



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 12:59 PM EDT

PDB ID : 7K9N  
Title : Co-crystal structure of alpha glucosidase with compound 2  
Authors : Karade, S.S.; Mariuzza, R.A.  
Deposited on : 2020-09-29  
Resolution : 2.07 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

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 : 2.35.1  
buster-report : 1.1.7 (2018)  
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) : 2.35.1

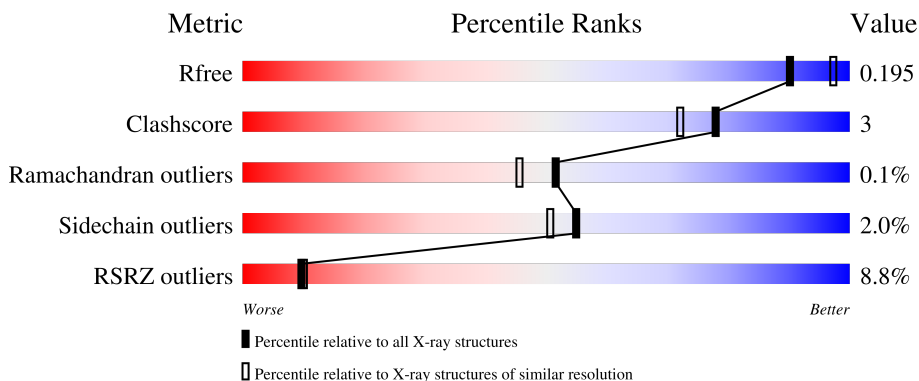
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.07 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	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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 of 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	977	 6% 13% 81% 6% 13%
1	C	977	 6% 13% 82% 5% 12%
2	B	547	 5% 13% 84%
2	D	547	 5% 15% 84%

## 2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 16462 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 glucosidase 2 alpha neutral subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	853	6903	4427	1188	1258	30	0	12	0
1	C	856	6865	4408	1184	1243	30	0	10	0

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	initiating methionine	UNP A1A4T2
A	3	GLY	-	expression tag	UNP A1A4T2
A	4	ILE	-	expression tag	UNP A1A4T2
A	5	LEU	-	expression tag	UNP A1A4T2
A	6	PRO	-	expression tag	UNP A1A4T2
A	7	SER	-	expression tag	UNP A1A4T2
A	8	PRO	-	expression tag	UNP A1A4T2
A	9	GLY	-	expression tag	UNP A1A4T2
A	10	MET	-	expression tag	UNP A1A4T2
A	11	PRO	-	expression tag	UNP A1A4T2
A	12	ALA	-	expression tag	UNP A1A4T2
A	13	LEU	-	expression tag	UNP A1A4T2
A	14	LEU	-	expression tag	UNP A1A4T2
A	15	SER	-	expression tag	UNP A1A4T2
A	16	LEU	-	expression tag	UNP A1A4T2
A	17	VAL	-	expression tag	UNP A1A4T2
A	18	SER	-	expression tag	UNP A1A4T2
A	19	LEU	-	expression tag	UNP A1A4T2
A	20	LEU	-	expression tag	UNP A1A4T2
A	21	SER	-	expression tag	UNP A1A4T2
A	22	VAL	-	expression tag	UNP A1A4T2
A	23	LEU	-	expression tag	UNP A1A4T2
A	24	LEU	-	expression tag	UNP A1A4T2
A	25	MET	-	expression tag	UNP A1A4T2
A	26	GLY	-	expression tag	UNP A1A4T2

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	CYS	-	expression tag	UNP A1A4T2
A	28	VAL	-	expression tag	UNP A1A4T2
A	29	ALA	-	expression tag	UNP A1A4T2
A	30	GLU	-	expression tag	UNP A1A4T2
A	31	THR	-	expression tag	UNP A1A4T2
A	32	GLY	-	expression tag	UNP A1A4T2
A	97	ASP	ASN	engineered mutation	UNP A1A4T2
A	967	SER	-	expression tag	UNP A1A4T2
A	968	ALA	-	expression tag	UNP A1A4T2
A	969	TRP	-	expression tag	UNP A1A4T2
A	970	SER	-	expression tag	UNP A1A4T2
A	971	HIS	-	expression tag	UNP A1A4T2
A	972	PRO	-	expression tag	UNP A1A4T2
A	973	GLN	-	expression tag	UNP A1A4T2
A	974	PHE	-	expression tag	UNP A1A4T2
A	975	GLU	-	expression tag	UNP A1A4T2
A	976	LYS	-	expression tag	UNP A1A4T2
A	977	LEU	-	expression tag	UNP A1A4T2
A	978	GLU	-	expression tag	UNP A1A4T2
C	2	MET	-	initiating methionine	UNP A1A4T2
C	3	GLY	-	expression tag	UNP A1A4T2
C	4	ILE	-	expression tag	UNP A1A4T2
C	5	LEU	-	expression tag	UNP A1A4T2
C	6	PRO	-	expression tag	UNP A1A4T2
C	7	SER	-	expression tag	UNP A1A4T2
C	8	PRO	-	expression tag	UNP A1A4T2
C	9	GLY	-	expression tag	UNP A1A4T2
C	10	MET	-	expression tag	UNP A1A4T2
C	11	PRO	-	expression tag	UNP A1A4T2
C	12	ALA	-	expression tag	UNP A1A4T2
C	13	LEU	-	expression tag	UNP A1A4T2
C	14	LEU	-	expression tag	UNP A1A4T2
C	15	SER	-	expression tag	UNP A1A4T2
C	16	LEU	-	expression tag	UNP A1A4T2
C	17	VAL	-	expression tag	UNP A1A4T2
C	18	SER	-	expression tag	UNP A1A4T2
C	19	LEU	-	expression tag	UNP A1A4T2
C	20	LEU	-	expression tag	UNP A1A4T2
C	21	SER	-	expression tag	UNP A1A4T2
C	22	VAL	-	expression tag	UNP A1A4T2
C	23	LEU	-	expression tag	UNP A1A4T2
C	24	LEU	-	expression tag	UNP A1A4T2

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	25	MET	-	expression tag	UNP A1A4T2
C	26	GLY	-	expression tag	UNP A1A4T2
C	27	CYS	-	expression tag	UNP A1A4T2
C	28	VAL	-	expression tag	UNP A1A4T2
C	29	ALA	-	expression tag	UNP A1A4T2
C	30	GLU	-	expression tag	UNP A1A4T2
C	31	THR	-	expression tag	UNP A1A4T2
C	32	GLY	-	expression tag	UNP A1A4T2
C	97	ASP	ASN	engineered mutation	UNP A1A4T2
C	967	SER	-	expression tag	UNP A1A4T2
C	968	ALA	-	expression tag	UNP A1A4T2
C	969	TRP	-	expression tag	UNP A1A4T2
C	970	SER	-	expression tag	UNP A1A4T2
C	971	HIS	-	expression tag	UNP A1A4T2
C	972	PRO	-	expression tag	UNP A1A4T2
C	973	GLN	-	expression tag	UNP A1A4T2
C	974	PHE	-	expression tag	UNP A1A4T2
C	975	GLU	-	expression tag	UNP A1A4T2
C	976	LYS	-	expression tag	UNP A1A4T2
C	977	LEU	-	expression tag	UNP A1A4T2
C	978	GLU	-	expression tag	UNP A1A4T2

- Molecule 2 is a protein called Glucosidase 2 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	87	609	359	102	138	10	0	0	0
2	D	87	621	370	100	141	10	0	0	0

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	MET	-	initiating methionine	UNP O08795
B	-15	GLY	-	expression tag	UNP O08795
B	-14	ILE	-	expression tag	UNP O08795
B	-13	LEU	-	expression tag	UNP O08795
B	-12	PRO	-	expression tag	UNP O08795
B	-11	SER	-	expression tag	UNP O08795
B	-10	PRO	-	expression tag	UNP O08795
B	-9	GLY	-	expression tag	UNP O08795
B	-8	MET	-	expression tag	UNP O08795

Continued on next page...

*Continued from previous page...*

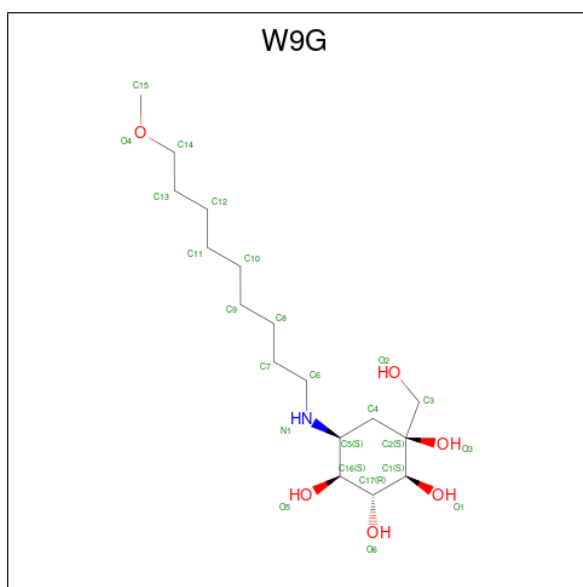
Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	PRO	-	expression tag	UNP O08795
B	-6	ALA	-	expression tag	UNP O08795
B	-5	LEU	-	expression tag	UNP O08795
B	-4	LEU	-	expression tag	UNP O08795
B	-3	SER	-	expression tag	UNP O08795
B	-2	LEU	-	expression tag	UNP O08795
B	-1	VAL	-	expression tag	UNP O08795
B	0	SER	-	expression tag	UNP O08795
B	1	LEU	-	expression tag	UNP O08795
B	2	LEU	-	expression tag	UNP O08795
B	3	SER	-	expression tag	UNP O08795
B	4	VAL	-	expression tag	UNP O08795
B	5	LEU	-	expression tag	UNP O08795
B	6	LEU	-	expression tag	UNP O08795
B	7	MET	-	expression tag	UNP O08795
B	8	GLY	-	expression tag	UNP O08795
B	9	CYS	-	expression tag	UNP O08795
B	10	VAL	-	expression tag	UNP O08795
B	11	ALA	-	expression tag	UNP O08795
B	12	GLU	-	expression tag	UNP O08795
B	13	THR	-	expression tag	UNP O08795
B	14	GLY	-	expression tag	UNP O08795
B	518	SER	-	expression tag	UNP O08795
B	519	ALA	-	expression tag	UNP O08795
B	520	TRP	-	expression tag	UNP O08795
B	521	LEU	-	expression tag	UNP O08795
B	522	GLU	-	expression tag	UNP O08795
B	523	THR	-	expression tag	UNP O08795
B	524	LYS	-	expression tag	UNP O08795
B	525	HIS	-	expression tag	UNP O08795
B	526	HIS	-	expression tag	UNP O08795
B	527	HIS	-	expression tag	UNP O08795
B	528	HIS	-	expression tag	UNP O08795
B	529	HIS	-	expression tag	UNP O08795
B	530	HIS	-	expression tag	UNP O08795
D	-16	MET	-	initiating methionine	UNP O08795
D	-15	GLY	-	expression tag	UNP O08795
D	-14	ILE	-	expression tag	UNP O08795
D	-13	LEU	-	expression tag	UNP O08795
D	-12	PRO	-	expression tag	UNP O08795
D	-11	SER	-	expression tag	UNP O08795
D	-10	PRO	-	expression tag	UNP O08795

*Continued on next page...*

*Continued from previous page...*

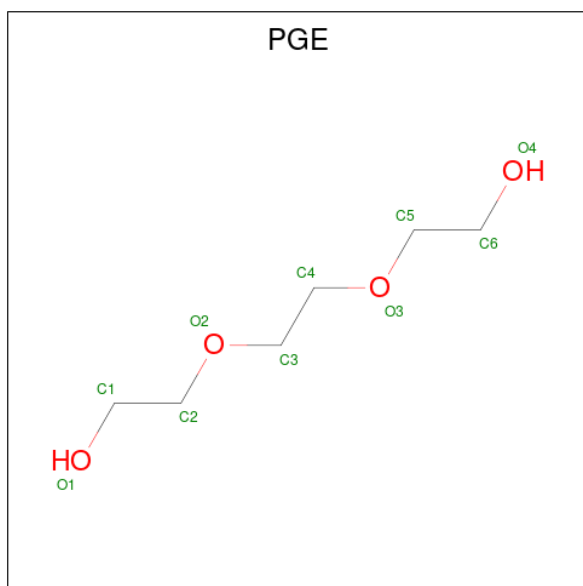
Chain	Residue	Modelled	Actual	Comment	Reference
D	-9	GLY	-	expression tag	UNP O08795
D	-8	MET	-	expression tag	UNP O08795
D	-7	PRO	-	expression tag	UNP O08795
D	-6	ALA	-	expression tag	UNP O08795
D	-5	LEU	-	expression tag	UNP O08795
D	-4	LEU	-	expression tag	UNP O08795
D	-3	SER	-	expression tag	UNP O08795
D	-2	LEU	-	expression tag	UNP O08795
D	-1	VAL	-	expression tag	UNP O08795
D	0	SER	-	expression tag	UNP O08795
D	1	LEU	-	expression tag	UNP O08795
D	2	LEU	-	expression tag	UNP O08795
D	3	SER	-	expression tag	UNP O08795
D	4	VAL	-	expression tag	UNP O08795
D	5	LEU	-	expression tag	UNP O08795
D	6	LEU	-	expression tag	UNP O08795
D	7	MET	-	expression tag	UNP O08795
D	8	GLY	-	expression tag	UNP O08795
D	9	CYS	-	expression tag	UNP O08795
D	10	VAL	-	expression tag	UNP O08795
D	11	ALA	-	expression tag	UNP O08795
D	12	GLU	-	expression tag	UNP O08795
D	13	THR	-	expression tag	UNP O08795
D	14	GLY	-	expression tag	UNP O08795
D	518	SER	-	expression tag	UNP O08795
D	519	ALA	-	expression tag	UNP O08795
D	520	TRP	-	expression tag	UNP O08795
D	521	LEU	-	expression tag	UNP O08795
D	522	GLU	-	expression tag	UNP O08795
D	523	THR	-	expression tag	UNP O08795
D	524	LYS	-	expression tag	UNP O08795
D	525	HIS	-	expression tag	UNP O08795
D	526	HIS	-	expression tag	UNP O08795
D	527	HIS	-	expression tag	UNP O08795
D	528	HIS	-	expression tag	UNP O08795
D	529	HIS	-	expression tag	UNP O08795
D	530	HIS	-	expression tag	UNP O08795

- Molecule 3 is (1S,2S,3R,4S,5S)-1-(hydroxymethyl)-5-[(9-methoxynonyl)amino]cyclohexane-1,2,3,4-tetrol (three-letter code: W9G) (formula: C<sub>17</sub>H<sub>35</sub>NO<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
3	A	1	Total	C	N	O	0	0
			24	17	1	6		
3	C	1	Total	C	N	O	0	0
			24	17	1	6		

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula:  $C_6H_{14}O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		

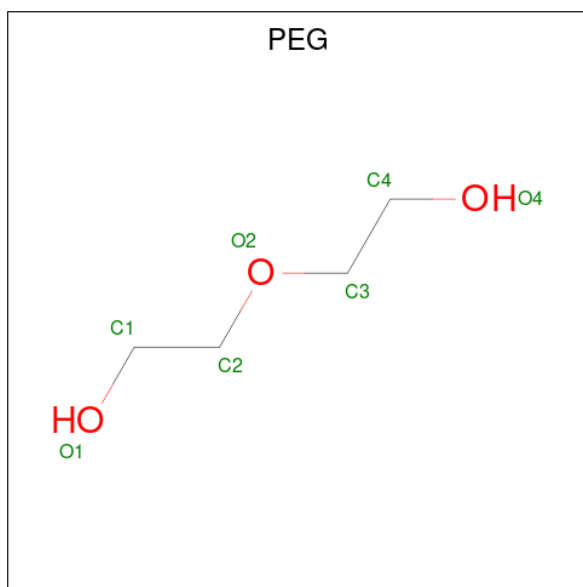
*Continued on next page...*



Continued from previous page...

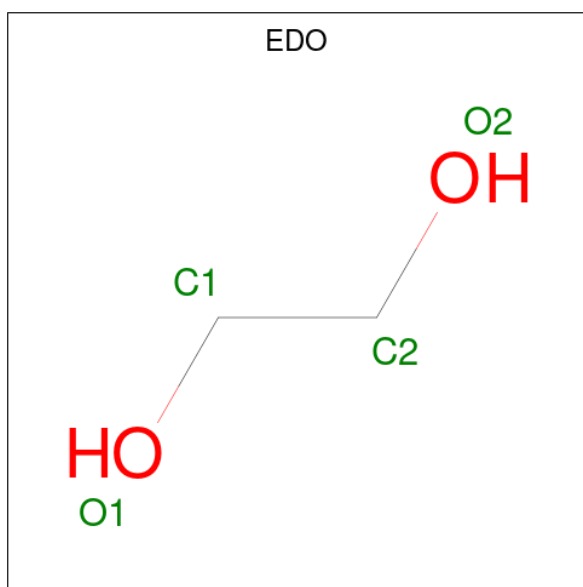
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 10 6 4	0	0
4	A	1	Total C O 10 6 4	0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0
5	C	1	Total C O 7 4 3	0	0

- Molecule 6 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
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0

*Continued on next page...*

*Continued from previous page...*

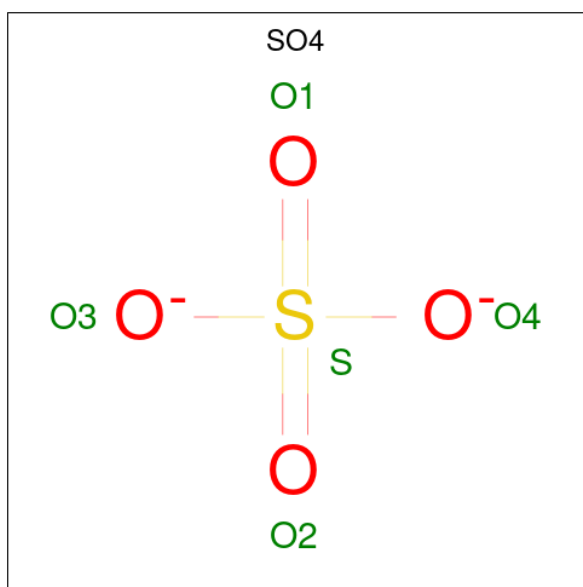
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	C	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0

- Molecule 7 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			13	8	5		
7	C	1	Total	C	O	0	0
			13	8	5		
7	D	1	Total	C	O	0	0
			13	8	5		

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

*Continued on next page...*

*Continued from previous page...*

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

- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	2	Total Ca 2 2	0	0
9	D	2	Total Ca 2 2	0	0

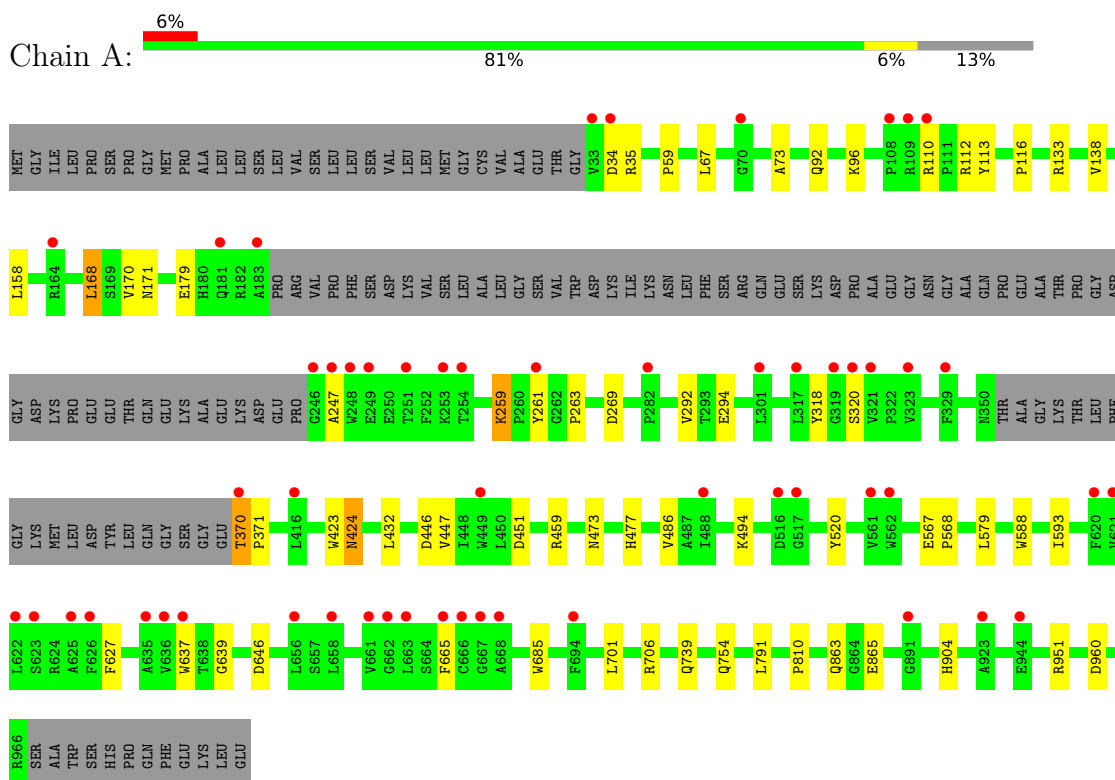
- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	563	Total O 563 563	0	0
10	B	44	Total O 44 44	0	0
10	C	485	Total O 485 485	0	0
10	D	33	Total O 33 33	0	0

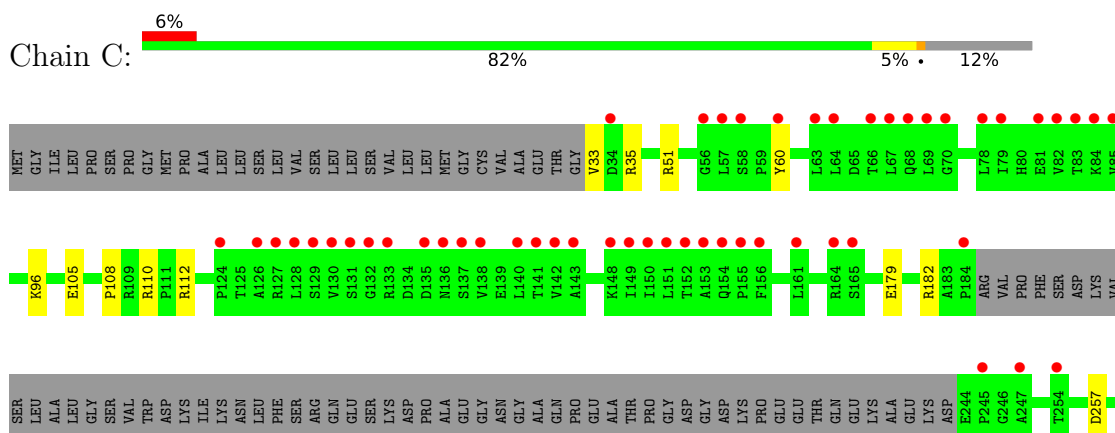
### 3 Residue-property plots [i](#)

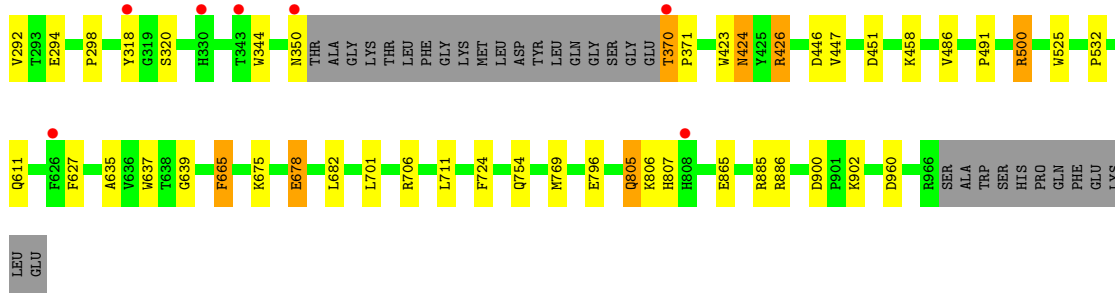
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 glucosidase 2 alpha neutral subunit

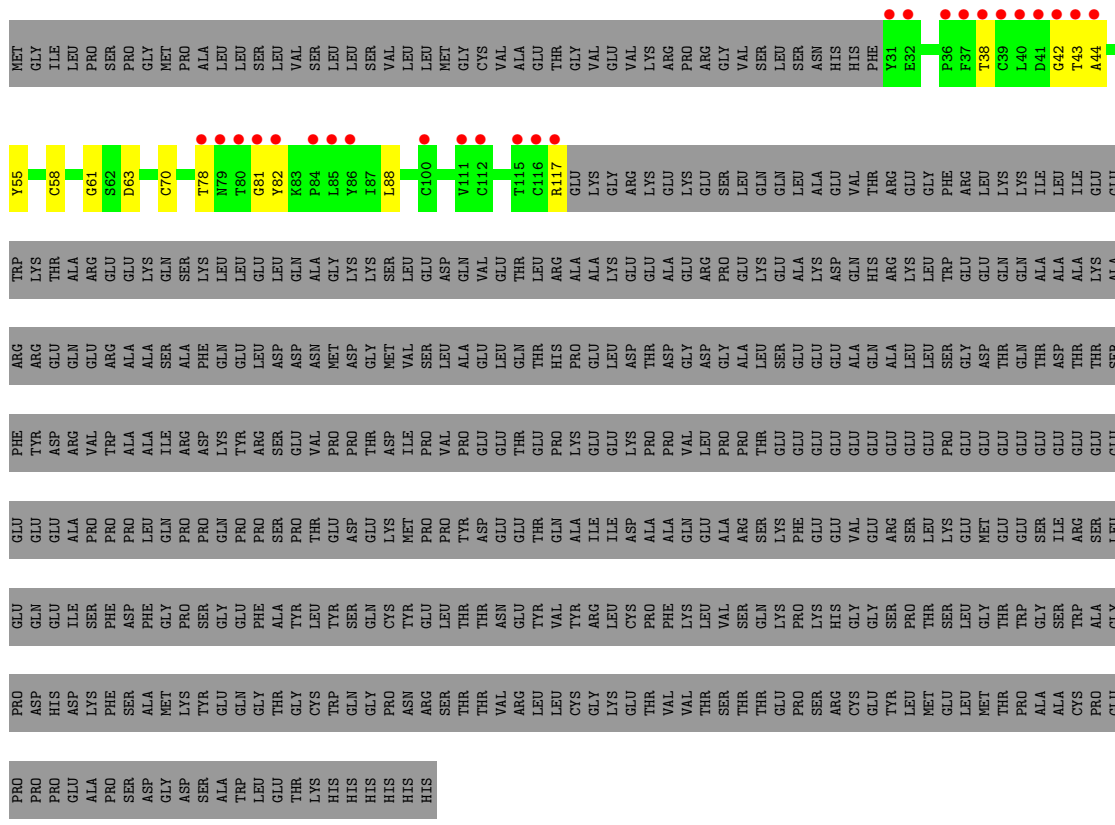


- Molecule 1: Alpha glucosidase 2 alpha neutral subunit

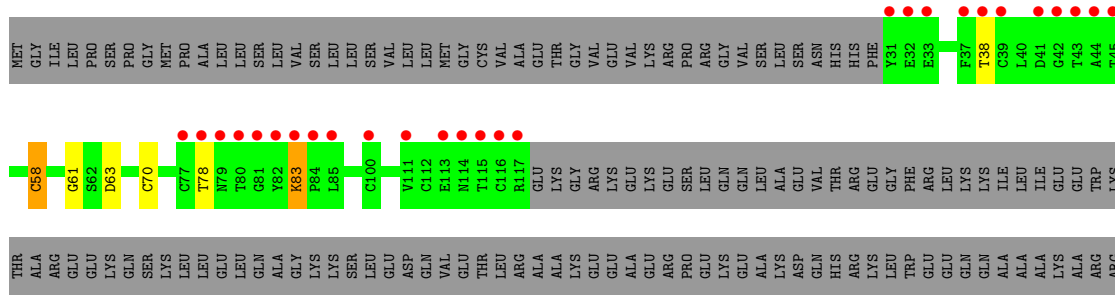




• Molecule 2: Glucosidase 2 subunit beta



• Molecule 2: Glucosidase 2 subunit beta



GLU ARG  
GLN GLU  
GLU ALA  
TRP ARG  
ALA ALA  
SER ALA  
ALA SER  
PHE ALA  
GLN GLU  
TYR TYR  
LEU LEU  
ASP SER  
ASN ASP

ASP ARG  
VAL TRP  
ALA ALA  
ILE ILE  
ARG ARG  
ASP LYS  
TYR TYR  
ARG ARG  
SER SER  
GLU GLU  
VAL VAL  
ASN ASN

GLU ALA  
ALA PRO  
PRO PRO  
LEU LEU  
GLN GLN  
PRO PRO  
GLN GLN  
PHE PHE  
SER SER  
PRO PRO

GLU ILE  
SER PHE  
ASP ASP  
PHE PHE  
GLY PRO  
SER SER  
GLY GLY  
GLU GLU  
PHE PHE  
ALA TYR  
TYR TYR  
CYS CYS  
TYR TYR

HIS ASP  
LYS PHE  
SER SER  
ALA MET  
LYS LYS  
TYR TYR  
GLU GLU  
GLN GLN  
TRP TRP  
LEU LEU  
THR THR  
GLY GLY  
CYS CYS  
TRP TRP  
ALA ALA

PRO PRO  
GLU GLU  
ALA ALA  
PRO PRO  
SER SER  
ASP ASP  
GLY GLY  
ASP ASP  
SER SER  
ALA ALA  
TRP TRP  
LEU LEU  
GLU GLU  
THR THR  
LYS LYS  
HIS HIS  
HIS HIS  
HIS HIS  
HIS HIS



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.79Å 102.79Å 240.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.75 – 2.07 43.77 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.9 (41.75-2.07) 94.8 (43.77-2.07)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.94 (at 2.06Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, $R_{free}$	0.170 , 0.195 0.170 , 0.195	Depositor DCC
$R_{free}$ test set	2011 reflections (1.16%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.1	Xtrriage
Anisotropy	0.124	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 53.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.013 for -h,-k,l 0.037 for h,-h-k,-l 0.023 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	16462	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.53% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, CA, EDO, PGE, W9G, PG4, SO4

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	0.36	0/7148	0.56	1/9733 (0.0%)
1	C	0.34	0/7105	0.54	0/9682
2	B	0.37	0/620	0.61	0/850
2	D	0.37	0/633	0.60	0/867
All	All	0.35	0/15506	0.56	1/21132 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	168	LEU	CA-CB-CG	5.54	128.04	115.30

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	6903	0	6650	34	0
1	C	6865	0	6594	39	0
2	B	609	0	486	7	0
2	D	621	0	506	3	0
3	A	24	0	0	0	0
3	C	24	0	0	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	40	0	52	3	0
5	A	21	0	30	1	0
5	B	7	0	10	1	0
5	C	28	0	40	1	0
6	A	60	0	89	5	0
6	B	8	0	12	1	0
6	C	36	0	54	4	0
6	D	8	0	12	0	0
7	A	13	0	18	2	0
7	C	13	0	18	0	0
7	D	13	0	18	1	0
8	A	25	0	0	1	0
8	C	15	0	0	1	0
9	B	2	0	0	0	0
9	D	2	0	0	0	0
10	A	563	0	0	4	0
10	B	44	0	0	2	0
10	C	485	0	0	14	0
10	D	33	0	0	0	0
All	All	16462	0	14589	87	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 3.

All (87) 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:739:GLN:HG2	6:A:1021:EDO:H22	1.61	0.82
1:A:59:PRO:HG3	7:A:1012:PG4:H41	1.60	0.81
1:C:350:ASN:ND2	10:C:1106:HOH:O	2.14	0.81
1:C:35:ARG:N	10:C:1102:HOH:O	2.00	0.74
1:C:960:ASP:HB3	5:C:1012:PEG:H22	1.70	0.73
2:B:42:GLY:O	2:B:44:ALA:N	2.21	0.71
1:C:796:GLU:OE1	10:C:1104:HOH:O	2.13	0.66
1:A:960:ASP:HB3	5:A:1013:PEG:H12	1.75	0.66
1:C:112:ARG:NH2	1:C:179:GLU:O	2.29	0.65
2:B:82:TYR:O	10:B:701:HOH:O	2.15	0.63
1:C:900:ASP:OD1	1:C:902:LYS:HG2	1.98	0.63
1:A:588:TRP:HE1	4:A:1017:PGE:H62	1.65	0.61
2:D:83:LYS:HD3	2:D:83:LYS:H	1.65	0.61
1:C:675:LYS:NZ	10:C:1112:HOH:O	2.33	0.60

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:865:GLU:H	6:C:1010:EDO:H22	1.65	0.60
1:C:182:ARG:NH1	10:C:1105:HOH:O	2.13	0.59
1:C:298:PRO:HG2	1:C:344:TRP:CE3	2.37	0.59
1:A:112:ARG:NH2	1:A:179:GLU:O	2.36	0.58
1:C:298:PRO:HG2	1:C:344:TRP:HE3	1.68	0.58
1:C:423:TRP:O	1:C:701:LEU:HA	2.05	0.57
2:B:88:LEU:HD23	6:B:603:EDO:H22	1.87	0.56
1:A:423:TRP:O	1:A:701:LEU:HA	2.06	0.56
1:C:500:ARG:HG3	10:C:1525:HOH:O	2.06	0.55
1:C:865:GLU:OE2	1:C:886:ARG:NH2	2.41	0.54
1:A:96:LYS:HB3	6:A:1023:EDO:H12	1.90	0.54
1:A:865:GLU:H	6:A:1015:EDO:H21	1.71	0.53
1:A:116:PRO:HG3	4:A:1017:PGE:H42	1.88	0.53
1:C:805:GLN:HG2	1:C:807:HIS:CE1	2.44	0.53
1:A:904:HIS:HB2	6:A:1004:EDO:H22	1.91	0.52
8:A:1028:SO4:O1	10:A:1101:HOH:O	2.18	0.52
2:B:58:CYS:HB2	2:B:63:ASP:OD1	2.10	0.52
1:C:678:GLU:OE1	10:C:1107:HOH:O	2.19	0.52
1:C:885:ARG:HH12	6:C:1014:EDO:C1	2.24	0.51
1:A:133[A]:ARG:HD2	1:A:138:VAL:HG22	1.92	0.51
1:C:426:ARG:NH2	10:C:1120:HOH:O	2.43	0.50
2:D:58:CYS:HB2	2:D:63:ASP:OD1	2.12	0.50
1:A:259:LYS:HD2	10:A:1329:HOH:O	2.12	0.49
1:A:247:ALA:HB1	1:A:263:PRO:HG3	1.95	0.49
1:C:105:GLU:HB2	1:C:108:PRO:HB3	1.94	0.48
1:C:292:VAL:HG12	1:C:294:GLU:H	1.79	0.48
5:B:605:PEG:H22	5:B:605:PEG:H41	1.61	0.47
1:C:447:VAL:HG11	1:C:486:VAL:HG23	1.97	0.47
1:C:491:PRO:O	1:C:532:PRO:HD2	2.15	0.46
1:C:426:ARG:NE	10:C:1101:HOH:O	1.96	0.46
7:D:1604:PG4:H22	7:D:1604:PG4:H42	1.66	0.46
2:D:61:GLY:HA2	2:D:70:CYS:SG	2.55	0.46
1:A:432:LEU:HD22	1:A:477[A]:HIS:ND1	2.31	0.46
2:B:81:GLY:N	10:B:701:HOH:O	2.48	0.46
1:A:320:SER:O	1:A:627:PHE:HA	2.16	0.46
1:C:51:ARG:CZ	1:C:298:PRO:HD3	2.47	0.45
1:C:257:ASP:HB2	8:C:1018:SO4:O2	2.17	0.45
1:C:370:THR:N	1:C:371:PRO:HD2	2.32	0.45
1:A:318:TYR:CE2	1:A:639:GLY:HA3	2.52	0.44
1:A:459:ARG:NH1	1:A:494:LYS:HE2	2.32	0.44
1:A:34:ASP:O	1:A:35:ARG:HD3	2.17	0.44

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:VAL:HG11	1:A:486:VAL:HG23	1.99	0.44
1:A:424:ASN:OD1	1:A:451:ASP:HB3	2.18	0.44
1:A:520:TYR:HE2	1:A:579:LEU:HD12	1.83	0.44
1:A:113:TYR:CZ	1:A:593:ILE:HG22	2.53	0.43
1:A:370:THR:N	1:A:371:PRO:HD2	2.33	0.43
1:A:754:GLN:HB3	10:A:1312:HOH:O	2.18	0.43
1:C:754:GLN:HB3	10:C:1181:HOH:O	2.16	0.43
1:C:682:LEU:HD23	1:C:711:LEU:HD11	2.00	0.43
1:A:292:VAL:HG12	1:A:294:GLU:H	1.83	0.43
1:C:320:SER:O	1:C:627:PHE:HA	2.19	0.43
2:B:61:GLY:HA2	2:B:70:CYS:SG	2.59	0.43
1:A:567:GLU:N	1:A:568:PRO:HA	2.34	0.43
1:C:611:GLN:OE1	10:C:1108:HOH:O	2.21	0.43
1:A:951:ARG:HG3	2:B:55:TYR:CE1	2.54	0.43
1:C:110:ARG:NH2	10:C:1117:HOH:O	2.40	0.43
1:C:318:TYR:CE2	1:C:639:GLY:HA3	2.55	0.42
1:A:171:ASN:HA	1:A:269:ASP:OD1	2.20	0.42
1:C:635:ALA:HB2	1:C:665:PHE:CD2	2.54	0.42
1:C:60:TYR:OH	10:C:1109:HOH:O	2.21	0.42
4:A:1024:PGE:H52	4:A:1024:PGE:H3	1.71	0.42
1:C:33:VAL:HG23	10:C:1310:HOH:O	2.20	0.42
1:C:902:LYS:NZ	6:C:1007:EDO:O2	2.52	0.42
1:A:791:LEU:O	1:A:810:PRO:HA	2.20	0.41
1:A:904:HIS:CB	6:A:1004:EDO:H22	2.51	0.41
1:A:646[B]:ASP:CG	10:A:1102:HOH:O	2.58	0.41
1:A:110:ARG:HH11	1:A:261:TYR:HD1	1.69	0.41
7:A:1012:PG4:H42	7:A:1012:PG4:H22	1.73	0.41
1:C:458:LYS:HG2	1:C:525:TRP:HB3	2.02	0.41
1:A:158:LEU:HB2	1:A:170:VAL:HB	2.02	0.41
1:A:73:ALA:HB2	1:A:92:GLN:HG2	2.03	0.40
1:C:424:ASN:OD1	1:C:451:ASP:HB3	2.21	0.40
1:C:724:PHE:CE2	6:C:1003:EDO:H22	2.56	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	859/977 (88%)	833 (97%)	26 (3%)	0	100	100
1	C	860/977 (88%)	834 (97%)	26 (3%)	0	100	100
2	B	85/547 (16%)	80 (94%)	4 (5%)	1 (1%)	13	4
2	D	85/547 (16%)	82 (96%)	3 (4%)	0	100	100
All	All	1889/3048 (62%)	1829 (97%)	59 (3%)	1 (0%)	51	45

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	43	THR

### 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	748/846 (88%)	736 (98%)	12 (2%)	62	59
1	C	735/846 (87%)	722 (98%)	13 (2%)	59	55
2	B	66/478 (14%)	63 (96%)	3 (4%)	27	20
2	D	69/478 (14%)	65 (94%)	4 (6%)	20	11
All	All	1618/2648 (61%)	1586 (98%)	32 (2%)	55	51

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	LEU
1	A	168	LEU
1	A	259	LYS
1	A	370	THR
1	A	424	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	446	ASP
1	A	473	ASN
1	A	637	TRP
1	A	665	PHE
1	A	685	TRP
1	A	706	ARG
1	A	863	GLN
2	B	38	THR
2	B	78	THR
2	B	117	ARG
1	C	96	LYS
1	C	370	THR
1	C	424	ASN
1	C	426	ARG
1	C	446	ASP
1	C	500	ARG
1	C	637	TRP
1	C	665	PHE
1	C	678	GLU
1	C	706	ARG
1	C	769	MET
1	C	805	GLN
1	C	806	LYS
2	D	38	THR
2	D	58	CYS
2	D	78	THR
2	D	83	LYS

Sometimes 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 [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 57 ligands modelled in this entry, 4 are monoatomic - leaving 53 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
6	EDO	D	1605	-	3,3,3	0.45	0	2,2,2	0.45	0
5	PEG	B	605	-	6,6,6	0.48	0	5,5,5	0.49	0
8	SO4	C	1017	-	4,4,4	0.16	0	6,6,6	0.22	0
6	EDO	B	603	-	3,3,3	0.53	0	2,2,2	0.24	0
6	EDO	A	1023	-	3,3,3	0.39	0	2,2,2	0.59	0
4	PGE	A	1002	-	9,9,9	0.40	0	8,8,8	0.28	0
6	EDO	A	1020	-	3,3,3	0.43	0	2,2,2	0.46	0
6	EDO	C	1008	-	3,3,3	0.53	0	2,2,2	0.26	0
8	SO4	A	1025	-	4,4,4	0.13	0	6,6,6	0.12	0
5	PEG	C	1012	-	6,6,6	0.48	0	5,5,5	0.31	0
6	EDO	C	1013	-	3,3,3	0.39	0	2,2,2	0.70	0
6	EDO	A	1011	-	3,3,3	0.44	0	2,2,2	0.50	0
6	EDO	A	1010	-	3,3,3	0.44	0	2,2,2	0.54	0
5	PEG	A	1013	-	6,6,6	0.49	0	5,5,5	0.31	0
6	EDO	C	1005	-	3,3,3	0.50	0	2,2,2	0.41	0
6	EDO	C	1003	-	3,3,3	0.38	0	2,2,2	0.61	0
8	SO4	C	1018	-	4,4,4	0.15	0	6,6,6	0.26	0
6	EDO	C	1014	-	3,3,3	0.48	0	2,2,2	0.27	0
6	EDO	A	1019	-	3,3,3	0.54	0	2,2,2	0.24	0
6	EDO	D	1601	-	3,3,3	0.51	0	2,2,2	1.26	0
8	SO4	C	1016	-	4,4,4	0.18	0	6,6,6	0.13	0
6	EDO	A	1005	-	3,3,3	0.53	0	2,2,2	0.27	0
5	PEG	A	1003	-	6,6,6	0.50	0	5,5,5	0.28	0
4	PGE	A	1017	-	9,9,9	0.30	0	8,8,8	0.39	0
5	PEG	A	1006	-	6,6,6	0.46	0	5,5,5	0.36	0
3	W9G	A	1001	-	24,24,24	0.78	1 (4%)	28,31,31	1.57	4 (14%)
6	EDO	A	1022	-	3,3,3	0.46	0	2,2,2	0.37	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	EDO	A	1004	-	3,3,3	0.44	0	2,2,2	0.24	0
6	EDO	C	1010	-	3,3,3	0.50	0	2,2,2	0.57	0
6	EDO	A	1018	-	3,3,3	0.54	0	2,2,2	0.17	0
6	EDO	A	1021	-	3,3,3	0.38	0	2,2,2	0.39	0
6	EDO	B	604	-	3,3,3	0.47	0	2,2,2	0.34	0
6	EDO	C	1007	-	3,3,3	0.52	0	2,2,2	0.30	0
8	SO4	A	1027	-	4,4,4	0.15	0	6,6,6	0.14	0
6	EDO	A	1015	-	3,3,3	0.52	0	2,2,2	0.58	0
6	EDO	C	1011	-	3,3,3	0.63	0	2,2,2	0.09	0
6	EDO	A	1007	-	3,3,3	0.55	0	2,2,2	0.31	0
3	W9G	C	1001	-	24,24,24	0.76	1 (4%)	28,31,31	1.62	4 (14%)
7	PG4	A	1012	-	12,12,12	0.51	0	11,11,11	0.32	0
7	PG4	C	1015	-	12,12,12	0.53	0	11,11,11	0.22	0
8	SO4	A	1029	-	4,4,4	0.14	0	6,6,6	0.06	0
8	SO4	A	1026	-	4,4,4	0.16	0	6,6,6	0.05	0
7	PG4	D	1604	-	12,12,12	0.52	0	11,11,11	0.24	0
8	SO4	A	1028	-	4,4,4	0.15	0	6,6,6	0.10	0
4	PGE	A	1024	-	9,9,9	0.35	0	8,8,8	0.33	0
5	PEG	C	1006	-	6,6,6	0.47	0	5,5,5	0.31	0
6	EDO	A	1014	-	3,3,3	0.52	0	2,2,2	0.31	0
6	EDO	A	1016	-	3,3,3	0.40	0	2,2,2	0.47	0
4	PGE	A	1008	-	9,9,9	0.30	0	8,8,8	0.34	0
6	EDO	C	1002	-	3,3,3	0.42	0	2,2,2	0.43	0
5	PEG	C	1009	-	6,6,6	0.47	0	5,5,5	0.27	0
6	EDO	A	1009	-	3,3,3	0.53	0	2,2,2	0.12	0
5	PEG	C	1004	-	6,6,6	0.47	0	5,5,5	0.24	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
6	EDO	D	1605	-	-	0/1/1/1	-
5	PEG	B	605	-	-	3/4/4/4	-
6	EDO	B	603	-	-	0/1/1/1	-
6	EDO	A	1023	-	-	0/1/1/1	-
4	PGE	A	1002	-	-	2/7/7/7	-
6	EDO	A	1020	-	-	0/1/1/1	-
6	EDO	C	1008	-	-	0/1/1/1	-
5	PEG	C	1012	-	-	2/4/4/4	-
6	EDO	C	1013	-	-	0/1/1/1	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	A	1011	-	-	0/1/1/1	-
6	EDO	A	1010	-	-	0/1/1/1	-
5	PEG	A	1013	-	-	3/4/4/4	-
6	EDO	C	1005	-	-	0/1/1/1	-
6	EDO	C	1003	-	-	1/1/1/1	-
6	EDO	C	1014	-	-	0/1/1/1	-
6	EDO	A	1019	-	-	0/1/1/1	-
6	EDO	D	1601	-	-	1/1/1/1	-
6	EDO	A	1005	-	-	1/1/1/1	-
5	PEG	A	1003	-	-	1/4/4/4	-
4	PGE	A	1017	-	-	5/7/7/7	-
5	PEG	A	1006	-	-	3/4/4/4	-
3	W9G	A	1001	-	-	7/15/38/38	0/1/1/1
6	EDO	A	1022	-	-	0/1/1/1	-
6	EDO	A	1004	-	-	0/1/1/1	-
6	EDO	C	1010	-	-	0/1/1/1	-
6	EDO	A	1018	-	-	1/1/1/1	-
6	EDO	A	1021	-	-	1/1/1/1	-
6	EDO	B	604	-	-	1/1/1/1	-
6	EDO	C	1007	-	-	0/1/1/1	-
6	EDO	A	1015	-	-	0/1/1/1	-
6	EDO	C	1011	-	-	0/1/1/1	-
6	EDO	A	1007	-	-	0/1/1/1	-
3	W9G	C	1001	-	-	7/15/38/38	0/1/1/1
7	PG4	A	1012	-	-	4/10/10/10	-
7	PG4	C	1015	-	-	5/10/10/10	-
7	PG4	D	1604	-	-	6/10/10/10	-
4	PGE	A	1024	-	-	4/7/7/7	-
5	PEG	C	1006	-	-	3/4/4/4	-
6	EDO	A	1014	-	-	0/1/1/1	-
6	EDO	A	1016	-	-	1/1/1/1	-
4	PGE	A	1008	-	-	3/7/7/7	-
6	EDO	C	1002	-	-	1/1/1/1	-
5	PEG	C	1009	-	-	0/4/4/4	-
6	EDO	A	1009	-	-	0/1/1/1	-
5	PEG	C	1004	-	-	3/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1001	W9G	O3-C2	-2.04	1.40	1.44
3	A	1001	W9G	O3-C2	-2.00	1.41	1.44

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1001	W9G	C16-C5-N1	5.09	118.93	109.66
3	A	1001	W9G	C16-C5-N1	4.22	117.35	109.66
3	C	1001	W9G	C17-C16-C5	-3.83	105.40	111.02
3	A	1001	W9G	C4-C5-N1	3.82	120.57	112.11
3	C	1001	W9G	C4-C5-C16	3.63	117.09	111.38
3	A	1001	W9G	C17-C16-C5	-3.62	105.72	111.02
3	A	1001	W9G	C4-C5-C16	3.07	116.21	111.38
3	C	1001	W9G	C4-C5-N1	2.61	117.88	112.11

There are no chirality outliers.

All (69) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1001	W9G	C4-C5-N1-C6
3	C	1001	W9G	C4-C5-N1-C6
4	A	1024	PGE	C3-C4-O3-C5
7	A	1012	PG4	C4-C3-O2-C2
4	A	1008	PGE	O3-C5-C6-O4
3	C	1001	W9G	C11-C10-C9-C8
7	C	1015	PG4	O2-C3-C4-O3
5	A	1006	PEG	O1-C1-C2-O2
5	B	605	PEG	C4-C3-O2-C2
4	A	1008	PGE	O2-C3-C4-O3
7	C	1015	PG4	O3-C5-C6-O4
7	D	1604	PG4	O2-C3-C4-O3
3	A	1001	W9G	C12-C13-C14-O4
4	A	1002	PGE	O3-C5-C6-O4
5	C	1006	PEG	O1-C1-C2-O2
3	A	1001	W9G	N1-C6-C7-C8
7	D	1604	PG4	C4-C3-O2-C2
3	A	1001	W9G	C11-C10-C9-C8
5	A	1003	PEG	O2-C3-C4-O4
5	A	1006	PEG	O2-C3-C4-O4
5	B	605	PEG	O2-C3-C4-O4
6	A	1005	EDO	O1-C1-C2-O2
6	A	1016	EDO	O1-C1-C2-O2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	C	1001	W9G	C6-C7-C8-C9
3	A	1001	W9G	C11-C12-C13-C14
3	C	1001	W9G	C12-C13-C14-O4
3	C	1001	W9G	C11-C12-C13-C14
5	A	1013	PEG	O1-C1-C2-O2
4	A	1024	PGE	O2-C3-C4-O3
4	A	1017	PGE	O1-C1-C2-O2
4	A	1024	PGE	O1-C1-C2-O2
5	C	1004	PEG	O2-C3-C4-O4
5	C	1006	PEG	O2-C3-C4-O4
7	C	1015	PG4	O4-C7-C8-O5
6	C	1002	EDO	O1-C1-C2-O2
3	A	1001	W9G	C13-C14-O4-C15
7	A	1012	PG4	O3-C5-C6-O4
3	A	1001	W9G	C6-C7-C8-C9
3	C	1001	W9G	C13-C14-O4-C15
5	C	1004	PEG	O1-C1-C2-O2
4	A	1017	PGE	C3-C4-O3-C5
7	D	1604	PG4	C5-C6-O4-C7
4	A	1008	PGE	C1-C2-O2-C3
7	C	1015	PG4	C4-C3-O2-C2
4	A	1002	PGE	C4-C3-O2-C2
7	A	1012	PG4	C1-C2-O2-C3
7	C	1015	PG4	C5-C6-O4-C7
4	A	1017	PGE	C6-C5-O3-C4
5	B	605	PEG	O1-C1-C2-O2
5	C	1012	PEG	C4-C3-O2-C2
5	A	1013	PEG	C4-C3-O2-C2
6	C	1003	EDO	O1-C1-C2-O2
6	D	1601	EDO	O1-C1-C2-O2
7	D	1604	PG4	C8-C7-O4-C6
7	D	1604	PG4	O1-C1-C2-O2
4	A	1017	PGE	O2-C3-C4-O3
6	A	1018	EDO	O1-C1-C2-O2
5	C	1006	PEG	C1-C2-O2-C3
5	C	1012	PEG	O2-C3-C4-O4
5	A	1013	PEG	O2-C3-C4-O4
3	C	1001	W9G	N1-C6-C7-C8
5	A	1006	PEG	C1-C2-O2-C3
7	A	1012	PG4	O2-C3-C4-O3
7	D	1604	PG4	O3-C5-C6-O4
4	A	1024	PGE	O3-C5-C6-O4

*Continued on next page...*

*Continued from previous page...*

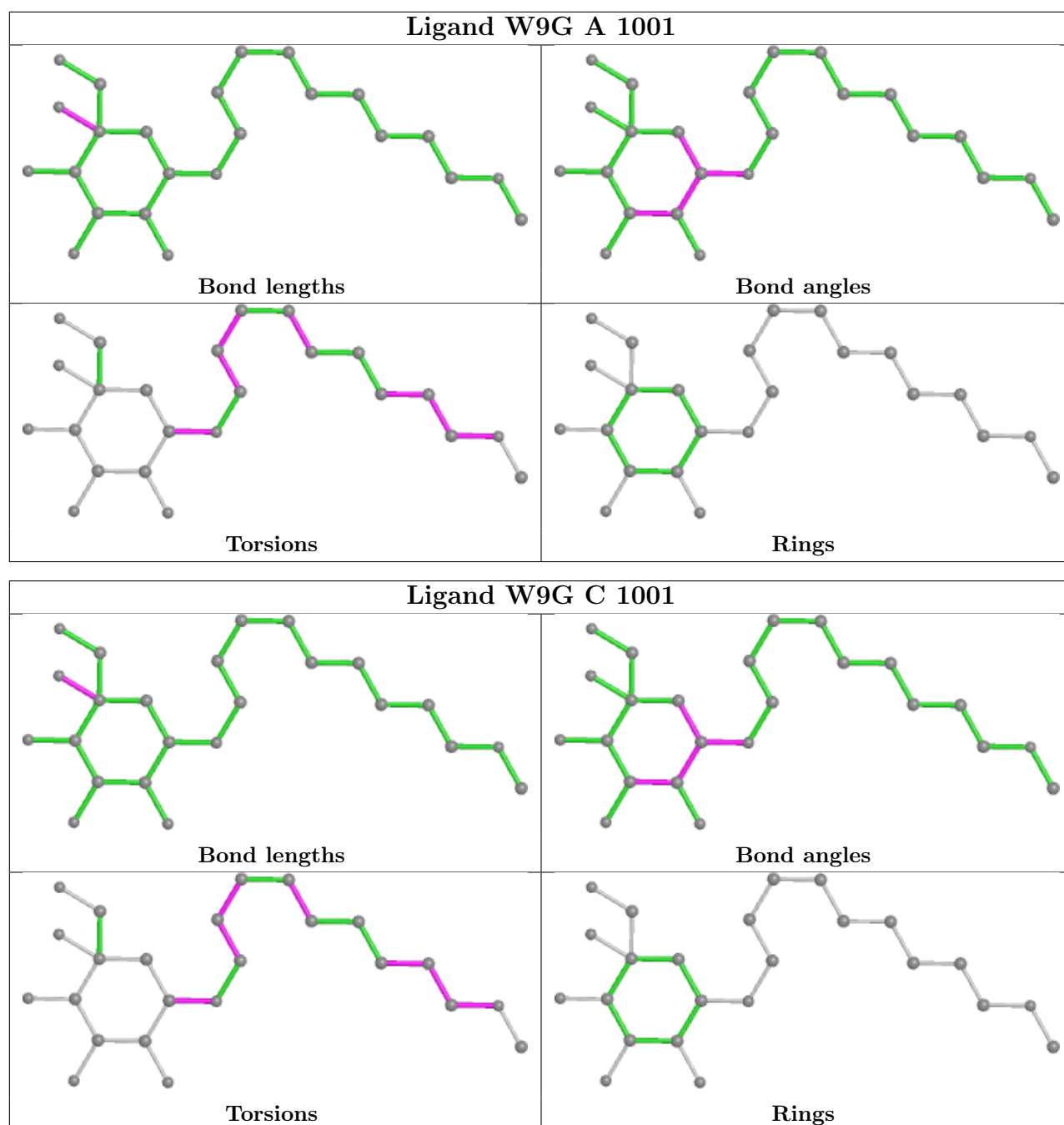
Mol	Chain	Res	Type	Atoms
5	C	1004	PEG	C1-C2-O2-C3
6	B	604	EDO	O1-C1-C2-O2
4	A	1017	PGE	C1-C2-O2-C3
6	A	1021	EDO	O1-C1-C2-O2

There are no ring outliers.

18 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	605	PEG	1	0
6	B	603	EDO	1	0
6	A	1023	EDO	1	0
5	C	1012	PEG	1	0
5	A	1013	PEG	1	0
6	C	1003	EDO	1	0
8	C	1018	SO4	1	0
6	C	1014	EDO	1	0
4	A	1017	PGE	2	0
6	A	1004	EDO	2	0
6	C	1010	EDO	1	0
6	A	1021	EDO	1	0
6	C	1007	EDO	1	0
6	A	1015	EDO	1	0
7	A	1012	PG4	2	0
7	D	1604	PG4	1	0
8	A	1028	SO4	1	0
4	A	1024	PGE	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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

### 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	853/977 (87%)	0.12	55 (6%) 19 19	22, 33, 56, 88	0
1	C	856/977 (87%)	0.16	59 (6%) 16 17	22, 37, 76, 117	0
2	B	87/547 (15%)	1.08	25 (28%) 0 0	30, 48, 86, 93	0
2	D	87/547 (15%)	1.10	27 (31%) 0 0	30, 50, 89, 96	0
All	All	1883/3048 (61%)	0.23	166 (8%) 10 10	22, 36, 74, 117	0

All (166) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	81	GLY	7.6
2	B	39	CYS	7.0
2	D	82	TYR	6.5
1	A	183	ALA	6.5
1	A	248	TRP	6.0
2	D	32	GLU	5.9
2	B	43	THR	5.8
2	D	80	THR	5.6
1	C	128	LEU	5.2
2	D	31	TYR	5.0
1	A	110	ARG	4.8
2	B	82	TYR	4.8
2	D	39	CYS	4.6
2	D	43	THR	4.5
2	B	84	PRO	4.4
1	C	143	ALA	4.4
1	C	141	THR	4.3
2	B	41	ASP	4.3
1	C	66	THR	4.3
1	C	132	GLY	4.3
2	B	117	ARG	4.2

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	247	ALA	4.2
2	B	80	THR	4.1
1	C	140	LEU	4.0
2	D	84	PRO	4.0
1	C	136	ASN	4.0
1	A	622	LEU	3.9
1	A	658	LEU	3.8
1	C	165	SER	3.8
1	A	33	VAL	3.8
2	D	116	CYS	3.7
2	B	81	GLY	3.7
1	C	69	LEU	3.7
1	A	636	VAL	3.7
1	C	156	PHE	3.7
1	C	370	THR	3.5
1	A	637	TRP	3.5
1	C	129	SER	3.5
2	D	100	CYS	3.5
1	C	135	ASP	3.5
1	C	184	PRO	3.5
1	C	82	VAL	3.5
2	D	78	THR	3.4
2	B	38	THR	3.4
1	C	85	VAL	3.4
1	A	34	ASP	3.4
1	A	251	THR	3.4
1	C	67	LEU	3.3
2	B	111	VAL	3.3
1	C	153	ALA	3.3
1	A	370	THR	3.3
2	B	85	LEU	3.3
1	C	63	LEU	3.3
2	B	116	CYS	3.2
2	B	40	LEU	3.2
2	B	79	ASN	3.2
1	C	81	GLU	3.2
1	C	155	PRO	3.2
1	C	83	THR	3.2
2	B	78	THR	3.2
2	B	31	TYR	3.1
1	C	79	ILE	3.1
1	C	142	VAL	3.1

*Continued on next page...*



*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	164	ARG	3.1
1	C	131	SER	3.0
1	A	665	PHE	3.0
2	D	83	LYS	3.0
1	A	626	PHE	3.0
1	C	138	VAL	3.0
2	D	79	ASN	3.0
1	A	663	LEU	3.0
2	D	117	ARG	2.9
1	C	56	GLY	2.9
1	A	667	GLY	2.9
1	A	254	THR	2.9
1	C	57	LEU	2.9
2	D	85	LEU	2.9
1	C	70	GLY	2.9
2	D	114	ASN	2.9
1	C	133	ARG	2.9
1	A	562	TRP	2.8
1	C	808	HIS	2.8
1	A	635	ALA	2.8
2	B	37	PHE	2.8
2	D	113	GLU	2.8
2	D	111	VAL	2.8
2	B	86	TYR	2.8
1	A	317	LEU	2.8
1	A	666	CYS	2.8
1	A	261	TYR	2.8
1	C	127	ARG	2.7
2	B	42	GLY	2.7
2	B	115	THR	2.7
2	D	38	THR	2.7
1	C	149	ILE	2.7
2	D	44	ALA	2.7
1	A	109	ARG	2.7
1	C	152	THR	2.7
2	B	100	CYS	2.7
1	C	58	SER	2.6
1	A	253	LYS	2.6
2	D	42	GLY	2.6
1	C	34	ASP	2.6
1	A	164	ARG	2.6
1	A	321	VAL	2.6

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	245	PRO	2.6
1	C	137	SER	2.6
2	D	45	THR	2.6
1	A	621	VAL	2.5
1	C	64	LEU	2.5
2	B	32	GLU	2.5
1	A	246	GLY	2.5
1	A	891	GLY	2.5
2	D	115	THR	2.5
1	A	319	GLY	2.5
2	B	44	ALA	2.5
1	A	923	ALA	2.4
2	D	37	PHE	2.4
1	C	350	ASN	2.4
1	A	694	PHE	2.4
1	A	944	GLU	2.4
1	A	181	GLN	2.4
1	C	84	LYS	2.4
2	B	112	CYS	2.4
1	C	126	ALA	2.3
1	C	148	LYS	2.3
1	C	154	GLN	2.3
1	A	516	ASP	2.3
1	A	662	GLY	2.3
1	C	343	THR	2.3
1	A	249	GLU	2.3
2	D	77	CYS	2.3
1	A	625	ALA	2.3
1	A	108	PRO	2.3
1	C	254	THR	2.3
1	C	68	GLN	2.2
1	A	301	LEU	2.2
1	A	661	VAL	2.2
2	B	36	PRO	2.2
1	C	151	LEU	2.2
1	A	449	TRP	2.1
1	C	60	TYR	2.1
1	A	416	LEU	2.1
1	A	517	GLY	2.1
1	A	623	SER	2.1
1	A	668	ALA	2.1
1	A	329	PHE	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	C	247	ALA	2.1
2	D	33	GLU	2.1
1	A	656	LEU	2.1
1	C	161	LEU	2.1
1	A	320	SER	2.1
1	A	282	PRO	2.1
1	C	124	PRO	2.1
1	C	330	HIS	2.1
1	C	318	TYR	2.0
1	C	78	LEU	2.0
1	A	323	VAL	2.0
1	A	561	VAL	2.0
1	A	620	PHE	2.0
1	C	626	PHE	2.0
2	D	41	ASP	2.0
1	A	488	ILE	2.0
1	C	150	ILE	2.0
1	A	70	GLY	2.0
1	C	130	VAL	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 monosaccharides 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(Å <sup>2</sup> )	Q<0.9
6	EDO	A	1018	4/4	0.64	0.18	49,54,61,64	0
6	EDO	C	1008	4/4	0.69	0.18	49,52,57,60	0
6	EDO	B	603	4/4	0.77	0.28	55,56,56,64	0
7	PG4	C	1015	13/13	0.79	0.28	52,63,75,84	0

*Continued on next page...*

*Continued from previous page...*

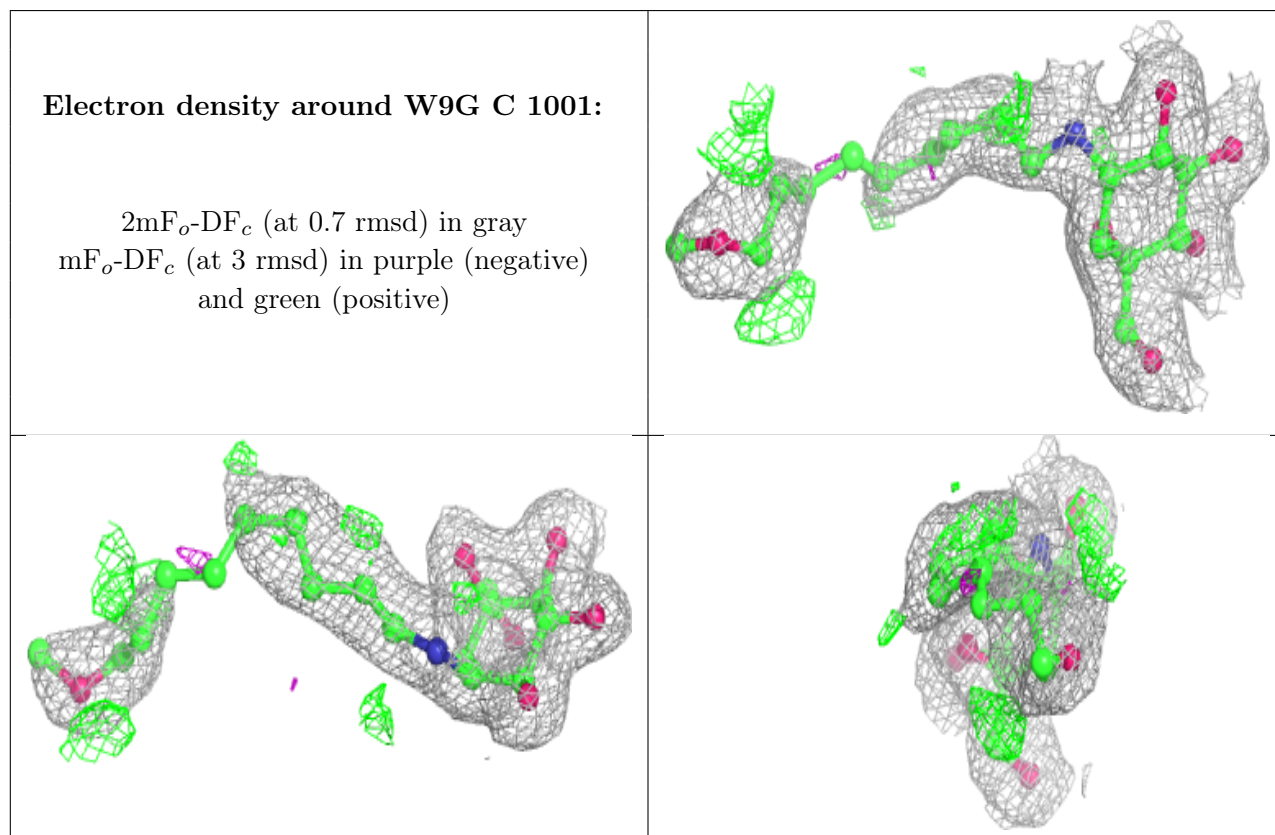
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	PG4	A	1012	13/13	0.80	0.20	52,57,63,68	0
5	PEG	B	605	7/7	0.81	0.18	43,56,61,66	0
4	PGE	A	1002	10/10	0.82	0.31	48,60,64,64	0
7	PG4	D	1604	13/13	0.83	0.14	48,61,65,74	0
6	EDO	A	1005	4/4	0.84	0.17	41,55,59,66	0
5	PEG	A	1003	7/7	0.85	0.14	54,55,57,63	0
6	EDO	D	1601	4/4	0.85	0.18	45,52,56,57	0
6	EDO	A	1014	4/4	0.85	0.43	59,59,61,72	0
5	PEG	C	1004	7/7	0.85	0.19	39,51,54,57	0
5	PEG	C	1006	7/7	0.85	0.18	57,61,70,73	0
6	EDO	A	1004	4/4	0.86	0.33	46,55,61,69	0
4	PGE	A	1008	10/10	0.86	0.16	42,56,69,76	0
8	SO4	A	1025	5/5	0.86	0.25	71,74,84,91	0
8	SO4	A	1028	5/5	0.86	0.33	78,84,97,104	0
8	SO4	A	1026	5/5	0.87	0.23	77,83,89,104	0
5	PEG	C	1009	7/7	0.88	0.21	48,57,64,65	0
4	PGE	A	1024	10/10	0.88	0.26	48,55,60,61	0
8	SO4	A	1029	5/5	0.88	0.30	98,99,117,121	0
8	SO4	C	1018	5/5	0.88	0.44	72,73,80,102	0
6	EDO	A	1009	4/4	0.89	0.17	53,57,57,61	0
6	EDO	C	1014	4/4	0.90	0.38	48,48,57,70	0
5	PEG	C	1012	7/7	0.90	0.17	45,50,59,67	0
6	EDO	C	1005	4/4	0.90	0.17	43,44,47,55	0
6	EDO	A	1020	4/4	0.90	0.33	47,49,50,57	0
6	EDO	C	1013	4/4	0.90	0.21	43,53,53,54	0
5	PEG	A	1013	7/7	0.91	0.18	48,50,61,63	0
6	EDO	D	1605	4/4	0.91	0.23	48,50,51,56	0
6	EDO	C	1010	4/4	0.91	0.16	32,34,47,49	0
6	EDO	A	1010	4/4	0.91	0.19	39,41,44,49	0
6	EDO	A	1019	4/4	0.91	0.19	35,43,47,50	0
6	EDO	A	1022	4/4	0.92	0.33	53,60,62,66	0
8	SO4	C	1016	5/5	0.92	0.13	60,65,71,84	0
6	EDO	C	1007	4/4	0.92	0.25	46,46,52,59	0
5	PEG	A	1006	7/7	0.93	0.19	43,54,60,62	0
6	EDO	B	604	4/4	0.93	0.07	54,58,59,63	0
6	EDO	A	1016	4/4	0.93	0.14	41,44,44,54	0
8	SO4	A	1027	5/5	0.93	0.39	69,73,81,92	0
6	EDO	C	1011	4/4	0.94	0.15	33,38,40,46	0
6	EDO	A	1021	4/4	0.94	0.14	41,46,49,51	0
4	PGE	A	1017	10/10	0.94	0.23	48,53,60,62	0
6	EDO	A	1015	4/4	0.94	0.11	35,37,43,43	0
3	W9G	C	1001	24/24	0.94	0.17	23,32,69,74	0

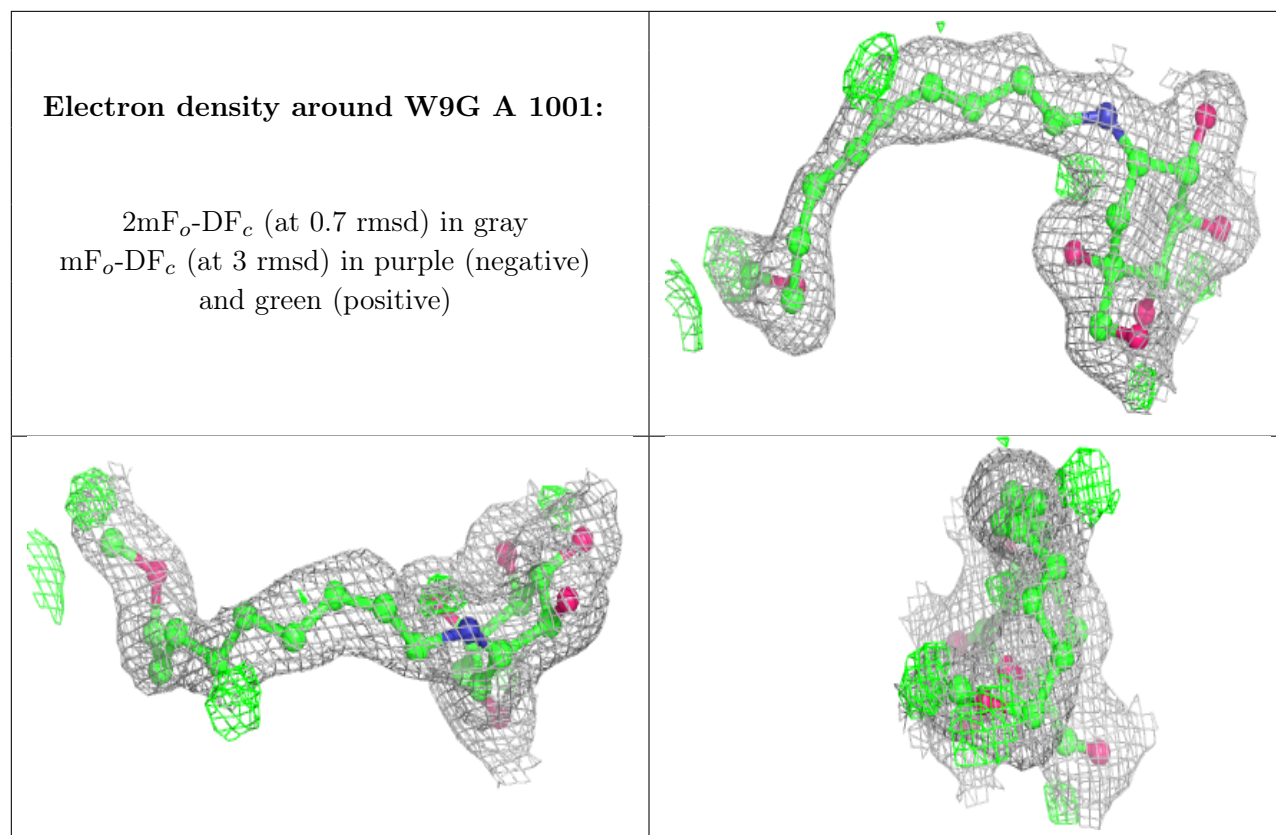
*Continued on next page...*

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	EDO	A	1007	4/4	0.95	0.21	38,42,45,54	0
3	W9G	A	1001	24/24	0.95	0.20	21,28,55,57	0
6	EDO	C	1002	4/4	0.96	0.10	45,45,48,55	0
8	SO4	C	1017	5/5	0.96	0.23	62,66,69,71	0
6	EDO	A	1023	4/4	0.96	0.14	46,48,48,50	0
9	CA	D	1602	1/1	0.96	0.07	40,40,40,40	0
9	CA	B	601	1/1	0.97	0.06	39,39,39,39	0
6	EDO	C	1003	4/4	0.97	0.12	42,47,49,54	0
6	EDO	A	1011	4/4	0.98	0.10	34,38,40,42	0
9	CA	B	602	1/1	0.99	0.06	33,33,33,33	0
9	CA	D	1603	1/1	0.99	0.05	31,31,31,31	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.