



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 5, 2023 – 05:00 AM EDT

PDB ID : 3U7Q  
Title : A. vinelandii nitrogenase MoFe protein at atomic resolution  
Authors : Spatzal, T.; Einsle, O.  
Deposited on : 2011-10-14  
Resolution : 1.00 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

<http://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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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) : 2.35

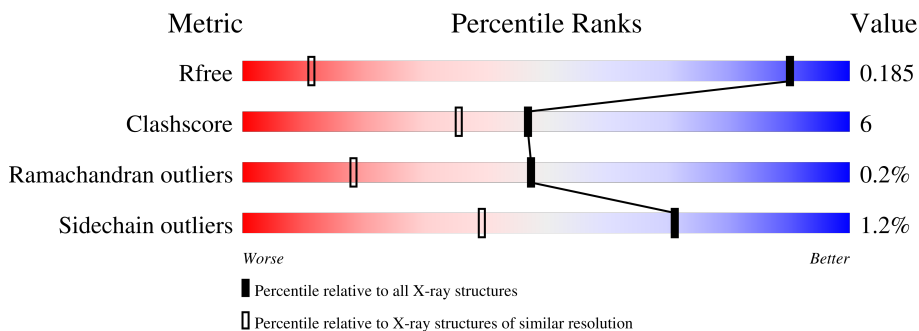
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.00 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	1050 (1.06-0.94)
Clashscore	141614	1117 (1.06-0.94)
Ramachandran outliers	138981	1043 (1.06-0.94)
Sidechain outliers	138945	1045 (1.06-0.94)

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	492	86% 10% ..
1	C	492	88% 8% ..
2	B	523	87% 13%
2	D	523	92% 7%

## 2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 18955 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.

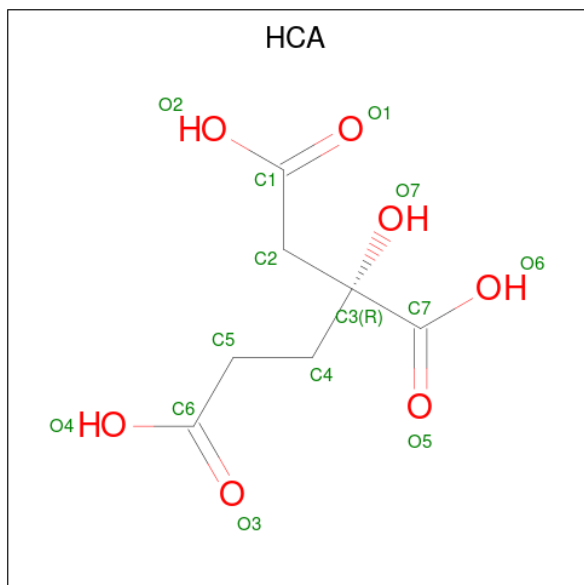
- Molecule 1 is a protein called Nitrogenase molybdenum-iron protein alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	477	Total 3811	C 2426	N 648	O 710	S 27	3	4	0
1	C	477	Total 3826	C 2438	N 648	O 712	S 28	33	8	0

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

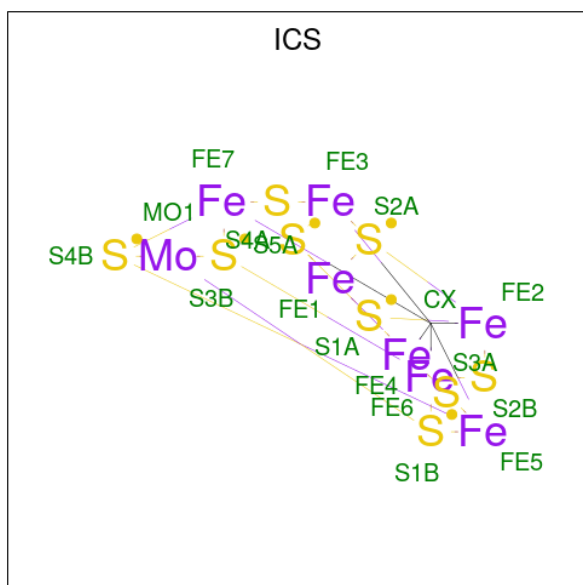
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	522	Total 4247	C 2722	N 707	O 783	S 35	28	14	0
2	D	522	Total 4301	C 2749	N 723	O 793	S 36	20	16	0

- Molecule 3 is 3-HYDROXY-3-CARBOXY-ADIPIC ACID (three-letter code: HCA) (formula: C<sub>7</sub>H<sub>10</sub>O<sub>7</sub>).



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:  $\text{CFe}_7\text{MoS}_9$ ).



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

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

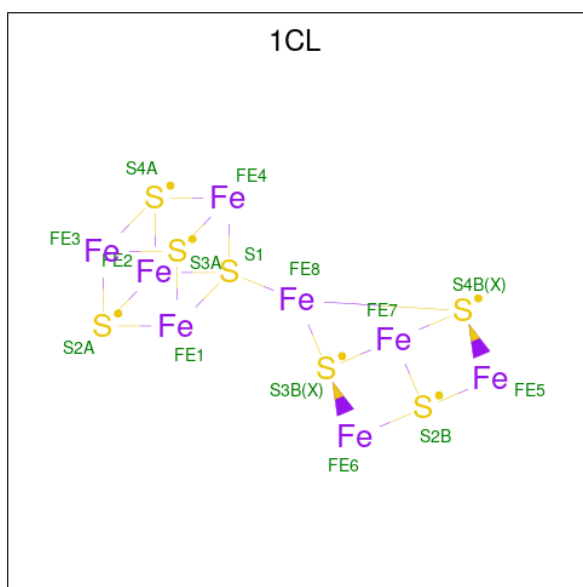


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N 5 3 2	0	0
5	A	1	Total C N 5 3 2	0	0
5	B	1	Total C N 5 3 2	0	0
5	B	1	Total C N 5 3 2	0	0
5	C	1	Total C N 5 3 2	0	0
5	C	1	Total C N 5 3 2	0	0
5	D	1	Total C N 5 3 2	0	0
5	D	1	Total C N 5 3 2	0	0

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

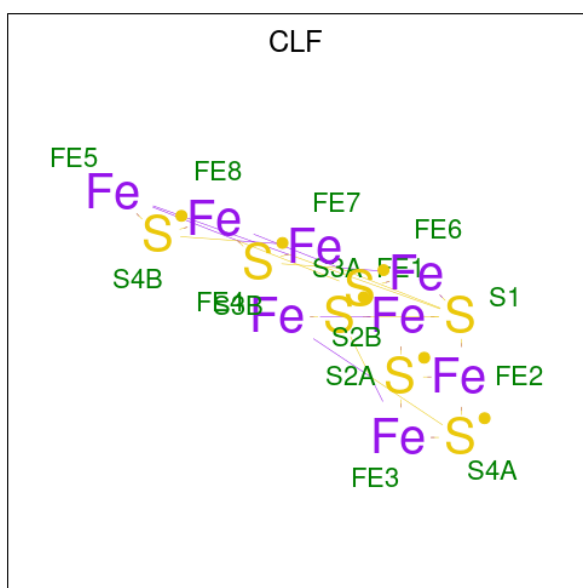
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	2	Total Ca 2 2	0	0

- 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	B	1	Total	Fe	S	0	1
			15	8	7		
7	D	1	Total	Fe	S	0	1
			15	8	7		

- Molecule 8 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
8	B	1	Total	Fe	S	0	1
			15	8	7		
8	D	1	Total	Fe	S	0	1
			15	8	7		

- 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
9	D	1	Total 1	Mg 1	0	0

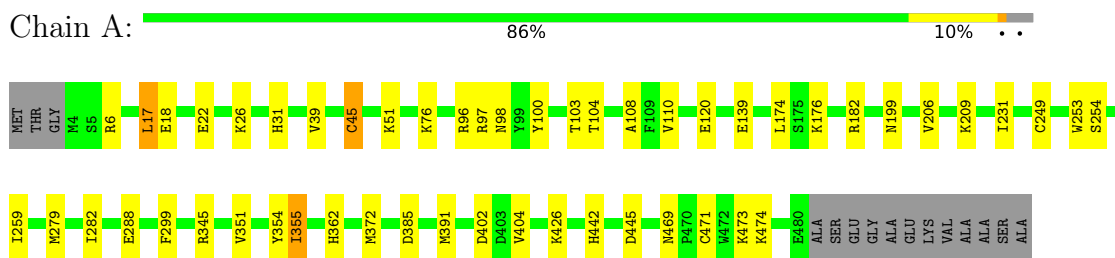
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	588	Total 588	O 588	0	0
10	B	726	Total 726	O 726	0	0
10	C	557	Total 557	O 557	0	0
10	D	731	Total 731	O 731	0	0

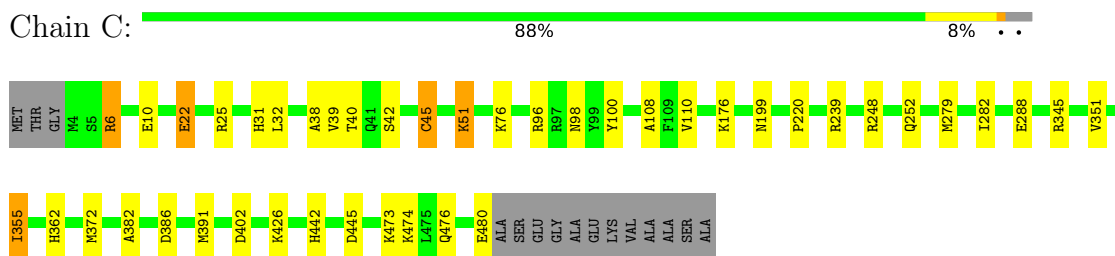
### 3 Residue-property plots [i](#)

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. 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. 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.

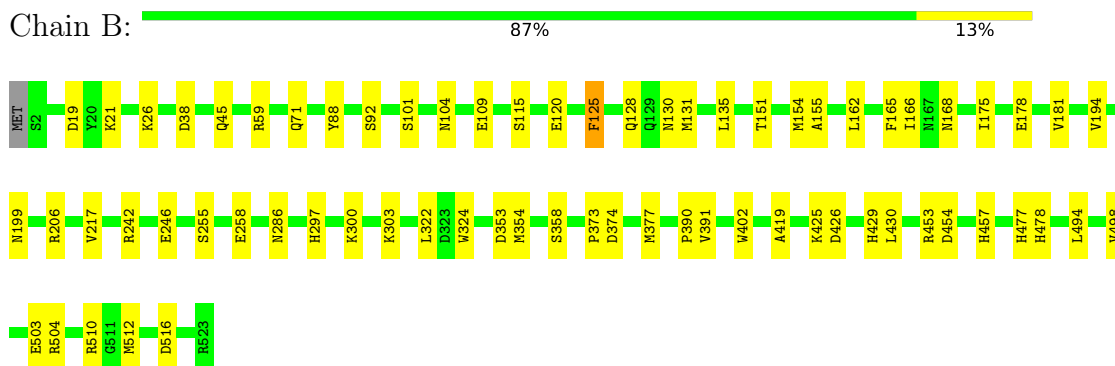
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



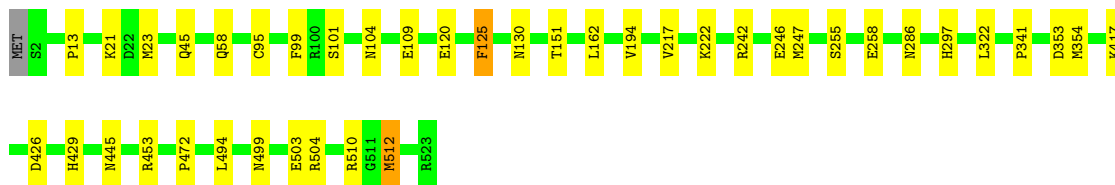
- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



- Molecule 2: Nitrogenase molybdenum-iron protein beta chain







## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.19Å 130.70Å 107.22Å 90.00° 110.67° 90.00°	Depositor
Resolution (Å)	47.46 – 1.00 47.46 – 1.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.46-1.00) 99.1 (47.46-1.00)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.54 (at 1.00Å)	Xtrriage
Refinement program	REFMAC 5.6.0113	Depositor
R, $R_{free}$	0.128 , 0.146 0.172 , 0.185	Depositor DCC
$R_{free}$ test set	55903 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	9.4	Xtrriage
Anisotropy	0.096	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 51.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.012 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	18955	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	10.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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: IMD, CA, CLF, 1CL, MG, ICS, HCA

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	0.65	2/3908 (0.1%)	0.84	6/5268 (0.1%)
1	C	0.73	5/3941 (0.1%)	0.86	8/5311 (0.2%)
2	B	0.62	2/4389 (0.0%)	0.79	5/5930 (0.1%)
2	D	0.61	1/4420 (0.0%)	0.79	3/5966 (0.1%)
All	All	0.65	10/16658 (0.1%)	0.82	22/22475 (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	1
1	C	0	1
2	B	0	1
2	D	0	1
All	All	0	4

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	10	GLU	CD-OE2	-14.01	1.10	1.25
1	C	22	GLU	CD-OE1	11.07	1.37	1.25
1	C	10	GLU	CD-OE1	7.80	1.34	1.25
1	C	45[A]	CYS	CB-SG	-7.60	1.69	1.82
1	C	45[B]	CYS	CB-SG	-7.60	1.69	1.82

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	51[A]	LYS	CD-CE-NZ	10.21	135.18	111.70
1	A	51[B]	LYS	CD-CE-NZ	10.21	135.18	111.70
1	C	6	ARG	NE-CZ-NH2	-10.21	115.20	120.30
1	C	248	ARG	NE-CZ-NH1	8.69	124.65	120.30
2	B	125	PHE	N-CA-CB	8.44	125.79	110.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	96	ARG	Sidechain
2	B	125	PHE	Peptide
1	C	96	ARG	Sidechain
2	D	125[B]	PHE	Peptide

## 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	3811	0	3763	51	0
1	C	3826	0	3797	30	0
2	B	4247	0	4202	93	0
2	D	4301	0	4227	57	0
3	A	14	0	6	2	0
3	C	14	0	6	2	0
4	A	18	0	0	0	0
4	C	18	0	0	0	0
5	A	10	0	10	1	0
5	B	10	0	10	1	0
5	C	10	0	10	3	0
5	D	10	0	10	1	0
6	B	2	0	0	0	0
7	B	15	0	0	0	0
7	D	15	0	0	0	0
8	B	15	0	0	0	0
8	D	15	0	0	0	0
9	B	1	0	0	0	0
9	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	A	588	0	0	13	1
10	B	726	0	0	31	0
10	C	557	0	0	9	0
10	D	731	0	0	16	0
All	All	18955	0	16041	201	1

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 6.

The worst 5 of 201 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:494:IMD:H5	10:D:878:HOH:O	1.29	1.29
1:A:249:CYS:HB3	10:A:1157:HOH:O	1.11	1.28
2:B:425:LYS:HE2	10:B:2302:HOH:O	1.28	1.28
1:A:182:ARG:HG3	10:A:2215:HOH:O	1.33	1.27
1:A:22:GLU:OE2	1:A:26:LYS:HE3	1.49	1.09

All (1) 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:A:1986:HOH:O	10:A:2381:HOH:O[2_646]	2.18	0.02

## 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	479/492 (97%)	462 (96%)	16 (3%)	1 (0%)	47 18
1	C	484/492 (98%)	464 (96%)	19 (4%)	1 (0%)	47 18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	534/523 (102%)	526 (98%)	7 (1%)	1 (0%)	47	18
2	D	537/523 (103%)	528 (98%)	8 (2%)	1 (0%)	47	18
All	All	2034/2030 (100%)	1980 (97%)	50 (2%)	4 (0%)	47	18

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 [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	411/415 (99%)	403 (98%)	8 (2%)	57	23
1	C	416/415 (100%)	407 (98%)	9 (2%)	52	18
2	B	468/455 (103%)	466 (100%)	2 (0%)	91	70
2	D	471/455 (104%)	466 (99%)	5 (1%)	73	43
All	All	1766/1740 (102%)	1742 (99%)	24 (1%)	71	34

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	176	LYS
1	C	362	HIS
1	C	355	ILE
1	C	445	ASP
1	A	445	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	294	GLN
2	D	363	HIS
2	D	499	ASN
2	B	294	GLN
2	B	286	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 4 are monoatomic - leaving 16 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
5	IMD	D	525	-	3,5,5	0.46	0	4,5,5	0.83	0
8	CLF	D	7499[B]	1,2	0,24,24	-	-	-		
4	ICS	C	7496	1	18,30,30	2.44	11 (61%)	-		
4	ICS	A	6496	1	18,30,30	2.44	10 (55%)	-		
5	IMD	A	493	-	3,5,5	0.40	0	4,5,5	0.82	0
3	HCA	A	6494	-	13,13,13	1.06	0	14,18,18	1.65	4 (28%)
5	IMD	B	525	-	3,5,5	0.36	0	4,5,5	0.42	0
7	1CL	D	7498[A]	1,2	0,22,22	-	-	-		
3	HCA	C	7494	-	13,13,13	1.01	0	14,18,18	1.72	4 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	CLF	B	6499[B]	1,2	0,24,24	-	-	-		
5	IMD	C	494	-	3,5,5	0.34	0	4,5,5	0.46	0
5	IMD	A	494	-	3,5,5	0.28	0	4,5,5	0.52	0
5	IMD	C	493	-	3,5,5	0.54	0	4,5,5	0.40	0
7	1CL	B	6498[A]	1,2	0,22,22	-	-	-		
5	IMD	D	524	-	3,5,5	0.44	0	4,5,5	0.46	0
5	IMD	B	524	-	3,5,5	0.15	0	4,5,5	0.77	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
5	IMD	D	525	-	-	-	0/1/1/1
8	CLF	D	7499[B]	1,2	-	-	0/12/10/10
5	IMD	A	493	-	-	-	0/1/1/1
3	HCA	A	6494	-	-	2/17/17/17	-
5	IMD	B	525	-	-	-	0/1/1/1
7	1CL	D	7498[A]	1,2	-	-	0/10/8/8
3	HCA	C	7494	-	-	2/17/17/17	-
8	CLF	B	6499[B]	1,2	-	-	0/12/10/10
5	IMD	C	494	-	-	-	0/1/1/1
5	IMD	A	494	-	-	-	0/1/1/1
5	IMD	C	493	-	-	-	0/1/1/1
7	1CL	B	6498[A]	1,2	-	-	0/10/8/8
5	IMD	D	524	-	-	-	0/1/1/1
5	IMD	B	524	-	-	-	0/1/1/1

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	6496	ICS	S3B-FE6	-4.08	2.22	2.32
4	A	6496	ICS	S4B-FE7	-4.04	2.22	2.32
4	C	7496	ICS	S3B-FE6	-4.03	2.22	2.32
4	C	7496	ICS	S4B-FE7	-4.01	2.22	2.32
4	A	6496	ICS	S1B-FE6	-3.44	2.23	2.32

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	7494	HCA	O5-C7-C3	-3.38	117.47	122.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	6494	HCA	O6-C7-C3	3.08	118.40	113.05
3	C	7494	HCA	O6-C7-C3	3.02	118.29	113.05
3	A	6494	HCA	C4-C5-C6	2.79	119.06	112.75
3	C	7494	HCA	C4-C5-C6	2.75	118.97	112.75

There are no chirality outliers.

All (4) torsion outliers are listed below:

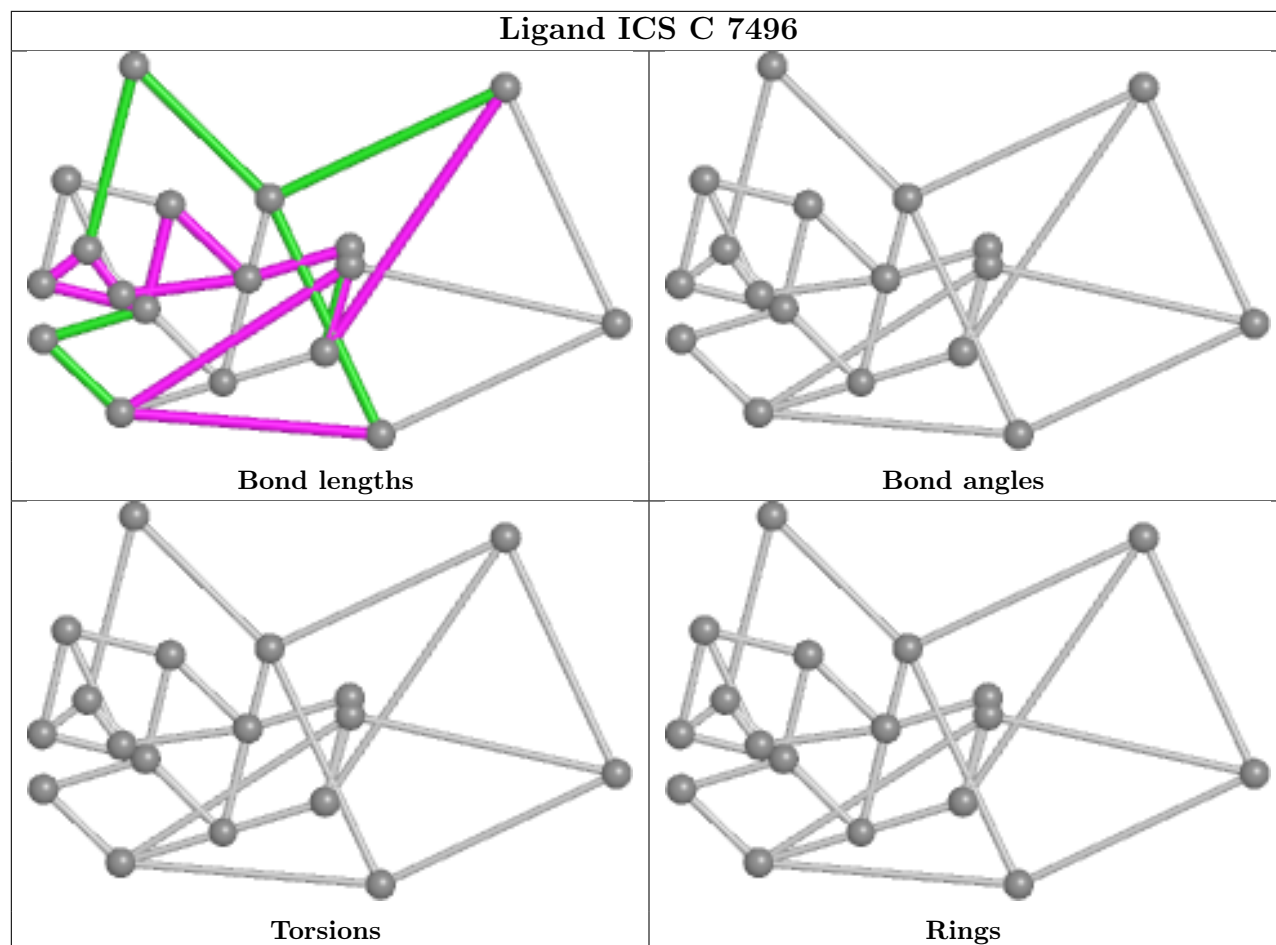
Mol	Chain	Res	Type	Atoms
3	C	7494	HCA	C4-C5-C6-O4
3	A	6494	HCA	C4-C5-C6-O4
3	A	6494	HCA	C4-C5-C6-O3
3	C	7494	HCA	C4-C5-C6-O3

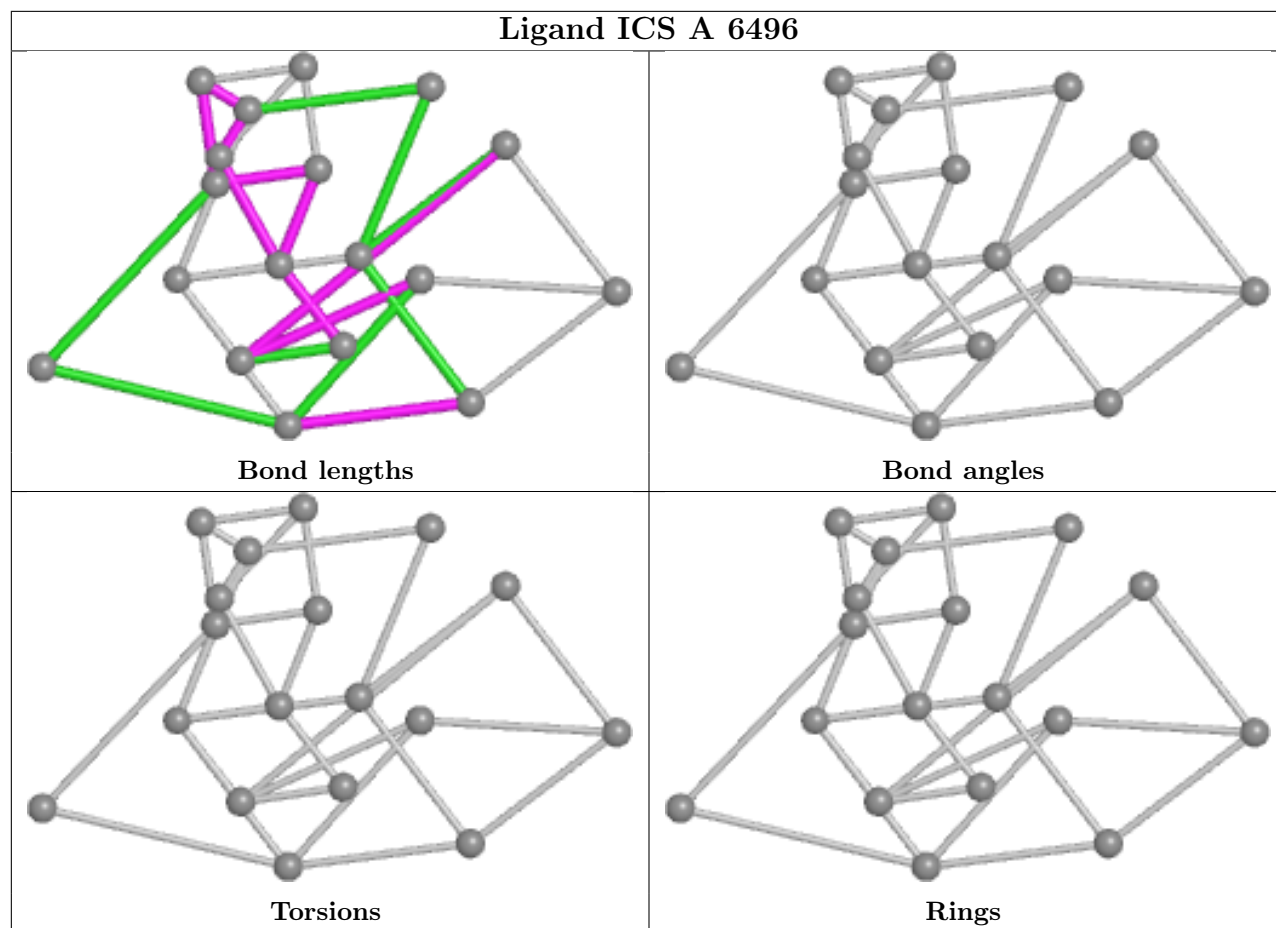
There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	6494	HCA	2	0
5	B	525	IMD	1	0
3	C	7494	HCA	2	0
5	C	494	IMD	1	0
5	A	494	IMD	1	0
5	C	493	IMD	2	0
5	D	524	IMD	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

### 6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

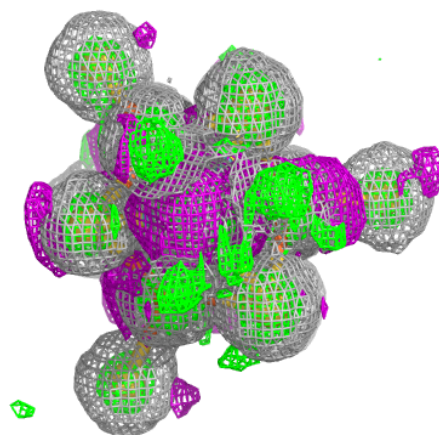
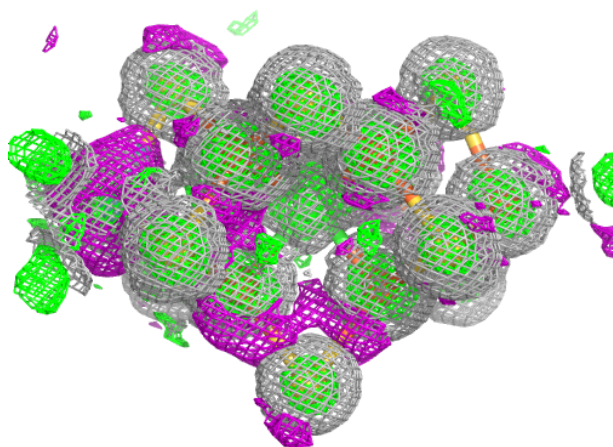
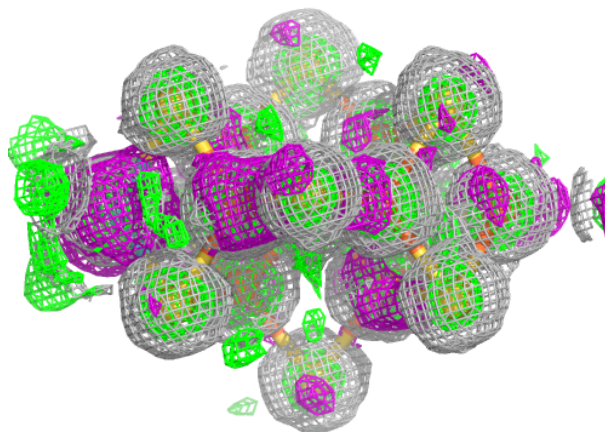
### 6.4 Ligands

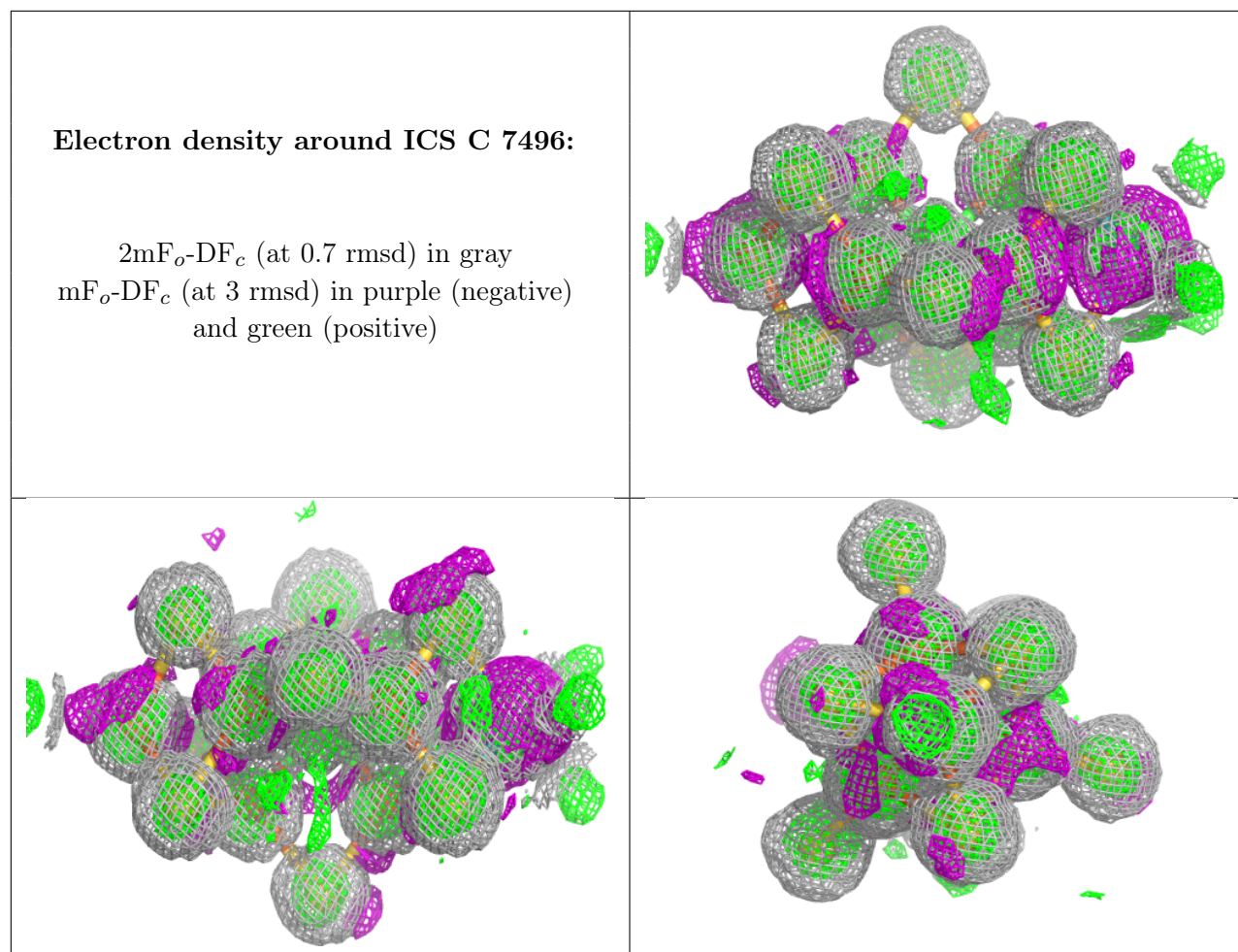
Unable to reproduce the depositors R factor - this section is therefore empty.

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 A 6496:**

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





## 6.5 Other polymers [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.