



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:26 AM GMT

PDB ID : 3EN1
Title : Crystal structure of Toluene 2,3-Dioxygenase
Authors : Friemann, R.; Lee, K.; Brown, E.N.; Gibson, D.T.; Eklund, H.; Ramaswamy, S.
Deposited on : 2008-09-25
Resolution : 3.20 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : **FAILED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

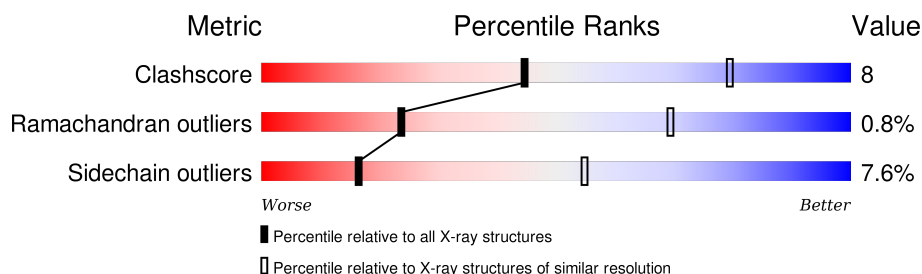
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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))
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)

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 ≥ 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.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	450	
2	B	187	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4917 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 Benzene 1,2-dioxygenase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	0	0
			3373	2131	585	636	21			

- Molecule 2 is a protein called Benzene 1,2-dioxygenase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	180	Total	C	N	O	S	0	0	0
			1499	947	267	280	5			

- Molecule 3 is FE (II) ION (three-letter code: FE2) (formula: Fe).

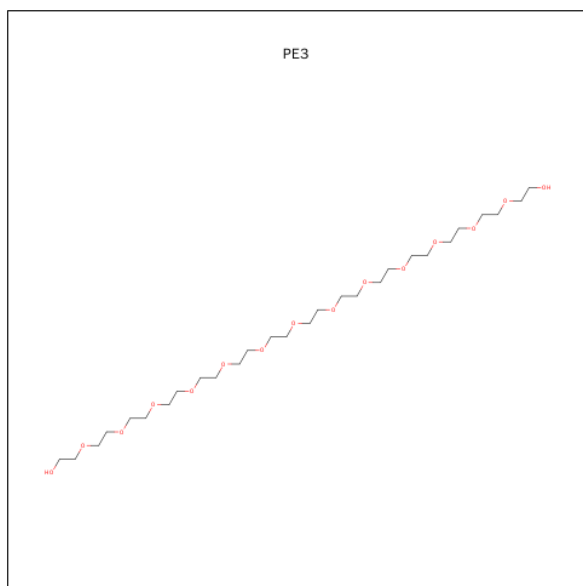
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Fe	0	0
			1	1		
3	A	1	Total	Fe	0	0
			1	1		

- Molecule 4 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



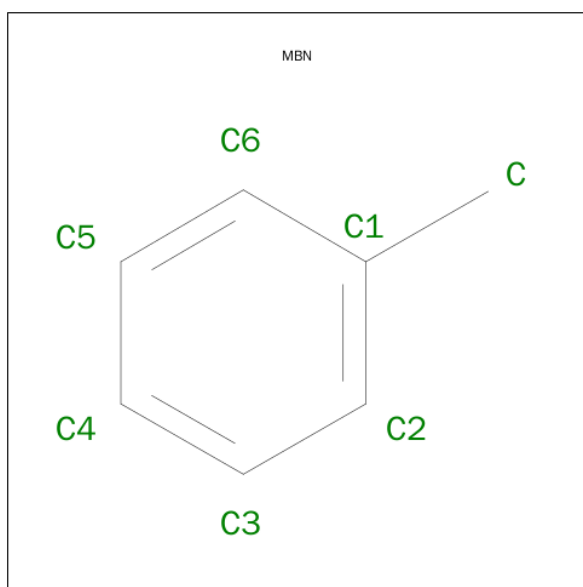
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 5 is 3,6,9,12,15,18,21,24,27,30,33,36,39-TRIDECAOXAHENTETRACONTANE-1,41-DIOL (three-letter code: PE3) (formula: $C_{28}H_{58}O_{15}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			14	9	5		

- Molecule 6 is TOLUENE (three-letter code: MBN) (formula: C_7H_8).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C 7 7	0	0

- Molecule 7 is water.

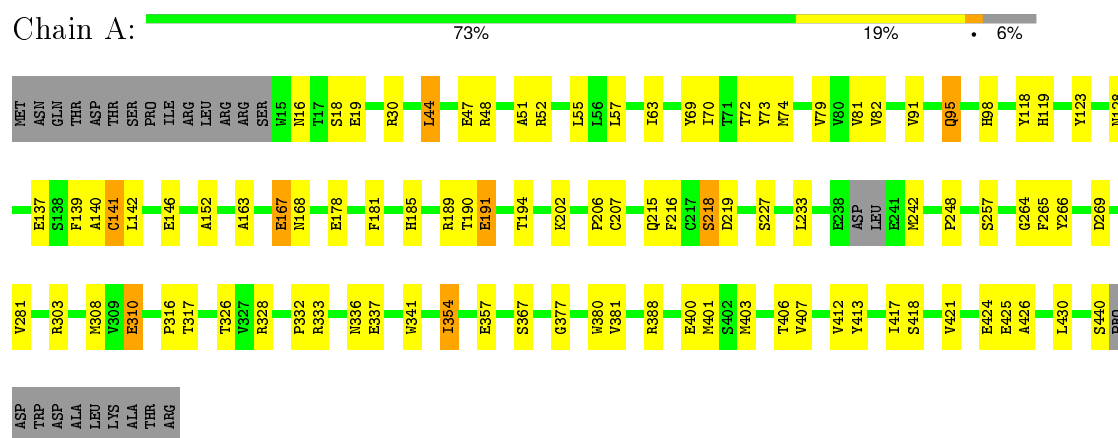
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	14	Total O 14 14	0	0
7	B	4	Total O 4 4	0	0

3 Residue-property plots

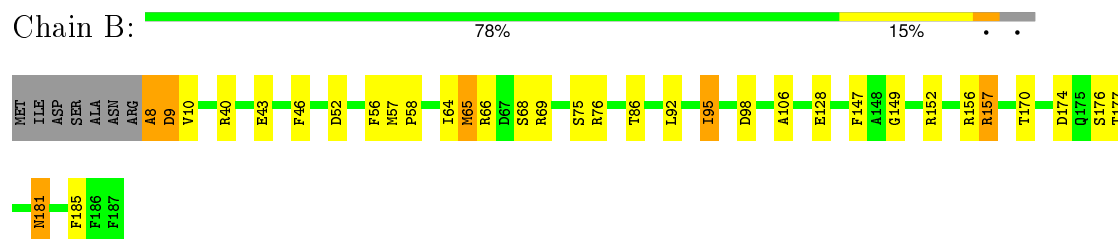
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS failed to run properly.

- Molecule 1: Benzene 1,2-dioxygenase subunit alpha



- Molecule 2: Benzene 1,2-dioxygenase subunit beta



4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 43 3 2	Depositor
Cell constants a, b, c, α , β , γ	234.53Å 234.53Å 234.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.20	Depositor
% Data completeness (in resolution range)	100.0 (20.00-3.20)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.18 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.185 , 0.208	Depositor
Wilson B-factor (Å ²)	65.2	Xtriage
Anisotropy	0.000	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 36830 reflections (0.003%)	Xtriage
Total number of atoms	4917	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.12% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MBN, FE2, FES, PE3

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	0.68	2/3465 (0.1%)	0.74	0/4706
2	B	0.68	0/1532	0.74	1/2067 (0.0%)
All	All	0.68	2/4997 (0.0%)	0.74	1/6773 (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
2	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	146	GLU	CB-CG	6.46	1.64	1.52
1	A	146	GLU	CG-CD	6.16	1.61	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	65	MET	CB-CG-SD	5.39	128.59	112.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	8	ALA	Peptide

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	3373	0	3201	59	0
2	B	1499	0	1451	17	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	4	0	0	1	0
5	A	14	0	17	3	0
6	A	7	0	8	1	0
7	A	14	0	0	0	0
7	B	4	0	0	0	0
All	All	4917	0	4677	76	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 8.

All (76) 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:A:72:THR:HG22	1:A:341:TRP:CZ3	1.77	1.18
1:A:218:SER:HB2	1:A:426:ALA:HB3	1.59	0.83
1:A:218:SER:CB	1:A:426:ALA:HB3	2.09	0.82
1:A:72:THR:HG22	1:A:341:TRP:CE3	2.15	0.82
2:B:181:ASN:H	2:B:181:ASN:HD22	1.26	0.79
1:A:336:ASN:OD1	5:A:456:PE3:H81	1.87	0.75
1:A:388:ARG:HA	5:A:456:PE3:H52	1.69	0.74
2:B:157:ARG:HH11	2:B:157:ARG:HG2	1.55	0.70
2:B:40:ARG:HD3	2:B:106:ALA:HB1	1.74	0.70
1:A:55:LEU:HD12	1:A:74:MET:HG2	1.75	0.69
2:B:157:ARG:CG	2:B:157:ARG:HH11	2.06	0.68
1:A:406:THR:HG21	1:A:425:GLU:HG2	1.76	0.67
1:A:74:MET:HE1	1:A:79:VAL:HG11	1.77	0.66
1:A:74:MET:CE	1:A:79:VAL:HG11	2.27	0.63
1:A:139:PHE:HB3	1:A:142:LEU:HB2	1.81	0.63
1:A:72:THR:CG2	1:A:341:TRP:CZ3	2.69	0.63
2:B:46:PHE:CD1	2:B:92:LEU:HD13	2.34	0.63
1:A:413:TYR:O	1:A:417:ILE:HD11	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:GLU:OE2	1:A:167:GLU:HA	2.01	0.61
1:A:264:GLY:O	1:A:310:GLU:HA	2.02	0.60
1:A:218:SER:HB3	1:A:426:ALA:HB3	1.82	0.59
1:A:72:THR:HG22	1:A:341:TRP:HZ3	1.54	0.58
1:A:119:HIS:HB2	4:A:452:FES:S2	2.44	0.58
2:B:8:ALA:N	2:B:152:ARG:HE	2.03	0.57
2:B:181:ASN:N	2:B:181:ASN:HD22	2.02	0.55
1:A:57:LEU:HD11	1:A:163:ALA:HB2	1.89	0.55
2:B:181:ASN:H	2:B:181:ASN:ND2	2.03	0.54
1:A:123:TYR:HA	1:A:128:ASN:O	2.08	0.54
1:A:140:ALA:O	1:A:141:CYS:SG	2.66	0.54
1:A:207:CYS:SG	1:A:380:TRP:HB3	2.48	0.54
1:A:137:GLU:N	1:A:137:GLU:OE1	2.39	0.53
1:A:401:MET:HB3	1:A:424:GLU:HB2	1.90	0.53
2:B:10:VAL:HG21	2:B:128:GLU:HG3	1.91	0.52
2:B:157:ARG:CG	2:B:157:ARG:NH1	2.69	0.52
1:A:47:GLU:O	1:A:51:ALA:HB3	2.10	0.51
1:A:191:GLU:CD	1:A:191:GLU:H	2.14	0.51
1:A:69:TYR:HB3	1:A:82:VAL:HG22	1.92	0.51
1:A:265:PHE:HB3	1:A:310:GLU:HB2	1.93	0.50
1:A:377:GLY:O	1:A:381:VAL:HG23	2.11	0.50
2:B:40:ARG:HD3	2:B:106:ALA:CB	2.40	0.49
1:A:95:GLN:HG3	1:A:95:GLN:O	2.12	0.49
2:B:149:GLY:HA2	2:B:174:ASP:OD2	2.13	0.49
1:A:81:VAL:HG22	1:A:91:VAL:HG22	1.94	0.48
2:B:56:PHE:O	2:B:170:THR:HA	2.13	0.48
1:A:400:GLU:O	1:A:403:MET:HG3	2.14	0.48
1:A:281:VAL:HG23	1:A:357:GLU:HG3	1.96	0.47
1:A:266:TYR:CE2	1:A:421:VAL:HG11	2.49	0.47
1:A:63:ILE:HD13	1:A:81:VAL:HG12	1.96	0.46
2:B:52:ASP:OD2	2:B:156:ARG:NH2	2.49	0.45
1:A:202:LYS:HD3	1:A:341:TRP:CE2	2.52	0.45
1:A:354:ILE:HA	1:A:354:ILE:HD12	1.87	0.45
1:A:98:HIS:CE1	1:A:119:HIS:ND1	2.83	0.45
1:A:265:PHE:HB3	1:A:310:GLU:CB	2.47	0.45
2:B:176:SER:OG	2:B:177:THR:N	2.50	0.45
1:A:215:GLN:HA	1:A:219:ASP:HB2	1.98	0.44
1:A:70:ILE:HG13	1:A:81:VAL:HB	1.99	0.44
1:A:72:THR:HB	1:A:73:TYR:H	1.32	0.44
1:A:266:TYR:HE2	1:A:421:VAL:HG11	1.82	0.44
1:A:206:PRO:HA	1:A:337:GLU:HA	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:PRO:HB3	1:A:269:ASP:HB3	1.99	0.43
1:A:44:LEU:HD12	1:A:48:ARG:HD2	1.99	0.43
1:A:216:PHE:CE1	6:A:457:MBN:H3	2.53	0.43
1:A:91:VAL:HG12	1:A:152:ALA:HB3	2.01	0.43
1:A:16:ASN:OD1	1:A:18:SER:HB2	2.19	0.43
2:B:57:MET:HA	2:B:58:PRO:HD2	1.83	0.43
1:A:181:PHE:CE2	1:A:303:ARG:NH1	2.87	0.43
1:A:57:LEU:HD11	1:A:163:ALA:CB	2.49	0.42
1:A:16:ASN:ND2	1:A:19:GLU:OE1	2.53	0.42
2:B:147:PHE:CE1	2:B:185:PHE:HZ	2.37	0.42
1:A:185:HIS:O	1:A:189:ARG:HD2	2.20	0.41
1:A:72:THR:CG2	1:A:341:TRP:HZ3	2.25	0.41
1:A:74:MET:HE3	1:A:79:VAL:HG11	2.01	0.41
1:A:74:MET:HB2	1:A:74:MET:HE3	1.55	0.41
1:A:332:PRO:O	1:A:333:ARG:HD3	2.21	0.40
1:A:388:ARG:HA	5:A:456:PE3:C5	2.46	0.40
1:A:316:PRO:HB2	1:A:317:THR:HG23	2.03	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	420/450 (93%)	381 (91%)	36 (9%)	3 (1%)	26	72
2	B	178/187 (95%)	166 (93%)	10 (6%)	2 (1%)	17	62
All	All	598/637 (94%)	547 (92%)	46 (8%)	5 (1%)	24	69

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	141	CYS

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Mol	Chain	Res	Type
2	B	9	ASP
2	B	95	ILE
1	A	167	GLU
1	A	310	GLU

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	352/376 (94%)	327 (93%)	25 (7%)	18	57
2	B	159/165 (96%)	145 (91%)	14 (9%)	12	45
All	All	511/541 (94%)	472 (92%)	39 (8%)	16	55

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	44	LEU
1	A	52	ARG
1	A	95	GLN
1	A	118	TYR
1	A	168	ASN
1	A	178	GLU
1	A	190	THR
1	A	191	GLU
1	A	194	THR
1	A	218	SER
1	A	227	SER
1	A	233	LEU
1	A	242	MET
1	A	257	SER
1	A	308	MET
1	A	326	THR
1	A	328	ARG
1	A	354	ILE

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Mol	Chain	Res	Type
1	A	367	SER
1	A	407	VAL
1	A	412	VAL
1	A	418	SER
1	A	430	LEU
1	A	440	SER
2	B	9	ASP
2	B	43	GLU
2	B	64	ILE
2	B	65	MET
2	B	66	ARG
2	B	68	SER
2	B	69	ARG
2	B	75	SER
2	B	76	ARG
2	B	86	THR
2	B	95	ILE
2	B	98	ASP
2	B	157	ARG
2	B	181	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	311	HIS
2	B	143	GLN
2	B	181	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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$
4	FES	A	452	1	0,4,4	0.00	-	0,4,4	0.00	-
5	PE3	A	456	-	13,13,42	2.03	4 (30%)	12,12,41	1.75	3 (25%)
6	MBN	A	457	-	7,7,7	0.71	0	8,8,8	0.49	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
4	FES	A	452	1	-	0/0/4/4	0/1/1/1
5	PE3	A	456	-	-	0/11/11/40	0/0/0/0
6	MBN	A	457	-	-	0/0/0/0	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	456	PE3	O4-C3	2.37	1.52	1.42
5	A	456	PE3	C11-C12	2.65	1.62	1.48
5	A	456	PE3	O13-C12	3.65	1.62	1.40
5	A	456	PE3	C5-C6	4.28	1.70	1.48

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	456	PE3	O10-C9-C8	2.10	119.68	110.36
5	A	456	PE3	O7-C6-C5	3.44	125.66	110.36
5	A	456	PE3	O1-C2-C3	3.58	134.15	112.03

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	452	FES	1	0
5	A	456	PE3	3	0
6	A	457	MBN	1	0

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 ⓘ

EDS failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.