



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 29, 2020 – 10:31 PM BST

PDB ID : 6OP3  
Title : Selenium incorporated FeMo-cofactor of nitrogenase from *Azotobacter vinelandii* with low concentration of selenium  
Authors : Arias, R.J.; Rees, D.C.  
Deposited on : 2019-04-24  
Resolution : 1.60 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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13  
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) : 2.13

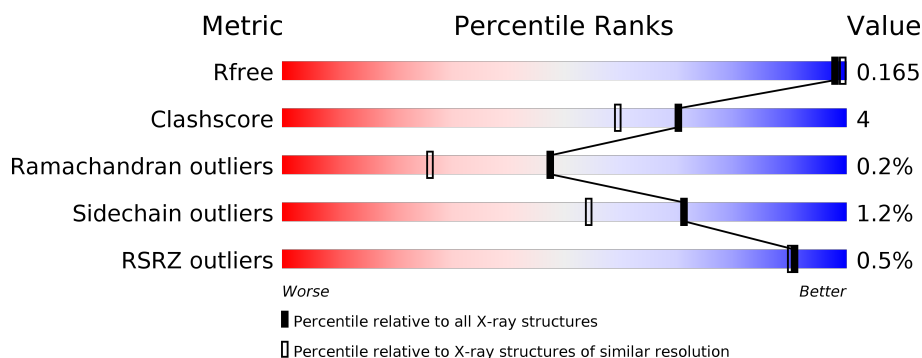
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 on 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	A	477	<div> <div>90%</div> <div>9%</div> </div>
1	C	477	<div> <div>%</div> <div>92%</div> <div>8%</div> </div>
2	B	522	<div> <div>92%</div> <div>6%</div> </div>
2	D	522	<div> <div>%</div> <div>92%</div> <div>7%</div> </div>



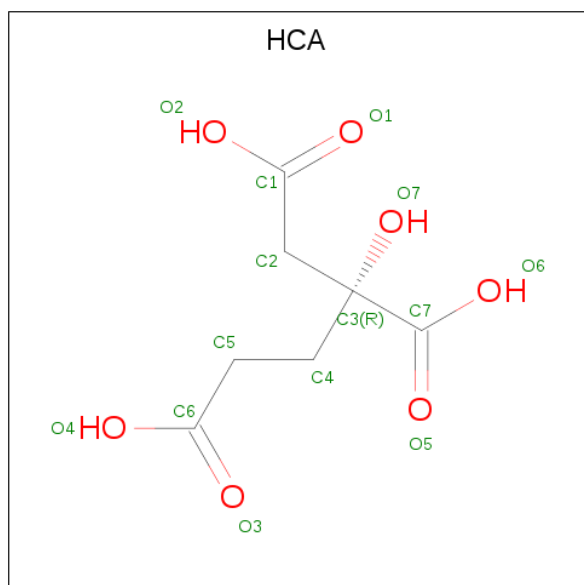
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total 3842	C 2442	N 656	O 718	S 26	0	6	0
1	C	477	Total 3819	C 2429	N 654	O 710	S 26	0	6	0

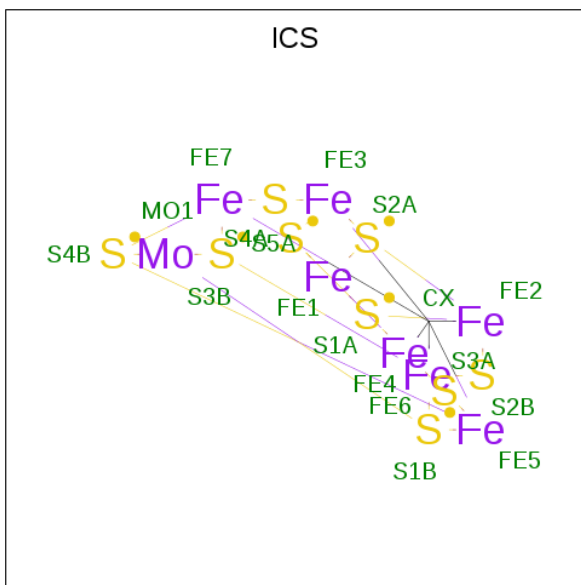
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	522	Total 4213	C 2690	N 712	O 783	S 28	0	7	0
2	D	522	Total 4193	C 2678	N 704	O 781	S 30	0	4	0

- Molecule 3 is 3-HYDROXY-3-CARBOXY-ADIPIIC ACID (three-letter code: HCA) (formula:  $C_7H_{10}O_7$ ).



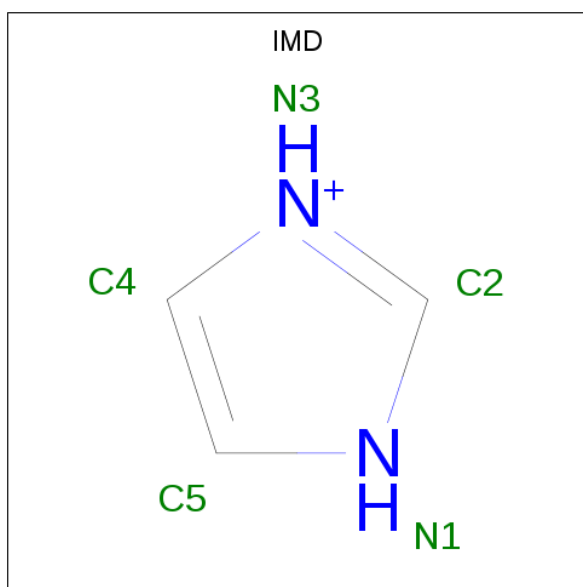
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			14	7	7		
3	C	1	Total	C	O	0	0
			14	7	7		

- Molecule 4 is iron-sulfur-molybdenum cluster with interstitial carbon (three-letter code: ICS) (formula:  $\text{CFe}_7\text{MoS}_9$ ) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	Mo	S	0	0
			17	1	7	1	8		
4	C	1	Total	C	Fe	Mo	S	0	0
			17	1	7	1	8		

- Molecule 5 is IMIDAZOLE (three-letter code: IMD) (formula:  $\text{C}_3\text{H}_5\text{N}_2$ ).

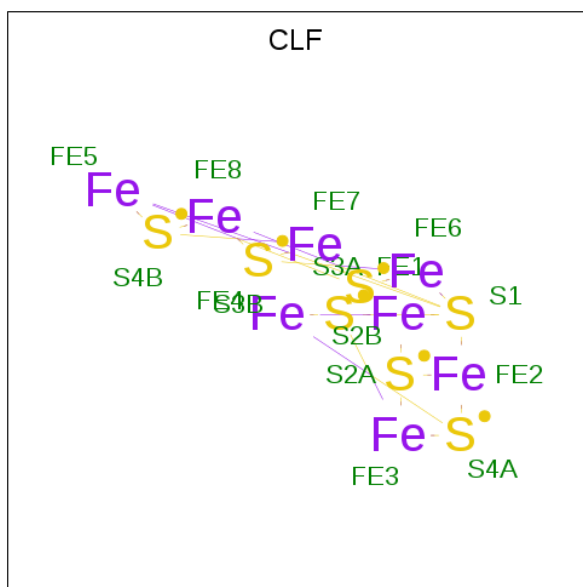


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	N	0	0
			5	3	2		
5	A	1	Total	C	N	0	0
			5	3	2		
5	B	1	Total	C	N	0	0
			5	3	2		
5	B	1	Total	C	N	0	0
			5	3	2		
5	B	1	Total	C	N	0	0
			5	3	2		
5	B	1	Total	C	N	0	0
			5	3	2		
5	C	1	Total	C	N	0	0
			5	3	2		
5	C	1	Total	C	N	0	0
			5	3	2		
5	D	1	Total	C	N	0	0
			5	3	2		
5	D	1	Total	C	N	0	0
			5	3	2		
5	D	1	Total	C	N	0	0
			5	3	2		

- Molecule 6 is SELENIUM ATOM (three-letter code: SE) (formula: Se).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Se 1 1	0	0
6	C	1	Total Se 1 1	0	0

- Molecule 7 is FE(8)-S(7) CLUSTER (three-letter code: CLF) (formula: Fe<sub>8</sub>S<sub>7</sub>).



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

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

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

- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total Ca 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	2	Total 2	Ca 2	0	0
9	C	1	Total 1	Ca 1	0	0

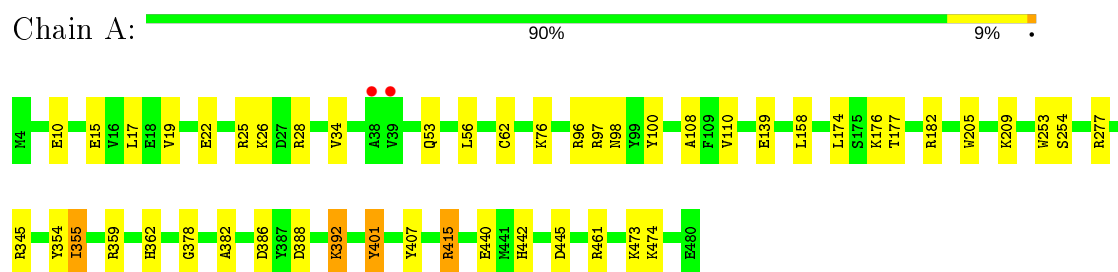
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	466	Total 466	O 466	0	0
10	B	604	Total 604	O 604	0	0
10	C	477	Total 477	O 477	0	0
10	D	603	Total 603	O 603	0	0

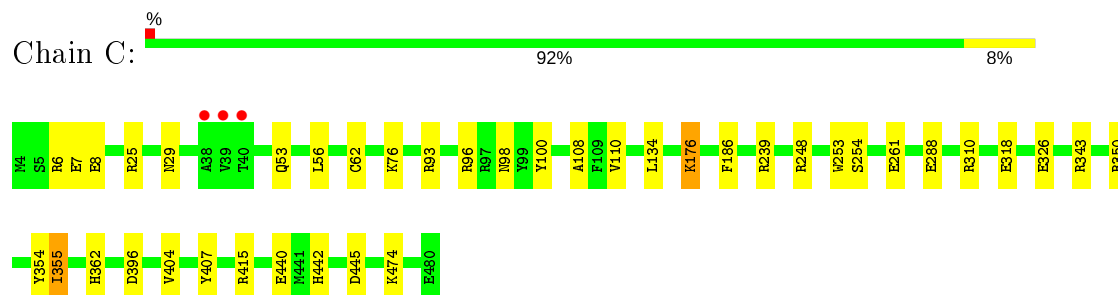
### 3 Residue-property plots

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.

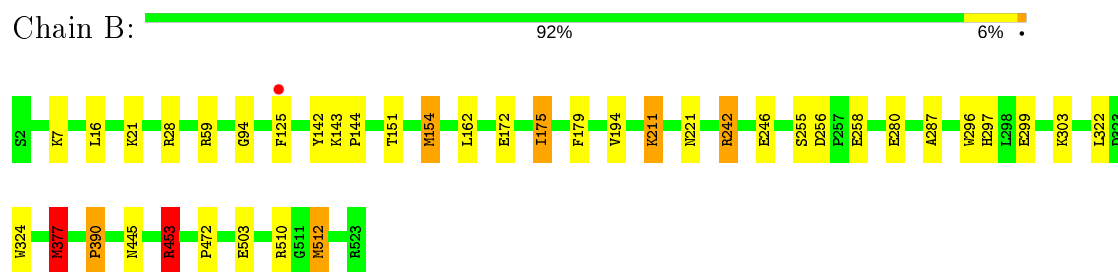
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



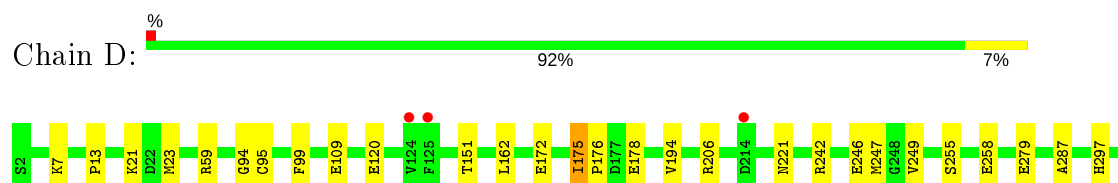
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



- Molecule 2: Nitrogenase molybdenum-iron protein beta chain







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.87Å 131.02Å 106.96Å 90.00° 110.62° 90.00°	Depositor
Resolution (Å)	37.85 – 1.60 38.62 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.6 (37.85-1.60) 98.6 (38.62-1.60)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.84 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, $R_{free}$	0.127 , 0.152 0.142 , 0.165	Depositor DCC
$R_{free}$ test set	13417 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	10.7	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	18377	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.68% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, IMD, CLF, HCA, ICS, CA, SE

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	0.77	1/3931 (0.0%)	0.91	8/5298 (0.2%)
1	C	0.77	4/3903 (0.1%)	0.92	8/5261 (0.2%)
2	B	0.74	0/4315	0.93	11/5831 (0.2%)
2	D	0.77	3/4299 (0.1%)	0.94	5/5814 (0.1%)
All	All	0.76	8/16448 (0.0%)	0.92	32/22204 (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
1	A	0	2
1	C	0	2
2	B	0	3
2	D	0	3
All	All	0	10

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	440	GLU	CD-OE2	10.08	1.36	1.25
1	A	440	GLU	CD-OE2	9.75	1.36	1.25
2	D	109	GLU	CD-OE1	-7.26	1.17	1.25
1	C	261	GLU	CD-OE2	7.08	1.33	1.25
2	D	178	GLU	CD-OE1	6.49	1.32	1.25

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	453	ARG	NE-CZ-NH2	15.32	127.96	120.30
2	D	453	ARG	NE-CZ-NH1	-14.53	113.03	120.30
2	B	453	ARG	NE-CZ-NH2	12.33	126.47	120.30
2	B	453	ARG	NE-CZ-NH1	-12.18	114.21	120.30
2	B	154	MET	CG-SD-CE	-10.74	83.01	100.20

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	415[A]	ARG	Sidechain
1	A	96	ARG	Sidechain
2	B	390	PRO	Mainchain
2	B	453	ARG	Sidechain
2	B	59	ARG	Sidechain

## 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	3842	0	3777	28	0
1	C	3819	0	3743	24	0
2	B	4213	0	4105	38	0
2	D	4193	0	4073	30	0
3	A	14	0	6	3	0
3	C	14	0	6	2	0
4	A	17	0	0	0	0
4	C	17	0	0	0	0
5	A	10	0	10	1	0
5	B	20	0	20	2	0
5	C	10	0	10	1	0
5	D	20	0	20	5	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
7	B	15	0	0	0	0
7	D	15	0	0	0	0
8	B	1	0	0	0	0
8	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	B	1	0	0	0	0
9	C	1	0	0	0	0
9	D	2	0	0	0	0
10	A	466	0	0	7	0
10	B	604	0	0	7	2
10	C	477	0	0	6	2
10	D	603	0	0	19	0
All	All	18377	0	15770	115	2

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 4.

The worst 5 of 115 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)
5:A:504:IMD:H5	10:D:830:HOH:O	1.34	1.27
2:B:503[B]:GLU:OE2	2:B:503[B]:GLU:OE1	1.65	1.14
2:B:21[B]:LYS:HE2	10:B:861:HOH:O	1.53	1.07
2:B:503[B]:GLU:CG	2:B:503[B]:GLU:OE1	2.04	1.05
2:D:172[B]:GLU:OE1	10:D:701:HOH:O	1.80	0.98

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B:1229:HOH:O	10:C:1047:HOH:O[1_556]	1.87	0.33
10:B:998:HOH:O	10:C:698:HOH:O[1_556]	2.01	0.19

## 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	481/477 (101%)	463 (96%)	17 (4%)	1 (0%)	47	26
1	C	481/477 (101%)	464 (96%)	16 (3%)	1 (0%)	47	26
2	B	527/522 (101%)	517 (98%)	9 (2%)	1 (0%)	47	26
2	D	524/522 (100%)	513 (98%)	10 (2%)	1 (0%)	47	26
All	All	2013/1998 (101%)	1957 (97%)	52 (3%)	4 (0%)	47	26

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	255	SER
2	D	255	SER
1	A	355	ILE
1	C	355	ILE

### 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	413/407 (102%)	406 (98%)	7 (2%)	60	38
1	C	405/407 (100%)	400 (99%)	5 (1%)	71	54
2	B	454/454 (100%)	449 (99%)	5 (1%)	73	57
2	D	452/454 (100%)	448 (99%)	4 (1%)	78	65
All	All	1724/1722 (100%)	1703 (99%)	21 (1%)	71	54

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	211	LYS
2	B	377	MET
2	D	7	LYS
2	B	175	ILE
2	D	13	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no

such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 26 ligands modelled in this entry, 8 are monoatomic - leaving 18 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	502	1,6	12,28,30	2.59	7 (58%)	-		
5	IMD	A	503	-	3,5,5	0.18	0	4,5,5	0.84	0
5	IMD	A	504	-	3,5,5	0.59	0	4,5,5	0.75	0
5	IMD	C	503	-	3,5,5	0.27	0	4,5,5	0.86	0
5	IMD	B	603	-	3,5,5	0.44	0	4,5,5	1.02	0
5	IMD	C	505	-	3,5,5	0.63	0	4,5,5	1.13	0
5	IMD	D	603	-	3,5,5	0.84	0	4,5,5	0.41	0
5	IMD	D	604	-	3,5,5	0.42	0	4,5,5	0.69	0
7	CLF	B	601	1,2	0,24,24	0.00	-	-		
7	CLF	D	602	1,2	0,24,24	0.00	-	-		
5	IMD	B	606	-	3,5,5	0.17	0	4,5,5	0.91	0
5	IMD	D	606	-	3,5,5	0.44	0	4,5,5	0.68	0
4	ICS	C	502	1,6	12,28,30	2.56	8 (66%)	-		
3	HCA	C	501	-	4,13,13	1.67	1 (25%)	4,18,18	3.04	3 (75%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	IMD	B	602	-	3,5,5	0.53	0	4,5,5	1.24	0
5	IMD	D	601	-	3,5,5	0.25	0	4,5,5	0.79	0
5	IMD	B	605	-	3,5,5	0.51	0	4,5,5	0.87	0
3	HCA	A	501	-	4,13,13	1.52	1 (25%)	4,18,18	3.12	1 (25%)

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
5	IMD	A	503	-	-	-	0/1/1/1
5	IMD	A	504	-	-	-	0/1/1/1
5	IMD	C	503	-	-	-	0/1/1/1
5	IMD	B	603	-	-	-	0/1/1/1
5	IMD	D	601	-	-	-	0/1/1/1
5	IMD	D	603	-	-	-	0/1/1/1
5	IMD	D	604	-	-	-	0/1/1/1
7	CLF	B	601	1,2	-	-	0/12/10/10
7	CLF	D	602	1,2	-	-	0/12/10/10
5	IMD	B	606	-	-	-	0/1/1/1
5	IMD	C	505	-	-	-	0/1/1/1
5	IMD	D	606	-	-	-	0/1/1/1
3	HCA	C	501	-	-	0/7/17/17	-
5	IMD	B	602	-	-	-	0/1/1/1
3	HCA	A	501	-	-	0/7/17/17	-
5	IMD	B	605	-	-	-	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	502	ICS	S4B-FE5	-4.67	2.20	2.32
4	C	502	ICS	S4B-FE7	-4.09	2.22	2.32
4	A	502	ICS	S4B-FE7	-3.99	2.22	2.32
4	C	502	ICS	S4B-FE5	-3.76	2.23	2.32
4	A	502	ICS	S3B-FE7	-3.30	2.24	2.32

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	HCA	C4-C5-C6	6.10	120.63	111.39
3	C	501	HCA	C4-C5-C6	4.91	118.83	111.39

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	501	HCA	C3-C2-C1	-2.60	110.83	114.98
3	C	501	HCA	C4-C3-C7	-2.19	107.67	111.52

There are no chirality outliers.

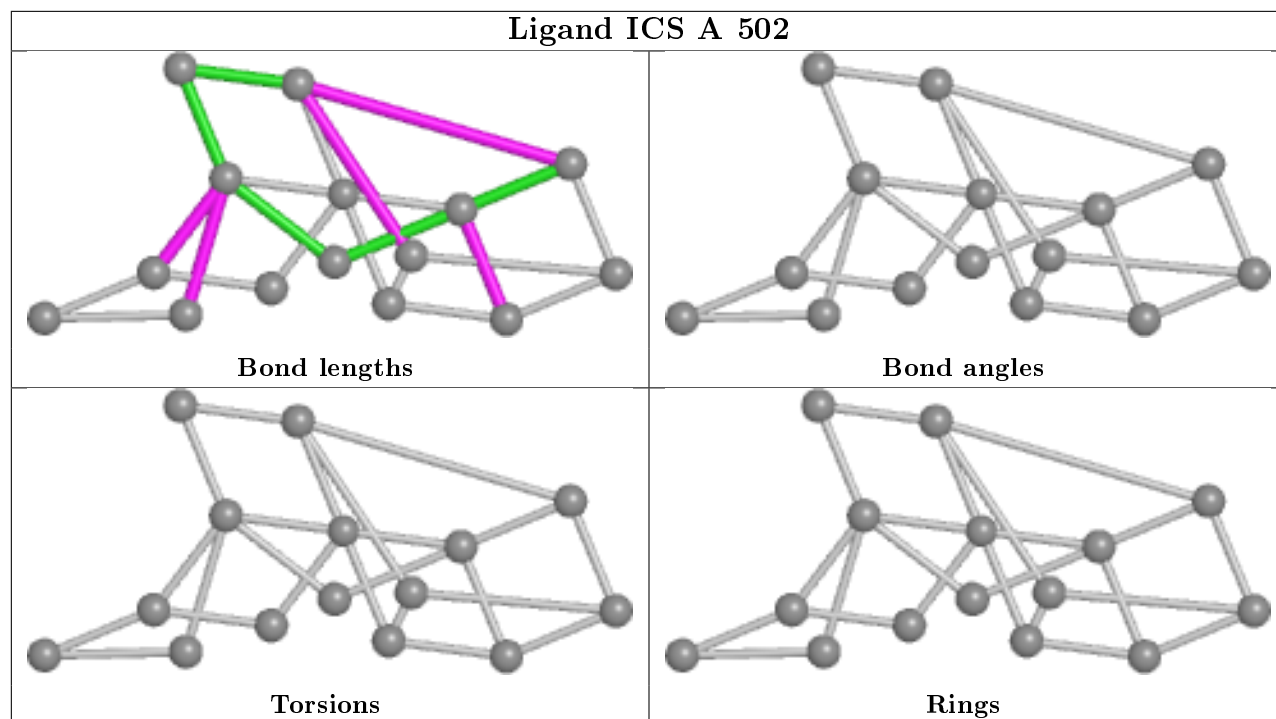
There are no torsion outliers.

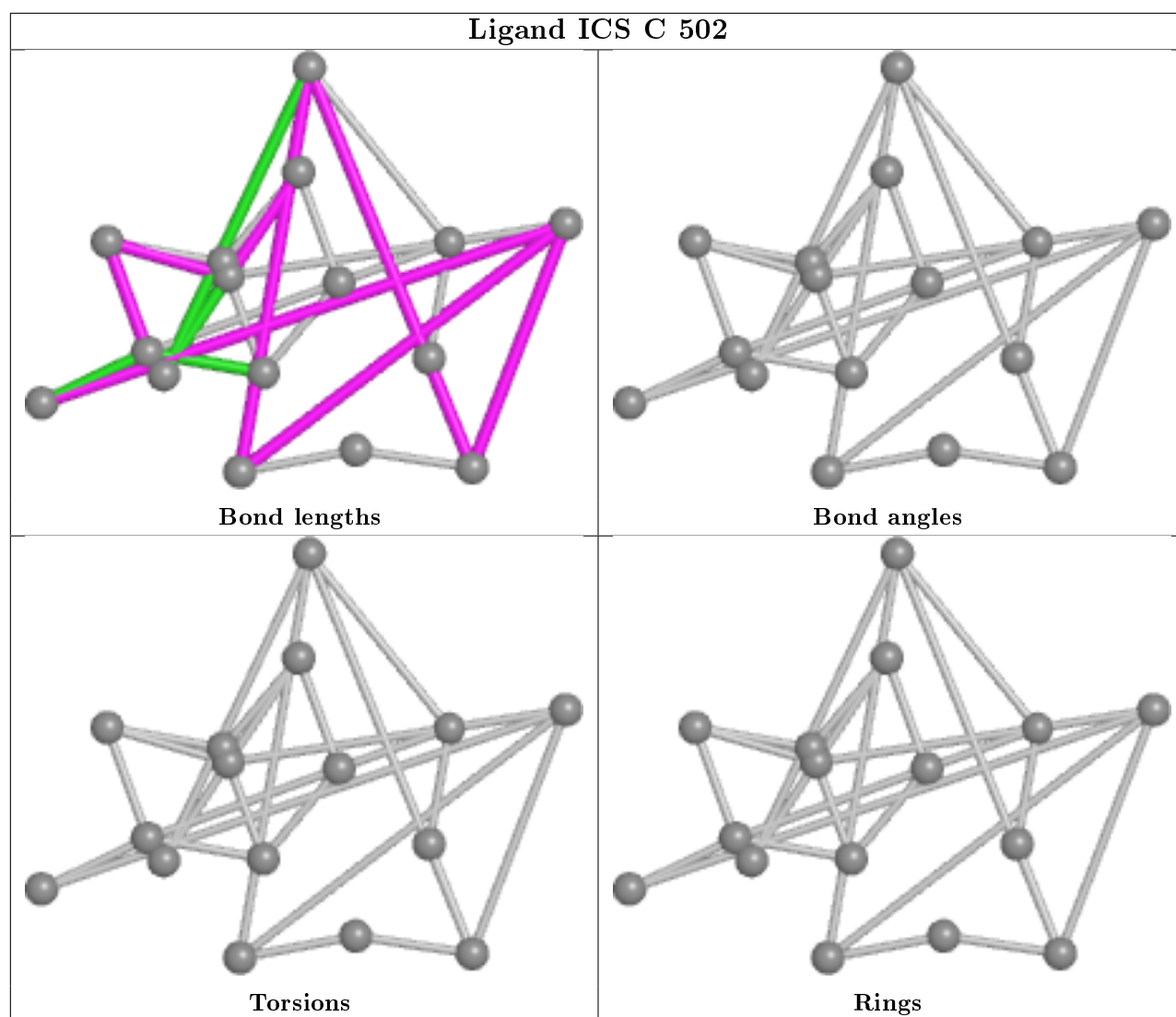
There are no ring outliers.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	504	IMD	1	0
5	C	505	IMD	1	0
5	D	603	IMD	1	0
5	D	606	IMD	3	0
3	C	501	HCA	2	0
5	D	601	IMD	1	0
5	B	605	IMD	2	0
3	A	501	HCA	3	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	A	477/477 (100%)	-0.26	2 (0%) 92 92	7, 12, 26, 41	0
1	C	477/477 (100%)	-0.26	3 (0%) 89 89	7, 11, 25, 42	0
2	B	522/522 (100%)	-0.35	1 (0%) 95 94	7, 11, 22, 46	0
2	D	522/522 (100%)	-0.34	3 (0%) 89 89	7, 12, 22, 42	0
All	All	1998/1998 (100%)	-0.30	9 (0%) 91 90	7, 12, 24, 46	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	125	PHE	6.9
2	D	125	PHE	4.5
1	A	38	ALA	4.5
1	C	38	ALA	4.4
1	C	39	VAL	3.4

### 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](#)

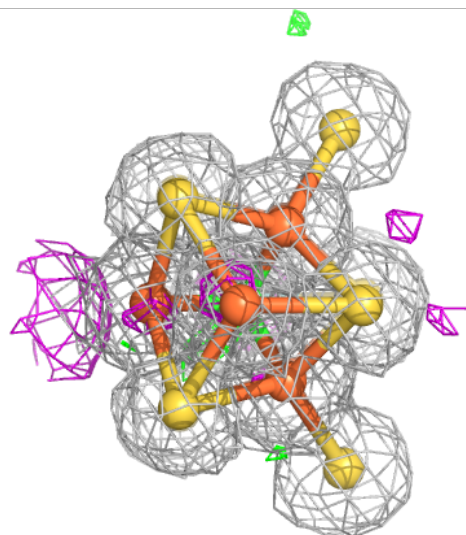
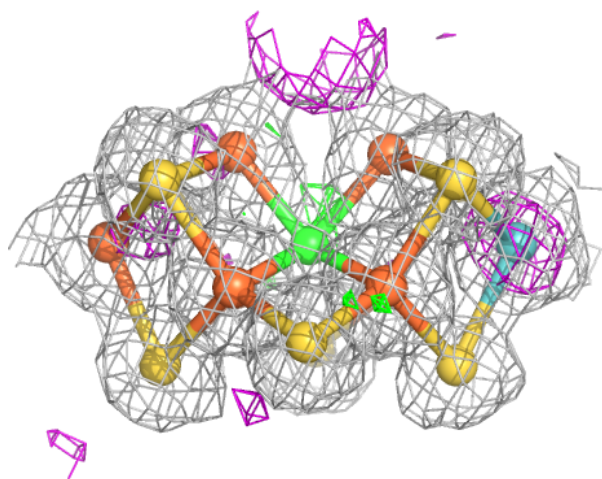
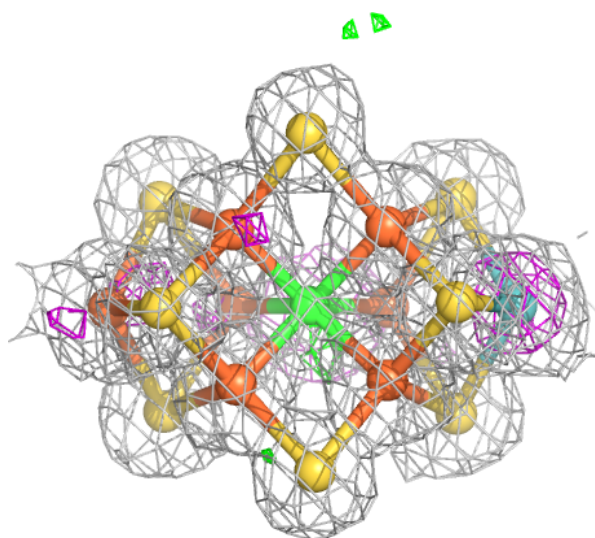
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 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	IMD	C	505	5/5	0.71	0.19	21,22,30,32	0
5	IMD	A	504	5/5	0.80	0.17	24,25,29,30	0
5	IMD	B	605	5/5	0.81	0.16	25,27,30,30	0
5	IMD	B	606	5/5	0.85	0.17	32,35,38,41	0
5	IMD	D	606	5/5	0.87	0.17	31,32,35,40	0
8	MG	B	604	1/1	0.90	0.10	45,45,45,45	0
5	IMD	D	601	5/5	0.91	0.13	22,23,25,27	0
8	MG	D	605	1/1	0.93	0.27	40,40,40,40	0
5	IMD	B	603	5/5	0.94	0.10	21,24,24,24	0
5	IMD	D	603	5/5	0.94	0.08	10,12,14,17	0
5	IMD	D	604	5/5	0.94	0.14	21,22,22,23	0
5	IMD	A	503	5/5	0.95	0.15	22,26,28,31	0
9	CA	D	607	1/1	0.96	0.12	35,35,35,35	0
5	IMD	B	602	5/5	0.96	0.09	11,12,13,16	0
5	IMD	C	503	5/5	0.97	0.13	21,23,24,25	0
3	HCA	C	501	14/14	0.98	0.09	7,8,12,12	0
3	HCA	A	501	14/14	0.98	0.10	6,8,12,12	0
7	CLF	B	601	15/15	0.99	0.07	7,7,8,9	0
9	CA	D	608	1/1	0.99	0.13	19,19,19,19	0
9	CA	B	607	1/1	0.99	0.13	19,19,19,19	0
9	CA	C	506	1/1	0.99	0.16	36,36,36,36	0
4	ICS	C	502	17/18	1.00	0.06	6,7,8,8	0
4	ICS	A	502	17/18	1.00	0.06	6,7,8,8	0
6	SE	C	504	1/1	1.00	0.15	9,9,9,9	0
7	CLF	D	602	15/15	1.00	0.06	7,8,8,9	0
6	SE	A	505	1/1	1.00	0.15	9,9,9,9	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.

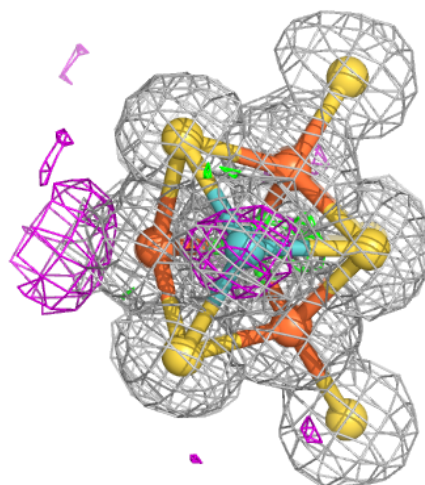
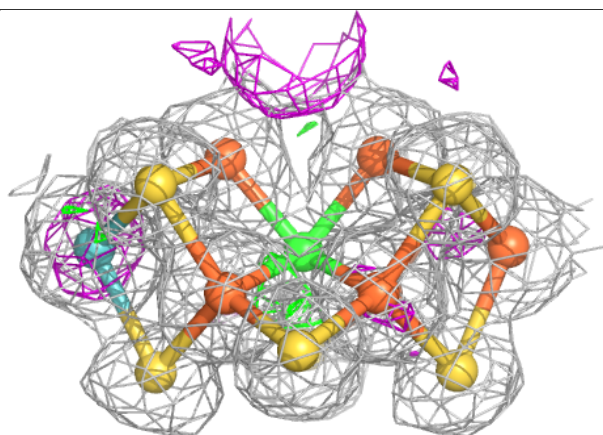
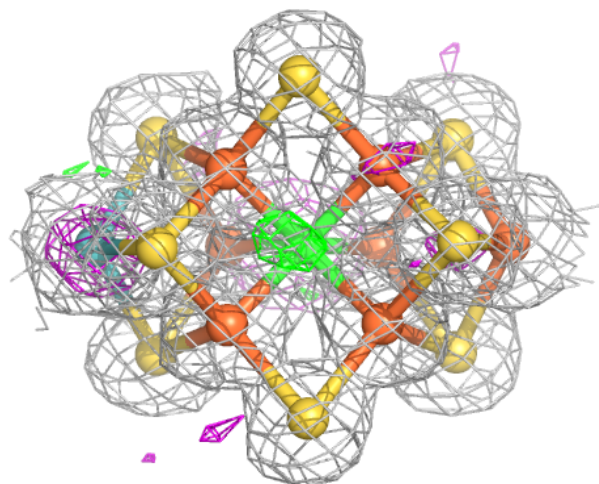
**Electron density around ICS C 502:**

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



**Electron density around ICS A 502:**

$2mF_o-DF_c$  (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.