



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 02:05 AM GMT

PDB ID : 2D0F  
Title : Crystal Structure of Thermoactinomyces vulgaris R-47 Alpha-Amylase 1 (TVAI) Mutant D356N complexed with P2, a pullulan model oligosaccharide  
Authors : Abe, A.; Yoshida, H.; Tono-zuka, T.; Sakano, Y.; Kamitori, S.  
Deposited on : 2005-08-02  
Resolution : 2.08 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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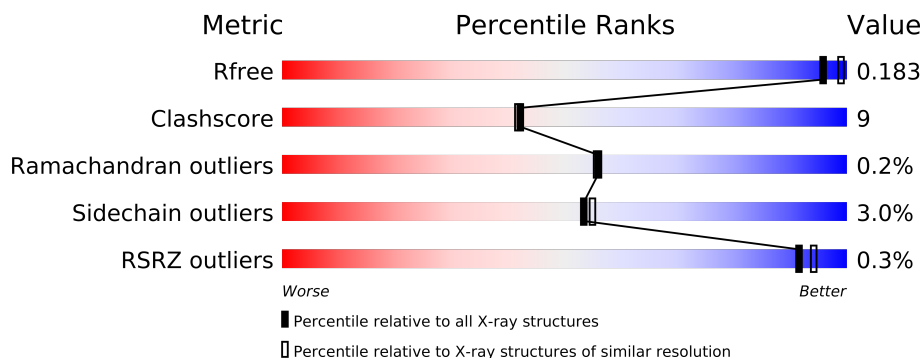
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance


The reported resolution of this entry is 2.08 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))
$R_{free}$	66092	3396 (2.10-2.06)
Clashscore	79885	4085 (2.10-2.06)
Ramachandran outliers	78287	4045 (2.10-2.06)
Sidechain outliers	78261	4046 (2.10-2.06)
RSRZ outliers	66119	3397 (2.10-2.06)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	637	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
5	MPD	A	1001	-	X
5	MPD	A	1002	-	X
5	MPD	A	1003	-	X
5	MPD	A	1004	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5615 atoms, of which 0 are hydrogen and 0 are deuterium.

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-amylase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	637	Total	C	N	O	S	0	0	0
			5038	3192	843	993	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	ASN	ASP	ENGINEERED	UNP Q60053

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	5	Total	C	O	0	0
			56	30	26		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	ASN	ASP	ENGINEERED	UNP Q60053

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	3	Total	C	O	0	0
			34	18	16		

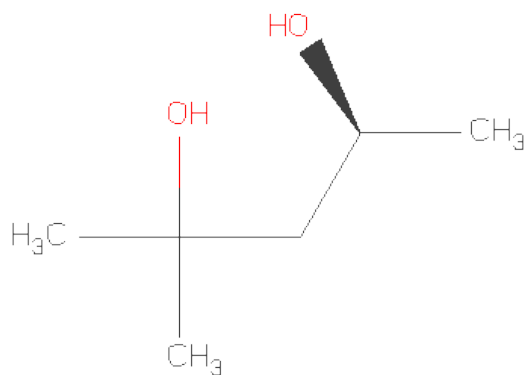
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	ASN	ASP	ENGINEERED	UNP Q60053

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Ca	0	0
			3	3		

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



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

- Molecule 6 is water.

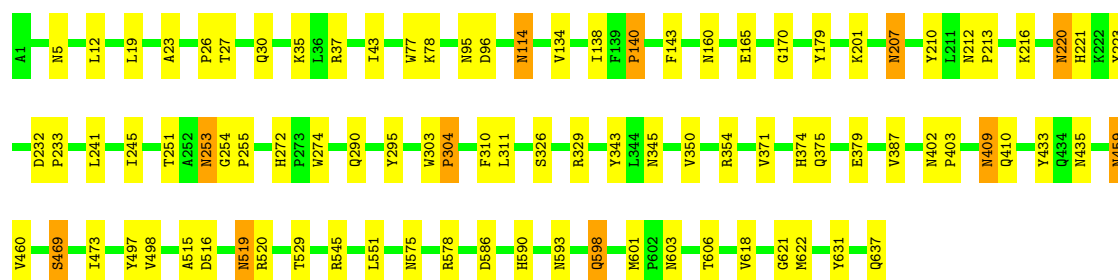
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	452	Total	O	0	0
			452	452		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: alpha-amylase I

Chain A: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.53Å 50.43Å 107.83Å 90.00° 104.30° 90.00°	Depositor
Resolution (Å)	46.00 – 2.08 46.36 – 2.08	Depositor EDS
% Data completeness (in resolution range)	(Not available) (46.00-2.08) 99.8 (46.36-2.08)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	11.20 (at 2.08Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.154 , 0.187 0.151 , 0.183	Depositor DCC
$R_{free}$ test set	3836 reflections (11.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	13.3	Xtriage
Anisotropy	0.346	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 42.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 38345 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5615	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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

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	0.32	0/5195	0.60	0/7108

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5038	0	4650	82	0
2	A	56	0	48	3	0
3	A	34	0	30	2	0
4	A	3	0	0	0	0
5	A	32	0	56	3	0
6	A	452	0	0	9	1
All	All	5615	0	4784	89	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (89) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:578:ARG:HE	1:A:637:GLN:HE21	1.17	0.93
1:A:272:HIS:HD2	1:A:274:TRP:H	1.17	0.90
1:A:603:ASN:HD21	1:A:621:GLY:H	1.16	0.88
3:A:801:GLC:H5	3:A:802:GLC:H62	1.62	0.80
1:A:37:ARG:HH22	1:A:598:GLN:HE22	1.30	0.76
1:A:603:ASN:ND2	1:A:621:GLY:H	1.85	0.74
1:A:207:ASN:H	1:A:207:ASN:HD22	1.33	0.74
1:A:603:ASN:HD21	1:A:621:GLY:N	1.85	0.73
1:A:221:HIS:CD2	1:A:223:TYR:H	2.08	0.72
1:A:221:HIS:HD2	1:A:223:TYR:H	1.36	0.71
1:A:220:ASN:HD22	1:A:221:HIS:N	1.92	0.67
1:A:519:ASN:ND2	1:A:520:ARG:HG3	2.10	0.66
1:A:606:THR:HG22	6:A:2350:HOH:O	1.97	0.63
1:A:201:LYS:HE3	1:A:255:PRO:O	1.97	0.63
2:A:701:GLC:H5	2:A:702:GLC:H62	1.81	0.61
3:A:801:GLC:C5	3:A:802:GLC:H62	2.30	0.60
1:A:586:ASP:OD1	1:A:590:HIS:HE1	1.83	0.60
1:A:578:ARG:HE	1:A:637:GLN:NE2	1.93	0.60
1:A:459:ASN:N	1:A:459:ASN:HD22	1.99	0.60
1:A:19:LEU:HD23	1:A:575:ASN:ND2	2.17	0.59
1:A:310:PHE:CE1	1:A:311:LEU:HD22	2.37	0.59
1:A:201:LYS:NZ	1:A:253:ASN:HD21	2.04	0.56
1:A:170:GLY:O	5:A:1002:MPD:HM1	2.08	0.54
1:A:345:ASN:ND2	1:A:387:VAL:HG13	2.22	0.54
1:A:409:ASN:H	1:A:409:ASN:HD22	1.56	0.54
1:A:272:HIS:CD2	1:A:274:TRP:H	2.10	0.53
1:A:143:PHE:HB3	6:A:2088:HOH:O	2.09	0.53
1:A:216:LYS:HE3	6:A:2370:HOH:O	2.08	0.53
1:A:578:ARG:NE	1:A:637:GLN:HE21	1.98	0.53
1:A:374:HIS:HE1	6:A:2028:HOH:O	1.92	0.52
1:A:37:ARG:NH2	1:A:598:GLN:HE22	2.04	0.51
1:A:37:ARG:HH22	1:A:598:GLN:NE2	2.05	0.51
1:A:114:ASN:C	1:A:114:ASN:HD22	2.13	0.50
1:A:78:LYS:NZ	1:A:78:LYS:HB3	2.27	0.49
1:A:253:ASN:H	1:A:253:ASN:ND2	2.11	0.49
1:A:519:ASN:ND2	1:A:519:ASN:H	2.12	0.48
1:A:343:TYR:O	1:A:350:VAL:HG22	2.14	0.47
1:A:23:ALA:O	1:A:26:PRO:HD3	2.14	0.47
1:A:303:TRP:CE2	1:A:304:PRO:HB3	2.49	0.47
1:A:545:ARG:HA	1:A:551:LEU:HD12	1.95	0.47
1:A:345:ASN:HD21	1:A:387:VAL:HG13	1.80	0.47
1:A:138:ILE:O	1:A:140:PRO:HD3	2.16	0.45
1:A:519:ASN:N	1:A:519:ASN:HD22	2.14	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:459:ASN:N	1:A:459:ASN:ND2	2.64	0.45
1:A:497:TYR:CG	1:A:498:VAL:N	2.85	0.45
1:A:402:ASN:HB3	1:A:403:PRO:HD3	1.98	0.45
5:A:1001:MPD:HM1	6:A:2408:HOH:O	2.16	0.45
1:A:134:VAL:H	1:A:207:ASN:ND2	2.15	0.44
1:A:216:LYS:HD3	1:A:233:PRO:CD	2.48	0.44
1:A:371:VAL:HG23	6:A:2294:HOH:O	2.16	0.44
1:A:354:ARG:HD3	1:A:354:ARG:C	2.38	0.44
1:A:326:SER:OG	1:A:329:ARG:HG3	2.16	0.44
2:A:705:BGC:H2	6:A:2010:HOH:O	2.17	0.44
1:A:603:ASN:HD22	1:A:618:VAL:HG12	1.83	0.43
1:A:253:ASN:H	1:A:253:ASN:HD22	1.66	0.43
1:A:519:ASN:H	1:A:519:ASN:HD22	1.67	0.43
1:A:459:ASN:HD22	1:A:460:VAL:H	1.66	0.43
5:A:1004:MPD:H32	6:A:2442:HOH:O	2.18	0.43
1:A:290:GLN:HA	1:A:295:TYR:CD1	2.54	0.43
1:A:375:GLN:O	1:A:379:GLU:HG3	2.18	0.43
1:A:603:ASN:HD22	1:A:603:ASN:HA	1.65	0.43
1:A:469:SER:HA	1:A:473:ILE:HD11	2.00	0.43
1:A:601:MET:HG2	1:A:637:GLN:NE2	2.34	0.43
1:A:43:ILE:HB	1:A:95:ASN:O	2.19	0.42
1:A:216:LYS:HD3	1:A:233:PRO:HD2	2.00	0.42
1:A:207:ASN:N	1:A:207:ASN:HD22	2.02	0.42
1:A:515:ALA:O	1:A:516:ASP:C	2.57	0.42
1:A:251:THR:HA	1:A:254:GLY:O	2.19	0.42
1:A:212:ASN:HB3	1:A:213:PRO:HD2	2.02	0.42
1:A:27:THR:H	1:A:30:GLN:HE21	1.67	0.42
1:A:593:ASN:HB3	1:A:622:MET:HE3	2.01	0.42
1:A:26:PRO:HA	1:A:30:GLN:NE2	2.35	0.42
1:A:593:ASN:HB3	1:A:622:MET:CE	2.50	0.42
1:A:374:HIS:HD2	1:A:410:GLN:OE1	2.03	0.41
1:A:12:LEU:HA	1:A:37:ARG:O	2.20	0.41
1:A:27:THR:H	1:A:30:GLN:NE2	2.19	0.41
1:A:216:LYS:HD2	1:A:232:ASP:OD2	2.21	0.41
1:A:345:ASN:HD22	1:A:345:ASN:HA	1.74	0.41
1:A:165:GLU:HB2	1:A:179:TYR:CD2	2.55	0.41
1:A:35:LYS:HA	1:A:77:TRP:O	2.20	0.41
1:A:114:ASN:C	1:A:114:ASN:ND2	2.73	0.41
2:A:701:GLC:H5	2:A:702:GLC:C6	2.48	0.41
1:A:201:LYS:HZ3	1:A:253:ASN:HD21	1.69	0.41
1:A:402:ASN:N	1:A:403:PRO:CD	2.84	0.41
1:A:5:ASN:HA	1:A:96:ASP:O	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:409:ASN:H	1:A:409:ASN:ND2	2.17	0.40
1:A:621:GLY:HA2	6:A:2320:HOH:O	2.21	0.40
1:A:220:ASN:HD22	1:A:220:ASN:C	2.24	0.40
1:A:241:LEU:O	1:A:245:ILE:HG13	2.21	0.40

All (1) 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	Distance(Å)	Clash(Å)
6:A:2178:HOH:O	6:A:2178:HOH:O[2_656]	1.10	1.10

## 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	635/637 (100%)	608 (96%)	26 (4%)	1 (0%)	56	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	140	PRO

### 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	540/540 (100%)	524 (97%)	16 (3%)	53	55

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	ASN
1	A	160	ASN
1	A	207	ASN
1	A	210	TYR
1	A	220	ASN
1	A	253	ASN
1	A	304	PRO
1	A	409	ASN
1	A	433	TYR
1	A	435	ASN
1	A	459	ASN
1	A	469	SER
1	A	519	ASN
1	A	529	THR
1	A	598	GLN
1	A	631	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	14	HIS
1	A	30	GLN
1	A	56	ASN
1	A	114	ASN
1	A	123	ASN
1	A	137	GLN
1	A	153	GLN
1	A	160	ASN
1	A	195	GLN
1	A	207	ASN
1	A	220	ASN
1	A	221	HIS
1	A	226	GLN
1	A	253	ASN
1	A	266	ASN
1	A	272	HIS
1	A	280	ASN
1	A	314	ASN
1	A	345	ASN
1	A	364	ASN
1	A	367	ASN
1	A	374	HIS

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Mol	Chain	Res	Type
1	A	409	ASN
1	A	410	GLN
1	A	435	ASN
1	A	459	ASN
1	A	494	GLN
1	A	512	GLN
1	A	519	ASN
1	A	539	GLN
1	A	546	ASN
1	A	547	GLN
1	A	575	ASN
1	A	585	ASN
1	A	590	HIS
1	A	598	GLN
1	A	603	ASN
1	A	614	HIS
1	A	637	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

8 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	$\# Z  > 2$
2	GLC	A	701	2	10,11,12	0.39	0	11,15,17	0.20	0
2	GLC	A	702	2	10,11,12	0.48	0	11,15,17	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GLC	A	703	2	10,11,12	0.44	0	11,15,17	0.32	0
2	GLC	A	704	2	10,11,12	0.50	0	11,15,17	0.27	0
2	BGC	A	705	2	12,12,12	0.41	0	17,17,17	0.75	0
3	GLC	A	801	3	10,11,12	0.40	0	11,15,17	0.23	0
3	GLC	A	802	3	10,11,12	0.46	0	11,15,17	0.20	0
3	BGC	A	803	3	12,12,12	0.36	0	17,17,17	0.34	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
2	GLC	A	701	2	-	0/2/19/22	0/1/1/1
2	GLC	A	702	2	-	0/2/19/22	0/1/1/1
2	GLC	A	703	2	-	0/2/19/22	0/1/1/1
2	GLC	A	704	2	-	0/2/19/22	0/1/1/1
2	BGC	A	705	2	-	0/2/22/22	0/1/1/1
3	GLC	A	801	3	-	0/2/19/22	0/1/1/1
3	GLC	A	802	3	-	0/2/19/22	0/1/1/1
3	BGC	A	803	3	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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
5	MPD	A	1001	-	7,7,7	0.55	0	10,10,10	0.55	0
5	MPD	A	1002	-	7,7,7	0.52	0	10,10,10	0.48	0
5	MPD	A	1003	-	7,7,7	0.47	0	10,10,10	0.40	0
5	MPD	A	1004	-	7,7,7	0.47	0	10,10,10	0.56	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
5	MPD	A	1001	-	-	0/5/5/5	0/0/0/0
5	MPD	A	1002	-	-	0/5/5/5	0/0/0/0
5	MPD	A	1003	-	-	0/5/5/5	0/0/0/0
5	MPD	A	1004	-	-	0/5/5/5	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	637/637 (100%)	-0.49	0 100 100	6, 11, 18, 24	0

There are no RSRZ outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	BGC	A	803	12/12	0.41	41.93	52,54,55,56	0
3	GLC	A	801	11/12	0.42	15.09	60,62,63,64	0
2	GLC	A	702	11/12	0.21	7.24	33,37,41,45	0
3	GLC	A	802	11/12	0.24	6.48	52,54,56,57	0
2	GLC	A	701	11/12	0.24	3.53	44,45,46,48	0
2	GLC	A	703	11/12	0.13	1.60	18,20,22,29	0
2	BGC	A	705	12/12	0.11	0.39	12,16,17,17	0
2	GLC	A	704	11/12	0.08	-0.64	11,14,15,16	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, 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	MPD	A	1004	8/8	0.41	12.71	71,71,71,72	0
5	MPD	A	1001	8/8	0.24	7.44	36,37,38,39	0
5	MPD	A	1002	8/8	0.23	5.09	35,36,38,39	0
5	MPD	A	1003	8/8	0.18	3.44	51,51,52,52	0
4	CA	A	2001	1/1	0.04	-2.35	11,11,11,11	0
4	CA	A	2003	1/1	0.02	-2.98	13,13,13,13	0
4	CA	A	2002	1/1	0.02	-9.05	11,11,11,11	0

## 6.5 Other polymers

There are no such residues in this entry.