



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 29, 2020 – 10:31 AM BST

PDB ID : 6A2C  
Title : Crystal structure of a synthase 2 from santalum album in complex with lig2  
Authors : Han, X.; Ko, T.P.; Liu, W.D.; Zheng, Y.Y.; Chen, C.C.; Guo, R.T.  
Deposited on : 2018-06-10  
Resolution : 1.94 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](mailto: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.

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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 : 2.13  
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) : 2.13

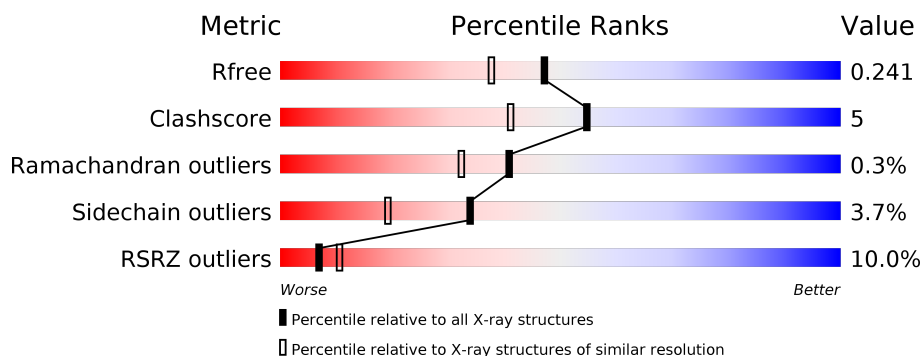
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.94 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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  $\geq 3$ , 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	566	<div> <div>3%</div> <div>83%</div> <div>7%</div> <div>8%</div> </div>
1	B	566	<div> <div>15%</div> <div>77%</div> <div>12%</div> <div>10%</div> </div>

## 2 Entry composition [i](#)

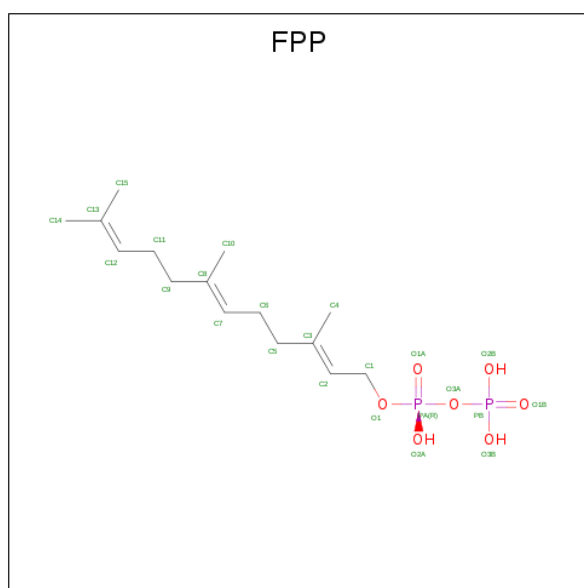
There are 4 unique types of molecules in this entry. The entry contains 9346 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Sesquisabinene B synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	518	Total	C	N	O	S	0	0	0
			4254	2743	703	789	19			
1	B	510	Total	C	N	O	S	0	0	0
			4158	2689	687	764	18			

- Molecule 2 is FARNESYL DIPHOSPHATE (three-letter code: FPP) (formula:  $C_{15}H_{28}O_7P_2$ ) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			24	15	7	2		
2	B	1	Total	C	O	P	0	0
			24	15	7	2		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total 3	Mg 3	0	0
3	A	3	Total 3	Mg 3	0	0

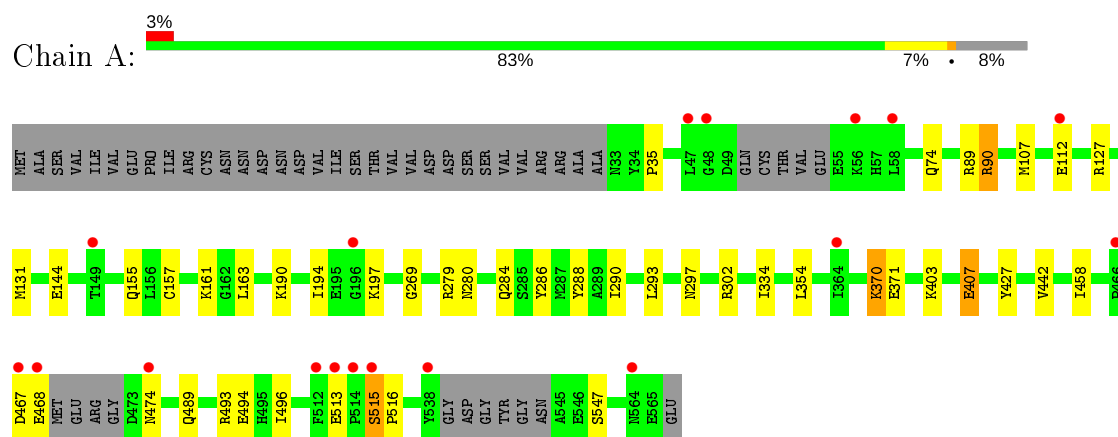
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	553	Total 553	O 553	0	0
4	B	327	Total 327	O 327	0	0

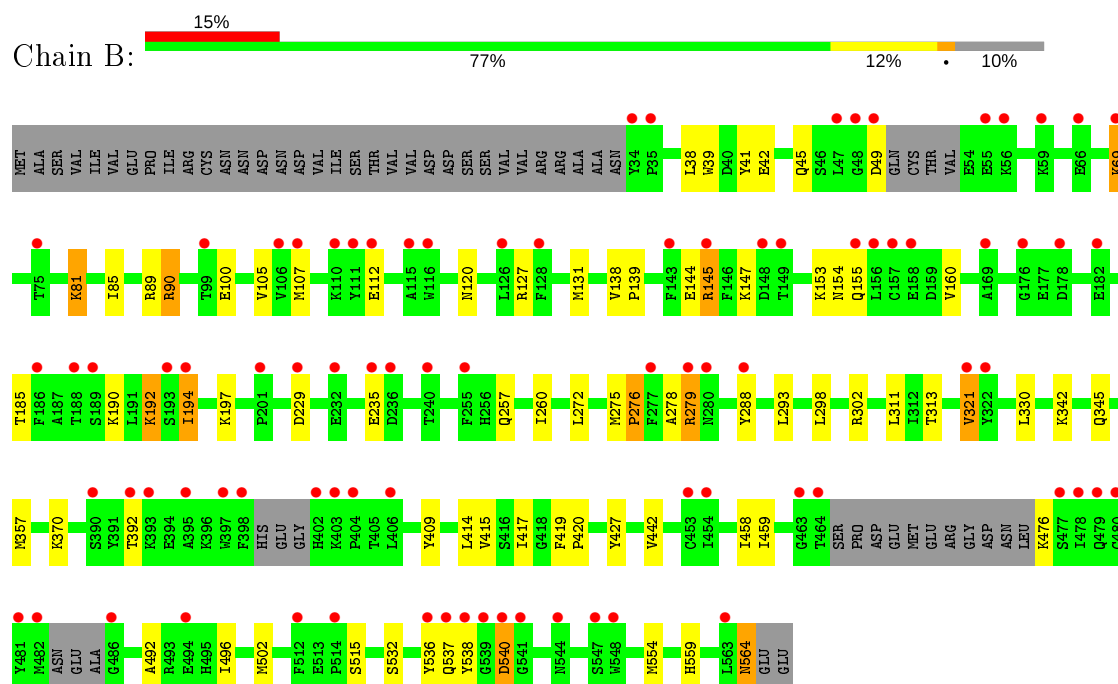
### 3 Residue-property plots [i](#)

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: Sesquisabinene B synthase 2



#### • Molecule 1: Sesquisabinene B synthase 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.05Å 133.05Å 142.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.94 – 1.94 24.92 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.9 (24.94-1.94) 100.0 (24.92-1.94)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.89 (at 1.93Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.192 , 0.238 0.204 , 0.241	Depositor DCC
$R_{free}$ test set	4597 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.0	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 51.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9346	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, FPP

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	0/4359	0.76	0/5901
1	B	0.68	0/4261	0.73	0/5769
All	All	0.69	0/8620	0.75	0/11670

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

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	4254	0	4191	30	0
1	B	4158	0	4083	56	0
2	A	24	0	25	2	0
2	B	24	0	25	3	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
4	A	553	0	0	7	0
4	B	327	0	0	10	0
All	All	9346	0	8324	88	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 5.

All (88) 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:515:SER:HB2	1:A:516:PRO:HD3	1.31	1.11
1:A:515:SER:CB	1:A:516:PRO:HD3	1.84	1.06
1:A:515:SER:HB2	1:A:516:PRO:CD	1.87	1.04
1:B:459:ILE:HG22	1:B:536:TYR:HD2	1.26	0.99
1:B:532:SER:HB3	1:B:536:TYR:CE2	1.99	0.96
1:B:185:THR:HG22	4:B:952:HOH:O	1.62	0.96
1:A:297:ASN:HB2	4:A:1413:HOH:O	1.71	0.89
1:B:532:SER:HB3	1:B:536:TYR:HE2	1.42	0.83
1:B:459:ILE:HG22	1:B:536:TYR:CD2	2.12	0.83
1:A:403:LYS:HE2	1:A:474:ASN:HD21	1.48	0.79
1:B:532:SER:CB	1:B:536:TYR:CE2	2.71	0.72
1:A:515:SER:HB3	1:A:516:PRO:HD3	1.72	0.72
1:B:459:ILE:CG2	1:B:536:TYR:HD2	2.03	0.72
1:B:38:LEU:HD23	1:B:39:TRP:CZ3	2.26	0.71
2:A:900:FPP:H52	4:A:1364:HOH:O	1.90	0.70
1:A:515:SER:CB	1:A:516:PRO:CD	2.49	0.70
1:A:403:LYS:HE2	1:A:474:ASN:ND2	2.07	0.69
1:B:536:TYR:HB2	4:B:720:HOH:O	1.93	0.67
1:B:257:GLN:O	1:B:260:ILE:HG22	1.98	0.62
1:A:494:GLU:HB3	4:A:1351:HOH:O	2.03	0.58
1:B:144:GLU:CG	4:B:742:HOH:O	2.53	0.57
1:B:409:TYR:HH	1:B:476:LYS:N	2.03	0.56
1:B:235:GLU:HG3	4:B:873:HOH:O	2.05	0.56
1:B:342:LYS:HE2	4:B:875:HOH:O	2.06	0.56
1:B:564:ASN:HD22	1:B:564:ASN:C	2.09	0.55
1:A:286:TYR:CE2	1:A:290:ILE:HD11	2.41	0.55
1:A:407:GLU:HB2	4:A:1055:HOH:O	2.07	0.54
1:A:157:CYS:HA	1:A:163:LEU:HD11	1.90	0.54
1:B:229:ASP:HB2	4:B:709:HOH:O	2.07	0.54
1:B:144:GLU:HG3	4:B:742:HOH:O	2.07	0.54
1:B:90:ARG:HD2	4:B:714:HOH:O	2.09	0.52
1:B:81:LYS:HE3	1:B:81:LYS:HA	1.91	0.52
1:B:160:VAL:HG22	1:B:194:ILE:HD12	1.92	0.51
1:A:458:ILE:HG23	1:A:496:ILE:CG2	2.40	0.51
1:B:564:ASN:ND2	1:B:564:ASN:C	2.65	0.50
1:A:489:GLN:HE22	1:A:493:ARG:HE	1.59	0.50
1:B:311:LEU:HD13	1:B:357:MET:HA	1.92	0.50
1:B:554:MET:CE	1:B:559:HIS:CE1	2.95	0.50
2:B:601:FPP:C2	2:B:601:FPP:H102	2.42	0.49
1:B:154:ASN:OD1	1:B:190:LYS:HE3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:415:VAL:HA	1:B:420:PRO:HG2	1.93	0.49
1:B:458:ILE:HG23	1:B:496:ILE:CG2	2.43	0.49
1:B:85:ILE:HD12	1:B:105:VAL:HG23	1.94	0.49
1:B:41:TYR:O	1:B:45:GLN:HG3	2.13	0.49
1:B:257:GLN:HA	1:B:260:ILE:HG22	1.95	0.48
1:B:257:GLN:O	1:B:260:ILE:CG2	2.62	0.48
1:B:313:THR:HG22	2:B:601:FPP:H103	1.95	0.48
1:B:492:ALA:O	1:B:496:ILE:HG12	2.13	0.48
1:A:370:LYS:HD2	1:A:370:LYS:C	2.34	0.47
1:B:69:LYS:HE2	1:B:100:GLU:OE2	2.14	0.47
1:A:288:TYR:CD1	2:A:900:FPP:H143	2.49	0.47
1:B:414:LEU:HD12	1:B:414:LEU:C	2.34	0.47
1:A:427:TYR:CD2	1:A:442:VAL:HG21	2.50	0.47
1:A:35:PRO:HB2	1:A:279:ARG:HD2	1.97	0.46
1:B:279:ARG:HB3	1:B:279:ARG:HE	1.46	0.46
1:B:554:MET:HE3	1:B:559:HIS:CE1	2.50	0.46
1:B:330:LEU:HD21	1:B:345:GLN:HB2	1.98	0.46
1:A:293:LEU:O	1:A:302:ARG:HD3	2.16	0.45
1:A:334:ILE:HG21	1:A:354:LEU:HD21	1.99	0.45
1:A:144:GLU:OE2	4:A:1001:HOH:O	2.20	0.44
1:B:272:LEU:HA	1:B:275:MET:HG2	1.99	0.44
1:B:276:PRO:O	1:B:278:ALA:N	2.51	0.44
1:B:145:ARG:HE	1:B:145:ARG:HB3	1.55	0.43
1:B:293:LEU:HD12	1:B:298:LEU:HB3	2.01	0.43
1:B:293:LEU:HD23	1:B:293:LEU:N	2.33	0.43
1:B:537:GLN:N	4:B:720:HOH:O	2.51	0.43
1:B:293:LEU:O	1:B:302:ARG:HD3	2.18	0.43
1:B:417:ILE:HD12	1:B:417:ILE:HA	1.94	0.43
1:B:537:GLN:HG3	1:B:538:TYR:CD2	2.54	0.43
2:B:601:FPP:H102	2:B:601:FPP:H2	2.00	0.43
1:B:540:ASP:N	1:B:540:ASP:OD1	2.52	0.43
1:B:419:PHE:N	1:B:420:PRO:CD	2.82	0.42
1:B:515:SER:HB2	4:B:771:HOH:O	2.19	0.42
1:A:370:LYS:HD2	1:A:371:GLU:N	2.34	0.42
1:A:90:ARG:HH11	1:A:90:ARG:HD2	1.65	0.42
1:B:427:TYR:CD2	1:B:442:VAL:HG21	2.55	0.42
1:A:280:ASN:O	1:A:284:GLN:HG3	2.20	0.42
1:A:197:LYS:HB2	1:A:197:LYS:HE2	1.67	0.42
1:B:120:ASN:OD1	1:B:120:ASN:C	2.58	0.42
1:B:127:ARG:O	1:B:131:MET:HG2	2.19	0.41
1:B:192:LYS:HB3	1:B:192:LYS:HE2	1.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:LYS:HA	1:A:190:LYS:HD3	1.91	0.41
1:B:138:VAL:HA	1:B:139:PRO:HD3	1.93	0.41
1:A:494:GLU:OE1	4:A:1002:HOH:O	2.22	0.41
1:B:147:LYS:HE2	1:B:147:LYS:HB2	1.89	0.41
1:A:127:ARG:O	1:A:131:MET:HG2	2.22	0.40
1:A:112:GLU:HG3	4:A:1335:HOH:O	2.21	0.40
1:A:269:GLY:O	1:B:370:LYS:HE2	2.21	0.40

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	510/566 (90%)	498 (98%)	11 (2%)	1 (0%)	47	39
1	B	500/566 (88%)	486 (97%)	12 (2%)	2 (0%)	34	24
All	All	1010/1132 (89%)	984 (97%)	23 (2%)	3 (0%)	41	32

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	515	SER
1	B	321	VAL
1	B	276	PRO

### 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	466/507 (92%)	453 (97%)	13 (3%)	43	29
1	B	449/507 (89%)	428 (95%)	21 (5%)	26	11
All	All	915/1014 (90%)	881 (96%)	34 (4%)	34	19

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	GLN
1	A	89	ARG
1	A	90	ARG
1	A	107	MET
1	A	155	GLN
1	A	161	LYS
1	A	194	ILE
1	A	370	LYS
1	A	407	GLU
1	A	467	ASP
1	A	468	GLU
1	A	513	GLU
1	A	547	SER
1	B	42	GLU
1	B	49	ASP
1	B	69	LYS
1	B	81	LYS
1	B	89	ARG
1	B	90	ARG
1	B	107	MET
1	B	112	GLU
1	B	145	ARG
1	B	153	LYS
1	B	155	GLN
1	B	192	LYS
1	B	194	ILE
1	B	197	LYS
1	B	279	ARG
1	B	288	TYR
1	B	321	VAL
1	B	392	THR
1	B	502	MET
1	B	540	ASP
1	B	564	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	155	GLN
1	A	489	GLN
1	A	552	GLN
1	B	559	HIS
1	B	564	ASN

### 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 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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	$\# Z  > 2$
2	FPP	A	900	3	21,23,23	0.60	0	27,31,31	1.44	4 (14%)
2	FPP	B	601	3	21,23,23	0.57	0	27,31,31	0.71	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
2	FPP	A	900	3	-	4/25/25/25	-
2	FPP	B	601	3	-	9/25/25/25	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	FPP	PA-O3A-PB	-4.58	117.11	132.83
2	A	900	FPP	O1-PA-O1A	-3.20	96.57	109.07
2	A	900	FPP	O2A-PA-O1	3.10	122.17	107.75
2	A	900	FPP	C1-C2-C3	-2.31	122.05	126.04

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	900	FPP	C1-O1-PA-O1A
2	A	900	FPP	C1-O1-PA-O2A
2	A	900	FPP	C1-O1-PA-O3A
2	B	601	FPP	O1-C1-C2-C3
2	B	601	FPP	C1-O1-PA-O1A
2	B	601	FPP	C3-C5-C6-C7
2	B	601	FPP	C12-C11-C9-C8
2	A	900	FPP	C12-C11-C9-C8
2	B	601	FPP	C10-C8-C9-C11
2	B	601	FPP	C7-C8-C9-C11
2	B	601	FPP	C5-C6-C7-C8
2	B	601	FPP	C1-O1-PA-O3A
2	B	601	FPP	C1-O1-PA-O2A

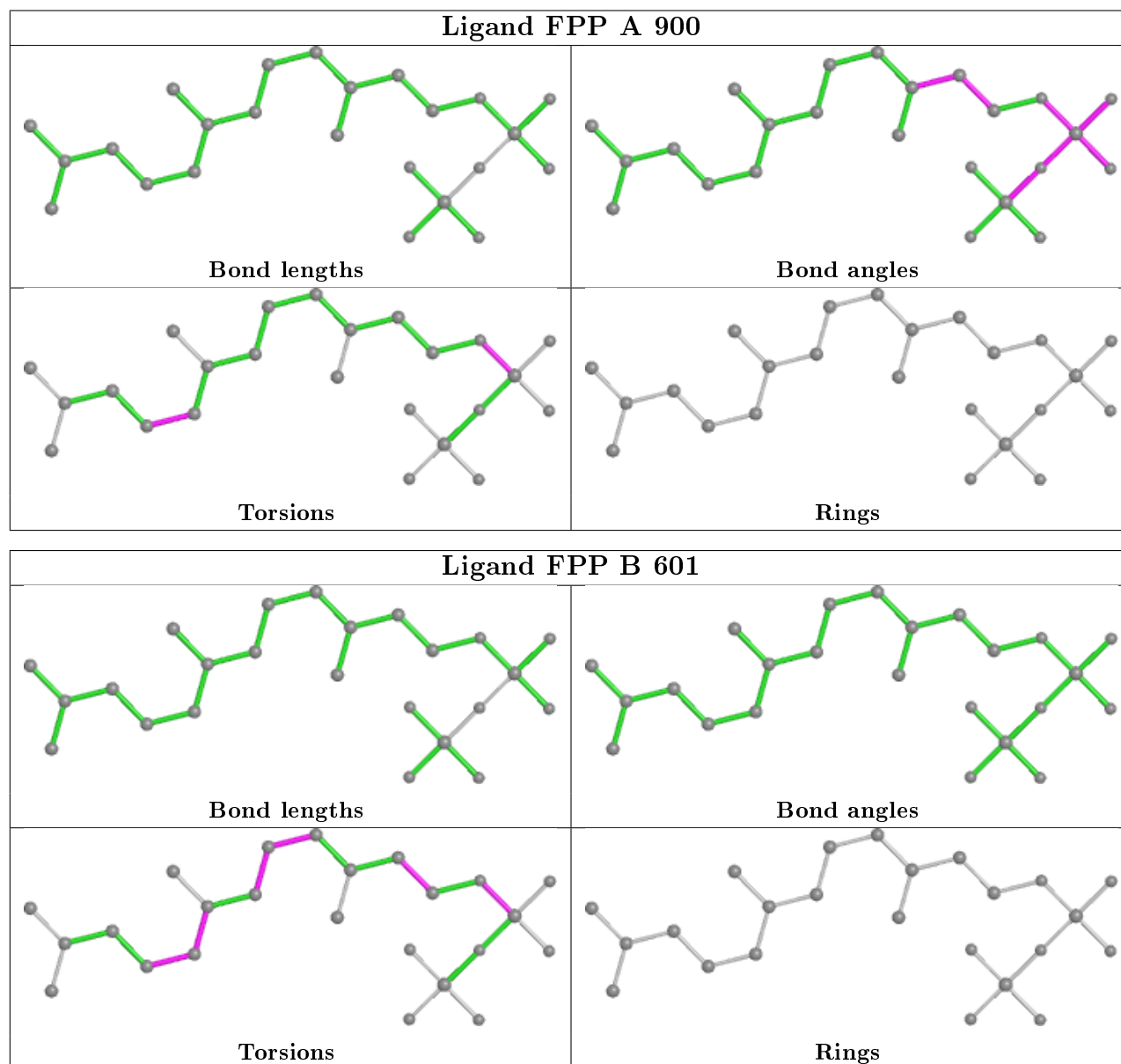
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	FPP	2	0
2	B	601	FPP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	518/566 (91%)	0.14	18 (3%) 44 51	17, 29, 60, 112	0
1	B	510/566 (90%)	0.86	85 (16%) 1 2	22, 46, 81, 119	0
All	All	1028/1132 (90%)	0.50	103 (10%) 7 10	17, 38, 75, 119	0

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	395	ALA	7.0
1	A	538	TYR	6.6
1	A	196	GLY	6.3
1	B	157	CYS	5.4
1	B	279	ARG	5.3
1	B	538	TYR	5.0
1	B	55	GLU	4.9
1	B	148	ASP	4.7
1	B	514	PRO	4.7
1	B	277	PHE	4.6
1	B	464	THR	4.6
1	B	34	TYR	4.5
1	B	156	LEU	4.4
1	B	56	LYS	4.2
1	B	403	LYS	4.1
1	B	280	ASN	4.1
1	B	486	GLY	4.1
1	B	482	MET	4.0
1	B	536	TYR	4.0
1	B	477	SER	3.9
1	B	111	TYR	3.8
1	A	48	GLY	3.8
1	B	186	PHE	3.8
1	B	494	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	541	GLY	3.6
1	B	397	TRP	3.5
1	B	481	TYR	3.5
1	B	155	GLN	3.5
1	B	540	ASP	3.5
1	A	467	ASP	3.4
1	A	474	ASN	3.4
1	B	75	THR	3.4
1	B	110	LYS	3.4
1	B	480	CYS	3.4
1	B	99	THR	3.4
1	B	537	GLN	3.3
1	B	49	ASP	3.3
1	B	539	GLY	3.3
1	B	194	ILE	3.3
1	A	564	ASN	3.2
1	A	514	PRO	3.2
1	B	106	VAL	3.2
1	B	115	ALA	3.2
1	B	149	THR	3.1
1	B	59	LYS	3.1
1	B	112	GLU	3.1
1	B	47	LEU	3.1
1	B	126	LEU	3.0
1	B	478	ILE	3.0
1	B	398	PHE	3.0
1	B	35	PRO	2.9
1	B	158	GLU	2.9
1	B	48	GLY	2.9
1	A	149	THR	2.9
1	B	548	TRP	2.8
1	B	402	HIS	2.8
1	B	107	MET	2.8
1	A	47	LEU	2.7
1	B	145	ARG	2.7
1	B	563	LEU	2.7
1	B	255	PHE	2.7
1	B	463	GLY	2.7
1	B	193	SER	2.6
1	B	390	SER	2.6
1	B	66	GLU	2.6
1	B	116	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	182	GLU	2.5
1	B	453	CYS	2.5
1	B	288	TYR	2.5
1	B	176	GLY	2.5
1	B	454	ILE	2.5
1	B	169	ALA	2.5
1	B	512	PHE	2.5
1	B	201	PRO	2.5
1	B	404	PRO	2.5
1	A	468	GLU	2.4
1	A	56	LYS	2.4
1	B	406	LEU	2.4
1	B	143	PHE	2.4
1	B	547	SER	2.4
1	B	321	VAL	2.4
1	A	513	GLU	2.3
1	A	58	LEU	2.3
1	B	189	SER	2.3
1	A	466	PRO	2.3
1	B	392	THR	2.3
1	A	364	ILE	2.3
1	A	512	PHE	2.2
1	B	178	ASP	2.2
1	B	236	ASP	2.2
1	B	229	ASP	2.2
1	B	69	LYS	2.2
1	B	393	LYS	2.2
1	B	479	GLN	2.2
1	B	544	ASN	2.1
1	B	322	TYR	2.1
1	A	112	GLU	2.1
1	B	128	PHE	2.1
1	B	188	THR	2.1
1	B	232	GLU	2.1
1	B	235	GLU	2.0
1	B	240	THR	2.0
1	A	515	SER	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates

There are no monosaccharides in this entry.

## 6.4 Ligands

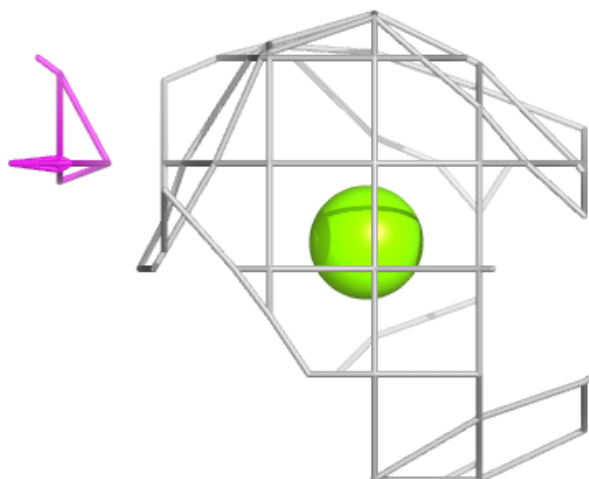
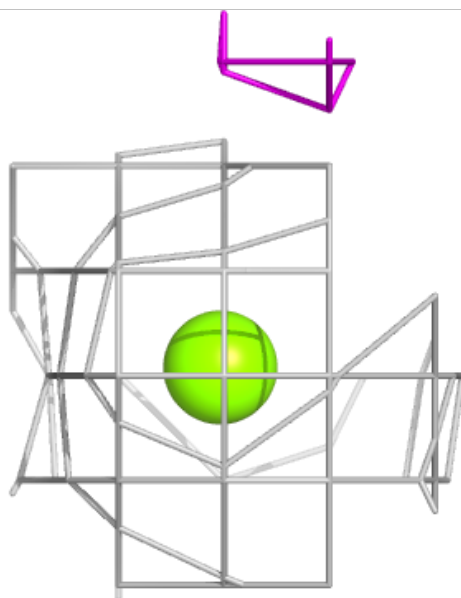
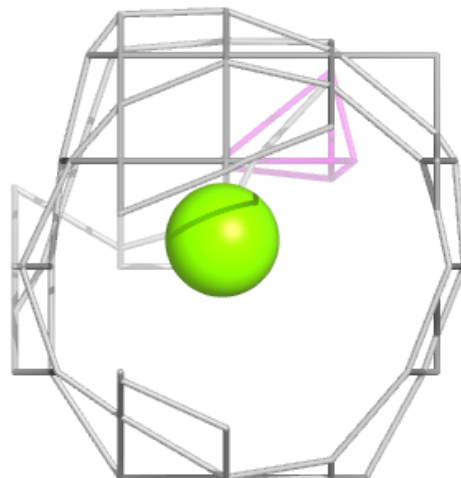
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	B	602	1/1	0.71	0.12	60,60,60,60	0
3	MG	B	604	1/1	0.76	0.07	49,49,49,49	0
3	MG	B	603	1/1	0.78	0.12	45,45,45,45	0
2	FPP	B	601	24/24	0.88	0.21	54,67,85,89	0
3	MG	A	902	1/1	0.90	0.11	40,40,40,40	0
3	MG	A	903	1/1	0.91	0.17	41,41,41,41	0
3	MG	A	901	1/1	0.94	0.07	32,32,32,32	0
2	FPP	A	900	24/24	0.94	0.16	30,44,62,63	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.

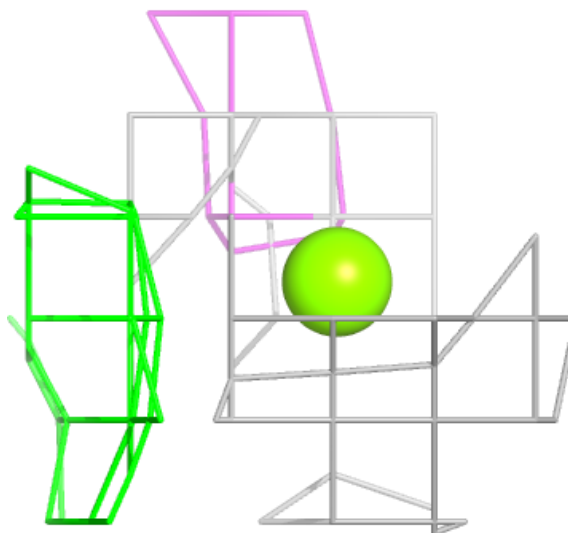
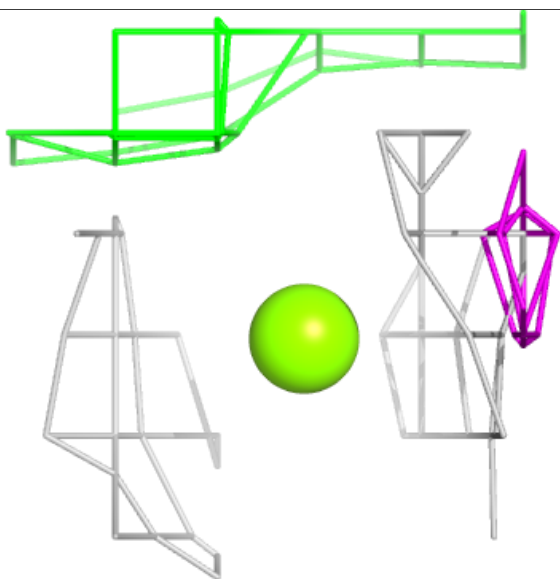
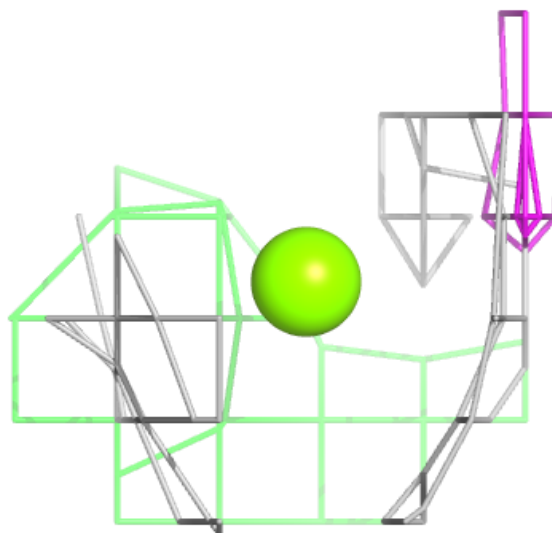
**Electron density around MG B 602:**

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



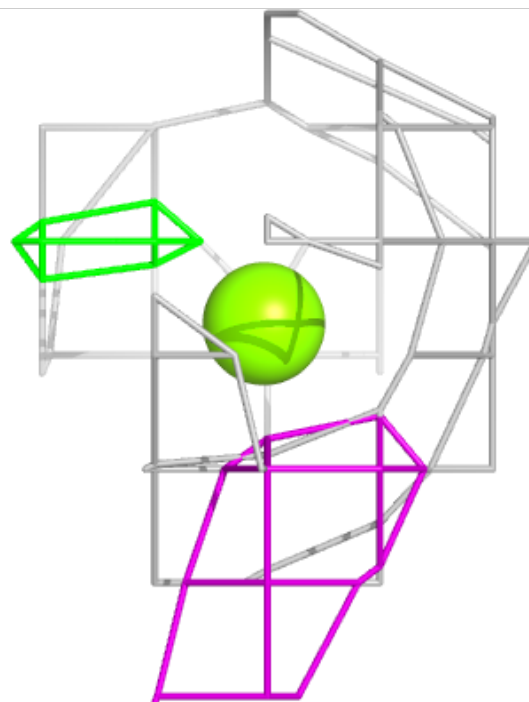
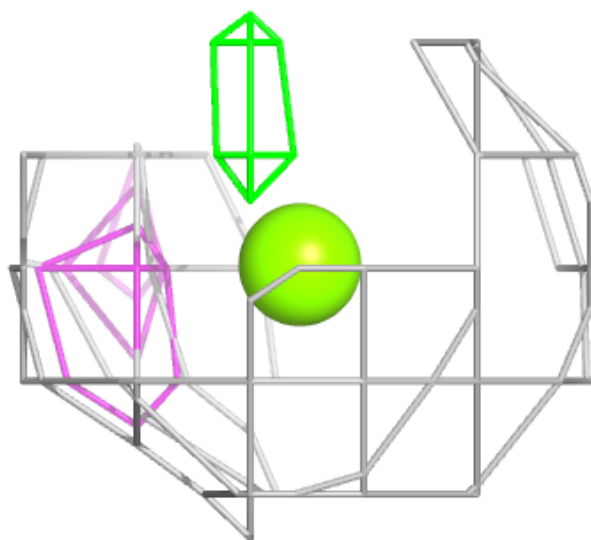
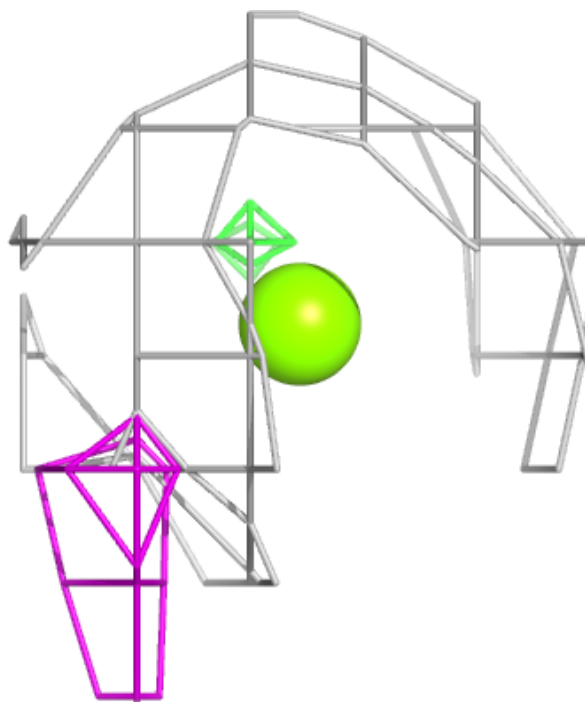
**Electron density around MG B 604:**

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



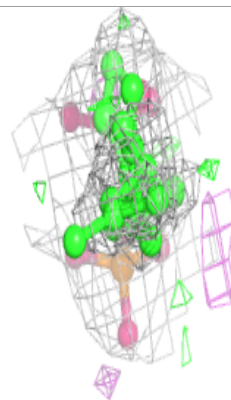
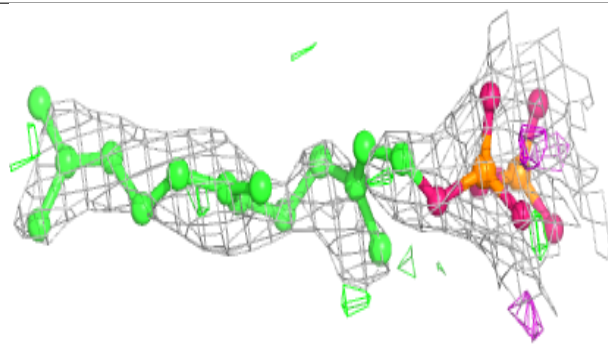
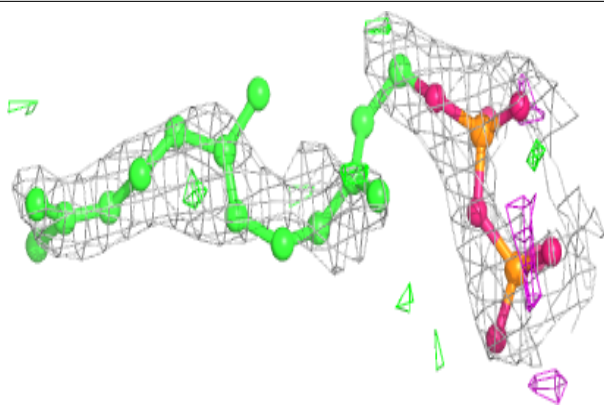
**Electron density around MG B 603:**

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



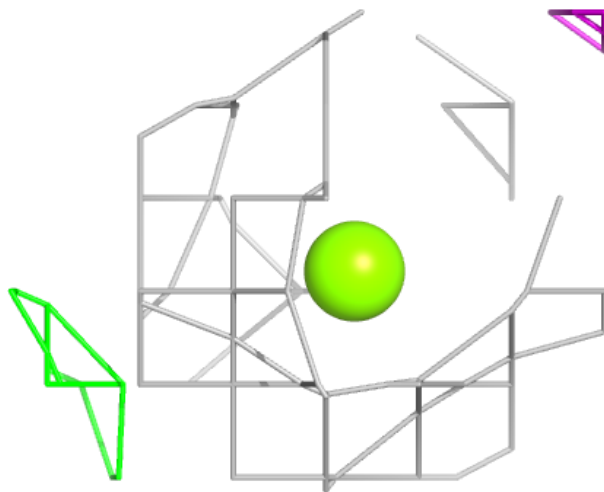
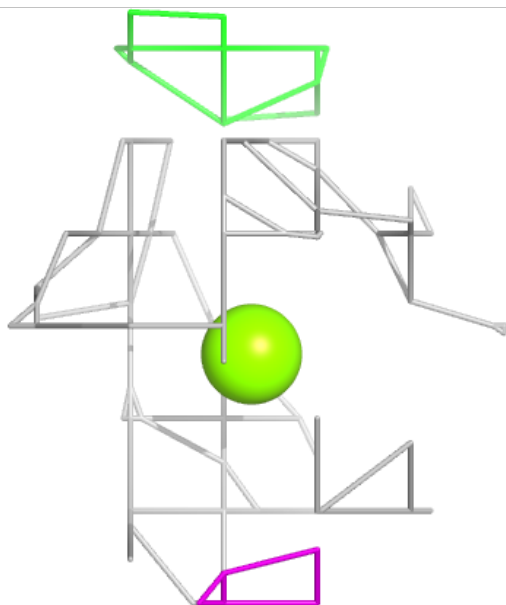
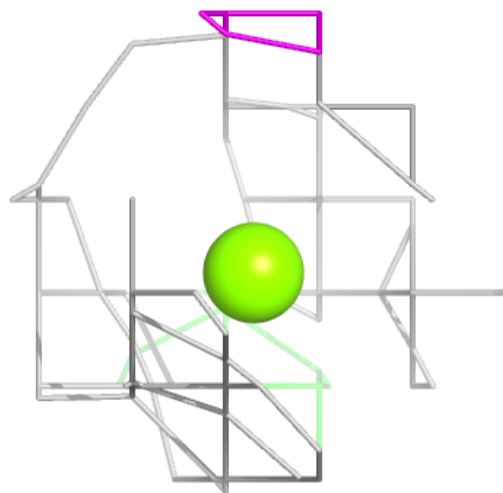
**Electron density around FPP B 601:**

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



**Electron density around MG A 902:**

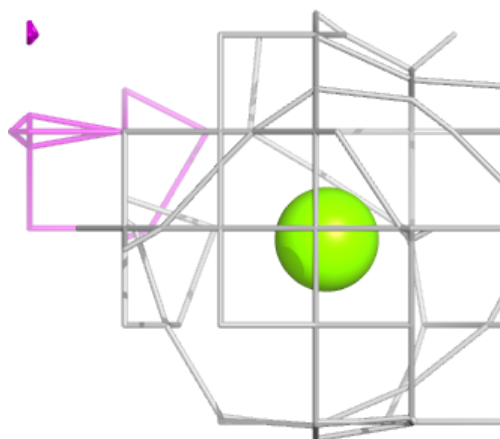
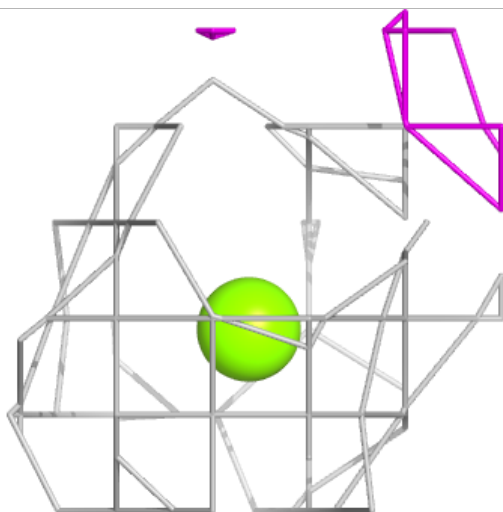
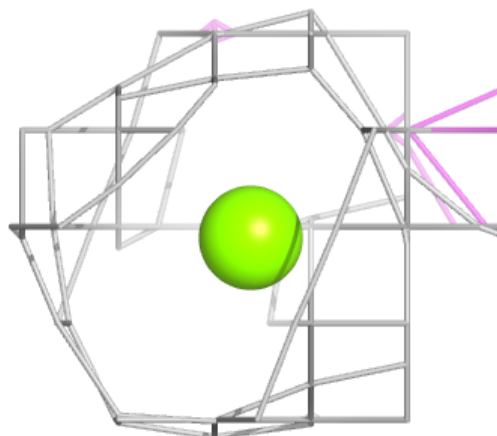
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





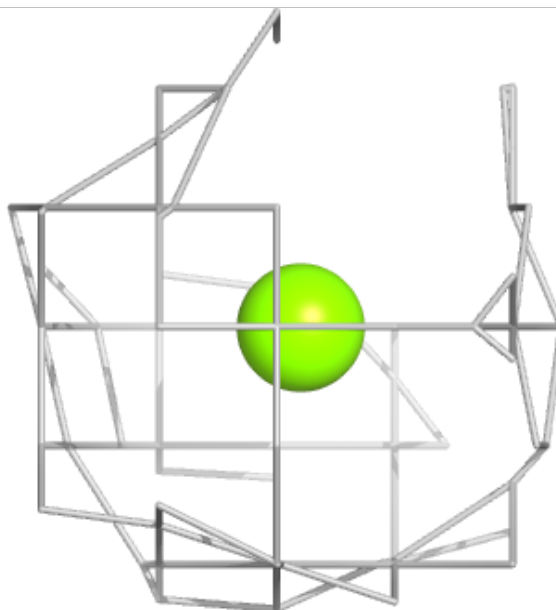
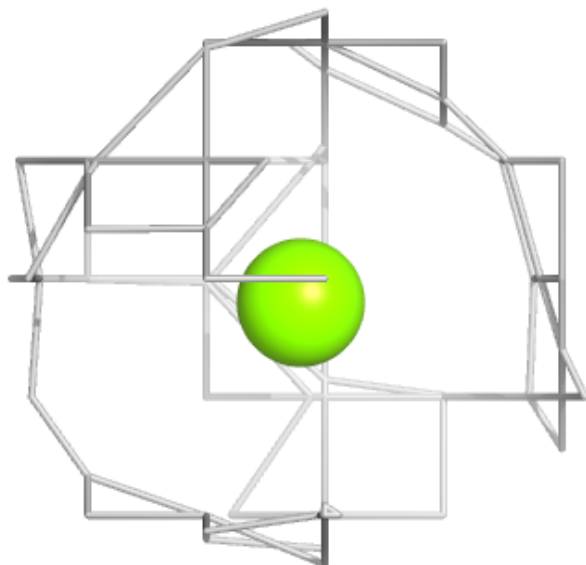
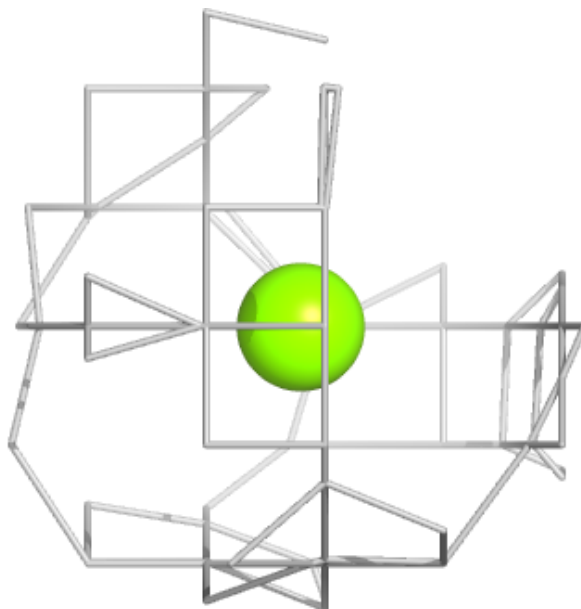
**Electron density around MG A 903:**

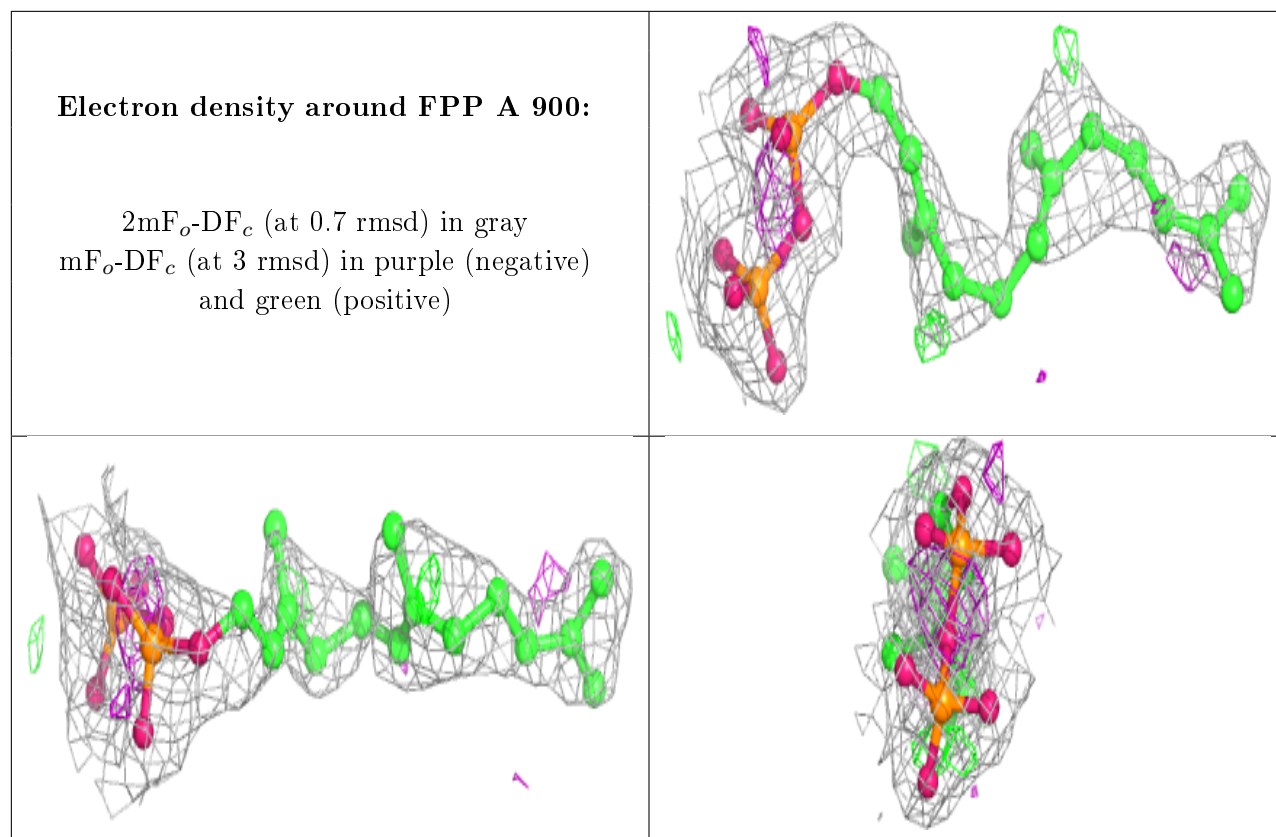
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around MG A 901:**

$2mF_o-DF_c$  (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.