115.17	112.25
3	C	2401	GAL	C1-O5-C5	2.42	115.32	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 3 are monoatomic - leaving 29 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	$\# Z > 2$
4	2NA	A	100	3	13,13,13	3.61	4 (30%)	17,17,17	0.66	0
2	UDH	A	399	6	25,33,33	1.80	2 (8%)	33,47,47	2.96	12 (36%)
7	GOL	A	417	-	5,5,5	0.64	0	5,5,5	0.63	0
7	GOL	A	420	-	5,5,5	0.37	0	5,5,5	0.23	0
5	SO4	A	602	-	4,4,4	3.20	2 (50%)	6,6,6	0.97	0
5	SO4	A	604	-	4,4,4	3.32	2 (50%)	6,6,6	0.96	0
5	SO4	A	607	-	4,4,4	3.40	2 (50%)	6,6,6	0.83	0
5	SO4	A	609	-	4,4,4	3.38	2 (50%)	6,6,6	0.88	0
5	SO4	A	610	-	4,4,4	3.26	2 (50%)	6,6,6	0.92	0
4	2NA	B	101	3	13,13,13	3.76	5 (38%)	17,17,17	0.57	0
2	UDH	B	1399	6	25,33,33	1.75	6 (24%)	33,47,47	2.85	12 (36%)
7	GOL	B	414	-	5,5,5	1.04	0	5,5,5	0.69	0
7	GOL	B	415	-	5,5,5	0.32	0	5,5,5	0.56	0
7	GOL	B	416	-	5,5,5	0.69	0	5,5,5	0.53	0
7	GOL	B	419	-	5,5,5	0.49	0	5,5,5	0.64	0
5	SO4	B	601	-	4,4,4	3.22	2 (50%)	6,6,6	0.97	0
5	SO4	B	603	-	4,4,4	3.17	2 (50%)	6,6,6	0.94	0
5	SO4	B	605	-	4,4,4	3.27	2 (50%)	6,6,6	0.97	0
5	SO4	B	606	-	4,4,4	3.27	2 (50%)	6,6,6	0.96	0
5	SO4	B	611	-	4,4,4	3.32	2 (50%)	6,6,6	0.89	0
5	SO4	B	613	-	4,4,4	3.37	2 (50%)	6,6,6	0.99	0
5	SO4	B	614	-	4,4,4	3.30	2 (50%)	6,6,6	1.01	0
4	2NA	C	102	3	13,13,13	3.49	4 (30%)	17,17,17	0.59	0
2	UDH	C	2399	6	25,33,33	1.79	4 (16%)	33,47,47	2.82	8 (24%)
7	GOL	C	418	-	5,5,5	0.45	0	5,5,5	0.49	0
8	DIO	C	435	-	6,6,6	0.92	0	6,6,6	1.64	2 (33%)
9	MES	C	436	-	11,12,12	1.31	2 (18%)	14,16,16	0.84	0
5	SO4	C	608	-	4,4,4	3.35	2 (50%)	6,6,6	0.98	0
5	SO4	C	612	-	4,4,4	3.20	2 (50%)	6,6,6	0.97	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	2NA	A	100	3	-	0/2/2/2	0/2/2/2
2	UDH	A	399	6	-	0/21/41/41	0/2/2/2
7	GOL	A	417	-	-	0/4/4/4	0/0/0/0
7	GOL	A	420	-	-	0/4/4/4	0/0/0/0
5	SO4	A	602	-	-	0/0/0/0	0/0/0/0
5	SO4	A	604	-	-	0/0/0/0	0/0/0/0
5	SO4	A	607	-	-	0/0/0/0	0/0/0/0
5	SO4	A	609	-	-	0/0/0/0	0/0/0/0
5	SO4	A	610	-	-	0/0/0/0	0/0/0/0
4	2NA	B	101	3	-	0/2/2/2	0/2/2/2
2	UDH	B	1399	6	-	0/21/41/41	0/2/2/2
7	GOL	B	414	-	-	0/4/4/4	0/0/0/0
7	GOL	B	415	-	-	0/4/4/4	0/0/0/0
7	GOL	B	416	-	-	0/4/4/4	0/0/0/0
7	GOL	B	419	-	-	0/4/4/4	0/0/0/0
5	SO4	B	601	-	-	0/0/0/0	0/0/0/0
5	SO4	B	603	-	-	0/0/0/0	0/0/0/0
5	SO4	B	605	-	-	0/0/0/0	0/0/0/0
5	SO4	B	606	-	-	0/0/0/0	0/0/0/0
5	SO4	B	611	-	-	0/0/0/0	0/0/0/0
5	SO4	B	613	-	-	0/0/0/0	0/0/0/0
5	SO4	B	614	-	-	0/0/0/0	0/0/0/0
4	2NA	C	102	3	-	0/2/2/2	0/2/2/2
2	UDH	C	2399	6	-	0/21/41/41	0/2/2/2
7	GOL	C	418	-	-	0/4/4/4	0/0/0/0
8	DIO	C	435	-	-	0/0/6/6	0/1/1/1
9	MES	C	436	-	-	0/6/14/14	0/1/1/1
5	SO4	C	608	-	-	0/0/0/0	0/0/0/0
5	SO4	C	612	-	-	0/0/0/0	0/0/0/0

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	609	SO4	O3-S	-4.61	1.30	1.47
5	A	602	SO4	O3-S	-4.59	1.30	1.47
5	A	607	SO4	O3-S	-4.57	1.30	1.47
5	B	603	SO4	O3-S	-4.53	1.31	1.47
5	C	608	SO4	O3-S	-4.49	1.31	1.47

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1399	UDH	O4'-C4B-C3B	-4.32	96.44	105.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	399	UDH	O4'-C4B-C3B	-4.27	96.54	105.15
2	C	2399	UDH	PB-O3A-PA	-3.94	121.65	132.73
2	A	399	UDH	PB-O3A-PA	-3.72	122.27	132.73
2	B	1399	UDH	PB-O3A-PA	-3.70	122.34	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	417	GOL	3	0
7	A	420	GOL	1	0
2	B	1399	UDH	1	0
7	B	414	GOL	3	0
7	B	415	GOL	1	0
7	B	416	GOL	6	0
5	B	611	SO4	1	0
7	C	418	GOL	1	0
8	C	435	DIO	1	0
9	C	436	MES	2	0

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	273/287 (95%)	-0.42	2 (0%) 89 88	23, 32, 51, 63	0
1	B	273/287 (95%)	-0.41	1 (0%) 93 93	22, 30, 44, 56	0
1	C	273/287 (95%)	-0.04	7 (2%) 59 58	29, 41, 61, 70	0
All	All	819/861 (95%)	-0.29	10 (1%) 81 80	22, 34, 55, 70	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	126	SER	3.4
1	C	126	SER	3.2
1	C	148	PRO	3.1
1	C	364	GLU	2.7
1	C	398	SER	2.7

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(Å ²)	Q<0.9
3	NAG	A	400	14/15	0.95	0.10	0.30	37,38,41,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	B	1400	14/15	0.96	0.09	-0.49	26,32,34,35	0
3	NAG	C	2400	14/15	0.92	0.10	-0.50	49,51,54,54	0
3	GAL	C	2401	11/12	0.85	0.15	-	59,64,68,71	0
3	GAL	A	401	11/12	0.84	0.14	-	45,52,57,61	0
3	GAL	B	1401	11/12	0.84	0.23	-	42,52,58,62	0

6.4 Ligands

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
5	SO4	B	614	5/5	0.76	0.40	31.96	87,88,89,90	0
7	GOL	B	415	6/6	0.74	0.43	21.04	70,71,74,74	0
4	2NA	B	101	12/12	0.79	0.28	19.02	57,59,59,60	0
7	GOL	A	417	6/6	0.76	0.27	15.78	59,61,62,63	0
9	MES	C	436	12/12	0.55	0.31	14.16	90,92,99,100	0
7	GOL	B	414	6/6	0.82	0.25	14.07	43,49,50,53	0
5	SO4	A	609	5/5	0.88	0.25	13.45	80,81,82,83	0
7	GOL	A	420	6/6	0.69	0.33	6.42	68,71,71,72	0
7	GOL	B	416	6/6	0.79	0.30	6.19	36,38,44,50	0
4	2NA	C	102	12/12	0.89	0.28	6.07	64,65,66,66	0
7	GOL	C	418	6/6	0.78	0.29	5.35	57,57,58,59	0
5	SO4	B	603	5/5	0.93	0.26	5.23	74,75,76,76	0
5	SO4	B	606	5/5	0.92	0.23	4.73	78,78,80,80	0
5	SO4	A	607	5/5	0.79	0.22	3.55	80,83,83,84	0
7	GOL	B	419	6/6	0.74	0.24	2.43	56,61,62,64	0
4	2NA	A	100	12/12	0.90	0.18	1.62	48,51,52,54	0
5	SO4	A	602	5/5	0.94	0.19	1.21	75,75,76,77	0
5	SO4	C	608	5/5	0.92	0.23	0.57	83,84,84,84	0
2	UDH	B	1399	32/32	0.97	0.12	-0.06	23,28,56,59	0
5	SO4	B	601	5/5	0.97	0.13	-0.07	74,75,75,75	0
2	UDH	C	2399	32/32	0.94	0.14	-0.16	37,46,59,63	0
2	UDH	A	399	32/32	0.97	0.11	-0.23	28,34,57,60	0
8	DIO	C	435	6/6	0.84	0.16	-0.36	67,69,69,69	0
5	SO4	A	604	5/5	0.92	0.10	-0.60	75,76,76,76	0
6	MN	A	611	1/1	1.00	0.07	-	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	SO4	A	610	5/5	0.94	0.27	-	85,86,86,86	0
5	SO4	B	613	5/5	0.92	0.15	-	78,78,80,80	0
6	MN	C	400	1/1	0.97	0.07	-	48,48,48,48	0
5	SO4	C	612	5/5	0.95	0.21	-	85,86,86,86	0
5	SO4	B	605	5/5	0.97	0.13	-	83,83,83,83	0
5	SO4	B	611	5/5	0.89	0.42	-	86,86,86,87	0
6	MN	B	400	1/1	0.99	0.09	-	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.