



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2020 – 02:23 AM BST

PDB ID : 6BBL  
Title : Crystal structure of the a-96Gln MoFe protein variant in the presence of the substrate acetylene  
Authors : Zadvornyy, O.A.; Keable, S.M.; Vertemara, J.; Eilers, B.J.; Karamatullah, D.; Rasmussen, A.J.; De Gioia, L.; Zampella, G.; Seefeldt, L.C.; Peters, J.W.  
Deposited on : 2017-10-18  
Resolution : 1.68 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 : 2.13.1  
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

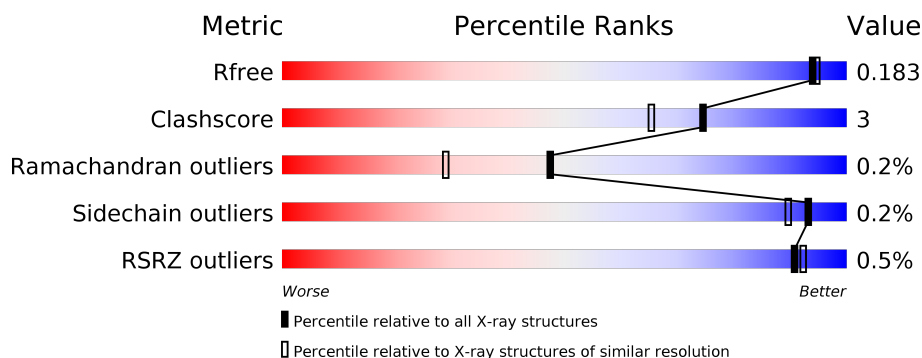
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.68 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	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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	492	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 1%, green 98%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>90%</span> <span>7%</span> </div> </div>
1	C	492	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, orange 0%, yellow 1%, green 99%);"></div> <div style="display: flex; justify-content: space-between; width: 88%; margin: 0 auto;"> <span>88%</span> <span>9%</span> </div> </div>
2	B	523	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, orange 0%, yellow 0%, green 96%);"></div> <div style="display: flex; justify-content: space-between; width: 96%; margin: 0 auto;"> <span>96%</span> <span></span> </div> </div>
2	D	523	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, orange 0%, yellow 0%, green 96%);"></div> <div style="display: flex; justify-content: space-between; width: 96%; margin: 0 auto;"> <span>96%</span> <span></span> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	C2H	A	501	-	X	-	-
3	C2H	C	501	-	X	X	-

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 33891 atoms, of which 15669 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 molybdenum-iron protein alpha chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	477	Total	C	H	N	O	S	0	2	0
			7525	2412	3731	645	711	26			
1	C	477	Total	C	H	N	O	S	0	2	0
			7525	2412	3731	645	711	26			

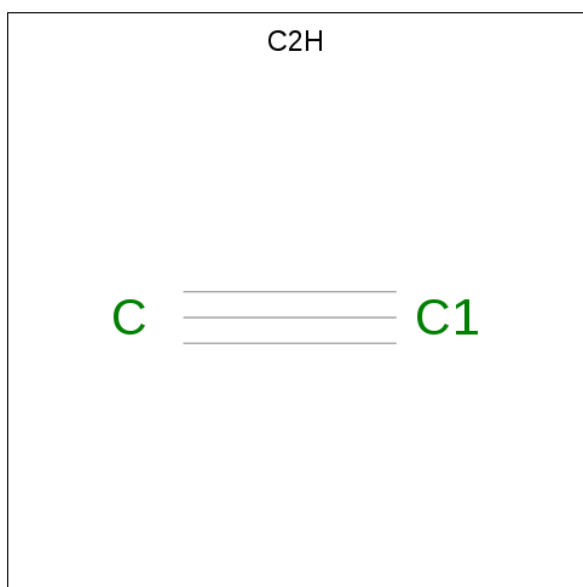
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	96	GLN	ARG	variant	UNP P07328
C	96	GLN	ARG	variant	UNP P07328

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

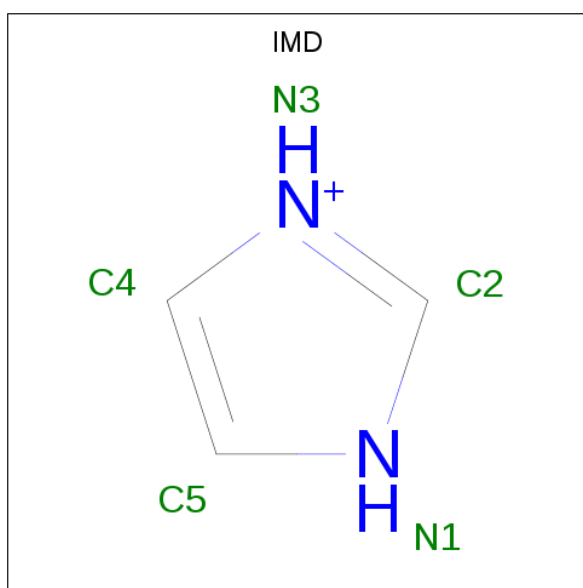
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	522	Total	C	H	N	O	S	0	0	0
			8262	2666	4088	705	775	28			
2	D	522	Total	C	H	N	O	S	0	0	0
			8262	2666	4088	705	775	28			

- Molecule 3 is acetylene (three-letter code: C2H) (formula: C<sub>2</sub>H<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	H	0	0
			4	2	2		
3	C	1	Total	C	H	0	0
			4	2	2		

- Molecule 4 is IMIDAZOLE (three-letter code: IMD) (formula:  $C_3H_5N_2$ ).



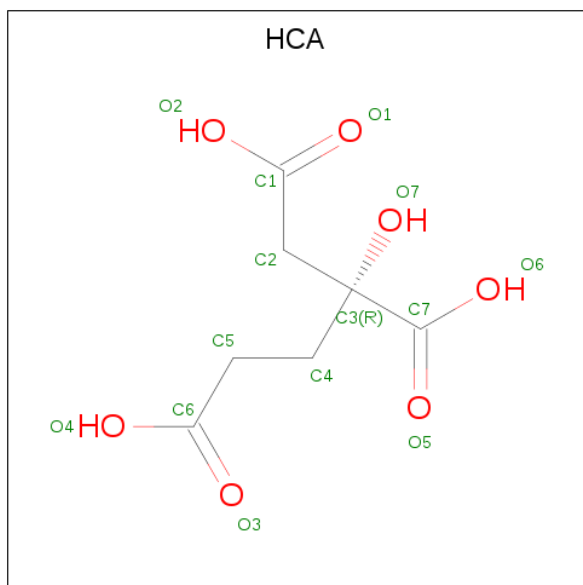
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	N	0	0
			10	3	5	2		
4	C	1	Total	C	H	N	0	0
			10	3	5	2		

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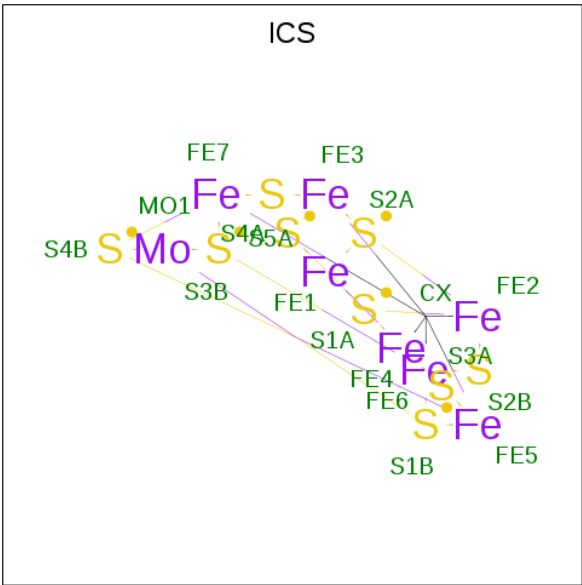
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	H	N	0	0
			10	3	5	2		

- Molecule 5 is 3-HYDROXY-3-CARBOXY-ADIPIC ACID (three-letter code: HCA) (formula:  $C_7H_{10}O_7$ ).



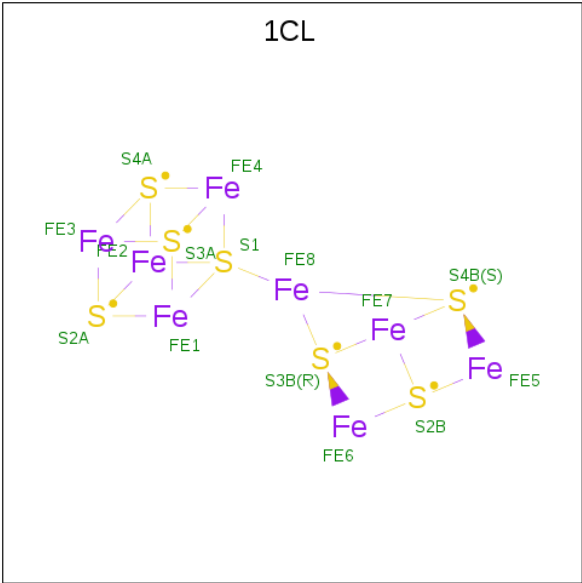
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			20	7	6	7		
5	C	1	Total	C	H	O	0	0
			20	7	6	7		

- Molecule 6 is iron-sulfur-molybdenum cluster with interstitial carbon (three-letter code: ICS) (formula:  $CFe_7MoS_9$ ).



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

- Molecule 7 is FE(8)-S(7) CLUSTER, OXIDIZED (three-letter code: 1CL) (formula: Fe<sub>8</sub>S<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	Fe	S	0	0
			15	8	7		
7	C	1	Total	Fe	S	0	0
			15	8	7		

- Molecule 8 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	2	Total 2	Fe 2	0	0

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	455	Total 455	O 455	0	0
10	B	620	Total 620	O 620	0	0
10	C	483	Total 483	O 483	0	0
10	D	612	Total 612	O 612	0	0





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.78Å 128.25Å 107.27Å 90.00° 109.11° 90.00°	Depositor
Resolution (Å)	39.76 – 1.68 49.92 – 1.68	Depositor EDS
% Data completeness (in resolution range)	91.9 (39.76-1.68) 91.9 (49.92-1.68)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.47 (at 1.68Å)	Xtriage
Refinement program	PHENIX (DEV_2880: ???)	Depositor
R, $R_{free}$	0.151 , 0.185 0.151 , 0.183	Depositor DCC
$R_{free}$ test set	10163 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.5	Xtriage
Anisotropy	0.378	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 48.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	33891	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.12% 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: MG, IMD, HCA, FE, ICS, C2H, 1CL

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	0.47	0/3889	0.60	0/5245
1	C	0.46	0/3889	0.61	0/5245
2	B	0.44	0/4280	0.60	0/5786
2	D	0.45	0/4280	0.61	1/5786 (0.0%)
All	All	0.45	0/16338	0.61	1/22062 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	19	ASP	CB-CG-OD1	6.49	124.14	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3794	3731	3720	32	0
1	C	3794	3731	3720	36	0
2	B	4174	4088	4088	19	0
2	D	4174	4088	4088	12	0
3	A	2	2	0	1	0
3	C	2	2	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	5	5	5	0	0
4	C	5	5	5	2	0
4	D	5	5	5	0	0
5	A	14	6	6	2	0
5	C	14	6	6	4	0
6	A	18	0	0	0	0
6	C	18	0	0	0	0
7	A	15	0	0	0	0
7	C	15	0	0	0	0
8	B	2	0	0	0	0
9	B	1	0	0	0	0
10	A	455	0	0	10	0
10	B	620	0	0	10	1
10	C	483	0	0	20	4
10	D	612	0	0	5	2
All	All	18222	15669	15643	101	4

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 3.

The worst 5 of 101 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:B:238:ARG:HG3	2:B:258:GLU:OE1	1.45	1.16
2:B:238:ARG:CG	2:B:258:GLU:OE1	1.96	1.12
2:B:312:GLU:OE2	10:B:701:HOH:O	1.81	0.99
1:C:326:GLU:OE1	10:C:601:HOH:O	1.80	0.97
2:B:21:LYS:NZ	10:B:703:HOH:O	2.01	0.93

All (4) 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:C:1013:HOH:O	10:C:1045:HOH:O[2_555]	1.88	0.32
10:B:1260:HOH:O	10:C:867:HOH:O[2_545]	1.99	0.21
10:C:967:HOH:O	10:D:872:HOH:O[1_655]	2.00	0.20
10:C:958:HOH:O	10:D:866:HOH:O[2_545]	2.18	0.02

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	477/492 (97%)	458 (96%)	18 (4%)	1 (0%)	47	29
1	C	477/492 (97%)	459 (96%)	17 (4%)	1 (0%)	47	29
2	B	520/523 (99%)	510 (98%)	9 (2%)	1 (0%)	47	29
2	D	520/523 (99%)	507 (98%)	12 (2%)	1 (0%)	47	29
All	All	1994/2030 (98%)	1934 (97%)	56 (3%)	4 (0%)	47	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	255	SER
2	B	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	409/415 (99%)	408 (100%)	1 (0%)	93	89
1	C	409/415 (99%)	407 (100%)	2 (0%)	88	83
2	B	454/455 (100%)	454 (100%)	0	100	100
2	D	454/455 (100%)	453 (100%)	1 (0%)	93	89
All	All	1726/1740 (99%)	1722 (100%)	4 (0%)	93	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	445	ASP
1	C	362	HIS
1	C	445	ASP
2	D	258	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	362	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 14 ligands modelled in this entry, 3 are monoatomic - leaving 11 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	$\# Z  > 2$
7	1CL	C	505	1,2	0,22,22	0.00	-	-		
7	1CL	A	505	1,2	0,22,22	0.00	-	-		
5	HCA	C	502	-	4,13,13	0.53	0	4,18,18	3.25	2 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	HCA	A	503	-	4,13,13	0.47	0	4,18,18	2.77	2 (50%)
3	C2H	C	501	-	1,1,1	2.22	1 (100%)	-		
4	IMD	D	601	-	3,5,5	0.42	0	4,5,5	0.62	0
3	C2H	A	501	-	1,1,1	2.22	1 (100%)	-		
4	IMD	C	504	-	3,5,5	0.67	0	4,5,5	0.83	0
4	IMD	A	502	-	3,5,5	0.47	0	4,5,5	0.58	0
6	ICS	C	503	1	18,30,30	6.59	12 (66%)	-		
6	ICS	A	504	1	18,30,30	6.80	12 (66%)	-		

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
7	1CL	C	505	1,2	-	-	0/9/8/8
7	1CL	A	505	1,2	-	-	0/9/8/8
4	IMD	A	502	-	-	-	0/1/1/1
5	HCA	A	503	-	-	4/7/17/17	-
4	IMD	D	601	-	-	-	0/1/1/1
4	IMD	C	504	-	-	-	0/1/1/1
5	HCA	C	502	-	-	4/7/17/17	-

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	504	ICS	S1B-FE6	-9.08	2.10	2.32
6	A	504	ICS	S3B-FE7	-8.98	2.10	2.32
6	C	503	ICS	S4B-FE7	-8.97	2.10	2.32
6	A	504	ICS	S4B-FE7	-8.91	2.10	2.32
6	C	503	ICS	S2A-FE2	-8.83	2.10	2.32

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	502	HCA	C4-C5-C6	5.91	120.33	111.39
5	A	503	HCA	C4-C5-C6	4.85	118.73	111.39
5	C	502	HCA	C3-C2-C1	-2.42	111.11	114.98
5	A	503	HCA	C3-C2-C1	-2.39	111.15	114.98

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	502	HCA	C2-C3-C4-C5
5	C	502	HCA	C7-C3-C4-C5
5	C	502	HCA	O7-C3-C4-C5
5	A	503	HCA	C2-C3-C4-C5
5	A	503	HCA	C7-C3-C4-C5

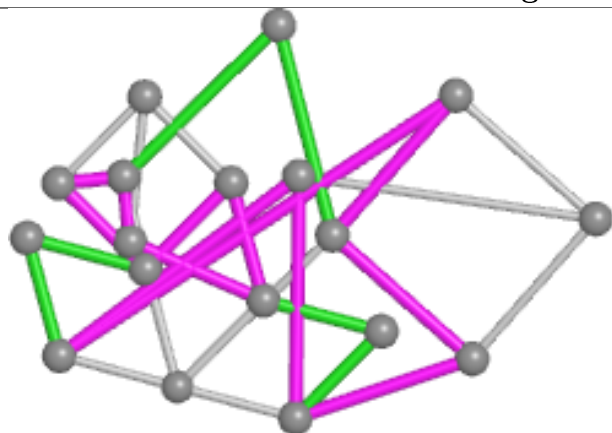
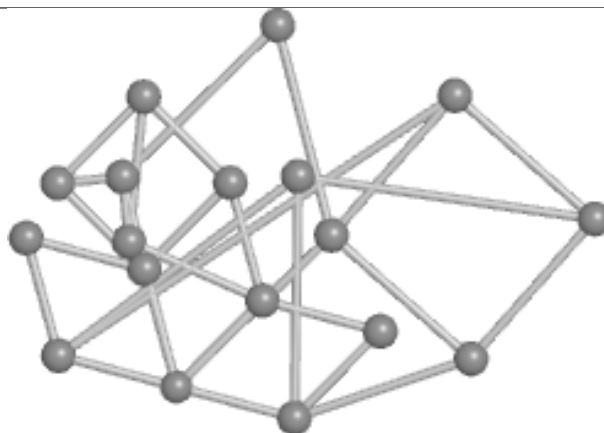
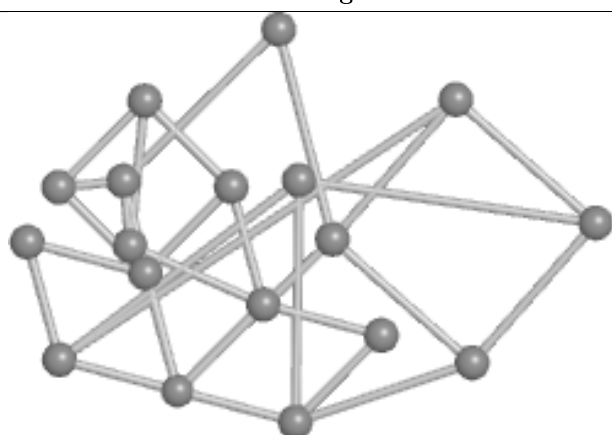
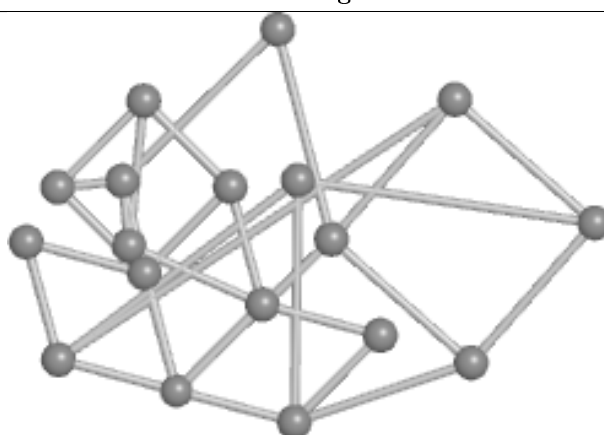
There are no ring outliers.

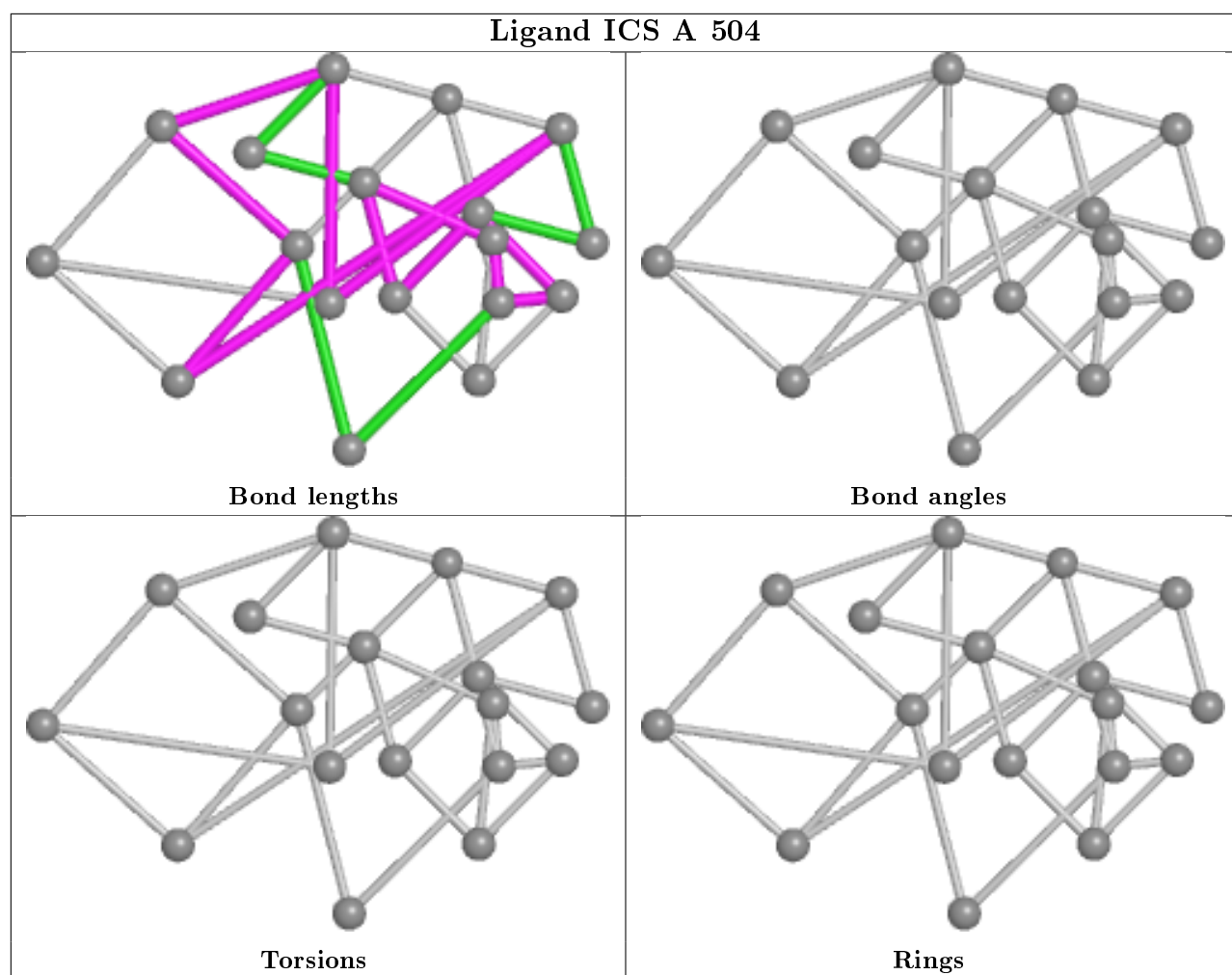
5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	502	HCA	4	0
5	A	503	HCA	2	0
3	C	501	C2H	2	0
3	A	501	C2H	1	0
4	C	504	IMD	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 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.



**Ligand ICS C 503****Bond lengths****Bond angles****Torsions****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 [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	477/492 (96%)	-0.38	5 (1%) 82 85	16, 21, 36, 55	9 (1%)
1	C	477/492 (96%)	-0.50	2 (0%) 92 93	15, 21, 38, 50	1 (0%)
2	B	522/523 (99%)	-0.55	2 (0%) 92 93	15, 20, 30, 49	3 (0%)
2	D	522/523 (99%)	-0.51	0 100 100	14, 19, 29, 39	3 (0%)
All	All	1998/2030 (98%)	-0.49	9 (0%) 91 92	14, 20, 34, 55	16 (0%)

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	39	VAL	4.9
2	B	124	VAL	4.2
1	A	174	LEU	3.6
1	A	38	ALA	3.5
1	C	4	MET	2.9

### 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](#)

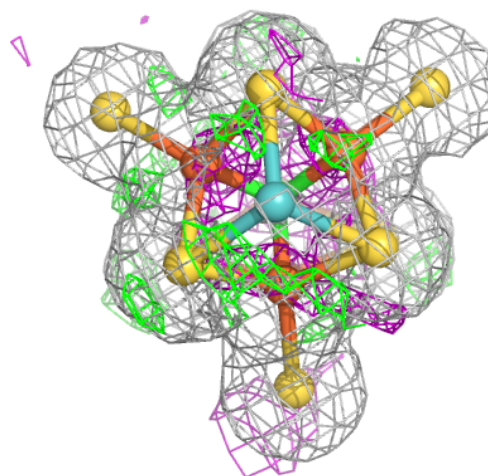
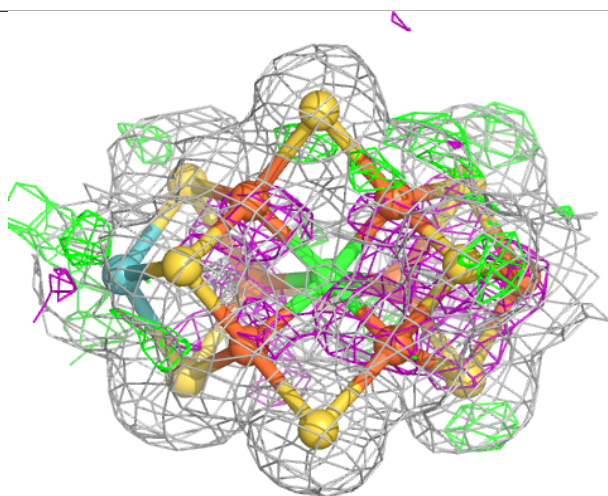
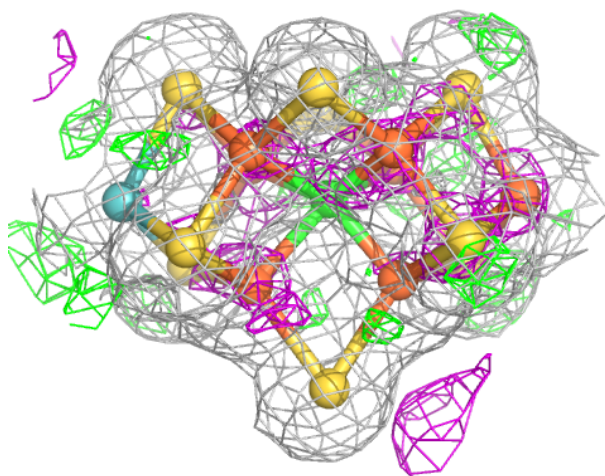
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 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
4	IMD	A	502	5/5	0.86	0.25	42,50,60,61	0
3	C2H	A	501	2/2	0.89	0.15	22,27,30,36	0
9	MG	B	602	1/1	0.91	0.15	42,42,42,42	0
4	IMD	D	601	5/5	0.93	0.07	39,44,52,53	0
4	IMD	C	504	5/5	0.94	0.19	16,30,46,47	0
5	HCA	C	502	14/14	0.94	0.10	16,20,23,23	0
3	C2H	C	501	2/2	0.94	0.13	24,26,29,31	0
5	HCA	A	503	14/14	0.96	0.09	18,22,27,27	0
7	1CL	A	505	15/15	0.97	0.08	14,16,26,28	0
7	1CL	C	505	15/15	0.98	0.08	14,16,26,28	0
6	ICS	C	503	18/18	0.99	0.07	11,17,18,18	1
6	ICS	A	504	18/18	0.99	0.06	10,17,19,19	3
8	FE	B	601	1/1	1.00	0.04	18,18,18,18	0
8	FE	B	603	1/1	1.00	0.02	21,21,21,21	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.

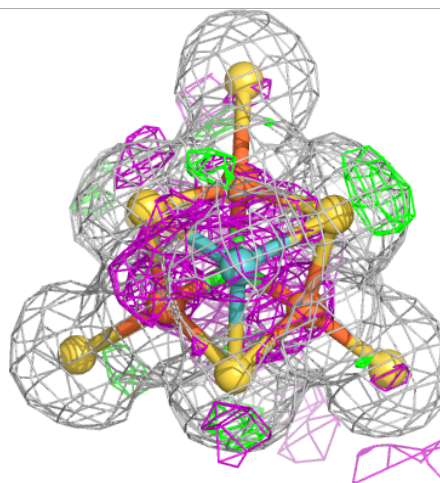
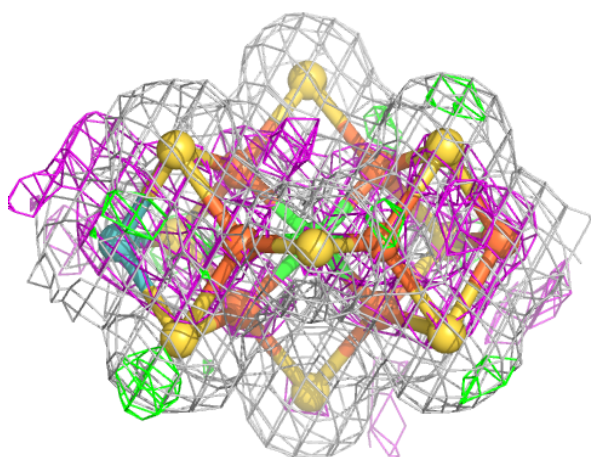
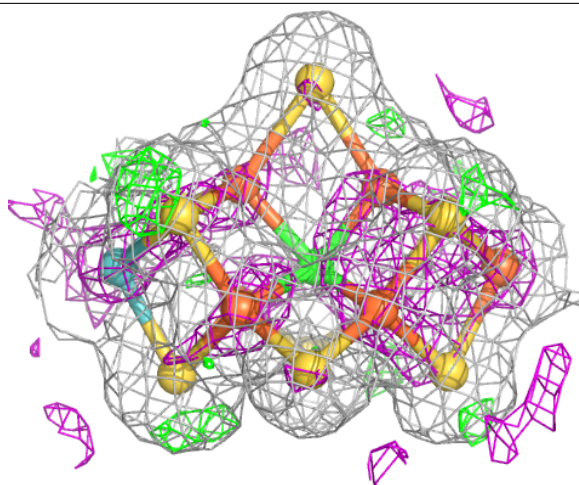
**Electron density around ICS C 503:**

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



**Electron density around ICS A 504:**

$2mF_o-DF_c$  (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.