



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:18 AM GMT

PDB ID : 2WNF  
Title : Crystal Structure of a Mammalian Sialyltransferase in complex with Gal-beta-1-3GalNAc-ortho-nitrophenol  
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Deposited on : 2009-07-09  
Resolution : 1.25 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](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) : 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

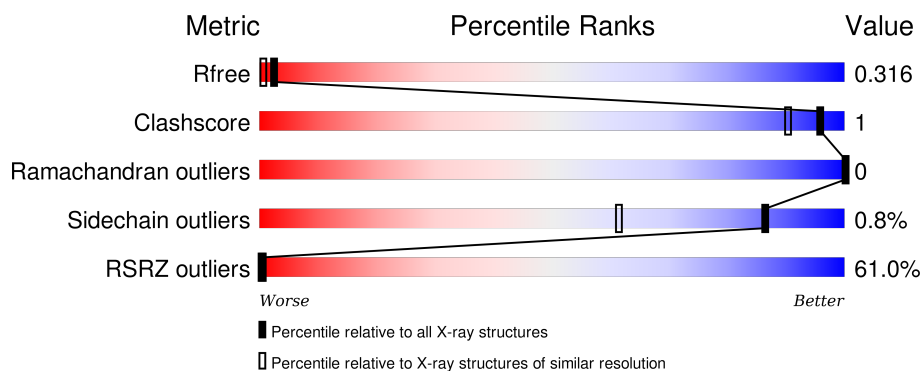
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 1.25 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	1442 (1.30-1.22)
Clashscore	102246	1530 (1.30-1.22)
Ramachandran outliers	100387	1467 (1.30-1.22)
Sidechain outliers	100360	1465 (1.30-1.22)
RSRZ outliers	91569	1442 (1.30-1.22)

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.

Mol	Chain	Length	Quality of chain
1	A	298	

## 2 Entry composition [i](#)

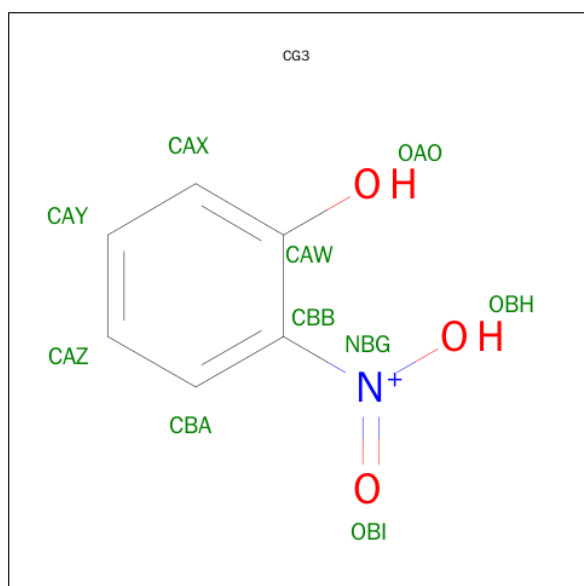
There are 4 unique types of molecules in this entry. The entry contains 2699 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	272	Total	C	N	O	S	Se	0	17	0
			2343	1493	415	424	8	3			

- Molecule 2 is HYDROXY(2-HYDROXYPHENYL)OXOAMMONIUM (three-letter code: CG3) (formula:  $C_6H_6NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	6	1	3		

- 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		

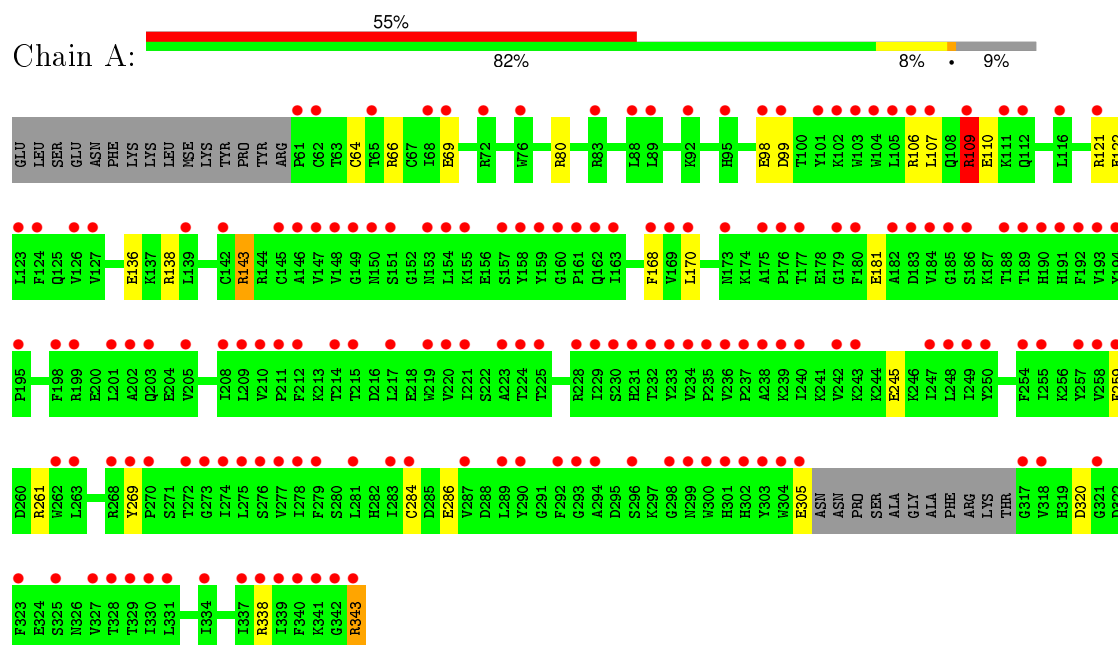
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	321	Total	O	0	0
			321	321		

### 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 ( $\text{RSRZ} > 2$ ). 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: CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.99Å 78.35Å 99.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.11 – 1.25 32.93 – 1.24	Depositor EDS
% Data completeness (in resolution range)	99.8 (33.11-1.25) 99.3 (32.93-1.24)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.39 (at 1.24Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, $R_{free}$	0.180 , 0.195 0.308 , 0.316	Depositor DCC
$R_{free}$ test set	4204 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	9.1	Xtriage
Anisotropy	0.409	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 30.8	EDS
Estimated twinning fraction	0.011 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 85219 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	2699	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.85% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: CG3, GAL, A2G

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	1.24	13/2423 (0.5%)	1.10	13/3271 (0.4%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	245	GLU	CD-OE1	8.41	1.34	1.25
1	A	110	GLU	CB-CG	-6.79	1.39	1.52
1	A	69	GLU	CD-OE2	-6.43	1.18	1.25
1	A	98	GLU	CD-OE1	6.14	1.32	1.25
1	A	69	GLU	CB-CG	-6.13	1.40	1.52
1	A	245	GLU	CB-CG	-6.10	1.40	1.52
1	A	305	GLU	CG-CD	5.95	1.60	1.51
1	A	136	GLU	CD-OE2	5.42	1.31	1.25
1	A	259	PHE	CD2-CE2	5.35	1.50	1.39
1	A	245	GLU	CD-OE2	5.22	1.31	1.25
1	A	338	ARG	CB-CG	-5.19	1.38	1.52
1	A	286	GLU	CD-OE2	-5.10	1.20	1.25
1	A	109	ARG	CG-CD	-5.02	1.39	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	343	ARG	NE-CZ-NH1	10.48	125.54	120.30
1	A	143	ARG	NE-CZ-NH2	-8.15	116.23	120.30
1	A	99	ASP	CB-CG-OD1	6.66	124.30	118.30
1	A	80	ARG	NE-CZ-NH2	-6.62	116.99	120.30
1	A	138	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	320	ASP	CB-CG-OD2	-5.80	113.08	118.30
1	A	168	PHE	CB-CG-CD1	5.59	124.71	120.80
1	A	121[A]	ARG	NE-CZ-NH2	-5.37	117.61	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	121[B]	ARG	NE-CZ-NH2	-5.37	117.61	120.30
1	A	170	LEU	CB-CG-CD2	5.28	119.97	111.00
1	A	343	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	A	261[A]	ARG	NE-CZ-NH1	5.17	122.89	120.30
1	A	261[B]	ARG	NE-CZ-NH1	5.17	122.89	120.30

There are no chirality outliers.

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	2343	0	2294	7	0
2	A	10	0	5	0	0
3	A	25	0	22	0	0
4	A	321	0	0	3	0
All	All	2699	0	2321	7	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 1.

All (7) 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:122[A]:GLU:HG2	4:A:2093:HOH:O	1.60	1.02
1:A:106:ARG:O	1:A:109:ARG:HD2	2.01	0.61
1:A:122[A]:GLU:CG	4:A:2093:HOH:O	2.35	0.57
1:A:181:GLU:HB2	4:A:2167:HOH:O	2.08	0.54
1:A:143:ARG:HG2	1:A:284[B]:CYS:SG	2.59	0.42
1:A:107:LEU:HD22	1:A:269:TYR:HB3	2.02	0.41
1:A:64:CYS:HB2	1:A:66:ARG:O	2.21	0.41

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	Percentiles	
1	A	285/298 (96%)	278 (98%)	7 (2%)	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	Rotameric	Outliers	Percentiles	
1	A	261/263 (99%)	259 (99%)	2 (1%)	86	61

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	ARG
1	A	343	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

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 ⓘ

2 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	A2G	A	1345	3,2	14,14,15	1.26	1 (7%)	15,19,21	1.46	2 (13%)
3	GAL	A	1346	3	11,11,12	1.41	2 (18%)	14,15,17	1.17	2 (14%)

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	A2G	A	1345	3,2	-	0/6/23/26	0/1/1/1
3	GAL	A	1346	3	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1346	GAL	O2-C2	2.13	1.48	1.43
3	A	1346	GAL	O5-C5	2.74	1.49	1.43
3	A	1345	A2G	C1-C2	3.27	1.57	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1346	GAL	C2-C3-C4	-2.22	107.27	111.04
3	A	1345	A2G	O3-C3-C2	-2.02	105.11	109.11
3	A	1346	GAL	C1-C2-C3	2.32	112.28	109.54
3	A	1345	A2G	C1-O-C5	3.09	116.17	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

1 ligand is 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	$\# Z  > 2$
2	CG3	A	1344	3	7,10,10	4.21	3 (42%)	6,13,13	3.25	4 (66%)

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	CG3	A	1344	3	-	0/2/4/4	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1344	CG3	OAO-CAW	2.68	1.42	1.36
2	A	1344	CG3	CAY-CAX	3.09	1.45	1.38
2	A	1344	CG3	OBI-NBG	10.09	1.42	1.22

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1344	CG3	CAY-CAX-CAW	-3.36	115.72	120.04
2	A	1344	CG3	CAZ-CBA-CBB	-2.88	113.75	118.63
2	A	1344	CG3	CAZ-CAY-CAX	-2.44	116.61	120.19
2	A	1344	CG3	CAY-CAZ-CBA	6.12	129.15	120.19

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	269/298 (90%)	2.39	164 (60%) 0 0	10, 13, 18, 26	0

All (164) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	317	GLY	7.3
1	A	300	TRP	5.8
1	A	158	TYR	5.1
1	A	232	THR	5.0
1	A	192	PHE	5.0
1	A	208	ILE	4.9
1	A	147	VAL	4.8
1	A	193	VAL	4.8
1	A	274	ILE	4.7
1	A	275	LEU	4.5
1	A	279	PHE	4.5
1	A	250	TYR	4.5
1	A	154	LEU	4.5
1	A	255	ILE	4.4
1	A	304	TRP	4.4
1	A	201	LEU	4.3
1	A	299	ASN	4.3
1	A	106	ARG	4.2
1	A	210	VAL	4.2
1	A	209	LEU	4.2
1	A	111	LYS	4.2
1	A	301	HIS	4.1
1	A	182	ALA	4.1
1	A	254	PHE	4.0
1	A	180	PHE	4.0
1	A	194	TYR	4.0
1	A	290	TYR	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	277	VAL	3.9
1	A	170	LEU	3.9
1	A	303	TYR	3.9
1	A	168	PHE	3.8
1	A	212	PHE	3.8
1	A	159	TYR	3.8
1	A	148	VAL	3.8
1	A	240	ILE	3.7
1	A	236	VAL	3.7
1	A	262	TRP	3.6
1	A	284[A]	CYS	3.6
1	A	318	VAL	3.6
1	A	278	ILE	3.6
1	A	104	TRP	3.6
1	A	145[A]	CYS	3.6
1	A	83	ARG	3.6
1	A	198	PHE	3.5
1	A	248	LEU	3.5
1	A	177	THR	3.5
1	A	188	THR	3.4
1	A	268	ARG	3.4
1	A	305	GLU	3.4
1	A	242	VAL	3.4
1	A	247	ILE	3.4
1	A	234	VAL	3.4
1	A	292	PHE	3.4
1	A	289	LEU	3.3
1	A	341[A]	LYS	3.3
1	A	219	TRP	3.3
1	A	229	ILE	3.3
1	A	272	THR	3.3
1	A	184	VAL	3.2
1	A	339	ILE	3.2
1	A	249	ILE	3.2
1	A	205	VAL	3.2
1	A	105	LEU	3.1
1	A	228[A]	ARG	3.1
1	A	103	TRP	3.1
1	A	112	GLN	3.1
1	A	169	VAL	3.1
1	A	203	GLN	3.1
1	A	340	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	163	ILE	3.1
1	A	221	ILE	3.0
1	A	160	GLY	3.0
1	A	281	LEU	3.0
1	A	185	GLY	3.0
1	A	233	TYR	3.0
1	A	189	THR	3.0
1	A	175	ALA	3.0
1	A	263	LEU	2.9
1	A	257	TYR	2.9
1	A	276[A]	SER	2.9
1	A	109	ARG	2.9
1	A	223	ALA	2.9
1	A	179	GLY	2.9
1	A	176	PRO	2.9
1	A	327	VAL	2.9
1	A	231[A]	HIS	2.8
1	A	146	ALA	2.8
1	A	259	PHE	2.8
1	A	258	VAL	2.8
1	A	343	ARG	2.7
1	A	283	ILE	2.7
1	A	287	VAL	2.7
1	A	153	ASN	2.6
1	A	191	HIS	2.6
1	A	337	ILE	2.6
1	A	331	LEU	2.6
1	A	269	TYR	2.6
1	A	220	VAL	2.6
1	A	121[A]	ARG	2.6
1	A	155	LYS	2.6
1	A	217	LEU	2.6
1	A	173	ASN	2.6
1	A	61	PRO	2.6
1	A	215	THR	2.6
1	A	89	LEU	2.5
1	A	123	LEU	2.5
1	A	342	GLY	2.5
1	A	294	ALA	2.5
1	A	68	ILE	2.5
1	A	142	CYS	2.5
1	A	88	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	230	SER	2.5
1	A	211	PRO	2.4
1	A	214	THR	2.4
1	A	224	THR	2.4
1	A	235	PRO	2.4
1	A	116	LEU	2.4
1	A	338	ARG	2.4
1	A	149	GLY	2.4
1	A	225	THR	2.4
1	A	92[A]	LYS	2.4
1	A	186[A]	SER	2.4
1	A	98	GLU	2.4
1	A	190	HIS	2.3
1	A	238	ALA	2.3
1	A	273	GLY	2.3
1	A	298	GLY	2.3
1	A	334	ILE	2.3
1	A	107	LEU	2.3
1	A	325[A]	SER	2.3
1	A	161	PRO	2.3
1	A	199	ARG	2.3
1	A	99	ASP	2.3
1	A	65	THR	2.3
1	A	296	SER	2.3
1	A	330	ILE	2.3
1	A	95[A]	HIS	2.3
1	A	293	GLY	2.2
1	A	151	SER	2.2
1	A	157	SER	2.2
1	A	328	THR	2.2
1	A	195	PRO	2.2
1	A	239	LYS	2.2
1	A	237	PRO	2.2
1	A	72	ARG	2.2
1	A	76	TRP	2.2
1	A	202	ALA	2.2
1	A	183	ASP	2.1
1	A	139	LEU	2.1
1	A	62	CYS	2.1
1	A	323	PHE	2.1
1	A	126	VAL	2.1
1	A	321	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	302	HIS	2.1
1	A	102	LYS	2.1
1	A	69	GLU	2.1
1	A	124	PHE	2.1
1	A	127	VAL	2.1
1	A	162	GLN	2.1
1	A	329	THR	2.1
1	A	101	TYR	2.1
1	A	270	PRO	2.0
1	A	243	LYS	2.0
1	A	150	ASN	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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	GAL	A	1346	11/12	0.80	0.20	1.68	13,14,16,18	0
3	A2G	A	1345	14/15	0.77	0.18	0.11	16,17,22,23	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	CG3	A	1344	10/10	0.69	0.24	-	20,23,28,28	0

## 6.5 Other polymers

There are no such residues in this entry.