



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 29, 2019 – 12:08 PM EDT

PDB ID : 6O7P  
Title : Nitrogenase MoFeP mutant F99Y from *Azotobacter vinelandii* in the dithionite reduced state  
Authors : Rutledge, H.L.; Williamson, L.M.; Tezcan, F.A.  
Deposited on : 2019-03-08  
Resolution : 1.70 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

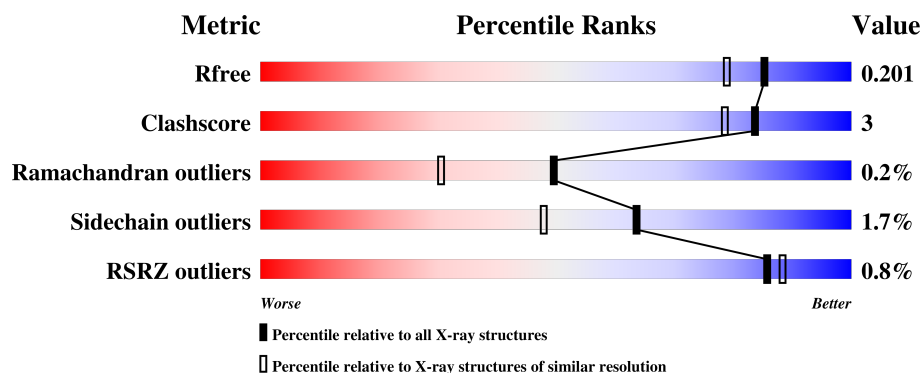
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	3793 (1.70-1.70)
Clashscore	122126	4167 (1.70-1.70)
Ramachandran outliers	120053	4100 (1.70-1.70)
Sidechain outliers	120020	4100 (1.70-1.70)
RSRZ outliers	108989	3718 (1.70-1.70)

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	 2% 88% 8% . .
1	C	492	 1% 89% 8% .
2	B	523	 94% 6%
2	D	523	 94% 6%

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 34126 atoms, of which 15592 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	476	Total	C	H	N	O	S	0	1	0
			7440	2392	3678	641	704	25			
1	C	478	Total	C	H	N	O	S	0	6	1
			7512	2415	3722	643	705	27			

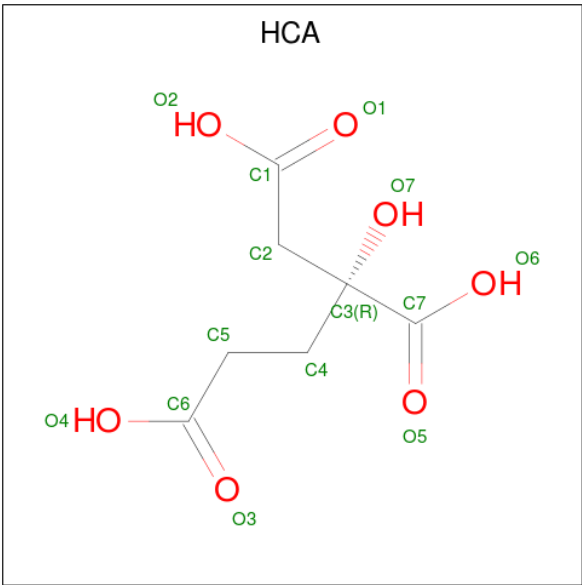
- Molecule 2 is a protein called Nitrogenase molybdenum-iron protein beta chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	522	Total	C	H	N	O	S	0	1	0
			8242	2661	4077	705	771	28			
2	D	522	Total	C	H	N	O	S	0	7	0
			8295	2683	4103	699	781	29			

There are 2 discrepancies between the modelled and reference sequences:

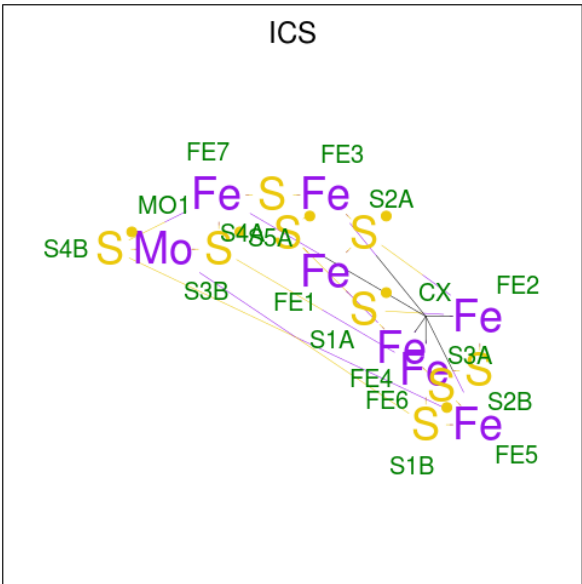
Chain	Residue	Modelled	Actual	Comment	Reference
B	99	TYR	PHE	engineered mutation	UNP P07329
D	99	TYR	PHE	engineered mutation	UNP P07329

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



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

- Molecule 4 is iron-sulfur-molybdenum cluster with interstitial carbon (three-letter code: ICS) (formula: CFe<sub>7</sub>MoS<sub>9</sub>).



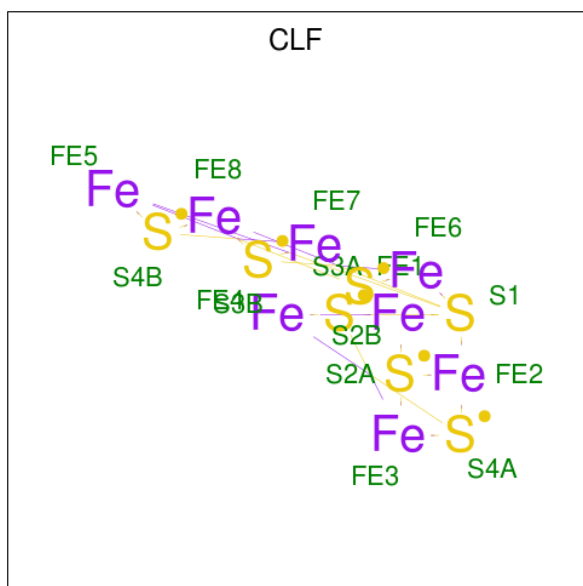
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	Mo	S	0	0
			18	1	7	1	9		

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

- Molecule 5 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
5	B	1	Total	Fe	S		
			15	8	7		
						0	0
5	D	1	Total	Fe	S		
			15	8	7		
						0	0

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

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	578	Total	O		
			578	578		
					0	0
7	B	725	Total	O		
			725	725		
					0	0

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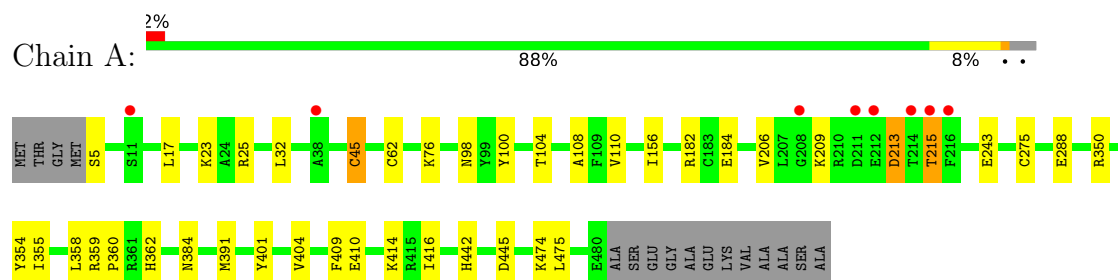
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	528	Total 528	O 528	0	0
7	D	698	Total 698	O 698	0	0

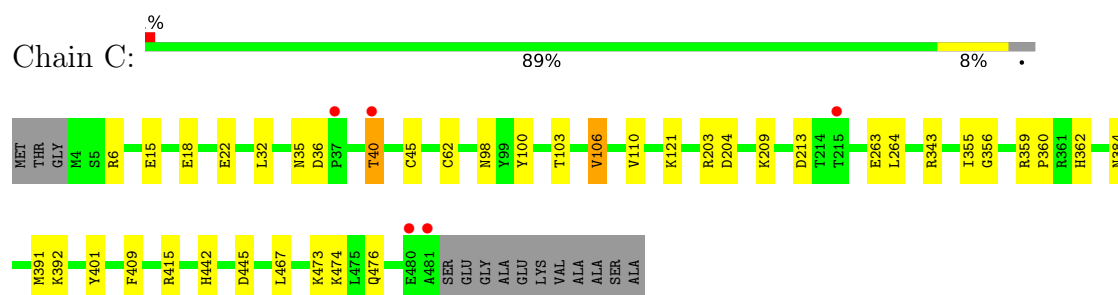
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

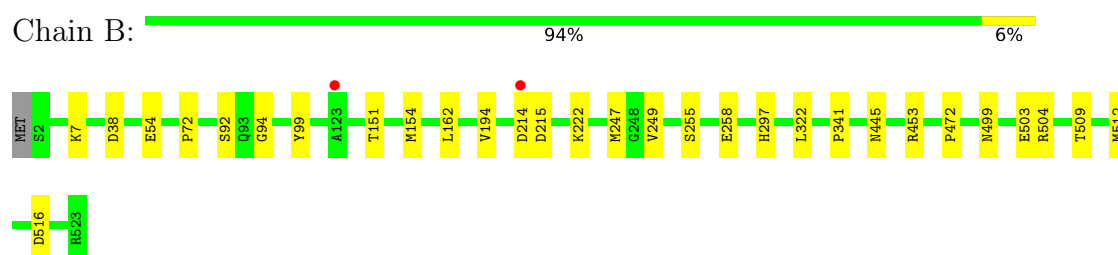
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



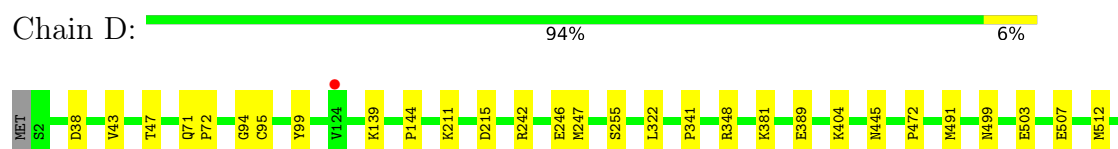
- Molecule 1: Nitrogenase molybdenum-iron protein alpha chain



- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



- Molecule 2: Nitrogenase molybdenum-iron protein beta chain



R523



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.85Å 128.44Å 107.71Å 90.00° 109.06° 90.00°	Depositor
Resolution (Å)	46.65 – 1.70 46.65 – 1.70	Depositor EDS
% Data completeness (in resolution range)	87.4 (46.65-1.70) 87.4 (46.65-1.70)	Depositor EDS
$R_{merge}$	0.24	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 1.70Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.168 , 0.201 0.168 , 0.201	Depositor DCC
$R_{free}$ test set	19044 reflections (10.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	12.5	Xtriage
Anisotropy	0.523	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 41.4	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	34126	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% 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	0.41	0/3853	0.54	1/5202 (0.0%)
1	C	0.37	0/3896	0.53	0/5258
2	B	0.38	0/4274	0.53	0/5779
2	D	0.38	0/4319	0.52	0/5844
All	All	0.39	0/16342	0.53	1/22083 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	213	ASP	CB-CG-OD1	7.09	124.68	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	3762	3678	3675	30	0
1	C	3790	3722	3722	20	0
2	B	4165	4077	4076	17	0
2	D	4192	4103	4103	19	0
3	A	14	6	6	2	0
3	C	14	6	6	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	18	0	0	0	0
4	C	18	0	0	1	0
5	B	15	0	0	0	0
5	D	15	0	0	0	0
6	B	1	0	0	0	0
6	D	1	0	0	0	0
7	A	578	0	0	11	2
7	B	725	0	0	4	1
7	C	528	0	0	6	2
7	D	698	0	0	4	1
All	All	18534	15592	15588	81	3

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.

All (81) 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:D:491:MET:SD	7:D:1003:HOH:O	2.28	0.91
1:A:209:LYS:NZ	7:A:601:HOH:O	2.10	0.85
1:A:23:LYS:NZ	7:A:602:HOH:O	2.10	0.82
1:C:121:LYS:NZ	7:C:602:HOH:O	2.16	0.78
1:A:5:SER:N	7:A:605:HOH:O	2.17	0.77
1:A:213:ASP:OD1	1:A:215:THR:HG22	1.87	0.75
2:B:54:GLU:OE1	7:B:701:HOH:O	2.08	0.70
1:A:5:SER:N	7:A:609:HOH:O	2.24	0.70
2:B:38:ASP:OD1	7:B:702:HOH:O	2.10	0.68
1:A:213:ASP:OD1	1:A:215:THR:CG2	2.42	0.68
1:A:288:GLU:OE1	7:A:604:HOH:O	2.15	0.65
1:C:476:GLN:O	7:C:601:HOH:O	2.14	0.64
2:B:222:LYS:O	7:B:703:HOH:O	2.15	0.64
1:A:215:THR:OG1	7:A:603:HOH:O	2.15	0.63
1:C:343:ARG:NH2	7:C:606:HOH:O	2.31	0.62
1:A:384:ASN:OD1	7:A:606:HOH:O	2.18	0.55
1:A:25:ARG:NH1	7:A:622:HOH:O	2.40	0.55
1:C:40:THR:O	1:C:391[B]:MET:SD	2.65	0.55
2:B:322:LEU:HD21	1:C:474:LYS:HB3	1.89	0.55
1:A:182:ARG:NH1	1:A:184:GLU:OE2	2.40	0.55
2:B:247:MET:HG2	2:B:341:PRO:HD3	1.89	0.55
2:D:507:GLU:OE2	7:D:701:HOH:O	2.17	0.53
1:A:32:LEU:O	7:A:607:HOH:O	2.19	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:TYR:CE1	1:A:110:VAL:HB	2.45	0.51
2:D:389:GLU:OE1	7:D:702:HOH:O	2.19	0.51
2:B:151:THR:HG23	2:B:162:LEU:HD11	1.93	0.51
1:A:275:CYS:HA	1:A:358:LEU:HD22	1.93	0.50
1:A:243:GLU:O	7:A:608:HOH:O	2.20	0.49
2:D:247:MET:HG2	2:D:341:PRO:HD3	1.95	0.48
1:C:203:ARG:HD2	1:C:204:ASP:OD1	2.12	0.48
1:C:391[B]:MET:HG2	1:C:392:LYS:N	2.29	0.48
2:B:214:ASP:OD1	2:B:215:ASP:N	2.46	0.47
2:B:247:MET:HB3	2:B:249:VAL:HG23	1.96	0.47
3:A:501:HCA:O7	3:A:501:HCA:O2	2.33	0.47
1:A:17:LEU:HB3	1:A:25:ARG:HG3	1.95	0.47
1:C:32:LEU:O	7:C:603:HOH:O	2.20	0.46
2:D:215:ASP:OD1	7:D:703:HOH:O	2.20	0.46
1:A:206:VAL:HA	1:A:209:LYS:HD2	1.98	0.46
1:A:156:ILE:HG22	1:A:182:ARG:HH12	1.81	0.45
1:C:209:LYS:NZ	1:C:263:GLU:OE2	2.47	0.45
1:A:442:HIS:CG	3:A:501:HCA:H52	2.53	0.44
2:D:43:VAL:O	2:D:47:THR:HG23	2.17	0.44
1:C:6:ARG:NH2	1:C:36:ASP:HB3	2.33	0.43
1:A:354:TYR:CZ	1:A:404:VAL:HG12	2.53	0.43
2:D:139:LYS:HA	2:D:144:PRO:HD2	2.00	0.43
2:B:453:ARG:HD3	2:D:512[B]:MET:SD	2.59	0.43
1:C:15:GLU:O	1:C:18:GLU:HG3	2.18	0.43
1:C:22:GLU:H	1:C:22:GLU:CD	2.22	0.43
2:B:72:PRO:HB2	2:B:99:TYR:CZ	2.53	0.43
1:A:410:GLU:HG2	1:A:414:LYS:HD2	2.01	0.43
1:A:182:ARG:NH2	7:A:642:HOH:O	2.50	0.43
1:C:359:ARG:N	1:C:360:PRO:CD	2.81	0.42
1:C:356:GLY:HA3	4:C:502:ICS:S1B	2.59	0.42
1:A:104:THR:HA	1:A:108:ALA:O	2.19	0.42
2:B:445:ASN:HB2	2:B:472:PRO:O	2.19	0.42
2:D:445:ASN:HB2	2:D:472:PRO:O	2.19	0.42
2:B:499:ASN:O	2:B:503:GLU:HG3	2.19	0.42
1:C:100:TYR:CE1	1:C:110:VAL:HB	2.54	0.42
2:B:194:VAL:HB	2:B:297:HIS:CG	2.55	0.42
2:B:509:THR:O	2:B:516:ASP:HA	2.19	0.42
1:A:474:LYS:HB3	2:D:322[A]:LEU:HD21	2.01	0.42
1:A:62:CYS:HB3	2:B:94:GLY:HA3	2.02	0.42
2:D:95:CYS:HB3	2:D:99:TYR:CZ	2.55	0.42
2:D:71:GLN:HB2	2:D:72:PRO:HD3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:103:THR:HG22	1:C:106:VAL:HG13	2.02	0.42
1:C:62:CYS:HB3	2:D:94:GLY:HA3	2.02	0.41
1:C:384:ASN:ND2	7:C:637:HOH:O	2.52	0.41
1:A:350:ARG:NH2	1:A:416:ILE:O	2.45	0.41
1:A:76:LYS:O	1:A:108:ALA:HA	2.20	0.41
2:D:242:ARG:HD3	2:D:246:GLU:OE2	2.21	0.41
2:B:453:ARG:HD3	2:D:512[A]:MET:CE	2.51	0.41
1:A:182:ARG:CZ	1:A:184:GLU:OE2	2.69	0.41
2:B:504:ARG:NH1	7:B:710:HOH:O	2.37	0.41
2:D:322[B]:LEU:HD21	2:D:348:ARG:NH2	2.36	0.41
1:A:359:ARG:N	1:A:360:PRO:CD	2.84	0.41
1:C:442:HIS:HB3	3:C:501:HCA:O5	2.20	0.41
2:D:211:LYS:HD2	2:D:211:LYS:HA	1.94	0.40
2:D:499:ASN:O	2:D:503:GLU:HG3	2.21	0.40
1:A:45:CYS:SG	1:A:391:MET:CE	3.10	0.40
1:C:415:ARG:NH1	7:C:639:HOH:O	2.54	0.40

All (3) 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)
7:A:1162:HOH:O	7:B:1356:HOH:O[2_546]	2.10	0.10
7:C:946:HOH:O	7:D:1048:HOH:O[2_555]	2.10	0.10
7:A:1001:HOH:O	7:C:1032:HOH:O[1_556]	2.17	0.03

## 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	475/492 (96%)	455 (96%)	19 (4%)	1 (0%)	49 30
1	C	482/492 (98%)	464 (96%)	17 (4%)	1 (0%)	49 30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	521/523 (100%)	510 (98%)	10 (2%)	1 (0%)	49 30
2	D	527/523 (101%)	513 (97%)	13 (2%)	1 (0%)	49 30
All	All	2005/2030 (99%)	1942 (97%)	59 (3%)	4 (0%)	49 30

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	401/415 (97%)	393 (98%)	8 (2%)	58 40
1	C	405/415 (98%)	392 (97%)	13 (3%)	42 21
2	B	451/455 (99%)	446 (99%)	5 (1%)	76 65
2	D	457/455 (100%)	454 (99%)	3 (1%)	85 79
All	All	1714/1740 (98%)	1685 (98%)	29 (2%)	63 48

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	CYS
1	A	98	ASN
1	A	215	THR
1	A	362	HIS
1	A	401	TYR
1	A	409	PHE
1	A	445	ASP
1	A	475	LEU

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Mol	Chain	Res	Type
2	B	7	LYS
2	B	92	SER
2	B	154	MET
2	B	258	GLU
2	B	512	MET
1	C	35	ASN
1	C	40	THR
1	C	45	CYS
1	C	98	ASN
1	C	106	VAL
1	C	213	ASP
1	C	264	LEU
1	C	362	HIS
1	C	401	TYR
1	C	409	PHE
1	C	445	ASP
1	C	467	LEU
1	C	473	LYS
2	D	38	ASP
2	D	381	LYS
2	D	404	LYS

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

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

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

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	HCA	A	501	-	4,13,13	0.91	0	4,18,18	2.05	2 (50%)
4	ICS	A	502	1	6,30,30	1.93	3 (50%)	-		
5	CLF	B	601	1,2	0,24,24	0.00	-	-		
3	HCA	C	501	-	4,13,13	0.54	0	4,18,18	2.15	2 (50%)
4	ICS	C	502	1	6,30,30	1.88	3 (50%)	-		
5	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	HCA	A	501	-	-	3/7/17/17	-
5	CLF	B	601	1,2	-	-	0/12/10/10
3	HCA	C	501	-	-	1/7/17/17	-
5	CLF	D	601	1,2	-	-	0/12/10/10

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	502	ICS	S5A-FE3	-2.80	2.18	2.24
4	A	502	ICS	S2B-FE6	-2.75	2.18	2.24
4	A	502	ICS	S5A-FE7	-2.48	2.19	2.24
4	A	502	ICS	S5A-FE3	-2.46	2.19	2.24
4	C	502	ICS	S2B-FE6	-2.43	2.19	2.24
4	C	502	ICS	S5A-FE7	-2.43	2.19	2.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	501	HCA	C4-C5-C6	3.37	116.49	111.39
3	A	501	HCA	C4-C5-C6	3.24	116.29	111.39

*Continued on next page...*



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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	HCA	C3-C2-C1	-2.22	111.43	114.98
3	C	501	HCA	C3-C2-C1	-2.17	111.50	114.98

There are no chirality outliers.

All (4) torsion outliers are listed below:

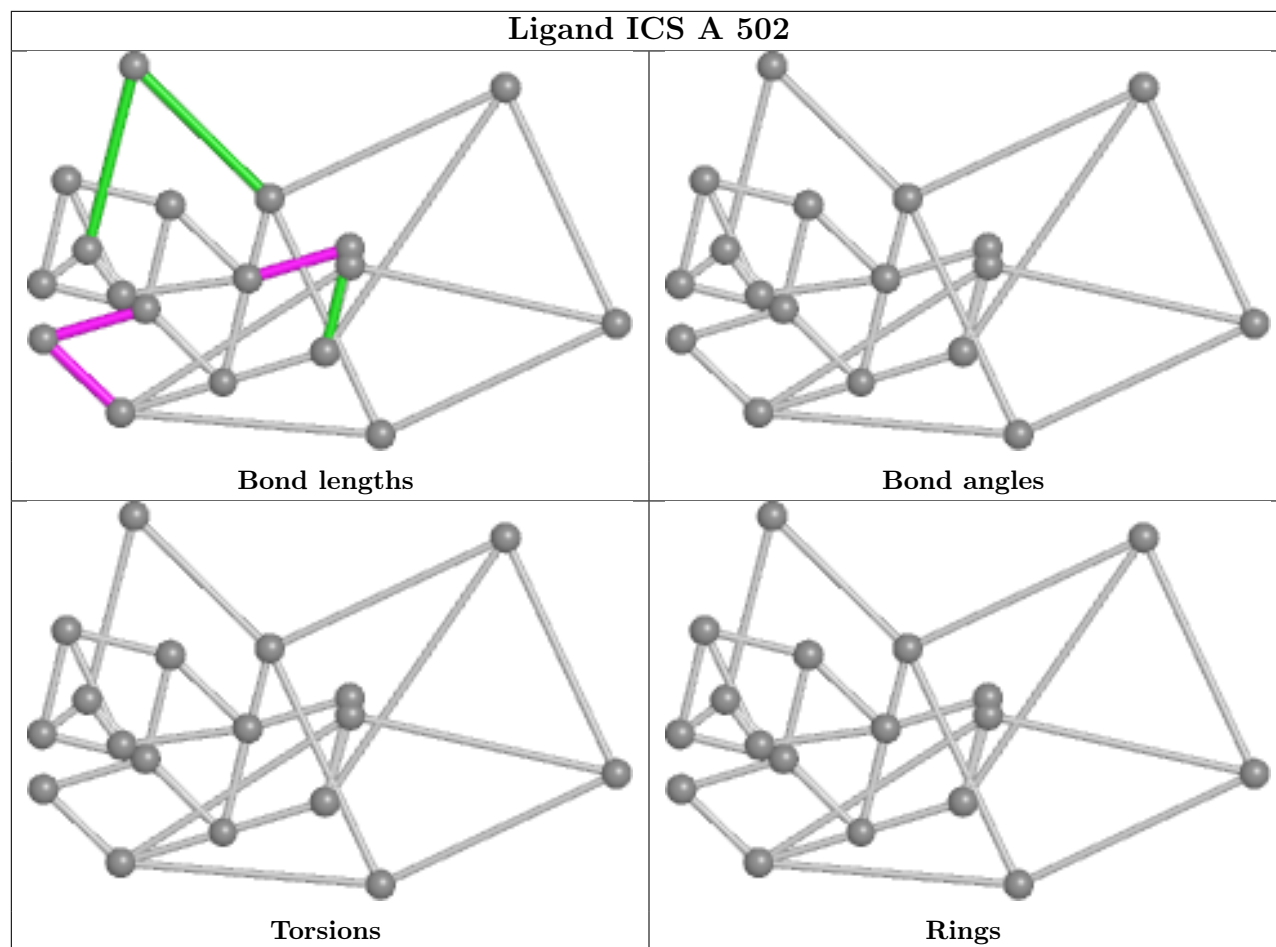
Mol	Chain	Res	Type	Atoms
3	C	501	HCA	C2-C3-C4-C5
3	A	501	HCA	C2-C3-C4-C5
3	A	501	HCA	O7-C3-C4-C5
3	A	501	HCA	C7-C3-C4-C5

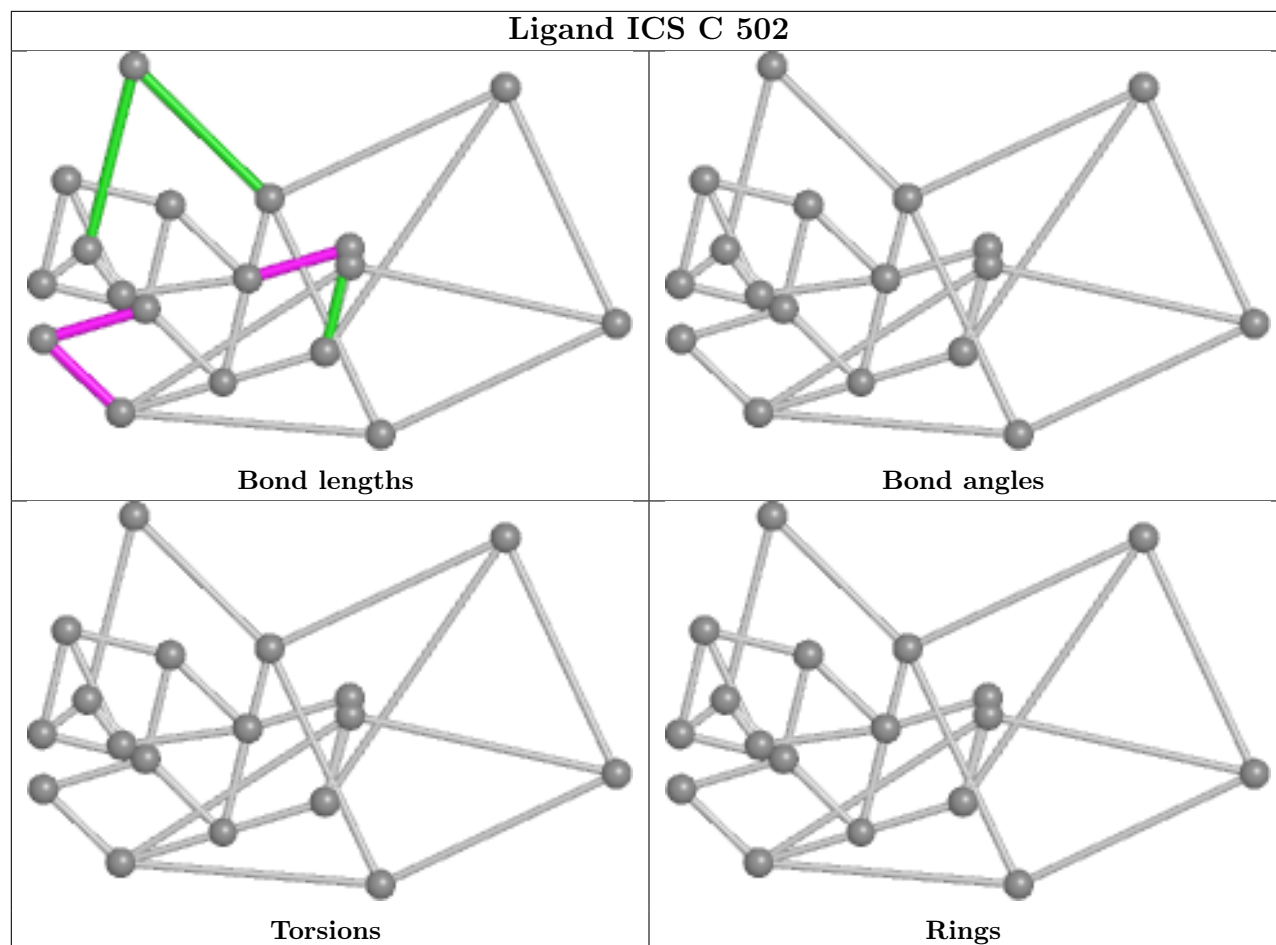
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	HCA	2	0
3	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.





## 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	476/492 (96%)	-0.42	8 (1%) 70 75	10, 17, 35, 53	0
1	C	478/492 (97%)	-0.36	5 (1%) 82 85	11, 17, 34, 48	0
2	B	522/523 (99%)	-0.52	2 (0%) 92 93	9, 14, 24, 42	0
2	D	522/523 (99%)	-0.52	1 (0%) 94 95	9, 15, 24, 39	0
All	All	1998/2030 (98%)	-0.46	16 (0%) 86 88	9, 16, 29, 53	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	214	THR	6.0
2	B	123	ALA	3.6
1	A	215	THR	3.4
2	D	124	VAL	3.1
2	B	214	ASP	3.1
1	A	208	GLY	3.0
1	C	37	PRO	3.0
1	C	481	ALA	2.9
1	C	480	GLU	2.8
1	A	38	ALA	2.7
1	C	40	THR	2.7
1	A	212	GLU	2.4
1	A	11	SER	2.4
1	A	211	ASP	2.3
1	C	215	THR	2.1
1	A	216	PHE	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](#)

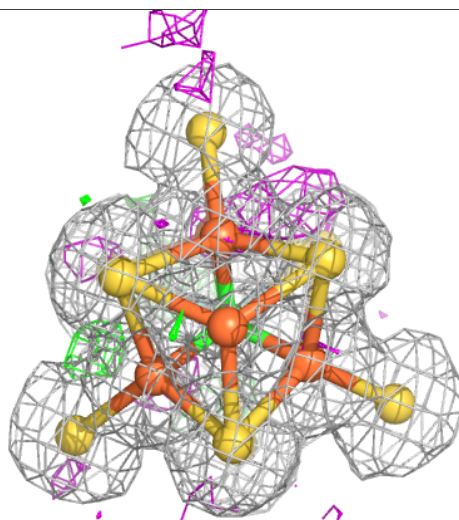
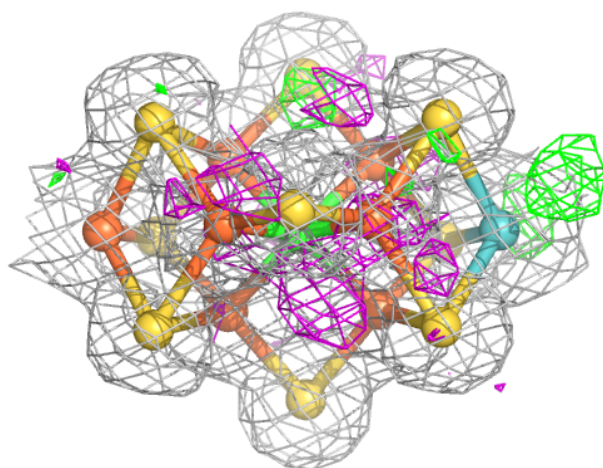
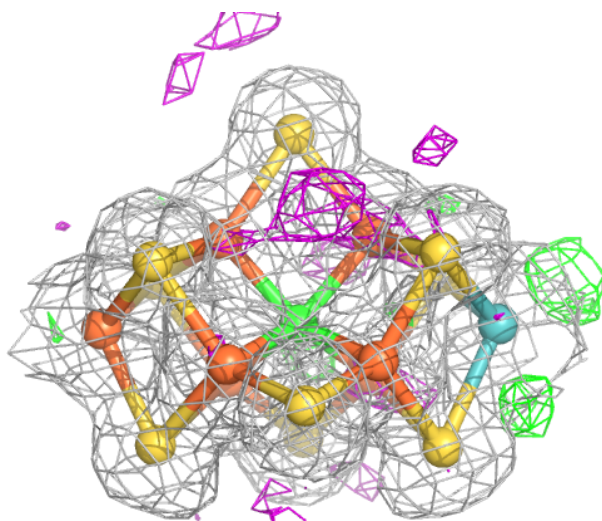
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	HCA	A	501	14/14	0.97	0.07	10,12,14,14	0
3	HCA	C	501	14/14	0.98	0.10	10,12,15,15	0
5	CLF	D	601	15/15	0.99	0.05	11,12,13,14	0
5	CLF	B	601	15/15	0.99	0.04	10,11,12,12	0
6	FE	D	602	1/1	1.00	0.04	12,12,12,12	1
4	ICS	A	502	18/18	1.00	0.04	8,10,13,13	0
6	FE	B	602	1/1	1.00	0.05	14,14,14,14	1
4	ICS	C	502	18/18	1.00	0.05	9,11,13,13	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.

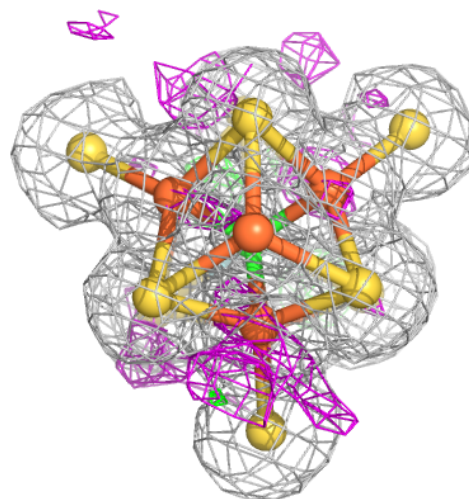
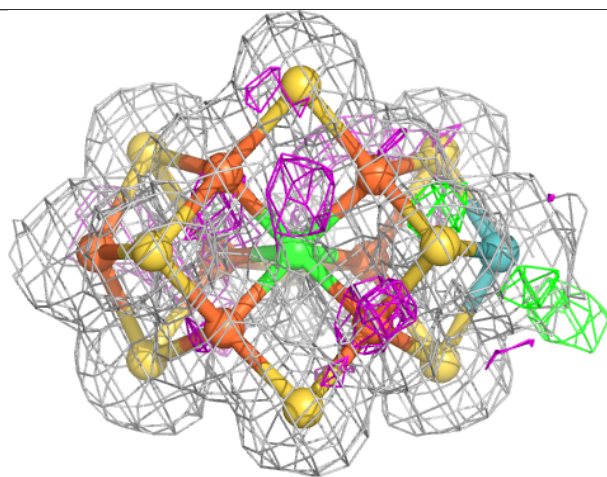
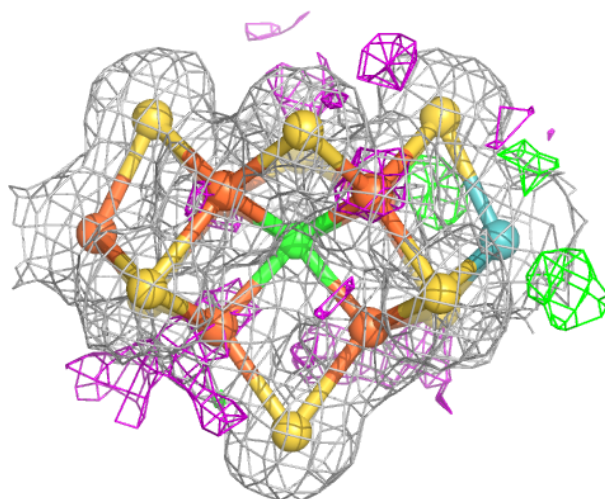
**Electron density around ICS A 502:**

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



**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)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.