



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 19, 2022 – 07:36 AM JST

PDB ID : 7VCM
Title : crystal structure of GINKO1
Authors : Wen, Y.; Campbell, R.E.; Lemieux, M.J.
Deposited on : 2021-09-03
Resolution : 1.85 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 : 4.02b-467
Mogul : ?? (???), CSD ??CSD?? (????)
Xtriage (Phenix) : 1.13
EDS : 2.29
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.29

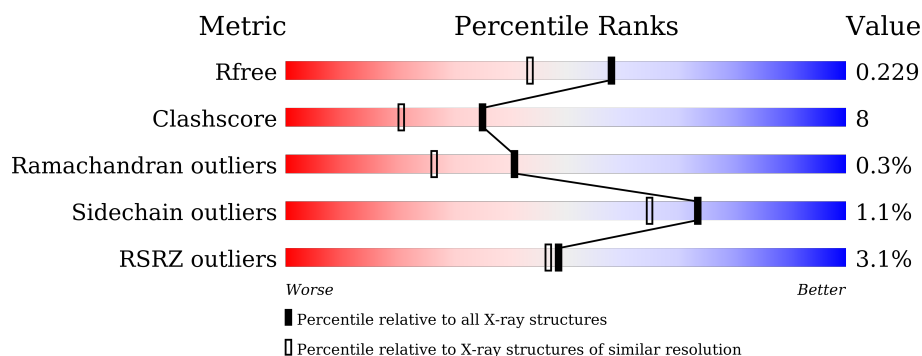
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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	386	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>13%</div> <div>••</div> </div> </div>
1	B	386	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>12%</div> <div>•</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6703 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 Green fluorescent protein,Potassium binding protein Kbp,Green fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	372	Total	C	N	O	S	0	0	0
			2910	1850	487	566	7			
1	B	370	Total	C	N	O	S	0	0	0
			2899	1844	485	563	7			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P42212
A	2	VAL	-	expression tag	UNP P42212
A	65	LEU	PHE	engineered mutation	UNP P42212
A	67	CRO	SER	chromophore	UNP P42212
A	67	CRO	TYR	chromophore	UNP P42212
A	67	CRO	GLY	chromophore	UNP P42212
A	94	ILE	VAL	engineered mutation	UNP P42212
A	146	LEU	-	linker	UNP P42212
A	147	PRO	-	linker	UNP P42212
A	148	ASP	-	linker	UNP P42212
A	297	LEU	-	linker	UNP P0ADE6
A	298	GLU	-	linker	UNP P0ADE6
A	303	LYS	MET	engineered mutation	UNP P42212
A	313	ALA	VAL	engineered mutation	UNP P42212
A	325	GLY	SER	engineered mutation	UNP P42212
A	330	TYR	ASP	engineered mutation	UNP P42212
A	353	VAL	THR	engineered mutation	UNP P42212
A	356	LYS	ALA	engineered mutation	UNP P42212
A	381	LEU	HIS	engineered mutation	UNP P42212
B	1	MET	-	initiating methionine	UNP P42212
B	2	VAL	-	expression tag	UNP P42212
B	65	LEU	PHE	engineered mutation	UNP P42212
B	67	CRO	SER	chromophore	UNP P42212
B	67	CRO	TYR	chromophore	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	67	CRO	GLY	chromophore	UNP P42212
B	94	ILE	VAL	engineered mutation	UNP P42212
B	146	LEU	-	linker	UNP P42212
B	147	PRO	-	linker	UNP P42212
B	148	ASP	-	linker	UNP P42212
B	297	LEU	-	linker	UNP P0ADE6
B	298	GLU	-	linker	UNP P0ADE6
B	303	LYS	MET	engineered mutation	UNP P42212
B	313	ALA	VAL	engineered mutation	UNP P42212
B	325	GLY	SER	engineered mutation	UNP P42212
B	330	TYR	ASP	engineered mutation	UNP P42212
B	353	VAL	THR	engineered mutation	UNP P42212
B	356	LYS	ALA	engineered mutation	UNP P42212
B	381	LEU	HIS	engineered mutation	UNP P42212

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total K 1 1	0	0
2	B	1	Total K 1 1	0	0

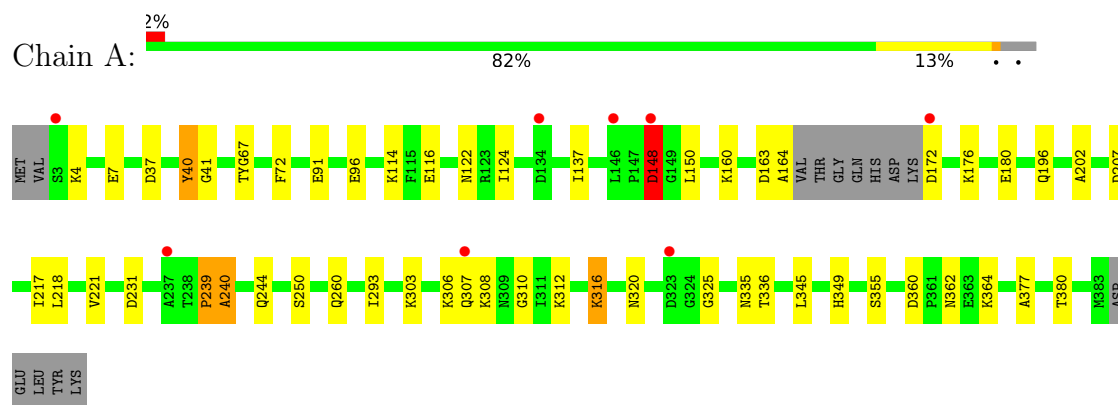
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	455	Total O 455 455	0	0
3	B	437	Total O 437 437	0	0

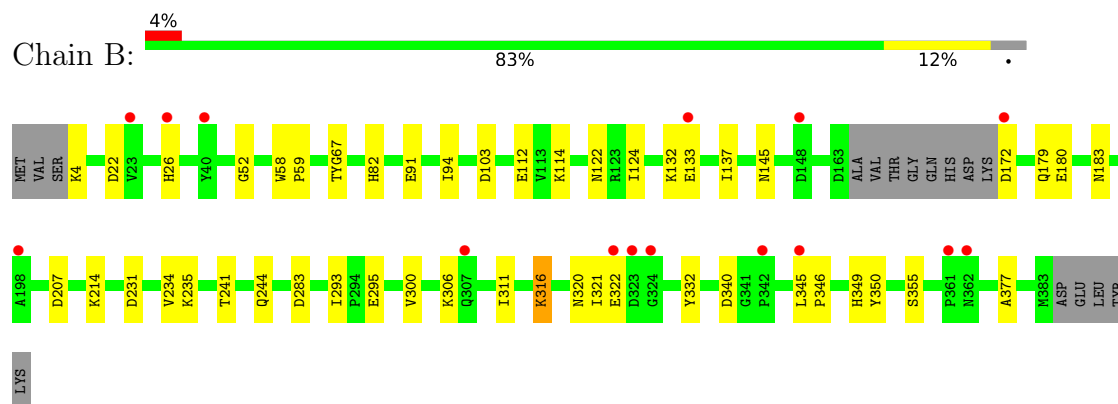
3 Residue-property plots [i](#)

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: Green fluorescent protein,Potassium binding protein Kbp,Green fluorescent protein



- Molecule 1: Green fluorescent protein,Potassium binding protein Kbp,Green fluorescent protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	46.83Å 49.32Å 83.68Å 89.96° 89.97° 80.95°	Depositor
Resolution (Å)	42.08 – 1.85 42.11 – 1.85	Depositor EDS
% Data completeness (in resolution range)	93.5 (42.08-1.85) 93.4 (42.11-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 1.86Å)	Xtriage
Refinement program	PHENIX 1.19	Depositor
R, R_{free}	0.195 , 0.225 0.203 , 0.229	Depositor DCC
R_{free} test set	1997 reflections (3.38%)	wwPDB-VP
Wilson B-factor (Å ²)	16.7	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 35.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.477 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6703	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CRO, 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	0.42	1/2944 (0.0%)	0.65	3/3978 (0.1%)
1	B	0.40	0/2933	0.56	0/3963
All	All	0.41	1/5877 (0.0%)	0.61	3/7941 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	250	SER	CB-OG	-6.81	1.33	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148	ASP	CB-CG-OD1	12.03	129.13	118.30
1	A	148	ASP	CB-CG-OD2	-10.85	108.53	118.30
1	A	40	TYR	CA-CB-CG	5.53	123.91	113.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2910	0	2877	52	0
1	B	2899	0	2867	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	455	0	0	25	6
3	B	437	0	0	29	3
All	All	6703	0	5744	95	6

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 8.

The worst 5 of 95 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:316:LYS:NZ	3:A:502:HOH:O	1.84	1.09
1:A:307:GLN:NE2	3:A:505:HOH:O	1.92	0.99
1:A:335:ASN:O	3:A:501:HOH:O	1.81	0.95
1:A:91:GLU:HG2	3:A:827:HOH:O	1.64	0.94
1:B:179:GLN:O	3:B:501:HOH:O	1.88	0.90

The worst 5 of 6 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:524:HOH:O	3:A:718:HOH:O[1_455]	1.70	0.50
3:A:865:HOH:O	3:A:928:HOH:O[1_565]	1.85	0.35
3:A:817:HOH:O	3:B:514:HOH:O[1_565]	2.00	0.20
3:A:875:HOH:O	3:B:529:HOH:O[1_564]	2.02	0.18
3:A:875:HOH:O	3:B:898:HOH:O[1_554]	2.06	0.14

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	365/386 (95%)	353 (97%)	10 (3%)	2 (0%)	29	15
1	B	363/386 (94%)	352 (97%)	11 (3%)	0	100	100
All	All	728/772 (94%)	705 (97%)	21 (3%)	2 (0%)	41	26

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	239	PRO
1	A	240	ALA

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	314/328 (96%)	310 (99%)	4 (1%)	69	58
1	B	313/328 (95%)	310 (99%)	3 (1%)	76	69
All	All	627/656 (96%)	620 (99%)	7 (1%)	73	65

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	355	SER
1	B	207	ASP
1	B	355	SER
1	B	316	LYS
1	A	316	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	244	GLN
1	A	320	ASN
1	B	309	ASN
1	B	320	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	371/386 (96%)	0.02	8 (2%) 62 61	7, 21, 48, 72	0
1	B	369/386 (95%)	0.09	15 (4%) 37 35	7, 22, 50, 88	0
All	All	740/772 (95%)	0.05	23 (3%) 49 47	7, 22, 49, 88	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	307	GLN	5.8
1	B	324	GLY	4.0
1	B	362	ASN	3.8
1	A	237	ALA	3.4
1	B	323	ASP	3.1

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	CRO	A	67	22/23	0.93	0.12	6,10,12,17	0
1	CRO	B	67	22/23	0.96	0.08	6,10,13,14	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands

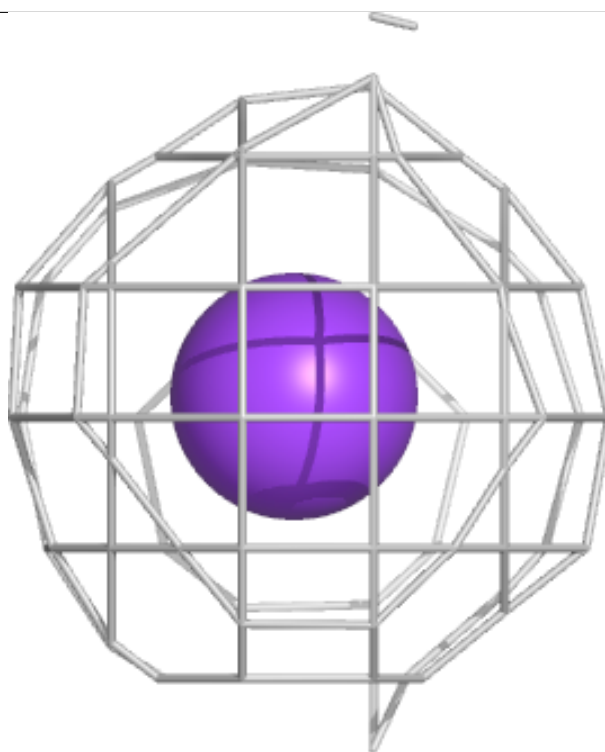
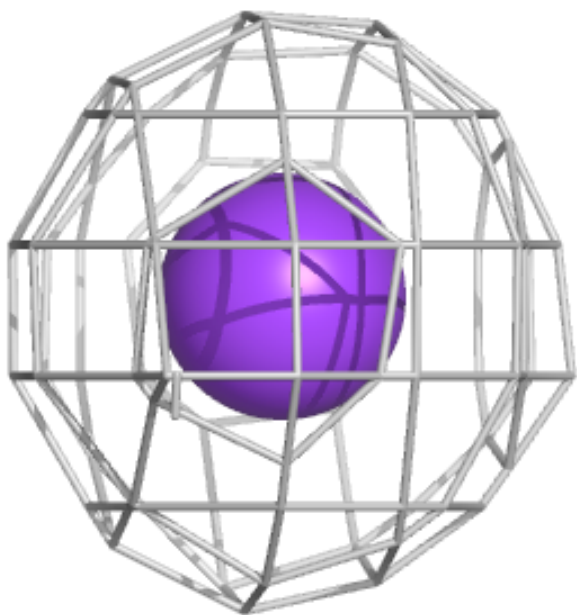
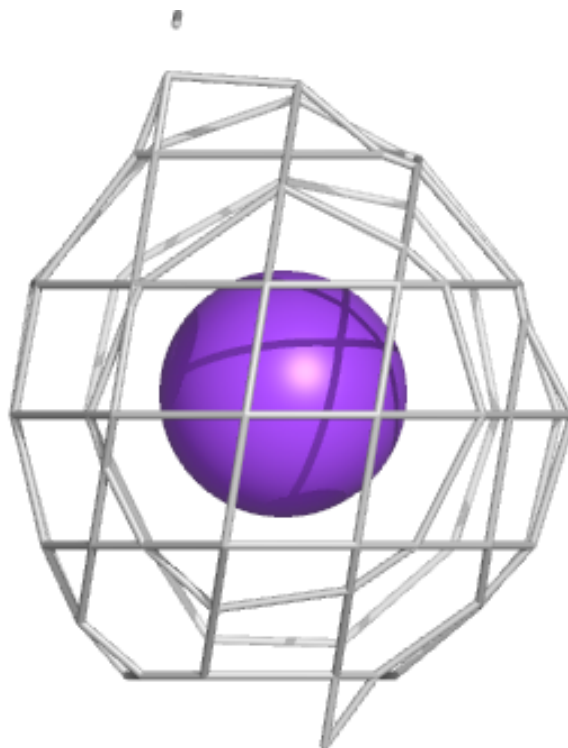
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

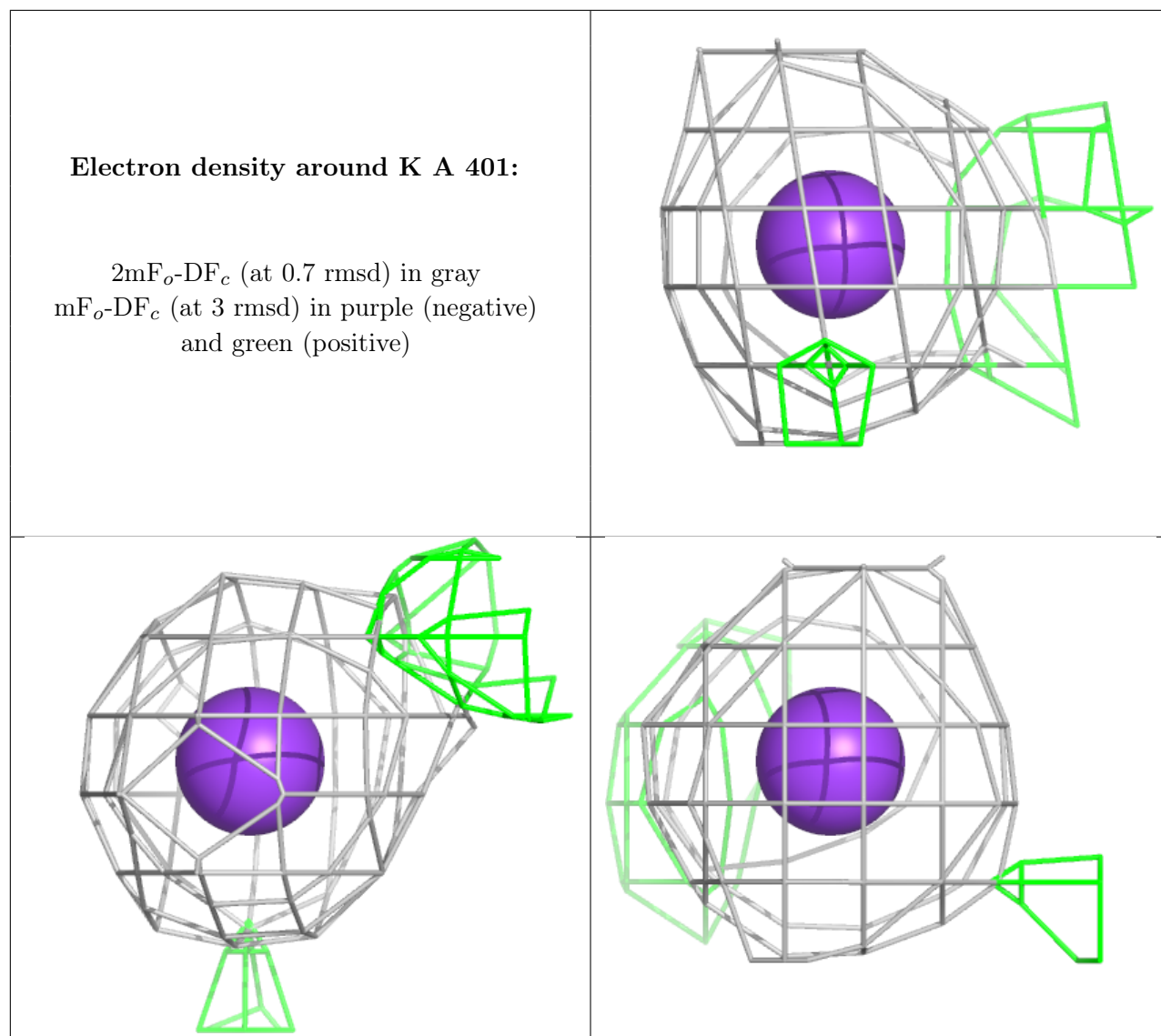
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	K	B	401	1/1	0.99	0.03	13,13,13,13	0
2	K	A	401	1/1	1.00	0.07	12,12,12,12	0

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 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.