



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2026 – 11:08 PM UTC

PDB ID : 8FAA / pdb\_00008faa  
Title : Crystal structure of Xanthomonas campestris GH35 beta-galactosidase  
Authors : Godoy, A.S.; Polikarpov, I.  
Deposited on : 2022-11-25  
Resolution : 2.50 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 : 4-5-2 with Phenix2.0  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

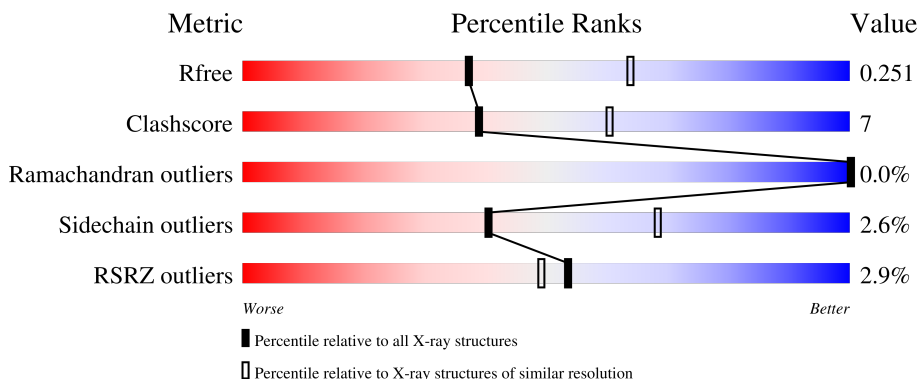
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	511	 85% 14% .
1	B	511	 2% 86% 13% .
1	C	511	 2% 86% 14% .
1	D	511	 4% 86% 12% .
1	E	511	 % 86% 13% .

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Mol	Chain	Length	Quality of chain
1	F	511	 % 85% 13%
1	G	511	 3% 85% 15%
1	H	511	 % 87% 13%
1	I	511	 4% 86% 13%
1	J	511	 3% 87% 12%
1	K	511	 4% 85% 15%
1	L	511	 5% 86% 12%
1	M	511	 3% 87% 13%
1	N	511	 5% 84% 15%
1	O	511	 7% 81% 17%
1	P	511	 2% 86% 13%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 65632 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-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	510	3921	2491	707	718	5	0	0	0
1	B	510	3921	2491	707	718	5	0	0	0
1	C	510	3921	2491	707	718	5	0	0	0
1	D	510	3921	2491	707	718	5	0	0	0
1	E	510	3921	2491	707	718	5	0	0	0
1	F	510	3921	2491	707	718	5	0	0	0
1	G	510	3921	2491	707	718	5	0	0	0
1	H	510	3921	2491	707	718	5	0	0	0
1	I	510	3921	2491	707	718	5	0	0	0
1	J	510	3921	2491	707	718	5	0	0	0
1	K	510	3921	2491	707	718	5	0	0	0
1	L	510	3921	2491	707	718	5	0	0	0
1	M	510	3921	2491	707	718	5	0	0	0
1	N	510	3921	2491	707	718	5	0	0	0
1	O	510	3921	2491	707	718	5	0	0	0
1	P	510	3921	2491	707	718	5	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	initiating methionine	UNP Q8P844
B	2	MET	-	initiating methionine	UNP Q8P844
C	2	MET	-	initiating methionine	UNP Q8P844
D	2	MET	-	initiating methionine	UNP Q8P844
E	2	MET	-	initiating methionine	UNP Q8P844
F	2	MET	-	initiating methionine	UNP Q8P844
G	2	MET	-	initiating methionine	UNP Q8P844
H	2	MET	-	initiating methionine	UNP Q8P844
I	2	MET	-	initiating methionine	UNP Q8P844
J	2	MET	-	initiating methionine	UNP Q8P844
K	2	MET	-	initiating methionine	UNP Q8P844
L	2	MET	-	initiating methionine	UNP Q8P844
M	2	MET	-	initiating methionine	UNP Q8P844
N	2	MET	-	initiating methionine	UNP Q8P844
O	2	MET	-	initiating methionine	UNP Q8P844
P	2	MET	-	initiating methionine	UNP Q8P844

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	242	Total O 242 242	0	0
2	B	157	Total O 157 157	0	0
2	C	186	Total O 186 186	0	0
2	D	186	Total O 186 186	0	0
2	E	200	Total O 200 200	0	0
2	F	203	Total O 203 203	0	0
2	G	196	Total O 196 196	0	0
2	H	188	Total O 188 188	0	0
2	I	215	Total O 215 215	0	0
2	J	198	Total O 198 198	0	0
2	K	185	Total O 185 185	0	0

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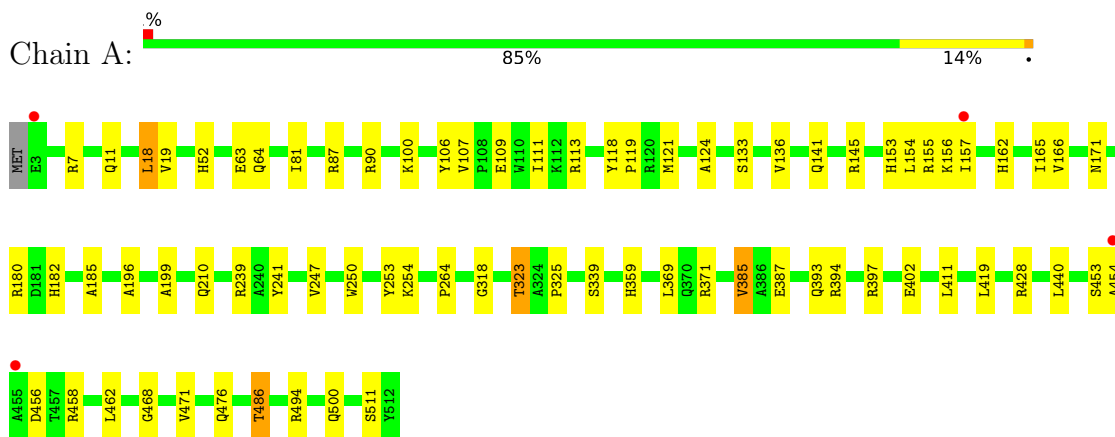
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
2	L	209	Total 209	O 209	0	0
2	M	129	Total 129	O 129	0	0
2	N	113	Total 113	O 113	0	0
2	O	94	Total 94	O 94	0	0
2	P	195	Total 195	O 195	0	0

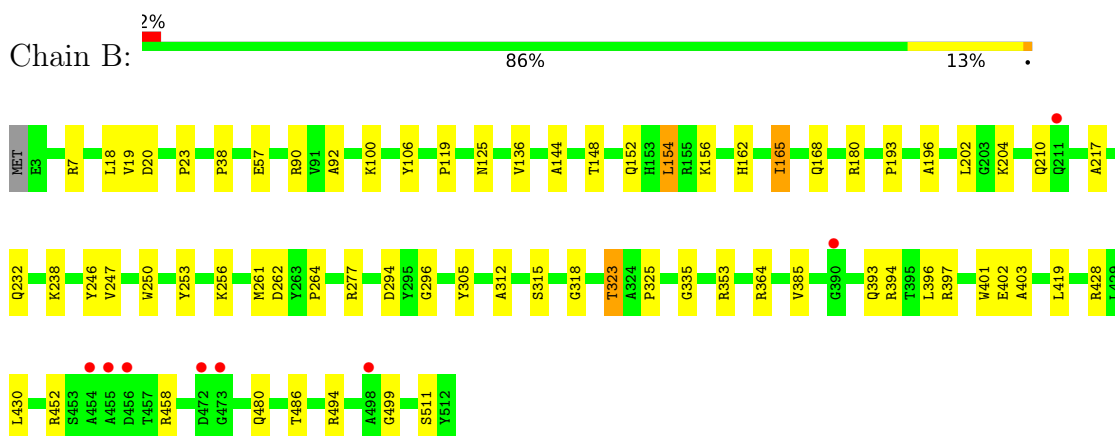
### 3 Residue-property plots [i](#)

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.

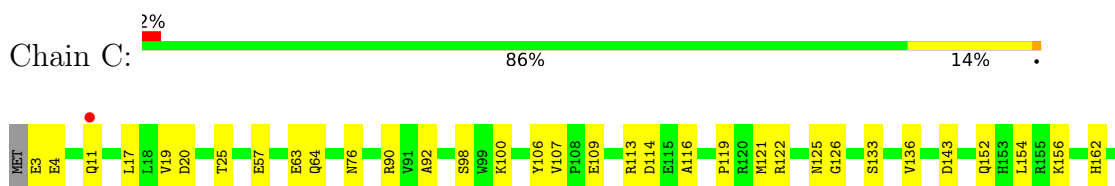
- Molecule 1: Beta-galactosidase

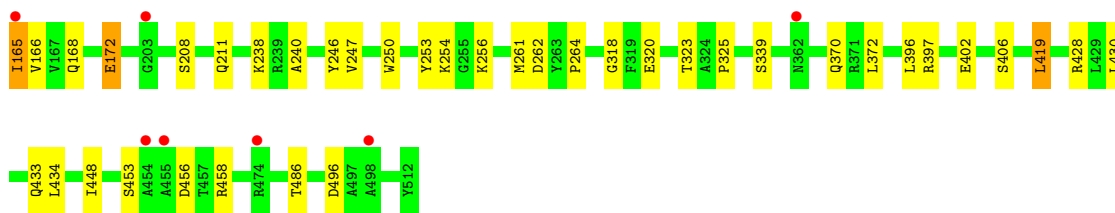


- Molecule 1: Beta-galactosidase

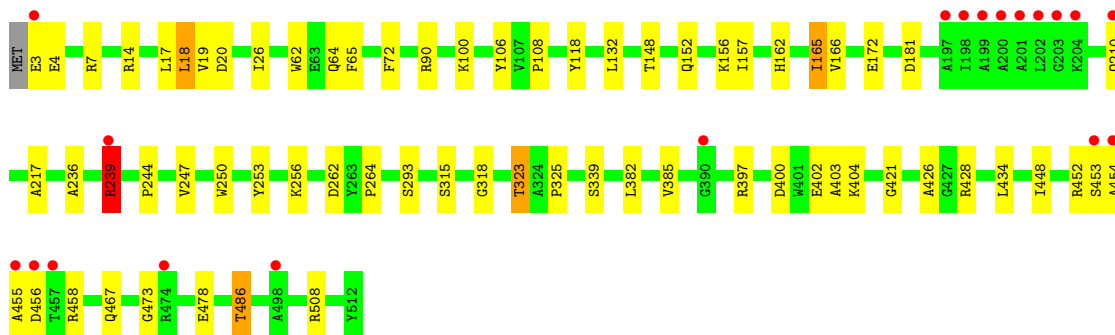
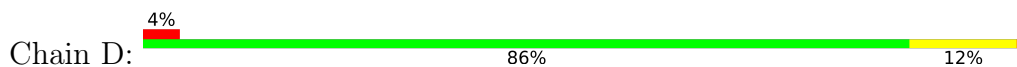


- Molecule 1: Beta-galactosidase

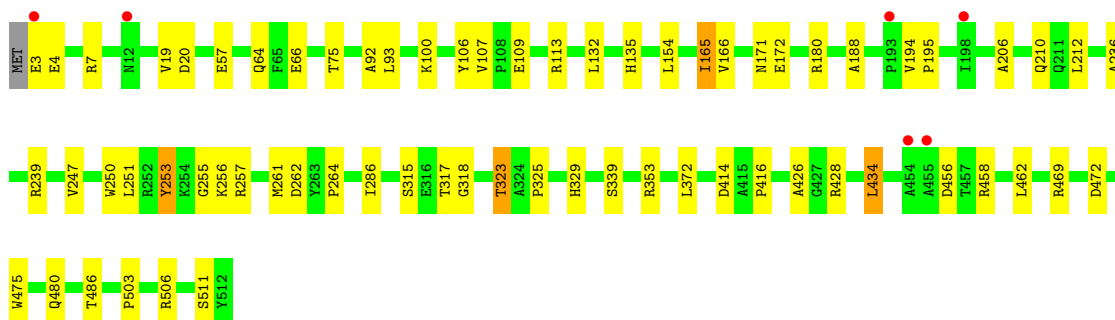
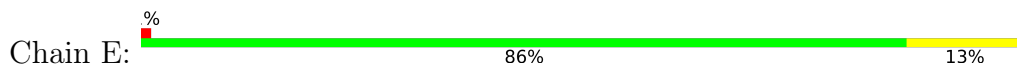




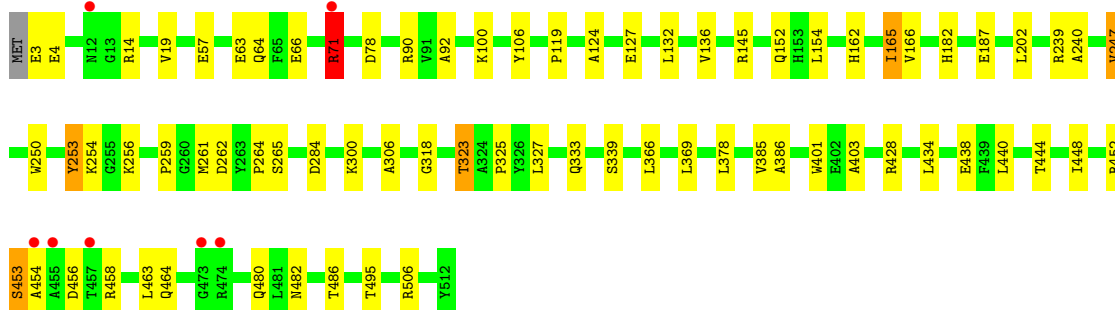
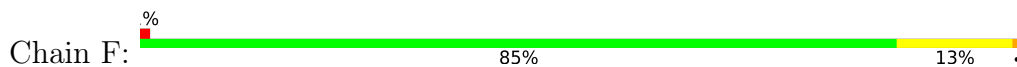
● Molecule 1: Beta-galactosidase



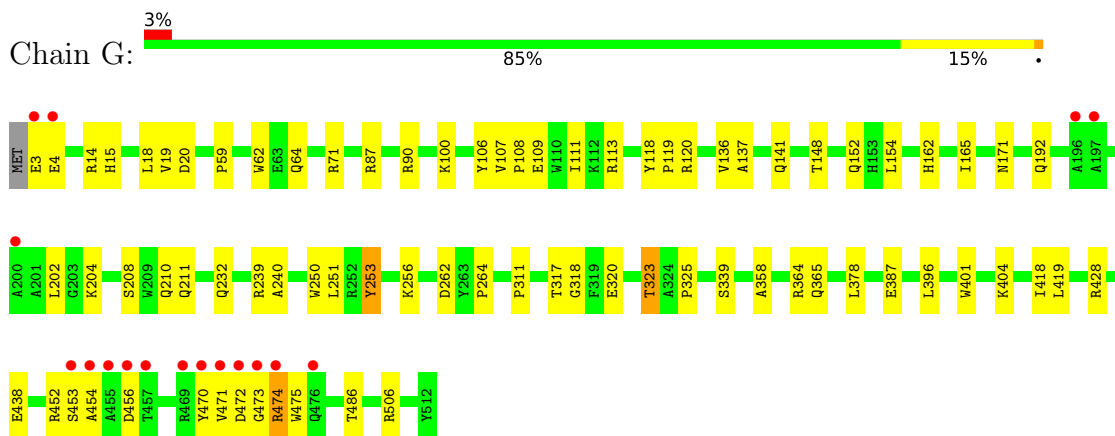
● Molecule 1: Beta-galactosidase



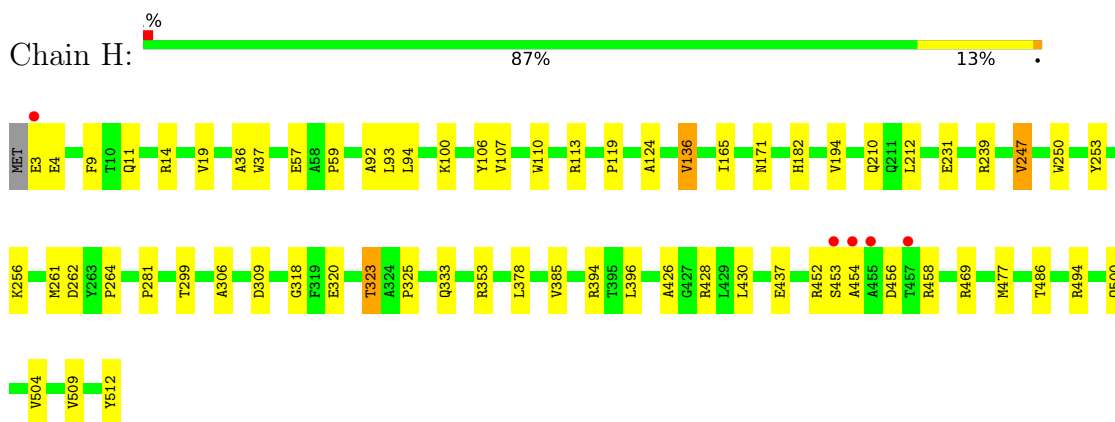
● Molecule 1: Beta-galactosidase



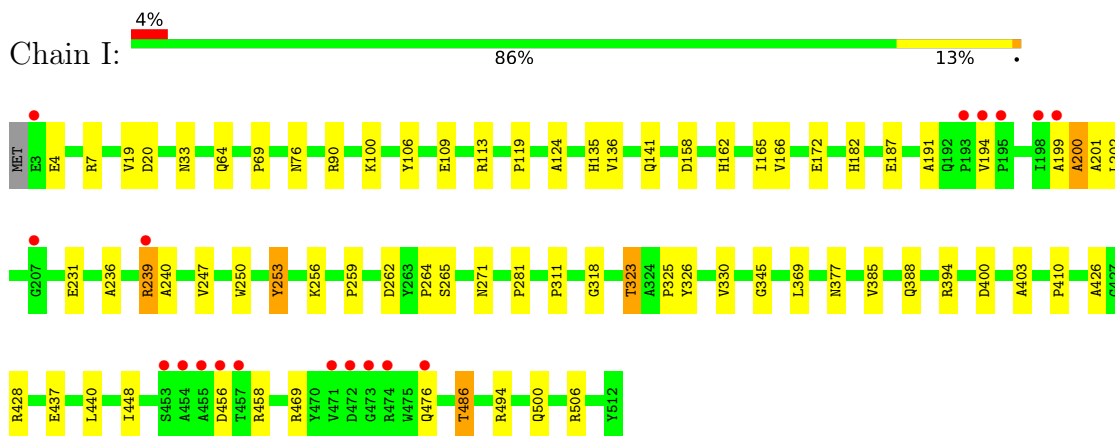
● Molecule 1: Beta-galactosidase



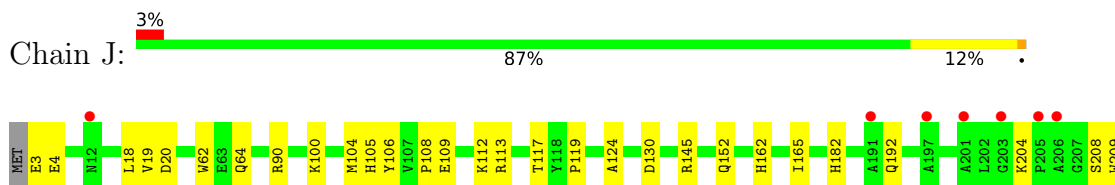
- Molecule 1: Beta-galactosidase

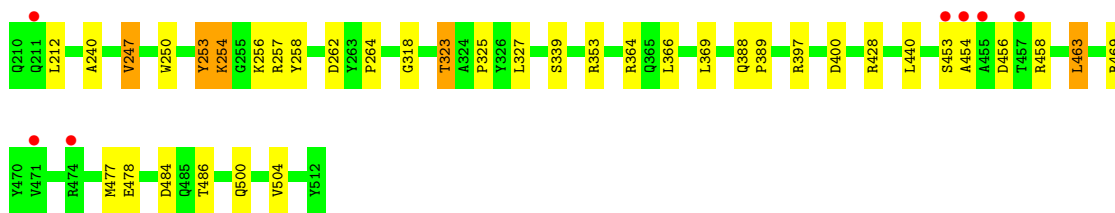


- Molecule 1: Beta-galactosidase

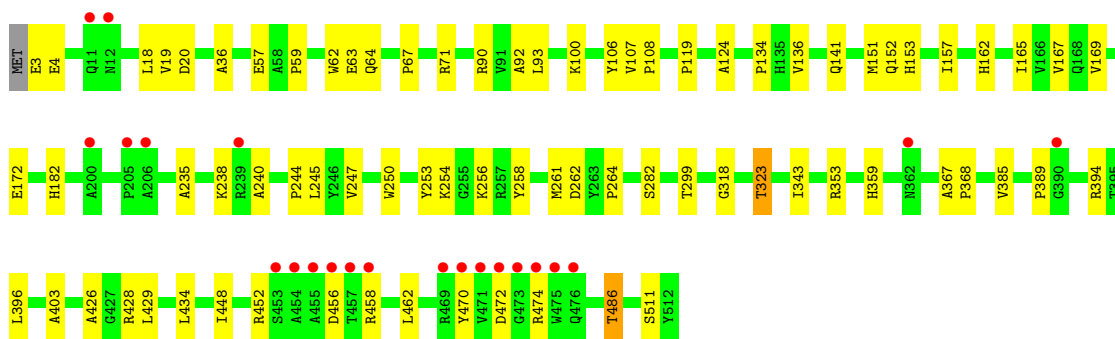
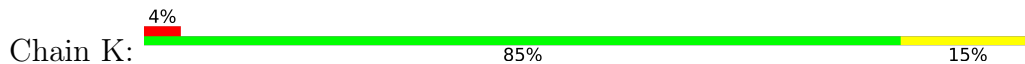


- Molecule 1: Beta-galactosidase

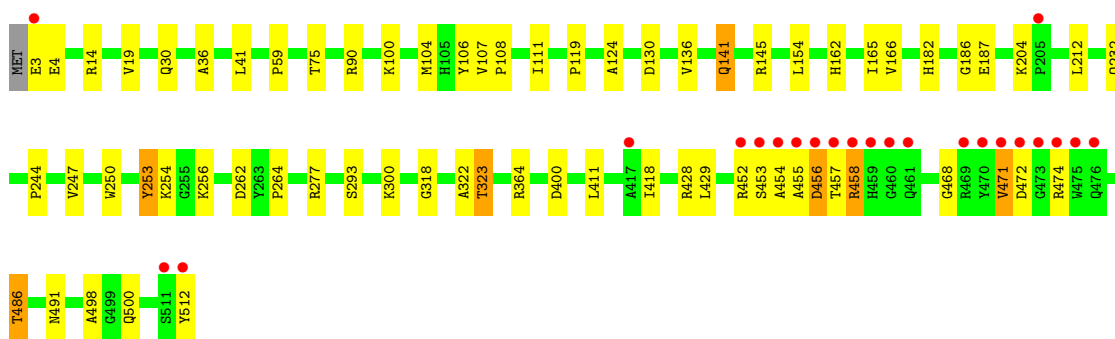
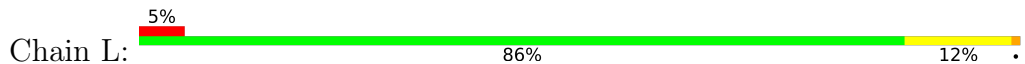




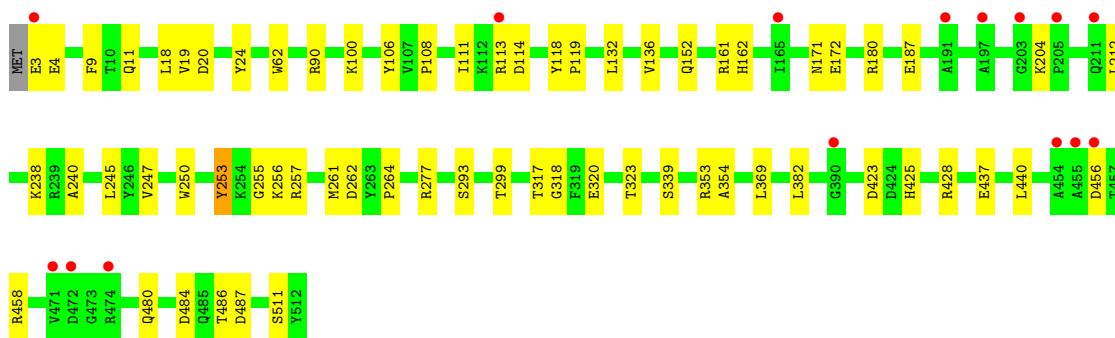
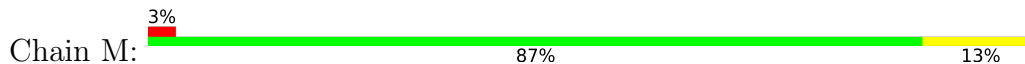
● Molecule 1: Beta-galactosidase



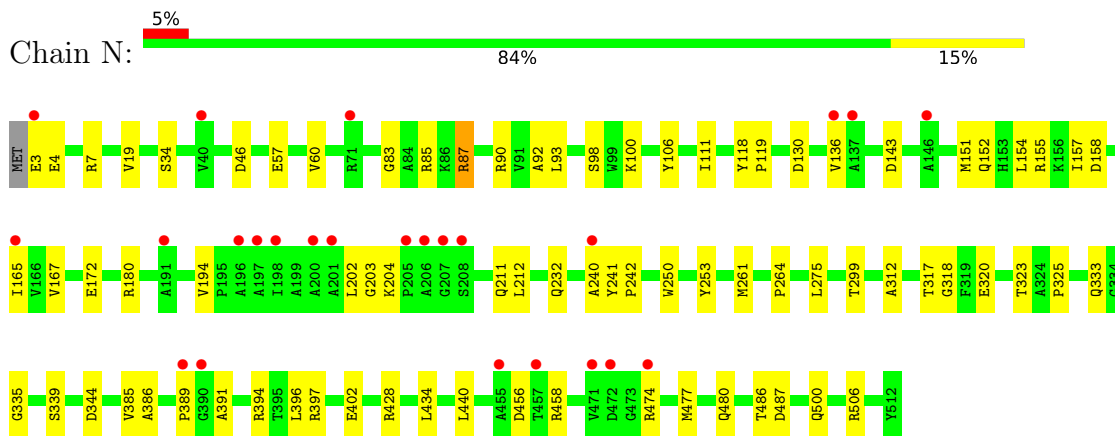
● Molecule 1: Beta-galactosidase



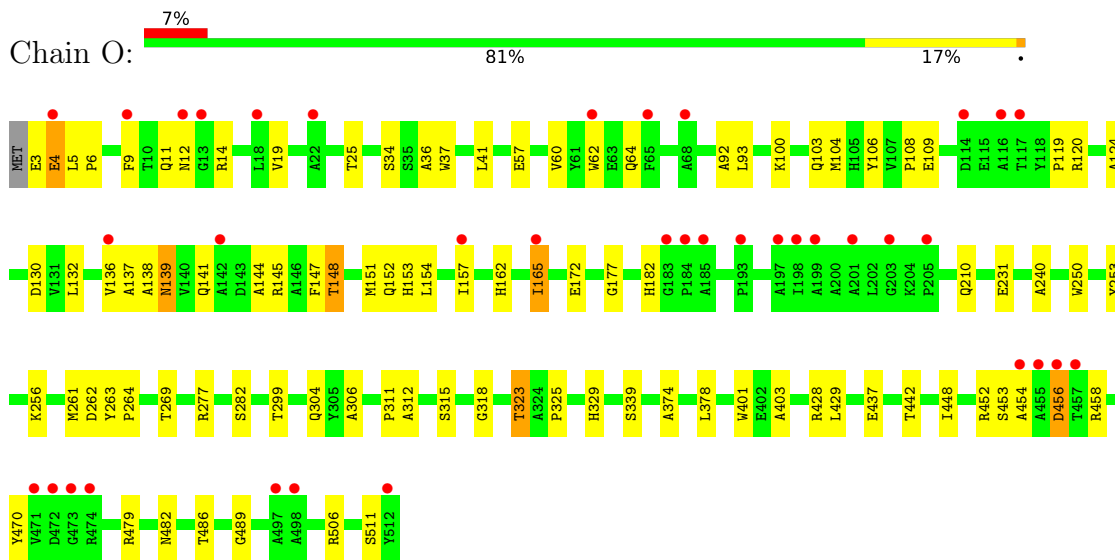
● Molecule 1: Beta-galactosidase



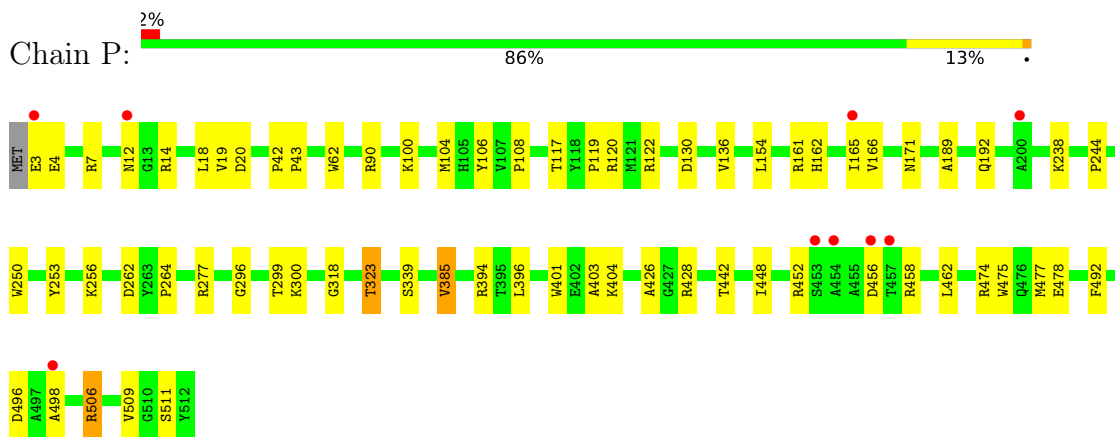
• Molecule 1: Beta-galactosidase



• Molecule 1: Beta-galactosidase



• Molecule 1: Beta-galactosidase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	128.27Å 162.99Å 235.48Å 90.00° 92.83° 90.00°	Depositor
Resolution (Å)	49.10 – 2.50 49.10 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.1 (49.10-2.50) 99.4 (49.10-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.29 (at 2.48Å)	Xtrriage
Refinement program	PHENIX v1	Depositor
R, $R_{free}$	0.211 , 0.251 0.211 , 0.251	Depositor DCC
$R_{free}$ test set	16771 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.4	Xtrriage
Anisotropy	0.453	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 35.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.020 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	65632	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	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 35.71 % 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 5.5908e-04. 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

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	0.30	0/4033	0.52	0/5508
1	B	0.25	0/4033	0.46	0/5508
1	C	0.29	1/4033 (0.0%)	0.47	0/5508
1	D	0.30	1/4033 (0.0%)	0.51	2/5508 (0.0%)
1	E	0.31	1/4033 (0.0%)	0.50	0/5508
1	F	0.29	0/4033	0.49	0/5508
1	G	0.27	0/4033	0.49	1/5508 (0.0%)
1	H	0.26	0/4033	0.47	0/5508
1	I	0.35	1/4033 (0.0%)	0.54	1/5508 (0.0%)
1	J	0.27	0/4033	0.47	0/5508
1	K	0.29	0/4033	0.49	0/5508
1	L	0.37	3/4033 (0.1%)	0.58	5/5508 (0.1%)
1	M	0.23	0/4033	0.43	0/5508
1	N	0.25	0/4033	0.45	0/5508
1	O	0.30	2/4033 (0.0%)	0.48	1/5508 (0.0%)
1	P	0.26	0/4033	0.45	0/5508
All	All	0.29	9/64528 (0.0%)	0.49	10/88128 (0.0%)

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	D	0	1
1	F	0	2
All	All	0	3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	172	GLU	C-O	8.57	1.28	1.23
1	C	172	GLU	C-O	8.40	1.27	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	172	GLU	C-O	7.94	1.27	1.23
1	L	458	ARG	CA-CB	7.54	1.66	1.53
1	O	4	GLU	CB-CG	-5.82	1.34	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	239	ARG	CB-CG-CD	-9.88	88.58	111.30
1	L	458	ARG	CD-NE-CZ	8.73	136.62	124.40
1	L	458	ARG	CA-CB-CG	8.26	130.62	114.10
1	D	239	ARG	CD-NE-CZ	-7.92	113.31	124.40
1	I	172	GLU	O-C-N	-6.39	118.59	121.53

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	239	ARG	Sidechain
1	F	71	ARG	Sidechain,Peptide

## 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	3921	0	3780	55	1
1	B	3921	0	3780	51	0
1	C	3921	0	3780	44	0
1	D	3921	0	3780	43	1
1	E	3921	0	3780	47	0
1	F	3921	0	3780	55	0
1	G	3921	0	3780	56	0
1	H	3921	0	3780	46	0
1	I	3921	0	3780	72	0
1	J	3921	0	3780	51	0
1	K	3921	0	3780	55	0
1	L	3921	0	3780	75	0
1	M	3921	0	3780	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	N	3921	0	3780	58	0
1	O	3921	0	3780	69	0
1	P	3921	0	3780	49	0
2	A	242	0	0	16	4
2	B	157	0	0	17	0
2	C	186	0	0	12	1
2	D	186	0	0	9	1
2	E	200	0	0	20	1
2	F	203	0	0	20	1
2	G	196	0	0	16	1
2	H	188	0	0	12	1
2	I	215	0	0	26	2
2	J	198	0	0	12	0
2	K	185	0	0	15	1
2	L	209	0	0	20	2
2	M	129	0	0	12	0
2	N	113	0	0	23	0
2	O	94	0	0	22	0
2	P	195	0	0	11	1
All	All	65632	0	60480	836	9

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 7.

The worst 5 of 836 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:I:239:ARG:HD2	1:L:458:ARG:HB3	1.27	1.13
1:G:364:ARG:NH2	2:G:1301:HOH:O	1.81	1.06
1:I:141:GLN:NE2	2:I:603:HOH:O	1.89	1.02
1:P:428:ARG:NH2	2:P:602:HOH:O	1.93	1.01
1:B:428:ARG:NH2	2:B:601:HOH:O	1.95	0.98

The worst 5 of 9 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:696:HOH:O	2:K:729:HOH:O[2_655]	1.59	0.61
2:A:794:HOH:O	2:G:1474:HOH:O[2_555]	1.96	0.24
2:H:716:HOH:O	2:L:604:HOH:O[1_655]	1.98	0.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:LYS:O	1:D:239:ARG:NH2[1_455]	2.03	0.17
2:A:606:HOH:O	2:P:692:HOH:O[1_565]	2.04	0.16

## 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	508/511 (99%)	491 (97%)	17 (3%)	0	100	100
1	B	508/511 (99%)	489 (96%)	19 (4%)	0	100	100
1	C	508/511 (99%)	489 (96%)	19 (4%)	0	100	100
1	D	508/511 (99%)	485 (96%)	22 (4%)	1 (0%)	43	63
1	E	508/511 (99%)	491 (97%)	16 (3%)	1 (0%)	43	63
1	F	508/511 (99%)	494 (97%)	14 (3%)	0	100	100
1	G	508/511 (99%)	490 (96%)	18 (4%)	0	100	100
1	H	508/511 (99%)	491 (97%)	17 (3%)	0	100	100
1	I	508/511 (99%)	490 (96%)	16 (3%)	2 (0%)	30	49
1	J	508/511 (99%)	493 (97%)	15 (3%)	0	100	100
1	K	508/511 (99%)	494 (97%)	14 (3%)	0	100	100
1	L	508/511 (99%)	491 (97%)	17 (3%)	0	100	100
1	M	508/511 (99%)	494 (97%)	14 (3%)	0	100	100
1	N	508/511 (99%)	491 (97%)	17 (3%)	0	100	100
1	O	508/511 (99%)	491 (97%)	17 (3%)	0	100	100
1	P	508/511 (99%)	493 (97%)	15 (3%)	0	100	100
All	All	8128/8176 (99%)	7857 (97%)	267 (3%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	200	ALA
1	I	201	ALA
1	D	239	ARG
1	E	195	PRO

### 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	381/382 (100%)	372 (98%)	9 (2%)	43	70
1	B	381/382 (100%)	372 (98%)	9 (2%)	43	70
1	C	381/382 (100%)	368 (97%)	13 (3%)	32	60
1	D	381/382 (100%)	367 (96%)	14 (4%)	30	57
1	E	381/382 (100%)	370 (97%)	11 (3%)	37	65
1	F	381/382 (100%)	371 (97%)	10 (3%)	40	68
1	G	381/382 (100%)	372 (98%)	9 (2%)	43	70
1	H	381/382 (100%)	372 (98%)	9 (2%)	43	70
1	I	381/382 (100%)	376 (99%)	5 (1%)	61	82
1	J	381/382 (100%)	372 (98%)	9 (2%)	43	70
1	K	381/382 (100%)	371 (97%)	10 (3%)	40	68
1	L	381/382 (100%)	371 (97%)	10 (3%)	40	68
1	M	381/382 (100%)	372 (98%)	9 (2%)	43	70
1	N	381/382 (100%)	373 (98%)	8 (2%)	47	74
1	O	381/382 (100%)	369 (97%)	12 (3%)	35	62
1	P	381/382 (100%)	370 (97%)	11 (3%)	37	65
All	All	6096/6112 (100%)	5938 (97%)	158 (3%)	40	68

5 of 158 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	471	VAL
1	O	339	SER

*Continued on next page...*

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Mol	Chain	Res	Type
1	M	161	ARG
1	N	299	THR
1	P	238	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 101 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	346	ASN
1	L	333	GLN
1	P	393	GLN
1	K	135	HIS
1	K	464	GLN

### 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](#)

There are no ligands in this entry.

### 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	510/511 (99%)	-0.20	4 (0%) 82 80	15, 25, 40, 66	0
1	B	510/511 (99%)	0.14	8 (1%) 70 67	21, 31, 48, 68	0
1	C	510/511 (99%)	-0.04	8 (1%) 70 67	19, 28, 43, 69	0
1	D	510/511 (99%)	0.04	19 (3%) 45 40	19, 27, 46, 71	0
1	E	510/511 (99%)	-0.16	6 (1%) 76 73	18, 25, 43, 64	0
1	F	510/511 (99%)	-0.01	7 (1%) 73 70	16, 27, 46, 70	0
1	G	510/511 (99%)	0.00	17 (3%) 49 45	17, 26, 45, 72	0
1	H	510/511 (99%)	0.03	5 (0%) 79 76	20, 29, 43, 68	0
1	I	510/511 (99%)	0.06	18 (3%) 47 42	17, 29, 47, 72	0
1	J	510/511 (99%)	0.06	14 (2%) 56 51	19, 29, 49, 69	0
1	K	510/511 (99%)	0.09	22 (4%) 40 35	19, 30, 45, 74	0
1	L	510/511 (99%)	0.15	23 (4%) 38 33	18, 28, 50, 78	0
1	M	510/511 (99%)	0.28	15 (2%) 53 49	25, 37, 55, 76	0
1	N	510/511 (99%)	0.65	25 (4%) 35 31	25, 42, 59, 84	0
1	O	510/511 (99%)	0.75	37 (7%) 21 19	27, 39, 56, 78	0
1	P	510/511 (99%)	-0.01	9 (1%) 67 64	19, 29, 46, 69	0
All	All	8160/8176 (99%)	0.11	237 (2%) 53 49	15, 30, 50, 84	0

The worst 5 of 237 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	471	VAL	11.1
1	K	471	VAL	8.5
1	L	476	GLN	8.1
1	K	472	ASP	7.8
1	L	457	THR	7.6

## 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 oligosaccharides in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.