



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 3, 2021 – 08:18 am BST

PDB ID : 7AIZ
Title : Vanadium nitrogenase VFe protein, high CO state
Authors : Rohde, M.; Einsle, O.
Deposited on : 2020-09-28
Resolution : 1.05 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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 : 2.19
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) : 2.19

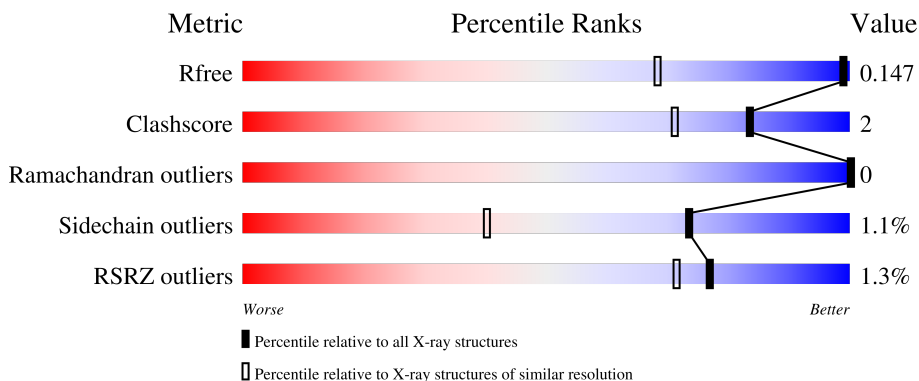
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.05 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.



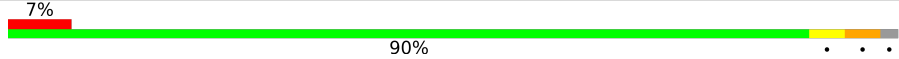
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1202 (1.10-1.02)
Clashscore	141614	1252 (1.10-1.02)
Ramachandran outliers	138981	1204 (1.10-1.02)
Sidechain outliers	138945	1202 (1.10-1.02)
RSRZ outliers	127900	1178 (1.10-1.02)

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 ≥ 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	474	 92% 6% .
1	D	474	 91% 8% .
2	B	475	 92% 5% ..
2	E	475	 91% 6% ..
3	C	113	 93% 5% ..

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Mol	Chain	Length	Quality of chain
3	F	113	 <p>7% 90%</p>

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 19918 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 vanadium-iron protein alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	473	3871	2466	664	713	28	0	11	0
1	D	473	3865	2464	658	715	28	0	11	0

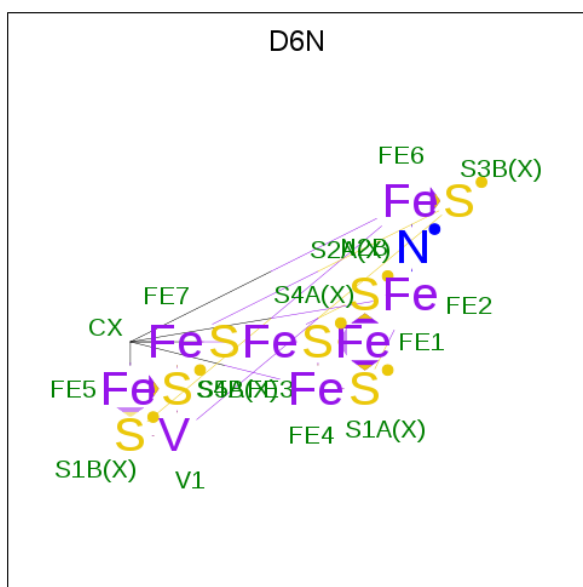
- Molecule 2 is a protein called Nitrogenase vanadium-iron protein beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	464	3721	2367	637	694	23	0	12	0
2	E	465	3756	2388	645	700	23	0	16	0

- Molecule 3 is a protein called Nitrogenase vanadium-iron protein delta chain.

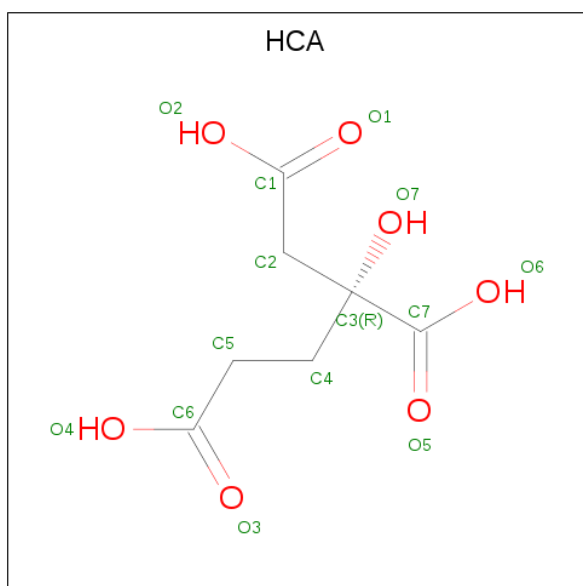
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	112	956	599	173	182	2	0	2	0
3	F	111	967	605	177	183	2	0	4	0

- Molecule 4 is FeV (three-letter code: D6N) (formula: CFe₇NS₇V) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	A	1	Total	C	Fe	S	V	0	0
			16	1	7	7	1		
4	D	1	Total	C	Fe	S	V	0	0
			16	1	7	7	1		

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



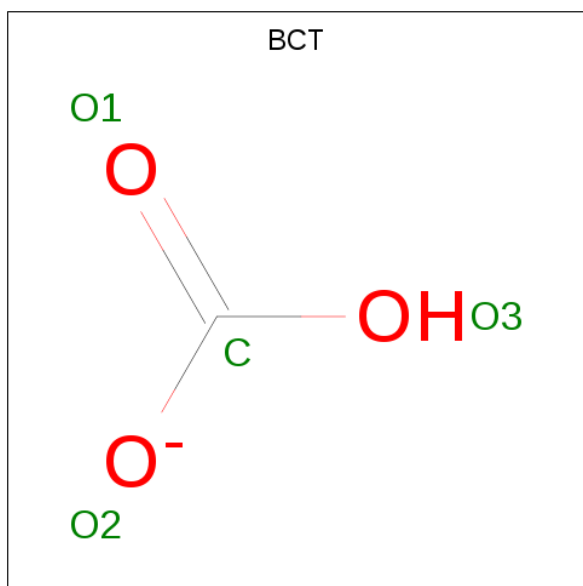
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
5	A	1	Total	C	O	0	0
			14	7	7		

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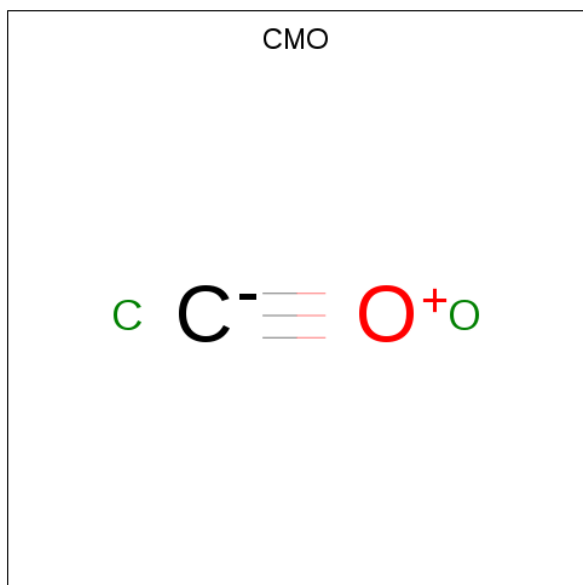
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	D	1	14	7	7	0	0

- Molecule 6 is BICARBONATE ION (three-letter code: BCT) (formula: CHO_3).



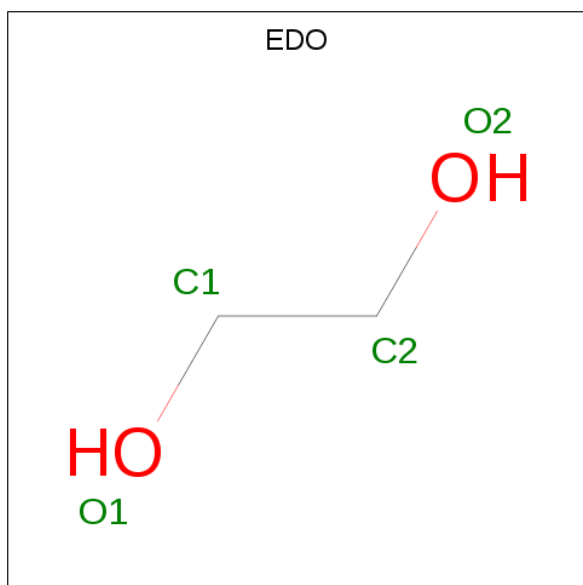
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	4	1	3	0	0
6	D	1	4	1	3	0	0

- Molecule 7 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO) (labeled as "Ligand of Interest" by depositor).



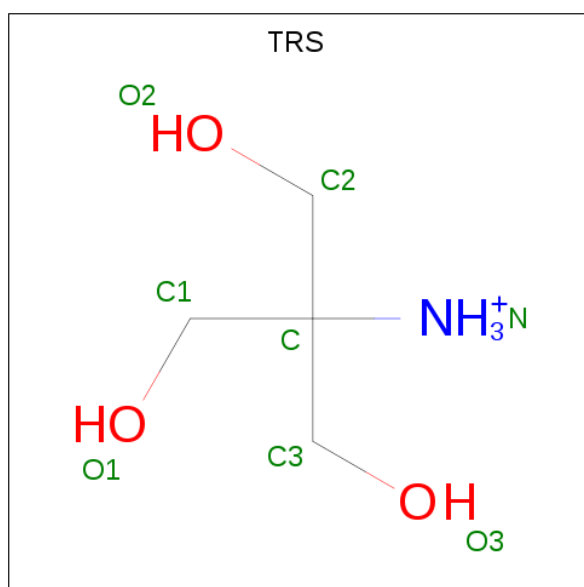
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			2	1	1		
7	A	1	Total	C	O	0	0
			2	1	1		
7	D	1	Total	C	O	0	0
			2	1	1		
7	D	1	Total	C	O	0	0
			2	1	1		

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\text{C}_2\text{H}_6\text{O}_2$).



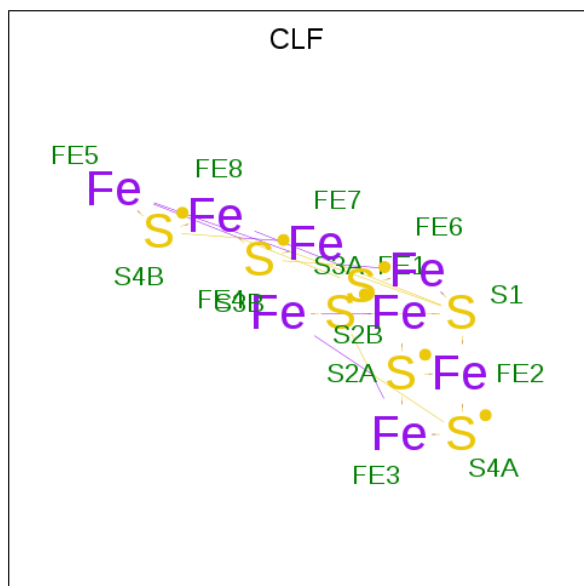
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 4 2 2	0	0
8	A	1	Total C O 4 2 2	0	0
8	B	1	Total C O 4 2 2	0	0
8	B	1	Total C O 4 2 2	0	0
8	B	1	Total C O 4 2 2	0	0
8	C	1	Total C O 4 2 2	0	0
8	E	1	Total C O 4 2 2	0	0
8	E	1	Total C O 4 2 2	0	0
8	E	1	Total C O 4 2 2	0	0
8	E	1	Total C O 4 2 2	0	0
8	F	1	Total C O 4 2 2	0	0

- Molecule 9 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C N O 8 4 1 3	0	0
9	A	1	Total C N O 8 4 1 3	0	0
9	D	1	Total C N O 8 4 1 3	0	0

- Molecule 10 is FE(8)-S(7) CLUSTER (three-letter code: CLF) (formula: Fe₈S₇).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	B	1	Total Fe S 16 9 7	0	1
10	E	1	Total Fe S 16 9 7	0	1

- Molecule 11 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	B	2	Total Mg 2 2	0	0
11	C	1	Total Mg 1 1	0	0
11	F	1	Total Mg 1 1	0	0

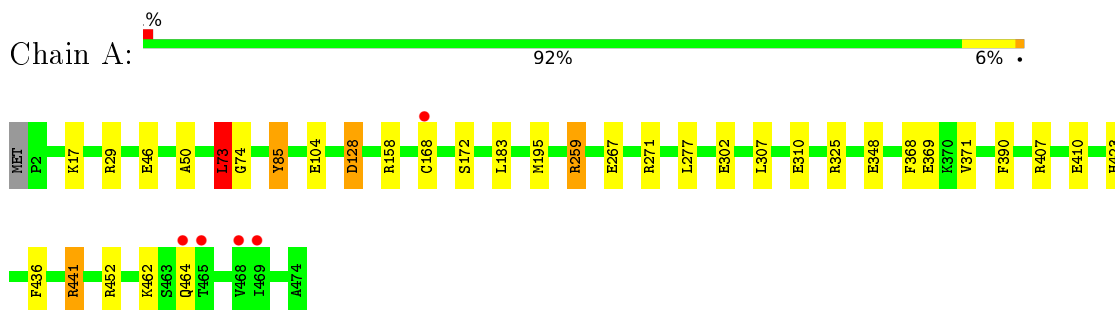
- Molecule 12 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	529	Total O 547 547	0	17
12	B	529	Total O 549 549	0	18
12	C	169	Total O 172 172	0	4
12	D	550	Total O 570 570	0	18
12	E	585	Total O 623 623	0	35
12	F	137	Total O 141 141	0	4

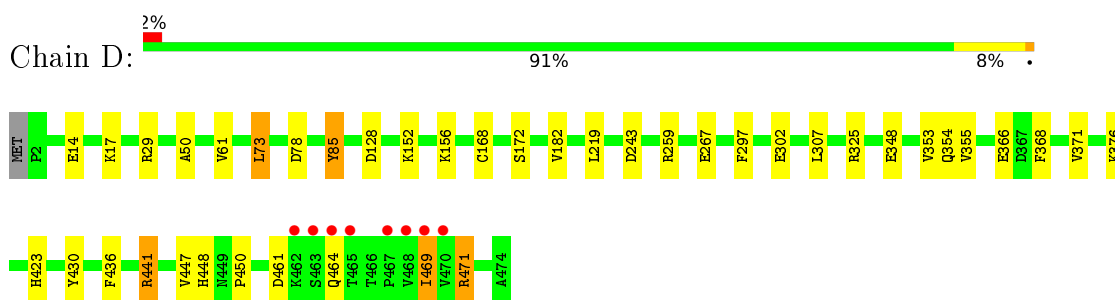
3 Residue-property plots [i](#)

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 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.

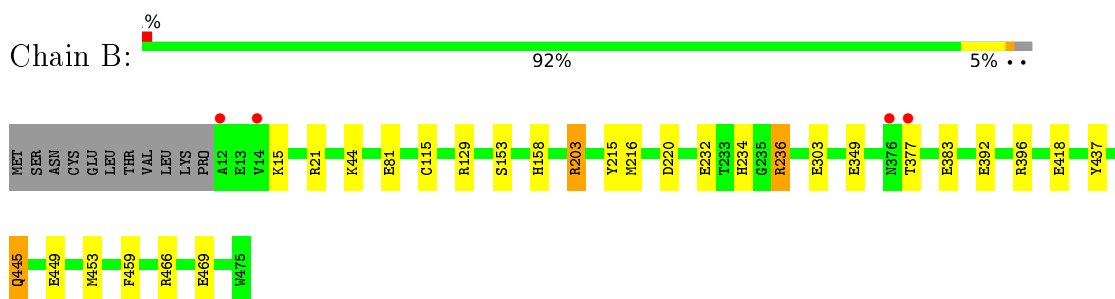
- Molecule 1: Nitrogenase vanadium-iron protein alpha chain



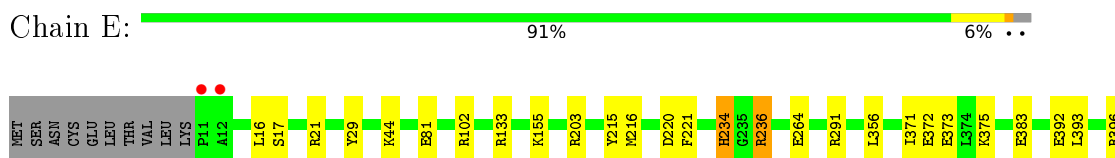
- Molecule 1: Nitrogenase vanadium-iron protein alpha chain



- Molecule 2: Nitrogenase vanadium-iron protein beta chain



- Molecule 2: Nitrogenase vanadium-iron protein beta chain





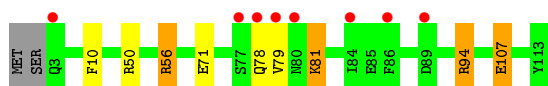
- Molecule 3: Nitrogenase vanadium-iron protein delta chain

Chain C: 93% 5% ..



- Molecule 3: Nitrogenase vanadium-iron protein delta chain

Chain F: 7% 90% . . .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	75.52Å 80.04Å 107.21Å 84.00° 72.48° 75.03°	Depositor
Resolution (Å)	48.39 – 1.05 48.34 – 1.05	Depositor EDS
% Data completeness (in resolution range)	93.2 (48.39-1.05) 93.2 (48.34-1.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 1.05Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.124 , 0.146 0.126 , 0.147	Depositor DCC
R_{free} test set	49972 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	10.9	Xtrriage
Anisotropy	0.389	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	19918	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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: CMO, MG, EDO, D6N, HCA, TRS, BCT, CLF

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	0.88	12/3970 (0.3%)	0.97	11/5363 (0.2%)
1	D	0.86	6/3972 (0.2%)	0.96	9/5366 (0.2%)
2	B	0.86	7/3818 (0.2%)	0.99	13/5165 (0.3%)
2	E	0.93	9/3848 (0.2%)	0.99	15/5206 (0.3%)
3	C	1.01	5/976 (0.5%)	0.98	2/1319 (0.2%)
3	F	0.93	2/987 (0.2%)	0.99	2/1333 (0.2%)
All	All	0.89	41/17571 (0.2%)	0.98	52/23752 (0.2%)

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	D	0	1
2	B	0	1
2	E	0	3
3	F	0	1
All	All	0	7

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	373	GLU	CD-OE1	-11.21	1.13	1.25
1	A	172	SER	CB-OG	-10.25	1.28	1.42
1	A	128	ASP	CG-OD1	10.05	1.48	1.25
2	E	392	GLU	CD-OE1	-9.58	1.15	1.25
1	D	267	GLU	CD-OE2	-9.32	1.15	1.25

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	236	ARG	NE-CZ-NH2	-12.61	113.99	120.30
2	B	236	ARG	NE-CZ-NH2	-12.56	114.02	120.30
2	B	466	ARG	NE-CZ-NH2	-11.10	114.75	120.30
1	A	271	ARG	NE-CZ-NH2	-9.46	115.57	120.30
3	C	41	ARG	NE-CZ-NH2	-9.20	115.70	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	441	ARG	Sidechain
2	B	445	GLN	Sidechain
1	D	441	ARG	Sidechain
2	E	234[A]	HIS	Sidechain
2	E	234[B]	HIS	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	3871	0	3783	14	0
1	D	3865	0	3781	24	0
2	B	3721	0	3706	18	0
2	E	3756	0	3740	14	0
3	C	956	0	915	5	0
3	F	967	0	926	9	0
4	A	16	0	0	0	0
4	D	16	0	0	0	0
5	A	14	0	6	1	0
5	D	14	0	6	1	0
6	A	4	0	0	0	0
6	D	4	0	0	0	0
7	A	4	0	0	0	0
7	D	4	0	0	0	0
8	A	8	0	12	0	0
8	B	12	0	18	0	0
8	C	4	0	6	0	0
8	E	16	0	23	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	F	4	0	6	0	0
9	A	16	0	24	1	0
9	D	8	0	12	1	0
10	B	16	0	0	0	0
10	E	16	0	0	0	0
11	B	2	0	0	0	0
11	C	1	0	0	0	0
11	F	1	0	0	0	0
12	A	547	0	0	2	0
12	B	549	0	0	2	0
12	C	172	0	0	4	0
12	D	570	0	0	6	0
12	E	623	0	0	6	0
12	F	141	0	0	3	0
All	All	19918	0	16964	82	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.

The worst 5 of 82 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:392[B]:GLU:OE2	2:B:396[B]:ARG:NH2	1.68	1.26
2:B:392[B]:GLU:CD	2:B:396[B]:ARG:HH22	1.58	1.07
2:B:392[B]:GLU:HG3	2:B:396[B]:ARG:NH2	1.70	1.06
2:B:392[B]:GLU:CG	2:B:396[B]:ARG:NH2	2.19	1.05
1:D:17:LYS:HG3	12:D:901:HOH:O	1.60	1.01

There are no symmetry-related clashes.

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	482/474 (102%)	465 (96%)	17 (4%)	0	100	100
1	D	483/474 (102%)	469 (97%)	14 (3%)	0	100	100
2	B	475/475 (100%)	467 (98%)	8 (2%)	0	100	100
2	E	479/475 (101%)	470 (98%)	9 (2%)	0	100	100
3	C	112/113 (99%)	107 (96%)	5 (4%)	0	100	100
3	F	113/113 (100%)	111 (98%)	2 (2%)	0	100	100
All	All	2144/2124 (101%)	2089 (97%)	55 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	414/404 (102%)	406 (98%)	8 (2%)	57	19
1	D	415/404 (103%)	408 (98%)	7 (2%)	60	23
2	B	400/398 (100%)	399 (100%)	1 (0%)	92	75
2	E	404/398 (102%)	402 (100%)	2 (0%)	88	66
3	C	103/102 (101%)	103 (100%)	0	100	100
3	F	104/102 (102%)	100 (96%)	4 (4%)	33	4
All	All	1840/1808 (102%)	1818 (99%)	22 (1%)	73	37

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	436	PHE
2	E	418[B]	GLU
2	E	418[A]	GLU
3	F	71	GLU
1	A	259	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	327	GLN
2	B	445	GLN
3	C	46	GLN
2	E	445	GLN
3	F	80	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 32 ligands modelled in this entry, 4 are monoatomic - leaving 28 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	$\# Z > 2$
8	EDO	A	506	-	3,3,3	0.37	0	2,2,2	0.57	0
5	HCA	A	502	4	4,13,13	1.09	0	4,18,18	0.96	0
9	TRS	A	509	-	7,7,7	0.26	0	9,9,9	0.31	0
6	BCT	D	503	4	0,3,3	0.00	-	0,3,3	0.00	-
7	CMO	D	505	-	0,1,1	0.00	-	-		
10	CLF	B	501[A]	2	0,24,24	0.00	-	-		
5	HCA	D	502	4	4,13,13	0.76	0	4,18,18	1.28	0
8	EDO	E	502	-	3,3,3	0.87	0	2,2,2	0.16	0
8	EDO	B	505	-	3,3,3	0.37	0	2,2,2	0.46	0
8	EDO	E	503	-	3,3,3	0.18	0	2,2,2	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	TRS	A	508	-	7,7,7	0.22	0	9,9,9	0.50	0
8	EDO	F	202	-	3,3,3	0.70	0	2,2,2	0.35	0
8	EDO	C	202	-	3,3,3	0.89	0	2,2,2	0.22	0
9	TRS	D	506	-	7,7,7	0.30	0	9,9,9	0.51	0
8	EDO	E	505	-	3,3,3	0.80	0	2,2,2	0.52	0
10	CLF	E	501[B]	2	0,24,24	0.00	-	-		
8	EDO	E	504	-	3,3,3	0.51	0	2,2,2	0.23	0
4	D6N	D	501	5,1,6,7	6,26,28	1.63	1 (16%)	-		
8	EDO	B	506	-	3,3,3	0.72	0	2,2,2	0.23	0
7	CMO	A	505	-	0,1,1	0.00	-	-		
8	EDO	A	507	-	3,3,3	0.41	0	2,2,2	0.53	0
6	BCT	A	503	4	0,3,3	0.00	-	0,3,3	0.00	-
7	CMO	A	504	4	0,1,1	0.00	-	-		
10	CLF	B	501[B]	2	0,24,24	0.00	-	-		
8	EDO	B	504	-	3,3,3	0.70	0	2,2,2	0.37	0
4	D6N	A	501	5,1,6,7	6,26,28	1.54	1 (16%)	-		
10	CLF	E	501[A]	2	0,24,24	0.00	-	-		
7	CMO	D	504	4	0,1,1	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
8	EDO	A	506	-	-	0/1/1/1	-
5	HCA	A	502	4	-	0/7/17/17	-
9	TRS	A	509	-	-	2/9/9/9	-
10	CLF	B	501[A]	2	-	-	0/12/10/10
5	HCA	D	502	4	-	0/7/17/17	-
8	EDO	E	502	-	-	0/1/1/1	-
8	EDO	B	505	-	-	0/1/1/1	-
8	EDO	E	503	-	-	0/1/1/1	-
9	TRS	A	508	-	-	0/9/9/9	-
8	EDO	F	202	-	-	0/1/1/1	-
8	EDO	C	202	-	-	0/1/1/1	-
9	TRS	D	506	-	-	0/9/9/9	-
8	EDO	E	505	-	-	0/1/1/1	-
10	CLF	E	501[B]	2	-	-	0/12/10/10
8	EDO	E	504	-	-	0/1/1/1	-
8	EDO	B	506	-	-	0/1/1/1	-
8	EDO	A	507	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	CLF	B	501[B]	2	-	-	0/12/10/10
8	EDO	B	504	-	-	0/1/1/1	-
10	CLF	E	501[A]	2	-	-	0/12/10/10

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	501	D6N	S4B-FE7	-2.42	2.23	2.31
4	A	501	D6N	S4B-FE7	-2.16	2.24	2.31

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

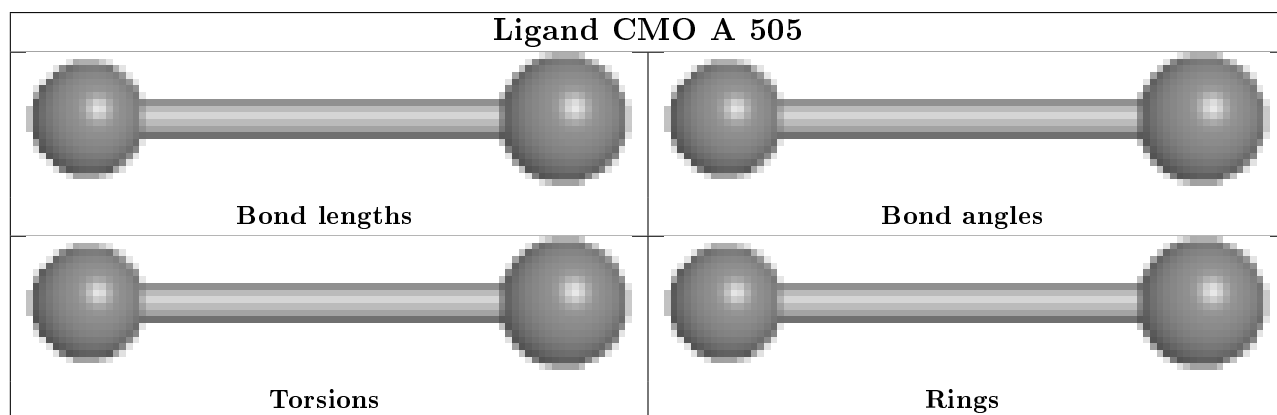
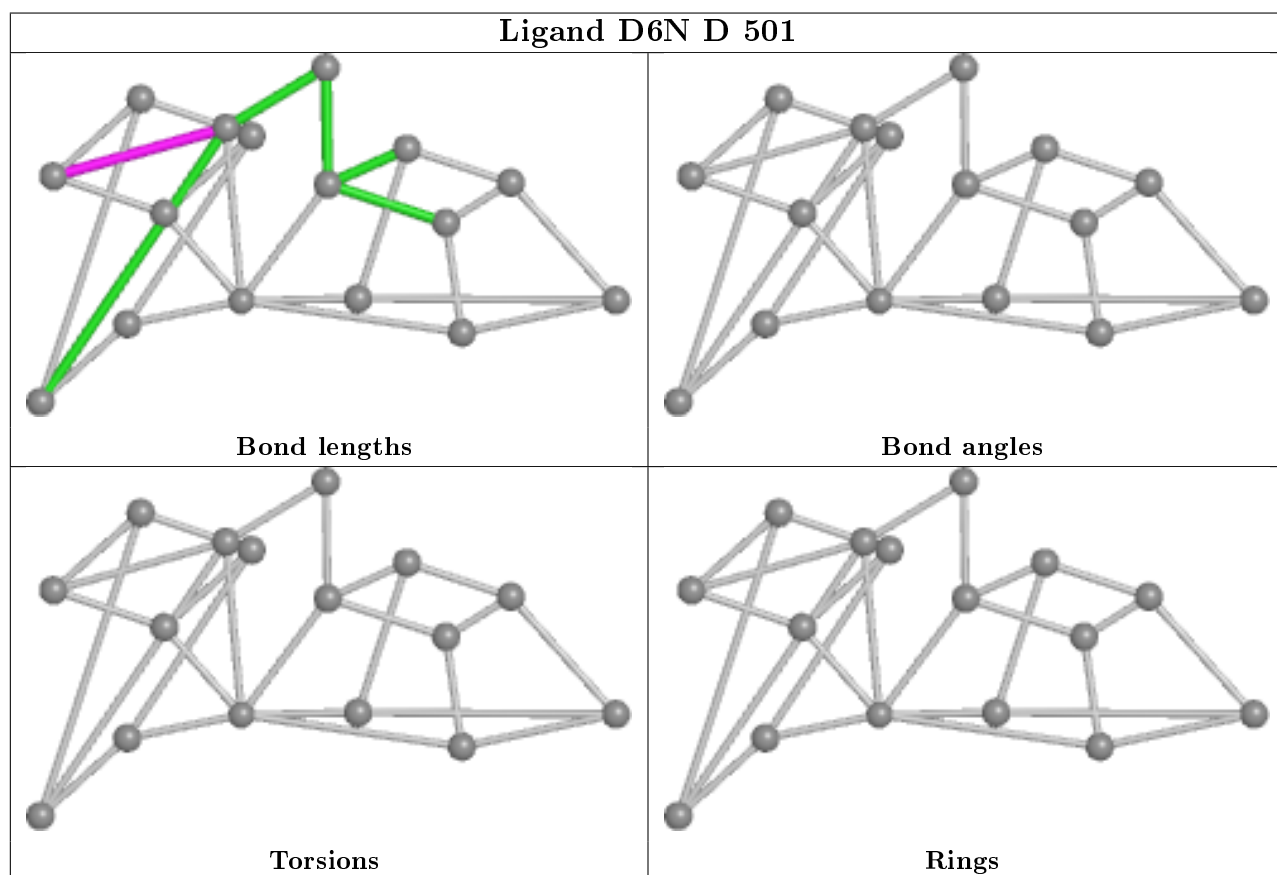
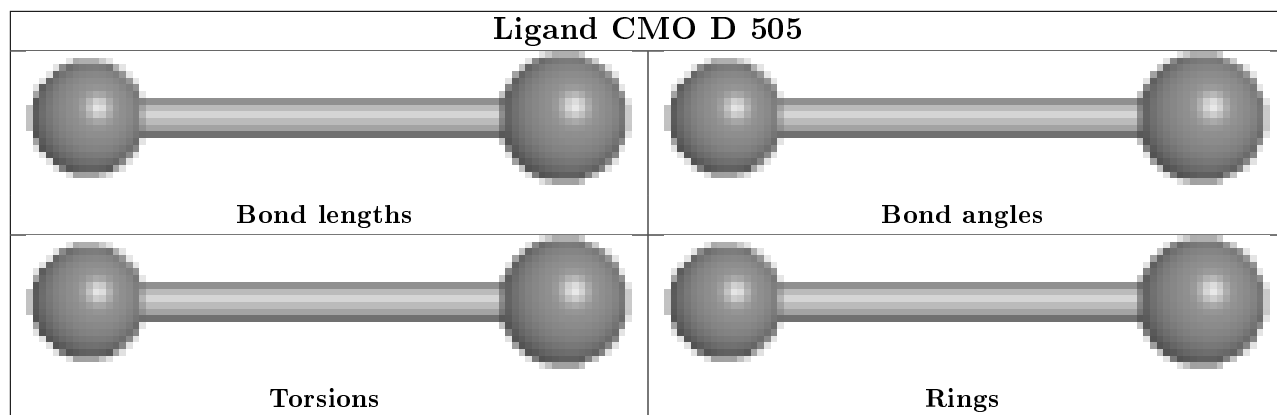
Mol	Chain	Res	Type	Atoms
9	A	509	TRS	N-C-C3-O3
9	A	509	TRS	C2-C-C3-O3

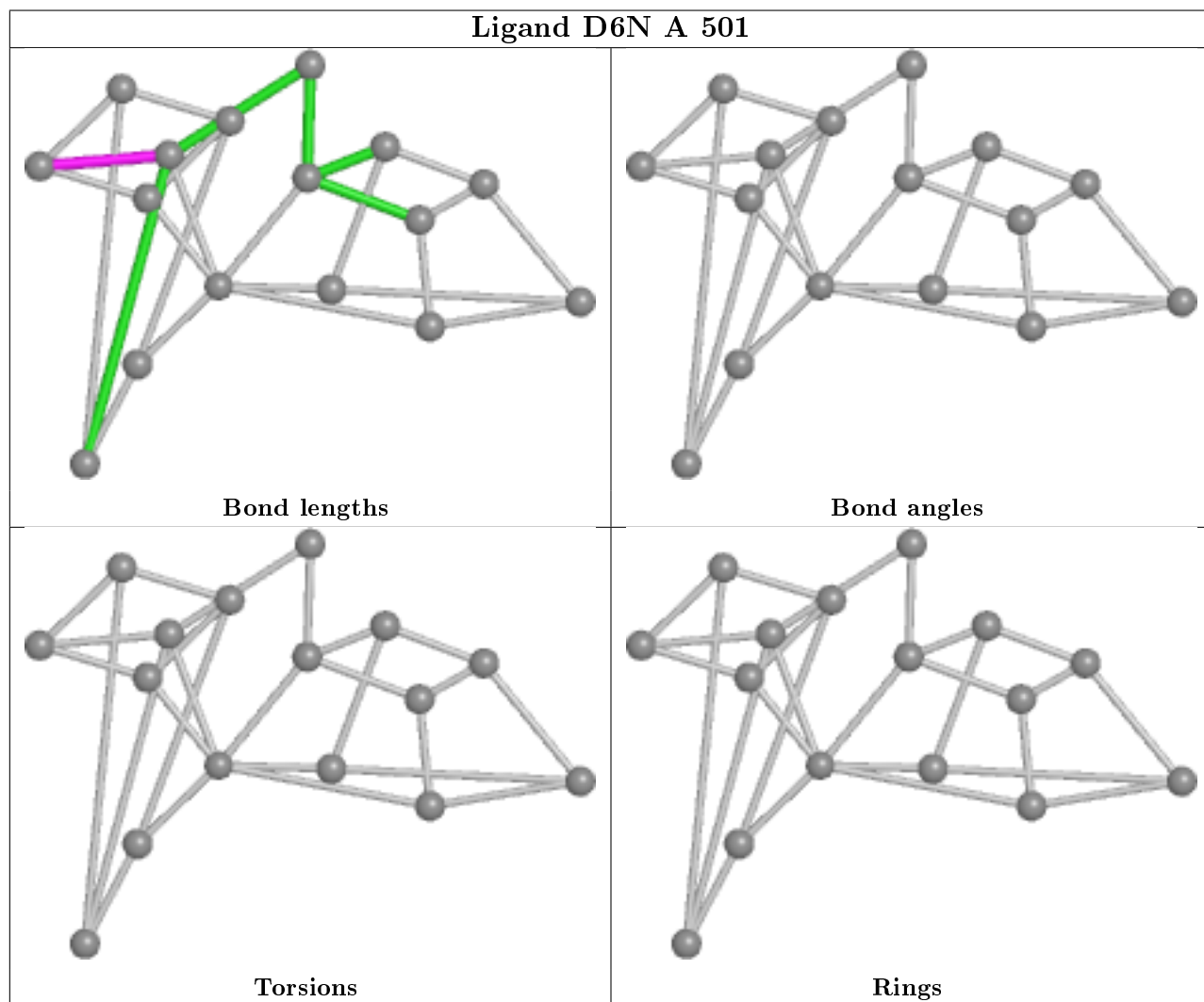
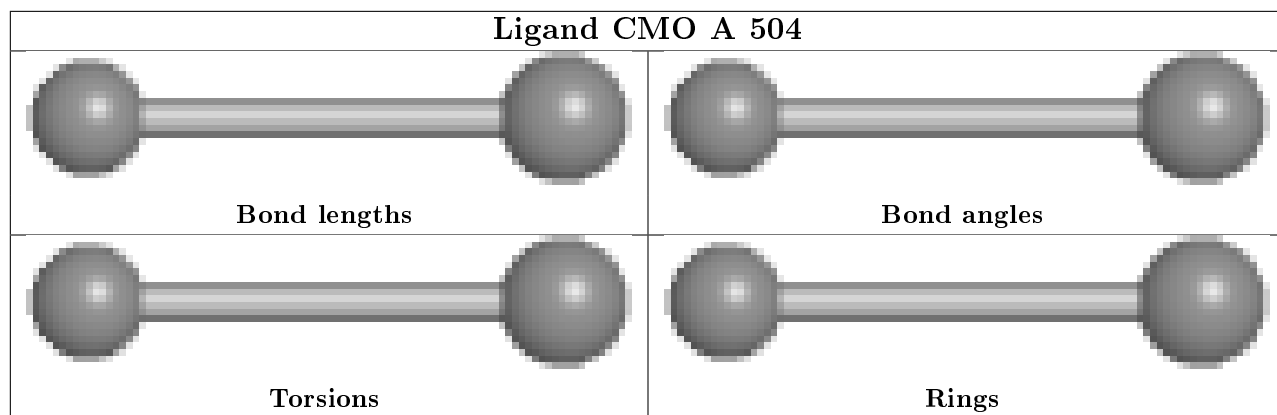
There are no ring outliers.

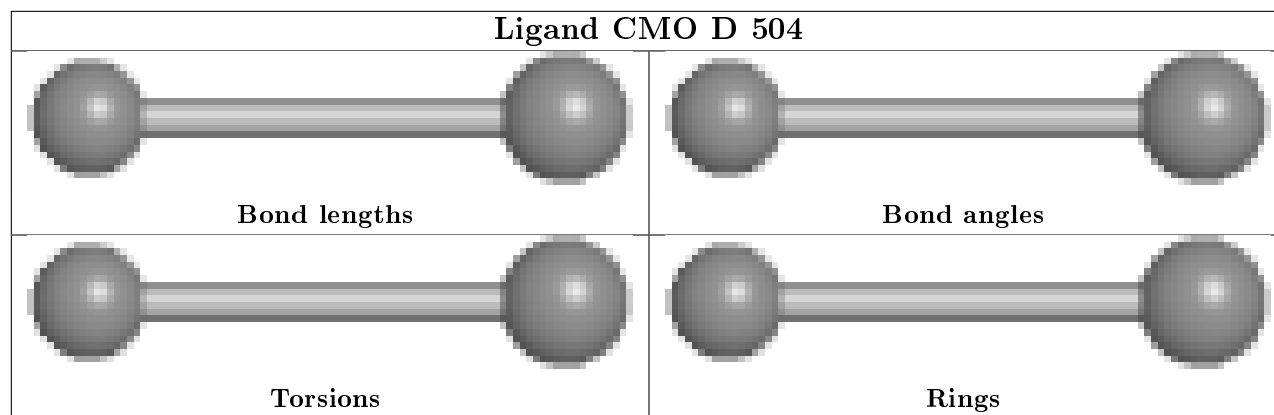
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	502	HCA	1	0
9	A	509	TRS	1	0
5	D	502	HCA	1	0
9	D	506	TRS	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, 95th 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 ²)	Q < 0.9
1	A	473/474 (99%)	-0.51	5 (1%) 80 75	9, 13, 23, 41	0
1	D	473/474 (99%)	-0.47	8 (1%) 70 63	8, 12, 24, 41	0
2	B	464/475 (97%)	-0.47	4 (0%) 84 80	9, 13, 24, 66	0
2	E	465/475 (97%)	-0.45	2 (0%) 92 89	8, 11, 22, 39	0
3	C	112/113 (99%)	-0.32	0 100 100	12, 16, 26, 38	0
3	F	111/113 (98%)	0.05	8 (7%) 15 16	11, 18, 40, 54	0
All	All	2098/2124 (98%)	-0.44	27 (1%) 77 71	8, 13, 25, 66	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	168[A]	CYS	4.7
3	F	79	VAL	4.6
3	F	84	ILE	4.0
3	F	80	ASN	3.9
1	D	468	VAL	3.9

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](#)

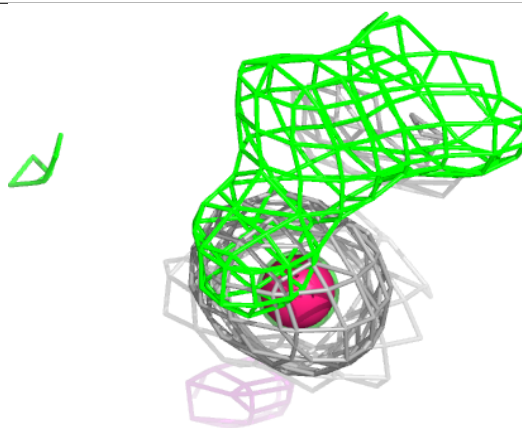
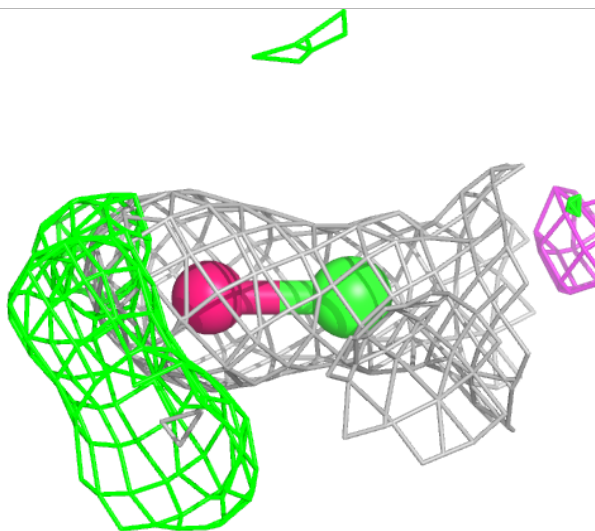
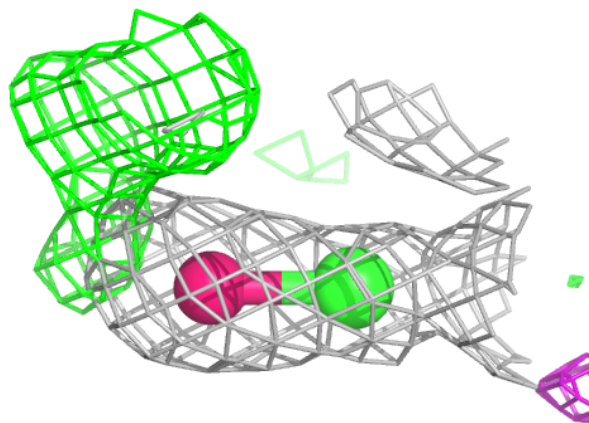
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	EDO	E	505	4/4	0.79	0.23	22,25,27,28	0
8	EDO	C	202	4/4	0.85	0.20	13,13,14,14	4
9	TRS	A	509	8/8	0.88	0.25	29,38,43,47	0
9	TRS	D	506	8/8	0.88	0.20	25,30,33,38	0
8	EDO	F	202	4/4	0.89	0.10	17,18,18,20	4
8	EDO	A	506	4/4	0.92	0.20	17,18,19,22	4
8	EDO	A	507	4/4	0.94	0.10	12,15,17,18	4
9	TRS	A	508	8/8	0.95	0.07	18,22,26,27	0
8	EDO	B	505	4/4	0.95	0.08	16,21,23,23	0
7	CMO	A	505	2/2	0.95	0.14	11,11,11,12	2
8	EDO	B	504	4/4	0.96	0.11	16,18,18,18	0
8	EDO	B	506	4/4	0.96	0.09	21,22,23,26	0
8	EDO	E	503	4/4	0.97	0.09	14,15,15,16	0
8	EDO	E	502	4/4	0.97	0.06	17,18,18,20	0
8	EDO	E	504	4/4	0.98	0.05	13,16,17,18	4
7	CMO	A	504	2/2	0.98	0.07	9,9,9,20	0
7	CMO	D	504	2/2	0.98	0.07	7,7,7,14	0
7	CMO	D	505	2/2	0.99	0.05	8,8,8,11	2
5	HCA	D	502	14/14	0.99	0.07	7,8,12,13	0
5	HCA	A	502	14/14	0.99	0.06	8,9,12,14	0
6	BCT	A	503	4/4	1.00	0.05	9,9,9,10	0
6	BCT	D	503	4/4	1.00	0.08	8,8,8,9	0
4	D6N	A	501	16/17	1.00	0.04	8,9,10,10	0
4	D6N	D	501	16/17	1.00	0.04	7,8,9,9	0
10	CLF	B	501[A]	15/15	1.00	0.03	8,9,10,10	1
10	CLF	B	501[B]	15/15	1.00	0.03	9,10,10,14	1
10	CLF	E	501[A]	15/15	1.00	0.04	7,8,8,8	1
10	CLF	E	501[B]	15/15	1.00	0.04	7,8,8,8	1
11	MG	B	502	1/1	1.00	0.03	10,10,10,10	0
11	MG	B	503	1/1	1.00	0.03	9,9,9,9	0
11	MG	C	201	1/1	1.00	0.05	15,15,15,15	0
11	MG	F	201	1/1	1.00	0.09	16,16,16,16	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.

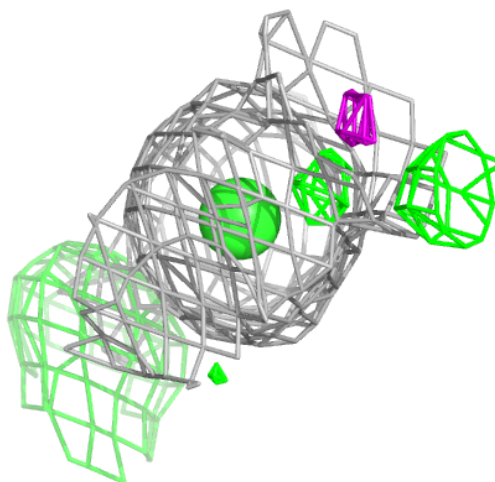
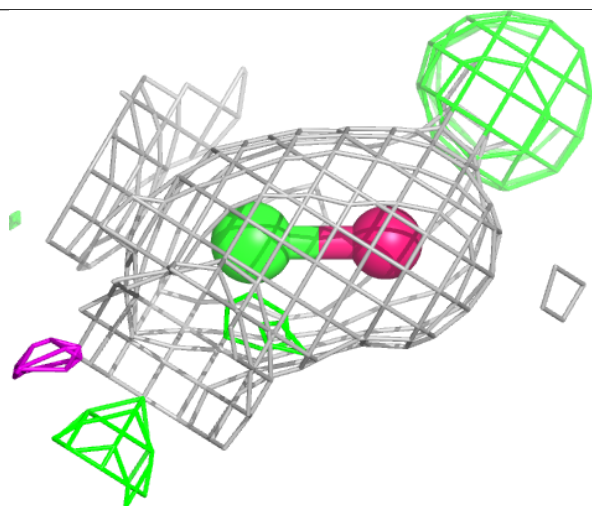
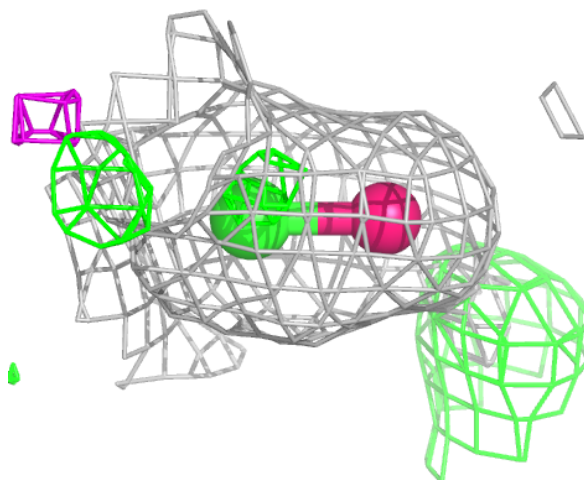
Electron density around CMO A 505:

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



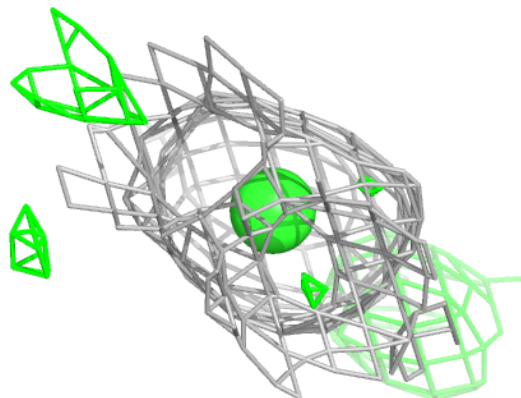
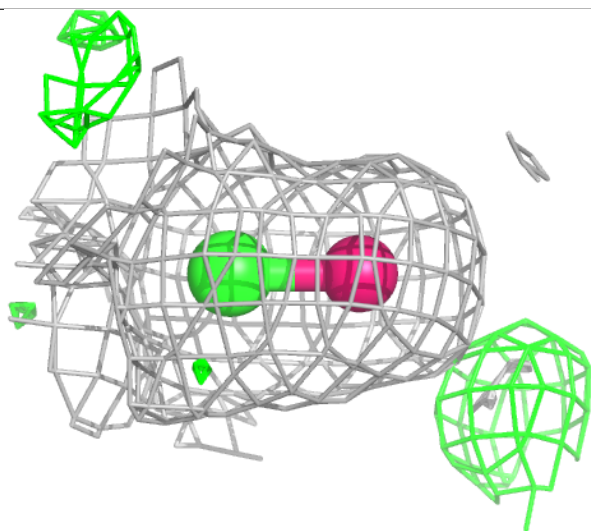
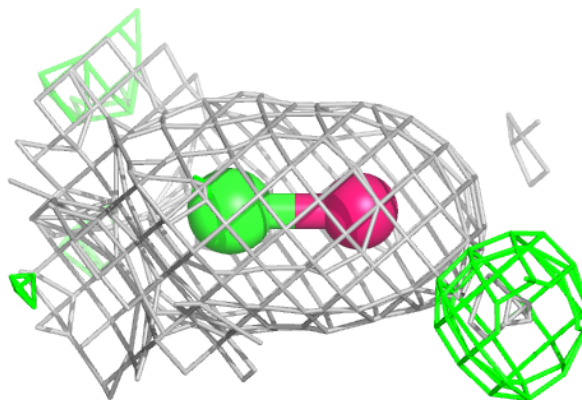
Electron density around CMO A 504:

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



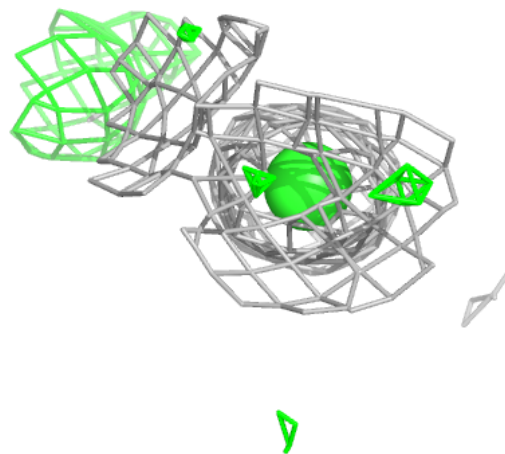
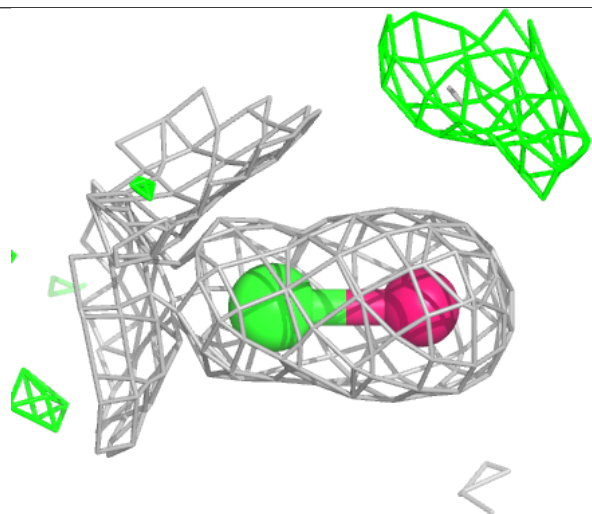
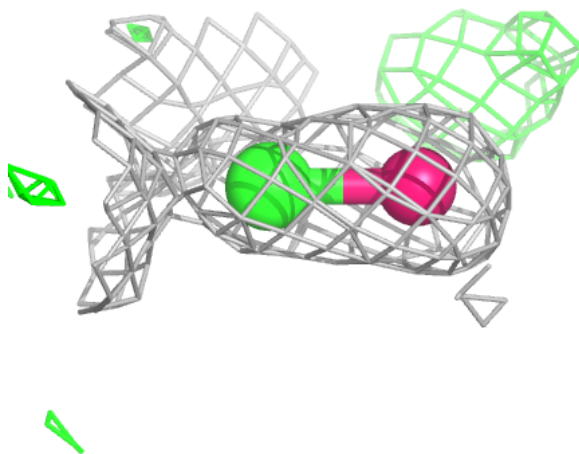
Electron density around CMO D 504:

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



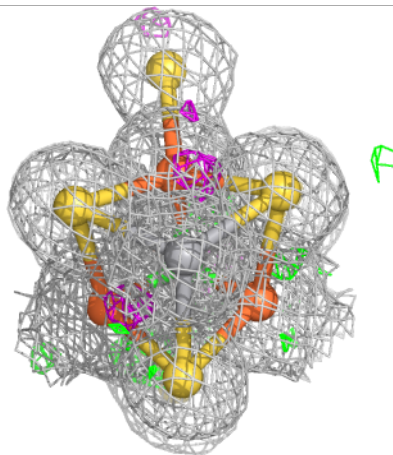
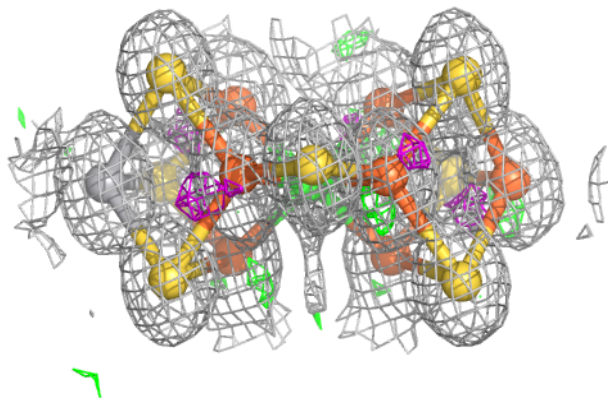
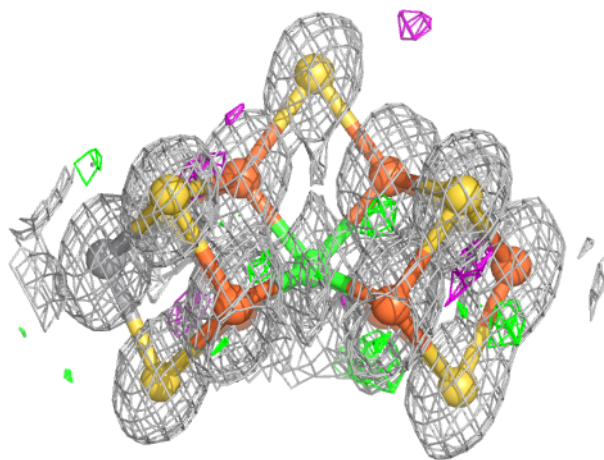
Electron density around CMO D 505:

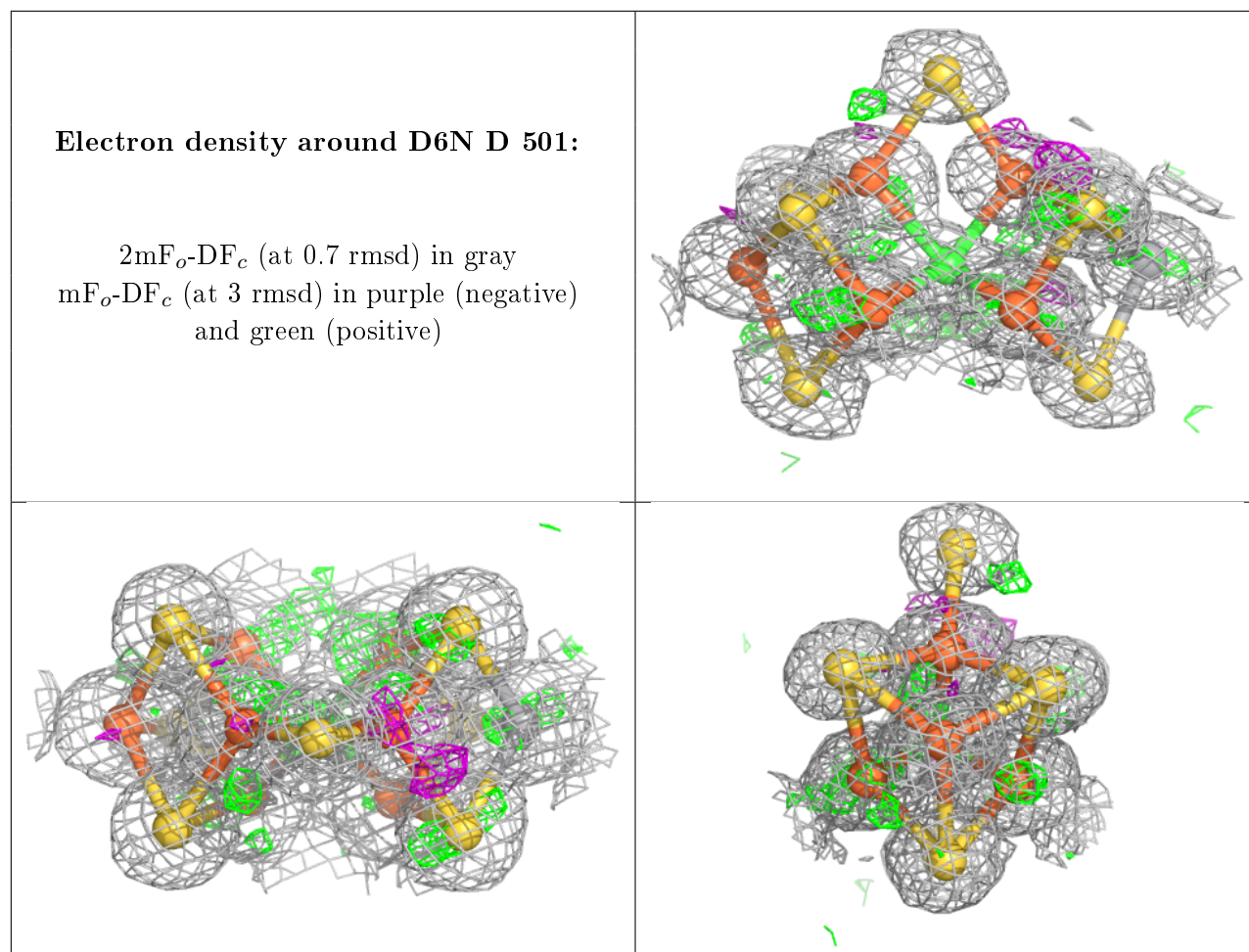
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around D6N A 501:

$2mF_o-DF_c$ (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.