



Full wwPDB X-ray Structure Validation Report ⓘ

May 7, 2026 – 08:11 AM EDT

PDB ID : 3DGZ / pdb_00003dgz
Title : Crystal Structure of Mouse Mitochondrial Thioredoxin Reductase, C-terminal 3-residue truncation
Authors : Eckenroth, B.E.; Hondal, R.J.; Everse, S.J.
Deposited on : 2008-06-16
Resolution : 2.25 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)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

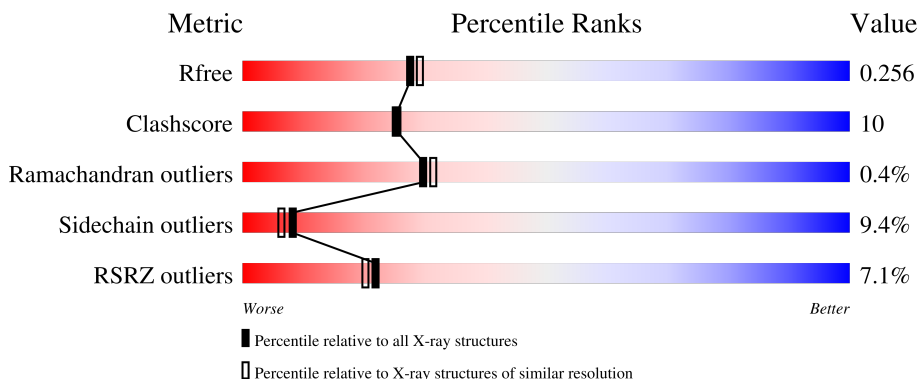
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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))
R_{free}	180053	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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 $\leq 5\%$. 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	Quality of chain
1	A	488	

2 Entry composition [i](#)

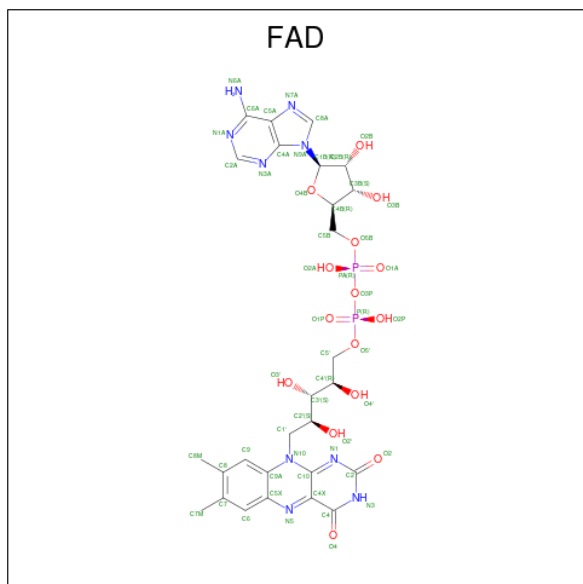
There are 4 unique types of molecules in this entry. The entry contains 3960 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 2.

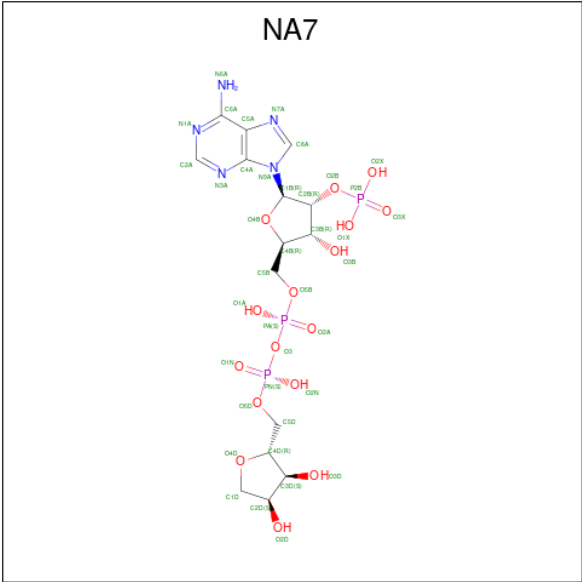
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	482	Total	C	N	O	S	0	0	0
			3679	2330	641	687	21			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 3 is [(2R,3R,4R,5R)-5-(6-AMINO-9H-PURIN-9-YL)-3-HYDROXY-4-(PHOSPHONOXY)TETRAHYDROFURAN-2-YL]METHYL [(2R,3S,4S)-3,4-DIHYDROXYTETRAHYDROFURAN-2-YL]METHYL DIHYDROGEN DIPHOSPHATE (CCD ID: NA7) (formula: $C_{15}H_{24}N_5O_{16}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			39	15	5	16	3		

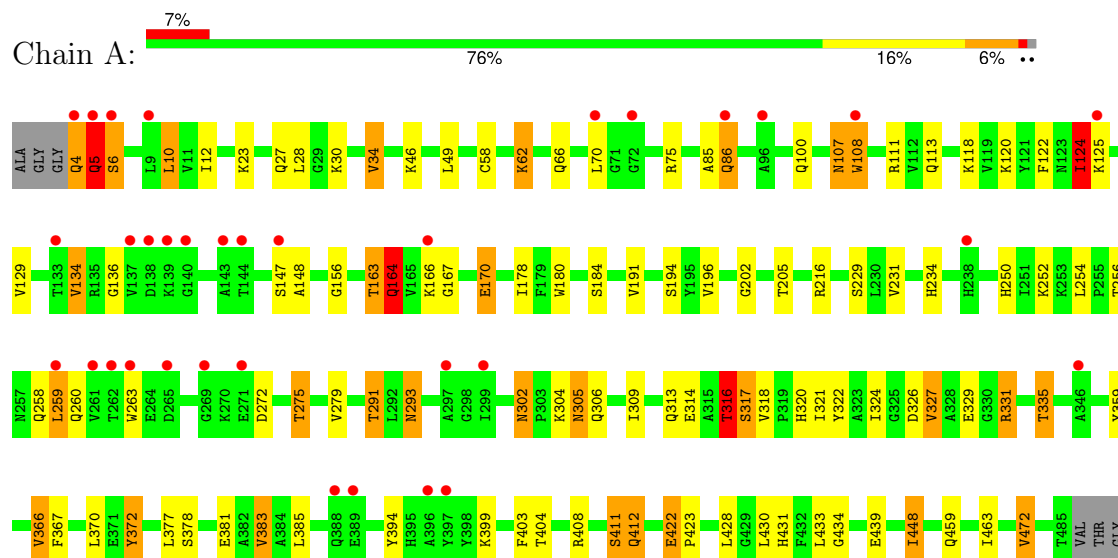
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	189	Total	O	0	0
			189	189		

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 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 2



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	110.51Å 110.51Å 208.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.45 – 2.25 15.45 – 2.25	Depositor EDS
% Data completeness (in resolution range)	95.2 (15.45-2.25) 95.2 (15.45-2.25)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.01 (at 2.25Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.193 , 0.258 0.191 , 0.256	Depositor DCC
R_{free} test set	2967 reflections (9.57%)	wwPDB-VP
Wilson B-factor (Å ²)	41.4	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3960	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: NA7, 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	1.45	24/3761 (0.6%)	1.34	33/5101 (0.6%)

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	1

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	412	GLN	N-CA	15.31	1.66	1.46
1	A	6	SER	CB-OG	10.00	1.62	1.42
1	A	6	SER	C-N	9.75	1.46	1.33
1	A	383	VAL	CA-CB	8.39	1.65	1.54
1	A	366	VAL	CA-CB	7.99	1.63	1.54
1	A	327	VAL	CA-CB	7.55	1.64	1.54
1	A	196	VAL	CA-CB	7.12	1.62	1.54
1	A	439	GLU	C-O	6.83	1.31	1.24
1	A	316	THR	CB-OG1	6.77	1.54	1.43
1	A	327	VAL	N-CA	6.62	1.54	1.46
1	A	411	SER	N-CA	6.46	1.54	1.46
1	A	202	GLY	N-CA	-6.32	1.38	1.45
1	A	191	VAL	CA-CB	6.25	1.61	1.54
1	A	108	TRP	NE1-CE2	6.11	1.44	1.37
1	A	6	SER	C-O	6.04	1.31	1.23
1	A	5	GLN	CA-CB	5.76	1.62	1.53
1	A	124	ILE	CA-CB	5.42	1.61	1.54
1	A	316	THR	CA-CB	5.41	1.62	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	317	SER	CB-OG	5.36	1.52	1.42
1	A	108	TRP	CG-CD1	5.33	1.50	1.36
1	A	394	TYR	CA-C	-5.28	1.46	1.52
1	A	372	TYR	C-O	-5.19	1.18	1.24
1	A	34	VAL	CA-CB	5.05	1.61	1.54
1	A	231	VAL	CA-CB	5.05	1.60	1.54

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	411	SER	CA-C-N	-9.44	103.52	121.54
1	A	411	SER	C-N-CA	-9.44	103.52	121.54
1	A	5	GLN	N-CA-C	8.27	115.56	108.78
1	A	302	ASN	CA-C-N	7.86	127.15	118.97
1	A	302	ASN	C-N-CA	7.86	127.15	118.97
1	A	86	GLN	CA-C-N	-7.82	110.06	119.84
1	A	86	GLN	C-N-CA	-7.82	110.06	119.84
1	A	305	ASN	CA-C-N	-7.49	110.52	122.95
1	A	305	ASN	C-N-CA	-7.49	110.52	122.95
1	A	411	SER	O-C-N	-7.37	113.39	122.82
1	A	412	GLN	N-CA-C	7.08	125.89	110.80
1	A	86	GLN	N-CA-C	6.57	124.33	109.81
1	A	448	ILE	N-CA-CB	6.52	118.17	110.55
1	A	366	VAL	CB-CA-C	6.32	118.61	110.96
1	A	335	THR	CA-C-N	-6.32	112.33	119.28
1	A	335	THR	C-N-CA	-6.32	112.33	119.28
1	A	463	ILE	CA-CB-CG1	6.17	120.89	110.40
1	A	205	THR	N-CA-C	-6.10	104.63	111.28
1	A	327	VAL	CB-CA-C	-6.08	96.67	111.02
1	A	107	ASN	N-CA-C	-5.75	104.92	111.07
1	A	6	SER	O-C-N	5.66	129.40	123.06
1	A	383	VAL	N-CA-CB	5.61	119.00	110.58
1	A	163	THR	CA-C-N	-5.56	118.13	126.86
1	A	163	THR	C-N-CA	-5.56	118.13	126.86
1	A	463	ILE	N-CA-CB	5.52	116.74	110.72
1	A	366	VAL	N-CA-CB	5.44	117.20	111.00
1	A	184	SER	CA-C-N	-5.43	114.22	119.87
1	A	184	SER	C-N-CA	-5.43	114.22	119.87
1	A	62	LYS	CD-CE-NZ	5.42	129.25	111.90
1	A	164	GLN	N-CA-CB	-5.40	108.70	114.10
1	A	124	ILE	CB-CA-C	5.17	118.45	110.28
1	A	472	VAL	CG1-CB-CG2	5.17	122.17	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	448	ILE	CG1-CB-CG2	-5.06	95.52	110.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	85	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	3679	0	3675	71	9
2	A	53	0	31	0	0
3	A	39	0	20	2	0
4	A	189	0	0	12	0
All	All	3960	0	3726	72	9

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 10.

All (72) 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:75:ARG:HD2	4:A:681:HOH:O	1.59	1.00
1:A:23:LYS:HZ3	1:A:113:GLN:HE21	0.99	0.93
1:A:75:ARG:CD	4:A:681:HOH:O	2.15	0.92
1:A:411:SER:O	1:A:412:GLN:HB2	1.67	0.92
1:A:23:LYS:HZ3	1:A:113:GLN:NE2	1.69	0.89
1:A:4:GLN:N	1:A:122:PHE:CZ	2.41	0.89
1:A:124:ILE:HG23	1:A:136:GLY:HA3	1.58	0.85
1:A:331:ARG:HH11	1:A:331:ARG:HG3	1.40	0.85
1:A:302:ASN:O	1:A:305:ASN:O	1.97	0.82
1:A:331:ARG:HH11	1:A:331:ARG:CG	1.91	0.81
1:A:23:LYS:NZ	1:A:113:GLN:HE21	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:SER:OG	1:A:381:GLU:HG3	1.81	0.79
1:A:23:LYS:NZ	1:A:113:GLN:NE2	2.32	0.78
1:A:411:SER:O	1:A:412:GLN:CB	2.27	0.75
1:A:66:GLN:O	1:A:70:LEU:HD23	1.89	0.72
1:A:163:THR:O	1:A:164:GLN:HB2	1.91	0.71
1:A:163:THR:O	1:A:164:GLN:CB	2.40	0.70
1:A:459:GLN:NE2	4:A:634:HOH:O	2.25	0.70
1:A:377:LEU:O	1:A:431:HIS:HE1	1.75	0.69
1:A:306:GLN:NE2	4:A:686:HOH:O	2.24	0.68
1:A:4:GLN:N	1:A:122:PHE:HZ	1.89	0.67
1:A:124:ILE:CG2	1:A:136:GLY:HA3	2.24	0.67
1:A:372:TYR:OH	1:A:431:HIS:HD2	1.81	0.63
1:A:166:LYS:HZ2	1:A:250:HIS:HB2	1.62	0.63
1:A:124:ILE:HD13	1:A:136:GLY:C	2.24	0.63
1:A:320:HIS:CD2	1:A:321:ILE:HG13	2.34	0.63
1:A:291:THR:HG22	4:A:684:HOH:O	1.99	0.62
1:A:62:LYS:HE3	1:A:367:PHE:CE2	2.35	0.62
1:A:194:SER:HB3	3:A:501:NA7:HC4'	1.84	0.60
1:A:316:THR:HG23	1:A:318:VAL:H	1.68	0.59
1:A:234:HIS:HE1	4:A:632:HOH:O	1.86	0.58
1:A:331:ARG:CG	1:A:331:ARG:NH1	2.61	0.57
1:A:66:GLN:O	1:A:70:LEU:CD2	2.52	0.55
1:A:124:ILE:HG23	1:A:136:GLY:CA	2.33	0.55
1:A:403:PHE:CG	1:A:408:ARG:HG3	2.44	0.53
1:A:30:LYS:NZ	4:A:568:HOH:O	2.43	0.52
1:A:260:GLN:HE22	1:A:275:THR:CG2	2.22	0.52
1:A:75:ARG:HD3	4:A:681:HOH:O	1.98	0.52
3:A:501:NA7:HC1'	4:A:582:HOH:O	2.10	0.51
1:A:291:THR:CG2	4:A:684:HOH:O	2.55	0.49
1:A:372:TYR:HB2	1:A:433:LEU:HD13	1.94	0.49
1:A:6:SER:HA	1:A:147:SER:O	2.13	0.49
1:A:260:GLN:NE2	1:A:275:THR:HB	2.28	0.48
1:A:12:ILE:HD11	1:A:134:VAL:HG21	1.96	0.47
1:A:313:GLN:C	1:A:314:GLU:HG2	2.40	0.47
1:A:322:TYR:N	1:A:322:TYR:CD1	2.81	0.47
1:A:370:LEU:HD11	1:A:434:GLY:HA2	1.97	0.47
1:A:302:ASN:OD1	1:A:302:ASN:C	2.58	0.47
1:A:5:GLN:HA	4:A:578:HOH:O	2.15	0.46
1:A:331:ARG:HD2	1:A:359:TYR:CZ	2.51	0.46
1:A:167:GLY:HA2	1:A:170:GLU:CG	2.47	0.45
1:A:316:THR:OG1	1:A:317:SER:N	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:LYS:HD3	1:A:404:THR:HG22	1.97	0.45
1:A:293:ASN:HD22	1:A:293:ASN:N	2.15	0.44
1:A:254:LEU:HD11	1:A:260:GLN:HE21	1.82	0.44
1:A:259:LEU:HD23	1:A:279:VAL:HG23	2.00	0.44
1:A:263:TRP:CE2	1:A:272:ASP:HB3	2.52	0.44
1:A:422:GLU:HA	1:A:423:PRO:HD3	1.90	0.43
1:A:107:ASN:HB3	1:A:111:ARG:HH12	1.83	0.43
1:A:156:GLY:HA2	1:A:326:ASP:HB2	2.00	0.42
1:A:66:GLN:OE1	1:A:70:LEU:HD21	2.19	0.42
1:A:314:GLU:OE2	1:A:331:ARG:NH1	2.53	0.42
1:A:23:LYS:O	1:A:27:GLN:HG3	2.20	0.42
1:A:331:ARG:HA	1:A:331:ARG:HD3	1.80	0.42
1:A:49:LEU:H	1:A:111:ARG:NH2	2.18	0.42
1:A:309:ILE:O	1:A:316:THR:HA	2.20	0.42
1:A:10:LEU:HB2	1:A:148:ALA:HB2	2.01	0.41
1:A:293:ASN:N	1:A:293:ASN:ND2	2.68	0.41
1:A:113:GLN:NE2	4:A:598:HOH:O	2.53	0.41
1:A:100:GLN:HG2	1:A:180:TRP:CZ3	2.56	0.41
1:A:256:THR:CB	1:A:258:GLN:HE21	2.34	0.40
1:A:293:ASN:HD22	1:A:293:ASN:H	1.70	0.40

All (9) 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)
1:A:108:TRP:CZ3	1:A:108:TRP:CZ3[16_664]	0.90	1.30
1:A:108:TRP:CE3	1:A:108:TRP:CE3[16_664]	1.10	1.10
1:A:108:TRP:CE3	1:A:108:TRP:CZ3[16_664]	1.11	1.09
1:A:108:TRP:CZ3	1:A:108:TRP:CH2[16_664]	1.54	0.66
1:A:108:TRP:CD2	1:A:108:TRP:CZ3[16_664]	1.79	0.41
1:A:108:TRP:CE3	1:A:108:TRP:CH2[16_664]	1.83	0.37
1:A:108:TRP:CD2	1:A:108:TRP:CE3[16_664]	1.87	0.33
1:A:108:TRP:CZ2	1:A:108:TRP:CZ3[16_664]	2.10	0.10
1:A:108:TRP:CE2	1:A:108:TRP:CZ3[16_664]	2.16	0.04

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	480/488 (98%)	458 (95%)	20 (4%)	2 (0%)	30	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	316	THR
1	A	304	LYS

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	394/396 (100%)	357 (91%)	37 (9%)	8	6

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLN
1	A	5	GLN
1	A	10	LEU
1	A	28	LEU
1	A	34	VAL
1	A	46	LYS
1	A	58	CYS
1	A	86	GLN
1	A	118	LYS

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Mol	Chain	Res	Type
1	A	120	LYS
1	A	124	ILE
1	A	125	LYS
1	A	129	VAL
1	A	134	VAL
1	A	164	GLN
1	A	170	GLU
1	A	178	ILE
1	A	216	ARG
1	A	229	SER
1	A	252	LYS
1	A	259	LEU
1	A	275	THR
1	A	291	THR
1	A	293	ASN
1	A	324	ILE
1	A	327	VAL
1	A	329	GLU
1	A	331	ARG
1	A	335	THR
1	A	366	VAL
1	A	383	VAL
1	A	385	LEU
1	A	422	GLU
1	A	428	LEU
1	A	430	LEU
1	A	448	ILE
1	A	472	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	A	55	ASN
1	A	89	GLN
1	A	113	GLN
1	A	164	GLN
1	A	234	HIS
1	A	250	HIS
1	A	258	GLN
1	A	260	GLN
1	A	293	ASN

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Mol	Chain	Res	Type
1	A	386	HIS
1	A	412	GLN
1	A	425	GLN
1	A	431	HIS
1	A	442	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	$\# Z > 2$
3	NA7	A	501	-	42,42,42	1.75	4 (9%)	60,65,65	2.14	14 (23%)
2	FAD	A	500	-	58,58,58	1.27	7 (12%)	85,89,89	1.87	24 (28%)

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	NA7	A	501	-	-	5/27/56/56	0/4/4/4
2	FAD	A	500	-	-	7/34/50/50	0/6/6/6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	NA7	PN-O3	6.42	1.66	1.59
3	A	501	NA7	PA-O3	6.04	1.66	1.59
2	A	500	FAD	C4X-N5	3.97	1.39	1.30
2	A	500	FAD	C9-C9A	3.39	1.45	1.39
3	A	501	NA7	C2A-N3A	3.12	1.39	1.33
2	A	500	FAD	PA-O3P	2.81	1.62	1.59
3	A	501	NA7	C2A-N1A	2.57	1.38	1.33
2	A	500	FAD	C10-N1	2.53	1.38	1.33
2	A	500	FAD	C2A-N3A	2.35	1.38	1.33
2	A	500	FAD	C2A-N1A	2.30	1.38	1.33
2	A	500	FAD	C1'-N10	2.17	1.53	1.47

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	NA7	N3A-C2A-N1A	-6.82	118.26	128.58
2	A	500	FAD	N3A-C2A-N1A	-6.44	118.83	128.58
3	A	501	NA7	C2B-C1B-N9A	-5.41	104.84	113.75
3	A	501	NA7	C5A-C4A-N3A	-5.16	119.61	126.72
3	A	501	NA7	O4B-C1B-N9A	4.68	117.07	108.09
3	A	501	NA7	O4D-C4D-C3D	4.30	108.60	104.63
3	A	501	NA7	C2A-N3A-C4A	4.22	122.13	111.83
2	A	500	FAD	C5A-C4A-N3A	-4.08	121.10	126.72
2	A	500	FAD	C5A-N7A-C8A	3.93	109.62	103.45
2	A	500	FAD	N9A-C8A-N7A	-3.82	108.52	113.94
3	A	501	NA7	N3A-C4A-N9A	3.76	133.56	127.17
2	A	500	FAD	C10-C4X-N5	-3.62	117.41	124.81
2	A	500	FAD	C4X-C10-N10	3.53	121.53	116.48
2	A	500	FAD	C4-N3-C2	-3.49	119.44	125.64
2	A	500	FAD	O3'-C3'-C4'	3.49	116.85	108.93
3	A	501	NA7	N9A-C8A-N7A	-3.44	109.06	113.94
2	A	500	FAD	O3B-C3B-C4B	-3.27	101.69	111.08
2	A	500	FAD	C2A-N3A-C4A	3.25	119.78	111.83
3	A	501	NA7	C5A-N7A-C8A	3.20	108.48	103.45
2	A	500	FAD	O3P-PA-O1A	3.15	120.17	110.70
2	A	500	FAD	N3A-C4A-N9A	3.00	132.27	127.17
2	A	500	FAD	C2A-N1A-C6A	2.90	123.49	118.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	FAD	C4-C4X-N5	2.86	122.16	118.21
2	A	500	FAD	C4A-C5A-N7A	-2.68	107.52	110.58
3	A	501	NA7	O2B-C2B-C3B	2.67	121.24	111.68
3	A	501	NA7	C1D-C2D-C3D	2.52	105.66	101.63
3	A	501	NA7	O3B-C3B-C2B	2.50	118.17	111.19
2	A	500	FAD	O4B-C1B-C2B	-2.49	101.28	106.62
3	A	501	NA7	O1A-PA-O3	2.41	113.78	107.27
2	A	500	FAD	C4X-C4-N3	2.33	119.19	113.25
2	A	500	FAD	O2-C2-N1	-2.30	117.98	121.80
2	A	500	FAD	O3P-P-O1P	2.26	117.50	110.70
2	A	500	FAD	C2B-C1B-N9A	2.25	118.89	113.30
2	A	500	FAD	O4-C4-C4X	-2.21	120.70	126.53
2	A	500	FAD	O4'-C4'-C3'	2.18	114.34	109.25
2	A	500	FAD	C4-C4X-C10	2.03	120.41	116.93
3	A	501	NA7	C5A-C6A-N6A	-2.03	118.27	123.29
2	A	500	FAD	C4X-C10-N1	-2.02	119.63	124.59

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	NA7	C5B-O5B-PA-O3
2	A	500	FAD	C5'-O5'-P-O1P
3	A	501	NA7	C5B-O5B-PA-O2A
3	A	501	NA7	C5D-O5D-PN-O2N
2	A	500	FAD	C3B-C4B-C5B-O5B
2	A	500	FAD	PA-O3P-P-O5'
3	A	501	NA7	O4D-C4D-C5D-O5D
2	A	500	FAD	O4B-C4B-C5B-O5B
2	A	500	FAD	P-O3P-PA-O2A
2	A	500	FAD	C2B-C1B-N9A-C8A
3	A	501	NA7	C3B-C2B-O2B-P2B
2	A	500	FAD	PA-O3P-P-O2P

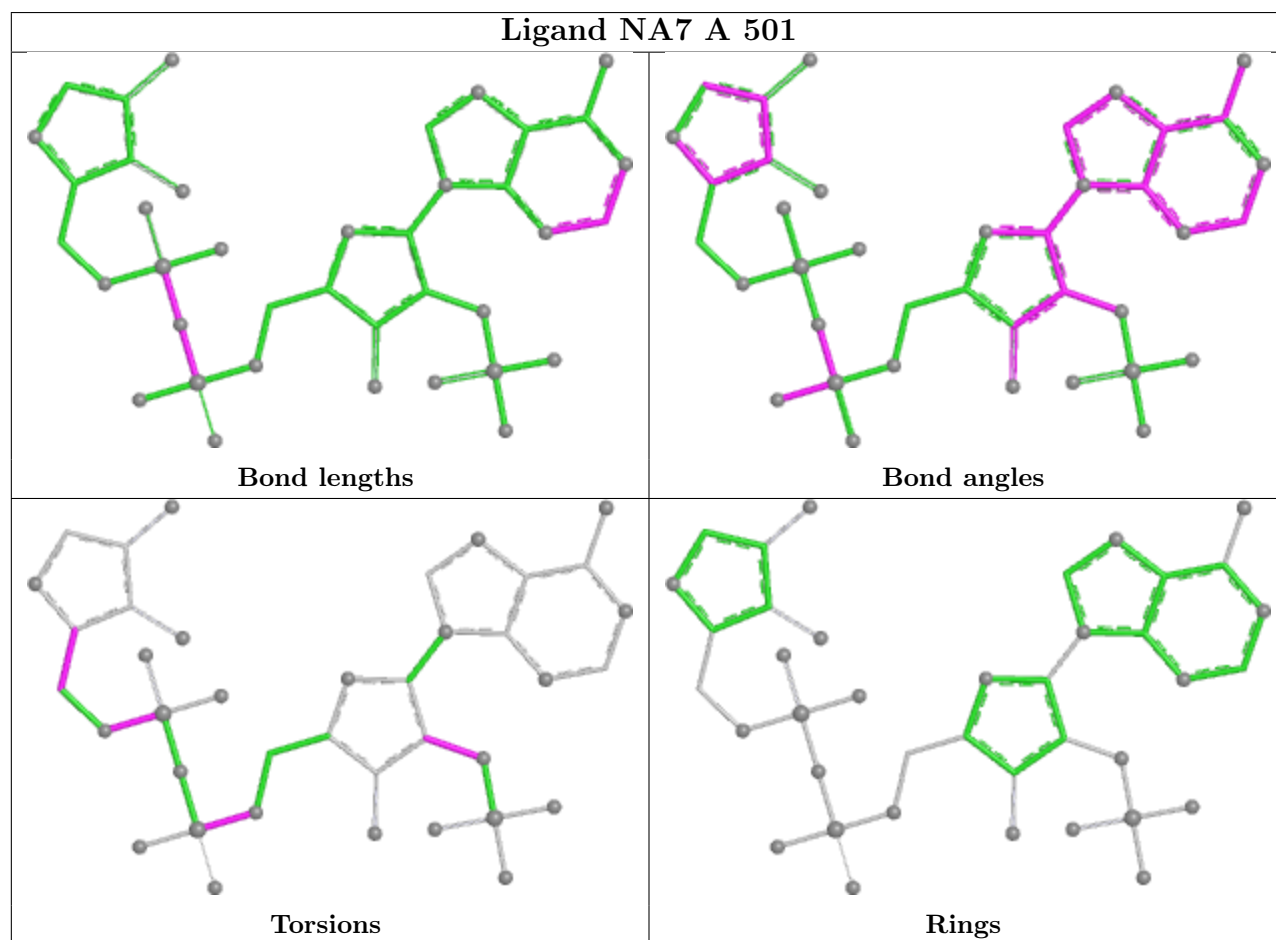
There are no ring outliers.

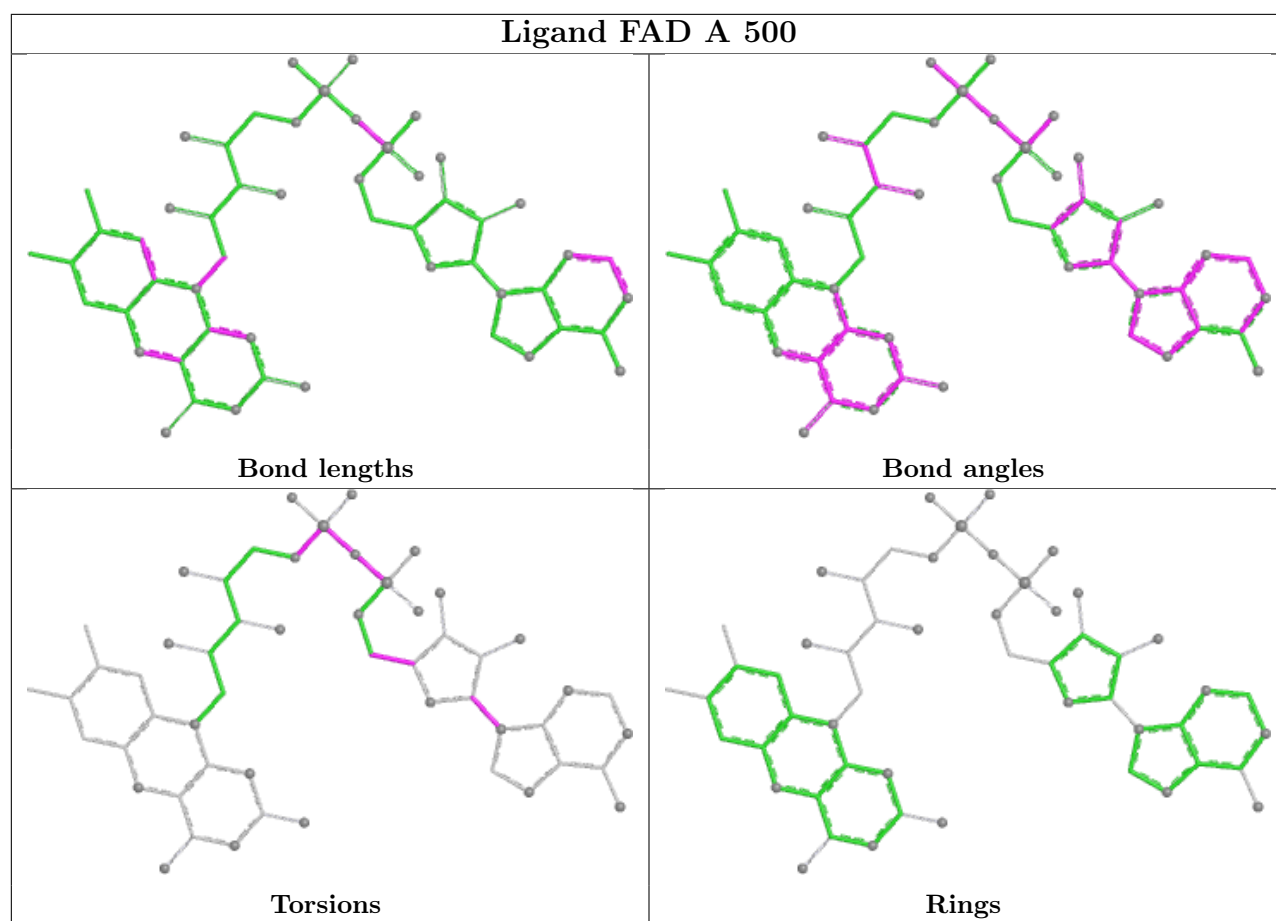
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	NA7	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 ⓘ

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, 95th 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	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	482/488 (98%)	0.60	34 (7%) 22 20	29, 39, 45, 59	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	108	TRP	4.7
1	A	263	TRP	3.9
1	A	265	ASP	3.8
1	A	133	THR	3.3
1	A	9	LEU	3.2
1	A	138	ASP	3.1
1	A	72	GLY	3.0
1	A	389	GLU	3.0
1	A	262	THR	2.9
1	A	397	TYR	2.9
1	A	297	ALA	2.8
1	A	259	LEU	2.8
1	A	5	GLN	2.7
1	A	396	ALA	2.7
1	A	137	VAL	2.7
1	A	346	ALA	2.7
1	A	144	THR	2.7
1	A	86	GLN	2.6
1	A	261	VAL	2.6
1	A	147	SER	2.5
1	A	4	GLN	2.4
1	A	96	ALA	2.4
1	A	166	LYS	2.4
1	A	238	HIS	2.3
1	A	6	SER	2.3
1	A	70	LEU	2.3
1	A	140	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	271	GLU	2.2
1	A	269	GLY	2.2
1	A	143	ALA	2.1
1	A	139	LYS	2.1
1	A	388	GLN	2.0
1	A	299	ILE	2.0
1	A	125	LYS	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

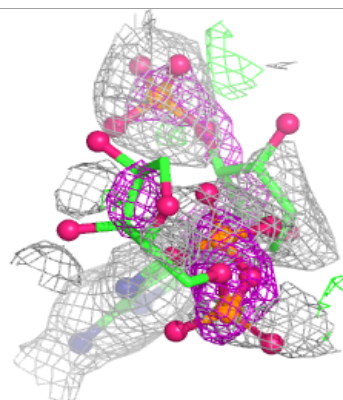
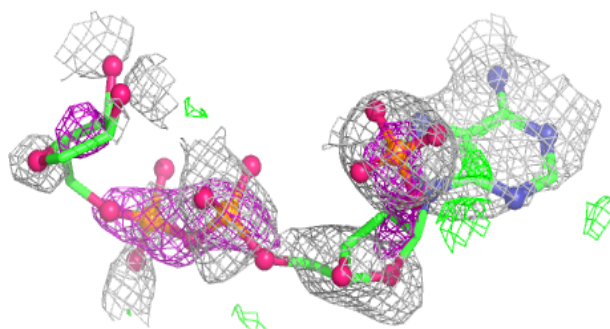
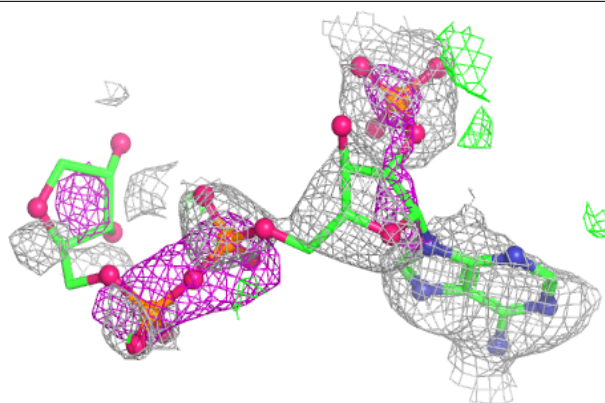
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NA7	A	501	39/39	0.73	0.17	70,80,111,112	0
2	FAD	A	500	53/53	0.85	0.14	28,35,39,40	0

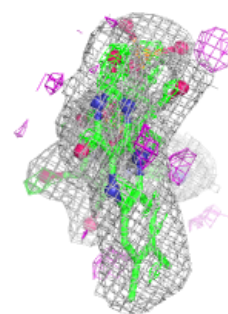
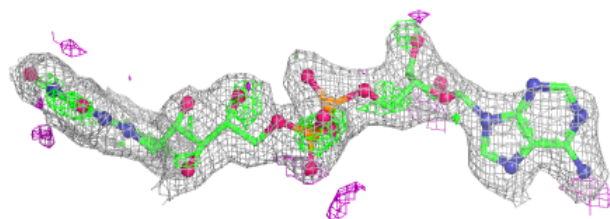
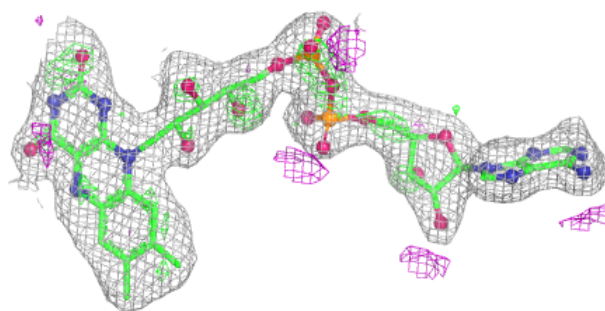
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NA7 A 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around FAD A 500:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.