



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 03:38 pm BST

PDB ID : 6QP4
Title : Structure of 299-452 fragment of the UspA1 protein from *Moraxella catarrhalis*
Authors : Mikula, K.M.; Kolodziejczyk, R.; Goldman, A.
Deposited on : 2019-02-13
Resolution : 2.50 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 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
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) : 2.11

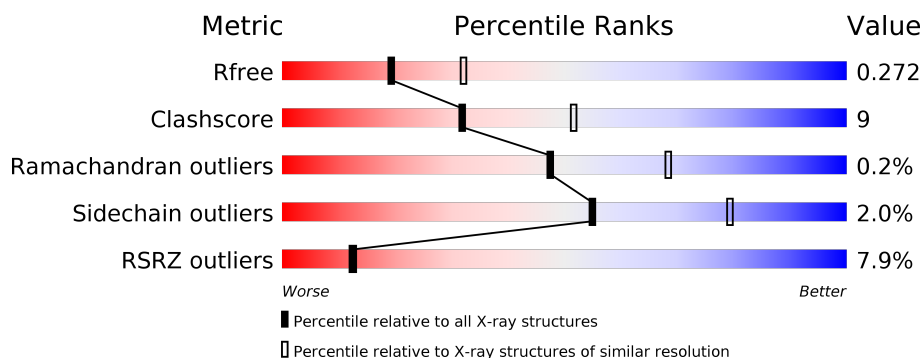
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 ≥ 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	158	<div> <div>14%</div> <div> <div></div> <div>80%</div> <div>17%</div> <div>..</div> </div> </div>
1	B	158	<div> <div>6%</div> <div> <div></div> <div>79%</div> <div>17%</div> <div>..</div> </div> </div>
1	C	158	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>18%</div> <div>..</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7461 atoms, of which 3634 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 UspA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	H	N	O	0	0	0
			2355	720	1169	209	257			
1	B	155	Total	C	H	N	O	0	0	0
			2314	710	1144	205	255			
1	C	155	Total	C	H	N	O	0	0	0
			2323	710	1153	205	255			

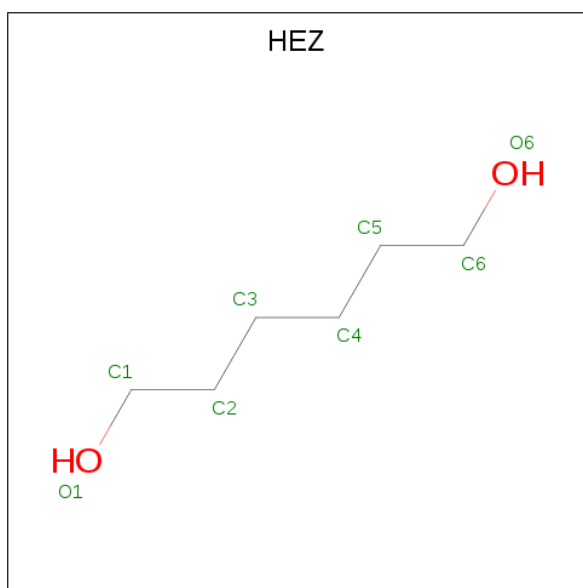
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	453	LEU	-	expression tag	UNP Q9XD56
A	454	VAL	-	expression tag	UNP Q9XD56
A	455	PRO	-	expression tag	UNP Q9XD56
A	456	ARG	-	expression tag	UNP Q9XD56
B	453	LEU	-	expression tag	UNP Q9XD56
B	454	VAL	-	expression tag	UNP Q9XD56
B	455	PRO	-	expression tag	UNP Q9XD56
B	456	ARG	-	expression tag	UNP Q9XD56
C	453	LEU	-	expression tag	UNP Q9XD56
C	454	VAL	-	expression tag	UNP Q9XD56
C	455	PRO	-	expression tag	UNP Q9XD56
C	456	ARG	-	expression tag	UNP Q9XD56

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		
2	A	3	Total	Cl	0	0
			3	3		

- Molecule 3 is HEXANE-1,6-DIOL (three-letter code: HEZ) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			22	6	14	2		
3	A	1	Total	C	H	O	0	0
			22	6	14	2		
3	A	1	Total	C	H	O	0	0
			22	6	14	2		
3	B	1	Total	C	H	O	0	0
			22	6	14	2		
3	B	1	Total	C	H	O	0	0
			22	6	14	2		
3	C	1	Total	C	H	O	0	0
			22	6	14	2		
3	C	1	Total	C	H	O	0	0
			22	6	14	2		
3	C	1	Total	C	H	O	0	0
			22	6	14	2		
3	C	1	Total	C	H	O	0	0
			22	6	14	2		
3	C	1	Total	C	H	O	0	0
			22	6	14	2		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Zn 1	0	0
4	C	1	Total 1	Zn 1	0	0

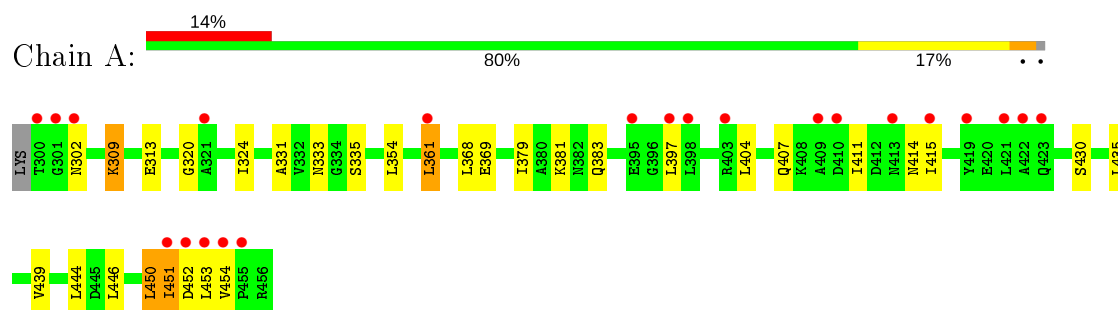
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	64	Total 64	O 64	0	0
5	B	66	Total 66	O 66	0	0
5	C	69	Total 69	O 69	0	0

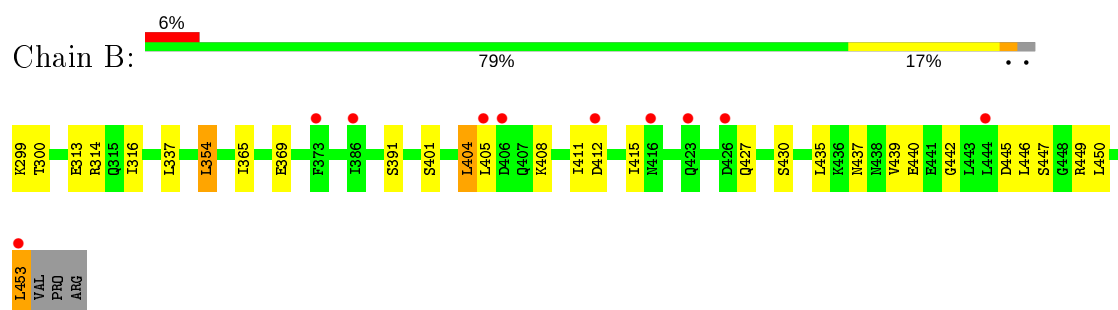
3 Residue-property plots [i](#)

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.

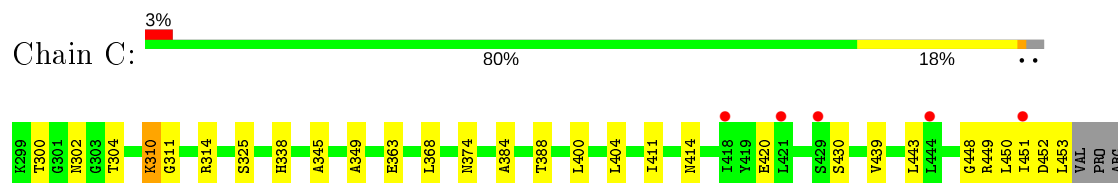
• Molecule 1: UspA1



• Molecule 1: UspA1



• Molecule 1: UspA1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.64Å 44.56Å 128.44Å 90.00° 92.07° 90.00°	Depositor
Resolution (Å)	46.00 – 2.50 46.01 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.3 (46.00-2.50) 98.5 (46.01-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.26 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.14 _3260: ???)	Depositor
R, R_{free}	0.212 , 0.272 0.212 , 0.272	Depositor DCC
R_{free} test set	1285 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	0.916	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 63.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.010 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7461	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.69% 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, HEZ, CL

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	0.70	0/1191	0.80	2/1608 (0.1%)
1	B	0.66	0/1174	0.84	3/1583 (0.2%)
1	C	0.69	1/1174 (0.1%)	0.77	1/1583 (0.1%)
All	All	0.68	1/3539 (0.0%)	0.80	6/4774 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	363	GLU	CG-CD	6.02	1.60	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	354	LEU	CB-CG-CD2	-5.39	101.84	111.00
1	A	450	LEU	CB-CG-CD1	5.31	120.02	111.00
1	A	361	LEU	CB-CG-CD2	5.20	119.84	111.00
1	B	404	LEU	CB-CG-CD1	-5.14	102.26	111.00
1	B	453	LEU	CA-CB-CG	-5.14	103.49	115.30
1	C	368	LEU	CB-CG-CD2	5.01	119.51	111.00

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	1186	1169	1169	35	2
1	B	1170	1144	1153	33	0
1	C	1170	1153	1153	24	2
2	A	3	0	0	0	0
2	B	1	0	0	0	0
3	A	24	42	42	1	0
3	B	16	28	28	2	0
3	C	56	98	98	4	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	64	0	0	2	0
5	B	66	0	0	3	0
5	C	69	0	0	3	0
All	All	3827	3634	3643	65	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 9.

All (65) 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:411:ILE:HD11	1:B:411:ILE:HD11	1.55	0.88
1:A:450:LEU:HD12	1:A:451:ILE:N	2.03	0.73
1:A:404:LEU:HD13	1:B:404:LEU:HD21	1.72	0.70
1:B:411:ILE:HD11	1:C:411:ILE:HD11	1.75	0.68
1:A:435:LEU:HD21	1:B:435:LEU:HD22	1.79	0.65
1:B:313:GLU:OE1	5:B:602:HOH:O	2.16	0.63
1:A:411:ILE:HD11	1:B:411:ILE:CD1	2.28	0.63
1:C:349:ALA:HB2	3:C:504:HEZ:H21	1.83	0.60
1:A:450:LEU:C	1:A:450:LEU:HD12	2.23	0.59
1:A:407:GLN:NE2	5:C:604:HOH:O	2.35	0.59
1:B:314:ARG:NE	5:B:601:HOH:O	2.03	0.58
1:B:450:LEU:O	1:B:450:LEU:HD23	2.03	0.58
1:A:324:ILE:HD12	1:B:337:LEU:HD23	1.86	0.57
1:A:411:ILE:HD11	1:C:411:ILE:HD11	1.87	0.57
5:B:601:HOH:O	1:C:302:ASN:C	2.44	0.56
1:A:407:GLN:OE1	1:B:408:LYS:HG3	2.06	0.56
1:A:452:ASP:OD1	1:B:453:LEU:HD22	2.05	0.56
1:A:446:LEU:HD21	1:B:447:SER:HB2	1.90	0.53
1:A:381:LYS:NZ	5:A:604:HOH:O	2.42	0.53
1:A:454:VAL:O	1:A:454:VAL:HG13	2.08	0.53
1:B:446:LEU:CD1	1:C:443:LEU:HD22	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:452:ASP:C	1:C:453:LEU:HD23	2.29	0.52
1:A:439:VAL:HG22	1:B:439:VAL:HG11	1.92	0.51
1:A:361:LEU:HD22	1:B:365:ILE:HD12	1.93	0.50
1:C:300:THR:O	1:C:304:THR:O	2.31	0.49
1:B:445:ASP:O	1:B:449:ARG:HG3	2.12	0.49
1:C:384:ALA:O	1:C:388:THR:HG23	2.13	0.49
1:A:368:LEU:HD21	1:B:369:GLU:CG	2.44	0.48
1:A:397:LEU:HD22	1:C:400:LEU:HD12	1.96	0.48
1:A:354:LEU:HD21	1:B:354:LEU:HB3	1.95	0.48
1:A:450:LEU:O	1:A:453:LEU:N	2.46	0.48
1:A:313:GLU:OE2	5:A:601:HOH:O	2.20	0.47
1:C:345:ALA:HB1	3:C:504:HEZ:H12	1.95	0.47
1:A:361:LEU:HD22	1:B:365:ILE:CD1	2.43	0.47
1:B:404:LEU:HG	1:C:404:LEU:HD21	1.97	0.47
1:B:427:GLN:O	1:B:430:SER:HB3	2.15	0.47
1:B:449:ARG:NH2	1:C:450:LEU:HD22	2.30	0.46
1:A:335:SER:HA	1:C:325:SER:O	2.15	0.46
1:A:379:ILE:O	1:A:383:GLN:HG3	2.16	0.46
1:B:300:THR:HB	3:B:503:HEZ:H52	1.98	0.46
1:C:345:ALA:O	3:C:504:HEZ:H21	2.17	0.45
1:B:450:LEU:O	1:B:450:LEU:CG	2.65	0.45
1:A:450:LEU:HD12	1:A:451:ILE:CA	2.47	0.44
1:A:439:VAL:HG11	1:C:439:VAL:HG12	1.98	0.44
1:C:448:GLY:O	1:C:451:ILE:HG13	2.17	0.44
1:A:414:ASN:HD21	1:B:415:ILE:HG13	1.83	0.44
1:B:450:LEU:CD2	1:B:450:LEU:O	2.64	0.44
1:C:420:GLU:HA	1:C:420:GLU:OE1	2.18	0.44
1:A:302:ASN:HA	1:C:314:ARG:HE	1.83	0.43
1:B:442:GLY:O	1:B:446:LEU:HD12	2.18	0.42
1:B:299:LYS:HB2	3:B:503:HEZ:O6	2.19	0.42
1:C:449:ARG:NH1	5:C:605:HOH:O	2.41	0.42
1:C:338:HIS:ND1	5:C:601:HOH:O	2.17	0.42
1:C:345:ALA:HA	3:C:504:HEZ:H31	2.01	0.42
1:A:320:GLY:HA2	3:A:504:HEZ:H11	2.02	0.42
1:C:302:ASN:CG	1:C:302:ASN:O	2.58	0.41
1:A:450:LEU:O	1:A:452:ASP:N	2.54	0.41
1:A:331:ALA:HB2	1:B:316:ILE:HB	2.01	0.41
1:A:404:LEU:CD1	1:B:404:LEU:HD21	2.45	0.41
1:C:310:LYS:HD2	1:C:311:GLY:N	2.36	0.41
1:A:333:ASN:C	1:A:333:ASN:OD1	2.59	0.41
1:B:437:ASN:HA	1:B:440:GLU:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:LEU:HD21	1:B:369:GLU:HG2	2.02	0.41
1:B:405:LEU:C	1:B:405:LEU:HD23	2.41	0.40
1:A:415:ILE:HG13	1:C:414:ASN:HD21	1.87	0.40

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	Interatomic distance (Å)	Clash overlap (Å)
1:A:309:LYS:HE3	1:C:374:ASN:HD22[2_656]	1.32	0.28
1:A:369:GLU:OE2	1:C:310:LYS:NZ[2_656]	2.13	0.07

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	155/158 (98%)	150 (97%)	4 (3%)	1 (1%)	25	43
1	B	153/158 (97%)	150 (98%)	3 (2%)	0	100	100
1	C	153/158 (97%)	147 (96%)	6 (4%)	0	100	100
All	All	461/474 (97%)	447 (97%)	13 (3%)	1 (0%)	47	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	451	ILE

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	132/133 (99%)	129 (98%)	3 (2%)	50	76
1	B	130/133 (98%)	127 (98%)	3 (2%)	50	76
1	C	130/133 (98%)	128 (98%)	2 (2%)	65	85
All	All	392/399 (98%)	384 (98%)	8 (2%)	55	79

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	309	LYS
1	A	430	SER
1	A	444	LEU
1	B	391	SER
1	B	401	SER
1	B	412	ASP
1	C	310	LYS
1	C	430	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	423	GLN
1	C	437	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 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 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	HEZ	C	501	-	7,7,7	0.35	0	6,6,6	0.82	0
3	HEZ	C	504	-	7,7,7	0.54	0	6,6,6	0.43	0
3	HEZ	A	504	-	7,7,7	0.45	0	6,6,6	1.07	1 (16%)
3	HEZ	B	502	-	7,7,7	0.48	0	6,6,6	0.64	0
3	HEZ	C	507	-	7,7,7	0.46	0	6,6,6	0.91	0
3	HEZ	C	503	-	7,7,7	0.37	0	6,6,6	0.59	0
3	HEZ	B	503	-	7,7,7	0.63	0	6,6,6	0.75	0
3	HEZ	A	506	-	7,7,7	0.39	0	6,6,6	0.57	0
3	HEZ	C	506	-	7,7,7	0.46	0	6,6,6	0.79	0
3	HEZ	C	505	-	7,7,7	0.30	0	6,6,6	0.87	0
3	HEZ	C	502	-	7,7,7	0.30	0	6,6,6	0.77	0
3	HEZ	A	505	-	7,7,7	0.58	0	6,6,6	0.43	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
3	HEZ	C	501	-	-	4/5/5/5	-
3	HEZ	C	504	-	-	3/5/5/5	-
3	HEZ	A	504	-	-	3/5/5/5	-
3	HEZ	B	502	-	-	2/5/5/5	-
3	HEZ	C	507	-	-	2/5/5/5	-
3	HEZ	C	503	-	-	3/5/5/5	-
3	HEZ	B	503	-	-	3/5/5/5	-
3	HEZ	A	506	-	-	2/5/5/5	-
3	HEZ	C	506	-	-	3/5/5/5	-
3	HEZ	C	505	-	-	2/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEZ	C	502	-	-	2/5/5/5	-
3	HEZ	A	505	-	-	3/5/5/5	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	504	HEZ	C5-C4-C3	-2.39	102.30	114.42

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	504	HEZ	C1-C2-C3-C4
3	C	502	HEZ	C3-C4-C5-C6
3	B	503	HEZ	C2-C3-C4-C5
3	C	501	HEZ	C2-C3-C4-C5
3	C	503	HEZ	C3-C4-C5-C6
3	A	505	HEZ	C1-C2-C3-C4
3	C	505	HEZ	C1-C2-C3-C4
3	C	501	HEZ	O1-C1-C2-C3
3	C	507	HEZ	O1-C1-C2-C3
3	B	503	HEZ	C4-C5-C6-O6
3	C	505	HEZ	C4-C5-C6-O6
3	B	503	HEZ	C3-C4-C5-C6
3	C	504	HEZ	O1-C1-C2-C3
3	A	506	HEZ	C4-C5-C6-O6
3	C	506	HEZ	C4-C5-C6-O6
3	A	505	HEZ	O1-C1-C2-C3
3	C	501	HEZ	C3-C4-C5-C6
3	A	504	HEZ	O1-C1-C2-C3
3	A	504	HEZ	C1-C2-C3-C4
3	A	504	HEZ	C2-C3-C4-C5
3	B	502	HEZ	C4-C5-C6-O6
3	C	504	HEZ	C3-C4-C5-C6
3	B	502	HEZ	C3-C4-C5-C6
3	C	503	HEZ	O1-C1-C2-C3
3	A	506	HEZ	C1-C2-C3-C4
3	C	506	HEZ	C2-C3-C4-C5
3	C	502	HEZ	C4-C5-C6-O6
3	C	503	HEZ	C1-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
3	C	501	HEZ	C4-C5-C6-O6
3	C	507	HEZ	C4-C5-C6-O6
3	A	505	HEZ	C2-C3-C4-C5
3	C	506	HEZ	C3-C4-C5-C6

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	504	HEZ	4	0
3	A	504	HEZ	1	0
3	B	503	HEZ	2	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, 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	157/158 (99%)	1.05	22 (14%) 2 2	22, 52, 103, 121	0
1	B	155/158 (98%)	0.82	10 (6%) 18 19	22, 58, 101, 113	0
1	C	155/158 (98%)	0.86	5 (3%) 47 51	23, 50, 97, 103	0
All	All	467/474 (98%)	0.91	37 (7%) 12 12	22, 55, 100, 121	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	300	THR	4.9
1	C	418	ILE	4.3
1	C	444	LEU	3.7
1	A	451	ILE	3.6
1	A	302	ASN	3.6
1	A	409	ALA	3.4
1	A	453	LEU	3.1
1	A	361	LEU	3.1
1	A	301	GLY	3.0
1	A	452	ASP	3.0
1	B	405	LEU	3.0
1	A	455	PRO	3.0
1	B	426	ASP	2.9
1	B	406	ASP	2.8
1	A	423	GLN	2.8
1	A	403	ARG	2.8
1	B	412	ASP	2.6
1	B	453	LEU	2.5
1	C	429	SER	2.5
1	A	421	LEU	2.5
1	B	373	PHE	2.4
1	A	454	VAL	2.4
1	C	421	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	395	GLU	2.3
1	A	413	ASN	2.3
1	A	397	LEU	2.3
1	A	410	ASP	2.2
1	A	422	ALA	2.2
1	A	415	ILE	2.2
1	B	416	ASN	2.1
1	B	444	LEU	2.1
1	A	321	ALA	2.1
1	B	386	ILE	2.1
1	A	398	LEU	2.1
1	A	419	TYR	2.0
1	C	451	ILE	2.0
1	B	423	GLN	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, 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(Å ²)	Q<0.9
3	HEZ	C	507	8/8	0.58	0.35	59,82,96,97	0
3	HEZ	A	506	8/8	0.68	0.30	66,90,97,98	0
3	HEZ	A	505	8/8	0.72	0.25	53,72,91,92	0
3	HEZ	C	504	8/8	0.73	0.32	47,66,77,85	0
3	HEZ	B	503	8/8	0.73	0.23	45,59,69,70	0
3	HEZ	B	502	8/8	0.74	0.31	44,67,83,102	0
3	HEZ	C	503	8/8	0.77	0.16	74,97,104,106	0
3	HEZ	C	501	8/8	0.78	0.18	75,95,104,104	0
3	HEZ	A	504	8/8	0.81	0.23	43,55,60,66	0

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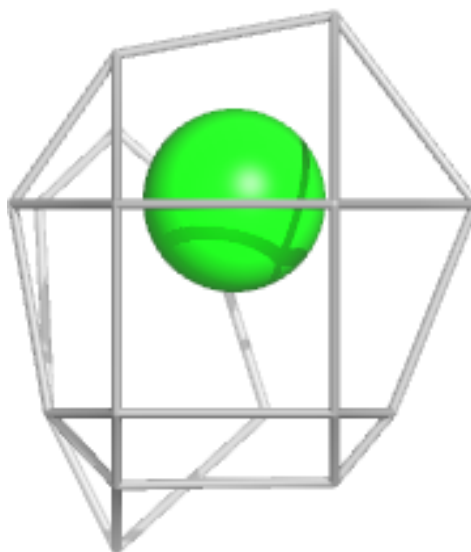
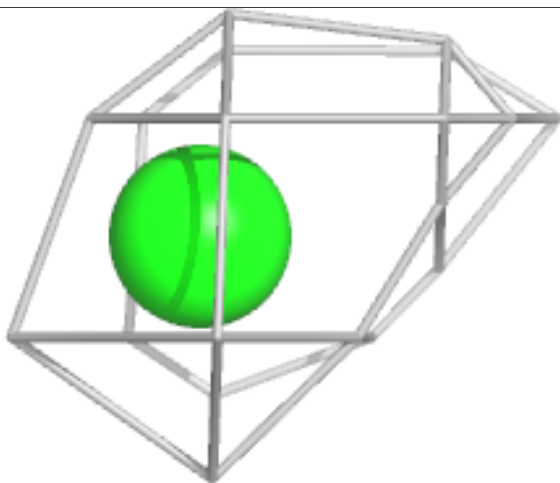
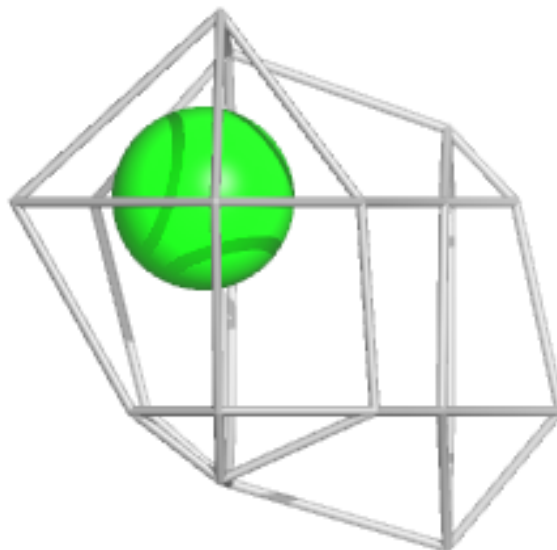
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	HEZ	C	502	8/8	0.82	0.12	74,91,98,106	0
3	HEZ	C	506	8/8	0.82	0.20	32,55,70,73	0
2	CL	B	501	1/1	0.83	0.37	56,56,56,56	1
3	HEZ	C	505	8/8	0.85	0.11	83,100,106,111	0
4	ZN	A	507	1/1	0.86	0.21	83,83,83,83	0
4	ZN	C	508	1/1	0.92	0.16	101,101,101,101	0
2	CL	A	501	1/1	0.99	0.21	35,35,35,35	0
2	CL	A	503	1/1	0.99	0.10	44,44,44,44	0
2	CL	A	502	1/1	0.99	0.19	38,38,38,38	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.

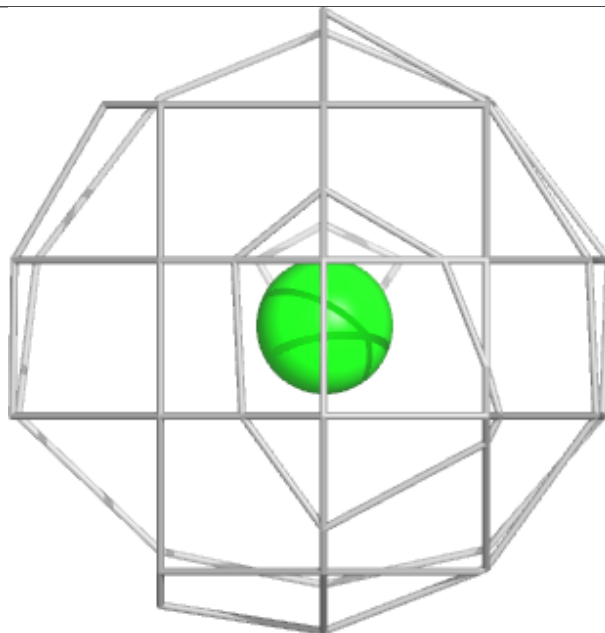
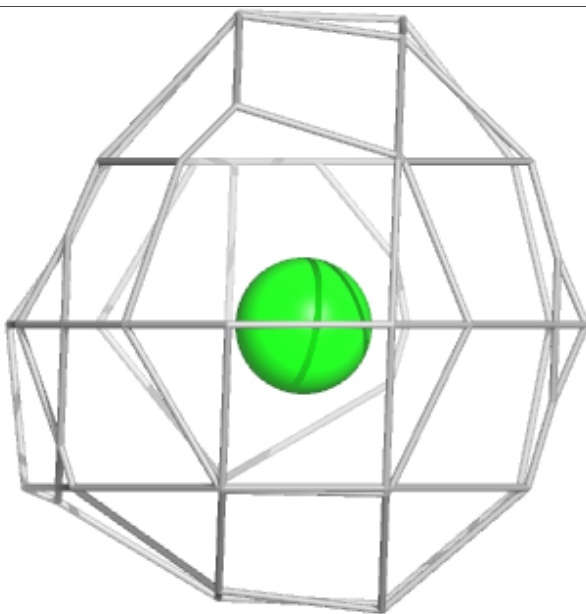
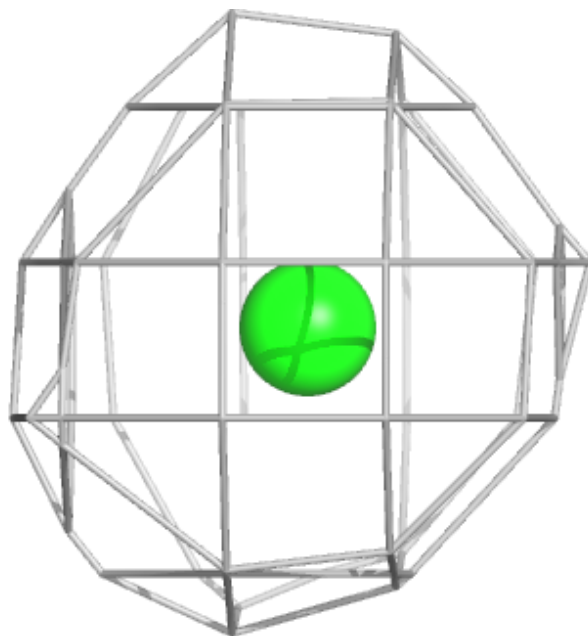
Electron density around CL B 501:

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



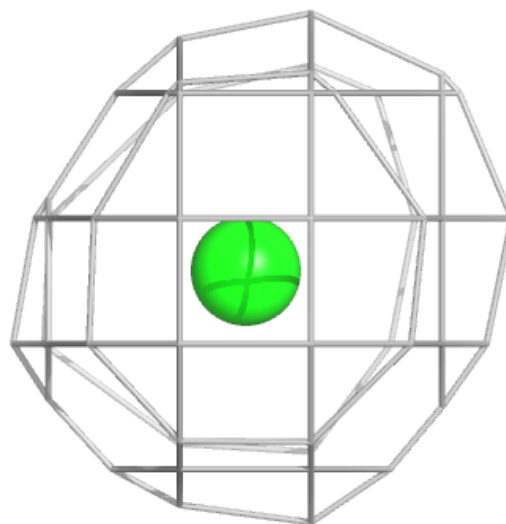
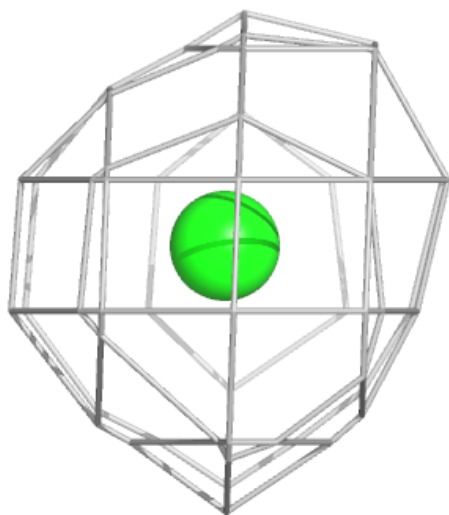
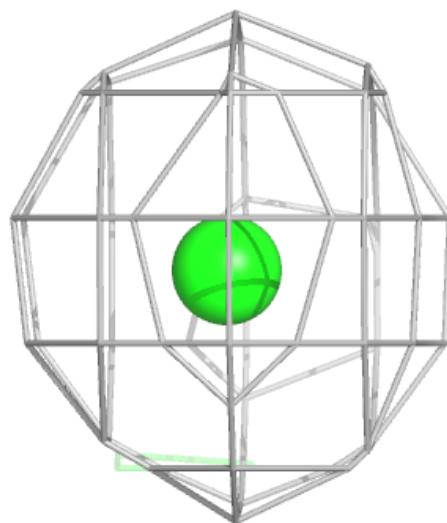
Electron density around CL A 501:

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



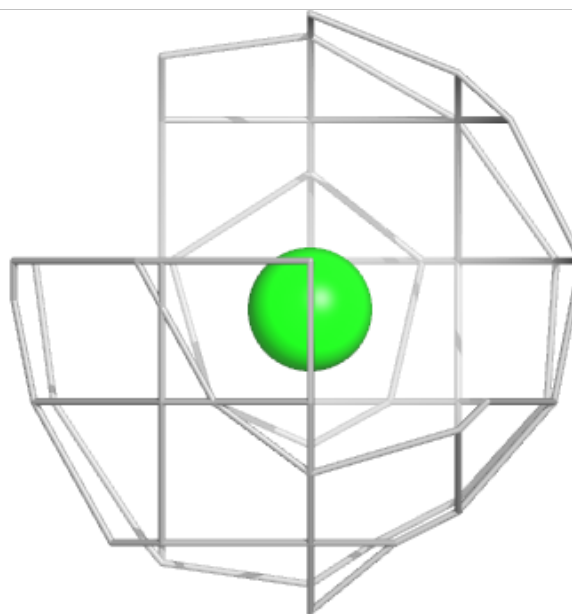
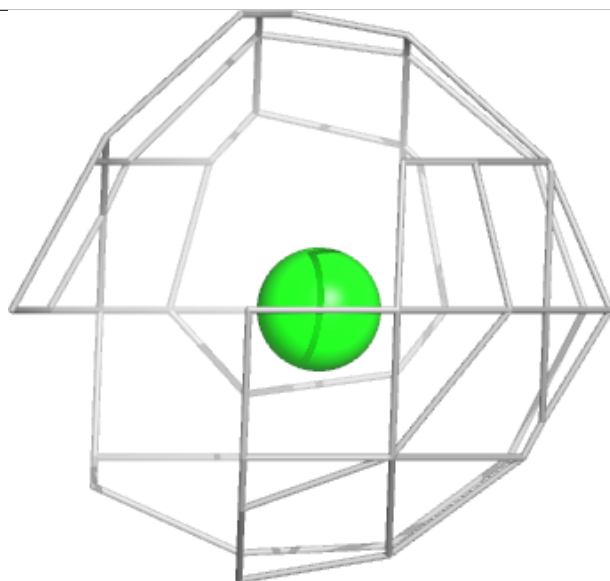
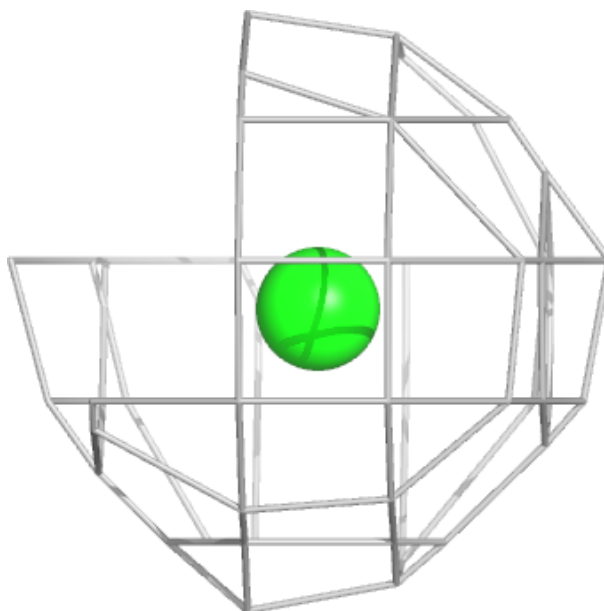
Electron density around CL A 503:

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



Electron density around CL A 502:

$2mF_o-DF_c$ (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.