



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:20 PM UTC

PDB ID : 7DSP / pdb_00007dsp
Title : Anthranilate phosphoribosyltransferase variant Ser121Ala from *Saccharomyces cerevisiae* with Mg bound
Authors : Wu, X.
Deposited on : 2020-12-31
Resolution : 1.95 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

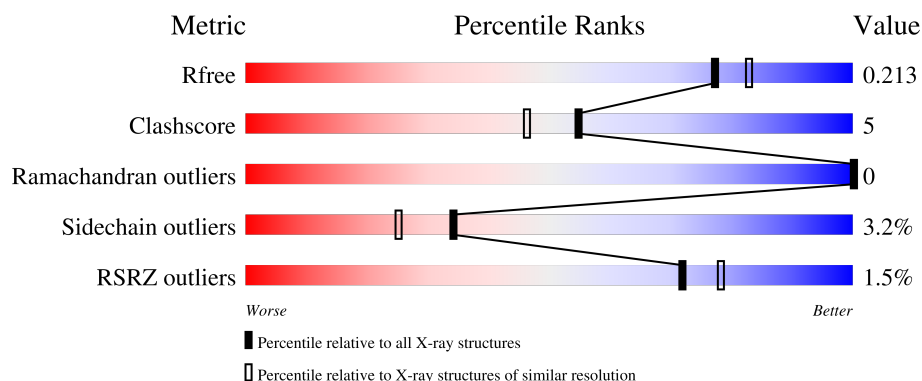
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	383	0% 82% 10% 7%
1	B	383	2% 82% 10% 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5917 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 Anthranilate phosphoribosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	357	Total	C	N	O	S	0	0	0
			2734	1757	458	508	11			
1	A	356	Total	C	N	O	S	0	0	0
			2739	1761	458	509	11			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	expression tag	UNP P07285
B	-1	HIS	-	expression tag	UNP P07285
B	0	HIS	-	expression tag	UNP P07285
B	121	ALA	SER	engineered mutation	UNP P07285
A	-2	HIS	-	expression tag	UNP P07285
A	-1	HIS	-	expression tag	UNP P07285
A	0	HIS	-	expression tag	UNP P07285
A	121	ALA	SER	engineered mutation	UNP P07285

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

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	205	Total	O	0	0
			205	205		

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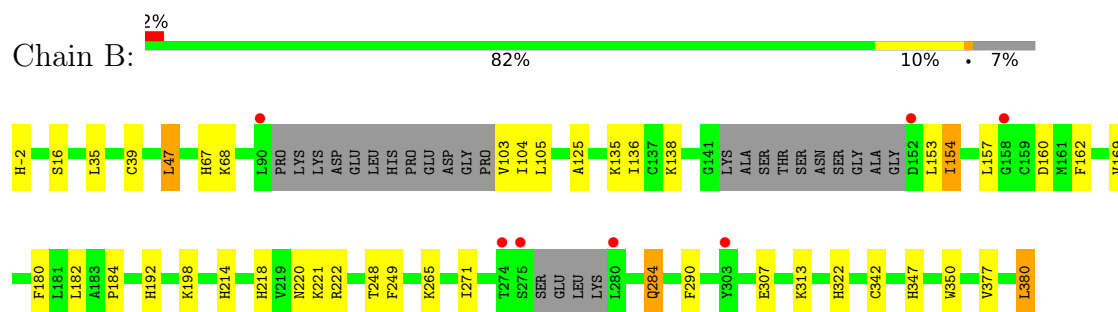
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	237	Total	O	0	0
			237	237		

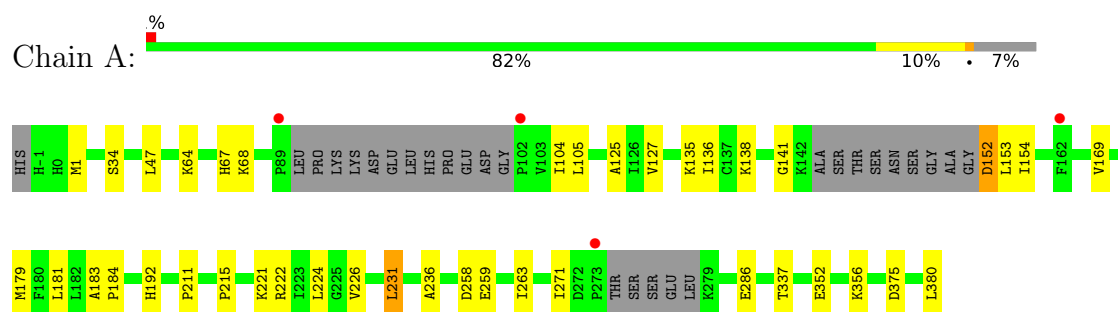
3 Residue-property plots [i](#)

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: Anthranilate phosphoribosyltransferase



- Molecule 1: Anthranilate phosphoribosyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.16Å 87.00Å 108.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.06 – 1.95 46.06 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.06-1.95) 99.9 (46.06-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.77 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.164 , 0.208 (Not available) , 0.213	Depositor DCC
R_{free} test set	2726 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 25.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5917	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.29% 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: MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.08	0/2801	1.24	2/3799 (0.1%)
1	B	1.07	1/2796 (0.0%)	1.25	2/3794 (0.1%)
All	All	1.07	1/5597 (0.0%)	1.24	4/7593 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	214	HIS	CE1-NE2	5.48	1.38	1.32

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	169	VAL	N-CA-CB	6.46	114.57	110.50
1	A	141	GLY	CA-C-O	-5.93	118.14	122.23
1	A	286	GLU	CB-CA-C	5.26	117.82	109.55
1	B	249	PHE	CA-CB-CG	5.17	118.97	113.80

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	2739	0	2748	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2734	0	2728	28	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	237	0	0	4	0
3	B	205	0	0	6	0
All	All	5917	0	5476	53	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 (53) 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:B:104:ILE:H	1:B:220:ASN:HD22	1.14	0.90
1:B:104:ILE:N	1:B:220:ASN:HD22	1.89	0.71
1:A:67:HIS:CD2	3:A:577:HOH:O	2.44	0.70
1:B:218:HIS:HD2	3:B:665:HOH:O	1.80	0.63
1:B:47:LEU:HD23	1:A:47:LEU:HD23	1.79	0.63
1:A:64:LYS:NZ	3:A:501:HOH:O	2.32	0.63
1:A:169:VAL:HG13	1:A:179:MET:HE1	1.79	0.62
1:B:160:ASP:HB3	1:B:162:PHE:CE2	2.35	0.61
1:A:236:ALA:HB1	1:A:271:ILE:HD11	1.84	0.60
1:B:67:HIS:HD2	3:B:681:HOH:O	1.84	0.60
1:B:-2:HIS:N	3:B:502:HOH:O	2.36	0.59
1:B:377:VAL:HA	1:B:380:LEU:HD22	1.85	0.58
1:A:152:ASP:N	1:A:152:ASP:OD1	2.36	0.58
1:B:153:LEU:C	1:B:153:LEU:HD23	2.29	0.57
1:A:192:HIS:HE1	3:A:664:HOH:O	1.88	0.56
1:B:182:LEU:HG	1:B:184:PRO:HD2	1.89	0.54
1:B:154:ILE:HA	1:B:157:LEU:HD12	1.90	0.53
1:B:125:ALA:HB1	1:B:136:ILE:HG21	1.93	0.51
1:B:67:HIS:CD2	3:B:681:HOH:O	2.61	0.51
1:B:290:PHE:CE2	1:B:350:TRP:HB3	2.47	0.50
1:B:105:LEU:HA	1:B:221:LYS:O	2.12	0.49
1:A:153:LEU:C	1:A:153:LEU:HD23	2.38	0.48
1:B:322:HIS:HD2	3:B:503:HOH:O	1.96	0.48
1:B:104:ILE:HA	1:B:135:LYS:O	2.13	0.48
1:B:248:THR:HB	1:B:271:ILE:HD12	1.95	0.48
1:B:104:ILE:H	1:B:220:ASN:ND2	1.96	0.47
1:A:352:GLU:OE1	1:A:356:LYS:NZ	2.40	0.47
1:B:138:LYS:HD2	1:B:180:PHE:CE2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:VAL:HG21	1:A:231:LEU:HD13	1.96	0.47
1:B:192:HIS:HE1	3:B:598:HOH:O	1.99	0.46
1:B:160:ASP:HB3	1:B:162:PHE:CD2	2.51	0.45
1:A:1:MET:HE3	1:A:34:SER:HB2	1.98	0.45
1:A:375:ASP:HB2	3:A:667:HOH:O	2.15	0.45
1:B:265:LYS:HD3	1:B:284:GLN:HE21	1.81	0.45
1:A:231:LEU:HD22	1:A:231:LEU:O	2.18	0.44
1:A:125:ALA:HB1	1:A:136:ILE:HG21	1.98	0.44
1:B:307:GLU:HA	1:B:307:GLU:OE2	2.19	0.43
1:A:183:ALA:HB3	1:A:184:PRO:HD3	1.99	0.43
1:A:211:PRO:HB3	1:A:224:LEU:HD22	1.99	0.43
1:B:153:LEU:C	1:B:153:LEU:CD2	2.92	0.43
1:A:105:LEU:HA	1:A:221:LYS:O	2.20	0.42
1:A:181:LEU:HD23	1:A:215:PRO:HG2	2.01	0.42
1:A:236:ALA:CB	1:A:271:ILE:HD11	2.50	0.42
1:A:68:LYS:HA	1:A:68:LYS:HD3	1.74	0.41
1:A:127:VAL:HG12	1:A:337:THR:HG21	2.03	0.41
1:B:342:CYS:HB3	1:B:347:HIS:O	2.20	0.41
1:B:265:LYS:CD	1:B:284:GLN:HE21	2.34	0.41
1:A:258:ASP:C	1:A:259:GLU:HG2	2.45	0.41
1:B:153:LEU:HD23	1:B:153:LEU:O	2.20	0.41
1:A:179:MET:HE2	1:A:179:MET:HB3	1.75	0.41
1:A:226:VAL:HG21	1:A:231:LEU:CD1	2.51	0.40
1:A:104:ILE:HA	1:A:135:LYS:O	2.21	0.40
1:A:226:VAL:CG2	1:A:231:LEU:HD12	2.52	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	348/383 (91%)	340 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	349/383 (91%)	343 (98%)	6 (2%)	0	100	100
All	All	697/766 (91%)	683 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	303/328 (92%)	296 (98%)	7 (2%)	44	38
1	B	300/328 (92%)	288 (96%)	12 (4%)	28	17
All	All	603/656 (92%)	584 (97%)	19 (3%)	34	25

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	16	SER
1	B	35	LEU
1	B	39	CYS
1	B	47	LEU
1	B	68	LYS
1	B	103	VAL
1	B	154	ILE
1	B	198	LYS
1	B	222	ARG
1	B	284	GLN
1	B	313	LYS
1	B	380	LEU
1	A	138	LYS
1	A	152	ASP
1	A	154	ILE
1	A	222	ARG
1	A	231	LEU
1	A	263	ILE

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Mol	Chain	Res	Type
1	A	380	LEU

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

Mol	Chain	Res	Type
1	B	0	HIS
1	B	19	GLN
1	B	26	HIS
1	B	192	HIS
1	B	220	ASN
1	B	284	GLN
1	B	322	HIS
1	A	19	GLN
1	A	192	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 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	356/383 (92%)	-0.24	4 (1%) 78 83	21, 29, 48, 65	0
1	B	357/383 (93%)	-0.12	7 (1%) 65 72	21, 30, 51, 74	0
All	All	713/766 (93%)	-0.18	11 (1%) 72 78	21, 29, 49, 74	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	158	GLY	4.3
1	A	273	PRO	3.1
1	A	162	PHE	3.1
1	B	274	THR	2.8
1	B	275	SER	2.8
1	B	90	LEU	2.6
1	B	152	ASP	2.5
1	A	89	PRO	2.5
1	B	303	TYR	2.3
1	B	280	LEU	2.2
1	A	102	PRO	2.2

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

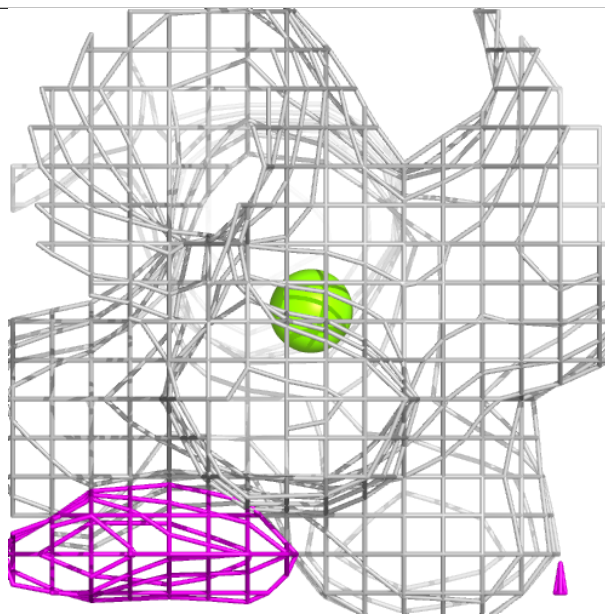
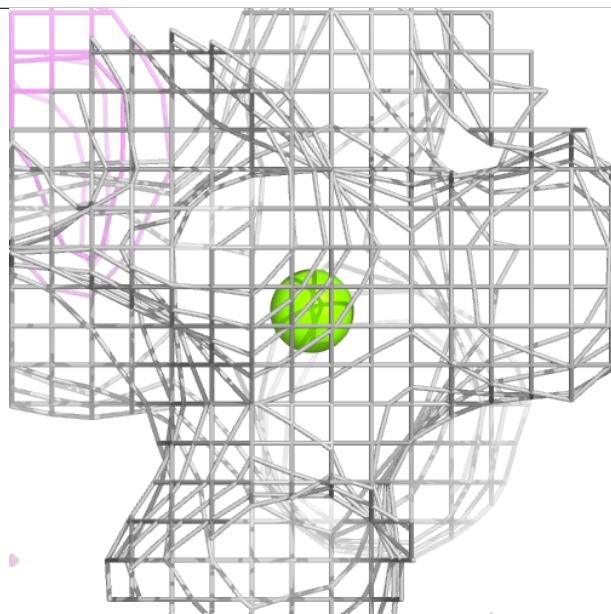
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MG	B	401	1/1	0.97	0.07	33,33,33,33	0
2	MG	A	401	1/1	0.99	0.04	28,28,28,28	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.

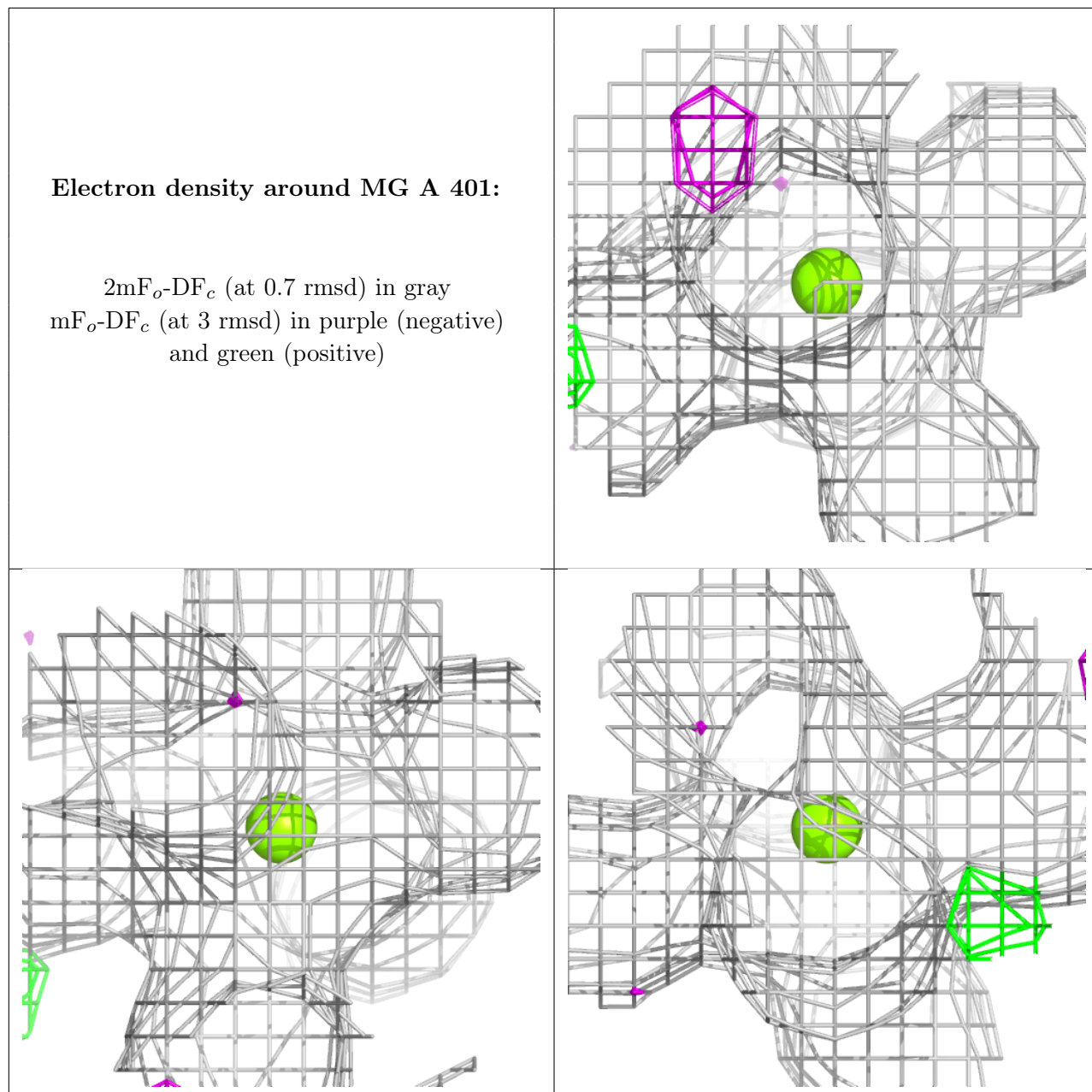
Electron density around MG B 401:

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



Electron density around MG 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.