



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2021 – 08:11 PM JST

PDB ID : 7D8N
Title : Structure of the inactive form of wild-type peptidylarginine deiminase type III (PAD3) crystallized under the condition with high concentrations of Ca²⁺
Authors : Funabashi, K.; Sawata, M.; Unno, M.
Deposited on : 2020-10-08
Resolution : 2.75 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.18
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)	:	2.18

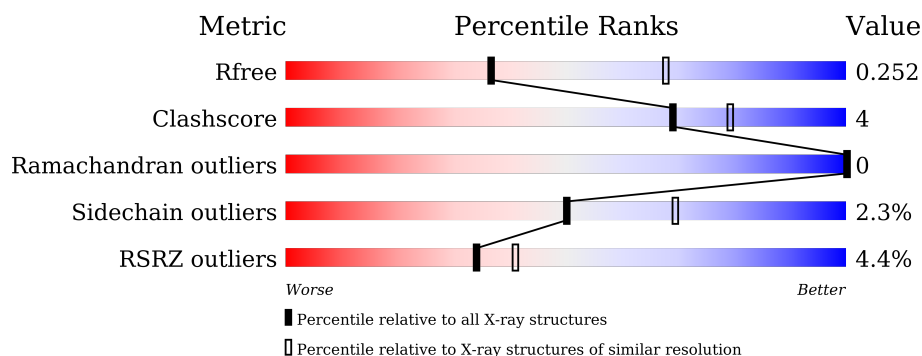
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	664	<div> <div>4%</div> <div> <div></div> <div>84%</div> <div>9%</div> <div>• 6%</div> </div> </div>
1	B	664	<div> <div>4%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>• 5%</div> </div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9874 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.

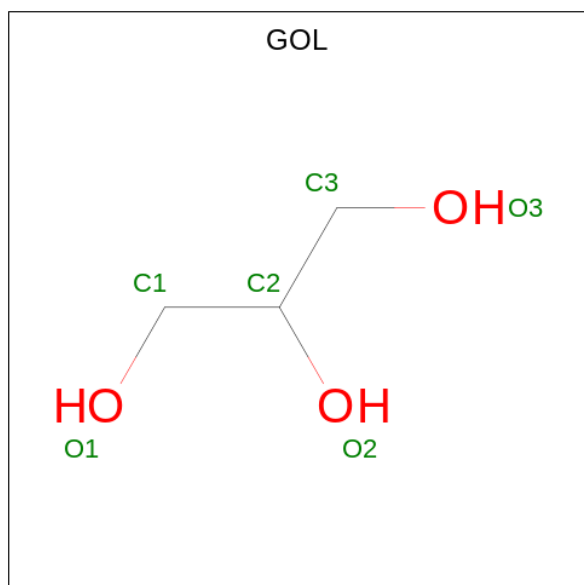
- Molecule 1 is a protein called Protein-arginine deiminase type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	625	Total	C	N	O	S	0	1	0
			4857	3102	821	902	32			
1	B	628	Total	C	N	O	S	0	0	0
			4838	3090	809	906	33			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	Ca	0	0
			5	5		
2	B	5	Total	Ca	0	0
			5	5		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

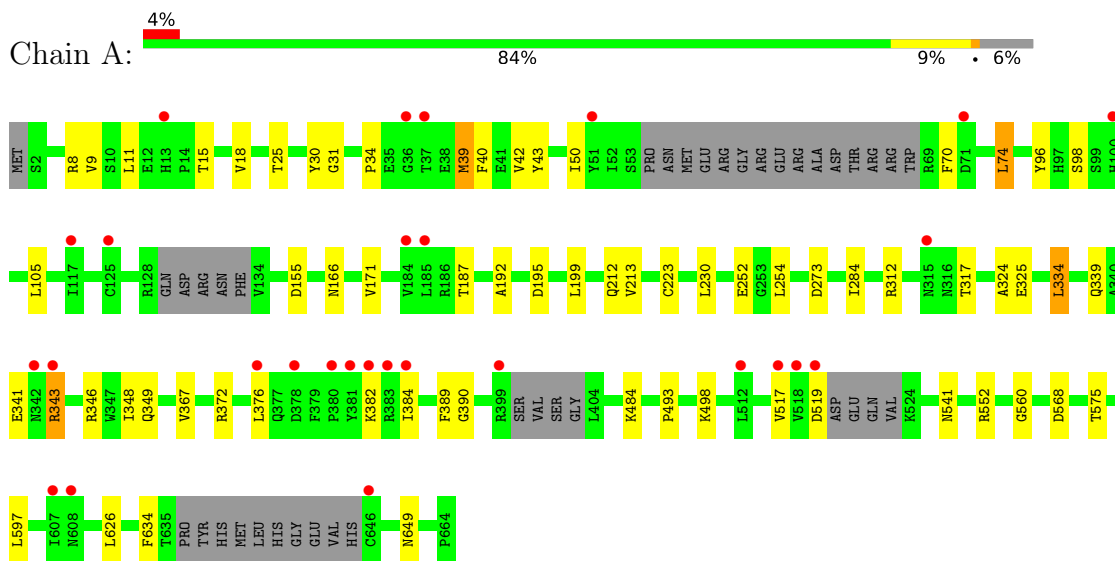
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	56	Total O 56 56	0	0
5	B	69	Total O 69 69	0	0

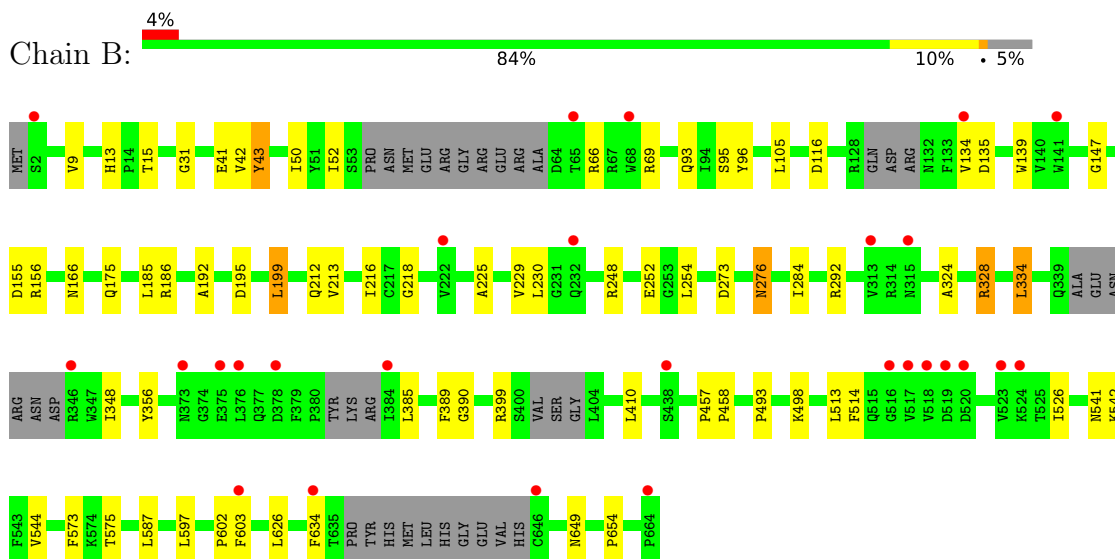
3 Residue-property plots [i](#)

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: Protein-arginine deiminase type-3



- Molecule 1: Protein-arginine deiminase type-3



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	178.87Å 108.11Å 93.56Å 90.00° 118.51° 90.00°	Depositor
Resolution (Å)	46.72 – 2.75 46.72 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.72-2.75) 99.4 (46.72-2.75)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.205 , 0.252 0.205 , 0.252	Depositor DCC
R_{free} test set	2079 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	61.5	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.177 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9874	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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: GOL, CA, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.26	0/4979	0.46	1/6775 (0.0%)
1	B	0.26	0/4955	0.45	0/6750
All	All	0.26	0/9934	0.46	1/13525 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	74	LEU	CA-CB-CG	5.29	127.47	115.30

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	4857	0	4702	34	0
1	B	4838	0	4651	39	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	18	0	24	1	0
3	B	24	0	32	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	56	0	0	1	0
5	B	69	0	0	2	0
All	All	9874	0	9409	70	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 (70) 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:372:ARG:HE	1:A:376:LEU:HD12	1.46	0.81
1:A:8:ARG:HH12	3:A:909:GOL:H12	1.57	0.69
1:A:597:LEU:HD11	1:A:626:LEU:HD13	1.78	0.66
1:B:155:ASP:HA	1:B:390:GLY:HA2	1.81	0.62
1:A:273:ASP:HB2	1:A:284:ILE:HD11	1.82	0.61
1:B:212:GLN:HG3	1:B:254:LEU:HD11	1.83	0.60
1:A:9:VAL:HA	1:A:15:THR:HG21	1.83	0.59
1:B:213:VAL:HB	1:B:230:LEU:HB2	1.86	0.58
1:B:273:ASP:HB2	1:B:284:ILE:HD11	1.86	0.58
1:A:552:ARG:NH2	1:A:568:ASP:OD1	2.37	0.57
1:A:213:VAL:HB	1:A:230:LEU:HB2	1.87	0.57
1:B:328:ARG:NH2	5:B:803:HOH:O	2.37	0.57
1:A:517:VAL:HG12	1:A:519:ASP:H	1.70	0.56
1:B:185:LEU:HD21	1:B:199:LEU:HD21	1.86	0.56
1:B:96:TYR:O	1:B:105:LEU:N	2.38	0.56
1:A:155:ASP:HA	1:A:390:GLY:HA2	1.88	0.55
1:A:42:VAL:HG12	1:A:50:ILE:HD13	1.88	0.55
1:A:348:ILE:HG22	1:A:649:ASN:HB2	1.87	0.55
1:B:348:ILE:HG22	1:B:649:ASN:HB2	1.87	0.55
1:A:312:ARG:HH12	1:A:317:THR:HG23	1.72	0.55
1:B:42:VAL:HG12	1:B:50:ILE:HD13	1.89	0.54
1:B:52:ILE:HG21	1:B:69:ARG:HE	1.72	0.54
1:B:597:LEU:HD11	1:B:626:LEU:HD13	1.89	0.54
1:A:346:ARG:NH2	5:A:1003:HOH:O	2.36	0.53
1:B:192:ALA:O	1:B:195:ASP:HB2	2.10	0.52
1:A:96:TYR:O	1:A:105:LEU:N	2.43	0.52
1:B:276:ASN:OD1	1:B:276:ASN:N	2.32	0.52
1:B:134:VAL:HG12	1:B:135:ASP:H	1.75	0.51
1:B:218:GLY:H	1:B:225:ALA:HB1	1.75	0.51
1:A:212:GLN:HG3	1:A:254:LEU:HD11	1.92	0.51
1:B:41:GLU:HB2	1:B:95:SER:OG	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:GLN:NE2	1:A:252:GLU:OE1	2.44	0.50
1:A:324:ALA:HA	1:A:334:LEU:HD13	1.92	0.50
1:A:498:LYS:NZ	1:B:31:GLY:O	2.45	0.50
1:B:324:ALA:HA	1:B:334:LEU:HD13	1.93	0.49
1:B:292:ARG:NH1	5:B:805:HOH:O	2.38	0.48
1:A:367:VAL:HG11	1:A:384:ILE:HG22	1.95	0.48
1:A:31:GLY:O	1:B:498:LYS:NZ	2.46	0.48
1:A:11:LEU:HD21	1:A:34:PRO:HD3	1.96	0.48
1:B:212:GLN:NE2	1:B:252:GLU:OE2	2.46	0.47
1:A:171:VAL:O	1:A:223:CYS:HB3	2.14	0.47
1:A:39:MET:HG2	1:A:40:PHE:N	2.30	0.47
1:B:493:PRO:HB3	1:B:541:ASN:HB3	1.95	0.47
1:A:484:LYS:NZ	1:A:560:GLY:O	2.48	0.47
1:B:356:TYR:CE2	1:B:654:PRO:HB3	2.51	0.46
1:A:341:GLU:O	1:A:343:ARG:HG3	2.15	0.45
1:A:343:ARG:O	1:A:343:ARG:HD2	2.16	0.45
1:A:346:ARG:HD2	1:A:349:GLN:HB3	1.97	0.45
1:A:493:PRO:HB3	1:A:541:ASN:HB3	1.98	0.45
1:A:98:SER:HB2	1:A:105:LEU:HD11	1.99	0.45
1:A:166:ASN:HB2	1:A:254:LEU:HD23	1.99	0.45
1:B:514:PHE:HA	1:B:603:PHE:HB3	2.00	0.43
1:A:187:THR:HG21	1:A:199:LEU:HD21	2.00	0.43
1:A:339:GLN:HE21	1:A:343:ARG:HB3	1.82	0.43
1:B:156:ARG:NH1	1:B:385:LEU:O	2.51	0.43
1:B:185:LEU:HD21	1:B:199:LEU:CD2	2.49	0.43
1:B:457:PRO:HA	1:B:458:PRO:HD3	1.90	0.43
1:B:13:HIS:CE1	1:B:15:THR:HG22	2.54	0.43
1:B:9:VAL:HA	1:B:15:THR:HG21	1.99	0.42
1:B:587:LEU:HD21	1:B:602:PRO:HG3	2.01	0.42
1:B:43:TYR:HD2	1:B:93:GLN:HB3	1.85	0.41
1:B:513:LEU:N	1:B:526:ILE:O	2.40	0.41
1:A:30:TYR:CE2	1:B:542:LYS:HB2	2.55	0.41
1:B:166:ASN:HB2	1:B:254:LEU:HD23	2.03	0.41
1:B:216:ILE:CG2	1:B:248:ARG:HB2	2.51	0.41
1:B:229:VAL:HG12	1:B:230:LEU:HG	2.02	0.41
1:B:116:ASP:OD2	1:B:186:ARG:NH1	2.54	0.40
1:A:192:ALA:O	1:A:195:ASP:HB2	2.21	0.40
1:B:139:TRP:CD1	1:B:147:GLY:HA3	2.56	0.40
1:B:544:VAL:HG11	1:B:573:PHE:CD1	2.56	0.40

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	614/664 (92%)	596 (97%)	18 (3%)	0	100	100
1	B	614/664 (92%)	598 (97%)	16 (3%)	0	100	100
All	All	1228/1328 (92%)	1194 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	535/588 (91%)	522 (98%)	13 (2%)	49	68
1	B	532/588 (90%)	520 (98%)	12 (2%)	50	69
All	All	1067/1176 (91%)	1042 (98%)	25 (2%)	50	69

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	VAL
1	A	25	THR
1	A	39	MET
1	A	43	TYR
1	A	70	PHE
1	A	74	LEU
1	A	325	GLU
1	A	334	LEU

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Mol	Chain	Res	Type
1	A	343	ARG
1	A	382	LYS
1	A	389	PHE
1	A	575	THR
1	A	634	PHE
1	B	43	TYR
1	B	66	ARG
1	B	175	GLN
1	B	199	LEU
1	B	276	ASN
1	B	328	ARG
1	B	334	LEU
1	B	389	PHE
1	B	399	ARG
1	B	410	LEU
1	B	575	THR
1	B	634	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	169	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 12 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	702	-	5,5,5	0.88	0	5,5,5	1.00	0
3	GOL	B	708	-	5,5,5	0.91	0	5,5,5	1.01	0
3	GOL	B	701	-	5,5,5	0.91	0	5,5,5	0.96	0
3	GOL	A	907	-	5,5,5	0.92	0	5,5,5	0.98	0
3	GOL	B	709	-	5,5,5	0.91	0	5,5,5	0.99	0
3	GOL	A	906	-	5,5,5	0.91	0	5,5,5	0.99	0
3	GOL	A	909	-	5,5,5	0.94	0	5,5,5	1.02	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	702	-	-	0/4/4/4	-
3	GOL	B	708	-	-	4/4/4/4	-
3	GOL	B	701	-	-	0/4/4/4	-
3	GOL	A	907	-	-	0/4/4/4	-
3	GOL	B	709	-	-	2/4/4/4	-
3	GOL	A	906	-	-	2/4/4/4	-
3	GOL	A	909	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	906	GOL	C1-C2-C3-O3
3	B	708	GOL	O1-C1-C2-C3
3	B	709	GOL	O1-C1-C2-O2
3	A	909	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
3	B	708	GOL	C1-C2-C3-O3
3	B	709	GOL	O1-C1-C2-C3
3	B	708	GOL	O2-C2-C3-O3
3	A	906	GOL	O2-C2-C3-O3
3	B	708	GOL	O1-C1-C2-O2
3	A	909	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	A	909	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 ⓘ

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	625/664 (94%)	0.28	28 (4%) 33 39	34, 57, 102, 166	0
1	B	628/664 (94%)	0.28	27 (4%) 35 42	35, 57, 108, 156	0
All	All	1253/1328 (94%)	0.28	55 (4%) 34 41	34, 57, 104, 166	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	37	THR	10.8
1	B	519	ASP	8.3
1	B	518	VAL	6.8
1	A	384	ILE	6.0
1	B	523	VAL	5.9
1	B	520	ASP	5.9
1	A	36	GLY	5.7
1	B	315	ASN	5.0
1	B	346	ARG	4.7
1	A	383	ARG	4.5
1	B	2	SER	4.1
1	B	134	VAL	4.1
1	A	399	ARG	3.6
1	B	222	VAL	3.6
1	A	343	ARG	3.4
1	A	381	TYR	3.3
1	A	608	ASN	3.2
1	B	376	LEU	3.1
1	A	607	ILE	2.9
1	A	100	HIS	2.9
1	A	315	ASN	2.9
1	A	517	VAL	2.9
1	B	646	CYS	2.8
1	B	141	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	438	SER	2.7
1	A	646	CYS	2.7
1	B	664	PRO	2.7
1	A	382	LYS	2.7
1	B	68	TRP	2.5
1	B	516	GLY	2.5
1	B	634	PHE	2.5
1	B	517	VAL	2.4
1	A	125	CYS	2.4
1	A	378	ASP	2.4
1	B	232	GLN	2.4
1	A	380	PRO	2.3
1	B	65	THR	2.3
1	A	342	ASN	2.3
1	B	378	ASP	2.3
1	B	375	GLU	2.2
1	B	603	PHE	2.2
1	A	13	HIS	2.2
1	A	184	VAL	2.2
1	B	384	ILE	2.2
1	B	373	ASN	2.2
1	A	71	ASP	2.2
1	A	376	LEU	2.2
1	A	117	ILE	2.1
1	A	519	ASP	2.1
1	A	185	LEU	2.1
1	A	512	LEU	2.1
1	A	518	VAL	2.1
1	B	313	VAL	2.0
1	A	51	TYR	2.0
1	B	524	LYS	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 ⓘ

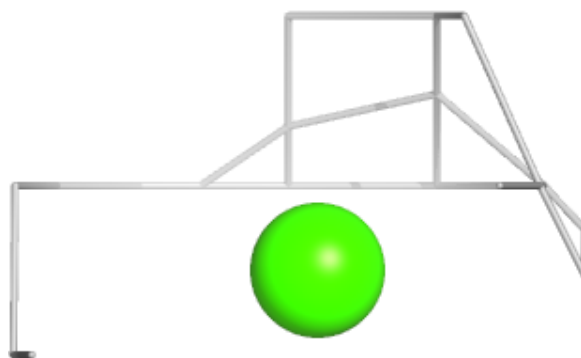
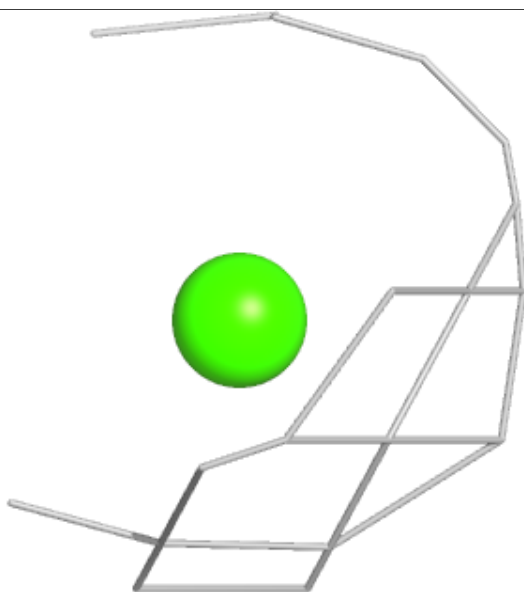
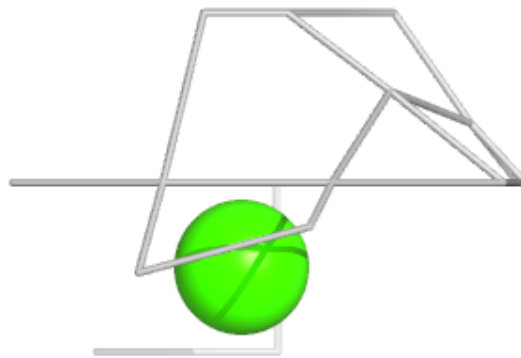
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	A	907	6/6	0.66	0.18	98,104,104,105	0
3	GOL	A	909	6/6	0.68	0.29	88,91,93,93	0
3	GOL	B	701	6/6	0.71	0.18	105,107,109,110	0
3	GOL	B	709	6/6	0.72	0.35	86,90,92,93	0
3	GOL	B	702	6/6	0.78	0.19	94,101,103,105	0
3	GOL	B	708	6/6	0.80	0.21	77,80,84,85	0
4	CL	B	710	1/1	0.83	0.15	78,78,78,78	0
3	GOL	A	906	6/6	0.85	0.21	74,80,83,83	0
2	CA	B	707	1/1	0.89	0.15	99,99,99,99	0
2	CA	B	703	1/1	0.92	0.19	54,54,54,54	0
2	CA	A	905	1/1	0.93	0.19	77,77,77,77	0
4	CL	A	908	1/1	0.94	0.16	74,74,74,74	0
2	CA	A	902	1/1	0.96	0.11	45,45,45,45	0
2	CA	A	901	1/1	0.97	0.13	51,51,51,51	0
2	CA	B	704	1/1	0.98	0.11	49,49,49,49	0
2	CA	B	705	1/1	0.98	0.18	74,74,74,74	0
2	CA	A	904	1/1	0.99	0.17	41,41,41,41	0
2	CA	B	706	1/1	0.99	0.17	41,41,41,41	0
2	CA	A	903	1/1	0.99	0.18	70,70,70,70	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.

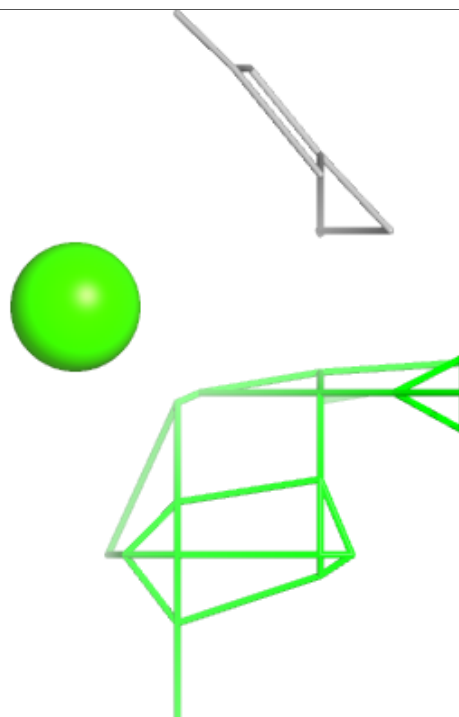
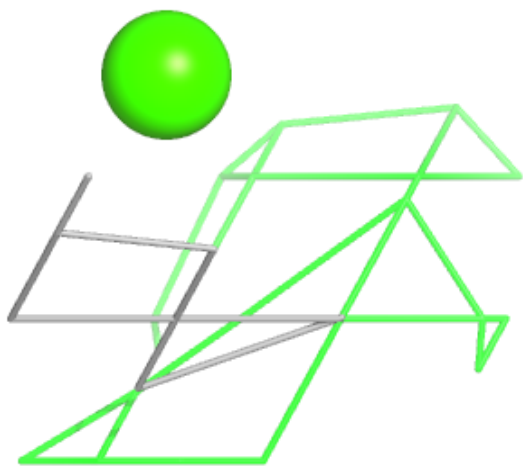
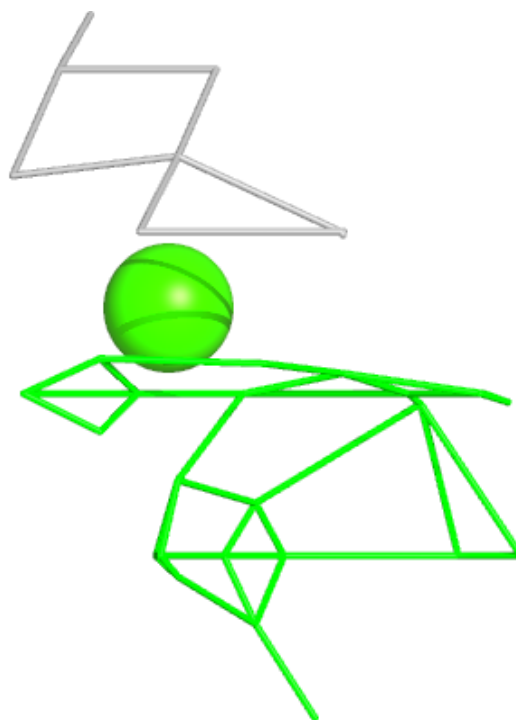
Electron density around CA B 707:

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



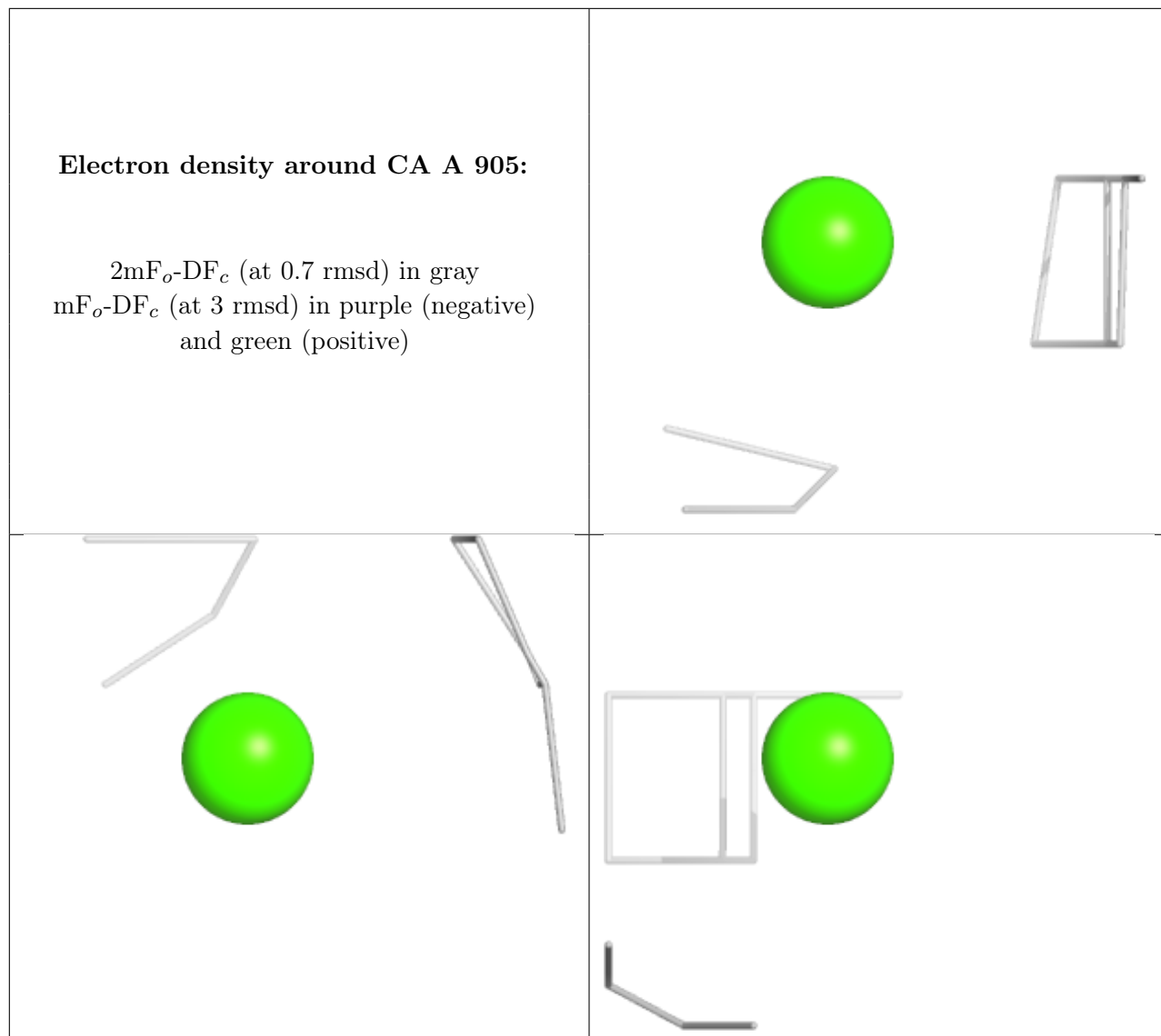
Electron density around CA B 703:

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



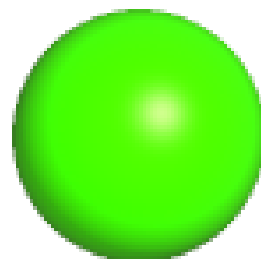
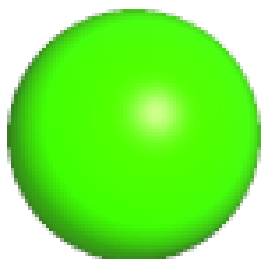
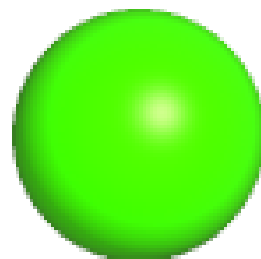
Electron density around CA A 905:

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



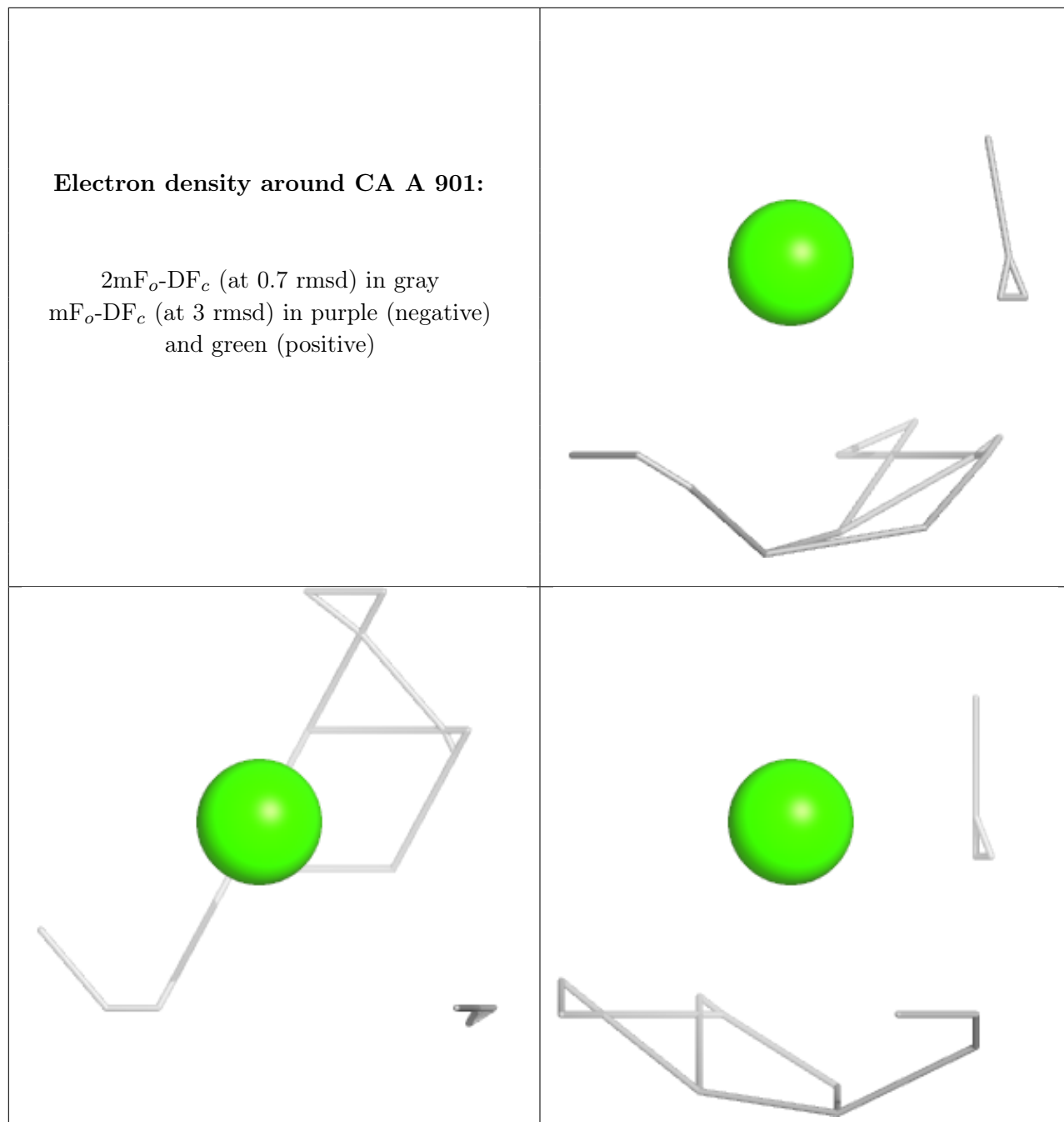
Electron density around CA A 902:

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



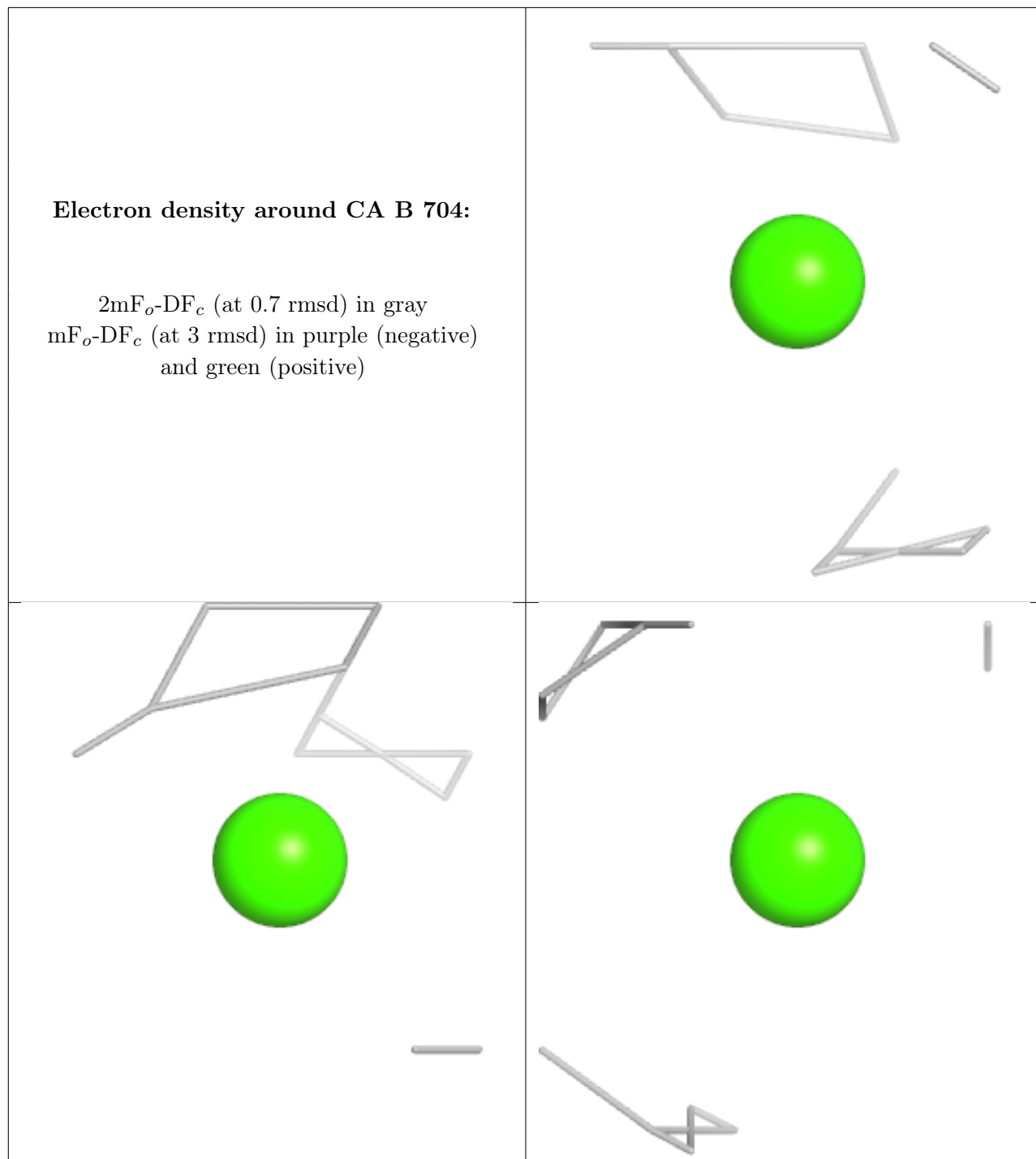
Electron density around CA A 901:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



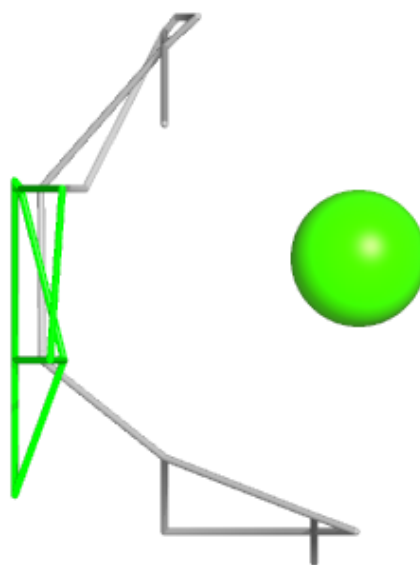
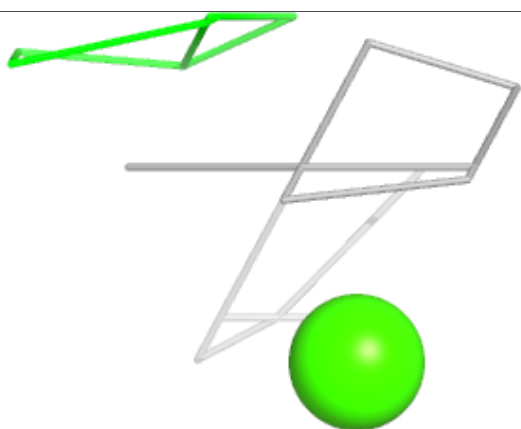
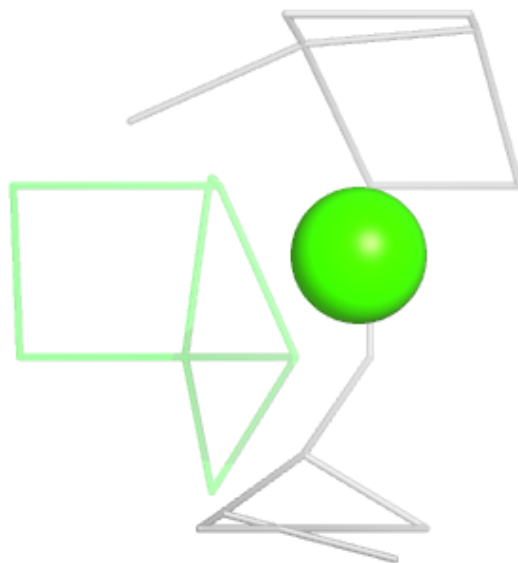
Electron density around CA B 704:

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



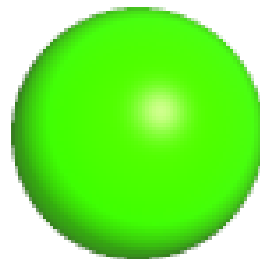
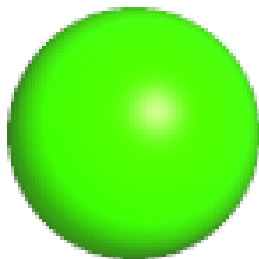
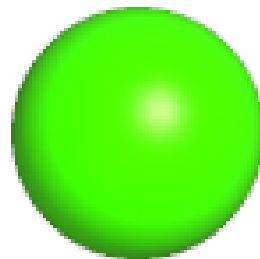
Electron density around CA B 705:

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



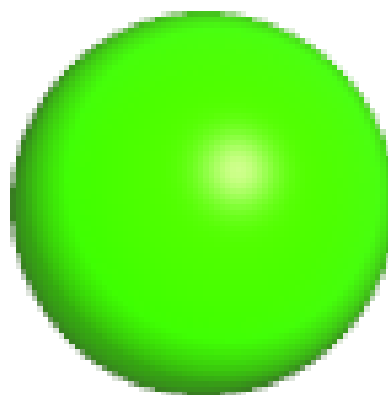
Electron density around CA A 904:

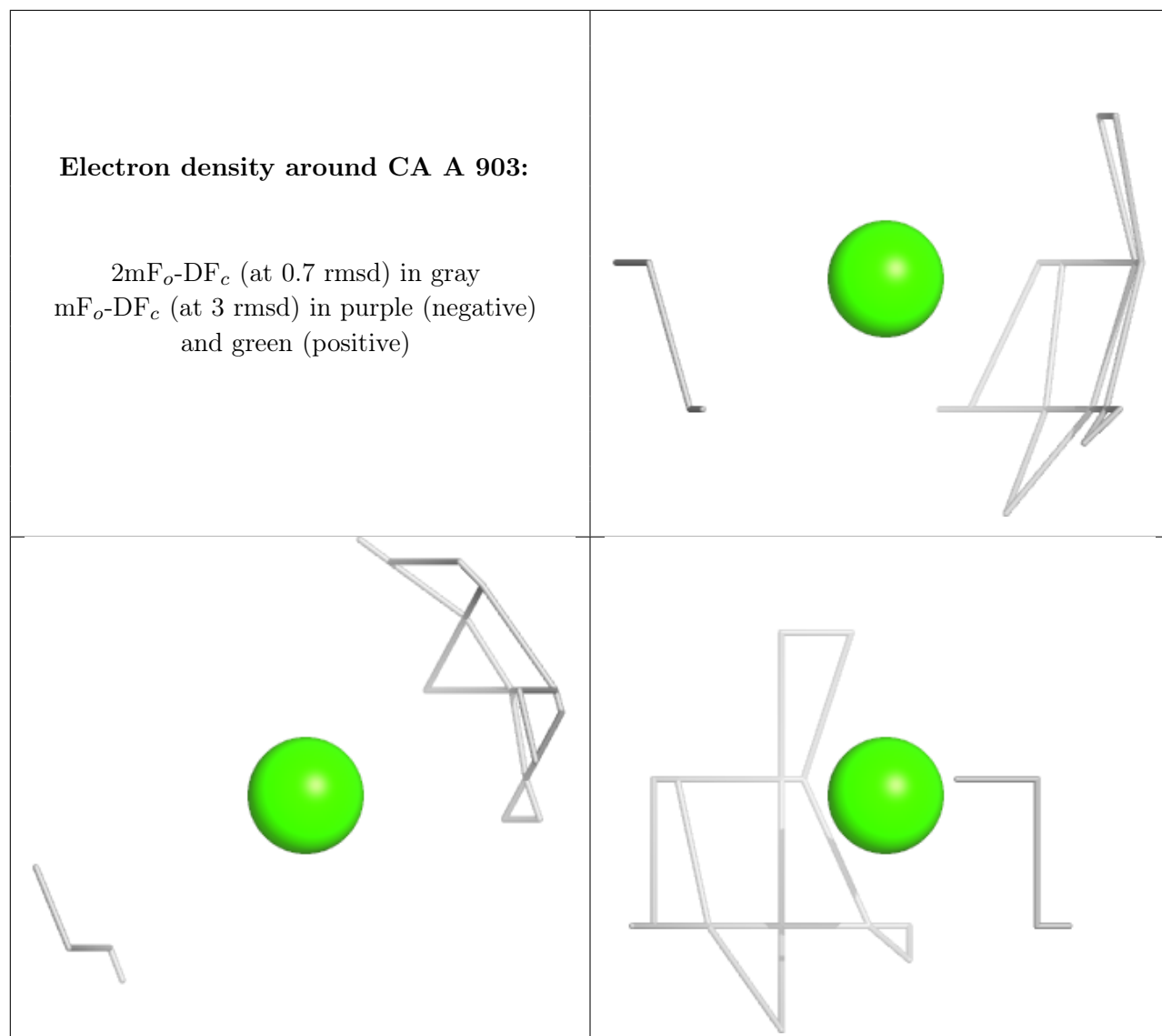
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CA B 706:

$2mF_o-DF_c$ (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.