



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 02:02 am GMT

PDB ID : 3AHX  
Title : Crystal structure of beta-glucosidase A from bacterium *Clostridium cellulovorans*  
Authors : Jeng, W.-Y.; Liu, C.-I.; Wang, A.H.-J.  
Deposited on : 2010-05-06  
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

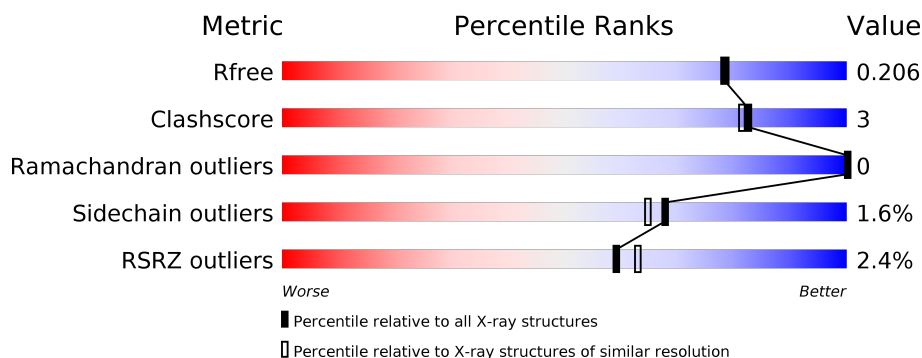
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
$R_{free}$	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	453	<div> <div>3%</div> <div> <div></div> <div>90%</div> <div>8%</div> <div>•</div> </div> </div>
1	B	453	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>6%</div> <div>••</div> </div> </div>
1	C	453	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>6%</div> <div>•</div> </div> </div>
1	D	453	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>6%</div> <div>•</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16719 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
1	A	444	Total	C	N	O	S	0	0	0
			3641	2345	605	679	12			
1	B	444	Total	C	N	O	S	0	0	0
			3641	2345	605	679	12			
1	C	441	Total	C	N	O	S	0	0	0
			3615	2329	601	674	11			
1	D	443	Total	C	N	O	S	0	0	0
			3633	2340	604	678	11			

There are 32 discrepancies between the modelled and reference sequences:

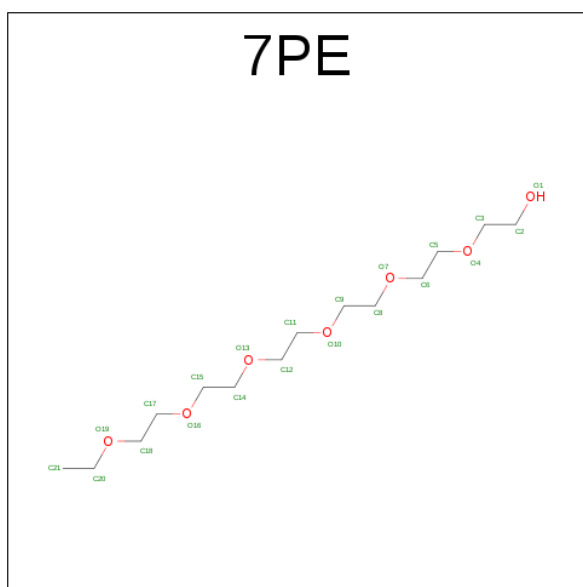
Chain	Residue	Modelled	Actual	Comment	Reference
A	446	LEU	-	EXPRESSION TAG	UNP Q53EH2
A	447	GLU	-	EXPRESSION TAG	UNP Q53EH2
A	448	HIS	-	EXPRESSION TAG	UNP Q53EH2
A	449	HIS	-	EXPRESSION TAG	UNP Q53EH2
A	450	HIS	-	EXPRESSION TAG	UNP Q53EH2
A	451	HIS	-	EXPRESSION TAG	UNP Q53EH2
A	452	HIS	-	EXPRESSION TAG	UNP Q53EH2
A	453	HIS	-	EXPRESSION TAG	UNP Q53EH2
B	446	LEU	-	EXPRESSION TAG	UNP Q53EH2
B	447	GLU	-	EXPRESSION TAG	UNP Q53EH2
B	448	HIS	-	EXPRESSION TAG	UNP Q53EH2
B	449	HIS	-	EXPRESSION TAG	UNP Q53EH2
B	450	HIS	-	EXPRESSION TAG	UNP Q53EH2
B	451	HIS	-	EXPRESSION TAG	UNP Q53EH2
B	452	HIS	-	EXPRESSION TAG	UNP Q53EH2
B	453	HIS	-	EXPRESSION TAG	UNP Q53EH2
C	446	LEU	-	EXPRESSION TAG	UNP Q53EH2
C	447	GLU	-	EXPRESSION TAG	UNP Q53EH2
C	448	HIS	-	EXPRESSION TAG	UNP Q53EH2
C	449	HIS	-	EXPRESSION TAG	UNP Q53EH2
C	450	HIS	-	EXPRESSION TAG	UNP Q53EH2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	451	HIS	-	EXPRESSION TAG	UNP Q53EH2
C	452	HIS	-	EXPRESSION TAG	UNP Q53EH2
C	453	HIS	-	EXPRESSION TAG	UNP Q53EH2
D	446	LEU	-	EXPRESSION TAG	UNP Q53EH2
D	447	GLU	-	EXPRESSION TAG	UNP Q53EH2
D	448	HIS	-	EXPRESSION TAG	UNP Q53EH2
D	449	HIS	-	EXPRESSION TAG	UNP Q53EH2
D	450	HIS	-	EXPRESSION TAG	UNP Q53EH2
D	451	HIS	-	EXPRESSION TAG	UNP Q53EH2
D	452	HIS	-	EXPRESSION TAG	UNP Q53EH2
D	453	HIS	-	EXPRESSION TAG	UNP Q53EH2

- Molecule 2 is 2-(2-(2-(2-(2-ETHOXYETHOXY)ETHOXY)ETHOXY)ETHOXY)ETHOXY)ETHANOL (three-letter code: 7PE) (formula: C<sub>14</sub>H<sub>30</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			21	14	7		
2	D	1	Total	C	O	0	0
			21	14	7		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	531	Total	O	0	0
			531	531		

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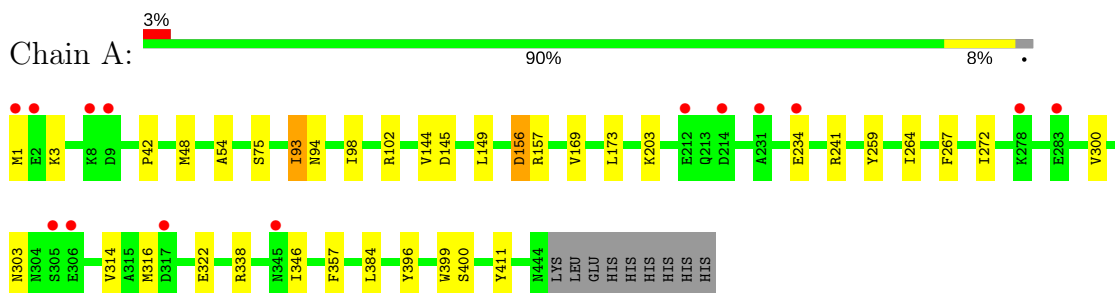
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	599	Total 599	O 599	0	0
3	C	529	Total 529	O 529	0	0
3	D	488	Total 488	O 488	0	0

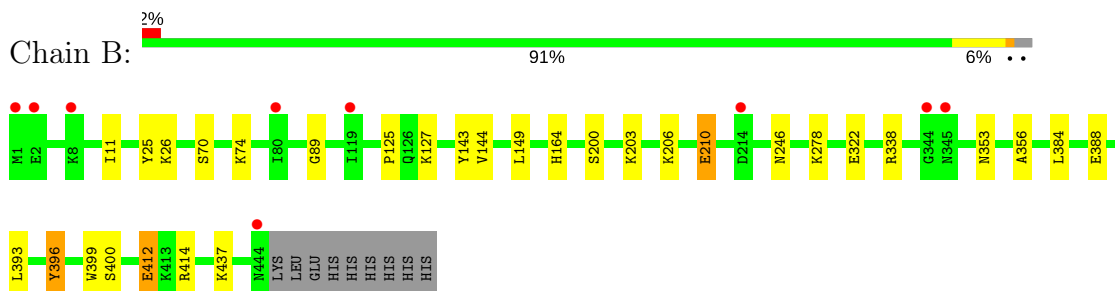
### 3 Residue-property plots [i](#)

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.

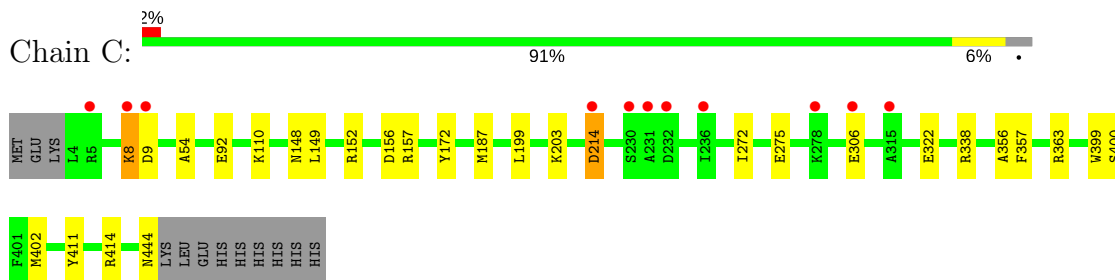
#### • Molecule 1: Beta-glucosidase A



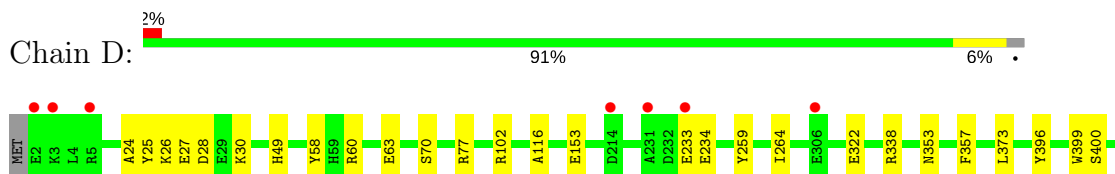
#### • Molecule 1: Beta-glucosidase A



#### • Molecule 1: Beta-glucosidase A



#### • Molecule 1: Beta-glucosidase A





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	128.50Å 128.50Å 264.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.30 – 1.90 28.31 – 1.90	Depositor EDS
% Data completeness (in resolution range)	92.0 (28.30-1.90) 92.1 (28.31-1.90)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.09 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.146 , 0.198 0.164 , 0.206	Depositor DCC
$R_{free}$ test set	7980 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.9	Xtriage
Anisotropy	0.791	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 42.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	16719	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.76% 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: 7PE

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	0.34	0/3743	0.70	0/5072
1	B	0.34	0/3743	0.70	0/5072
1	C	0.33	0/3717	0.68	0/5039
1	D	0.31	0/3735	0.68	0/5062
All	All	0.33	0/14938	0.69	0/20245

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	A	3641	0	3487	29	0
1	B	3641	0	3487	17	0
1	C	3615	0	3456	17	0
1	D	3633	0	3475	18	0
2	C	21	0	30	0	0
2	D	21	0	30	5	0
3	A	531	0	0	3	0
3	B	599	0	0	3	0
3	C	529	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	488	0	0	4	0
All	All	16719	0	13965	83	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 (83) 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:D:28:ASP:OD1	1:D:58:TYR:OH	1.81	0.97
1:A:322:GLU:HG2	1:A:357:PHE:HA	1.49	0.93
1:D:422:TYR:HB3	2:D:4002:7PE:H152	1.56	0.87
1:C:322:GLU:HG2	1:C:357:PHE:HA	1.65	0.77
1:A:300:VAL:HG21	1:A:316:MET:SD	2.29	0.73
1:A:93:ILE:HD11	1:A:98:ILE:CD1	2.19	0.73
2:D:4002:7PE:H151	3:D:1624:HOH:O	1.90	0.70
1:A:300:VAL:HG23	1:A:314:VAL:HB	1.76	0.68
1:B:206:LYS:O	1:B:210:GLU:HG2	1.95	0.66
1:C:444:ASN:O	3:C:992:HOH:O	2.13	0.65
1:D:322:GLU:HG2	1:D:357:PHE:HA	1.79	0.65
1:B:70:SER:O	1:B:437:LYS:HE2	1.96	0.65
1:D:422:TYR:CB	2:D:4002:7PE:H152	2.28	0.64
1:D:49:HIS:CD2	1:D:411:TYR:H	2.18	0.60
1:A:322:GLU:CG	1:A:357:PHE:HA	2.26	0.60
1:D:49:HIS:HD2	1:D:411:TYR:H	1.50	0.59
1:A:75:SER:HB3	3:A:573:HOH:O	2.01	0.59
1:A:3:LYS:HD3	3:A:2186:HOH:O	2.02	0.59
1:B:384:LEU:O	1:B:388:GLU:HG2	2.02	0.59
1:D:60:ARG:O	1:D:63:GLU:HG2	2.04	0.58
1:D:259:TYR:HB2	1:D:264:ILE:HD11	1.88	0.55
1:A:93:ILE:HD11	1:A:98:ILE:HD12	1.88	0.55
1:B:144:VAL:HG21	1:B:203:LYS:HB3	1.88	0.54
1:A:93:ILE:HD13	1:A:94:ASN:N	2.23	0.54
1:A:93:ILE:CD1	1:A:98:ILE:HD12	2.39	0.53
1:A:156:ASP:OD1	1:A:157:ARG:NH1	2.41	0.53
1:D:444:ASN:HD22	1:D:444:ASN:C	2.12	0.53
1:B:412:GLU:HB2	3:B:1962:HOH:O	2.08	0.53
1:B:11:ILE:HA	1:B:74:LYS:HD3	1.90	0.52
1:B:25:TYR:CZ	1:B:26:LYS:HE3	2.44	0.52
1:C:172:TYR:HE1	1:C:187:MET:CE	2.21	0.52
1:C:172:TYR:HE1	1:C:187:MET:HE3	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:ASP:OD1	1:A:157:ARG:HG3	2.11	0.50
1:A:259:TYR:HB2	1:A:264:ILE:HD11	1.93	0.50
1:A:346:ILE:N	3:A:2093:HOH:O	2.44	0.50
1:B:25:TYR:CE2	1:B:26:LYS:HE3	2.47	0.50
1:C:187:MET:HG2	1:C:272:ILE:HD12	1.94	0.50
1:D:24:ALA:HB1	1:D:27:GLU:HG3	1.93	0.49
1:B:144:VAL:HG21	1:B:203:LYS:HE3	1.93	0.49
1:C:149:LEU:C	1:C:149:LEU:HD23	2.34	0.49
1:A:144:VAL:HG21	1:A:203:LYS:HB3	1.96	0.48
1:A:267:PHE:CD1	1:A:272:ILE:HD11	2.49	0.48
1:A:234:GLU:HG2	1:A:303:ASN:CB	2.44	0.47
2:D:4002:7PE:H213	3:D:1624:HOH:O	2.13	0.47
1:C:322:GLU:CG	1:C:357:PHE:HA	2.42	0.47
1:B:246:ASN:HB3	3:B:767:HOH:O	2.14	0.47
1:A:42:PRO:HA	1:A:48:MET:SD	2.55	0.47
1:A:1:MET:HG3	1:C:363:ARG:HB2	1.97	0.46
1:A:98:ILE:HD11	1:A:149:LEU:HD11	1.98	0.46
1:D:373:LEU:HD23	1:D:373:LEU:C	2.37	0.46
1:B:164:HIS:HE1	1:B:200:SER:OG	1.97	0.45
1:B:278:LYS:HG3	3:B:845:HOH:O	2.15	0.45
1:A:399:TRP:HA	1:A:400:SER:HA	1.74	0.45
1:A:169:VAL:HG13	1:A:173:LEU:HD22	1.99	0.45
1:A:241:ARG:HH22	1:A:303:ASN:ND2	2.16	0.44
1:A:98:ILE:HG22	1:A:102:ARG:NH2	2.33	0.44
1:D:233:GLU:HG3	1:D:234:GLU:N	2.33	0.44
1:D:25:TYR:OH	1:D:26:LYS:HE2	2.18	0.44
1:A:93:ILE:CD1	1:A:98:ILE:CD1	2.92	0.43
1:D:399:TRP:HA	1:D:400:SER:HA	1.84	0.43
1:B:399:TRP:HA	1:B:400:SER:HA	1.83	0.43
1:C:148:ASN:O	1:C:152:ARG:HG3	2.19	0.43
1:C:214:ASP:OD2	1:C:214:ASP:N	2.50	0.43
1:B:143:TYR:CD2	1:B:200:SER:HB2	2.54	0.43
2:D:4002:7PE:H182	3:D:900:HOH:O	2.19	0.43
1:C:8:LYS:NZ	1:C:9:ASP:HB3	2.33	0.43
1:A:54:ALA:HA	1:A:411:TYR:OH	2.19	0.42
1:A:93:ILE:HD11	1:A:98:ILE:CG1	2.50	0.42
1:C:110:LYS:C	1:C:110:LYS:HD3	2.40	0.42
1:D:77:ARG:HA	1:D:116:ALA:O	2.19	0.42
1:B:356:ALA:HA	1:B:414:ARG:O	2.19	0.42
1:D:30:LYS:HE3	3:D:1258:HOH:O	2.18	0.42
1:A:3:LYS:HA	1:A:3:LYS:HD3	1.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:ILE:HD11	1:A:98:ILE:HG13	2.01	0.41
1:C:399:TRP:HA	1:C:400:SER:HA	1.79	0.41
1:B:89:GLY:HA2	1:B:125:PRO:HG2	2.03	0.41
1:D:102:ARG:NH2	1:D:153:GLU:OE1	2.54	0.41
1:C:156:ASP:OD1	1:C:157:ARG:HG3	2.20	0.41
1:C:199:LEU:O	1:C:203:LYS:HG3	2.22	0.40
1:D:353:ASN:ND2	1:D:396:TYR:OH	2.54	0.40
1:B:353:ASN:ND2	1:B:396:TYR:OH	2.54	0.40
1:C:54:ALA:HA	1:C:411:TYR:OH	2.22	0.40
1:C:356:ALA:HA	1:C:414:ARG:O	2.22	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	A	442/453 (98%)	433 (98%)	9 (2%)	0	100	100
1	B	442/453 (98%)	432 (98%)	10 (2%)	0	100	100
1	C	439/453 (97%)	426 (97%)	13 (3%)	0	100	100
1	D	441/453 (97%)	431 (98%)	10 (2%)	0	100	100
All	All	1764/1812 (97%)	1722 (98%)	42 (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	A	377/386 (98%)	371 (98%)	6 (2%)	68	65
1	B	377/386 (98%)	369 (98%)	8 (2%)	59	53
1	C	374/386 (97%)	367 (98%)	7 (2%)	62	57
1	D	376/386 (97%)	373 (99%)	3 (1%)	85	85
All	All	1504/1544 (97%)	1480 (98%)	24 (2%)	68	65

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	93	ILE
1	A	145	ASP
1	A	156	ASP
1	A	338	ARG
1	A	384	LEU
1	A	396	TYR
1	B	127	LYS
1	B	149	LEU
1	B	210	GLU
1	B	322	GLU
1	B	338	ARG
1	B	393	LEU
1	B	396	TYR
1	B	412	GLU
1	C	8	LYS
1	C	92	GLU
1	C	214	ASP
1	C	275	GLU
1	C	306	GLU
1	C	338	ARG
1	C	402	MET
1	D	70	SER
1	D	338	ARG
1	D	444	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	121	HIS

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Mol	Chain	Res	Type
1	B	164	HIS
1	B	229	ASN
1	B	353	ASN
1	C	229	ASN
1	D	49	HIS
1	D	353	ASN
1	D	444	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 ⓘ

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	7PE	C	4001	-	20,20,20	0.66	0	19,19,19	0.41	0
2	7PE	D	4002	-	20,20,20	0.67	0	19,19,19	1.13	1 (5%)

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	7PE	C	4001	-	-	0/18/18/18	0/0/0/0
2	7PE	D	4002	-	-	0/18/18/18	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	D	4002	7PE	O16-C15-C14	3.67	127.24	110.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	4002	7PE	5	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 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	444/453 (98%)	-0.04	14 (3%) 48 51	10, 15, 30, 46	0
1	B	444/453 (98%)	-0.12	9 (2%) 65 69	10, 16, 28, 43	0
1	C	441/453 (97%)	-0.12	11 (2%) 58 62	11, 16, 28, 39	0
1	D	443/453 (97%)	-0.01	8 (1%) 69 72	14, 20, 32, 46	0
All	All	1772/1812 (97%)	-0.07	42 (2%) 59 63	10, 17, 30, 46	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	345	ASN	4.0
1	A	214	ASP	3.9
1	B	214	ASP	3.8
1	B	1	MET	3.6
1	C	306	GLU	3.4
1	A	1	MET	3.4
1	D	214	ASP	3.4
1	D	233	GLU	3.3
1	C	9	ASP	2.9
1	B	444	ASN	2.9
1	C	8	LYS	2.8
1	C	278	LYS	2.7
1	D	444	ASN	2.6
1	D	3	LYS	2.6
1	A	2	GLU	2.6
1	C	214	ASP	2.6
1	A	306	GLU	2.6
1	C	315	ALA	2.5
1	A	345	ASN	2.5
1	A	283	GLU	2.5
1	A	278	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	9	ASP	2.4
1	C	231	ALA	2.4
1	B	2	GLU	2.4
1	A	234	GLU	2.4
1	B	344	GLY	2.4
1	A	8	LYS	2.3
1	A	317	ASP	2.3
1	B	8	LYS	2.3
1	D	2	GLU	2.3
1	C	230	SER	2.3
1	D	231	ALA	2.3
1	D	306	GLU	2.2
1	A	305	SER	2.2
1	A	212	GLU	2.1
1	A	231	ALA	2.1
1	C	5	ARG	2.1
1	B	80	ILE	2.1
1	B	119	ILE	2.1
1	C	232	ASP	2.1
1	C	236	ILE	2.1
1	D	5	ARG	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	7PE	D	4002	21/21	0.92	0.11	0.40	26,29,34,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	7PE	C	4001	21/21	0.92	0.14	0.32	28,32,44,47	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.