

wwPDB X-ray Structure Validation Summary Report (i)

Mar 10, 2024 – 12:15 AM EST

PDB ID 3ILF

> Title Crystal structure of porphyranase A (PorA) in complex with neo-

> > porphyrotetraose

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Μ.

2009-08-07 Deposited on

1.80 Å(reported) Resolution

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 A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13

EDS 2.36

20191225.v01 (using entries in the PDB archive December 25th 2019) Percentile statistics

> Refmac 5.8.0158

CCP4 7.0.044 (Gargrove)

Ideal geometry (proteins) Engh & Huber (2001) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

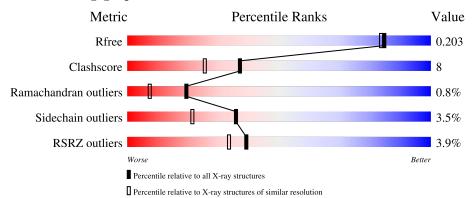
Validation Pipeline (wwPDB-VP) 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 1.80 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}({\rm \AA})) \end{array}$
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 >=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 <=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	268	83%	11% • •		
2	В	4	75%	25%		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	L6S	В	4	X	-	-	-
6	ACT	A	282	-	-	X	-



2 Entry composition (i)

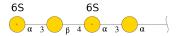
There are 7 unique types of molecules in this entry. The entry contains 2556 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 porphyranase A.

\mathbf{Mol}	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	257	Total 2159	C 1386	N 367	O 400	S 6	0	8	0

• Molecule 2 is an oligosaccharide called 6-O-sulfo-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-6-O-sulfo-alpha-L-galactopyranose-(1-3)-alpha-D-galactopyranose.



Mol	Chain	Residues	A	Aton	ns		ZeroOcc	AltConf	Trace
9	B	4	Total	С	О	S	0	0	0
	Ъ	4	53	24	27	2	0	0	

• Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0

• Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

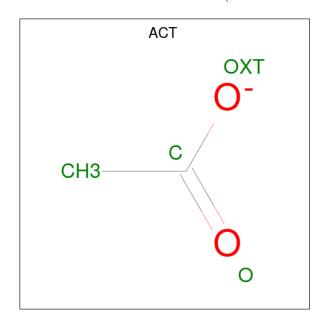
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mg 1 1	0	0

• Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Cl 2 2	0	0



 \bullet Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: $\mathrm{C_2H_3O_2}).$



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

• Molecule 7 is water.

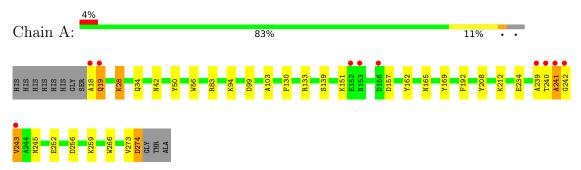
\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
7	A	324	Total O 324 324	0	0



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: porphyranase A



• Molecule 2: 6-O-sulfo-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-6-O-sulfo-alpha-L-galactopyranose-(1-3)-alpha-D-galactopyranose

Chain B: 75% 25%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	62.09Å 68.38Å 71.27Å	Donositon
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.34 - 1.80	Depositor
Resolution (A)	18.37 - 1.80	EDS
% Data completeness	94.0 (49.34-1.80)	Depositor
(in resolution range)	94.1 (18.37-1.80)	EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) > 1$	6.93 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
D.D.	0.157 , 0.205	Depositor
R, R_{free}	0.158 , 0.203	DCC
R_{free} test set	1381 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	11.2	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 48.5	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.018 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2556	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.86% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: ACT, GLA, GAL, L6S, MG, CL, CA

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 Chair		Boı	nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	1.30	5/2236~(0.2%)	1.07	2/3032 (0.1%)	

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(Å)
1	A	234	GLU	CD-OE2	5.97	1.32	1.25
1	A	192	PHE	CD2-CE2	5.67	1.50	1.39
1	A	169	TYR	CD2-CE2	5.35	1.47	1.39
1	A	208	TYR	CD1-CE1	5.34	1.47	1.39
1	A	34	GLN	CG-CD	5.15	1.62	1.51

All (2) bond angle outliers are listed below:

Mo	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	130	PHE	CB-CG-CD2	-5.38	117.03	120.80
1	A	256	ASP	CB-CG-OD2	-5.09	113.72	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2159	0	2063	34	0

Continued on next page...



Continued	trom	mmoninonic	maaa
COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	В	53	0	36	1	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	2	0	0	0	0
6	A	16	0	12	5	0
7	A	324	0	0	6	2
All	All	2556	0	2111	34	2

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 8.

The worst 5 of 34 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:18:ALA:HB2	7:A:449:HOH:O	1.60	1.00
1:A:240[B]:THR:HG23	1:A:241[B]:ALA:N	1.83	0.93
1:A:266:TRP:HE1	6:A:285:ACT:H2	1.33	0.91
1:A:259:LYS:HZ3	6:A:282:ACT:H3	1.39	0.84
1:A:259:LYS:NZ	6:A:282:ACT:H3	1.91	0.84

All (2) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
7:A:565:HOH:O	7:A:567:HOH:O[2_554]	1.74	0.46
7:A:558:HOH:O	7:A:561:HOH:O[4_555]	2.17	0.03

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	263/268 (98%)	247 (94%)	13 (5%)	3 (1%)	14 4

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	241[A]	ALA
1	A	241[B]	ALA
1	A	243	VAL

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	232/234 (99%)	223 (96%)	9 (4%)	32 17

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	252[B]	GLU
1	A	274	ASP
1	A	162	TYR
1	A	165	ASN
1	A	212	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	42	ASN
1	A	165	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)

4 monosaccharides 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	Mal Trung (Res	Link	Во	Bond lengths			Bond angles		
WIOI	Type	Chain	rtes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
2	GLA	В	1	2	12,12,12	1.05	0	17,17,17	3.26	6 (35%)	
2	L6S	В	2	2	15,15,16	1.10	3 (20%)	20,22,24	3.30	8 (40%)	
2	GAL	В	3	2	11,11,12	1.43	1 (9%)	15,15,17	3.01	6 (40%)	
2	L6S	В	4	2	15,15,16	1.95	2 (13%)	20,22,24	5.23	11 (55%)	

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	GLA	В	1	2	-	0/2/22/22	0/1/1/1
2	L6S	В	2	2	-	0/6/23/26	0/1/1/1
2	GAL	В	3	2	-	0/2/19/22	0/1/1/1
2	L6S	В	4	2	1/1/5/6	2/6/23/26	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$Ideal(\AA)$
2	В	4	L6S	C2-C3	-5.23	1.44	1.52
2	В	4	L6S	O5-C1	4.39	1.50	1.43
2	В	3	GAL	O3-C3	3.62	1.51	1.43
2	В	2	L6S	O5-C1	-2.57	1.39	1.43
2	В	2	L6S	C1-C2	-2.33	1.46	1.52



The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	4	L6S	C1-C2-C3	-16.91	88.88	109.67
2	В	1	GLA	C1-C2-C3	-8.84	91.97	110.31
2	В	2	L6S	O4-C4-C3	-8.70	90.24	110.35
2	В	4	L6S	C1-O5-C5	-8.56	100.60	112.19
2	В	3	GAL	O3-C3-C4	8.39	129.74	110.35

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	В	4	L6S	C1

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	4	L6S	C4-C5-C6-O6
2	В	4	L6S	O5-C5-C6-O6

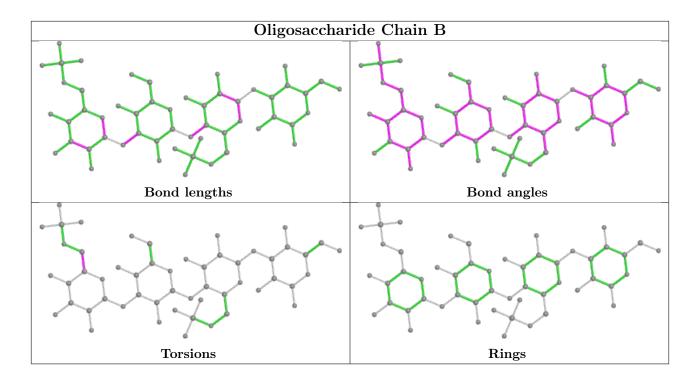
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	2	L6S	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 oligosaccharide.





5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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).

Mal	Mal Tara Chair Das		Dag	Link	Bond lengths			Bond angles		
Mol	Type	Chain	Res	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	ACT	A	283	-	3,3,3	1.16	0	3,3,3	1.13	0
6	ACT	A	282	-	3,3,3	0.92	0	3,3,3	2.40	2 (66%)
6	ACT	A	284	-	3,3,3	0.71	0	3,3,3	1.69	1 (33%)
6	ACT	A	285	-	3,3,3	0.90	0	3,3,3	1.54	0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	${f Atoms}$	\mathbf{Z}	$\operatorname{Observed}(^{o})$	$ \operatorname{Ideal}(^o) $
6	A	282	ACT	OXT-C-CH3	3.00	127.60	115.18
6	A	282	ACT	OXT-C-O	-2.84	111.58	122.05
6	A	284	ACT	OXT-C-CH3	2.20	124.29	115.18



There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	282	ACT	4	0
6	A	285	ACT	1	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 (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^{th} 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	257/268 (95%)	-0.37	10 (3%) 39 33	4, 9, 23, 39	5 (1%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	239	ALA	11.0
1	A	242[A]	GLY	8.5
1	A	241[A]	ALA	8.3
1	A	18	ALA	6.4
1	A	240[A]	THR	6.3

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

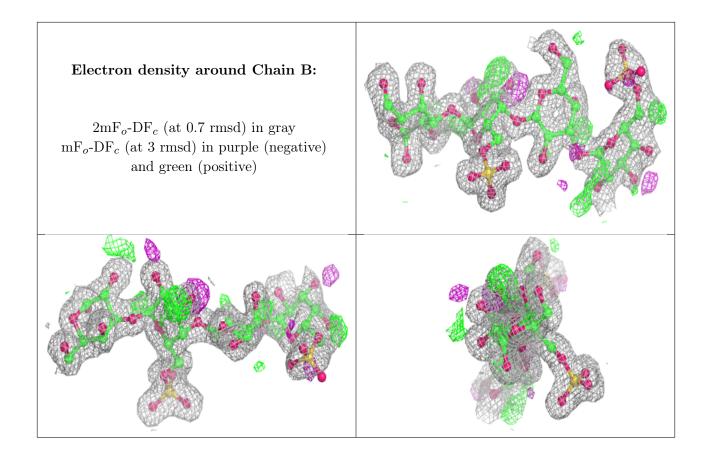
6.3 Carbohydrates (i)

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^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	L6S	В	4	15/16	0.79	0.23	33,39,57,58	0
2	GAL	В	3	11/12	0.93	0.10	10,13,20,26	0
2	L6S	В	2	15/16	0.96	0.08	4,6,9,10	0
2	GLA	В	1	12/12	0.97	0.06	2,5,10,14	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





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^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
6	ACT	A	284	4/4	0.58	0.24	62,62,63,63	0
6	ACT	A	285	4/4	0.80	0.16	28,31,31,31	0
6	ACT	A	282	4/4	0.90	0.13	29,29,31,32	0
6	ACT	A	283	4/4	0.96	0.15	23,25,25,26	0
4	MG	A	279	1/1	0.99	0.24	7,7,7,7	0
5	CL	A	280	1/1	0.99	0.17	25,25,25,25	0
3	CA	A	278	1/1	1.00	0.03	8,8,8,8	0
5	CL	A	281	1/1	1.00	0.03	8,8,8,8	0

6.5 Other polymers (i)

There are no such residues in this entry.

