



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2025 – 08:46 PM JST

PDB ID : 7VB4 / pdb_00007vb4
Title : A crystal structure of alphavirus nonstructural protein 4 (nsP4) reveals an intrinsically dynamic RNA-dependent RNA polymerase
Authors : Tan, Y.B.; Luo, D.
Deposited on : 2021-08-30
Resolution : 1.86 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

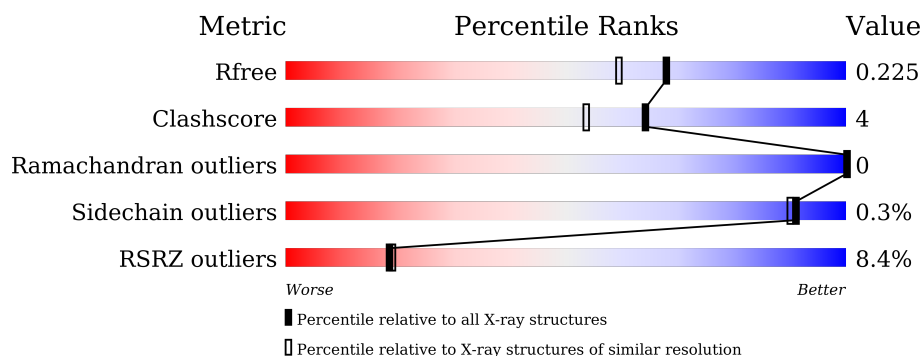
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.86 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}	164625	3097 (1.86-1.86)
Clashscore	180529	3359 (1.86-1.86)
Ramachandran outliers	177936	3335 (1.86-1.86)
Sidechain outliers	177891	3335 (1.86-1.86)
RSRZ outliers	164620	3097 (1.86-1.86)

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	520	<div> <div>8%</div> <div>80%</div> <div>8%</div> <div>12%</div> </div>
1	B	520	<div> <div>7%</div> <div>81%</div> <div>8%</div> <div>11%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8064 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.

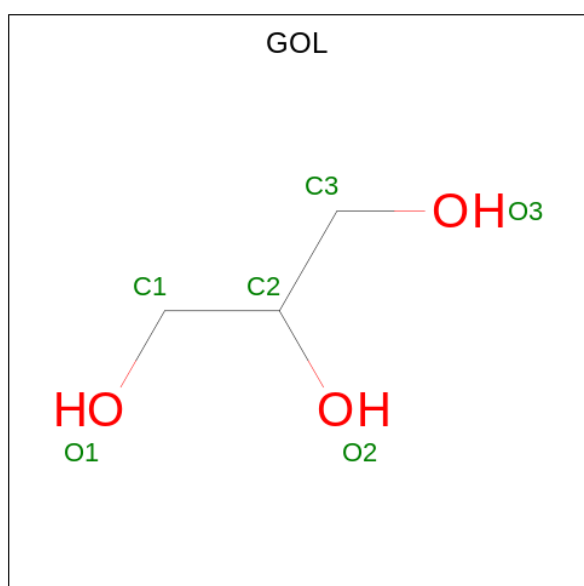
- Molecule 1 is a protein called RNA-directed RNA polymerase nsP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	456	Total	C	N	O	S	0	0	0
			3560	2263	599	675	23			
1	B	461	Total	C	N	O	S	0	0	0
			3600	2290	606	680	24			

- 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	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 6	C 3	O 3	0	0
3	A	1	Total 6	C 3	O 3	0	0
3	B	1	Total 6	C 3	O 3	0	0
3	B	1	Total 6	C 3	O 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	435	Total 435	O 435	0	0
4	B	441	Total 441	O 441	0	0

- Molecule 1: RNA-directed RNA polymerase nsP4



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	67.00Å 68.29Å 71.07Å 115.97° 106.71° 95.90°	Depositor
Resolution (Å)	45.00 – 1.86 45.00 – 1.86	Depositor EDS
% Data completeness (in resolution range)	89.4 (45.00-1.86) 89.6 (45.00-1.86)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 1.86Å)	Xtriage
Refinement program	PHENIX 1.19.2	Depositor
R, R_{free}	0.187 , 0.225 0.187 , 0.225	Depositor DCC
R_{free} test set	85892 reflections (2.44%)	wwPDB-VP
Wilson B-factor (Å ²)	18.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 53.9	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	0.95	EDS
Total number of atoms	8064	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.83% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 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	0.15	0/3629	0.34	0/4929
1	B	0.15	0/3669	0.35	0/4984
All	All	0.15	0/7298	0.34	0/9913

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	3560	0	3534	32	0
1	B	3600	0	3586	29	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	12	0	16	0	0
3	B	12	0	16	1	0
4	A	435	0	0	2	0
4	B	441	0	0	3	0
All	All	8064	0	7152	54	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 4.

All (54) 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:B:384:LEU:HG	1:B:388:MET:HE3	1.52	0.90
1:A:586:ARG:HE	1:A:590:GLN:HE21	1.31	0.79
1:A:353:ASP:HB3	1:B:104:PRO:HG3	1.66	0.74
1:A:384:LEU:HG	1:A:388:MET:HE3	1.74	0.69
1:A:423:PHE:HA	1:A:427:MET:HE2	1.75	0.69
1:A:185:ALA:O	4:A:801:HOH:O	2.12	0.67
1:B:590:GLN:NE2	4:B:802:HOH:O	2.28	0.65
1:A:410:ILE:HD11	1:A:426:MET:HG3	1.84	0.60
1:A:557:PHE:CE1	1:B:112:ALA:HB3	2.41	0.56
1:B:287:MET:HE2	1:B:311:ILE:HG12	1.88	0.55
1:B:420:ARG:NH2	1:B:536:PRO:HG3	2.22	0.54
1:A:362:GLN:HB2	1:A:511:GLN:HE22	1.73	0.53
1:B:407:PHE:HD1	1:B:410:ILE:HD12	1.74	0.52
1:A:191:GLN:HE21	1:A:378:GLN:HE22	1.58	0.52
1:B:420:ARG:HH22	1:B:536:PRO:HG3	1.75	0.51
1:B:544:ASP:OD1	1:B:547:ARG:NH2	2.44	0.50
1:A:152:ASP:HB3	1:A:183:ARG:HB3	1.92	0.50
1:B:422:LYS:NZ	3:B:703:GOL:O3	2.45	0.50
1:B:423:PHE:HA	1:B:427:MET:HE2	1.93	0.49
1:B:152:ASP:HB3	1:B:183:ARG:HB3	1.93	0.49
1:B:434:THR:OG1	4:B:801:HOH:O	2.19	0.49
1:A:109:SER:HA	1:B:558:ARG:HA	1.96	0.47
1:A:586:ARG:HG3	1:B:113:ASN:HB3	1.96	0.47
1:A:362:GLN:HB2	1:A:511:GLN:NE2	2.29	0.47
1:A:414:HIS:CE1	1:B:532:GLY:HA3	2.51	0.46
1:A:586:ARG:HE	1:A:590:GLN:NE2	2.07	0.46
1:B:248:THR:HA	1:B:279:GLU:HA	1.98	0.45
1:B:387:LEU:HD11	1:B:400:LEU:HD11	1.99	0.45
1:A:586:ARG:O	1:A:590:GLN:HG3	2.16	0.44
1:A:478:MET:HG2	1:A:492:ILE:HD13	1.99	0.44
1:B:419:THR:O	1:B:420:ARG:HG2	2.18	0.44
1:A:586:ARG:NE	1:A:590:GLN:HE21	2.08	0.44
1:A:532:GLY:HA3	1:B:414:HIS:CE1	2.53	0.44
1:A:375:ASP:OD1	1:A:378:GLN:NE2	2.51	0.44
1:A:191:GLN:HE21	1:A:378:GLN:NE2	2.16	0.44
1:A:558:ARG:HA	1:B:109:SER:HA	2.00	0.44
1:A:214:LEU:N	1:A:215:PRO:HD2	2.33	0.43
1:A:387:LEU:HD11	1:A:400:LEU:HD11	2.01	0.43
1:B:399:LEU:HD12	1:B:399:LEU:HA	1.86	0.43
1:A:478:MET:HE3	1:A:478:MET:HB2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:458:ARG:NH2	4:B:804:HOH:O	2.36	0.43
1:A:327:ARG:NH1	4:A:827:HOH:O	2.52	0.43
1:A:427:MET:HE3	1:A:427:MET:HB3	1.81	0.43
1:A:272:TYR:OH	1:A:314:ALA:HA	2.19	0.43
1:B:501:PRO:HG3	1:B:568:ALA:HB1	1.99	0.43
1:B:105:LEU:HD12	1:B:105:LEU:HA	1.86	0.42
1:B:461:ALA:O	1:B:467:ASN:HA	2.21	0.41
1:A:282:MET:O	1:A:286:VAL:HG13	2.21	0.41
1:A:230:TYR:CD2	1:A:451:GLU:HA	2.56	0.41
1:B:377:SER:HB2	1:B:378:GLN:NE2	2.35	0.41
1:B:458:ARG:HE	1:B:458:ARG:HB2	1.69	0.41
1:A:194:LEU:HD21	1:A:407:PHE:CD2	2.56	0.40
1:B:410:ILE:HD11	1:B:426:MET:HE3	2.04	0.40
1:A:550:LEU:O	1:A:554:LYS:HG3	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	448/520 (86%)	435 (97%)	13 (3%)	0	100	100
1	B	453/520 (87%)	441 (97%)	12 (3%)	0	100	100
All	All	901/1040 (87%)	876 (97%)	25 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	385/446 (86%)	384 (100%)	1 (0%)	91	90
1	B	390/446 (87%)	389 (100%)	1 (0%)	91	90
All	All	775/892 (87%)	773 (100%)	2 (0%)	91	90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	367	LEU
1	B	308	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	191	GLN
1	A	205	ASN
1	A	511	GLN
1	A	590	GLN
1	B	118	GLN
1	B	326	HIS
1	B	397	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	704	-	5,5,5	0.53	0	5,5,5	0.38	0
3	GOL	B	703	-	5,5,5	0.51	0	5,5,5	0.48	0
3	GOL	A	703	-	5,5,5	0.55	0	5,5,5	0.37	0
3	GOL	A	704	-	5,5,5	0.51	0	5,5,5	0.39	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	704	-	-	0/4/4/4	-
3	GOL	B	703	-	-	2/4/4/4	-
3	GOL	A	703	-	-	4/4/4/4	-
3	GOL	A	704	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

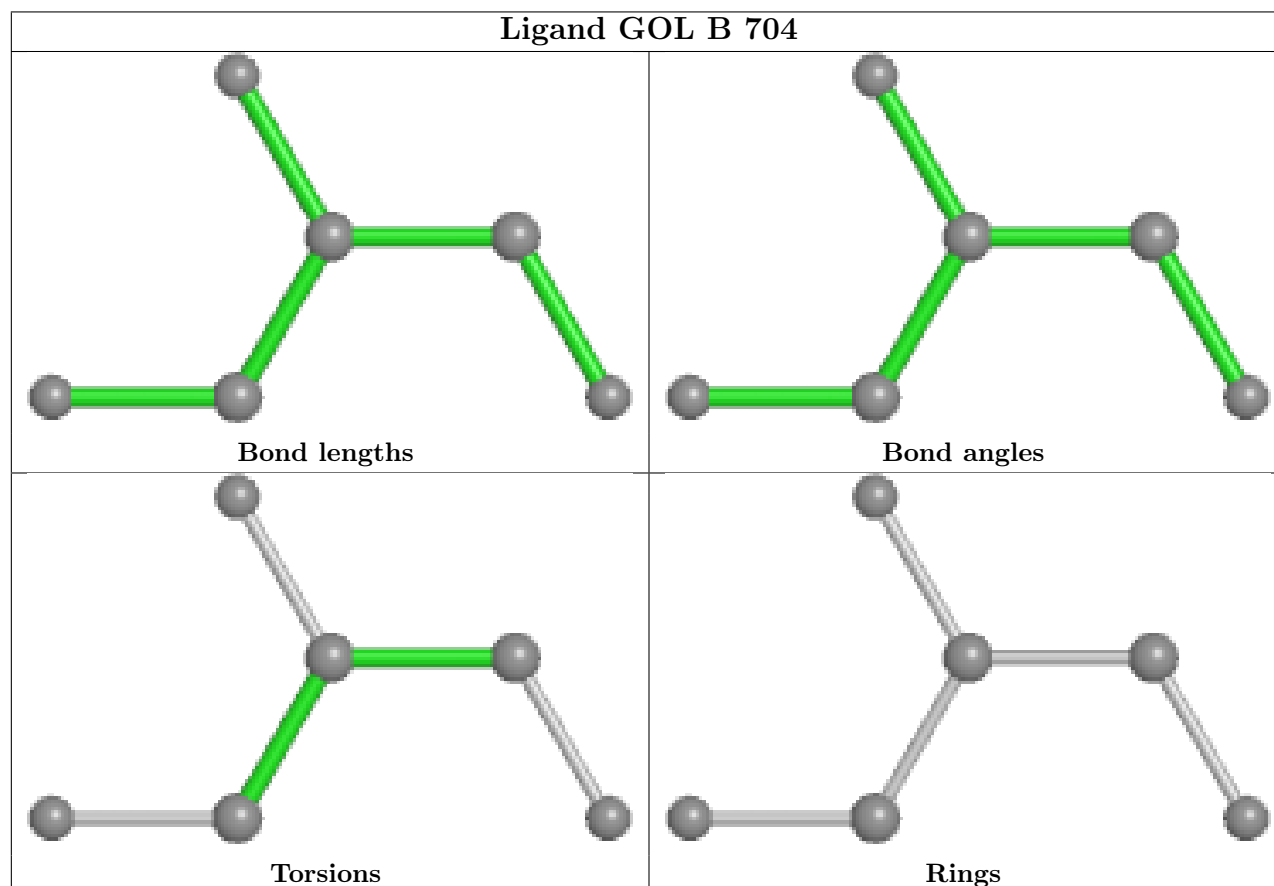
Mol	Chain	Res	Type	Atoms
3	A	703	GOL	C1-C2-C3-O3
3	A	704	GOL	C1-C2-C3-O3
3	A	703	GOL	O2-C2-C3-O3
3	A	704	GOL	O2-C2-C3-O3
3	B	703	GOL	O2-C2-C3-O3
3	A	703	GOL	O1-C1-C2-C3
3	B	703	GOL	C1-C2-C3-O3
3	A	703	GOL	O1-C1-C2-O2

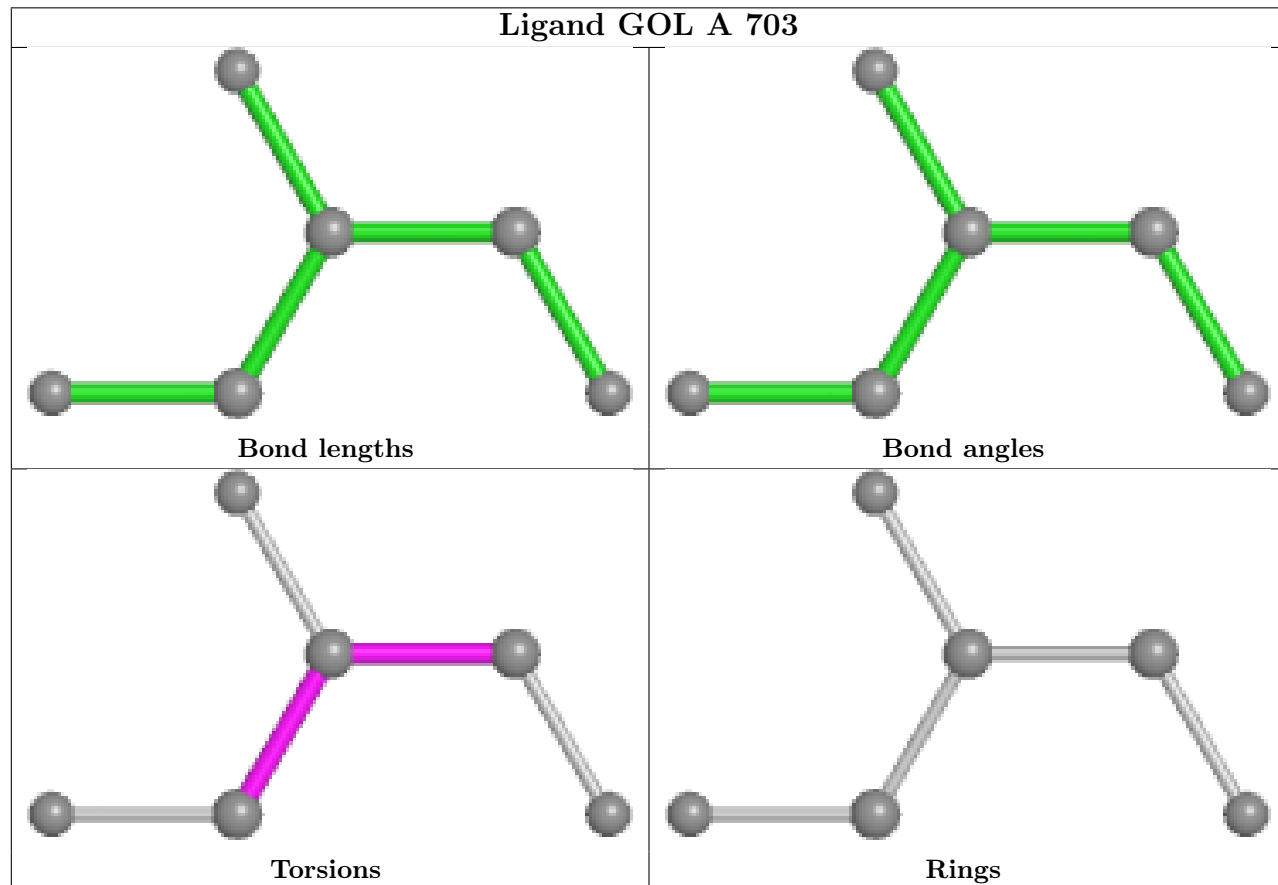
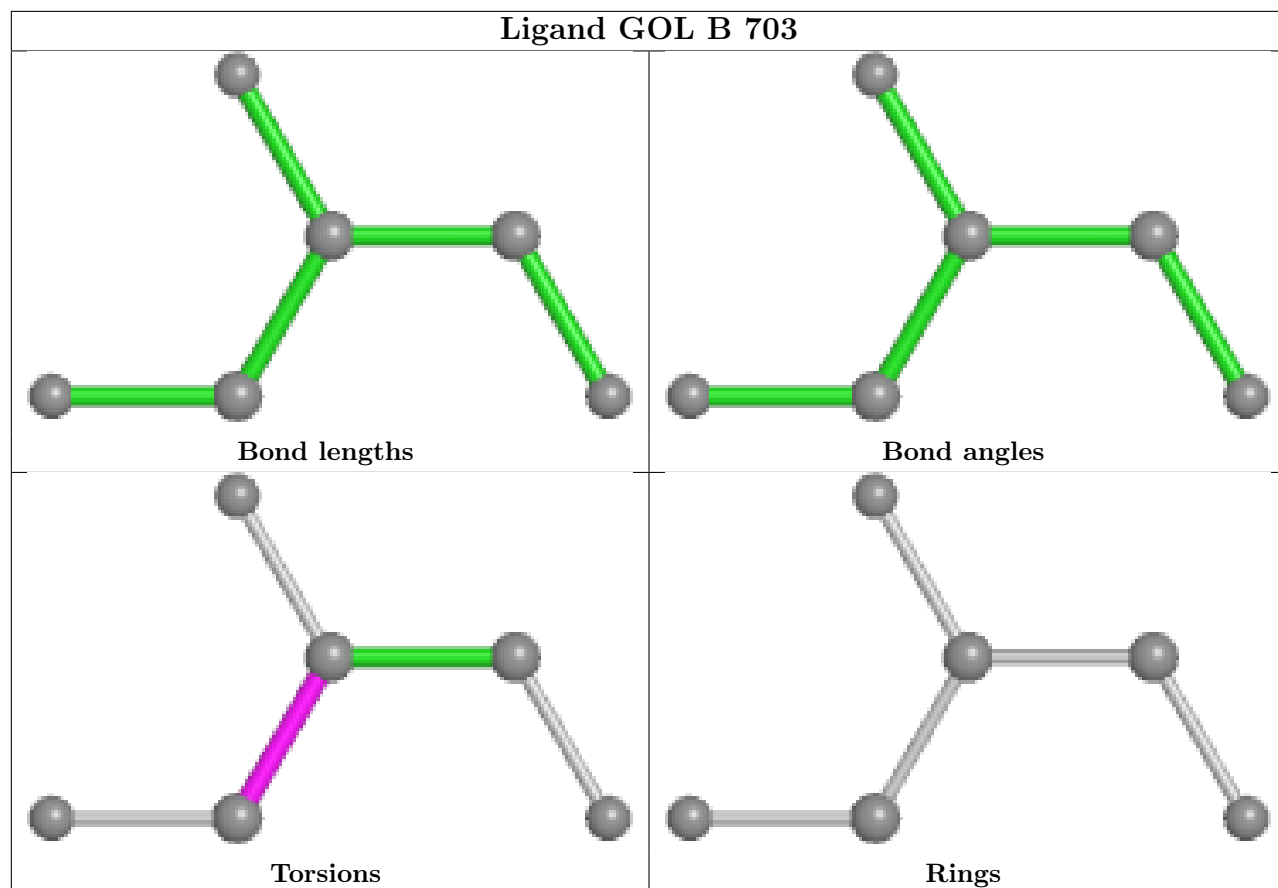
There are no ring outliers.

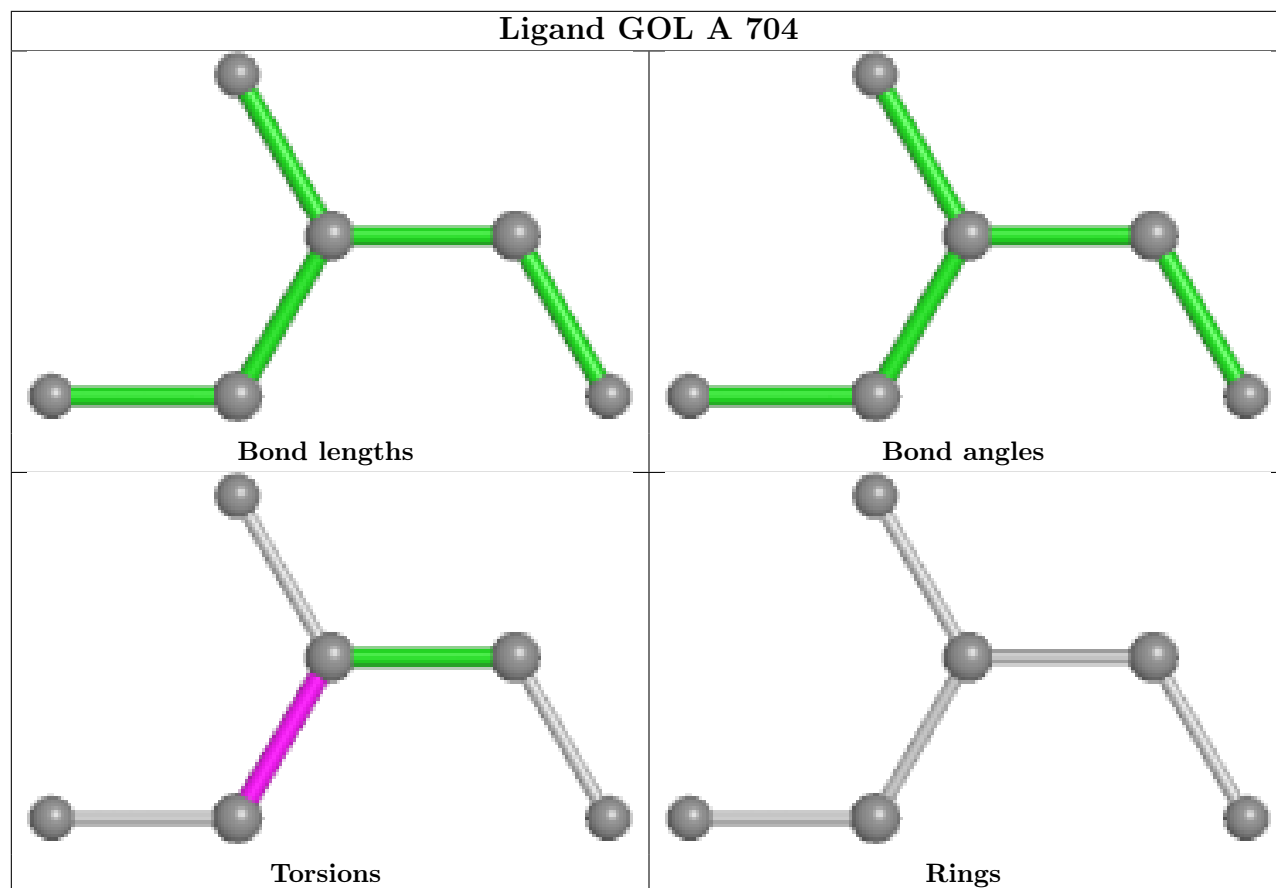
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	703	GOL	1	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 [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	456/520 (87%)	0.30	43 (9%)	15 15	8, 24, 64, 84	0
1	B	461/520 (88%)	0.15	34 (7%)	22 23	8, 21, 56, 76	0
All	All	917/1040 (88%)	0.22	77 (8%)	18 19	8, 23, 61, 84	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	313	ALA	6.1
1	A	166	ALA	5.9
1	B	112	ALA	5.9
1	A	286	VAL	5.6
1	B	105	LEU	5.6
1	A	602	ILE	5.6
1	A	104	PRO	5.4
1	B	166	ALA	4.9
1	A	110	VAL	4.6
1	B	110	VAL	4.3
1	A	287	MET	4.3
1	B	308	VAL	4.3
1	A	259	LEU	4.2
1	B	111	PRO	4.2
1	A	261	GLY	4.1
1	B	160	THR	4.0
1	A	314	ALA	3.8
1	B	104	PRO	3.7
1	B	179	ALA	3.5
1	A	160	THR	3.3
1	A	165	PRO	3.3
1	A	162	THR	3.3
1	A	488	MET	3.2
1	B	163	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	267	LEU	3.2
1	B	261	GLY	3.1
1	B	211	MET	3.1
1	B	499	GLU	3.0
1	B	287	MET	3.0
1	A	105	LEU	3.0
1	A	258	ARG	3.0
1	A	285	PHE	3.0
1	A	272	TYR	3.0
1	A	214	LEU	3.0
1	B	311	ILE	2.9
1	A	349	ALA	2.9
1	A	205	ASN	2.8
1	A	410	ILE	2.8
1	A	163	PHE	2.7
1	A	407	PHE	2.7
1	A	157	CYS	2.7
1	B	162	THR	2.7
1	A	268	PHE	2.6
1	B	286	VAL	2.6
1	B	488	MET	2.6
1	A	288	ASP	2.6
1	B	346	ASP	2.6
1	B	106	TYR	2.5
1	A	212	ARG	2.5
1	B	259	LEU	2.5
1	A	264	ALA	2.5
1	B	310	VAL	2.5
1	A	266	ALA	2.4
1	A	111	PRO	2.4
1	A	161	ALA	2.4
1	A	346	ASP	2.3
1	B	262	PRO	2.3
1	A	262	PRO	2.3
1	B	108	SER	2.3
1	A	213	GLU	2.3
1	B	205	ASN	2.2
1	B	114	TYR	2.2
1	B	161	ALA	2.2
1	B	314	ALA	2.2
1	A	158	LEU	2.2
1	A	180	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	267	LEU	2.2
1	B	283	ASP	2.1
1	A	270	LYS	2.1
1	A	181	ASN	2.1
1	A	164	CYS	2.1
1	B	312	GLN	2.1
1	B	277	LEU	2.1
1	B	115	SER	2.1
1	A	109	SER	2.0
1	B	487	ASN	2.0
1	A	282	MET	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 [i](#)

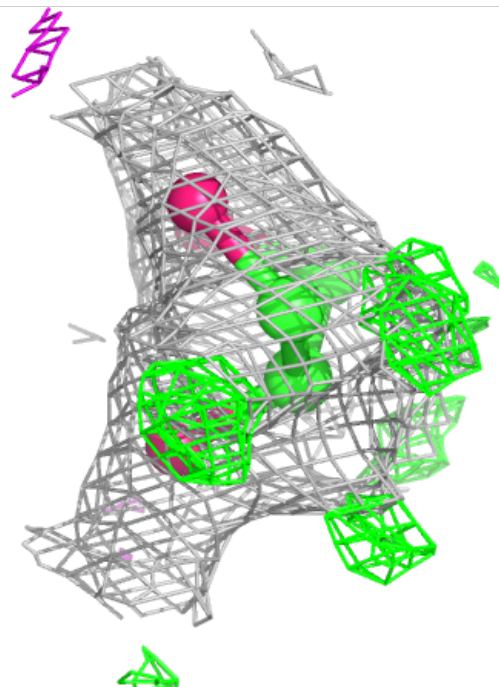
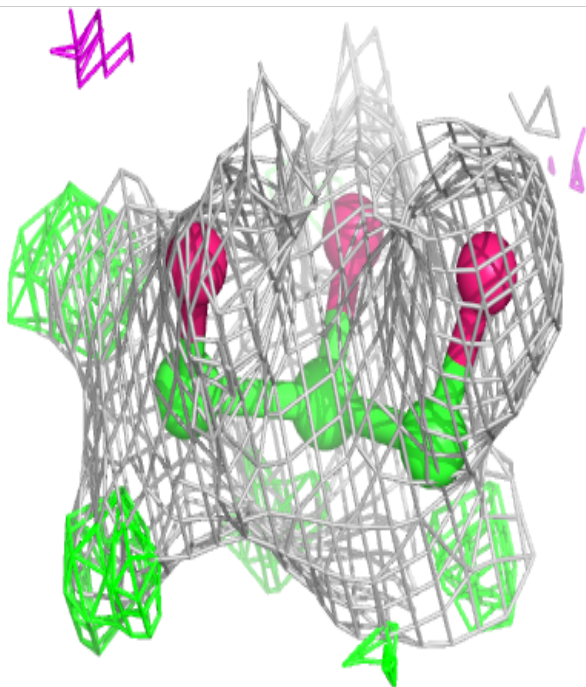
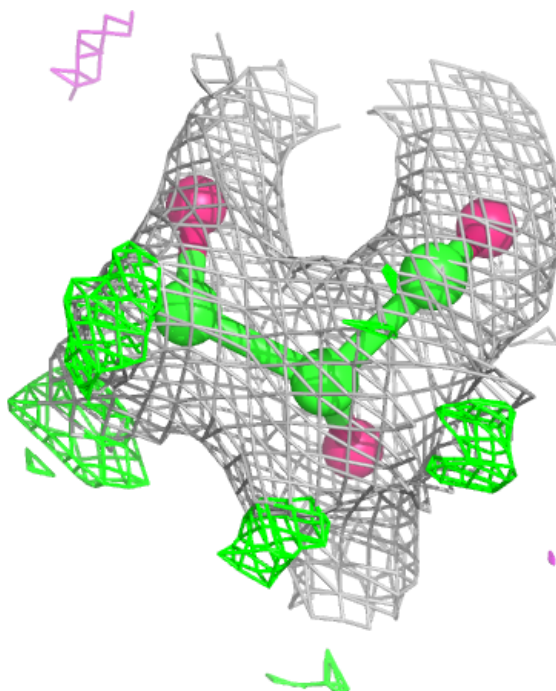
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	GOL	A	704	6/6	0.68	0.16	31,39,39,48	0
3	GOL	B	703	6/6	0.84	0.15	22,31,35,46	0
3	GOL	A	703	6/6	0.85	0.14	25,26,35,45	0
3	GOL	B	704	6/6	0.87	0.16	25,33,38,42	0
2	MG	A	701	1/1	0.94	0.06	27,27,27,27	0
2	MG	B	701	1/1	0.95	0.10	26,26,26,26	0
2	MG	A	702	1/1	0.97	0.05	18,18,18,18	0
2	MG	B	702	1/1	0.97	0.06	19,19,19,19	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.

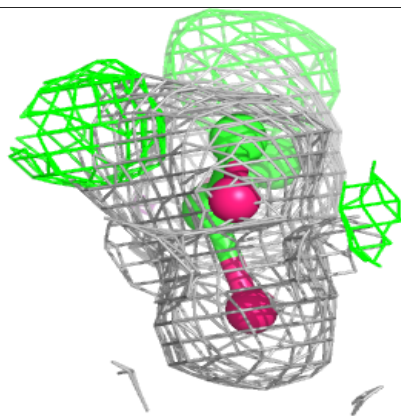
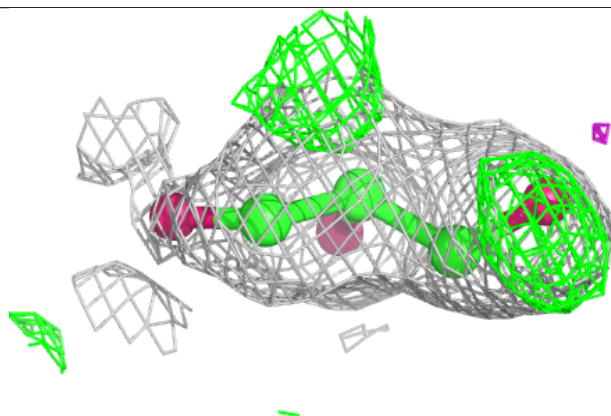
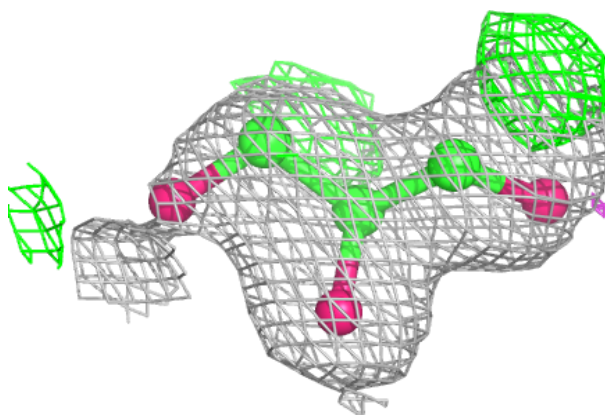
Electron density around GOL A 704:

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

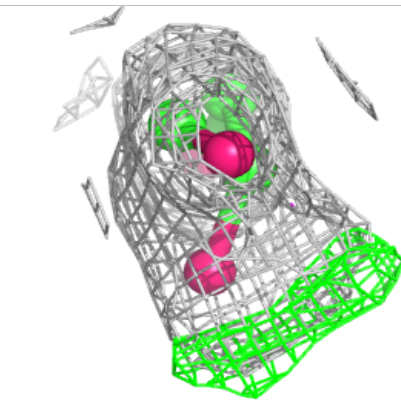
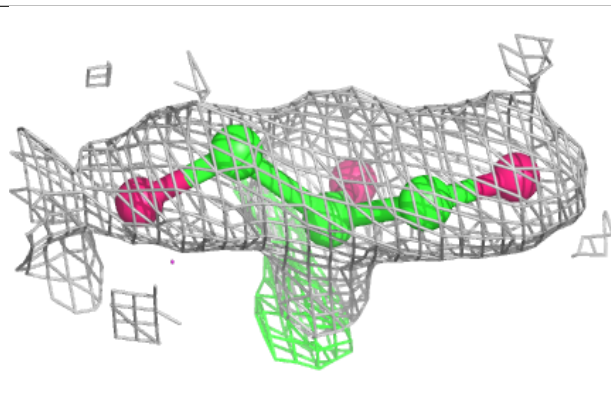
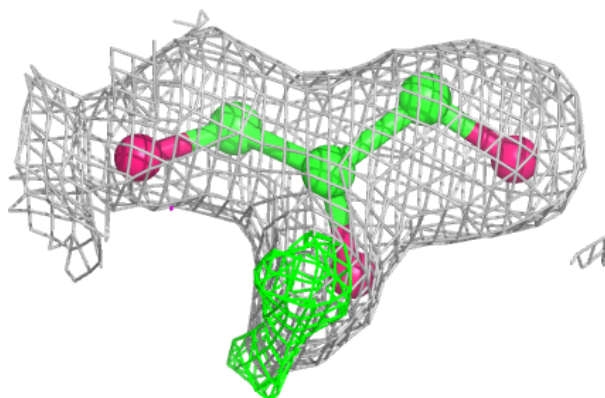


Electron density around GOL B 703:

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

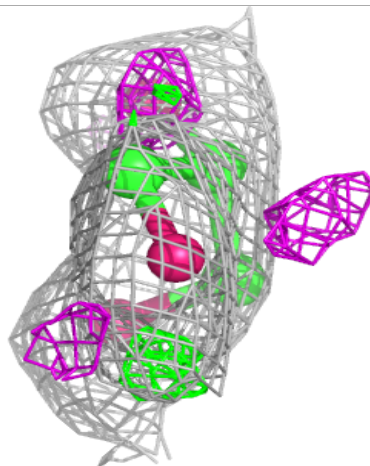
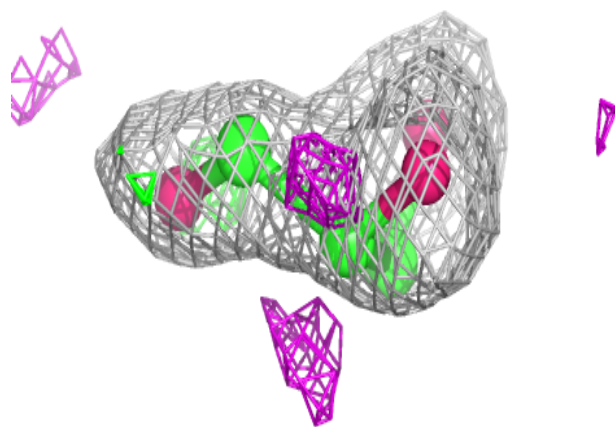
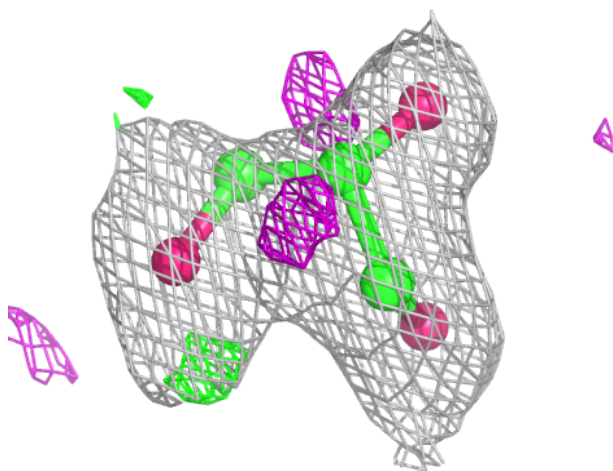
**Electron density around GOL A 703:**

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



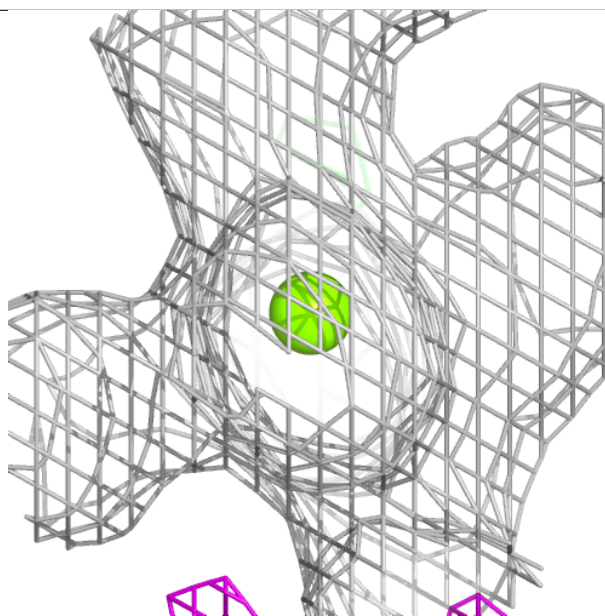
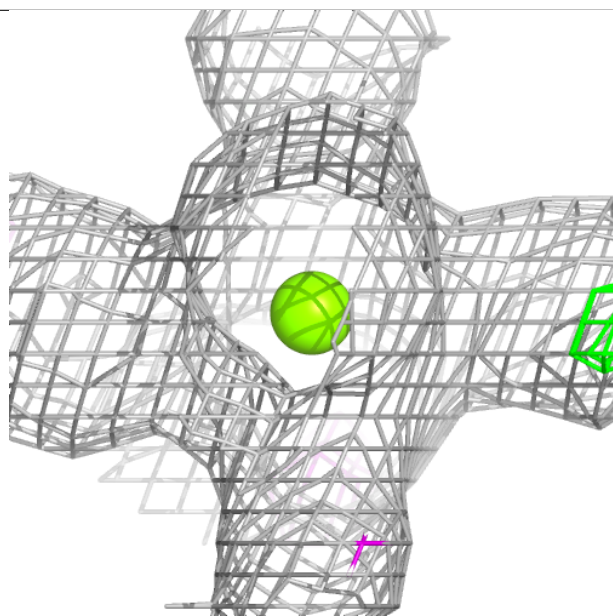
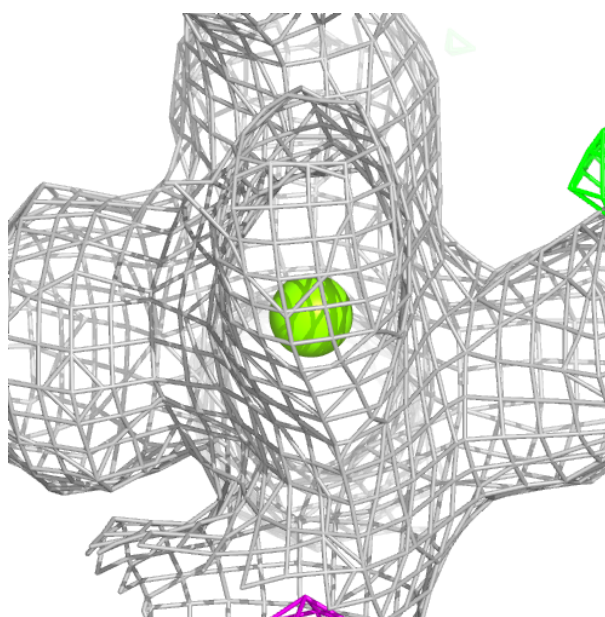
Electron density around GOL B 704:

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



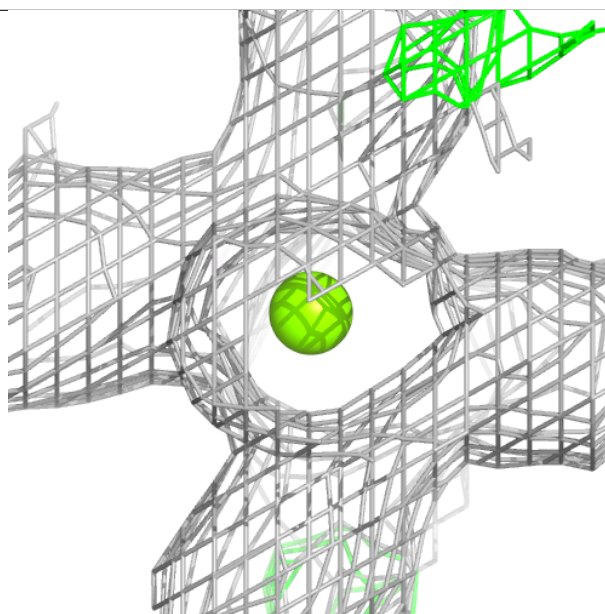
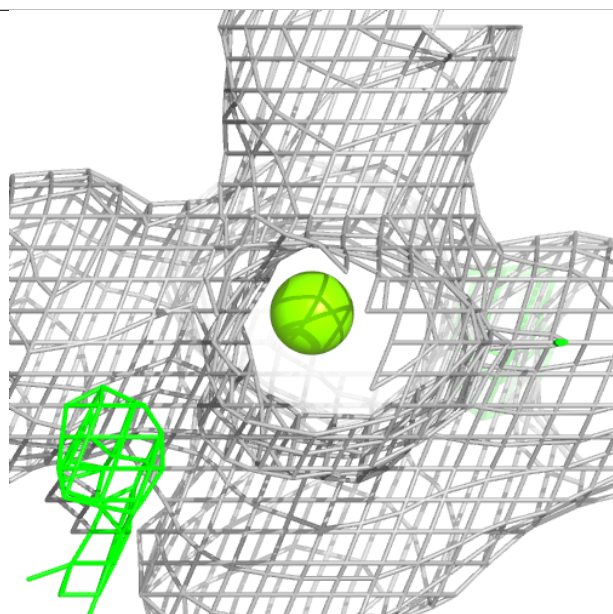
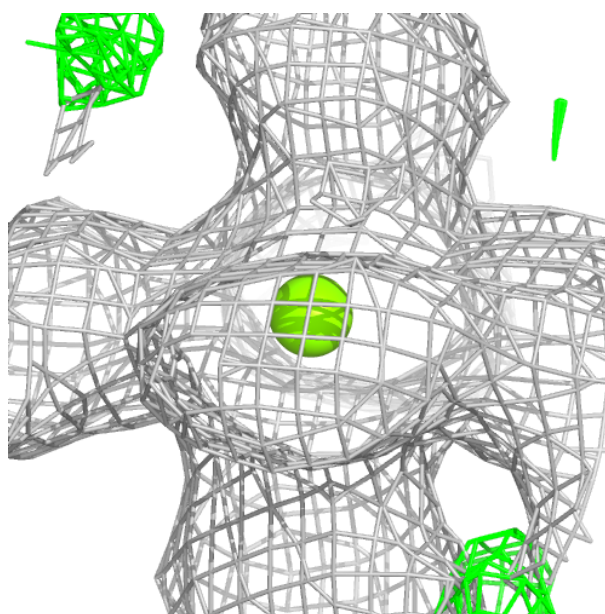
Electron density around MG A 701:

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



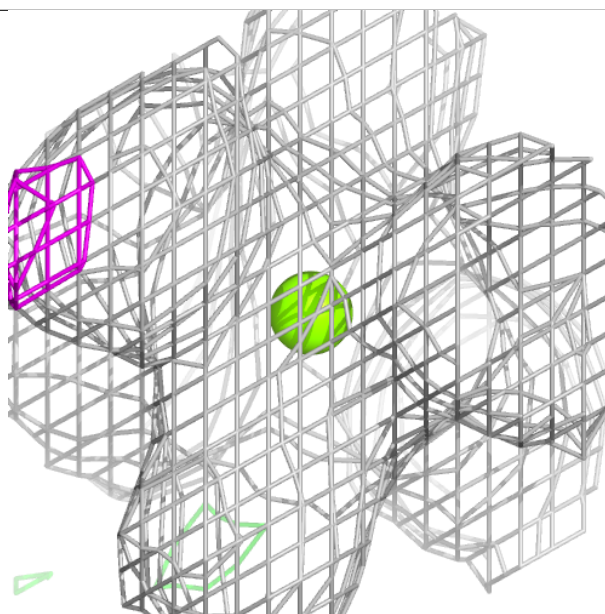
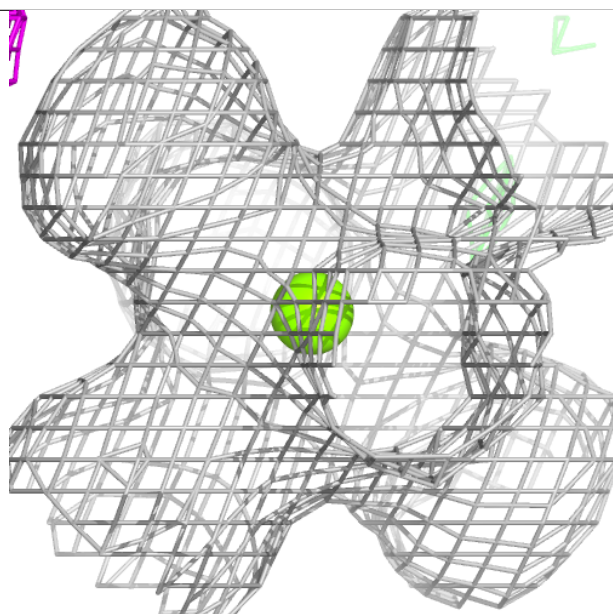
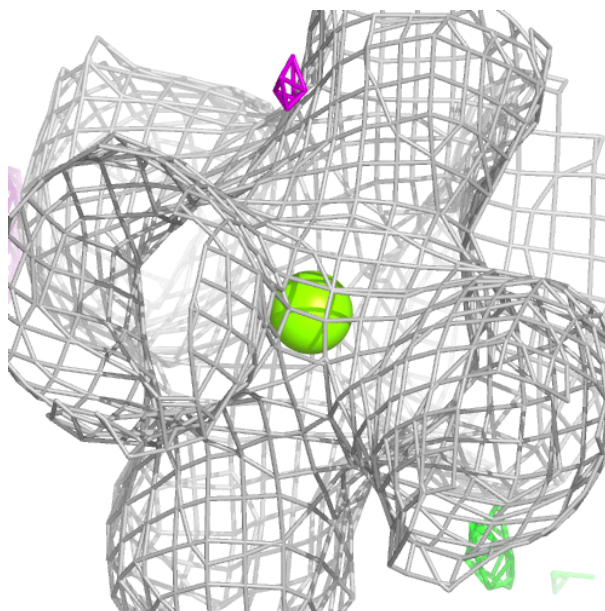
Electron density around MG B 701:

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



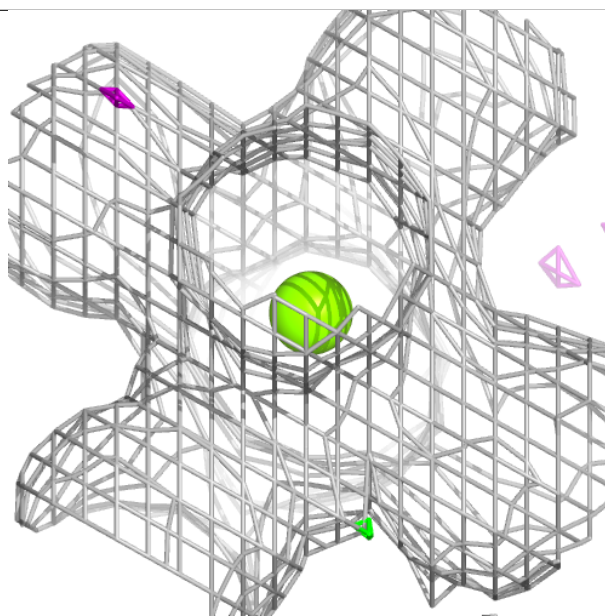
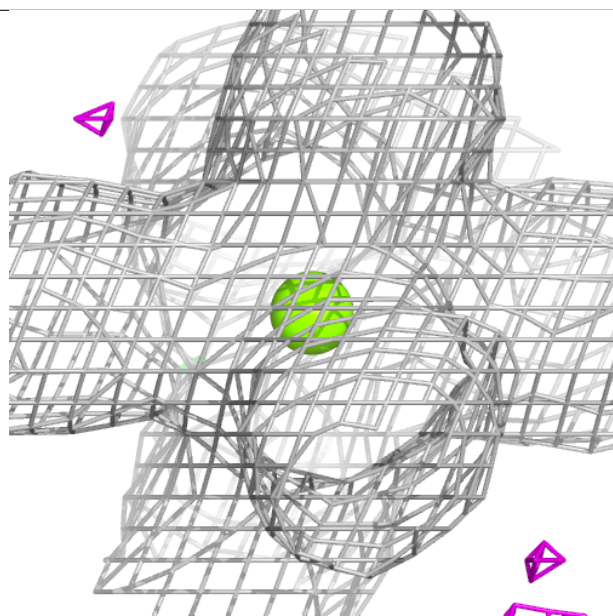
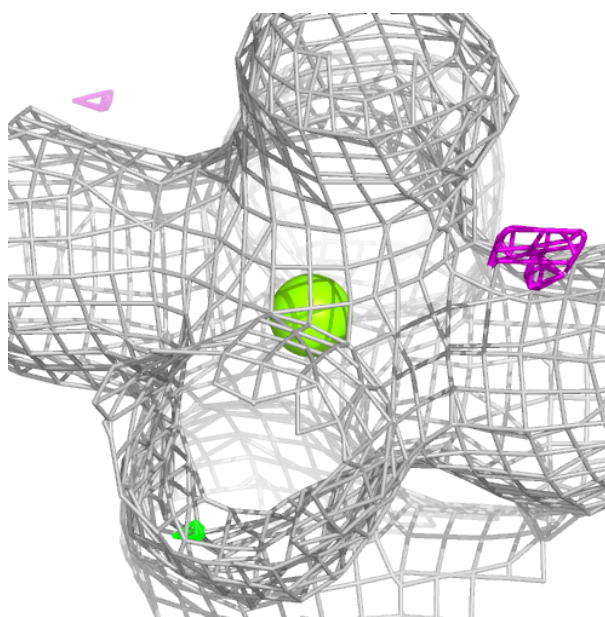
Electron density around MG A 702:

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



Electron density around MG B 702:

$2mF_o-DF_c$ (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.