

# Full wwPDB X-ray Structure Validation Report (i)

#### May 23, 2020 – 08:53 pm BST

PDB ID : 5MH4

Title : Crystal Structure of Lactococcus lactis Thioredoxin Reductase (FR conforma-

tion)

Authors: Skjoldager, N.; Bang, M.B.; Svensson, B.; Hagglund, P.; Harris, P.

Deposited on : 2016-11-23

Resolution : 2.14 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.11

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

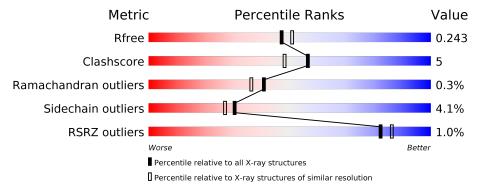
Validation Pipeline (wwPDB-VP) : 2.11

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	130704	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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 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 <=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	• •			
			% ■			
1	A	327	79%	12%	•	7%



# 2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2631 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 Thioredoxin reductase.

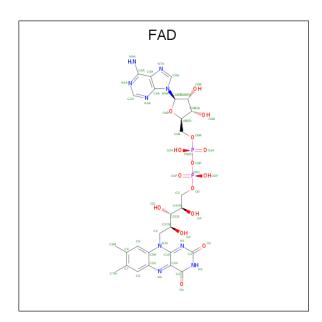
Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace		
1	Λ	303	Total	С	N	О	S	0	0	0
1	A	303	2347	1486	390	459	12	0	U	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	=	expression tag	UNP A0A166TWQ7
A	-17	SER	-	expression tag	UNP A0A166TWQ7
A	-16	SER	_	expression tag	UNP A0A166TWQ7
A	-15	HIS	_	expression tag	UNP A0A166TWQ7
A	-14	HIS	_	expression tag	UNP A0A166TWQ7
A	-13	HIS	_	expression tag	UNP A0A166TWQ7
A	-12	HIS	_	expression tag	UNP A0A166TWQ7
A	-11	HIS	_	expression tag	UNP A0A166TWQ7
A	-10	HIS	-	expression tag	UNP A0A166TWQ7
A	-9	SER	-	expression tag	UNP A0A166TWQ7
A	-8	SER	-	expression tag	UNP A0A166TWQ7
A	-7	GLY	-	expression tag	UNP A0A166TWQ7
A	-6	LEU	_	expression tag	UNP A0A166TWQ7
A	-5	VAL	-	expression tag	UNP A0A166TWQ7
A	-4	PRO	_	expression tag	UNP A0A166TWQ7
A	-3	ARG	=	expression tag	UNP A0A166TWQ7
A	-2	GLY	-	expression tag	UNP A0A166TWQ7
A	-1	SER	=	expression tag	UNP A0A166TWQ7
A	0	HIS	-	expression tag	UNP A0A166TWQ7

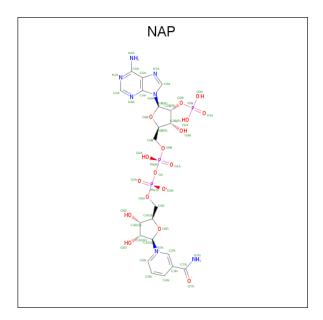
• Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).





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

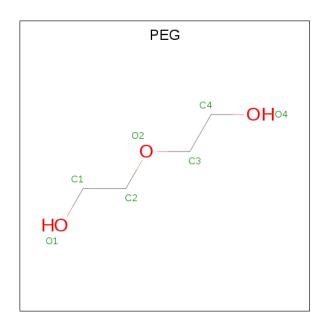
• Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula:  $C_{21}H_{28}N_7O_{17}P_3$ ).



Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf
3	A	1	Total 48			O 17	P 3	0	0

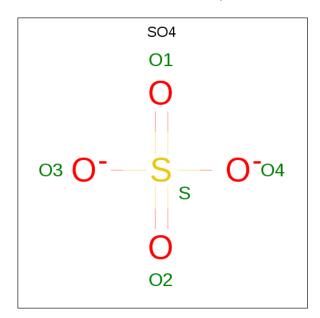
• Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).





Mo	l Cha	in	Residues	Atoms			ZeroOcc	AltConf
4	A		1	Total 7	C 4	O 3	0	0

 $\bullet$  Molecule 5 is SULFATE ION (three-letter code: SO4) (formula:  $\mathrm{O_4S}).$ 



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

• Molecule 6 is water.



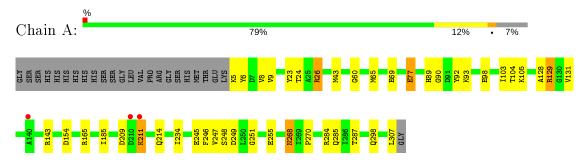
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	166	Total O 166 166	0	0



# 3 Residue-property plots (i)

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 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: Thioredoxin reductase





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	120.54Å 120.54Å 60.47Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.37 - 2.14	Depositor
Resolution (A)	49.32 - 2.14	EDS
% Data completeness	99.9 (49.37-2.14)	Depositor
(in resolution range)	99.9 (49.32-2.14)	EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.75 (at 2.14Å)	Xtriage
Refinement program	REFMAC 6.3	Depositor
P. P.	0.177 , $0.237$	Depositor
$R, R_{free}$	0.185 , $0.243$	DCC
$R_{free}$ test set	1195 reflections $(4.76\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.6	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36, 45.5	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2631	wwPDB-VP
Average B, all atoms $(Å^2)$	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.16% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $< L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

## 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: NAP, PEG, SO4, 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	Boı	nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.88	$1/2388 \ (0.0\%)$	0.95	4/3222 (0.1%)	

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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

#### All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
1	A	23	TYR	CB-CG	5.03	1.59	1.51

#### All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	A	268	ASN	CB-CA-C	-7.81	94.77	110.40
1	A	26	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	A	26	ARG	NE-CZ-NH1	5.79	123.20	120.30
1	A	154	ASP	CB-CG-OD1	5.37	123.13	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	128	ALA	Peptide



### 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	2347	0	2308	24	1
2	A	53	0	31	0	0
3	A	48	0	25	1	0
4	A	7	0	10	0	0
5	A	10	0	0	0	0
6	A	166	0	0	4	1
All	All	2631	0	2374	24	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 5.

All (24) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{ll}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{array}$	Clash overlap (Å)
1:A:93:LYS:NZ	6:A:504:HOH:O	2.29	0.65
1:A:92:TYR:HD2	1:A:103:ILE:HG23	1.65	0.61
1:A:246:PHE:CD1	1:A:247:VAL:HG13	2.38	0.58
1:A:185:ILE:HG13	6:A:599:HOH:O	2.04	0.58
1:A:255:GLU:H	1:A:255:GLU:CD	2.10	0.53
1:A:6:TYR:OH	1:A:77:GLU:OE1	2.20	0.53
1:A:8:VAL:HG11	1:A:24:THR:HG21	1.91	0.53
1:A:131:VAL:HG22	1:A:234:ILE:CG2	2.39	0.52
1:A:9:VAL:HG23	1:A:104:THR:HB	1.95	0.48
1:A:165:ARG:HB2	1:A:165:ARG:HH11	1.78	0.48
1:A:129:ARG:HG2	1:A:211:LYS:O	2.13	0.48
1:A:89:HIS:HB2	1:A:92:TYR:CE1	2.49	0.47
1:A:92:TYR:CD2	1:A:103:ILE:HG23	2.49	0.45
1:A:65:MET:CE	6:A:664:HOH:O	2.64	0.45
1:A:43:MET:O	1:A:60:GLY:HA3	2.17	0.45
1:A:246:PHE:HD1	1:A:247:VAL:HG13	1.81	0.44
1:A:209:ASP:HB3	1:A:214:GLN:HE22	1.82	0.44
1:A:284:ARG:O	3:A:402:NAP:H1D	2.17	0.44
1:A:287:THR:HG23	6:A:561:HOH:O	2.16	0.44
1:A:268:ASN:O	1:A:270:PRO:HD3	2.19	0.43
1:A:249:ASP:OD1	1:A:249:ASP:N	2.51	0.42

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Atom-1	Atom-2	$egin{array}{c}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{array}$	Clash overlap (Å)
1:A:245:GLU:N	1:A:245:GLU:OE1	2.41	0.41
1:A:105:LYS:HD3	1:A:307:LEU:HD23	2.03	0.41
1:A:251:GLY:O	1:A:268:ASN:ND2	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	$egin{array}{c}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{array}$	$egin{array}{c}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{array}$
1:A:98:GLU:OE2	1:A:98:GLU:OE2[8_554]	1.54	0.66
6:A:514:HOH:O	6:A:568:HOH:O[8_555]	2.02	0.18

### 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	301/327 (92%)	289 (96%)	11 (4%)	1 (0%)	41 36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	90	GLY

### 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	245/265 (92%)	235 (96%)	10 (4%)	30 27

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	26	ARG
1	A	69	GLU
1	A	77	GLU
1	A	129	ARG
1	A	143	ARG
1	A	211	LYS
1	A	248	SER
1	A	285	GLN
1	A	298	GLN

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	285	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 carbohydrates in this entry.

## 5.6 Ligand geometry (i)

5 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	Mol Type Chain Res		Link	Bond lengths			Bond angles			
MIOI	Type	Chain	nes	Link	Counts	RMSZ	$\mid \# Z  > 2$	Counts	RMSZ	# Z >2
4	PEG	A	403	_	6,6,6	0.51	0	5,5,5	0.80	0
5	SO4	A	404	-	4,4,4	0.46	0	6,6,6	1.23	0
3	NAP	A	402	_	45,52,52	1.27	5 (11%)	56,80,80	1.60	9 (16%)
5	SO4	A	405	-	4,4,4	0.46	0	6,6,6	0.61	0
2	FAD	A	401	-	51,58,58	1.56	8 (15%)	60,89,89	2.35	16 (26%)

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	$\mathbf{Type}$	Chain	Res	Link	Chirals	${f Torsions}$	Rings
4	PEG	A	403	_	-	1/4/4/4	-
3	NAP	A	402	-	-	2/31/67/67	0/5/5/5
2	FAD	A	401	_	ı	2/30/50/50	0/6/6/6

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$Ideal(\AA)$
2	A	401	FAD	C4X-C10	5.44	1.44	1.38
2	A	401	FAD	C2-N3	-3.63	1.31	1.38
2	A	401	FAD	C4-C4X	3.40	1.47	1.41
2	A	401	FAD	O4B-C1B	3.29	1.45	1.41
3	A	402	NAP	P2B-O2B	3.17	1.65	1.59
2	A	401	FAD	C9A-N10	3.14	1.42	1.38
3	A	402	NAP	C4A-N3A	3.12	1.40	1.35
3	A	402	NAP	C7N-N7N	-2.95	1.27	1.33
3	A	402	NAP	O7N-C7N	-2.94	1.18	1.24
2	A	401	FAD	C2B-C1B	-2.70	1.49	1.53
3	A	402	NAP	C2D-C1D	-2.52	1.49	1.53
2	A	401	FAD	C9A-C5X	2.29	1.47	1.42
2	A	401	FAD	C2A-N3A	2.11	1.35	1.32

All (25) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\mathbf{Ideal}(^o)$
2	A	401	FAD	C1'-N10-C9A	8.70	125.14	118.29
2	A	401	FAD	C4-N3-C2	7.65	121.61	115.14
2	A	401	FAD	C4-C4X-C10	-7.14	115.22	119.95
2	A	401	FAD	N3A-C2A-N1A	-4.59	121.50	128.68
3	A	402	NAP	N3A-C2A-N1A	-4.48	121.67	128.68
3	A	402	NAP	C1B-N9A-C4A	-3.68	120.18	126.64
3	A	402	NAP	O7N-C7N-N7N	-3.57	117.51	122.58
3	A	402	NAP	O4D-C1D-C2D	-3.36	102.02	106.93
2	A	401	FAD	C4X-N5-C5X	3.35	120.12	116.77
2	A	401	FAD	N6A-C6A-N1A	3.32	125.47	118.57
2	A	401	FAD	C1B-N9A-C4A	-3.07	121.25	126.64
2	A	401	FAD	C4-C4X-N5	2.92	121.94	118.60
3	A	402	NAP	C5N-C4N-C3N	-2.67	117.19	120.34
2	A	401	FAD	C2A-N1A-C6A	2.66	123.31	118.75
2	A	401	FAD	C5A-C6A-N6A	-2.57	116.45	120.35
2	A	401	FAD	C9A-N10-C10	-2.53	118.60	121.91
2	A	401	FAD	P-O3P-PA	-2.49	124.29	132.83
2	A	401	FAD	C1'-N10-C10	-2.40	116.26	118.41
3	A	402	NAP	C3N-C7N-N7N	2.37	120.59	117.75
2	A	401	FAD	C10-C4X-N5	2.28	122.84	121.26
3	A	402	NAP	O2B-P2B-O1X	-2.26	100.68	109.39
2	A	401	FAD	C8M-C8-C7	-2.20	116.23	120.74
3	A	402	NAP	C5A-C6A-N6A	-2.19	117.03	120.35
3	A	402	NAP	C3B-C2B-C1B	-2.17	98.80	102.89
2	A	401	FAD	C4X-C4-N3	-2.11	120.55	123.43

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	NAP	C3B-C2B-O2B-P2B
4	A	403	PEG	O2-C3-C4-O4
2	A	401	FAD	PA-O3P-P-O5'
3	A	402	NAP	O4B-C4B-C5B-O5B
2	A	401	FAD	O4B-C4B-C5B-O5B

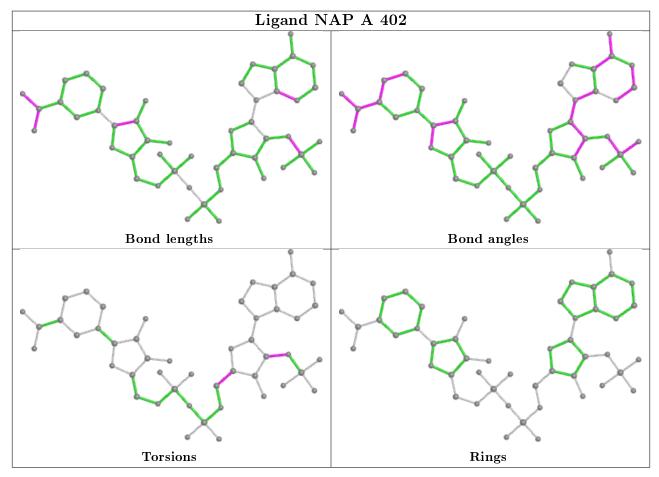
There are no ring outliers.

1 monomer is involved in 1 short contact:

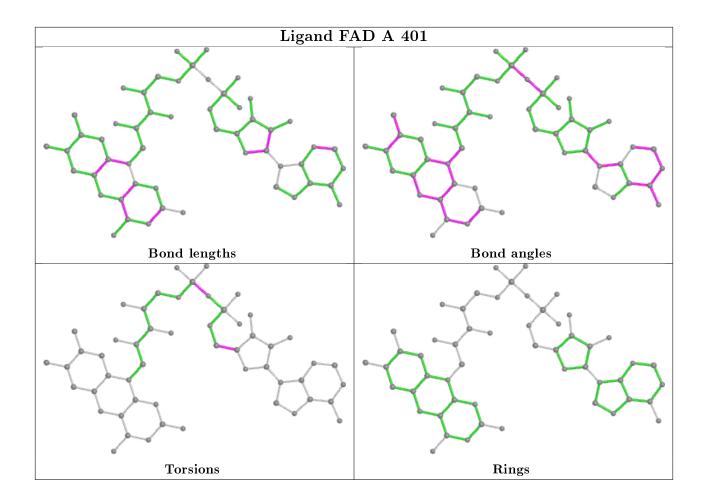
$\mathbf{Mol}$	Chain	${ m Res}$	Type	Clashes	Symm-Clashes
3	A	402	NAP	1	0



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 then 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 (i)

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

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,  $95^{th}$  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	$\langle { m RSRZ} \rangle$	$\# \mathrm{RSRZ} {>} 2$	$OWAB(A^2)$	Q < 0.9
1	A	303/327 (92%)	-0.28	3 (0%) 82 86	27, 41, 66, 95	0

All (3) RSRZ outliers are listed below:

Mol	Chain	$\operatorname{Res}$	Type	RSRZ
1	A	210	ASP	2.5
1	A	211	LYS	2.1
1	A	140	ALA	2.0

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

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

### 6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

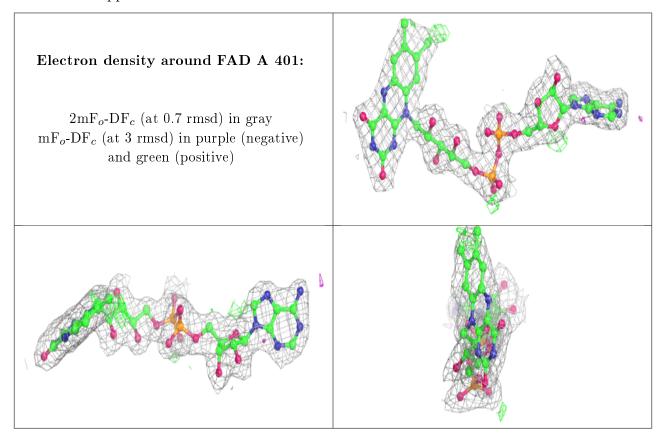
### 6.4 Ligands (i)

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,  $95^{th}$  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.

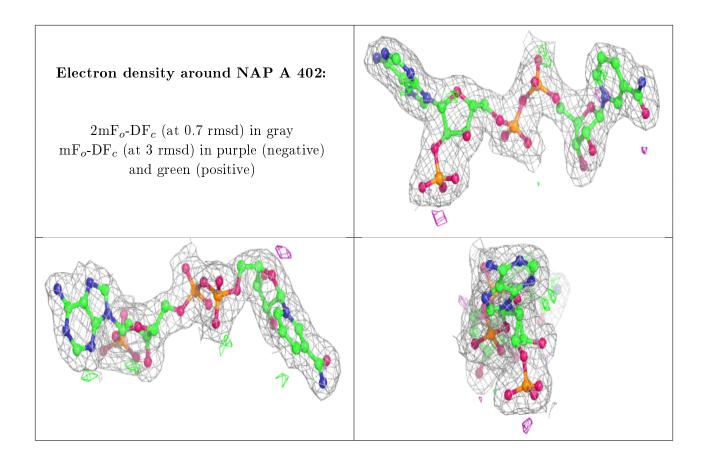
Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B\text{-factors}}({f \AA}^2)$	Q < 0.9
5	SO4	Α	405	5/5	0.89	0.20	60,66,82,91	5
4	PEG	A	403	7/7	0.90	0.14	47,51,59,71	0
5	SO4	A	404	5/5	0.94	0.10	53,54,60,69	5
2	FAD	A	401	53/53	0.98	0.10	25,33,49,57	0
3	NAP	A	402	48/48	0.99	0.10	28,34,39,41	0



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.







# 6.5 Other polymers (i)

There are no such residues in this entry.

