



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 12:47 pm BST

PDB ID : 6F8Z  
Title : Structure of the family GH92 alpha-mannosidase BT3130 from *Bacteroides thetaiotaomicron*  
Authors : Thompson, A.J.; Spears, R.J.; Zhu, Y.; Suits, M.D.L.; Williams, S.J.; Gilbert, H.J.; Davies, G.J.  
Deposited on : 2017-12-13  
Resolution : 2.50 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 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) : 2.11

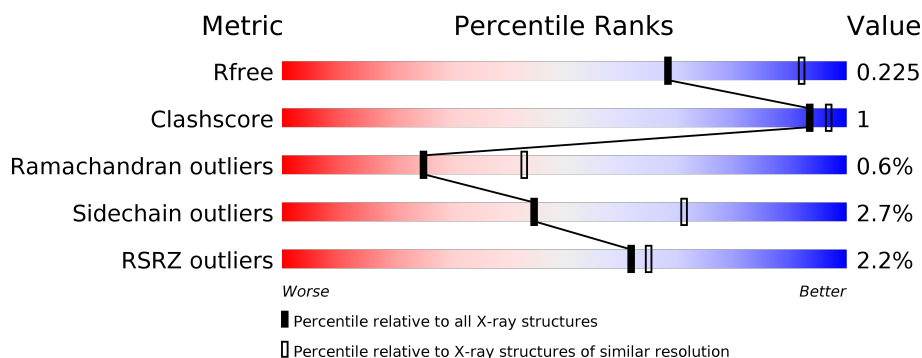
# 1 Overall quality at a glance

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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 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  $\leq 5\%$ . 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	727	<div> <div>%</div> <div> <div></div> <div>93%</div> <div></div> </div> <div>...</div> </div>
1	B	727	<div> <div>%</div> <div> <div></div> <div>92%</div> <div></div> </div> <div>...</div> </div>
1	C	727	<div> <div>5%</div> <div> <div></div> <div>91%</div> <div></div> </div> <div>5%</div> <div>.</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17983 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 Alpha-1,2-mannosidase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	715	Total	C	N	O	S	0	2	0
			5678	3610	963	1078	27			
1	B	703	Total	C	N	O	S	0	5	0
			5588	3565	939	1058	26			
1	C	700	Total	C	N	O	S	0	4	0
			5417	3438	918	1034	27			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	MET	-	initiating methionine	UNP A0A174L250
A	18	GLY	-	expression tag	UNP A0A174L250
A	736	LEU	-	expression tag	UNP A0A174L250
A	737	GLU	-	expression tag	UNP A0A174L250
A	738	HIS	-	expression tag	UNP A0A174L250
A	739	HIS	-	expression tag	UNP A0A174L250
A	740	HIS	-	expression tag	UNP A0A174L250
A	741	HIS	-	expression tag	UNP A0A174L250
A	742	HIS	-	expression tag	UNP A0A174L250
A	743	HIS	-	expression tag	UNP A0A174L250
B	17	MET	-	initiating methionine	UNP A0A174L250
B	18	GLY	-	expression tag	UNP A0A174L250
B	736	LEU	-	expression tag	UNP A0A174L250
B	737	GLU	-	expression tag	UNP A0A174L250
B	738	HIS	-	expression tag	UNP A0A174L250
B	739	HIS	-	expression tag	UNP A0A174L250
B	740	HIS	-	expression tag	UNP A0A174L250
B	741	HIS	-	expression tag	UNP A0A174L250
B	742	HIS	-	expression tag	UNP A0A174L250
B	743	HIS	-	expression tag	UNP A0A174L250
C	17	MET	-	initiating methionine	UNP A0A174L250
C	18	GLY	-	expression tag	UNP A0A174L250
C	736	LEU	-	expression tag	UNP A0A174L250

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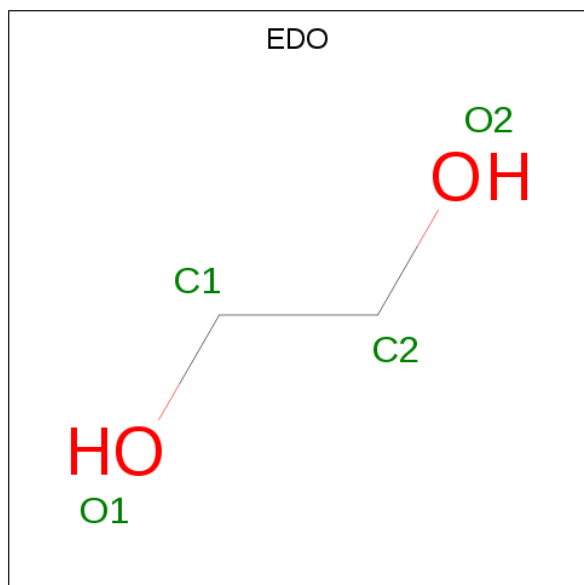
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Chain	Residue	Modelled	Actual	Comment	Reference
C	737	GLU	-	expression tag	UNP A0A174L250
C	738	HIS	-	expression tag	UNP A0A174L250
C	739	HIS	-	expression tag	UNP A0A174L250
C	740	HIS	-	expression tag	UNP A0A174L250
C	741	HIS	-	expression tag	UNP A0A174L250
C	742	HIS	-	expression tag	UNP A0A174L250
C	743	HIS	-	expression tag	UNP A0A174L250

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0

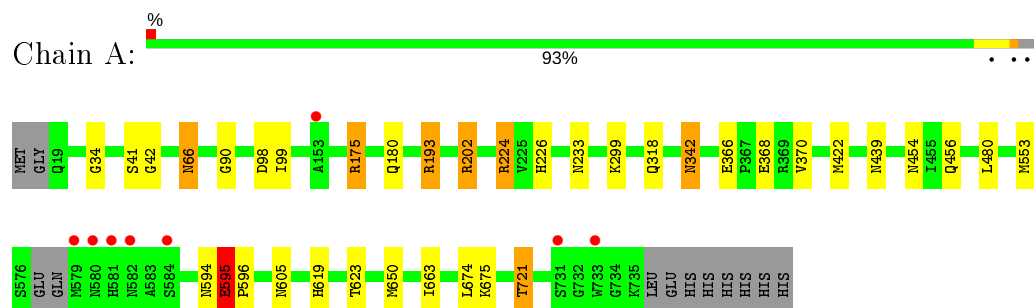
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	668	Total 668	O 668	0	0
4	B	417	Total 417	O 417	0	0
4	C	208	Total 208	O 208	0	0

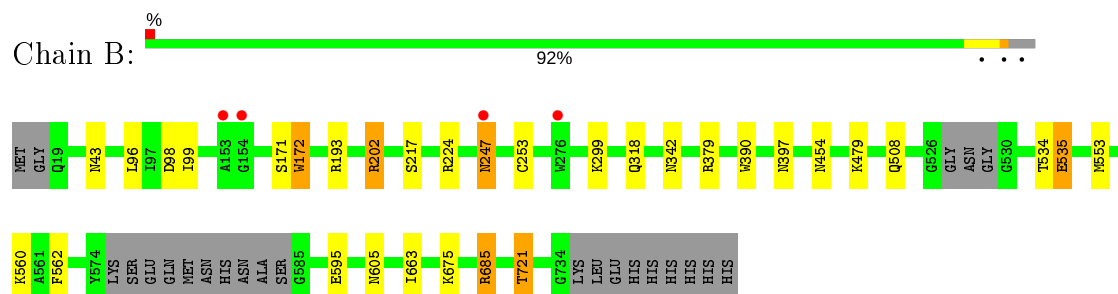
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

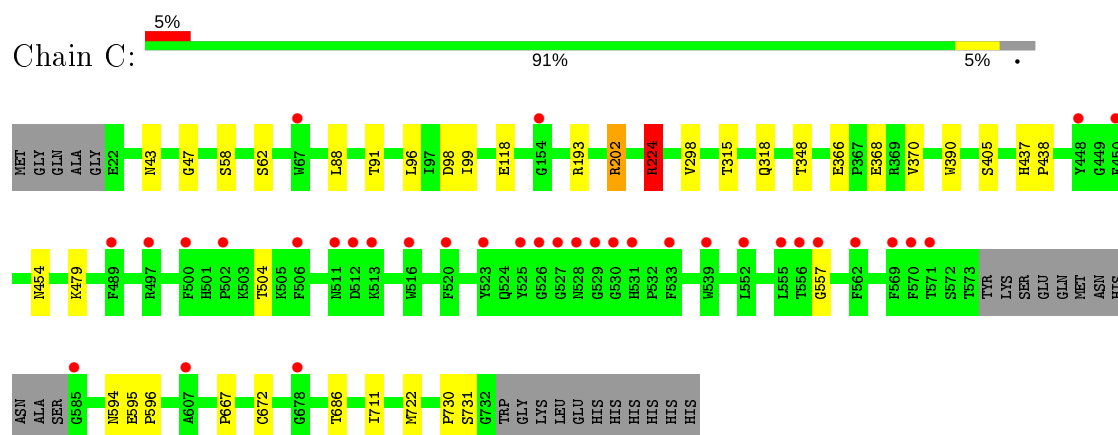
- Molecule 1: Alpha-1,2-mannosidase, putative



- Molecule 1: Alpha-1,2-mannosidase, putative



- Molecule 1: Alpha-1,2-mannosidase, putative



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	272.30Å 272.30Å 190.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.67 – 2.50 49.32 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.67-2.50) 99.8 (49.32-2.50)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.44 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.181 , 0.222 0.185 , 0.225	Depositor DCC
$R_{free}$ test set	7011 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.2	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 48.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	17983	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.10% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, EDO

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	0.49	0/5848	0.71	5/7949 (0.1%)
1	B	0.47	0/5761	0.67	4/7834 (0.1%)
1	C	0.48	0/5589	0.64	4/7624 (0.1%)
All	All	0.48	0/17198	0.67	13/23407 (0.1%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	202	ARG	NE-CZ-NH2	-9.32	115.64	120.30
1	A	202	ARG	NE-CZ-NH1	7.92	124.26	120.30
1	C	202	ARG	NE-CZ-NH1	6.76	123.68	120.30
1	B	202	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	C	224	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	C	224	ARG	NE-CZ-NH2	-5.89	117.36	120.30
1	C	202	ARG	NE-CZ-NH2	-5.61	117.50	120.30
1	A	175	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	A	224	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	B	685	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	B	202	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	A	193	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	B	379	ARG	NE-CZ-NH1	5.13	122.87	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	5678	0	5300	22	0
1	B	5588	0	5201	9	0
1	C	5417	0	4861	15	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	4	0	6	1	0
4	A	668	0	0	4	3
4	B	417	0	0	4	0
4	C	208	0	0	2	0
All	All	17983	0	15368	46	3

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 (46) 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:439:ASN:HD22	1:A:456:GLN:HE22	1.41	0.67
1:A:619:HIS:O	1:A:623:THR:HB	1.95	0.67
1:C:98:ASP:OD2	1:C:202:ARG:NH2	2.36	0.57
1:A:422:MET:HE2	1:A:480:LEU:HD21	1.87	0.55
1:A:202:ARG:HD3	4:A:1096:HOH:O	2.08	0.53
1:A:66:ASN:HD22	3:A:802:EDO:H12	1.74	0.52
1:C:202:ARG:HD3	4:C:1037:HOH:O	2.11	0.51
1:A:342:ASN:N	1:A:342:ASN:HD22	2.09	0.49
1:B:534:THR:O	1:B:535:GLU:C	2.50	0.49
1:B:98:ASP:OD2	1:B:202:ARG:NH2	2.46	0.49
1:A:342:ASN:ND2	1:A:342:ASN:H	2.11	0.49
1:B:202:ARG:HD3	4:B:1110:HOH:O	2.12	0.49
1:A:180:GLN:HE21	1:A:233:ASN:HD21	1.61	0.48
1:A:342:ASN:H	1:A:342:ASN:HD22	1.59	0.48
1:A:98:ASP:OD2	1:A:202:ARG:NH2	2.47	0.47
1:C:298:VAL:HG12	1:C:672:CYS:CB	2.44	0.47
1:C:224:ARG:NH2	4:C:1001:HOH:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:650:MET:SD	1:A:674:LEU:HD11	2.54	0.47
4:A:1154:HOH:O	1:B:721:THR:HG21	2.15	0.47
1:A:721:THR:HG22	4:A:1462:HOH:O	2.15	0.46
1:A:721:THR:HG21	4:B:1105:HOH:O	2.15	0.46
1:B:171[A]:SER:O	1:B:172:TRP:CG	2.69	0.46
1:C:437:HIS:HB2	1:C:438:PRO:CD	2.46	0.46
1:C:47:GLY:HA3	1:C:58:SER:HB2	1.99	0.45
1:A:224:ARG:NH2	4:A:907:HOH:O	2.50	0.45
1:C:711:ILE:HG21	1:C:722:MET:CE	2.46	0.45
1:C:98:ASP:CG	1:C:202:ARG:HH22	2.20	0.44
1:C:88:LEU:HD13	1:C:91:THR:HG21	1.99	0.44
1:A:34:GLY:O	1:A:41:SER:HB2	2.17	0.44
1:B:553:MET:HG2	1:B:562:PHE:CG	2.53	0.43
1:A:439:ASN:ND2	1:A:456:GLN:HE22	2.13	0.43
1:C:366:GLU:O	1:C:370:VAL:HG23	2.17	0.43
1:A:366:GLU:O	1:A:370:VAL:HG23	2.19	0.43
1:C:595:GLU:N	1:C:596:PRO:CD	2.82	0.43
1:B:224:ARG:NH2	4:B:1004:HOH:O	2.51	0.43
1:C:298:VAL:HG12	1:C:672:CYS:HB2	2.01	0.42
1:A:224:ARG:HE	1:A:226:HIS:CE1	2.37	0.42
1:C:667:PRO:HB2	1:C:686:THR:HG21	2.01	0.42
1:C:298:VAL:HG12	1:C:672:CYS:HB3	2.02	0.42
1:B:508:GLN:NE2	4:B:1010:HOH:O	2.53	0.41
1:A:42:GLY:O	1:A:90:GLY:HA2	2.20	0.41
1:A:595:GLU:N	1:A:596:PRO:CD	2.83	0.41
1:B:605:ASN:HD22	1:B:663:ILE:CG2	2.34	0.41
1:C:711:ILE:HG21	1:C:722:MET:HE1	2.02	0.41
1:A:605:ASN:HD22	1:A:663:ILE:CG2	2.33	0.40
1:A:553:MET:HG2	1:A:562:PHE:CG	2.56	0.40

All (3) 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)
4:A:962:HOH:O	4:A:962:HOH:O[10_664]	1.88	0.32
4:A:1081:HOH:O	4:A:1081:HOH:O[10_664]	1.96	0.24
4:A:1410:HOH:O	4:A:1410:HOH:O[10_664]	2.05	0.15

## 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	713/727 (98%)	688 (96%)	23 (3%)	2 (0%)	41	61
1	B	702/727 (97%)	672 (96%)	26 (4%)	4 (1%)	25	43
1	C	700/727 (96%)	662 (95%)	32 (5%)	6 (1%)	17	31
All	All	2115/2181 (97%)	2022 (96%)	81 (4%)	12 (1%)	25	43

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	172	TRP
1	B	247	ASN
1	B	535	GLU
1	C	731	SER
1	C	348	THR
1	C	118	GLU
1	A	99	ILE
1	B	99	ILE
1	C	99	ILE
1	C	730	PRO
1	A	595	GLU
1	C	557	GLY

### 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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	590/618 (96%)	577 (98%)	13 (2%)	52 77
1	B	578/618 (94%)	560 (97%)	18 (3%)	40 67
1	C	537/618 (87%)	523 (97%)	14 (3%)	46 72
All	All	1705/1854 (92%)	1660 (97%)	45 (3%)	44 72

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	ASN
1	A	175	ARG
1	A	193	ARG
1	A	299	LYS
1	A	318	GLN
1	A	342	ASN
1	A	368	GLU
1	A	454	ASN
1	A	560	LYS
1	A	594	ASN
1	A	595	GLU
1	A	675	LYS
1	A	721	THR
1	B	43	ASN
1	B	96	LEU
1	B	193	ARG
1	B	217	SER
1	B	247	ASN
1	B	253	CYS
1	B	299	LYS
1	B	318	GLN
1	B	342	ASN
1	B	390	TRP
1	B	397	ASN
1	B	454	ASN
1	B	479	LYS
1	B	560	LYS
1	B	595	GLU
1	B	675	LYS
1	B	685	ARG
1	B	721	THR

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Mol	Chain	Res	Type
1	C	43	ASN
1	C	62	SER
1	C	96	LEU
1	C	193	ARG
1	C	224	ARG
1	C	315	THR
1	C	318	GLN
1	C	368	GLU
1	C	390	TRP
1	C	405	SER
1	C	454	ASN
1	C	479	LYS
1	C	504	THR
1	C	594	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	ASN
1	A	66	ASN
1	A	147	HIS
1	A	180	GLN
1	A	226	HIS
1	A	233	ASN
1	A	267	GLN
1	A	292	GLN
1	A	318	GLN
1	A	342	ASN
1	A	391	GLN
1	A	403	ASN
1	A	439	ASN
1	A	454	ASN
1	A	466	GLN
1	A	487	GLN
1	A	498	ASN
1	A	501	HIS
1	A	508	GLN
1	A	531	HIS
1	A	619	HIS
1	B	43	ASN
1	B	44	ASN
1	B	147	HIS

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Mol	Chain	Res	Type
1	B	267	GLN
1	B	292	GLN
1	B	318	GLN
1	B	342	ASN
1	B	391	GLN
1	B	397	ASN
1	B	403	ASN
1	B	439	ASN
1	B	454	ASN
1	B	456	GLN
1	B	487	GLN
1	B	498	ASN
1	B	622	ASN
1	B	635	ASN
1	B	713	HIS
1	C	43	ASN
1	C	44	ASN
1	C	147	HIS
1	C	238	HIS
1	C	267	GLN
1	C	292	GLN
1	C	403	ASN
1	C	437	HIS
1	C	454	ASN
1	C	466	GLN
1	C	605	ASN
1	C	619	HIS
1	C	622	ASN
1	C	713	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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 4 ligands modelled in this entry, 3 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	$\# Z  > 2$
3	EDO	A	802	-	3,3,3	0.60	0	2,2,2	0.55	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
3	EDO	A	802	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	802	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	EDO	1	0

## 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	715/727 (98%)	-0.46	8 (1%) 80 82	25, 34, 59, 128	0
1	B	703/727 (96%)	-0.35	4 (0%) 89 90	31, 46, 75, 107	0
1	C	700/727 (96%)	0.18	35 (5%) 28 30	37, 71, 99, 138	0
All	All	2118/2181 (97%)	-0.21	47 (2%) 62 65	25, 48, 90, 138	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	582	ASN	5.3
1	C	527	GLY	5.1
1	C	529	GLY	4.6
1	A	579	MET	4.2
1	C	528	ASN	4.2
1	C	555	LEU	3.9
1	C	562	PHE	3.6
1	C	520	PHE	3.5
1	C	539	TRP	3.4
1	C	530	GLY	3.4
1	B	247	ASN	3.2
1	C	585	GLY	3.1
1	C	154	GLY	3.0
1	C	516	TRP	2.9
1	B	153	ALA	2.9
1	A	580	ASN	2.8
1	C	552	LEU	2.8
1	C	571	THR	2.8
1	C	448	TYR	2.7
1	C	557	GLY	2.6
1	A	581	HIS	2.6
1	C	500	PHE	2.5
1	C	678	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	733	TRP	2.5
1	C	525	TYR	2.5
1	C	506	PHE	2.5
1	C	512	ASP	2.4
1	C	502	PRO	2.4
1	C	607	ALA	2.3
1	A	153	ALA	2.3
1	A	584	SER	2.3
1	C	67	TRP	2.3
1	A	731	SER	2.3
1	C	497	ARG	2.3
1	C	569	PHE	2.3
1	C	450	PHE	2.2
1	C	531	HIS	2.2
1	B	154	GLY	2.2
1	C	523	TYR	2.2
1	B	276	TRP	2.1
1	C	526	GLY	2.1
1	C	556	THR	2.1
1	C	570	PHE	2.1
1	C	513	LYS	2.1
1	C	533	PHE	2.1
1	C	511	ASN	2.1
1	C	489	PHE	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 carbohydrates 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<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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CA	A	801	1/1	0.81	0.07	58,58,58,58	0
3	EDO	A	802	4/4	0.91	0.13	44,44,47,48	0
2	CA	C	900	1/1	0.94	0.06	81,81,81,81	0
2	CA	B	900	1/1	0.95	0.03	49,49,49,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.