



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:25 AM GMT

PDB ID : 2D0G  
Title : Crystal Structure of Thermoactinomyces vulgaris R-47 Alpha-Amylase 1 (TVAI) Mutant D356N/E396Q complexed with P5, a pullulan model oligosaccharide  
Authors : Abe, A.; Yoshida, H.; Tono-zuka, T.; Sakano, Y.; Kamitori, S.  
Deposited on : 2005-08-02  
Resolution : 2.60 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

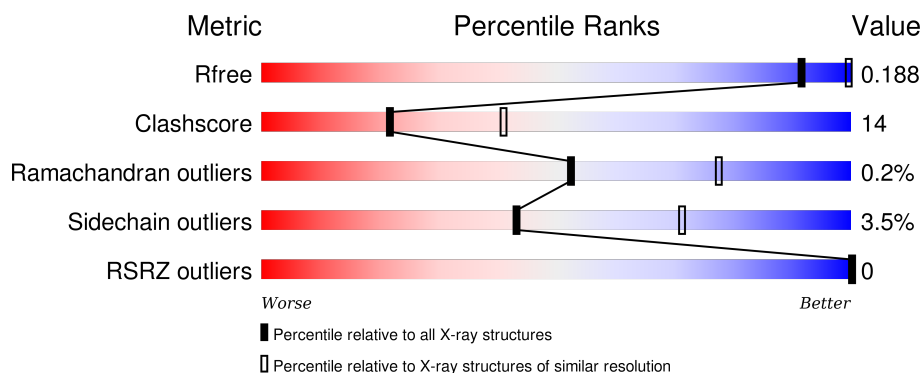
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	637	<div> <div></div> <div>76%</div> <div>22%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLC	A	705	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BGC	A	801	-	-	-	X
5	BGC	A	904	-	-	-	X
6	BGC	A	910	-	-	-	X
8	MPD	A	1001	-	-	-	X

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 5737 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-amylase I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	637	Total	C	N	O	S	0	0	0
			5038	3192	844	992	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	ASN	ASP	ENGINEERED	UNP Q60053
A	396	GLN	GLU	ENGINEERED	UNP Q60053

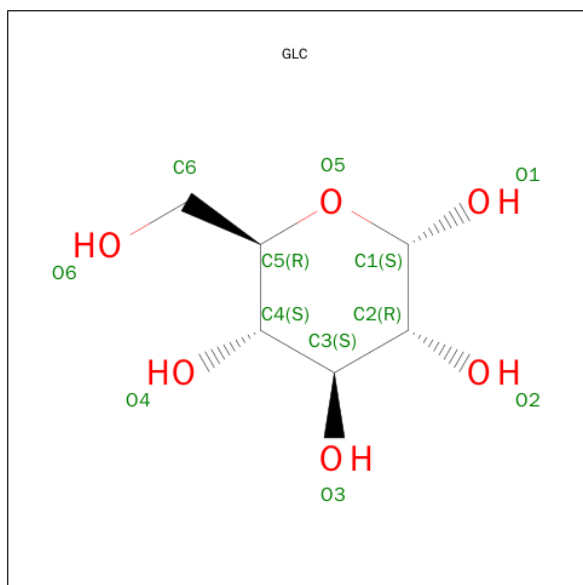
- Molecule 2 is a polymer of unknown type called SUGAR (10-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	10	Total	C	O	0	0
			111	60	51		

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	2	Total	C	O	0	0
			23	12	11		

- Molecule 4 is SUGAR (GLUCOSE) (three-letter code: GLC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).

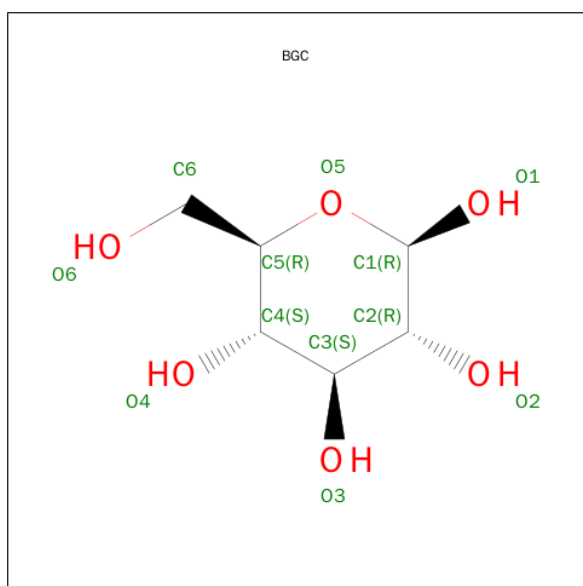


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		

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

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

- Molecule 6 is SUGAR (BETA-D-GLUCOSE) (three-letter code: BGC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).

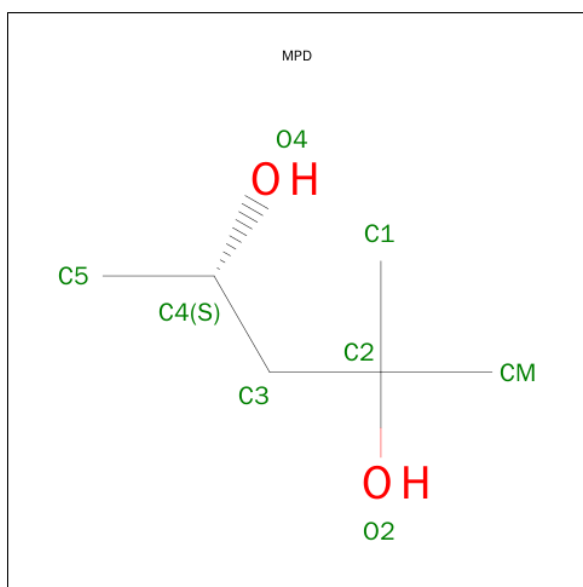


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 8 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
8	A	1	Total	C	O	0	0
			8	6	2		

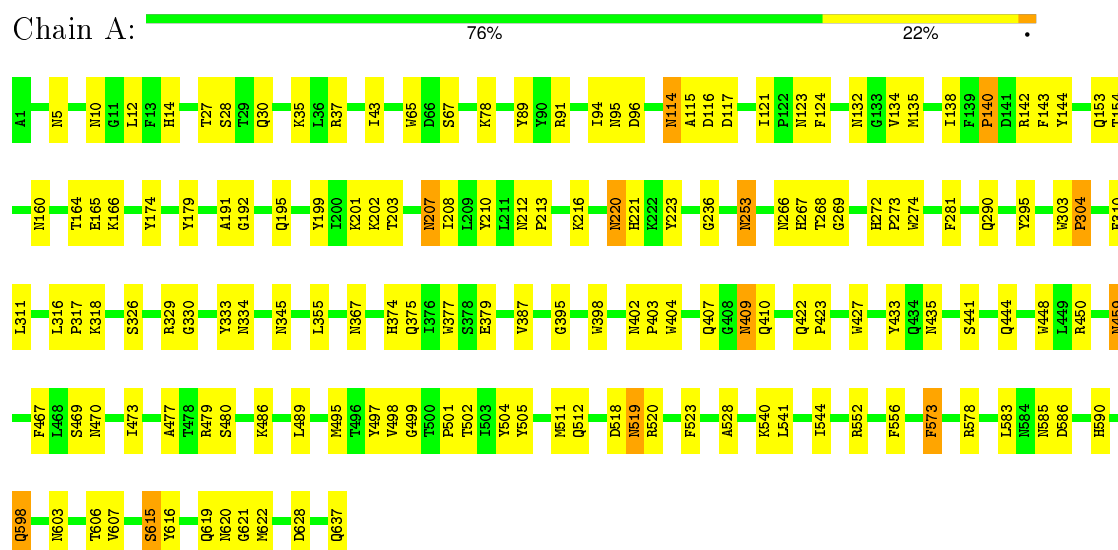
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	474	Total	O	0	0
			474	474		

### 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 ( $\text{RSRZ} > 2$ ). 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: alpha-amylase I



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	120.89Å 50.70Å 108.01Å 90.00° 103.43° 90.00°	Depositor
Resolution (Å)	35.00 – 2.60 35.31 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (35.00-2.60) 96.8 (35.31-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.45 (at 2.61Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.150 , 0.190 0.149 , 0.188	Depositor DCC
$R_{free}$ test set	1899 reflections (10.93%)	DCC
Wilson B-factor (Å <sup>2</sup> )	14.4	Xtriage
Anisotropy	0.386	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 48.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 19275 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5737	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.38% 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

### 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	0.35	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 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	5038	0	4652	136	0
2	A	111	0	93	5	0
3	A	23	0	21	1	0
4	A	12	0	12	1	0
5	A	56	0	48	3	0
6	A	12	0	12	0	0
7	A	3	0	0	0	0
8	A	8	0	14	0	0
9	A	474	0	0	13	0
All	All	5737	0	4852	142	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 14.

All (142) 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:578:ARG:HE	1:A:637:GLN:HE21	1.12	0.94
1:A:603:ASN:HD21	1:A:621:GLY:H	1.12	0.91
1:A:272:HIS:HD2	1:A:274:TRP:H	1.17	0.86
1:A:207:ASN:H	1:A:207:ASN:HD22	1.22	0.84
1:A:578:ARG:HE	1:A:637:GLN:NE2	1.81	0.78
2:A:703:BGC:C1	2:A:704:BGC:H6C1	2.16	0.75
1:A:27:THR:H	1:A:30:GLN:HE21	1.38	0.71
1:A:114:ASN:C	1:A:114:ASN:HD22	1.94	0.71
1:A:266:ASN:HD21	1:A:318:LYS:HE2	1.57	0.69
1:A:578:ARG:NE	1:A:637:GLN:HE21	1.87	0.69
1:A:469:SER:HA	1:A:473:ILE:HD11	1.74	0.68
1:A:459:ASN:HD22	1:A:459:ASN:N	1.92	0.67
1:A:403:PRO:HG2	1:A:404:TRP:CE3	2.31	0.66
1:A:134:VAL:H	1:A:207:ASN:HD21	1.44	0.66
1:A:619:GLN:HA	1:A:619:GLN:HE21	1.62	0.65
1:A:272:HIS:CD2	1:A:274:TRP:H	2.08	0.64
1:A:409:ASN:HD21	1:A:410:GLN:HE21	1.43	0.64
1:A:619:GLN:HA	1:A:619:GLN:NE2	2.12	0.63
1:A:202:LYS:HE2	1:A:253:ASN:O	1.98	0.62
1:A:221:HIS:HD2	1:A:223:TYR:H	1.47	0.62
1:A:221:HIS:CD2	1:A:223:TYR:H	2.18	0.62
1:A:615:SER:HB2	9:A:2117:HOH:O	2.00	0.61
1:A:329:ARG:HH12	1:A:375:GLN:NE2	1.99	0.60
1:A:134:VAL:H	1:A:207:ASN:ND2	2.00	0.59
1:A:519:ASN:ND2	1:A:519:ASN:H	2.01	0.59
1:A:519:ASN:H	1:A:519:ASN:HD22	1.51	0.59
1:A:174:TYR:OH	1:A:518:ASP:HB2	2.03	0.57
1:A:28:SER:H	1:A:123:ASN:HD21	1.53	0.57
1:A:586:ASP:OD1	1:A:590:HIS:HE1	1.86	0.57
1:A:495:MET:HG3	1:A:541:LEU:HB3	1.86	0.56
1:A:236:GLY:HA2	9:A:2239:HOH:O	2.05	0.56
1:A:409:ASN:ND2	1:A:410:GLN:HG3	2.21	0.55
1:A:165:GLU:HB2	1:A:179:TYR:CD2	2.41	0.55
1:A:519:ASN:N	1:A:519:ASN:HD22	2.03	0.55
1:A:499:GLY:O	1:A:501:PRO:HD3	2.07	0.55
1:A:441:SER:OG	1:A:444:GLN:HG3	2.08	0.54
1:A:138:ILE:O	1:A:140:PRO:HD3	2.07	0.54
1:A:179:TYR:HB3	9:A:2137:HOH:O	2.07	0.54
1:A:330:GLY:HA2	1:A:334:ASN:HB2	1.89	0.54
1:A:556:PHE:HB3	9:A:2258:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:345:ASN:ND2	1:A:387:VAL:HG13	2.22	0.54
1:A:153:GLN:HE22	1:A:166:LYS:HD3	1.71	0.54
1:A:43:ILE:HB	1:A:95:ASN:O	2.08	0.54
1:A:114:ASN:HD22	1:A:115:ALA:N	2.05	0.54
1:A:519:ASN:ND2	1:A:520:ARG:HG3	2.23	0.53
1:A:402:ASN:N	1:A:403:PRO:HD2	2.23	0.53
1:A:329:ARG:HH12	1:A:375:GLN:HE22	1.57	0.52
1:A:480:SER:HB2	1:A:486:LYS:HD2	1.91	0.52
1:A:220:ASN:HD22	1:A:221:HIS:N	2.07	0.52
1:A:267:HIS:CD2	1:A:316:LEU:HD22	2.45	0.52
1:A:403:PRO:HG2	1:A:404:TRP:CZ3	2.45	0.52
1:A:5:ASN:HA	1:A:96:ASP:O	2.09	0.51
1:A:303:TRP:CE2	1:A:304:PRO:HB3	2.46	0.51
1:A:114:ASN:C	1:A:114:ASN:ND2	2.62	0.51
1:A:345:ASN:HD21	1:A:387:VAL:HG13	1.74	0.50
1:A:142:ARG:HG3	1:A:520:ARG:O	2.11	0.50
1:A:573:PHE:N	1:A:573:PHE:CD2	2.80	0.50
1:A:329:ARG:HD3	1:A:333:TYR:OH	2.12	0.50
1:A:477:ALA:HB3	1:A:511:MET:O	2.11	0.50
1:A:489:LEU:HD11	1:A:583:LEU:HB3	1.94	0.50
1:A:374:HIS:HD2	1:A:410:GLN:OE1	1.95	0.50
1:A:94:ILE:HD12	1:A:94:ILE:N	2.27	0.50
1:A:409:ASN:H	1:A:409:ASN:HD22	1.60	0.49
1:A:12:LEU:HA	1:A:37:ARG:O	2.12	0.49
1:A:115:ALA:O	1:A:116:ASP:HB2	2.11	0.49
1:A:269:GLY:HA3	9:A:2182:HOH:O	2.13	0.49
1:A:27:THR:HA	1:A:123:ASN:ND2	2.28	0.49
5:A:904:BGC:O5	5:A:905:BGC:H6C2	2.12	0.49
1:A:37:ARG:HH22	1:A:598:GLN:HE22	1.60	0.49
1:A:14:HIS:HD2	1:A:35:LYS:O	1.95	0.49
1:A:201:LYS:NZ	1:A:253:ASN:HD21	2.11	0.49
1:A:326:SER:OG	1:A:329:ARG:HG3	2.12	0.49
1:A:459:ASN:N	1:A:459:ASN:ND2	2.61	0.48
1:A:448:TRP:CE2	4:A:810:GLC:H2	2.48	0.48
1:A:598:GLN:HE21	1:A:598:GLN:CA	2.27	0.48
1:A:89:TYR:CD1	3:A:802:BGC:H4	2.47	0.48
1:A:355:LEU:HB2	1:A:395:GLY:HA2	1.96	0.48
1:A:65:TRP:CZ2	1:A:67:SER:HA	2.49	0.48
1:A:427:TRP:CZ2	1:A:585:ASN:HB2	2.48	0.48
2:A:703:BGC:C5	2:A:704:BGC:H6C1	2.44	0.48
2:A:703:BGC:C1	2:A:704:BGC:C6	2.84	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:ASN:H	1:A:220:ASN:ND2	2.12	0.48
1:A:78:LYS:NZ	1:A:78:LYS:HB3	2.29	0.48
1:A:290:GLN:HA	1:A:295:TYR:CD1	2.50	0.47
1:A:65:TRP:CZ2	5:A:905:BGC:H4	2.50	0.47
1:A:132:ASN:HA	1:A:552:ARG:HG2	1.97	0.47
1:A:253:ASN:HD22	1:A:253:ASN:C	2.17	0.47
1:A:191:ALA:O	1:A:195:GLN:HG3	2.14	0.47
1:A:144:TYR:O	1:A:192:GLY:HA3	2.14	0.47
1:A:310:PHE:CZ	1:A:311:LEU:HD22	2.50	0.46
1:A:329:ARG:NH1	1:A:375:GLN:HE22	2.13	0.46
1:A:207:ASN:N	1:A:207:ASN:HD22	1.94	0.46
1:A:207:ASN:H	1:A:207:ASN:ND2	2.03	0.46
1:A:495:MET:HG3	1:A:541:LEU:CB	2.46	0.46
1:A:153:GLN:NE2	1:A:166:LYS:HD3	2.30	0.46
1:A:459:ASN:HD22	1:A:459:ASN:H	1.62	0.45
1:A:523:PHE:CE1	1:A:528:ALA:HB2	2.52	0.45
2:A:703:BGC:H5	2:A:704:BGC:H6C1	1.97	0.45
1:A:334:ASN:HB3	9:A:2054:HOH:O	2.17	0.45
1:A:511:MET:HG2	1:A:512:GLN:N	2.30	0.45
1:A:467:PHE:HA	1:A:502:THR:O	2.17	0.45
1:A:28:SER:N	1:A:123:ASN:HD21	2.14	0.44
1:A:450:ARG:NH2	9:A:2324:HOH:O	2.50	0.44
1:A:497:TYR:CG	1:A:498:VAL:N	2.86	0.44
1:A:598:GLN:HA	1:A:598:GLN:HE21	1.82	0.44
2:A:703:BGC:O5	2:A:704:BGC:H6C1	2.17	0.44
1:A:212:ASN:HB3	1:A:213:PRO:CD	2.48	0.44
1:A:398:TRP:CD1	1:A:398:TRP:N	2.85	0.44
1:A:620:ASN:O	1:A:622:MET:HG2	2.17	0.44
1:A:207:ASN:N	1:A:207:ASN:ND2	2.65	0.44
1:A:212:ASN:HB3	1:A:213:PRO:HD2	2.00	0.44
1:A:27:THR:N	1:A:30:GLN:HE21	2.11	0.44
1:A:504:TYR:O	1:A:505:TYR:C	2.56	0.44
1:A:135:MET:HA	1:A:208:ILE:HB	1.99	0.43
1:A:540:LYS:HE3	1:A:540:LYS:HB2	1.82	0.43
1:A:621:GLY:HA2	9:A:2064:HOH:O	2.16	0.43
1:A:469:SER:O	1:A:504:TYR:HB2	2.18	0.43
1:A:407:GLN:HG3	9:A:2203:HOH:O	2.18	0.43
1:A:523:PHE:HE1	1:A:528:ALA:HB2	1.83	0.43
1:A:615:SER:CB	9:A:2117:HOH:O	2.65	0.43
1:A:91:ARG:NH2	1:A:117:ASP:OD1	2.51	0.43
1:A:220:ASN:HD22	1:A:221:HIS:H	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:519:ASN:ND2	1:A:519:ASN:N	2.62	0.42
1:A:216:LYS:HD2	9:A:2392:HOH:O	2.18	0.42
1:A:143:PHE:HB3	9:A:2037:HOH:O	2.18	0.42
1:A:603:ASN:HD22	1:A:603:ASN:HA	1.67	0.42
1:A:355:LEU:HD13	1:A:377:TRP:CZ3	2.55	0.42
1:A:154:THR:HA	1:A:164:THR:O	2.20	0.42
1:A:374:HIS:HE1	9:A:2278:HOH:O	2.03	0.42
1:A:345:ASN:HA	1:A:345:ASN:HD22	1.68	0.42
1:A:469:SER:HB3	1:A:479:ARG:NH2	2.35	0.42
1:A:422:GLN:HB3	1:A:423:PRO:CD	2.50	0.42
1:A:607:VAL:HG12	1:A:616:TYR:HB2	2.01	0.42
1:A:65:TRP:CH2	5:A:905:BGC:H4	2.55	0.41
1:A:121:ILE:HG22	1:A:124:PHE:HB2	2.02	0.41
1:A:273:PRO:HD3	1:A:281:PHE:CZ	2.55	0.41
1:A:199:TYR:O	1:A:203:THR:HB	2.19	0.41
1:A:375:GLN:O	1:A:379:GLU:HG3	2.20	0.41
1:A:268:THR:O	1:A:317:PRO:HD2	2.21	0.41
1:A:470:ASN:HA	1:A:504:TYR:CG	2.56	0.41
1:A:253:ASN:H	1:A:253:ASN:HD22	1.68	0.40
1:A:540:LYS:O	1:A:544:ILE:HG13	2.20	0.40

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	635/637 (100%)	593 (93%)	41 (6%)	1 (0%)	52 77

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%)	521 (96%)	19 (4%)	43 71

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
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	367	ASN
1	A	409	ASN
1	A	433	TYR
1	A	435	ASN
1	A	459	ASN
1	A	519	ASN
1	A	573	PHE
1	A	598	GLN
1	A	606	THR
1	A	615	SER
1	A	628	ASP

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	3	ASN
1	A	14	HIS
1	A	30	GLN
1	A	56	ASN
1	A	114	ASN
1	A	123	ASN

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Mol	Chain	Res	Type
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	242	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
1	A	375	GLN
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	575	ASN
1	A	585	ASN
1	A	590	HIS
1	A	598	GLN
1	A	603	ASN
1	A	619	GLN
1	A	637	GLN

### 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 ⓘ

17 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	BGC	A	701	2	11,11,12	0.63	0	14,15,17	0.88	1 (7%)
2	GLC	A	702	2	11,11,12	0.48	0	14,15,17	0.61	0
2	BGC	A	703	2	11,11,12	0.67	0	14,15,17	0.85	1 (7%)
2	BGC	A	704	2	11,11,12	0.64	0	14,15,17	0.85	1 (7%)
2	GLC	A	705	2	11,11,12	0.59	0	14,15,17	1.27	2 (14%)
2	GLC	A	706	2	11,11,12	0.63	0	14,15,17	0.54	0
2	GLC	A	707	2	11,11,12	0.51	0	14,15,17	0.60	0
2	GLC	A	708	2	11,11,12	0.49	0	14,15,17	0.72	0
2	GLC	A	709	2	11,11,12	0.52	0	14,15,17	0.70	1 (7%)
2	GLC	A	710	2	12,12,12	0.34	0	17,17,17	0.50	0
3	BGC	A	801	3	11,11,12	0.59	0	14,15,17	0.70	0
3	BGC	A	802	3	12,12,12	0.60	0	17,17,17	0.54	0
5	GLC	A	901	5	11,11,12	0.45	0	14,15,17	0.67	1 (7%)
5	BGC	A	902	5	11,11,12	0.56	0	14,15,17	0.73	0
5	BGC	A	903	5	11,11,12	0.61	0	14,15,17	0.71	0
5	BGC	A	904	5	11,11,12	0.49	0	14,15,17	1.09	1 (7%)
5	BGC	A	905	5	12,12,12	0.51	0	17,17,17	0.81	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	BGC	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	BGC	A	703	2	-	0/2/19/22	0/1/1/1
2	BGC	A	704	2	-	0/2/19/22	0/1/1/1
2	GLC	A	705	2	-	0/2/19/22	0/1/1/1
2	GLC	A	706	2	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	A	707	2	-	0/2/19/22	0/1/1/1
2	GLC	A	708	2	-	0/2/19/22	0/1/1/1
2	GLC	A	709	2	-	0/2/19/22	0/1/1/1
2	GLC	A	710	2	-	0/2/22/22	0/1/1/1
3	BGC	A	801	3	-	0/2/19/22	0/1/1/1
3	BGC	A	802	3	-	0/2/22/22	0/1/1/1
5	GLC	A	901	5	-	0/2/19/22	0/1/1/1
5	BGC	A	902	5	-	0/2/19/22	0/1/1/1
5	BGC	A	903	5	-	0/2/19/22	0/1/1/1
5	BGC	A	904	5	-	0/2/19/22	0/1/1/1
5	BGC	A	905	5	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	705	GLC	C2-C3-C4	-2.78	106.31	111.04
2	A	703	BGC	C1-C2-C3	-2.73	106.31	109.54
2	A	704	BGC	C1-O5-C5	2.15	114.97	112.25
2	A	709	GLC	C1-O5-C5	2.15	114.98	112.25
5	A	901	GLC	C1-O5-C5	2.26	115.12	112.25
5	A	904	BGC	C1-O5-C5	2.62	115.57	112.25
2	A	705	GLC	C1-O5-C5	2.70	115.68	112.25
2	A	701	BGC	C1-O5-C5	2.75	115.74	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	703	BGC	5	0
2	A	704	BGC	5	0
3	A	802	BGC	1	0
5	A	904	BGC	1	0
5	A	905	BGC	3	0

## 5.6 Ligand geometry

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	$\# Z  > 2$
8	MPD	A	1001	-	6,7,7	0.44	0	7,10,10	0.48	0
4	GLC	A	810	-	12,12,12	0.36	0	17,17,17	0.32	0
6	BGC	A	910	-	12,12,12	0.41	0	17,17,17	0.40	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
8	MPD	A	1001	-	-	0/5/5/5	0/0/0/0
4	GLC	A	810	-	-	0/2/22/22	0/1/1/1
6	BGC	A	910	-	-	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	810	GLC	1	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, 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%)	-0.69	0 100 100	5, 13, 23, 33	0

There are no RSRZ outliers to report.

### 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
2	GLC	A	705	11/12	0.94	0.18	3.70	25,27,28,29	0
3	BGC	A	801	11/12	0.81	0.29	3.32	44,47,49,50	0
5	BGC	A	904	11/12	0.92	0.23	2.99	26,28,33,38	0
2	BGC	A	703	11/12	0.91	0.18	1.90	35,38,43,48	0
3	BGC	A	802	12/12	0.89	0.22	1.85	36,40,42,45	0
2	GLC	A	709	11/12	0.97	0.13	0.75	16,18,19,19	0
2	GLC	A	708	11/12	0.97	0.14	0.52	13,14,17,17	0
2	GLC	A	707	11/12	0.97	0.11	-0.63	14,17,18,22	0
5	GLC	A	901	11/12	0.84	0.31	-	52,53,55,56	0
5	BGC	A	902	11/12	0.89	0.43	-	51,53,53,55	0
2	GLC	A	706	11/12	0.96	0.11	-	22,23,25,26	0
2	GLC	A	710	12/12	0.94	0.14	-	23,26,28,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	BGC	A	905	12/12	0.87	0.28	-	28,31,32,33	0
5	BGC	A	903	11/12	0.81	0.36	-	41,44,48,50	0
2	BGC	A	704	11/12	0.93	0.14	-	23,27,30,34	0
2	GLC	A	702	11/12	0.89	0.26	-	52,55,58,62	0
2	BGC	A	701	11/12	0.77	0.36	-	64,66,68,69	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( $\text{\AA}^2$ )	Q<0.9
8	MPD	A	1001	8/8	0.89	0.25	6.52	59,59,60,60	0
6	BGC	A	910	12/12	0.67	0.34	5.84	74,77,78,79	0
7	CA	A	2001	1/1	0.99	0.03	-3.00	13,13,13,13	0
7	CA	A	2002	1/1	0.99	0.04	-3.66	22,22,22,22	0
7	CA	A	2003	1/1	0.99	0.02	-5.23	14,14,14,14	0
4	GLC	A	810	12/12	0.76	0.33	-	74,77,78,78	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.