



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:44 AM UTC

PDB ID : 7UHQ / pdb_00007uhq
Title : Time-Resolved Structure of Metallo Beta-Lactamase L1 in a Complex with Cleaved Moxalactam (4000 ms Snapshot)
Authors : Wilamowski, M.; Kim, Y.; Sherrell, D.A.; Lavens, A.; Henning, R.; Maltseva, N.; Endres, M.; Babnigg, G.; Srajer, V.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2022-03-27
Resolution : 2.20 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 ⓘ 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

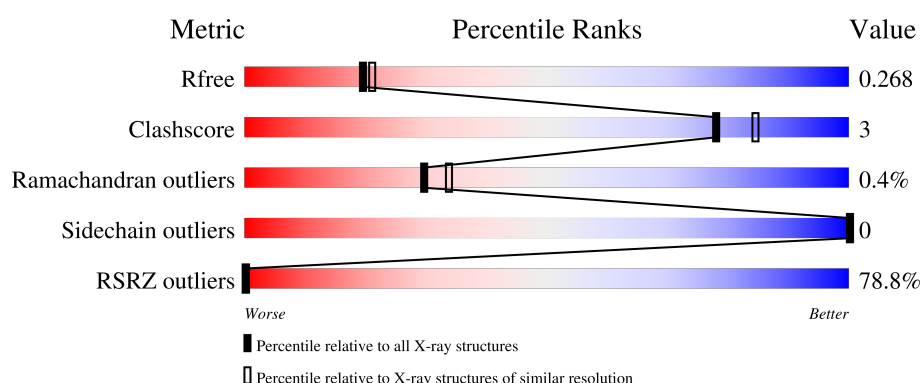
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 $\leq 5\%$. 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	275	76% 88%8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2070 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 Putative metallo-beta-lactamase 11 (Beta-lactamase type ii) (Ec 3.5.2.6) (Penicillinase).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	0	0
			1986	1251	355	372	8			

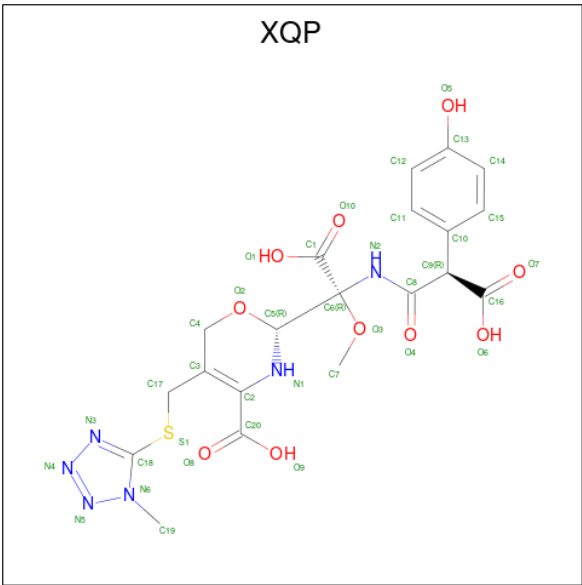
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	SER	-	expression tag	UNP B2FTM1
A	17	ASN	-	expression tag	UNP B2FTM1
A	18	ALA	-	expression tag	UNP B2FTM1

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is (2R)-2-[(R)-carboxy{[(2R)-2-carboxy-2-(4-hydroxyphenyl)acetyl]amino}methoxymethyl]-5-[[[(1-methyl-1H-tetrazol-5-yl)sulfanyl]methyl]-3,6-dihydro-2H-1,3-oxazine-4-carboxylic acid (CCD ID: XQP) (formula: C₂₀H₂₂N₆O₁₀S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			24	13	2	9		

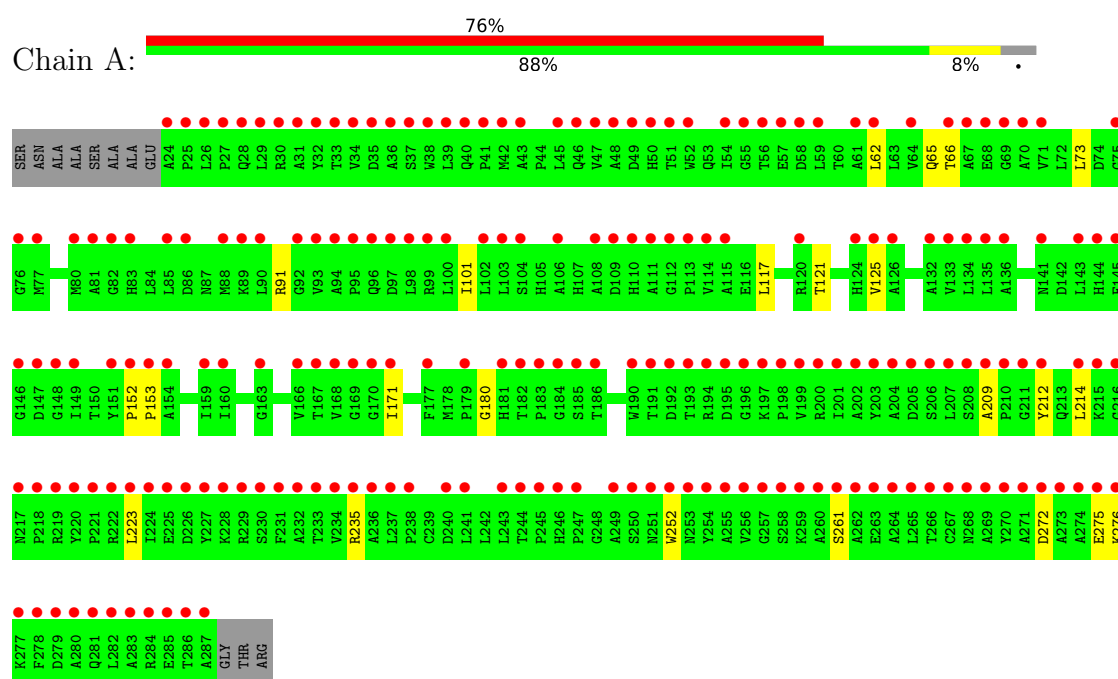
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	58	Total	O	0	0
			58	58		

3 Residue-property plots

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: Putative metallo-beta-lactamase 11 (Beta-lactamase type ii) (Ec 3.5.2.6) (Penicillinase)



4 Data and refinement statistics

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, α , β , γ	105.85Å 105.85Å 99.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.65 – 2.20 33.65 – 2.20	Depositor EDS
% Data completeness (in resolution range)	67.6 (33.65-2.20) 67.9 (33.65-2.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.72 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.233 , 0.264 0.234 , 0.268	Depositor DCC
R_{free} test set	543 reflections (3.18%)	wwPDB-VP
Wilson B-factor (Å ²)	7.0	Xtriage
Anisotropy	0.633	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 27.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.64	EDS
Total number of atoms	2070	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: ZN, XQP

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	0.10	0/2036	0.28	0/2782

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	1986	0	1949	11	0
2	A	2	0	0	0	0
3	A	24	0	0	0	0
4	A	58	0	0	0	0
All	All	2070	0	1949	11	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 (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)
1:A:235:ARG:NH1	1:A:275:GLU:OE1	2.37	0.53
1:A:101:ILE:HB	1:A:125:VAL:HG22	1.92	0.52
1:A:117:LEU:O	1:A:121:THR:OG1	2.26	0.48
1:A:66:THR:HG22	1:A:171:ILE:HD12	1.95	0.47
1:A:252:TRP:CH2	1:A:261:SER:HB3	2.49	0.46
1:A:65:GLN:OE1	1:A:91:ARG:NH1	2.41	0.44
1:A:272:ASP:O	1:A:276:LYS:HG3	2.19	0.42
1:A:62:LEU:HB2	1:A:73:LEU:HB2	2.01	0.42
1:A:214:LEU:HA	1:A:223:LEU:HD22	2.02	0.41
1:A:152:PRO:HA	1:A:153:PRO:HD3	1.84	0.41
1:A:209:ALA:HB1	1:A:212:TYR:HB2	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	A	262/275 (95%)	247 (94%)	14 (5%)	1 (0%)	30	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	180	GLY

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	200/206 (97%)	200 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 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	$\# Z > 2$
3	XQP	A	303	2	21,24,39	1.33	3 (14%)	18,35,56	1.08	2 (11%)

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
3	XQP	A	303	2	-	5/18/45/54	0/1/1/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	303	XQP	O9-C20	-3.11	1.22	1.30
3	A	303	XQP	C2-C20	3.10	1.53	1.48
3	A	303	XQP	O6-C16	-2.91	1.21	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	303	XQP	O8-C20-C2	-2.56	115.75	120.20
3	A	303	XQP	C17-C3-C2	2.18	126.12	123.50

There are no chirality outliers.

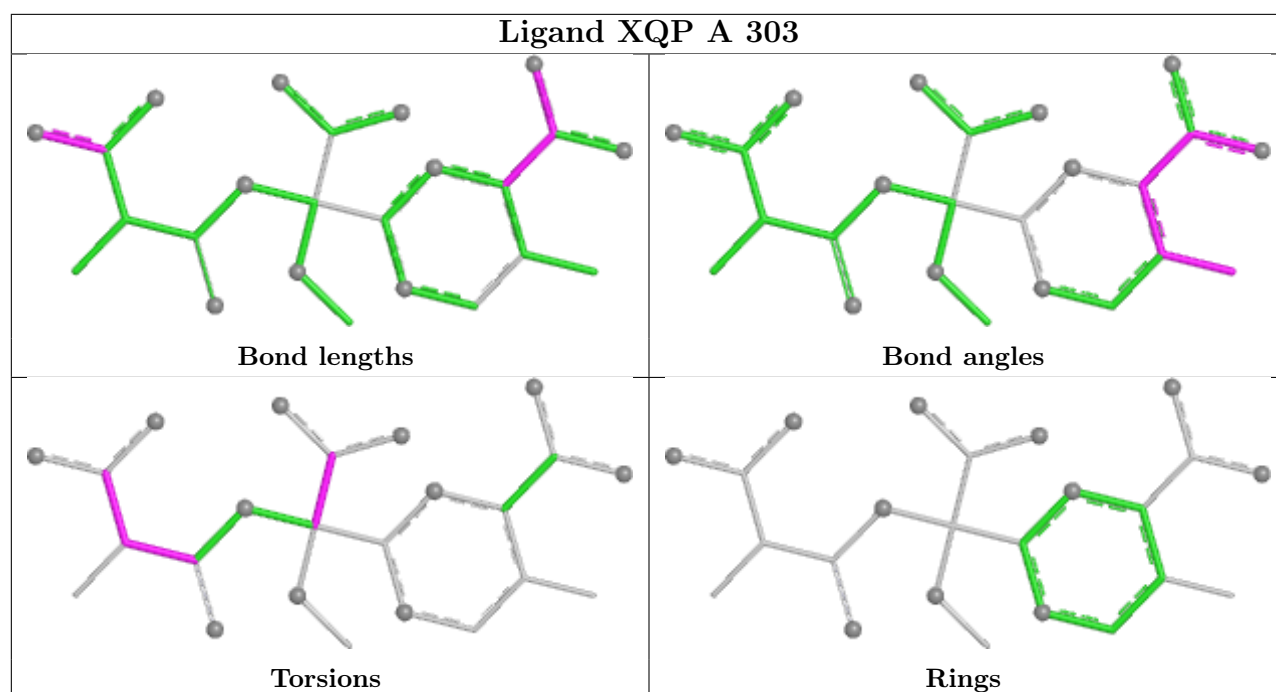
All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	XQP	N2-C8-C9-C16
3	A	303	XQP	O4-C8-C9-C16
3	A	303	XQP	O6-C16-C9-C10
3	A	303	XQP	O7-C16-C9-C10
3	A	303	XQP	O1-C1-C6-N2

There are no ring outliers.

No monomer is involved in short contacts.

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 than 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 ⓘ

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, 95th 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	A	264/275 (96%)	3.04	208 (78%) 0 0	9, 24, 42, 67	0

All (208) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	286	THR	9.3
1	A	287	ALA	8.7
1	A	195	ASP	6.8
1	A	204	ALA	6.7
1	A	259	LYS	6.6
1	A	32	TYR	6.4
1	A	36	ALA	6.2
1	A	196	GLY	6.1
1	A	194	ARG	5.9
1	A	35	ASP	5.9
1	A	26	LEU	5.8
1	A	262	ALA	5.7
1	A	285	GLU	5.6
1	A	30	ARG	5.4
1	A	75	GLY	5.4
1	A	260	ALA	5.3
1	A	234	VAL	5.2
1	A	201	ILE	5.0
1	A	24	ALA	5.0
1	A	34	VAL	5.0
1	A	146	GLY	5.0
1	A	232	ALA	4.9
1	A	39	LEU	4.9
1	A	258	SER	4.8
1	A	47	VAL	4.8
1	A	38	TRP	4.8
1	A	134	LEU	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	145	PHE	4.8
1	A	93	VAL	4.7
1	A	94	ALA	4.7
1	A	284	ARG	4.6
1	A	268	ASN	4.6
1	A	272	ASP	4.6
1	A	219	ARG	4.5
1	A	256	VAL	4.4
1	A	261	SER	4.4
1	A	271	ALA	4.3
1	A	193	THR	4.3
1	A	223	LEU	4.3
1	A	265	LEU	4.3
1	A	255	ALA	4.3
1	A	25	PRO	4.3
1	A	229	ARG	4.2
1	A	96	GLN	4.2
1	A	263	GLU	4.2
1	A	33	THR	4.2
1	A	41	PRO	4.2
1	A	236	ALA	4.1
1	A	199	VAL	4.1
1	A	276	LYS	4.0
1	A	197	LYS	4.0
1	A	216	GLY	4.0
1	A	253	ASN	4.0
1	A	37	SER	4.0
1	A	283	ALA	4.0
1	A	67	ALA	3.9
1	A	254	TYR	3.9
1	A	274	ALA	3.9
1	A	241	LEU	3.9
1	A	51	THR	3.9
1	A	95	PRO	3.8
1	A	269	ALA	3.8
1	A	267	CYS	3.8
1	A	52	TRP	3.8
1	A	235	ARG	3.8
1	A	224	ILE	3.7
1	A	90	LEU	3.7
1	A	257	GLY	3.7
1	A	247	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	278	PHE	3.7
1	A	154	ALA	3.7
1	A	143	LEU	3.6
1	A	202	ALA	3.6
1	A	207	LEU	3.6
1	A	111	ALA	3.6
1	A	203	TYR	3.5
1	A	82	GLY	3.5
1	A	282	LEU	3.5
1	A	279	ASP	3.5
1	A	231	PHE	3.5
1	A	133	VAL	3.4
1	A	70	ALA	3.4
1	A	27	PRO	3.4
1	A	29	LEU	3.4
1	A	48	ALA	3.4
1	A	205	ASP	3.4
1	A	270	TYR	3.3
1	A	251	ASN	3.3
1	A	198	PRO	3.3
1	A	222	ARG	3.3
1	A	81	ALA	3.3
1	A	280	ALA	3.3
1	A	97	ASP	3.3
1	A	277	LYS	3.3
1	A	210	PRO	3.3
1	A	43	ALA	3.2
1	A	31	ALA	3.2
1	A	264	ALA	3.2
1	A	153	PRO	3.2
1	A	57	GLU	3.2
1	A	151	TYR	3.2
1	A	252	TRP	3.2
1	A	214	LEU	3.2
1	A	56	THR	3.2
1	A	28	GLN	3.1
1	A	40	GLN	3.1
1	A	182	THR	3.1
1	A	64	VAL	3.1
1	A	152	PRO	3.1
1	A	218	PRO	3.1
1	A	191	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	217	ASN	3.0
1	A	103	LEU	3.0
1	A	68	GLU	3.0
1	A	54	ILE	3.0
1	A	149	ILE	3.0
1	A	171	ILE	3.0
1	A	233	THR	3.0
1	A	49	ASP	3.0
1	A	179	PRO	3.0
1	A	160	ILE	3.0
1	A	148	GLY	3.0
1	A	136	ALA	3.0
1	A	230	SER	3.0
1	A	58	ASP	2.9
1	A	132	ALA	2.9
1	A	249	ALA	2.9
1	A	92	GLY	2.9
1	A	181	HIS	2.8
1	A	273	ALA	2.8
1	A	89	LYS	2.8
1	A	237	LEU	2.8
1	A	114	VAL	2.8
1	A	66	THR	2.8
1	A	246	HIS	2.8
1	A	86	ASP	2.8
1	A	220	TYR	2.8
1	A	206	SER	2.7
1	A	77	MET	2.7
1	A	50	HIS	2.7
1	A	183	PRO	2.7
1	A	80	MET	2.7
1	A	144	HIS	2.7
1	A	113	PRO	2.7
1	A	238	PRO	2.7
1	A	275	GLU	2.7
1	A	147	ASP	2.7
1	A	245	PRO	2.7
1	A	243	LEU	2.7
1	A	62	LEU	2.6
1	A	250	SER	2.6
1	A	135	LEU	2.6
1	A	186	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	266	THR	2.6
1	A	46	GLN	2.5
1	A	240	ASP	2.5
1	A	59	LEU	2.5
1	A	108	ALA	2.5
1	A	112	GLY	2.5
1	A	244	THR	2.5
1	A	177	PHE	2.5
1	A	126	ALA	2.5
1	A	215	LYS	2.5
1	A	225	GLU	2.5
1	A	45	LEU	2.5
1	A	42	MET	2.5
1	A	55	GLY	2.5
1	A	120	ARG	2.4
1	A	228	LYS	2.4
1	A	102	LEU	2.4
1	A	281	GLN	2.4
1	A	221	PRO	2.4
1	A	76	GLY	2.4
1	A	99	ARG	2.4
1	A	124	HIS	2.4
1	A	109	ASP	2.3
1	A	163	GLY	2.3
1	A	125	VAL	2.3
1	A	168	VAL	2.3
1	A	200	ARG	2.3
1	A	170	GLY	2.3
1	A	184	GLY	2.3
1	A	106	ALA	2.3
1	A	71	VAL	2.3
1	A	212	TYR	2.3
1	A	167	THR	2.3
1	A	100	LEU	2.3
1	A	69	GLY	2.3
1	A	169	GLY	2.3
1	A	159	ILE	2.3
1	A	141	ASN	2.2
1	A	98	LEU	2.2
1	A	209	ALA	2.2
1	A	227	TYR	2.2
1	A	190	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	192	ASP	2.2
1	A	115	ALA	2.2
1	A	88	MET	2.2
1	A	211	GLY	2.1
1	A	185	SER	2.1
1	A	208	SER	2.1
1	A	85	LEU	2.1
1	A	104	SER	2.1
1	A	83	HIS	2.1
1	A	166	VAL	2.1
1	A	61	ALA	2.0
1	A	110	HIS	2.0
1	A	226	ASP	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

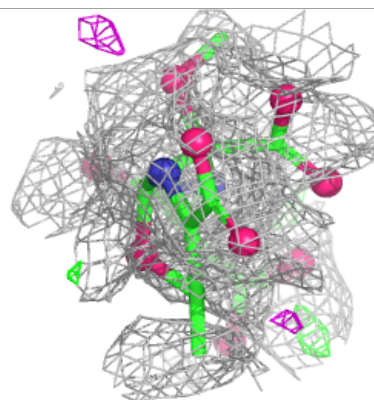
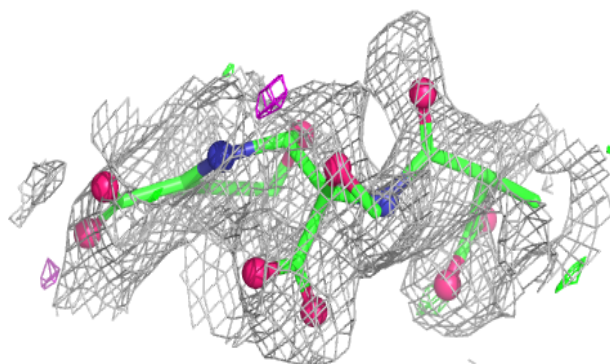
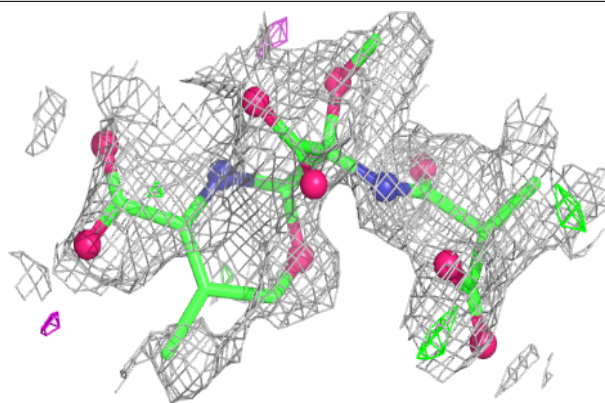
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	XQP	A	303	24/37	0.57	0.29	28,28,30,31	24
2	ZN	A	301	1/1	0.88	0.10	27,27,27,27	1
2	ZN	A	302	1/1	0.92	0.05	14,14,14,14	1

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.

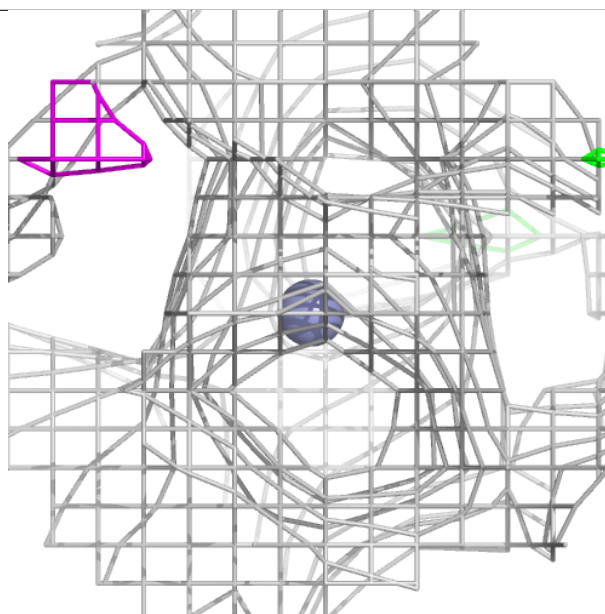
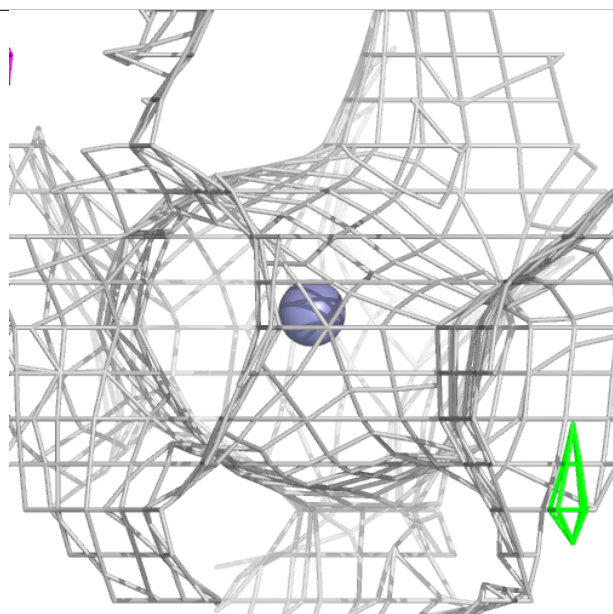
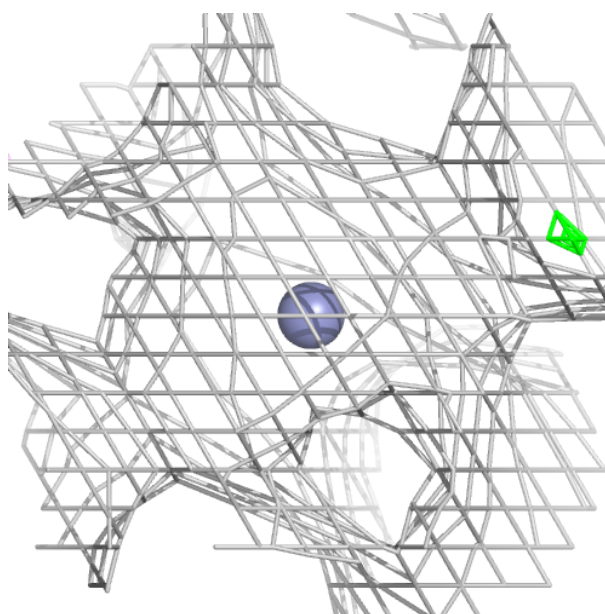
Electron density around XQP A 303:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



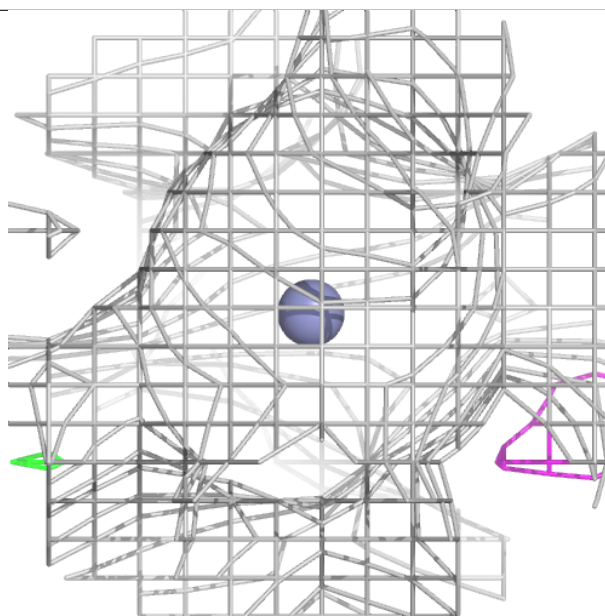
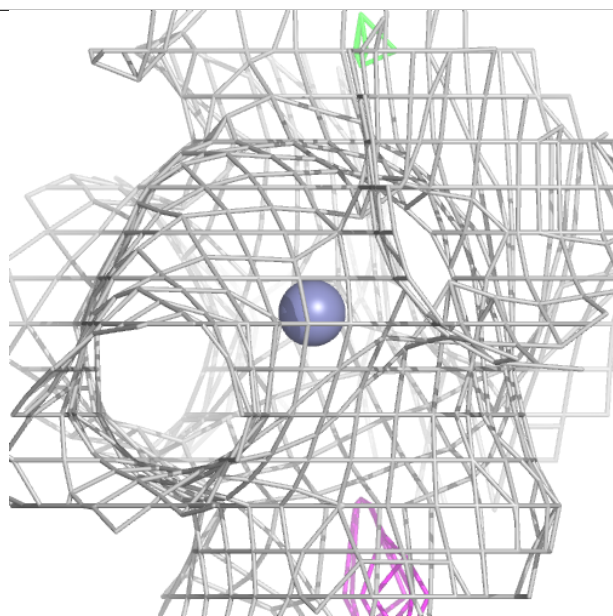
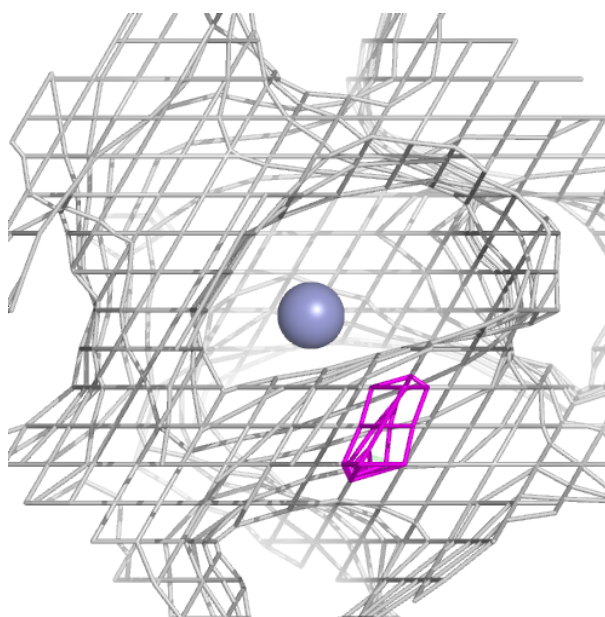
Electron density around ZN A 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN A 302:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.