



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 31, 2023 – 10:02 PM EDT

PDB ID : 2OAT
Title : ORNITHINE AMINOTRANSFERASE COMPLEXED WITH 5-FLUOROMETHYLORNITHINE
Authors : Storici, P.; Schirmer, T.
Deposited on : 1998-05-07
Resolution : 1.95 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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.34

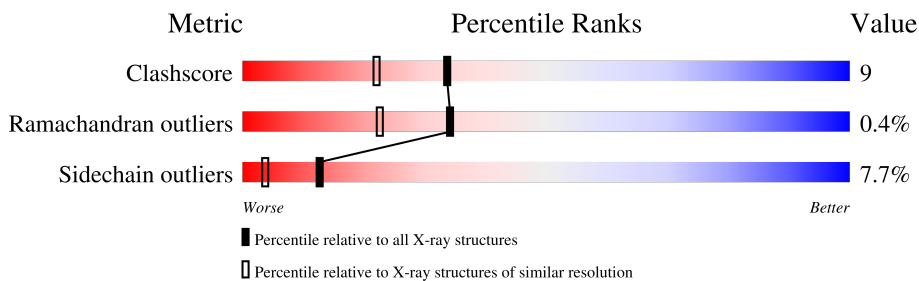
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	439	
1	B	439	
1	C	439	

2 Entry composition i

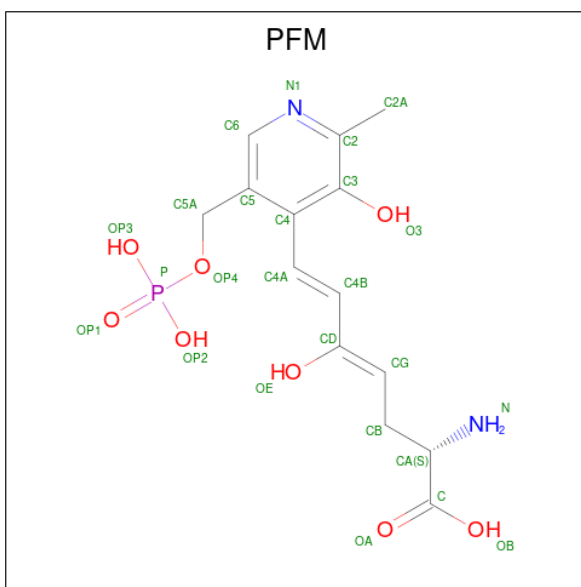
There are 3 unique types of molecules in this entry. The entry contains 10302 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ORNITHINE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	404	Total 3161	C 2030	N 533	O 586	S 12	0	0	0
1	B	404	Total 3161	C 2030	N 533	O 586	S 12	0	0	0
1	C	404	Total 3161	C 2030	N 533	O 586	S 12	0	0	0

- Molecule 2 is 1-AMINO-7-(2-METHYL-3-OXIDO-5-((PHOSPHONOXY)METHYL)-4-PYRIDOXAL-5-OXO-6-HEPTENATE (three-letter code: PFM) (formula: C₁₄H₁₉N₂O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 25	C 14	N 2	O 8	P 1	0	0
2	B	1	Total 25	C 14	N 2	O 8	P 1	0	0
2	C	1	Total 25	C 14	N 2	O 8	P 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	236	Total 236	O 236	2	0
3	B	250	Total 250	O 250	0	0
3	C	258	Total 258	O 258	1	0

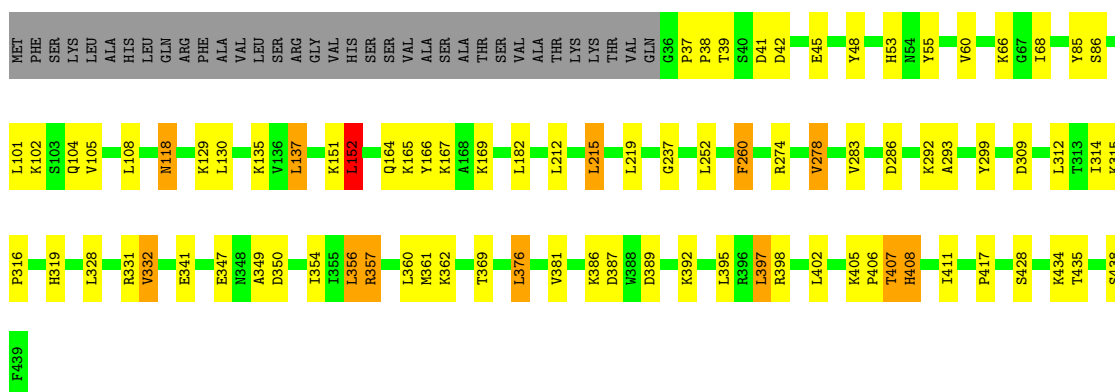
3 Residue-property plots [i](#)

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. 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. 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 was not executed.

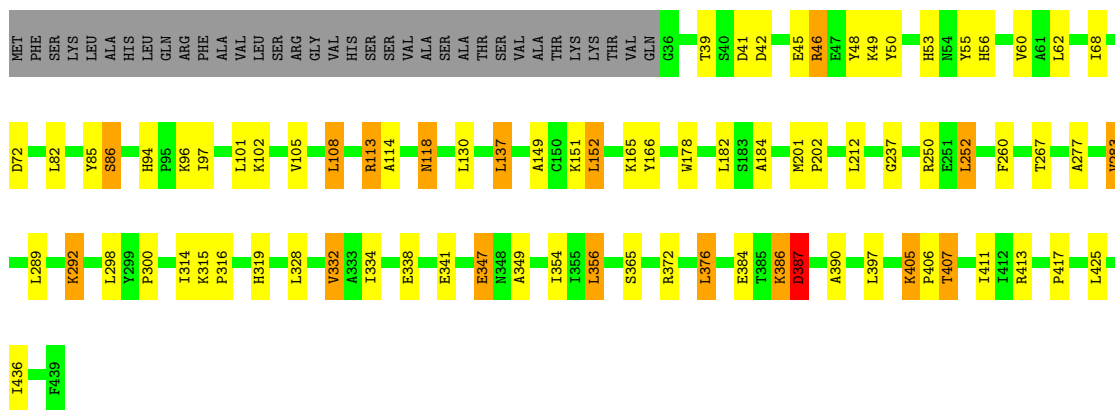
- Molecule 1: ORNITHINE AMINOTRANSFERASE

Chain A: 



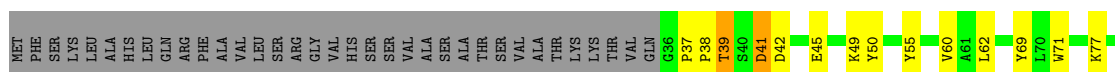
- Molecule 1: ORNITHINE AMINOTRANSFERASE

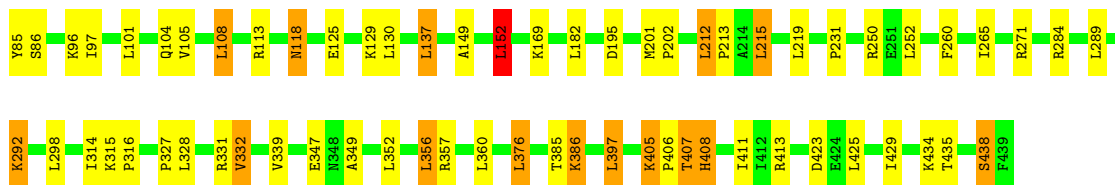
Chain B: 



- Molecule 1: ORNITHINE AMINOTRANSFERASE

Chain C: 





4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	115.28Å 115.28Å 186.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.60 – 1.95	Depositor
% Data completeness (in resolution range)	97.0 (19.60-1.95)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	REFMAC, X-PLOR	Depositor
R, R_{free}	0.204 , 0.232	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	10302	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

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: PFM

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	0.62	0/3235	0.98	6/4393 (0.1%)
1	B	0.64	0/3235	1.02	8/4393 (0.2%)
1	C	0.65	0/3235	1.04	11/4393 (0.3%)
All	All	0.64	0/9705	1.02	25/13179 (0.2%)

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	413	ARG	CD-NE-CZ	11.92	140.29	123.60
1	C	113	ARG	NE-CZ-NH1	-6.95	116.83	120.30
1	C	413	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	B	252	LEU	CA-CB-CG	6.53	130.33	115.30
1	B	413	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	C	357	ARG	CD-NE-CZ	6.10	132.14	123.60
1	B	387	ASP	CB-CG-OD1	6.09	123.78	118.30
1	A	286	ASP	CB-CG-OD1	-6.00	112.90	118.30
1	A	260	PHE	CB-CG-CD1	5.88	124.91	120.80
1	C	137	LEU	CA-CB-CG	5.78	128.59	115.30
1	B	137	LEU	CA-CB-CG	5.61	128.20	115.30
1	A	137	LEU	CA-CB-CG	5.54	128.04	115.30
1	B	46	ARG	CD-NE-CZ	5.52	131.33	123.60
1	C	152	LEU	CA-CB-CG	5.48	127.91	115.30
1	C	55	TYR	CA-CB-CG	5.42	123.70	113.40
1	A	274	ARG	CD-NE-CZ	5.41	131.17	123.60
1	C	423	ASP	CB-CG-OD1	5.41	123.17	118.30
1	A	152	LEU	CA-CB-CG	5.38	127.67	115.30
1	C	195	ASP	CB-CG-OD1	5.34	123.10	118.30
1	B	413	ARG	CD-NE-CZ	5.33	131.06	123.60
1	C	284	ARG	NE-CZ-NH1	-5.30	117.65	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	357	ARG	CD-NE-CZ	5.11	130.75	123.60
1	B	113	ARG	NE-CZ-NH1	-5.06	117.77	120.30
1	B	108	LEU	CA-CB-CG	5.05	126.91	115.30
1	C	231	PRO	C-N-CA	5.05	134.32	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3161	0	3165	57	0
1	B	3161	0	3165	58	0
1	C	3161	0	3165	50	0
2	A	25	0	15	2	0
2	B	25	0	14	1	0
2	C	25	0	16	3	0
3	A	236	0	0	4	0
3	B	250	0	0	14	0
3	C	258	0	0	7	0
All	All	10302	0	9540	163	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 9.

All (163) 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:309:ASP:HB3	3:A:659:HOH:O	1.65	0.95
1:C:101:LEU:O	1:C:105:VAL:HG23	1.68	0.92
1:C:250:ARG:HD2	3:C:649:HOH:O	1.69	0.91
1:C:407:THR:HB	3:C:669:HOH:O	1.71	0.90
1:B:101:LEU:HD12	1:B:328:LEU:HD11	1.55	0.88
1:C:349:ALA:HA	1:C:376:LEU:HD22	1.53	0.88
1:B:101:LEU:O	1:B:105:VAL:HG23	1.75	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:LEU:HD12	1:C:328:LEU:HD11	1.61	0.82
1:A:101:LEU:O	1:A:105:VAL:HG23	1.79	0.81
1:B:407:THR:HG22	1:B:411:ILE:HB	1.63	0.80
1:C:405:LYS:NZ	3:C:694:HOH:O	2.16	0.79
1:B:86:SER:HB2	3:B:651:HOH:O	1.83	0.77
1:B:283:VAL:HG13	3:B:640:HOH:O	1.84	0.76
1:A:349:ALA:HA	1:A:376:LEU:HD22	1.66	0.76
1:B:39:THR:HG23	1:B:42:ASP:H	1.50	0.75
1:B:250:ARG:HD2	3:B:640:HOH:O	1.87	0.73
1:A:405:LYS:HG3	1:A:406:PRO:HD2	1.71	0.73
2:C:440:PFM:OA	3:C:556:HOH:O	2.07	0.73
1:A:357:ARG:O	1:A:361:MET:HG3	1.88	0.72
1:A:39:THR:HG23	1:A:42:ASP:H	1.53	0.71
1:A:101:LEU:HD23	1:B:105:VAL:HG21	1.72	0.71
1:B:349:ALA:HA	1:B:376:LEU:HD22	1.72	0.70
1:C:397:LEU:HD13	1:C:435:THR:HG21	1.75	0.69
1:C:85:TYR:O	1:C:86:SER:HB2	1.93	0.69
1:C:407:THR:HG23	1:C:407:THR:O	1.92	0.68
1:C:328:LEU:O	1:C:332:VAL:HG13	1.93	0.68
1:C:405:LYS:HD3	1:C:406:PRO:HD2	1.75	0.68
1:C:39:THR:HG22	1:C:42:ASP:H	1.57	0.68
1:A:407:THR:HG22	1:A:411:ILE:HB	1.76	0.67
1:A:85:TYR:O	1:A:86:SER:HB2	1.95	0.66
1:A:151:LYS:NZ	1:A:319:HIS:HD2	1.94	0.65
1:B:82:LEU:HD12	3:B:664:HOH:O	1.96	0.65
1:B:151:LYS:HZ3	1:B:319:HIS:HD2	1.44	0.64
1:B:151:LYS:NZ	1:B:319:HIS:HD2	1.96	0.63
1:A:354:ILE:HD13	1:A:357:ARG:NH2	2.14	0.62
1:C:352:LEU:HB3	1:C:425:LEU:HD22	1.82	0.61
1:B:384:GLU:HB3	3:B:547:HOH:O	2.00	0.60
1:C:118:ASN:H	1:C:118:ASN:HD22	1.49	0.60
1:B:356:LEU:HG	1:B:425:LEU:HD11	1.82	0.60
1:A:151:LYS:HZ3	1:A:319:HIS:HD2	1.50	0.60
1:B:237:GLY:HA2	1:B:407:THR:HG21	1.83	0.59
1:A:101:LEU:CD2	1:B:105:VAL:HG21	2.34	0.58
1:A:48:TYR:O	1:A:53:HIS:HE1	1.86	0.58
1:C:101:LEU:HD13	1:C:332:VAL:HG11	1.85	0.58
1:B:46:ARG:HD3	3:B:636:HOH:O	2.02	0.58
1:C:407:THR:O	1:C:407:THR:CG2	2.51	0.58
2:A:440:PFM:OE	2:A:440:PFM:HA	2.04	0.57
1:B:118:ASN:HD22	1:B:118:ASN:H	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:LEU:HD13	1:B:314:ILE:HD12	1.86	0.57
1:A:118:ASN:HD22	1:A:118:ASN:H	1.51	0.56
1:A:169:LYS:HD3	3:A:631:HOH:O	2.06	0.56
1:C:405:LYS:CD	1:C:406:PRO:HD2	2.35	0.55
1:C:169:LYS:HD3	3:C:654:HOH:O	2.06	0.55
1:A:39:THR:HG22	1:A:42:ASP:CG	2.26	0.55
1:C:39:THR:HG23	1:C:41:ASP:H	1.72	0.55
1:A:315:LYS:HB3	1:A:316:PRO:HD2	1.90	0.54
1:A:356:LEU:HD22	1:A:360:LEU:CD1	2.37	0.54
1:B:390:ALA:HB1	1:B:406:PRO:HB3	1.89	0.54
2:C:440:PFM:H4B	2:C:440:PFM:O3	2.06	0.54
1:A:68:ILE:HG12	3:A:674:HOH:O	2.07	0.53
1:A:105:VAL:HG22	1:A:328:LEU:HD11	1.88	0.53
1:C:101:LEU:HD22	1:C:298:LEU:HD23	1.91	0.53
1:B:48:TYR:O	1:B:53:HIS:HE1	1.92	0.52
1:B:49:LYS:HD3	1:B:50:TYR:CZ	2.44	0.52
2:C:440:PFM:HG	3:C:556:HOH:O	2.08	0.52
1:A:152:LEU:HD13	1:A:314:ILE:HD12	1.92	0.52
1:B:151:LYS:HZ3	1:B:319:HIS:CD2	2.26	0.52
1:A:39:THR:CG2	1:A:42:ASP:H	2.22	0.51
1:B:372:ARG:HD2	3:B:681:HOH:O	2.08	0.51
1:C:386:LYS:H	1:C:386:LYS:CE	2.24	0.51
1:C:152:LEU:HD13	1:C:314:ILE:CD1	2.41	0.51
1:C:152:LEU:HD13	1:C:314:ILE:HD12	1.91	0.51
1:C:407:THR:HG22	1:C:411:ILE:HB	1.92	0.51
1:B:39:THR:HG22	1:B:42:ASP:CG	2.30	0.51
1:B:149:ALA:HB2	1:B:289:LEU:HD21	1.93	0.51
1:C:386:LYS:H	1:C:386:LYS:CD	2.23	0.51
1:A:237:GLY:HA2	1:A:407:THR:HG21	1.92	0.51
1:A:278:VAL:HG13	1:A:283:VAL:O	2.10	0.50
1:A:356:LEU:HD22	1:A:360:LEU:HD11	1.91	0.50
1:B:96:LYS:HE2	1:B:338:GLU:OE1	2.11	0.50
1:B:386:LYS:HE3	1:B:386:LYS:H	1.76	0.50
1:C:385:THR:HB	1:C:386:LYS:NZ	2.26	0.50
1:B:55:TYR:OH	2:B:440:PFM:N	2.44	0.50
1:A:397:LEU:HD13	1:A:435:THR:HG21	1.94	0.50
1:C:125:GLU:HG2	1:C:129:LYS:HE2	1.93	0.50
1:A:405:LYS:HG3	1:A:406:PRO:CD	2.42	0.49
1:C:425:LEU:O	1:C:429:ILE:HG13	2.11	0.49
1:B:152:LEU:HD13	1:B:314:ILE:CD1	2.41	0.49
1:B:277:ALA:HB2	3:B:455:HOH:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:178:TRP:CZ2	1:B:184:ALA:HA	2.48	0.48
1:C:71:TRP:CZ2	1:C:77:LYS:HD2	2.48	0.48
1:A:86:SER:O	1:A:293:ALA:HB2	2.13	0.48
1:A:402:LEU:CD1	1:A:428:SER:HB3	2.43	0.48
1:C:202:PRO:HB3	3:C:664:HOH:O	2.13	0.48
1:A:102:LYS:HD3	1:B:102:LYS:HD3	1.95	0.48
1:B:386:LYS:HE3	1:B:386:LYS:N	2.29	0.48
1:A:407:THR:O	1:A:407:THR:HG23	2.13	0.48
1:B:277:ALA:N	3:B:455:HOH:O	2.47	0.48
1:B:267:THR:O	3:B:455:HOH:O	2.20	0.47
1:A:405:LYS:CG	1:A:406:PRO:HD2	2.40	0.47
1:C:97:ILE:HG22	1:C:298:LEU:HD22	1.96	0.47
1:A:395:LEU:O	1:A:398:ARG:HB3	2.15	0.47
1:A:151:LYS:NZ	1:A:319:HIS:CD2	2.80	0.46
1:A:215:LEU:HD22	1:A:219:LEU:HG	1.96	0.46
1:C:104:GLN:HB2	1:C:331:ARG:HG3	1.98	0.46
1:A:37:PRO:HA	1:A:38:PRO:HD3	1.87	0.46
1:A:105:VAL:HG11	1:B:101:LEU:HD23	1.97	0.46
1:C:212:LEU:N	1:C:213:PRO:CD	2.79	0.46
1:A:105:VAL:HG22	1:A:328:LEU:CD1	2.46	0.45
1:A:55:TYR:CE2	1:B:113:ARG:HG3	2.52	0.45
1:A:316:PRO:HB3	1:B:56:HIS:HB2	1.97	0.45
1:A:101:LEU:HD13	1:A:332:VAL:HG11	1.99	0.45
1:B:405:LYS:HG3	1:B:406:PRO:HD2	1.98	0.45
1:C:85:TYR:HB3	1:C:292:LYS:HZ3	1.81	0.45
1:C:356:LEU:HD22	1:C:360:LEU:HD11	1.99	0.45
1:A:68:ILE:HA	1:A:417:PRO:HG2	1.97	0.45
1:A:299:TYR:CZ	1:B:300:PRO:HD3	2.52	0.44
1:A:381:VAL:HG22	1:A:411:ILE:HG12	1.98	0.44
1:C:96:LYS:HD3	1:C:339:VAL:HG23	1.99	0.44
1:B:62:LEU:HA	1:B:72:ASP:HA	2.00	0.44
1:C:315:LYS:HB3	1:C:316:PRO:CD	2.48	0.44
1:B:151:LYS:NZ	1:B:319:HIS:CD2	2.82	0.44
1:C:101:LEU:HD12	1:C:328:LEU:CD1	2.40	0.44
1:C:149:ALA:HB2	1:C:289:LEU:HD21	1.98	0.44
1:A:164:GLN:HB3	1:A:167:LYS:HD2	2.00	0.43
1:A:376:LEU:HD12	1:A:376:LEU:HA	1.92	0.43
1:A:315:LYS:HB3	1:A:316:PRO:CD	2.48	0.43
1:A:407:THR:O	1:A:408:HIS:CG	2.71	0.43
1:C:49:LYS:HD3	1:C:50:TYR:CZ	2.53	0.43
1:A:350:ASP:HA	3:A:450:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:68:ILE:HA	1:B:417:PRO:HG2	2.01	0.43
1:C:69:TYR:CG	1:C:77:LYS:HE3	2.54	0.43
1:A:165:LYS:HA	1:A:166:TYR:HA	1.76	0.43
1:A:328:LEU:O	1:A:332:VAL:HG13	2.19	0.43
1:B:94:HIS:HA	3:B:453:HOH:O	2.18	0.43
1:C:37:PRO:HA	1:C:38:PRO:HD3	1.84	0.43
1:B:85:TYR:HB3	1:B:292:LYS:NZ	2.34	0.42
1:A:389:ASP:OD1	1:A:392:LYS:HG3	2.19	0.42
1:C:108:LEU:HD13	1:C:327:PRO:HG3	2.00	0.42
1:C:315:LYS:HB3	1:C:316:PRO:HD2	2.00	0.42
1:B:387:ASP:OD1	1:B:387:ASP:C	2.58	0.42
1:A:135:LYS:HE2	1:A:312:LEU:HD21	2.00	0.42
1:B:113:ARG:HA	1:B:113:ARG:HD2	1.76	0.42
1:C:356:LEU:O	1:C:360:LEU:HG	2.20	0.42
1:B:315:LYS:HB3	1:B:316:PRO:HD2	2.02	0.41
1:A:104:GLN:HB2	1:A:331:ARG:HG3	2.01	0.41
1:B:334:ILE:O	1:B:338:GLU:HG3	2.21	0.41
1:B:165:LYS:HA	1:B:166:TYR:HA	1.77	0.41
1:B:386:LYS:H	1:B:386:LYS:CE	2.33	0.41
2:A:440:PFM:H4B	2:A:440:PFM:O3	2.20	0.41
1:B:97:ILE:HG22	1:B:298:LEU:HD22	2.02	0.41
1:B:347:GLU:HB2	3:B:541:HOH:O	2.20	0.41
1:C:407:THR:O	1:C:408:HIS:CG	2.74	0.41
1:B:390:ALA:CB	1:B:406:PRO:HB3	2.52	0.40
1:A:434:LYS:O	1:A:438:SER:HB3	2.21	0.40
1:B:114:ALA:HA	3:B:456:HOH:O	2.21	0.40
1:C:265:ILE:HG22	1:C:292:LYS:HD2	2.02	0.40
1:C:434:LYS:O	1:C:438:SER:HB3	2.20	0.40
1:C:201:MET:SD	1:C:202:PRO:HD2	2.61	0.40
1:C:215:LEU:HD22	1:C:219:LEU:HG	2.02	0.40
1:B:201:MET:SD	1:B:202:PRO:HD2	2.61	0.40
1:B:328:LEU:O	1:B:332:VAL:HG13	2.22	0.40
1:A:66:LYS:HE2	3:B:448:HOH:O	2.22	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	402/439 (92%)	387 (96%)	13 (3%)	2 (0%)	29	17
1	B	402/439 (92%)	388 (96%)	13 (3%)	1 (0%)	47	38
1	C	402/439 (92%)	382 (95%)	18 (4%)	2 (0%)	29	17
All	All	1206/1317 (92%)	1157 (96%)	44 (4%)	5 (0%)	34	22

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	408	HIS
1	A	408	HIS
1	A	292	LYS
1	C	292	LYS
1	B	292	LYS

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	337/366 (92%)	311 (92%)	26 (8%)	13	4
1	B	337/366 (92%)	310 (92%)	27 (8%)	12	3
1	C	337/366 (92%)	312 (93%)	25 (7%)	13	4
All	All	1011/1098 (92%)	933 (92%)	78 (8%)	13	4

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ASP
1	A	45	GLU
1	A	60	VAL
1	A	108	LEU
1	A	118	ASN
1	A	129	LYS
1	A	130	LEU
1	A	137	LEU
1	A	152	LEU
1	A	182	LEU
1	A	212	LEU
1	A	215	LEU
1	A	252	LEU
1	A	260	PHE
1	A	278	VAL
1	A	332	VAL
1	A	341	GLU
1	A	347	GLU
1	A	356	LEU
1	A	362	LYS
1	A	369	THR
1	A	376	LEU
1	A	386	LYS
1	A	387	ASP
1	A	397	LEU
1	A	407	THR
1	B	41	ASP
1	B	45	GLU
1	B	60	VAL
1	B	86	SER
1	B	108	LEU
1	B	118	ASN
1	B	130	LEU
1	B	137	LEU
1	B	152	LEU
1	B	182	LEU
1	B	212	LEU
1	B	252	LEU
1	B	260	PHE
1	B	283	VAL
1	B	332	VAL
1	B	341	GLU
1	B	347	GLU

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Mol	Chain	Res	Type
1	B	354	ILE
1	B	356	LEU
1	B	365	SER
1	B	376	LEU
1	B	386	LYS
1	B	387	ASP
1	B	397	LEU
1	B	405	LYS
1	B	407	THR
1	B	436	ILE
1	C	39	THR
1	C	41	ASP
1	C	45	GLU
1	C	60	VAL
1	C	62	LEU
1	C	108	LEU
1	C	118	ASN
1	C	130	LEU
1	C	137	LEU
1	C	152	LEU
1	C	182	LEU
1	C	212	LEU
1	C	215	LEU
1	C	252	LEU
1	C	260	PHE
1	C	271	ARG
1	C	332	VAL
1	C	347	GLU
1	C	356	LEU
1	C	376	LEU
1	C	386	LYS
1	C	397	LEU
1	C	405	LYS
1	C	407	THR
1	C	438	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	HIS
1	A	118	ASN
1	A	132	ASN

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Mol	Chain	Res	Type
1	A	282	ASN
1	A	319	HIS
1	A	400	ASN
1	B	53	HIS
1	B	118	ASN
1	B	132	ASN
1	B	319	HIS
1	B	400	ASN
1	C	118	ASN
1	C	132	ASN
1	C	400	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](#)

3 ligands are modelled in this entry.

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
2	PFM	A	440	-	24,25,25	6.11	3 (12%)	30,35,35	1.44	4 (13%)
2	PFM	B	440	-	24,25,25	6.36	6 (25%)	30,35,35	1.42	6 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PFM	C	440	-	24,25,25	7.20	8 (33%)	30,35,35	3.11	6 (20%)

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
2	PFM	A	440	-	-	10/18/20/20	0/1/1/1
2	PFM	B	440	-	-	8/18/20/20	0/1/1/1
2	PFM	C	440	-	-	3/18/20/20	0/1/1/1

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	440	PFM	CG-CD	32.66	1.54	1.32
2	B	440	PFM	CG-CD	29.42	1.52	1.32
2	A	440	PFM	CG-CD	28.09	1.51	1.32
2	C	440	PFM	C4B-CD	-9.41	1.33	1.45
2	A	440	PFM	C4B-CD	-6.83	1.36	1.45
2	B	440	PFM	C4B-CD	-6.57	1.37	1.45
2	C	440	PFM	C4-C4A	-6.26	1.34	1.47
2	A	440	PFM	C4-C4A	-5.75	1.35	1.47
2	B	440	PFM	C4-C4A	-5.34	1.36	1.47
2	C	440	PFM	C3-C2	-3.74	1.37	1.40
2	C	440	PFM	C2A-C2	2.57	1.54	1.50
2	C	440	PFM	C2-N1	2.46	1.38	1.33
2	C	440	PFM	C6-N1	2.17	1.39	1.34
2	B	440	PFM	C2-N1	2.15	1.37	1.33
2	B	440	PFM	C4-C5	-2.13	1.39	1.42
2	B	440	PFM	C2A-C2	2.08	1.53	1.50
2	C	440	PFM	OE-CD	2.06	1.39	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	440	PFM	CB-CG-CD	-10.07	110.70	126.25
2	C	440	PFM	OE-CD-CG	-9.80	112.36	121.11
2	C	440	PFM	OE-CD-C4B	6.90	124.76	116.85
2	C	440	PFM	OB-C-CA	3.75	126.17	113.38
2	A	440	PFM	OE-CD-C4B	3.55	120.92	116.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	440	PFM	OE-CD-C4B	3.40	120.75	116.85
2	A	440	PFM	OE-CD-CG	-2.99	118.44	121.11
2	B	440	PFM	OP2-P-OP4	-2.98	98.81	106.73
2	B	440	PFM	CB-CG-CD	-2.51	122.37	126.25
2	B	440	PFM	C4B-CD-CG	-2.50	118.87	122.19
2	A	440	PFM	CB-CG-CD	-2.21	122.84	126.25
2	C	440	PFM	OB-C-OA	-2.17	119.16	124.09
2	C	440	PFM	OA-C-CA	-2.13	114.61	122.14
2	B	440	PFM	C6-C5-C4	2.09	122.00	118.15
2	B	440	PFM	OP3-P-OP1	2.09	118.85	110.68
2	A	440	PFM	C5-C6-N1	-2.05	120.40	123.82

There are no chirality outliers.

All (21) torsion outliers are listed below:

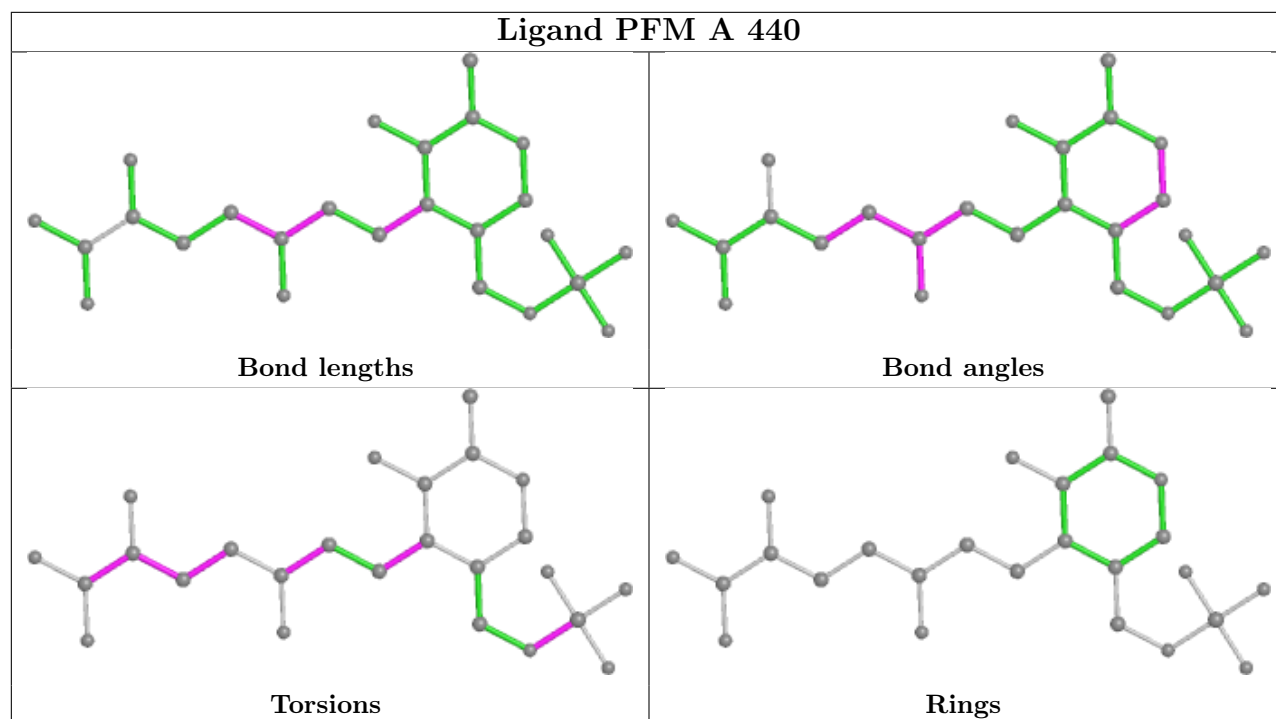
Mol	Chain	Res	Type	Atoms
2	A	440	PFM	OA-C-CA-N
2	A	440	PFM	N-CA-CB-CG
2	A	440	PFM	C-CA-CB-CG
2	A	440	PFM	CA-CB-CG-CD
2	A	440	PFM	C4A-C4B-CD-CG
2	B	440	PFM	C-CA-CB-CG
2	B	440	PFM	C4A-C4B-CD-CG
2	B	440	PFM	C4A-C4B-CD-OE
2	C	440	PFM	C4A-C4B-CD-CG
2	C	440	PFM	C4A-C4B-CD-OE
2	A	440	PFM	OB-C-CA-N
2	B	440	PFM	CA-CB-CG-CD
2	A	440	PFM	OB-C-CA-CB
2	A	440	PFM	OA-C-CA-CB
2	B	440	PFM	N-CA-CB-CG
2	B	440	PFM	OA-C-CA-N
2	C	440	PFM	C5-C4-C4A-C4B
2	A	440	PFM	C5A-OP4-P-OP3
2	B	440	PFM	C3-C4-C4A-C4B
2	B	440	PFM	OB-C-CA-N
2	A	440	PFM	C5-C4-C4A-C4B

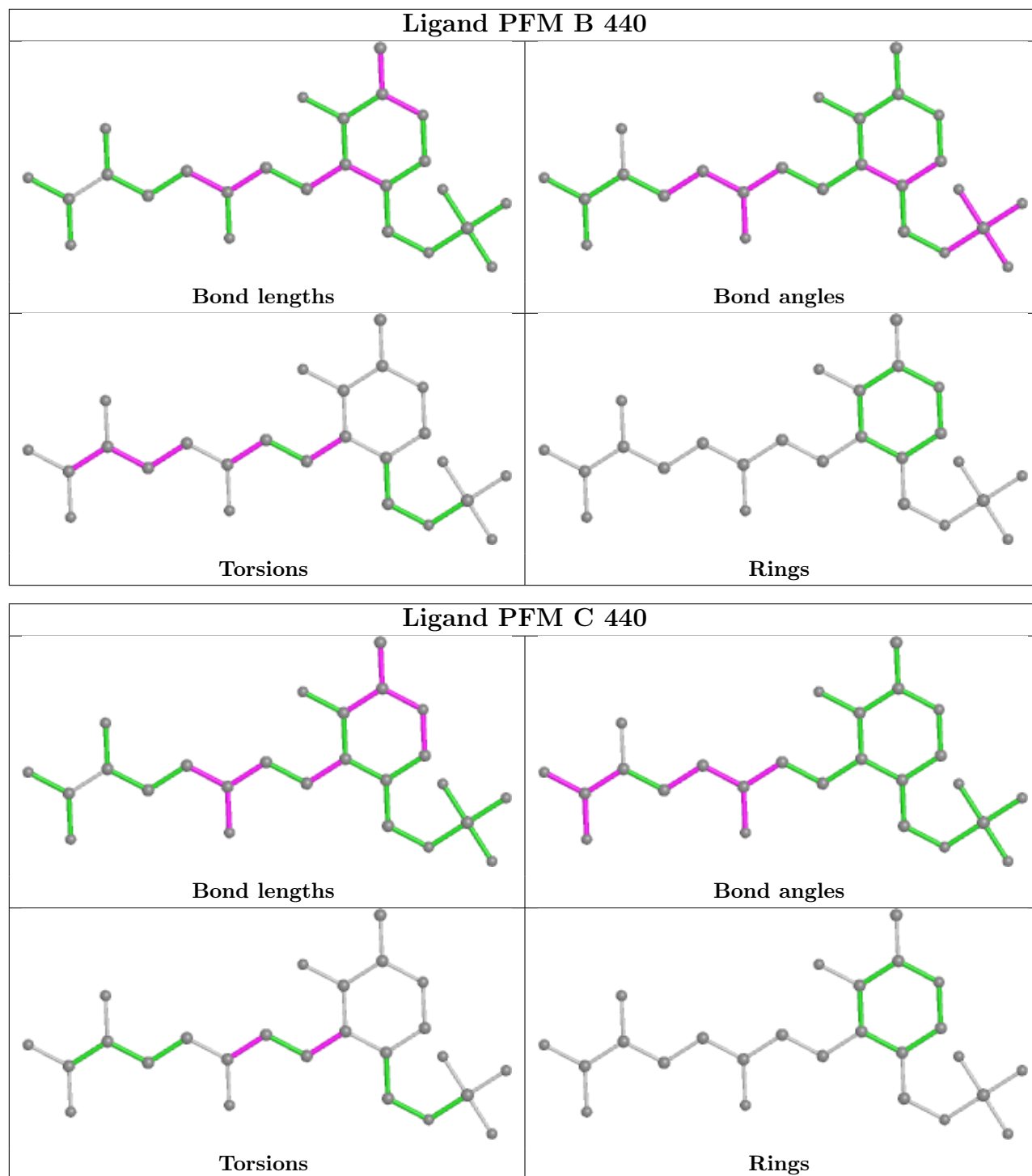
There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	440	PFM	2	0
2	B	440	PFM	1	0
2	C	440	PFM	3	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

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.