



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 29, 2019 – 12:15 PM EDT

PDB ID : 6O7Q  
Title : Nitrogenase MoFeP mutant S188A from *Azotobacter vinelandii* in the dithionite reduced state after redox cycling  
Authors : Rutledge, H.L.; Tezcan, F.A.  
Deposited on : 2019-03-08  
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : 2.3.2  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.3.2

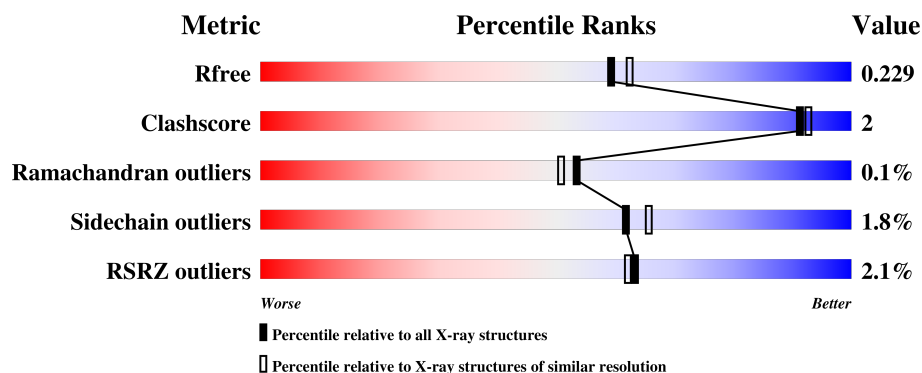
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	111664	7193 (2.00-2.00)
Clashscore	122126	8267 (2.00-2.00)
Ramachandran outliers	120053	8166 (2.00-2.00)
Sidechain outliers	120020	8165 (2.00-2.00)
RSRZ outliers	108989	7011 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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>4%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div>.</div> </div> </div>
1	C	492	<div> <div>2%</div> <div> <div></div> <div>90%</div> <div>7%</div> <div>.</div> </div> </div>
2	B	523	<div> <div>%</div> <div> <div></div> <div>96%</div> <div>.</div> </div> </div>
2	D	523	<div> <div>%</div> <div> <div></div> <div>96%</div> <div>.</div> </div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 32582 atoms, of which 15358 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	473	Total	C	H	N	O	S	0	1	1
			7337	2371	3616	628	697	25			
1	C	475	Total	C	H	N	O	S	0	1	0
			7392	2383	3646	639	699	25			

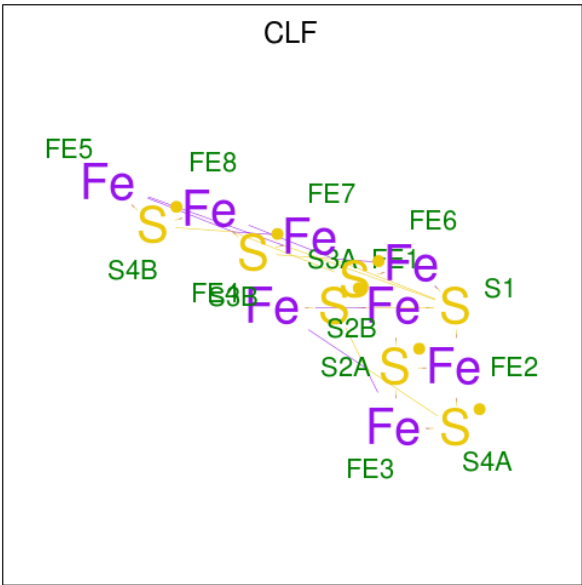
- Molecule 2 is a protein called Nitrogenase molybdenum-iron protein beta chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	522	Total	C	H	N	O	S	0	0	0
			8170	2649	4024	699	770	28			
2	D	522	Total	C	H	N	O	S	0	0	0
			8224	2660	4060	702	774	28			

There are 2 discrepancies between the modelled and reference sequences:

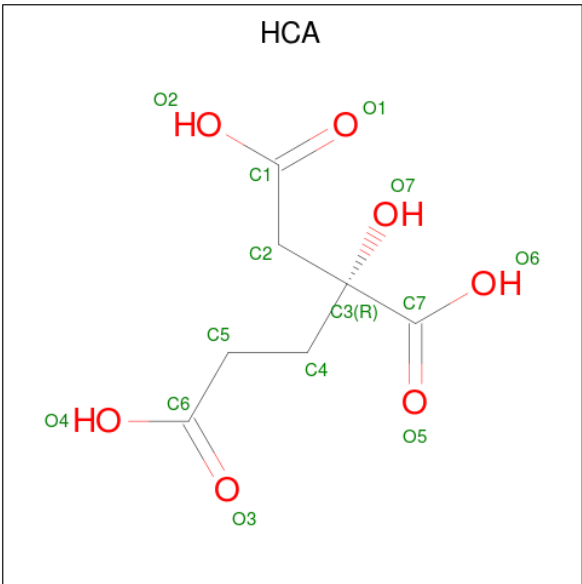
Chain	Residue	Modelled	Actual	Comment	Reference
B	188	ALA	SER	engineered mutation	UNP P07329
D	188	ALA	SER	engineered mutation	UNP P07329

- Molecule 3 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
3	A	1	Total	Fe	S	0	0
			15	8	7		
3	D	1	Total	Fe	S	0	0
			15	8	7		

- Molecule 4 is 3-HYDROXY-3-CARBOXY-ADIPIC ACID (three-letter code: HCA) (formula: C<sub>7</sub>H<sub>10</sub>O<sub>7</sub>).



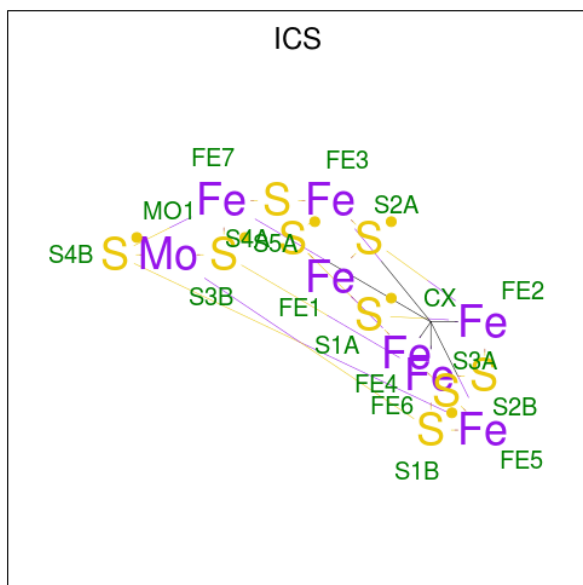
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			20	7	6	7		

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

- Molecule 5 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
5	A	1	Total	C	Fe	Mo	S	0
			18	1	7	1	9	
5	C	1	Total	C	Fe	Mo	S	0
			18	1	7	1	9	

- Molecule 6 is FE (III) ION (three-letter code: FE) (formula: Fe).

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	261	Total	O	0	0
			261	261		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	399	Total 399	O 399	0	0
7	C	272	Total 272	O 272	0	0
7	D	419	Total 419	O 419	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	77.44Å 130.41Å 107.75Å 90.00° 109.09° 90.00°	Depositor
Resolution (Å)	48.68 – 2.00 48.68 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.68-2.00) 99.9 (48.68-2.00)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.71 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.186 , 0.229 0.185 , 0.229	Depositor DCC
$R_{free}$ test set	13211 reflections (9.72%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.1	Xtriage
Anisotropy	0.544	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 44.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.031 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	32582	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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: ICS, CLF, HCA, FE

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	0.25	0/3811	0.44	0/5144
1	C	0.26	0/3836	0.44	0/5177
2	B	0.25	0/4252	0.43	0/5756
2	D	0.25	0/4270	0.42	0/5776
All	All	0.25	0/16169	0.43	0/21853

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [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	3721	3616	3616	16	0
1	C	3746	3646	3652	15	0
2	B	4146	4024	4024	9	0
2	D	4164	4060	4061	13	0
3	A	15	0	0	0	0
3	D	15	0	0	0	0
4	A	14	6	6	1	0
4	C	14	6	6	1	0
5	A	18	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	18	0	0	0	0
6	B	1	0	0	0	0
6	D	1	0	0	0	0
7	A	261	0	0	5	0
7	B	399	0	0	3	0
7	C	272	0	0	3	0
7	D	419	0	0	6	0
All	All	17224	15358	15365	55	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (55) 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)
1:C:6:ARG:NH2	1:C:396:ASP:OD1	2.12	0.81
2:D:315:LYS:NZ	7:D:704:HOH:O	2.18	0.76
1:A:476:GLN:O	7:A:601:HOH:O	2.08	0.71
1:A:42:SER:OG	1:A:384:ASN:OD1	2.08	0.71
2:D:211:LYS:NZ	7:D:706:HOH:O	2.22	0.71
2:D:516:ASP:OD2	7:D:701:HOH:O	2.11	0.69
1:C:213:ASP:OD2	1:C:215:THR:OG1	2.07	0.69
2:B:33:GLU:OE1	7:B:701:HOH:O	2.09	0.69
2:D:280:GLU:OE1	7:D:702:HOH:O	2.12	0.66
2:D:178:GLU:O	7:D:703:HOH:O	2.14	0.64
1:A:42:SER:N	7:A:603:HOH:O	2.33	0.61
2:D:90:HIS:ND1	2:D:116:ASP:OD2	2.30	0.60
2:D:369:LEU:HD22	2:D:379:LEU:HD12	1.83	0.59
1:C:29:ASN:O	7:C:602:HOH:O	2.17	0.56
2:D:9:LYS:NZ	7:D:718:HOH:O	2.40	0.55
1:C:276:TYR:OH	1:C:284:ARG:NH2	2.40	0.53
4:A:502:HCA:O7	4:A:502:HCA:O1	2.26	0.53
1:A:480:GLU:N	1:A:480:GLU:OE1	2.42	0.53
1:A:60:ARG:NH2	7:A:610:HOH:O	2.44	0.48
2:B:151:THR:HG23	2:B:162:LEU:HD11	1.96	0.48
2:B:90:HIS:ND1	2:B:116:ASP:OD2	2.45	0.48
1:C:176:LYS:NZ	7:C:619:HOH:O	2.46	0.47
2:B:6:ASP:OD1	2:B:6:ASP:N	2.44	0.47
1:A:96:ARG:NH1	5:A:503:ICS:S5A	2.84	0.47
1:C:98:ASN:O	1:C:98:ASN:ND2	2.48	0.47
2:D:217:VAL:HG13	2:D:220:SER:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:399:ASN:ND2	7:B:729:HOH:O	2.49	0.46
4:C:501:HCA:O2	4:C:501:HCA:O7	2.34	0.46
2:B:510:ARG:NH2	7:B:728:HOH:O	2.48	0.45
1:A:176:LYS:NZ	7:A:622:HOH:O	2.48	0.45
1:A:253:TRP:HA	1:A:254:SER:HA	1.79	0.45
1:A:42:SER:N	1:A:388:ASP:OD1	2.51	0.44
1:A:210:ARG:NH1	7:A:619:HOH:O	2.48	0.44
1:A:359:ARG:N	1:A:360:PRO:CD	2.81	0.44
1:C:59:ILE:HD12	1:C:427:GLU:OE2	2.17	0.43
1:A:350:ARG:NH2	1:A:416:ILE:O	2.49	0.43
2:B:499:ASN:O	2:B:503:GLU:HG3	2.18	0.43
2:B:358:SER:HB3	2:B:498:VAL:HG21	2.00	0.42
1:C:359:ARG:N	1:C:360:PRO:CD	2.82	0.42
1:C:209:LYS:NZ	1:C:263:GLU:OE2	2.46	0.42
1:A:467:LEU:O	1:A:467:LEU:HD12	2.19	0.42
2:D:494:LEU:HD23	2:D:494:LEU:C	2.39	0.42
1:C:382:ALA:HB1	1:C:386:ASP:HB2	2.02	0.42
2:D:18:GLN:NE2	2:D:22:ASP:OD1	2.49	0.42
2:D:254:LEU:O	2:D:255:SER:HB3	2.20	0.41
2:B:394:LEU:HD13	2:B:430:LEU:HB2	2.02	0.41
1:C:27:ASP:OD1	7:C:603:HOH:O	2.22	0.41
1:C:253:TRP:HA	1:C:254:SER:HA	1.81	0.41
1:C:124:VAL:HG23	1:C:125:PHE:CD2	2.55	0.41
2:D:86:MET:HG2	2:D:138:CYS:SG	2.61	0.41
1:A:354:TYR:CZ	1:A:404:VAL:HG12	2.54	0.41
1:C:133:LYS:HB3	1:C:133:LYS:NZ	2.35	0.41
1:A:213:ASP:O	1:A:267:LYS:NZ	2.52	0.41
1:A:447:SER:OG	1:A:448:GLY:N	2.54	0.41
1:C:277:ARG:HD2	1:C:386:ASP:OD2	2.21	0.40

There are no symmetry-related clashes.

## 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	470/492 (96%)	446 (95%)	23 (5%)	1 (0%)	49	46
1	C	472/492 (96%)	452 (96%)	19 (4%)	1 (0%)	49	46
2	B	520/523 (99%)	503 (97%)	17 (3%)	0	100	100
2	D	520/523 (99%)	505 (97%)	15 (3%)	0	100	100
All	All	1982/2030 (98%)	1906 (96%)	74 (4%)	2 (0%)	53	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
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	393/415 (95%)	383 (98%)	10 (2%)	50	52
1	C	397/415 (96%)	387 (98%)	10 (2%)	50	52
2	B	445/454 (98%)	437 (98%)	8 (2%)	62	66
2	D	450/454 (99%)	447 (99%)	3 (1%)	85	89
All	All	1685/1738 (97%)	1654 (98%)	31 (2%)	62	66

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	SER
1	A	98	ASN
1	A	212	GLU
1	A	264	LEU
1	A	318	GLU
1	A	362	HIS
1	A	401	TYR
1	A	409	PHE
1	A	445	ASP

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Mol	Chain	Res	Type
1	A	467	LEU
2	B	6	ASP
2	B	38	ASP
2	B	80	LEU
2	B	92	SER
2	B	115	SER
2	B	177	ASP
2	B	369	LEU
2	B	512	MET
1	C	45	CYS
1	C	98	ASN
1	C	315	LYS
1	C	318	GLU
1	C	322	LYS
1	C	362	HIS
1	C	401	TYR
1	C	409	PHE
1	C	445	ASP
1	C	474	LYS
2	D	177	ASP
2	D	258	GLU
2	D	505	LEU

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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	CLF	A	501	1,2	0,24,24	0.00	-	-		
4	HCA	A	502	-	4,13,13	0.76	0	4,18,18	1.47	1 (25%)
5	ICS	A	503	1	6,30,30	1.48	1 (16%)	-		
4	HCA	C	501	-	4,13,13	0.77	0	4,18,18	1.59	1 (25%)
5	ICS	C	502	1	6,30,30	1.53	1 (16%)	-		
3	CLF	D	601	1,2	0,24,24	0.00	-	-		

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	CLF	A	501	1,2	-	-	0/10/10/10
4	HCA	A	502	-	-	2/7/17/17	-
4	HCA	C	501	-	-	1/7/17/17	-
3	CLF	D	601	1,2	-	-	0/10/10/10

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	502	ICS	S2B-FE6	-2.68	2.18	2.24
5	A	503	ICS	S2B-FE6	-2.61	2.18	2.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	501	HCA	C3-C2-C1	-2.36	111.21	114.98
4	A	502	HCA	C3-C2-C1	-2.08	111.66	114.98

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	502	HCA	C1-C2-C3-C4
4	C	501	HCA	C1-C2-C3-C4
4	A	502	HCA	C1-C2-C3-O7

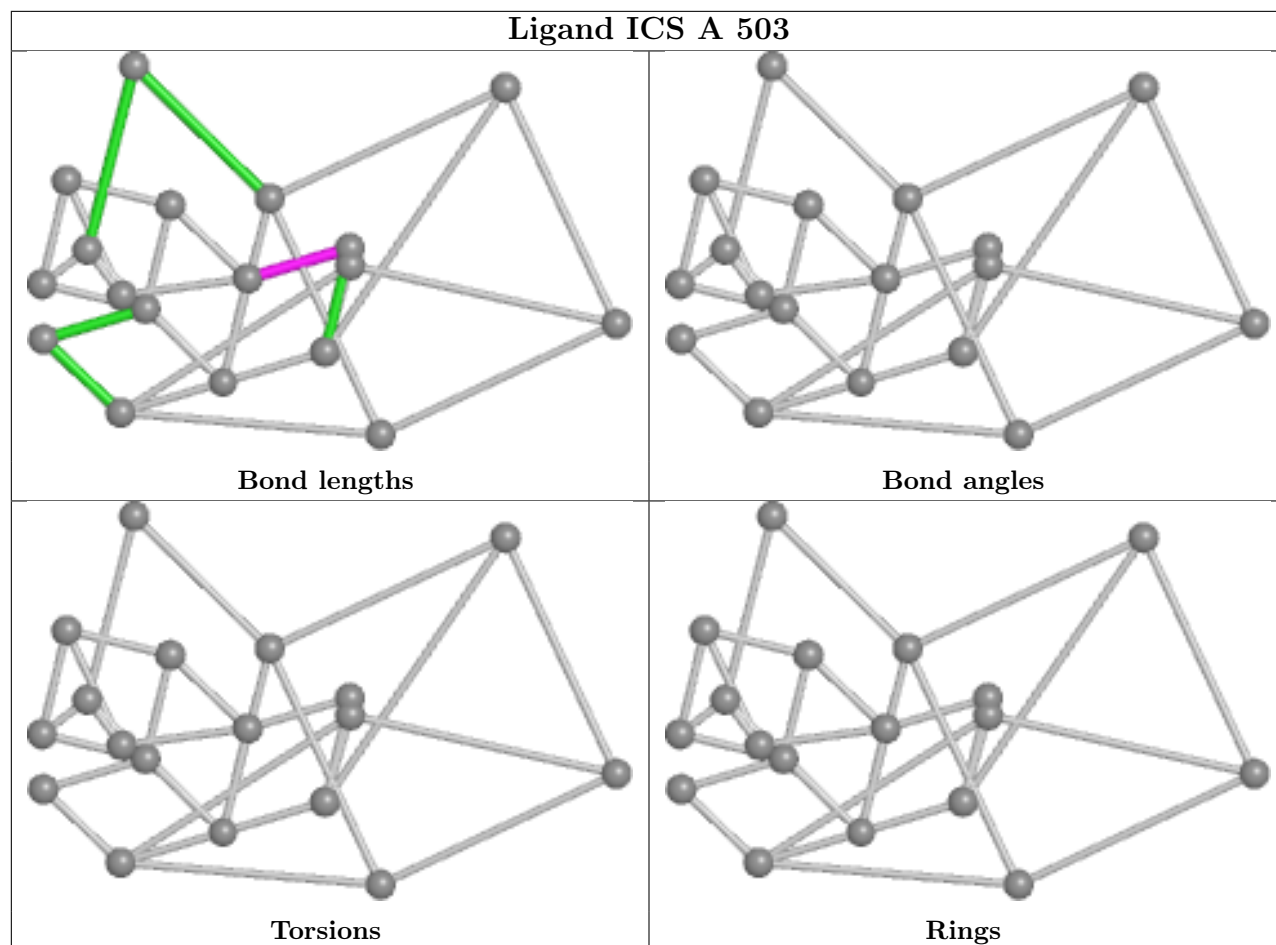
There are no ring outliers.

2 monomers are involved in 2 short contacts:

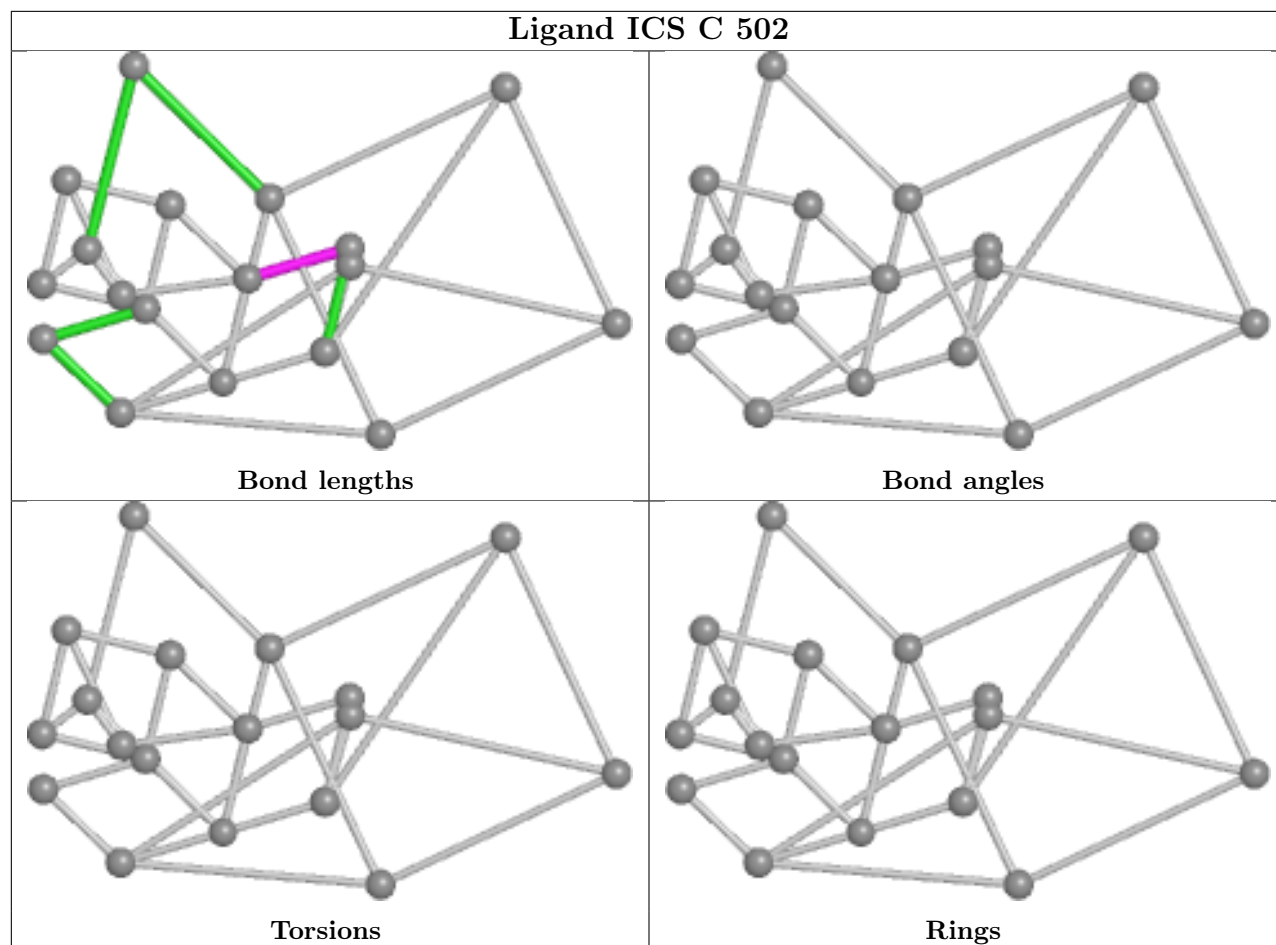
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502	HCA	1	0
4	C	501	HCA	1	0

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.

## Ligand ICS A 503







## 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	473/492 (96%)	0.13	21 (4%) 34 33	17, 28, 49, 66	0
1	C	475/492 (96%)	0.05	11 (2%) 60 59	16, 27, 49, 64	0
2	B	522/523 (99%)	-0.09	4 (0%) 86 85	15, 24, 39, 55	0
2	D	522/523 (99%)	-0.12	5 (0%) 82 81	13, 23, 37, 52	0
All	All	1992/2030 (98%)	-0.01	41 (2%) 63 62	13, 26, 43, 66	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	37	PRO	7.3
1	C	45	CYS	4.9
1	C	481	ALA	4.8
1	A	214	THR	4.6
1	C	37	PRO	3.7
1	A	212	GLU	3.6
1	A	213	ASP	3.3
1	A	14	GLN	3.3
1	A	36	ASP	3.0
1	C	9	VAL	2.9
2	B	215	ASP	2.9
1	C	41	GLN	2.9
1	A	91	TYR	2.8
1	A	174	LEU	2.8
2	B	124	VAL	2.7
1	A	19	VAL	2.7
1	A	17	LEU	2.7
1	C	36	ASP	2.6
1	A	18	GLU	2.6
1	A	215	THR	2.6
2	D	125	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	214	ASP	2.6
2	D	102	TYR	2.5
1	A	45	CYS	2.5
1	A	43	LYS	2.5
2	D	124	VAL	2.4
1	A	159	ILE	2.4
1	A	125	PHE	2.4
2	B	98	TYR	2.4
1	C	318	GLU	2.4
1	A	87	GLY	2.4
1	C	396	ASP	2.3
1	C	214	THR	2.3
1	A	4	MET	2.3
1	C	125	PHE	2.3
1	A	391	MET	2.2
2	D	215	ASP	2.2
1	A	169	VAL	2.2
2	D	521	LEU	2.1
1	A	397	SER	2.0
1	C	91	TYR	2.0

## 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 carbohydrates 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(Å <sup>2</sup> )	Q<0.9
4	HCA	C	501	14/14	0.93	0.15	12,20,26,26	0
3	CLF	A	501	15/15	0.94	0.07	16,21,31,33	0
4	HCA	A	502	14/14	0.94	0.15	14,19,25,25	0

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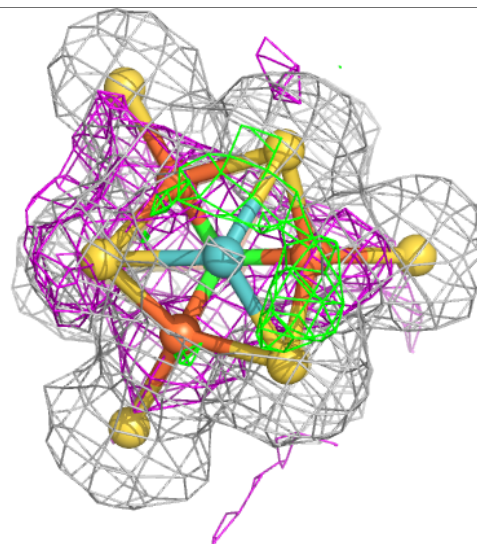
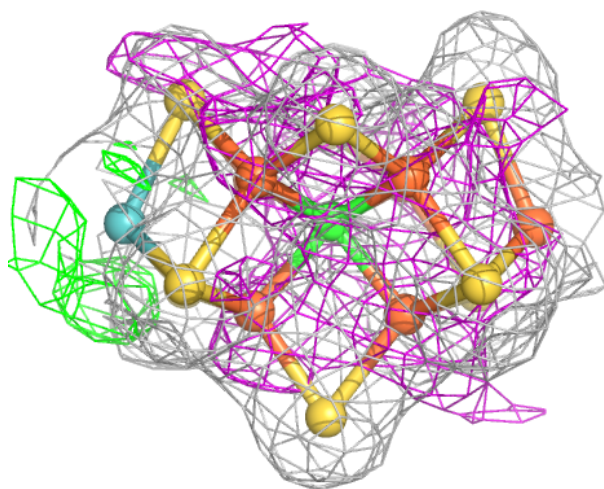
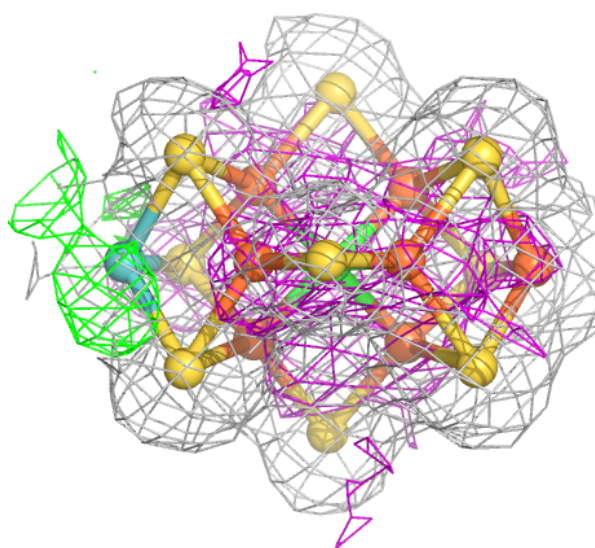
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CLF	D	601	15/15	0.95	0.07	16,20,29,30	0
5	ICS	C	502	18/18	0.97	0.07	9,17,27,29	0
5	ICS	A	503	18/18	0.97	0.07	7,18,28,29	0
6	FE	D	602	1/1	0.98	0.10	24,24,24,24	1
6	FE	B	601	1/1	0.99	0.10	27,27,27,27	1

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.

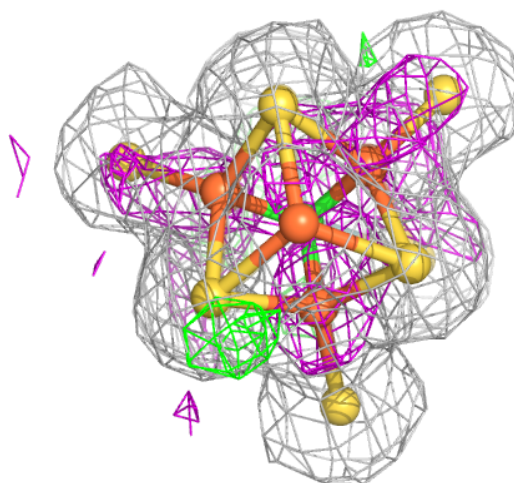
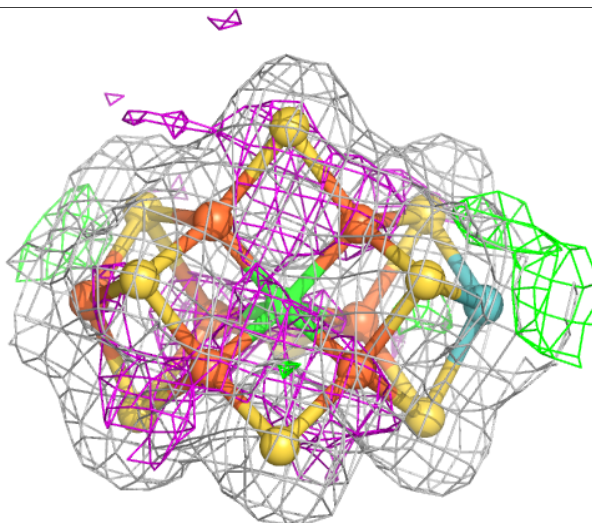
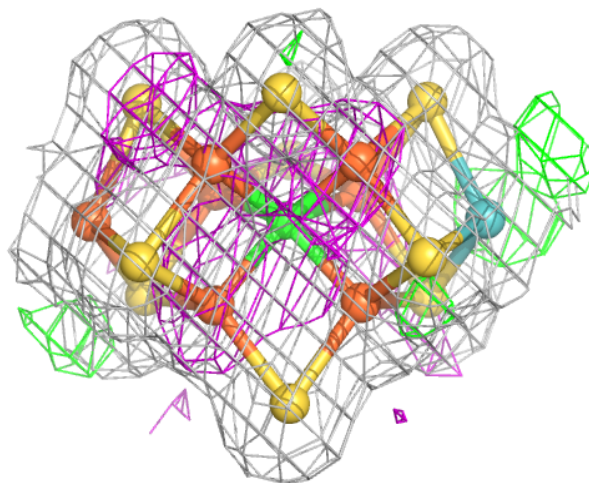
**Electron density around ICS C 502:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around ICS A 503:**

$2mF_o-DF_c$  (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.