



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 09:38 pm BST

PDB ID : 6UKI  
Title : HhaI endonuclease in Complex with DNA in space group P212121 (pH 6.0)  
Authors : Horton, J.R.; Cheng, X.  
Deposited on : 2019-10-04  
Resolution : 2.70 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.

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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) : 1.13  
EDS : 2.11  
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) : 2.11

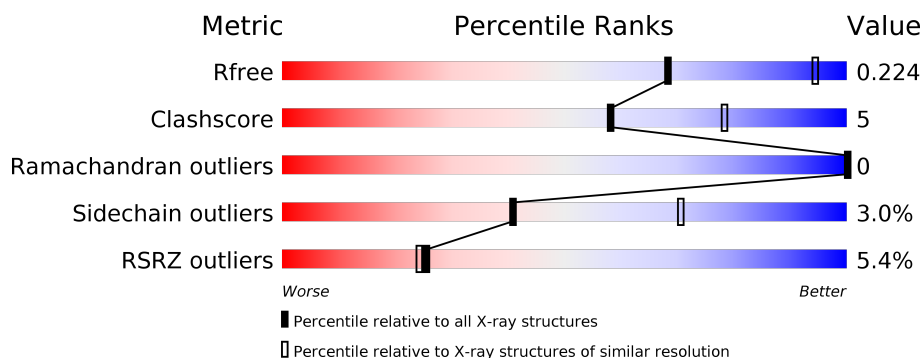
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria 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	X	258	<div> <div></div> <div> <div></div> <div>86%</div> <div>13%</div> </div> </div>
1	Y	258	<div> <div>11%</div> <div> <div></div> <div>86%</div> <div>14%</div> </div> </div>
2	A	14	<div> <div></div> <div> <div></div> <div>71%</div> <div>29%</div> </div> </div>
2	D	14	<div> <div></div> <div> <div></div> <div>57%</div> <div>43%</div> </div> </div>
3	B	14	<div> <div></div> <div> <div></div> <div>86%</div> <div>14%</div> </div> </div>
3	E	14	<div> <div></div> <div> <div></div> <div>71%</div> <div>29%</div> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5256 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 HhaI Restriction Endonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	258	Total	C	N	O	S	0	0	0
			2069	1341	340	380	8			
1	Y	258	Total	C	N	O	S	0	0	0
			2020	1311	330	372	7			

- Molecule 2 is a DNA chain called DNA (5'-D(\*CP\*TP\*GP\*TP\*TP\*GP\*CP\*GP\*CP\*TP\*TP\*GP\*GP\*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	14	Total	C	N	O	P	0	0	0
			285	137	49	86	13			
2	D	14	Total	C	N	O	P	0	0	0
			285	137	49	86	13			

- Molecule 3 is a DNA chain called DNA (5'-D(\*TP\*CP\*CP\*AP\*AP\*GP\*CP\*GP\*CP\*AP\*AP\*CP\*AP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	14	Total	C	N	O	P	0	0	0
			283	135	57	78	13			
3	E	14	Total	C	N	O	P	0	0	0
			283	135	57	78	13			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	X	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		
4	D	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	Y	1	Total	Ca	0	0
			1	1		

- Molecule 5 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
5	B	1	Total	C	O	0	0
			4	2	2		

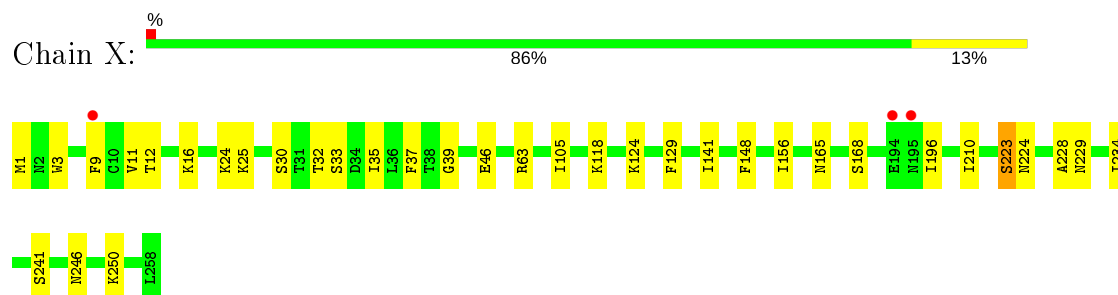
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	X	6	Total	O	0	0
			6	6		
6	A	6	Total	O	0	0
			6	6		
6	B	2	Total	O	0	0
			2	2		
6	Y	5	Total	O	0	0
			5	5		
6	D	3	Total	O	0	0
			3	3		
6	E	1	Total	O	0	0
			1	1		

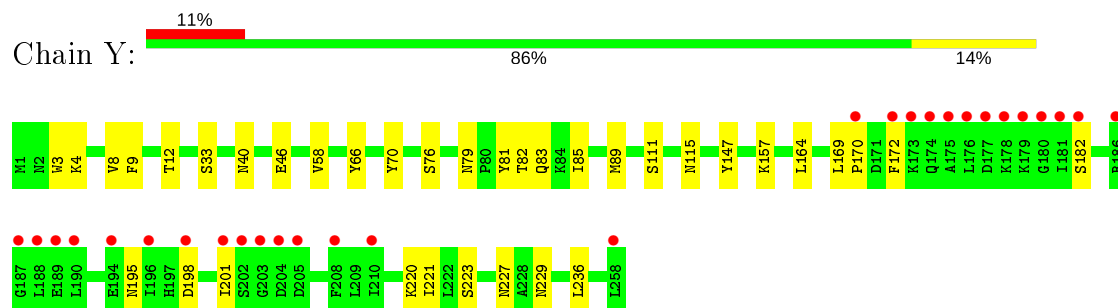
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

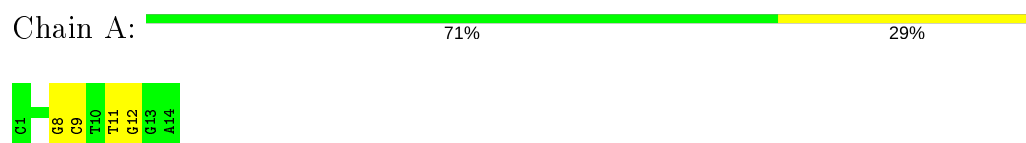
- Molecule 1: HhaI Restriction Endonuclease



- Molecule 1: HhaI Restriction Endonuclease



- Molecule 2: DNA (5'-D(\*CP\*TP\*GP\*TP\*TP\*GP\*CP\*GP\*CP\*TP\*TP\*GP\*GP\*A)-3')



- Molecule 2: DNA (5'-D(\*CP\*TP\*GP\*TP\*TP\*GP\*CP\*GP\*CP\*TP\*TP\*GP\*GP\*A)-3')



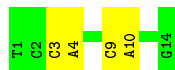
- Molecule 3: DNA (5'-D(\*TP\*CP\*CP\*AP\*AP\*GP\*CP\*GP\*CP\*AP\*AP\*CP\*AP\*G)-3')





- Molecule 3: DNA (5'-D(\*TP\*CP\*CP\*AP\*AP\*GP\*CP\*GP\*CP\*AP\*AP\*CP\*AP\*G)-3')

Chain E:  71% 29%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.41Å 95.00Å 97.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.97 – 2.70 48.93 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.4 (33.97-2.70) 92.8 (48.93-2.70)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.47 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, $R_{free}$	0.180 , 0.224 0.180 , 0.224	Depositor DCC
$R_{free}$ test set	1201 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	56.9	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 47.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.022 for -h,l,k 0.024 for -l,-k,-h 0.019 for k,h,-l 0.000 for k,l,h 0.000 for l,h,k	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5256	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.55% 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: CA, EDO

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	X	0.31	0/2123	0.45	0/2863
1	Y	0.30	0/2074	0.46	0/2808
2	A	0.67	0/318	1.00	0/490
2	D	0.65	0/318	0.97	0/490
3	B	0.65	0/318	0.79	0/488
3	E	0.71	0/318	0.75	0/488
All	All	0.42	0/5469	0.60	0/7627

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [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	X	2069	0	2004	19	0
1	Y	2020	0	1903	19	0
2	A	285	0	161	4	0
2	D	285	0	161	5	0
3	B	283	0	157	1	0
3	E	283	0	157	2	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1	0	0	0	0
4	X	1	0	0	0	0
4	Y	1	0	0	0	0
5	B	4	0	6	0	0
6	A	6	0	0	0	0
6	B	2	0	0	0	0
6	D	3	0	0	0	0
6	E	1	0	0	0	0
6	X	6	0	0	0	0
6	Y	5	0	0	0	0
All	All	5256	0	4549	45	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 5.

All (45) 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:X:25:LYS:HZ2	1:X:32:THR:HG21	1.58	0.67
1:X:11:VAL:HG21	1:X:24:LYS:HG3	1.78	0.64
1:X:196:ILE:HG13	1:X:210:ILE:HG21	1.78	0.64
1:X:118:LYS:HA	1:X:141:ILE:HD11	1.84	0.59
1:Y:3:TRP:CE3	2:D:9:DC:H4'	2.39	0.58
1:Y:79:ASN:OD1	1:Y:82:THR:N	2.36	0.58
1:Y:79:ASN:ND2	1:Y:82:THR:OG1	2.38	0.55
1:Y:33:SER:OG	1:Y:46:GLU:HG2	2.10	0.51
1:Y:8:VAL:O	1:Y:12:THR:HG23	2.11	0.51
1:Y:164:LEU:HA	1:Y:221:ILE:HD11	1.92	0.50
1:X:3:TRP:CE3	2:A:9:DC:H4'	2.47	0.50
1:Y:172:PHE:CE1	1:Y:201:ILE:HD11	2.48	0.49
2:D:11:DT:H2''	2:D:12:DG:C8	2.49	0.48
1:X:148:PHE:CE1	1:X:234:ILE:HD12	2.48	0.48
2:A:8:DG:H2'	2:A:9:DC:C6	2.49	0.48
1:X:37:PHE:CZ	1:X:39:GLY:HA3	2.49	0.48
2:A:11:DT:H2''	2:A:12:DG:C8	2.49	0.47
2:D:1:DC:H2'	2:D:2:DT:H72	1.96	0.46
1:Y:58:VAL:HG22	1:Y:229:ASN:HB3	1.97	0.46
1:X:124:LYS:HE3	1:Y:40:ASN:OD1	2.17	0.45
1:Y:169:LEU:HB3	1:Y:170:PRO:HD3	1.99	0.44
1:Y:198:ASP:N	1:Y:198:ASP:OD1	2.51	0.44
1:Y:227:ASN:ND2	2:D:6:DG:OP2	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:33:SER:OG	1:X:46:GLU:OE2	2.33	0.43
1:Y:85:ILE:O	1:Y:89:MET:HG3	2.17	0.43
3:B:9:DC:H2'	3:B:10:DA:C8	2.54	0.43
3:E:9:DC:H2'	3:E:10:DA:C8	2.54	0.43
1:Y:157:LYS:HB3	1:Y:229:ASN:HD21	1.84	0.43
1:X:11:VAL:HG22	1:X:35:ILE:HG12	2.01	0.43
1:Y:164:LEU:HD12	1:Y:221:ILE:HD11	2.01	0.43
1:X:246:ASN:O	1:X:250:LYS:HG2	2.18	0.42
1:Y:147:TYR:O	1:Y:236:LEU:HD12	2.19	0.42
1:X:156:ILE:HA	1:X:228:ALA:HA	2.02	0.42
1:Y:70:TYR:OH	1:Y:76:SER:O	2.21	0.42
1:X:12:THR:O	1:X:16:LYS:HG3	2.21	0.41
1:X:3:TRP:CD2	2:A:9:DC:H4'	2.54	0.41
1:X:129:PHE:HE1	1:X:141:ILE:HD13	1.86	0.41
1:X:223:SER:OG	1:X:224:ASN:N	2.53	0.41
1:X:105:ILE:HD12	1:X:105:ILE:H	1.84	0.41
2:D:1:DC:H2'	2:D:2:DT:C7	2.51	0.41
3:E:3:DC:H2''	3:E:4:DA:C8	2.55	0.41
1:X:165:ASN:OD1	1:X:168:SER:OG	2.35	0.40
1:Y:81:TYR:CE2	1:Y:115:ASN:HB3	2.56	0.40
1:X:1:MET:HE1	1:X:9:PHE:HD2	1.87	0.40
1:Y:83:GLN:HB2	1:Y:83:GLN:HE21	1.73	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	X	256/258 (99%)	253 (99%)	3 (1%)	0	100	100
1	Y	256/258 (99%)	246 (96%)	10 (4%)	0	100	100
All	All	512/516 (99%)	499 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	X	224/237 (94%)	219 (98%)	5 (2%)	52	79
1	Y	211/237 (89%)	203 (96%)	8 (4%)	33	62
All	All	435/474 (92%)	422 (97%)	13 (3%)	41	70

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	30	SER
1	X	63	ARG
1	X	223	SER
1	X	229	ASN
1	X	241	SER
1	Y	4	LYS
1	Y	9	PHE
1	Y	66	TYR
1	Y	111	SER
1	Y	182	SER
1	Y	195	ASN
1	Y	220	LYS
1	Y	223	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	Y	41	ASN
1	Y	83	GLN
1	Y	195	ASN
1	Y	229	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	EDO	B	101	-	3,3,3	0.48	0	2,2,2	0.32	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	B	101	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	X	258/258 (100%)	0.01	3 (1%) 79 80	37, 69, 121, 150	0
1	Y	258/258 (100%)	0.34	28 (10%) 5 4	42, 73, 145, 189	0
2	A	14/14 (100%)	-0.47	0 100 100	41, 69, 100, 110	0
2	D	14/14 (100%)	-0.56	0 100 100	50, 71, 110, 119	0
3	B	14/14 (100%)	-0.53	0 100 100	51, 73, 118, 132	0
3	E	14/14 (100%)	-0.57	0 100 100	53, 86, 120, 120	0
All	All	572/572 (100%)	0.11	31 (5%) 25 24	37, 71, 133, 189	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Y	175	ALA	5.9
1	Y	201	ILE	4.9
1	Y	203	GLY	4.7
1	Y	208	PHE	4.0
1	Y	172	PHE	4.0
1	Y	179	LYS	4.0
1	Y	258	LEU	3.9
1	Y	204	ASP	3.7
1	Y	189	GLU	3.4
1	Y	188	LEU	3.4
1	Y	174	GLN	3.3
1	Y	202	SER	3.2
1	Y	194	GLU	3.2
1	Y	190	LEU	3.1
1	Y	176	LEU	3.0
1	Y	205	ASP	2.9
1	Y	187	GLY	2.8
1	Y	210	ILE	2.8
1	Y	198	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	Y	178	LYS	2.6
1	Y	177	ASP	2.5
1	X	194	GLU	2.5
1	X	195	ASN	2.5
1	Y	173	LYS	2.5
1	Y	196	ILE	2.4
1	Y	186	ARG	2.3
1	Y	180	GLY	2.3
1	Y	170	PRO	2.1
1	Y	181	ILE	2.1
1	Y	182	SER	2.1
1	X	9	PHE	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 carbohydrates 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
5	EDO	B	101	4/4	0.89	0.22	87,87,88,91	0
4	CA	X	301	1/1	0.95	0.22	55,55,55,55	0
4	CA	D	101	1/1	0.98	0.17	63,63,63,63	0
4	CA	Y	301	1/1	0.98	0.11	52,52,52,52	0
4	CA	A	101	1/1	0.99	0.19	54,54,54,54	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.