wwPDB X-ray Structure Validation Summary Report (i)

Sep 20, 2026 – 09:39 pm BST

PDB ID	:	8BTS / pdb_00008bts
Title	:	Nitrogenase MoFe protein from A. vinelandii alpha double mutant C45A/L158C
Authors	:	Wagner, T.; Maslac, N.
Deposited on	:	2022-11-29
Resolution	:	3.03 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 (i) 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 (i)) were used in the production of this report:

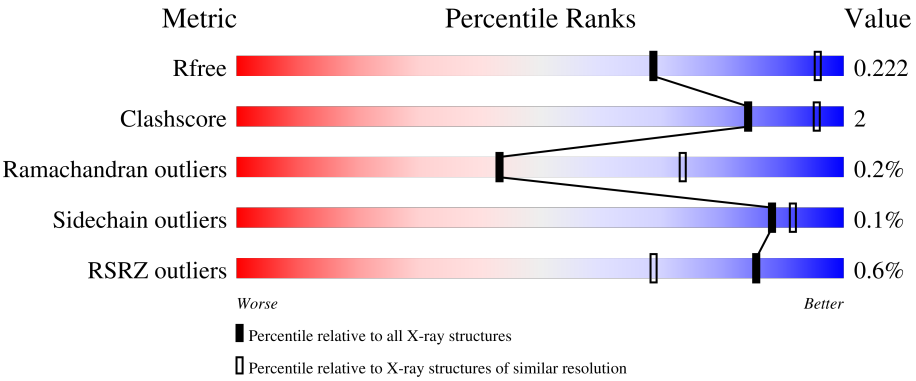
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

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 3.03 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	3685 (3.08-3.00)
Clashscore	190562	4007 (3.08-3.00)
Ramachandran outliers	187476	3834 (3.08-3.00)
Sidechain outliers	187428	3836 (3.08-3.00)
RSRZ outliers	180081	3684 (3.08-3.00)

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	500	91% · 5%
1	C	500	2% 90% 6% 5%
1	H	500	2% 91% · 5%
1	J	500	88% 8% 5%
2	B	523	94% 6%

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Mol	Chain	Length	Quality of chain
2	D	523	94% 6%
2	I	523	% 93% 7%
2	L	523	93% 7%

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
6	SO4	D	704	-	-	X	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 32158 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 Nitrogenase protein alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total 3787	C 2407	N 647	O 708	S 25	0	0	0
1	C	477	Total 3787	C 2407	N 647	O 708	S 25	0	0	0
1	H	477	Total 3787	C 2407	N 647	O 708	S 25	0	0	0
1	J	477	Total 3787	C 2407	N 647	O 708	S 25	0	0	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP C1DGZ7
A	-6	THR	-	expression tag	UNP C1DGZ7
A	-5	HIS	-	expression tag	UNP C1DGZ7
A	-4	HIS	-	expression tag	UNP C1DGZ7
A	-3	HIS	-	expression tag	UNP C1DGZ7
A	-2	HIS	-	expression tag	UNP C1DGZ7
A	-1	HIS	-	expression tag	UNP C1DGZ7
A	0	HIS	-	expression tag	UNP C1DGZ7
A	1	HIS	-	expression tag	UNP C1DGZ7
A	2	HIS	-	expression tag	UNP C1DGZ7
A	45	ALA	CYS	engineered mutation	UNP C1DGZ7
A	158	CYS	LEU	engineered mutation	UNP C1DGZ7
C	-7	MET	-	initiating methionine	UNP C1DGZ7
C	-6	THR	-	expression tag	UNP C1DGZ7
C	-5	HIS	-	expression tag	UNP C1DGZ7
C	-4	HIS	-	expression tag	UNP C1DGZ7
C	-3	HIS	-	expression tag	UNP C1DGZ7
C	-2	HIS	-	expression tag	UNP C1DGZ7
C	-1	HIS	-	expression tag	UNP C1DGZ7
C	0	HIS	-	expression tag	UNP C1DGZ7
C	1	HIS	-	expression tag	UNP C1DGZ7

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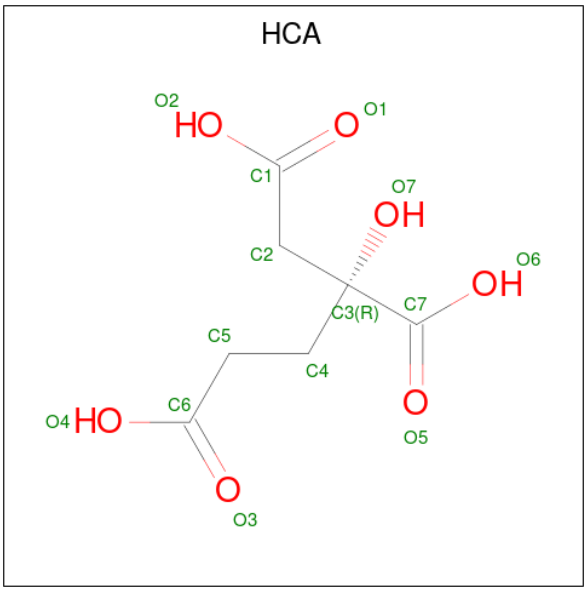
Chain	Residue	Modelled	Actual	Comment	Reference
C	2	HIS	-	expression tag	UNP C1DGZ7
C	45	ALA	CYS	engineered mutation	UNP C1DGZ7
C	158	CYS	LEU	engineered mutation	UNP C1DGZ7
H	-7	MET	-	initiating methionine	UNP C1DGZ7
H	-6	THR	-	expression tag	UNP C1DGZ7
H	-5	HIS	-	expression tag	UNP C1DGZ7
H	-4	HIS	-	expression tag	UNP C1DGZ7
H	-3	HIS	-	expression tag	UNP C1DGZ7
H	-2	HIS	-	expression tag	UNP C1DGZ7
H	-1	HIS	-	expression tag	UNP C1DGZ7
H	0	HIS	-	expression tag	UNP C1DGZ7
H	1	HIS	-	expression tag	UNP C1DGZ7
H	2	HIS	-	expression tag	UNP C1DGZ7
H	45	ALA	CYS	engineered mutation	UNP C1DGZ7
H	158	CYS	LEU	engineered mutation	UNP C1DGZ7
J	-7	MET	-	initiating methionine	UNP C1DGZ7
J	-6	THR	-	expression tag	UNP C1DGZ7
J	-5	HIS	-	expression tag	UNP C1DGZ7
J	-4	HIS	-	expression tag	UNP C1DGZ7
J	-3	HIS	-	expression tag	UNP C1DGZ7
J	-2	HIS	-	expression tag	UNP C1DGZ7
J	-1	HIS	-	expression tag	UNP C1DGZ7
J	0	HIS	-	expression tag	UNP C1DGZ7
J	1	HIS	-	expression tag	UNP C1DGZ7
J	2	HIS	-	expression tag	UNP C1DGZ7
J	45	ALA	CYS	engineered mutation	UNP C1DGZ7
J	158	CYS	LEU	engineered mutation	UNP C1DGZ7

- Molecule 2 is a protein called Nitrogenase molybdenum-iron protein beta chain.

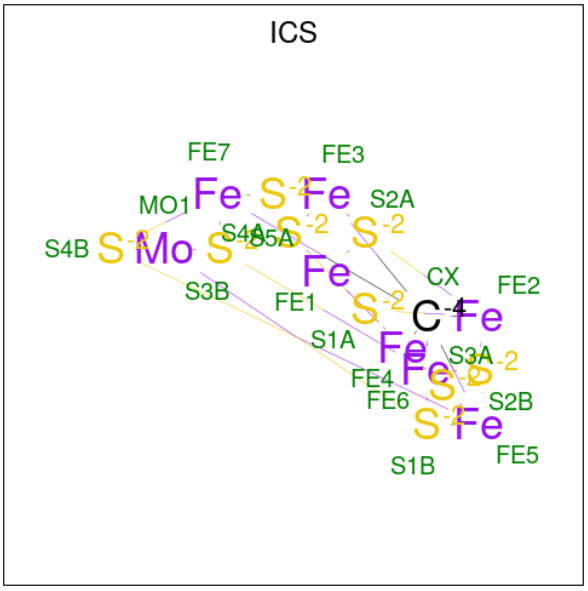
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	522	Total	C	N	O	S	0	0	0
			4174	2666	705	775	28			
2	D	522	Total	C	N	O	S	0	0	0
			4174	2666	705	775	28			
2	I	522	Total	C	N	O	S	0	0	0
			4174	2666	705	775	28			
2	L	522	Total	C	N	O	S	0	0	0
			4174	2666	705	775	28			

- Molecule 3 is 3-HYDROXY-3-CARBOXY-ADIPIC ACID (CCD ID: HCA) (formula: $C_7H_{10}O_7$) (labeled as "Ligand of Interest" by depositor).



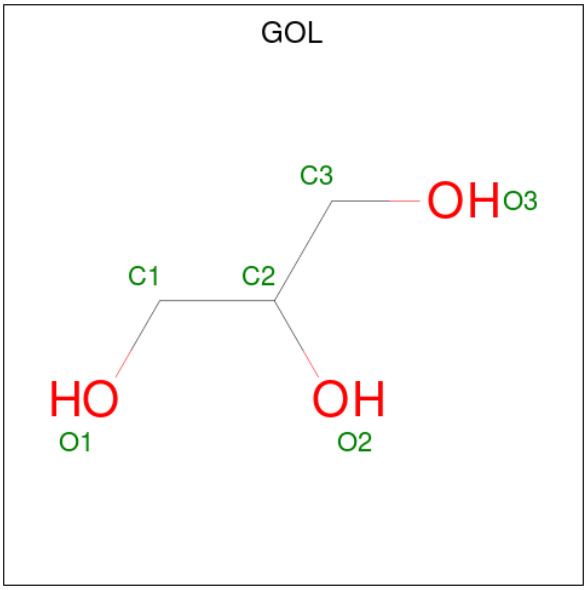
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 14 7 7	0	0
3	C	1	Total C O 14 7 7	0	0
3	H	1	Total C O 14 7 7	0	0
3	J	1	Total C O 14 7 7	0	0

- Molecule 4 is iron-sulfur-molybdenum cluster with interstitial carbon (CCD ID: ICS) (formula: CFe_7MoS_9) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C Fe Mo S 18 1 7 1 9	0	0
4	C	1	Total C Fe Mo S 18 1 7 1 9	0	0
4	H	1	Total C Fe Mo S 18 1 7 1 9	0	0
4	J	1	Total C Fe Mo S 18 1 7 1 9	0	0

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

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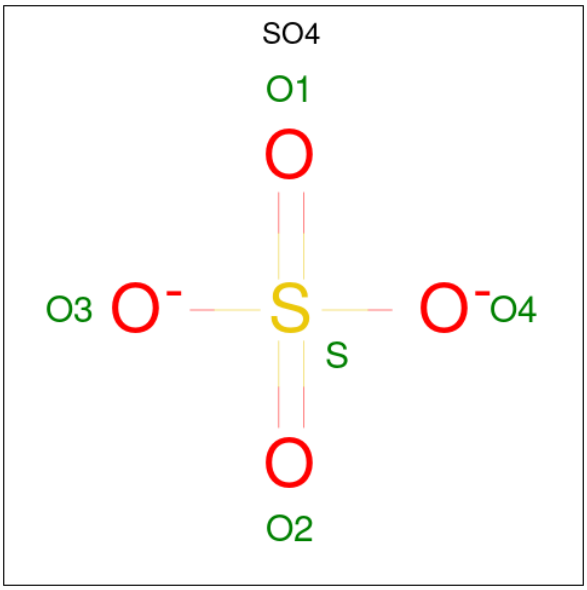
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	1	Total C O 6 3 3	0	0
5	D	1	Total C O 6 3 3	0	0
5	J	1	Total C O 6 3 3	0	0
5	L	1	Total C O 6 3 3	0	0

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0
6	C	1	Total O S 5 4 1	0	0
6	D	1	Total O S 5 4 1	0	0
6	H	1	Total O S 5 4 1	0	0
6	I	1	Total O S 5 4 1	0	0

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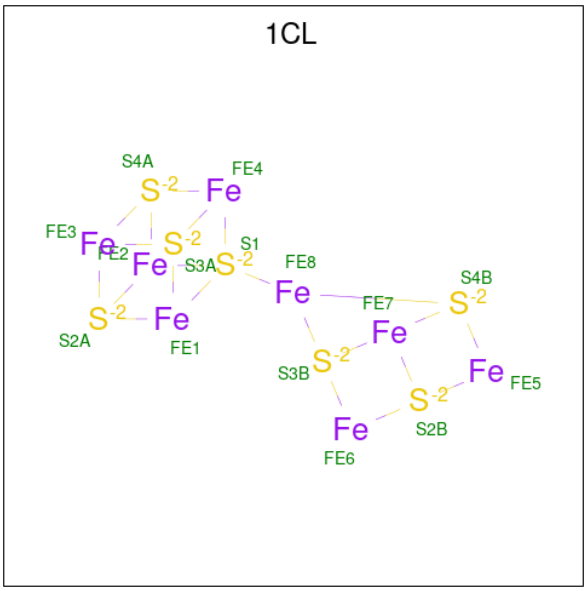
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	J	1	Total O S 5 4 1	0	0
6	L	1	Total O S 5 4 1	0	0
6	L	1	Total O S 5 4 1	0	0

- Molecule 7 is FE(8)-S(7) CLUSTER, OXIDIZED (CCD ID: 1CL) (formula: Fe_8S_7) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Fe S 15 8 7	0	0
7	D	1	Total Fe S 15 8 7	0	0
7	I	1	Total Fe S 15 8 7	0	0
7	L	1	Total Fe S 15 8 7	0	0

- Molecule 8 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total Fe 1 1	0	0
8	D	1	Total Fe 1 1	0	0

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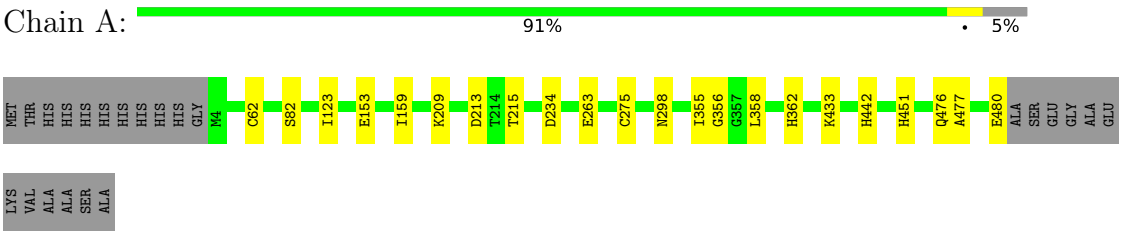
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	I	1	Total Fe 1 1	0	0
8	L	1	Total Fe 1 1	0	0

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.

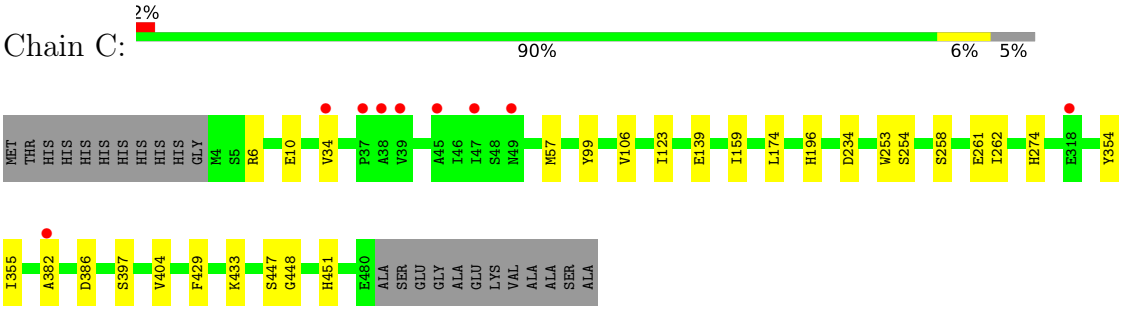
• Molecule 1: Nitrogenase protein alpha chain

Chain A:



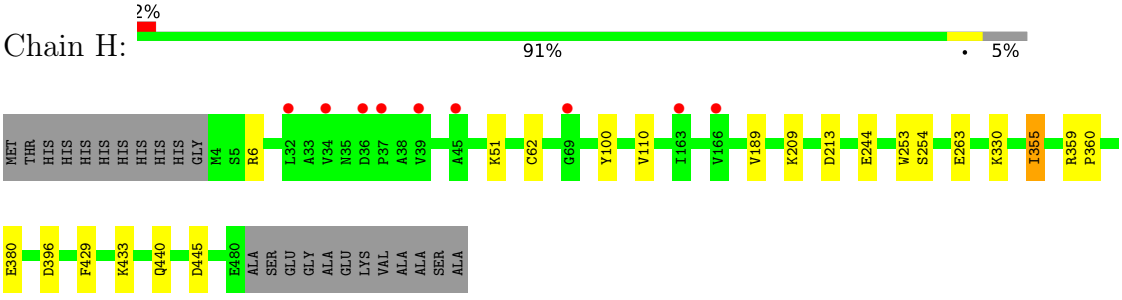
• Molecule 1: Nitrogenase protein alpha chain

Chain C:



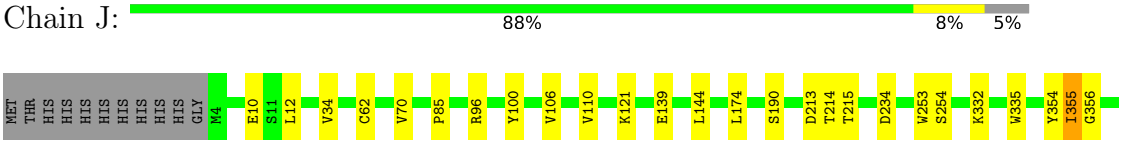
• Molecule 1: Nitrogenase protein alpha chain

Chain H:



• Molecule 1: Nitrogenase protein alpha chain

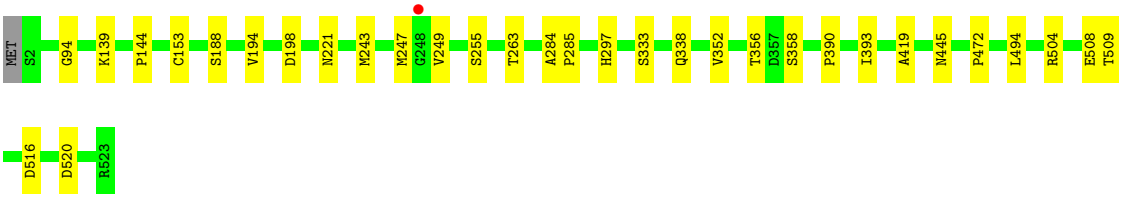
Chain J:





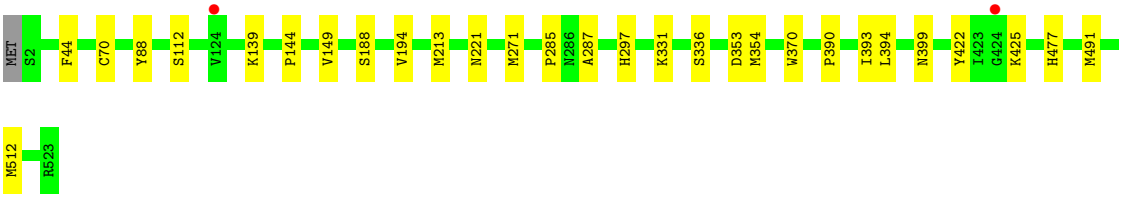
• Molecule 2: Nitrogenase molybdenum-iron protein beta chain

Chain B:



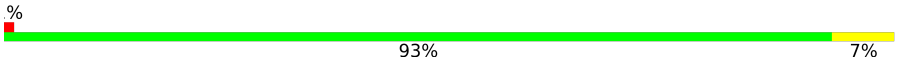
• Molecule 2: Nitrogenase molybdenum-iron protein beta chain

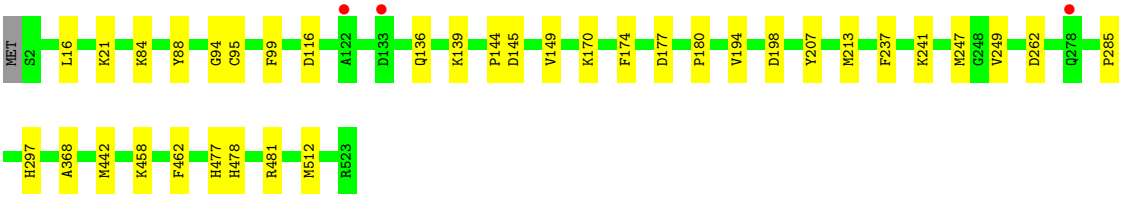
Chain D:



• Molecule 2: Nitrogenase molybdenum-iron protein beta chain

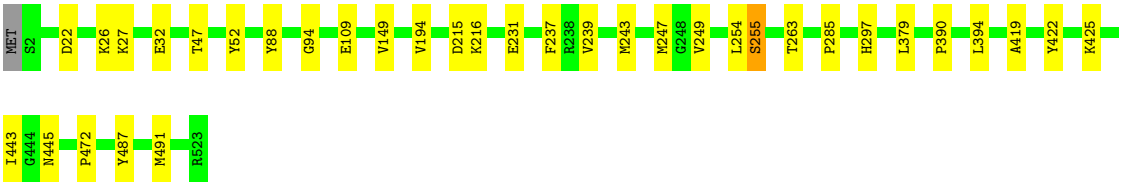
Chain I:





• Molecule 2: Nitrogenase molybdenum-iron protein beta chain

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	148.39Å 73.44Å 211.25Å 90.00° 104.76° 90.00°	Depositor
Resolution (Å)	95.50 – 3.03 95.50 – 3.03	Depositor EDS
% Data completeness (in resolution range)	46.2 (95.50-3.03) 46.2 (95.50-3.03)	Depositor EDS
R_{merge}	0.30	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.82 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.20.1-4487, BUSTER 2.10.4	Depositor
R, R_{free}	0.204 , 0.223 0.204 , 0.222	Depositor DCC
R_{free} test set	1947 reflections (2.25%)	wwPDB-VP
Wilson B-factor (Å^2)	25.2	Xtriage
Anisotropy	0.315	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 26.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.41$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	32158	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.33% 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: SO4, HCA, FE, ICS, 1CL, 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	0.18	0/3875	0.38	0/5225
1	C	0.15	0/3875	0.36	0/5225
1	H	0.15	0/3875	0.35	0/5225
1	J	0.19	0/3875	0.39	0/5225
2	B	0.18	0/4280	0.36	0/5786
2	D	0.16	0/4280	0.35	0/5786
2	I	0.14	0/4280	0.33	0/5786
2	L	0.15	0/4280	0.34	0/5786
All	All	0.16	0/32620	0.35	0/44044

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	3787	0	3725	15	0
1	C	3787	0	3725	19	0
1	H	3787	0	3725	12	0
1	J	3787	0	3725	25	0
2	B	4174	0	4087	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	4174	0	4089	24	0
2	I	4174	0	4087	20	0
2	L	4174	0	4088	20	0
3	A	14	0	6	2	0
3	C	14	0	7	1	0
3	H	14	0	7	1	0
3	J	14	0	6	2	0
4	A	18	0	0	1	0
4	C	18	0	0	0	0
4	H	18	0	0	0	0
4	J	18	0	0	1	0
5	A	12	0	16	0	0
5	B	30	0	40	0	0
5	C	6	0	8	2	0
5	D	12	0	16	1	0
5	J	6	0	8	0	0
5	L	6	0	8	0	0
6	A	5	0	0	0	0
6	B	10	0	0	0	0
6	C	5	0	0	0	0
6	D	5	0	0	2	0
6	H	5	0	0	0	0
6	I	5	0	0	0	0
6	J	5	0	0	0	0
6	L	10	0	0	0	0
7	B	15	0	0	0	0
7	D	15	0	0	2	0
7	I	15	0	0	0	0
7	L	15	0	0	1	0
8	B	1	0	0	0	0
8	D	1	0	0	0	0
8	I	1	0	0	0	0
8	L	1	0	0	0	0
All	All	32158	0	31373	147	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 2.

The worst 5 of 147 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)
2:I:213:MET:HE1	2:I:285:PRO:HB3	1.88	0.55
1:A:433:LYS:NZ	2:B:263:THR:O	2.35	0.53
2:D:188:SER:OG	7:D:701:1CL:S2B	2.62	0.53
1:J:85:PRO:HB2	7:L:701:1CL:S2B	2.48	0.53
1:A:442:HIS:CG	3:A:601:HCA:H52	2.44	0.53

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	475/500 (95%)	452 (95%)	22 (5%)	1 (0%)	43	73
1	C	475/500 (95%)	453 (95%)	21 (4%)	1 (0%)	43	73
1	H	475/500 (95%)	455 (96%)	19 (4%)	1 (0%)	43	73
1	J	475/500 (95%)	455 (96%)	19 (4%)	1 (0%)	43	73
2	B	520/523 (99%)	507 (98%)	12 (2%)	1 (0%)	43	73
2	D	520/523 (99%)	507 (98%)	13 (2%)	0	100	100
2	I	520/523 (99%)	507 (98%)	13 (2%)	0	100	100
2	L	520/523 (99%)	508 (98%)	11 (2%)	1 (0%)	43	73
All	All	3980/4092 (97%)	3844 (97%)	130 (3%)	6 (0%)	43	73

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	255	SER
2	B	255	SER
1	C	355	ILE
1	H	355	ILE
1	J	355	ILE

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	406/422 (96%)	405 (100%)	1 (0%)	87 90
1	C	406/422 (96%)	406 (100%)	0	100 100
1	H	406/422 (96%)	406 (100%)	0	100 100
1	J	406/422 (96%)	405 (100%)	1 (0%)	87 90
2	B	454/455 (100%)	454 (100%)	0	100 100
2	D	454/455 (100%)	454 (100%)	0	100 100
2	I	454/455 (100%)	454 (100%)	0	100 100
2	L	454/455 (100%)	454 (100%)	0	100 100
All	All	3440/3508 (98%)	3438 (100%)	2 (0%)	88 91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	476	GLN
1	J	214	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	294	GLN
2	L	18	GLN
2	L	513	GLN
2	L	163	ASN
1	J	29	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 38 ligands modelled in this entry, 4 are monoatomic - leaving 34 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	$\#\|Z\| > 2$
4	ICS	A	602	3,1	18,30,30	2.49	10 (55%)	-		
6	SO4	D	704	-	4,4,4	0.40	0	6,6,6	0.05	0
3	HCA	C	601	4	13,13,13	1.22	1 (7%)	14,18,18	1.40	2 (14%)
5	GOL	B	703	-	5,5,5	0.09	0	5,5,5	0.31	0
6	SO4	B	708	-	4,4,4	0.40	0	6,6,6	0.05	0
5	GOL	L	702	-	5,5,5	0.97	0	5,5,5	0.90	0
5	GOL	J	603	-	5,5,5	1.09	0	5,5,5	0.79	0
5	GOL	D	703	-	5,5,5	0.09	0	5,5,5	0.32	0
5	GOL	C	603	-	5,5,5	0.85	0	5,5,5	0.91	0
4	ICS	C	602	3,1	18,30,30	2.35	10 (55%)	-		
5	GOL	B	702	-	5,5,5	0.92	0	5,5,5	0.89	0
5	GOL	B	705	-	5,5,5	0.09	0	5,5,5	0.32	0
4	ICS	J	602	3,1	18,30,30	2.55	10 (55%)	-		
5	GOL	D	702	-	5,5,5	0.08	0	5,5,5	0.31	0
5	GOL	B	706	-	5,5,5	0.09	0	5,5,5	0.32	0
3	HCA	A	601	4	13,13,13	0.95	0	14,18,18	1.83	4 (28%)
5	GOL	B	704	-	5,5,5	0.08	0	5,5,5	0.32	0
3	HCA	H	601	4	13,13,13	1.00	0	14,18,18	1.58	1 (7%)
6	SO4	A	605	-	4,4,4	0.14	0	6,6,6	0.09	0
7	1CL	B	701	2,1	0,22,22	-	-	-		
5	GOL	A	604	-	5,5,5	0.86	0	5,5,5	0.89	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
6	SO4	L	703	-	4,4,4	0.14	0	6,6,6	0.11	0
4	ICS	H	602	3,1	18,30,30	2.37	9 (50%)	-		
6	SO4	I	702	-	4,4,4	0.14	0	6,6,6	0.10	0
7	1CL	L	701	2,1	0,22,22	-	-	-		
5	GOL	A	603	-	5,5,5	0.91	0	5,5,5	1.00	0
6	SO4	J	604	-	4,4,4	0.15	0	6,6,6	0.06	0
6	SO4	L	704	-	4,4,4	0.14	0	6,6,6	0.10	0
6	SO4	C	604	-	4,4,4	0.14	0	6,6,6	0.13	0
6	SO4	B	707	-	4,4,4	0.13	0	6,6,6	0.09	0
7	1CL	I	701	2,1	0,22,22	-	-	-		
3	HCA	J	601	4	13,13,13	0.98	0	14,18,18	1.84	4 (28%)
6	SO4	H	603	-	4,4,4	0.14	0	6,6,6	0.08	0
7	1CL	D	701	2,1	0,22,22	-	-	-		

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	HCA	C	601	4	-	5/17/17/17	-
5	GOL	B	703	-	-	0/4/4/4	-
5	GOL	L	702	-	-	4/4/4/4	-
5	GOL	J	603	-	-	2/4/4/4	-
5	GOL	D	703	-	-	0/4/4/4	-
5	GOL	C	603	-	-	0/4/4/4	-
5	GOL	B	702	-	-	2/4/4/4	-
5	GOL	B	705	-	-	0/4/4/4	-
5	GOL	D	702	-	-	2/4/4/4	-
5	GOL	B	706	-	-	2/4/4/4	-
3	HCA	A	601	4	-	11/17/17/17	-
5	GOL	B	704	-	-	4/4/4/4	-
3	HCA	H	601	4	-	6/17/17/17	-
7	1CL	B	701	2,1	-	-	0/10/8/8
5	GOL	A	604	-	-	2/4/4/4	-
7	1CL	L	701	2,1	-	-	0/10/8/8
5	GOL	A	603	-	-	1/4/4/4	-
7	1CL	I	701	2,1	-	-	0/10/8/8
3	HCA	J	601	4	-	10/17/17/17	-
7	1CL	D	701	2,1	-	-	0/10/8/8

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J	602	ICS	S3B-FE6	-4.19	2.22	2.32
4	J	602	ICS	S4B-FE7	-4.15	2.22	2.32
4	A	602	ICS	S4B-FE7	-4.06	2.22	2.32
4	C	602	ICS	S4B-FE7	-4.02	2.22	2.32
4	A	602	ICS	S3B-FE6	-4.01	2.22	2.32

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	J	601	HCA	O6-C7-C3	4.67	121.16	113.05
3	A	601	HCA	O6-C7-C3	4.62	121.07	113.05
3	H	601	HCA	O6-C7-C3	3.92	119.86	113.05
3	C	601	HCA	O5-C7-C3	-3.21	117.71	122.25
3	A	601	HCA	O4-C6-C5	2.38	121.69	114.03

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	HCA	C2-C3-C4-C5
3	C	601	HCA	C1-C2-C3-C4
3	C	601	HCA	C1-C2-C3-C7
3	C	601	HCA	C3-C4-C5-C6
3	H	601	HCA	C2-C3-C4-C5

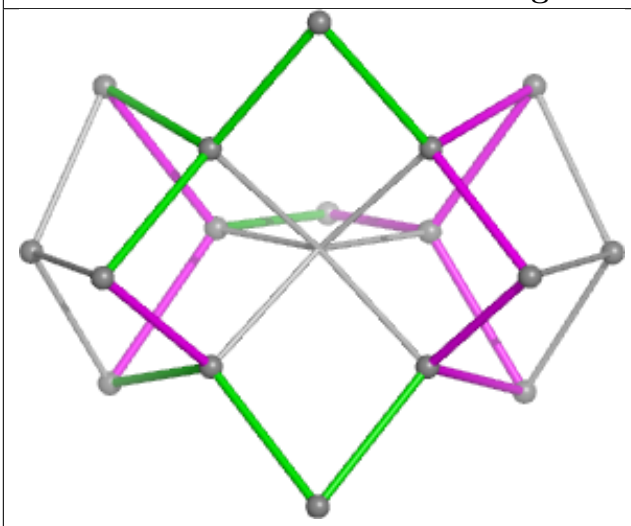
There are no ring outliers.

11 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	602	ICS	1	0
6	D	704	SO4	2	0
3	C	601	HCA	1	0
5	C	603	GOL	2	0
4	J	602	ICS	1	0
5	D	702	GOL	1	0
3	A	601	HCA	2	0
3	H	601	HCA	1	0
7	L	701	1CL	1	0
3	J	601	HCA	2	0
7	D	701	1CL	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand ICS A 602



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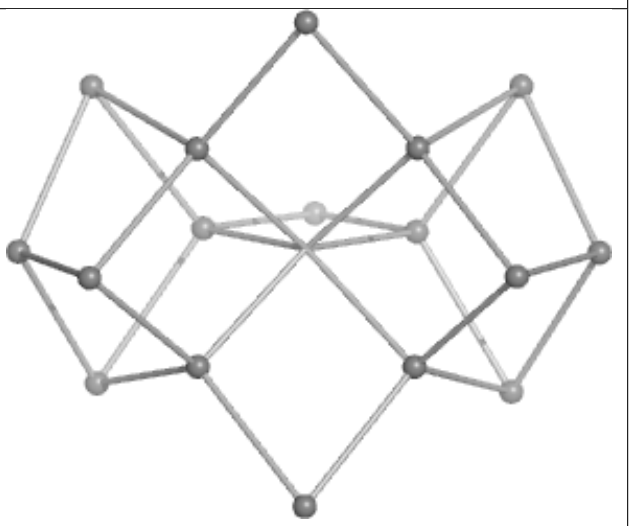
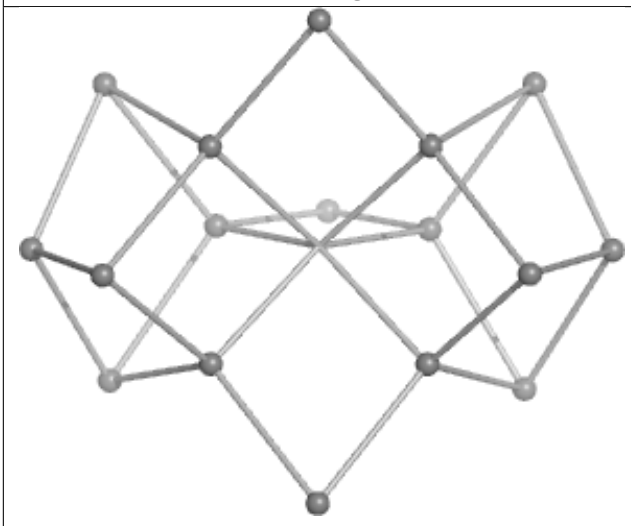
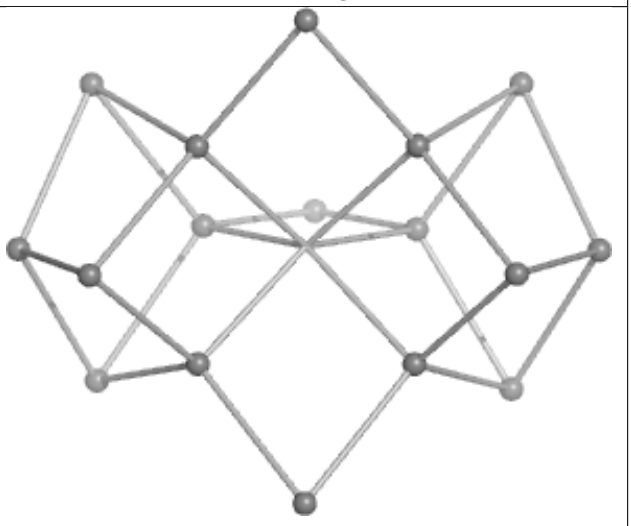


Bond angles

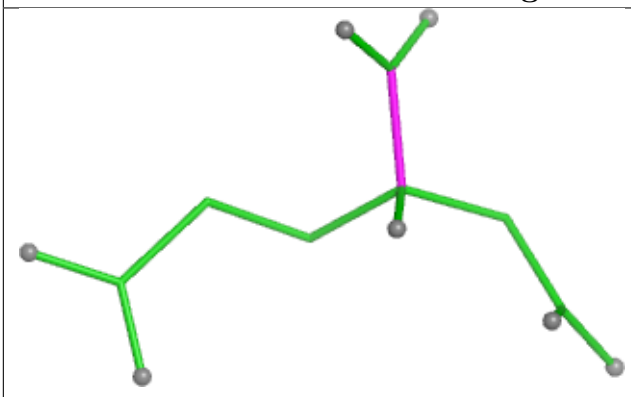


Torsions



Rings

Ligand HCA C 601



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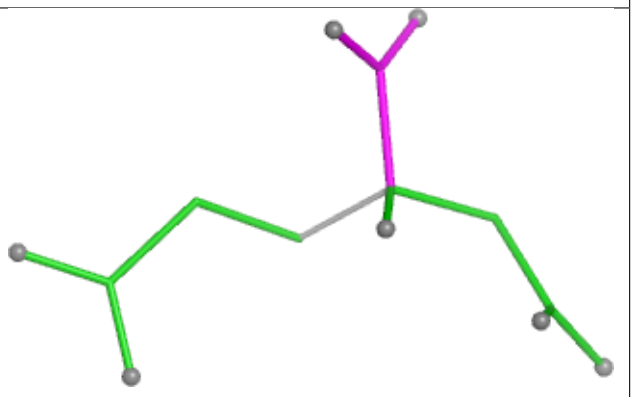

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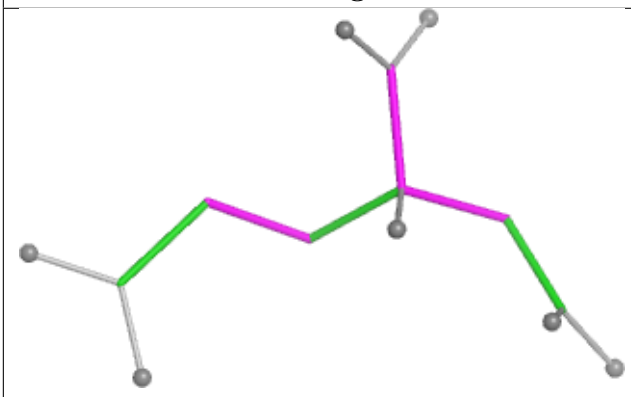

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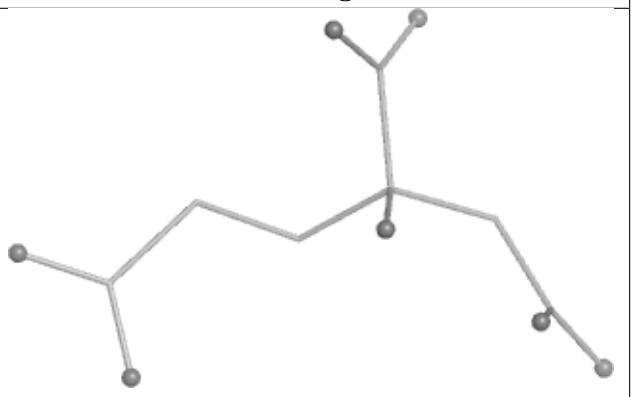
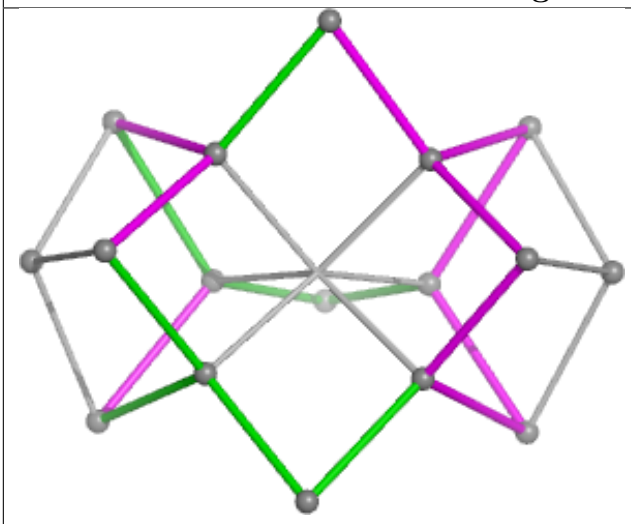


Rings

Ligand ICS C 602



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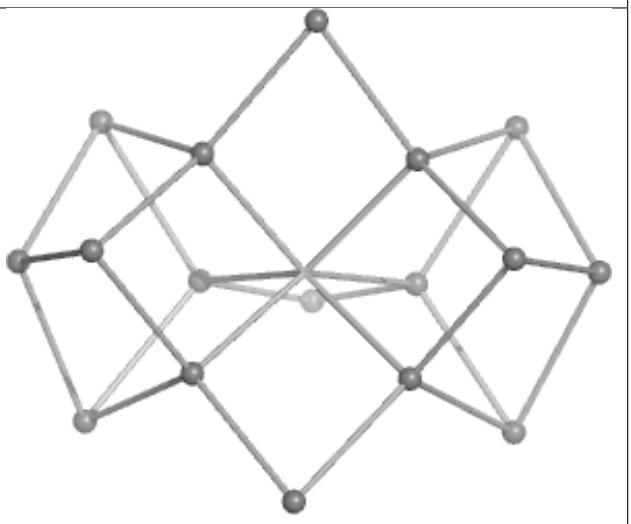

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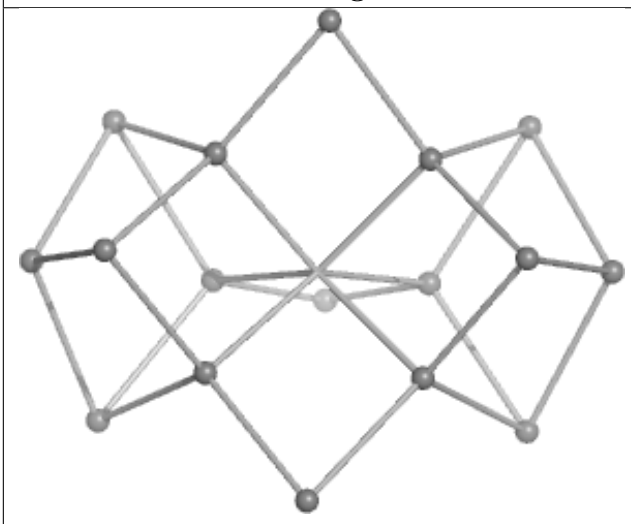

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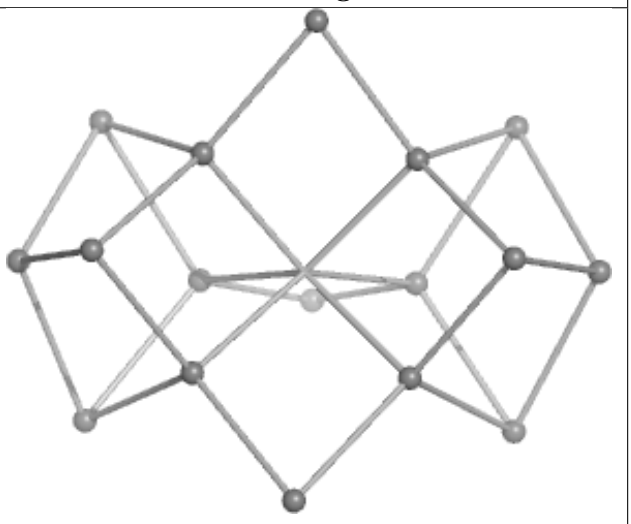
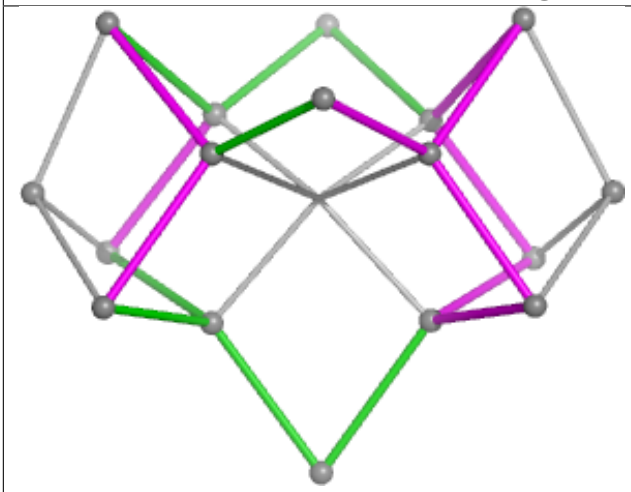


Rings

Ligand ICS J 602



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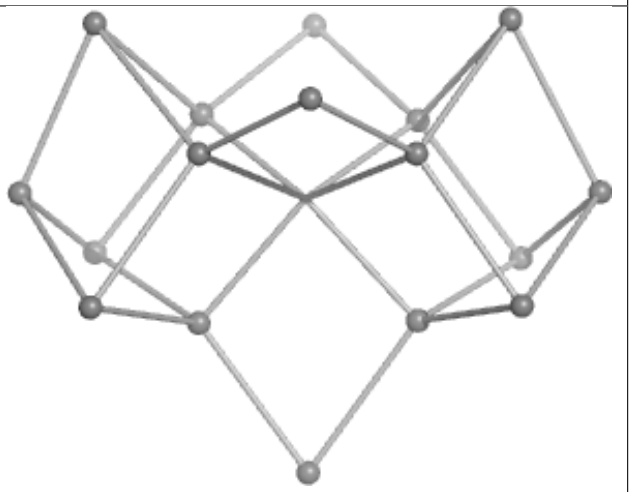

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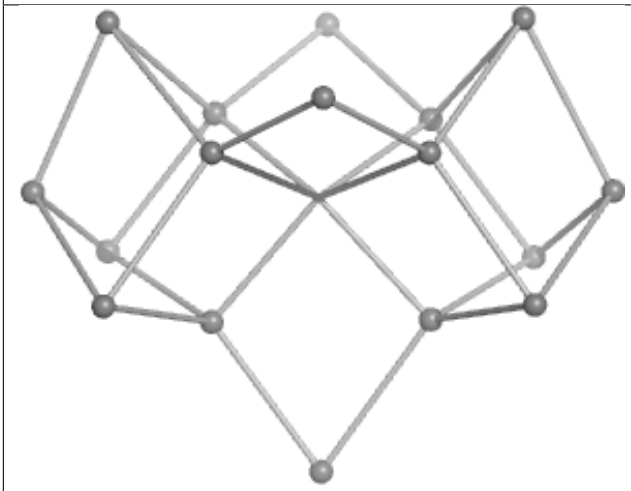

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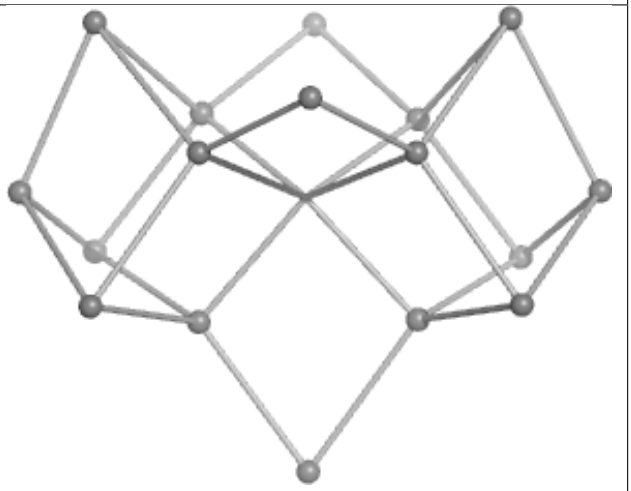
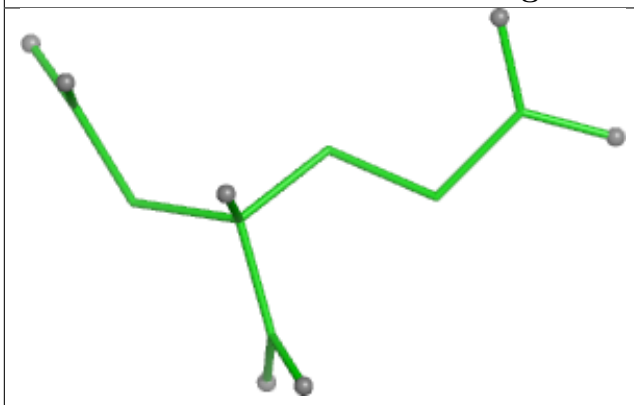


Rings

Ligand HCA A 601



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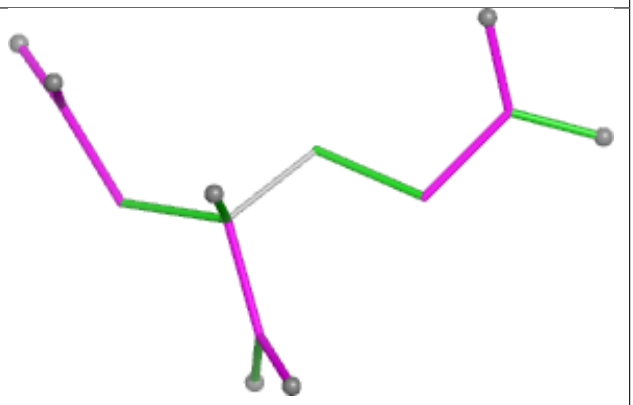

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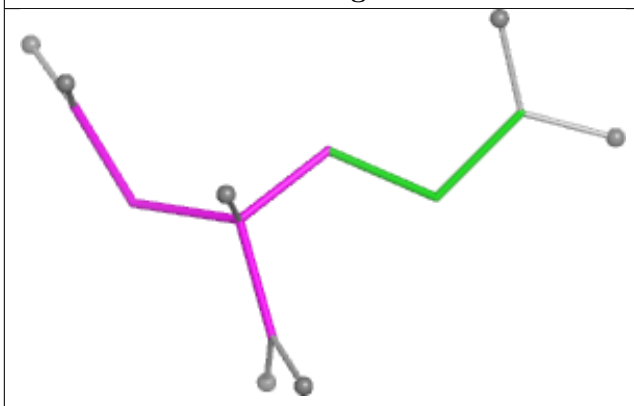

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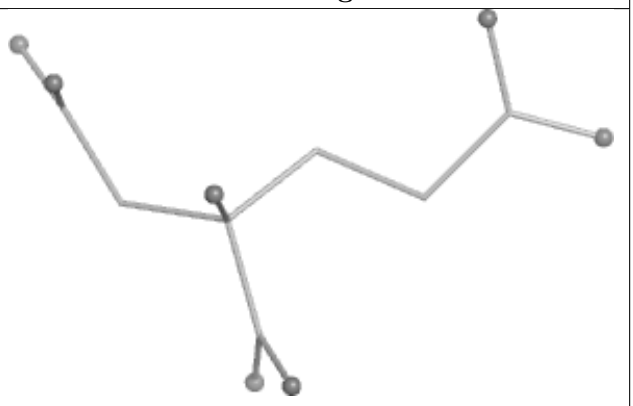

Rings

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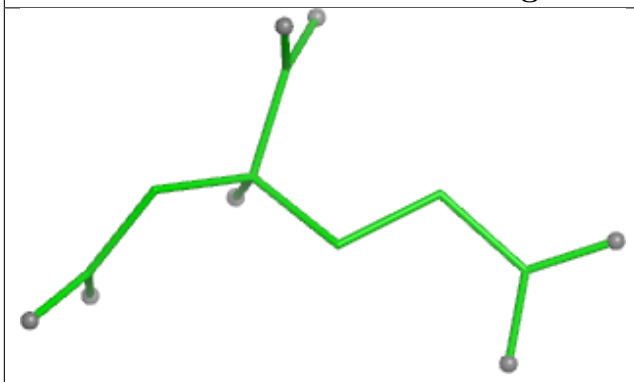

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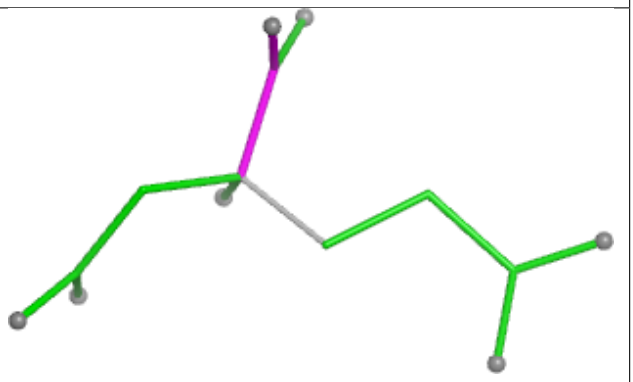
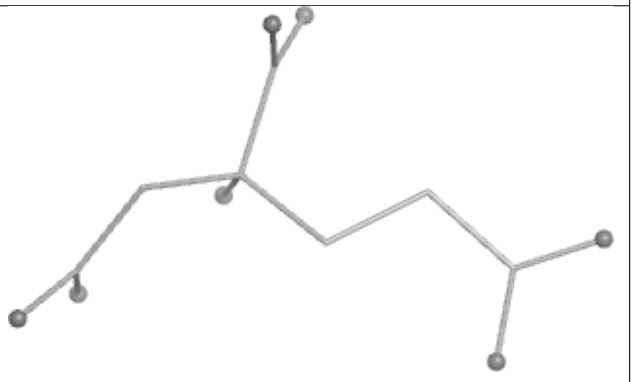


Bond angles

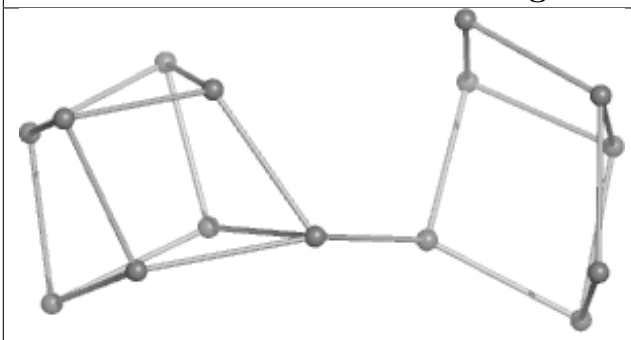


Torsions



Rings

Ligand 1CL B 701



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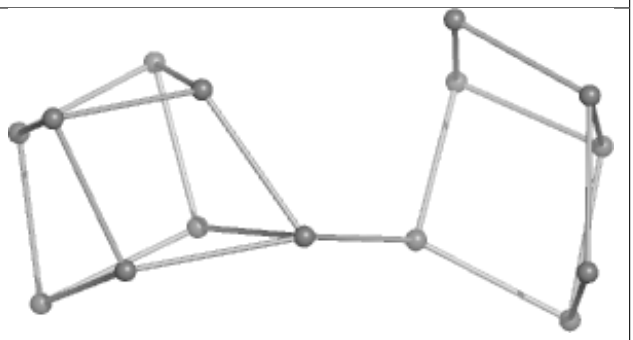
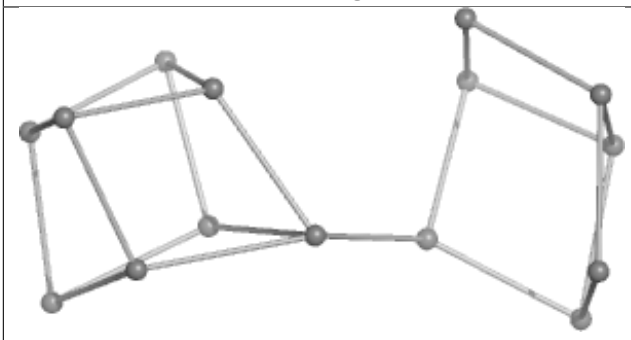


Bond angles



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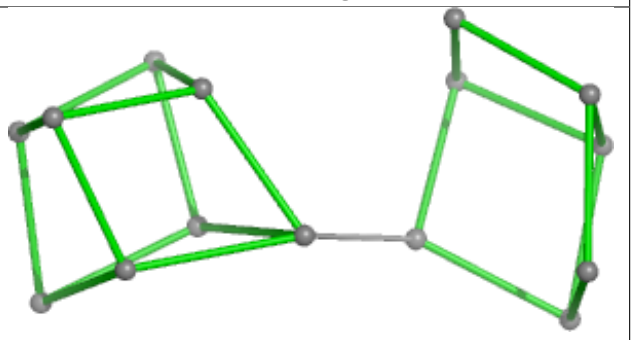
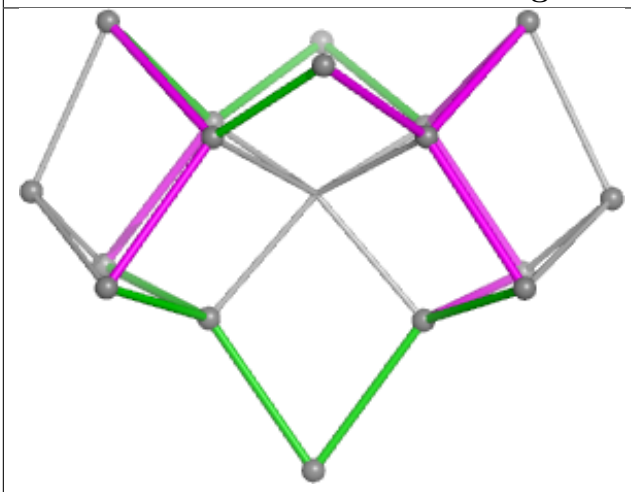


Rings

Ligand ICS H 602



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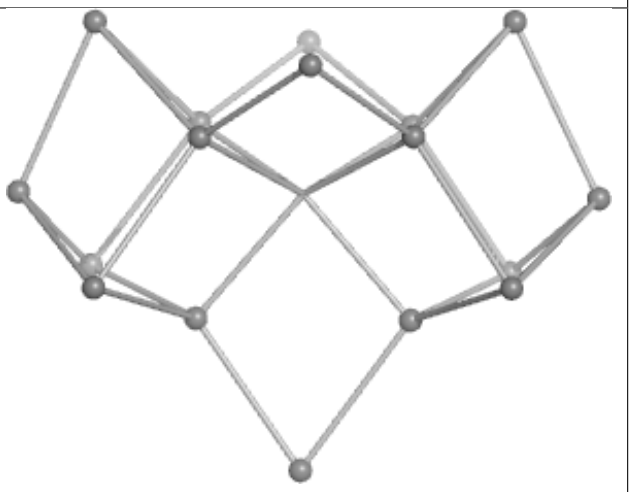

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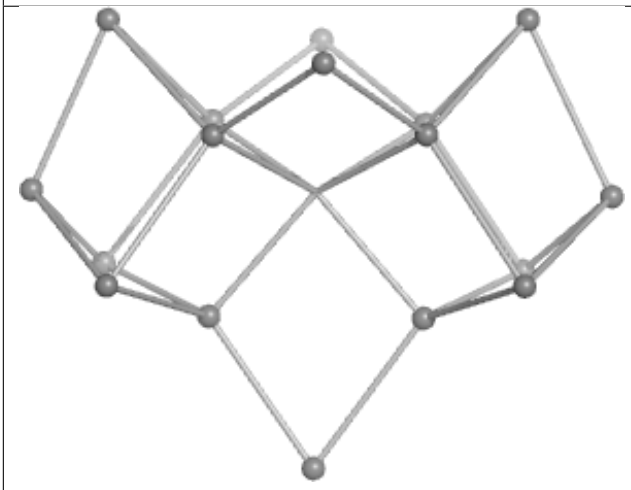
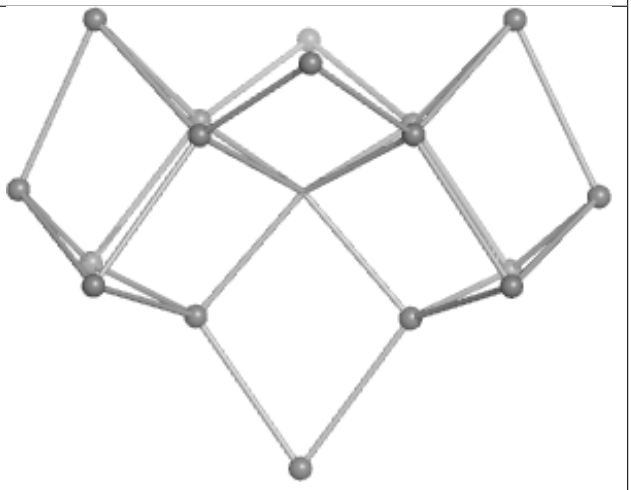
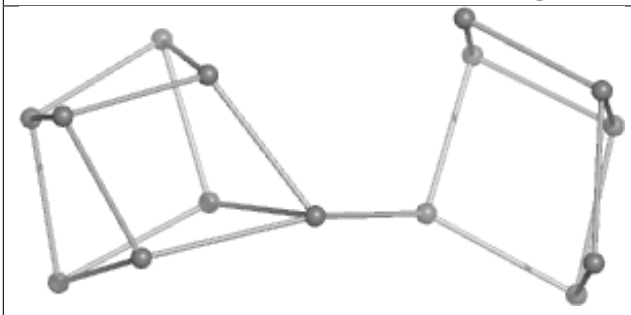


Torsions

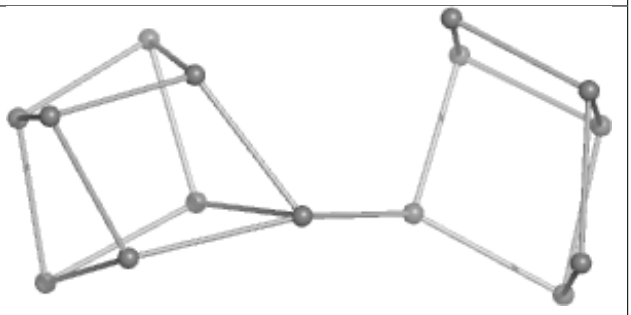


Rings

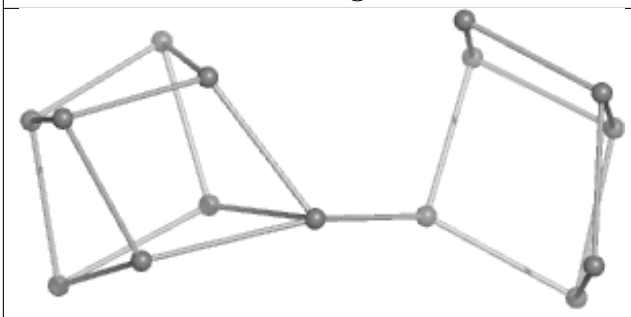
Ligand 1CL L 701



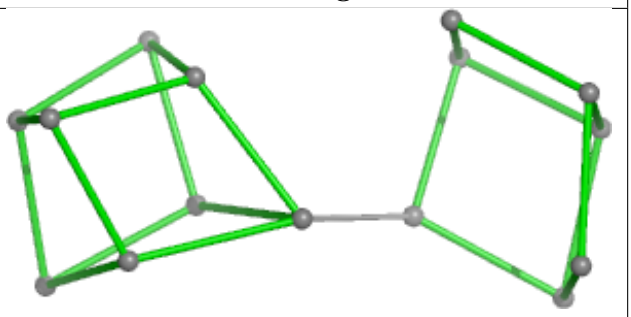
Bond lengths



Bond angles

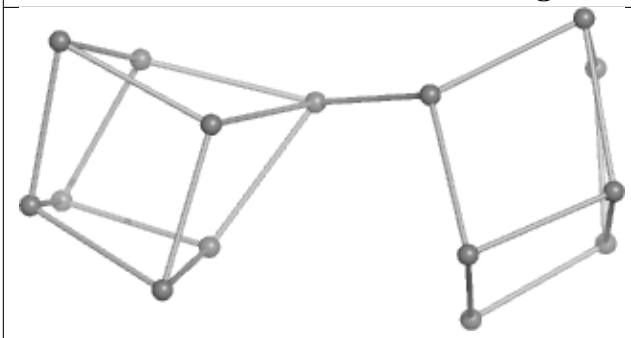


Torsions

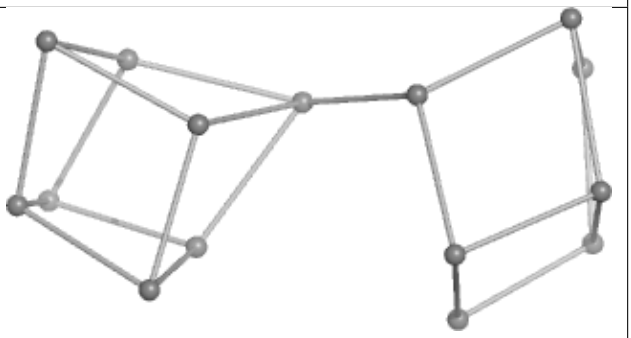


Rings

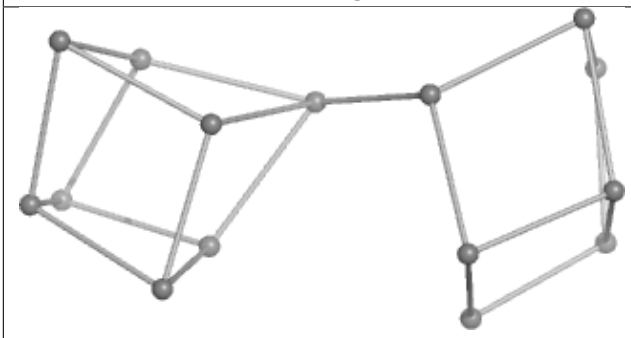
Ligand 1CL I 701



Bond lengths



Bond angles



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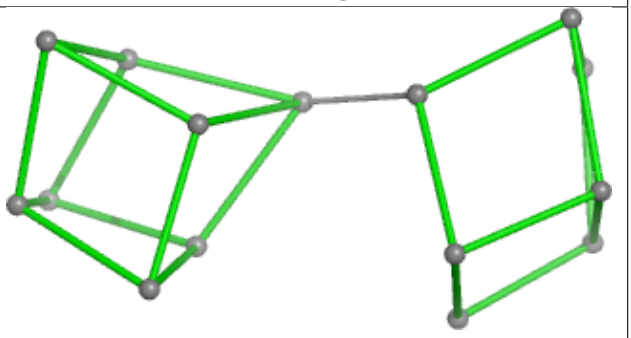
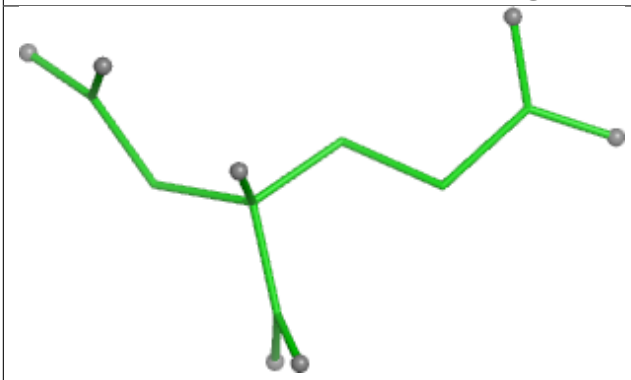
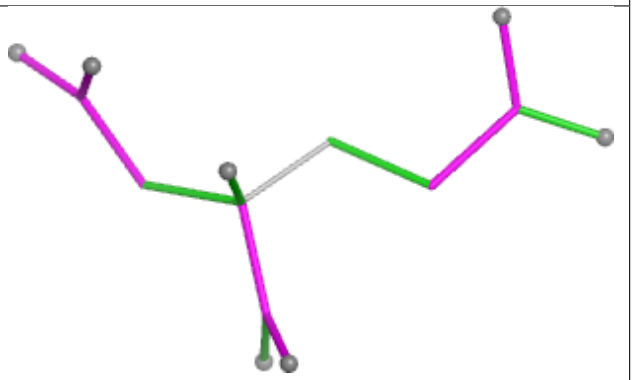


Rings

Ligand HCA J 601



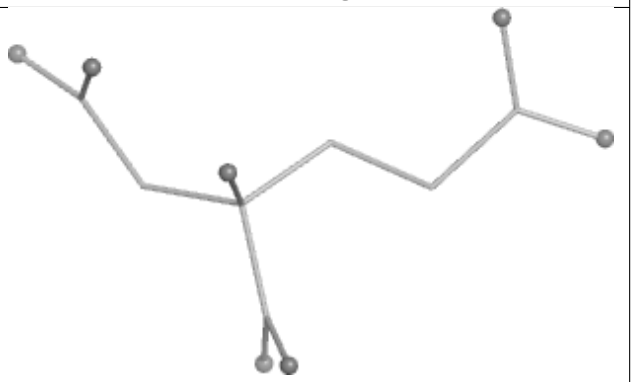
Bond lengths



Bond angles

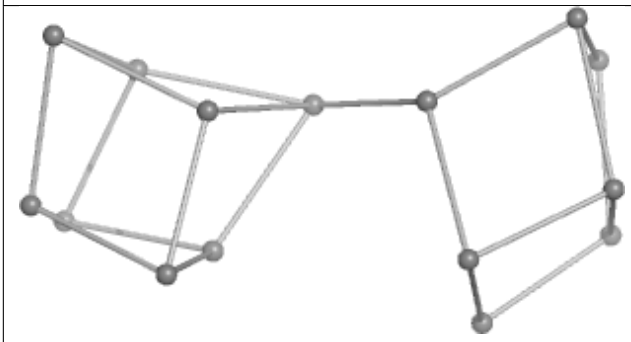


Torsions

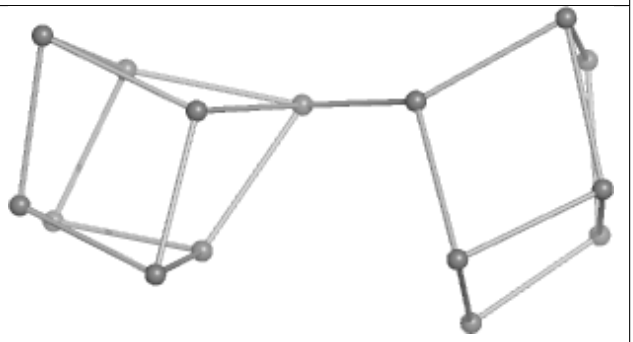


Rings

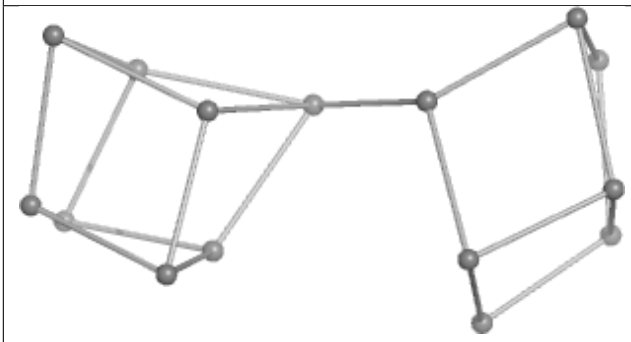
Ligand 1CL D 701



Bond lengths



Bond angles



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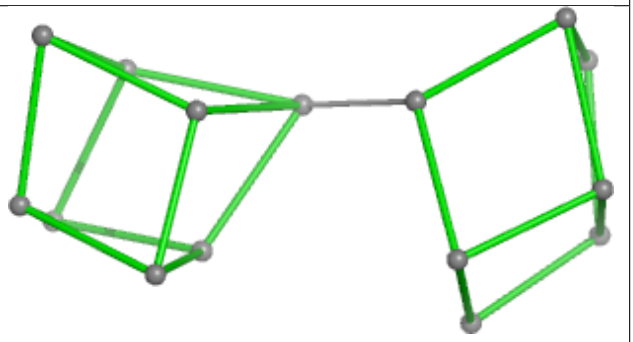

Rings

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

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	477/500 (95%)	-0.24	0 100 100	10, 20, 35, 55	0
1	C	477/500 (95%)	0.33	9 (1%) 66 42	27, 48, 74, 88	0
1	H	477/500 (95%)	0.38	9 (1%) 66 42	28, 51, 90, 103	0
1	J	477/500 (95%)	-0.25	0 100 100	9, 24, 41, 56	0
2	B	522/523 (99%)	-0.33	1 (0%) 91 83	9, 20, 34, 40	0
2	D	522/523 (99%)	0.04	2 (0%) 88 76	12, 38, 68, 78	0
2	I	522/523 (99%)	0.26	3 (0%) 85 69	14, 45, 78, 87	0
2	L	522/523 (99%)	-0.28	0 100 100	10, 22, 40, 49	0
All	All	3996/4092 (97%)	-0.02	24 (0%) 85 69	9, 31, 69, 103	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	38	ALA	3.6
2	D	424	GLY	3.6
1	H	36	ASP	2.9
1	C	37	PRO	2.9
1	H	69	GLY	2.8

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 (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
6	SO4	I	702	5/5	0.55	0.15	79,79,79,79	0
6	SO4	L	704	5/5	0.55	0.20	89,89,89,89	0
5	GOL	A	603	6/6	0.68	0.18	28,28,28,28	0
5	GOL	L	702	6/6	0.68	0.18	24,24,24,24	0
5	GOL	C	603	6/6	0.69	0.17	55,55,55,55	0
5	GOL	B	705	6/6	0.70	0.13	20,20,20,20	0
6	SO4	B	707	5/5	0.74	0.20	72,72,72,72	0
5	GOL	B	706	6/6	0.79	0.14	20,20,20,20	0
6	SO4	C	604	5/5	0.79	0.12	66,66,66,66	0
6	SO4	H	603	5/5	0.82	0.10	60,60,60,60	0
3	HCA	H	601	14/14	0.83	0.12	51,51,51,51	0
6	SO4	L	703	5/5	0.87	0.11	58,58,58,58	0
5	GOL	J	603	6/6	0.88	0.10	26,26,26,26	0
5	GOL	D	702	6/6	0.88	0.14	20,20,20,20	0
5	GOL	B	702	6/6	0.89	0.09	25,25,25,25	0
3	HCA	C	601	14/14	0.89	0.18	36,36,36,36	0
6	SO4	B	708	5/5	0.89	0.18	30,30,30,30	0
5	GOL	A	604	6/6	0.89	0.11	13,13,13,13	0
8	FE	L	705	1/1	0.89	0.12	77,77,77,77	0
8	FE	D	705	1/1	0.90	0.10	59,59,59,59	0
5	GOL	B	704	6/6	0.91	0.10	24,24,24,24	0
6	SO4	D	704	5/5	0.91	0.25	30,30,30,30	0
3	HCA	J	601	14/14	0.92	0.14	16,16,16,16	0
5	GOL	B	703	6/6	0.93	0.13	31,31,31,31	0
6	SO4	A	605	5/5	0.93	0.07	41,41,41,41	0
5	GOL	D	703	6/6	0.94	0.09	20,20,20,20	0
8	FE	B	709	1/1	0.94	0.05	54,54,54,54	0
7	1CL	I	701	15/15	0.95	0.07	73,74,74,74	0
8	FE	I	703	1/1	0.95	0.12	53,53,53,53	0
6	SO4	J	604	5/5	0.95	0.06	65,65,65,65	0
3	HCA	A	601	14/14	0.96	0.10	10,10,11,11	0
7	1CL	D	701	15/15	0.97	0.06	61,61,62,62	0
4	ICS	H	602	18/18	0.97	0.05	61,62,62,62	0
4	ICS	C	602	18/18	0.98	0.05	56,56,56,56	0
7	1CL	B	701	15/15	0.99	0.05	17,18,18,18	0
4	ICS	A	602	18/18	0.99	0.05	12,12,12,12	0
4	ICS	J	602	18/18	0.99	0.06	15,15,15,15	0

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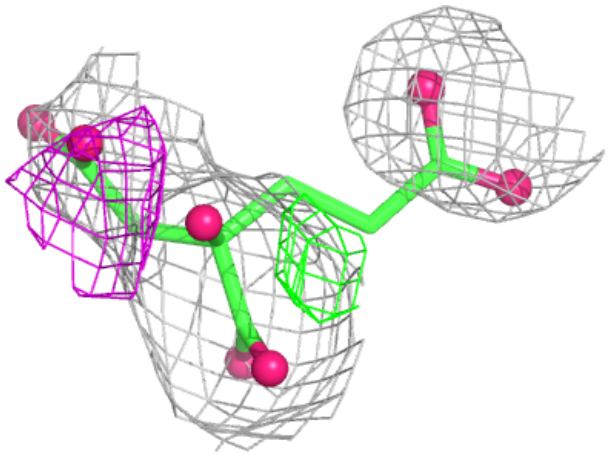
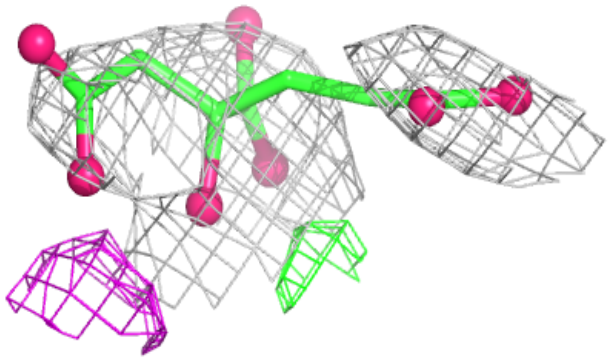
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	1CL	L	701	15/15	0.99	0.04	16,16,17,17	0

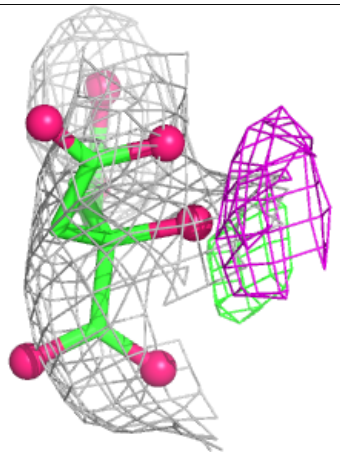
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around HCA H 601:

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

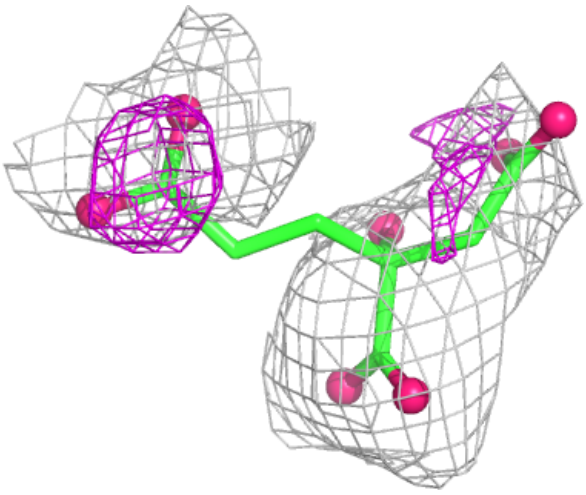


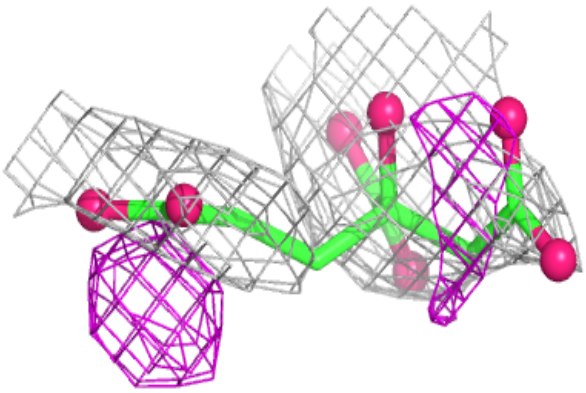


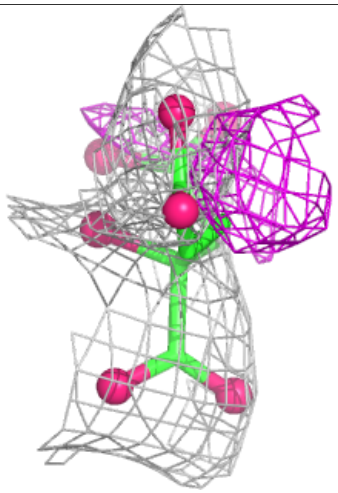


Electron density around HCA C 601:

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

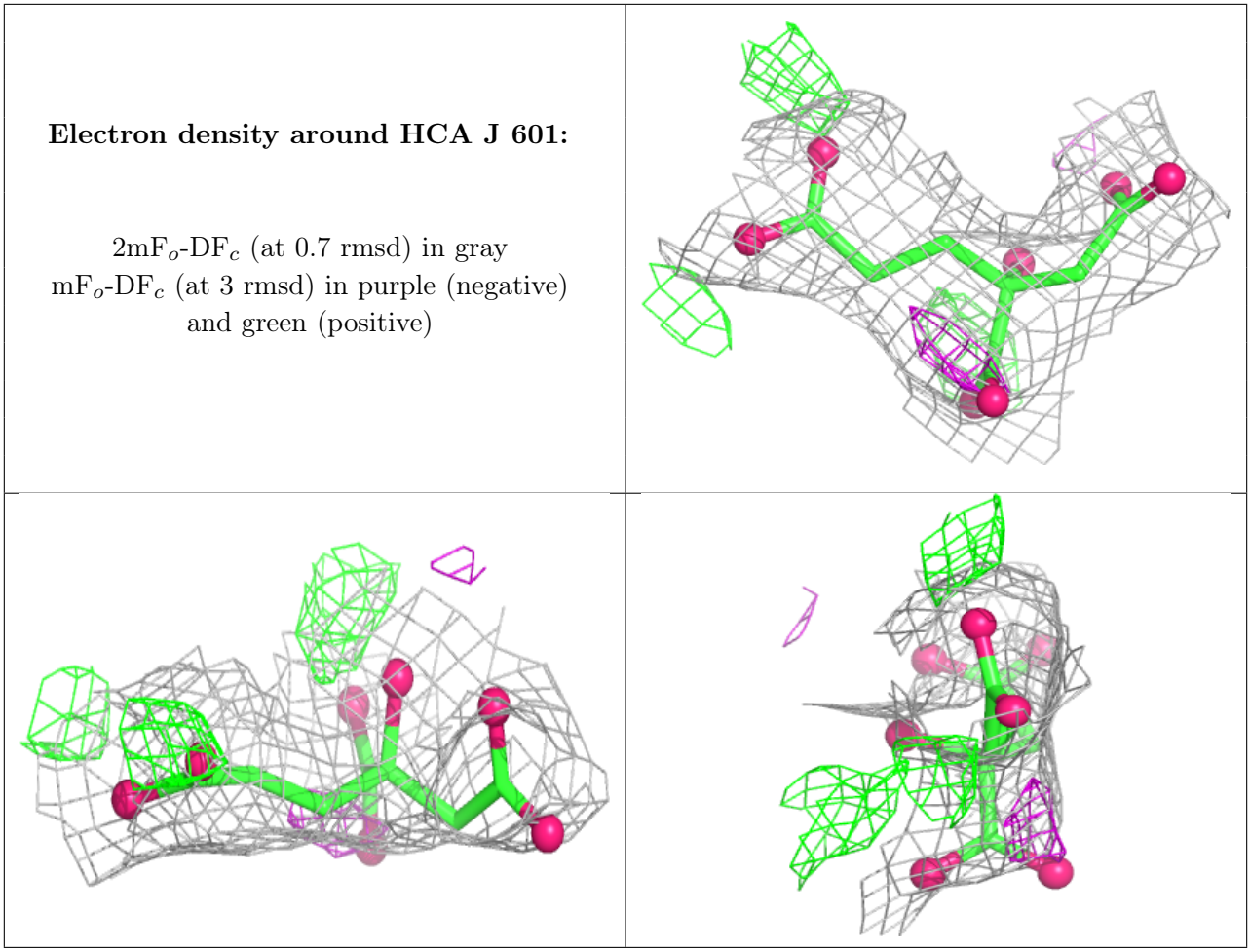






Electron density around HCA J 601:

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



Electron density around 1CL I 701:

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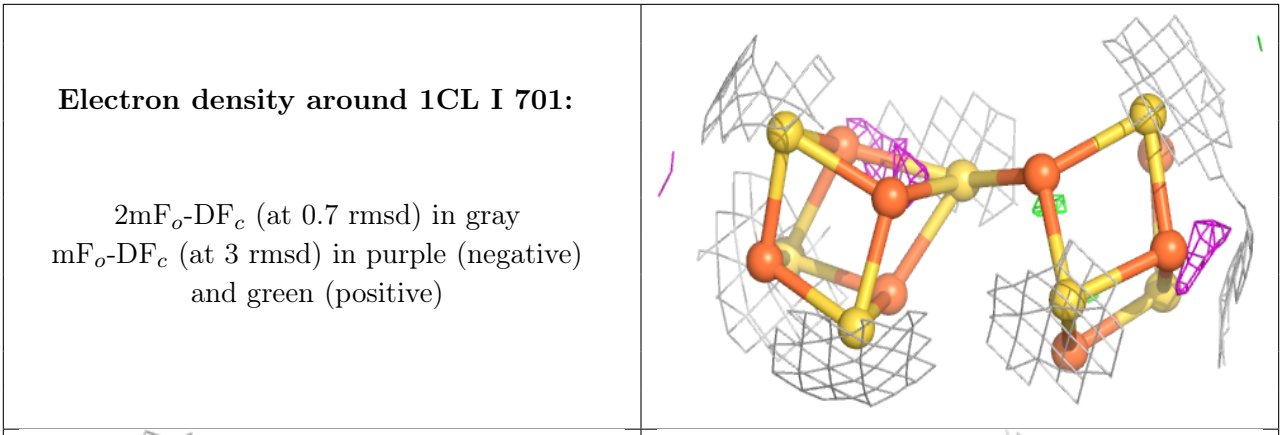
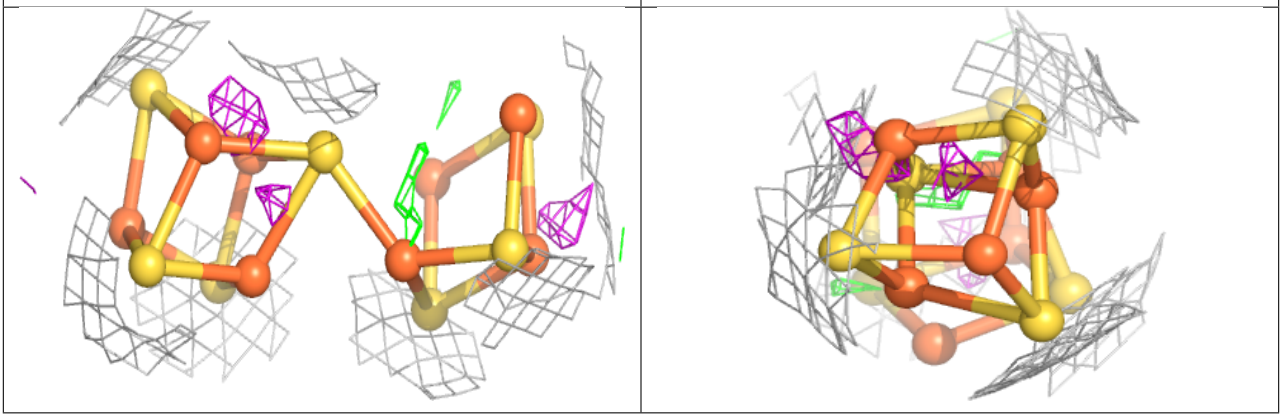
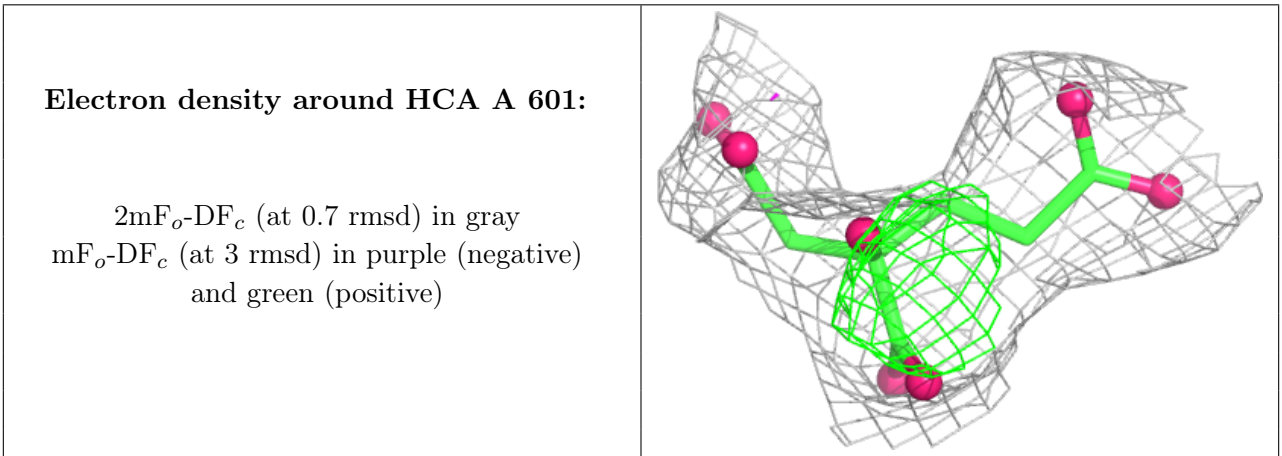
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

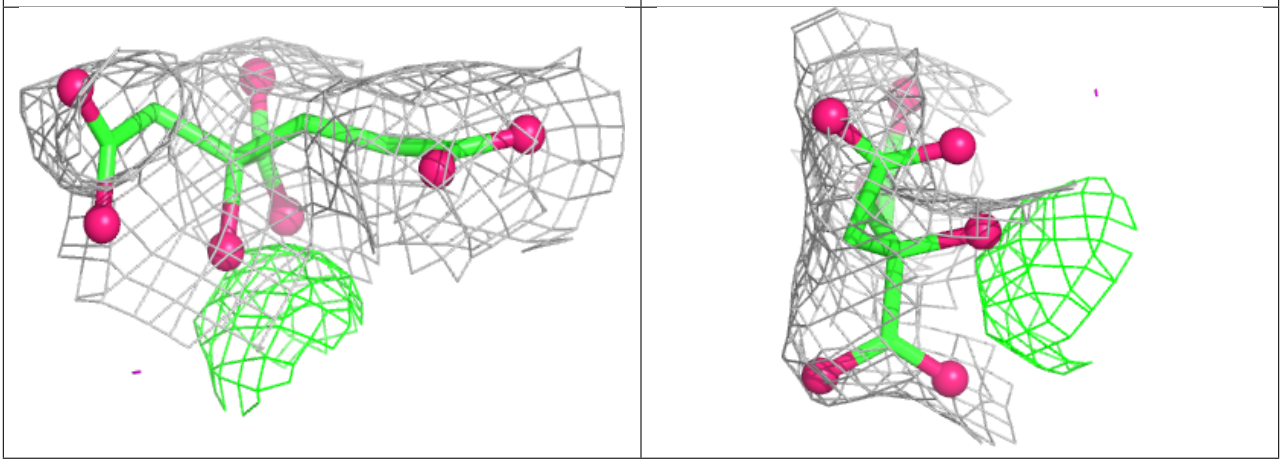




Electron density around HCA A 601:

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





Electron density around 1CL D 701:

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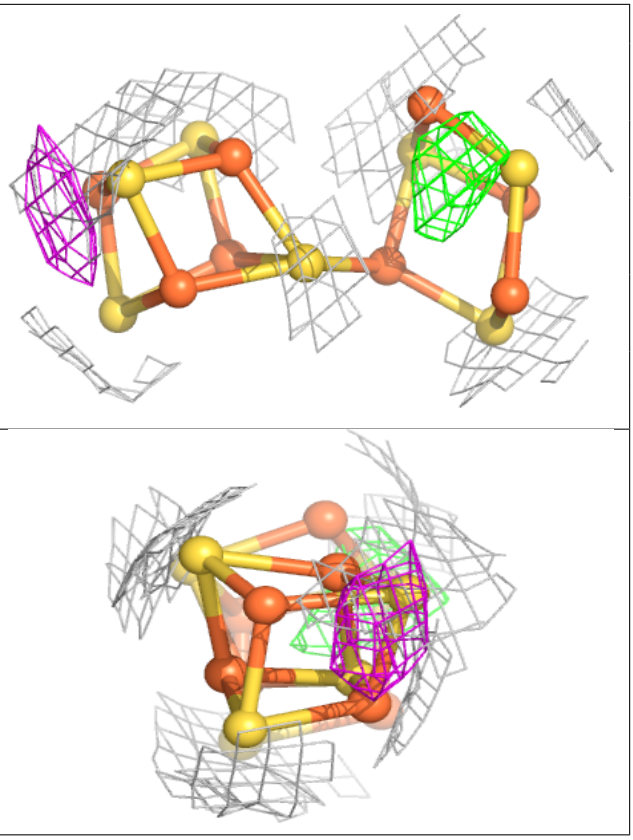
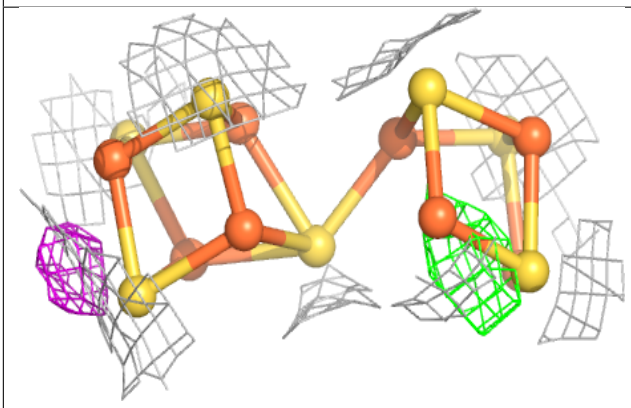
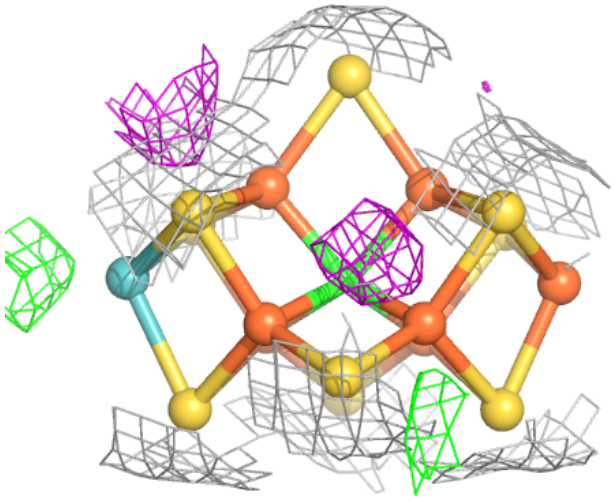
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

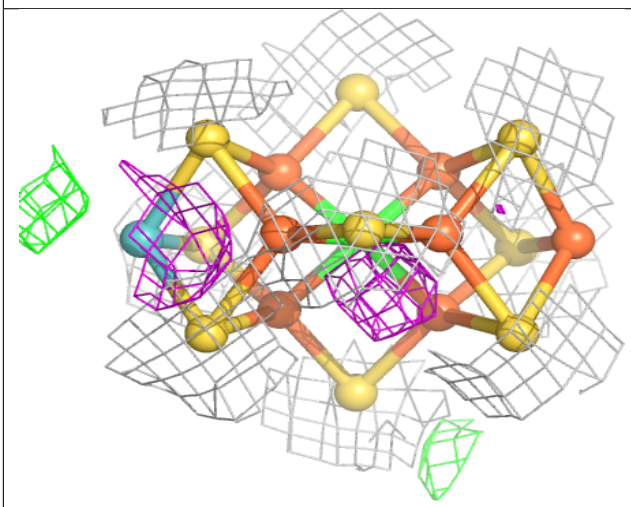


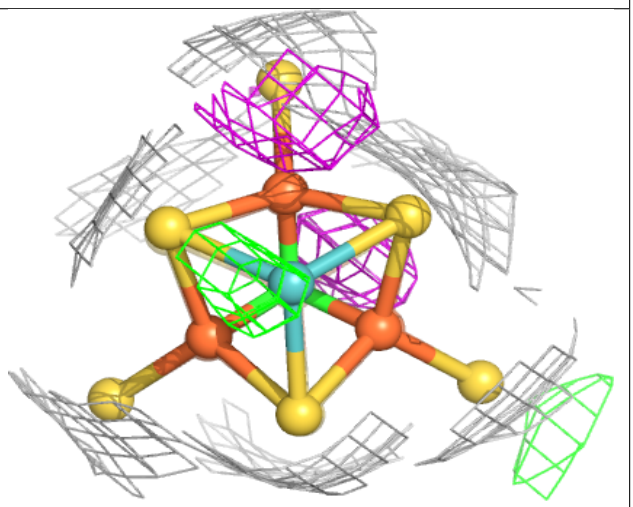


Electron density around ICS H 602:

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

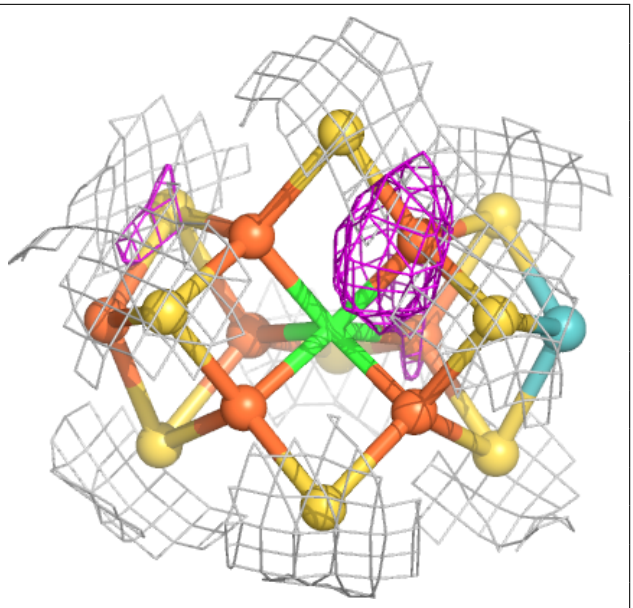


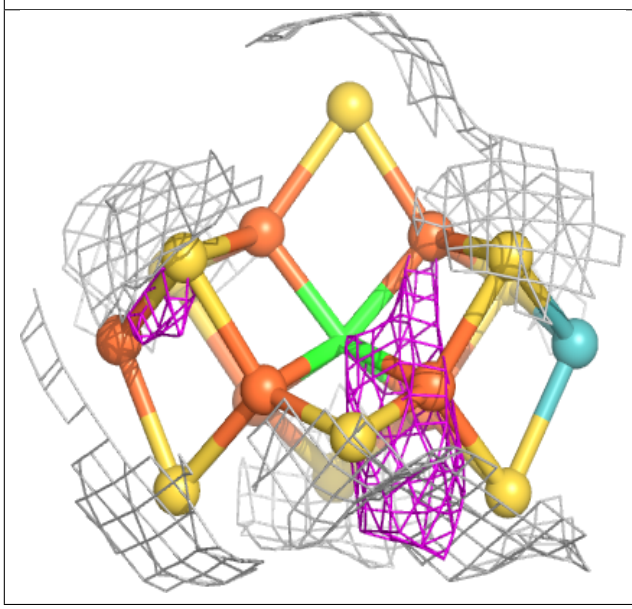


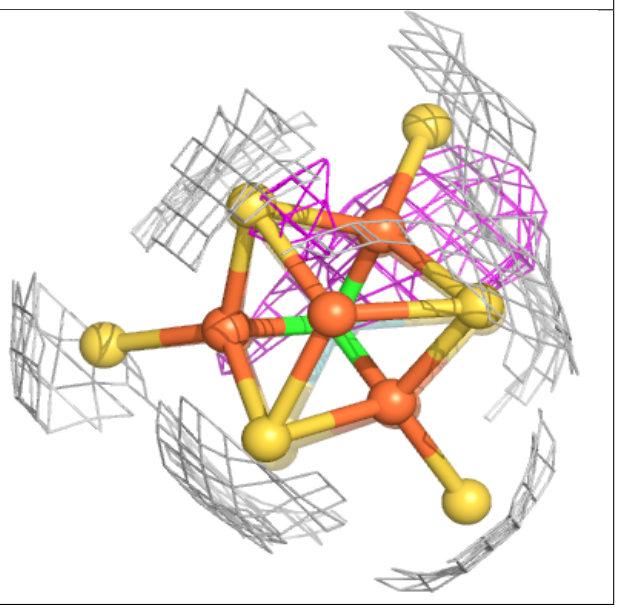


Electron density around ICS C 602:

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







Electron density around 1CL B 701:

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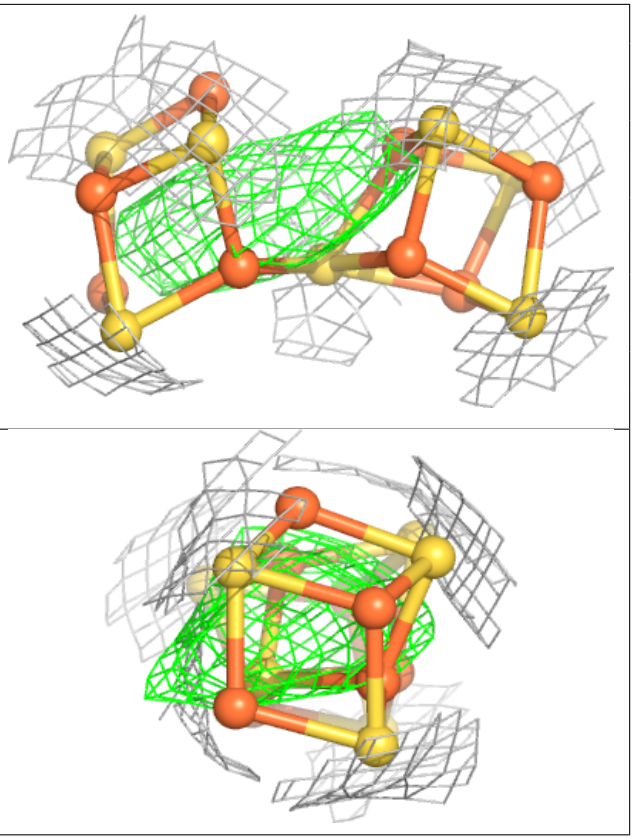
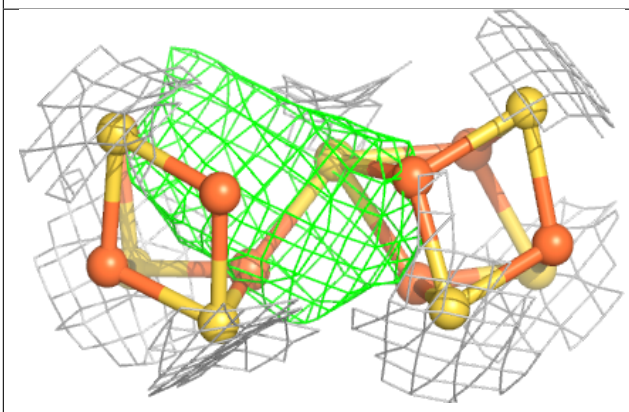
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around ICS A 602:

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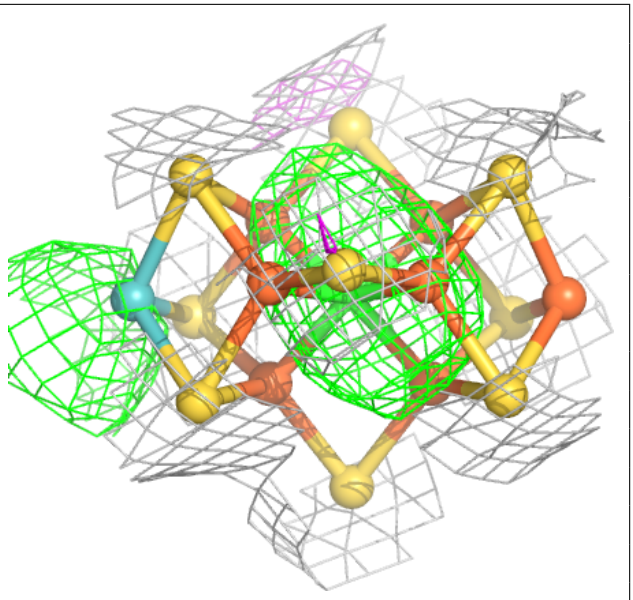
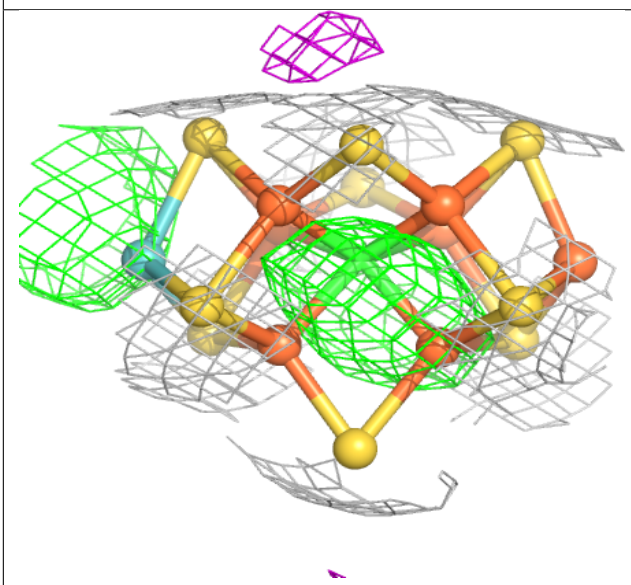
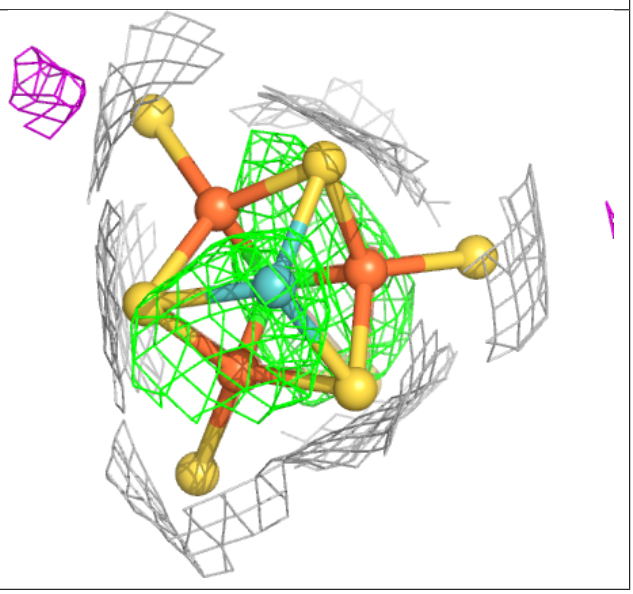
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

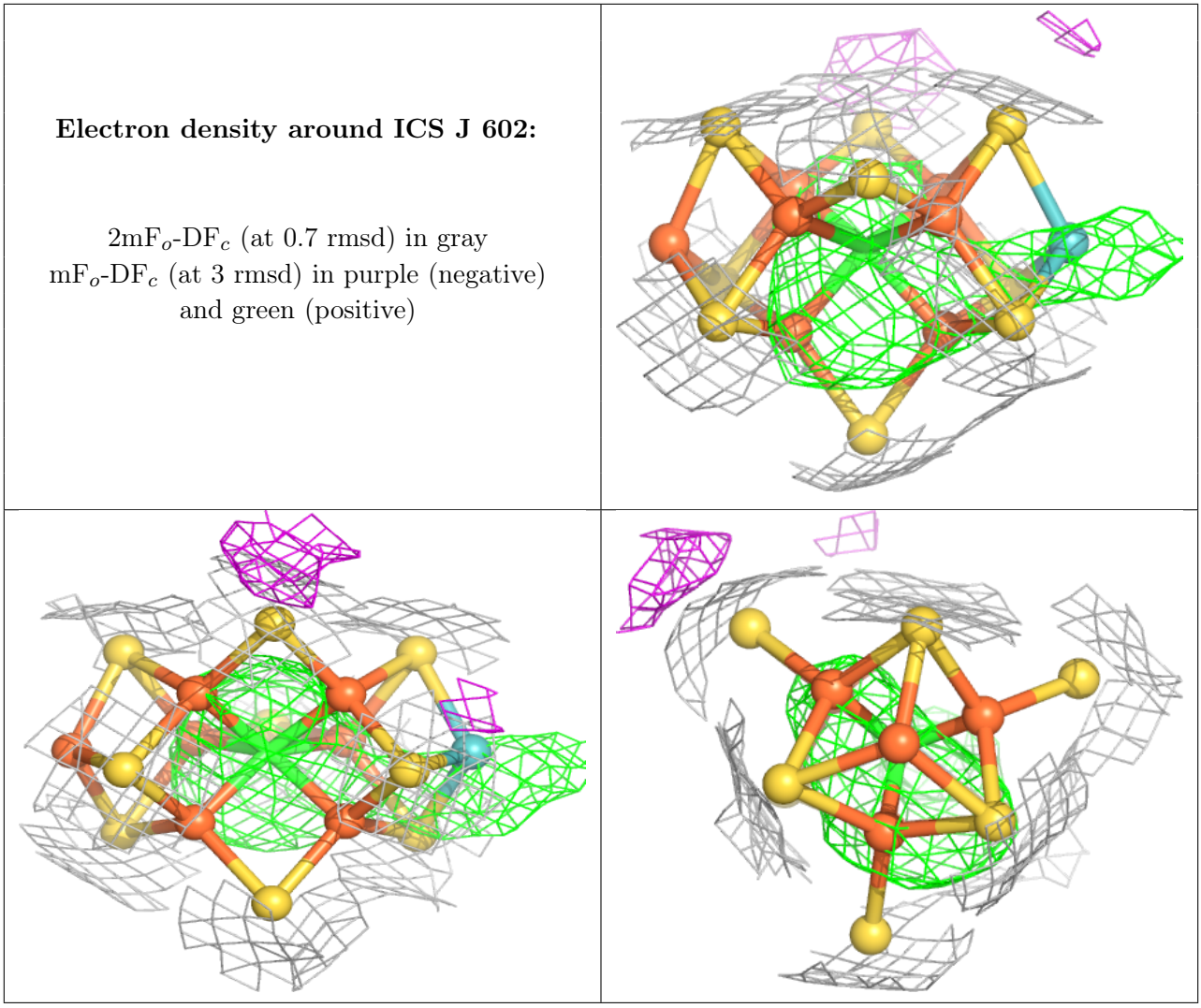






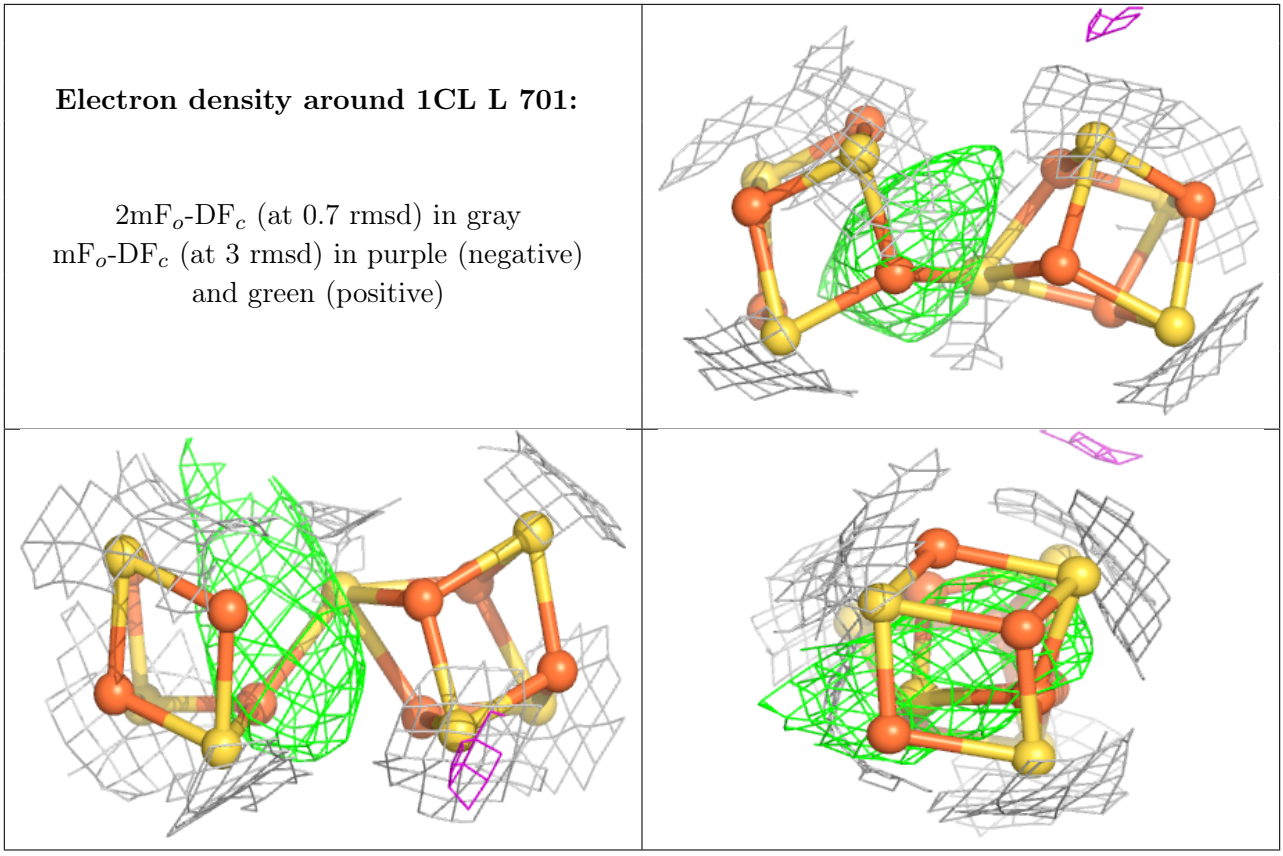
Electron density around ICS J 602:

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



Electron density around 1CL L 701:

$2mF_o$-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.