



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:21 AM UTC

PDB ID : 1GRH / pdb_00001grh
Title : INHIBITION OF HUMAN GLUTATHIONE REDUCTASE BY THE NITROSOUREA DRUGS 1,3-BIS(2-CHLOROETHYL)-1-NITROSOUREA AND 1-(2-CHLOROETHYL)-3-(2-HYDROXYETHYL)-1-NITROSOUREA
Authors : Karplus, P.A.; Schulz, G.E.
Deposited on : 1992-12-15
Resolution : 3.00 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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

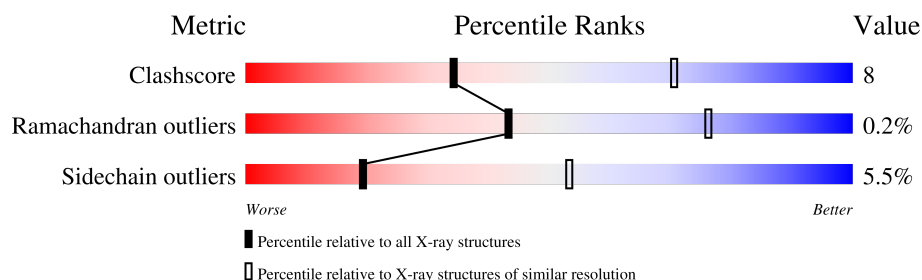
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)

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	478	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EOH	A	482	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4080 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 GLUTATHIONE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	461	3499	2212	603	660	24	0	0	0

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



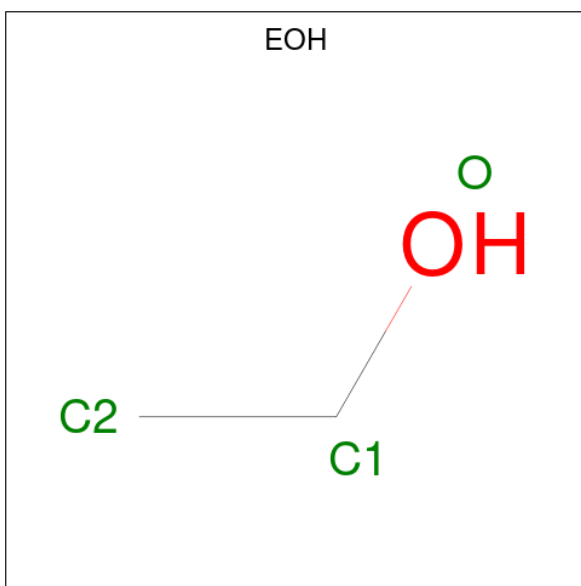
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	A	1	5	4	1	0	0

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 4 is ETHANOL (CCD ID: EOH) (formula: $\text{C}_2\text{H}_6\text{O}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			3	2	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	520	Total 520	O 520	0	0

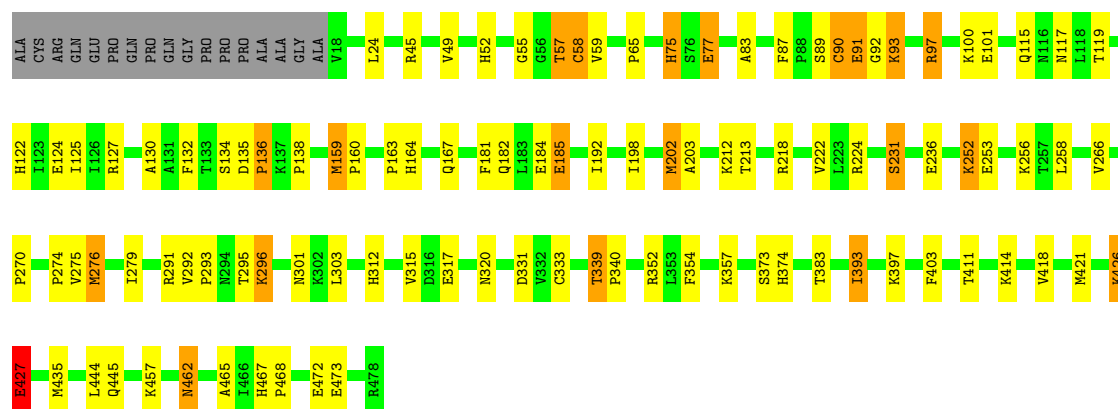
3 Residue-property plots

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: GLUTATHIONE REDUCTASE

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	B 1 1 2	Depositor
Cell constants a, b, c, α , β , γ	119.80Å 84.50Å 63.20Å 90.00° 90.00° 58.70°	Depositor
Resolution (Å)	(Not available) – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4080	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, EOH, FAD

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	1.17	3/3566 (0.1%)	1.58	41/4824 (0.8%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	57	THR	C-N	-15.05	1.14	1.33
1	A	58	CYS	C-N	13.33	1.51	1.33
1	A	339	THR	C-O	-5.37	1.19	1.24

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	91	GLU	CA-C-N	-20.50	99.26	122.42
1	A	91	GLU	C-N-CA	-20.50	99.26	122.42
1	A	159	MET	CB-CA-C	-11.30	95.31	110.22
1	A	92	GLY	N-CA-C	8.76	128.64	110.69
1	A	57	THR	O-C-N	6.95	129.25	122.03
1	A	331	ASP	CA-CB-CG	6.60	119.20	112.60
1	A	462	ASN	CA-CB-CG	-6.58	106.02	112.60
1	A	91	GLU	N-CA-C	6.52	121.32	113.23
1	A	97	ARG	N-CA-CB	6.33	120.09	110.28
1	A	393	ILE	CB-CA-C	-6.28	103.81	112.04
1	A	52	HIS	CA-CB-CG	-6.26	107.54	113.80
1	A	181	PHE	CA-CB-CG	-6.17	107.63	113.80
1	A	75	HIS	CA-CB-CG	-6.13	107.67	113.80
1	A	55	GLY	N-CA-C	-6.10	106.32	114.25
1	A	291	ARG	NE-CZ-NH1	-6.05	115.45	121.50
1	A	231	SER	N-CA-CB	5.96	118.88	110.12
1	A	122	HIS	CA-CB-CG	-5.93	107.87	113.80
1	A	445	GLN	N-CA-C	5.84	118.11	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	159	MET	CA-CB-CG	5.77	125.63	114.10
1	A	274	PRO	N-CA-CB	5.67	108.28	103.35
1	A	444	LEU	N-CA-C	5.65	117.52	111.36
1	A	77	GLU	CB-CA-C	-5.63	101.28	110.85
1	A	163	PRO	N-CA-CB	5.57	108.51	103.33
1	A	58	CYS	CA-C-N	5.51	129.37	120.55
1	A	58	CYS	C-N-CA	5.51	129.37	120.55
1	A	58	CYS	O-C-N	-5.41	115.89	122.11
1	A	91	GLU	O-C-N	-5.34	115.14	122.46
1	A	279	ILE	N-CA-CB	5.32	118.48	111.40
1	A	75	HIS	ND1-CG-CD2	5.29	111.39	106.10
1	A	97	ARG	NE-CZ-NH2	5.29	123.96	119.20
1	A	295	THR	CA-C-N	5.25	127.58	120.38
1	A	295	THR	C-N-CA	5.25	127.58	120.38
1	A	270	PRO	N-CA-CB	5.18	108.16	103.34
1	A	352	ARG	NE-CZ-NH2	5.15	123.84	119.20
1	A	354	PHE	CA-CB-CG	-5.13	108.67	113.80
1	A	383	THR	N-CA-C	-5.08	103.98	110.53
1	A	65	PRO	N-CA-CB	5.08	108.92	103.33
1	A	213	THR	N-CA-C	5.08	117.76	109.59
1	A	75	HIS	CB-CA-C	-5.03	102.45	110.79
1	A	301	ASN	CA-CB-CG	-5.02	107.58	112.60
1	A	427	GLU	CB-CG-CD	5.00	121.10	112.60

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	3499	0	3538	54	1
2	A	5	0	0	0	0
3	A	53	0	31	0	0
4	A	3	0	4	4	0
5	A	520	0	0	13	1
All	All	4080	0	3573	54	2

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 (54) 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:59:VAL:HG23	4:A:482:EOH:H22	1.60	0.81
1:A:202:MET:HA	1:A:202:MET:HE2	1.61	0.81
1:A:59:VAL:CG2	4:A:482:EOH:H22	2.16	0.75
1:A:224:ARG:HD2	5:A:992:HOH:O	1.87	0.73
1:A:296:LYS:HB2	5:A:589:HOH:O	1.87	0.72
1:A:77:GLU:OE2	1:A:374:HIS:ND1	2.24	0.70
1:A:127:ARG:HD2	5:A:729:HOH:O	1.92	0.68
1:A:93:LYS:O	1:A:93:LYS:HG2	1.95	0.66
1:A:185:GLU:HG3	5:A:814:HOH:O	1.96	0.66
1:A:266:VAL:HG22	1:A:276:MET:HG2	1.76	0.66
1:A:164:HIS:HB2	5:A:932:HOH:O	1.96	0.65
1:A:293:PRO:HG3	1:A:312:HIS:CD2	2.32	0.65
1:A:115:GLN:O	1:A:119:THR:HG23	2.02	0.58
1:A:315:VAL:HA	1:A:320:ASN:O	2.04	0.57
1:A:59:VAL:CG2	4:A:482:EOH:C2	2.82	0.57
1:A:236:GLU:HG2	5:A:936:HOH:O	2.05	0.56
1:A:373:SER:HB2	5:A:999:HOH:O	2.07	0.54
1:A:339:THR:HB	1:A:340:PRO:HD3	1.90	0.53
1:A:100:LYS:O	1:A:100:LYS:HG2	2.06	0.53
1:A:59:VAL:HG22	4:A:482:EOH:C2	2.39	0.51
1:A:159:MET:HB3	1:A:160:PRO:CD	2.42	0.50
1:A:198:ILE:O	1:A:202:MET:HG2	2.11	0.50
1:A:91:GLU:O	1:A:91:GLU:HG3	2.09	0.50
1:A:421:MET:SD	1:A:457:LYS:HD3	2.51	0.49
1:A:218:ARG:HG3	5:A:600:HOH:O	2.12	0.48
1:A:465:ALA:HB1	1:A:472:GLU:HB2	1.95	0.48
1:A:192:ILE:HD13	1:A:203:ALA:HA	1.95	0.47
1:A:258:LEU:HD23	1:A:258:LEU:HA	1.81	0.47
1:A:292:VAL:HG23	1:A:293:PRO:HD2	1.97	0.46
1:A:159:MET:HB3	1:A:160:PRO:HD2	1.98	0.45
1:A:411:THR:O	1:A:414:LYS:HE2	2.16	0.45
1:A:132:PHE:CD1	1:A:303:LEU:HD12	2.52	0.45
1:A:393:ILE:O	1:A:393:ILE:HG22	2.15	0.44
1:A:49:VAL:HG11	1:A:130:ALA:HB2	1.99	0.44
1:A:426:LYS:HB3	1:A:426:LYS:HE3	1.74	0.44
1:A:57:THR:O	1:A:58:CYS:C	2.60	0.43
1:A:45:ARG:HH22	1:A:124:GLU:HB2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:ILE:HG22	1:A:127:ARG:HD3	2.00	0.43
1:A:462:ASN:ND2	5:A:1005:HOH:O	2.51	0.43
1:A:117:ASN:HD22	1:A:117:ASN:HA	1.51	0.43
1:A:403:PHE:CE1	1:A:473:GLU:HG3	2.54	0.42
1:A:222:VAL:O	1:A:231:SER:HB2	2.19	0.42
1:A:418:VAL:O	1:A:435:MET:HA	2.20	0.42
1:A:427:GLU:H	1:A:427:GLU:HG2	1.30	0.42
1:A:467:HIS:HA	1:A:468:PRO:HA	1.88	0.42
1:A:138:PRO:HA	5:A:587:HOH:O	2.19	0.42
1:A:202:MET:HA	1:A:202:MET:CE	2.41	0.41
1:A:357:LYS:NZ	5:A:798:HOH:O	2.52	0.41
1:A:252:LYS:HG3	5:A:982:HOH:O	2.19	0.41
1:A:135:ASP:HB3	1:A:136:PRO:HD2	2.03	0.40
1:A:333:CYS:HB2	5:A:530:HOH:O	2.21	0.40
1:A:83:ALA:HA	1:A:87:PHE:O	2.22	0.40
1:A:24:LEU:HA	1:A:24:LEU:HD23	1.83	0.40
1:A:97:ARG:NH2	1:A:101:GLU:OE2	2.54	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:585:HOH:O	5:A:585:HOH:O[2_665]	0.64	1.56
1:A:90:CYS:SG	1:A:90:CYS:SG[2_665]	1.56	0.64

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	459/478 (96%)	441 (96%)	17 (4%)	1 (0%)	43 76

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	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	382/393 (97%)	361 (94%)	21 (6%)	19 53

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	HIS
1	A	89	SER
1	A	90	CYS
1	A	93	LYS
1	A	134	SER
1	A	167	GLN
1	A	182	GLN
1	A	184	GLU
1	A	185	GLU
1	A	202	MET
1	A	212	LYS
1	A	252	LYS
1	A	253	GLU
1	A	256	LYS
1	A	275	VAL
1	A	276	MET
1	A	296	LYS
1	A	317	GLU
1	A	397	LYS
1	A	426	LYS
1	A	427	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	HIS
1	A	116	ASN
1	A	117	ASN
1	A	164	HIS
1	A	182	GLN
1	A	306	GLN
1	A	366	ASN
1	A	425	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
4	EOH	A	482	1	2,2,2	0.41	0	1,1,1	0.42	0
2	PO4	A	480	-	4,4,4	1.48	0	6,6,6	0.43	0
3	FAD	A	479	-	58,58,58	1.61	9 (15%)	85,89,89	1.24	9 (10%)

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	FAD	A	479	-	-	4/34/50/50	0/6/6/6

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	479	FAD	PA-O3P	-6.26	1.52	1.59
3	A	479	FAD	P-O2P	-4.45	1.34	1.55
3	A	479	FAD	PA-O1A	2.83	1.60	1.50
3	A	479	FAD	P-O3P	-2.74	1.56	1.59
3	A	479	FAD	C6-C7	-2.54	1.36	1.39
3	A	479	FAD	O2-C2	-2.30	1.19	1.24
3	A	479	FAD	O4B-C1B	2.20	1.47	1.42
3	A	479	FAD	O5'-C5'	2.19	1.52	1.44
3	A	479	FAD	C1'-C2'	2.10	1.55	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	479	FAD	O2A-PA-O3P	4.31	118.91	107.27
3	A	479	FAD	O4B-C1B-N9A	-3.85	100.70	108.09
3	A	479	FAD	O2A-PA-O5B	-3.01	93.94	107.57
3	A	479	FAD	O4B-C1B-C2B	-2.17	101.98	106.62
3	A	479	FAD	C2A-N1A-C6A	2.16	122.28	118.73
3	A	479	FAD	O2P-P-O1P	2.11	122.24	112.44
3	A	479	FAD	O5'-P-O1P	-2.07	100.73	108.94
3	A	479	FAD	O2P-P-O5'	2.07	116.93	107.57
3	A	479	FAD	O3B-C3B-C4B	2.06	117.01	111.08

There are no chirality outliers.

All (4) torsion outliers are listed below:

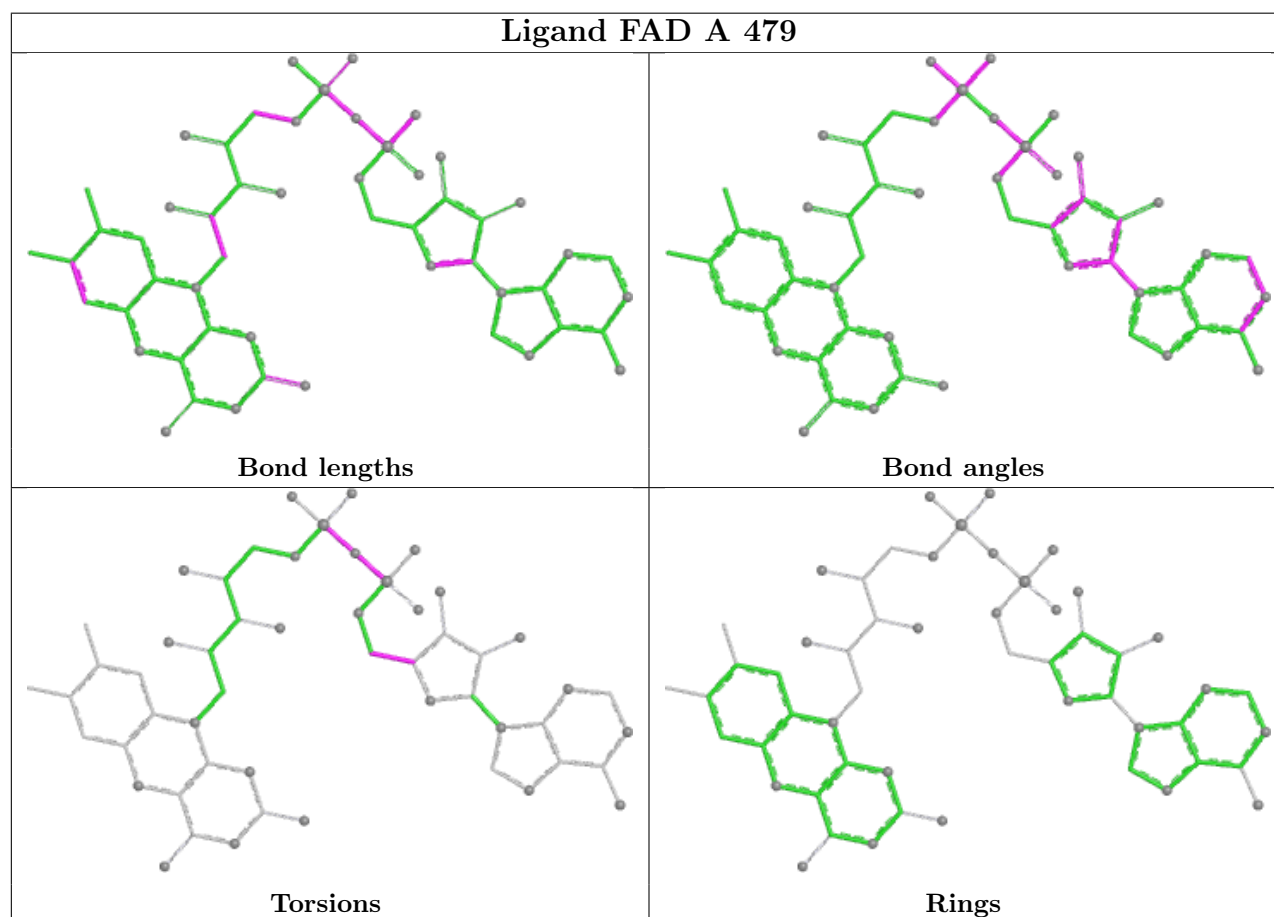
Mol	Chain	Res	Type	Atoms
3	A	479	FAD	P-O3P-PA-O1A
3	A	479	FAD	PA-O3P-P-O5'
3	A	479	FAD	P-O3P-PA-O2A
3	A	479	FAD	O4B-C4B-C5B-O5B

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	482	EOH	4	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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	57:THR	C	58:CYS	N	1.14

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.