Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:47 AM UTC

PDB ID	:	8DFB / pdb_00008dfb
Title	:	Structure of M. kandleri topoisomerase V in complex with DNA. 39 base pair symmetric DNA complex
Authors	:	Osterman, A.; Mondragon, A.
Deposited on	:	2022-06-21
Resolution	:	3.17 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:

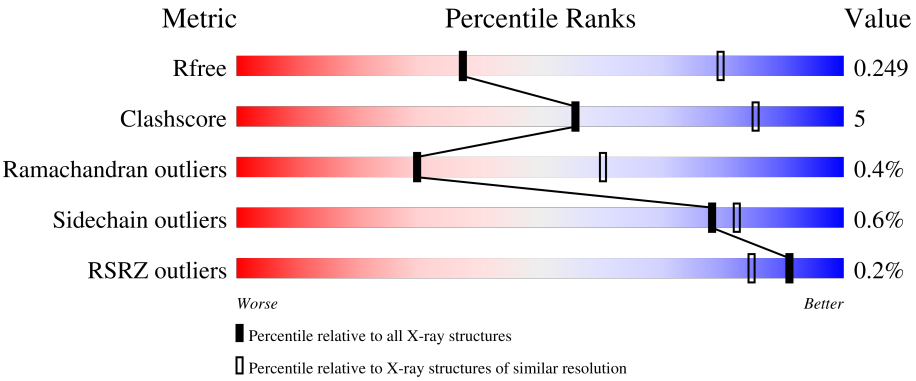
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 3.17 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	2001 (3.20-3.16)
Clashscore	190562	2119 (3.20-3.16)
Ramachandran outliers	187476	2070 (3.20-3.16)
Sidechain outliers	187428	2069 (3.20-3.16)
RSRZ outliers	180081	2001 (3.20-3.16)

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 <=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	854	86% 14%
1	B	854	87% 13%
2	U	40	62% 38%
3	V	40	62% 38%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 15225 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 Topoisomerase V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	850	Total	C	N	O	S	0	0	0
			6802	4255	1222	1315	10			
1	B	850	Total	C	N	O	S	0	0	0
			6802	4255	1222	1315	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	809	ALA	LYS	engineered mutation	UNP Q977W1
A	820	ALA	LYS	engineered mutation	UNP Q977W1
A	831	ALA	LYS	engineered mutation	UNP Q977W1
A	835	ALA	LYS	engineered mutation	UNP Q977W1
A	846	ALA	LYS	engineered mutation	UNP Q977W1
A	851	ALA	LYS	engineered mutation	UNP Q977W1
B	809	ALA	LYS	engineered mutation	UNP Q977W1
B	820	ALA	LYS	engineered mutation	UNP Q977W1
B	831	ALA	LYS	engineered mutation	UNP Q977W1
B	835	ALA	LYS	engineered mutation	UNP Q977W1
B	846	ALA	LYS	engineered mutation	UNP Q977W1
B	851	ALA	LYS	engineered mutation	UNP Q977W1

- Molecule 2 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	U	40	Total	C	N	O	P	0	0	0
			808	384	146	238	40			

- Molecule 3 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	V	40	Total	C	N	O	P	0	0	0
			809	384	149	236	40			

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

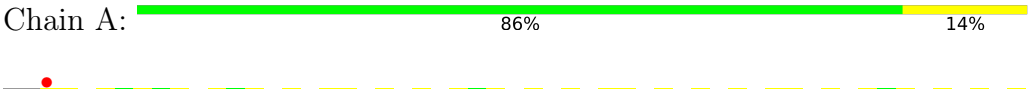
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total K 2 2	0	0
4	B	2	Total K 2 2	0	0

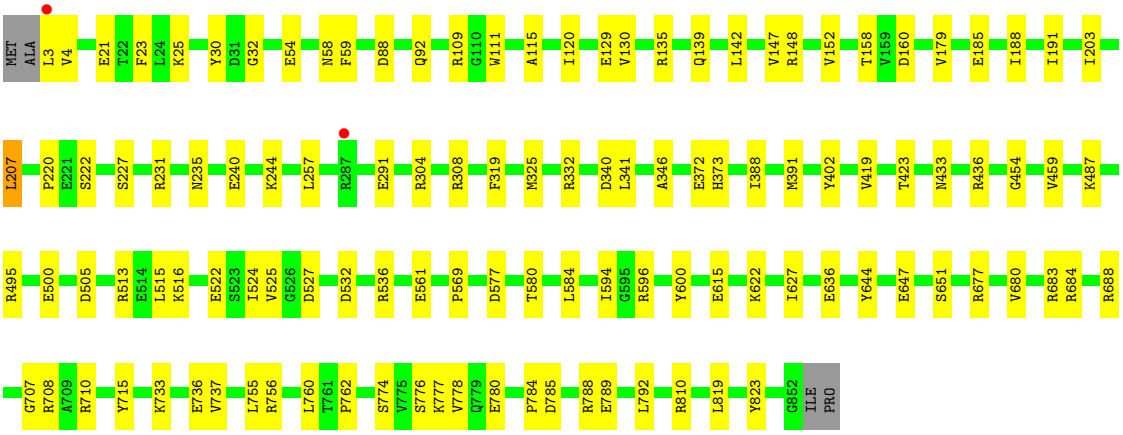
3 Residue-property plots (i)

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: Topoisomerase V

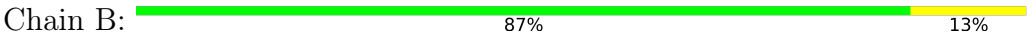
Chain A:

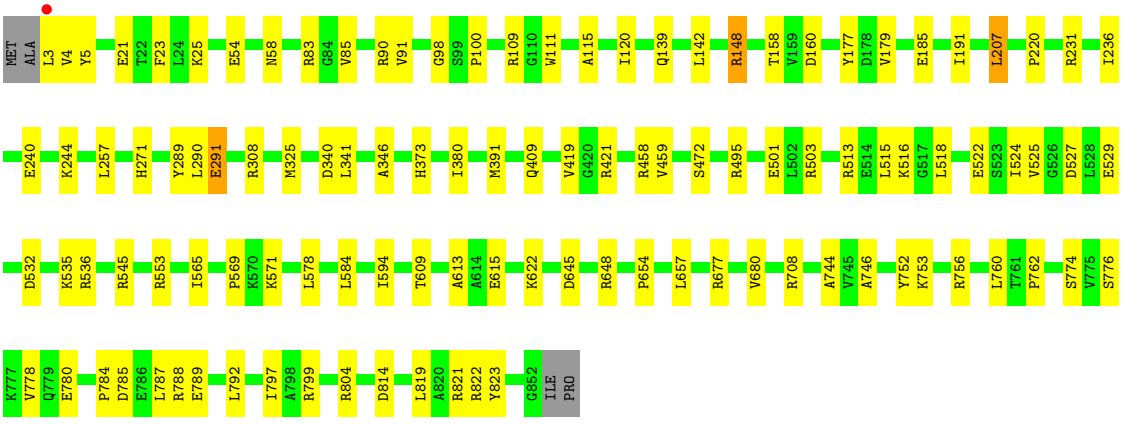




• Molecule 1: Topoisomerase V

Chain B:

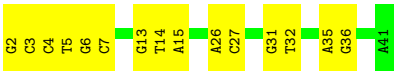




• Molecule 2: DNA (40-MER)

Chain U:

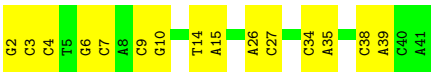




• Molecule 3: DNA (40-MER)

Chain V:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	121.56Å 121.56Å 497.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.04 – 3.17 59.04 – 3.17	Depositor EDS
% Data completeness (in resolution range)	82.4 (59.04-3.17) 82.4 (59.04-3.17)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.56 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.19.1_4122: ???)	Depositor
R, R_{free}	0.218 , 0.251 0.216 , 0.249	Depositor DCC
R_{free} test set	2690 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å^2)	108.6	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 72.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	15225	wwPDB-VP
Average B, all atoms (Å^2)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.85% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: K

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	0.08	0/6898	0.23	0/9292
1	B	0.08	0/6898	0.24	0/9292
2	U	0.20	0/905	0.38	0/1393
3	V	0.19	0/907	0.38	0/1396
All	All	0.10	0/15608	0.26	0/21373

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6802	0	6864	66	0
1	B	6802	0	6864	63	0
2	U	808	0	445	12	0
3	V	809	0	444	12	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
All	All	15225	0	14617	139	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 5.

All (139) 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:V:38:DC:H2"	3:V:39:DA:H5'	1.59	0.85
1:B:513:ARG:HD3	1:B:522:GLU:HG3	1.73	0.69
1:A:513:ARG:HD3	1:A:522:GLU:HG3	1.74	0.69
1:A:21:GLU:HG2	1:A:25:LYS:HE3	1.78	0.66
1:B:799:ARG:HD3	1:B:804:ARG:HH21	1.62	0.66
1:B:753:LYS:NZ	2:U:13:DG:OP2	2.30	0.65
1:B:495:ARG:O	1:B:516:LYS:NZ	2.31	0.64
1:B:784:PRO:HB2	1:B:788:ARG:HH21	1.61	0.64
1:B:21:GLU:HG2	1:B:25:LYS:HE3	1.82	0.61
3:V:26:DA:H4'	3:V:27:DC:H5'	1.85	0.59
1:A:615:GLU:HA	1:A:622:LYS:HE2	1.85	0.58
1:A:240:GLU:HG3	1:A:244:LYS:HE2	1.86	0.57
1:B:760:LEU:HD21	1:B:792:LEU:HD21	1.85	0.57
1:A:135:ARG:NH1	3:V:39:DA:OP2	2.38	0.57
1:A:419:VAL:HG22	1:A:459:VAL:HG13	1.88	0.56
1:B:654:PRO:HA	1:B:657:LEU:HD13	1.87	0.56
1:A:683:ARG:NH2	2:U:35:DA:OP1	2.35	0.56
1:A:109:ARG:HD3	2:U:2:DG:C6	2.41	0.56
1:A:600:TYR:N	1:A:636:GLU:OE2	2.36	0.55
3:V:34:DC:H2"	3:V:35:DA:C8	2.41	0.55
2:U:26:DA:H4'	2:U:27:DC:H5'	1.88	0.55
1:A:784:PRO:HB2	1:A:788:ARG:HH21	1.72	0.55
1:B:220:PRO:HB3	1:B:231:ARG:HG2	1.87	0.54
1:B:308:ARG:NH2	1:B:340:ASP:O	2.40	0.54
1:B:419:VAL:HG22	1:B:459:VAL:HG13	1.88	0.54
1:A:760:LEU:HD21	1:A:792:LEU:HD21	1.90	0.54
2:U:5:DT:H2"	2:U:6:DG:C8	2.43	0.54
1:A:115:ALA:HA	1:A:120:ILE:HD12	1.90	0.54
1:B:615:GLU:HA	1:B:622:LYS:HE2	1.89	0.54
1:A:23:PHE:HZ	1:A:111:TRP:HB2	1.73	0.53
1:A:373:HIS:CG	1:A:391:MET:HE1	2.41	0.53
1:B:569:PRO:HB3	2:U:7:DC:H5"	1.89	0.53
1:B:503:ARG:NH1	1:B:529:GLU:OE2	2.41	0.53
1:A:54:GLU:O	1:A:58:ASN:ND2	2.41	0.52
1:B:115:ALA:HA	1:B:120:ILE:HD12	1.92	0.52
1:A:191:ILE:HD11	1:A:207:LEU:HD13	1.92	0.52
2:U:6:DG:H2"	2:U:7:DC:O5'	2.10	0.51
1:A:584:LEU:HB3	1:A:594:ILE:HD12	1.93	0.51
1:A:495:ARG:O	1:A:516:LYS:NZ	2.45	0.50
1:B:584:LEU:HB3	1:B:594:ILE:HD12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:PRO:HB3	1:A:231:ARG:HG2	1.92	0.49
1:A:524:ILE:HG22	1:A:525:VAL:HG23	1.94	0.49
1:A:487:LYS:NZ	1:A:505:ASP:OD1	2.45	0.49
1:A:708:ARG:NH2	1:B:325:MET:SD	2.85	0.49
1:A:776:SER:O	1:A:780:GLU:HG2	2.12	0.49
1:A:569:PRO:HB3	3:V:7:DC:H5"	1.94	0.49
1:B:98:GLY:HA3	1:B:148:ARG:HH22	1.78	0.49
2:U:3:DC:H2"	2:U:4:DC:H5'	1.94	0.49
1:A:819:LEU:O	1:A:823:TYR:HB2	2.13	0.48
1:B:158:THR:HG22	1:B:160:ASP:H	1.78	0.48
3:V:6:DG:H2"	3:V:7:DC:O5'	2.13	0.48
1:B:524:ILE:HG22	1:B:525:VAL:HG23	1.95	0.48
1:B:518:LEU:HD21	1:B:535:LYS:HD2	1.95	0.48
1:B:819:LEU:O	1:B:823:TYR:HB2	2.14	0.48
1:B:54:GLU:O	1:B:58:ASN:ND2	2.45	0.48
1:A:304:ARG:HG2	1:B:472:SER:HB2	1.97	0.47
1:A:185:GLU:OE1	1:A:231:ARG:NH2	2.48	0.47
1:A:810:ARG:HH12	1:B:501:GLU:CD	2.23	0.47
1:A:684:ARG:O	1:A:688:ARG:HB2	2.15	0.47
1:A:332:ARG:NH2	1:A:372:GLU:OE2	2.44	0.46
1:A:774:SER:OG	1:A:777:LYS:HD3	2.15	0.46
1:B:85:VAL:HG11	1:B:90:ARG:HH11	1.80	0.46
1:B:109:ARG:HD3	3:V:2:DG:C5	2.50	0.46
1:A:707:GLY:O	1:A:710:ARG:HG2	2.16	0.46
1:B:821:ARG:HH12	1:B:822:ARG:HE	1.64	0.46
1:B:185:GLU:OE1	1:B:231:ARG:NH2	2.48	0.45
1:B:191:ILE:HD11	1:B:207:LEU:HD13	1.97	0.45
1:B:708:ARG:HH11	1:B:744:ALA:HB2	1.81	0.45
1:B:774:SER:O	1:B:778:VAL:HG23	2.17	0.45
1:B:58:ASN:HB3	1:B:257:LEU:HD11	1.99	0.45
1:B:677:ARG:HA	1:B:680:VAL:HG22	1.98	0.45
1:A:3:LEU:HG	1:A:4:VAL:HG23	1.99	0.45
1:A:185:GLU:CD	1:A:231:ARG:HH22	2.24	0.45
1:A:774:SER:O	1:A:778:VAL:HG23	2.17	0.45
1:B:3:LEU:HG	1:B:4:VAL:HG23	1.98	0.45
1:B:290:LEU:O	1:B:291:GLU:HB2	2.17	0.45
1:B:380:ILE:O	1:B:409:GLN:NE2	2.40	0.45
1:B:787:LEU:HD12	1:B:797:ILE:HG23	1.98	0.45
1:A:308:ARG:NH2	1:A:340:ASP:O	2.43	0.45
1:A:109:ARG:HD3	2:U:2:DG:C5	2.51	0.44
1:A:755:LEU:HD22	1:A:760:LEU:HD22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:746:ALA:HA	1:B:752:TYR:HB3	1.99	0.44
1:A:715:TYR:CD2	1:A:737:VAL:HG22	2.52	0.44
2:U:36:DG:H1	3:V:4:DC:H42	1.64	0.44
1:B:109:ARG:HD3	3:V:2:DG:C6	2.52	0.44
1:B:545:ARG:HG2	1:B:565:ILE:HG23	1.98	0.44
1:A:388:ILE:HG22	1:A:402:TYR:HD1	1.81	0.44
3:V:9:DC:H2"	3:V:10:DG:C8	2.53	0.44
1:B:240:GLU:HG3	1:B:244:LYS:HE2	2.00	0.43
2:U:14:DT:H2"	2:U:15:DA:C8	2.53	0.43
1:A:525:VAL:HG12	1:A:527:ASP:H	1.84	0.43
1:B:23:PHE:HZ	1:B:111:TRP:HB2	1.82	0.43
2:U:31:DG:C8	2:U:32:DT:H72	2.53	0.43
1:B:373:HIS:CG	1:B:391:MET:HE1	2.53	0.43
3:V:14:DT:H2"	3:V:15:DA:C8	2.53	0.43
1:A:423:THR:HG22	1:A:454:GLY:HA3	2.00	0.43
1:B:341:LEU:HD21	1:B:346:ALA:HB2	2.00	0.43
1:B:785:ASP:O	1:B:789:GLU:HG2	2.19	0.43
1:A:130:VAL:HG21	1:A:147:VAL:HG11	2.01	0.43
1:A:231:ARG:O	1:A:235:ASN:ND2	2.51	0.43
1:B:5:TYR:OH	1:B:83:ARG:NH1	2.51	0.43
1:B:525:VAL:HG12	1:B:527:ASP:H	1.84	0.43
1:A:756:ARG:NH1	1:A:762:PRO:HD3	2.34	0.43
1:B:571:LYS:HD3	1:B:615:GLU:HB3	2.01	0.43
1:A:158:THR:HG22	1:A:160:ASP:H	1.83	0.42
1:A:677:ARG:HA	1:A:680:VAL:HG22	2.00	0.42
1:B:495:ARG:NH1	1:B:515:LEU:O	2.52	0.42
1:B:139:GLN:HB3	1:B:142:LEU:HB3	2.00	0.42
1:B:185:GLU:CD	1:B:231:ARG:HH22	2.26	0.42
1:A:188:ILE:HG23	1:A:203:ILE:HG21	2.02	0.42
1:A:58:ASN:HB3	1:A:257:LEU:HD11	2.01	0.42
1:A:561:GLU:HG3	1:B:271:HIS:CD2	2.55	0.42
1:A:341:LEU:HD21	1:A:346:ALA:HB2	2.02	0.42
3:V:3:DC:H2"	3:V:4:DC:H5'	2.02	0.42
1:A:785:ASP:O	1:A:789:GLU:HG2	2.20	0.42
1:A:30:TYR:CE1	1:A:129:GLU:HB2	2.55	0.41
1:B:645:ASP:HB3	1:B:648:ARG:HB2	2.02	0.41
1:A:319:PHE:HD2	1:A:325:MET:HG2	1.85	0.41
1:A:733:LYS:O	1:A:736:GLU:HG2	2.20	0.41
1:A:139:GLN:HB3	1:A:142:LEU:HB3	2.01	0.41
1:A:433:ASN:OD1	1:A:436:ARG:N	2.47	0.41
1:B:421:ARG:HE	1:B:421:ARG:HB3	1.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:756:ARG:NH1	1:B:762:PRO:HD3	2.35	0.41
1:B:609:THR:O	1:B:613:ALA:N	2.39	0.41
1:A:500:GLU:CD	1:A:500:GLU:H	2.29	0.41
1:A:647:GLU:O	1:A:651:SER:OG	2.34	0.41
1:A:32:GLY:HA3	1:A:59:PHE:CE1	2.55	0.41
1:B:91:VAL:HG21	1:B:100:PRO:HA	2.03	0.41
1:B:148:ARG:HE	1:B:148:ARG:C	2.29	0.41
1:A:596:ARG:HG3	1:A:644:TYR:CD1	2.56	0.41
1:B:177:TYR:CZ	1:B:236:ILE:HG12	2.56	0.41
1:B:532:ASP:O	1:B:536:ARG:HG2	2.20	0.41
1:B:776:SER:O	1:B:780:GLU:HG2	2.20	0.41
1:A:577:ASP:OD1	1:A:580:THR:OG1	2.27	0.40
1:A:88:ASP:OD2	1:A:92:GLN:NE2	2.55	0.40
1:A:222:SER:HB3	1:A:227:SER:HB2	2.03	0.40
1:A:495:ARG:NH1	1:A:515:LEU:O	2.55	0.40
1:A:532:ASP:O	1:A:536:ARG:HG2	2.22	0.40
1:B:788:ARG:NH2	1:B:814:ASP:OD1	2.48	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	848/854 (99%)	812 (96%)	33 (4%)	3 (0%)	30	60
1	B	848/854 (99%)	813 (96%)	32 (4%)	3 (0%)	30	60
All	All	1696/1708 (99%)	1625 (96%)	65 (4%)	6 (0%)	30	60

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	291	GLU

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Mol	Chain	Res	Type
1	B	291	GLU
1	A	207	LEU
1	B	207	LEU
1	A	179	VAL
1	B	179	VAL

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	712/715 (100%)	709 (100%)	3 (0%)	84 85
1	B	712/715 (100%)	707 (99%)	5 (1%)	76 81
All	All	1424/1430 (100%)	1416 (99%)	8 (1%)	78 82

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	148	ARG
1	A	152	VAL
1	A	627	ILE
1	B	148	ARG
1	B	289	TYR
1	B	458	ARG
1	B	553	ARG
1	B	578	LEU

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

Mol	Chain	Res	Type
1	A	92	GLN
1	A	195	ASN
1	A	281	HIS
1	B	57	GLN
1	B	195	ASN

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Mol	Chain	Res	Type
1	B	281	HIS
1	B	511	GLN

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 4 ligands modelled in this entry, 4 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

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	850/854 (99%)	-0.22	2 (0%)	91	85	47, 101, 156, 196	0
1	B	850/854 (99%)	-0.24	1 (0%)	92	88	44, 103, 165, 205	0
2	U	40/40 (100%)	-0.02	0	100	100	97, 119, 143, 156	0
3	V	40/40 (100%)	-0.02	0	100	100	80, 119, 135, 145	0
All	All	1780/1788 (99%)	-0.22	3 (0%)	91	85	44, 104, 160, 205	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	LEU	3.3
1	B	3	LEU	2.6
1	A	287	ARG	2.3

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

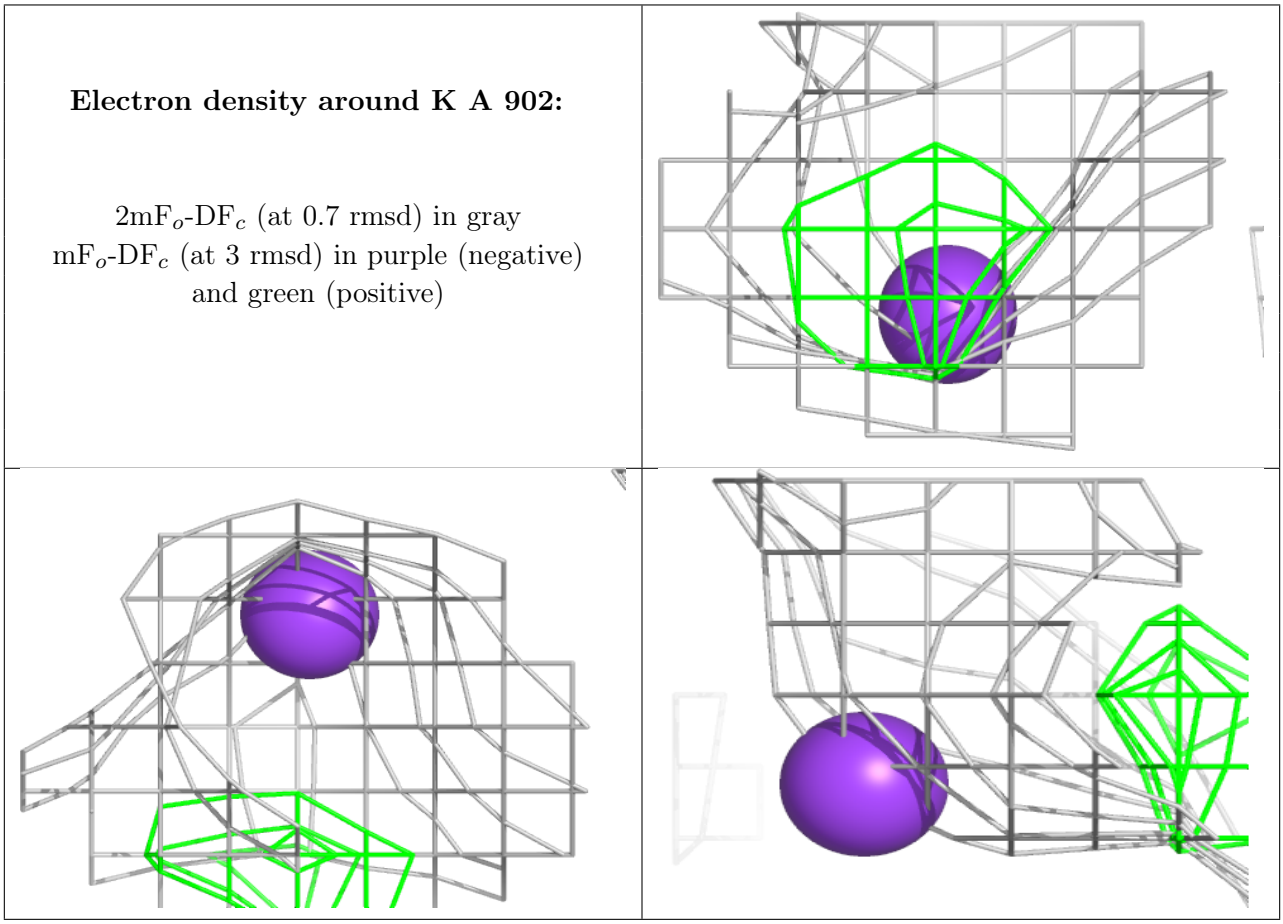
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	K	A	902	1/1	0.51	0.20	137,137,137,137	0
4	K	B	901	1/1	0.78	0.16	127,127,127,127	0
4	K	B	902	1/1	0.82	0.14	118,118,118,118	0
4	K	A	901	1/1	0.91	0.10	101,101,101,101	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.

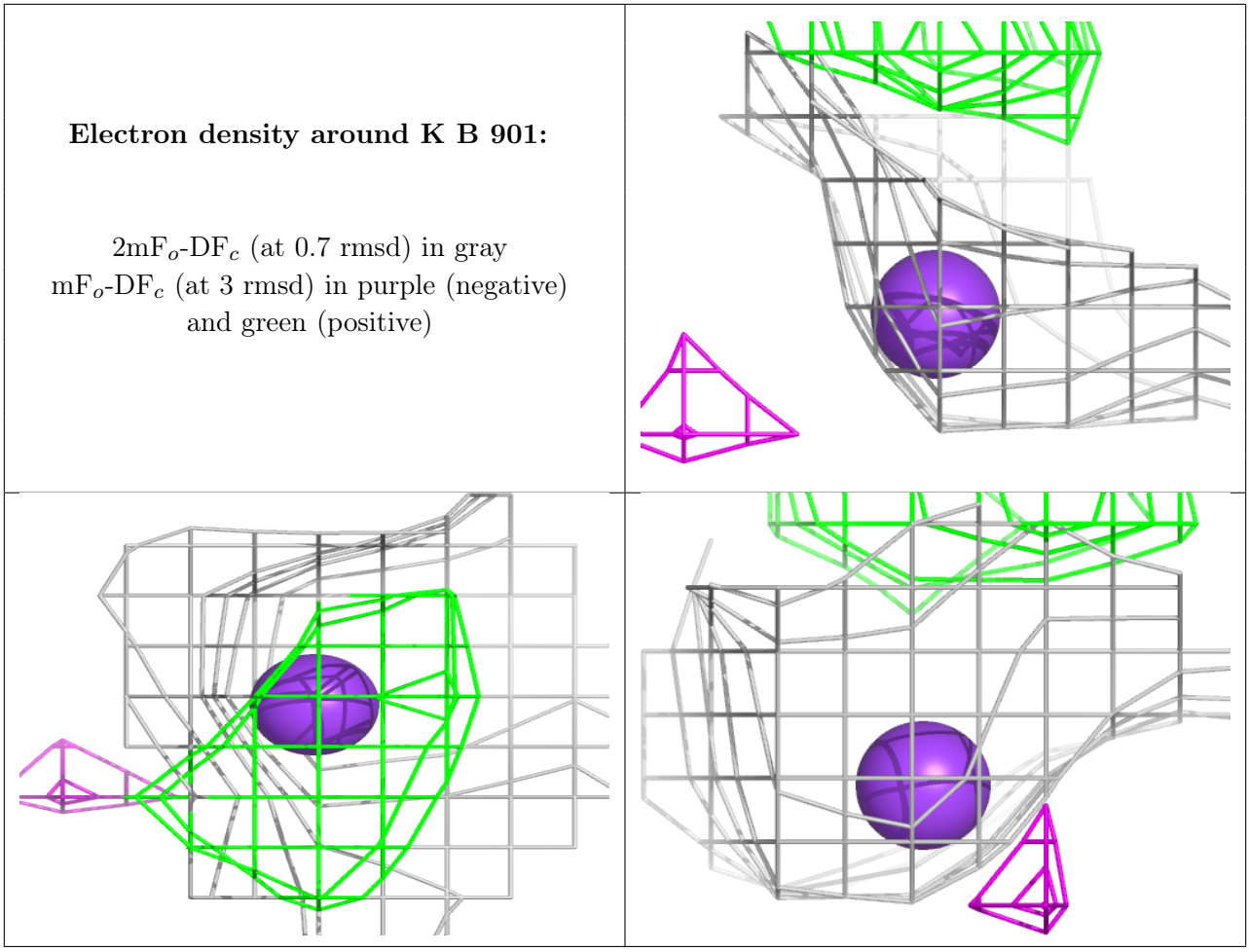
Electron density around K A 902:

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



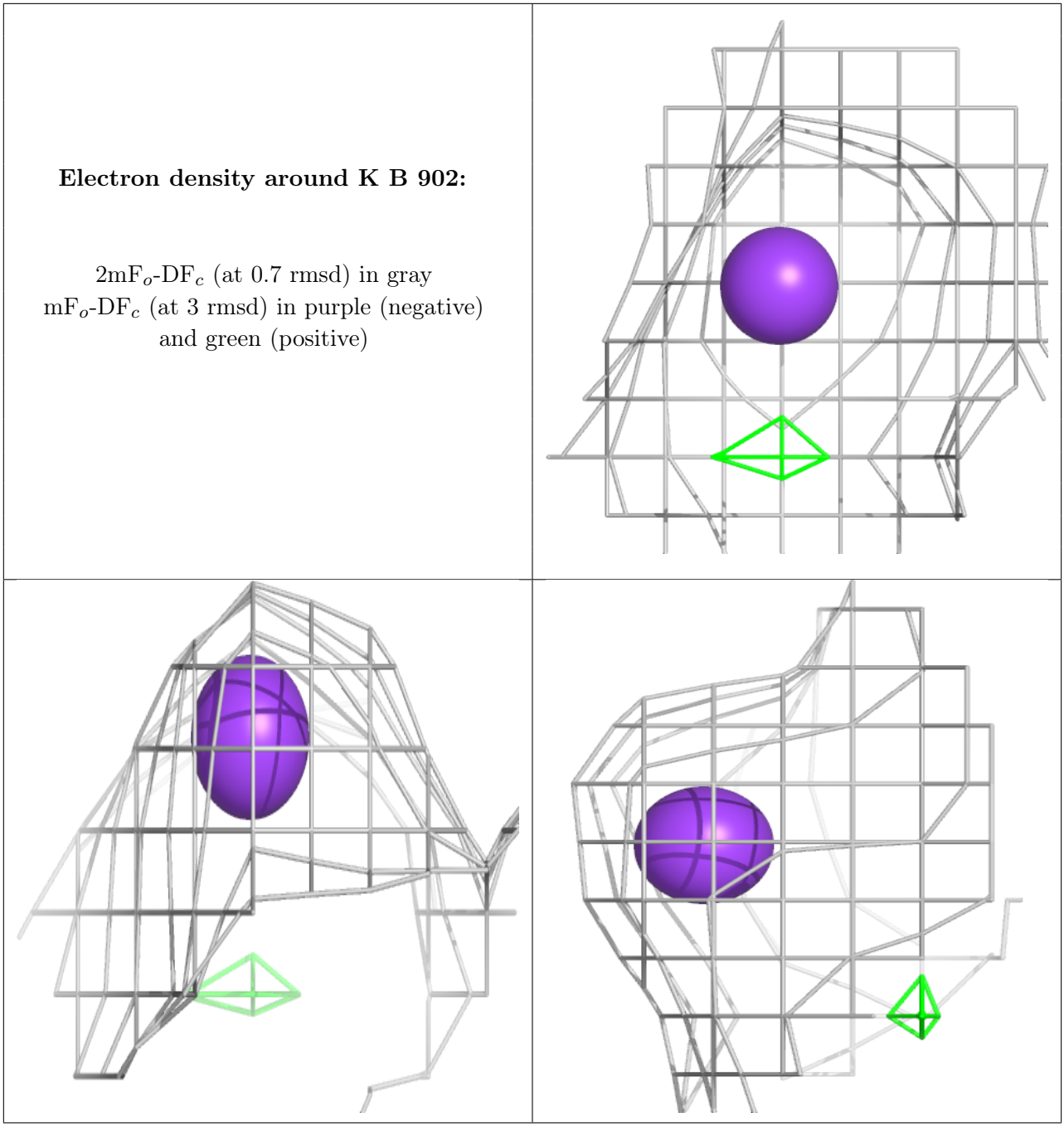
Electron density around K B 901:

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



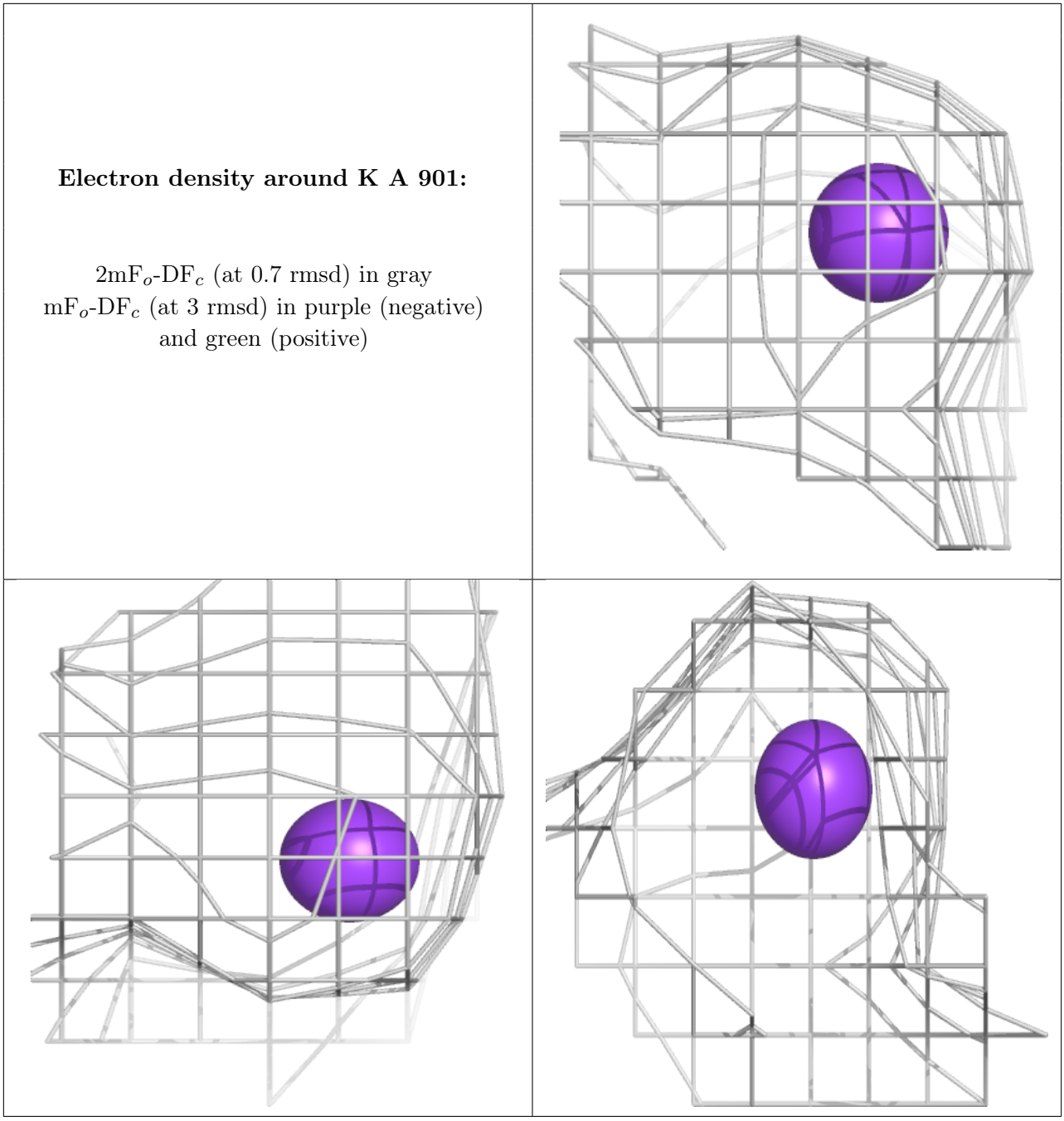
Electron density around K B 902:

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



Electron density around K A 901:

$2mF_o$-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.