

# Full wwPDB X-ray Structure Validation Report (i)

Dec 13, 2023 – 03:32 am GMT

PDB ID	:	4CVC
Title	:	Crystal structure of quinone-dependent alcohol dehydrogenase from Pseu-
		dogluconobacter saccharoketogenenes with zinc in the active site
Authors	:	Rozeboom, H.J.; Yu, S.; Mikkelsen, R.; Nikolaev, I.; Mulder, H.; Dijkstra,
		B.W.
Deposited on	:	2014-03-25
Resolution	:	1.83  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* 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 (i)) were used in the production of this report:

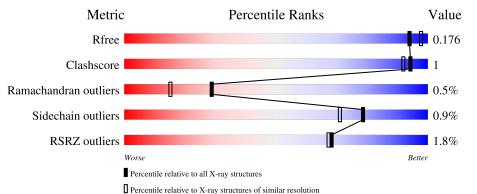
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as $541$ be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.83 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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	А	572	2% 93%	5% •



#### 4CVC

# 2 Entry composition (i)

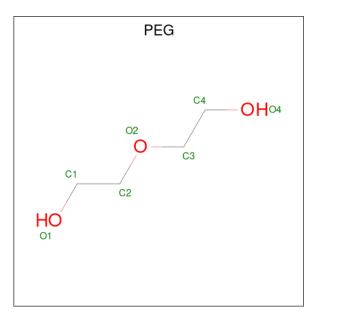
There are 7 unique types of molecules in this entry. The entry contains 4884 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ALCOHOL DEHYDROGENASE.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	562	Total	С	N	0	S	0	3	0
			4269	2687	714	853	15		Ū	

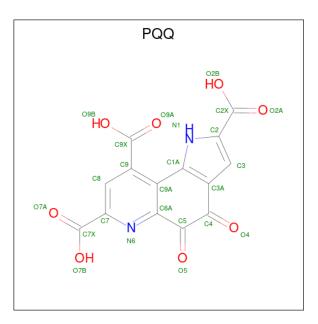
• Molecule 2 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
2	А	1	Total 7	$\begin{array}{c} \mathrm{C} \\ 4 \end{array}$	O 3	0	0

• Molecule 3 is PYRROLOQUINOLINE QUINONE (three-letter code: PQQ) (formula:  $C_{14}H_6N_2O_8$ ).





M	ol	Chain	Residues	A	Aton	ns		ZeroOcc	AltConf
3	×	А	1	Total	С	Ν	0	0	0
	,	11	1	24	14	2	8	0	Ū

• Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

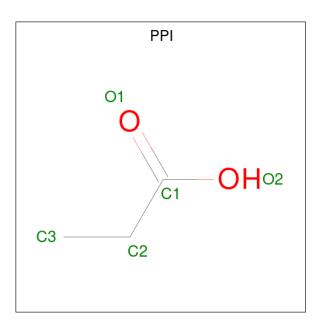
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	7	Total Zn 7 7	0	0

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

[	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	5	А	1	Total Cl 1 1	0	0

• Molecule 6 is PROPANOIC ACID (three-letter code: PPI) (formula:  $C_3H_6O_2$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	А	1	Total 5	${ m C} { m 3}$	O 2	0	0

• Molecule 7 is water.

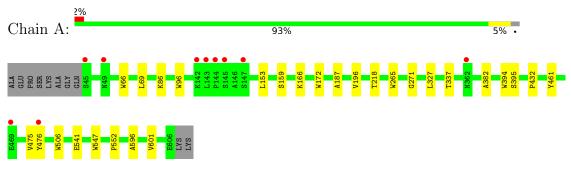
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	571	Total O 571 571	0	0



# 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: ALCOHOL DEHYDROGENASE





### 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	128.22Å 87.16Å 57.00Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.29^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	72.08 - 1.83	Depositor
Resolution (A)	32.05 - 1.84	EDS
% Data completeness	99.9(72.08-1.83)	Depositor
(in resolution range)	100.0 (32.05 - 1.84)	EDS
R <sub>merge</sub>	0.08	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.26 (at 1.83 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
P. P.	0.161 , $0.184$	Depositor
$R, R_{free}$	0.162 , $0.176$	DCC
$R_{free}$ test set	5404 reflections $(9.86\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	10.1	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.38 , $44.3$	EDS
L-test for twinning <sup>2</sup>	$< L >=0.48, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4884	wwPDB-VP
Average B, all atoms $(Å^2)$	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.45% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: PEG, CL, PQQ, ZN, PPI

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	Boi	nd lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.52	6/4374~(0.1%)	0.57	0/5969	

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	А	506	TRP	CD2-CE2	5.37	1.47	1.41
1	А	265	TRP	CD2-CE2	5.11	1.47	1.41
1	А	172	TRP	CD2-CE2	5.08	1.47	1.41
1	А	547	TRP	CD2-CE2	5.08	1.47	1.41
1	А	394	TRP	CD2-CE2	5.04	1.47	1.41
1	А	66	TRP	CD2-CE2	5.03	1.47	1.41

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	А	4269	0	4064	8	0	
2	А	7	0	10	3	0	
3	А	24	0	3	3	0	
4	А	7	0	0	0	0	
5	А	1	0	0	0	0	

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	А	5	0	5	0	0
7	А	571	0	0	0	0
All	All	4884	0	4082	11	0

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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 1.

All (11) 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)
2:A:1607:PEG:H21	3:A:1608:PQQ:C4	2.34	0.56
2:A:1607:PEG:O1	3:A:1608:PQQ:O5	2.31	0.48
1:A:86:LYS:NZ	1:A:541:GLU:OE1	2.48	0.47
1:A:166:LYS:HE3	1:A:187:ALA:CB	2.46	0.45
1:A:271:GLY:HA3	1:A:337:THR:O	2.17	0.45
3:A:1608:PQQ:O9B	3:A:1608:PQQ:N1	2.46	0.44
1:A:153:LEU:HD11	2:A:1607:PEG:H42	1.99	0.44
1:A:69:LEU:HD13	1:A:159:SER:HB3	2.01	0.42
1:A:382:ALA:O	1:A:395:SER:HA	2.19	0.42
1:A:96:TRP:CZ2	1:A:601:VAL:HG21	2.55	0.42
1:A:552:PRO:HB2	1:A:596:ALA:HB3	2.02	0.41

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	А	563/572~(98%)	546 (97%)	14 (2%)	3~(0%)	29 15	

All (3) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	А	432	PRO
1	А	196	VAL
1	А	475	VAL

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	449/453~(99%)	445~(99%)	4 (1%)	78 71	

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	218	THR
1	А	327	LEU
1	А	461	TYR
1	А	476	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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 monosaccharides in this entry.



#### Ligand geometry (i) 5.6

Of 11 ligands modelled in this entry, 8 are monoatomic - leaving 3 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	Turne	ype Chain	hain Res	tes Link	Bo	Bond lengths			Bond angles		
	Moi Type				Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
6	PPI	А	1617	4	4,4,4	1.03	0	4,4,4	0.81	0	
2	PEG	А	1607	-	$6,\!6,\!6$	0.47	0	$5,\!5,\!5$	0.28	0	
3	PQQ	А	1608	4	23,26,26	2.24	3 (13%)	29,40,40	2.56	12 (41%)	

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
6	PPI	А	1617	4	-	2/2/2/2	-
2	PEG	А	1607	-	-	2/4/4/4	-
3	PQQ	А	1608	4	-	4/10/28/28	0/3/3/3

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А		÷ -	O4-C4		( )	1.23
3	А	1608	PQQ	C6A-C9A	5.22	1.48	1.42

C9-C9A

All (3) bond length outliers are listed below:

All (12) bond angle outliers are listed below:

PQQ

1608

3

А

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	А	1608	PQQ	C9-C9A-C1A	6.10	127.88	122.88
3	А	1608	PQQ	O4-C4-C3A	-5.20	112.21	122.23
3	А	1608	PQQ	O4-C4-C5	-4.92	110.77	119.31
3	А	1608	PQQ	C9-C9A-C6A	-4.71	115.38	121.68
3	А	1608	PQQ	C6A-N6-C7	3.49	123.78	117.91
3	А	1608	PQQ	C2-N1-C1A	2.81	109.67	103.90

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1.41



4.28

1.50

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	1608	PQQ	O2B-C2X-C2	2.65	120.72	114.69
3	А	1608	PQQ	O9B-C9X-C9	2.61	121.79	114.39
3	А	1608	PQQ	O9A-C9X-C9	-2.59	115.31	122.23
3	А	1608	PQQ	O2A-C2X-C2	-2.53	116.10	121.24
3	А	1608	PQQ	C2-C3-C3A	-2.41	102.78	105.98
3	А	1608	PQQ	C3A-C1A-C9A	2.14	124.38	121.54

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There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	1608	PQQ	С9А-С9-С9Х-О9В
3	А	1608	PQQ	С9А-С9-С9Х-О9А
3	А	1608	PQQ	C8-C9-C9X-O9A
3	А	1608	PQQ	С8-С9-С9Х-О9В
2	А	1607	PEG	C1-C2-O2-C3
2	А	1607	PEG	C4-C3-O2-C2
6	А	1617	PPI	O1-C1-C2-C3
6	А	1617	PPI	O2-C1-C2-C3

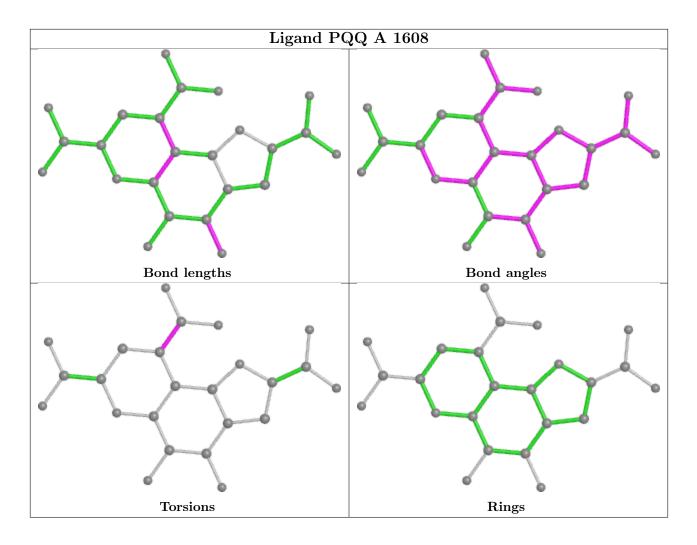
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	1607	PEG	3	0
3	А	1608	PQQ	3	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 then 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,  $95^{th}$  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 $>$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	562/572~(98%)	-0.18	10 (1%) 68 67	5, 10, 22, 30	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	362	ASN	4.0
1	А	49	ASN	3.9
1	А	476	TYR	3.3
1	А	144	PRO	3.1
1	А	143	LEU	3.0
1	А	45	SER	2.8
1	А	147	SER	2.8
1	А	145	SER	2.5
1	А	142	LYS	2.4
1	А	469	GLU	2.1

### 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.

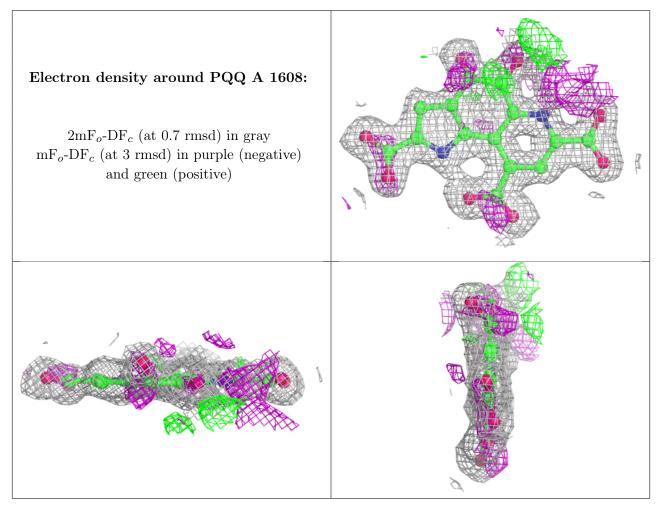
#### 6.4 Ligands (i)

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,  $95^{th}$  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	$B$ -factors( $Å^2$ )	Q<0.9
2	PEG	А	1607	7/7	0.69	0.28	$25,\!28,\!31,\!33$	0
4	ZN	А	1615	1/1	0.88	0.14	23,23,23,23	1
5	CL	А	1616	1/1	0.92	0.11	12,12,12,12	0
6	PPI	А	1617	5/5	0.92	0.18	10,10,10,11	0
3	PQQ	А	1608	24/24	0.93	0.12	10,11,12,13	0
4	ZN	А	1613	1/1	0.96	0.10	12,12,12,12	1
4	ZN	А	1614	1/1	0.98	0.06	14,14,14,14	1
4	ZN	А	1610	1/1	0.98	0.09	20,20,20,20	0
4	ZN	А	1612	1/1	0.99	0.04	14,14,14,14	0
4	ZN	А	1609	1/1	0.99	0.02	9,9,9,9	0
4	ZN	А	1611	1/1	0.99	0.03	9,9,9,9	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.

