



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 13, 2024 – 01:28 pm GMT

PDB ID : 6SYX  
Title : Hydrogenase-2 variant R479K - reduced sample exposed to pure oxygen  
Authors : Carr, S.B.; Beaton, S.E.; Evans, R.M.; Armstrong, F.A.  
Deposited on : 2019-10-01  
Resolution : 1.30 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](mailto: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

<https://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

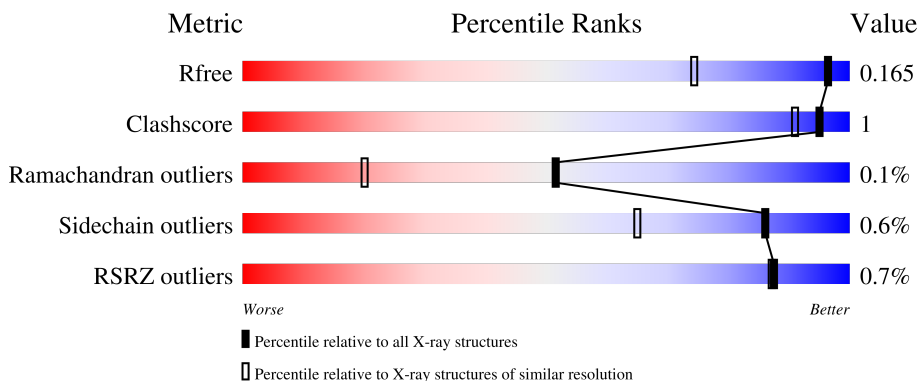
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*





The reported resolution of this entry is 1.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1058 (1.30-1.30)
Clashscore	141614	1101 (1.30-1.30)
Ramachandran outliers	138981	1058 (1.30-1.30)
Sidechain outliers	138945	1058 (1.30-1.30)
RSRZ outliers	127900	1029 (1.30-1.30)

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  $\geq 3$ , 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	SSS	298	 88% 10%
1	TTT	298	 88% 10%
2	LLL	567	 92% 5%
2	MMM	567	 94%

## 2 Entry composition i

There are 11 unique types of molecules in this entry. The entry contains 14669 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 Hydrogenase-2 small chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	SSS	268	2064	1308	362	381	13	0	4	0
1	TTT	268	2050	1300	361	376	13	0	2	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SSS	291	HIS	-	expression tag	UNP P69741
SSS	292	HIS	-	expression tag	UNP P69741
SSS	293	HIS	-	expression tag	UNP P69741
SSS	294	HIS	-	expression tag	UNP P69741
SSS	295	HIS	-	expression tag	UNP P69741
SSS	296	HIS	-	expression tag	UNP P69741
TTT	291	HIS	-	expression tag	UNP P69741
TTT	292	HIS	-	expression tag	UNP P69741
TTT	293	HIS	-	expression tag	UNP P69741
TTT	294	HIS	-	expression tag	UNP P69741
TTT	295	HIS	-	expression tag	UNP P69741
TTT	296	HIS	-	expression tag	UNP P69741

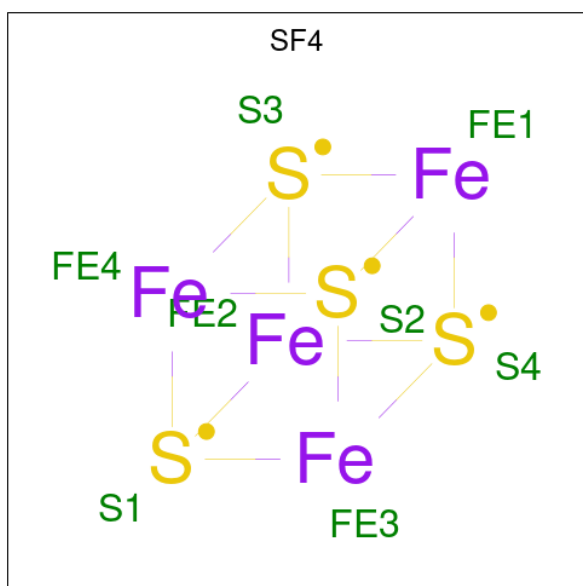
- Molecule 2 is a protein called Hydrogenase-2 large chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	LLL	551	4313	2747	738	810	18	0	6	0
2	MMM	551	4319	2750	741	810	18	0	6	0

There are 2 discrepancies between the modelled and reference sequences:

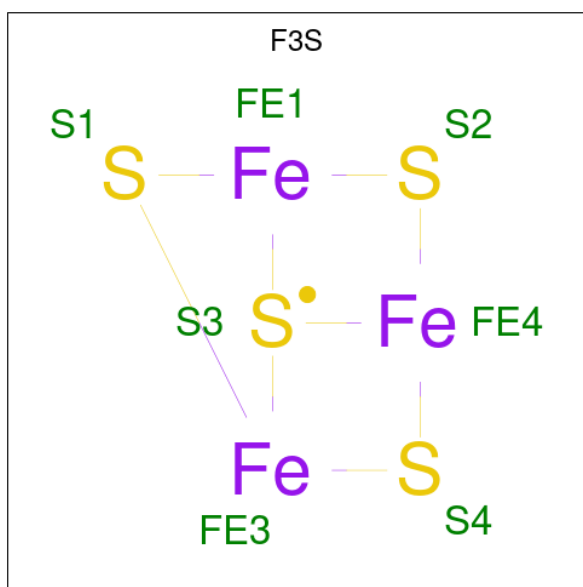
Chain	Residue	Modelled	Actual	Comment	Reference
LLL	479	LYS	ARG	engineered mutation	UNP V0V766
MMM	479	LYS	ARG	engineered mutation	UNP V0V766

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	SSS	1	Total Fe S 8 4 4	0	0
3	SSS	1	Total Fe S 8 4 4	0	0
3	TTT	1	Total Fe S 8 4 4	0	0
3	TTT	1	Total Fe S 8 4 4	0	0

- Molecule 4 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe<sub>3</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	SSS	1	Total Fe S 7 3 4	0	0
4	TTT	1	Total Fe S 7 3 4	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



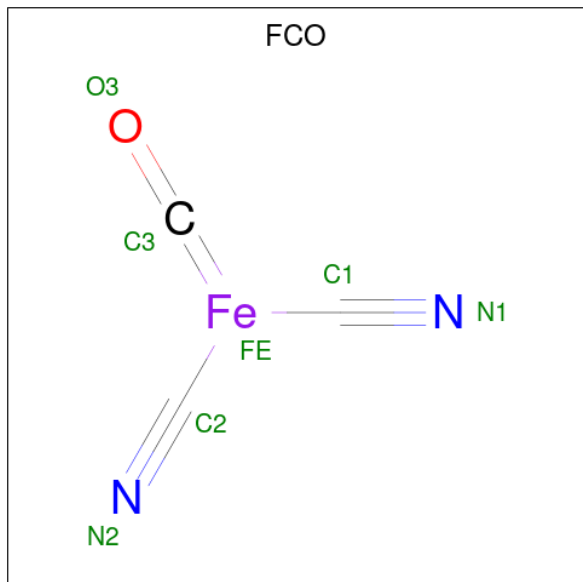
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	SSS	1	Total C O 6 3 3	0	0
5	SSS	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	LLL	1	Total	C	O	0	0
			6	3	3		
5	LLL	1	Total	C	O	0	0
			6	3	3		
5	TTT	1	Total	C	O	0	0
			6	3	3		
5	MMM	1	Total	C	O	0	0
			6	3	3		
5	MMM	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is CARBONMONOXIDE-(DICYANO) IRON (three-letter code: FCO) (formula:  $C_3FeN_2O$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	LLL	1	Total	C	Fe	N	O	0	0
			7	3	1	2	1		
6	MMM	1	Total	C	Fe	N	O	0	0
			7	3	1	2	1		

- Molecule 7 is NICKEL (II) ION (three-letter code: NI) (formula: Ni) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	LLL	1	Total	Ni	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	MMM	1	Total Ni 1 1	0	0

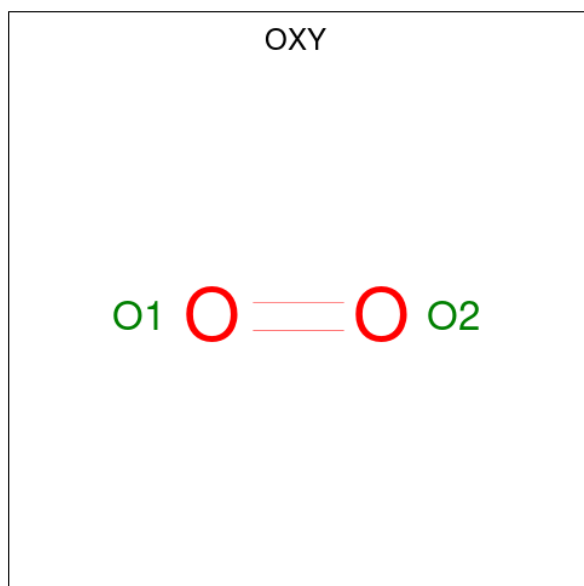
- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	LLL	2	Total Mg 2 2	0	0
8	TTT	1	Total Mg 1 1	0	0
8	MMM	1	Total Mg 1 1	0	0

- Molecule 9 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	LLL	1	Total Cl 1 1	0	0
9	MMM	1	Total Cl 1 1	0	0

- Molecule 10 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	LLL	1	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	MMM	1	Total O 2 2	0	0

- Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	SSS	321	Total O 321 321	0	0
11	LLL	618	Total O 618 618	0	0
11	TTT	294	Total O 294 294	0	0
11	MMM	576	Total O 576 576	0	0



### 3 Residue-property plots [i](#)

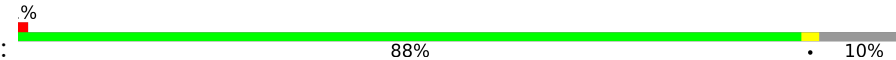
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

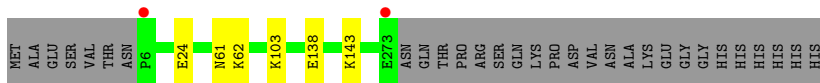
- Molecule 1: Hydrogenase-2 small chain

Chain SSS:  88% 10%



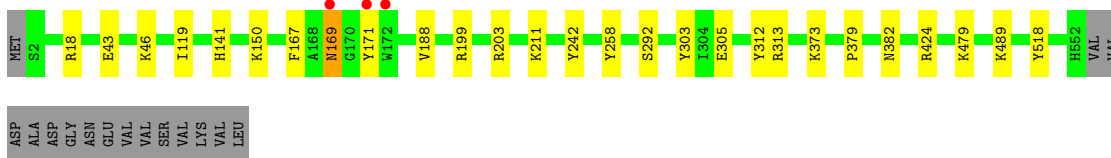
- Molecule 1: Hydrogenase-2 small chain

Chain TTT:  88% 10%



- Molecule 2: Hydrogenase-2 large chain

Chain LLL:  92% 5%



- Molecule 2: Hydrogenase-2 large chain

Chain MMM:  94%



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.73Å 101.33Å 170.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	87.13 – 1.30 87.13 – 1.30	Depositor EDS
% Data completeness (in resolution range)	99.5 (87.13-1.30) 99.5 (87.13-1.30)	Depositor EDS
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.75 (at 1.30Å)	Xtrriage
Refinement program	REFMAC 5.8.0253	Depositor
R, $R_{free}$	0.147 , 0.163 0.149 , 0.165	Depositor DCC
$R_{free}$ test set	20792 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	9.7	Xtrriage
Anisotropy	0.038	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.007 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	14669	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: F3S, MG, CL, OXY, NI, FCO, SF4, 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	SSS	1.04	2/2131 (0.1%)	0.91	0/2900
1	TTT	1.04	2/2114 (0.1%)	0.92	0/2877
2	LLL	0.96	1/4438 (0.0%)	0.94	10/6047 (0.2%)
2	MMM	0.97	1/4441 (0.0%)	0.94	8/6052 (0.1%)
All	All	0.99	6/13124 (0.0%)	0.93	18/17876 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	LLL	0	1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	SSS	24	GLU	CD-OE2	6.12	1.32	1.25
2	LLL	43	GLU	CD-OE1	6.12	1.32	1.25
2	MMM	535	GLU	CD-OE2	5.83	1.32	1.25
1	SSS	193	GLU	CD-OE2	5.25	1.31	1.25
1	TTT	138	GLU	CD-OE1	5.25	1.31	1.25

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	LLL	203	ARG	NE-CZ-NH2	-7.90	116.35	120.30
2	MMM	424	ARG	NE-CZ-NH1	7.29	123.95	120.30
2	LLL	242	TYR	CB-CG-CD1	7.27	125.36	121.00
2	LLL	424	ARG	NE-CZ-NH1	7.15	123.87	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	MMM	12	ARG	NE-CZ-NH1	6.60	123.60	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	LLL	171	TYR	Sidechain

## 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	SSS	2064	0	1990	8	0
1	TTT	2050	0	1981	4	0
2	LLL	4313	0	4267	15	0
2	MMM	4319	0	4270	8	0
3	SSS	16	0	0	1	0
3	TTT	16	0	0	0	0
4	SSS	7	0	0	0	0
4	TTT	7	0	0	0	0
5	LLL	12	0	16	0	0
5	MMM	12	0	16	0	0
5	SSS	12	0	16	0	0
5	TTT	6	0	8	0	0
6	LLL	7	0	0	0	0
6	MMM	7	0	0	0	0
7	LLL	1	0	0	0	0
7	MMM	1	0	0	0	0
8	LLL	2	0	0	0	0
8	MMM	1	0	0	0	0
8	TTT	1	0	0	0	0
9	LLL	1	0	0	0	0
9	MMM	1	0	0	0	0
10	LLL	2	0	0	0	0
10	MMM	2	0	0	0	0
11	LLL	618	0	0	7	0
11	MMM	576	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	SSS	321	0	0	5	0
11	TTT	294	0	0	2	0
All	All	14669	0	12564	31	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 1.

The worst 5 of 31 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:MMM:379:PRO:HB2	11:MMM:907:HOH:O	1.71	0.89
1:TTT:61:ASN:HD21	2:MMM:169:ASN:HB3	1.39	0.86
2:LLL:379:PRO:HB2	11:LLL:938:HOH:O	1.83	0.76
1:TTT:62:LYS:HE2	11:TTT:829:HOH:O	1.89	0.72
2:LLL:169:ASN:O	11:LLL:701:HOH:O	2.09	0.71

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	SSS	270/298 (91%)	261 (97%)	9 (3%)	0	100	100
1	TTT	268/298 (90%)	260 (97%)	8 (3%)	0	100	100
2	LLL	555/567 (98%)	531 (96%)	23 (4%)	1 (0%)	47	19
2	MMM	555/567 (98%)	531 (96%)	23 (4%)	1 (0%)	47	19
All	All	1648/1730 (95%)	1583 (96%)	63 (4%)	2 (0%)	51	20

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	LLL	211	LYS
2	MMM	211	LYS

### 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	SSS	217/239 (91%)	217 (100%)	0	100	100
1	TTT	215/239 (90%)	214 (100%)	1 (0%)	88	69
2	LLL	471/479 (98%)	467 (99%)	4 (1%)	81	58
2	MMM	471/479 (98%)	468 (99%)	3 (1%)	86	65
All	All	1374/1436 (96%)	1366 (99%)	8 (1%)	86	65

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	MMM	479	LYS
2	MMM	312	TYR
1	TTT	143	LYS
2	LLL	479	LYS
2	MMM	141	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 25 ligands modelled in this entry, 8 are monoatomic - leaving 17 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	SF4	TTT	604	1	0,12,12	-	-	-		
5	GOL	LLL	601	-	5,5,5	0.29	0	5,5,5	0.49	0
3	SF4	SSS	403	1	0,12,12	-	-	-		
4	F3S	TTT	603	1	0,9,9	-	-	-		
10	OXY	LLL	608	7	1,1,1	0.19	0	-		
5	GOL	LLL	605	-	5,5,5	0.15	0	5,5,5	0.32	0
4	F3S	SSS	402	1	0,9,9	-	-	-		
5	GOL	TTT	601	-	5,5,5	0.26	0	5,5,5	0.69	0
5	GOL	SSS	404	-	5,5,5	0.41	0	5,5,5	0.81	0
3	SF4	TTT	602	1	0,12,12	-	-	-		
5	GOL	MMM	601	-	5,5,5	0.35	0	5,5,5	0.76	0
3	SF4	SSS	401	1	0,12,12	-	-	-		
6	FCO	LLL	602	2	0,6,6	-	-	-		
10	OXY	MMM	607	-	1,1,1	0.14	0	-		
5	GOL	SSS	405	-	5,5,5	0.25	0	5,5,5	0.39	0
6	FCO	MMM	602	2	0,6,6	-	-	-		
5	GOL	MMM	605	-	5,5,5	0.29	0	5,5,5	1.01	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	SF4	TTT	604	1	-	-	0/6/5/5
5	GOL	LLL	601	-	-	2/4/4/4	-
3	SF4	SSS	403	1	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	F3S	TTT	603	1	-	-	0/3/3/3
5	GOL	LLL	605	-	-	0/4/4/4	-
4	F3S	SSS	402	1	-	-	0/3/3/3
5	GOL	TTT	601	-	-	2/4/4/4	-
5	GOL	SSS	404	-	-	1/4/4/4	-
5	GOL	MMM	601	-	-	0/4/4/4	-
3	SF4	TTT	602	1	-	-	0/6/5/5
3	SF4	SSS	401	1	-	-	0/6/5/5
5	GOL	SSS	405	-	-	0/4/4/4	-
5	GOL	MMM	605	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	LLL	601	GOL	C1-C2-C3-O3
5	TTT	601	GOL	C1-C2-C3-O3
5	MMM	605	GOL	O1-C1-C2-C3
5	MMM	605	GOL	O1-C1-C2-O2
5	LLL	601	GOL	O2-C2-C3-O3

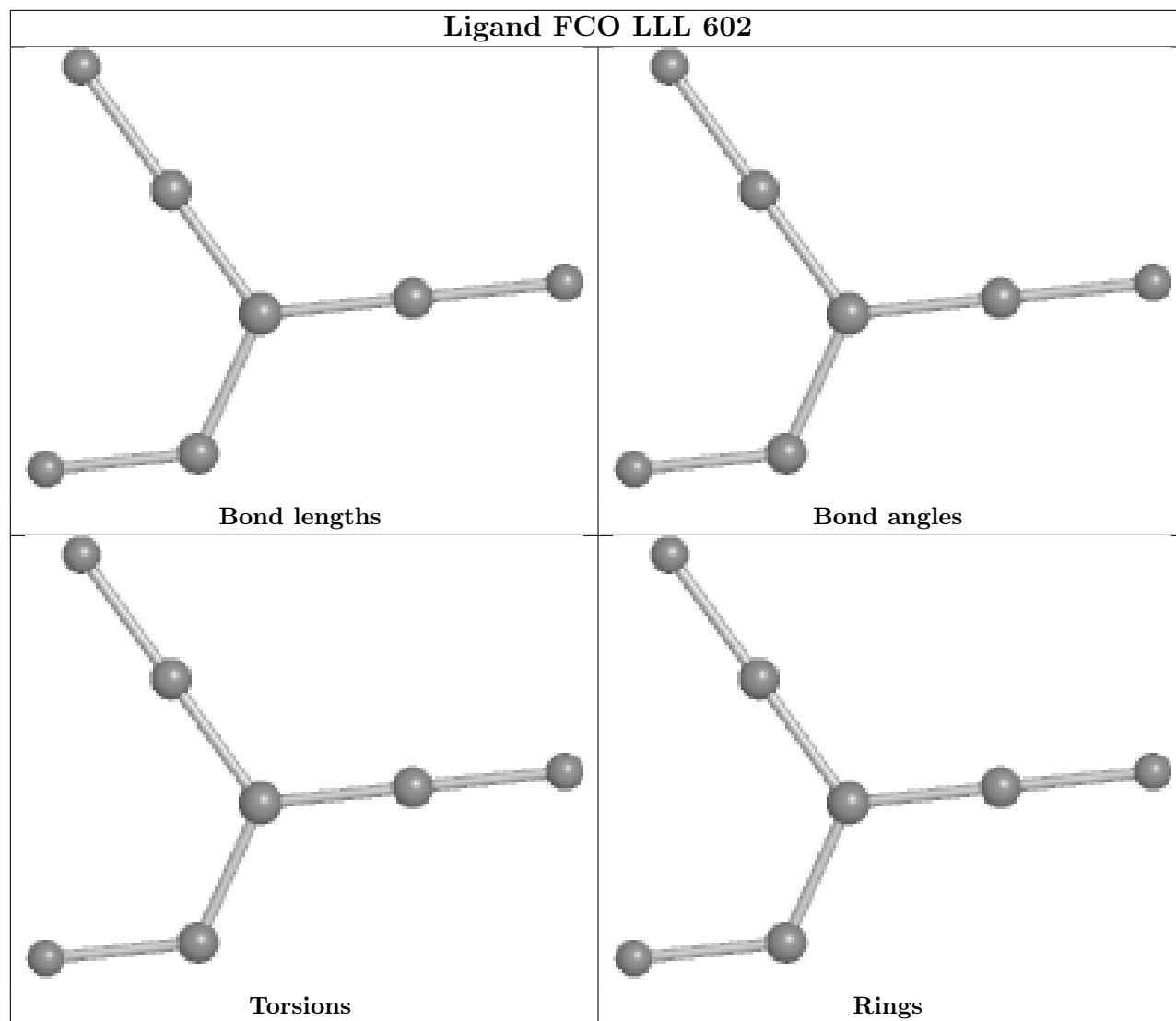
There are no ring outliers.

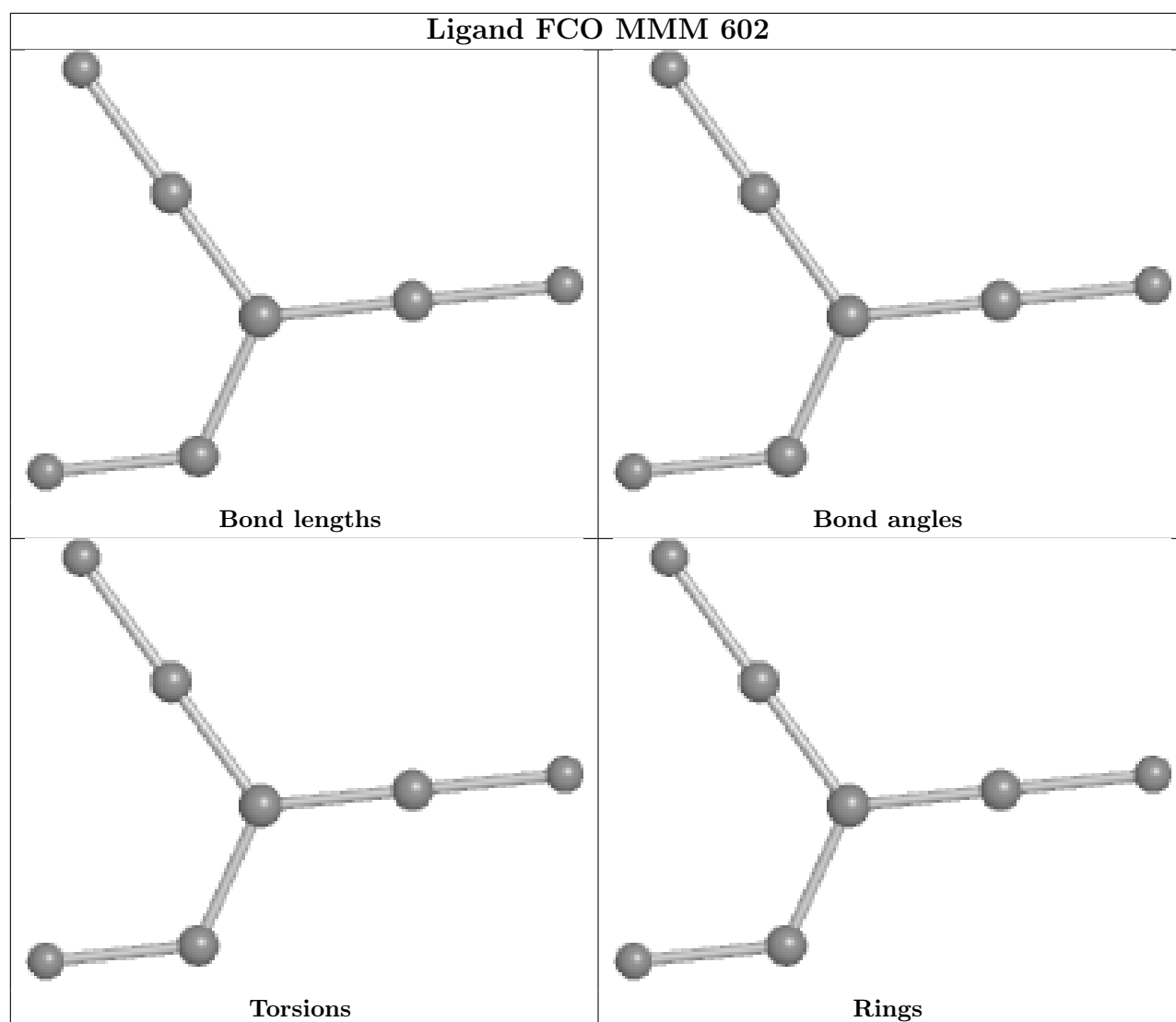
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	SSS	403	SF4	1	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 than 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.







## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	SSS	268/298 (89%)	-0.47	1 (0%) 92 91	6, 10, 23, 38	0
1	TTT	268/298 (89%)	-0.38	2 (0%) 87 87	7, 12, 26, 51	0
2	LLL	551/567 (97%)	-0.48	3 (0%) 91 91	6, 10, 23, 40	0
2	MMM	551/567 (97%)	-0.39	6 (1%) 80 82	6, 12, 27, 64	0
All	All	1638/1730 (94%)	-0.43	12 (0%) 87 87	6, 11, 25, 64	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	MMM	172	TRP	6.4
2	LLL	172	TRP	6.0
2	LLL	171	TYR	4.4
2	MMM	171	TYR	3.9
1	TTT	6	PRO	3.2

### 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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

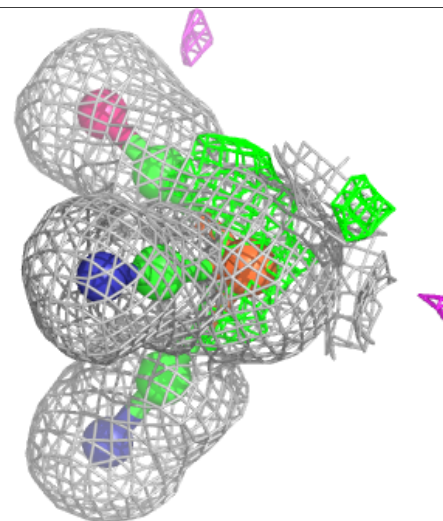
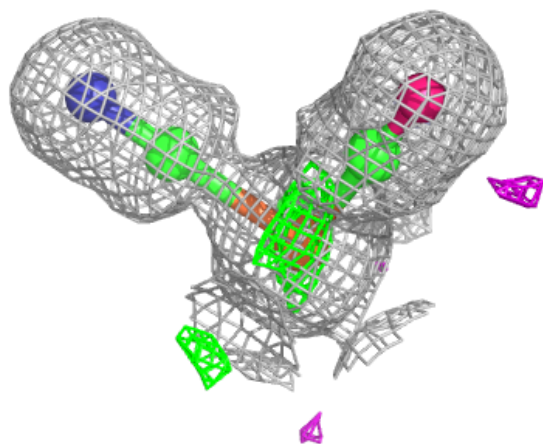
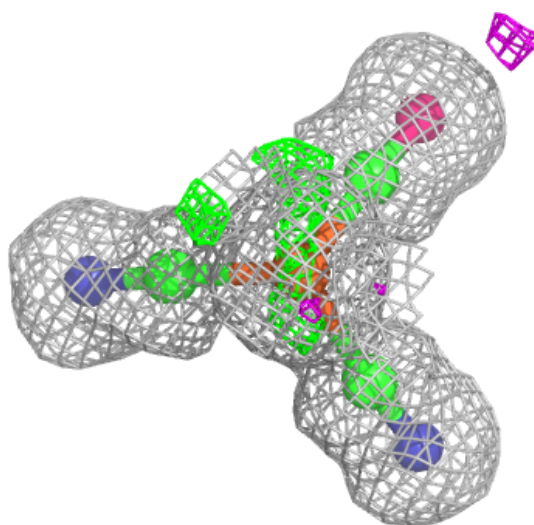
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	GOL	MMM	605	6/6	0.79	0.15	31,33,34,37	0
5	GOL	SSS	405	6/6	0.80	0.18	23,28,28,33	0
5	GOL	SSS	404	6/6	0.81	0.19	20,27,29,30	0
5	GOL	LLL	605	6/6	0.84	0.18	25,29,33,36	0
5	GOL	TTT	601	6/6	0.85	0.14	26,31,32,34	0
5	GOL	LLL	601	6/6	0.86	0.23	18,28,33,44	0
5	GOL	MMM	601	6/6	0.93	0.16	18,23,29,37	0
8	MG	LLL	606	1/1	0.95	0.21	29,29,29,29	0
9	CL	LLL	607	1/1	0.98	0.05	16,16,16,16	0
10	OXY	LLL	608	2/2	0.98	0.19	12,12,12,14	2
8	MG	TTT	605	1/1	0.99	0.16	18,18,18,18	0
9	CL	MMM	606	1/1	0.99	0.05	15,15,15,15	0
8	MG	MMM	604	1/1	0.99	0.06	6,6,6,6	0
10	OXY	MMM	607	2/2	0.99	0.16	14,14,14,17	2
6	FCO	MMM	602	7/7	1.00	0.05	7,7,7,8	0
7	NI	LLL	603	1/1	1.00	0.04	7,7,7,7	0
7	NI	MMM	603	1/1	1.00	0.04	8,8,8,8	0
8	MG	LLL	604	1/1	1.00	0.07	5,5,5,5	0
3	SF4	SSS	403	8/8	1.00	0.05	6,6,6,7	0
3	SF4	TTT	602	8/8	1.00	0.05	7,8,8,9	0
3	SF4	TTT	604	8/8	1.00	0.05	7,7,8,8	0
4	F3S	SSS	402	7/7	1.00	0.05	6,7,7,7	0
4	F3S	TTT	603	7/7	1.00	0.05	7,7,7,7	0
3	SF4	SSS	401	8/8	1.00	0.05	8,8,8,8	0
6	FCO	LLL	602	7/7	1.00	0.04	6,6,7,8	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.

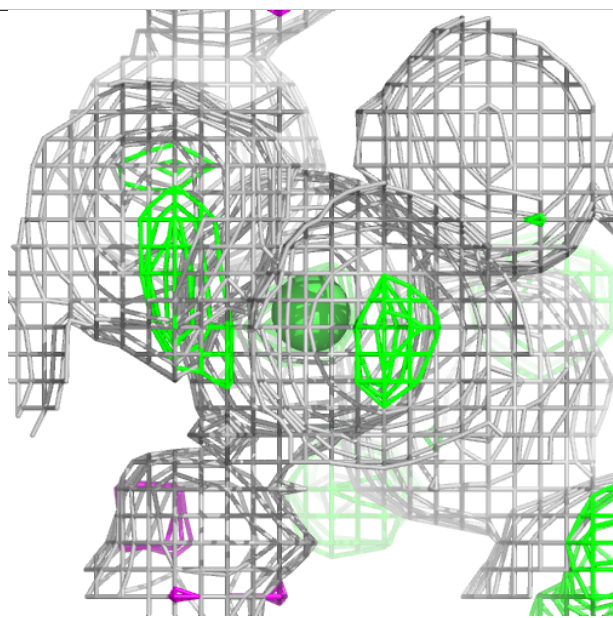
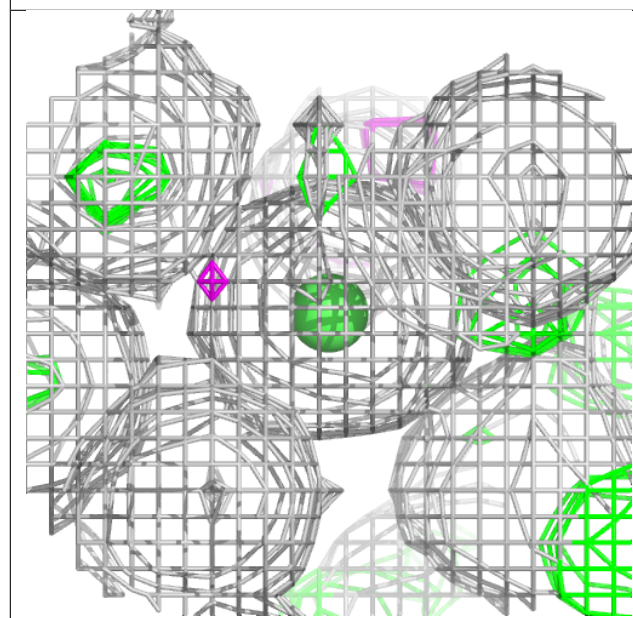
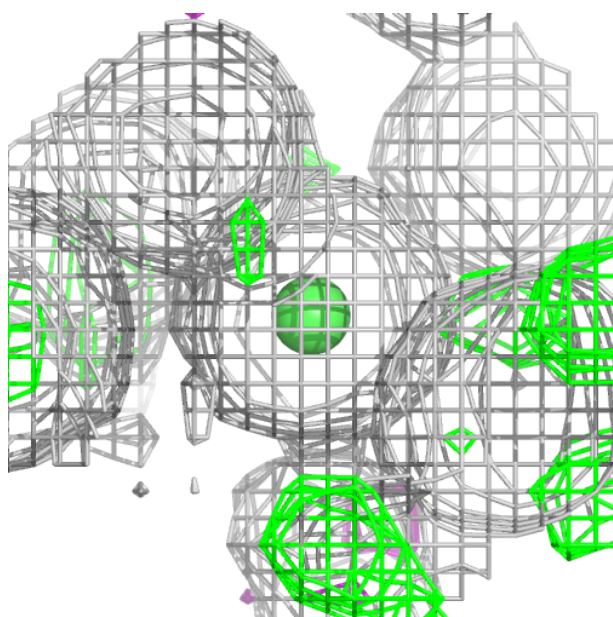
**Electron density around FCO MMM 602:**

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



**Electron density around NI LLL 603:**

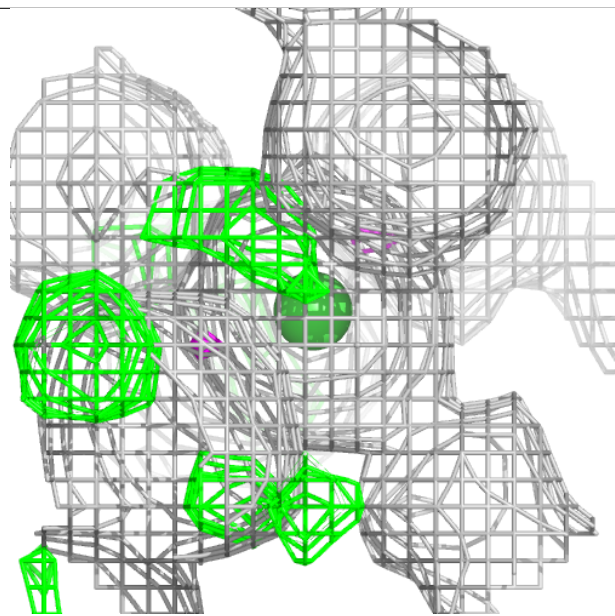
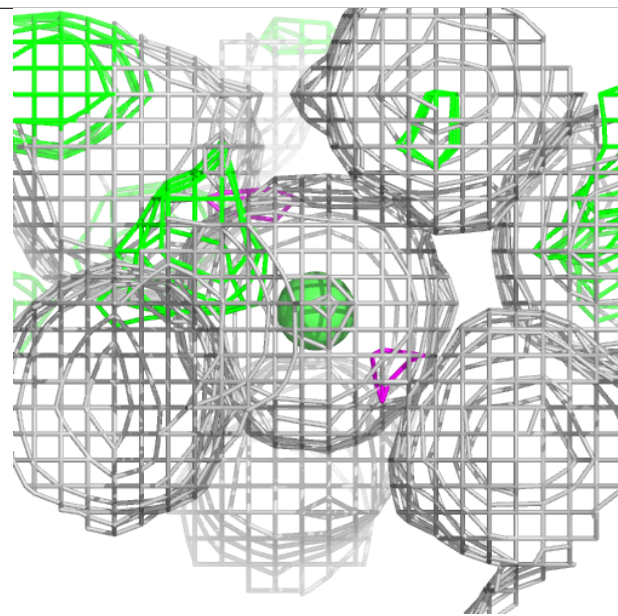
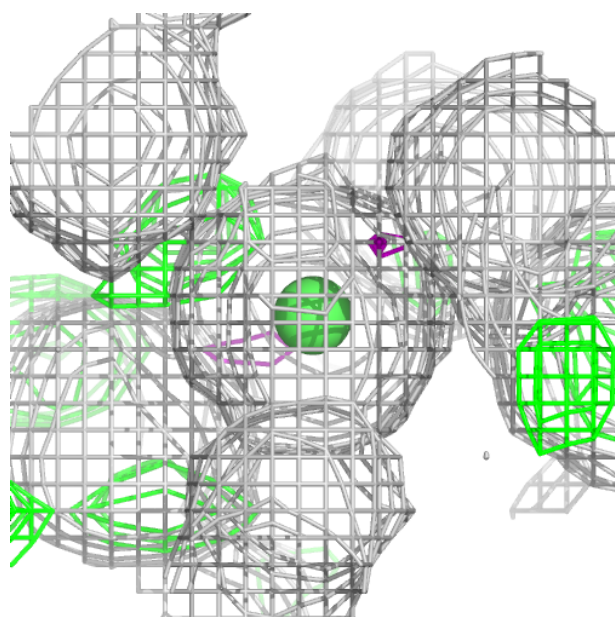
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

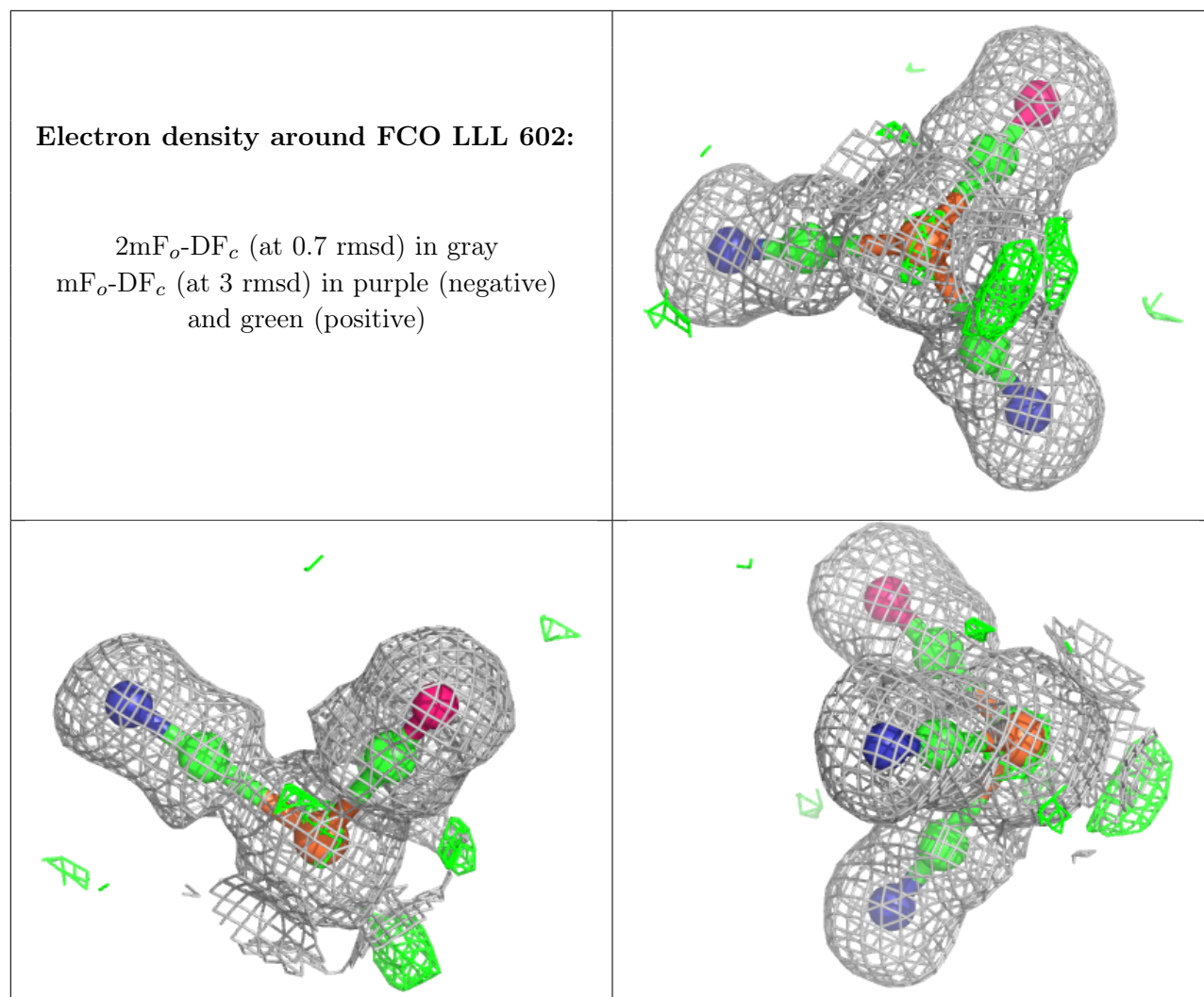




**Electron density around NI MMM 603:**

$2mF_o-DF_c$  (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.