



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 8, 2025 – 04:22 PM JST

PDB ID : 9IQB  
Title : Crystal structure of beta-glucosidase from *Acetivibrio thermocellus*  
Authors : Kamale, C.; Bhaumik, P.  
Deposited on : 2024-07-12  
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.21  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.004 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

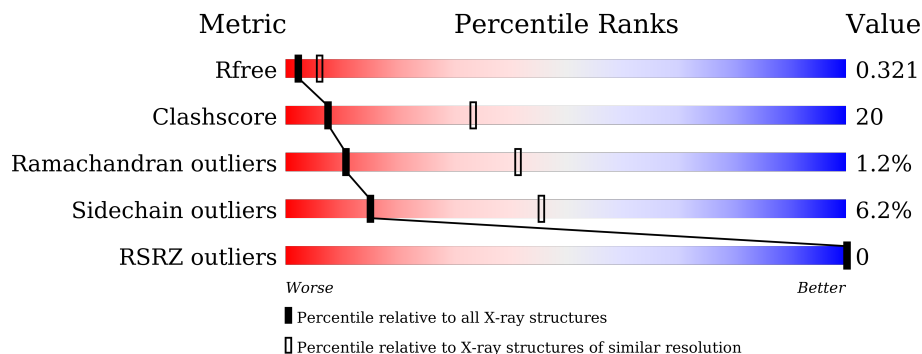
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 3.00 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))
$R_{free}$	164625	2511 (3.00-3.00)
Clashscore	180529	2866 (3.00-3.00)
Ramachandran outliers	177936	2778 (3.00-3.00)
Sidechain outliers	177891	2781 (3.00-3.00)
RSRZ outliers	164620	2523 (3.00-3.00)

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	456	 69% 26% ..
1	B	456	 69% 27% ..
1	C	456	 72% 24% ..
1	D	456	 73% 23% ..
1	E	456	 70% 27% ..
1	F	456	 70% 25% ..

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Mol	Chain	Length	Quality of chain
1	G	456	 64% 30% 5% .
1	H	456	 65% 30% . .
1	I	456	 62% 32% 5% .
1	J	456	 66% 28% 5% .
1	K	456	 59% 34% 6% .
1	L	456	 53% 38% 7% .

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 44214 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 Beta-glucosidase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	B	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	C	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	D	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	E	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	F	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	G	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	H	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	I	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	J	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	K	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0
1	L	449	Total 3658	C 2369	N 601	O 682	S 6	0	0	0

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	449	LEU	-	expression tag	UNP P26208
A	450	GLU	-	expression tag	UNP P26208
A	451	HIS	-	expression tag	UNP P26208
A	452	HIS	-	expression tag	UNP P26208
A	453	HIS	-	expression tag	UNP P26208

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Chain	Residue	Modelled	Actual	Comment	Reference
A	454	HIS	-	expression tag	UNP P26208
A	455	HIS	-	expression tag	UNP P26208
A	456	HIS	-	expression tag	UNP P26208
B	449	LEU	-	expression tag	UNP P26208
B	450	GLU	-	expression tag	UNP P26208
B	451	HIS	-	expression tag	UNP P26208
B	452	HIS	-	expression tag	UNP P26208
B	453	HIS	-	expression tag	UNP P26208
B	454	HIS	-	expression tag	UNP P26208
B	455	HIS	-	expression tag	UNP P26208
B	456	HIS	-	expression tag	UNP P26208
C	449	LEU	-	expression tag	UNP P26208
C	450	GLU	-	expression tag	UNP P26208
C	451	HIS	-	expression tag	UNP P26208
C	452	HIS	-	expression tag	UNP P26208
C	453	HIS	-	expression tag	UNP P26208
C	454	HIS	-	expression tag	UNP P26208
C	455	HIS	-	expression tag	UNP P26208
C	456	HIS	-	expression tag	UNP P26208
D	449	LEU	-	expression tag	UNP P26208
D	450	GLU	-	expression tag	UNP P26208
D	451	HIS	-	expression tag	UNP P26208
D	452	HIS	-	expression tag	UNP P26208
D	453	HIS	-	expression tag	UNP P26208
D	454	HIS	-	expression tag	UNP P26208
D	455	HIS	-	expression tag	UNP P26208
D	456	HIS	-	expression tag	UNP P26208
E	449	LEU	-	expression tag	UNP P26208
E	450	GLU	-	expression tag	UNP P26208
E	451	HIS	-	expression tag	UNP P26208
E	452	HIS	-	expression tag	UNP P26208
E	453	HIS	-	expression tag	UNP P26208
E	454	HIS	-	expression tag	UNP P26208
E	455	HIS	-	expression tag	UNP P26208
E	456	HIS	-	expression tag	UNP P26208
F	449	LEU	-	expression tag	UNP P26208
F	450	GLU	-	expression tag	UNP P26208
F	451	HIS	-	expression tag	UNP P26208
F	452	HIS	-	expression tag	UNP P26208
F	453	HIS	-	expression tag	UNP P26208
F	454	HIS	-	expression tag	UNP P26208
F	455	HIS	-	expression tag	UNP P26208

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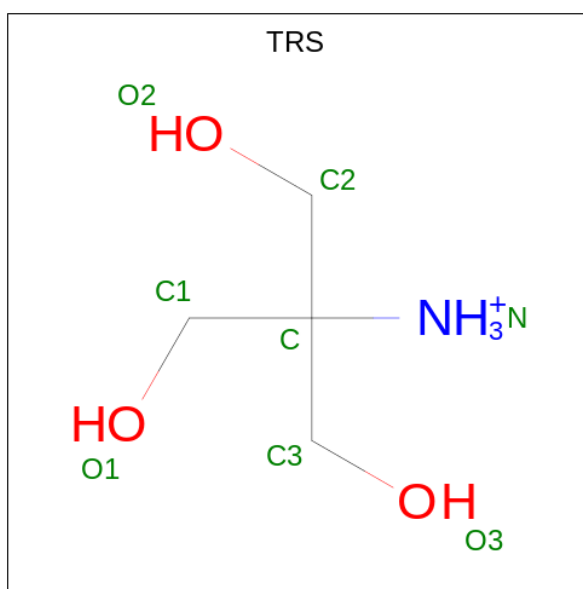
Chain	Residue	Modelled	Actual	Comment	Reference
F	456	HIS	-	expression tag	UNP P26208
G	449	LEU	-	expression tag	UNP P26208
G	450	GLU	-	expression tag	UNP P26208
G	451	HIS	-	expression tag	UNP P26208
G	452	HIS	-	expression tag	UNP P26208
G	453	HIS	-	expression tag	UNP P26208
G	454	HIS	-	expression tag	UNP P26208
G	455	HIS	-	expression tag	UNP P26208
G	456	HIS	-	expression tag	UNP P26208
H	449	LEU	-	expression tag	UNP P26208
H	450	GLU	-	expression tag	UNP P26208
H	451	HIS	-	expression tag	UNP P26208
H	452	HIS	-	expression tag	UNP P26208
H	453	HIS	-	expression tag	UNP P26208
H	454	HIS	-	expression tag	UNP P26208
H	455	HIS	-	expression tag	UNP P26208
H	456	HIS	-	expression tag	UNP P26208
I	449	LEU	-	expression tag	UNP P26208
I	450	GLU	-	expression tag	UNP P26208
I	451	HIS	-	expression tag	UNP P26208
I	452	HIS	-	expression tag	UNP P26208
I	453	HIS	-	expression tag	UNP P26208
I	454	HIS	-	expression tag	UNP P26208
I	455	HIS	-	expression tag	UNP P26208
I	456	HIS	-	expression tag	UNP P26208
J	449	LEU	-	expression tag	UNP P26208
J	450	GLU	-	expression tag	UNP P26208
J	451	HIS	-	expression tag	UNP P26208
J	452	HIS	-	expression tag	UNP P26208
J	453	HIS	-	expression tag	UNP P26208
J	454	HIS	-	expression tag	UNP P26208
J	455	HIS	-	expression tag	UNP P26208
J	456	HIS	-	expression tag	UNP P26208
K	449	LEU	-	expression tag	UNP P26208
K	450	GLU	-	expression tag	UNP P26208
K	451	HIS	-	expression tag	UNP P26208
K	452	HIS	-	expression tag	UNP P26208
K	453	HIS	-	expression tag	UNP P26208
K	454	HIS	-	expression tag	UNP P26208
K	455	HIS	-	expression tag	UNP P26208
K	456	HIS	-	expression tag	UNP P26208
L	449	LEU	-	expression tag	UNP P26208

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Chain	Residue	Modelled	Actual	Comment	Reference
L	450	GLU	-	expression tag	UNP P26208
L	451	HIS	-	expression tag	UNP P26208
L	452	HIS	-	expression tag	UNP P26208
L	453	HIS	-	expression tag	UNP P26208
L	454	HIS	-	expression tag	UNP P26208
L	455	HIS	-	expression tag	UNP P26208
L	456	HIS	-	expression tag	UNP P26208

- Molecule 2 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			8	4	1	3		
2	B	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	24	Total	O	0	0
			24	24		
3	B	38	Total	O	0	0
			38	38		
3	C	27	Total	O	0	0
			27	27		

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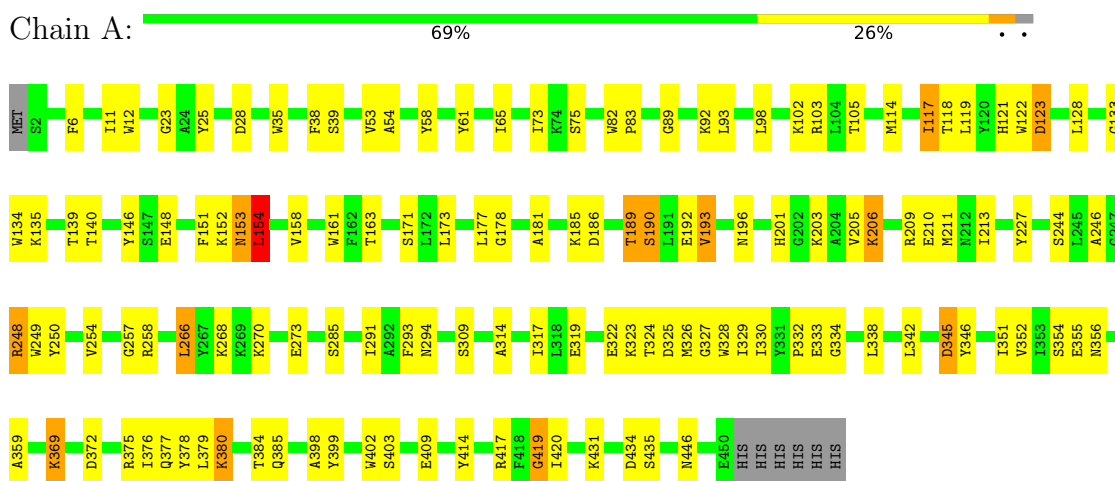
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
3	D	29	Total O 29 29	0	0
3	E	26	Total O 26 26	0	0
3	F	24	Total O 24 24	0	0
3	G	23	Total O 23 23	0	0
3	H	17	Total O 17 17	0	0
3	I	25	Total O 25 25	0	0
3	J	25	Total O 25 25	0	0
3	K	27	Total O 27 27	0	0
3	L	17	Total O 17 17	0	0



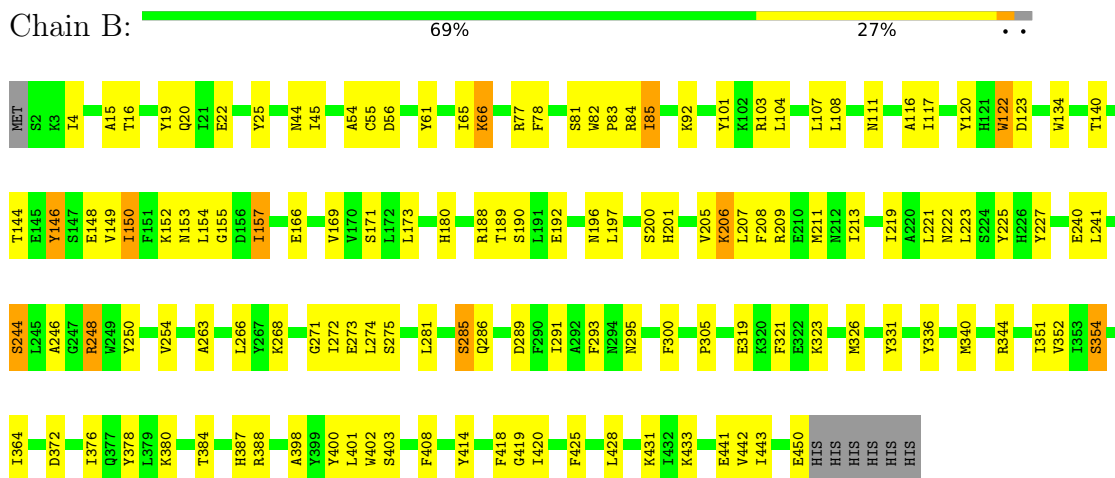
### 3 Residue-property plots [i](#)

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: Beta-glucosidase A

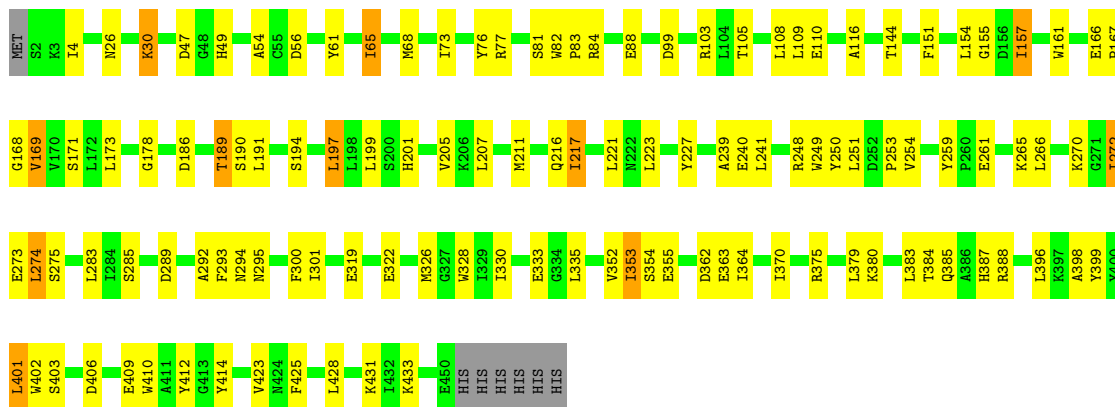


- Molecule 1: Beta-glucosidase A



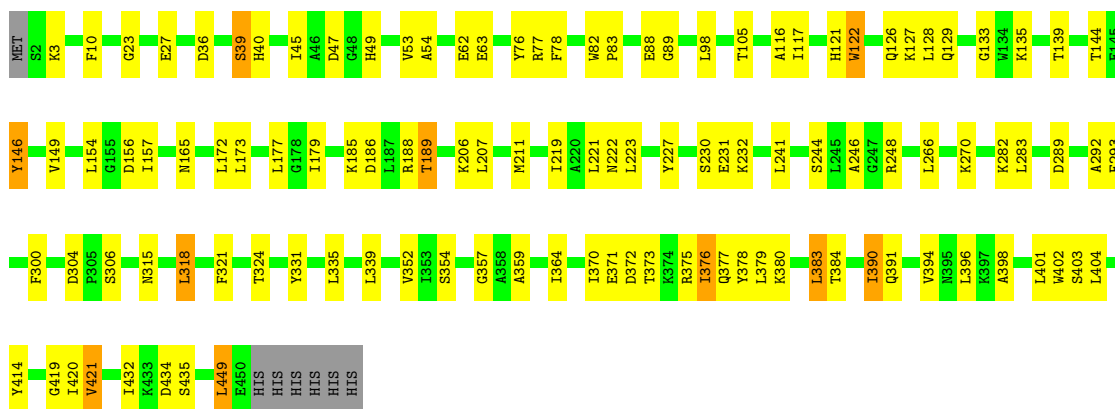
- Molecule 1: Beta-glucosidase A





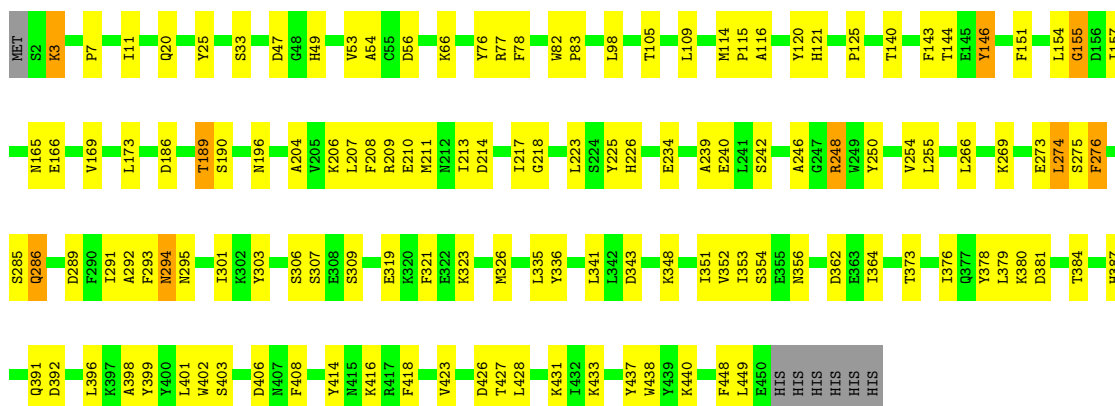
- Molecule 1: Beta-glucosidase A

Chain D: 73% 23% ..



- Molecule 1: Beta-glucosidase A

Chain E: 70% 27% ..

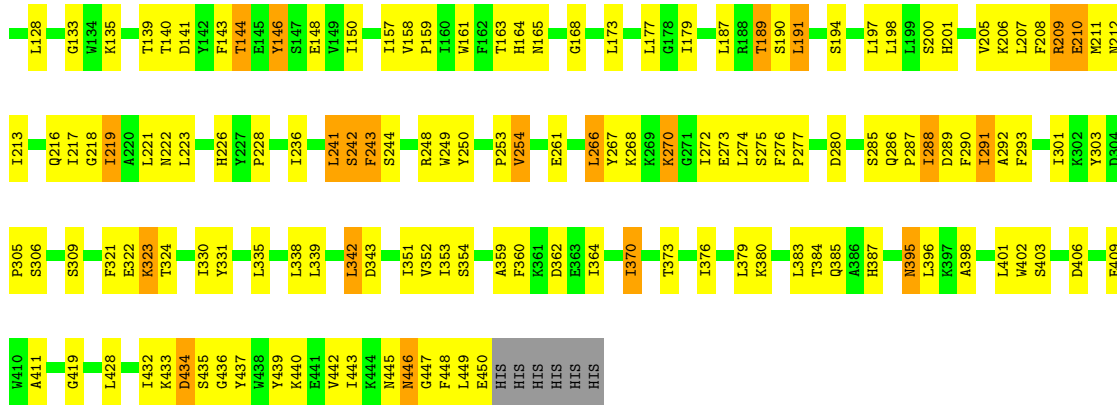


- Molecule 1: Beta-glucosidase A

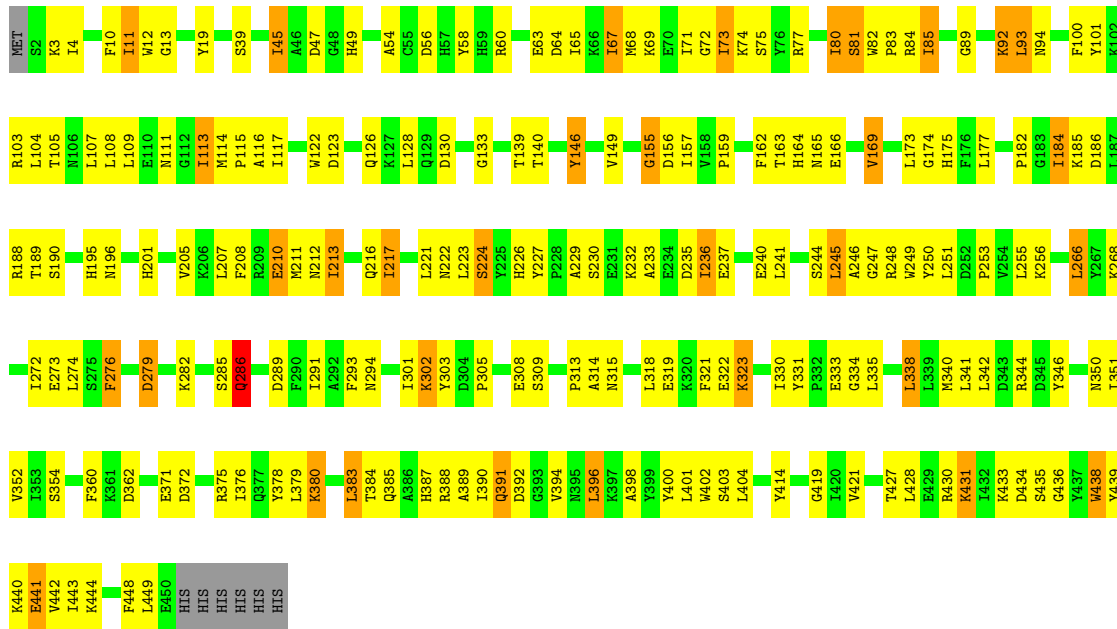
Chain F: 70% 25% ..







• Molecule 1: Beta-glucosidase A



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.93Å 158.62Å 158.91Å 60.12° 88.19° 87.48°	Depositor
Resolution (Å)	34.99 – 3.00 34.99 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.1 (34.99-3.00) 82.1 (34.99-3.00)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.43 (at 3.00Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.300 , 0.350 0.311 , 0.321	Depositor DCC
$R_{free}$ test set	8755 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.9	Xtrriage
Anisotropy	0.039	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 12.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.075 for h,l,-k+1 0.075 for h,k-l,k 0.045 for h,-k+1,-k 0.045 for h,-l,k-l 0.094 for h,-k,-l 0.028 for -h,k,k-l 0.009 for -h,-k+1,l 0.009 for -h,l,k 0.012 for -h,-l,-k 0.030 for -h,-k,-k+1 0.011 for -h,k-l,-l	Xtrriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	44214	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 25.89 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9141e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: TRS

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	0.65	0/3760	0.79	0/5088
1	B	0.65	0/3760	0.78	0/5088
1	C	0.65	0/3760	0.77	0/5088
1	D	0.65	0/3760	0.79	0/5088
1	E	0.65	0/3760	0.81	0/5088
1	F	0.65	0/3760	0.80	0/5088
1	G	0.65	0/3760	0.78	0/5088
1	H	0.65	0/3760	0.79	0/5088
1	I	0.65	0/3760	0.78	0/5088
1	J	0.65	0/3760	0.78	0/5088
1	K	0.65	0/3760	0.78	0/5088
1	L	0.66	0/3760	0.80	0/5088
All	All	0.65	0/45120	0.79	0/61056

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	D	0	1
1	H	0	2
1	I	0	3
1	L	0	1
All	All	0	8

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	325	ASP	Peptide
1	D	419	GLY	Peptide
1	H	241	LEU	Peptide
1	H	449	LEU	Peptide
1	I	112	GLY	Peptide

## 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	3658	0	3558	117	0
1	B	3658	0	3558	111	0
1	C	3658	0	3558	111	0
1	D	3658	0	3558	95	0
1	E	3658	0	3558	103	0
1	F	3658	0	3558	123	0
1	G	3658	0	3558	168	0
1	H	3658	0	3558	155	0
1	I	3658	0	3558	158	0
1	J	3658	0	3558	141	0
1	K	3658	0	3558	220	0
1	L	3658	0	3558	238	0
2	A	8	0	12	1	0
2	B	8	0	12	1	0
3	A	24	0	0	8	0
3	B	38	0	0	28	0
3	C	27	0	0	6	0
3	D	29	0	0	5	0
3	E	26	0	0	8	0
3	F	24	0	0	8	0
3	G	23	0	0	9	0
3	H	17	0	0	5	0
3	I	25	0	0	9	0
3	J	25	0	0	14	0
3	K	27	0	0	10	0
3	L	17	0	0	6	0
All	All	44214	0	42720	1724	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 20.

The worst 5 of 1724 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:E:82:TRP:CH2	1:E:146:TYR:HB3	1.37	1.29
1:J:315:ASN:HA	1:J:318:LEU:CD1	1.69	1.23
1:A:403:SER:O	1:A:419:GLY:O	1.58	1.20
1:K:339:LEU:CA	1:K:342:LEU:HD21	1.73	1.19
1:I:199:LEU:HA	1:I:284:ILE:HD11	1.25	1.16

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	447/456 (98%)	415 (93%)	26 (6%)	6 (1%)	10	39
1	B	447/456 (98%)	418 (94%)	26 (6%)	3 (1%)	19	54
1	C	447/456 (98%)	410 (92%)	35 (8%)	2 (0%)	30	66
1	D	447/456 (98%)	417 (93%)	26 (6%)	4 (1%)	14	49
1	E	447/456 (98%)	412 (92%)	29 (6%)	6 (1%)	10	39
1	F	447/456 (98%)	420 (94%)	24 (5%)	3 (1%)	19	54
1	G	447/456 (98%)	407 (91%)	37 (8%)	3 (1%)	19	54
1	H	447/456 (98%)	409 (92%)	28 (6%)	10 (2%)	5	27
1	I	447/456 (98%)	405 (91%)	30 (7%)	12 (3%)	4	22
1	J	447/456 (98%)	414 (93%)	31 (7%)	2 (0%)	30	66
1	K	447/456 (98%)	400 (90%)	39 (9%)	8 (2%)	7	32
1	L	447/456 (98%)	406 (91%)	34 (8%)	7 (2%)	8	34
All	All	5364/5472 (98%)	4933 (92%)	365 (7%)	66 (1%)	11	41

5 of 66 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	154	LEU
1	A	420	ILE
1	D	122	TRP
1	D	373	THR
1	E	276	PHE

### 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	388/395 (98%)	370 (95%)	18 (5%)	23	56
1	B	388/395 (98%)	366 (94%)	22 (6%)	17	49
1	C	388/395 (98%)	374 (96%)	14 (4%)	30	64
1	D	388/395 (98%)	372 (96%)	16 (4%)	26	60
1	E	388/395 (98%)	373 (96%)	15 (4%)	27	61
1	F	388/395 (98%)	365 (94%)	23 (6%)	16	47
1	G	388/395 (98%)	358 (92%)	30 (8%)	10	37
1	H	388/395 (98%)	366 (94%)	22 (6%)	17	49
1	I	388/395 (98%)	363 (94%)	25 (6%)	14	44
1	J	388/395 (98%)	358 (92%)	30 (8%)	10	37
1	K	388/395 (98%)	358 (92%)	30 (8%)	10	37
1	L	388/395 (98%)	344 (89%)	44 (11%)	4	21
All	All	4656/4740 (98%)	4367 (94%)	289 (6%)	15	45

5 of 289 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	254	VAL
1	L	431	LYS
1	K	323	LYS
1	L	184	ILE

*Continued on next page...*

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Mol	Chain	Res	Type
1	F	286	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	415	ASN
1	K	356	ASN
1	J	94	ASN
1	J	387	HIS
1	L	196	ASN

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 ligands 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	TRS	B	501	-	7,7,7	0.21	0	9,9,9	0.53	0
2	TRS	A	501	-	7,7,7	0.12	0	9,9,9	0.36	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	TRS	B	501	-	-	3/9/9/9	-
2	TRS	A	501	-	-	9/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

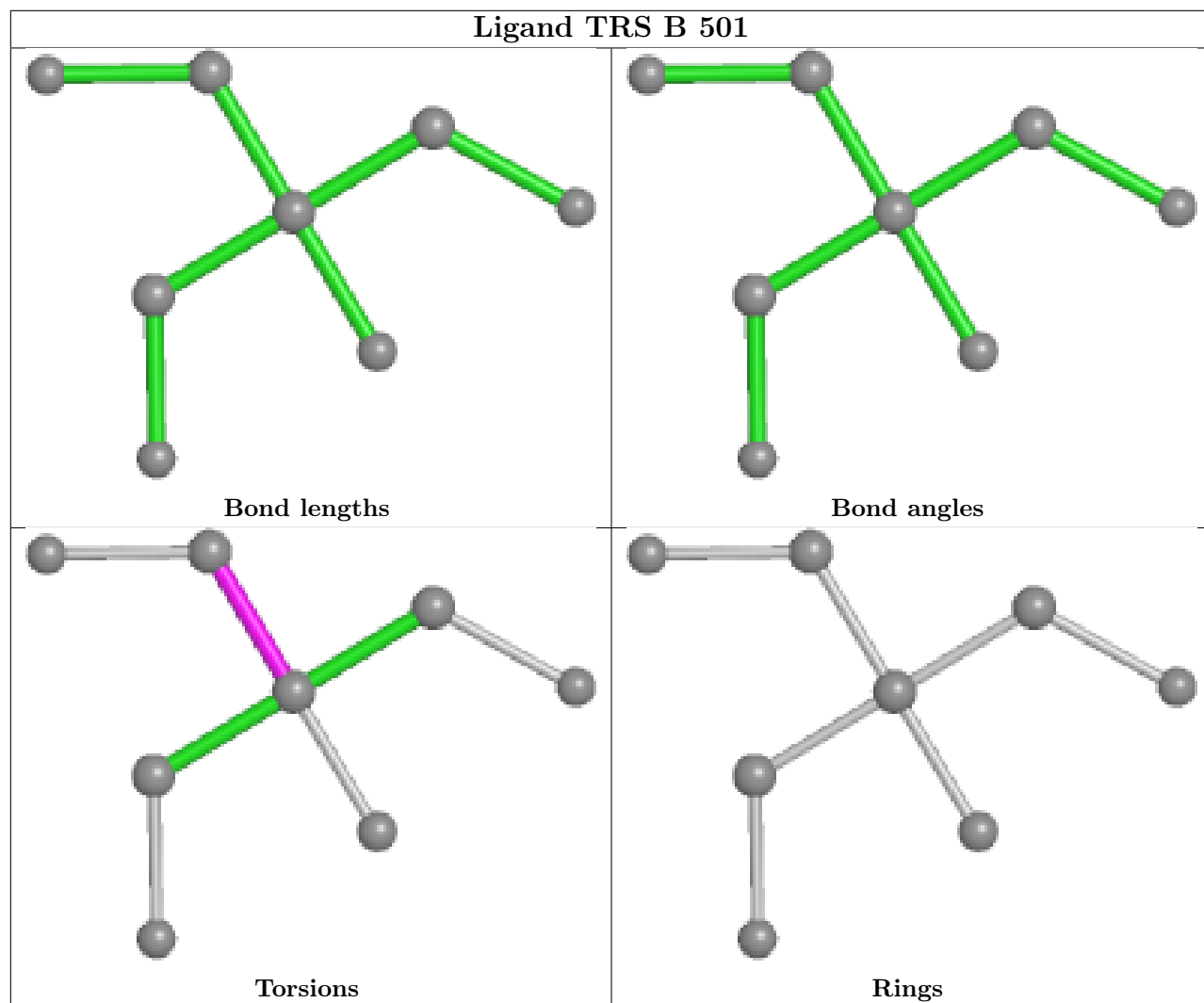
Mol	Chain	Res	Type	Atoms
2	A	501	TRS	C2-C-C1-O1
2	A	501	TRS	C3-C-C1-O1
2	A	501	TRS	N-C-C1-O1
2	A	501	TRS	C1-C-C2-O2
2	A	501	TRS	C3-C-C2-O2

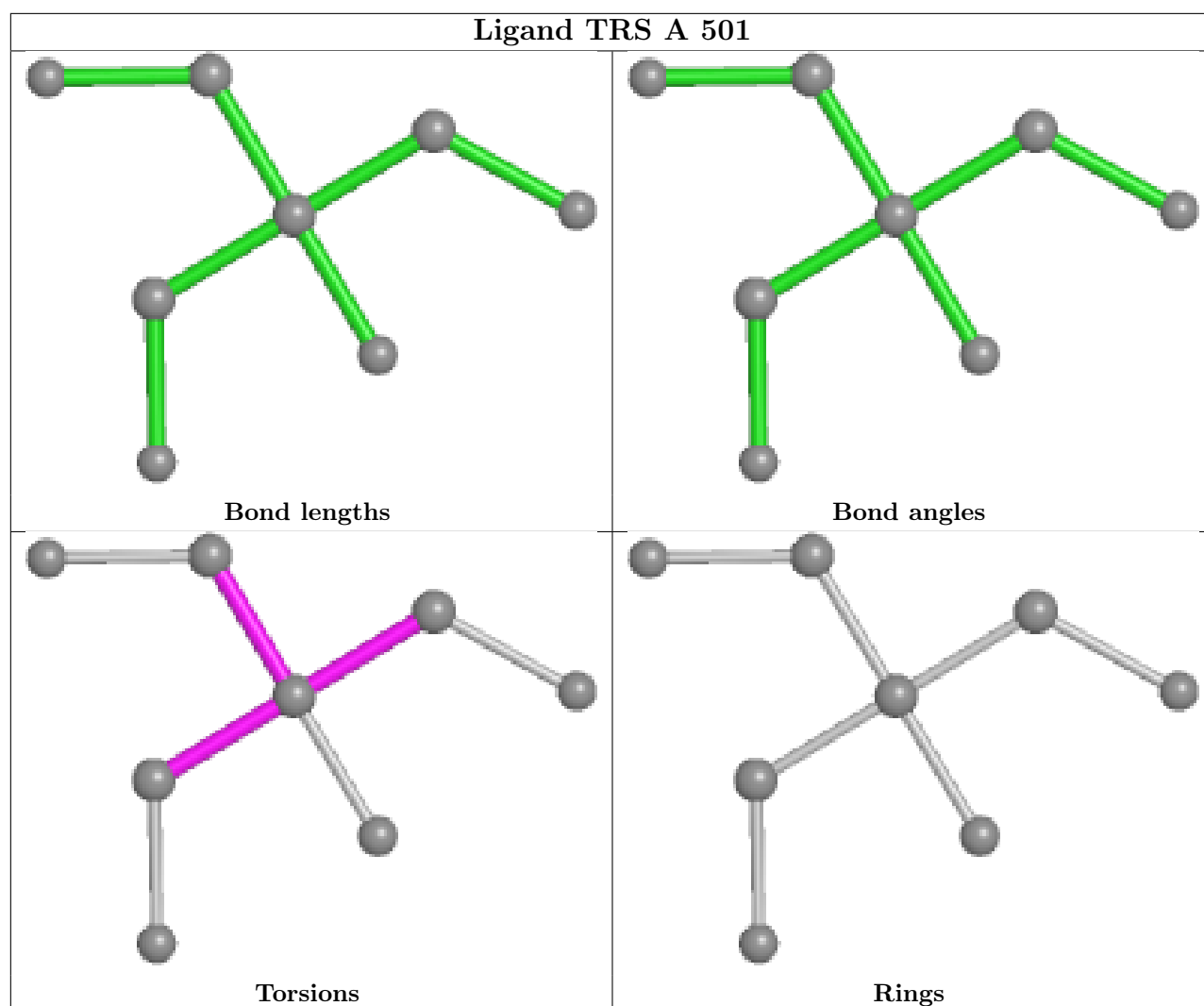
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	TRS	1	0
2	A	501	TRS	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 [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	449/456 (98%)	-1.45	0 100 100	16, 35, 58, 80	0
1	B	449/456 (98%)	-1.43	0 100 100	16, 33, 57, 74	0
1	C	449/456 (98%)	-1.44	0 100 100	19, 37, 60, 93	0
1	D	449/456 (98%)	-1.44	0 100 100	18, 42, 66, 81	0
1	E	449/456 (98%)	-1.48	0 100 100	17, 29, 46, 70	0
1	F	449/456 (98%)	-1.44	0 100 100	17, 38, 57, 81	0
1	G	449/456 (98%)	-1.42	0 100 100	19, 42, 65, 75	0
1	H	449/456 (98%)	-1.42	0 100 100	17, 42, 67, 86	0
1	I	449/456 (98%)	-1.38	0 100 100	19, 47, 69, 82	0
1	J	449/456 (98%)	-1.36	0 100 100	19, 43, 73, 100	0
1	K	449/456 (98%)	-1.33	0 100 100	21, 54, 75, 92	0
1	L	449/456 (98%)	-1.34	0 100 100	21, 52, 79, 107	0
All	All	5388/5472 (98%)	-1.41	0 100 100	16, 40, 68, 107	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](#)

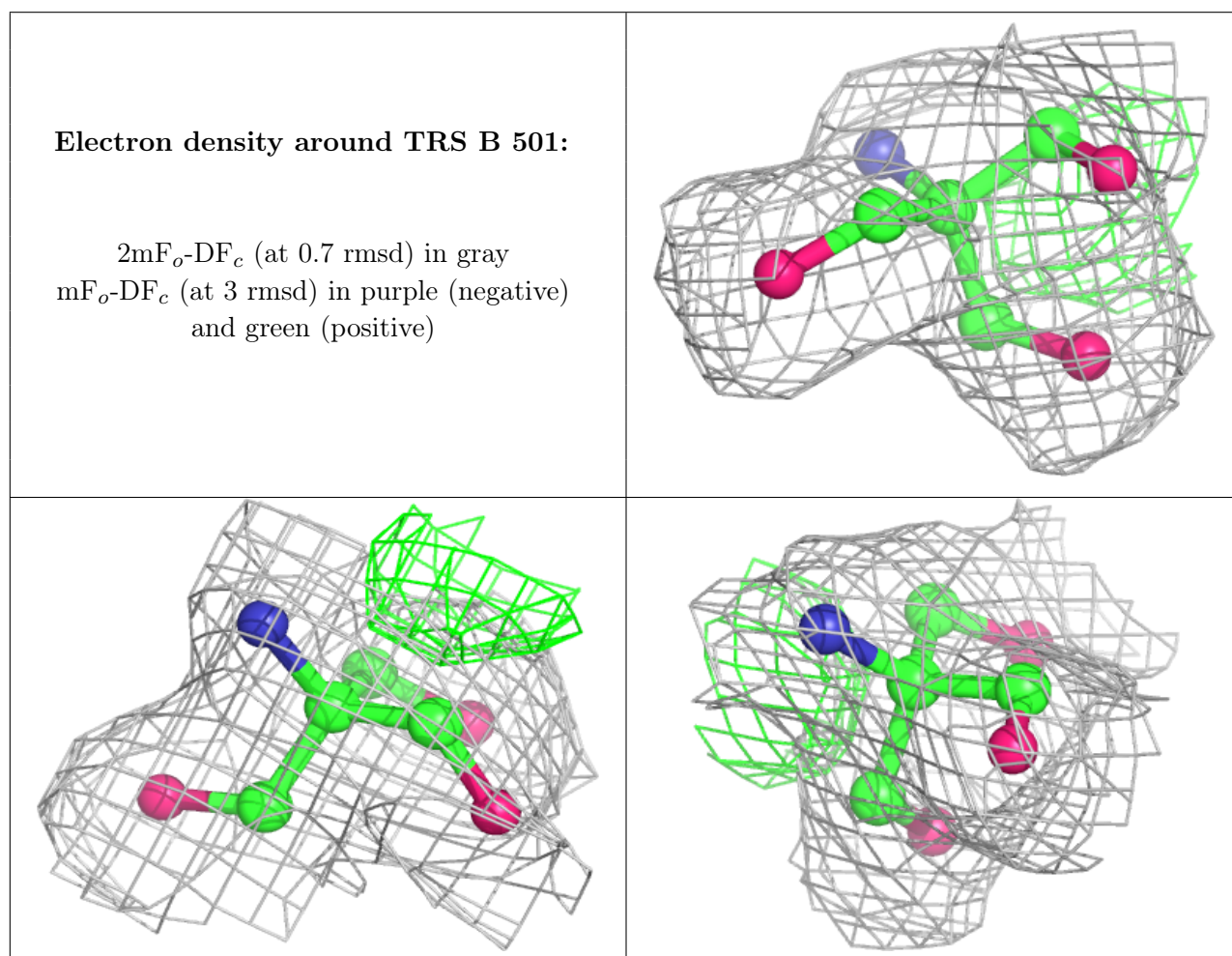
There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

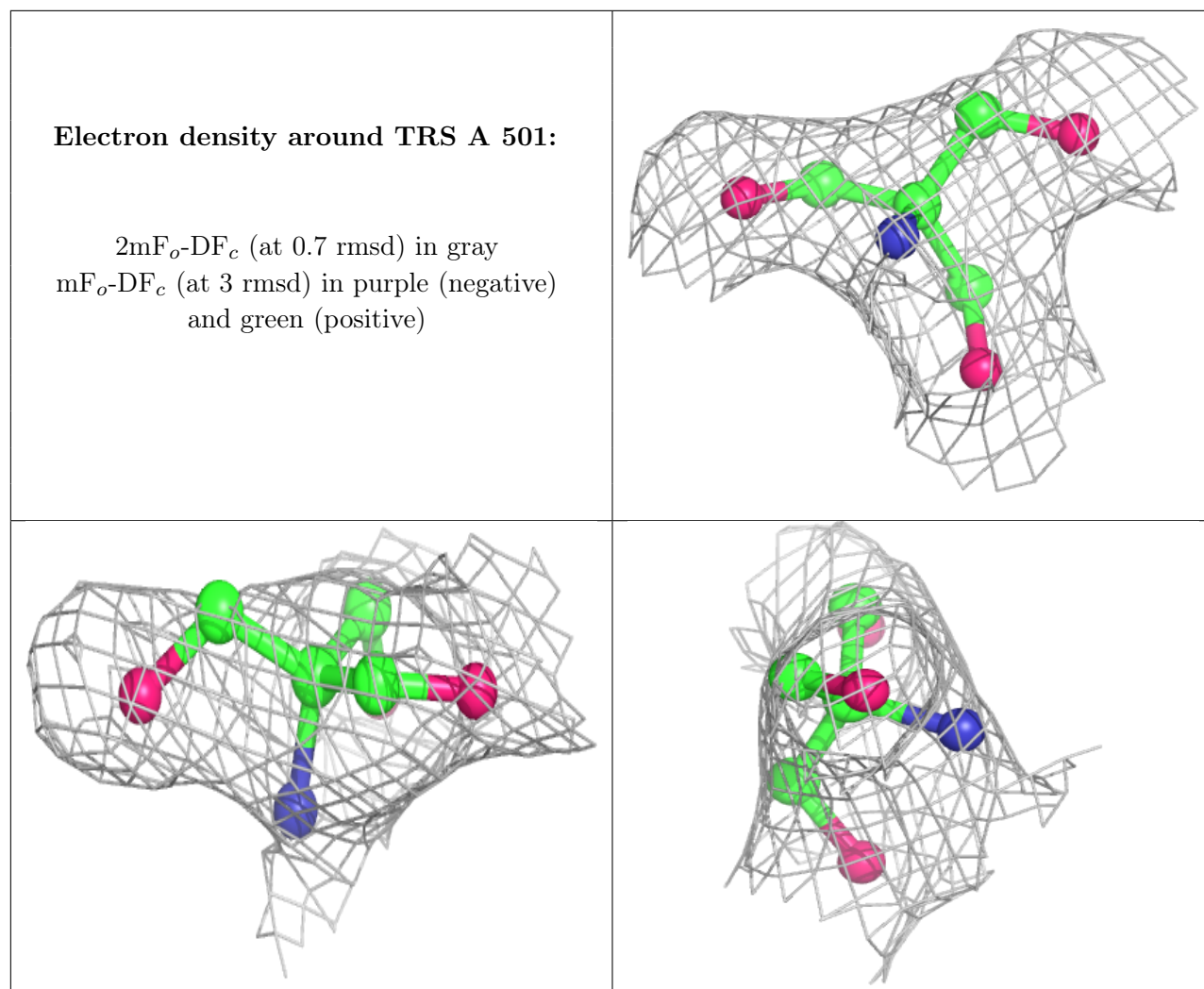
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<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
2	TRS	B	501	8/8	0.98	0.05	21,23,24,24	0
2	TRS	A	501	8/8	0.99	0.04	19,20,20,21	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.