



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 2, 2021 – 10:11 AM EST

PDB ID : 6WEE
Title : Copper-bound M88I variant of Campylobacter jejuni P19
Authors : Chan, A.C.; Murphy, M.E.
Deposited on : 2020-04-02
Resolution : 2.30 Å(reported)

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 ⓘ 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	:	2.16
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)	:	2.16

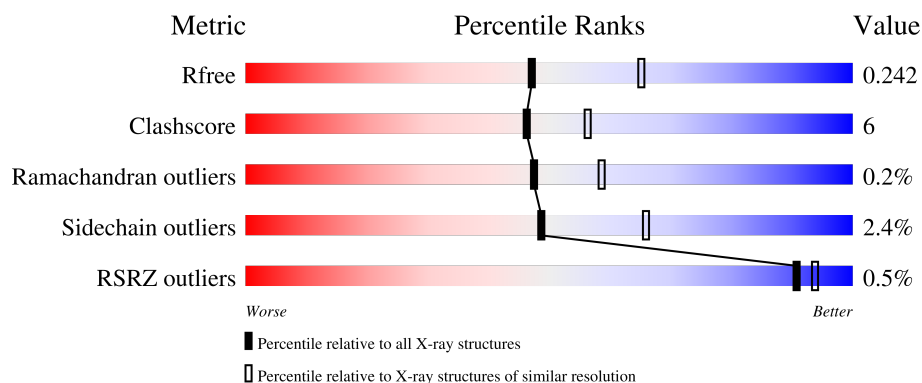
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	159	<div> <div>76%</div> <div>22%</div> <div>..</div> </div>
1	B	159	<div> <div>94%</div> <div>6%</div> </div>
1	C	159	<div> <div>89%</div> <div>11%</div> <div>.</div> </div>
1	D	159	<div> <div>84%</div> <div>16%</div> </div>
1	E	159	<div> <div>%</div> <div>87%</div> <div>13%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	159	<div><div></div><div>3%</div><div>79%</div><div>17%</div><div>••</div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 14857 atoms, of which 7076 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	157	Total	C	H	N	O	S	0	0	0
			2373	783	1160	193	232	5			
1	B	159	Total	C	H	N	O	S	0	0	0
			2423	795	1190	198	235	5			
1	C	158	Total	C	H	N	O	S	0	0	0
			2400	790	1175	196	234	5			
1	D	159	Total	C	H	N	O	S	0	2	0
			2430	797	1191	200	236	6			
1	E	159	Total	C	H	N	O	S	0	4	0
			2468	806	1214	205	237	6			
1	F	154	Total	C	H	N	O	S	0	0	0
			2302	761	1119	192	225	5			

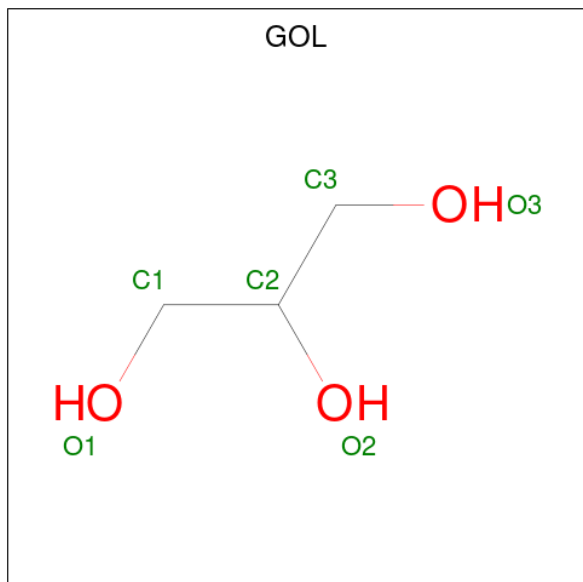
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP A0A0H3PA01
A	88	ILE	MET	engineered mutation	UNP A0A0H3PA01
B	1	GLY	-	expression tag	UNP A0A0H3PA01
B	88	ILE	MET	engineered mutation	UNP A0A0H3PA01
C	1	GLY	-	expression tag	UNP A0A0H3PA01
C	88	ILE	MET	engineered mutation	UNP A0A0H3PA01
D	1	GLY	-	expression tag	UNP A0A0H3PA01
D	88	ILE	MET	engineered mutation	UNP A0A0H3PA01
E	1	GLY	-	expression tag	UNP A0A0H3PA01
E	88	ILE	MET	engineered mutation	UNP A0A0H3PA01
F	1	GLY	-	expression tag	UNP A0A0H3PA01
F	88	ILE	MET	engineered mutation	UNP A0A0H3PA01

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Cu 1 1	0	0
2	E	1	Total Cu 1 1	0	0
2	B	1	Total Cu 1 1	0	0
2	C	1	Total Cu 1 1	0	0
2	A	1	Total Cu 1 1	0	0
2	F	1	Total Cu 1 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



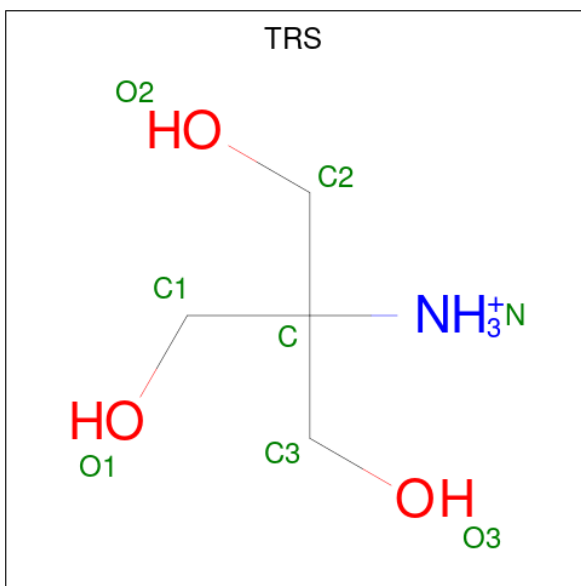
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C H O 9 3 3 3	0	0
3	B	1	Total C H O 9 3 3 3	0	0
3	D	1	Total C H O 9 3 3 3	0	0
3	F	1	Total C H O 9 3 3 3	0	0
3	F	1	Total C H O 9 3 3 3	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	O	S		0	0
			5	4	1			

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	E	1	Total	C	H	N	O	0	0
			20	4	12	1	3		

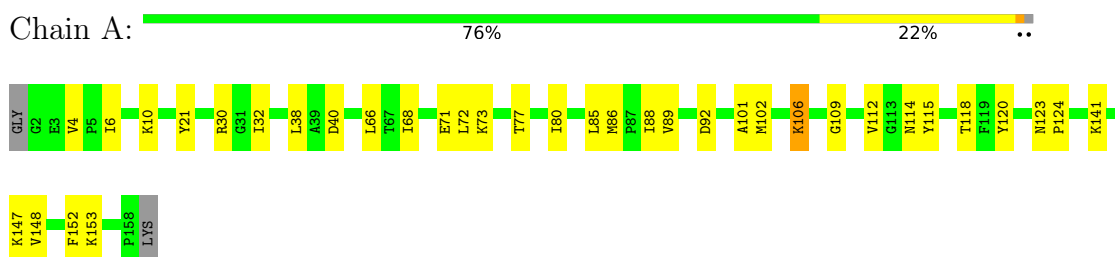
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	48	Total 48	O 48	0	0
6	B	71	Total 71	O 71	0	0
6	C	70	Total 70	O 70	0	0
6	D	77	Total 77	O 77	0	0
6	E	80	Total 80	O 80	0	0
6	F	39	Total 39	O 39	0	0

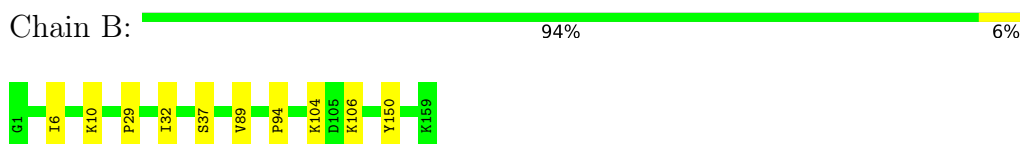
3 Residue-property plots [i](#)

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.

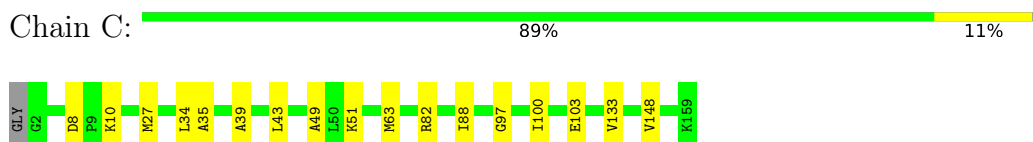
- Molecule 1: Uncharacterized protein



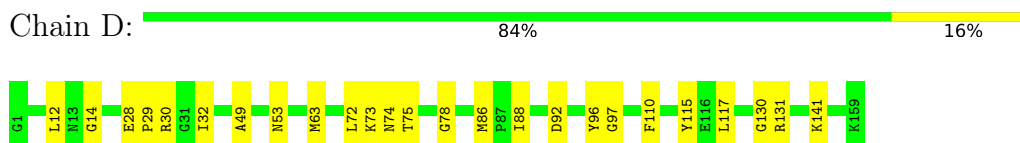
- Molecule 1: Uncharacterized protein



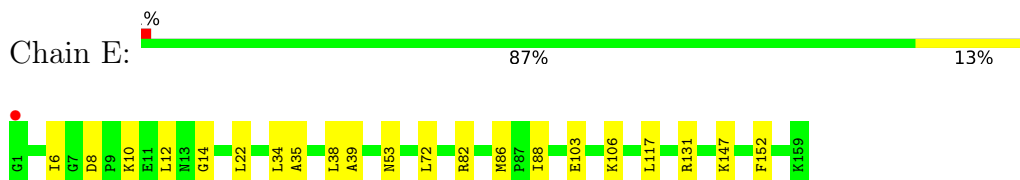
- Molecule 1: Uncharacterized protein



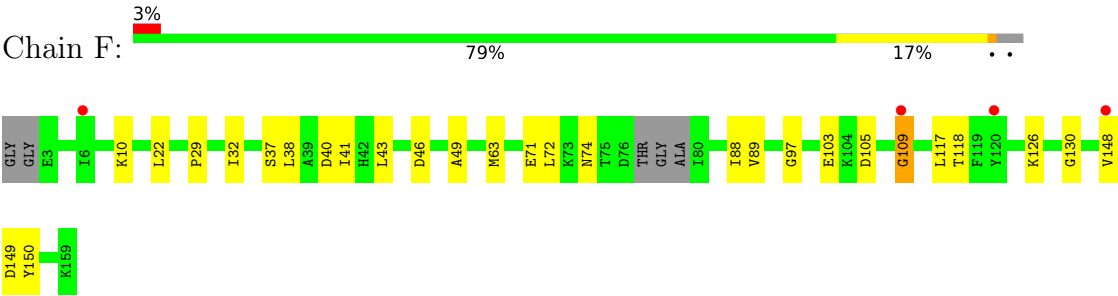
- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



● Molecule 1: Uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, α , β , γ	132.97Å 132.97Å 104.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.55 – 2.30 30.55 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.7 (30.55-2.30) 83.2 (30.55-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.55 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.235 , 0.277 0.212 , 0.242	Depositor DCC
R_{free} test set	1996 reflections (4.37%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.443	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 25.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.489 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.500 for h,-h-k,-l	Depositor
Outliers	1 of 45675 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14857	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.15 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.7676e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GOL, TRS, SO4, CU

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	0.31	0/1248	0.50	0/1694
1	B	0.26	0/1268	0.45	0/1718
1	C	0.26	0/1260	0.46	0/1709
1	D	0.42	0/1283	0.49	0/1739
1	E	0.26	0/1302	0.45	0/1762
1	F	0.32	0/1216	0.46	0/1650
All	All	0.31	0/7577	0.47	0/10272

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	1213	1160	1154	35	0
1	B	1233	1190	1188	4	0
1	C	1225	1175	1171	13	0
1	D	1239	1191	1180	15	0
1	E	1254	1214	1201	12	0
1	F	1183	1119	1108	17	0
2	A	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	B	12	6	16	0	0
3	D	6	3	8	0	0
3	F	12	6	16	1	0
4	D	5	0	0	0	0
5	E	8	12	12	1	0
6	A	48	0	0	2	0
6	B	71	0	0	0	0
6	C	70	0	0	3	0
6	D	77	0	0	0	0
6	E	80	0	0	2	0
6	F	39	0	0	0	0
All	All	7781	7076	7054	91	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 6.

The worst 5 of 91 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:E:34:LEU:HD12	1:E:39:ALA:HB2	1.57	0.85
1:D:29:PRO:HG2	1:D:32:ILE:HD12	1.64	0.80
1:C:34:LEU:HD12	1:C:39:ALA:HB2	1.64	0.80
1:A:114:ASN:OD1	1:A:153:LYS:HD2	1.82	0.79
1:A:73:LYS:HA	1:A:80:ILE:HG13	1.67	0.75

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	155/159 (98%)	147 (95%)	8 (5%)	0	100	100
1	B	157/159 (99%)	153 (98%)	4 (2%)	0	100	100
1	C	156/159 (98%)	150 (96%)	6 (4%)	0	100	100
1	D	159/159 (100%)	151 (95%)	8 (5%)	0	100	100
1	E	161/159 (101%)	157 (98%)	4 (2%)	0	100	100
1	F	150/159 (94%)	142 (95%)	6 (4%)	2 (1%)	12	12
All	All	938/954 (98%)	900 (96%)	36 (4%)	2 (0%)	47	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	105	ASP
1	F	109	GLY

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	123/127 (97%)	118 (96%)	5 (4%)	30	43
1	B	126/127 (99%)	124 (98%)	2 (2%)	62	78
1	C	125/127 (98%)	125 (100%)	0	100	100
1	D	127/127 (100%)	123 (97%)	4 (3%)	40	55
1	E	129/127 (102%)	125 (97%)	4 (3%)	40	55
1	F	118/127 (93%)	115 (98%)	3 (2%)	47	65
All	All	748/762 (98%)	730 (98%)	18 (2%)	49	66

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	30	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	92	ASP
1	E	106	LYS
1	B	106	LYS
1	D	12	LEU

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.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 6 are monoatomic - leaving 7 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	GOL	B	202	-	5,5,5	0.90	0	5,5,5	1.02	0
5	TRS	E	202	-	7,7,7	0.15	0	9,9,9	0.33	0
3	GOL	F	202	-	5,5,5	0.90	0	5,5,5	1.02	0
3	GOL	B	203	-	5,5,5	0.90	0	5,5,5	1.02	0
3	GOL	D	203	-	5,5,5	0.89	0	5,5,5	1.04	0
4	SO4	D	202	-	4,4,4	0.14	0	6,6,6	0.05	0
3	GOL	F	203	-	5,5,5	0.89	0	5,5,5	1.01	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	GOL	B	202	-	-	2/4/4/4	-
5	TRS	E	202	-	-	5/9/9/9	-
3	GOL	F	202	-	-	1/4/4/4	-
3	GOL	B	203	-	-	0/4/4/4	-
3	GOL	D	203	-	-	2/4/4/4	-
3	GOL	F	203	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	202	TRS	N-C-C2-O2
5	E	202	TRS	N-C-C3-O3
3	B	202	GOL	O2-C2-C3-O3
3	D	203	GOL	O2-C2-C3-O3
5	E	202	TRS	C3-C-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	202	TRS	1	0
3	F	202	GOL	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, 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	157/159 (98%)	0.01	0 100 100	25, 49, 79, 97	0
1	B	159/159 (100%)	-0.30	0 100 100	21, 37, 54, 70	0
1	C	158/159 (99%)	-0.27	0 100 100	18, 36, 57, 68	0
1	D	159/159 (100%)	-0.24	0 100 100	18, 39, 57, 91	0
1	E	159/159 (100%)	-0.23	1 (0%) 89 92	24, 39, 62, 76	0
1	F	154/159 (96%)	0.10	4 (2%) 56 63	25, 54, 81, 124	0
All	All	946/954 (99%)	-0.16	5 (0%) 91 94	18, 40, 69, 124	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1	GLY	3.0
1	F	120	TYR	2.7
1	F	109	GLY	2.1
1	F	6	ILE	2.0
1	F	148	VAL	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 monosaccharides in this entry.

6.4 Ligands

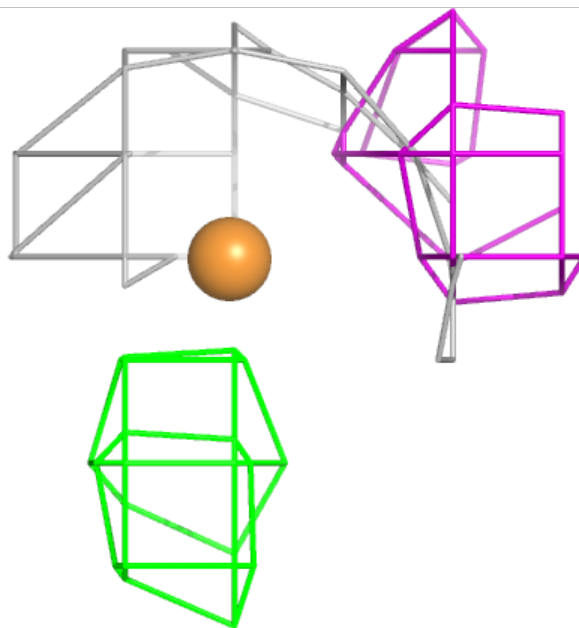
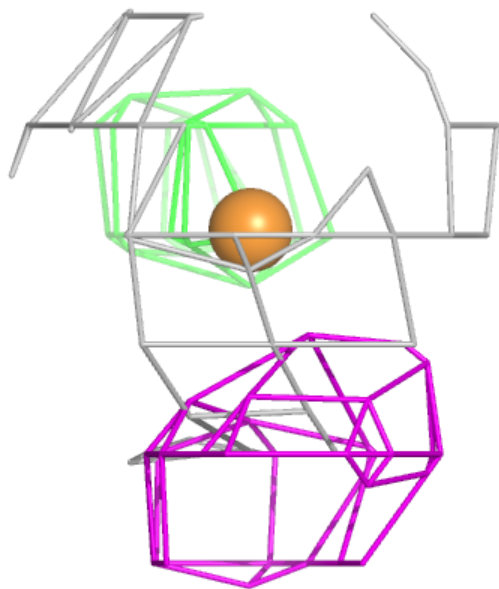
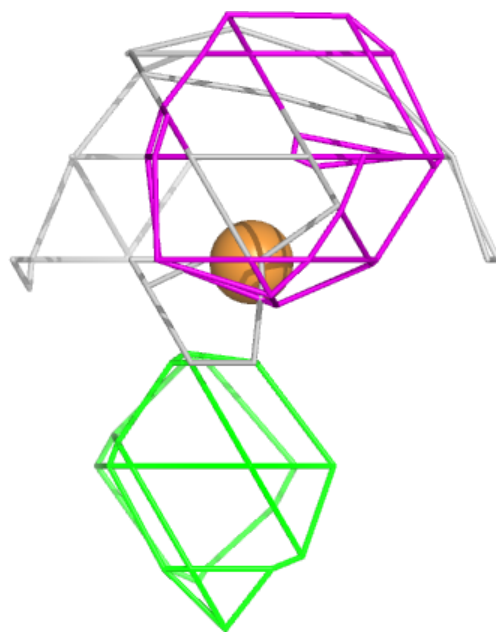
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	GOL	F	203	6/6	0.86	0.18	42,44,53,56	0
5	TRS	E	202	8/8	0.87	0.18	42,55,65,65	0
3	GOL	F	202	6/6	0.88	0.17	22,28,32,38	0
3	GOL	B	203	6/6	0.89	0.16	43,46,57,62	0
2	CU	D	201	1/1	0.90	0.10	49,49,49,49	1
3	GOL	D	203	6/6	0.92	0.14	28,31,38,41	0
2	CU	B	201	1/1	0.92	0.11	45,45,45,45	1
3	GOL	B	202	6/6	0.93	0.15	26,30,37,44	0
2	CU	A	201	1/1	0.93	0.09	51,51,51,51	1
2	CU	F	201	1/1	0.94	0.07	103,103,103,103	0
2	CU	C	201	1/1	0.94	0.10	41,41,41,41	0
4	SO4	D	202	5/5	0.96	0.10	54,56,58,60	0
2	CU	E	201	1/1	0.99	0.08	33,33,33,33	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.

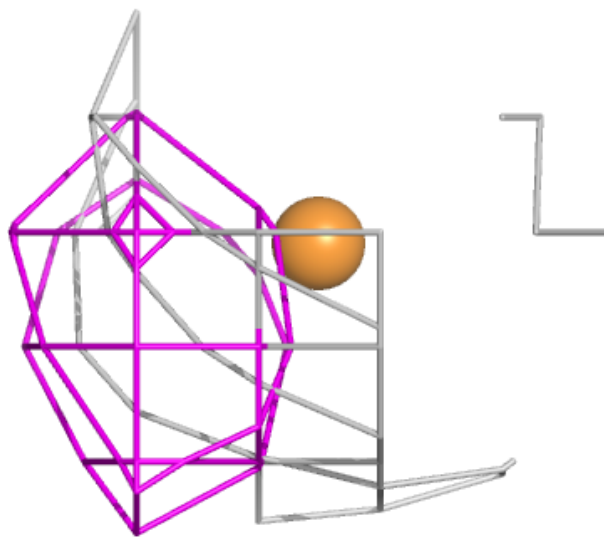
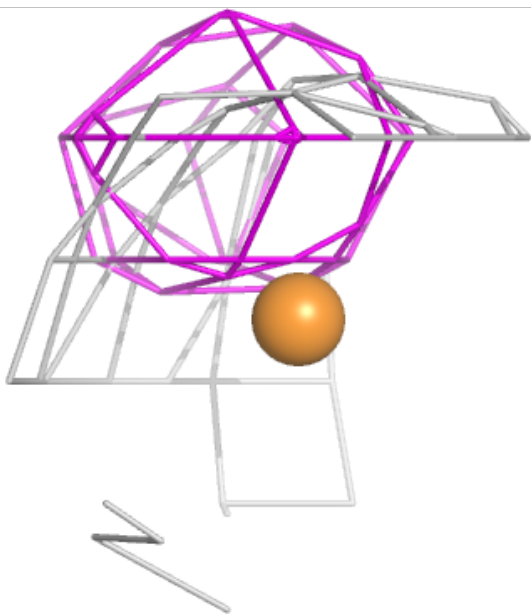
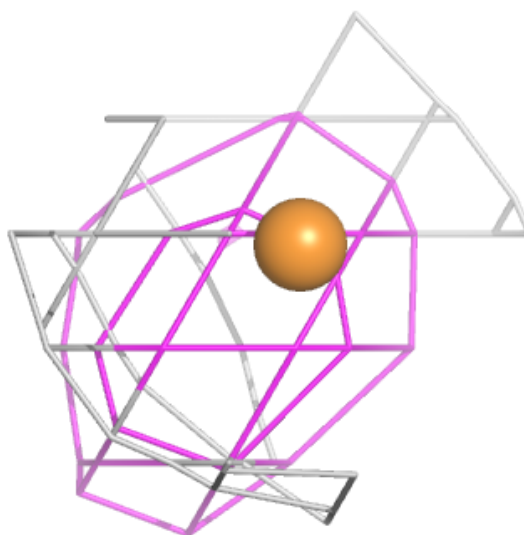
Electron density around CU D 201:

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



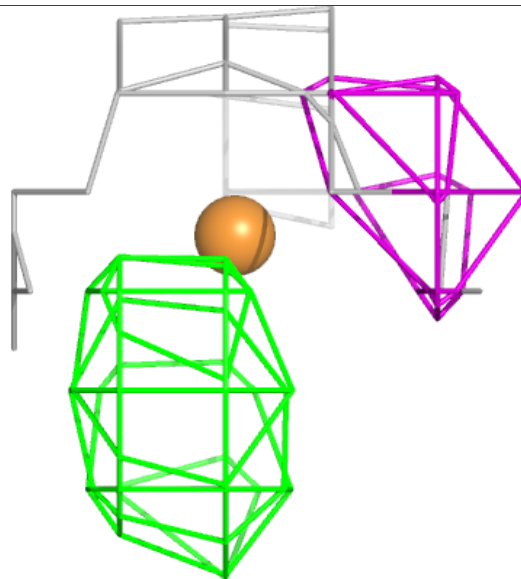
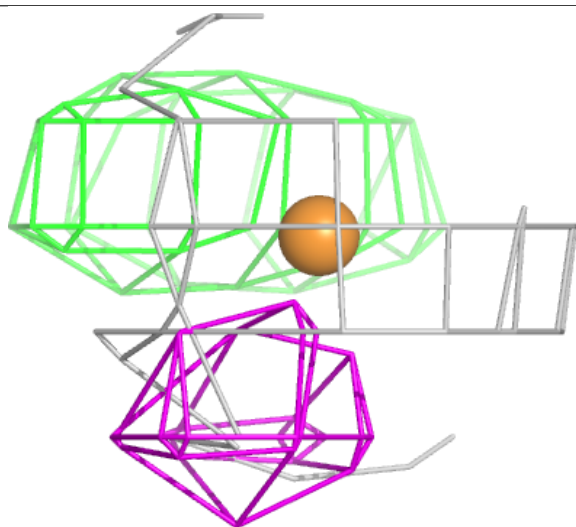
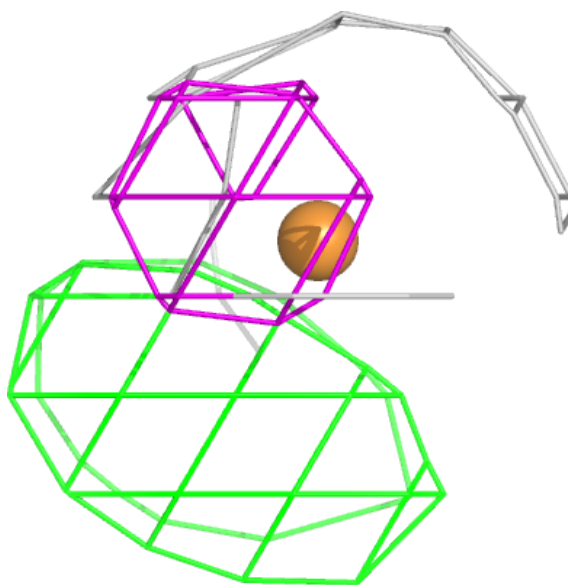
Electron density around CU B 201:

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



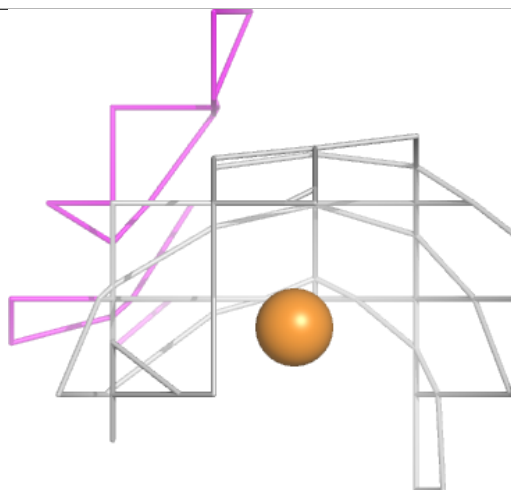
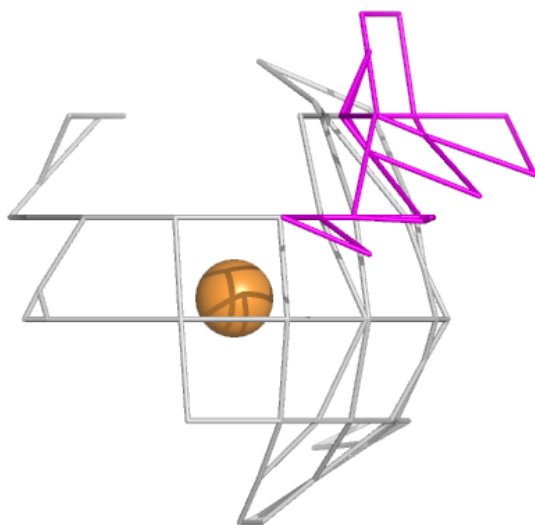
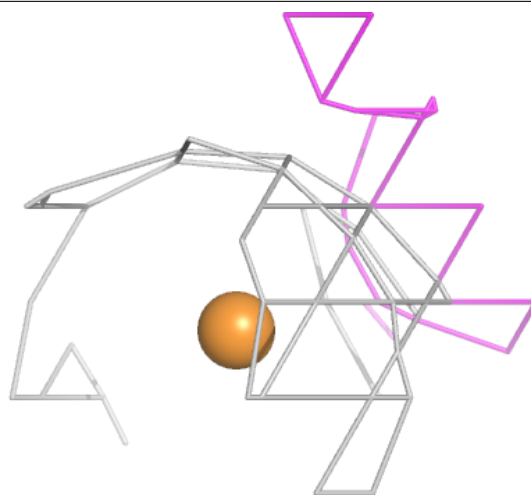
Electron density around CU A 201:

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



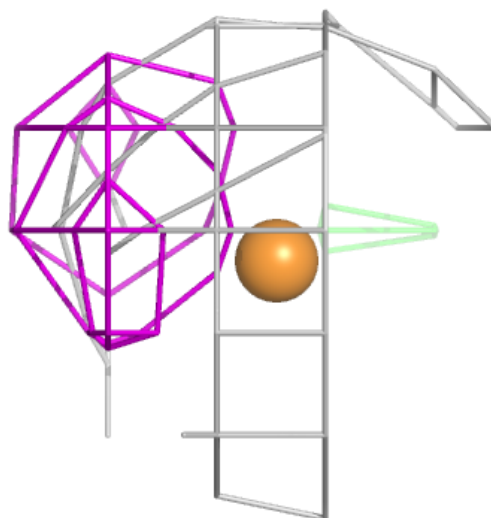
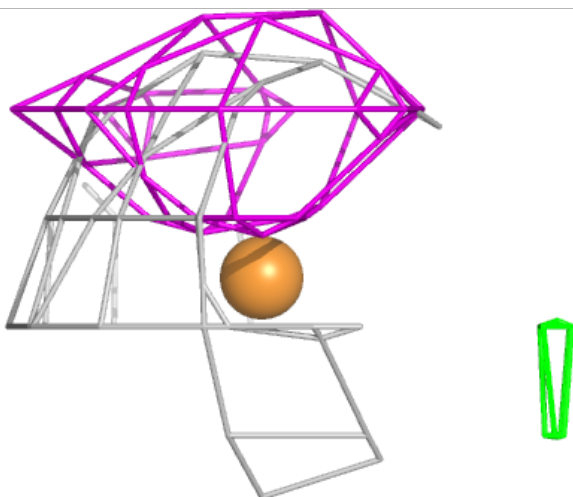
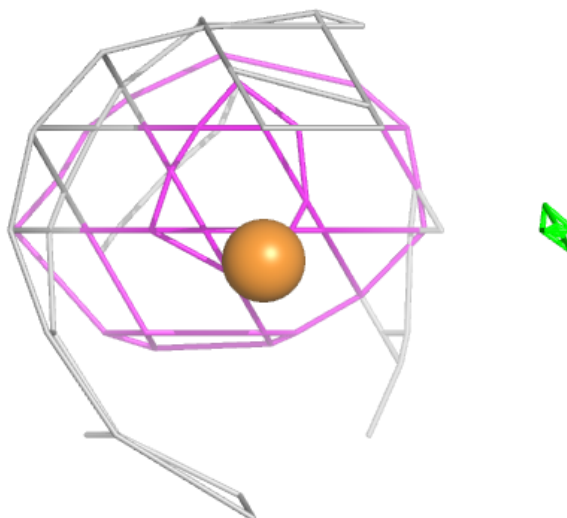
Electron density around CU F 201:

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



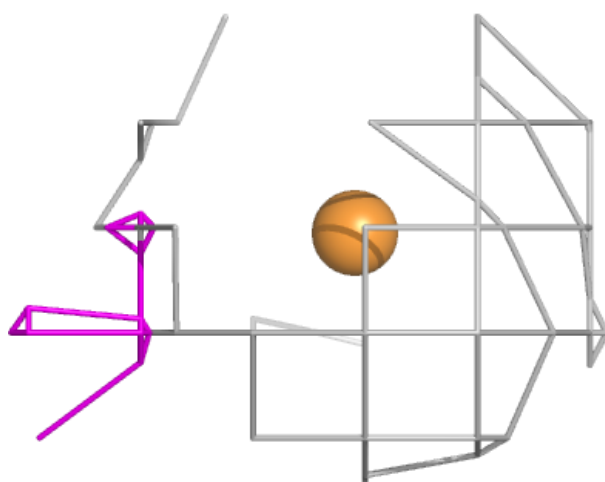
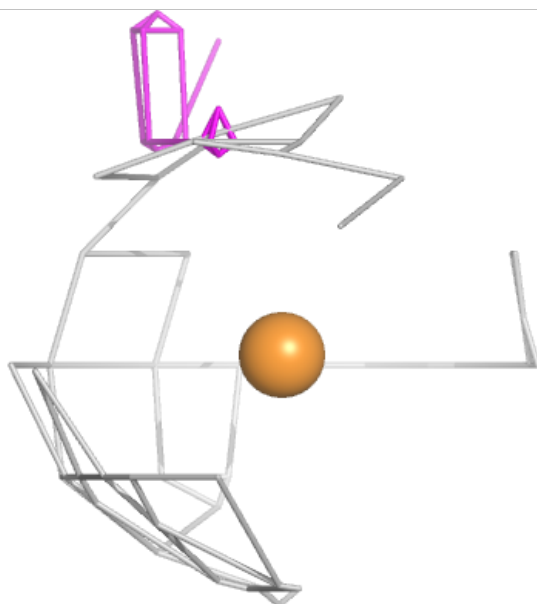
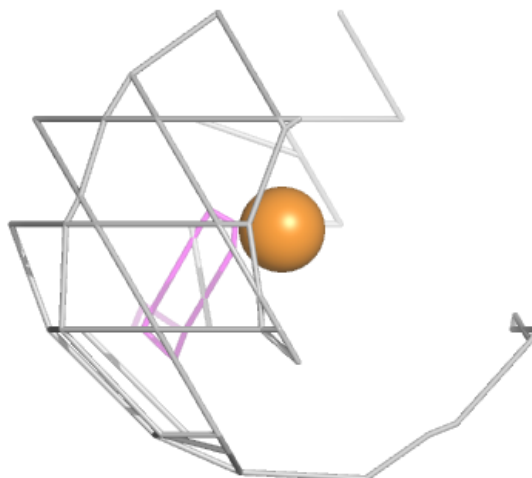
Electron density around CU C 201:

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



Electron density around CU E 201:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.