



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 05:11 PM JST

PDB ID : 6LL1 / pdb_00006ll1
Title : Oxygen-exposed reduced terminal oxygenase in carbazole 1,9a-dioxygenase
Authors : Wang, Y.X.; Suzuki-Minakuchi, C.; Nojiri, H.
Deposited on : 2019-12-21
Resolution : 2.15 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 : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

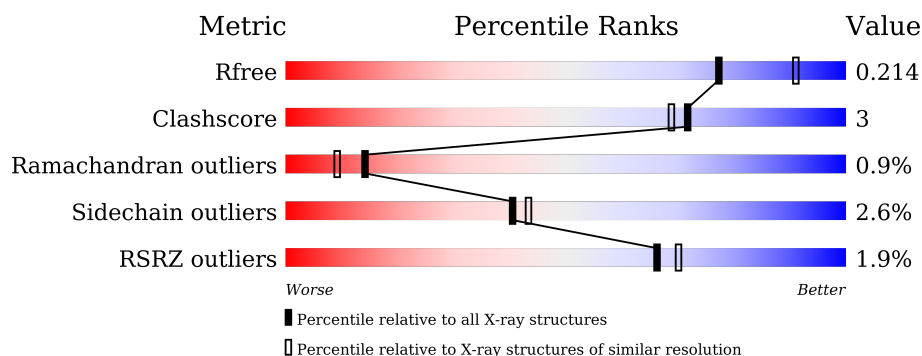
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	392	2% 87% 11% .
1	B	392	2% 86% 10% ...
1	C	392	2% 86% 11% .

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 9852 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 Terminal oxygenase component of carbazole.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	383	Total	C	N	O	S	0	0	0
			3081	1970	523	575	13			
1	B	383	Total	C	N	O	S	0	1	0
			3084	1972	523	576	13			
1	C	383	Total	C	N	O	S	0	0	0
			3081	1970	523	575	13			

There are 24 discrepancies between the modelled and reference sequences:

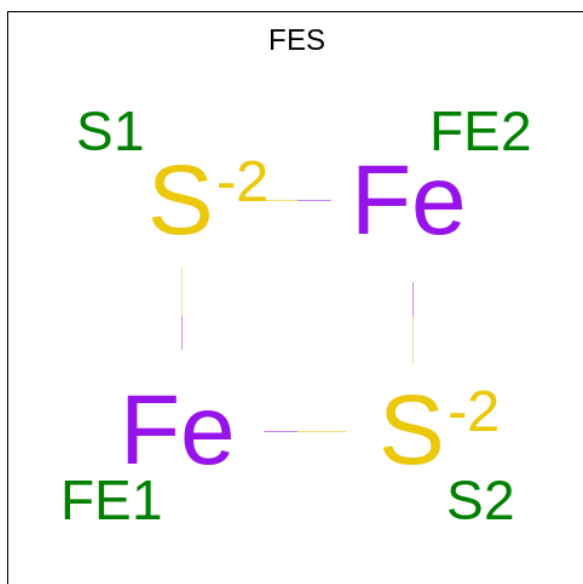
Chain	Residue	Modelled	Actual	Comment	Reference
A	385	LEU	-	expression tag	UNP Q84II6
A	386	GLU	-	expression tag	UNP Q84II6
A	387	HIS	-	expression tag	UNP Q84II6
A	388	HIS	-	expression tag	UNP Q84II6
A	389	HIS	-	expression tag	UNP Q84II6
A	390	HIS	-	expression tag	UNP Q84II6
A	391	HIS	-	expression tag	UNP Q84II6
A	392	HIS	-	expression tag	UNP Q84II6
B	385	LEU	-	expression tag	UNP Q84II6
B	386	GLU	-	expression tag	UNP Q84II6
B	387	HIS	-	expression tag	UNP Q84II6
B	388	HIS	-	expression tag	UNP Q84II6
B	389	HIS	-	expression tag	UNP Q84II6
B	390	HIS	-	expression tag	UNP Q84II6
B	391	HIS	-	expression tag	UNP Q84II6
B	392	HIS	-	expression tag	UNP Q84II6
C	385	LEU	-	expression tag	UNP Q84II6
C	386	GLU	-	expression tag	UNP Q84II6
C	387	HIS	-	expression tag	UNP Q84II6
C	388	HIS	-	expression tag	UNP Q84II6
C	389	HIS	-	expression tag	UNP Q84II6
C	390	HIS	-	expression tag	UNP Q84II6
C	391	HIS	-	expression tag	UNP Q84II6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	392	HIS	-	expression tag	UNP Q84II6

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



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

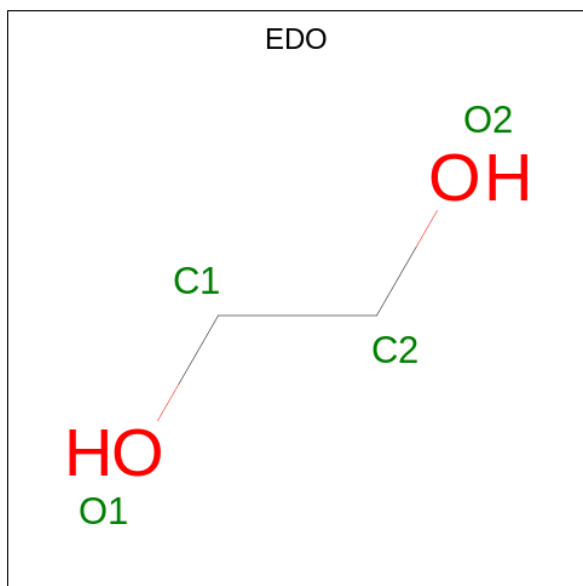
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is FE (II) ION (CCD ID: FE2) (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 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



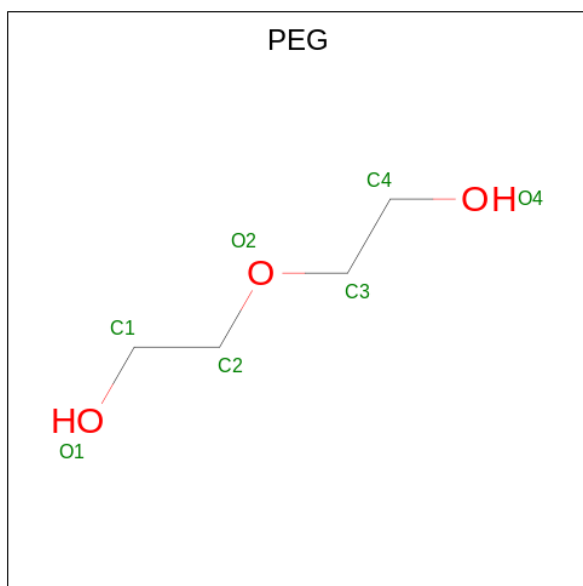
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

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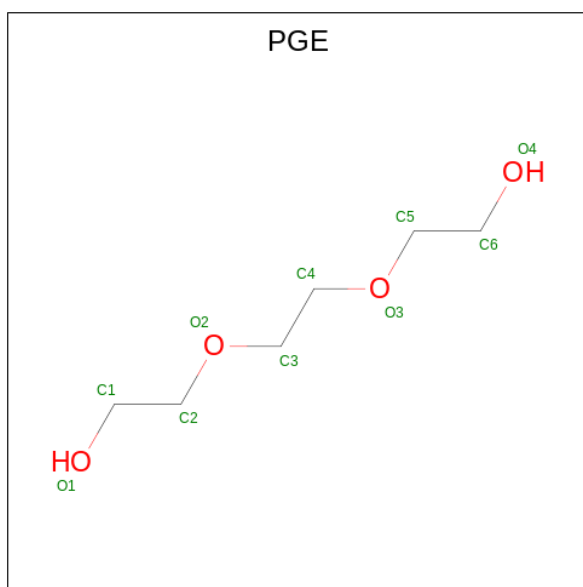
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



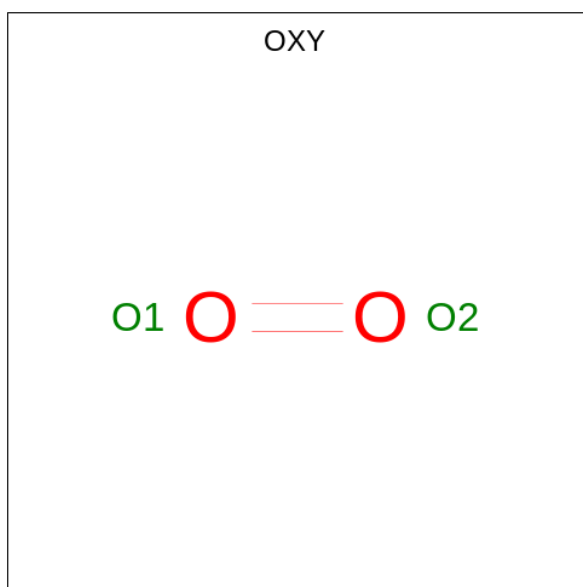
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	C	1	Total	C	O	0	0
			7	4	3		
6	C	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



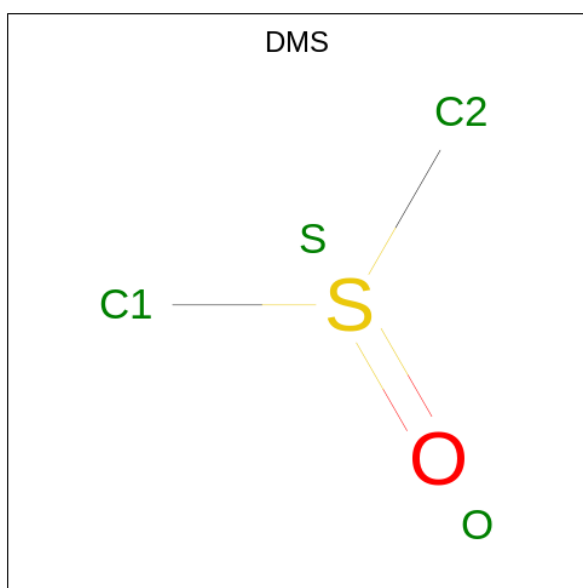
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			10	6	4		
7	B	1	Total	C	O	0	0
			10	6	4		
7	B	1	Total	C	O	0	0
			10	6	4		
7	C	1	Total	C	O	0	0
			10	6	4		
7	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 8 is OXYGEN MOLECULE (CCD ID: OXY) (formula: O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	O	0	0
			2	2		
8	C	1	Total	O	0	0
			2	2		

- Molecule 9 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total	C	O	S	0	0
			4	2	1	1		

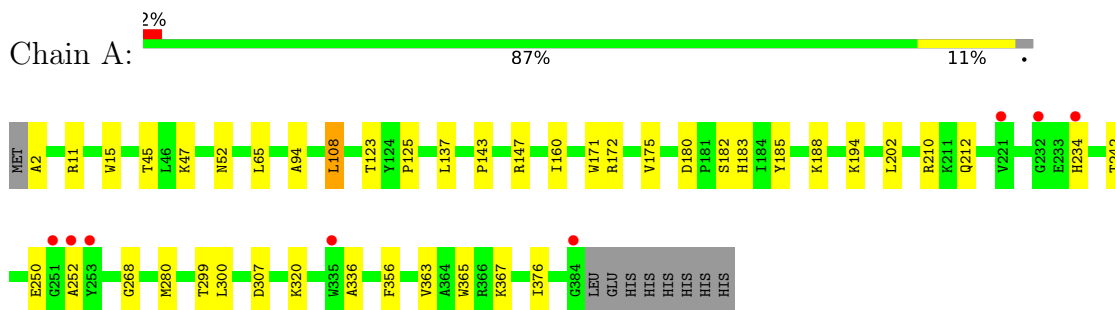
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	135	Total 135	O 135	0	0
10	B	170	Total 170	O 170	0	0
10	C	143	Total 143	O 143	0	0

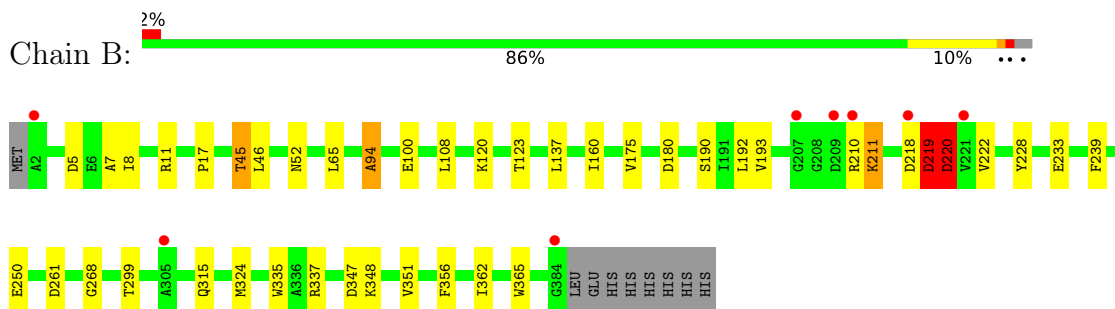
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

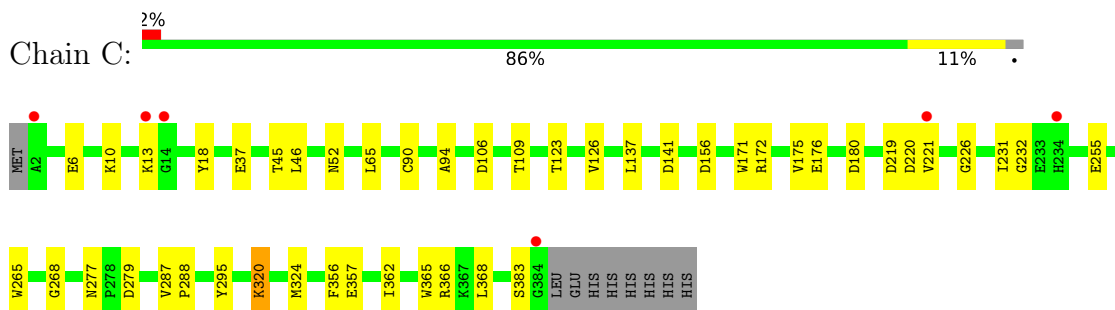
- Molecule 1: Terminal oxygenase component of carbazole



- Molecule 1: Terminal oxygenase component of carbazole



- Molecule 1: Terminal oxygenase component of carbazole



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	91.74Å 91.74Å 240.02Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	79.45 – 2.15 79.45 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.3 (79.45-2.15) 98.3 (79.45-2.15)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.80 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.153 , 0.209 0.162 , 0.214	Depositor DCC
R_{free} test set	3074 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	22.7	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.054 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9852	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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: OXY, DMS, MG, FES, EDO, PEG, PGE, FE2

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	1.09	3/3163 (0.1%)	1.06	3/4294 (0.1%)
1	B	1.20	2/3169 (0.1%)	1.11	3/4302 (0.1%)
1	C	1.10	2/3163 (0.1%)	1.06	1/4294 (0.0%)
All	All	1.13	7/9495 (0.1%)	1.08	7/12890 (0.1%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	335	TRP	CB-CG	-6.10	1.31	1.50
1	C	320	LYS	CA-C	5.58	1.57	1.52
1	B	17	PRO	CA-C	5.19	1.59	1.52
1	A	376	ILE	C-O	-5.17	1.18	1.24
1	A	336	ALA	N-CA	5.11	1.52	1.46
1	A	252	ALA	CA-C	5.03	1.59	1.52
1	C	357	GLU	N-CA	5.00	1.52	1.46

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	220	ASP	N-CA-C	-6.26	97.46	110.80
1	C	126	VAL	CB-CA-C	-5.92	101.39	110.50
1	A	182	SER	N-CA-C	5.58	119.93	113.18
1	B	337	ARG	CB-CA-C	-5.46	102.25	110.92
1	A	250	GLU	N-CA-C	5.37	117.23	109.07
1	A	242	THR	N-CA-C	5.27	118.15	109.72
1	B	94	ALA	N-CA-C	5.15	118.83	112.24

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	3081	0	2992	20	0
1	B	3084	0	2997	22	0
1	C	3081	0	2992	20	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	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	28	0	42	2	0
5	B	8	0	12	1	0
5	C	4	0	6	0	0
6	A	14	0	20	0	0
6	B	14	0	20	1	0
6	C	14	0	20	1	0
7	A	10	0	14	0	0
7	B	20	0	28	0	0
7	C	20	0	28	1	0
8	B	2	0	0	0	0
8	C	2	0	0	0	0
9	C	4	0	6	1	0
10	A	135	0	0	1	0
10	B	170	0	0	2	0
10	C	143	0	0	1	0
All	All	9852	0	9177	61	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 3.

All (61) 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:45:THR:OG1	10:C:501:HOH:O	1.83	0.92
1:B:45:THR:OG1	10:B:501:HOH:O	1.76	0.81
1:B:192:LEU:HD12	1:B:324:MET:HE3	1.73	0.68
1:C:255:GLU:OE1	9:C:410:DMS:S	2.52	0.67
1:C:65:LEU:HD23	1:C:123:THR:HG22	1.82	0.62
1:A:2:ALA:N	10:A:505:HOH:O	2.36	0.58
1:A:185:TYR:CZ	1:A:188:LYS:HE3	2.38	0.58
1:A:194:LYS:O	5:A:410:EDO:C1	2.56	0.54
1:B:210:ARG:O	1:B:210:ARG:HD3	2.07	0.53
1:B:348:LYS:O	1:B:351:VAL:HG22	2.08	0.53
1:C:52:ASN:HD21	6:C:406:PEG:H31	1.74	0.53
1:A:280:MET:HE1	1:A:300:LEU:HD13	1.92	0.52
1:C:320:LYS:HG2	1:C:324:MET:HE2	1.91	0.52
1:A:47:LYS:HE3	1:A:52:ASN:HD21	1.74	0.52
1:C:226:GLY:HA3	1:C:265:TRP:CE3	2.46	0.50
1:A:94:ALA:HB1	1:A:108:LEU:HB2	1.92	0.50
1:A:175:VAL:HG11	1:A:365:TRP:CE2	2.47	0.50
1:B:7:ALA:O	1:B:11:ARG:HG3	2.11	0.50
1:B:192:LEU:CD1	1:B:324:MET:HE3	2.41	0.50
1:B:218:ASP:C	1:B:219:ASP:O	2.53	0.50
1:B:65:LEU:HD23	1:B:123:THR:HG22	1.92	0.49
1:B:94:ALA:HB1	1:B:108:LEU:HB2	1.94	0.49
1:A:65:LEU:HD23	1:A:123:THR:HG22	1.94	0.48
1:B:52:ASN:HD21	6:B:407:PEG:H12	1.77	0.48
1:A:15:TRP:CZ3	1:A:363:VAL:HG13	2.48	0.48
1:C:171:TRP:CE2	1:C:172:ARG:HG3	2.50	0.47
1:C:231:ILE:HG23	1:C:232:GLY:N	2.30	0.47
1:A:47:LYS:HE3	1:A:52:ASN:ND2	2.30	0.47
1:B:175:VAL:HG11	1:B:365:TRP:CE2	2.50	0.47
1:C:287:VAL:HB	1:C:295:TYR:HB2	1.96	0.46
1:C:277:ASN:HB3	1:C:279:ASP:OD1	2.16	0.46
1:A:202:LEU:O	1:C:109:THR:HG22	2.16	0.46
1:A:160:ILE:HG23	1:A:299:THR:HB	1.99	0.45
1:B:218:ASP:C	1:B:218:ASP:OD1	2.59	0.45
1:B:228:TYR:HE2	1:B:261:ASP:OD1	2.00	0.44
1:A:180:ASP:HB3	1:A:183:HIS:HB3	1.99	0.44
1:C:37:GLU:HB3	7:C:408:PGE:H6	2.00	0.44
1:B:219:ASP:O	1:B:220:ASP:CB	2.66	0.43
1:C:18:TYR:CE2	1:C:366:ARG:HG2	2.53	0.43
1:B:190[B]:SER:OG	1:B:193:VAL:HG23	2.18	0.43
1:B:160:ILE:HG23	1:B:299:THR:HB	1.99	0.43
1:A:94:ALA:CB	1:A:108:LEU:HB2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:TRP:CG	1:C:288:PRO:HG3	2.54	0.42
1:B:210:ARG:NH1	5:B:406:EDO:O1	2.45	0.42
1:C:175:VAL:HG11	1:C:365:TRP:CE2	2.55	0.42
1:A:171:TRP:CE2	1:A:172:ARG:HG3	2.54	0.42
1:C:180:ASP:HB2	1:C:362:ILE:HD11	2.01	0.42
1:C:279:ASP:OD1	1:C:279:ASP:N	2.31	0.42
1:B:5:ASP:OD2	1:B:7:ALA:HB3	2.19	0.41
1:B:8:ILE:HD13	1:B:347:ASP:HB2	2.01	0.41
1:A:125:PRO:HA	5:A:408:EDO:C2	2.51	0.41
1:A:143:PRO:HG3	1:A:147:ARG:CZ	2.51	0.41
1:B:315:GLN:NE2	10:B:513:HOH:O	2.49	0.41
1:A:212:GLN:OE1	1:A:234:HIS:NE2	2.54	0.41
1:C:176:GLU:O	1:C:180:ASP:HB2	2.21	0.41
1:C:90:CYS:O	1:C:94:ALA:HA	2.21	0.40
1:A:185:TYR:CE1	1:A:188:LYS:HE3	2.56	0.40
1:A:363:VAL:HG12	1:A:367:LYS:HE2	2.03	0.40
1:B:180:ASP:HB2	1:B:362:ILE:HD11	2.04	0.40
1:B:239:PHE:O	1:B:250:GLU:HA	2.20	0.40
1:C:6:GLU:O	1:C:10:LYS:HG3	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	381/392 (97%)	365 (96%)	15 (4%)	1 (0%)	36	34
1	B	382/392 (97%)	356 (93%)	22 (6%)	4 (1%)	12	8
1	C	381/392 (97%)	362 (95%)	14 (4%)	5 (1%)	9	5
All	All	1144/1176 (97%)	1083 (95%)	51 (4%)	10 (1%)	14	9

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	219	ASP
1	B	220	ASP
1	C	13	LYS
1	A	268	GLY
1	C	221	VAL
1	C	268	GLY
1	B	211	LYS
1	B	268	GLY
1	C	219	ASP
1	C	220	ASP

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	330/339 (97%)	322 (98%)	8 (2%)	43	47
1	B	331/339 (98%)	321 (97%)	10 (3%)	36	38
1	C	330/339 (97%)	322 (98%)	8 (2%)	43	47
All	All	991/1017 (97%)	965 (97%)	26 (3%)	40	43

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ARG
1	A	45	THR
1	A	108	LEU
1	A	137	LEU
1	A	210	ARG
1	A	307	ASP
1	A	320	LYS
1	A	356	PHE
1	B	45	THR
1	B	46	LEU
1	B	100	GLU
1	B	120	LYS
1	B	137	LEU

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Mol	Chain	Res	Type
1	B	211	LYS
1	B	219	ASP
1	B	222	VAL
1	B	233	GLU
1	B	356	PHE
1	C	46	LEU
1	C	106	ASP
1	C	137	LEU
1	C	141	ASP
1	C	156	ASP
1	C	356	PHE
1	C	368	LEU
1	C	383	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	213	GLN
1	A	273	ASN
1	A	372	HIS
1	A	379	GLN
1	B	177	ASN
1	B	213	GLN
1	B	372	HIS
1	C	52	ASN
1	C	75	GLN
1	C	213	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 33 ligands modelled in this entry, 6 are monoatomic - leaving 27 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	EDO	A	409	-	3,3,3	0.40	0	2,2,2	0.40	0
5	EDO	B	406	-	3,3,3	0.37	0	2,2,2	0.72	0
7	PGE	A	413	-	9,9,9	0.63	0	8,8,8	0.78	0
6	PEG	B	408	-	6,6,6	0.36	0	5,5,5	0.80	0
7	PGE	C	409	-	9,9,9	0.78	0	8,8,8	0.78	0
5	EDO	A	407	-	3,3,3	0.52	0	2,2,2	0.24	0
7	PGE	B	409	-	9,9,9	0.57	0	8,8,8	0.65	0
2	FES	B	401	1	0,4,4	-	-	-	-	-
5	EDO	A	406	-	3,3,3	0.38	0	2,2,2	0.36	0
6	PEG	C	406	-	6,6,6	0.39	0	5,5,5	1.11	0
6	PEG	A	412	-	6,6,6	0.53	0	5,5,5	1.06	0
8	OXY	C	404	4	1,1,1	0.18	0	-	-	-
5	EDO	A	404	-	3,3,3	0.34	0	2,2,2	0.52	0
5	EDO	A	408	-	3,3,3	0.53	0	2,2,2	0.68	0
2	FES	A	401	1	0,4,4	-	-	-	-	-
9	DMS	C	410	-	3,3,3	0.48	0	3,3,3	0.85	0
5	EDO	C	405	-	3,3,3	0.42	0	2,2,2	0.44	0
8	OXY	B	404	4	1,1,1	0.03	0	-	-	-
2	FES	C	401	1	0,4,4	-	-	-	-	-
6	PEG	B	407	-	6,6,6	0.53	0	5,5,5	1.42	1 (20%)
5	EDO	B	405	-	3,3,3	0.39	0	2,2,2	0.77	0
7	PGE	B	410	-	9,9,9	0.96	0	8,8,8	0.98	0
5	EDO	A	405	-	3,3,3	0.55	0	2,2,2	0.14	0
6	PEG	C	407	-	6,6,6	0.50	0	5,5,5	0.59	0
5	EDO	A	410	-	3,3,3	0.41	0	2,2,2	0.28	0
7	PGE	C	408	-	9,9,9	0.51	0	8,8,8	0.40	0
6	PEG	A	411	-	6,6,6	0.43	0	5,5,5	0.51	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	A	409	-	-	1/1/1/1	-
5	EDO	B	406	-	-	1/1/1/1	-
7	PGE	A	413	-	-	2/7/7/7	-
6	PEG	B	408	-	-	1/4/4/4	-
7	PGE	C	409	-	-	3/7/7/7	-
5	EDO	A	407	-	-	0/1/1/1	-
7	PGE	B	409	-	-	5/7/7/7	-
2	FES	B	401	1	-	-	0/1/1/1
5	EDO	A	406	-	-	1/1/1/1	-
6	PEG	C	406	-	-	3/4/4/4	-
6	PEG	A	412	-	-	3/4/4/4	-
5	EDO	A	404	-	-	0/1/1/1	-
5	EDO	A	408	-	-	1/1/1/1	-
2	FES	A	401	1	-	-	0/1/1/1
5	EDO	C	405	-	-	0/1/1/1	-
2	FES	C	401	1	-	-	0/1/1/1
6	PEG	B	407	-	-	2/4/4/4	-
5	EDO	B	405	-	-	0/1/1/1	-
7	PGE	B	410	-	-	3/7/7/7	-
5	EDO	A	405	-	-	0/1/1/1	-
6	PEG	C	407	-	-	2/4/4/4	-
5	EDO	A	410	-	-	0/1/1/1	-
7	PGE	C	408	-	-	2/7/7/7	-
6	PEG	A	411	-	-	2/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	407	PEG	C3-O2-C2	2.73	125.12	113.29

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	412	PEG	C4-C3-O2-C2
6	B	407	PEG	C1-C2-O2-C3
6	A	412	PEG	O1-C1-C2-O2
6	C	406	PEG	O1-C1-C2-O2
6	B	408	PEG	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
7	C	409	PGE	O3-C5-C6-O4
6	A	411	PEG	O1-C1-C2-O2
7	A	413	PGE	O2-C3-C4-O3
6	A	411	PEG	O2-C3-C4-O4
6	A	412	PEG	O2-C3-C4-O4
7	A	413	PGE	O1-C1-C2-O2
7	B	409	PGE	O2-C3-C4-O3
5	A	409	EDO	O1-C1-C2-O2
7	B	409	PGE	C1-C2-O2-C3
7	B	409	PGE	C6-C5-O3-C4
6	C	407	PEG	C1-C2-O2-C3
7	C	408	PGE	C3-C4-O3-C5
7	C	409	PGE	C4-C3-O2-C2
6	C	406	PEG	C1-C2-O2-C3
7	B	410	PGE	C4-C3-O2-C2
7	C	409	PGE	C1-C2-O2-C3
6	B	407	PEG	C4-C3-O2-C2
5	A	408	EDO	O1-C1-C2-O2
5	B	406	EDO	O1-C1-C2-O2
6	C	407	PEG	O2-C3-C4-O4
7	B	409	PGE	O3-C5-C6-O4
7	B	409	PGE	O1-C1-C2-O2
6	C	406	PEG	C4-C3-O2-C2
7	B	410	PGE	O2-C3-C4-O3
7	C	408	PGE	C4-C3-O2-C2
5	A	406	EDO	O1-C1-C2-O2
7	B	410	PGE	O1-C1-C2-O2

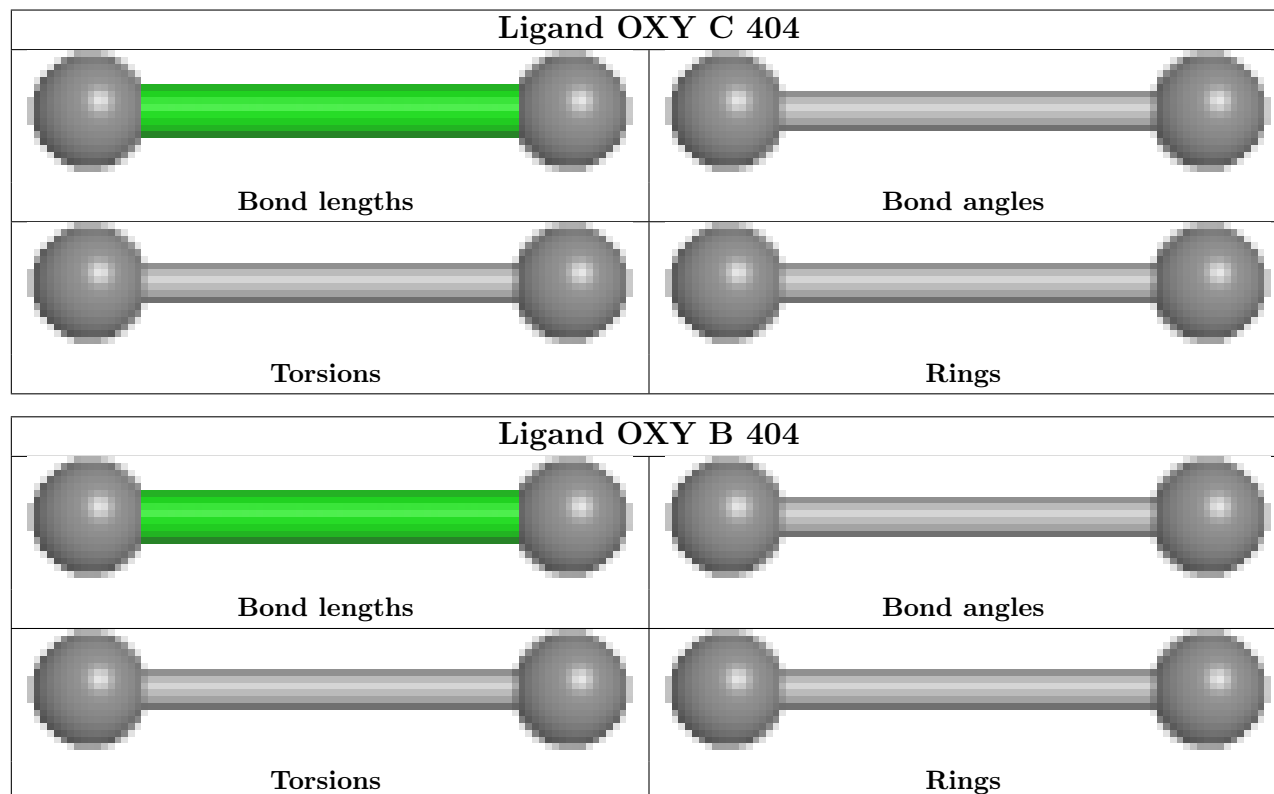
There are no ring outliers.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	406	EDO	1	0
6	C	406	PEG	1	0
5	A	408	EDO	1	0
9	C	410	DMS	1	0
6	B	407	PEG	1	0
5	A	410	EDO	1	0
7	C	408	PGE	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	383/392 (97%)	-0.11	8 (2%) 63 67	12, 27, 58, 85	0
1	B	383/392 (97%)	-0.35	8 (2%) 63 67	11, 21, 47, 103	1 (0%)
1	C	383/392 (97%)	-0.12	6 (1%) 70 74	15, 27, 57, 75	0
All	All	1149/1176 (97%)	-0.19	22 (1%) 66 70	11, 25, 57, 103	1 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	251	GLY	4.9
1	B	384	GLY	3.9
1	B	221	VAL	3.5
1	C	384	GLY	3.4
1	A	252	ALA	3.2
1	B	2	ALA	3.2
1	B	218	ASP	3.2
1	A	221	VAL	3.0
1	B	209	ASP	3.0
1	A	384	GLY	2.9
1	B	207	GLY	2.8
1	C	221	VAL	2.8
1	A	335	TRP	2.6
1	A	253	TYR	2.4
1	C	14	GLY	2.4
1	B	210	ARG	2.3
1	C	13	LYS	2.3
1	B	305	ALA	2.2
1	C	234	HIS	2.1
1	A	232	GLY	2.1
1	A	234	HIS	2.1
1	C	2	ALA	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides 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.

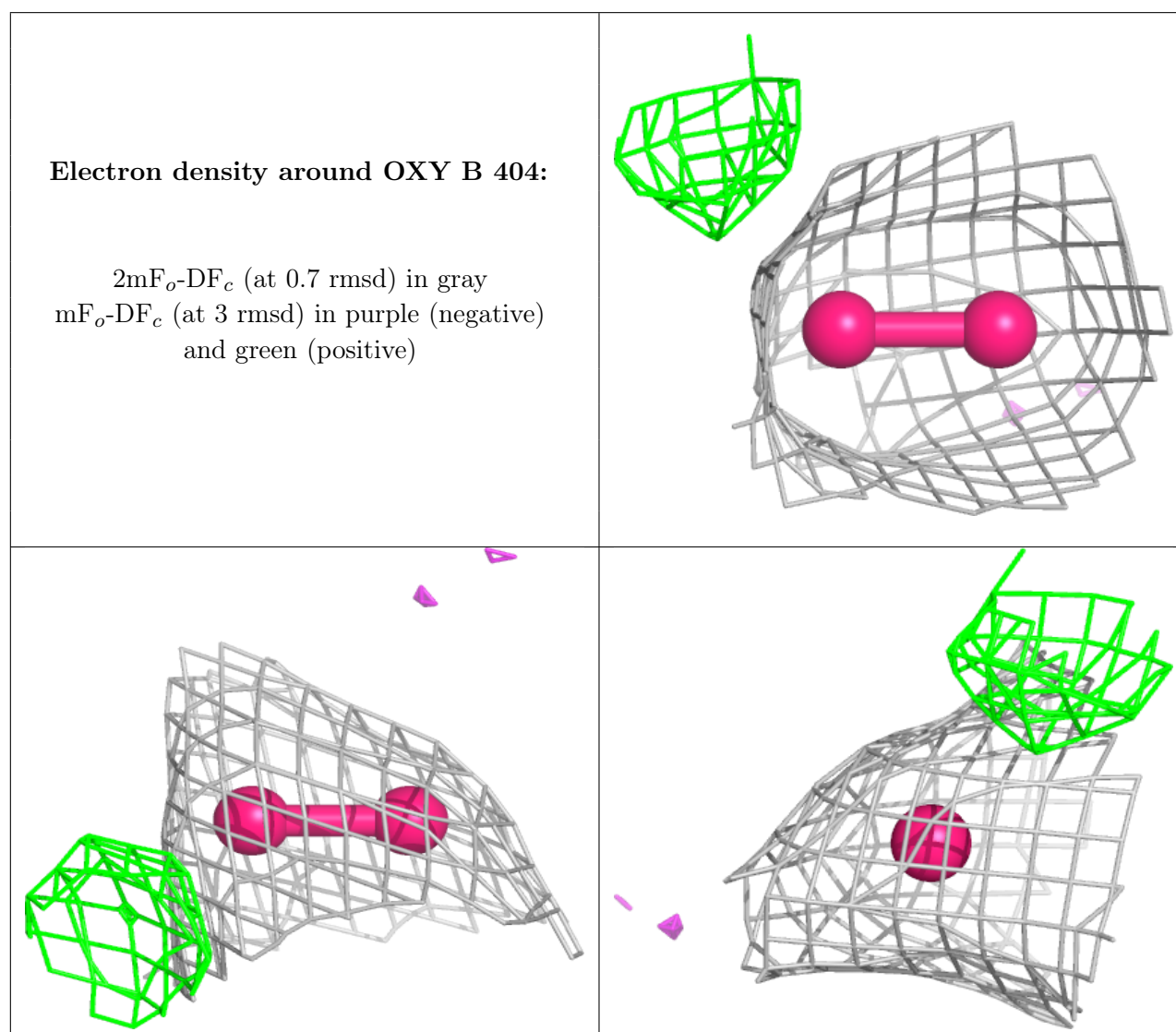
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	A	410	4/4	0.70	0.16	57,59,62,65	0
6	PEG	C	407	7/7	0.72	0.16	57,62,64,67	0
7	PGE	C	409	10/10	0.74	0.21	35,53,56,58	0
7	PGE	A	413	10/10	0.77	0.16	53,56,59,61	0
5	EDO	A	405	4/4	0.78	0.13	50,53,54,56	0
7	PGE	B	410	10/10	0.81	0.18	41,47,50,59	0
9	DMS	C	410	4/4	0.83	0.17	72,72,78,79	0
6	PEG	C	406	7/7	0.85	0.13	33,38,45,50	0
6	PEG	B	408	7/7	0.88	0.12	41,43,47,50	0
7	PGE	C	408	10/10	0.88	0.12	46,52,54,54	0
5	EDO	A	409	4/4	0.89	0.11	49,51,51,53	0
5	EDO	B	406	4/4	0.90	0.16	41,42,45,47	0
6	PEG	B	407	7/7	0.90	0.12	31,34,46,50	0
5	EDO	C	405	4/4	0.91	0.10	35,39,41,51	0
5	EDO	A	408	4/4	0.91	0.10	27,29,33,38	0
5	EDO	A	406	4/4	0.91	0.11	42,45,46,47	0
7	PGE	B	409	10/10	0.91	0.10	44,47,49,50	0
5	EDO	B	405	4/4	0.92	0.12	31,33,39,43	0
6	PEG	A	412	7/7	0.92	0.12	41,43,48,54	0
6	PEG	A	411	7/7	0.93	0.09	31,36,48,52	0
5	EDO	A	407	4/4	0.93	0.11	48,48,52,53	0
8	OXY	B	404	2/2	0.96	0.08	30,30,30,37	0
3	MG	C	402	1/1	0.96	0.06	40,40,40,40	0
8	OXY	C	404	2/2	0.97	0.10	28,28,28,30	0
5	EDO	A	404	4/4	0.97	0.06	23,28,30,34	0
3	MG	B	402	1/1	0.98	0.03	36,36,36,36	0
3	MG	A	402	1/1	0.98	0.06	26,26,26,26	0

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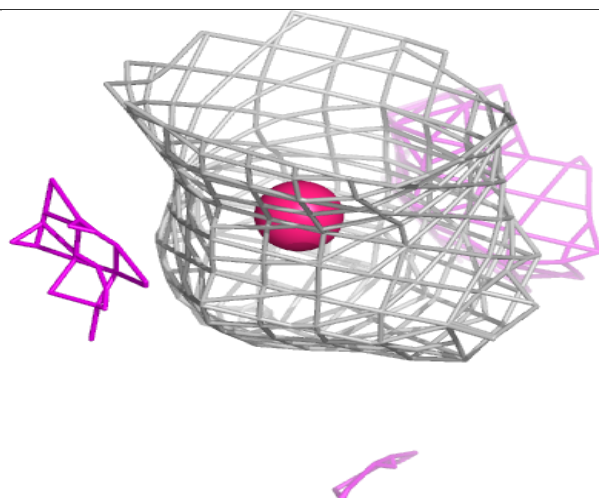
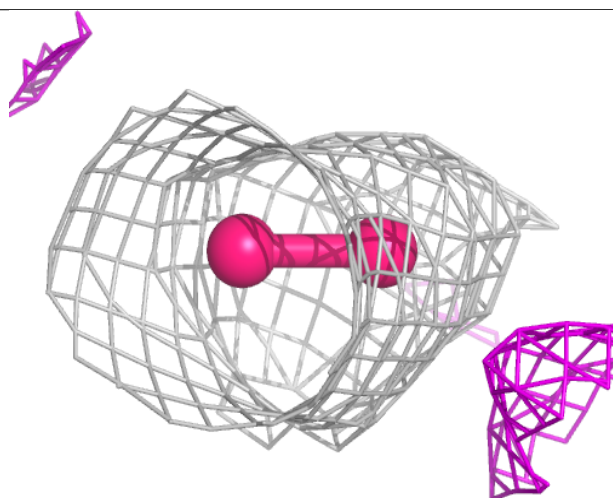
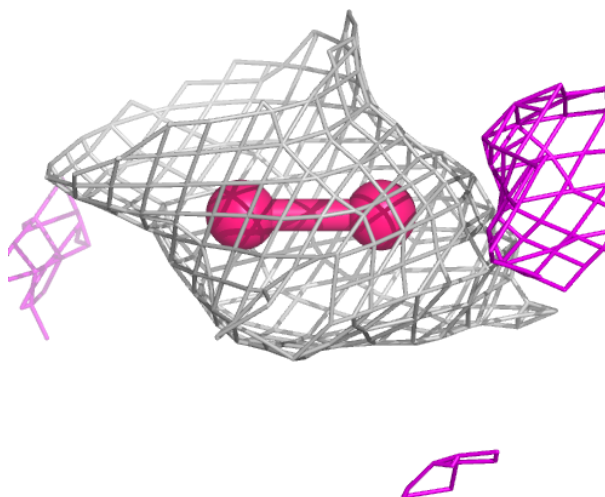
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FES	C	401	4/4	0.99	0.04	20,22,23,24	0
4	FE2	C	403	1/1	1.00	0.02	19,19,19,19	0
2	FES	A	401	4/4	1.00	0.02	12,12,14,14	0
2	FES	B	401	4/4	1.00	0.02	14,15,16,16	0
4	FE2	A	403	1/1	1.00	0.01	25,25,25,25	0
4	FE2	B	403	1/1	1.00	0.02	16,16,16,16	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.



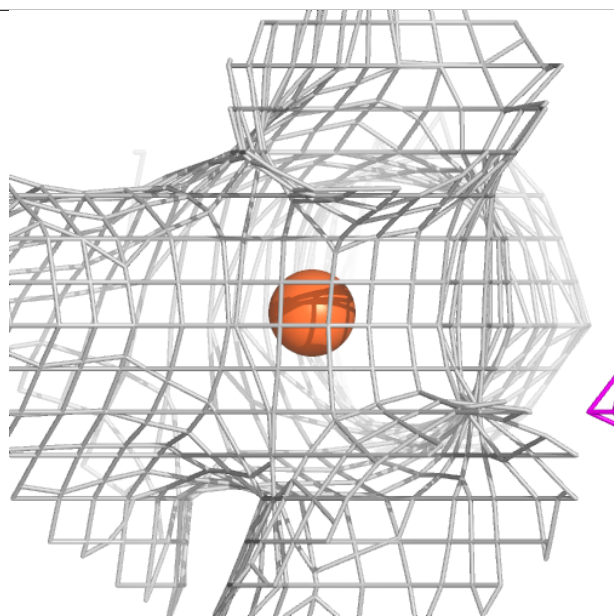
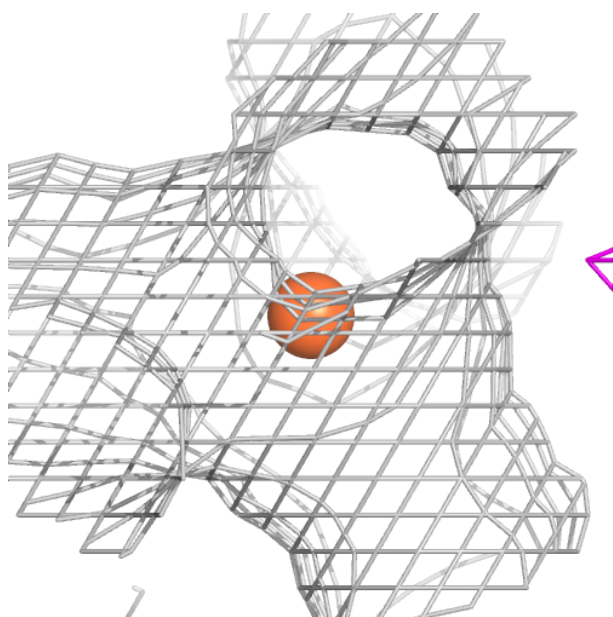
Electron density around OXY C 404:

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



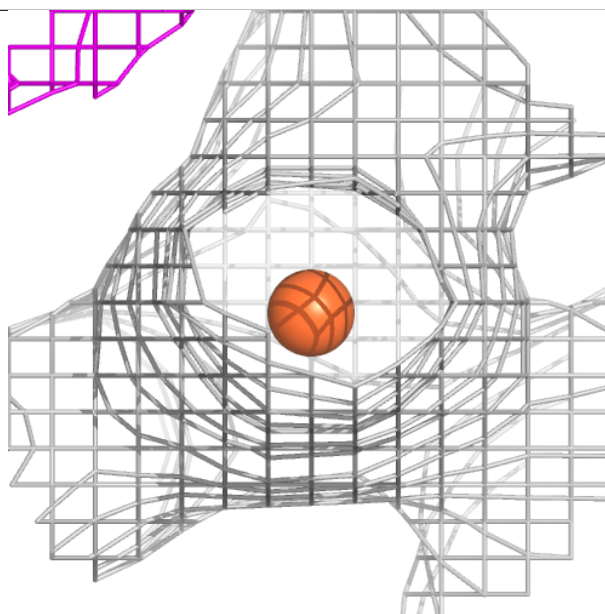
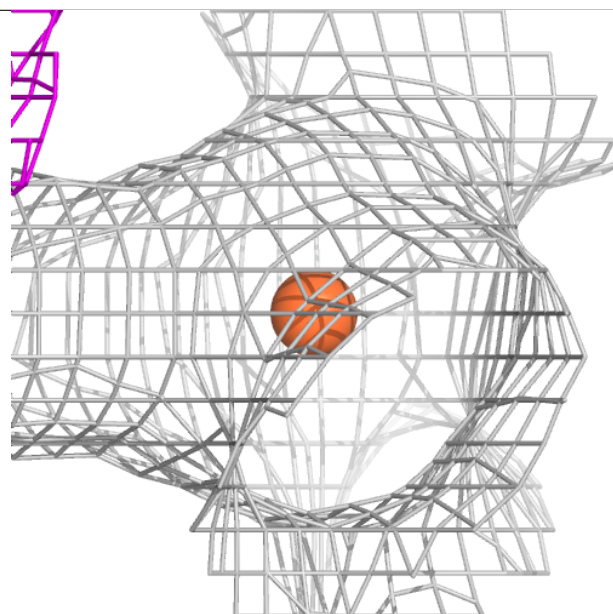
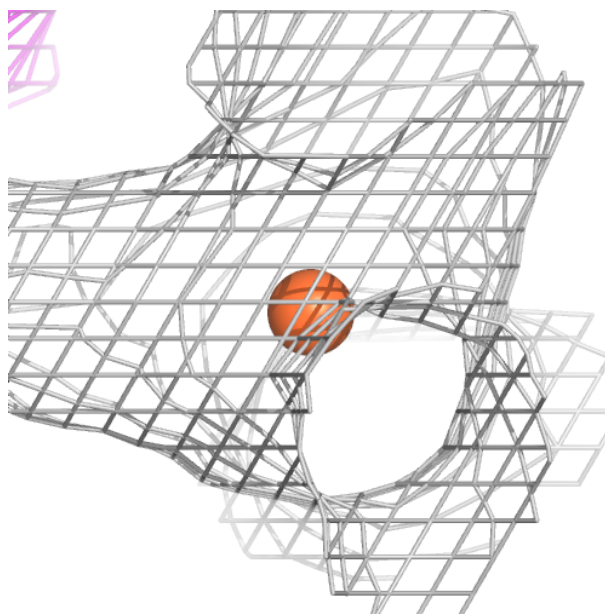
Electron density around FE2 C 403:

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



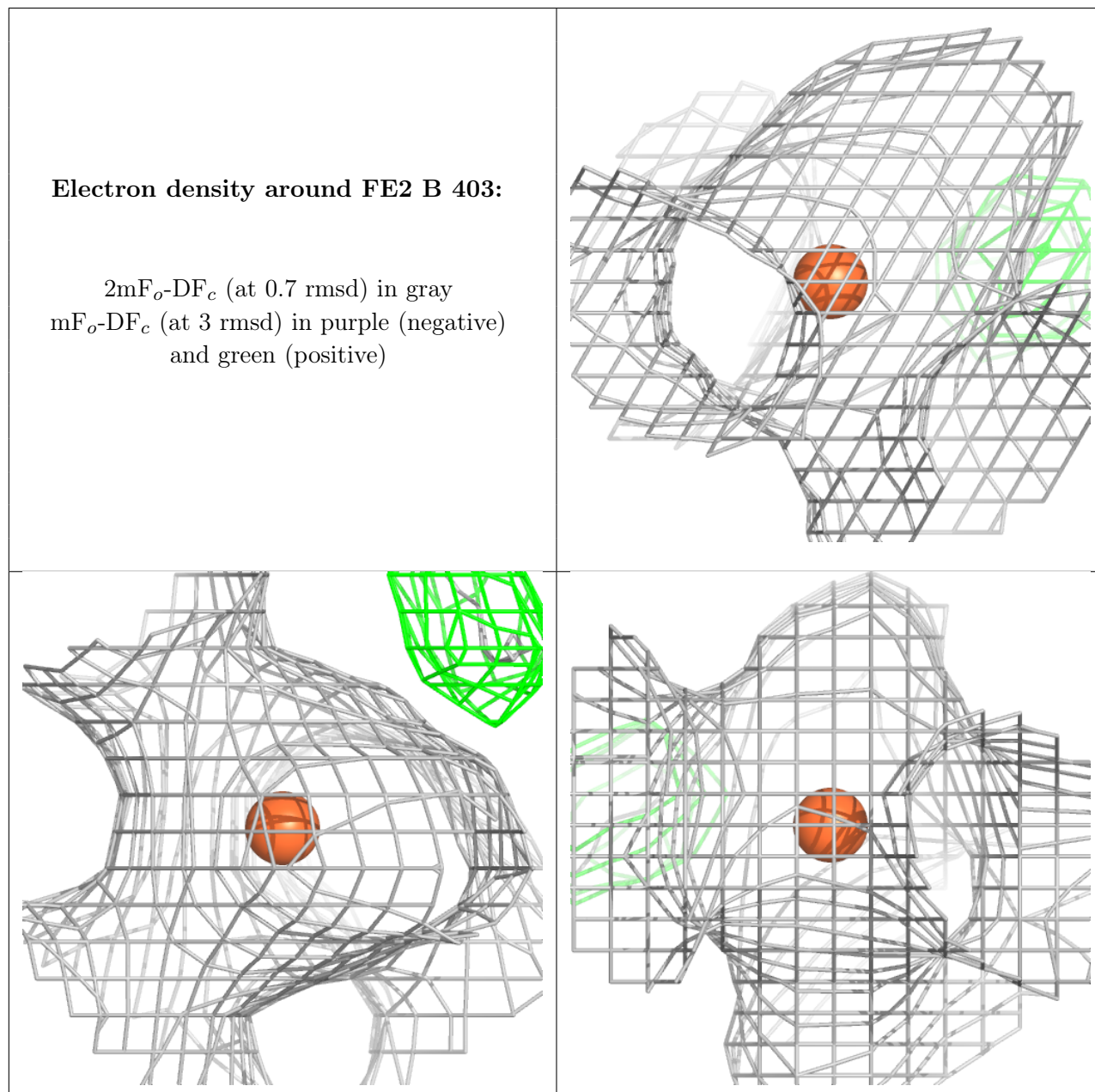
Electron density around FE2 A 403:

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



Electron density around FE2 B 403:

$2mF_o-DF_c$ (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.