



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 15, 2026 – 12:46 AM UTC

PDB ID : 9NWH / pdb_00009nwh
Title : Long-wavelength SAD Crystal Structure of the Third Immunoglobulin-Like Domain of Human Muscle-Specific Kinase (MuSK)
Authors : Canciani, A.; Palamini, M.; Forneris, F.
Deposited on : 2025-03-22
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

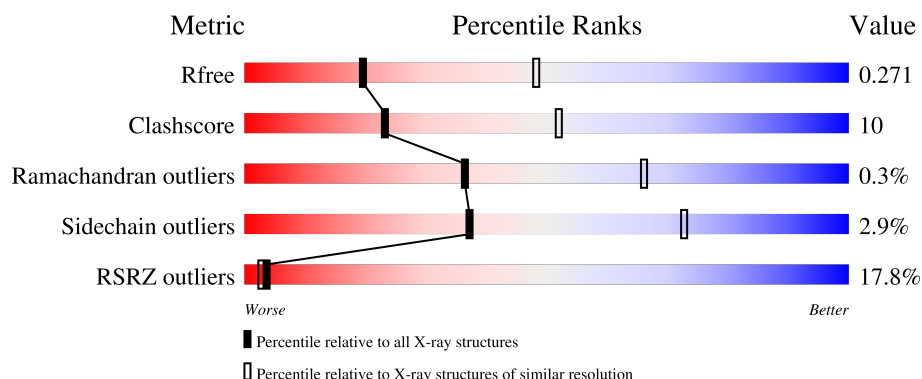
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	104	<div> <div>12%</div> <div>74%</div> <div>19%</div> <div>• •</div> </div>
1	B	104	<div> <div>25%</div> <div>61%</div> <div>29%</div> <div>• 8%</div> </div>
1	C	104	<div> <div>20%</div> <div>76%</div> <div>14%</div> <div>• 7%</div> </div>
1	D	104	<div> <div>12%</div> <div>70%</div> <div>20%</div> <div>• 9%</div> </div>
1	E	104	<div> <div>17%</div> <div>75%</div> <div>17%</div> <div>• 7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	104	
1	G	104	
1	H	104	
1	I	104	
1	J	104	

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
3	BR	D	403	-	-	X	-
4	PEG	D	405	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7348 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 Muscle, skeletal receptor tyrosine-protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	100	Total	C	N	O	S	0	5	0
			774	492	136	144	2			
1	B	96	Total	C	N	O	S	0	1	0
			719	452	127	138	2			
1	C	97	Total	C	N	O	S	0	1	0
			726	458	127	139	2			
1	D	95	Total	C	N	O	S	0	1	0
			716	451	128	135	2			
1	E	97	Total	C	N	O	S	0	0	0
			721	453	127	139	2			
1	F	94	Total	C	N	O	S	0	0	0
			703	443	124	134	2			
1	G	96	Total	C	N	O	S	0	0	0
			714	449	126	137	2			
1	H	97	Total	C	N	O	S	0	0	0
			719	452	127	138	2			
1	I	96	Total	C	N	O	S	0	1	0
			722	454	127	139	2			
1	J	98	Total	C	N	O	S	0	0	0
			726	456	128	140	2			

There are 110 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	204	THR	-	expression tag	UNP O15146
A	205	GLY	-	expression tag	UNP O15146
A	206	GLU	-	expression tag	UNP O15146
A	207	PHE	-	expression tag	UNP O15146
A	208	THR	-	expression tag	UNP O15146
A	209	SER	-	expression tag	UNP O15146
A	210	GLY	-	expression tag	UNP O15146
A	211	SER	-	expression tag	UNP O15146
A	305	ALA	-	expression tag	UNP O15146

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Chain	Residue	Modelled	Actual	Comment	Reference
A	306	ALA	-	expression tag	UNP O15146
A	307	ALA	-	expression tag	UNP O15146
B	204	THR	-	expression tag	UNP O15146
B	205	GLY	-	expression tag	UNP O15146
B	206	GLU	-	expression tag	UNP O15146
B	207	PHE	-	expression tag	UNP O15146
B	208	THR	-	expression tag	UNP O15146
B	209	SER	-	expression tag	UNP O15146
B	210	GLY	-	expression tag	UNP O15146
B	211	SER	-	expression tag	UNP O15146
B	305	ALA	-	expression tag	UNP O15146
B	306	ALA	-	expression tag	UNP O15146
B	307	ALA	-	expression tag	UNP O15146
C	204	THR	-	expression tag	UNP O15146
C	205	GLY	-	expression tag	UNP O15146
C	206	GLU	-	expression tag	UNP O15146
C	207	PHE	-	expression tag	UNP O15146
C	208	THR	-	expression tag	UNP O15146
C	209	SER	-	expression tag	UNP O15146
C	210	GLY	-	expression tag	UNP O15146
C	211	SER	-	expression tag	UNP O15146
C	305	ALA	-	expression tag	UNP O15146
C	306	ALA	-	expression tag	UNP O15146
C	307	ALA	-	expression tag	UNP O15146
D	204	THR	-	expression tag	UNP O15146
D	205	GLY	-	expression tag	UNP O15146
D	206	GLU	-	expression tag	UNP O15146
D	207	PHE	-	expression tag	UNP O15146
D	208	THR	-	expression tag	UNP O15146
D	209	SER	-	expression tag	UNP O15146
D	210	GLY	-	expression tag	UNP O15146
D	211	SER	-	expression tag	UNP O15146
D	305	ALA	-	expression tag	UNP O15146
D	306	ALA	-	expression tag	UNP O15146
D	307	ALA	-	expression tag	UNP O15146
E	204	THR	-	expression tag	UNP O15146
E	205	GLY	-	expression tag	UNP O15146
E	206	GLU	-	expression tag	UNP O15146
E	207	PHE	-	expression tag	UNP O15146
E	208	THR	-	expression tag	UNP O15146
E	209	SER	-	expression tag	UNP O15146
E	210	GLY	-	expression tag	UNP O15146

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Chain	Residue	Modelled	Actual	Comment	Reference
E	211	SER	-	expression tag	UNP O15146
E	305	ALA	-	expression tag	UNP O15146
E	306	ALA	-	expression tag	UNP O15146
E	307	ALA	-	expression tag	UNP O15146
F	204	THR	-	expression tag	UNP O15146
F	205	GLY	-	expression tag	UNP O15146
F	206	GLU	-	expression tag	UNP O15146
F	207	PHE	-	expression tag	UNP O15146
F	208	THR	-	expression tag	UNP O15146
F	209	SER	-	expression tag	UNP O15146
F	210	GLY	-	expression tag	UNP O15146
F	211	SER	-	expression tag	UNP O15146
F	305	ALA	-	expression tag	UNP O15146
F	306	ALA	-	expression tag	UNP O15146
F	307	ALA	-	expression tag	UNP O15146
G	204	THR	-	expression tag	UNP O15146
G	205	GLY	-	expression tag	UNP O15146
G	206	GLU	-	expression tag	UNP O15146
G	207	PHE	-	expression tag	UNP O15146
G	208	THR	-	expression tag	UNP O15146
G	209	SER	-	expression tag	UNP O15146
G	210	GLY	-	expression tag	UNP O15146
G	211	SER	-	expression tag	UNP O15146
G	305	ALA	-	expression tag	UNP O15146
G	306	ALA	-	expression tag	UNP O15146
G	307	ALA	-	expression tag	UNP O15146
H	204	THR	-	expression tag	UNP O15146
H	205	GLY	-	expression tag	UNP O15146
H	206	GLU	-	expression tag	UNP O15146
H	207	PHE	-	expression tag	UNP O15146
H	208	THR	-	expression tag	UNP O15146
H	209	SER	-	expression tag	UNP O15146
H	210	GLY	-	expression tag	UNP O15146
H	211	SER	-	expression tag	UNP O15146
H	305	ALA	-	expression tag	UNP O15146
H	306	ALA	-	expression tag	UNP O15146
H	307	ALA	-	expression tag	UNP O15146
I	204	THR	-	expression tag	UNP O15146
I	205	GLY	-	expression tag	UNP O15146
I	206	GLU	-	expression tag	UNP O15146
I	207	PHE	-	expression tag	UNP O15146
I	208	THR	-	expression tag	UNP O15146

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Chain	Residue	Modelled	Actual	Comment	Reference
I	209	SER	-	expression tag	UNP O15146
I	210	GLY	-	expression tag	UNP O15146
I	211	SER	-	expression tag	UNP O15146
I	305	ALA	-	expression tag	UNP O15146
I	306	ALA	-	expression tag	UNP O15146
I	307	ALA	-	expression tag	UNP O15146
J	204	THR	-	expression tag	UNP O15146
J	205	GLY	-	expression tag	UNP O15146
J	206	GLU	-	expression tag	UNP O15146
J	207	PHE	-	expression tag	UNP O15146
J	208	THR	-	expression tag	UNP O15146
J	209	SER	-	expression tag	UNP O15146
J	210	GLY	-	expression tag	UNP O15146
J	211	SER	-	expression tag	UNP O15146
J	305	ALA	-	expression tag	UNP O15146
J	306	ALA	-	expression tag	UNP O15146
J	307	ALA	-	expression tag	UNP O15146

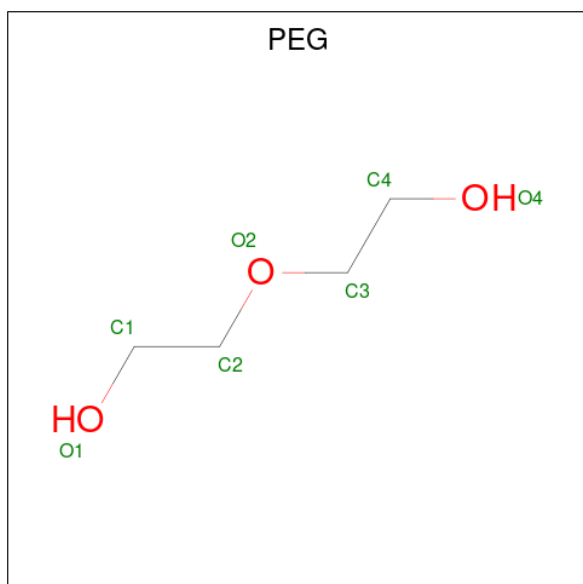
- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	5	Total K 5 5	0	0
2	B	2	Total K 2 2	0	0
2	C	3	Total K 3 3	0	0
2	D	2	Total K 2 2	0	0
2	E	3	Total K 3 3	0	0
2	F	1	Total K 1 1	0	0
2	G	3	Total K 3 3	0	0
2	H	2	Total K 2 2	0	0
2	I	3	Total K 3 3	0	0
2	J	2	Total K 2 2	0	0

- Molecule 3 is BROMIDE ION (CCD ID: BR) (formula: Br).

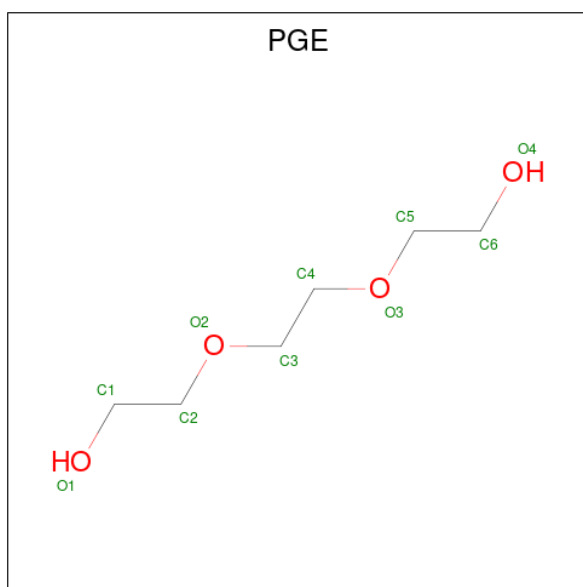
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Br	0	0
			1	1		
3	D	2	Total	Br	0	0
			2	2		
3	H	1	Total	Br	0	0
			1	1		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		
4	I	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	I	1	Total	C	O	0	0
			10	6	4		

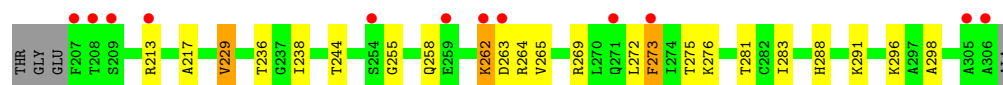
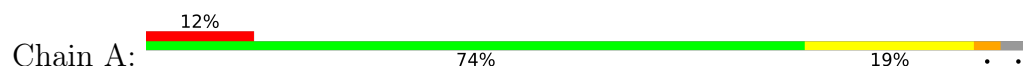
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	O	0	0
			3	3		
6	B	5	Total	O	0	0
			5	5		
6	C	2	Total	O	0	0
			2	2		
6	D	5	Total	O	0	0
			5	5		
6	E	11	Total	O	0	0
			11	11		
6	F	3	Total	O	0	0
			3	3		
6	G	1	Total	O	0	0
			1	1		
6	H	5	Total	O	0	0
			5	5		
6	I	2	Total	O	0	0
			2	2		
6	J	10	Total	O	0	0
			10	10		

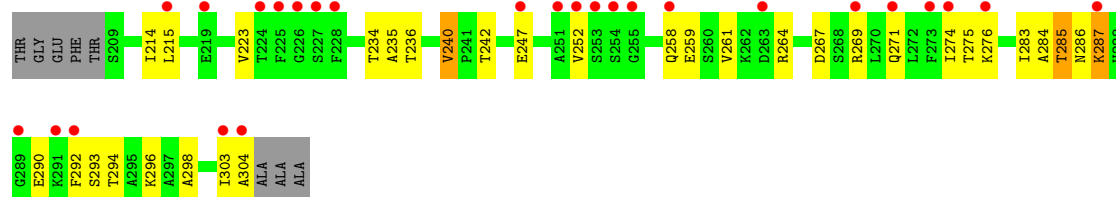
3 Residue-property plots [i](#)

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.

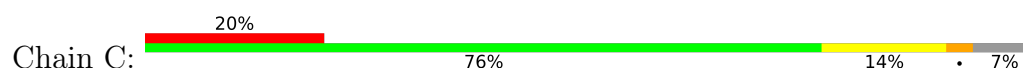
- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase



- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase



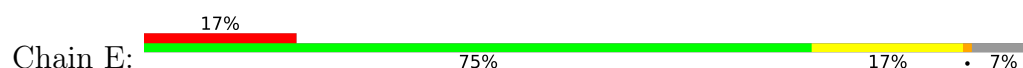
- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase

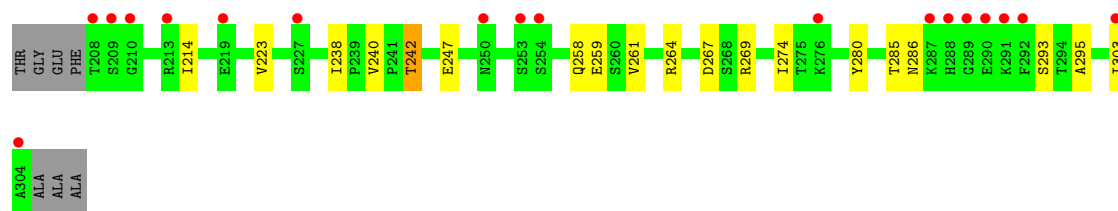


- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase

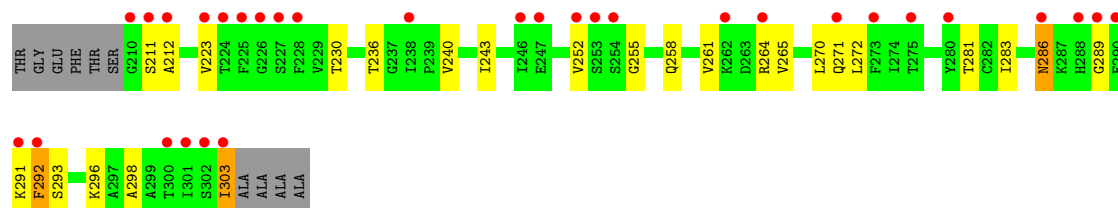


- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase

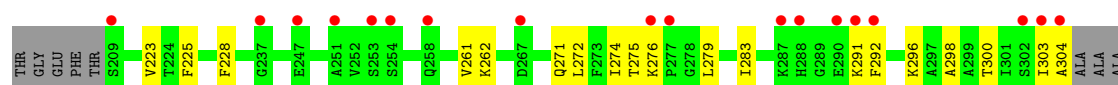
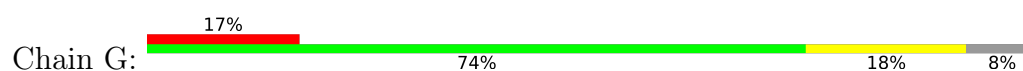




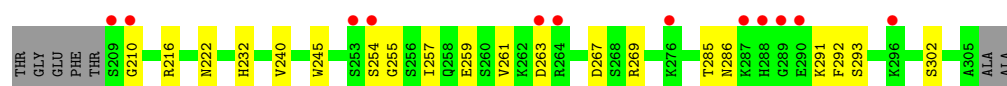
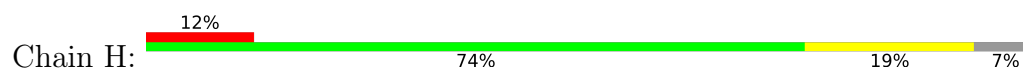
- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase



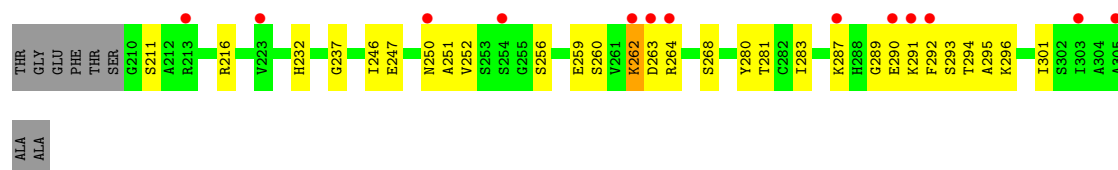
- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase



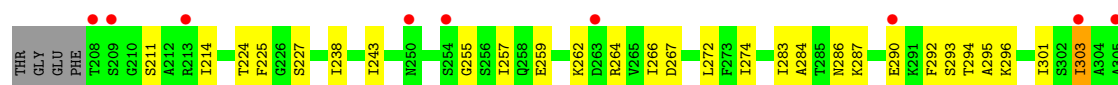
- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase



- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase



- Molecule 1: Muscle, skeletal receptor tyrosine-protein kinase



ALA
ALA

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.16Å 49.53Å 143.76Å 90.00° 92.21° 90.00°	Depositor
Resolution (Å)	47.88 – 2.80 47.88 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.88-2.80) 99.7 (47.88-2.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	50.70 (at 2.82Å)	Xtriage
Refinement program	PHENIX (1.20_4459: ???)	Depositor
R, R_{free}	0.239 , 0.268 0.246 , 0.271	Depositor DCC
R_{free} test set	1433 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for h,-k,-l	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	7348	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.98% 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: PEG, K, PGE, BR

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	0.35	0/804	0.61	0/1091
1	B	0.43	0/735	0.68	0/999
1	C	0.30	0/742	0.53	0/1009
1	D	0.41	0/732	0.62	0/994
1	E	0.37	0/734	0.61	0/998
1	F	0.46	1/716 (0.1%)	0.65	0/973
1	G	0.35	0/727	0.55	0/988
1	H	0.39	0/732	0.58	0/995
1	I	0.43	0/735	0.61	0/999
1	J	0.39	0/739	0.64	0/1005
All	All	0.39	1/7396 (0.0%)	0.61	0/10051

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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	264	ARG	CD-NE	5.22	1.53	1.46

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	213	ARG	Sidechain

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	774	0	798	16	0
1	B	719	0	728	20	0
1	C	726	0	740	14	0
1	D	716	0	730	14	0
1	E	721	0	729	10	0
1	F	703	0	712	17	0
1	G	714	0	722	12	0
1	H	719	0	726	17	0
1	I	722	0	726	24	0
1	J	726	0	734	20	0
2	A	5	0	0	0	0
2	B	2	0	0	0	0
2	C	3	0	0	0	0
2	D	2	0	0	0	0
2	E	3	0	0	0	0
2	F	1	0	0	0	0
2	G	3	0	0	0	0
2	H	2	0	0	0	0
2	I	3	0	0	0	0
2	J	2	0	0	0	0
3	A	1	0	0	0	0
3	D	2	0	0	4	0
3	H	1	0	0	1	0
4	D	14	0	20	6	0
4	I	7	0	10	0	0
5	I	10	0	13	1	0
6	A	3	0	0	4	0
6	B	5	0	0	0	0
6	C	2	0	0	0	0
6	D	5	0	0	0	0
6	E	11	0	0	2	0
6	F	3	0	0	0	0
6	G	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	H	5	0	0	1	0
6	I	2	0	0	0	0
6	J	10	0	0	0	0
All	All	7348	0	7388	151	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 10.

The worst 5 of 151 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)
3:D:403:BR:BR	4:D:405:PEG:H41	2.13	1.02
1:H:269:ARG:HD2	3:H:403:BR:BR	2.31	0.84
1:B:247:GLU:HB2	1:B:252:VAL:HG12	1.62	0.82
3:D:403:BR:BR	4:D:405:PEG:C4	2.83	0.80
3:D:403:BR:BR	4:D:405:PEG:H21	2.39	0.77

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	103/104 (99%)	99 (96%)	3 (3%)	1 (1%)	12	38
1	B	95/104 (91%)	93 (98%)	2 (2%)	0	100	100
1	C	96/104 (92%)	94 (98%)	1 (1%)	1 (1%)	12	38
1	D	94/104 (90%)	92 (98%)	2 (2%)	0	100	100
1	E	95/104 (91%)	93 (98%)	2 (2%)	0	100	100
1	F	92/104 (88%)	89 (97%)	3 (3%)	0	100	100
1	G	94/104 (90%)	92 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	95/104 (91%)	93 (98%)	2 (2%)	0	100	100
1	I	95/104 (91%)	94 (99%)	0	1 (1%)	11	36
1	J	96/104 (92%)	94 (98%)	2 (2%)	0	100	100
All	All	955/1040 (92%)	933 (98%)	19 (2%)	3 (0%)	36	66

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	264	ARG
1	C	264	ARG
1	I	263	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	86/83 (104%)	82 (95%)	4 (5%)	23	57
1	B	80/83 (96%)	74 (92%)	6 (8%)	12	37
1	C	81/83 (98%)	78 (96%)	3 (4%)	30	65
1	D	79/83 (95%)	76 (96%)	3 (4%)	29	64
1	E	80/83 (96%)	78 (98%)	2 (2%)	42	76
1	F	78/83 (94%)	75 (96%)	3 (4%)	29	64
1	G	79/83 (95%)	77 (98%)	2 (2%)	42	76
1	H	79/83 (95%)	79 (100%)	0	100	100
1	I	79/83 (95%)	78 (99%)	1 (1%)	61	86
1	J	80/83 (96%)	79 (99%)	1 (1%)	61	86
All	All	801/830 (96%)	776 (97%)	25 (3%)	37	70

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	246	ILE
1	E	285	THR
1	J	303	ILE
1	E	242	THR
1	F	286	ASN

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

Mol	Chain	Res	Type
1	A	232	HIS
1	D	232	HIS
1	E	232	HIS
1	H	288	HIS
1	J	222	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 30 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
5	PGE	I	404	2	9,9,9	0.35	0	8,8,8	0.52	0
4	PEG	D	406	-	6,6,6	0.21	0	5,5,5	0.16	0
4	PEG	D	405	-	6,6,6	0.16	0	5,5,5	0.14	0
4	PEG	I	405	2	6,6,6	0.16	0	5,5,5	0.10	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
5	PGE	I	404	2	-	3/7/7/7	-
4	PEG	D	406	-	-	1/4/4/4	-
4	PEG	D	405	-	-	1/4/4/4	-
4	PEG	I	405	2	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	I	404	PGE	O3-C5-C6-O4
4	D	405	PEG	C4-C3-O2-C2
4	I	405	PEG	O1-C1-C2-O2
4	I	405	PEG	O2-C3-C4-O4
4	I	405	PEG	C4-C3-O2-C2

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	404	PGE	1	0
4	D	406	PEG	1	0
4	D	405	PEG	5	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	100/104 (96%)	0.95	12 (12%) 9 6	14, 28, 58, 77	5 (5%)
1	B	96/104 (92%)	1.24	26 (27%) 1 1	13, 37, 67, 78	1 (1%)
1	C	97/104 (93%)	1.22	21 (21%) 2 2	19, 37, 73, 83	1 (1%)
1	D	95/104 (91%)	0.62	12 (12%) 8 6	14, 25, 55, 67	1 (1%)
1	E	97/104 (93%)	0.79	18 (18%) 3 2	16, 28, 68, 91	0
1	F	94/104 (90%)	1.60	31 (32%) 1 1	21, 43, 77, 92	0
1	G	96/104 (92%)	1.14	18 (18%) 3 2	23, 39, 77, 87	0
1	H	97/104 (93%)	0.86	12 (12%) 8 6	24, 32, 69, 84	0
1	I	96/104 (92%)	0.95	13 (13%) 7 5	18, 34, 61, 77	1 (1%)
1	J	98/104 (94%)	0.53	9 (9%) 14 10	12, 24, 51, 66	0
All	All	966/1040 (92%)	0.99	172 (17%) 4 3	12, 32, 69, 92	9 (0%)

The worst 5 of 172 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	273	PHE	8.2
1	H	288	HIS	6.6
1	C	263	ASP	6.3
1	C	228	PHE	6.1
1	E	291	LYS	5.8

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

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

6.3 Carbohydrates ⓘ

There are no 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.

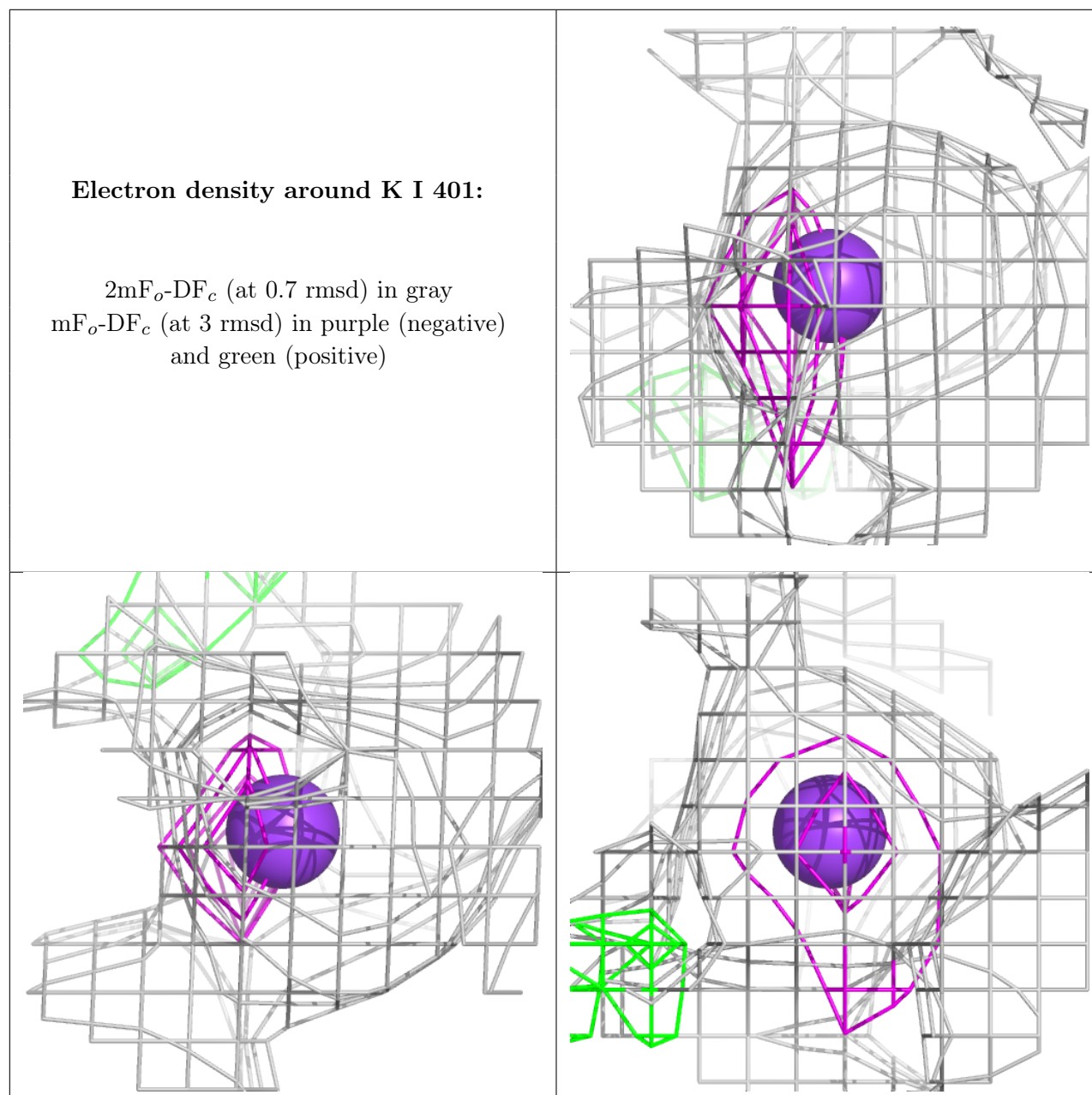
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	PEG	I	405	7/7	0.72	0.22	29,36,54,68	0
5	PGE	I	404	10/10	0.72	0.18	30,37,48,57	0
2	K	I	401	1/1	0.76	0.20	25,25,25,25	0
2	K	C	402	1/1	0.78	0.25	88,88,88,88	0
4	PEG	D	405	7/7	0.80	0.21	24,33,41,59	0
2	K	E	403	1/1	0.81	0.18	68,68,68,68	0
2	K	J	402	1/1	0.82	0.14	48,48,48,48	0
4	PEG	D	406	7/7	0.84	0.15	29,32,36,38	0
2	K	A	403	1/1	0.84	0.17	66,66,66,66	0
2	K	E	401	1/1	0.84	0.14	42,42,42,42	0
2	K	I	403	1/1	0.86	0.10	50,50,50,50	0
2	K	H	402	1/1	0.86	0.16	65,65,65,65	0
2	K	I	402	1/1	0.86	0.21	43,43,43,43	1
2	K	B	402	1/1	0.88	0.10	57,57,57,57	0
2	K	E	402	1/1	0.88	0.18	36,36,36,36	0
2	K	A	404	1/1	0.89	0.10	55,55,55,55	0
2	K	G	401	1/1	0.89	0.18	73,73,73,73	0
2	K	G	403	1/1	0.89	0.13	60,60,60,60	0
2	K	A	405	1/1	0.90	0.13	53,53,53,53	0
2	K	A	402	1/1	0.91	0.10	24,24,24,24	0
2	K	D	402	1/1	0.92	0.12	55,55,55,55	0
2	K	C	403	1/1	0.92	0.14	52,52,52,52	0
2	K	H	401	1/1	0.92	0.12	25,25,25,25	0
3	BR	A	406	1/1	0.93	0.20	55,55,55,55	0
2	K	D	401	1/1	0.95	0.13	20,20,20,20	0
2	K	J	401	1/1	0.95	0.15	19,19,19,19	0
3	BR	D	403	1/1	0.95	0.20	50,50,50,50	0
3	BR	H	403	1/1	0.95	0.16	38,38,38,38	0
2	K	C	401	1/1	0.96	0.16	19,19,19,19	0
3	BR	D	404	1/1	0.97	0.23	39,39,39,39	0
2	K	F	401	1/1	0.97	0.14	11,11,11,11	0
2	K	B	401	1/1	0.97	0.06	4,4,4,4	0

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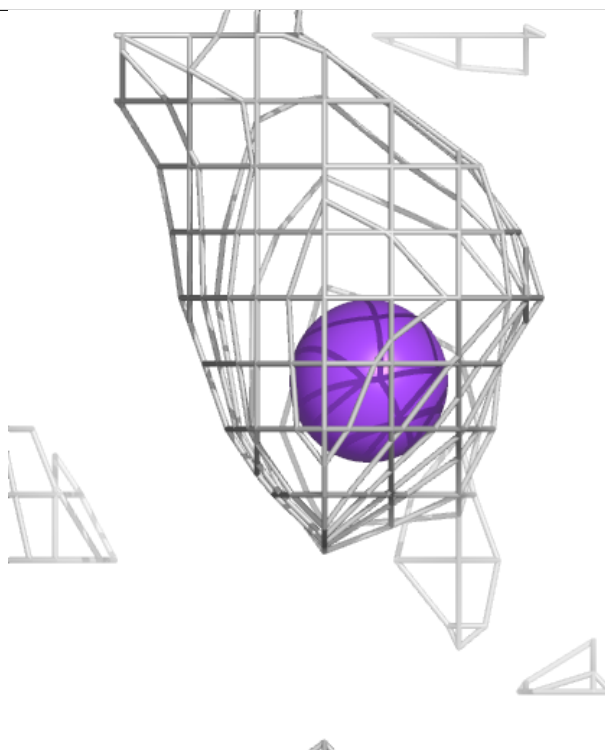
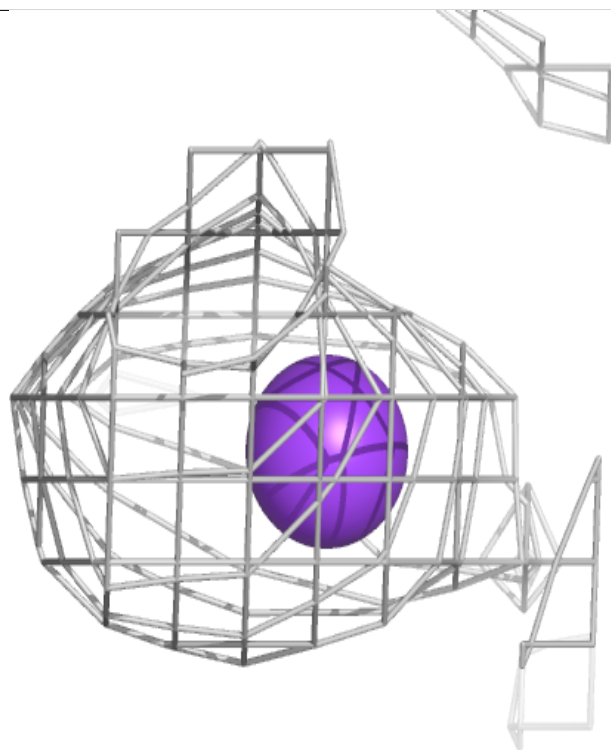
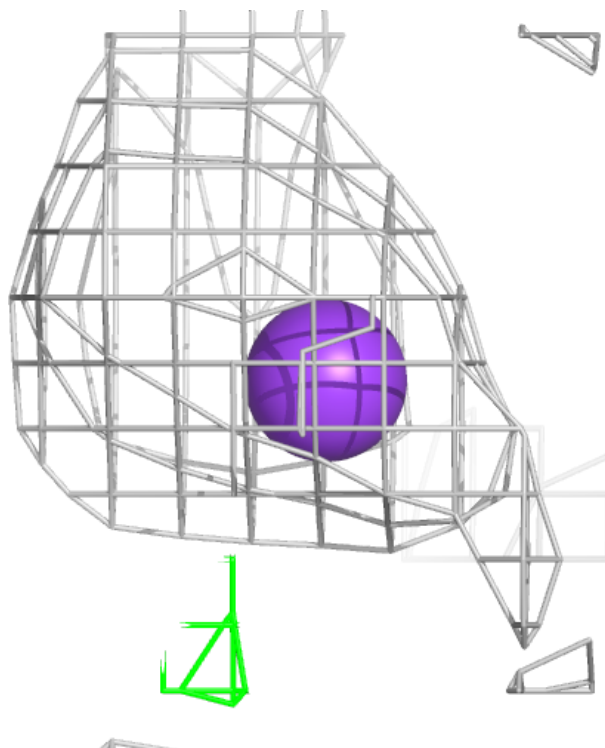
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	K	A	401	1/1	0.98	0.11	1,1,1,1	0
2	K	G	402	1/1	0.98	0.05	2,2,2,2	0

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.



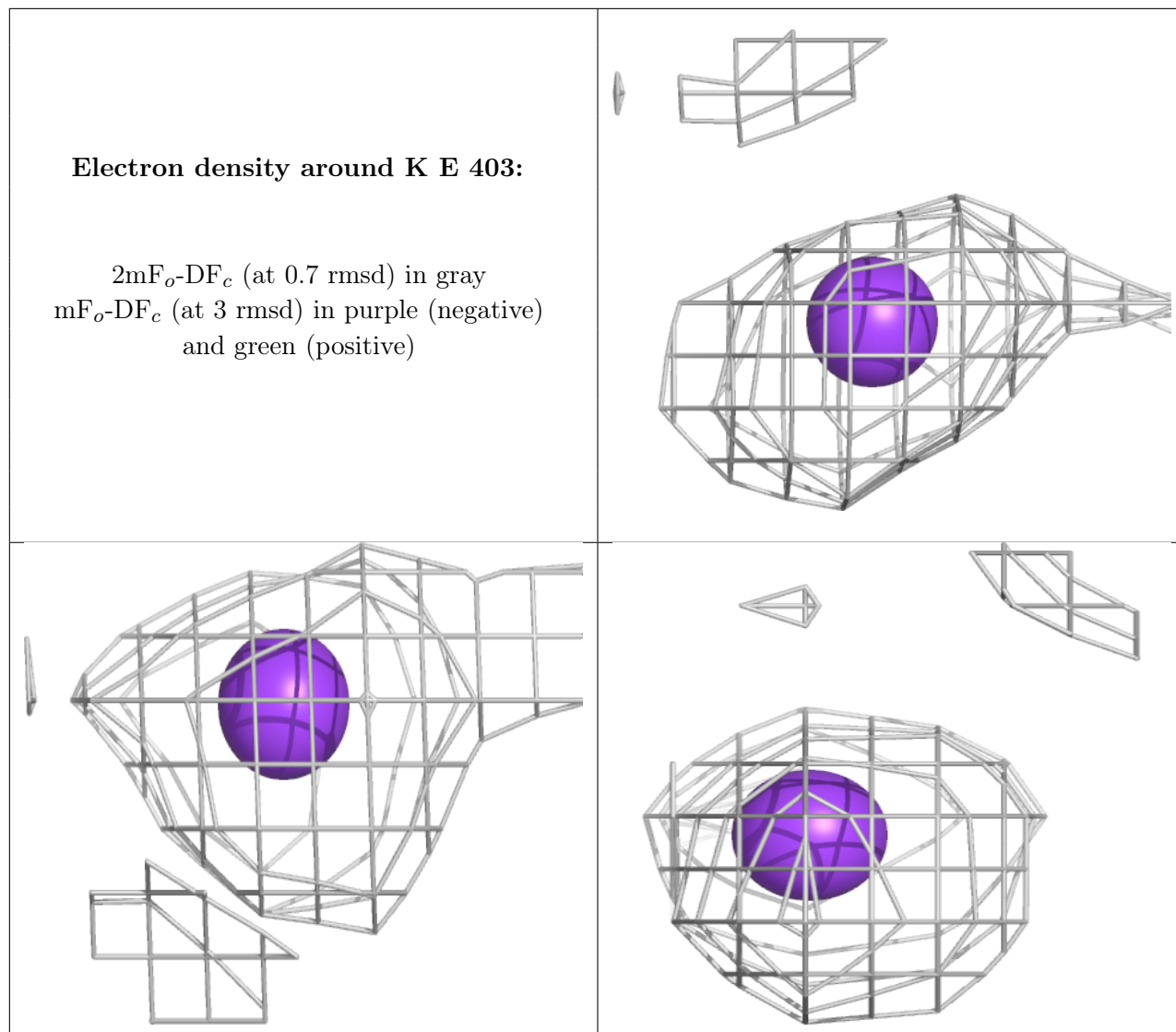
Electron density around K C 402:

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



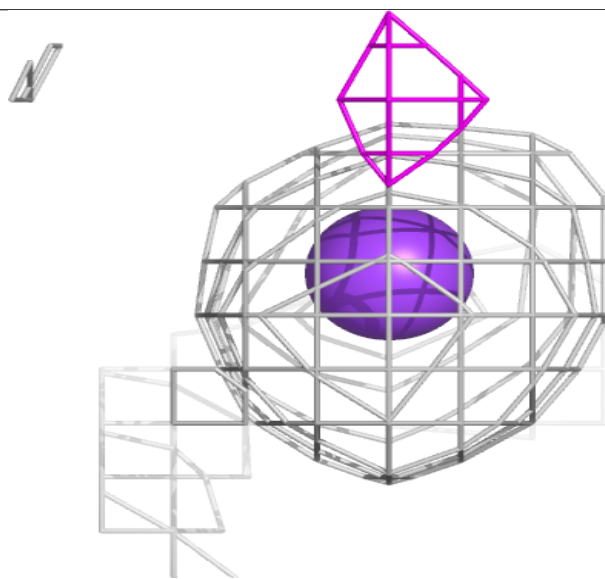
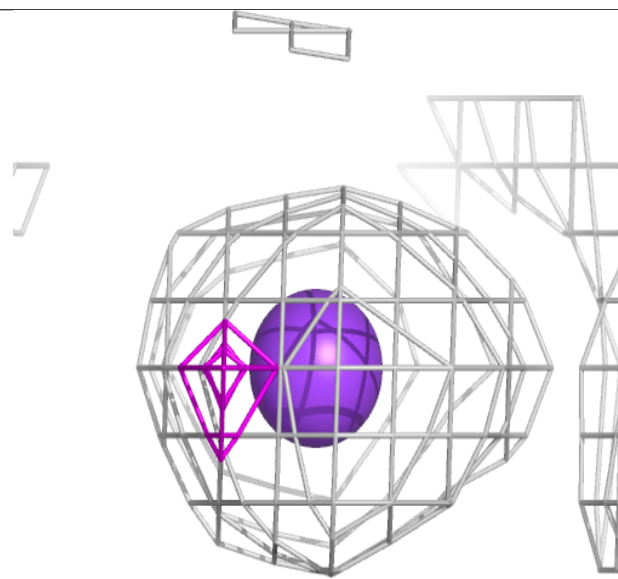
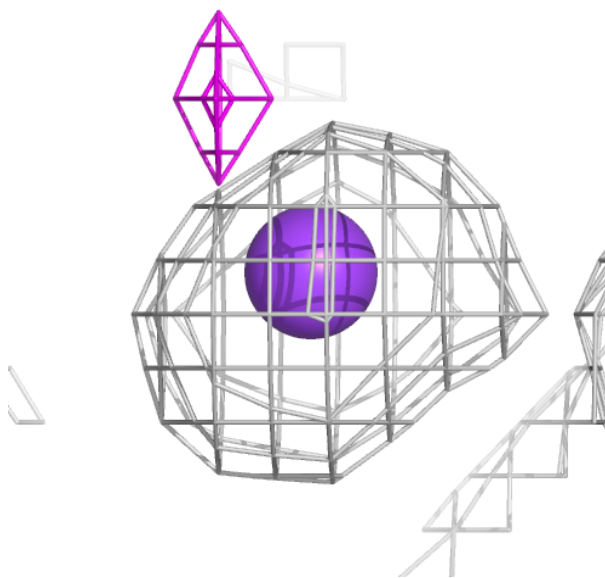
Electron density around K E 403:

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



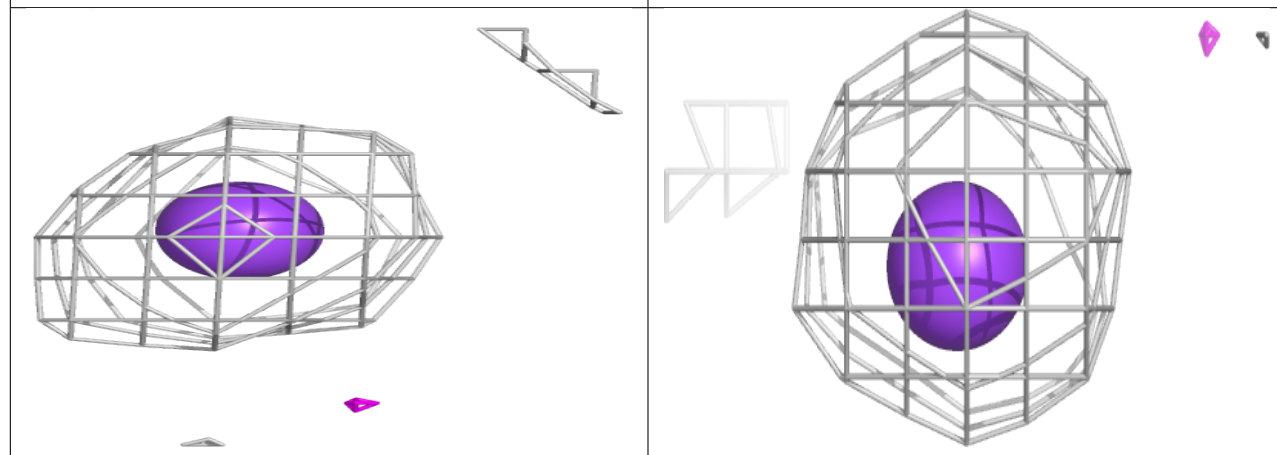
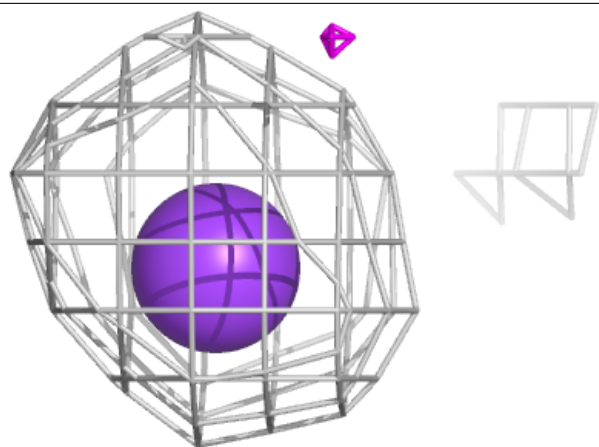
Electron density around K J 402:

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and green (positive)



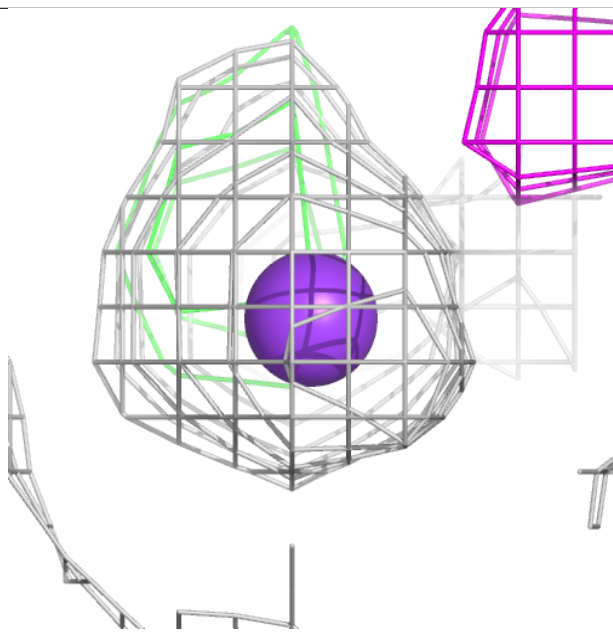
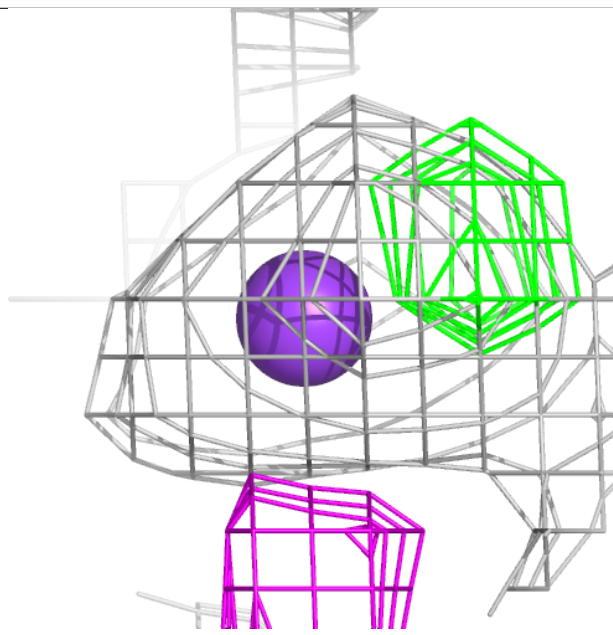
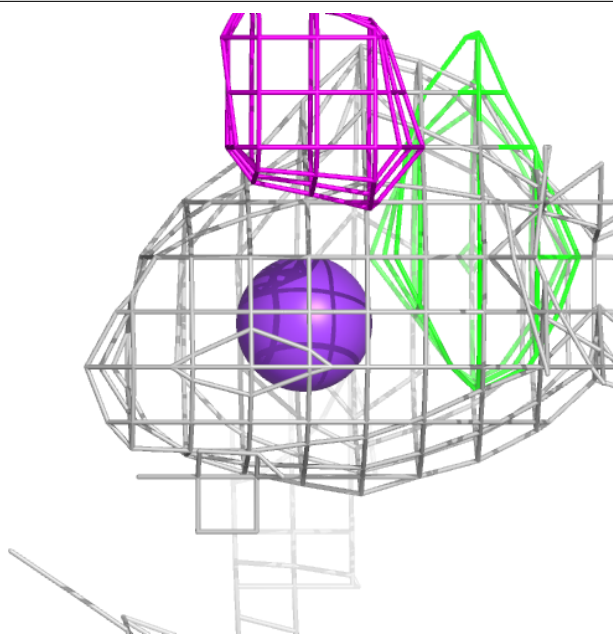
Electron density around K A 403:

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and green (positive)



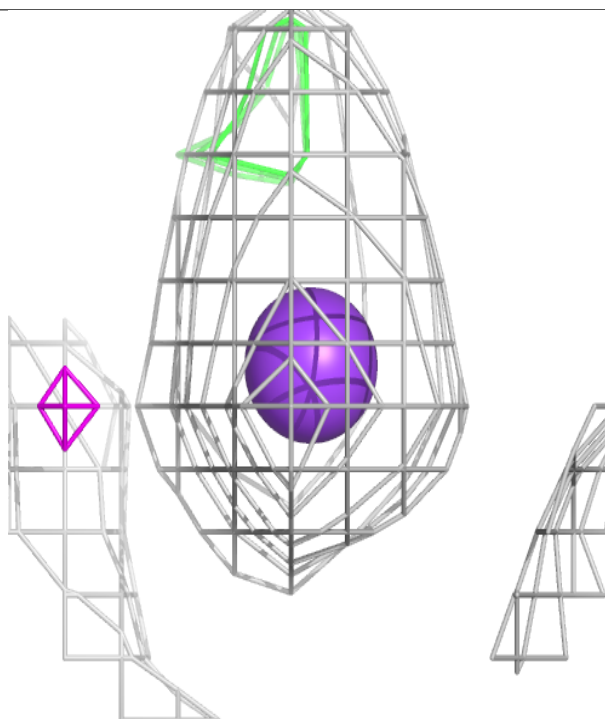
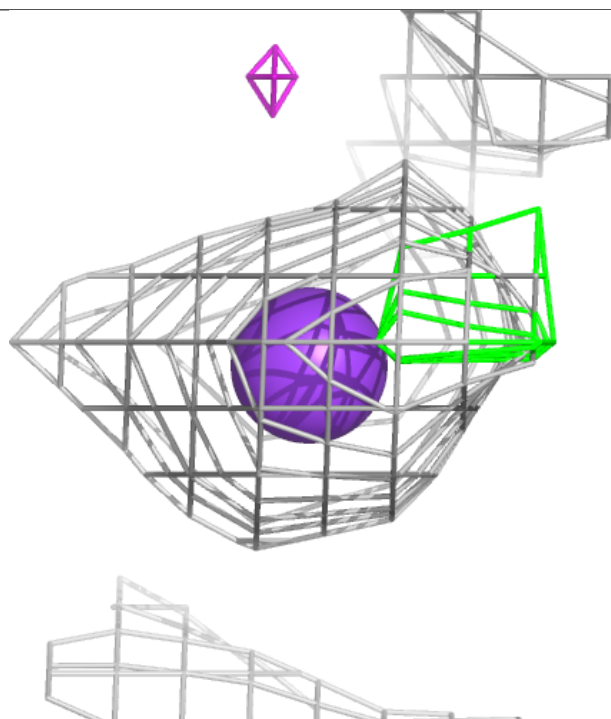
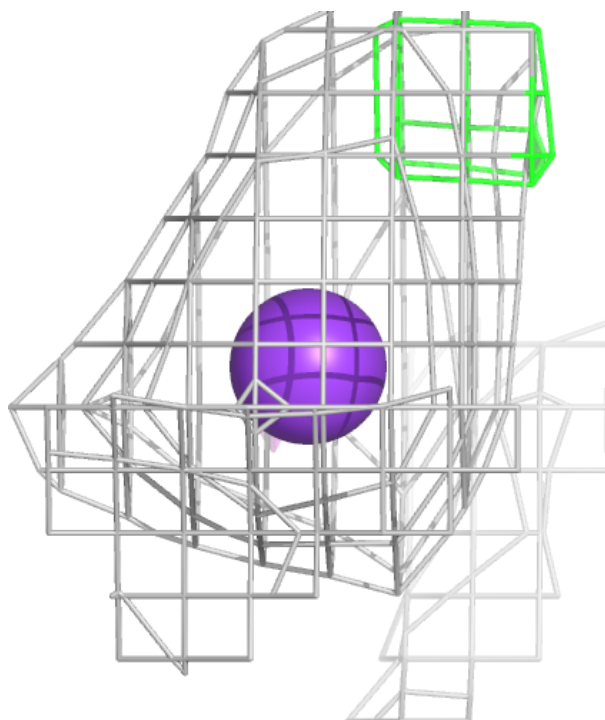
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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



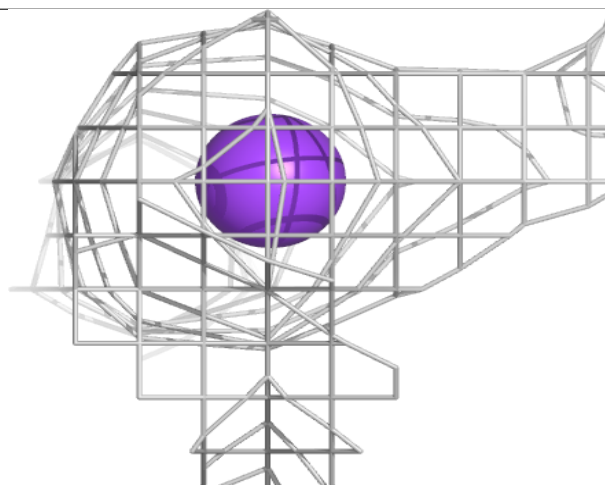
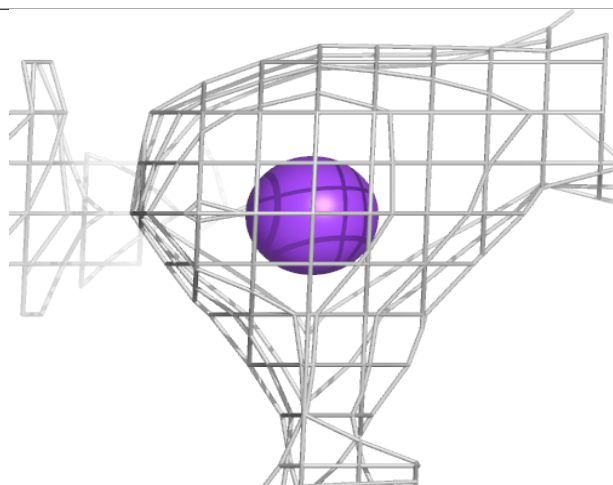
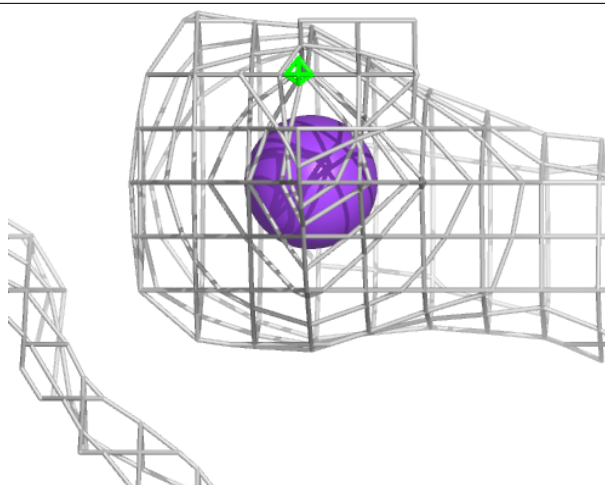
Electron density around K I 403:

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and green (positive)



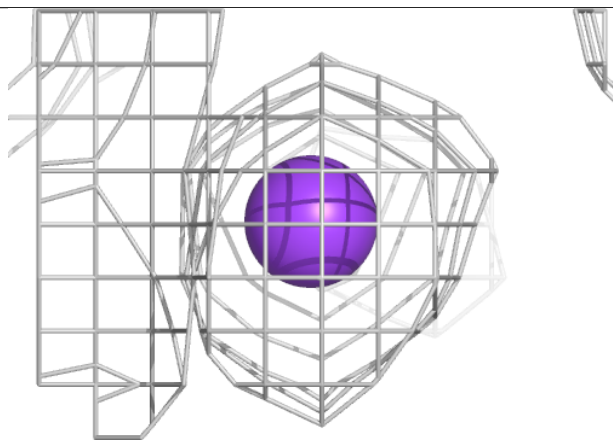
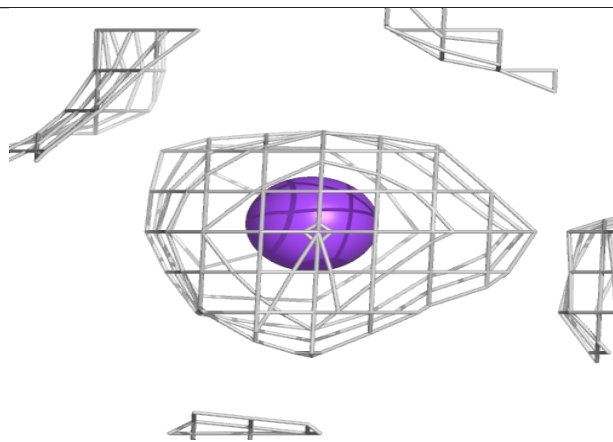
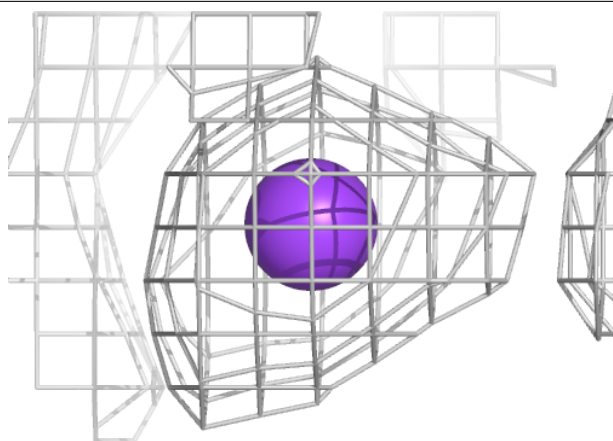
Electron density around K H 402:

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and green (positive)



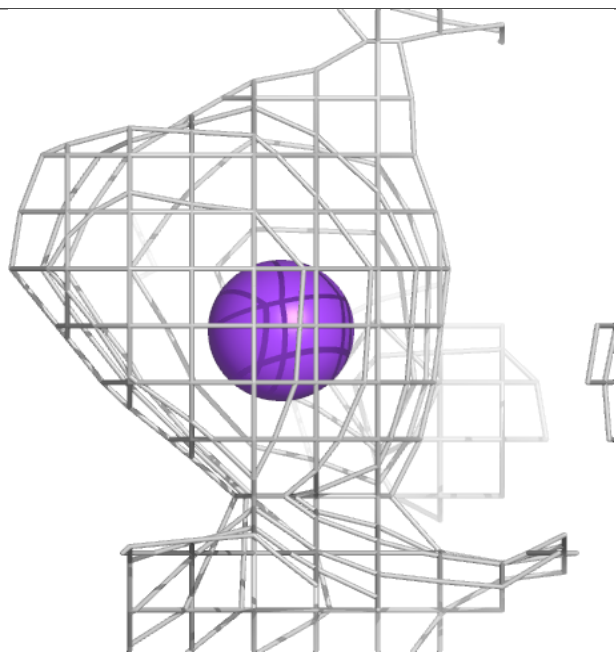
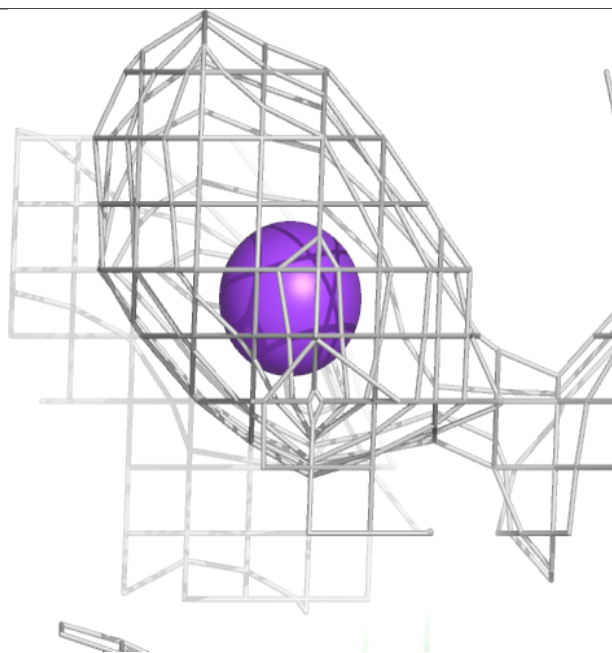
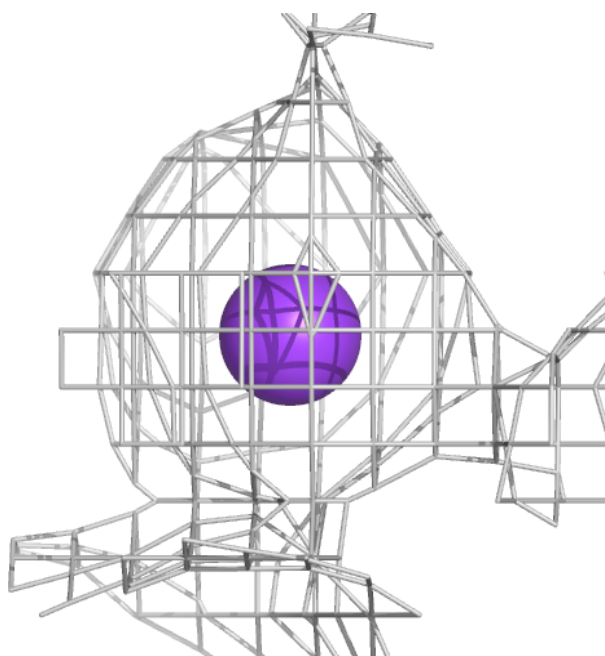
Electron density around K I 402:

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



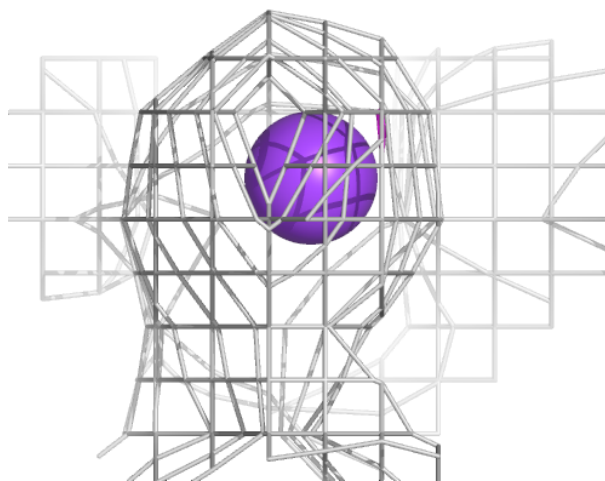
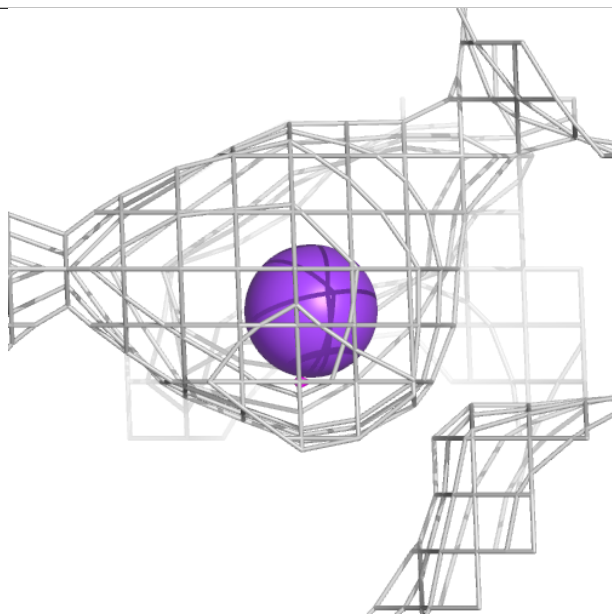
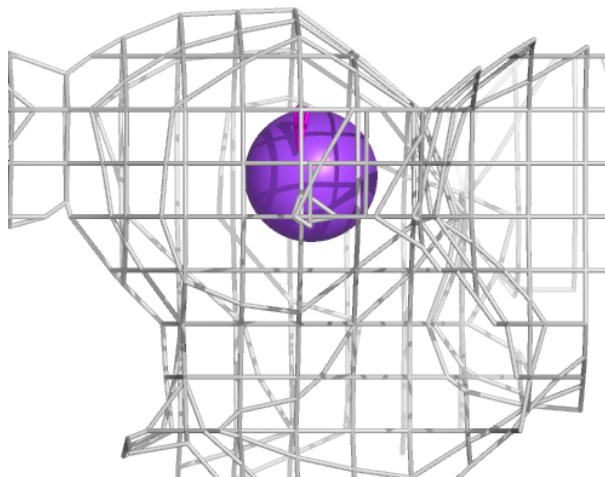
Electron density around K B 402:

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and green (positive)



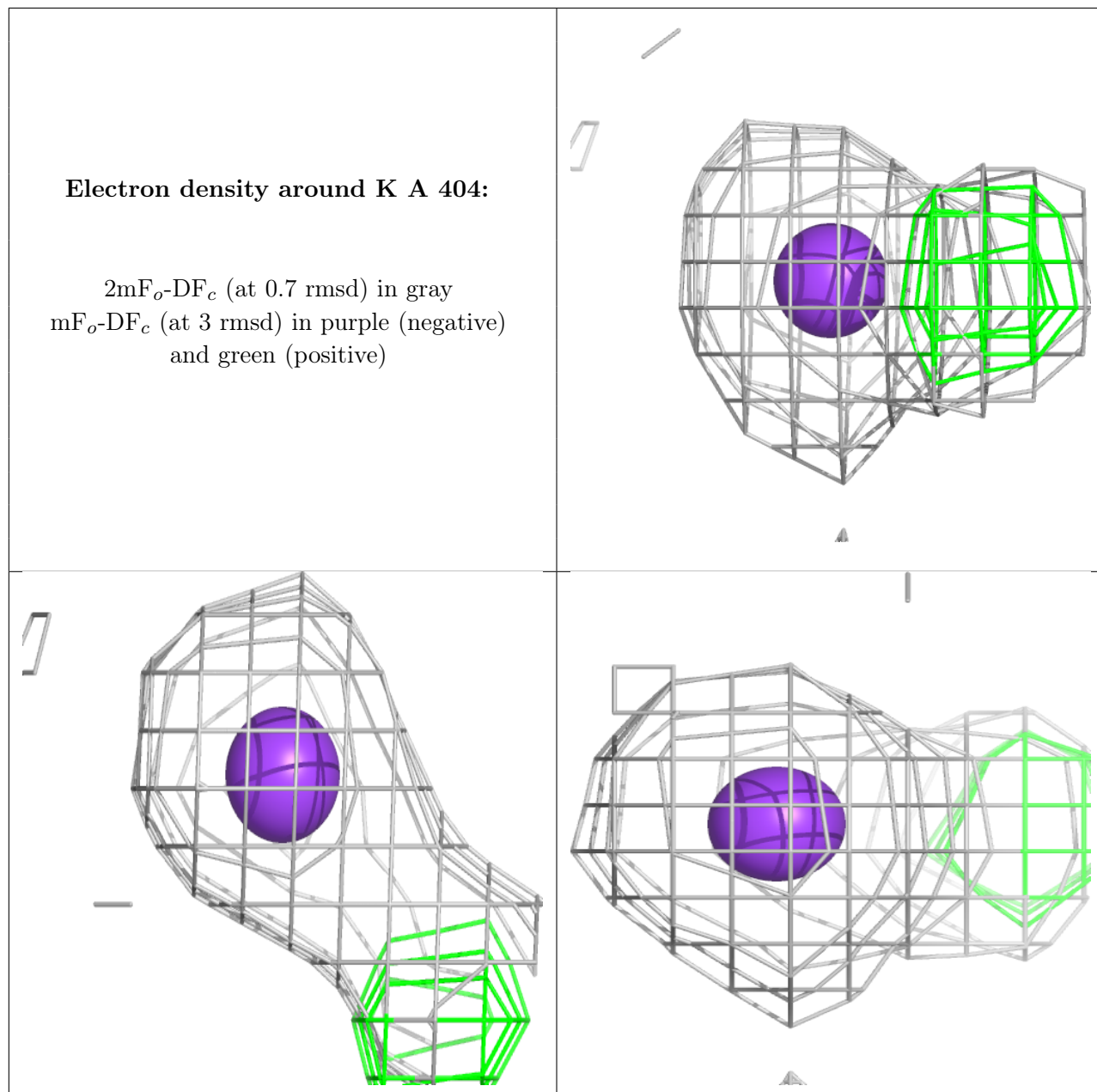
Electron density around K E 402:

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and green (positive)



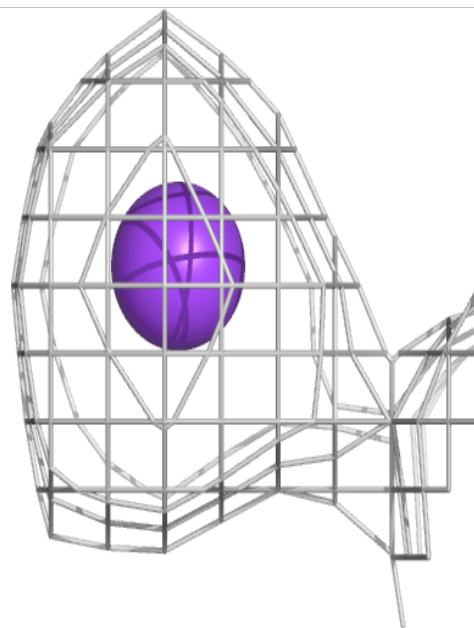
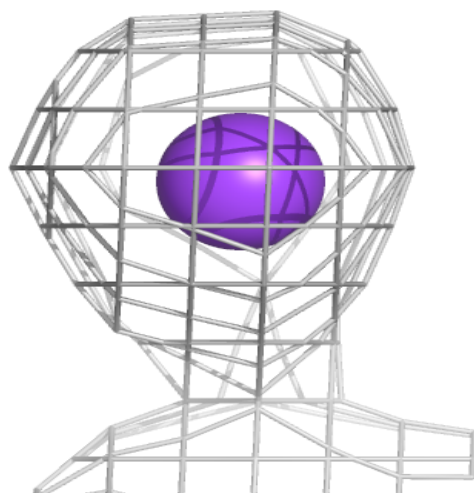
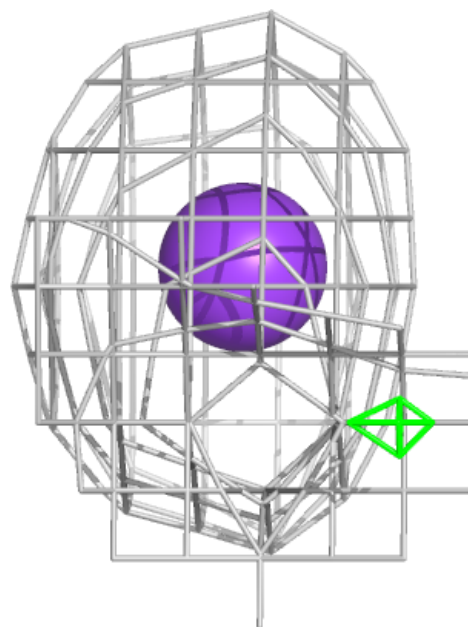
Electron density around K A 404:

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and green (positive)



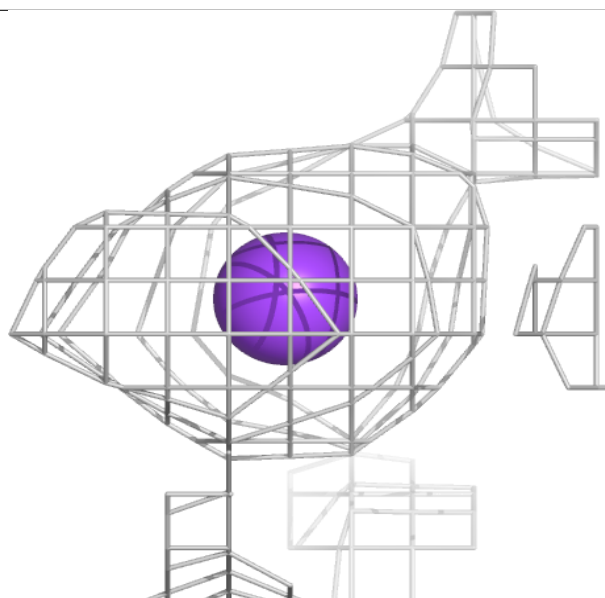
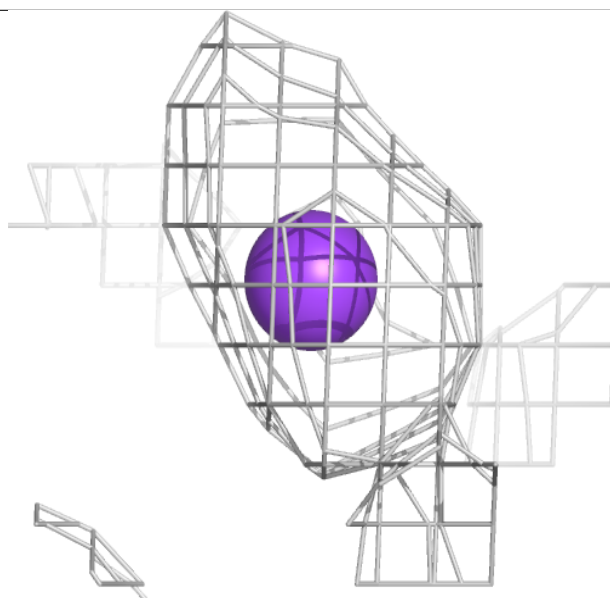
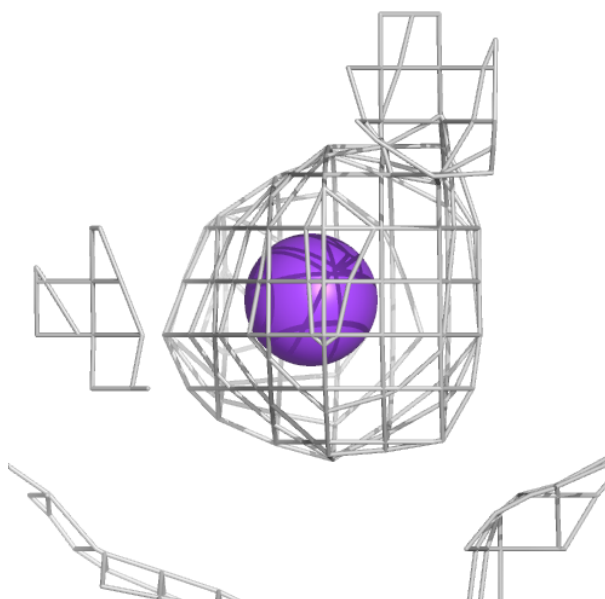
Electron density around K G 401:

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and green (positive)



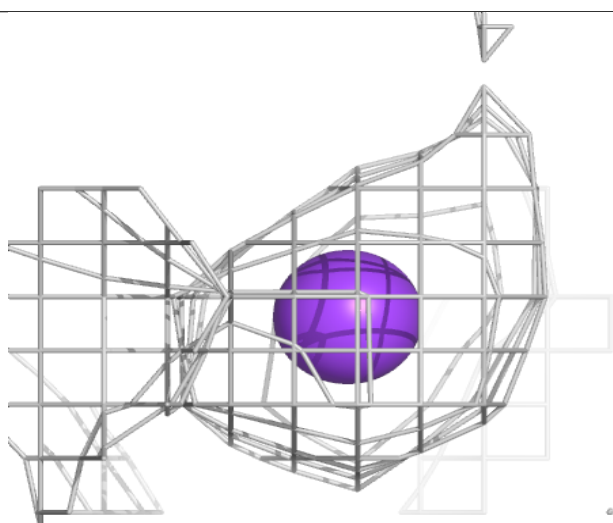
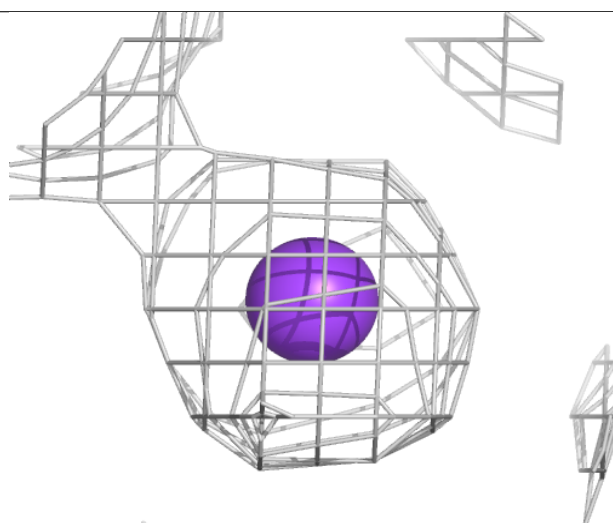
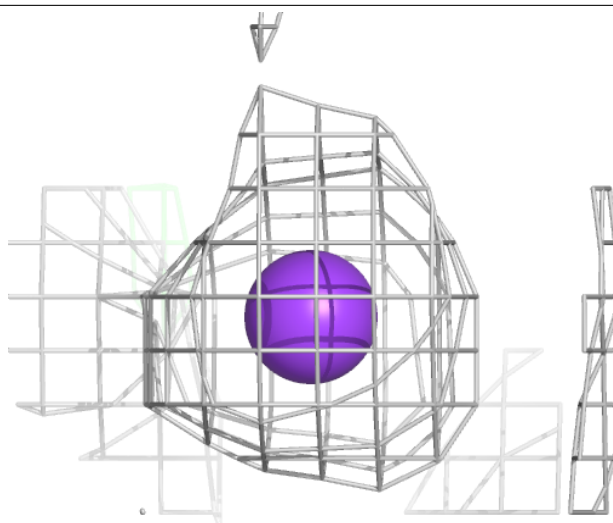
Electron density around K G 403:

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



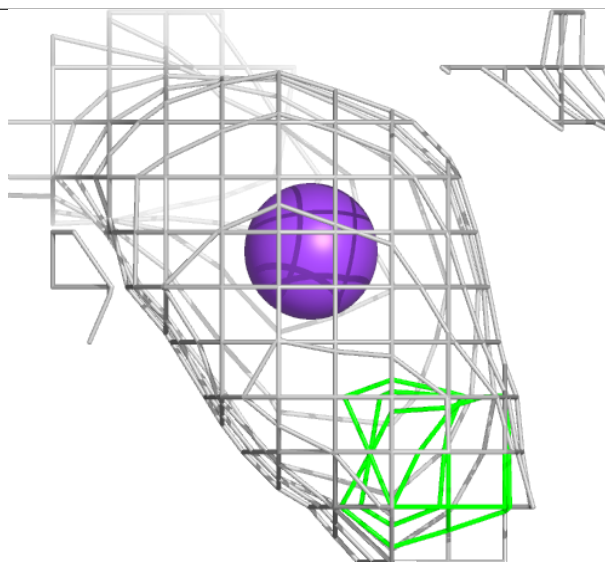
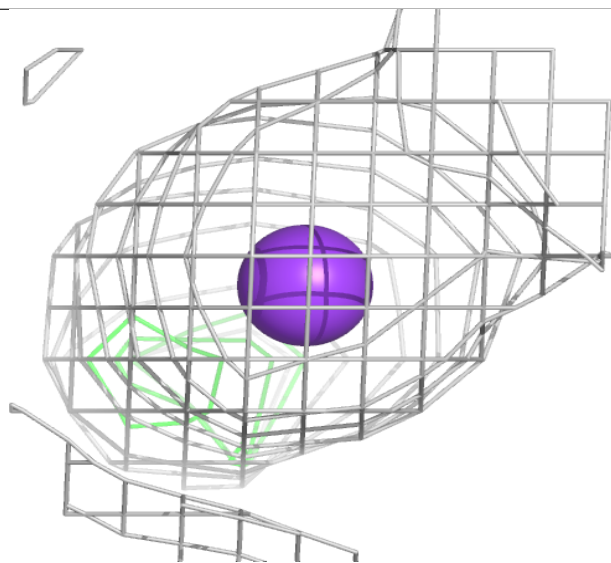
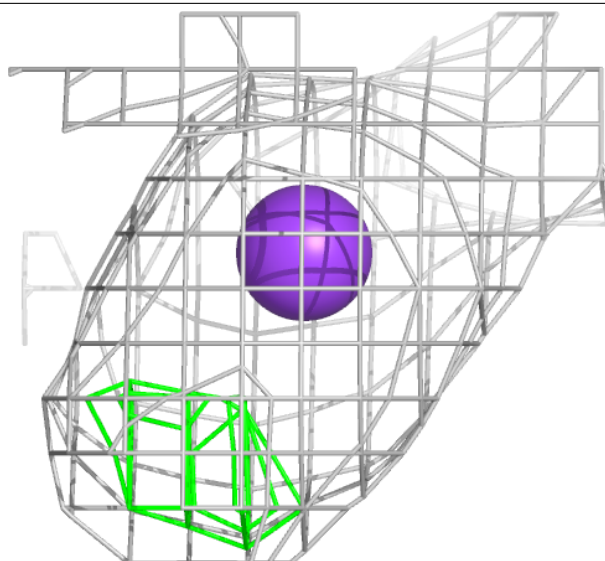
Electron density around K A 405:

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



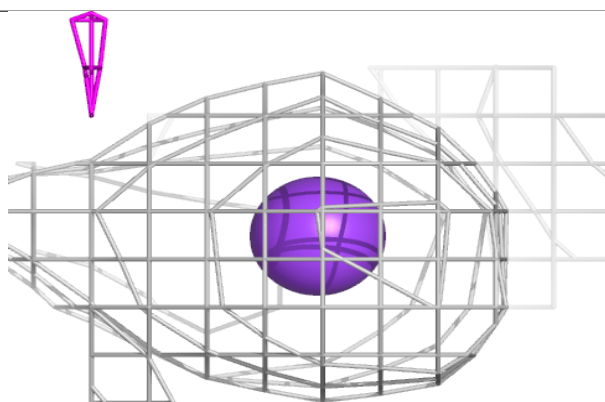
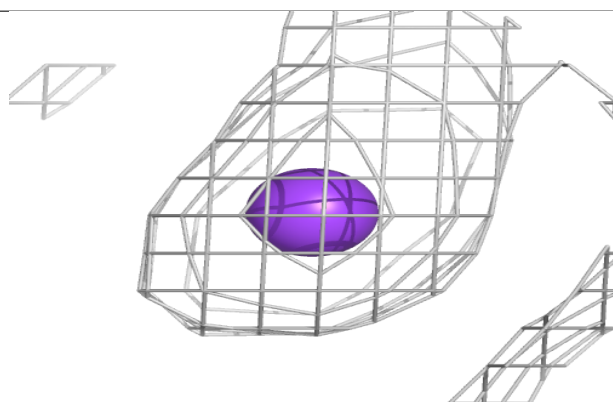
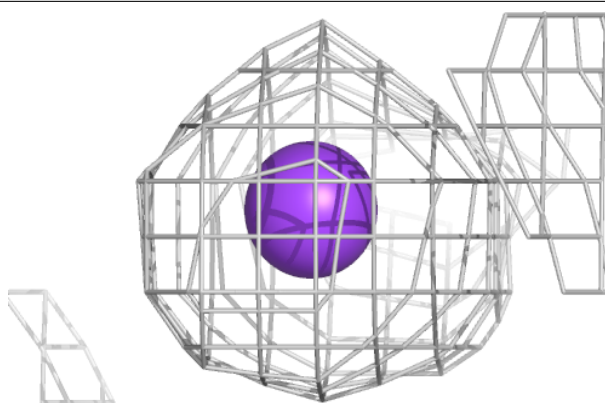
Electron density around K A 402:

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



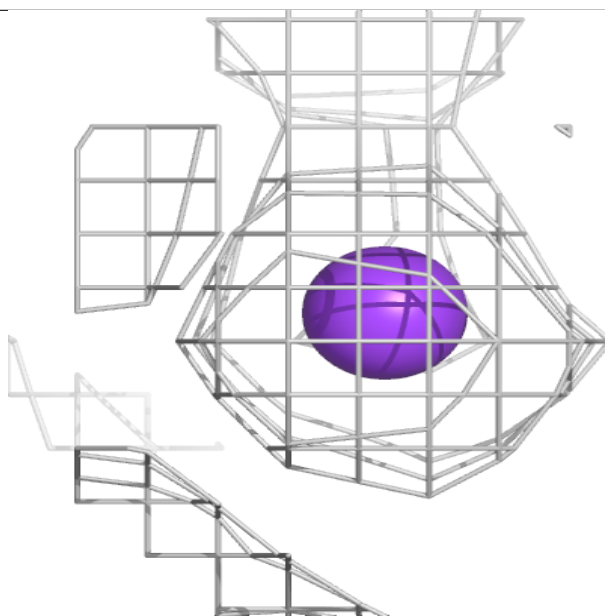
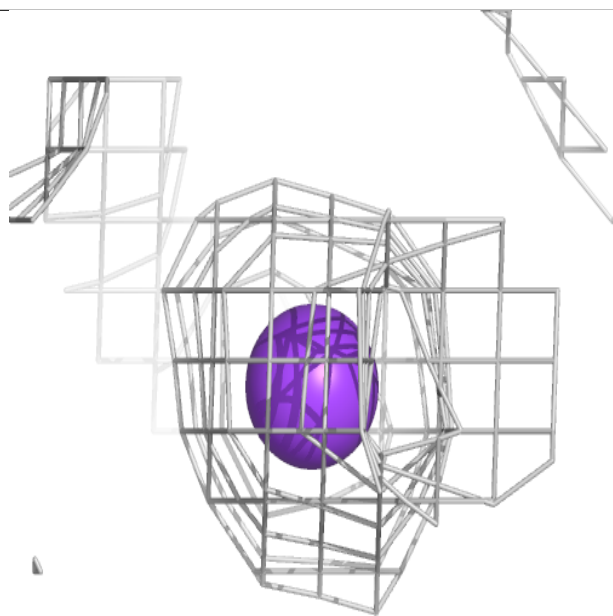
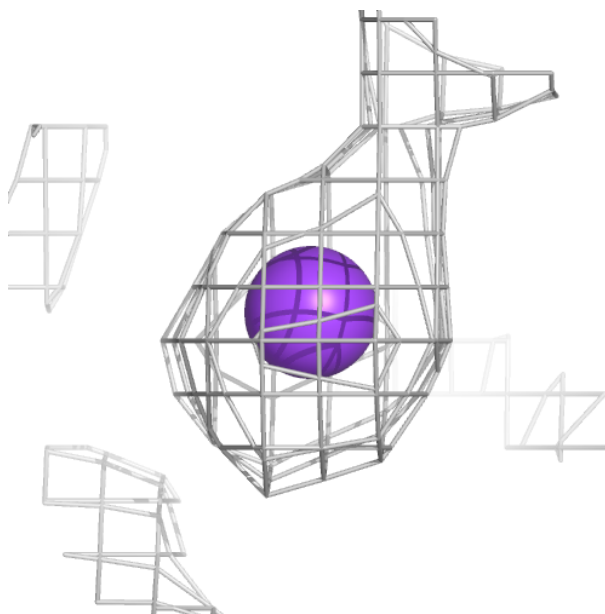
Electron density around K D 402:

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



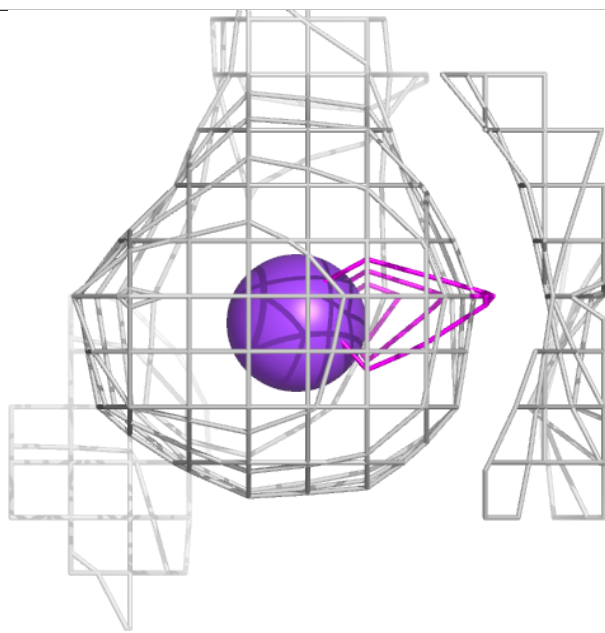
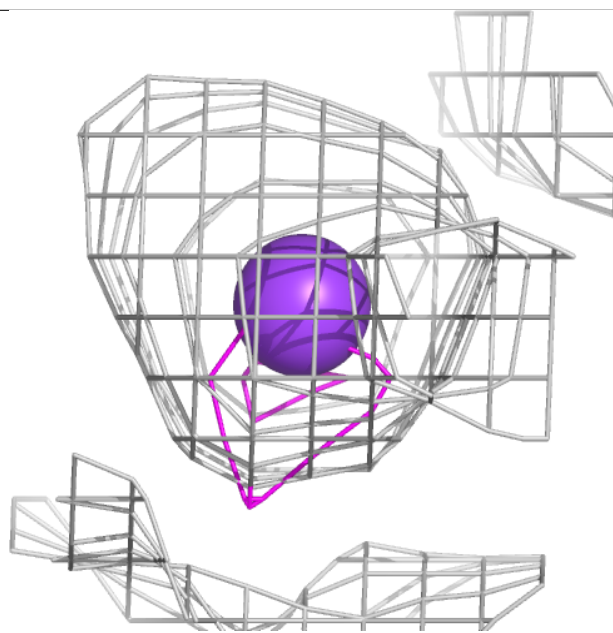
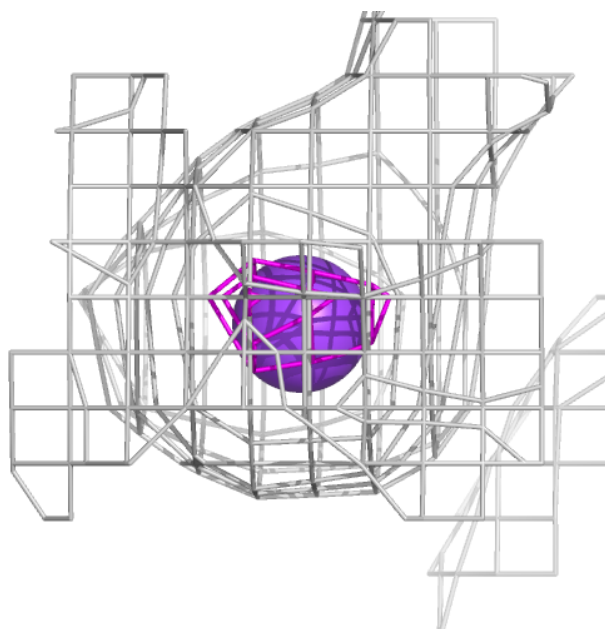
Electron density around K C 403:

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



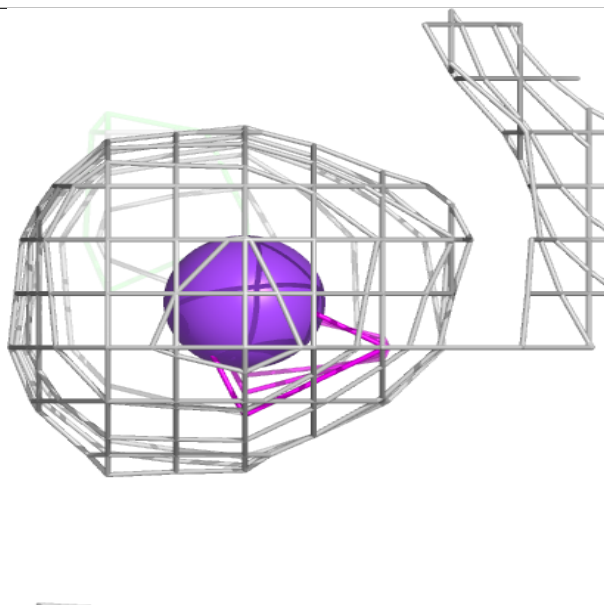
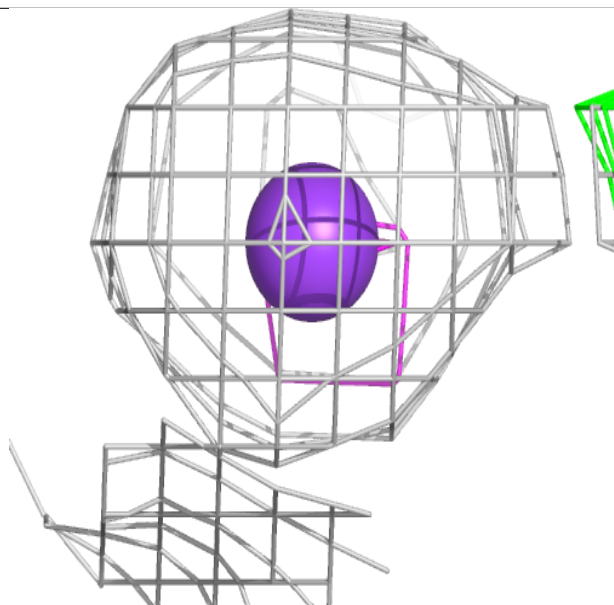
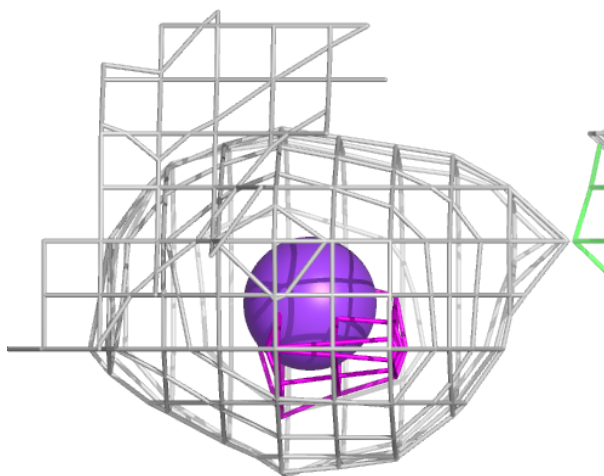
Electron density around K H 401:

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



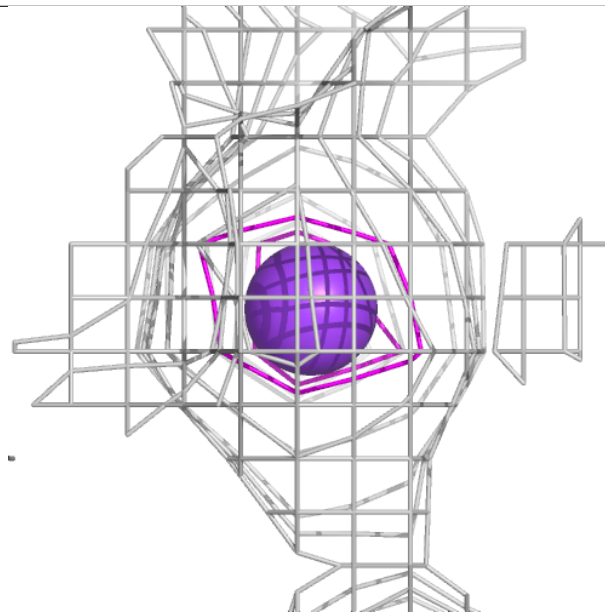
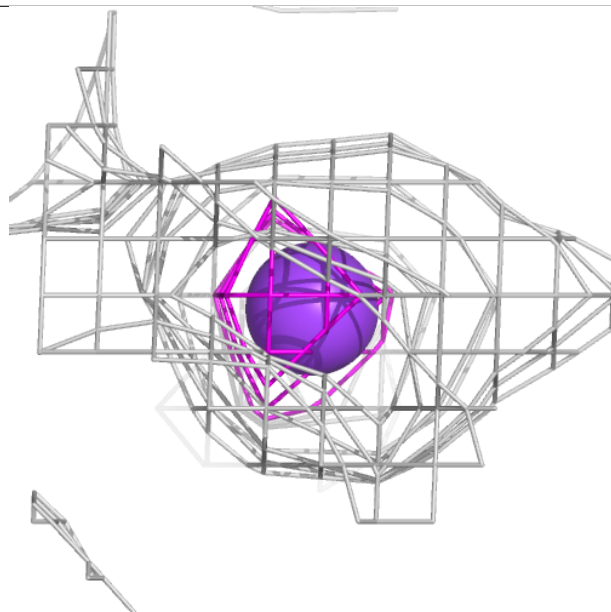
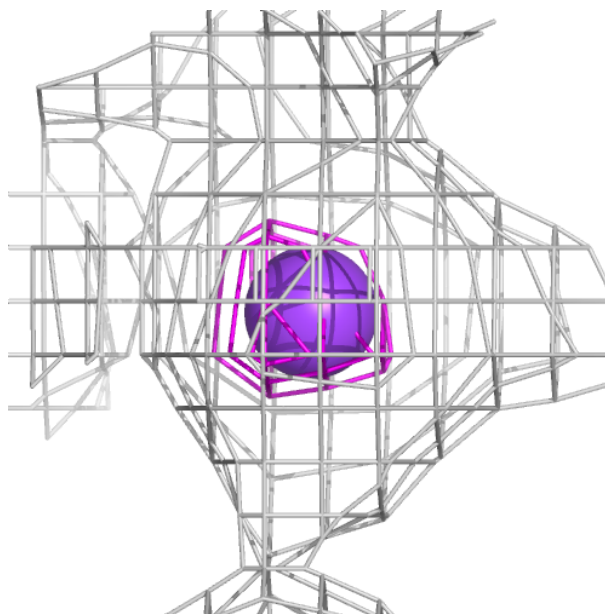
Electron density around K D 401:

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



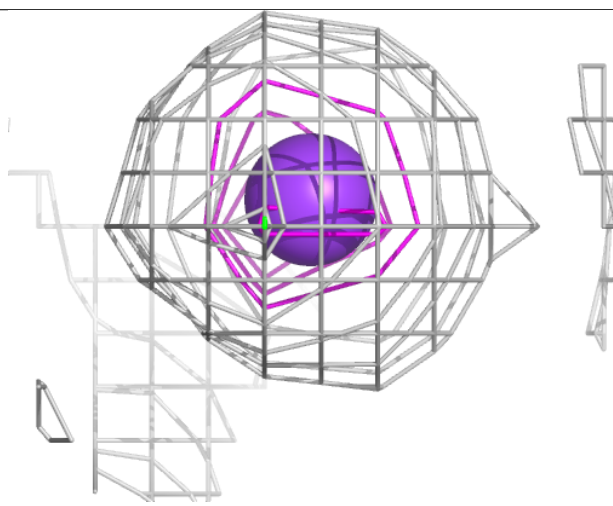
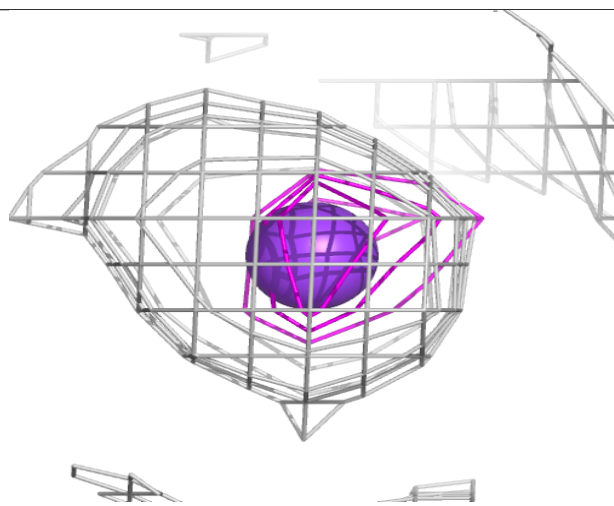
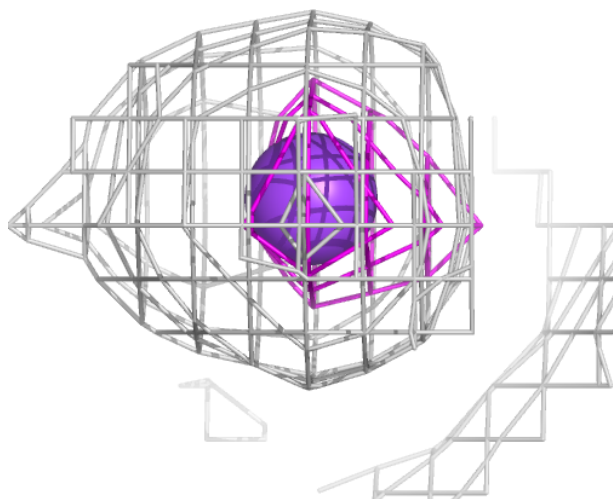
Electron density around K J 401:

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



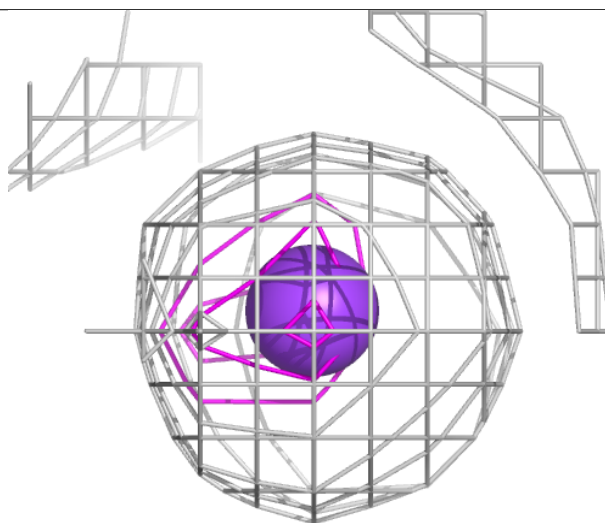
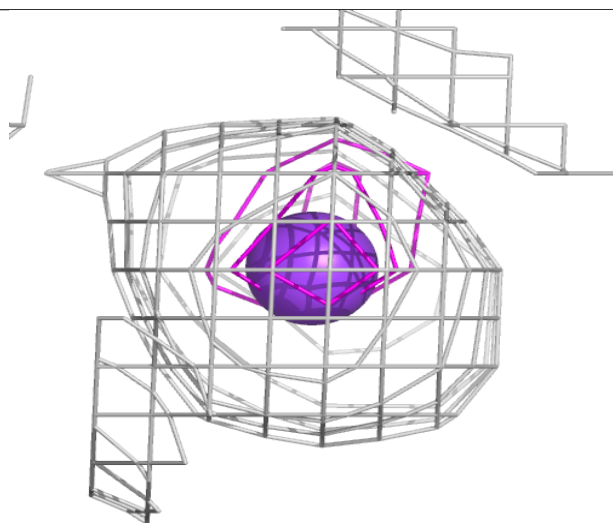
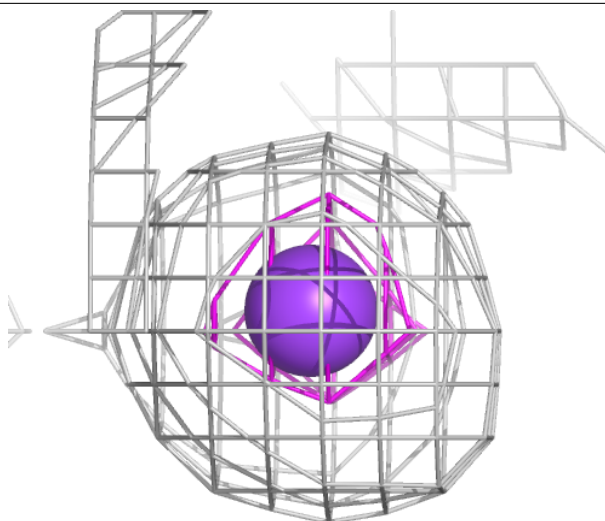
Electron density around K C 401:

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



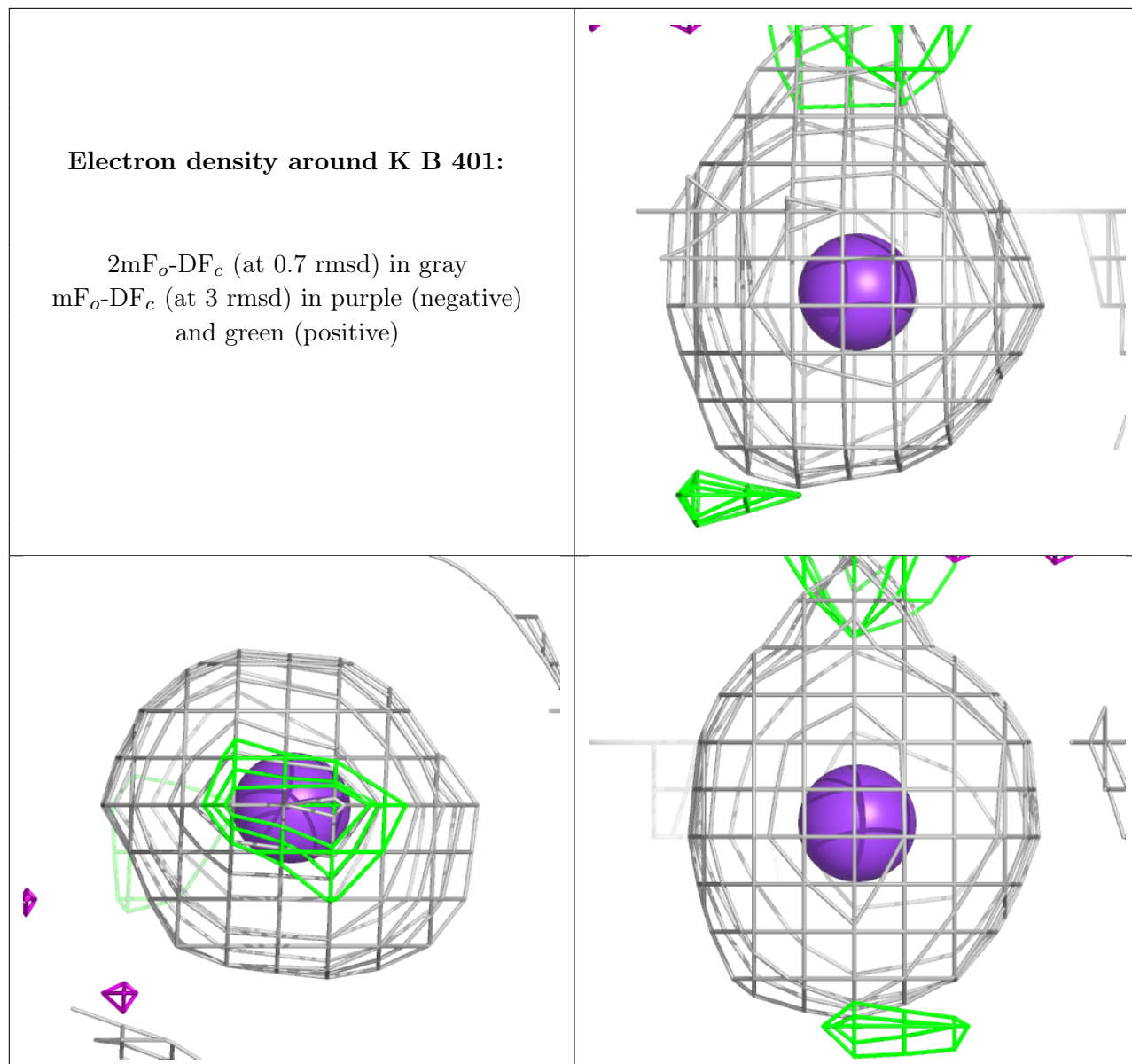
Electron density around K F 401:

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



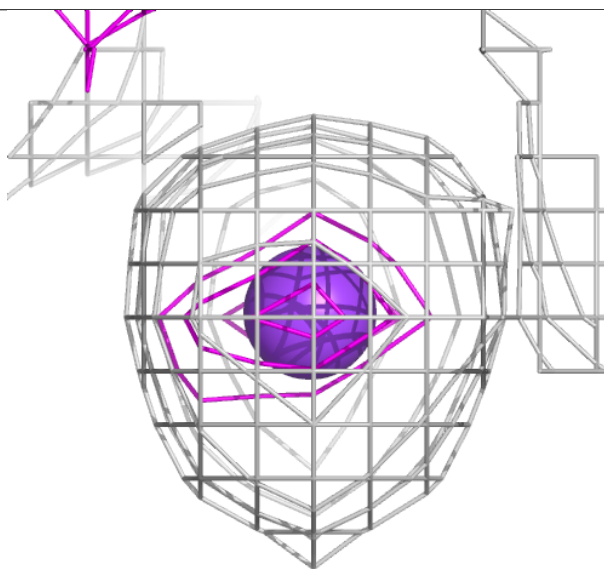
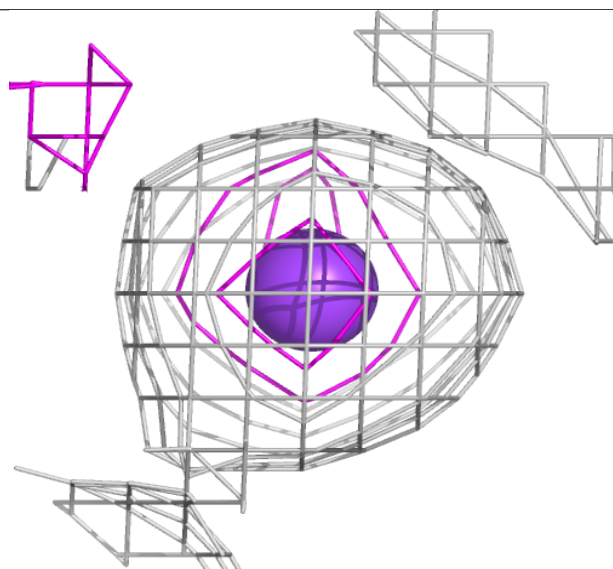
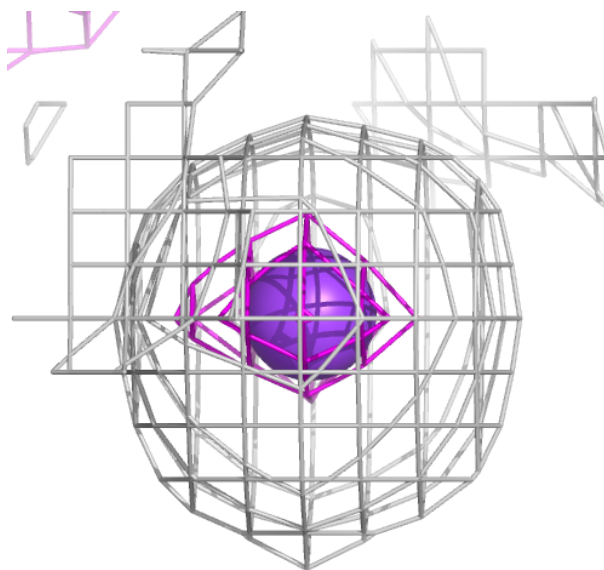
Electron density around K B 401:

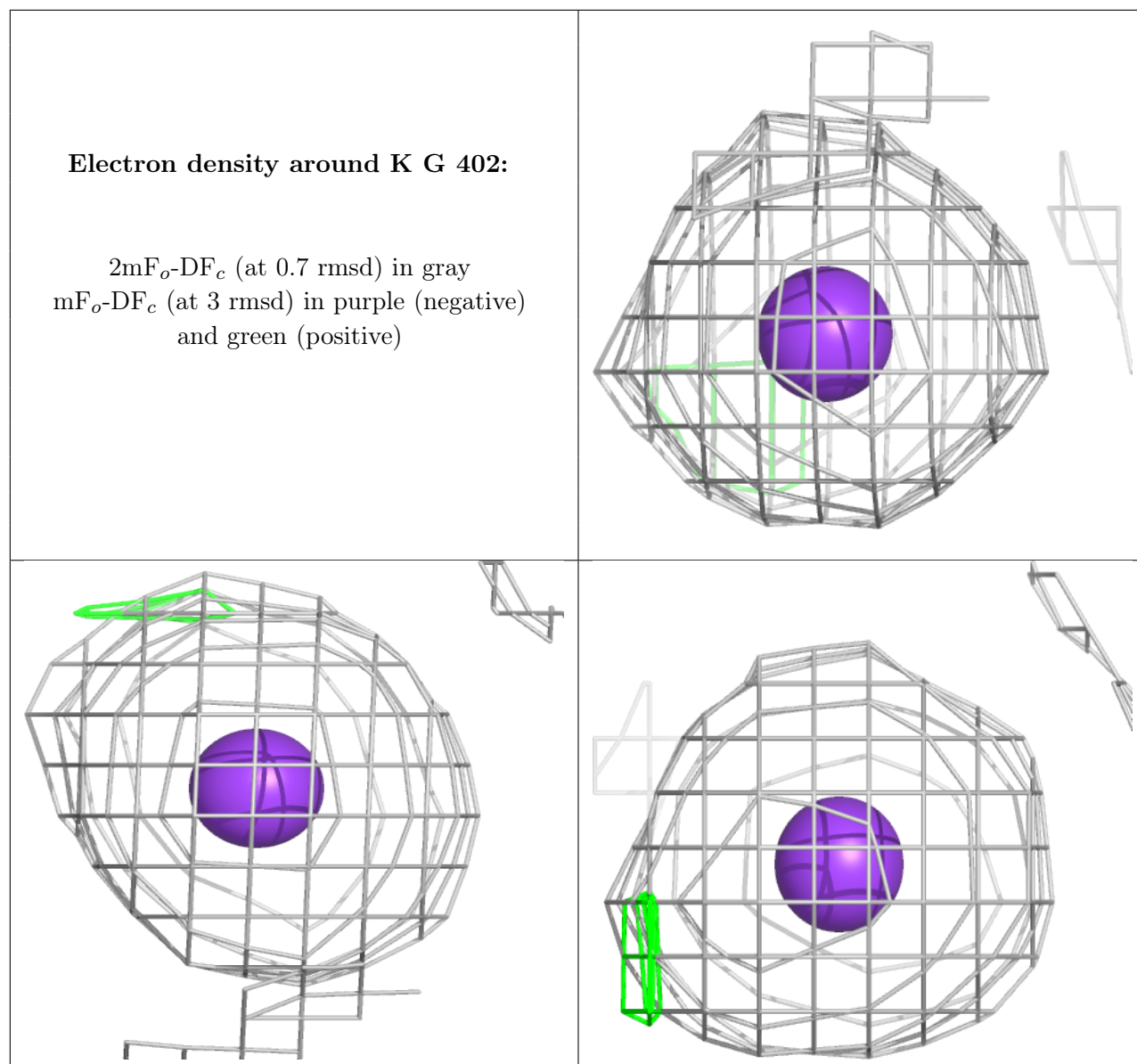
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around K A 401:

$2mF_o-DF_c$ (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.