



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:07 PM UTC

PDB ID : 7PJD / pdb_00007pjd
Title : The X-ray structure of juvenile hormone diol kinase from the silk worm *Bombyx mori*.
Authors : Guo, J.; Cooper, J.; Keegan, R.M.
Deposited on : 2021-08-23
Resolution : 1.99 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:

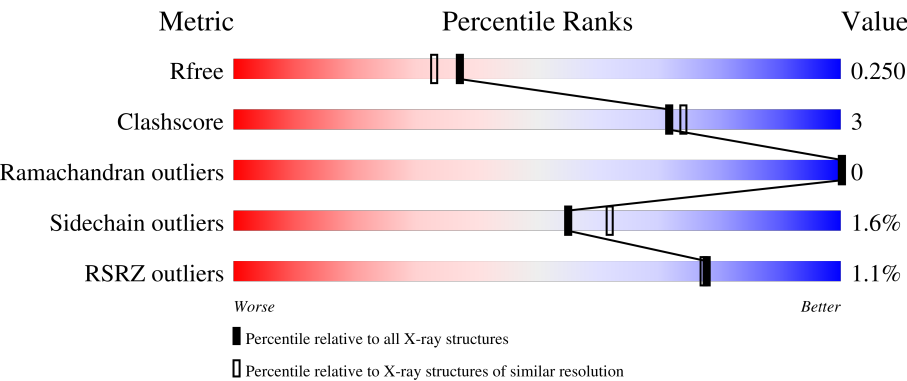
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	184	92%7%..
1	B	184	% 90%9%.
1	C	184	2% 82%13%..
1	D	184	2% 88%10%..
1	E	184	% 86%12%..

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Mol	Chain	Length	Quality of chain
1	F	184	2% 88% 10% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9287 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 Juvenile hormone diol kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	183	Total	C	N	O	S	0	2	0
			1479	942	239	294	4			
1	B	184	Total	C	N	O	S	0	0	0
			1472	939	239	290	4			
1	C	178	Total	C	N	O	S	0	2	0
			1438	915	234	285	4			
1	D	183	Total	C	N	O	S	0	4	0
			1493	953	241	295	4			
1	E	182	Total	C	N	O	S	0	4	0
			1482	946	241	292	3			
1	F	182	Total	C	N	O	S	0	0	0
			1458	932	237	286	3			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP Q6URH4
B	0	HIS	-	expression tag	UNP Q6URH4
C	0	HIS	-	expression tag	UNP Q6URH4
D	0	HIS	-	expression tag	UNP Q6URH4
E	0	HIS	-	expression tag	UNP Q6URH4
F	0	HIS	-	expression tag	UNP Q6URH4

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Ca	0	0
			3	3		
2	B	3	Total	Ca	0	0
			3	3		
2	C	3	Total	Ca	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	3	Total 3	Ca 3	0	0
2	E	3	Total 3	Ca 3	0	0
2	F	3	Total 3	Ca 3	0	0

- Molecule 3 is water.

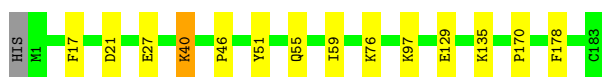
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	86	Total 86	O 86	0	0
3	B	87	Total 87	O 87	0	0
3	C	74	Total 74	O 74	0	0
3	D	58	Total 58	O 58	0	0
3	E	68	Total 68	O 68	0	0
3	F	74	Total 74	O 74	0	0

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.

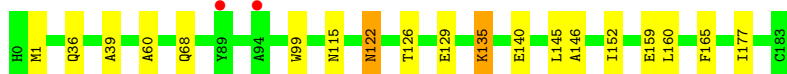
- Molecule 1: Juvenile hormone diol kinase

Chain A:  92% 7% ..



- Molecule 1: Juvenile hormone diol kinase

Chain B:  90% 9% .



- Molecule 1: Juvenile hormone diol kinase

Chain C:  82% 13% . .



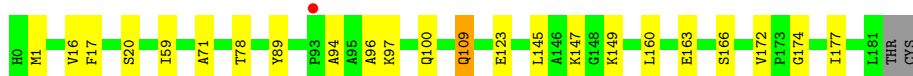
- Molecule 1: Juvenile hormone diol kinase

Chain D:  88% 10% ..

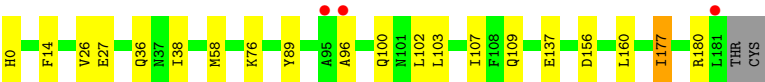
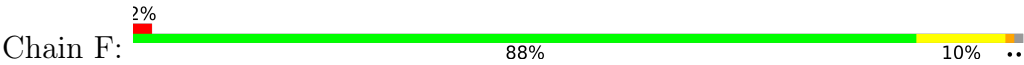


- Molecule 1: Juvenile hormone diol kinase

Chain E:  86% 12% ..



- Molecule 1: Juvenile hormone diol kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.64Å 79.43Å 100.93Å 90.00° 91.60° 90.00°	Depositor
Resolution (Å)	50.50 – 1.99 50.50 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.50-1.99) 99.9 (50.50-1.99)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.190 , 0.248 0.194 , 0.250	Depositor DCC
R_{free} test set	3471 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9287	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% 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: CA

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	1.16	1/1514 (0.1%)	1.43	3/2047 (0.1%)
1	B	1.16	1/1508 (0.1%)	1.52	6/2039 (0.3%)
1	C	1.20	5/1470 (0.3%)	1.46	5/1985 (0.3%)
1	D	1.20	2/1528 (0.1%)	1.52	2/2067 (0.1%)
1	E	1.15	0/1524	1.51	7/2061 (0.3%)
1	F	1.18	1/1494 (0.1%)	1.46	1/2021 (0.0%)
All	All	1.17	10/9038 (0.1%)	1.48	24/12220 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	170	PRO	C-O	-5.59	1.16	1.24
1	C	147	LYS	C-O	5.54	1.30	1.23
1	D	46	PRO	C-O	-5.43	1.17	1.23
1	C	76	LYS	C-O	5.36	1.30	1.23
1	C	167	SER	C-O	5.32	1.30	1.24
1	B	39	ALA	C-O	5.29	1.30	1.24
1	C	159	GLU	CD-OE1	5.21	1.35	1.25
1	C	155	ALA	CA-C	5.11	1.59	1.52
1	F	0	HIS	CE1-NE2	5.09	1.37	1.32
1	D	103	LEU	C-O	5.01	1.29	1.24

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	156	ASP	N-CA-C	-7.56	102.71	112.23
1	B	122	ASN	CA-CB-CG	-6.68	105.92	112.60
1	E	17	PHE	CA-CB-CG	-6.64	107.16	113.80
1	B	165	PHE	CA-CB-CG	-6.05	107.75	113.80
1	E	59	ILE	N-CA-C	-5.78	104.88	110.72
1	A	21	ASP	N-CA-C	-5.72	105.97	113.17
1	E	78	THR	CA-CB-OG1	-5.67	101.09	109.60
1	D	32	GLU	CA-C-O	-5.60	114.61	120.55
1	B	115	ASN	CB-CA-C	-5.41	103.17	111.66
1	E	20	SER	CA-C-O	-5.37	114.83	120.63
1	C	150	ASP	CA-CB-CG	5.31	117.91	112.60
1	C	1	MET	CA-C-N	5.30	130.37	123.06
1	C	1	MET	C-N-CA	5.30	130.37	123.06
1	F	36	GLN	CB-CG-CD	-5.19	103.77	112.60
1	C	155	ALA	N-CA-C	-5.18	104.90	111.11
1	D	134	ASN	CB-CA-C	5.17	118.49	109.65
1	A	40	LYS	CA-C-O	-5.09	115.47	120.82
1	B	159	GLU	CA-C-O	-5.09	115.02	120.42
1	B	60	ALA	CA-C-O	-5.09	115.16	120.55
1	E	71	ALA	CA-C-O	-5.03	114.42	120.10
1	B	36	GLN	CB-CA-C	5.01	119.10	110.79
1	A	97	LYS	CA-C-O	-5.01	115.56	120.82
1	E	123	GLU	CA-C-N	5.00	126.94	120.44
1	E	123	GLU	C-N-CA	5.00	126.94	120.44

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	145	LEU	Peptide

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	1479	0	1405	5	0
1	B	1472	0	1402	9	0
1	C	1438	0	1368	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1493	0	1426	10	0
1	E	1482	0	1415	15	0
1	F	1458	0	1392	10	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	3	0	0	0	0
2	F	3	0	0	0	0
3	A	86	0	0	0	0
3	B	87	0	0	1	0
3	C	74	0	0	1	0
3	D	58	0	0	1	0
3	E	68	0	0	5	0
3	F	74	0	0	3	0
All	All	9287	0	8408	57	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 3.

All (57) 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:109[A]:GLN:NE2	3:E:301:HOH:O	2.06	0.88
1:E:1:MET:HA	1:E:1:MET:HE2	1.61	0.81
1:D:32:GLU:HG3	1:D:59[B]:ILE:HD11	1.68	0.75
1:B:145:LEU:HD11	1:B:177:ILE:HA	1.67	0.74
1:B:1:MET:HA	1:B:1:MET:HE2	1.70	0.73
1:E:100[A]:GLN:NE2	3:E:303:HOH:O	2.22	0.72
1:B:146:ALA:HB2	1:B:152:ILE:HD11	1.71	0.72
1:E:100[B]:GLN:NE2	1:E:100[B]:GLN:HA	2.13	0.63
1:F:76:LYS:NZ	3:F:303:HOH:O	2.32	0.62
1:B:122:ASN:O	1:B:126:THR:HG23	2.02	0.59
1:B:140:GLU:HG3	3:B:339:HOH:O	2.02	0.59
1:E:145:LEU:HD22	1:E:160:LEU:HD13	1.84	0.58
1:E:160:LEU:HB3	1:E:177:ILE:HD12	1.85	0.58
1:F:109:GLN:OE1	3:F:301:HOH:O	2.17	0.57
1:C:11:LEU:HD21	1:C:83:LEU:HD11	1.86	0.57
1:C:180:ARG:CZ	1:C:182:THR:HB	2.37	0.55
3:C:323:HOH:O	1:D:12:HIS:HD2	1.93	0.51
1:F:156:ASP:OD2	3:F:302:HOH:O	2.19	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:100[B]:GLN:HG3	3:E:303:HOH:O	2.10	0.51
1:C:8:LYS:HD3	1:D:182:THR:HG21	1.92	0.51
1:B:145:LEU:HD22	1:B:160:LEU:HD13	1.92	0.50
1:C:129:GLU:OE2	1:C:135:LYS:HB2	2.11	0.49
1:F:89:TYR:CG	1:F:96:ALA:HB2	2.48	0.49
1:D:26:VAL:HA	1:D:30:ASP:OD2	2.12	0.48
1:D:145:LEU:HD11	1:D:177:ILE:HA	1.95	0.48
1:E:1:MET:HA	1:E:1:MET:CE	2.40	0.48
1:F:14:PHE:CZ	1:F:26:VAL:HG23	2.48	0.48
1:A:46:PRO:HA	1:A:51:TYR:CD2	2.50	0.47
1:D:22:LYS:NZ	3:D:302:HOH:O	2.47	0.47
1:D:124:TYR:CZ	1:D:128:HIS:CE1	3.03	0.46
1:C:99:TRP:CH2	1:C:103:LEU:HD22	2.50	0.46
1:F:137:GLU:OE2	1:F:180:ARG:NH1	2.49	0.46
1:D:1:MET:HG2	1:D:87:ASP:OD1	2.17	0.45
1:E:109[A]:GLN:HE21	1:E:109[A]:GLN:HA	1.82	0.45
1:B:146:ALA:CB	1:B:152:ILE:HD11	2.44	0.45
1:E:163:GLU:HB3	1:E:174:GLY:HA3	1.99	0.44
1:A:27:GLU:HG2	1:A:76:LYS:HG2	1.98	0.44
1:E:149:LYS:HE3	3:E:352:HOH:O	2.18	0.43
1:F:160:LEU:HB3	1:F:177:ILE:HD12	2.01	0.43
1:C:14:PHE:CZ	1:C:26:VAL:HG23	2.52	0.43
1:F:96:ALA:HB1	1:F:100:GLN:OE1	2.19	0.43
1:E:94:ALA:HA	1:E:97:LYS:HE3	2.01	0.43
1:E:16:VAL:O	3:E:302:HOH:O	2.21	0.43
1:A:55:GLN:O	1:A:59:ILE:HG12	2.19	0.42
1:D:35:ALA:HB3	1:D:55:GLN:NE2	2.33	0.42
1:F:38:ILE:HD12	1:F:58:MET:CE	2.49	0.42
1:B:68:GLN:HG3	1:B:99:TRP:CD2	2.55	0.42
1:C:177:ILE:HD12	1:C:178:PHE:CE2	2.54	0.42
1:A:17:PHE:CE1	1:A:178:PHE:HB3	2.55	0.42
1:F:103:LEU:O	1:F:107:ILE:HG12	2.19	0.41
1:E:89:TYR:CG	1:E:96:ALA:HB2	2.56	0.41
1:C:74:ASP:OD2	1:C:76:LYS:CE	2.69	0.41
1:A:129[A]:GLU:OE1	1:A:135:LYS:HD2	2.21	0.41
1:C:124:TYR:CZ	1:C:128:HIS:CE1	3.09	0.41
1:E:163:GLU:HG2	1:E:172:VAL:HG21	2.03	0.41
1:B:129:GLU:OE1	1:B:135:LYS:HB2	2.21	0.40
1:D:14:PHE:CZ	1:D:26:VAL:HG23	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	183/184 (100%)	183 (100%)	0	0	100	100
1	B	182/184 (99%)	181 (100%)	1 (0%)	0	100	100
1	C	176/184 (96%)	175 (99%)	1 (1%)	0	100	100
1	D	185/184 (100%)	184 (100%)	1 (0%)	0	100	100
1	E	184/184 (100%)	182 (99%)	2 (1%)	0	100	100
1	F	180/184 (98%)	179 (99%)	1 (1%)	0	100	100
All	All	1090/1104 (99%)	1084 (99%)	6 (1%)	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	158/157 (101%)	157 (99%)	1 (1%)	78	85
1	B	157/157 (100%)	156 (99%)	1 (1%)	78	85
1	C	154/157 (98%)	150 (97%)	4 (3%)	40	44
1	D	160/157 (102%)	157 (98%)	3 (2%)	50	56
1	E	159/157 (101%)	154 (97%)	5 (3%)	35	37
1	F	155/157 (99%)	152 (98%)	3 (2%)	50	56
All	All	943/942 (100%)	926 (98%)	17 (2%)	55	58

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	LYS
1	B	135	LYS
1	C	97	LYS
1	C	100	GLN
1	C	177	ILE
1	C	182	THR
1	D	143	LYS
1	D	152	ILE
1	D	177	ILE
1	E	109[A]	GLN
1	E	109[B]	GLN
1	E	147	LYS
1	E	166[A]	SER
1	E	166[B]	SER
1	F	27	GLU
1	F	102	LEU
1	F	177	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	68	GLN
1	A	158	GLN
1	B	36	GLN
1	B	68	GLN
1	B	111	GLN
1	B	158	GLN
1	C	128	HIS
1	C	158	GLN
1	D	12	HIS
1	D	55	GLN
1	D	109	GLN
1	D	128	HIS
1	D	158	GLN
1	E	29	GLN
1	E	36	GLN
1	F	66	GLN
1	F	68	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 18 ligands modelled in this entry, 18 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	183/184 (99%)	-0.07	0 100 100	18, 38, 56, 66	2 (1%)
1	B	184/184 (100%)	-0.09	2 (1%) 78 77	28, 38, 63, 85	0
1	C	178/184 (96%)	0.07	3 (1%) 69 68	19, 41, 67, 93	2 (1%)
1	D	183/184 (99%)	0.15	3 (1%) 70 70	18, 43, 69, 87	4 (2%)
1	E	182/184 (98%)	0.06	1 (0%) 87 87	21, 44, 69, 90	4 (2%)
1	F	182/184 (98%)	0.07	3 (1%) 70 70	32, 45, 69, 81	0
All	All	1092/1104 (98%)	0.03	12 (1%) 78 77	18, 42, 67, 93	12 (1%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	94	ALA	3.2
1	D	170	PRO	3.1
1	B	89	TYR	2.9
1	C	96	ALA	2.8
1	E	93	PRO	2.5
1	F	96	ALA	2.4
1	D	172	VAL	2.3
1	C	1	MET	2.2
1	F	181	LEU	2.2
1	D	149	LYS	2.2
1	B	94	ALA	2.1
1	F	95	ALA	2.1

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

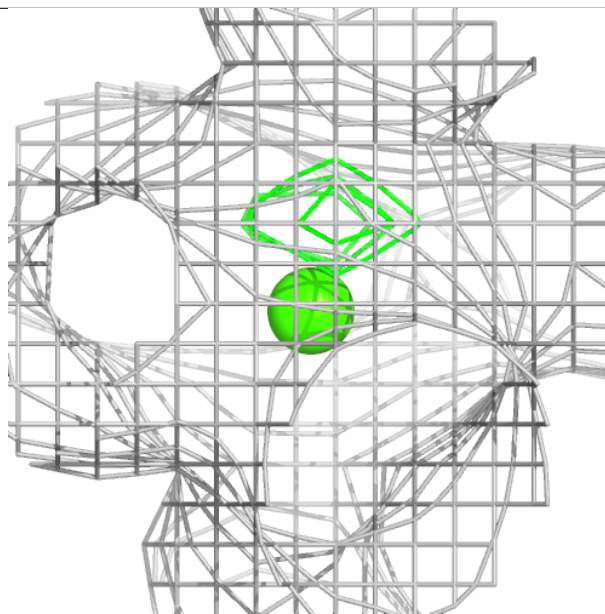
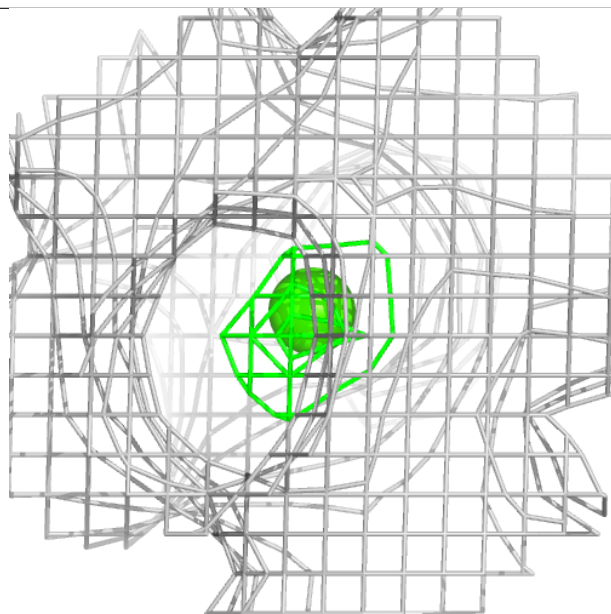
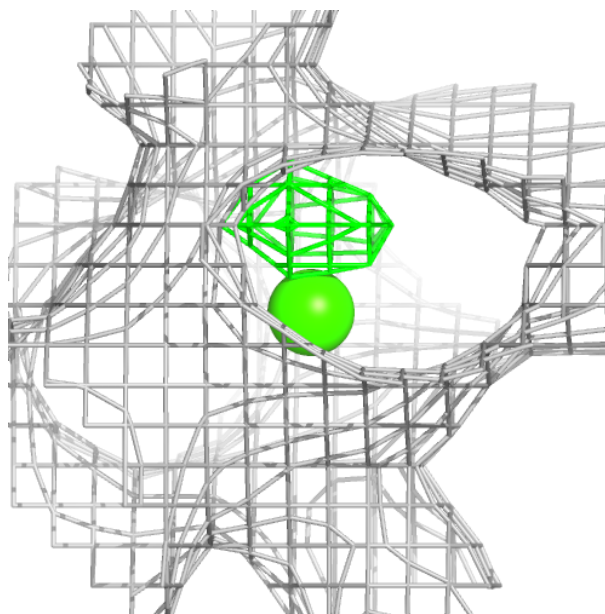
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	E	203	1/1	0.95	0.07	60,60,60,60	0
2	CA	F	202	1/1	0.95	0.06	44,44,44,44	0
2	CA	E	202	1/1	0.98	0.03	38,38,38,38	0
2	CA	B	203	1/1	0.99	0.04	31,31,31,31	0
2	CA	C	202	1/1	0.99	0.04	38,38,38,38	0
2	CA	C	203	1/1	0.99	0.03	39,39,39,39	0
2	CA	D	201	1/1	0.99	0.03	35,35,35,35	0
2	CA	D	202	1/1	0.99	0.03	36,36,36,36	0
2	CA	D	203	1/1	0.99	0.03	49,49,49,49	0
2	CA	A	203	1/1	0.99	0.04	34,34,34,34	0
2	CA	B	201	1/1	0.99	0.02	36,36,36,36	0
2	CA	F	201	1/1	0.99	0.05	41,41,41,41	0
2	CA	B	202	1/1	0.99	0.03	39,39,39,39	0
2	CA	F	203	1/1	0.99	0.03	48,48,48,48	0
2	CA	A	201	1/1	1.00	0.01	33,33,33,33	0
2	CA	A	202	1/1	1.00	0.02	34,34,34,34	0
2	CA	E	201	1/1	1.00	0.01	32,32,32,32	0
2	CA	C	201	1/1	1.00	0.02	32,32,32,32	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.

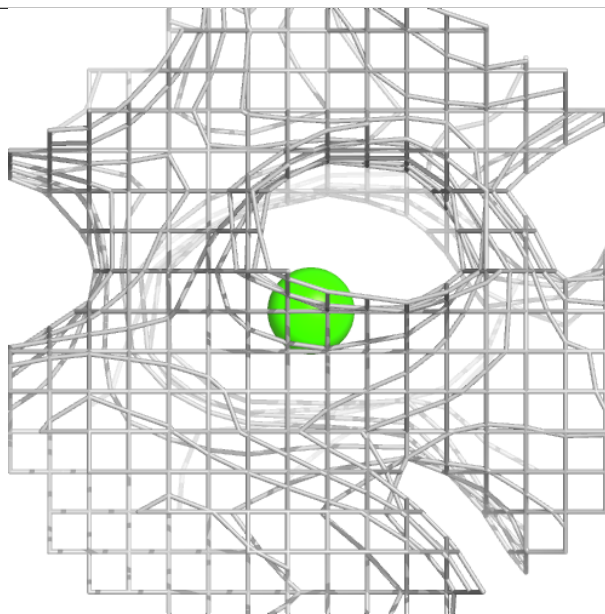
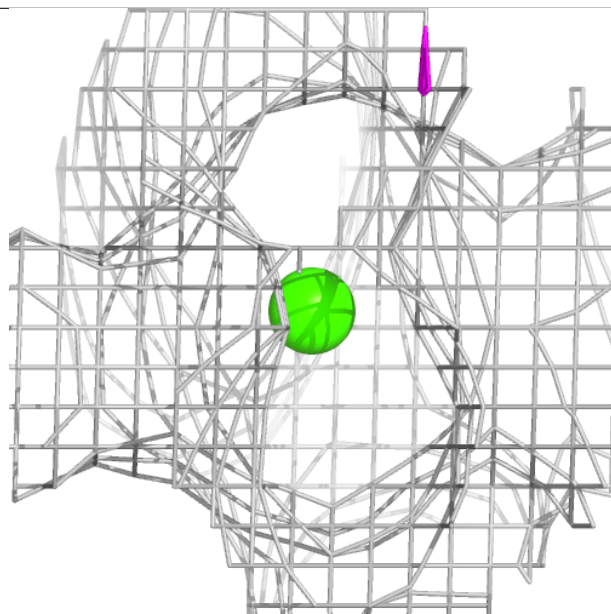
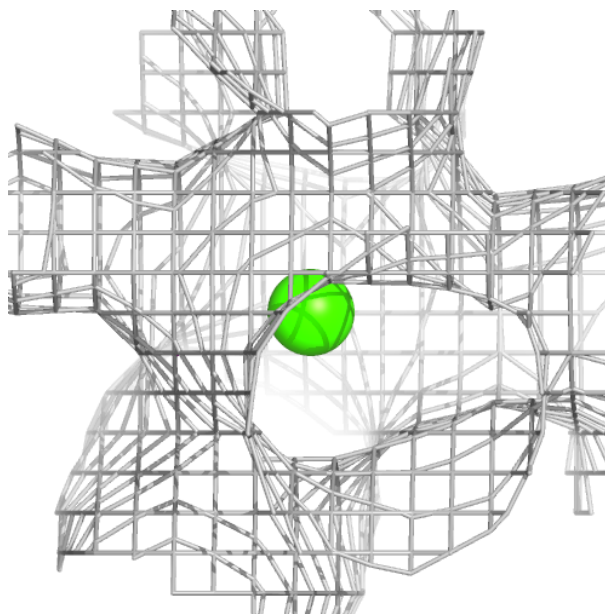
Electron density around CA E 203:

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



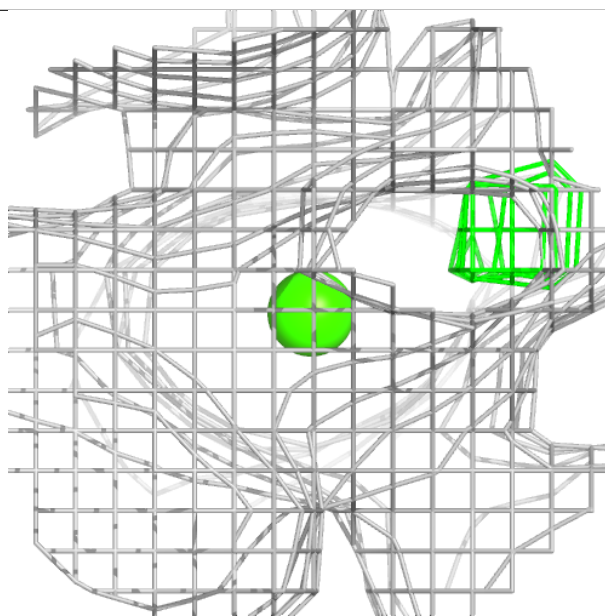
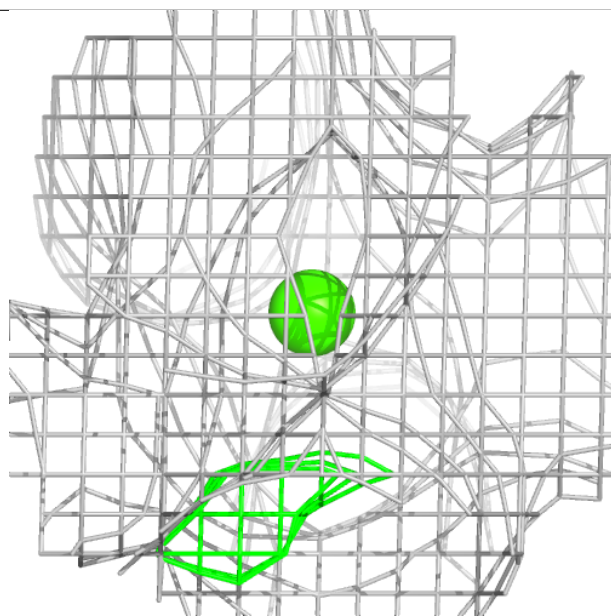
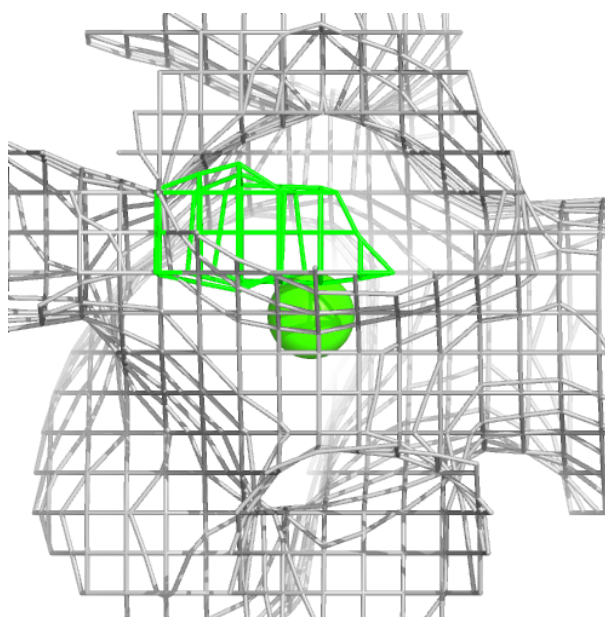
Electron density around CA F 202:

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and green (positive)



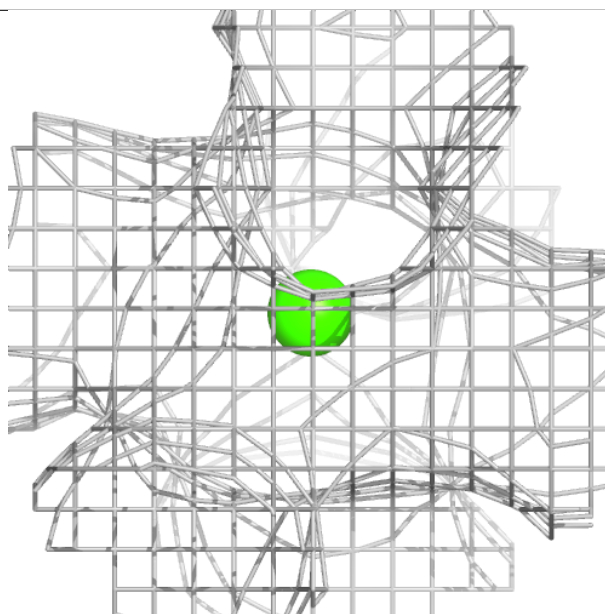
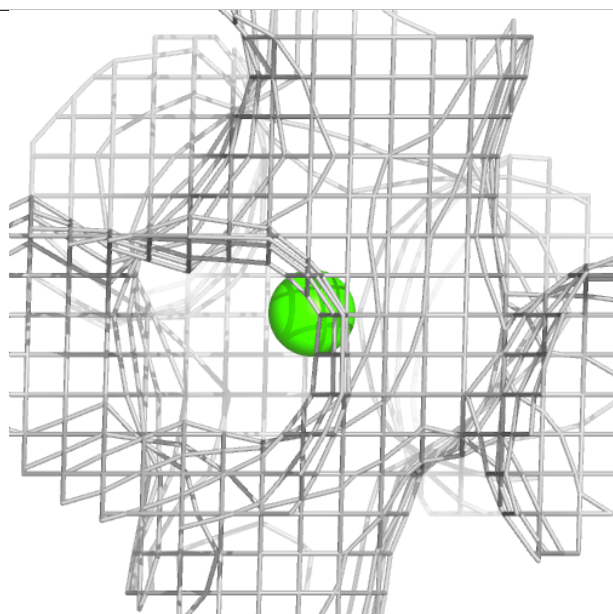
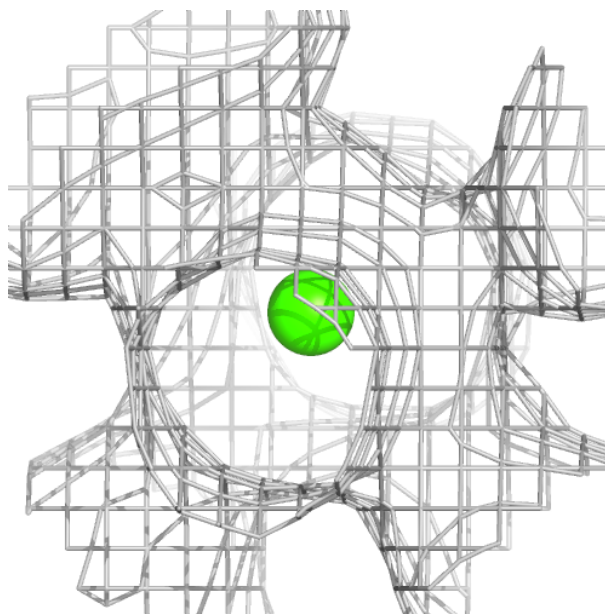
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and green (positive)



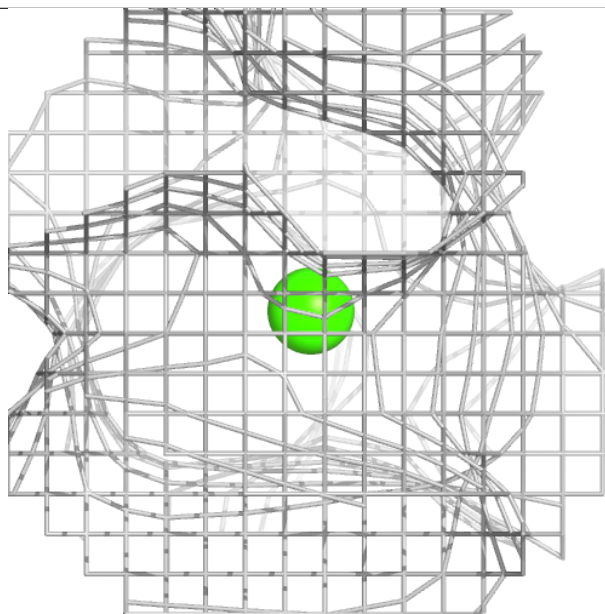
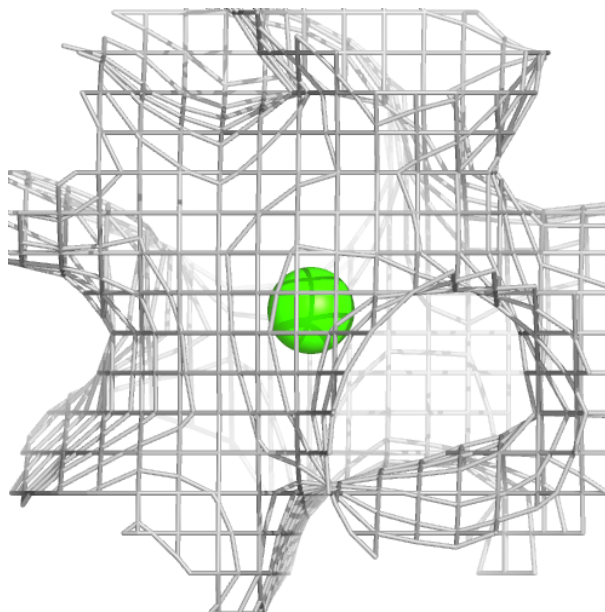
Electron density around CA B 203:

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and green (positive)



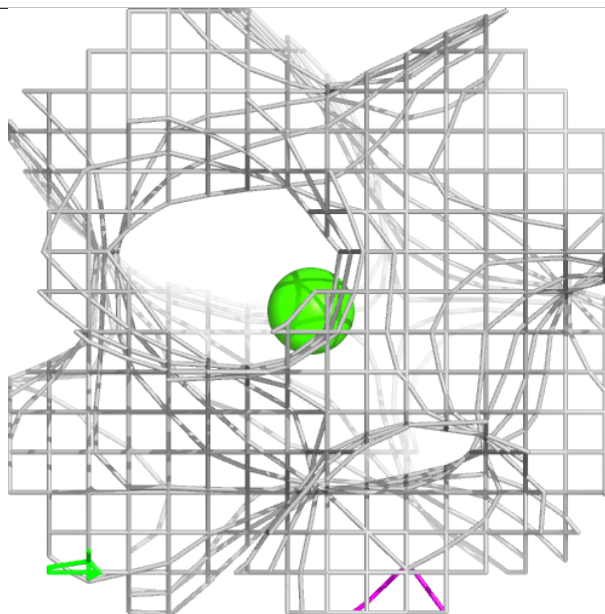
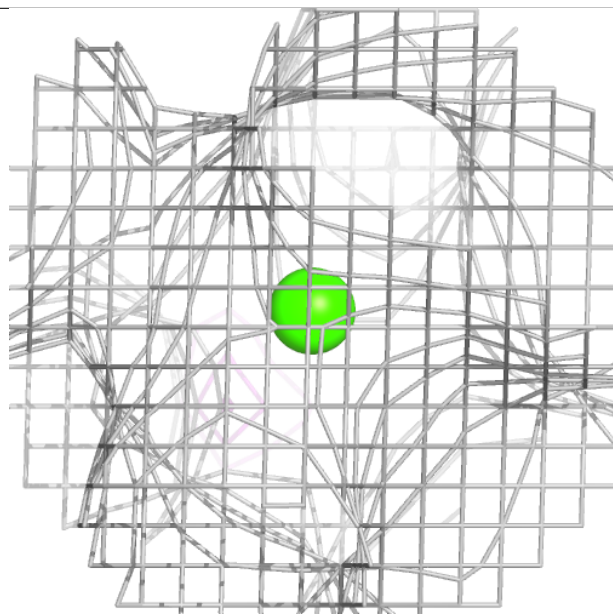
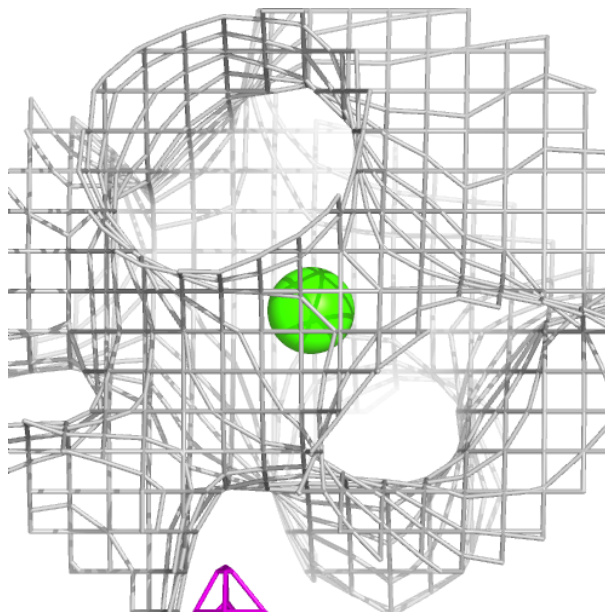
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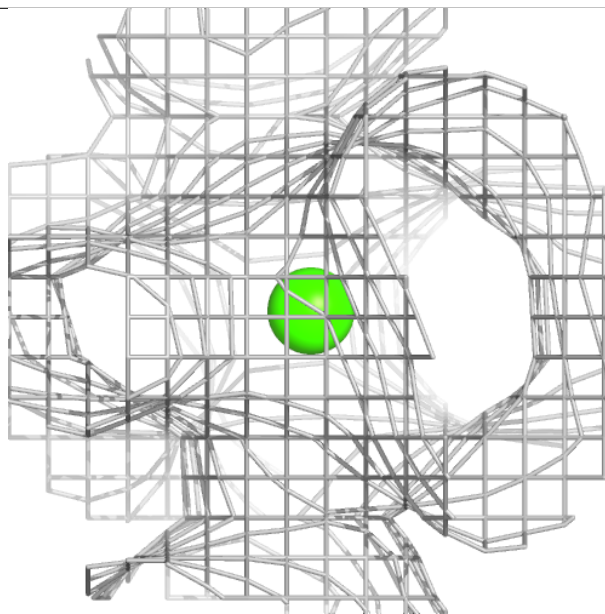
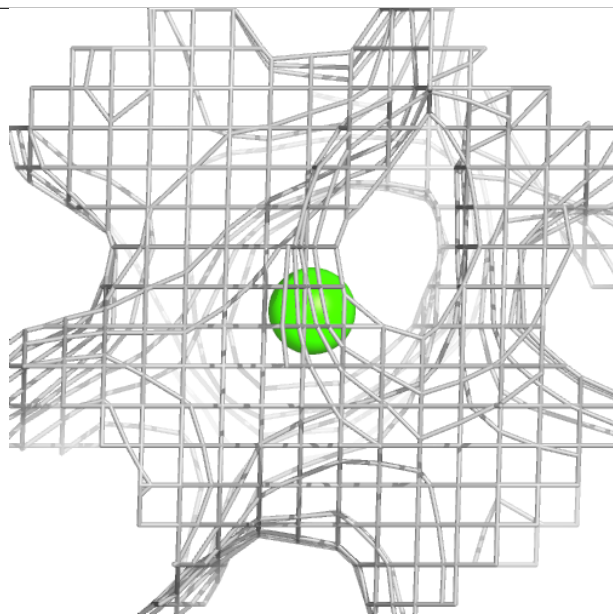
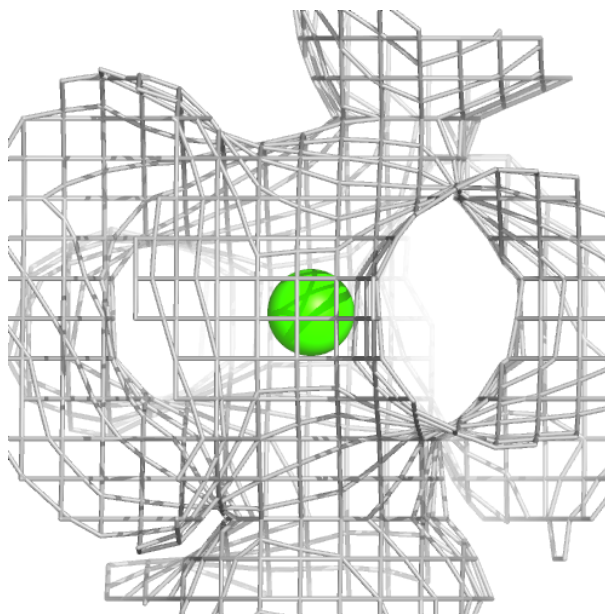
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and green (positive)



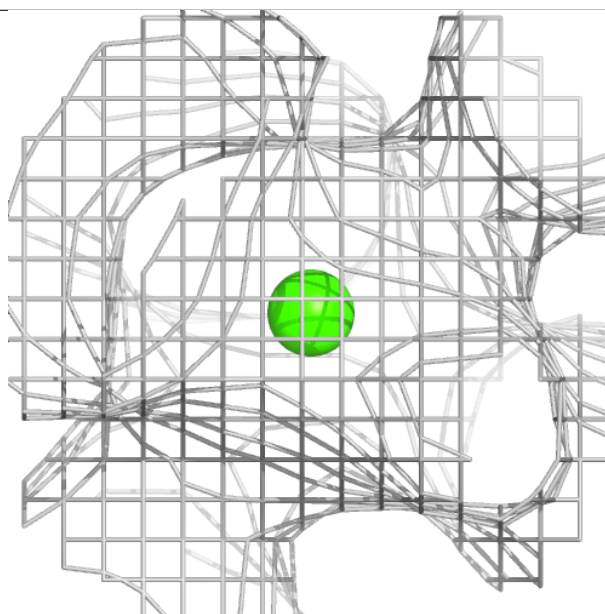
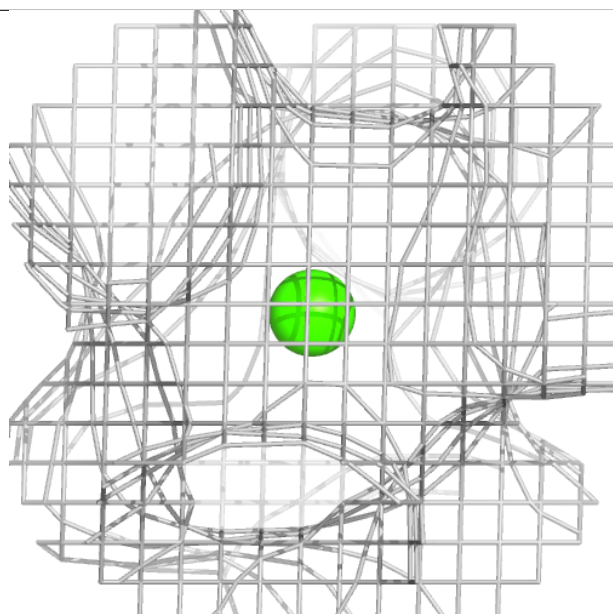
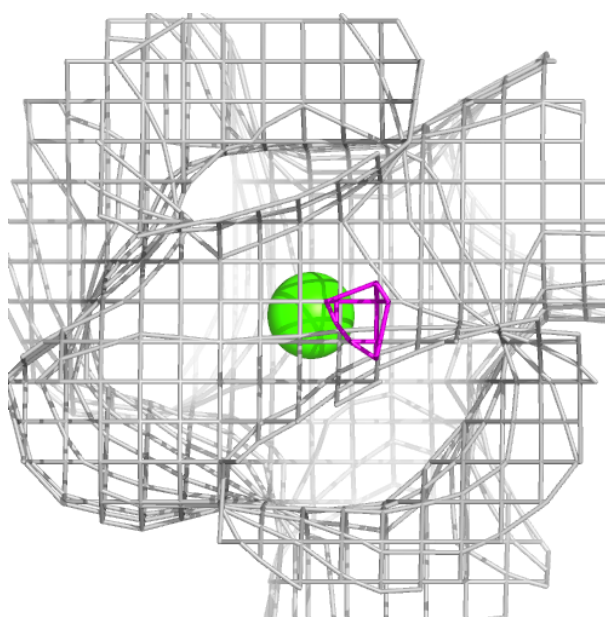
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and green (positive)



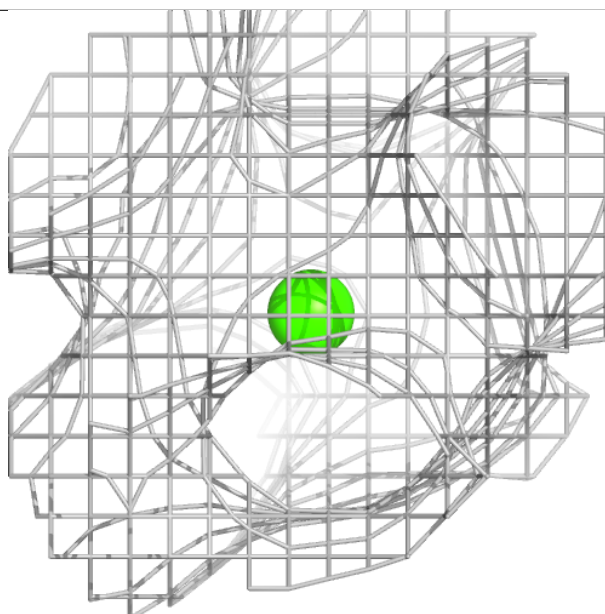
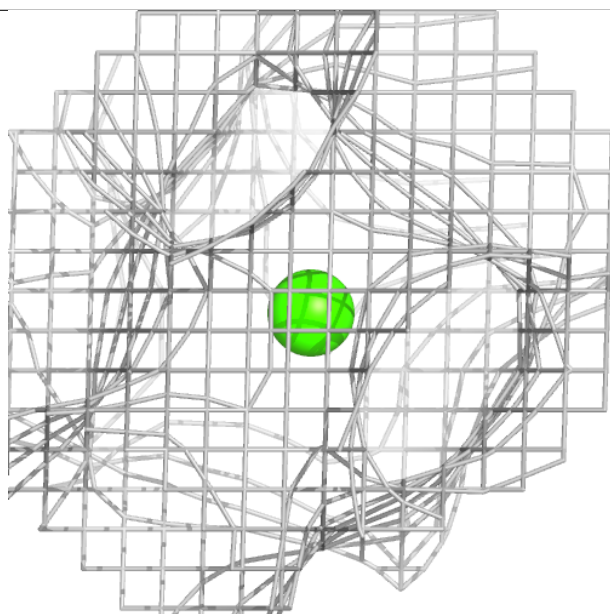
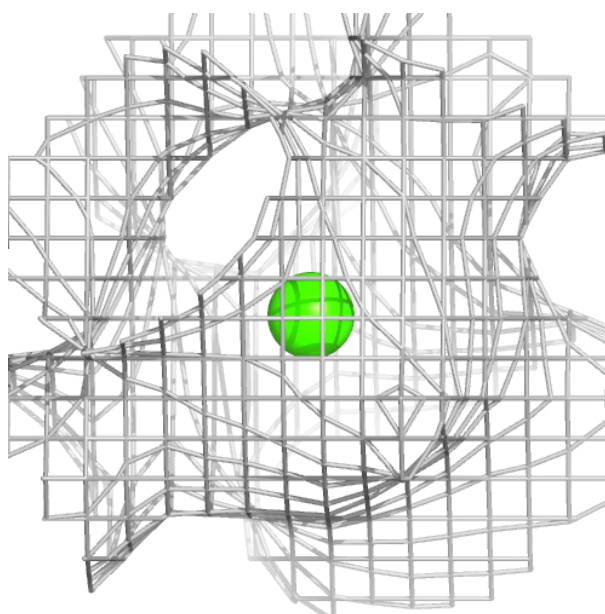
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and green (positive)



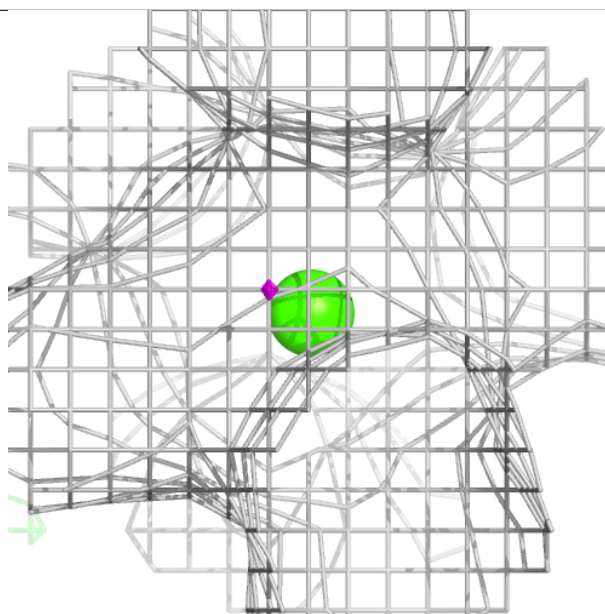
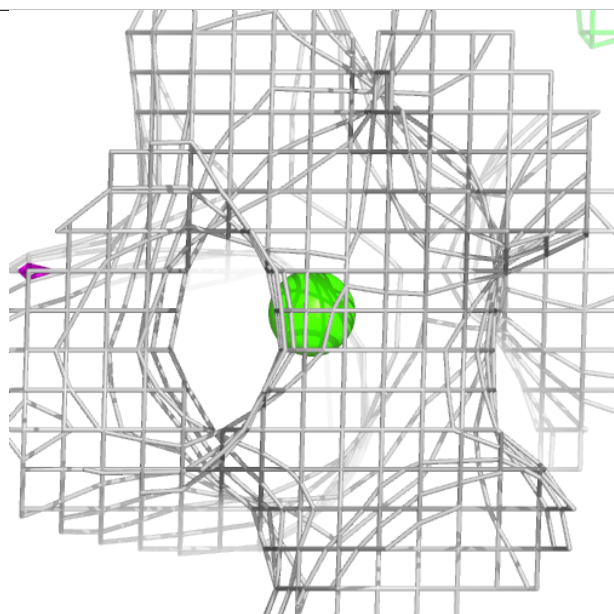
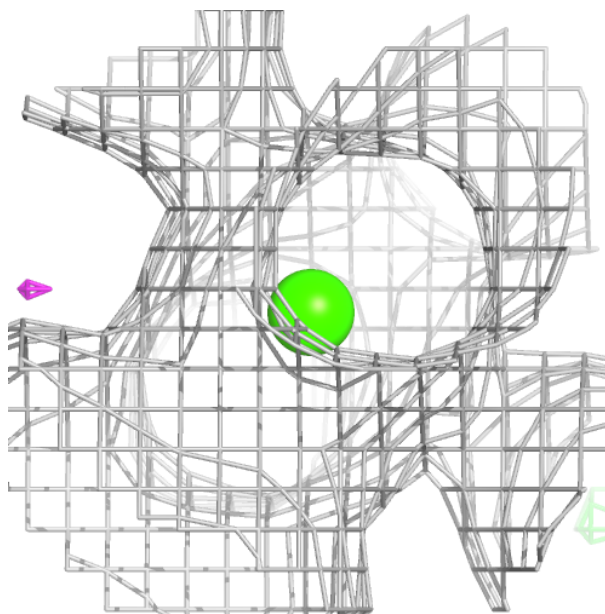
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and green (positive)



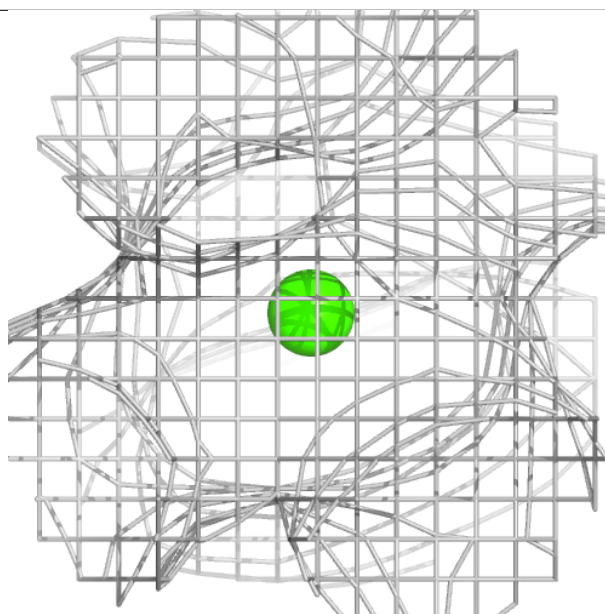
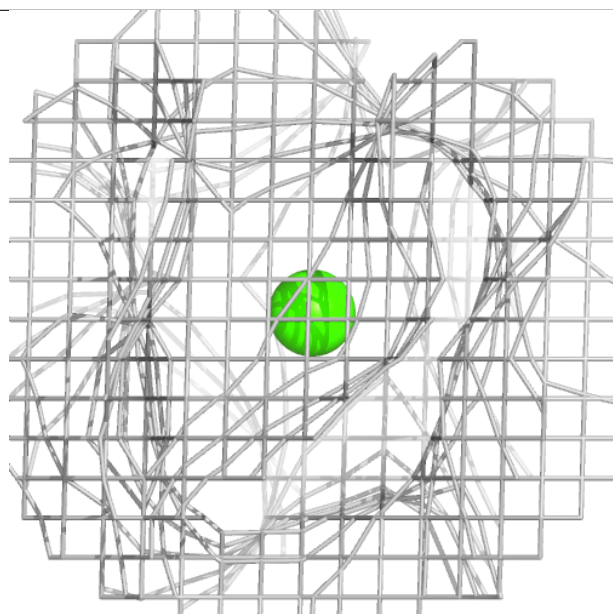
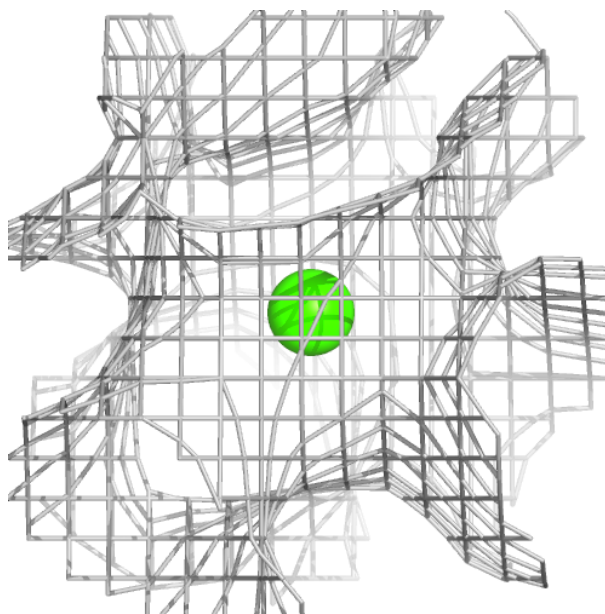
Electron density around CA A 203:

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and green (positive)



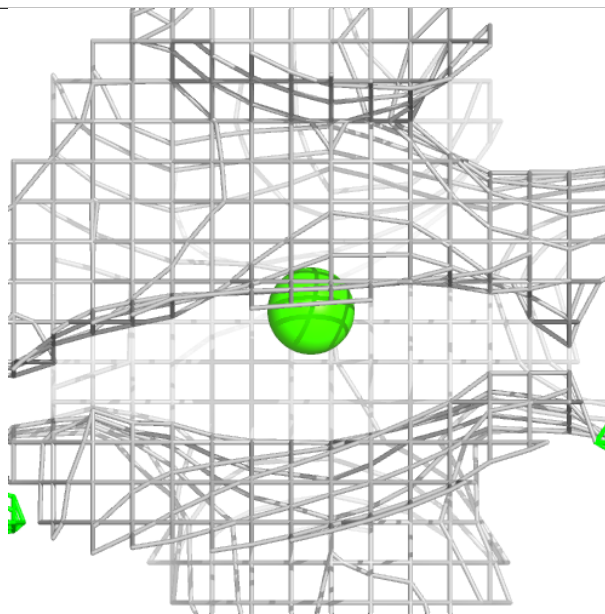
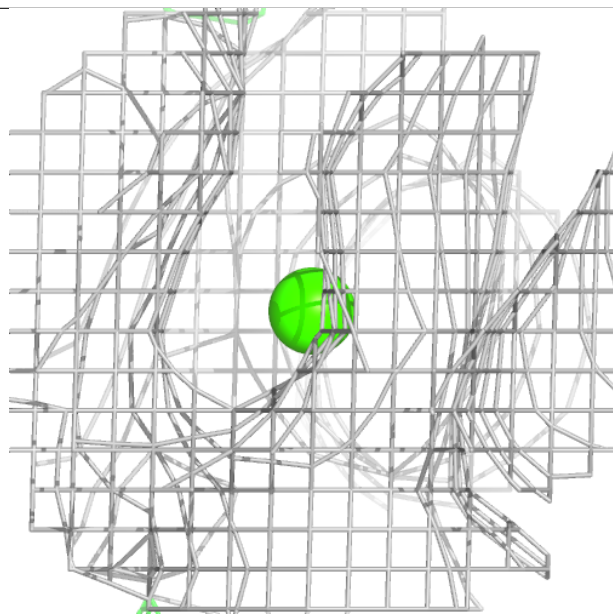
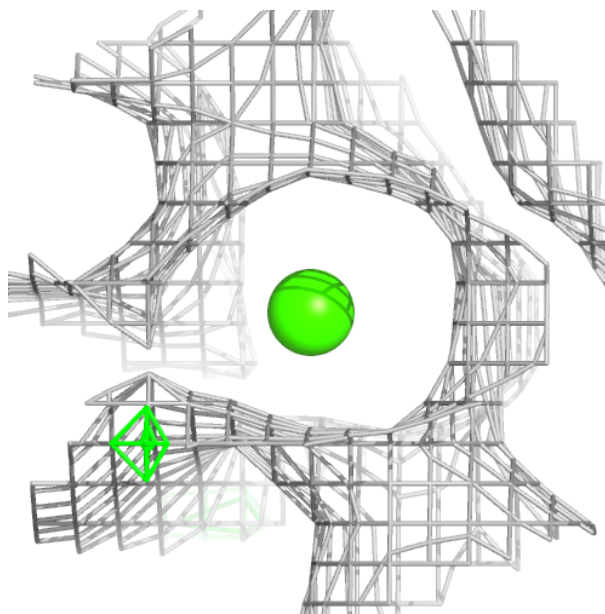
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and green (positive)



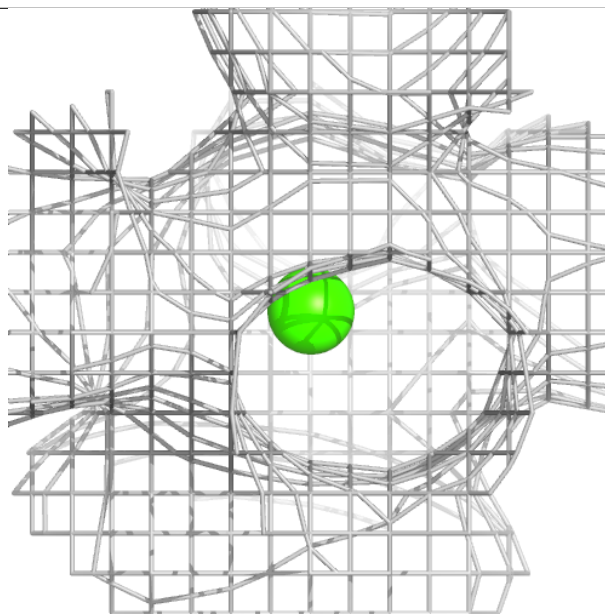
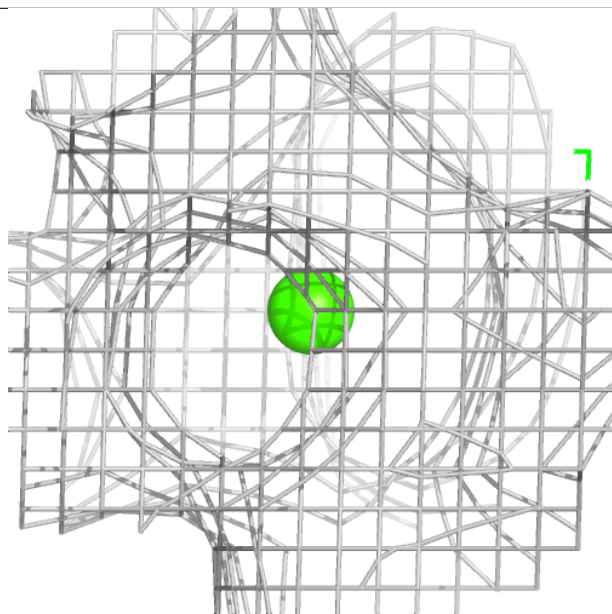
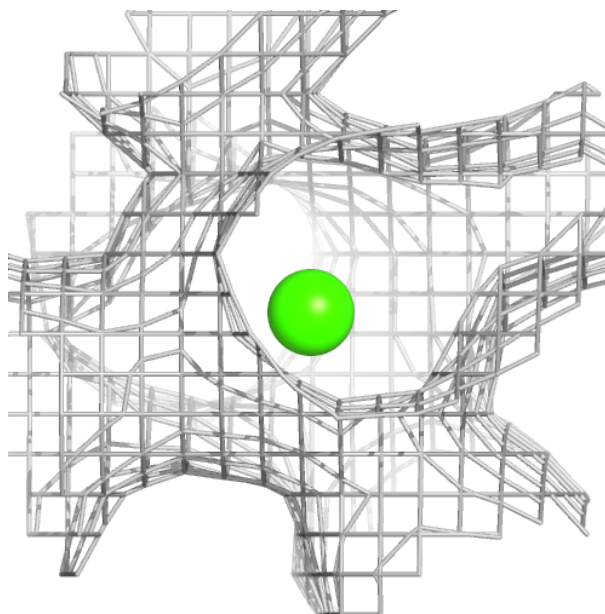
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and green (positive)



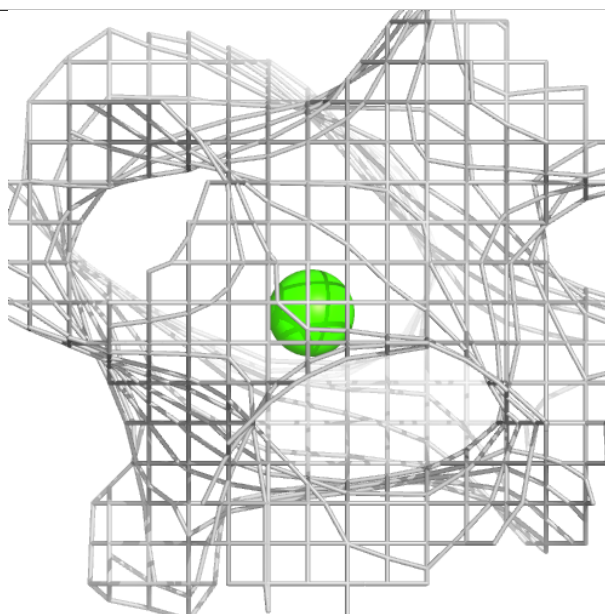
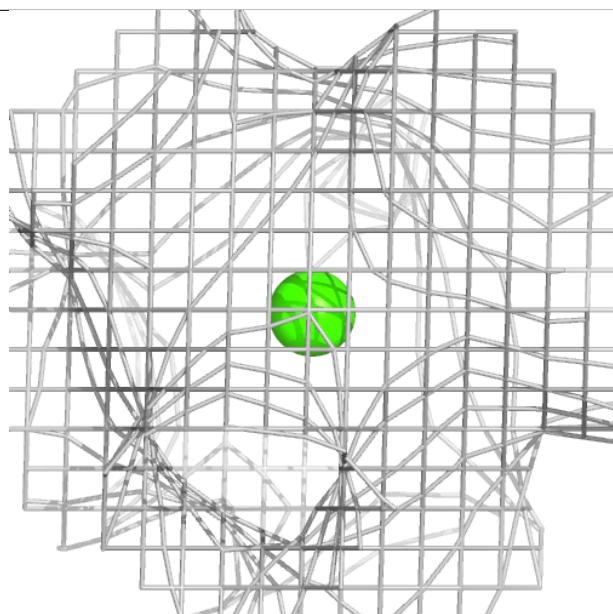
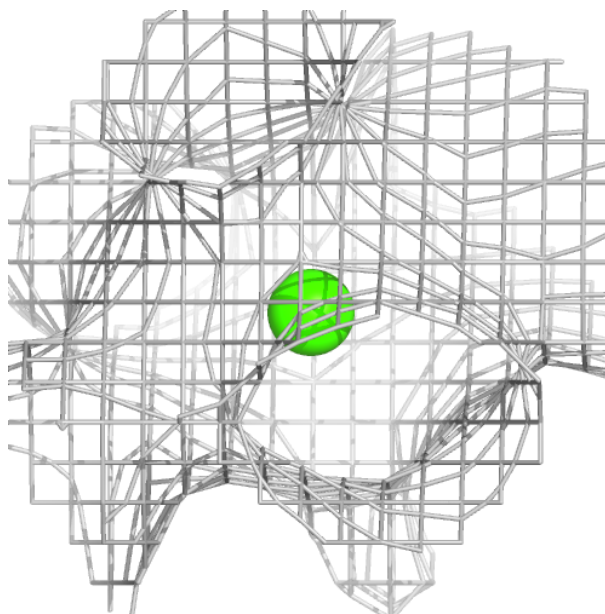
Electron density around CA B 202:

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and green (positive)



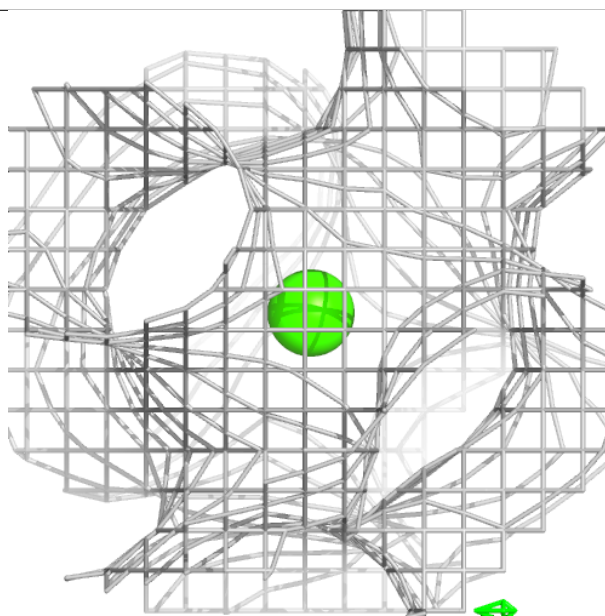
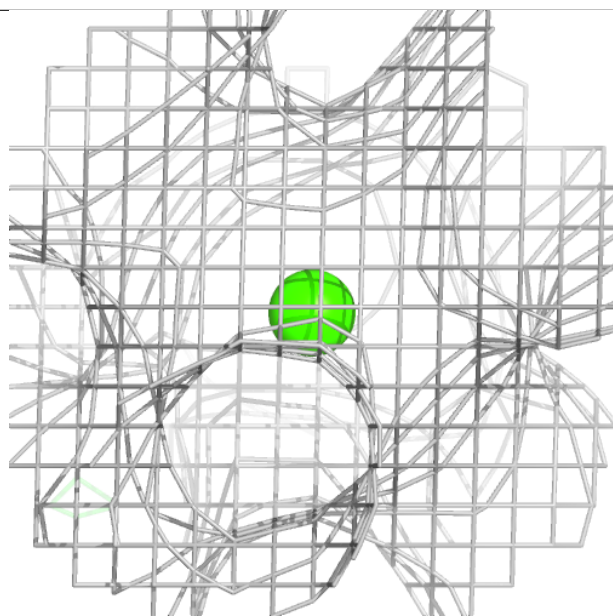
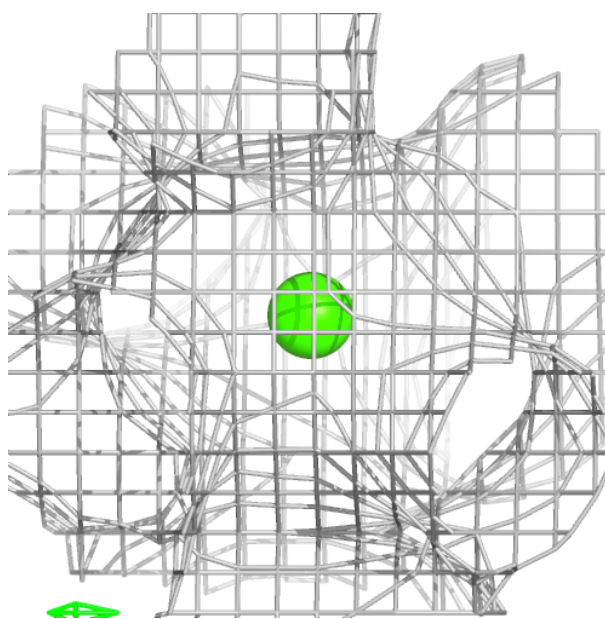
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and green (positive)



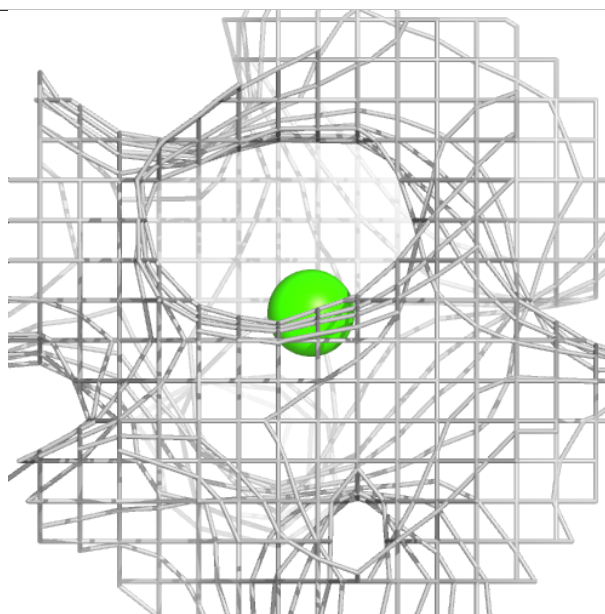
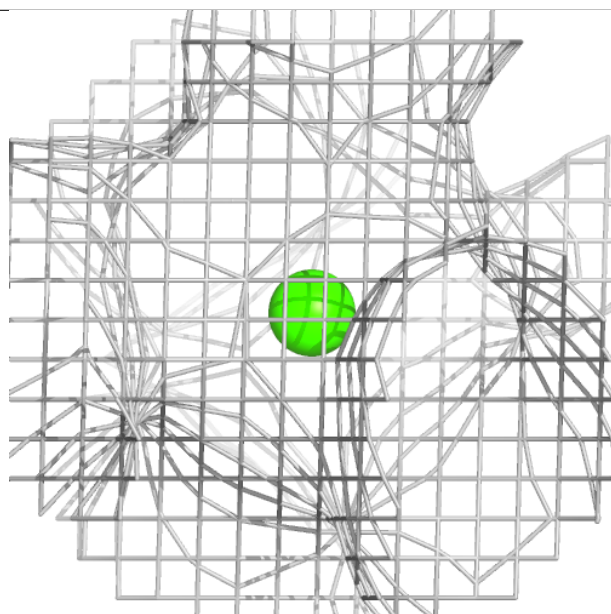
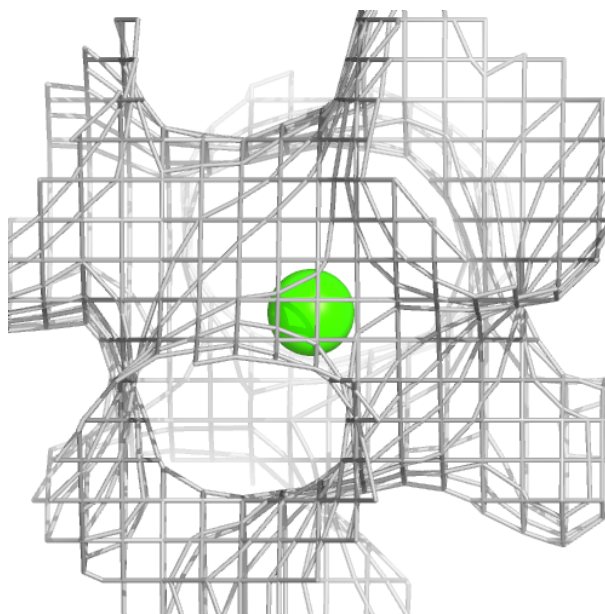
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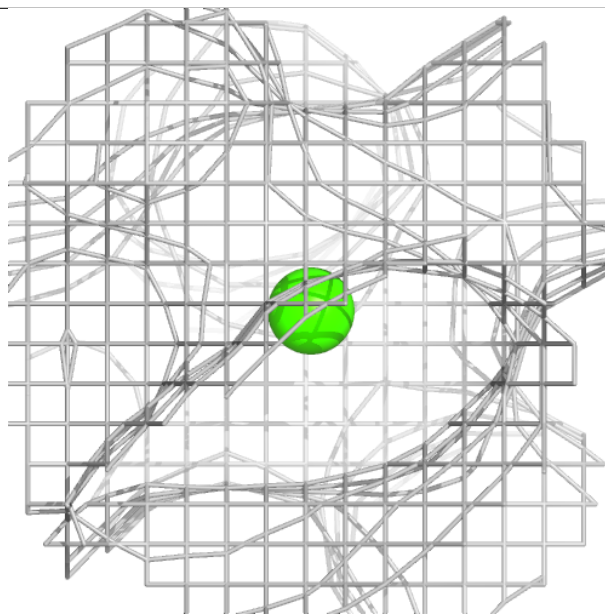
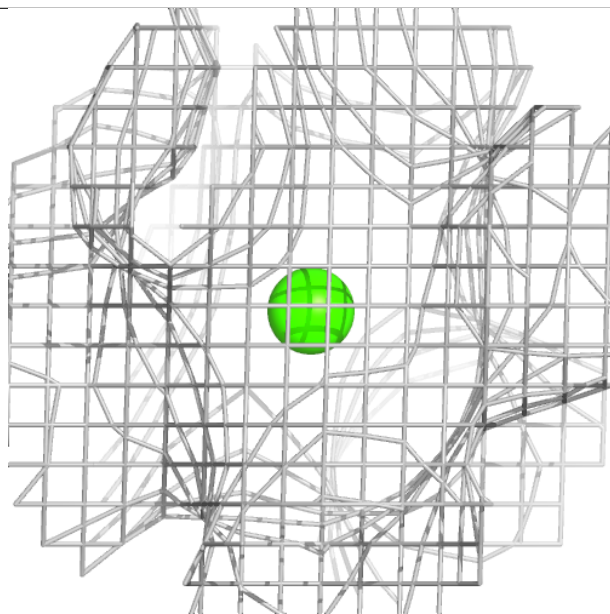
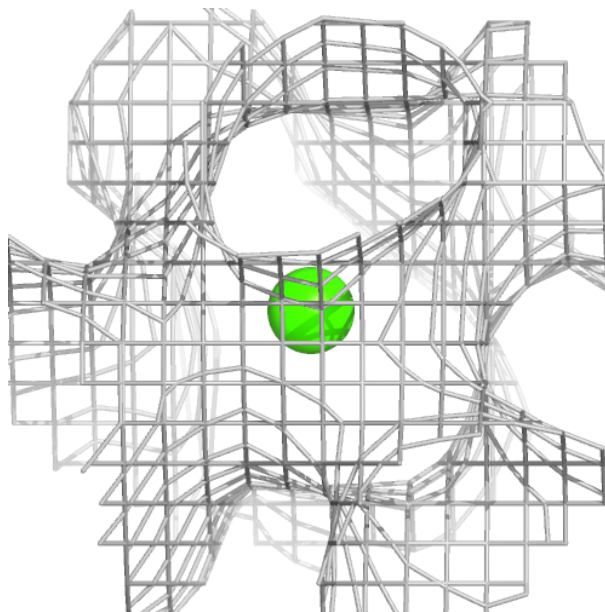
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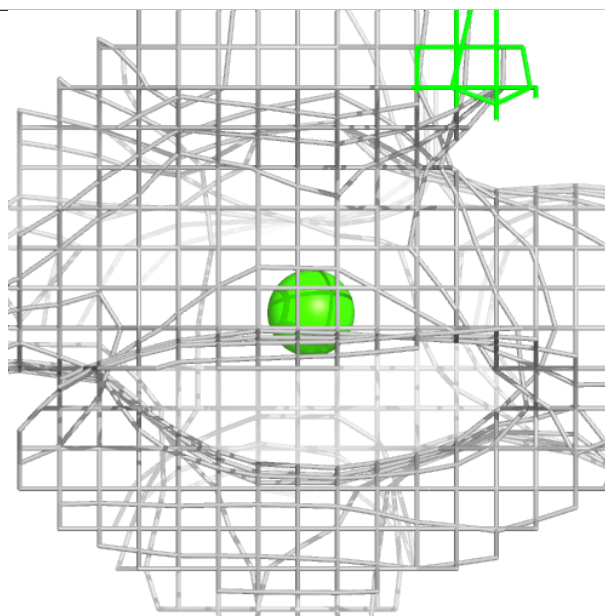
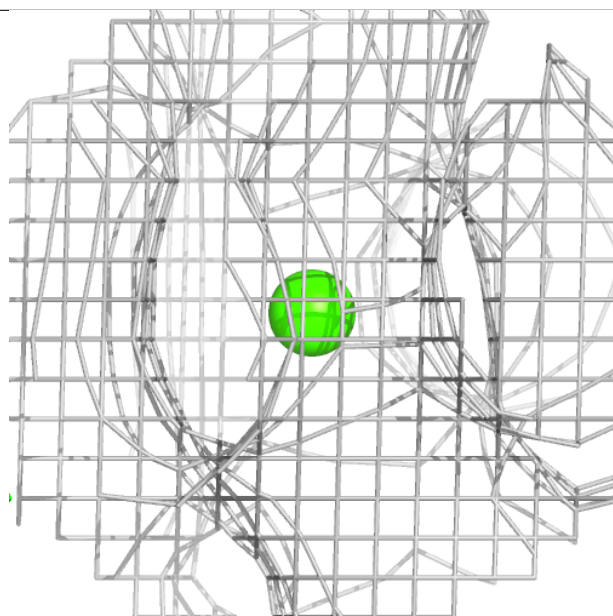
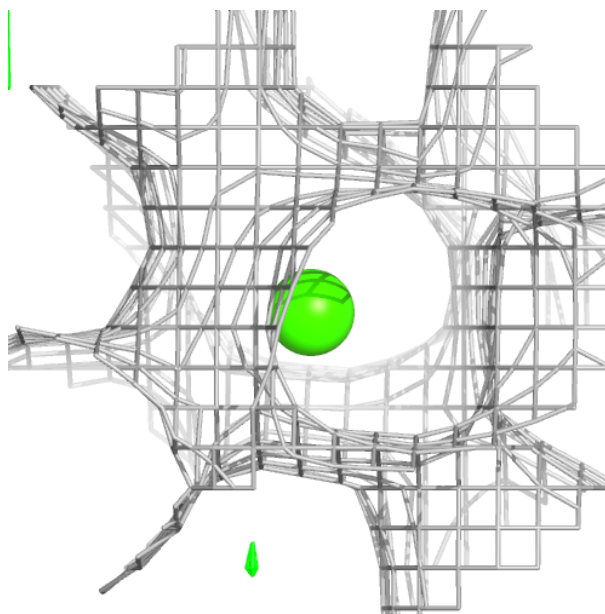
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and green (positive)



Electron density around CA C 201:

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 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.