



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 10:05 AM EDT

PDB ID : 7YH5 / pdb_00007yh5
Title : MazG(Mycobacterium tuberculosis)
Authors : Li, J.; Wang, S.
Deposited on : 2022-07-12
Resolution : 2.70 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

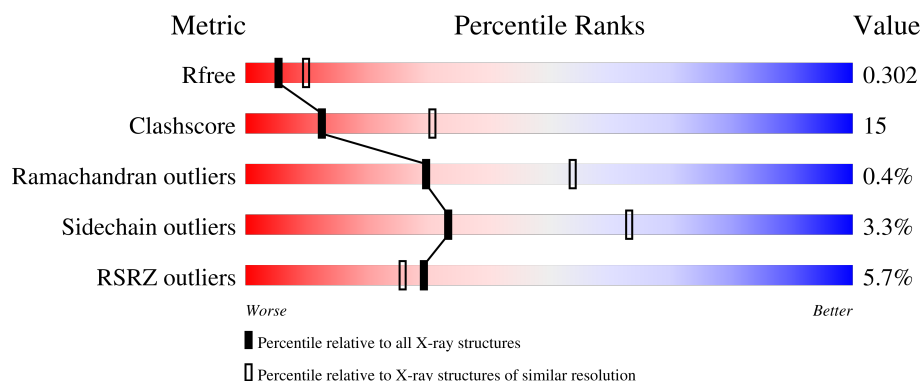
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	185	
1	B	185	
1	C	185	
1	D	185	
1	E	185	

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Mol	Chain	Length	Quality of chain
1	F	185	17%46%14%.36%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7117 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 Nucleoside triphosphate pyrophosphohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	169	Total	C	N	O	S	0	0	0
			1265	798	208	254	5			
1	B	177	Total	C	N	O	S	0	0	0
			1314	824	225	260	5			
1	C	176	Total	C	N	O	S	0	0	0
			1306	822	224	255	5			
1	D	176	Total	C	N	O	S	0	0	0
			1278	804	211	258	5			
1	E	165	Total	C	N	O	S	0	0	0
			1108	707	184	213	4			
1	F	118	Total	C	N	O	S	0	0	0
			805	501	134	169	1			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

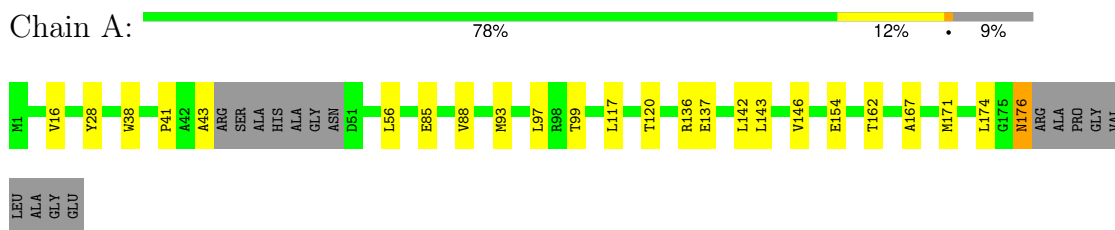
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	12	Total 12	O 12	0	0
3	B	6	Total 6	O 6	0	0
3	C	5	Total 5	O 5	0	0
3	D	6	Total 6	O 6	0	0
3	E	4	Total 4	O 4	0	0
3	F	2	Total 2	O 2	0	0

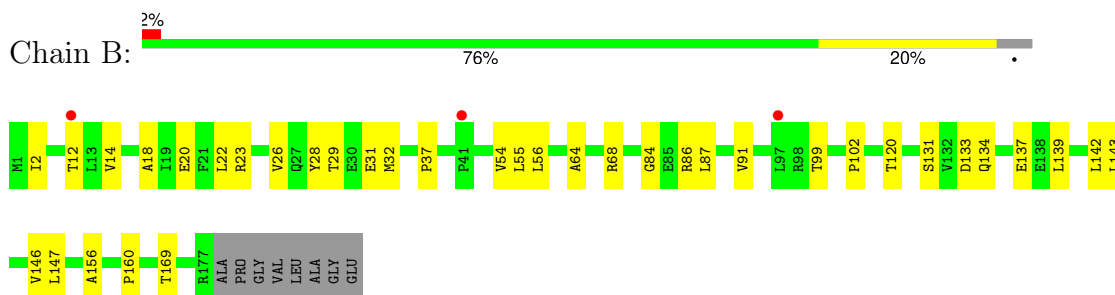
3 Residue-property plots

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.

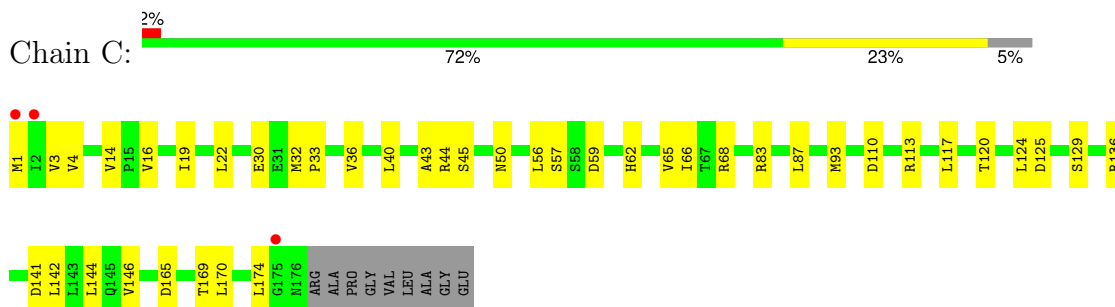
- Molecule 1: Nucleoside triphosphate pyrophosphohydrolase



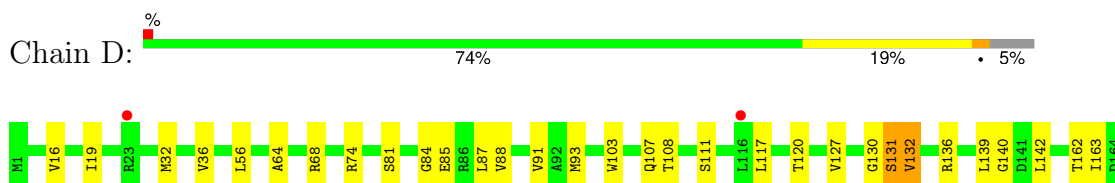
- Molecule 1: Nucleoside triphosphate pyrophosphohydrolase



- Molecule 1: Nucleoside triphosphate pyrophosphohydrolase



- Molecule 1: Nucleoside triphosphate pyrophosphohydrolase



D165
V166
A167
D168
T169
L170
M171
R172
K173
L174
G175
N176
ARG
ALA
PRO
GLY
VAL
LEU
ALA
GLY
GLU

• Molecule 1: Nucleoside triphosphate pyrophosphohydrolase

Chain E: 9% 58% 26% 5% 11%

M1
I2
V3
V4
L5
V6
R10
P11
T12
L13
V16
I19
E20
F21
L22
R23
G24
E25
V26
Q27
T28
Y29
E30
E31
K32
A35
V36
P37
W38
S39
L40
P41
R44
S45
A46
H47
GLY
N50
S51
A52
P53
V54
L55
L56
S57
P60
A64
V65
T66
T67
R68
L69

A70
A73
R74
L75
I76
S77
L87
V88
D89
A90
V91
A92
M93
M94
L97
R98
R99
THR
ALA
GLY
PRO
TRP
GLU
SER
GLN
Q107
L116
T120
L144
L147
F148
A153
S157
Q158
S159
P160
F161
T162
I163
D164
D165
V166
G175
ASN
ARG
ALA
PRO
GLY
VAL
LEU
ALA

GLY
GLU

• Molecule 1: Nucleoside triphosphate pyrophosphohydrolase

Chain F: 17% 46% 14% 36%

MET
ILE
VAL
VAL
LEU
VAL
ASP
PRO
R9
R10
P11
THR
LEU
V14
P15
V16
E17
A18
I19
E20
F21
L22
R23
GLY
GLU
VAL
GLN
TYR
THR
GLU
GLU
MET
PRO
VAL
ALA
VAL
PRO
TRP
SER
LEU
PRO
ALA
ALA
ARG
SER
HIS
ALA
GLY
ASN
ASP
ALA
PRO
VAL
LEU
LEU
SER
SER
ASP
PRO

ASN
HIS
PRO
ALA
VAL
ILE
THR
ARG
ARG
ALA
A71
G72
A73
R74
L75
I76
S77
A78
P79
D80
S81
Q82
L87
V88
D89
A90
T99
A100
T108
H109
L112
L117
L123
L124
V127
R128
S129
G130
S131
V132
D133
Q134
L139
L143
A150
R151
A156
P160

F161
T162
I163
D164
D165
T169
L170
M171
L174
G175
ASN
ARG
ALA
PRO
GLY
VAL
LEU
ALA
GLY
GLU

4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	109.31Å 109.31Å 242.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.86 – 2.70 35.86 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (35.86-2.70) 99.9 (35.86-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.68Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.258 , 0.296 0.260 , 0.302	Depositor DCC
R_{free} test set	2082 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	87.7	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7117	wwPDB-VP
Average B, all atoms (Å ²)	90.0	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: MG

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	0.24	0/1287	0.44	1/1763 (0.1%)
1	B	0.29	0/1338	0.47	1/1833 (0.1%)
1	C	0.34	0/1330	0.47	0/1820
1	D	0.42	0/1301	0.65	3/1786 (0.2%)
1	E	0.57	0/1122	0.87	3/1546 (0.2%)
1	F	0.65	0/814	0.96	4/1115 (0.4%)
All	All	0.42	0/7192	0.64	12/9863 (0.1%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	132	VAL	N-CA-C	-10.94	99.98	111.58
1	D	131	SER	N-CA-C	-8.45	97.82	110.24
1	E	160	PRO	N-CA-CB	7.08	109.91	103.33
1	E	41	PRO	N-CA-CB	6.72	110.31	103.25
1	B	102	PRO	N-CA-CB	6.43	110.00	103.25

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	1265	0	1218	23	0
1	B	1314	0	1259	30	0
1	C	1306	0	1269	52	0
1	D	1278	0	1216	41	0
1	E	1108	0	1013	73	0
1	F	805	0	684	27	0
2	A	1	0	0	0	0
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	A	12	0	0	2	0
3	B	6	0	0	1	0
3	C	5	0	0	3	0
3	D	6	0	0	0	0
3	E	4	0	0	0	0
3	F	2	0	0	0	0
All	All	7117	0	6659	210	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 15.

The worst 5 of 210 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:94:MET:CE	1:E:148:PHE:HA	1.59	1.29
1:E:153:ALA:CB	1:E:161:PHE:HE2	1.58	1.15
1:E:94:MET:CE	1:E:148:PHE:CA	2.26	1.13
1:E:163:ILE:H	1:E:163:ILE:HD12	1.16	1.09
1:E:94:MET:HE3	1:E:148:PHE:HA	1.07	1.06

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	165/185 (89%)	163 (99%)	2 (1%)	0	100	100
1	B	175/185 (95%)	170 (97%)	5 (3%)	0	100	100
1	C	174/185 (94%)	171 (98%)	3 (2%)	0	100	100
1	D	174/185 (94%)	170 (98%)	4 (2%)	0	100	100
1	E	159/185 (86%)	146 (92%)	12 (8%)	1 (1%)	21	44
1	F	112/185 (60%)	96 (86%)	13 (12%)	3 (3%)	4	10
All	All	959/1110 (86%)	916 (96%)	39 (4%)	4 (0%)	30	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	19	ILE
1	E	41	PRO
1	F	15	PRO
1	F	79	PRO

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	134/153 (88%)	133 (99%)	1 (1%)	76	90
1	B	136/153 (89%)	135 (99%)	1 (1%)	76	90
1	C	135/153 (88%)	135 (100%)	0	100	100
1	D	132/153 (86%)	130 (98%)	2 (2%)	57	81
1	E	99/153 (65%)	88 (89%)	11 (11%)	6	15
1	F	70/153 (46%)	62 (89%)	8 (11%)	5	14
All	All	706/918 (77%)	683 (97%)	23 (3%)	33	63

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	166	VAL
1	F	75	LEU
1	F	74	ARG
1	F	129	SER
1	E	6	VAL

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

Mol	Chain	Res	Type
1	C	176	ASN
1	F	145	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	169/185 (91%)	0.18	0	100 100	64, 77, 98, 114	0
1	B	177/185 (95%)	0.36	3 (1%)	69 67	63, 82, 105, 114	0
1	C	176/185 (95%)	0.25	3 (1%)	69 67	66, 81, 103, 116	0
1	D	176/185 (95%)	0.24	2 (1%)	78 76	60, 78, 106, 119	0
1	E	165/185 (89%)	0.96	17 (10%)	12 10	96, 114, 132, 145	0
1	F	118/185 (63%)	1.35	31 (26%)	1 1	30, 119, 137, 139	0
All	All	981/1110 (88%)	0.51	56 (5%)	29 26	30, 87, 127, 145	0

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	16	VAL	5.3
1	F	76	ILE	4.6
1	F	18	ALA	4.4
1	F	21	PHE	4.4
1	F	90	ALA	4.3

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

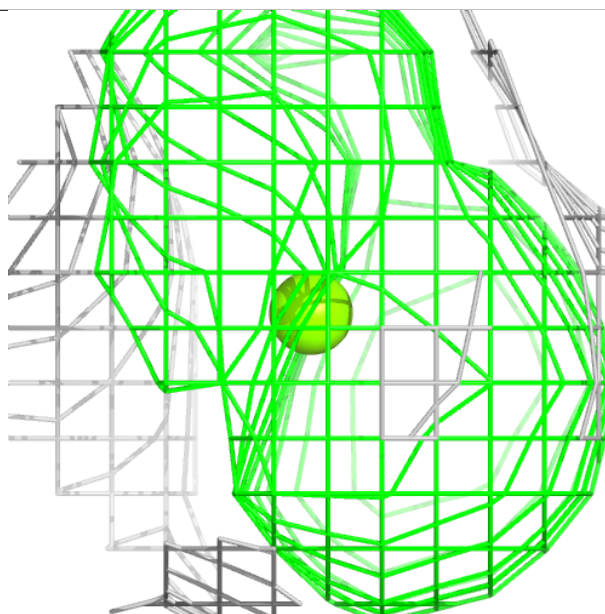
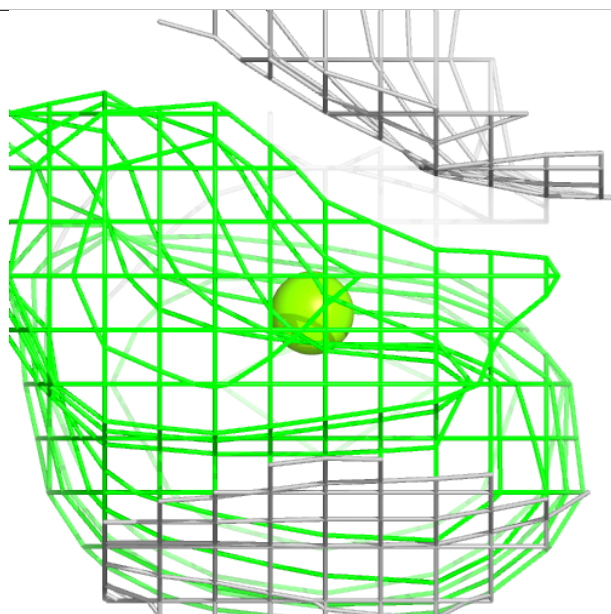
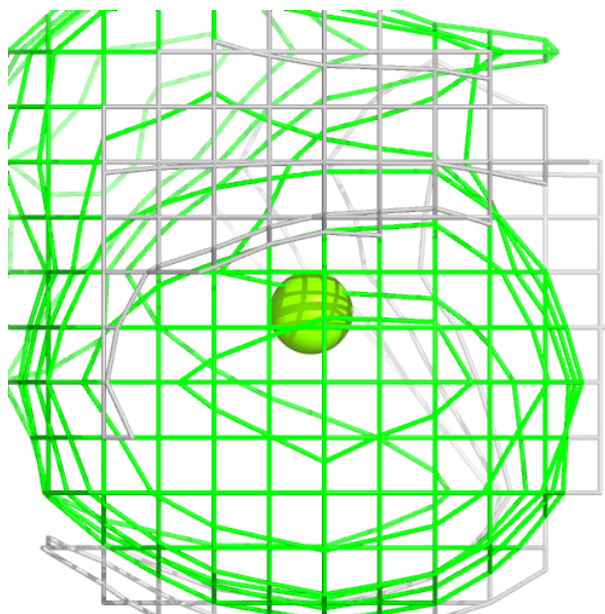
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MG	C	201	1/1	0.58	0.25	77,77,77,77	0
2	MG	D	201	1/1	0.70	0.34	80,80,80,80	0
2	MG	E	201	1/1	0.79	0.31	94,94,94,94	0
2	MG	B	201	1/1	0.87	0.18	85,85,85,85	0
2	MG	F	201	1/1	0.87	0.21	96,96,96,96	0
2	MG	A	201	1/1	0.90	0.15	83,83,83,83	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.

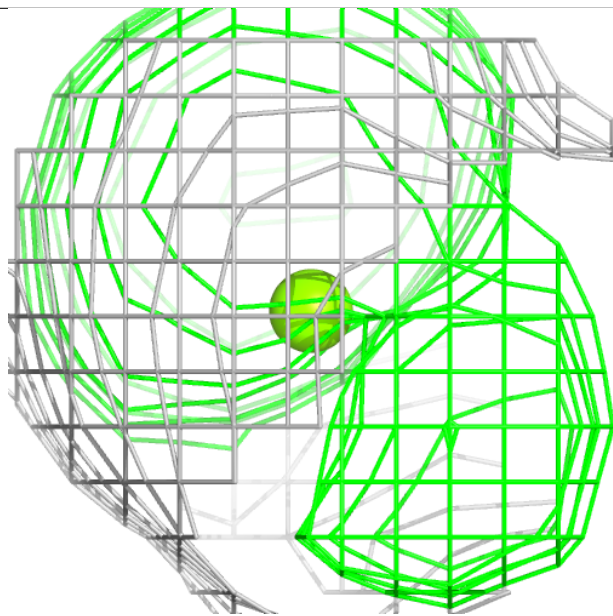
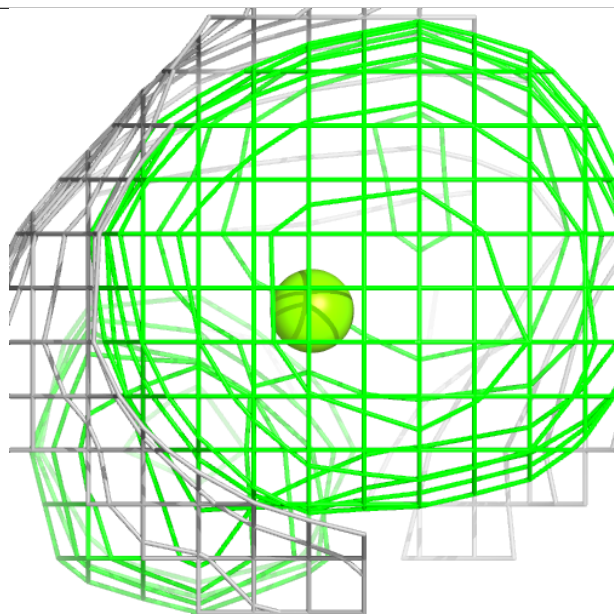
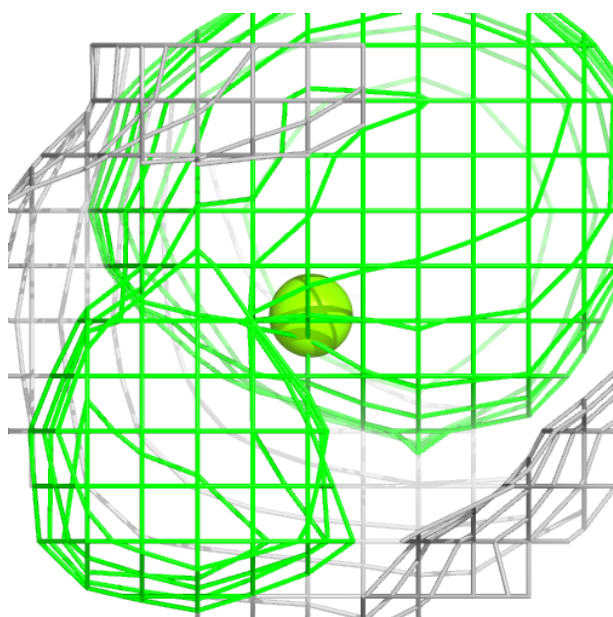
Electron density around MG C 201:

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



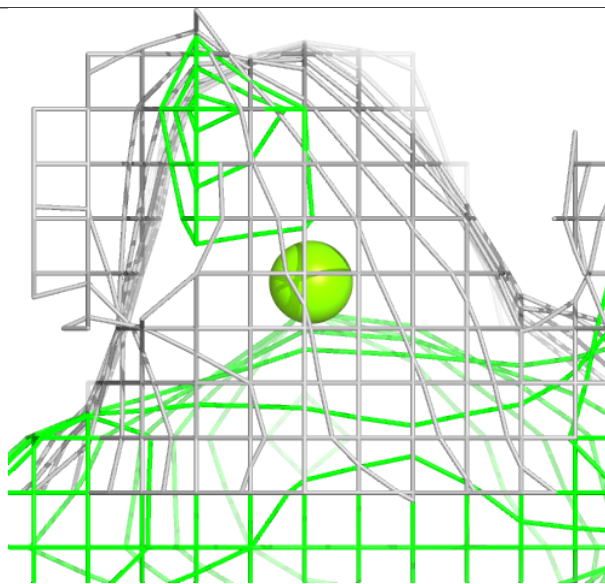
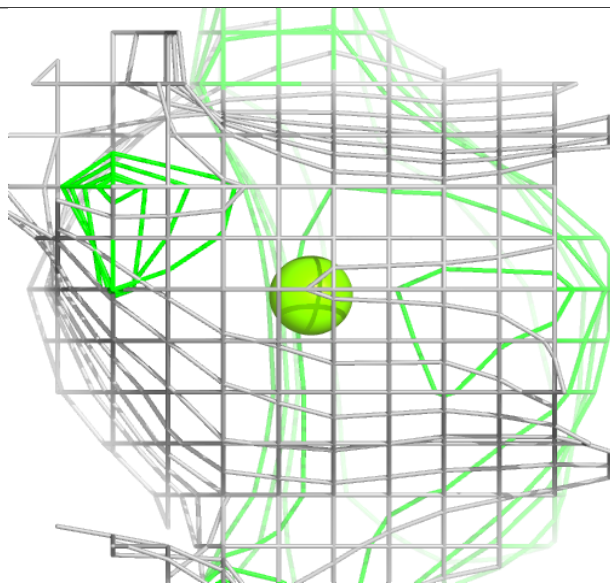
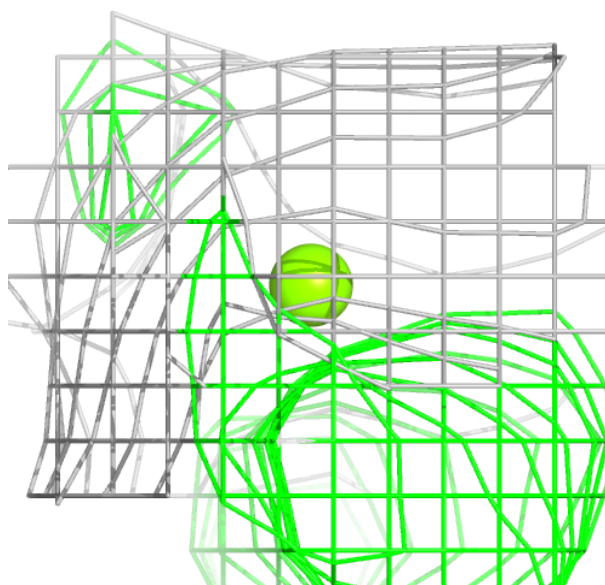
Electron density around MG D 201:

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



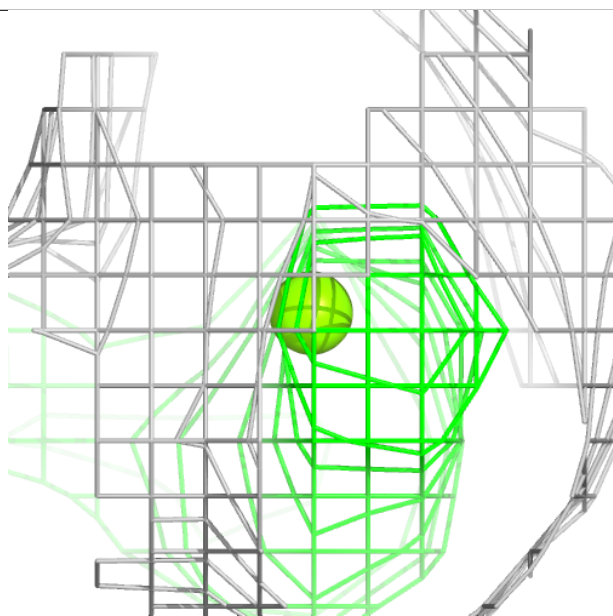
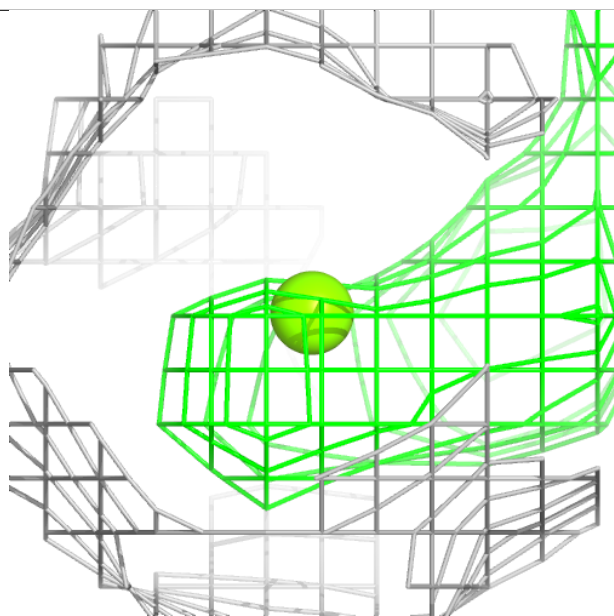
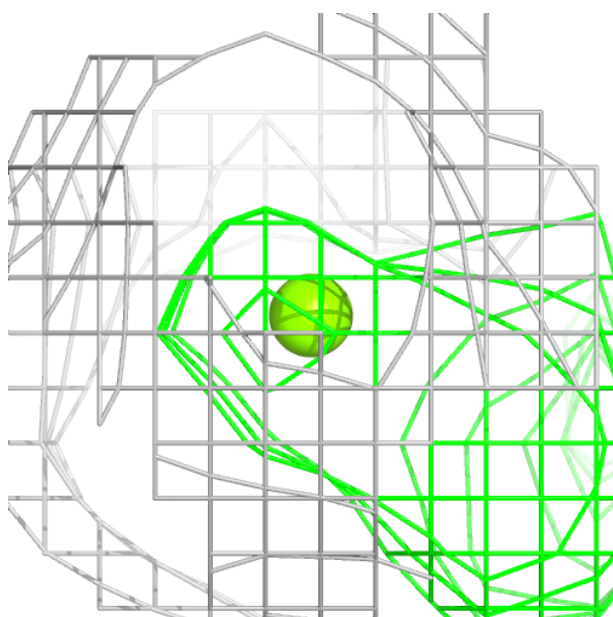
Electron density around MG E 201:

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



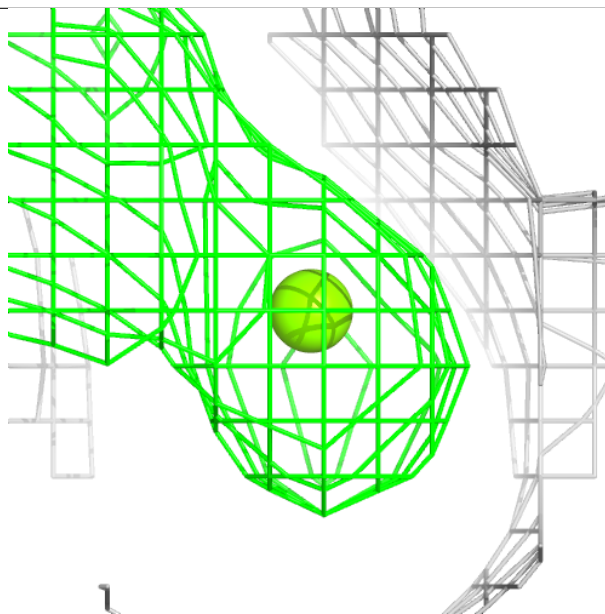
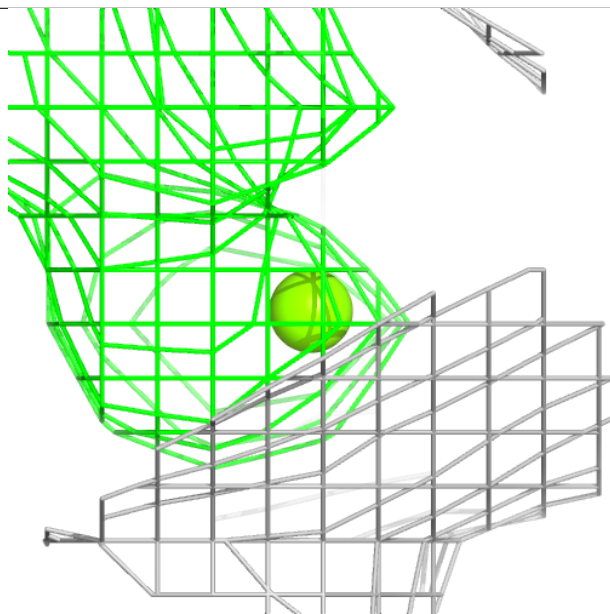
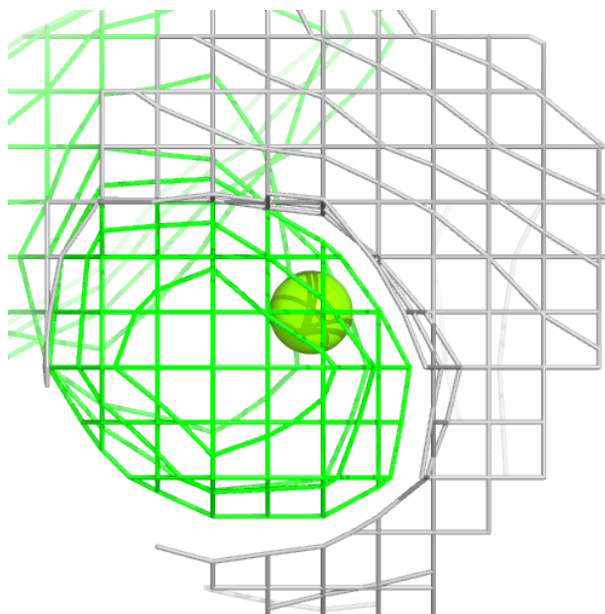
Electron density around MG B 201:

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



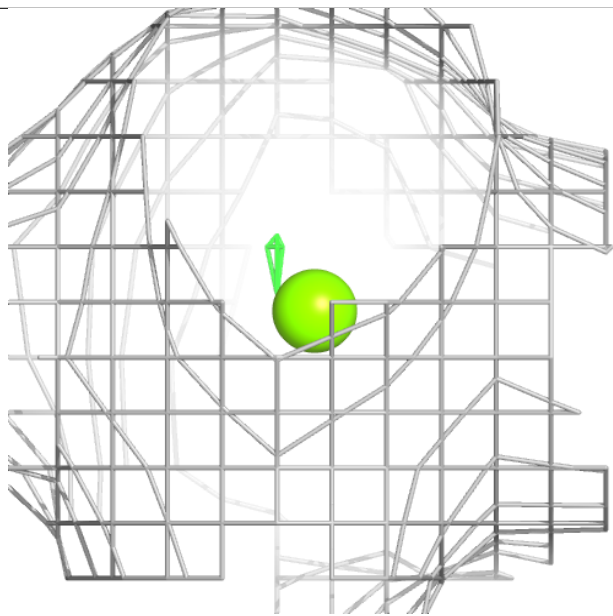
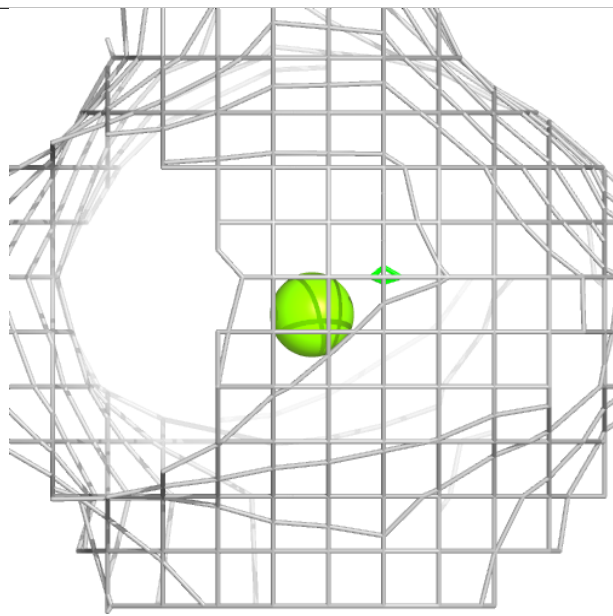
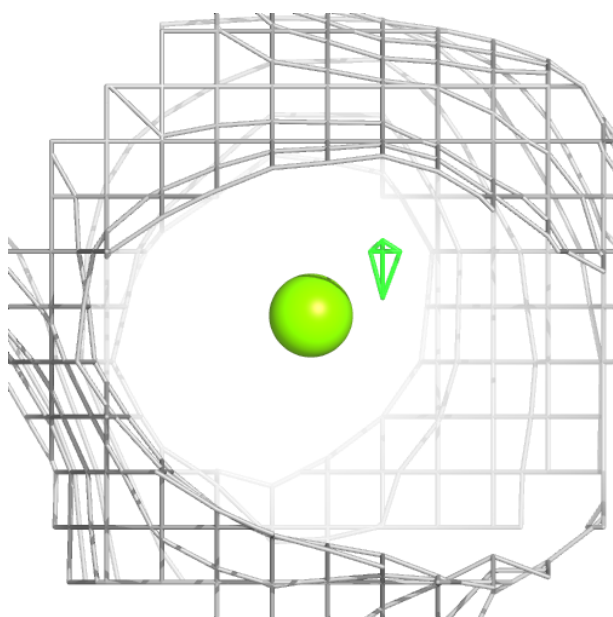
Electron density around MG F 201:

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



Electron density around MG 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)



6.5 Other polymers ⓘ

There are no such residues in this entry.