



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 07:21 am BST

PDB ID : 3NOS  
Title : HUMAN ENDOTHELIAL NITRIC OXIDE SYNTHASE WITH ARGININE  
SUBSTRATE  
Authors : Fischmann, T.O.; Weber, P.C.  
Deposited on : 1999-02-03  
Resolution : 2.40 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](mailto: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.

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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) : **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) : 2.11

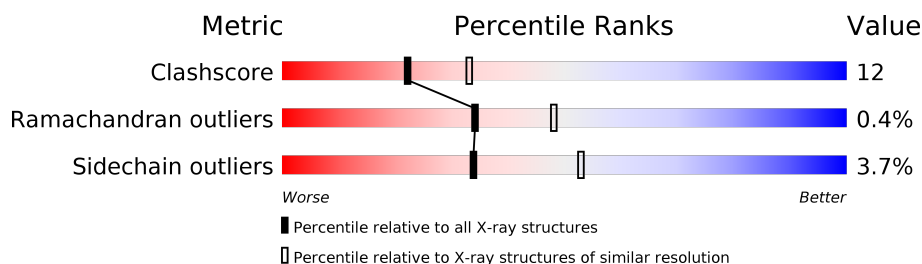
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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  $\geq 3$ , 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	427	
1	B	427	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7042 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.

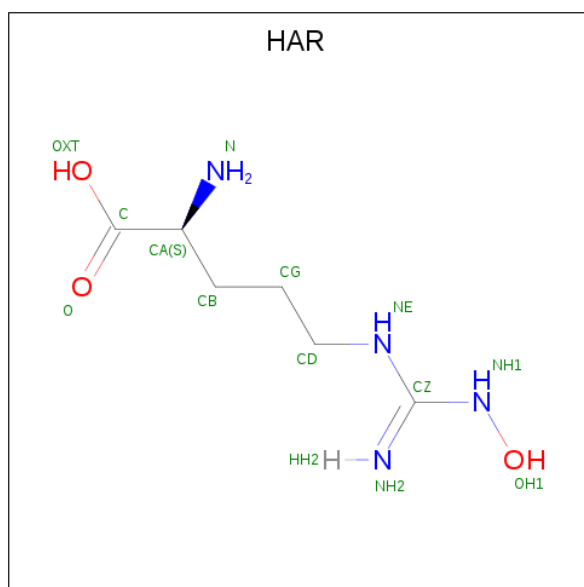
- Molecule 1 is a protein called ENDOTHELIAL NITRIC-OXIDE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	0	0	0
			3198	2037	566	579	16			
1	B	400	Total	C	N	O	S	0	0	0
			3198	2037	566	579	16			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is N-OMEGA-HYDROXY-L-ARGININE (three-letter code: HAR) (formula: C<sub>6</sub>H<sub>14</sub>N<sub>4</sub>O<sub>3</sub>).



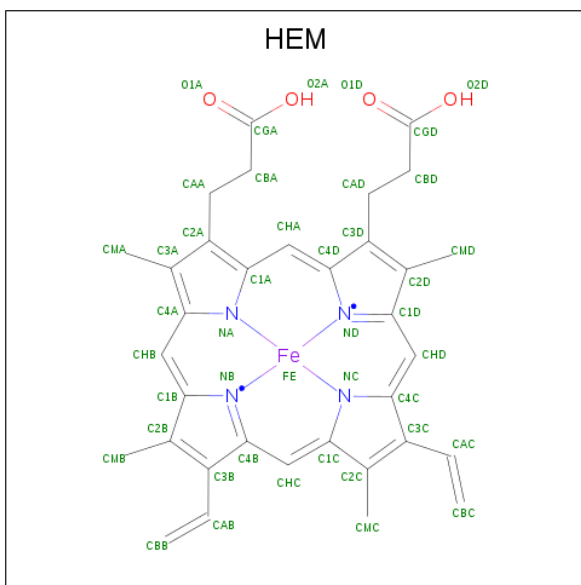
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			13	6	4	3		

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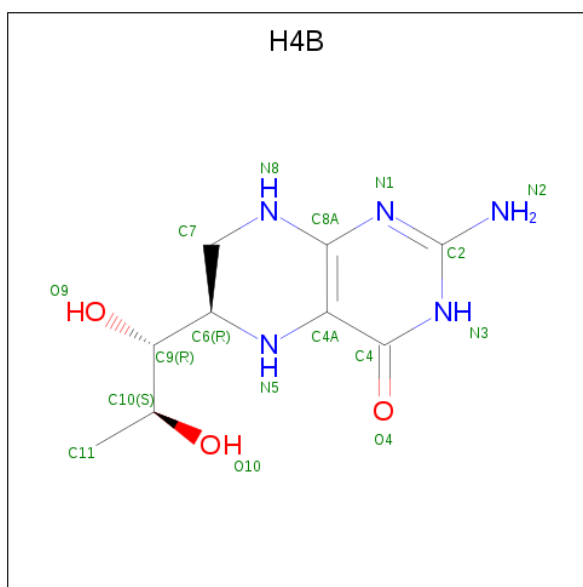
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			13	6	4	3		

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
4	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 5 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula:  $\text{C}_9\text{H}_{15}\text{N}_5\text{O}_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total 17	C 9	N 5	O 3	0	0
5	B	1	Total 17	C 9	N 5	O 3	0	0

- Molecule 6 is water.

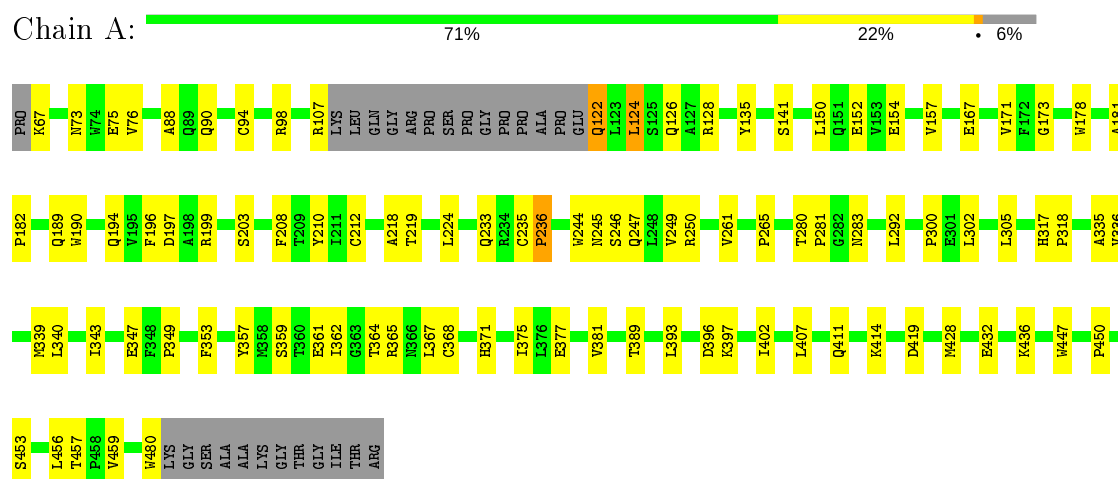
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	253	Total O 253 253	0	0
6	B	246	Total O 246 246	0	0

### 3 Residue-property plots

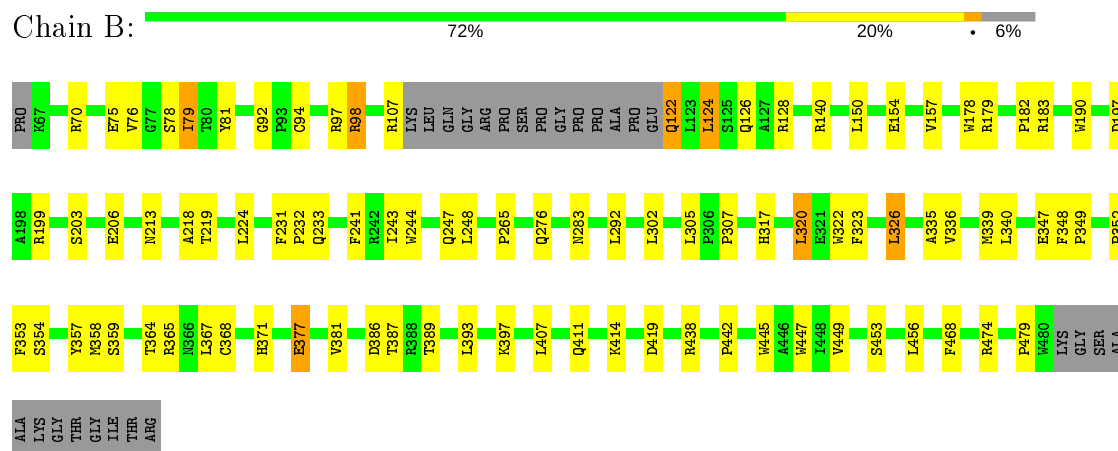
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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: ENDOTHELIAL NITRIC-OXIDE SYNTHASE



#### • Molecule 1: ENDOTHELIAL NITRIC-OXIDE SYNTHASE



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.86 Å 93.26 Å 156.12 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.40	Depositor
% Data completeness (in resolution range)	90.0 (8.00-2.40)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.193 , 0.308	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7042	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	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: HEM, ZN, HAR, H4B

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	0.50	0/3289	0.68	0/4481
1	B	0.49	0/3289	0.69	0/4481
All	All	0.49	0/6578	0.69	0/8962

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	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	135	TYR	Sidechain
1	A	210	TYR	Sidechain

### 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	3198	0	3106	75	0
1	B	3198	0	3106	75	0
2	A	1	0	0	0	0
3	A	13	0	12	2	0
3	B	13	0	12	2	0
4	A	43	0	30	11	0
4	B	43	0	30	8	0
5	A	17	0	15	2	0
5	B	17	0	15	2	0
6	A	253	0	0	7	0
6	B	246	0	0	6	0
All	All	7042	0	6326	150	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 12.

All (150) 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:152:GLU:HG2	6:A:1224:HOH:O	1.59	1.00
1:B:339:MET:HE1	4:B:1010:HEM:HBD2	1.54	0.89
4:A:510:HEM:HBC2	4:A:510:HEM:HMC2	1.58	0.85
1:A:428:MET:HE3	1:A:459:VAL:HG12	1.59	0.81
1:A:339:MET:HE1	4:A:510:HEM:HBD2	1.71	0.72
1:B:124:LEU:HD22	1:B:157:VAL:HG11	1.72	0.71
1:B:70:ARG:HD2	1:B:79:ILE:HD12	1.73	0.69
1:A:197:ASP:OD1	1:A:199:ARG:HD3	1.92	0.69
1:A:219:THR:HA	1:A:224:LEU:HD23	1.74	0.68
1:B:197:ASP:OD1	1:B:199:ARG:HD3	1.93	0.68
1:B:323:PHE:O	1:B:326:LEU:HB2	1.93	0.67
1:B:339:MET:HE3	1:B:353:PHE:HZ	1.60	0.67
4:B:1010:HEM:HBC2	4:B:1010:HEM:HMC2	1.76	0.66
1:A:428:MET:HE3	1:A:459:VAL:CG1	2.26	0.66
1:A:124:LEU:HD22	1:A:157:VAL:HG11	1.76	0.66
1:A:339:MET:HE3	1:A:353:PHE:HZ	1.61	0.65
1:A:244:TRP:HB2	1:A:292:LEU:HB3	1.80	0.64
1:B:213:ASN:HB3	6:B:1248:HOH:O	1.98	0.63
1:A:361:GLU:OE1	3:A:512:HAR:HB3	2.01	0.60
1:B:231:PHE:HB3	1:B:232:PRO:CD	2.33	0.59
1:B:124:LEU:O	1:B:128:ARG:HG3	2.02	0.58
1:A:292:LEU:HD13	1:A:302:LEU:HD23	1.86	0.58
1:A:336:VAL:HG11	1:A:339:MET:HE2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:SER:OG	1:B:206:GLU:HG3	2.03	0.58
1:B:244:TRP:HB2	1:B:292:LEU:HB3	1.86	0.58
1:A:428:MET:CE	1:A:459:VAL:HG12	2.32	0.58
1:B:243:ILE:HD12	1:B:352:PRO:HG3	1.85	0.58
1:A:189:GLN:HB3	6:A:1099:HOH:O	2.04	0.57
1:A:219:THR:HA	1:A:224:LEU:CD2	2.34	0.57
1:B:393:LEU:O	1:B:397:LYS:HG3	2.05	0.56
1:B:183:ARG:HD3	1:B:447:TRP:CD2	2.41	0.56
1:A:124:LEU:O	1:A:128:ARG:HG3	2.06	0.56
1:A:339:MET:CE	1:A:353:PHE:HZ	2.19	0.55
1:A:173:GLY:HA3	1:A:343:ILE:HD13	1.88	0.55
1:B:357:TYR:HE1	3:B:1012:HAR:O	1.89	0.55
1:B:359:SER:OG	1:B:419:ASP:HA	2.06	0.55
1:A:178:TRP:CZ2	4:A:510:HEM:HBB2	2.42	0.55
1:A:94:CYS:HB3	1:B:94:CYS:HB3	1.88	0.55
1:A:371:HIS:HD2	1:B:75:GLU:O	1.89	0.55
1:A:292:LEU:HD13	1:A:302:LEU:CD2	2.36	0.55
1:B:76:VAL:HG23	1:B:78:SER:H	1.73	0.54
4:A:510:HEM:CHA	4:A:510:HEM:HBA1	2.38	0.54
1:B:231:PHE:HB3	1:B:232:PRO:HD2	1.89	0.54
1:B:365:ARG:HH12	5:B:1011:H4B:C4	2.21	0.54
1:A:393:LEU:O	1:A:397:LYS:HG3	2.07	0.54
1:A:371:HIS:CD2	1:B:75:GLU:O	2.61	0.54
1:B:414:LYS:HE2	6:B:1189:HOH:O	2.08	0.53
1:B:453:SER:HB3	1:B:456:LEU:HD12	1.91	0.53
1:A:357:TYR:CD2	1:A:362:ILE:HD11	2.43	0.53
1:A:218:ALA:O	1:A:224:LEU:HA	2.08	0.52
1:B:218:ALA:O	1:B:224:LEU:HA	2.10	0.52
1:B:140:ARG:NH2	6:B:1240:HOH:O	2.42	0.52
1:A:67:LYS:HG2	1:B:98:ARG:HH21	1.74	0.52
1:A:88:ALA:O	1:B:97:ARG:NH1	2.43	0.51
4:A:510:HEM:HHA	4:A:510:HEM:HBA1	1.92	0.51
1:B:122:GLN:O	1:B:126:GLN:HG3	2.11	0.51
1:A:453:SER:HB3	1:A:456:LEU:HD12	1.93	0.50
1:B:317:HIS:CE1	1:B:320:LEU:HD22	2.46	0.50
1:A:432:GLU:O	1:A:436:LYS:HE2	2.12	0.50
1:A:245:ASN:HB3	6:A:1193:HOH:O	2.12	0.50
1:A:407:LEU:O	1:A:411:GLN:HG3	2.12	0.50
1:B:265:PRO:HB2	1:B:371:HIS:O	2.12	0.50
1:B:320:LEU:HG	1:B:322:TRP:CZ2	2.47	0.49
1:B:407:LEU:O	1:B:411:GLN:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:474:ARG:HD2	6:B:1038:HOH:O	2.12	0.49
1:A:122:GLN:O	1:A:126:GLN:HG3	2.12	0.49
1:B:447:TRP:CZ3	4:B:1010:HEM:HBA2	2.47	0.49
1:A:94:CYS:CB	1:B:94:CYS:HB3	2.42	0.49
1:B:386:ASP:OD2	1:B:389:THR:HG22	2.13	0.49
4:A:510:HEM:HHC	4:A:510:HEM:CBB	2.44	0.48
1:A:340:LEU:HD21	1:A:347:GLU:HG2	1.95	0.48
1:B:150:LEU:O	1:B:154:GLU:HG3	2.13	0.48
1:B:232:PRO:HG2	1:B:241:PHE:CE2	2.48	0.48
1:B:243:ILE:CD1	1:B:352:PRO:HG3	2.43	0.48
1:B:377:GLU:O	1:B:381:VAL:HG23	2.13	0.48
1:A:94:CYS:HB3	1:B:94:CYS:CB	2.44	0.47
1:B:339:MET:CE	4:B:1010:HEM:HMD1	2.45	0.47
1:B:340:LEU:HD11	1:B:347:GLU:HB3	1.95	0.47
1:B:445:TRP:O	1:B:449:VAL:HG23	2.15	0.47
1:A:189:GLN:NE2	6:A:1126:HOH:O	2.47	0.47
1:A:208:PHE:CZ	1:A:212:CYS:SG	3.08	0.46
1:B:364:THR:O	1:B:368:CYS:HB2	2.16	0.46
1:A:150:LEU:O	1:A:154:GLU:HG3	2.15	0.46
1:B:183:ARG:HD3	1:B:447:TRP:CE2	2.51	0.46
1:A:246:SER:OG	1:A:250:ARG:HD2	2.16	0.46
1:A:377:GLU:O	1:A:381:VAL:HG23	2.16	0.46
1:A:90:GLN:HG2	1:B:97:ARG:HB2	1.97	0.46
1:B:178:TRP:CE3	1:B:190:TRP:HA	2.51	0.45
1:A:357:TYR:HE1	3:A:512:HAR:OXT	1.99	0.45
1:A:359:SER:OG	1:A:419:ASP:HA	2.16	0.45
1:B:339:MET:CE	1:B:353:PHE:HZ	2.27	0.45
4:A:510:HEM:HHC	4:A:510:HEM:HBB2	1.99	0.45
1:B:447:TRP:CE3	4:B:1010:HEM:HBA2	2.52	0.45
3:B:1012:HAR:HG2	4:B:1010:HEM:O1A	2.17	0.45
1:B:124:LEU:HA	1:B:124:LEU:HD13	1.76	0.44
1:B:339:MET:HE1	4:B:1010:HEM:HMD1	1.99	0.44
1:A:339:MET:HE3	1:A:353:PHE:CZ	2.47	0.44
1:B:124:LEU:HD11	1:B:154:GLU:HG2	2.00	0.44
1:A:375:ILE:HD11	1:A:402:ILE:HD13	1.99	0.44
1:B:178:TRP:HZ2	4:B:1010:HEM:HBB2	1.80	0.44
1:B:292:LEU:HD13	1:B:302:LEU:CD2	2.47	0.44
1:B:365:ARG:HG3	6:B:1131:HOH:O	2.18	0.44
1:A:244:TRP:CH2	1:A:480:TRP:HB3	2.52	0.44
1:B:233:GLN:HB3	1:B:348:PHE:CE2	2.52	0.44
1:B:70:ARG:HG3	1:B:81:TYR:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:TRP:CE3	1:A:190:TRP:HA	2.53	0.44
1:B:447:TRP:HA	5:B:1011:H4B:N1	2.32	0.43
1:A:450:PRO:HG3	1:A:457:THR:HG21	2.00	0.43
1:B:335:ALA:HA	1:B:354:SER:HB3	1.99	0.43
1:A:364:THR:O	1:A:368:CYS:HB2	2.18	0.43
1:A:411:GLN:O	1:A:414:LYS:HD2	2.18	0.43
4:A:510:HEM:HBC2	4:A:510:HEM:CMC	2.40	0.43
1:A:167:GLU:O	1:A:171:VAL:HG23	2.19	0.43
1:B:339:MET:HE3	1:B:353:PHE:CZ	2.46	0.43
1:A:67:LYS:CG	1:B:98:ARG:HH21	2.30	0.43
4:A:510:HEM:HHA	4:A:510:HEM:CBA	2.49	0.43
1:B:276:GLN:O	1:B:276:GLN:HG2	2.19	0.43
1:A:244:TRP:CZ2	1:A:300:PRO:HG2	2.54	0.43
1:A:247:GLN:HA	1:A:335:ALA:O	2.18	0.43
1:B:219:THR:HA	1:B:224:LEU:HD22	2.01	0.42
1:A:447:TRP:HA	5:A:511:H4B:N1	2.34	0.42
1:B:122:GLN:NE2	6:B:1137:HOH:O	2.52	0.42
1:A:233:GLN:HG2	6:A:1058:HOH:O	2.19	0.42
1:A:124:LEU:HD13	1:A:124:LEU:HA	1.73	0.42
1:A:339:MET:CE	4:A:510:HEM:HMD1	2.50	0.42
1:B:248:LEU:HD12	1:B:335:ALA:CB	2.49	0.42
1:A:414:LYS:HD2	1:A:414:LYS:N	2.33	0.42
1:B:336:VAL:HG11	1:B:339:MET:HE2	2.01	0.42
1:A:244:TRP:CZ3	1:A:480:TRP:HB3	2.54	0.42
1:A:141:SER:HB3	6:A:1223:HOH:O	2.19	0.41
1:B:347:GLU:O	1:B:349:PRO:HD3	2.20	0.41
1:B:247:GLN:HA	1:B:335:ALA:O	2.20	0.41
1:A:280:THR:HA	1:A:281:PRO:HD2	1.90	0.41
1:A:178:TRP:CH2	4:A:510:HEM:HMC1	2.55	0.41
1:A:203:SER:HB2	6:A:1064:HOH:O	2.21	0.41
1:A:365:ARG:HH12	5:A:511:H4B:C4	2.33	0.41
1:B:179:ARG:CZ	1:B:438:ARG:HD2	2.50	0.41
1:A:347:GLU:O	1:A:349:PRO:HD3	2.20	0.41
1:B:182:PRO:HA	1:B:442:PRO:O	2.20	0.41
1:A:261:VAL:HG11	1:A:265:PRO:HA	2.03	0.41
1:A:194:GLN:HG3	1:A:196:PHE:CE1	2.56	0.41
1:B:292:LEU:HD13	1:B:302:LEU:HD23	2.03	0.40
1:B:244:TRP:CD1	1:B:479:PRO:HG3	2.56	0.40
1:B:92:GLY:HA2	1:B:468:PHE:HE2	1.86	0.40
1:A:432:GLU:HG2	1:A:436:LYS:HE2	2.03	0.40
1:A:124:LEU:HD11	1:A:154:GLU:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:HIS:CG	1:A:318:PRO:HD2	2.56	0.40
1:A:181:ALA:HA	1:A:182:PRO:HD3	1.96	0.40
1:A:397:LYS:HE2	1:A:397:LYS:HB3	1.92	0.40
1:A:73:ASN:OD1	1:A:76:VAL:HG13	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	396/427 (93%)	377 (95%)	17 (4%)	2 (0%)	29	41
1	B	396/427 (93%)	380 (96%)	15 (4%)	1 (0%)	41	55
All	All	792/854 (93%)	757 (96%)	32 (4%)	3 (0%)	34	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	ASN
1	B	283	ASN
1	A	236	PRO

### 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	340/359 (95%)	328 (96%)	12 (4%)	36	55
1	B	340/359 (95%)	327 (96%)	13 (4%)	33	51
All	All	680/718 (95%)	655 (96%)	25 (4%)	34	53

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	GLU
1	A	98	ARG
1	A	107	ARG
1	A	122	GLN
1	A	124	LEU
1	A	235	CYS
1	A	236	PRO
1	A	249	VAL
1	A	305	LEU
1	A	367	LEU
1	A	389	THR
1	A	396	ASP
1	B	79	ILE
1	B	98	ARG
1	B	107	ARG
1	B	122	GLN
1	B	124	LEU
1	B	305	LEU
1	B	307	PRO
1	B	320	LEU
1	B	326	LEU
1	B	358	MET
1	B	367	LEU
1	B	377	GLU
1	B	387	THR

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

Mol	Chain	Res	Type
1	A	371	HIS

### 5.3.3 RNA ⓘ

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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 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	HAR	A	512	-	7,12,12	0.92	0	6,14,14	0.88	0
4	HEM	B	1010	1	27,50,50	1.85	8 (29%)	17,82,82	1.81	6 (35%)
5	H4B	A	511	-	16,18,18	2.03	4 (25%)	11,26,26	4.15	7 (63%)
4	HEM	A	510	1	27,50,50	1.87	7 (25%)	17,82,82	1.83	5 (29%)
5	H4B	B	1011	-	16,18,18	2.19	5 (31%)	11,26,26	4.09	7 (63%)
3	HAR	B	1012	-	7,12,12	0.86	0	6,14,14	0.44	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	HAR	A	512	-	-	2/7/13/13	-
4	HEM	B	1010	1	-	3/6/54/54	-
5	H4B	A	511	-	-	2/8/17/17	0/2/2/2
4	HEM	A	510	1	-	3/6/54/54	-
5	H4B	B	1011	-	-	2/8/17/17	0/2/2/2
3	HAR	B	1012	-	-	0/7/13/13	-

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1011	H4B	C4-N3	5.83	1.43	1.33
5	A	511	H4B	C4-N3	5.44	1.42	1.33
5	B	1011	H4B	C7-C6	-4.29	1.48	1.52
4	A	510	HEM	C3C-C2C	-3.90	1.35	1.40
4	B	1010	HEM	C3C-CAC	3.84	1.55	1.47
4	A	510	HEM	CBC-CAC	3.84	1.54	1.29
4	A	510	HEM	CBB-CAB	3.79	1.54	1.29
4	B	1010	HEM	CBC-CAC	3.75	1.54	1.29
4	B	1010	HEM	CBB-CAB	3.68	1.53	1.29
5	A	511	H4B	C7-C6	-3.59	1.48	1.52
4	A	510	HEM	C3B-C2B	-3.00	1.36	1.40
4	B	1010	HEM	C3C-C2C	-2.87	1.36	1.40
4	A	510	HEM	C3B-CAB	2.81	1.53	1.47
4	A	510	HEM	C3C-CAC	2.59	1.53	1.47
5	A	511	H4B	C4A-C8A	2.57	1.46	1.41
4	B	1010	HEM	C1C-C2C	2.43	1.48	1.42
5	A	511	H4B	C6-N5	2.41	1.50	1.45
4	B	1010	HEM	C3B-CAB	2.41	1.52	1.47
4	A	510	HEM	C1C-C2C	2.30	1.47	1.42
5	B	1011	H4B	C4A-C8A	2.28	1.45	1.41
4	B	1010	HEM	C3B-C2B	-2.18	1.37	1.40
4	B	1010	HEM	C1D-ND	2.17	1.40	1.36
5	B	1011	H4B	C8A-N1	2.12	1.38	1.34
5	B	1011	H4B	C6-N5	2.11	1.50	1.45

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1011	H4B	C4-C4A-C8A	10.17	123.61	114.57
5	A	511	H4B	C4-C4A-C8A	10.12	123.56	114.57
5	A	511	H4B	C4-N3-C2	5.09	124.03	115.93
5	B	1011	H4B	C4-N3-C2	4.96	123.80	115.93
4	B	1010	HEM	CBD-CAD-C3D	-4.66	103.89	112.48
4	A	510	HEM	CBD-CAD-C3D	-4.52	104.16	112.48
5	B	1011	H4B	N3-C2-N1	-3.80	119.47	125.42
5	A	511	H4B	N3-C2-N1	-3.66	119.68	125.42
5	A	511	H4B	C2-N1-C8A	3.61	122.62	114.54
5	B	1011	H4B	C2-N1-C8A	3.53	122.45	114.54
5	A	511	H4B	C4A-C4-N3	-3.46	114.17	124.01
5	B	1011	H4B	C4A-C4-N3	-3.34	114.52	124.01
5	A	511	H4B	C4-C4A-N5	3.16	121.77	119.12
4	A	510	HEM	CMC-C2C-C3C	2.97	130.23	124.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1010	HEM	CMC-C2C-C3C	2.70	129.74	124.68
4	B	1010	HEM	CMB-C2B-C3B	2.67	129.67	124.68
4	A	510	HEM	CMA-C3A-C4A	-2.65	124.39	128.46
4	A	510	HEM	CMD-C2D-C1D	-2.56	124.52	128.46
5	A	511	H4B	N2-C2-N3	2.53	121.19	117.25
5	B	1011	H4B	C4-C4A-N5	2.41	121.14	119.12
5	B	1011	H4B	N2-C2-N3	2.37	120.94	117.25
4	B	1010	HEM	CAA-CBA-CGA	2.18	116.33	112.67
4	B	1010	HEM	CMA-C3A-C4A	-2.13	125.18	128.46
4	A	510	HEM	CMB-C2B-C3B	2.11	128.62	124.68
4	B	1010	HEM	CMD-C2D-C1D	-2.06	125.31	128.46

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	512	HAR	C-CA-CB-CG
4	B	1010	HEM	C1A-C2A-CAA-CBA
4	B	1010	HEM	C2A-CAA-CBA-CGA
4	A	510	HEM	C1A-C2A-CAA-CBA
4	A	510	HEM	C3A-C2A-CAA-CBA
4	A	510	HEM	C2A-CAA-CBA-CGA
3	A	512	HAR	CA-CB-CG-CD
5	A	511	H4B	C7-C6-C9-C10
5	A	511	H4B	C7-C6-C9-O9
4	B	1010	HEM	C3A-C2A-CAA-CBA
5	B	1011	H4B	C7-C6-C9-O9
5	B	1011	H4B	C7-C6-C9-C10

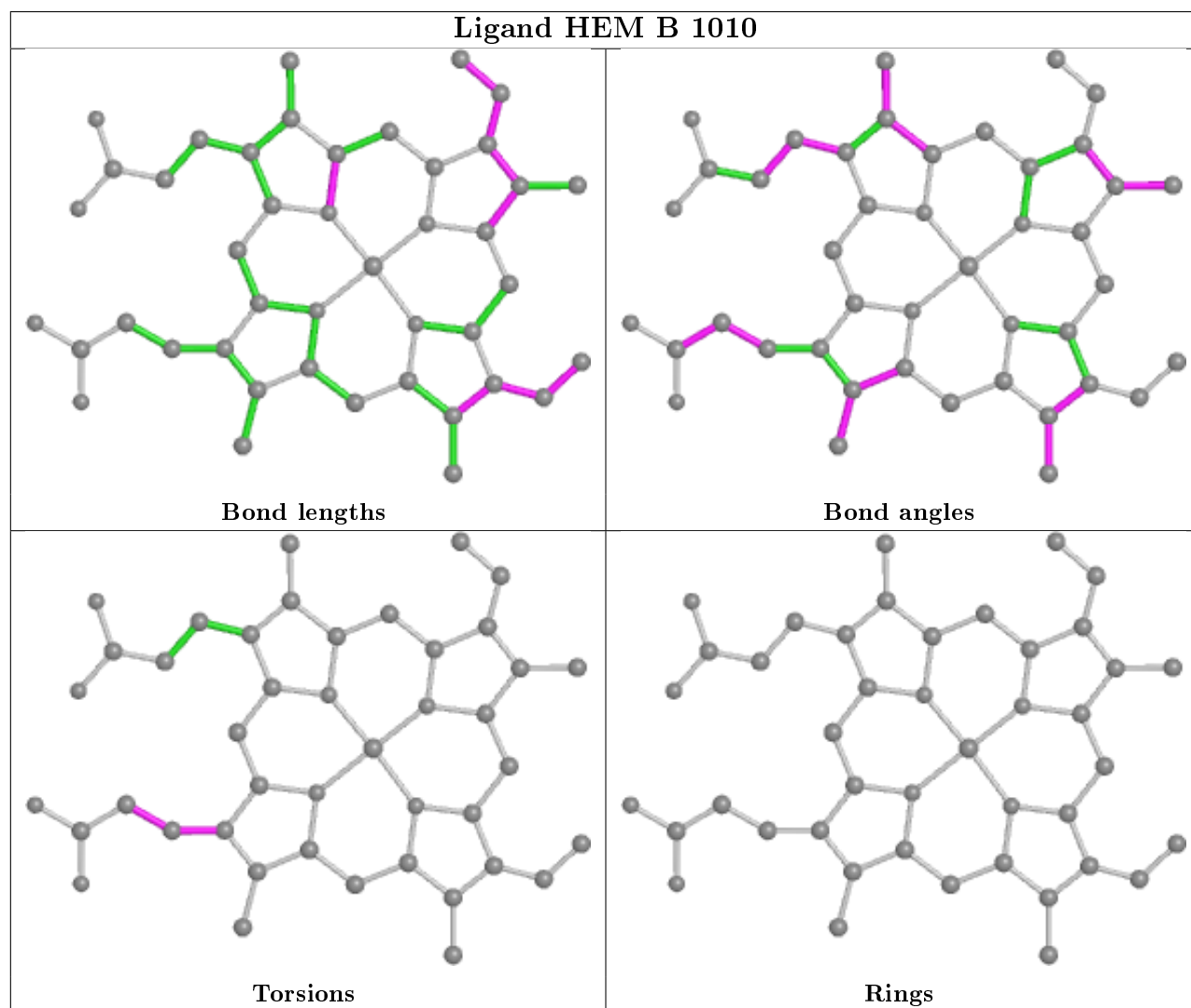
There are no ring outliers.

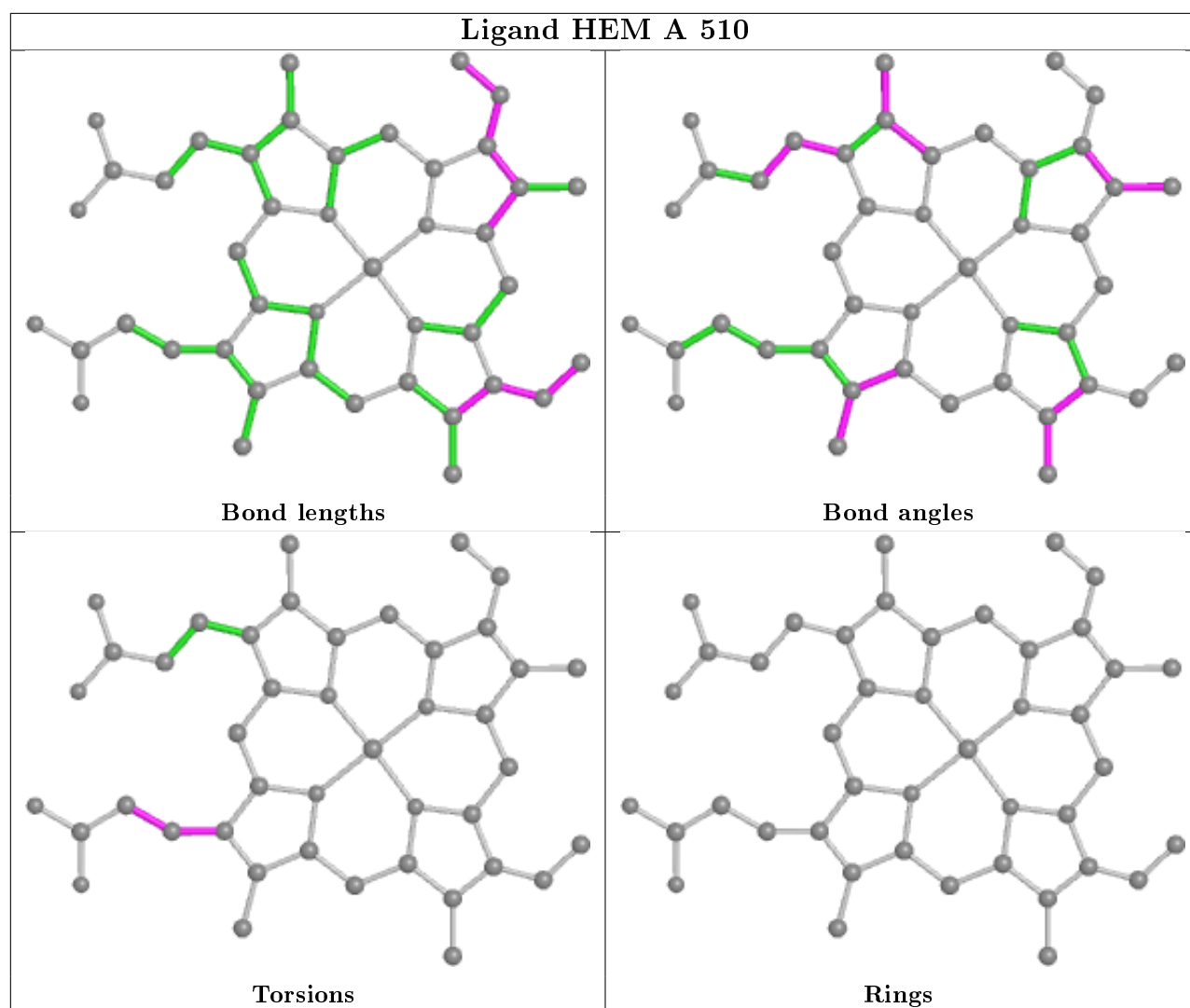
6 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	512	HAR	2	0
4	B	1010	HEM	8	0
5	A	511	H4B	2	0
4	A	510	HEM	11	0
5	B	1011	H4B	2	0
3	B	1012	HAR	2	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.