



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 11:14 PM EDT

PDB ID : 6WNC
Title : Structure of the Rieske non-heme iron oxygenase GxtA
Authors : Bridwell-Rabb, J.; Liu, J.
Deposited on : 2020-04-22
Resolution : 2.20 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

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>.

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 : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

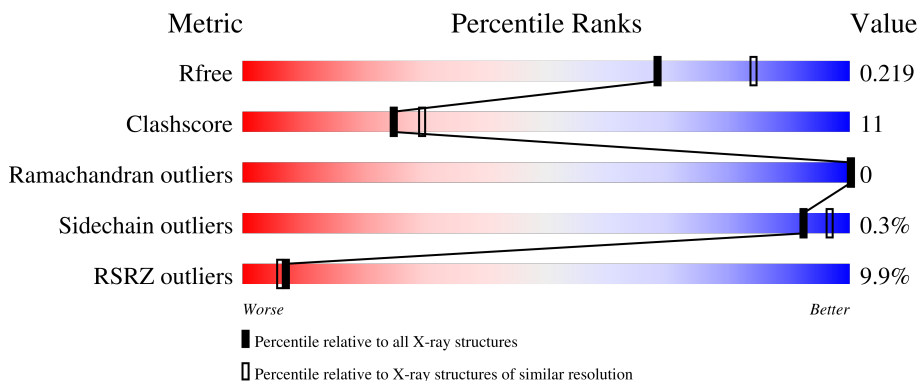
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	334	 10% 78% 14% • 7%
1	B	334	 9% 75% 21% • •
1	C	334	 10% 80% 17% • •

2 Entry composition [i](#)

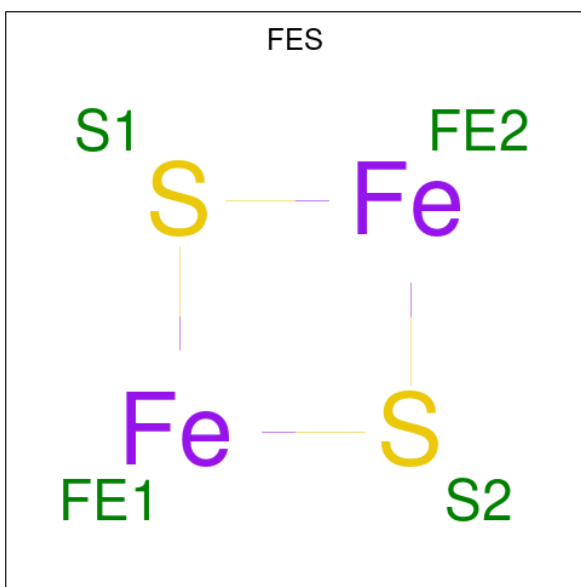
There are 5 unique types of molecules in this entry. The entry contains 8131 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 SxtDIOX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	311	Total 2504	C 1593	N 429	O 463	S 19	0	1	0
1	B	321	Total 2605	C 1651	N 448	O 486	S 20	0	4	0
1	C	325	Total 2638	C 1671	N 455	O 492	S 20	0	4	0

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
2	A	1	Total 4	Fe 2	S 2	0	0
2	B	1	Total 4	Fe 2	S 2	0	0
2	C	1	Total 4	Fe 2	S 2	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



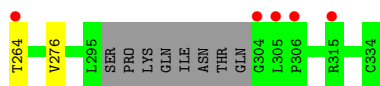
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0

- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Fe 1 1	0	0
4	B	1	Total Fe 1 1	0	0
4	C	1	Total Fe 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	120	Total O 120 120	0	0
5	B	112	Total O 112 112	0	0
5	C	125	Total O 125 125	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.73Å 96.93Å 80.81Å 90.00° 106.97° 90.00°	Depositor
Resolution (Å)	38.65 – 2.20 38.65 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.5 (38.65-2.20) 96.5 (38.65-2.20)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.20Å)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.194 , 0.219 0.194 , 0.219	Depositor DCC
R_{free} test set	2701 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	36.9	Xtrriage
Anisotropy	0.377	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 53.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8131	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: FE, GOL, FES

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	0.55	0/2571	0.73	1/3507 (0.0%)
1	B	0.58	1/2677 (0.0%)	0.81	1/3655 (0.0%)
1	C	0.55	0/2711	0.78	2/3700 (0.1%)
All	All	0.56	1/7959 (0.0%)	0.77	4/10862 (0.0%)

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	B	0	3
1	C	0	3
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	55	CYS	C-N	7.90	1.49	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	21	CYS	O-C-N	5.93	132.19	122.70
1	C	86	LYS	O-C-N	5.43	131.39	122.70
1	A	175	ASP	CB-CG-OD1	5.12	122.91	118.30
1	C	243	VAL	O-C-N	-5.08	114.57	122.70

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	243	VAL	Mainchain
1	B	228[A]	CYS	Mainchain
1	B	228[B]	CYS	Mainchain
1	B	73	VAL	Mainchain
1	C	159[A]	SER	Mainchain
1	C	159[B]	SER	Mainchain
1	C	75[B]	PRO	Mainchain

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	2504	0	2434	51	0
1	B	2605	0	2519	67	0
1	C	2638	0	2549	48	0
2	A	4	0	0	1	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
3	A	6	0	8	1	0
3	C	6	0	8	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	120	0	0	0	0
5	B	112	0	0	2	0
5	C	125	0	0	0	0
All	All	8131	0	7518	165	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 11.

All (165) 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:73:VAL:HG22	1:C:80:ARG:HD3	1.28	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:73:VAL:CG2	1:C:80:ARG:HD3	1.92	0.99
1:A:273:TYR:O	1:A:277:ILE:HG13	1.62	0.98
1:A:200:VAL:HG13	1:A:214:MET:HB3	1.47	0.95
1:C:169:HIS:CE1	1:C:276:VAL:HG13	2.06	0.90
1:B:188:VAL:CG2	1:B:193:LEU:HD12	2.06	0.86
1:B:111:GLU:HG2	5:B:670:HOH:O	1.74	0.85
1:B:323:TRP:O	1:B:327:LEU:HG	1.74	0.85
1:A:199:GLN:OE1	1:A:215:VAL:HG22	1.77	0.85
1:B:200:VAL:CG1	1:B:214:MET:HB2	2.09	0.83
1:A:172:ILE:HD11	1:A:275:GLN:OE1	1.79	0.82
1:B:32:LEU:HD12	1:B:120:LEU:HD12	1.61	0.82
1:A:268:LYS:HA	1:A:268:LYS:HE2	1.61	0.81
1:B:209:THR:HG22	1:B:233:SER:HB3	1.62	0.79
1:A:235:MET:HE1	1:A:259:TRP:HD1	1.48	0.79
1:B:73:VAL:HG22	1:B:80:ARG:HG2	1.64	0.79
1:A:200:VAL:CG1	1:A:214:MET:HB3	2.14	0.77
1:C:73:VAL:HG22	1:C:80:ARG:CD	2.13	0.76
1:B:188:VAL:HG22	1:B:193:LEU:HD12	1.68	0.76
1:A:262:SER:OG	1:A:264:THR:HG22	1.87	0.75
1:C:65:GLY:CA	1:C:75[A]:PRO:HD3	2.17	0.74
1:B:295:LEU:HD11	1:B:318:VAL:HG13	1.70	0.72
1:B:172:ILE:HD11	1:B:275:GLN:OE1	1.89	0.71
1:B:323:TRP:CE2	1:B:327:LEU:HD11	2.28	0.69
1:B:209:THR:HG22	1:B:233:SER:CB	2.22	0.69
1:B:305:LEU:HB2	1:B:306:PRO:CD	2.23	0.68
1:A:241:MET:SD	1:A:243:VAL:HG13	2.34	0.68
1:B:305:LEU:CB	1:B:306:PRO:CD	2.73	0.65
1:A:136:PRO:HB2	1:C:88:VAL:HG23	1.81	0.61
1:C:187:LYS:HE2	1:C:194:THR:HB	1.83	0.61
1:B:139:HIS:CE1	1:B:263:LYS:HG3	2.36	0.60
1:B:38:LEU:HD12	1:B:38:LEU:N	2.17	0.60
1:C:38:LEU:HD12	1:C:38:LEU:N	2.17	0.59
1:B:305:LEU:CB	1:B:306:PRO:HD3	2.31	0.59
1:B:235:MET:SD	1:B:265:LEU:CD1	2.90	0.59
1:B:41:SER:HB2	1:B:70:ASN:OD1	2.03	0.58
1:C:65:GLY:HA3	1:C:75[A]:PRO:HD3	1.85	0.58
1:A:186:VAL:CG1	1:A:315:ARG:HG2	2.34	0.58
1:B:195:MET:CE	1:B:198:TYR:CD1	2.86	0.58
1:A:14:VAL:HG21	1:A:242:VAL:HG21	1.86	0.57
1:B:305:LEU:HB3	1:B:306:PRO:HD3	1.87	0.57
1:A:235:MET:HE3	1:A:261:GLY:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:MET:CE	1:A:261:GLY:H	2.18	0.56
1:B:195:MET:HG3	1:B:316:CYS:SG	2.46	0.56
1:B:193:LEU:HD23	1:B:220:LEU:HD13	1.87	0.55
1:A:186:VAL:HG12	1:A:315:ARG:HD2	1.89	0.55
1:C:246:ILE:HD11	1:C:252:VAL:HG23	1.88	0.55
1:B:305:LEU:HB2	1:B:306:PRO:HD2	1.88	0.55
1:A:235:MET:HE1	1:A:259:TRP:CD1	2.36	0.54
1:A:39:TRP:CD1	1:A:72:LEU:HD22	2.43	0.54
1:B:209:THR:CG2	1:B:233:SER:HA	2.38	0.54
1:C:64:MET:HB2	1:C:75[B]:PRO:HG3	1.89	0.54
1:B:195:MET:HE1	1:B:198:TYR:CD1	2.42	0.54
1:B:186:VAL:H	1:B:315:ARG:HH21	1.55	0.54
1:A:246:ILE:HD11	1:A:252:VAL:CG2	2.39	0.53
1:B:17:LYS:HE3	1:B:19:GLU:OE2	2.08	0.53
1:B:41:SER:OG	1:B:43:GLU:HB2	2.09	0.53
1:B:202:THR:HG21	1:B:214:MET:SD	2.48	0.53
1:B:241:MET:HB2	1:B:255:TYR:CE2	2.42	0.53
1:B:41:SER:OG	1:B:46:SER:HB3	2.09	0.53
1:B:74[A]:CYS:SG	1:B:75[A]:PRO:HD2	2.49	0.53
1:B:225:CYS:SG	1:B:240:LEU:HD11	2.49	0.53
1:A:186:VAL:HG11	1:A:315:ARG:HG2	1.90	0.53
1:A:200:VAL:CG1	1:A:214:MET:CG	2.86	0.53
1:A:200:VAL:CG1	1:A:214:MET:CB	2.85	0.52
1:A:200:VAL:HG13	1:A:214:MET:CB	2.30	0.52
1:B:209:THR:HG22	1:B:233:SER:HA	1.90	0.52
1:A:246:ILE:HD11	1:A:252:VAL:HG23	1.90	0.52
1:A:9:ILE:HG22	1:A:121:GLY:HA3	1.92	0.52
1:C:73:VAL:CG2	1:C:80:ARG:CD	2.80	0.51
1:A:268:LYS:HA	1:A:268:LYS:CE	2.30	0.51
1:B:200:VAL:O	1:B:213:SER:HA	2.12	0.50
1:C:38:LEU:HG	1:C:50:VAL:HG22	1.94	0.50
1:B:323:TRP:NE1	1:B:327:LEU:HD21	2.26	0.50
1:C:144:LYS:HE2	1:C:146:TYR:CE2	2.47	0.50
1:A:235:MET:HE2	1:A:259:TRP:HB2	1.94	0.50
1:A:73:VAL:HG22	1:A:80:ARG:HG2	1.94	0.49
1:A:243:VAL:HG23	1:A:243:VAL:O	2.12	0.49
1:B:195:MET:HE2	1:B:198:TYR:CD1	2.47	0.49
1:C:222:HIS:CE1	1:C:224:LEU:HB2	2.47	0.49
1:B:41:SER:OG	1:B:46:SER:CB	2.60	0.49
1:B:200:VAL:HG13	1:B:214:MET:HB2	1.91	0.49
1:A:160:ILE:HD11	1:A:220:LEU:HD21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:SER:O	1:B:203:SER:OG	2.17	0.49
1:C:222:HIS:HE1	1:C:224:LEU:HB2	1.77	0.49
1:C:202:THR:HG21	1:C:212:ASP:HB2	1.95	0.49
1:C:117:TRP:CG	1:C:127:ILE:HD13	2.48	0.48
1:B:43:GLU:HB2	1:B:46:SER:HB3	1.96	0.48
1:B:225:CYS:SG	1:B:242:VAL:HG12	2.54	0.48
1:C:234:GLU:HG2	1:C:234:GLU:O	2.14	0.48
1:A:237:THR:HG23	1:A:259:TRP:HB3	1.96	0.48
1:C:198:TYR:CZ	1:C:216:ASN:HB2	2.49	0.48
1:B:112:ARG:NH2	1:B:127:ILE:HD12	2.29	0.47
1:A:175:ASP:O	1:A:175:ASP:OD1	2.32	0.47
1:C:65:GLY:HA2	1:C:75[A]:PRO:HD3	1.96	0.47
1:C:38:LEU:HA	1:C:49:GLN:O	2.14	0.47
1:A:51:TRP:CD1	1:A:106:THR:HG22	2.51	0.46
1:A:159:SER:OG	1:A:226:GLN:OE1	2.30	0.46
1:B:209:THR:HG22	1:B:233:SER:CA	2.45	0.46
1:A:186:VAL:HG12	1:A:315:ARG:CD	2.45	0.46
1:B:151:SER:O	1:B:155:VAL:HG23	2.16	0.46
1:C:222:HIS:CE1	1:C:224:LEU:H	2.33	0.46
1:B:235:MET:SD	1:B:265:LEU:HD13	2.55	0.46
1:C:7:ILE:HG23	1:C:8:LEU:N	2.30	0.46
1:C:235:MET:HE1	1:C:259:TRP:CD1	2.51	0.46
1:B:189:ASP:OD1	1:B:191:ASP:N	2.49	0.45
1:C:241:MET:SD	1:C:255:TYR:CZ	3.10	0.45
1:C:4:ALA:HB3	1:C:9:ILE:HD11	1.99	0.45
1:C:5:ASP:HB2	1:C:7:ILE:HG22	1.98	0.45
1:C:202:THR:OG1	1:C:203:SER:N	2.47	0.45
1:C:74[B]:CYS:SG	1:C:76:TYR:N	2.85	0.45
1:B:305:LEU:HD23	1:B:305:LEU:N	2.32	0.45
1:A:228[B]:CYS:SG	3:A:502:GOL:H2	2.57	0.45
1:A:160:ILE:HG22	1:A:160:ILE:O	2.17	0.44
1:A:30:HIS:HB3	1:A:246:ILE:HG23	2.00	0.44
1:B:325:LYS:NZ	5:B:607:HOH:O	2.50	0.44
1:C:86:LYS:O	1:C:88:VAL:HG13	2.17	0.44
1:A:200:VAL:HG11	1:A:214:MET:SD	2.58	0.44
1:B:230:THR:O	1:B:230:THR:HG23	2.17	0.44
1:C:17:LYS:NZ	1:C:143:THR:O	2.41	0.44
1:B:74[B]:CYS:O	1:B:78:GLY:HA2	2.18	0.44
1:C:206:ASN:HB3	1:C:209:THR:OG1	2.18	0.44
1:C:37:VAL:C	1:C:38:LEU:HD12	2.38	0.44
1:B:22:ARG:HB3	1:B:23:PRO:CD	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:VAL:HG22	1:B:80:ARG:CG	2.40	0.43
1:C:7:ILE:CG2	1:C:8:LEU:N	2.80	0.43
1:C:170:GLU:HG3	1:C:175:ASP:HA	1.99	0.43
1:A:77:HIS:HB2	2:A:501:FES:S1	2.59	0.43
1:A:105:LYS:HA	1:A:105:LYS:HD2	1.72	0.43
1:A:195:MET:HE3	1:A:198:TYR:CE1	2.53	0.43
1:A:305:LEU:HD12	1:A:305:LEU:N	2.33	0.43
1:B:189:ASP:OD1	1:B:191:ASP:HB2	2.17	0.43
1:C:41:SER:HB3	1:C:46:SER:HB3	1.99	0.43
1:B:110:GLN:HE21	1:B:112:ARG:HH21	1.66	0.43
1:C:241:MET:SD	1:C:255:TYR:OH	2.73	0.43
1:A:160:ILE:HD11	1:A:220:LEU:CD2	2.49	0.43
1:B:132:GLU:OE2	1:B:236:ARG:NH1	2.46	0.43
1:B:155:VAL:HG21	1:B:251[B]:SER:OG	2.19	0.43
1:C:62:LEU:HD23	1:C:74[A]:CYS:HB2	2.00	0.43
1:B:209:THR:CG2	1:B:233:SER:HB3	2.43	0.42
1:B:244:THR:HB	1:B:252:VAL:HB	2.02	0.42
1:C:65:GLY:HA3	1:C:73:VAL:O	2.20	0.42
1:A:273:TYR:O	1:A:277:ILE:CG1	2.52	0.42
1:B:240:LEU:HG	1:B:242:VAL:HG13	2.02	0.42
1:B:323:TRP:HE1	1:B:327:LEU:HD21	1.84	0.41
1:A:160:ILE:CG2	1:A:316:CYS:SG	3.09	0.41
1:A:162:VAL:HG11	1:A:195:MET:CE	2.49	0.41
1:C:169:HIS:NE2	1:C:276:VAL:HG13	2.32	0.41
1:A:195:MET:CE	1:A:198:TYR:CE1	3.02	0.41
1:B:110:GLN:HB2	1:B:127:ILE:HD11	2.02	0.41
1:C:240:LEU:HD12	1:C:240:LEU:HA	1.90	0.41
1:C:73:VAL:HG21	1:C:80:ARG:HD3	1.90	0.41
1:C:262:SER:OG	1:C:264:THR:HG23	2.21	0.41
1:A:200:VAL:CG1	1:A:214:MET:HG2	2.50	0.41
1:C:41:SER:HB3	1:C:46:SER:CB	2.51	0.41
1:C:70:ASN:OD1	1:C:83:GLN:HG3	2.21	0.41
1:A:170:GLU:O	1:A:170:GLU:CD	2.60	0.41
1:A:200:VAL:HG11	1:A:214:MET:CG	2.49	0.41
1:B:17:LYS:CE	1:B:19:GLU:OE2	2.69	0.41
1:C:156:MET:SD	1:C:220:LEU:HD21	2.61	0.41
1:B:169:HIS:CE1	1:B:276:VAL:HG13	2.56	0.40
1:B:226:GLN:HG2	1:B:228[B]:CYS:SG	2.60	0.40
1:A:272:ASP:O	1:A:276:VAL:HG22	2.21	0.40
1:C:235:MET:CE	1:C:259:TRP:CD1	3.03	0.40
1:B:294:LEU:HD23	1:B:294:LEU:HA	1.87	0.40

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	304/334 (91%)	292 (96%)	12 (4%)	0	100	100
1	B	319/334 (96%)	311 (98%)	8 (2%)	0	100	100
1	C	325/334 (97%)	310 (95%)	15 (5%)	0	100	100
All	All	948/1002 (95%)	913 (96%)	35 (4%)	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	282/304 (93%)	282 (100%)	0	100	100
1	B	296/304 (97%)	295 (100%)	1 (0%)	92	97
1	C	299/304 (98%)	297 (99%)	2 (1%)	84	91
All	All	877/912 (96%)	874 (100%)	3 (0%)	92	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	76	TYR
1	C	76	TYR

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Mol	Chain	Res	Type
1	C	89	GLN

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

Mol	Chain	Res	Type
1	B	110	GLN

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 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 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	GOL	C	502	-	5,5,5	0.10	0	5,5,5	0.40	0
2	FES	A	501	1	0,4,4	-	-	-		
2	FES	C	501	1	0,4,4	-	-	-		
2	FES	B	501	1	0,4,4	-	-	-		
3	GOL	A	502	-	5,5,5	0.08	0	5,5,5	0.63	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
3	GOL	C	502	-	-	2/4/4/4	-
2	FES	A	501	1	-	-	0/1/1/1
2	FES	C	501	1	-	-	0/1/1/1
2	FES	B	501	1	-	-	0/1/1/1
3	GOL	A	502	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

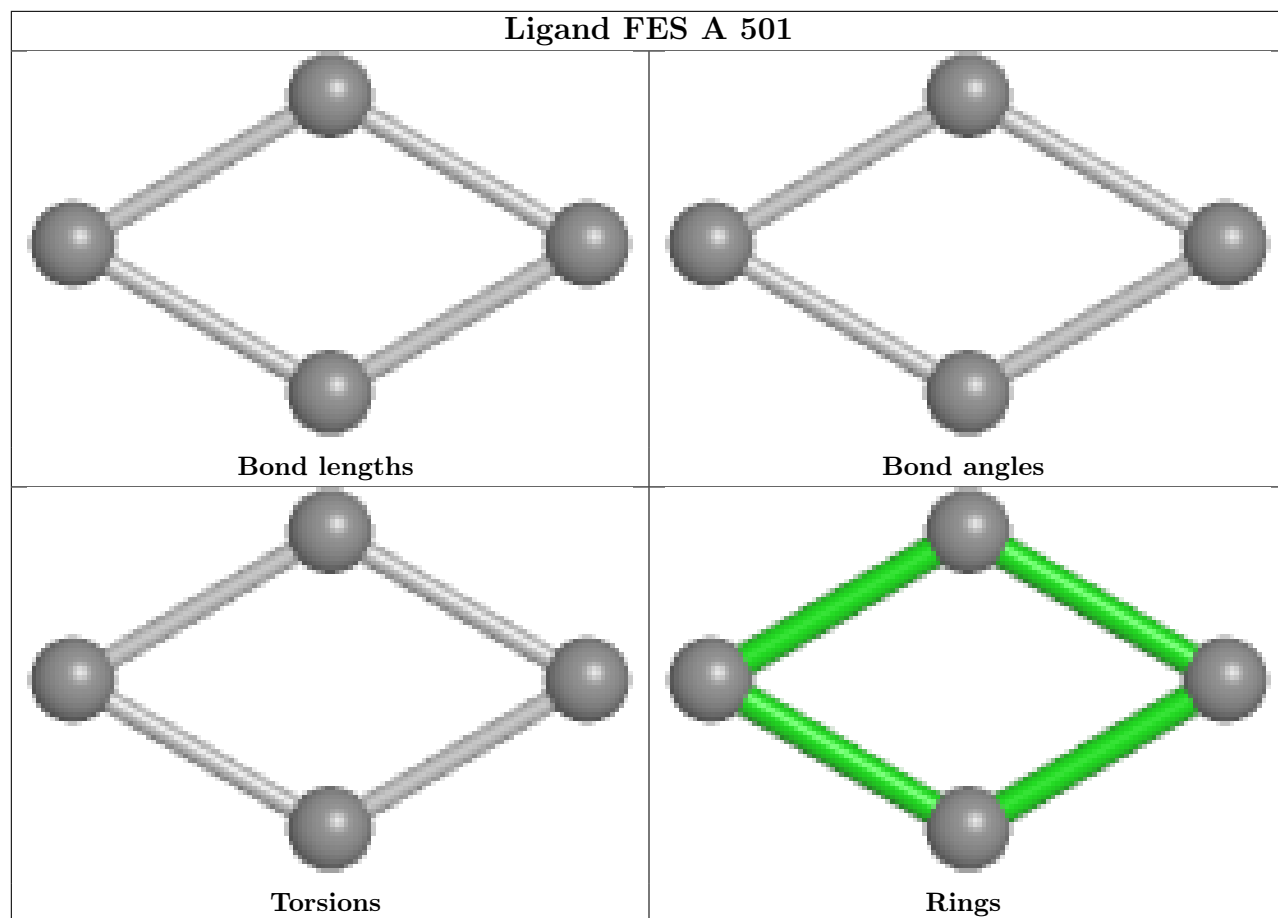
Mol	Chain	Res	Type	Atoms
3	A	502	GOL	O1-C1-C2-C3
3	C	502	GOL	O1-C1-C2-O2
3	A	502	GOL	C1-C2-C3-O3
3	C	502	GOL	O1-C1-C2-C3
3	A	502	GOL	O1-C1-C2-O2
3	A	502	GOL	O2-C2-C3-O3

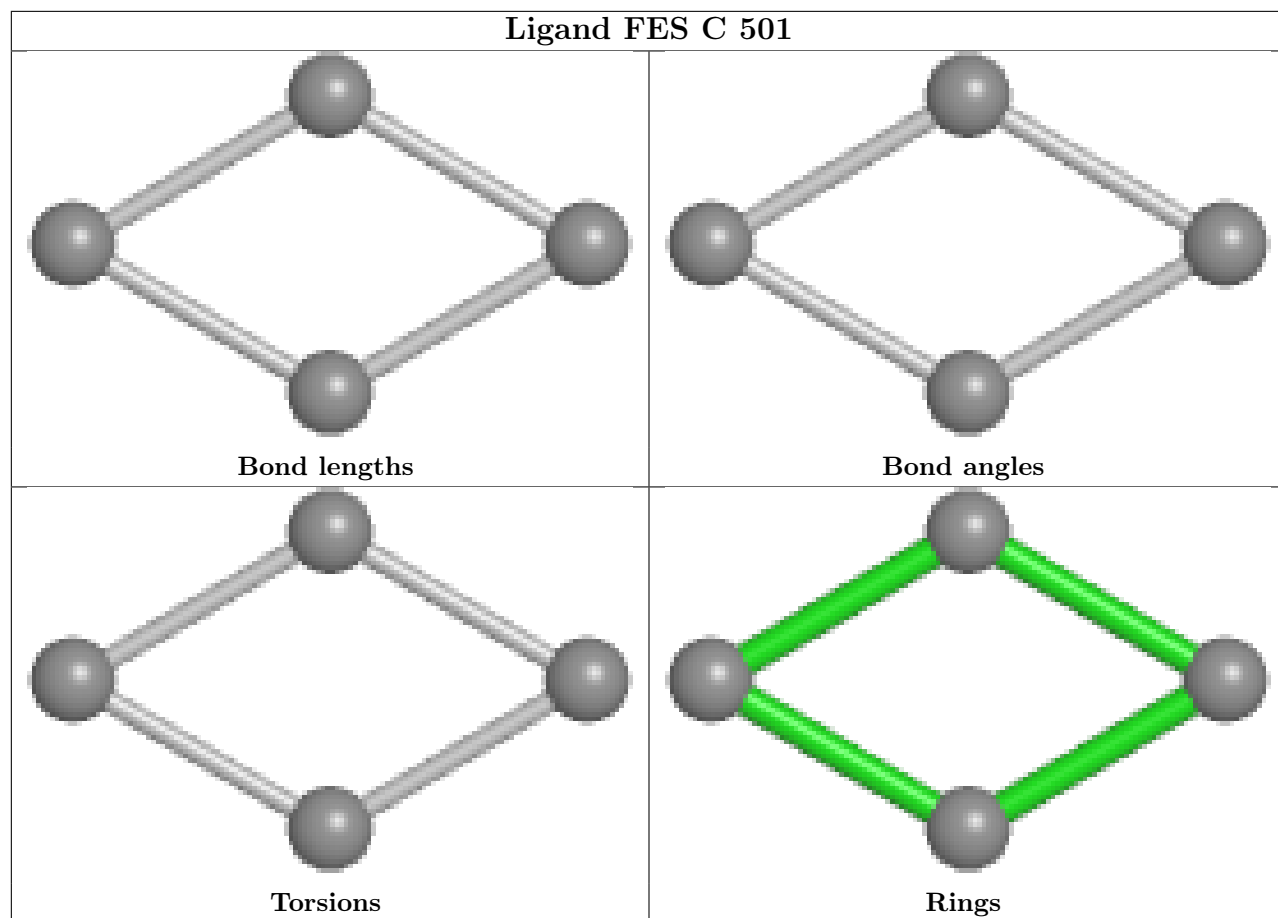
There are no ring outliers.

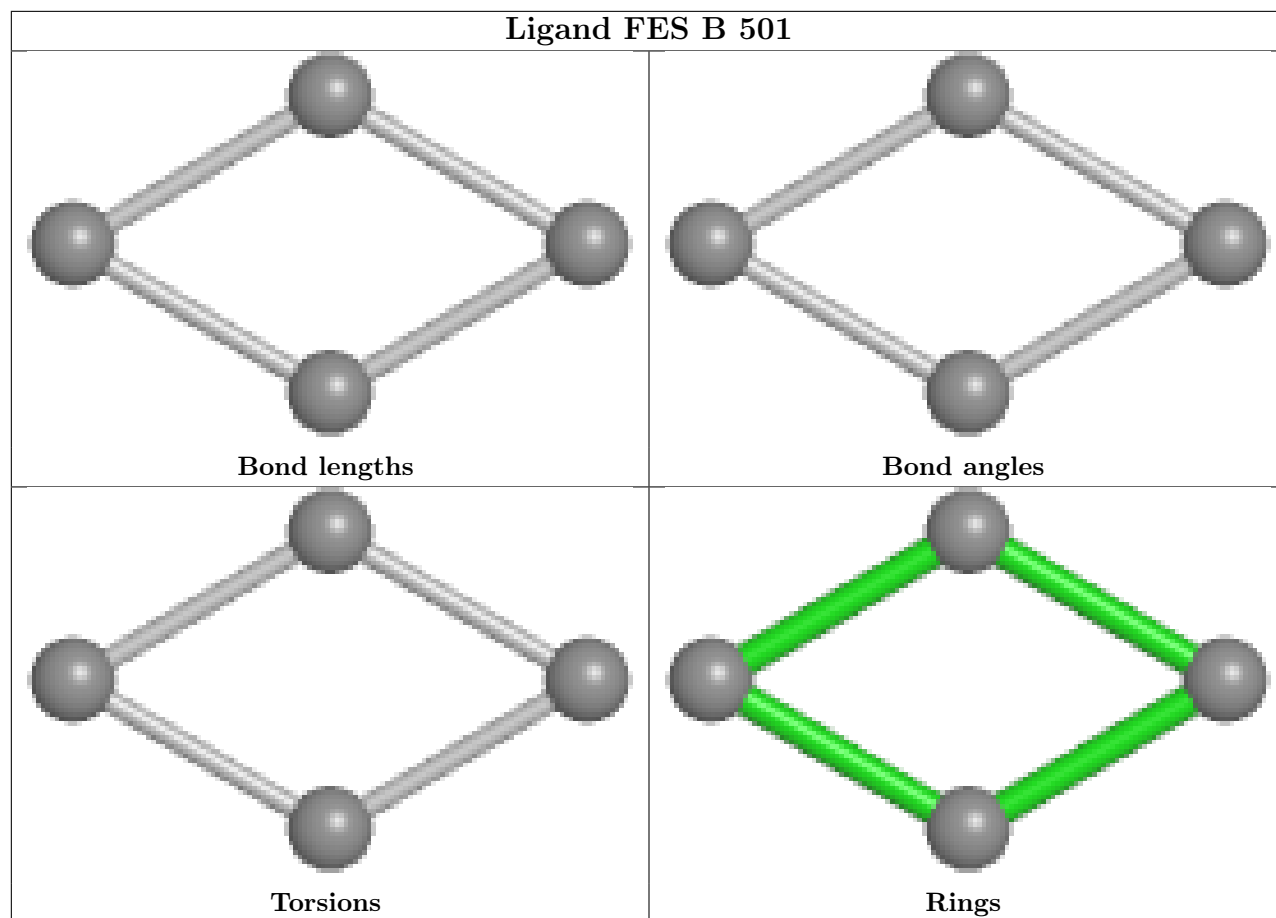
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	FES	1	0
3	A	502	GOL	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

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	311/334 (93%)	0.57	32 (10%) 6 5	27, 39, 70, 95	0
1	B	321/334 (96%)	0.62	31 (9%) 7 6	27, 41, 71, 99	0
1	C	325/334 (97%)	0.61	32 (9%) 7 6	26, 40, 68, 98	0
All	All	957/1002 (95%)	0.60	95 (9%) 7 6	26, 40, 71, 99	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	209	THR	9.0
1	B	234	GLU	8.4
1	C	304	GLY	7.2
1	C	177	ASN	6.7
1	A	233	SER	6.6
1	A	200	VAL	6.2
1	B	211	ASP	6.1
1	B	212	ASP	6.0
1	B	210	LYS	5.8
1	A	232	ALA	5.6
1	C	234	GLU	5.6
1	A	175	ASP	5.2
1	B	232	ALA	5.2
1	A	305	LEU	4.7
1	A	88	VAL	4.5
1	C	210	LYS	4.4
1	C	233	SER	4.4
1	B	201	HIS	4.3
1	B	307	GLN	4.2
1	B	191	ASP	4.2
1	A	234	GLU	4.1
1	A	97	VAL	4.0
1	B	203	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	C	306	PRO	3.8
1	A	334	CYS	3.8
1	C	212	ASP	3.8
1	A	176	ARG	3.7
1	A	2	THR	3.7
1	C	199	GLN	3.6
1	C	137	ASN	3.6
1	C	232	ALA	3.6
1	C	183	ASP	3.6
1	B	9	ILE	3.6
1	B	297	PRO	3.6
1	A	306	PRO	3.6
1	C	176	ARG	3.5
1	C	201	HIS	3.5
1	A	43	GLU	3.5
1	A	214	MET	3.5
1	B	235	MET	3.5
1	A	171	GLY	3.5
1	A	304	GLY	3.4
1	C	211	ASP	3.4
1	C	231	GLU	3.3
1	B	327	LEU	3.2
1	A	95	ASP	3.2
1	C	217	TRP	3.1
1	B	189	ASP	3.1
1	C	175	ASP	3.0
1	B	198	TYR	3.0
1	B	111	GLU	3.0
1	B	182	GLU	2.9
1	B	190	LYS	2.9
1	A	3	THR	2.9
1	A	190	LYS	2.9
1	B	3	THR	2.8
1	B	199	GLN	2.8
1	B	202	THR	2.8
1	A	243	VAL	2.7
1	B	134	ASP	2.7
1	B	233	SER	2.7
1	B	284	LEU	2.7
1	C	214	MET	2.7
1	B	214	MET	2.5
1	C	264	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	123	PRO	2.5
1	C	186	VAL	2.5
1	A	69	ASN	2.4
1	C	75[A]	PRO	2.4
1	B	43	GLU	2.4
1	C	235	MET	2.4
1	C	305	LEU	2.4
1	A	242	VAL	2.3
1	C	222	HIS	2.3
1	C	315	ARG	2.3
1	A	170	GLU	2.3
1	A	160	ILE	2.3
1	A	198	TYR	2.3
1	B	44	GLN	2.3
1	C	198	TYR	2.3
1	B	24	GLY	2.2
1	A	89	GLN	2.2
1	A	42	HIS	2.2
1	C	187	LYS	2.1
1	B	326	GLU	2.1
1	C	134	ASP	2.1
1	C	243	VAL	2.1
1	C	255	TYR	2.1
1	C	241	MET	2.1
1	A	165	PHE	2.1
1	A	173	LEU	2.0
1	A	307	GLN	2.0
1	C	143	THR	2.0
1	A	86	LYS	2.0
1	B	197	LYS	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 monosaccharides in this entry.

6.4 Ligands

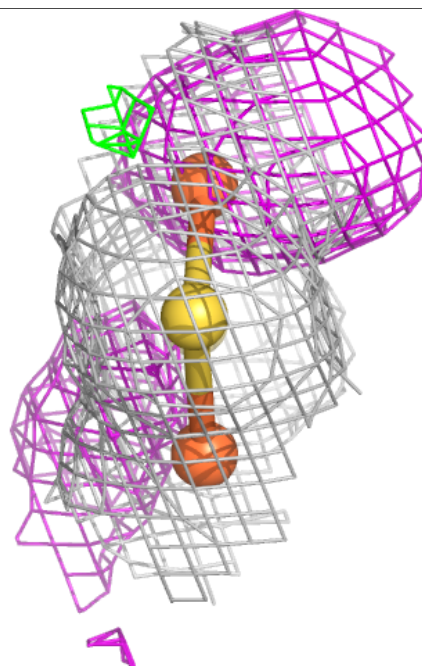
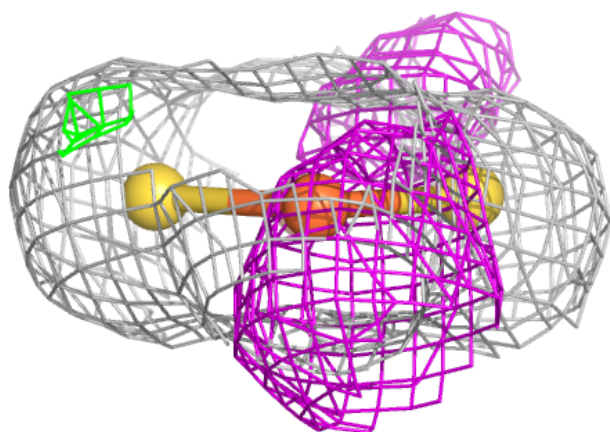
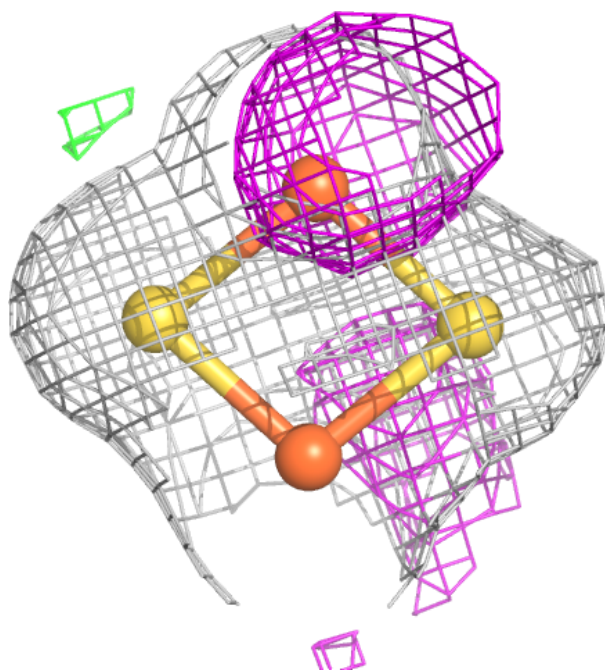
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GOL	A	502	6/6	0.82	0.17	49,61,64,70	0
3	GOL	C	502	6/6	0.82	0.32	63,67,71,81	0
2	FES	A	501	4/4	0.97	0.12	27,27,31,31	0
4	FE	A	503	1/1	0.97	0.09	35,35,35,35	0
2	FES	C	501	4/4	0.99	0.12	26,27,30,32	0
2	FES	B	501	4/4	0.99	0.09	31,32,33,35	0
4	FE	B	502	1/1	0.99	0.16	32,32,32,32	0
4	FE	C	503	1/1	0.99	0.13	32,32,32,32	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.

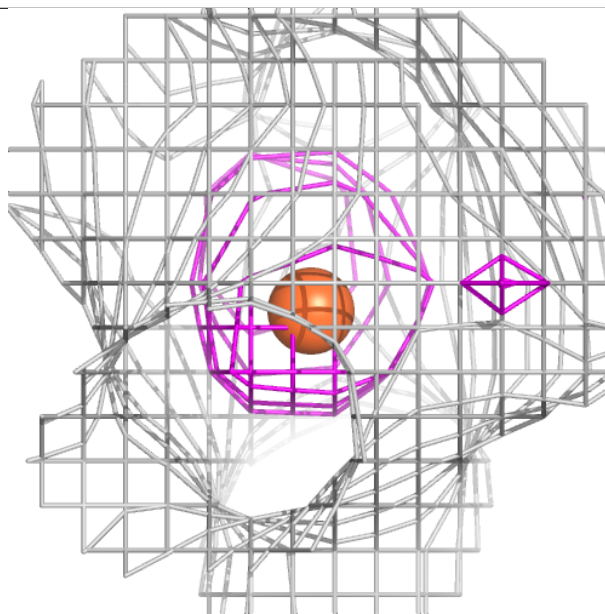
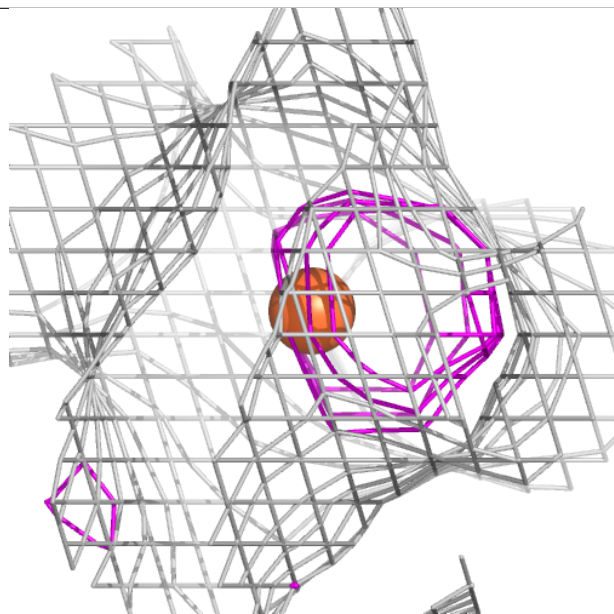
Electron density around FES A 501:

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



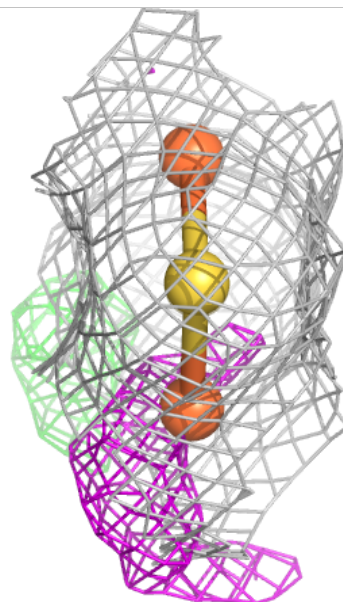
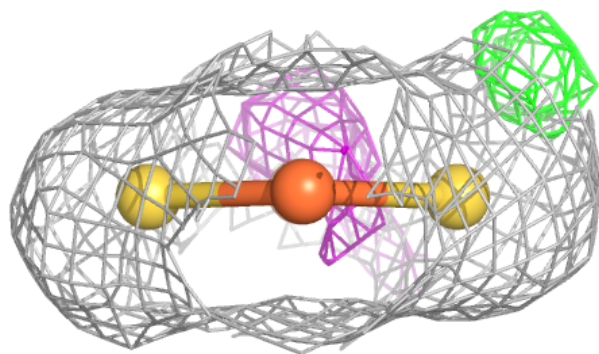
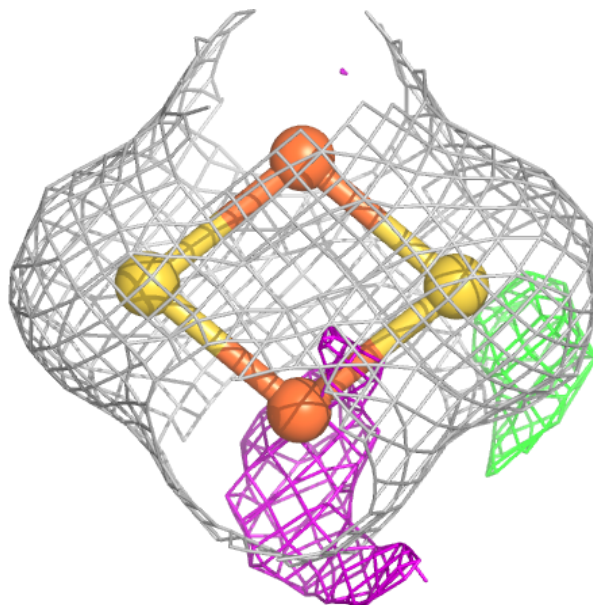
Electron density around FE A 503:

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



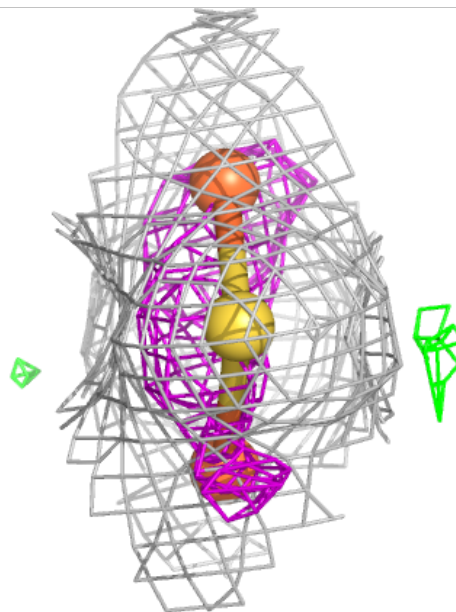
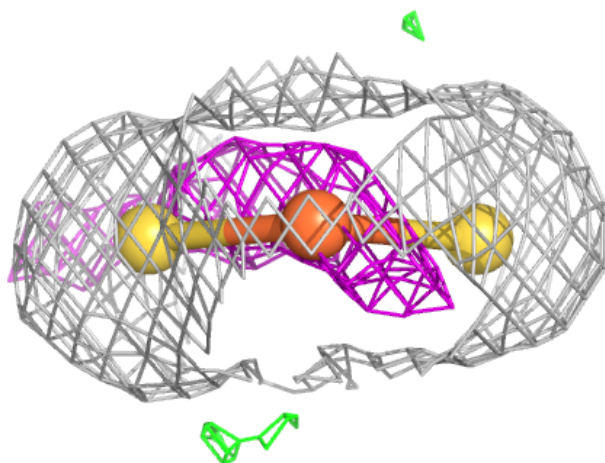
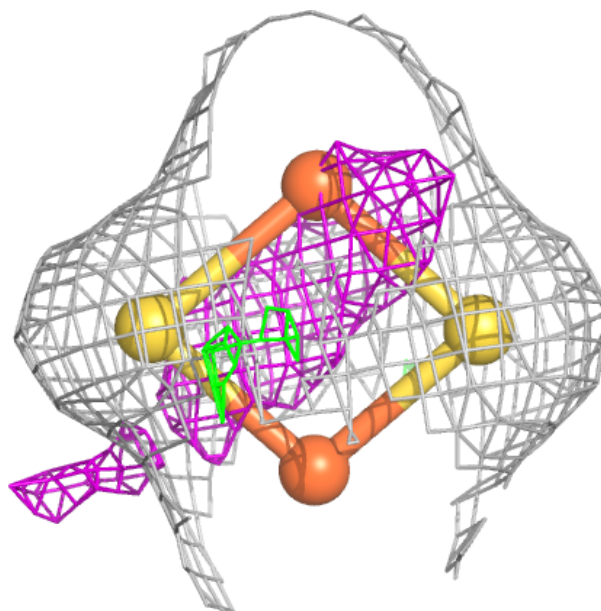
Electron density around FES C 501:

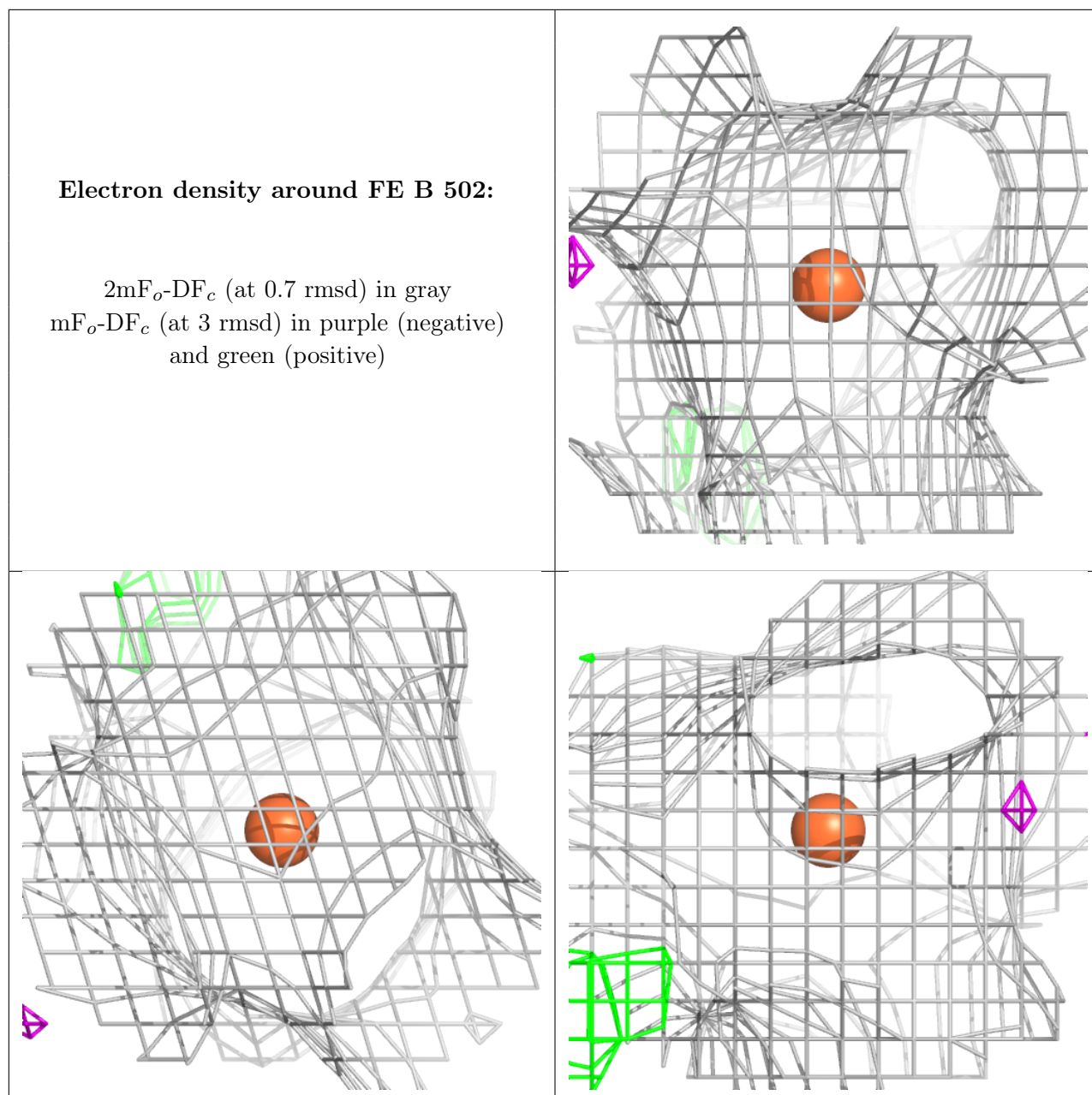
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

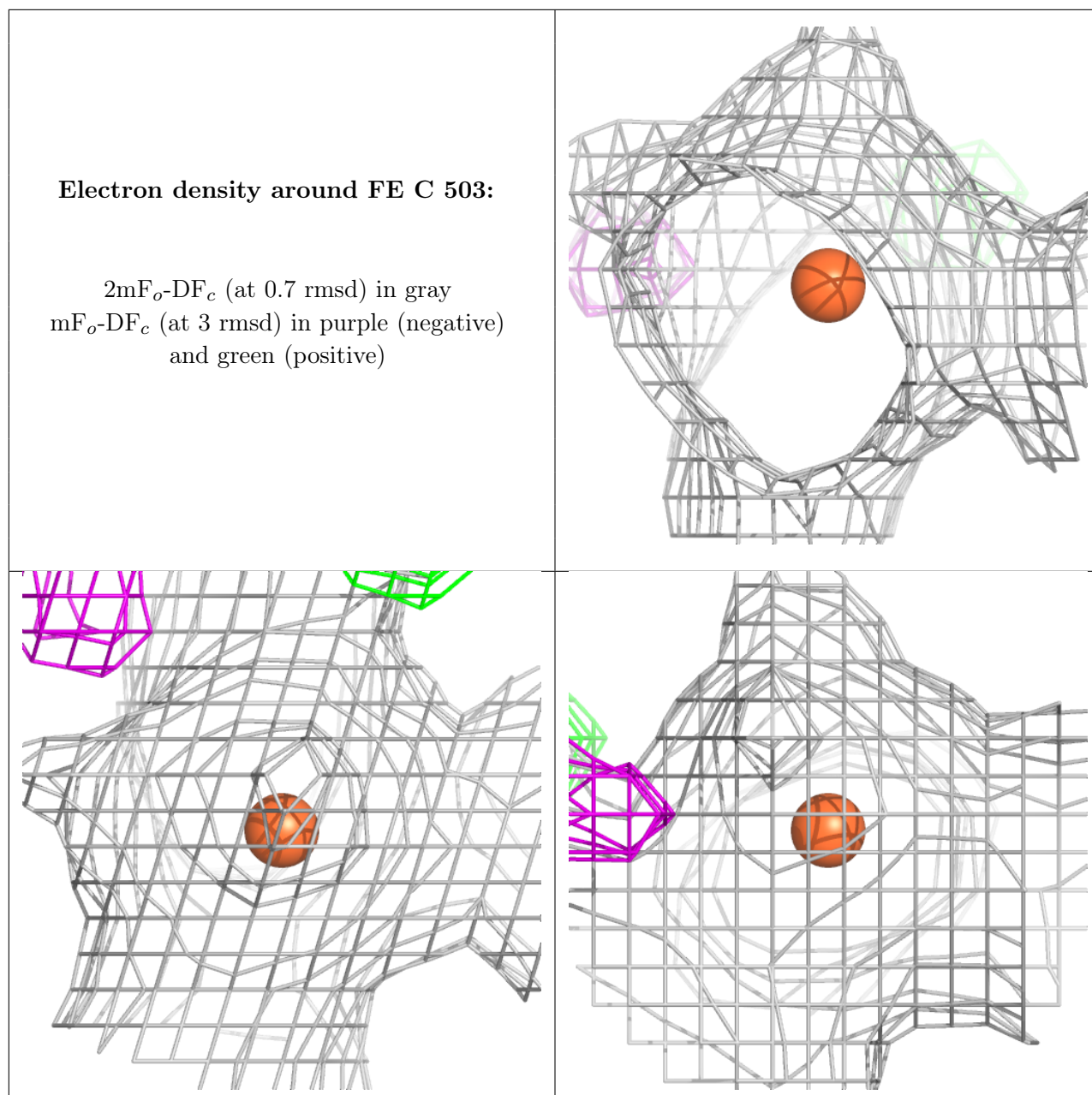


Electron density around FES B 501:

$2mF_o-DF_c$ (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.