



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:45 PM UTC

PDB ID : 6KAK / pdb_00006kak
Title : Crystal structure of FKRP in complex with Mg ion
Authors : Kuwabara, N.
Deposited on : 2019-06-23
Resolution : 2.06 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
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

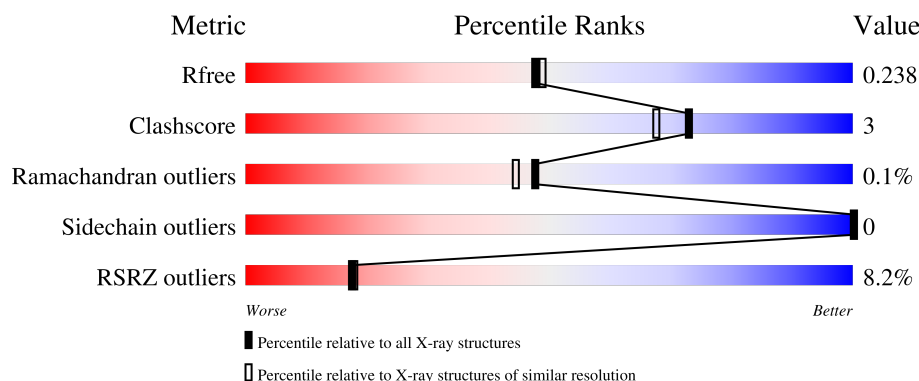
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	455	8% 89% 8% .
1	B	455	9% 90% 6% .
1	C	455	7% 91% 6% .
1	D	455	9% 87% 7% 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MG	A	505	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14589 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 Fukutin-related protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	443	Total	C	N	O	S	0	0	0
			3416	2191	606	610	9			
1	B	439	Total	C	N	O	S	0	0	0
			3379	2170	593	607	9			
1	C	441	Total	C	N	O	S	0	0	0
			3410	2190	602	609	9			
1	D	430	Total	C	N	O	S	0	1	0
			3318	2128	584	597	9			

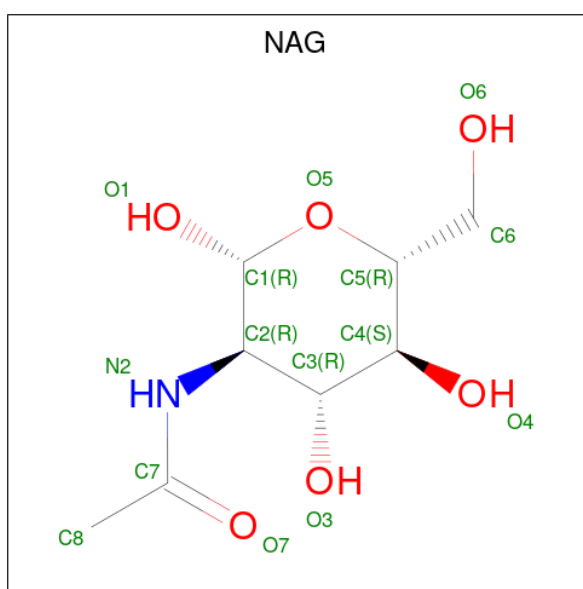
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	GLY	-	expression tag	UNP Q9H9S5
A	42	GLY	-	expression tag	UNP Q9H9S5
A	43	ARG	-	expression tag	UNP Q9H9S5
A	44	PRO	-	expression tag	UNP Q9H9S5
B	41	GLY	-	expression tag	UNP Q9H9S5
B	42	GLY	-	expression tag	UNP Q9H9S5
B	43	ARG	-	expression tag	UNP Q9H9S5
B	44	PRO	-	expression tag	UNP Q9H9S5
C	41	GLY	-	expression tag	UNP Q9H9S5
C	42	GLY	-	expression tag	UNP Q9H9S5
C	43	ARG	-	expression tag	UNP Q9H9S5
C	44	PRO	-	expression tag	UNP Q9H9S5
D	41	GLY	-	expression tag	UNP Q9H9S5
D	42	GLY	-	expression tag	UNP Q9H9S5
D	43	ARG	-	expression tag	UNP Q9H9S5
D	44	PRO	-	expression tag	UNP Q9H9S5

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

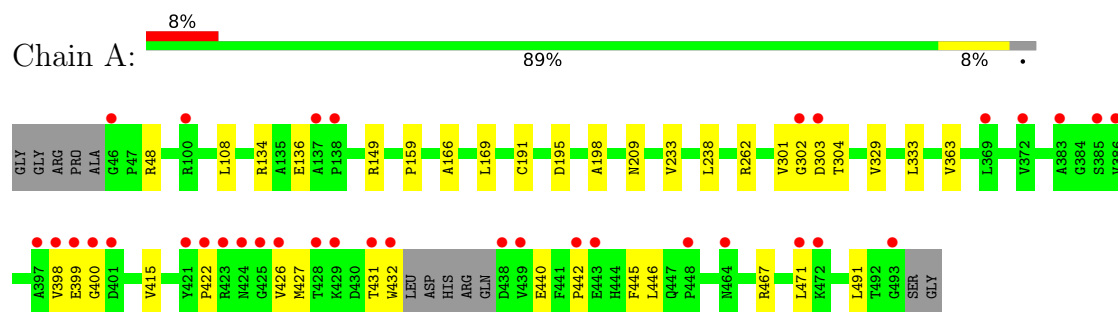
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	269	Total	O	0	0
			269	269		
5	B	192	Total	O	0	0
			192	192		
5	C	260	Total	O	0	0
			260	260		
5	D	222	Total	O	0	0
			222	222		

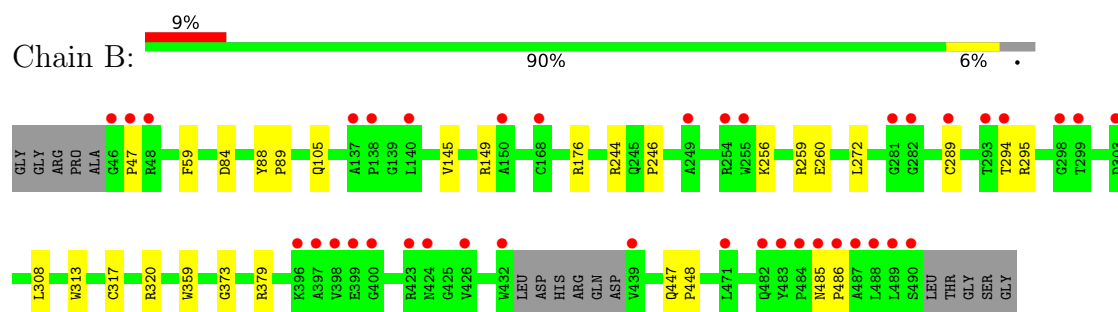
3 Residue-property plots [i](#)

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.

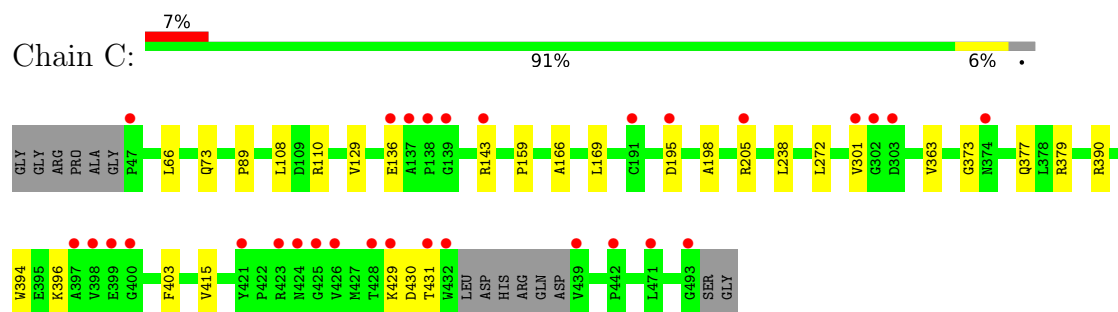
- Molecule 1: Fukutin-related protein



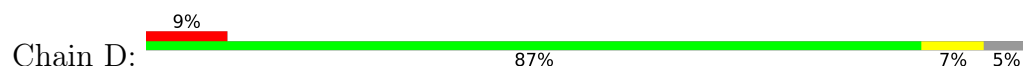
- Molecule 1: Fukutin-related protein

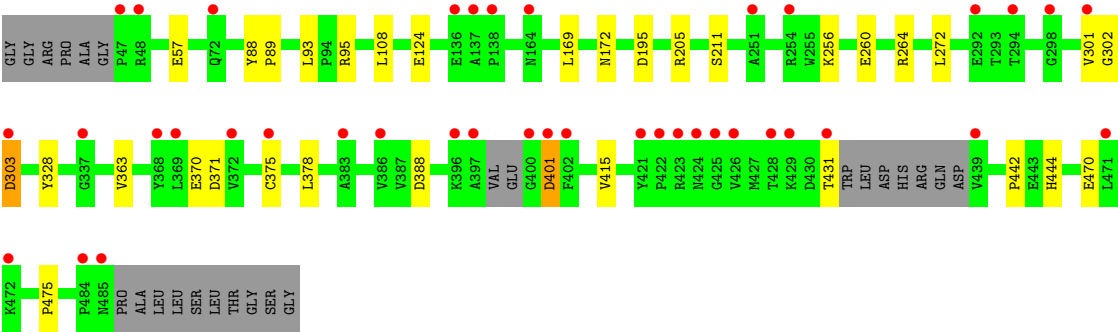


- Molecule 1: Fukutin-related protein



- Molecule 1: Fukutin-related protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.82Å 119.42Å 258.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.41 – 2.06 49.41 – 2.06	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.41-2.06) 99.7 (49.41-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 2.05Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.196 , 0.227 0.208 , 0.238	Depositor DCC
R_{free} test set	7466 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtriage
Anisotropy	0.395	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.6	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	14589	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.07 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.1437e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.16	0/3510	0.41	0/4809
1	B	0.14	0/3473	0.39	0/4761
1	C	0.13	0/3504	0.37	0/4798
1	D	0.14	0/3412	0.38	0/4674
All	All	0.14	0/13899	0.39	0/19042

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	D	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	401	ASP	Peptide

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	3416	0	3347	27	0
1	B	3379	0	3297	18	0
1	C	3410	0	3354	24	0
1	D	3318	0	3230	23	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	28	0	26	0	0
3	B	28	0	26	0	0
3	C	28	0	26	1	0
3	D	28	0	26	3	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0
4	D	2	0	0	0	0
5	A	269	0	0	2	0
5	B	192	0	0	1	0
5	C	260	0	0	2	0
5	D	222	0	0	1	0
All	All	14589	0	13332	85	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 (85) 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:467:ARG:O	1:A:471:LEU:CD2	2.28	0.81
1:D:470:GLU:HG2	1:D:475:PRO:HA	1.64	0.80
1:A:467:ARG:O	1:A:471:LEU:HD22	1.83	0.79
1:C:373:GLY:O	1:C:379:ARG:NH1	2.15	0.79
1:D:401:ASP:OD2	1:D:431:THR:HB	1.92	0.70
1:A:427:MET:HE3	1:A:446:LEU:HD12	1.73	0.69
1:D:124:GLU:OE1	5:D:601:HOH:O	2.11	0.69
1:C:143:ARG:HG2	1:C:238:LEU:HD11	1.75	0.67
1:D:328:TYR:OH	1:D:388:ASP:OD2	2.12	0.66
1:A:398:VAL:HG23	1:A:399:GLU:H	1.62	0.65
1:D:57:GLU:OE2	1:D:264:ARG:NH2	2.33	0.62
1:A:467:ARG:O	1:A:471:LEU:HD23	2.01	0.61
1:D:363:VAL:HB	1:D:415:VAL:HG22	1.81	0.61
1:A:262:ARG:NH2	5:A:603:HOH:O	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:205:ARG:HA	3:D:503:NAG:H83	1.84	0.60
1:D:375:CYS:HB3	1:D:378:LEU:HD23	1.83	0.60
1:C:390:ARG:NH2	5:C:605:HOH:O	2.34	0.59
1:D:93:LEU:O	1:D:95:ARG:NH1	2.36	0.59
1:A:108:LEU:HD21	1:B:272:LEU:HD13	1.84	0.58
1:B:294:THR:HG22	1:B:295:ARG:O	2.03	0.57
1:A:48:ARG:NH2	1:A:149:ARG:HH12	2.03	0.57
1:C:169:LEU:HD11	1:C:195:ASP:HB2	1.86	0.56
1:A:432:TRP:HH2	1:A:440:GLU:HB3	1.70	0.56
1:C:73:GLN:NE2	1:C:136:GLU:O	2.39	0.56
1:C:143:ARG:CZ	1:C:238:LEU:HD21	2.38	0.53
1:B:47:PRO:HB3	1:B:145:VAL:HG11	1.91	0.52
1:C:89:PRO:HB3	1:D:301:VAL:HG21	1.90	0.52
1:C:108:LEU:HD21	1:D:272:LEU:HD13	1.92	0.52
1:B:289:CYS:HB2	1:B:317:CYS:HB2	1.93	0.51
1:A:467:ARG:C	1:A:471:LEU:CD2	2.84	0.51
1:B:84:ASP:O	1:B:105:GLN:HB3	2.11	0.51
1:C:301:VAL:O	5:C:601:HOH:O	2.19	0.50
1:C:429:LYS:NZ	1:C:431:THR:O	2.38	0.49
1:A:467:ARG:C	1:A:471:LEU:HD23	2.38	0.49
1:C:301:VAL:HG21	1:D:89:PRO:HB3	1.93	0.49
1:D:172:ASN:HB2	3:D:502:NAG:N2	2.27	0.48
1:B:320:ARG:NE	5:B:611:HOH:O	2.44	0.48
1:D:256:LYS:O	1:D:260:GLU:HG2	2.13	0.48
1:A:422:PRO:HG3	1:A:427:MET:HE1	1.95	0.48
1:A:169:LEU:HD11	1:A:195:ASP:HB2	1.96	0.47
1:C:363:VAL:HB	1:C:415:VAL:HG22	1.96	0.47
1:C:159:PRO:HD2	1:C:238:LEU:O	2.15	0.46
1:D:169:LEU:HD11	1:D:195:ASP:HB2	1.96	0.46
1:C:143:ARG:NE	1:C:238:LEU:HD21	2.31	0.46
1:A:400:GLY:HA2	1:A:431:THR:HG21	1.97	0.46
1:C:429:LYS:HB3	1:C:429:LYS:HE3	1.78	0.46
1:B:244:ARG:O	1:B:246:PRO:HD3	2.15	0.45
1:D:370:GLU:HG2	1:D:371:ASP:OD1	2.15	0.45
1:A:442:PRO:HG2	1:A:445:PHE:CE2	2.52	0.45
1:A:491:LEU:HD12	3:C:503:NAG:O6	2.16	0.45
1:B:88:TYR:HA	1:B:89:PRO:C	2.41	0.45
1:C:272:LEU:HD13	1:D:108:LEU:HD21	1.98	0.45
1:A:134:ARG:HG2	1:A:136:GLU:HG2	1.99	0.45
1:D:172:ASN:HB2	3:D:502:NAG:HN2	1.83	0.44
1:A:301:VAL:HG22	1:B:88:TYR:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:PRO:HD2	1:A:238:LEU:O	2.17	0.44
1:A:302:GLY:O	1:A:304:THR:N	2.51	0.44
1:D:57:GLU:CD	1:D:264:ARG:HH22	2.26	0.44
1:A:166:ALA:CB	1:A:198:ALA:HB2	2.48	0.43
1:B:256:LYS:O	1:B:260:GLU:HG3	2.17	0.43
1:A:166:ALA:HB2	1:A:198:ALA:HB2	2.01	0.43
1:B:176:ARG:HD2	1:B:313:TRP:CE2	2.53	0.43
1:A:209:ASN:HB3	5:A:662:HOH:O	2.17	0.43
1:A:422:PRO:HA	1:A:426:VAL:O	2.19	0.43
1:B:145:VAL:O	1:B:149:ARG:HG3	2.18	0.43
1:C:166:ALA:HB2	1:C:198:ALA:HB2	2.01	0.43
1:B:59:PHE:CE2	1:B:256:LYS:HE3	2.54	0.43
1:C:110:ARG:O	1:D:211:SER:HB2	2.18	0.43
1:B:485:ASN:HA	1:B:486:PRO:HD3	1.77	0.42
1:C:205:ARG:HD2	1:C:205:ARG:HA	1.84	0.42
1:D:302:GLY:O	1:D:303:ASP:C	2.62	0.42
1:A:363:VAL:HB	1:A:415:VAL:HG22	2.02	0.42
1:D:88:TYR:HA	1:D:89:PRO:C	2.44	0.42
1:B:256:LYS:O	1:B:259:ARG:HG2	2.19	0.42
1:A:191:CYS:HB2	1:A:233:VAL:HG13	2.02	0.41
1:A:329:VAL:O	1:A:333:LEU:HG	2.19	0.41
1:C:396:LYS:HD3	1:C:403:PHE:CE1	2.56	0.41
1:B:373:GLY:O	1:B:379:ARG:HD3	2.19	0.41
1:B:308:LEU:HD21	1:B:359:TRP:HB2	2.03	0.41
1:C:166:ALA:CB	1:C:198:ALA:HB2	2.51	0.41
1:C:429:LYS:HG2	1:C:430:ASP:N	2.36	0.41
1:D:442:PRO:HB2	1:D:444:HIS:CD2	2.55	0.41
1:C:377:GLN:HB3	1:C:394:TRP:CD2	2.57	0.40
1:B:447:GLN:HA	1:B:448:PRO:HA	1.84	0.40
1:C:66:LEU:HD11	1:C:129:VAL:HG12	2.03	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	439/455 (96%)	427 (97%)	11 (2%)	1 (0%)	43	38
1	B	435/455 (96%)	422 (97%)	13 (3%)	0	100	100
1	C	437/455 (96%)	430 (98%)	7 (2%)	0	100	100
1	D	425/455 (93%)	419 (99%)	5 (1%)	1 (0%)	43	38
All	All	1736/1820 (95%)	1698 (98%)	36 (2%)	2 (0%)	48	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	303	ASP
1	D	303	ASP

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	342/357 (96%)	342 (100%)	0	100	100
1	B	338/357 (95%)	338 (100%)	0	100	100
1	C	343/357 (96%)	343 (100%)	0	100	100
1	D	332/357 (93%)	332 (100%)	0	100	100
All	All	1355/1428 (95%)	1355 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	GLN
1	A	252	HIS
1	A	464	ASN
1	B	406	GLN

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Mol	Chain	Res	Type
1	B	460	GLN
1	B	485	ASN
1	C	414	HIS
1	D	164	ASN
1	D	252	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 11 are monoatomic - leaving 8 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	NAG	A	502	1	14,14,15	0.39	0	17,19,21	0.40	0
3	NAG	B	503	1	14,14,15	0.42	0	17,19,21	0.61	1 (5%)
3	NAG	D	503	1	14,14,15	0.23	0	17,19,21	0.55	0
3	NAG	C	502	1	14,14,15	0.39	0	17,19,21	0.72	0
3	NAG	B	502	1	14,14,15	0.41	0	17,19,21	0.41	0
3	NAG	A	503	1	14,14,15	0.27	0	17,19,21	0.71	1 (5%)
3	NAG	C	503	1	14,14,15	0.17	0	17,19,21	0.58	0
3	NAG	D	502	1	14,14,15	0.85	1 (7%)	17,19,21	0.80	1 (5%)

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	NAG	A	502	1	-	2/6/23/26	0/1/1/1
3	NAG	B	503	1	-	1/6/23/26	0/1/1/1
3	NAG	D	503	1	-	2/6/23/26	0/1/1/1
3	NAG	C	502	1	-	0/6/23/26	0/1/1/1
3	NAG	B	502	1	-	2/6/23/26	0/1/1/1
3	NAG	A	503	1	-	2/6/23/26	0/1/1/1
3	NAG	C	503	1	-	2/6/23/26	0/1/1/1
3	NAG	D	502	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	502	NAG	C1-C2	2.99	1.56	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	502	NAG	C1-O5-C5	2.72	115.84	112.19
3	A	503	NAG	C1-O5-C5	2.20	115.14	112.19
3	B	503	NAG	C1-O5-C5	2.01	114.88	112.19

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	503	NAG	C4-C5-C6-O6
3	D	503	NAG	C8-C7-N2-C2
3	D	503	NAG	O7-C7-N2-C2
3	C	503	NAG	O5-C5-C6-O6
3	B	502	NAG	C4-C5-C6-O6
3	A	503	NAG	C4-C5-C6-O6
3	A	502	NAG	C4-C5-C6-O6
3	A	502	NAG	O5-C5-C6-O6
3	B	503	NAG	O5-C5-C6-O6
3	A	503	NAG	O5-C5-C6-O6
3	B	502	NAG	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	503	NAG	1	0
3	C	503	NAG	1	0
3	D	502	NAG	2	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	443/455 (97%)	0.32	35 (7%)	18 19	24, 40, 79, 116	0
1	B	439/455 (96%)	0.50	39 (8%)	15 16	25, 43, 84, 117	0
1	C	441/455 (96%)	0.29	30 (6%)	23 23	24, 40, 75, 109	0
1	D	430/455 (94%)	0.45	40 (9%)	14 14	22, 43, 84, 120	1 (0%)
All	All	1753/1820 (96%)	0.39	144 (8%)	17 18	22, 41, 83, 120	1 (0%)

All (144) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	47	PRO	5.6
1	C	302	GLY	5.4
1	D	397	ALA	5.4
1	D	471	LEU	5.4
1	A	398	VAL	5.3
1	B	489	LEU	5.3
1	D	439	VAL	5.3
1	B	488	LEU	5.1
1	B	487	ALA	5.0
1	C	137	ALA	5.0
1	A	422	PRO	4.9
1	A	438	ASP	4.8
1	B	432	TRP	4.8
1	B	439	VAL	4.5
1	B	486	PRO	4.4
1	D	400	GLY	4.4
1	D	431	THR	4.3
1	B	483	TYR	4.2
1	C	439	VAL	4.1
1	B	484	PRO	3.9
1	C	432	TRP	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	398	VAL	3.9
1	C	398	VAL	3.9
1	D	137	ALA	3.9
1	A	399	GLU	3.9
1	C	47	PRO	3.9
1	B	47	PRO	3.8
1	D	401	ASP	3.8
1	C	138	PRO	3.8
1	B	46	GLY	3.8
1	B	289	CYS	3.7
1	A	471	LEU	3.6
1	B	399	GLU	3.6
1	B	490	SER	3.5
1	A	439	VAL	3.5
1	D	485	ASN	3.5
1	A	425	GLY	3.5
1	A	428	THR	3.5
1	D	396	LYS	3.5
1	B	282	GLY	3.4
1	B	485	ASN	3.4
1	D	429	LYS	3.4
1	C	303	ASP	3.3
1	D	425	GLY	3.3
1	B	423	ARG	3.3
1	A	432	TRP	3.2
1	B	426	VAL	3.2
1	D	422	PRO	3.2
1	A	369	LEU	3.1
1	B	48	ARG	3.1
1	B	168	CYS	3.1
1	D	294	THR	3.1
1	B	137	ALA	3.0
1	A	431	THR	3.0
1	C	493	GLY	2.9
1	C	429	LYS	2.9
1	A	137	ALA	2.9
1	C	301	VAL	2.9
1	D	423	ARG	2.9
1	A	397	ALA	2.9
1	B	400	GLY	2.9
1	B	298	GLY	2.9
1	C	423	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	368	TYR	2.8
1	B	397	ALA	2.8
1	A	138	PRO	2.8
1	C	425	GLY	2.8
1	B	294	THR	2.8
1	A	426	VAL	2.8
1	A	448	PRO	2.7
1	D	369	LEU	2.7
1	B	138	PRO	2.7
1	A	443	GLU	2.6
1	D	375	CYS	2.6
1	C	397	ALA	2.6
1	D	424	ASN	2.6
1	C	431	THR	2.6
1	B	482	GLN	2.6
1	C	421	TYR	2.6
1	D	72	GLN	2.6
1	D	301	VAL	2.6
1	D	426	VAL	2.6
1	B	255	TRP	2.6
1	D	428	THR	2.5
1	D	402	PHE	2.5
1	C	139	GLY	2.5
1	A	46	GLY	2.5
1	A	472	LYS	2.5
1	D	164	ASN	2.5
1	A	401	ASP	2.5
1	D	484	PRO	2.5
1	C	426	VAL	2.4
1	A	386	VAL	2.4
1	B	299	THR	2.4
1	D	48	ARG	2.4
1	A	442	PRO	2.4
1	B	424	ASN	2.4
1	A	429	LYS	2.4
1	D	138	PRO	2.4
1	A	421	TYR	2.3
1	A	302	GLY	2.3
1	A	303	ASP	2.3
1	D	303	ASP	2.3
1	A	372	VAL	2.3
1	C	424	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	400	GLY	2.3
1	D	298	GLY	2.3
1	A	423	ARG	2.3
1	A	424	ASN	2.2
1	C	195	ASP	2.2
1	D	383	ALA	2.2
1	B	471	LEU	2.2
1	D	421	TYR	2.2
1	A	100	ARG	2.2
1	D	386	VAL	2.2
1	C	205	ARG	2.2
1	B	281	GLY	2.2
1	B	150	ALA	2.2
1	D	251	ALA	2.2
1	B	140	LEU	2.2
1	D	254	ARG	2.2
1	A	493	GLY	2.1
1	A	383	ALA	2.1
1	C	191	CYS	2.1
1	C	471	LEU	2.1
1	C	428	THR	2.1
1	B	396	LYS	2.1
1	D	292	GLU	2.1
1	C	136	GLU	2.1
1	A	464	ASN	2.1
1	B	254	ARG	2.1
1	C	143	ARG	2.1
1	D	337	GLY	2.1
1	A	385	SER	2.1
1	B	249	ALA	2.1
1	D	136	GLU	2.0
1	C	374	ASN	2.0
1	B	303	ASP	2.0
1	C	442	PRO	2.0
1	D	472	LYS	2.0
1	C	399	GLU	2.0
1	D	372	VAL	2.0
1	B	293	THR	2.0
1	A	400	GLY	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

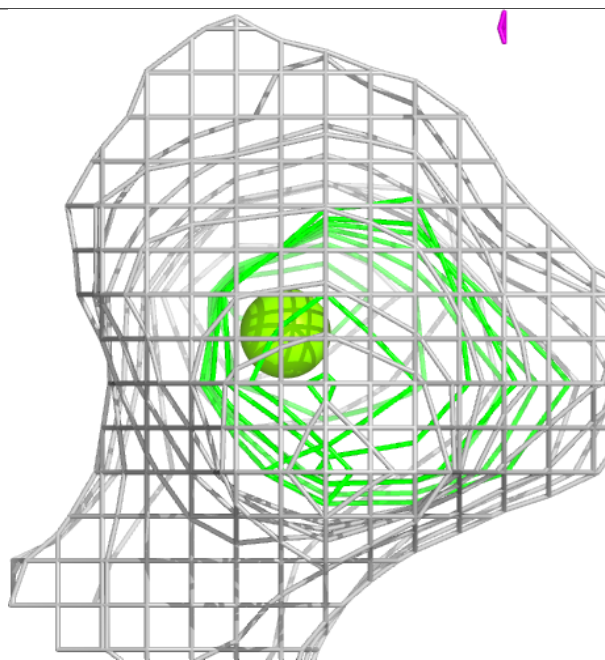
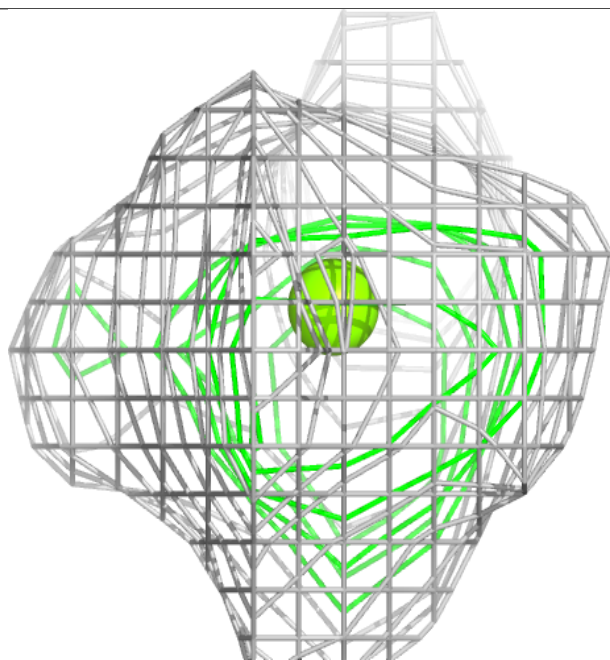
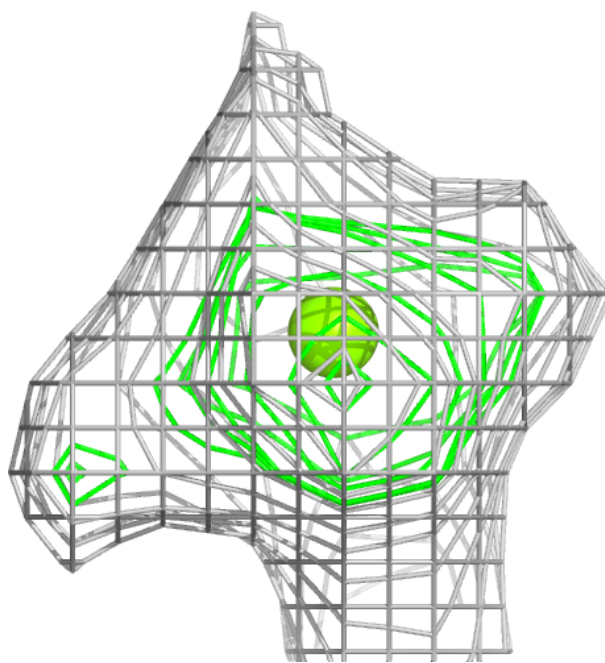
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MG	D	505	1/1	0.32	0.32	108,108,108,108	0
3	NAG	B	503	14/15	0.59	0.19	73,81,88,89	0
3	NAG	D	503	14/15	0.64	0.16	61,66,69,71	0
4	MG	A	505	1/1	0.65	0.65	124,124,124,124	0
3	NAG	D	502	14/15	0.69	0.16	77,83,87,87	0
4	MG	D	504	1/1	0.71	0.24	87,87,87,87	0
3	NAG	B	502	14/15	0.79	0.11	62,70,76,76	0
3	NAG	C	503	14/15	0.83	0.12	44,47,57,58	0
3	NAG	C	502	14/15	0.86	0.14	49,58,78,82	0
4	MG	B	504	1/1	0.86	0.10	56,56,56,56	0
4	MG	C	504	1/1	0.88	0.14	60,60,60,60	0
3	NAG	A	502	14/15	0.88	0.10	44,54,62,63	0
3	NAG	A	503	14/15	0.88	0.12	46,49,60,62	0
4	MG	B	505	1/1	0.92	0.15	61,61,61,61	0
4	MG	A	504	1/1	0.95	0.08	70,70,70,70	0
2	ZN	B	501	1/1	0.98	0.04	38,38,38,38	0
2	ZN	A	501	1/1	0.99	0.02	29,29,29,29	0
2	ZN	D	501	1/1	1.00	0.02	33,33,33,33	0
2	ZN	C	501	1/1	1.00	0.03	30,30,30,30	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.

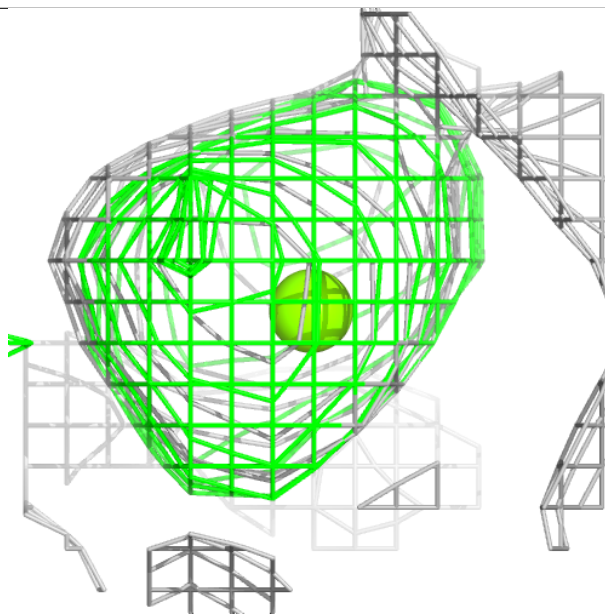
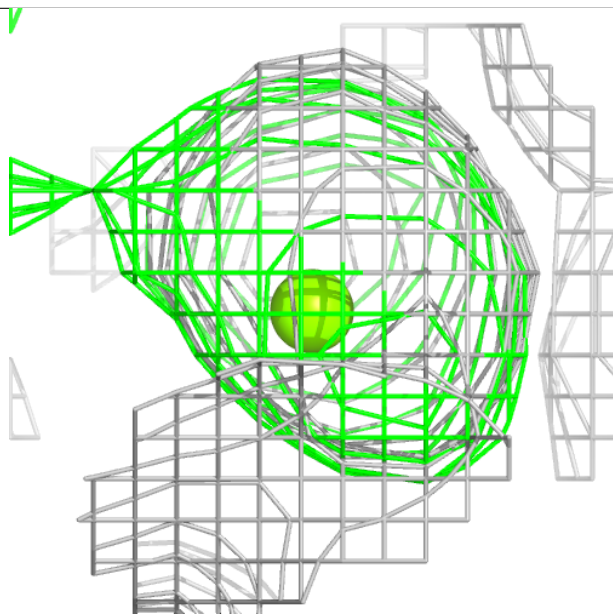
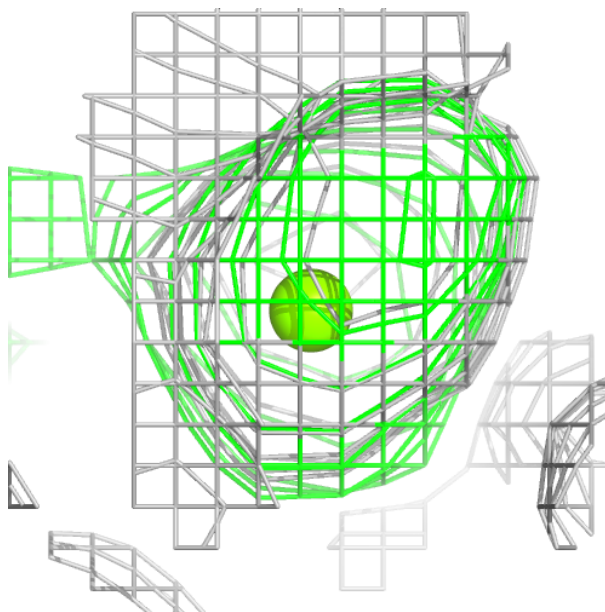
Electron density around MG D 505:

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



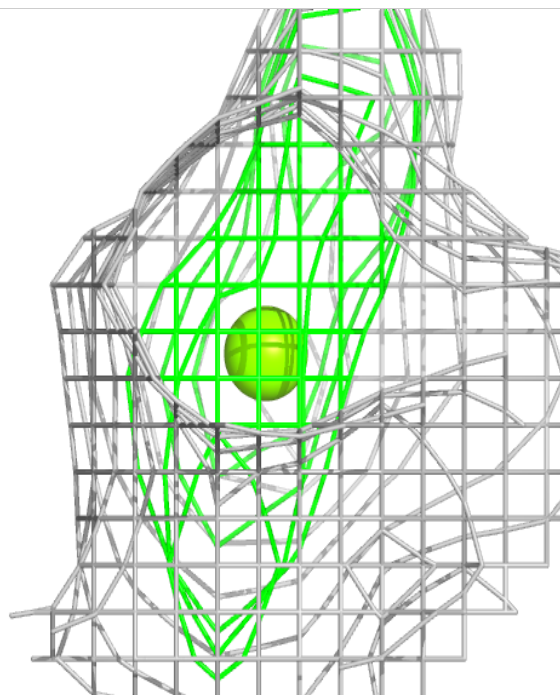
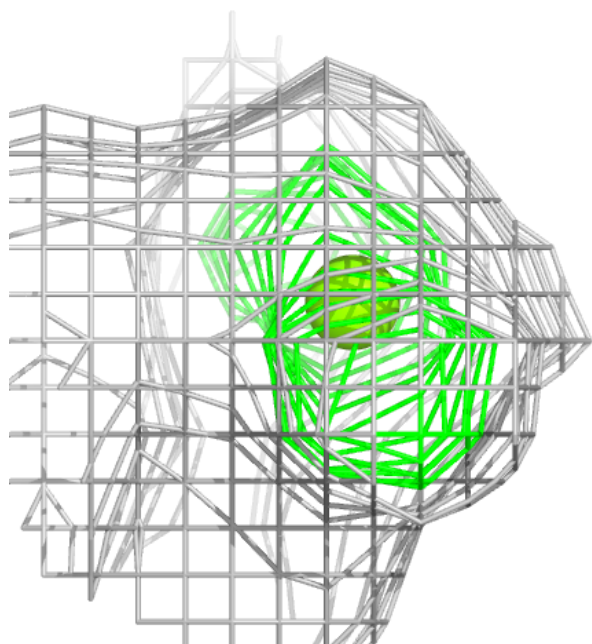
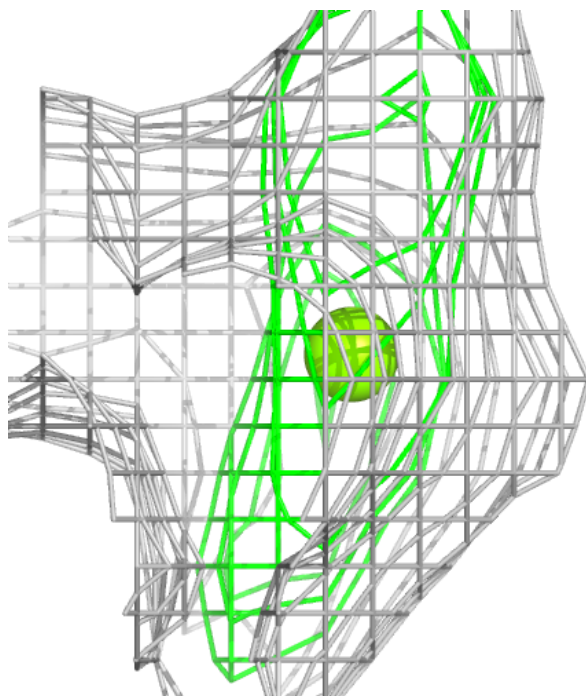
Electron density around MG A 505:

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and green (positive)



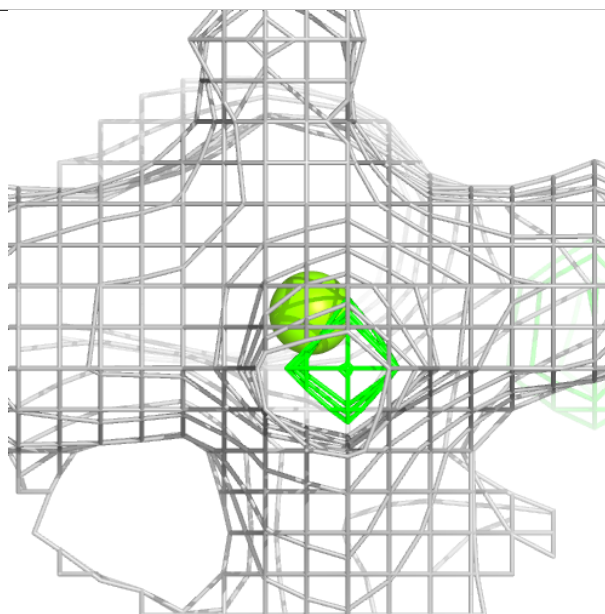
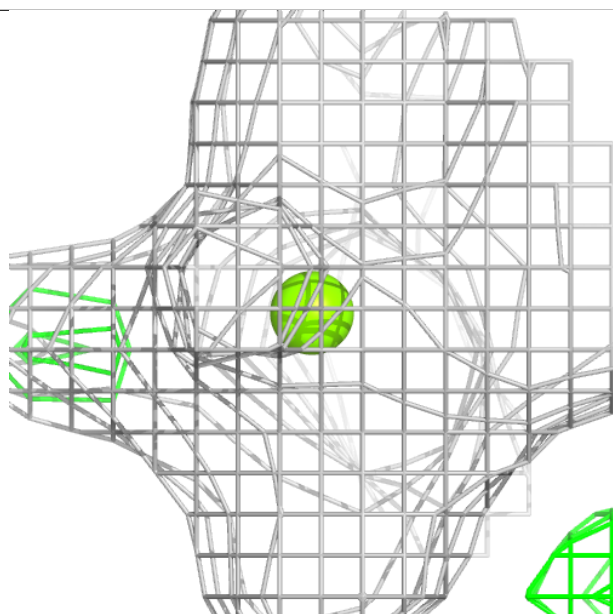
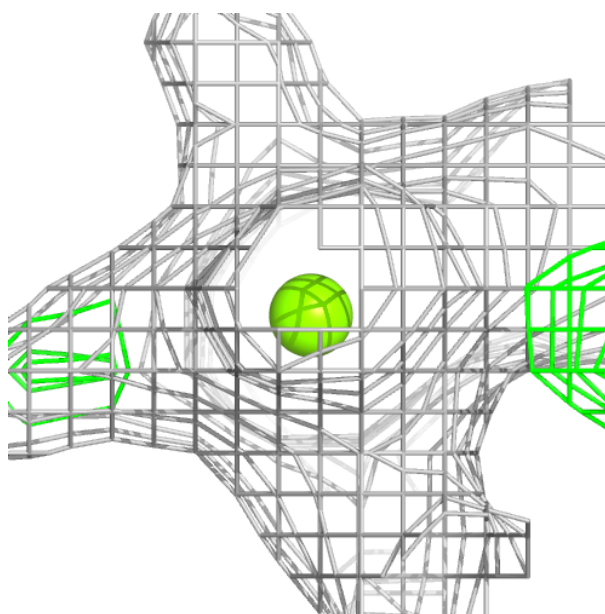
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and green (positive)



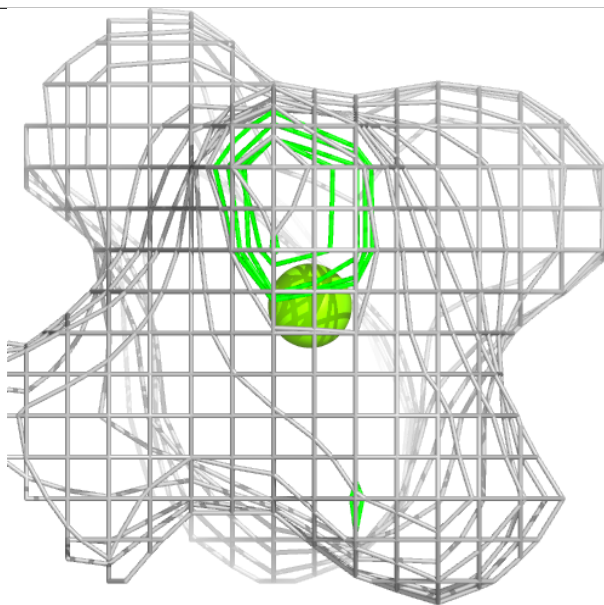
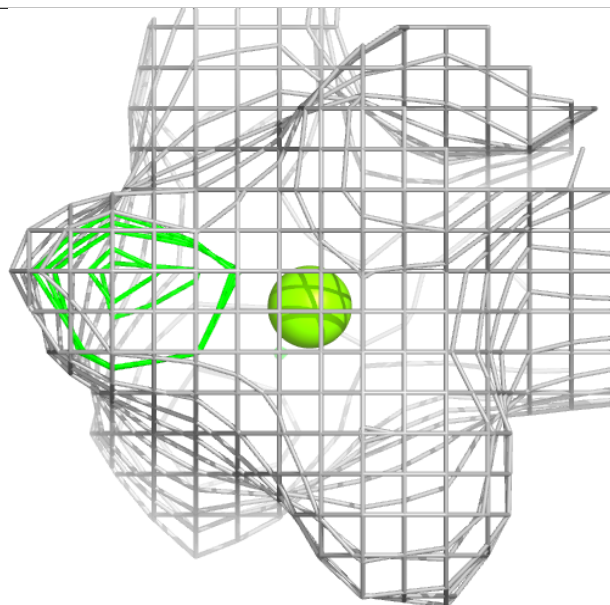
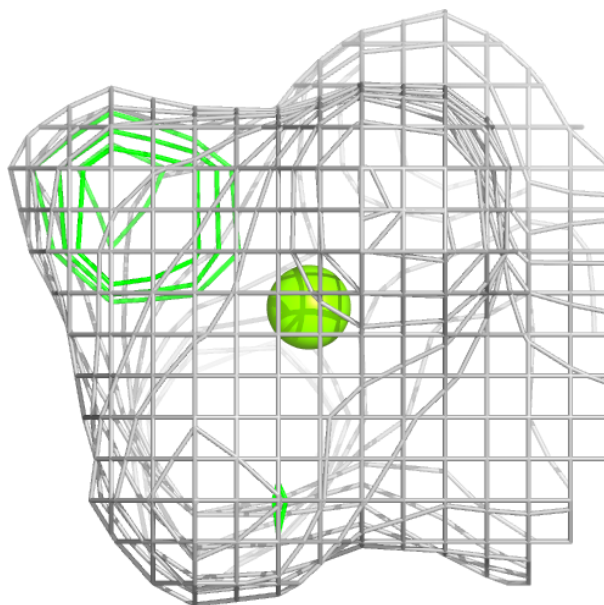
Electron density around MG B 504:

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



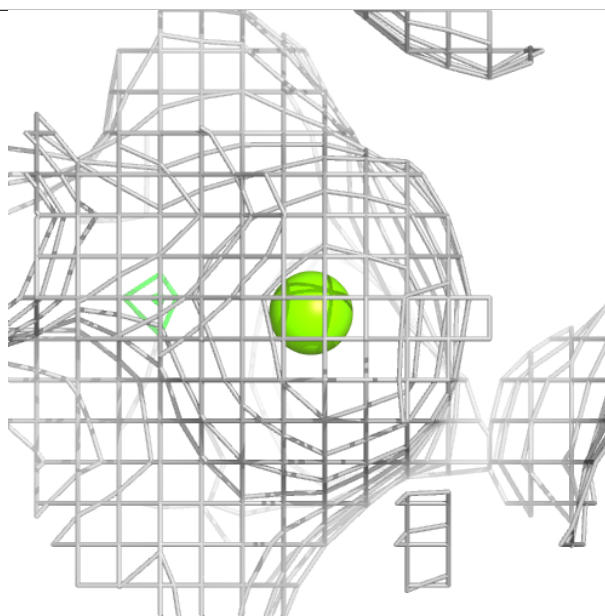
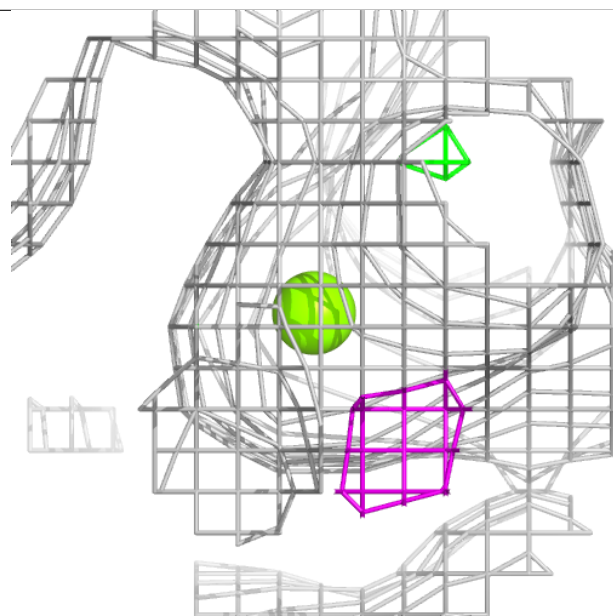
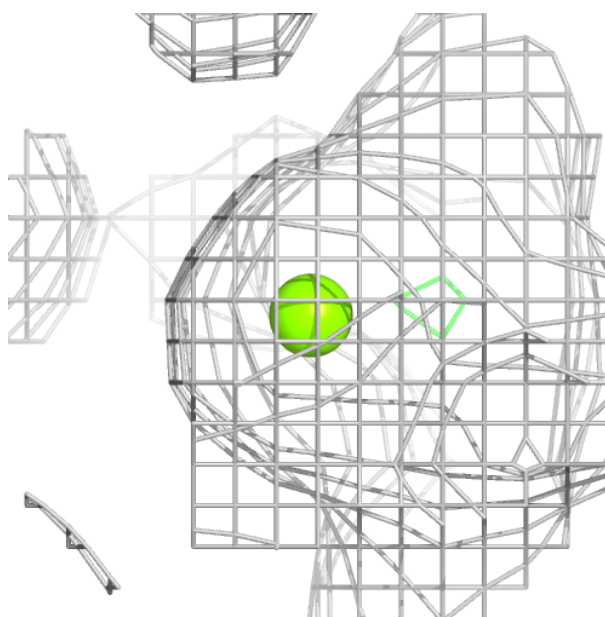
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and green (positive)



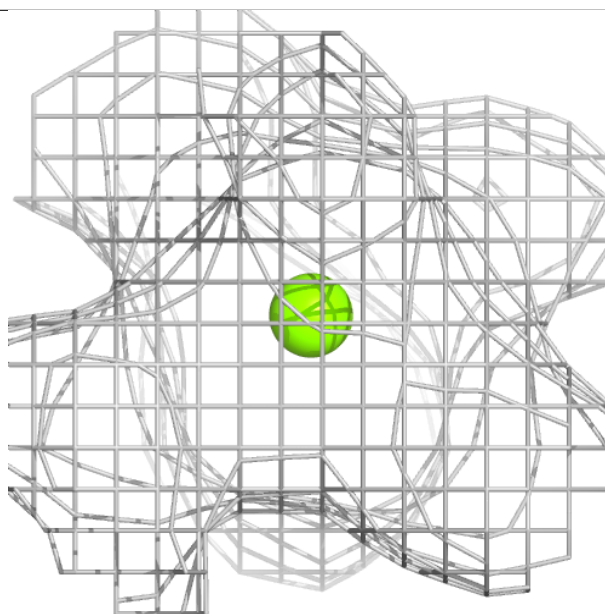
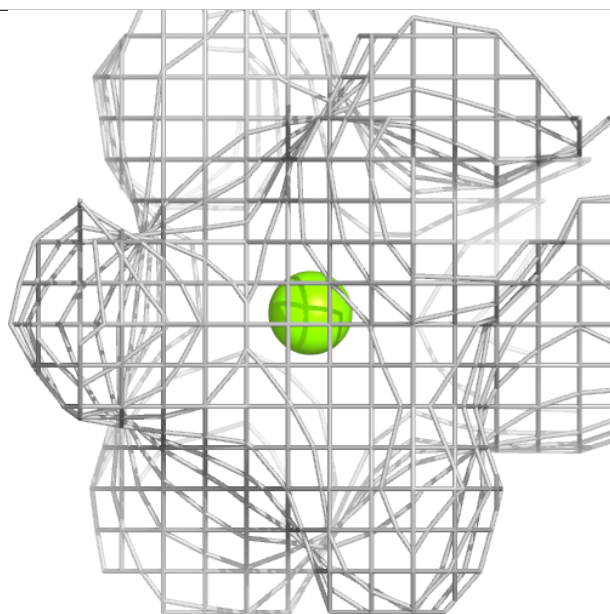
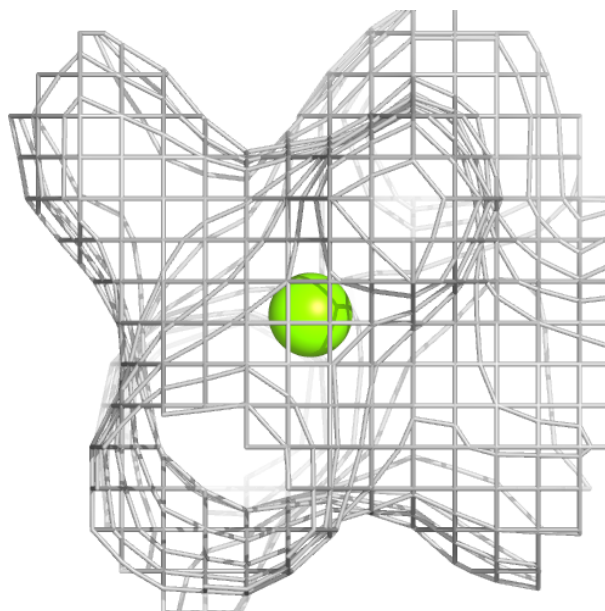
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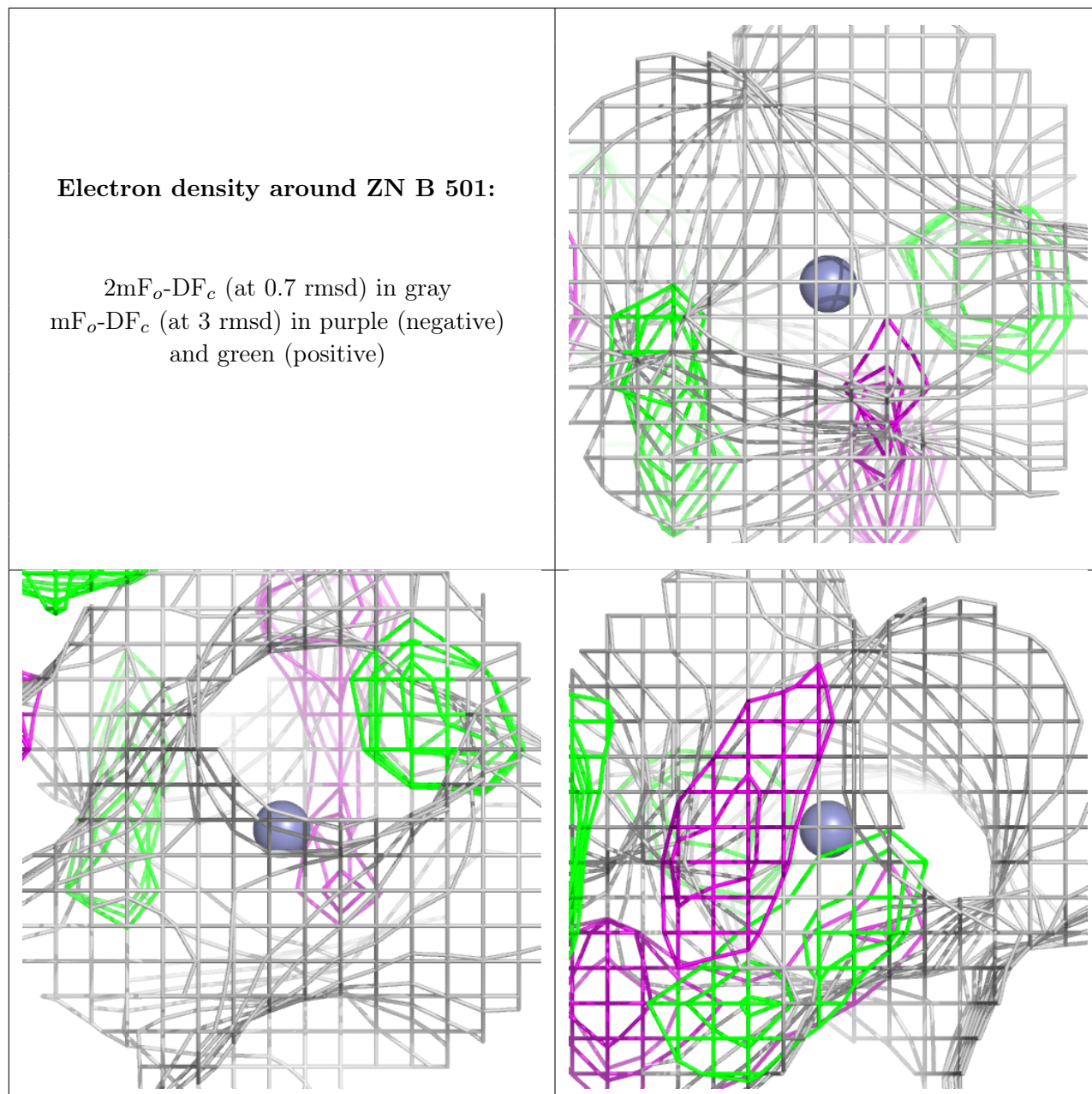
Electron density around MG A 504:

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and green (positive)



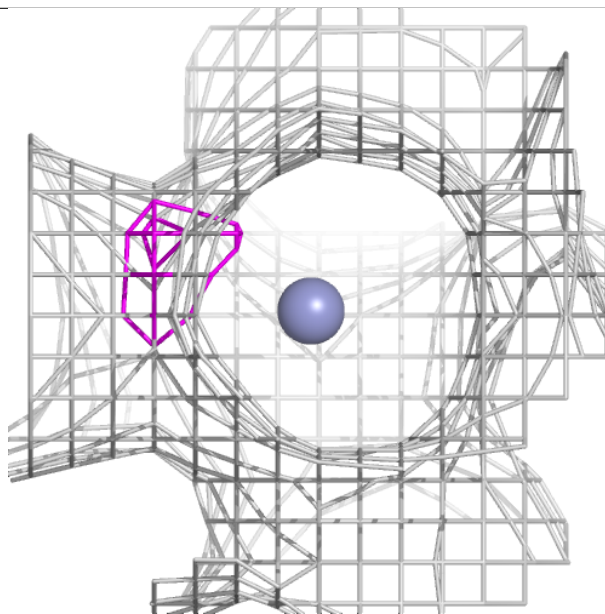
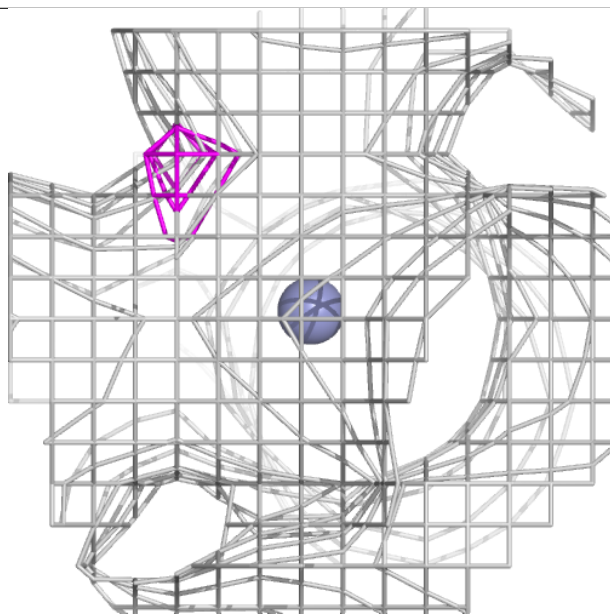
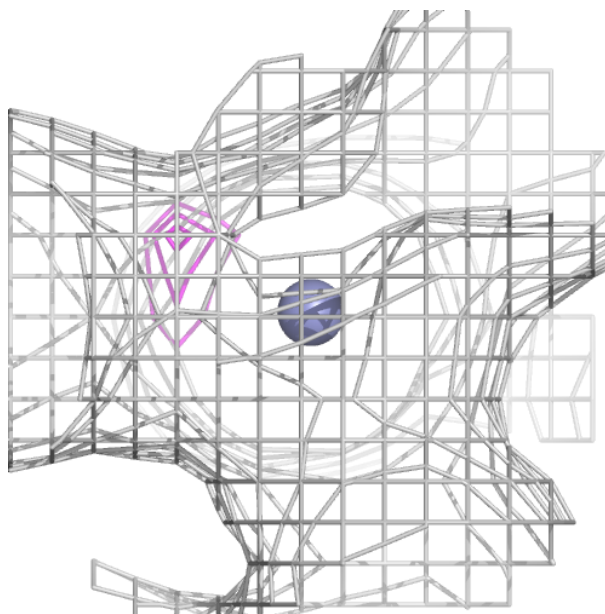
Electron density around ZN B 501:

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and green (positive)



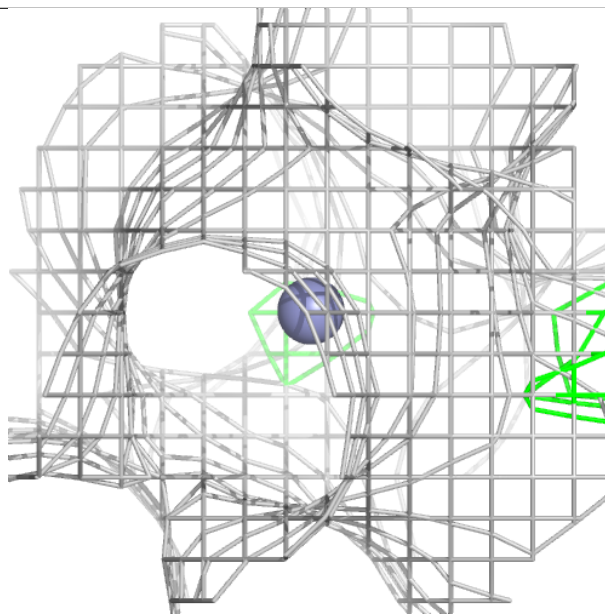
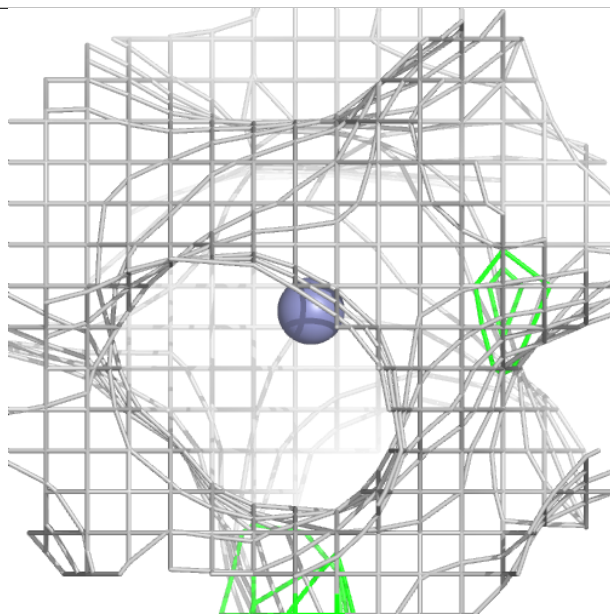
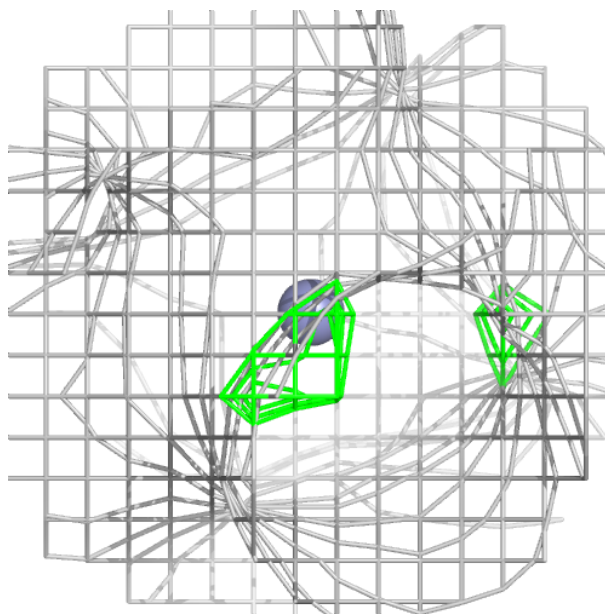
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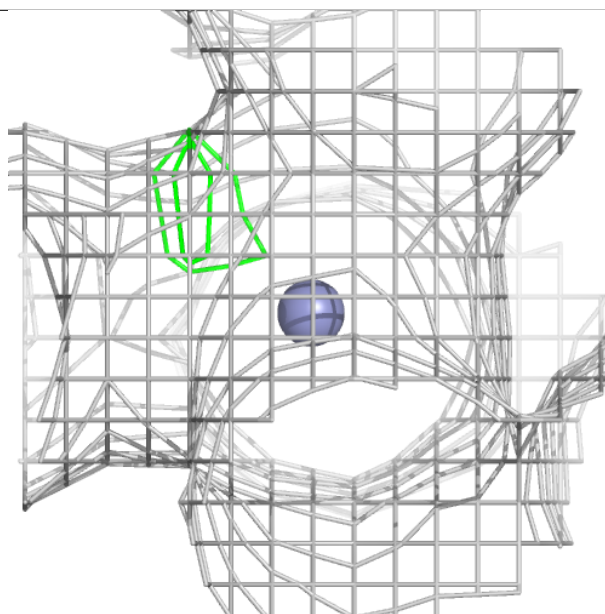
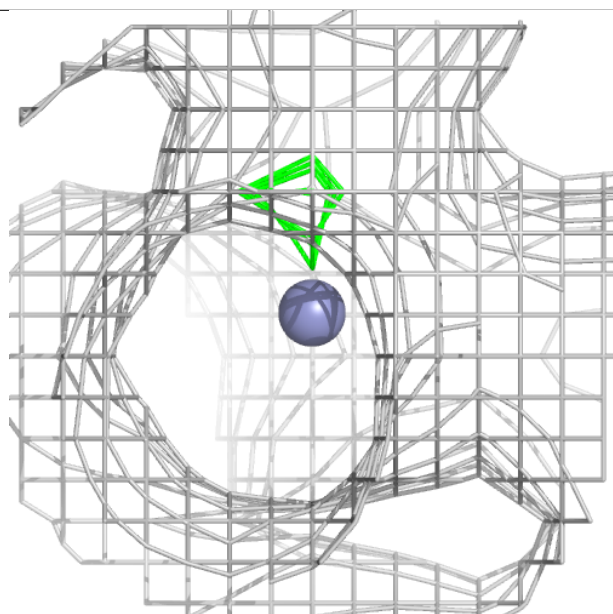
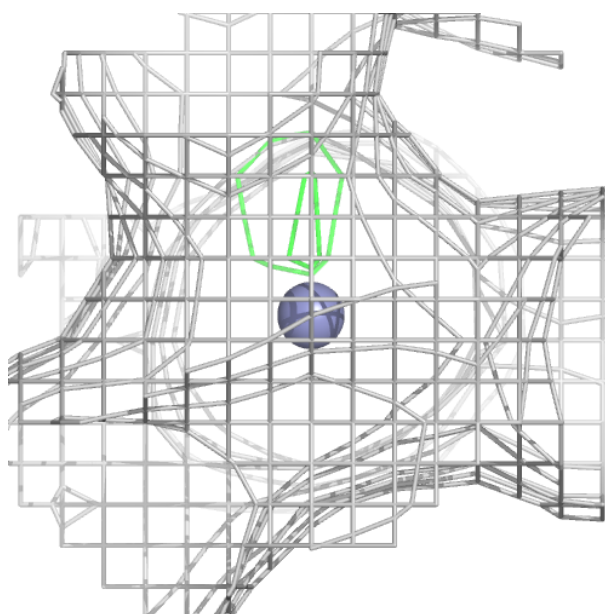
Electron density around ZN D 501:

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and green (positive)



Electron density around ZN C 501:

$2mF_o-DF_c$ (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.