



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 01:03 AM UTC

PDB ID : 7CWV / pdb_00007cwv
Title : Crystal structure of Arabinose isomerase from hyper thermophilic bacterium
Thermotoga maritima (TMAI) wt
Authors : Hoang, N.K.Q.; Dhanasingh, I.; Cao, T.P.; Sung, J.Y.; Shin, S.M.; Lee, D.W.;
Lee, S.H.
Deposited on : 2020-08-31
Resolution : 3.53 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

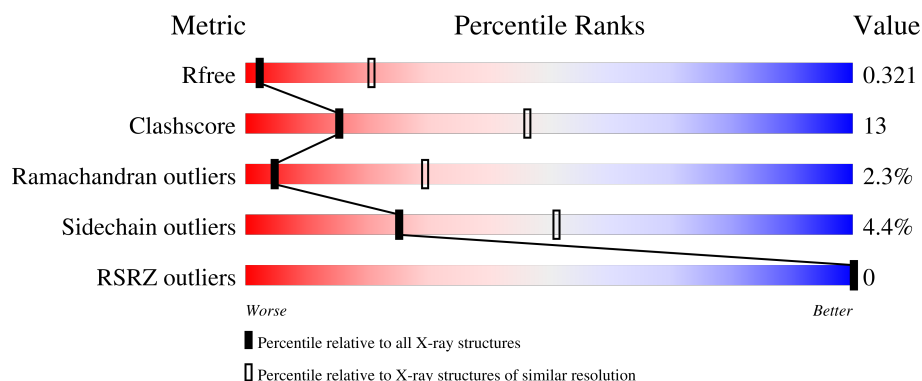
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.53 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	1008 (3.58-3.50)
Clashscore	190562	1062 (3.58-3.50)
Ramachandran outliers	187476	1033 (3.58-3.50)
Sidechain outliers	187428	1034 (3.58-3.50)
RSRZ outliers	180081	1007 (3.58-3.50)

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	496	61% 35% ..
1	B	496	70% 27% .
1	C	496	59% 37% ..
1	D	496	65% 32% .
1	E	496	62% 35% .

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Mol	Chain	Length	Quality of chain
1	F	496	 64% 31% 5%
1	G	496	 65% 32% •
1	H	496	 67% 30% •
1	I	496	 68% 30% •
1	J	496	 63% 34% •
1	K	496	 67% 31% •
1	L	496	 72% 26% •

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 47714 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 L-arabinose isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	0	0	0
			3943	2534	675	715	19			
1	B	494	Total	C	N	O	S	0	0	0
			3973	2552	678	725	18			
1	C	487	Total	C	N	O	S	0	0	0
			3930	2524	670	717	19			
1	D	495	Total	C	N	O	S	0	0	0
			3981	2557	679	726	19			
1	E	495	Total	C	N	O	S	0	0	0
			3981	2557	679	726	19			
1	F	495	Total	C	N	O	S	0	0	0
			3981	2557	679	726	19			
1	G	495	Total	C	N	O	S	0	0	0
			3981	2557	679	726	19			
1	H	495	Total	C	N	O	S	0	0	0
			3981	2557	679	726	19			
1	I	495	Total	C	N	O	S	0	0	0
			3981	2557	679	726	19			
1	J	495	Total	C	N	O	S	0	0	0
			3981	2557	679	726	19			
1	K	495	Total	C	N	O	S	0	0	0
			3981	2557	679	726	19			
1	L	495	Total	C	N	O	S	0	0	0
			3981	2557	679	726	19			

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

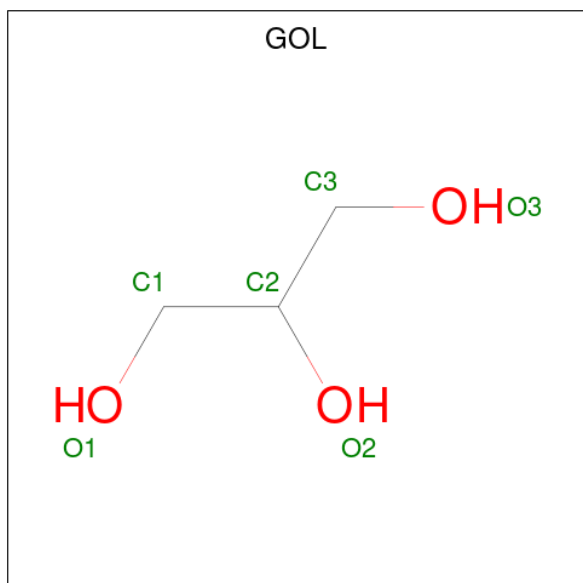
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		
2	B	1	Total	Mn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total	Mn	0	0
			1	1		
2	D	1	Total	Mn	0	0
			1	1		
2	E	1	Total	Mn	0	0
			1	1		
2	F	1	Total	Mn	0	0
			1	1		
2	G	1	Total	Mn	0	0
			1	1		
2	H	1	Total	Mn	0	0
			1	1		
2	I	1	Total	Mn	0	0
			1	1		
2	J	1	Total	Mn	0	0
			1	1		
2	K	1	Total	Mn	0	0
			1	1		
2	L	1	Total	Mn	0	0
			1	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			6	3	3		

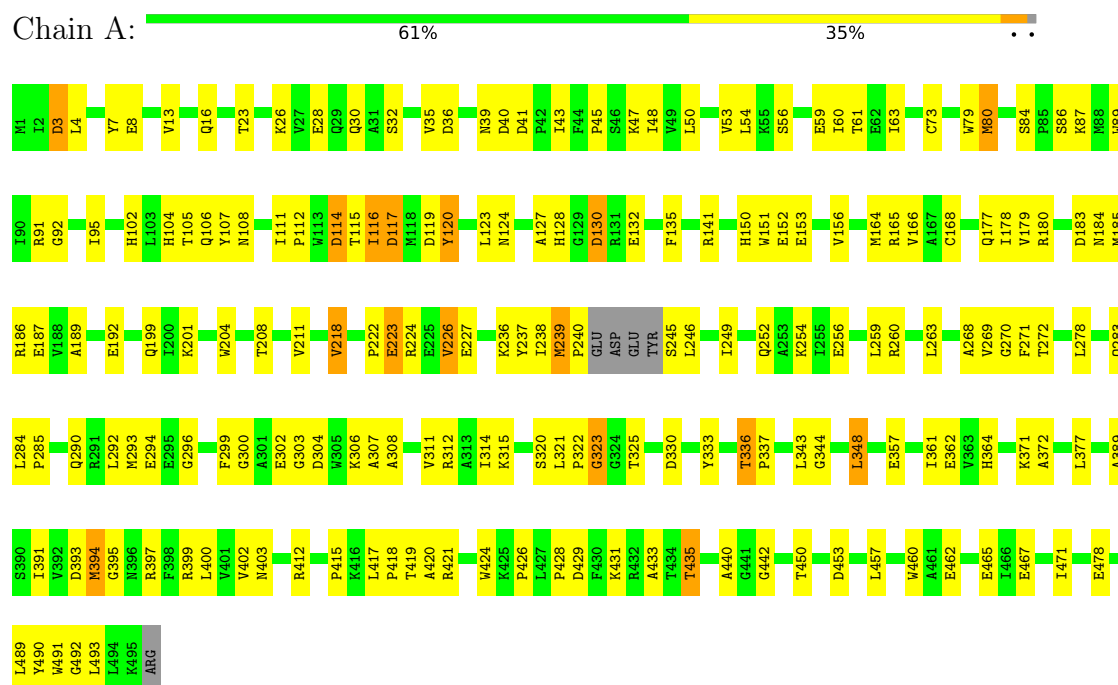
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total 5	O 5	0	0
4	B	1	Total 1	O 1	0	0
4	C	1	Total 1	O 1	0	0
4	D	1	Total 1	O 1	0	0
4	F	2	Total 2	O 2	0	0
4	G	4	Total 4	O 4	0	0
4	H	1	Total 1	O 1	0	0
4	I	1	Total 1	O 1	0	0
4	J	2	Total 2	O 2	0	0
4	K	2	Total 2	O 2	0	0
4	L	1	Total 1	O 1	0	0

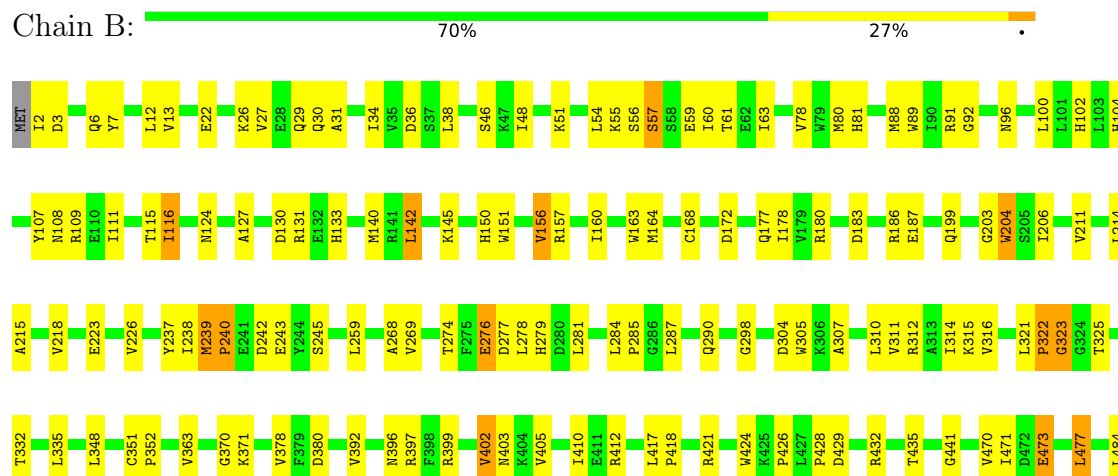
3 Residue-property plots

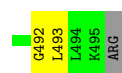
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: L-arabinose isomerase



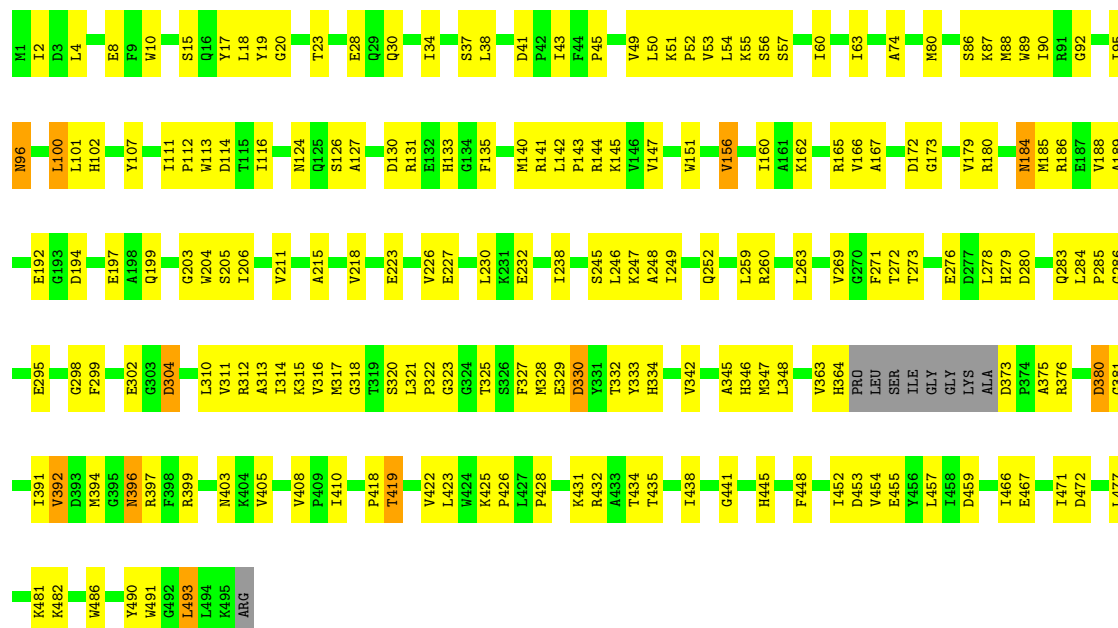
• Molecule 1: L-arabinose isomerase





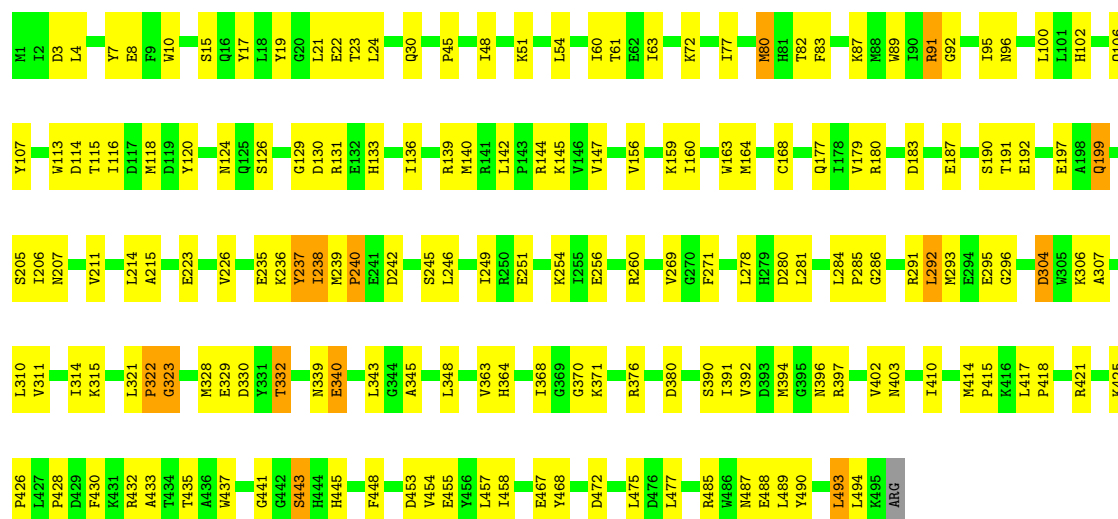
- Molecule 1: L-arabinose isomerase

Chain C: 59% 37%



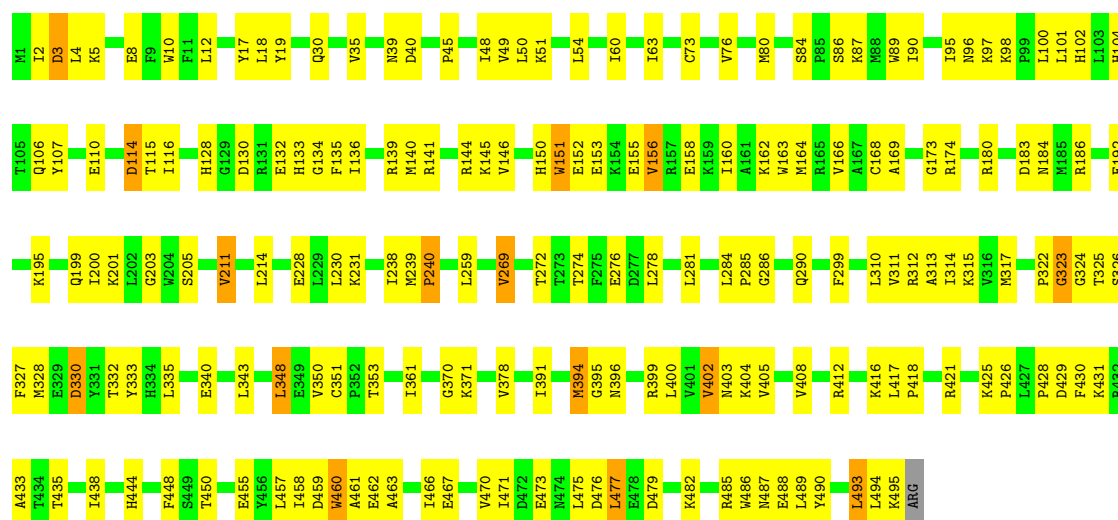
- Molecule 1: L-arabinose isomerase

Chain D: 65% 32%



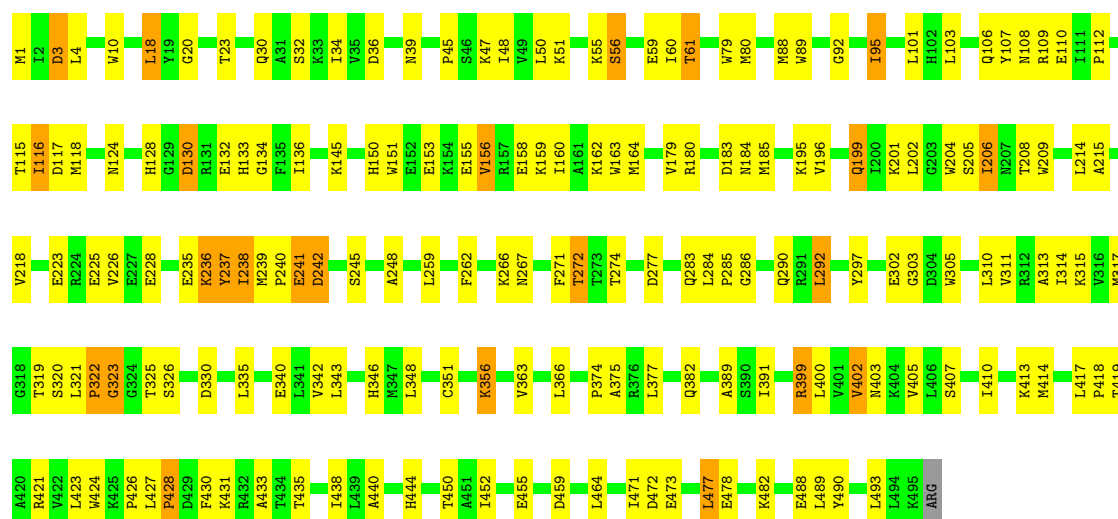
- Molecule 1: L-arabinose isomerase

Chain E: 62% 35%



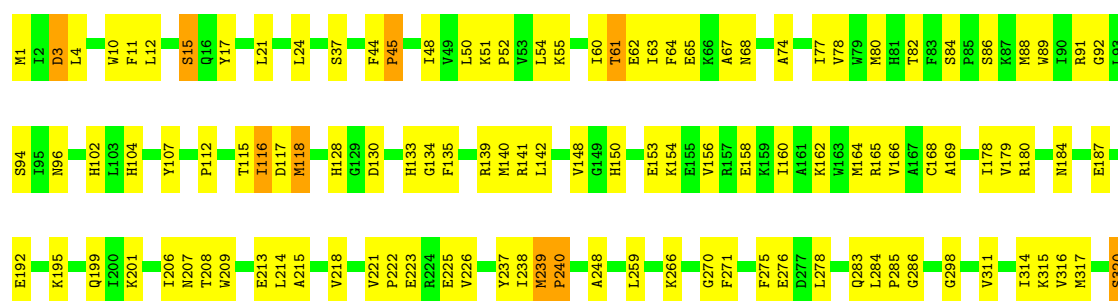
• Molecule 1: L-arabinose isomerase

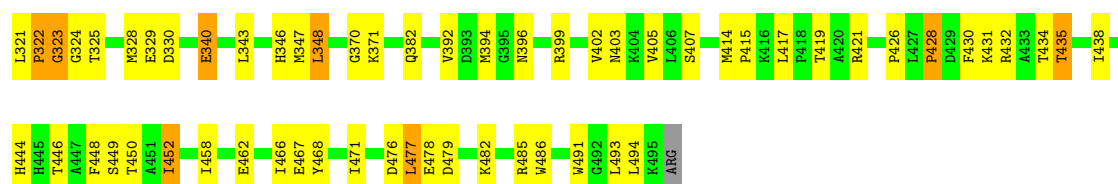
Chain F: 64% 31% 5%



• Molecule 1: L-arabinose isomerase

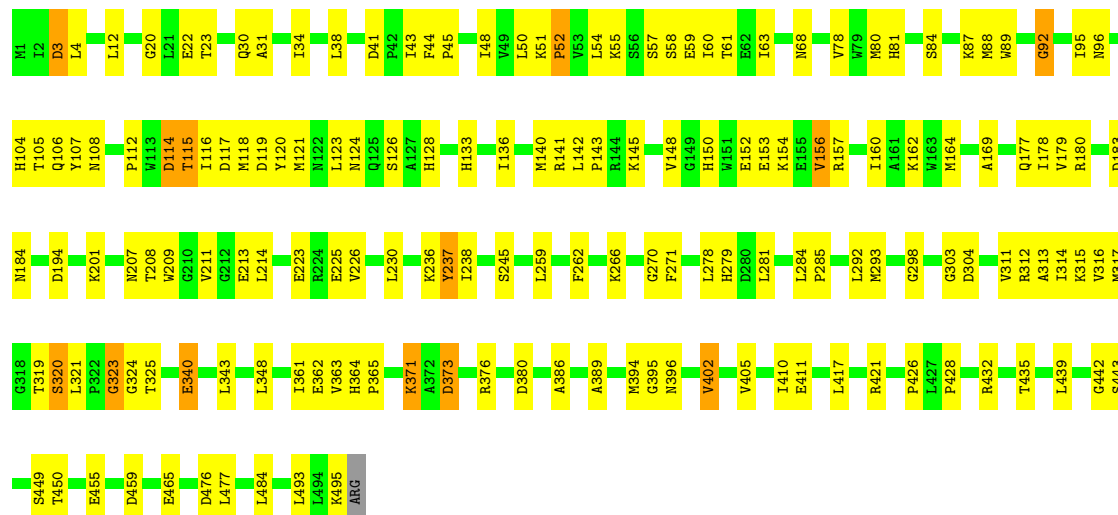
Chain G: 65% 32% 3%





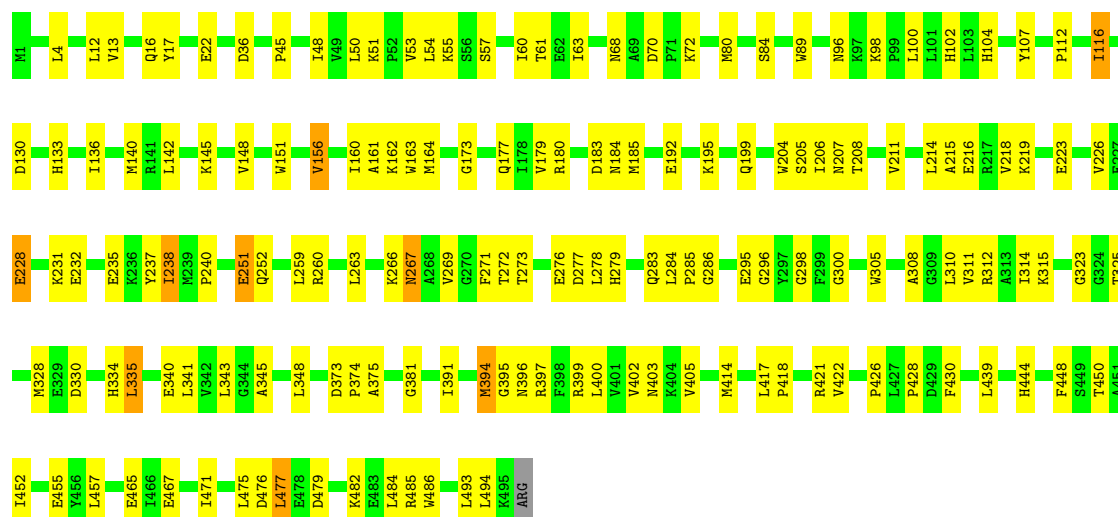
• Molecule 1: L-arabinose isomerase

Chain H: 67% 30%



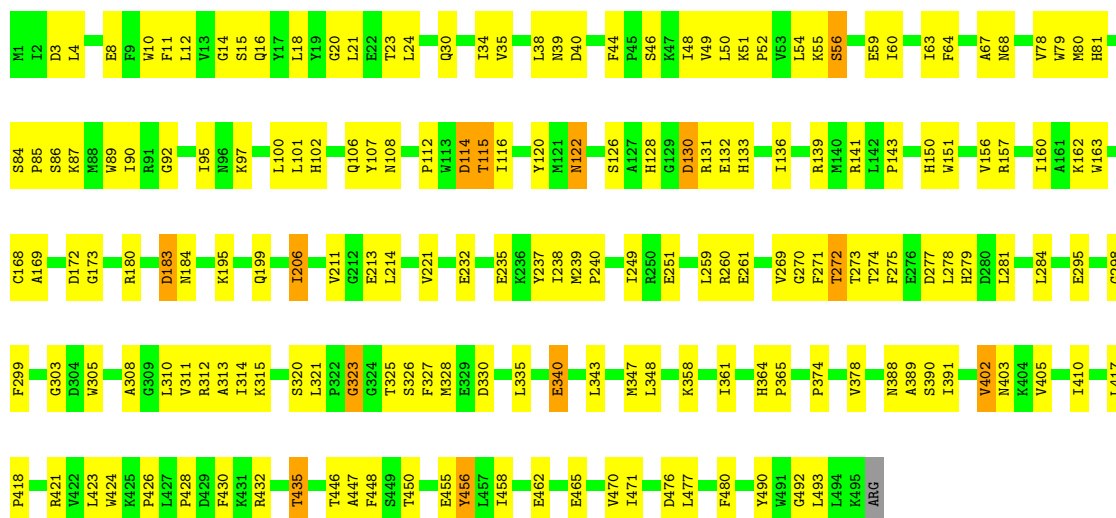
• Molecule 1: L-arabinose isomerase

Chain I: 68% 30%



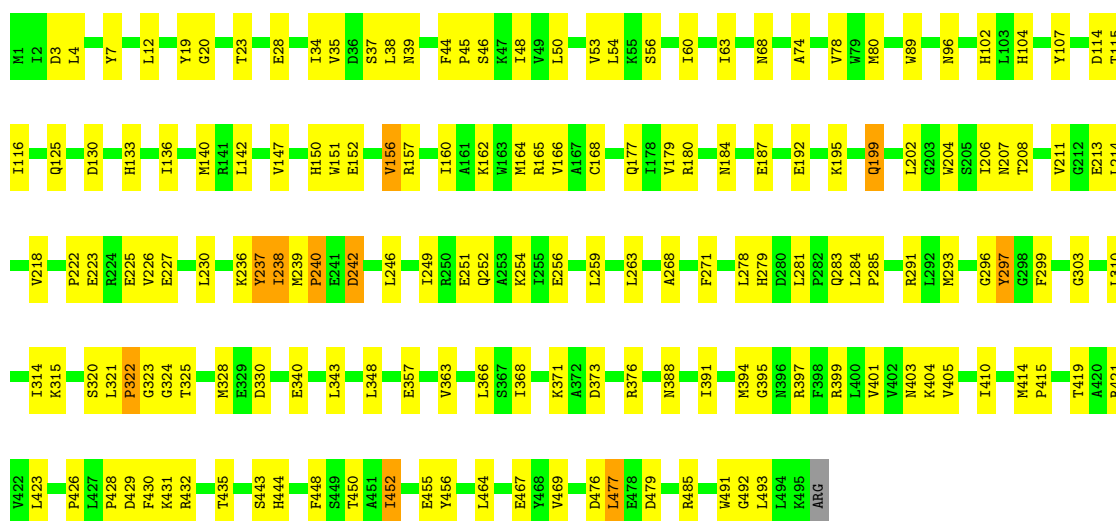
• Molecule 1: L-arabinose isomerase

Chain J: 63% 34%



• Molecule 1: L-arabinose isomerase

Chain K: 67% 31% .



• Molecule 1: L-arabinose isomerase

Chain L: 72% 26% .



T353	E357	K371	A372	D373	V392	D393	N396	R397	F398	R399	V402	N403	M414	R421	P428	D429	F430	T435	F448	S449	T450	A451	I452	I458	D459	E462	E465	V470	I471	D472	L477	F480	E483	L484	W491	G492	L493	L494	K495	ARG
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	85.97Å 109.43Å 153.85Å 98.14° 98.18° 89.97°	Depositor
Resolution (Å)	49.74 – 3.53 49.74 – 3.53	Depositor EDS
% Data completeness (in resolution range)	91.6 (49.74-3.53) 91.8 (49.74-3.53)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 3.48Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.222 , 0.332 0.218 , 0.321	Depositor DCC
R_{free} test set	3146 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	88.6	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 74.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	47714	wwPDB-VP
Average B, all atoms (Å ²)	118.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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: MN, GOL

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	1.02	0/4036	1.46	5/5459 (0.1%)
1	B	1.01	0/4068	1.44	4/5505 (0.1%)
1	C	1.02	0/4023	1.48	7/5442 (0.1%)
1	D	1.02	0/4076	1.47	7/5515 (0.1%)
1	E	1.02	0/4076	1.44	7/5515 (0.1%)
1	F	1.02	0/4076	1.45	6/5515 (0.1%)
1	G	1.01	1/4076 (0.0%)	1.47	6/5515 (0.1%)
1	H	1.02	0/4076	1.46	5/5515 (0.1%)
1	I	1.01	0/4076	1.46	0/5515
1	J	1.01	1/4076 (0.0%)	1.44	3/5515 (0.1%)
1	K	1.02	0/4076	1.46	4/5515 (0.1%)
1	L	1.02	0/4076	1.46	3/5515 (0.1%)
All	All	1.02	2/48811 (0.0%)	1.46	57/66041 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	221	VAL	N-CA	5.36	1.50	1.45
1	J	221	VAL	N-CA	5.31	1.50	1.45

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	269	VAL	N-CA-C	-6.12	106.98	112.12
1	B	3	ASP	CA-CB-CG	5.83	118.43	112.60
1	B	131	ARG	N-CA-C	-5.80	105.86	113.12
1	G	478	GLU	CA-C-N	5.57	128.02	120.44
1	G	478	GLU	C-N-CA	5.57	128.02	120.44

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	3943	0	3971	139	0
1	B	3973	0	3985	100	0
1	C	3930	0	3938	144	0
1	D	3981	0	3997	118	0
1	E	3981	0	3997	131	0
1	F	3981	0	3997	127	0
1	G	3981	0	3997	124	0
1	H	3981	0	3997	104	0
1	I	3981	0	3997	98	0
1	J	3981	0	3997	119	0
1	K	3981	0	3997	107	0
1	L	3981	0	3997	88	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	C	6	0	8	0	0
4	A	5	0	0	1	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	F	2	0	0	0	0
4	G	4	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	J	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	K	2	0	0	0	0
4	L	1	0	0	0	0
All	All	47714	0	47875	1287	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 13.

The worst 5 of 1287 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:I:162:LYS:HD2	1:I:455:GLU:HG2	1.57	0.87
1:J:403:ASN:HD21	1:J:426:PRO:HB3	1.42	0.84
1:C:180:ARG:NH2	1:C:184:ASN:OD1	2.12	0.83
1:L:278:LEU:O	1:L:371:LYS:NZ	2.11	0.83
1:E:145:LYS:HD3	1:E:459:ASP:OD1	1.81	0.80

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	487/496 (98%)	412 (85%)	67 (14%)	8 (2%)	7	36
1	B	492/496 (99%)	433 (88%)	48 (10%)	11 (2%)	5	30
1	C	483/496 (97%)	426 (88%)	46 (10%)	11 (2%)	5	29
1	D	493/496 (99%)	434 (88%)	44 (9%)	15 (3%)	3	25
1	E	493/496 (99%)	430 (87%)	49 (10%)	14 (3%)	4	25
1	F	493/496 (99%)	428 (87%)	53 (11%)	12 (2%)	4	29
1	G	493/496 (99%)	427 (87%)	56 (11%)	10 (2%)	6	32
1	H	493/496 (99%)	428 (87%)	55 (11%)	10 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	493/496 (99%)	426 (86%)	54 (11%)	13 (3%)	4	27
1	J	493/496 (99%)	426 (86%)	56 (11%)	11 (2%)	5	30
1	K	493/496 (99%)	432 (88%)	50 (10%)	11 (2%)	5	30
1	L	493/496 (99%)	439 (89%)	45 (9%)	9 (2%)	6	34
All	All	5899/5952 (99%)	5141 (87%)	623 (11%)	135 (2%)	5	29

5 of 135 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	323	GLY
1	B	323	GLY
1	C	238	ILE
1	D	242	ASP
1	D	323	GLY

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	421/426 (99%)	400 (95%)	21 (5%)	22	49
1	B	424/426 (100%)	409 (96%)	15 (4%)	32	57
1	C	420/426 (99%)	402 (96%)	18 (4%)	26	51
1	D	425/426 (100%)	411 (97%)	14 (3%)	33	58
1	E	425/426 (100%)	407 (96%)	18 (4%)	26	52
1	F	425/426 (100%)	400 (94%)	25 (6%)	18	45
1	G	425/426 (100%)	404 (95%)	21 (5%)	22	49
1	H	425/426 (100%)	403 (95%)	22 (5%)	21	48
1	I	425/426 (100%)	410 (96%)	15 (4%)	32	57
1	J	425/426 (100%)	404 (95%)	21 (5%)	22	49
1	K	425/426 (100%)	410 (96%)	15 (4%)	32	57
1	L	425/426 (100%)	407 (96%)	18 (4%)	26	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	5090/5112 (100%)	4867 (96%)	223 (4%)	25	51

5 of 223 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	61	THR
1	L	472	ASP
1	H	245	SER
1	L	450	THR
1	K	373	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	403	ASN
1	J	177	GLN
1	I	39	ASN
1	I	184	ASN
1	J	403	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 13 ligands modelled in this entry, 12 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	GOL	C	501	-	5,5,5	0.18	0	5,5,5	0.43	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
3	GOL	C	501	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	501	GOL	O1-C1-C2-O2
3	C	501	GOL	O1-C1-C2-C3

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	491/496 (98%)	-0.76	0 100 100	56, 102, 159, 278	0
1	B	494/496 (99%)	-0.75	0 100 100	70, 113, 180, 228	0
1	C	487/496 (98%)	-0.75	0 100 100	65, 108, 171, 216	0
1	D	495/496 (99%)	-0.77	0 100 100	64, 112, 191, 271	0
1	E	495/496 (99%)	-0.75	0 100 100	60, 111, 179, 213	0
1	F	495/496 (99%)	-0.75	0 100 100	49, 102, 158, 222	0
1	G	495/496 (99%)	-0.73	0 100 100	49, 105, 199, 283	0
1	H	495/496 (99%)	-0.76	0 100 100	64, 114, 171, 207	0
1	I	495/496 (99%)	-0.75	0 100 100	68, 118, 184, 296	0
1	J	495/496 (99%)	-0.76	0 100 100	68, 115, 184, 241	0
1	K	495/496 (99%)	-0.76	0 100 100	67, 115, 188, 236	0
1	L	495/496 (99%)	-0.74	0 100 100	67, 121, 184, 243	0
All	All	5927/5952 (99%)	-0.75	0 100 100	49, 111, 181, 296	0

There are no RSRZ outliers to report.

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

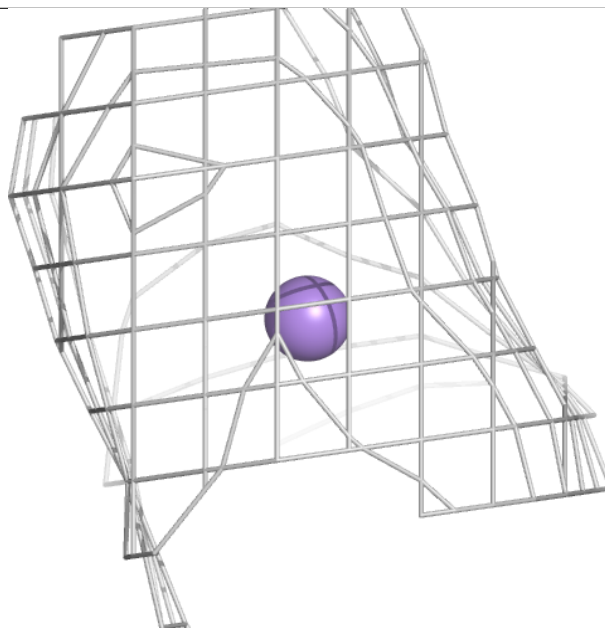
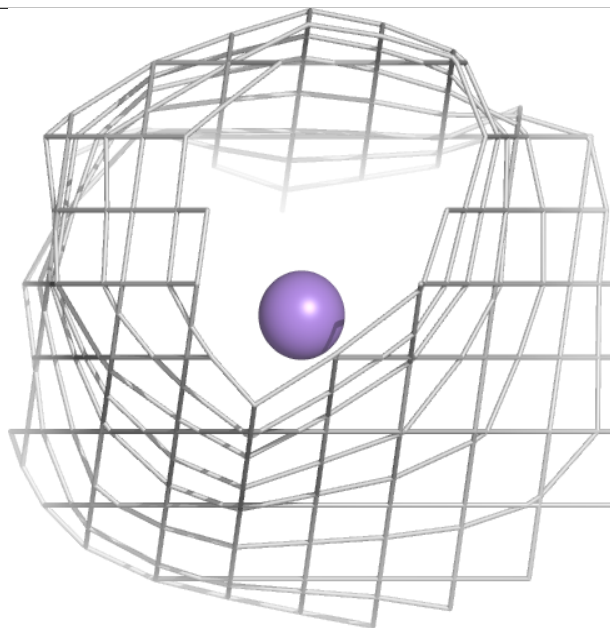
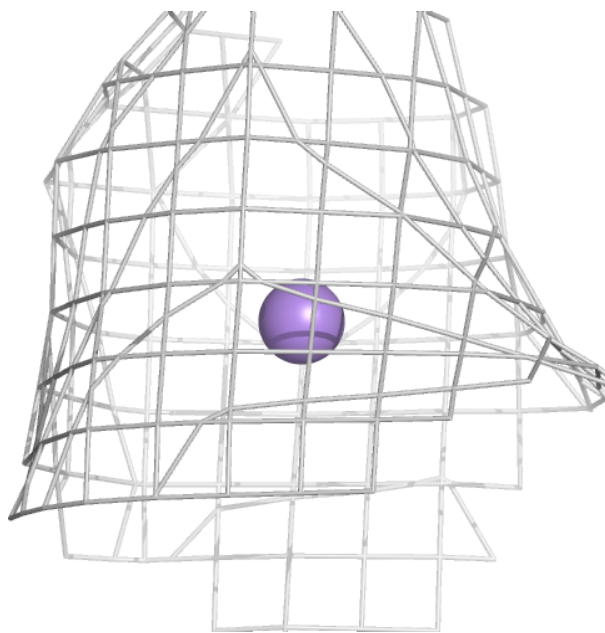
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MN	D	501	1/1	0.89	0.06	135,135,135,135	0
3	GOL	C	501	6/6	0.89	0.08	76,89,94,107	0
2	MN	E	501	1/1	0.97	0.04	115,115,115,115	0
2	MN	F	501	1/1	0.97	0.04	84,84,84,84	0
2	MN	G	501	1/1	0.97	0.03	99,99,99,99	0
2	MN	H	501	1/1	0.97	0.04	109,109,109,109	0
2	MN	K	501	1/1	0.97	0.03	117,117,117,117	0
2	MN	B	501	1/1	0.97	0.04	112,112,112,112	0
2	MN	I	501	1/1	0.98	0.03	112,112,112,112	0
2	MN	J	501	1/1	0.98	0.03	115,115,115,115	0
2	MN	C	502	1/1	0.99	0.02	112,112,112,112	0
2	MN	L	501	1/1	0.99	0.03	85,85,85,85	0
2	MN	A	501	1/1	0.99	0.04	84,84,84,84	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.

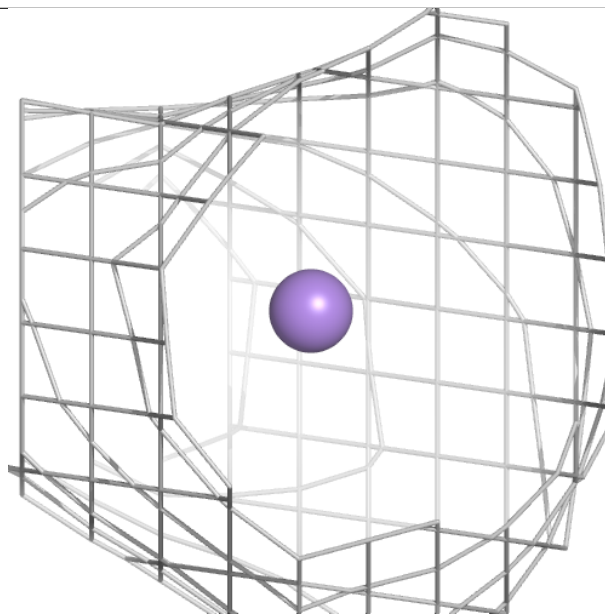
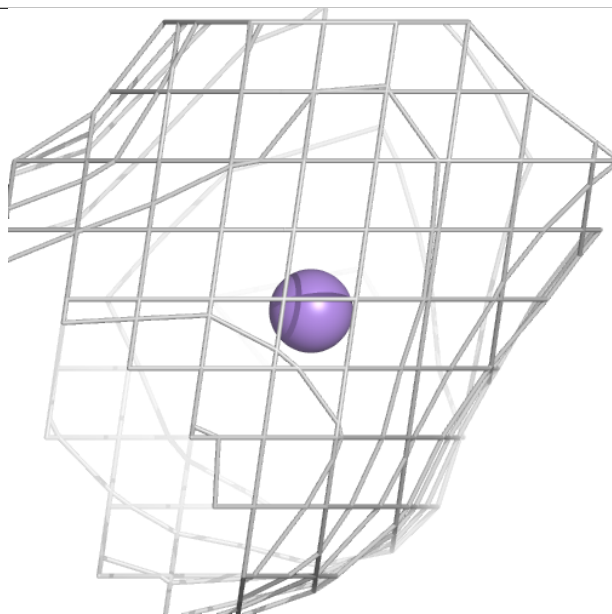
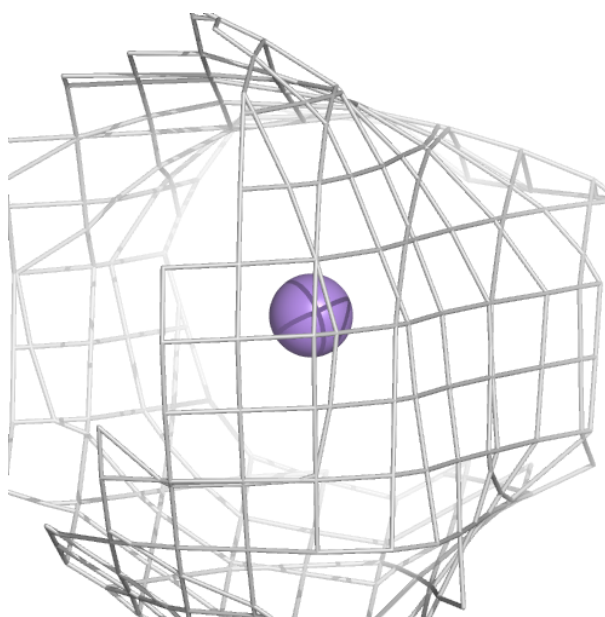
Electron density around MN D 501:

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



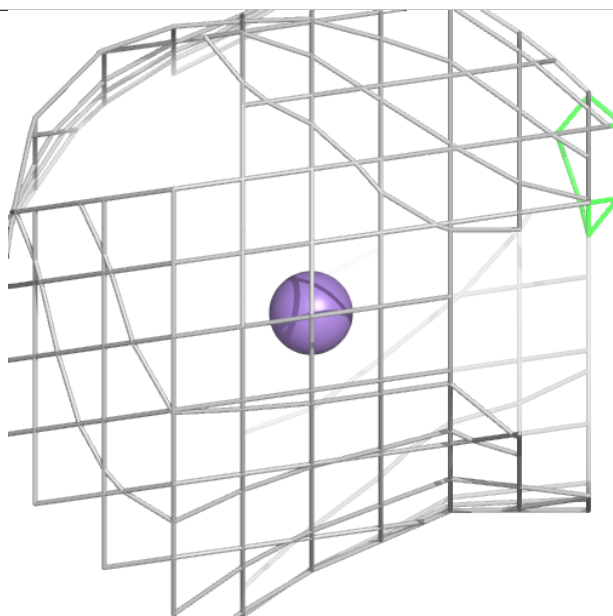
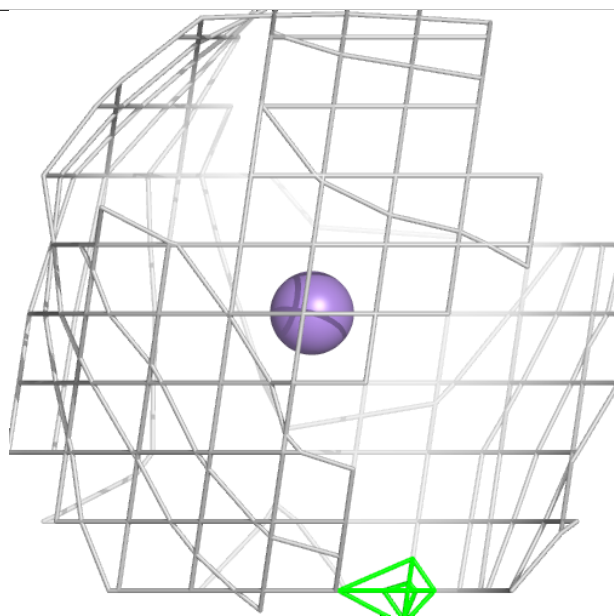
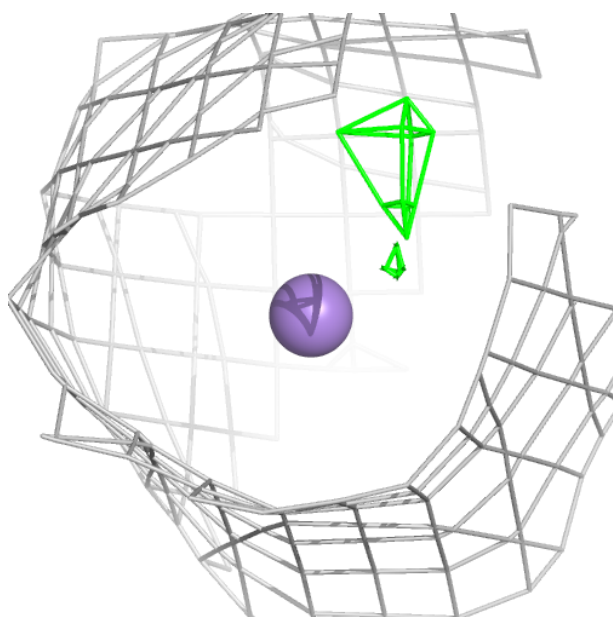
Electron density around MN E 501:

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



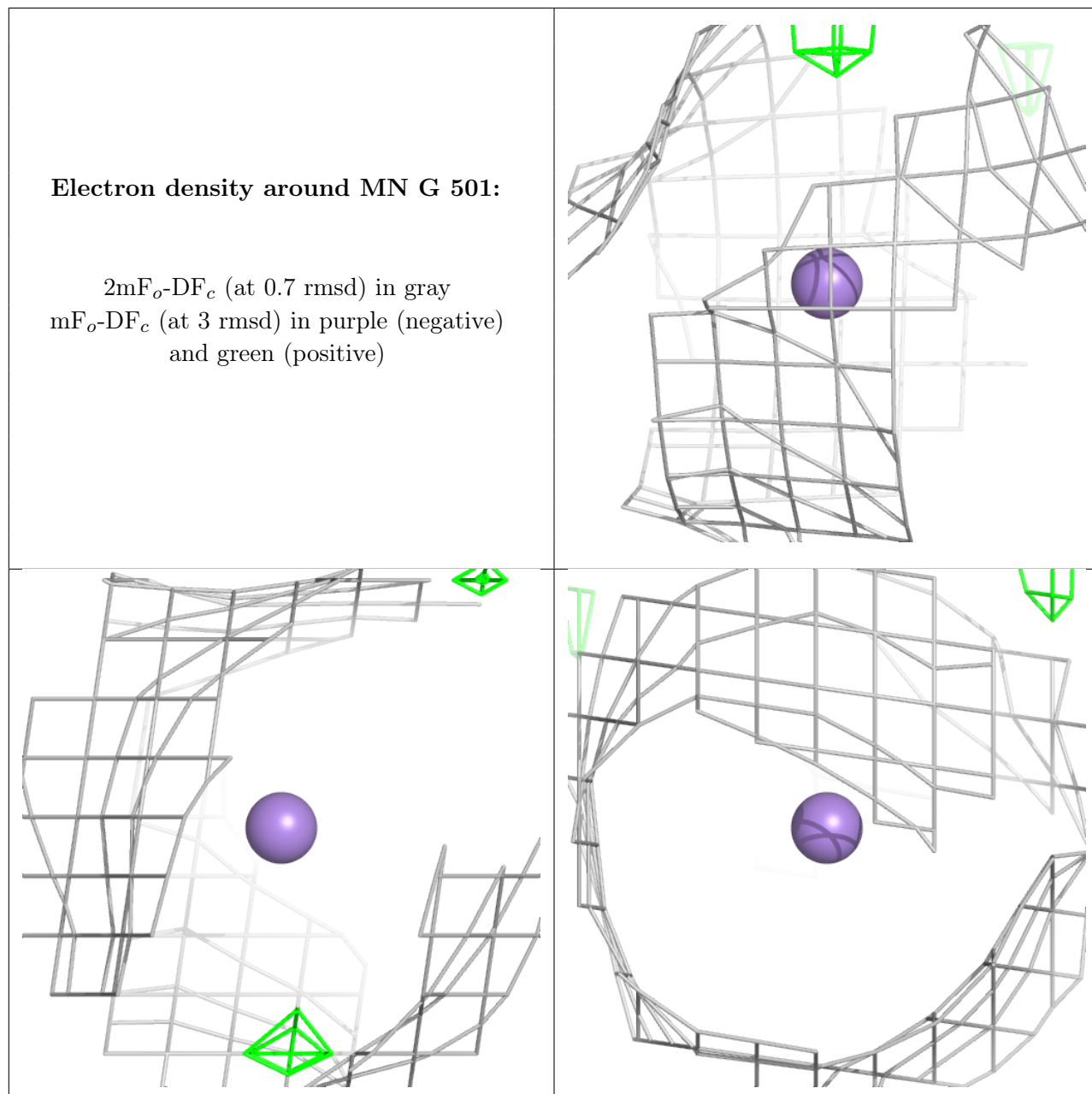
Electron density around MN F 501:

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



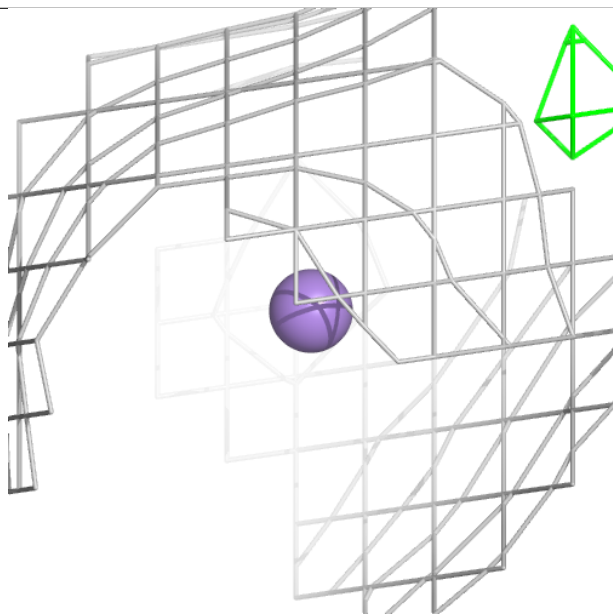
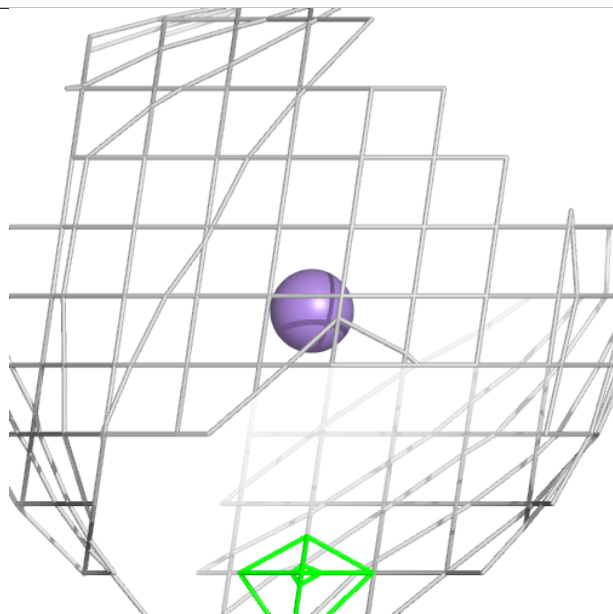
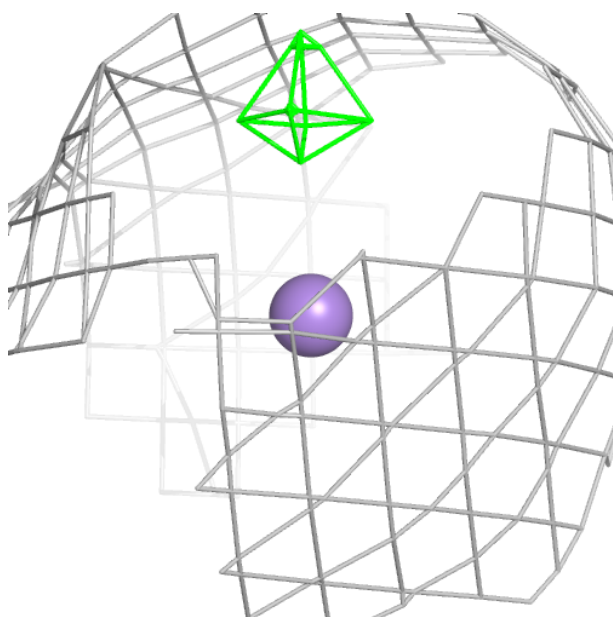
Electron density around MN G 501:

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and green (positive)



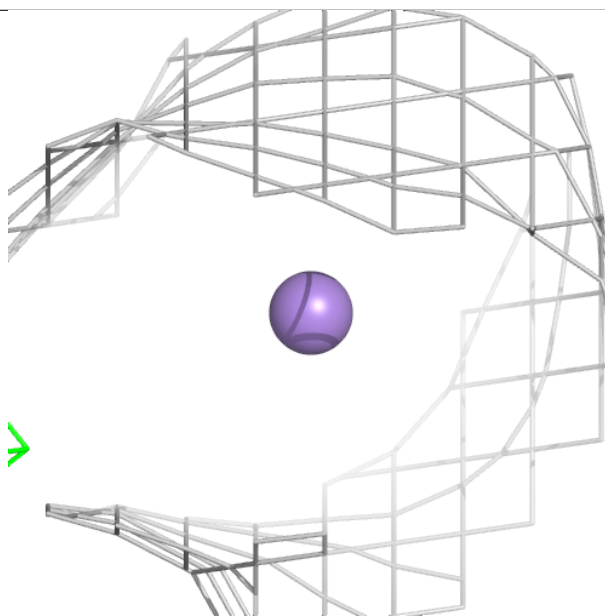
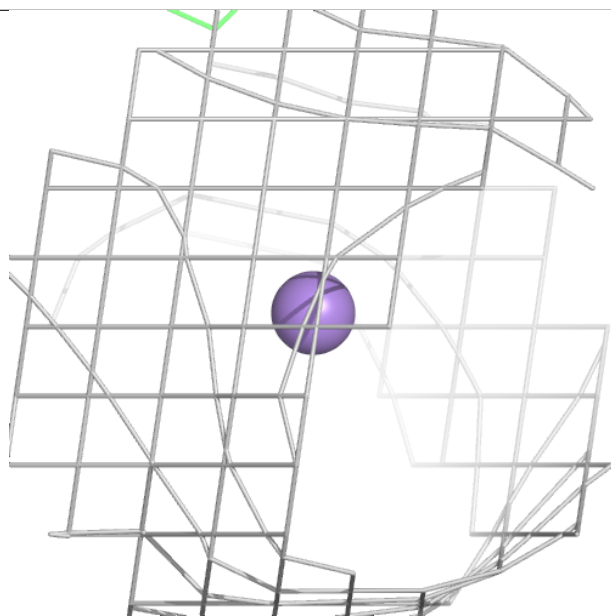
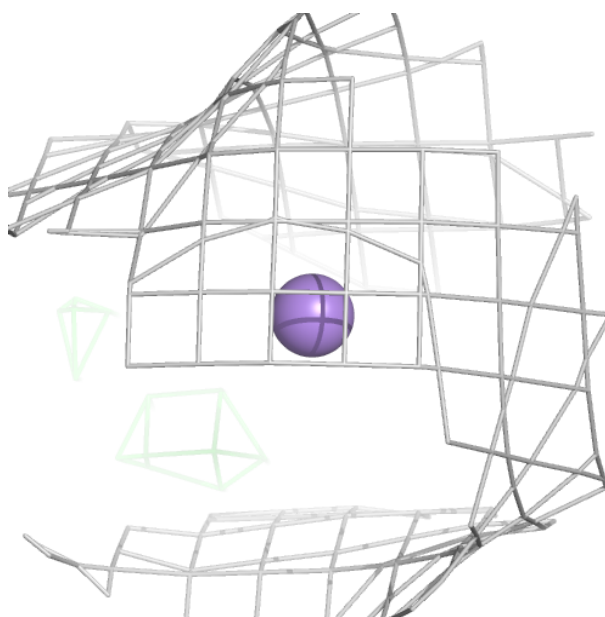
Electron density around MN H 501:

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



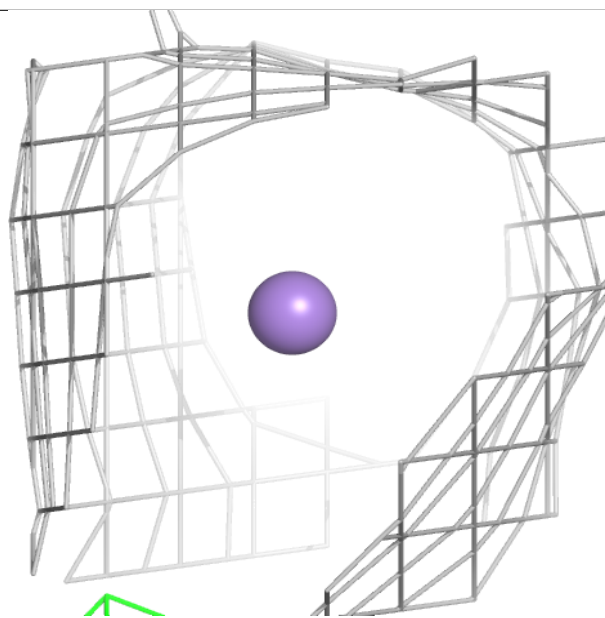
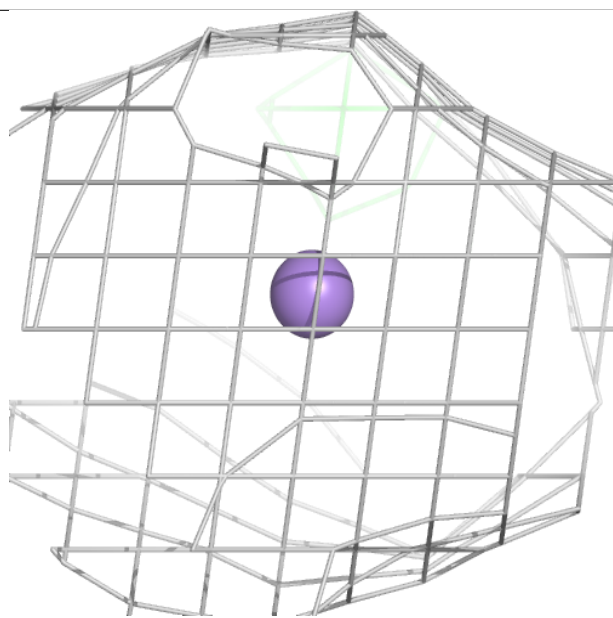
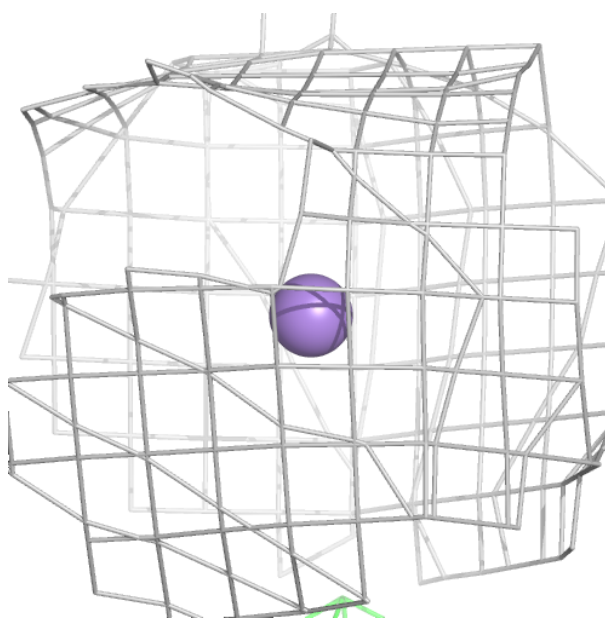
Electron density around MN K 501:

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



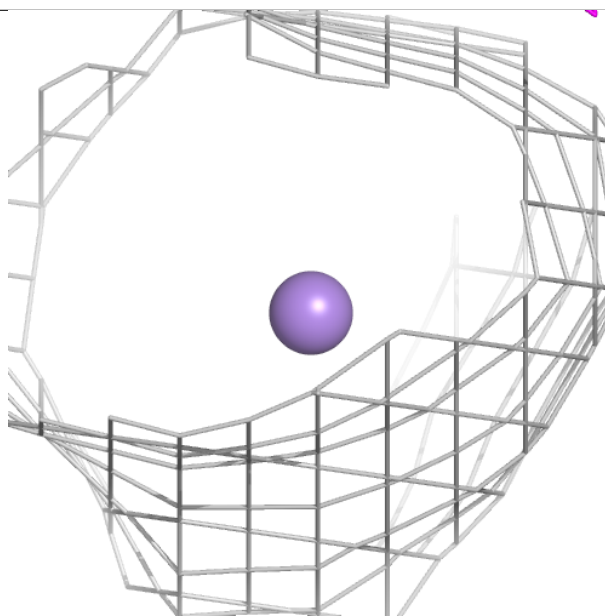
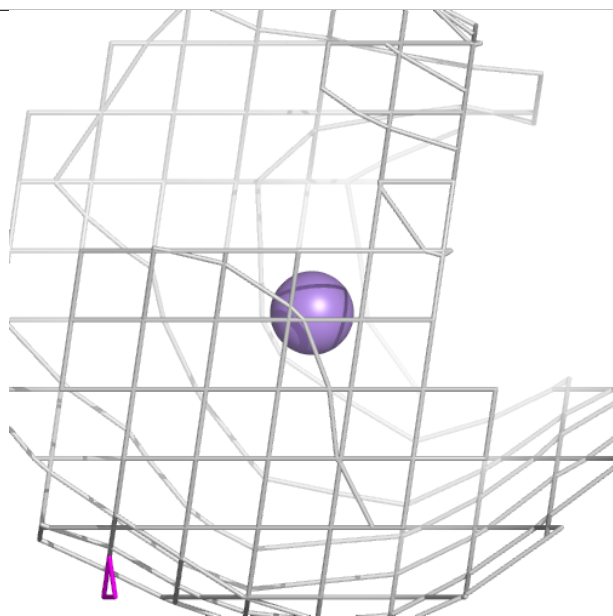
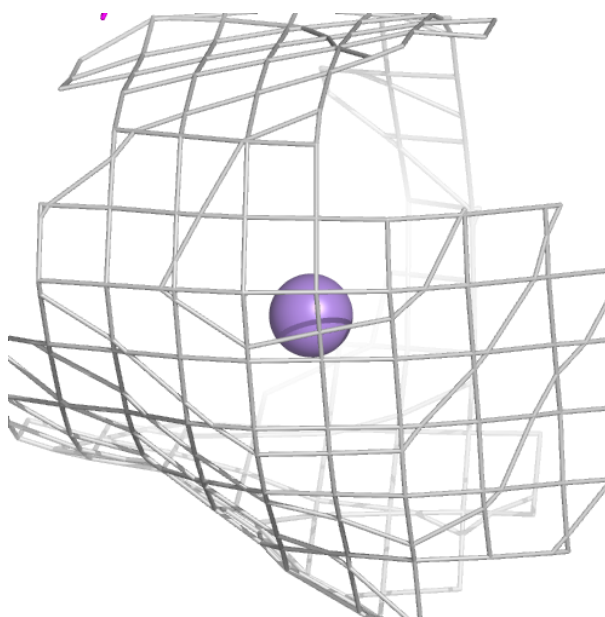
Electron density around MN B 501:

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



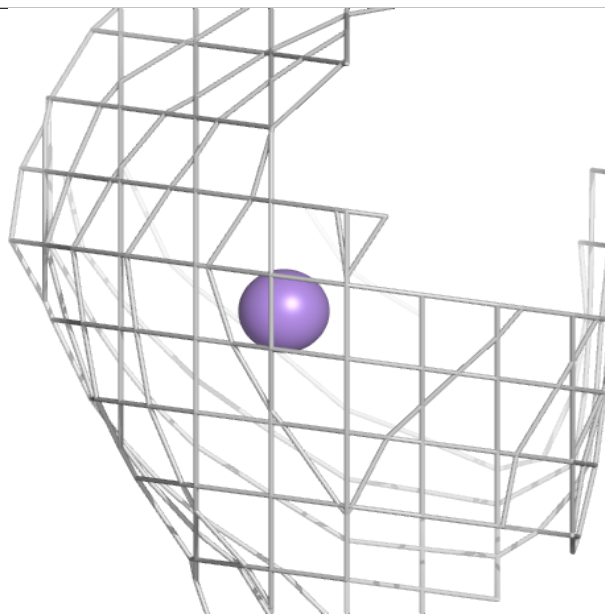
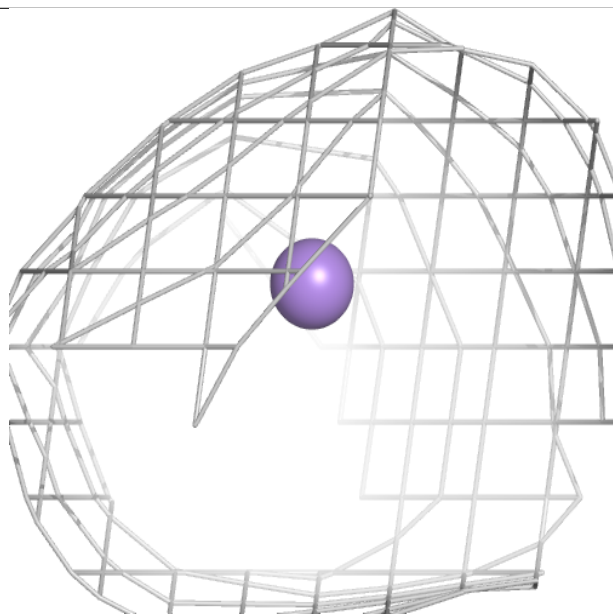
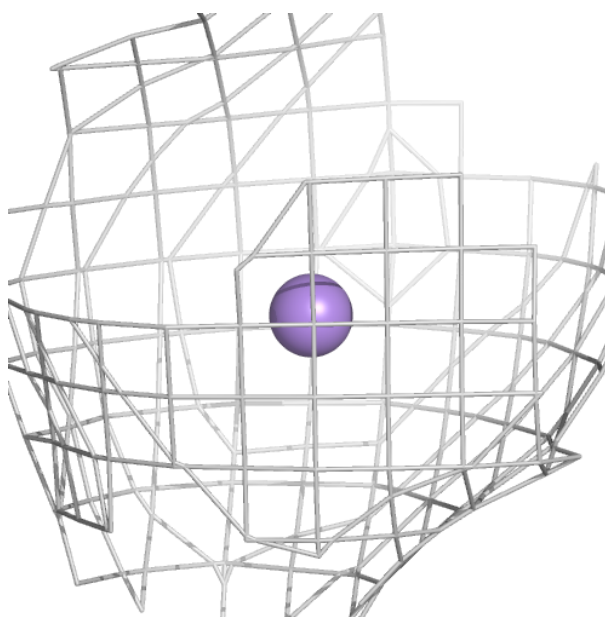
Electron density around MN I 501:

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



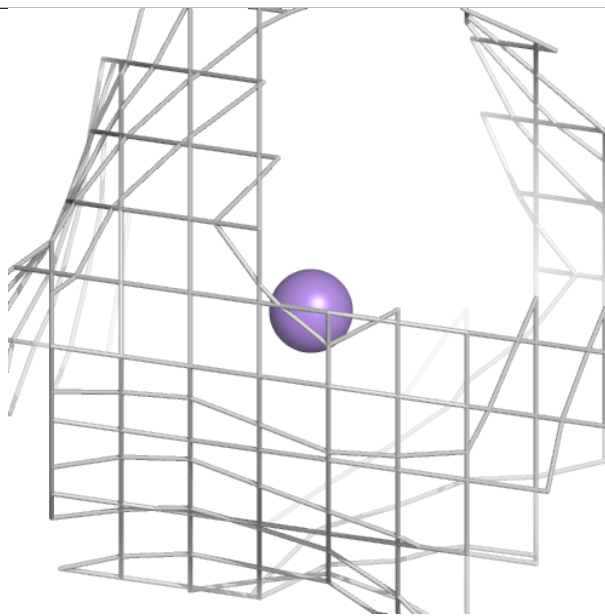
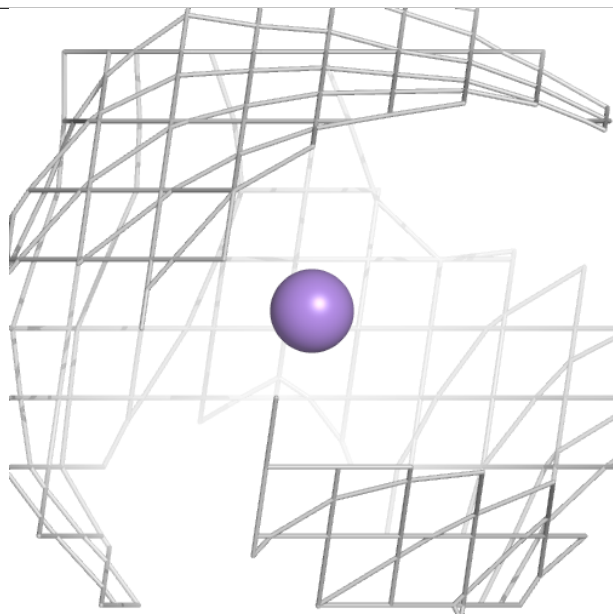
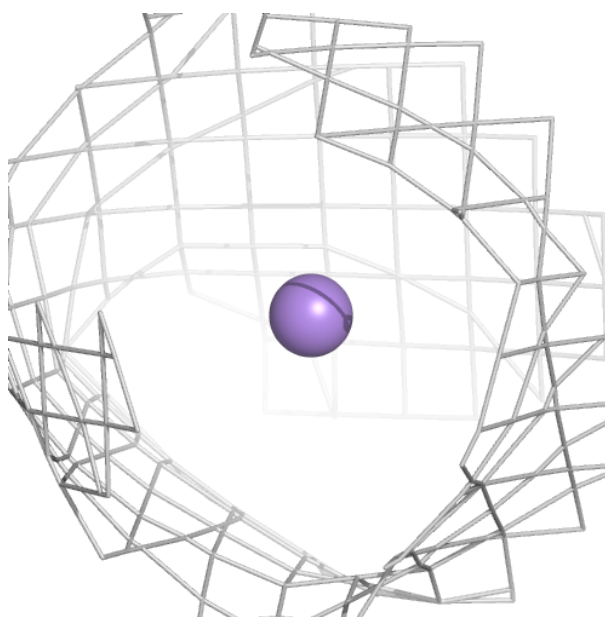
Electron density around MN J 501:

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



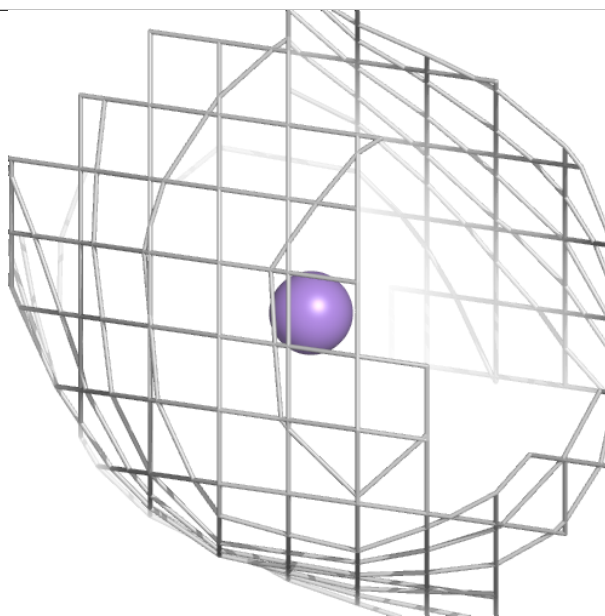
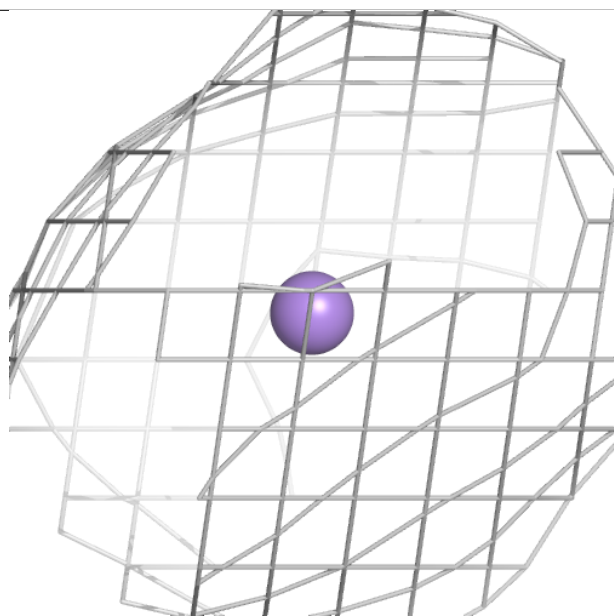
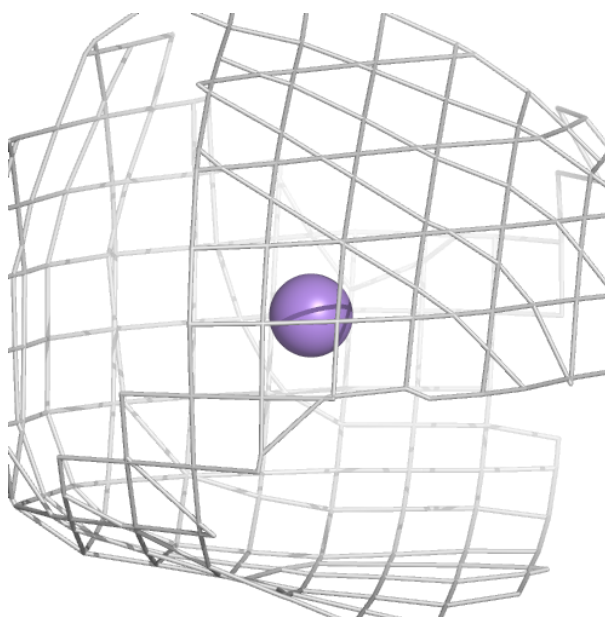
Electron density around MN C 502:

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



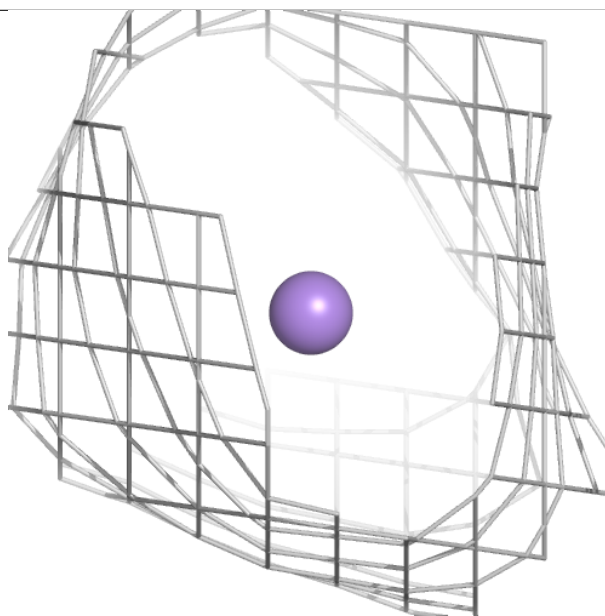
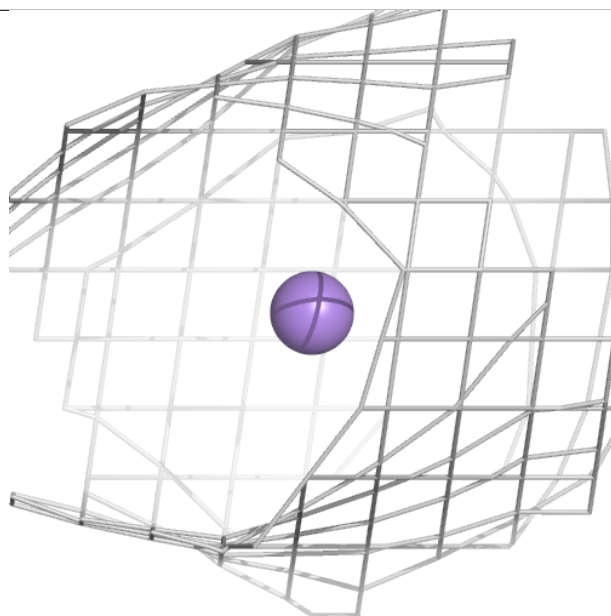
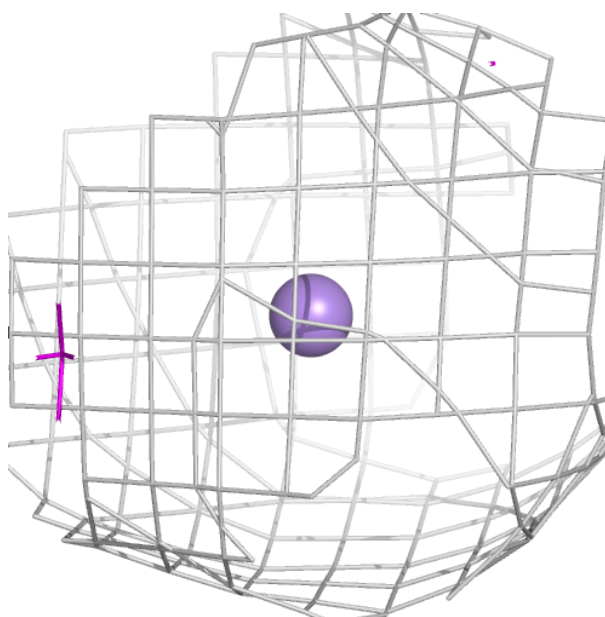
Electron density around MN L 501:

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



Electron density around MN A 501:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.