



Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 09:12 am BST

PDB ID : 3OJX
Title : Disulfide crosslinked cytochrome P450 reductase inactive
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Waskell, L.; Kim, J.-J.P.
Deposited on : 2010-08-23
Resolution : 2.50 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 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) : 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

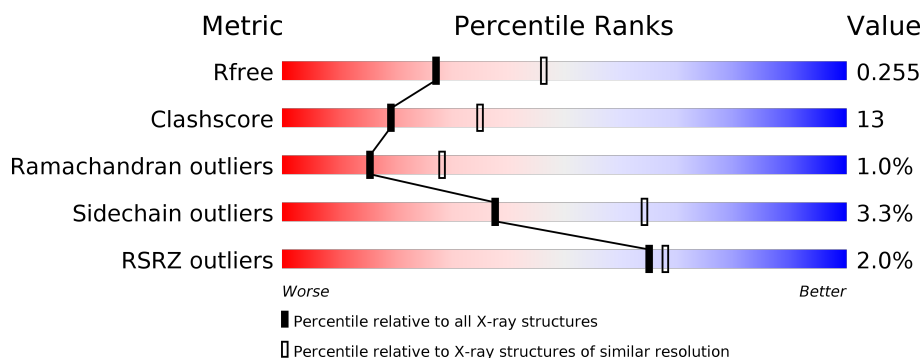
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 $\leq 5\%$. 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	622	<div> <div>2%</div> <div>68%</div> <div>28%</div> <div>..</div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5057 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.

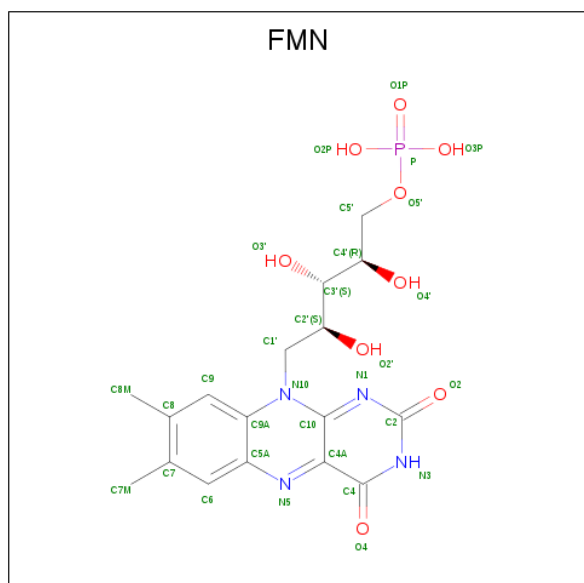
- Molecule 1 is a protein called NADPH-Cytochrome P450 Reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	607	4855	3079	831	926	19	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

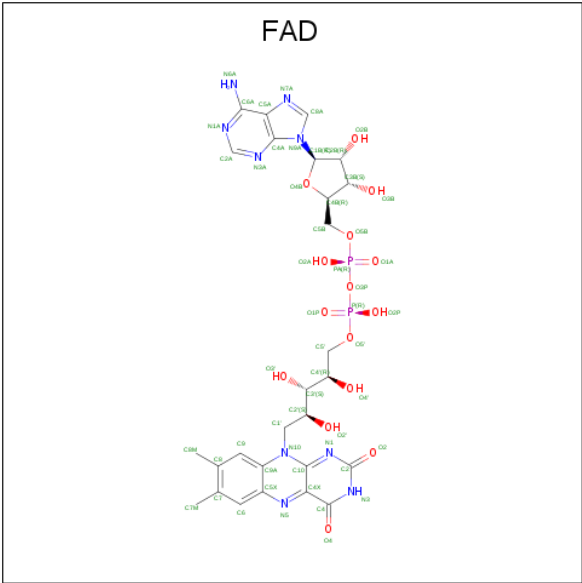
Chain	Residue	Modelled	Actual	Comment	Reference
A	136	ALA	CYS	ENGINEERED MUTATION	UNP P00388
A	147	CYS	ASP	ENGINEERED MUTATION	UNP P00388
A	228	ALA	CYS	ENGINEERED MUTATION	UNP P00388
A	363	THR	CYS	ENGINEERED MUTATION	UNP P00388
A	445	LEU	CYS	ENGINEERED MUTATION	UNP P00388
A	472	THR	CYS	ENGINEERED MUTATION	UNP P00388
A	514	CYS	ARG	ENGINEERED MUTATION	UNP P00388
A	566	ALA	CYS	ENGINEERED MUTATION	UNP P00388

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	70	Total	O	0	0
			70	70		

- Molecule 1: NADPH-Cytochrome P450 Reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.41 Å 73.27 Å 137.49 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	21.54 – 2.50 21.54 – 2.50	Depositor EDS
% Data completeness (in resolution range)	92.7 (21.54-2.50) 92.8 (21.54-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.50 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.209 , 0.267 0.201 , 0.255	Depositor DCC
R_{free} test set	1061 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	35.0	Xtriage
Anisotropy	0.690	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 29.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5057	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% 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: FMN, NAP, 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	0.37	0/4971	0.61	0/6731

There are no bond length outliers.

There are no bond angle outliers.

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	4855	0	4699	125	1
2	A	31	0	18	0	0
3	A	53	0	31	0	0
4	A	48	0	25	4	0
5	A	70	0	0	0	0
All	All	5057	0	4773	126	1

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 13.

All (126) 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:578:GLU:HA	1:A:581:ARG:HH12	1.36	0.90
4:A:753:NAP:H51A	4:A:753:NAP:H5N	1.60	0.81
1:A:606:GLN:HE21	1:A:606:GLN:H	1.33	0.76
1:A:578:GLU:HA	1:A:581:ARG:NH1	2.00	0.75
1:A:526:THR:HG21	1:A:626:HIS:HD2	1.50	0.75
1:A:376:ASP:HB3	1:A:449:PRO:HG2	1.72	0.72
1:A:295:GLY:HA3	1:A:571:GLU:OE1	1.90	0.72
1:A:86:SER:HB2	1:A:91:ALA:HB3	1.72	0.71
1:A:242:ILE:HG22	1:A:243:ARG:N	2.06	0.71
1:A:426:HIS:HD2	1:A:429:ALA:H	1.43	0.66
1:A:236:THR:HG23	1:A:238:GLU:H	1.61	0.65
1:A:266:LEU:HD12	1:A:267:LYS:H	1.62	0.65
1:A:606:GLN:H	1:A:606:GLN:NE2	1.95	0.65
1:A:606:GLN:HE22	4:A:753:NAP:H2A	1.62	0.64
1:A:292:LEU:HD11	1:A:302:HIS:HB2	1.80	0.64
1:A:529:ILE:HD13	1:A:616:LEU:HD22	1.80	0.63
1:A:310:SER:O	1:A:311:LYS:HB2	1.99	0.63
1:A:147:CYS:SG	1:A:514:CYS:HB3	2.39	0.63
1:A:313:ARG:HH11	1:A:313:ARG:HG3	1.64	0.63
1:A:243:ARG:O	1:A:351:LEU:HD12	1.99	0.62
1:A:606:GLN:N	1:A:606:GLN:HE21	1.98	0.62
1:A:120:ALA:HA	1:A:155:TRP:CZ2	2.35	0.61
1:A:300:LEU:HD13	1:A:574:LEU:HD21	1.83	0.61
1:A:633:ALA:HA	1:A:637:ALA:HB3	1.82	0.60
1:A:332:ASN:ND2	1:A:368:ARG:HH12	1.99	0.60
1:A:298:ARG:NH2	4:A:753:NAP:O1N	2.38	0.57
1:A:535:THR:HG1	1:A:677:TRP:HZ3	1.53	0.57
1:A:409:SER:O	1:A:413:LYS:HG3	2.05	0.57
1:A:413:LYS:O	1:A:417:LEU:HG	2.05	0.56
1:A:266:LEU:HD12	1:A:267:LYS:N	2.20	0.56
1:A:633:ALA:HB2	1:A:676:VAL:HB	1.86	0.56
1:A:239:GLU:O	1:A:240:SER:CB	2.54	0.55
1:A:334:ILE:O	1:A:337:ILE:HG22	2.05	0.55
1:A:105:TYR:CE2	1:A:224:TRP:HB3	2.41	0.54
1:A:302:HIS:HD2	1:A:575:TYR:OH	1.91	0.54
1:A:543:PHE:O	1:A:547:ARG:HG2	2.08	0.54
1:A:526:THR:HG21	1:A:626:HIS:CD2	2.39	0.54
1:A:567:ARG:HG3	1:A:572:ASP:OD2	2.07	0.53
1:A:276:PHE:CG	1:A:282:PHE:HB2	2.43	0.53
1:A:381:PRO:HG2	1:A:430:ILE:HD12	1.91	0.53
1:A:147:CYS:HG	1:A:514:CYS:CB	2.22	0.53
1:A:577:GLU:H	1:A:577:GLU:CD	2.12	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:GLY:C	1:A:182:ASN:HD21	2.12	0.53
1:A:665:LYS:O	1:A:669:LYS:HB2	2.09	0.53
1:A:667:MET:HG2	1:A:672:TYR:HB3	1.90	0.52
1:A:341:ASP:HB3	1:A:344:VAL:HG23	1.91	0.52
1:A:257:LYS:HB2	1:A:257:LYS:NZ	2.25	0.52
1:A:145:PRO:HB3	1:A:184:MET:SD	2.49	0.52
1:A:428:LEU:O	1:A:432:GLN:HG3	2.10	0.51
1:A:479:GLU:HG2	1:A:485:VAL:HG22	1.91	0.51
1:A:332:ASN:HD21	1:A:368:ARG:HH12	1.57	0.51
1:A:236:THR:HG23	1:A:238:GLU:N	2.24	0.51
1:A:308:SER:O	1:A:309:ASP:HB2	2.11	0.51
1:A:76:THR:OG1	1:A:78:ARG:HG2	2.10	0.51
1:A:173:LEU:N	1:A:173:LEU:HD12	2.27	0.50
1:A:236:THR:CG2	1:A:238:GLU:HB2	2.42	0.50
1:A:250:HIS:HB3	1:A:253:MET:HG2	1.93	0.50
1:A:82:VAL:HG22	1:A:134:VAL:HB	1.93	0.49
1:A:81:ILE:CD1	1:A:110:MET:HG3	2.42	0.49
1:A:363:THR:HB	1:A:364:PRO:HA	1.93	0.49
1:A:242:ILE:CG2	1:A:243:ARG:N	2.76	0.49
1:A:300:LEU:HD23	1:A:474:VAL:HA	1.95	0.49
1:A:160:ASP:O	1:A:160:ASP:OD1	2.31	0.48
1:A:426:HIS:CD2	1:A:429:ALA:H	2.29	0.48
1:A:80:ILE:O	1:A:109:GLY:HA2	2.12	0.48
1:A:236:THR:CG2	1:A:238:GLU:H	2.24	0.48
1:A:304:GLU:HG2	1:A:470:HIS:CD2	2.49	0.47
1:A:79:ASN:O	1:A:131:SER:HA	2.15	0.47
1:A:125:LEU:N	1:A:126:PRO:CD	2.78	0.47
1:A:361:PHE:HB2	1:A:362:PRO:HD2	1.96	0.47
1:A:152:PHE:CZ	1:A:156:LEU:HD11	2.50	0.46
1:A:493:TRP:CH2	1:A:509:VAL:HG13	2.49	0.46
1:A:252:ASP:O	1:A:253:MET:HB2	2.14	0.46
1:A:626:HIS:HB3	1:A:628:TYR:CE1	2.50	0.46
1:A:318:ASP:OD1	1:A:515:LYS:HA	2.16	0.46
1:A:145:PRO:HB3	1:A:184:MET:CE	2.45	0.46
1:A:286:VAL:HG23	1:A:507:ALA:O	2.16	0.46
1:A:80:ILE:HG12	1:A:132:LEU:HB3	1.98	0.46
1:A:388:GLU:HG3	1:A:447:LEU:HD21	1.97	0.46
1:A:394:SER:OG	1:A:436:SER:HB2	2.16	0.45
1:A:388:GLU:O	1:A:391:GLN:HG2	2.17	0.45
1:A:213:GLU:O	1:A:217:ILE:HG12	2.16	0.45
1:A:598:GLU:O	1:A:599:GLN:CB	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:ALA:HA	1:A:481:LYS:HB2	1.97	0.45
1:A:652:GLY:N	1:A:653:PRO:HA	2.32	0.45
1:A:241:SER:O	1:A:242:ILE:HB	2.16	0.45
1:A:620:ILE:CD1	1:A:627:ILE:HD11	2.47	0.45
1:A:133:VAL:HG13	1:A:133:VAL:O	2.18	0.44
1:A:405:MET:CG	1:A:415:LEU:HG	2.47	0.44
1:A:390:ALA:HB1	1:A:403:HIS:CE1	2.52	0.44
1:A:535:THR:C	1:A:537:ILE:H	2.20	0.44
1:A:434:TYR:O	1:A:437:LEU:HB3	2.18	0.44
1:A:499:PRO:O	1:A:500:ALA:C	2.56	0.44
1:A:636:MET:HG2	4:A:753:NAP:C2A	2.48	0.44
1:A:361:PHE:HB2	1:A:362:PRO:CD	2.48	0.44
1:A:645:TYR:OH	1:A:664:LYS:HE3	2.18	0.43
1:A:620:ILE:HD11	1:A:627:ILE:HD11	2.01	0.43
1:A:266:LEU:O	1:A:267:LYS:HB2	2.18	0.43
1:A:568:ARG:HA	1:A:598:GLU:HG3	2.00	0.43
1:A:145:PRO:HD3	1:A:184:MET:HE1	2.00	0.43
1:A:382:ARG:HG2	1:A:382:ARG:HH11	1.84	0.43
1:A:265:ARG:HB3	1:A:268:SER:HB3	2.01	0.42
1:A:497:LYS:HD2	1:A:507:ALA:HB1	2.00	0.42
1:A:262:GLU:HG3	1:A:269:TYR:HB2	2.01	0.42
1:A:588:LEU:HD22	1:A:590:GLN:O	2.19	0.42
1:A:536:GLY:HA2	1:A:677:TRP:CH2	2.55	0.42
1:A:314:TYR:CD1	1:A:314:TYR:C	2.93	0.42
1:A:549:TRP:O	1:A:553:GLN:HG2	2.20	0.42
1:A:119:LEU:HG	1:A:152:PHE:CD1	2.55	0.42
1:A:493:TRP:HH2	1:A:509:VAL:HG13	1.85	0.42
1:A:441:ILE:O	1:A:445:LEU:HD13	2.20	0.41
1:A:550:LEU:O	1:A:555:LYS:HB2	2.20	0.41
1:A:474:VAL:HG13	1:A:474:VAL:O	2.20	0.41
1:A:528:VAL:HG12	1:A:530:MET:HG3	2.02	0.41
1:A:253:MET:HA	1:A:253:MET:CE	2.50	0.41
1:A:374:TYR:O	1:A:375:LEU:HD23	2.20	0.41
1:A:441:ILE:HG12	1:A:445:LEU:HD13	2.03	0.41
1:A:291:LYS:HE3	1:A:293:ASN:O	2.20	0.41
1:A:313:ARG:CG	1:A:313:ARG:HH11	2.33	0.41
1:A:147:CYS:SG	1:A:514:CYS:SG	3.19	0.40
1:A:81:ILE:HD12	1:A:110:MET:HG3	2.03	0.40
1:A:254:ASP:O	1:A:257:LYS:N	2.41	0.40
1:A:370:ALA:HA	1:A:374:TYR:HD2	1.86	0.40
1:A:273:LYS:HA	1:A:274:PRO:HD2	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:LEU:HD21	1:A:474:VAL:HB	2.04	0.40
1:A:238:GLU:OE1	1:A:238:GLU:HA	2.21	0.40

All (1) 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:104:ARG:NH2	1:A:158:GLU:OE1[3_555]	2.19	0.01

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	603/622 (97%)	566 (94%)	31 (5%)	6 (1%)	15 28

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	SER
1	A	407	SER
1	A	599	GLN
1	A	253	MET
1	A	255	VAL
1	A	141	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	515/528 (98%)	498 (97%)	17 (3%)	38 64

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	167	LYS
1	A	190	GLN
1	A	218	THR
1	A	346	MET
1	A	350	ASN
1	A	353	GLU
1	A	356	ASN
1	A	422	GLU
1	A	484	ARG
1	A	567	ARG
1	A	572	ASP
1	A	573	TYR
1	A	588	LEU
1	A	606	GLN
1	A	672	TYR
1	A	674	LEU
1	A	676	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	ASN
1	A	150	GLN
1	A	180	HIS
1	A	182	ASN
1	A	250	HIS
1	A	271	ASN
1	A	280	ASN
1	A	294	GLN
1	A	302	HIS
1	A	332	ASN
1	A	350	ASN
1	A	426	HIS
1	A	467	ASN
1	A	470	HIS

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Mol	Chain	Res	Type
1	A	486	ASN
1	A	517	GLN
1	A	590	GLN
1	A	592	ASN
1	A	606	GLN
1	A	626	HIS

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 carbohydrates 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	$\# Z > 2$
3	FAD	A	752	-	51,58,58	2.93	21 (41%)	60,89,89	2.83	15 (25%)
4	NAP	A	753	-	45,52,52	2.26	16 (35%)	56,80,80	1.40	9 (16%)
2	FMN	A	751	-	31,33,33	3.33	12 (38%)	40,50,50	3.52	17 (42%)

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	752	-	-	3/30/50/50	0/6/6/6
4	NAP	A	753	-	-	6/31/67/67	0/5/5/5
2	FMN	A	751	-	-	0/18/18/18	0/3/3/3

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	751	FMN	O4'-C4'	-9.12	1.24	1.43
3	A	752	FAD	C9A-N10	8.39	1.49	1.38
2	A	751	FMN	C9A-N10	6.96	1.47	1.38
3	A	752	FAD	C4A-N3A	6.61	1.44	1.35
3	A	752	FAD	C4X-C10	6.61	1.45	1.38
4	A	753	NAP	C7N-N7N	6.38	1.45	1.33
2	A	751	FMN	C8M-C8	-6.29	1.38	1.51
4	A	753	NAP	C4A-N3A	6.04	1.44	1.35
3	A	752	FAD	C4-N3	5.99	1.43	1.33
3	A	752	FAD	C4X-N5	5.56	1.41	1.33
2	A	751	FMN	C4A-N5	5.49	1.41	1.33
2	A	751	FMN	C10-N1	5.42	1.40	1.33
4	A	753	NAP	C2N-C3N	5.40	1.47	1.39
3	A	752	FAD	C8-C7	5.36	1.54	1.40
3	A	752	FAD	C10-N1	5.28	1.40	1.33
2	A	751	FMN	C4A-C10	5.26	1.44	1.38
3	A	752	FAD	C5X-N5	4.10	1.42	1.35
2	A	751	FMN	C4-N3	4.08	1.40	1.33
4	A	753	NAP	C4N-C3N	4.06	1.46	1.39
3	A	752	FAD	C4-C4X	3.93	1.48	1.41
3	A	752	FAD	C9A-C5X	3.70	1.50	1.42
4	A	753	NAP	C2N-N1N	3.57	1.39	1.35
3	A	752	FAD	C2A-N1A	3.52	1.40	1.33
3	A	752	FAD	C6-C5X	3.52	1.47	1.41
3	A	752	FAD	C2A-N3A	3.51	1.37	1.32
2	A	751	FMN	C8-C7	3.36	1.49	1.40
2	A	751	FMN	C1'-N10	-3.29	1.44	1.48
2	A	751	FMN	C9-C9A	3.24	1.47	1.40
4	A	753	NAP	C2A-N3A	3.19	1.37	1.32
4	A	753	NAP	C6N-N1N	3.18	1.43	1.35
4	A	753	NAP	O4D-C1D	3.10	1.45	1.41
3	A	752	FAD	C5'-C4'	3.01	1.56	1.51
4	A	753	NAP	C3N-C7N	2.83	1.54	1.50
4	A	753	NAP	P2B-O1X	2.80	1.59	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	751	FMN	C5A-N5	2.80	1.40	1.35
4	A	753	NAP	C2A-N1A	2.74	1.39	1.33
3	A	752	FAD	C9-C9A	2.63	1.46	1.40
3	A	752	FAD	C6-C7	2.57	1.44	1.37
3	A	752	FAD	O4B-C1B	2.53	1.44	1.41
4	A	753	NAP	PN-O1N	-2.27	1.42	1.50
3	A	752	FAD	C2'-C3'	2.26	1.57	1.53
4	A	753	NAP	C6N-C5N	2.22	1.43	1.38
4	A	753	NAP	PA-O2A	-2.21	1.44	1.55
4	A	753	NAP	C5N-C4N	2.19	1.43	1.38
3	A	752	FAD	C2-N3	2.18	1.42	1.38
2	A	751	FMN	C9A-C5A	2.18	1.46	1.42
4	A	753	NAP	PN-O2N	-2.13	1.45	1.55
3	A	752	FAD	C8M-C8	2.11	1.55	1.51
3	A	752	FAD	PA-O2A	-2.09	1.45	1.55

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	751	FMN	C4-N3-C2	14.44	127.33	115.14
3	A	752	FAD	C4-N3-C2	13.88	126.86	115.14
3	A	752	FAD	C1'-N10-C9A	8.49	124.97	118.29
2	A	751	FMN	C10-C4A-N5	8.35	127.03	121.26
2	A	751	FMN	C4-C4A-C10	-7.05	115.28	119.95
3	A	752	FAD	C4X-C4-N3	-6.30	114.81	123.43
3	A	752	FAD	C10-C4X-N5	5.23	124.88	121.26
2	A	751	FMN	C4A-C4-N3	-4.93	116.69	123.43
3	A	752	FAD	C1'-N10-C10	-4.34	114.52	118.41
3	A	752	FAD	C5X-C9A-N10	-4.25	114.64	117.72
2	A	751	FMN	C4A-C10-N10	-4.03	116.16	120.30
4	A	753	NAP	O7N-C7N-N7N	-3.91	117.02	122.58
2	A	751	FMN	P-O5'-C5'	3.90	129.04	118.30
2	A	751	FMN	O4'-C4'-C3'	-3.64	100.26	109.10
3	A	752	FAD	C4-C4X-C10	-3.63	117.55	119.95
4	A	753	NAP	C4A-C5A-N7A	3.34	112.88	109.40
4	A	753	NAP	C3D-C2D-C1D	3.32	105.98	100.98
3	A	752	FAD	C4A-C5A-N7A	3.28	112.82	109.40
4	A	753	NAP	O7N-C7N-C3N	3.26	123.54	119.63
3	A	752	FAD	C4X-C10-N10	-3.16	117.05	120.30
2	A	751	FMN	C6-C5A-N5	-3.13	115.60	119.05
4	A	753	NAP	C6N-N1N-C2N	-3.02	119.22	121.97
2	A	751	FMN	C5A-C9A-N10	-2.94	115.58	117.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	751	FMN	O3P-P-O5'	-2.80	99.28	106.73
2	A	751	FMN	C9A-C5A-N5	2.76	126.67	122.36
4	A	753	NAP	N3A-C2A-N1A	-2.66	124.51	128.68
3	A	752	FAD	N3A-C2A-N1A	-2.65	124.54	128.68
3	A	752	FAD	C4'-C3'-C2'	2.62	118.82	113.36
2	A	751	FMN	C8M-C8-C7	2.55	125.96	120.74
4	A	753	NAP	C3N-C2N-N1N	2.47	122.84	120.43
2	A	751	FMN	C4A-N5-C5A	-2.41	114.37	116.77
3	A	752	FAD	O2'-C2'-C1'	2.39	115.34	109.59
2	A	751	FMN	O2P-P-O1P	2.38	120.00	110.68
2	A	751	FMN	C4'-C3'-C2'	-2.37	108.43	113.36
2	A	751	FMN	C1'-N10-C10	2.36	120.52	118.41
4	A	753	NAP	C2N-C3N-C4N	-2.22	115.74	118.26
3	A	752	FAD	C6-C5X-N5	-2.20	116.62	119.05
3	A	752	FAD	O5'-C5'-C4'	2.16	115.12	109.36
3	A	752	FAD	C9A-C5X-N5	2.09	125.63	122.36
4	A	753	NAP	PN-O3-PA	-2.08	125.68	132.83
2	A	751	FMN	C5'-C4'-C3'	2.03	116.13	112.20

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	752	FAD	C3'-C4'-C5'-O5'
4	A	753	NAP	O4B-C4B-C5B-O5B
4	A	753	NAP	O4D-C4D-C5D-O5D
4	A	753	NAP	C2B-O2B-P2B-O1X
3	A	752	FAD	PA-O3P-P-O1P
4	A	753	NAP	PA-O3-PN-O1N
4	A	753	NAP	C3D-C4D-C5D-O5D
3	A	752	FAD	PA-O3P-P-O2P
4	A	753	NAP	C5D-O5D-PN-O2N

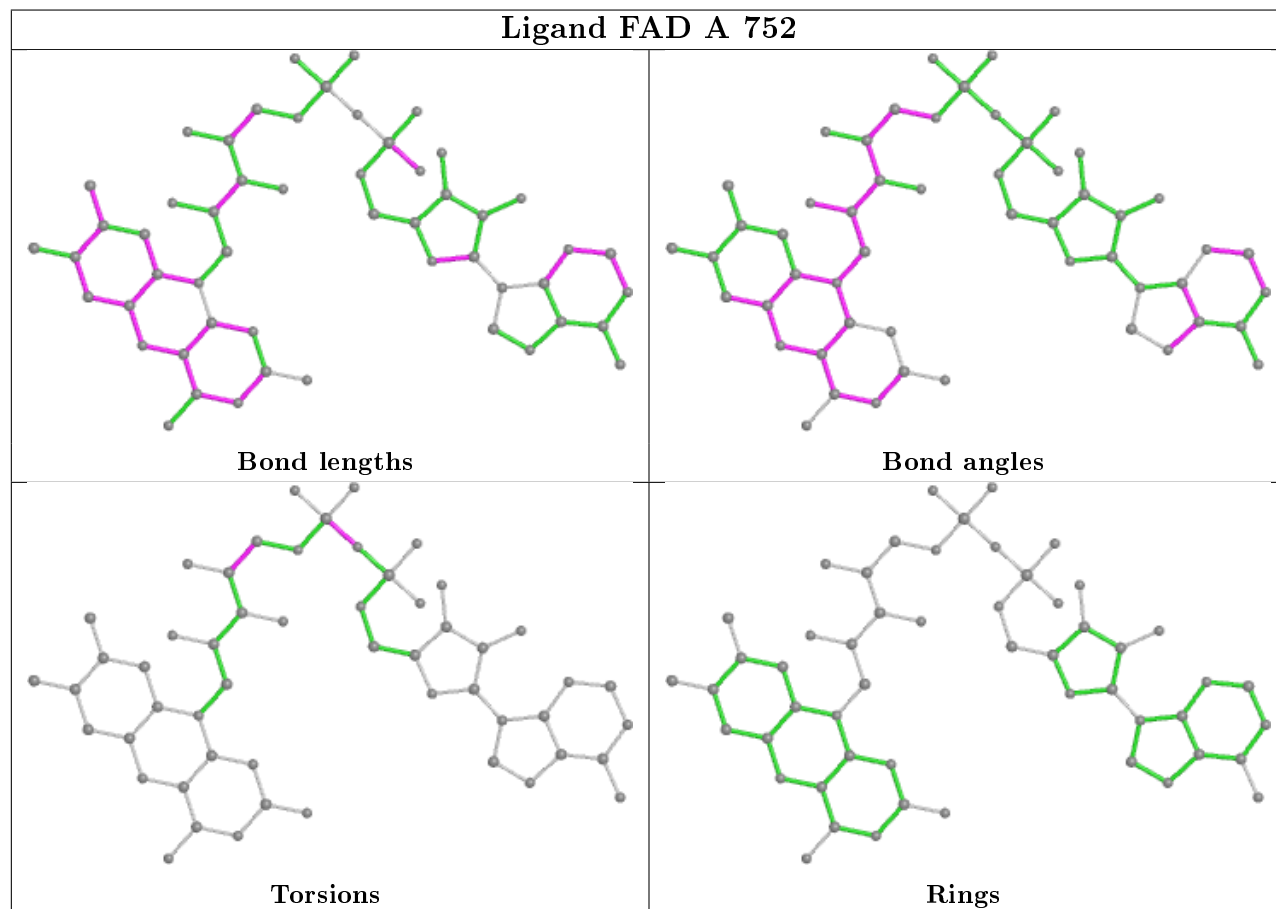
There are no ring outliers.

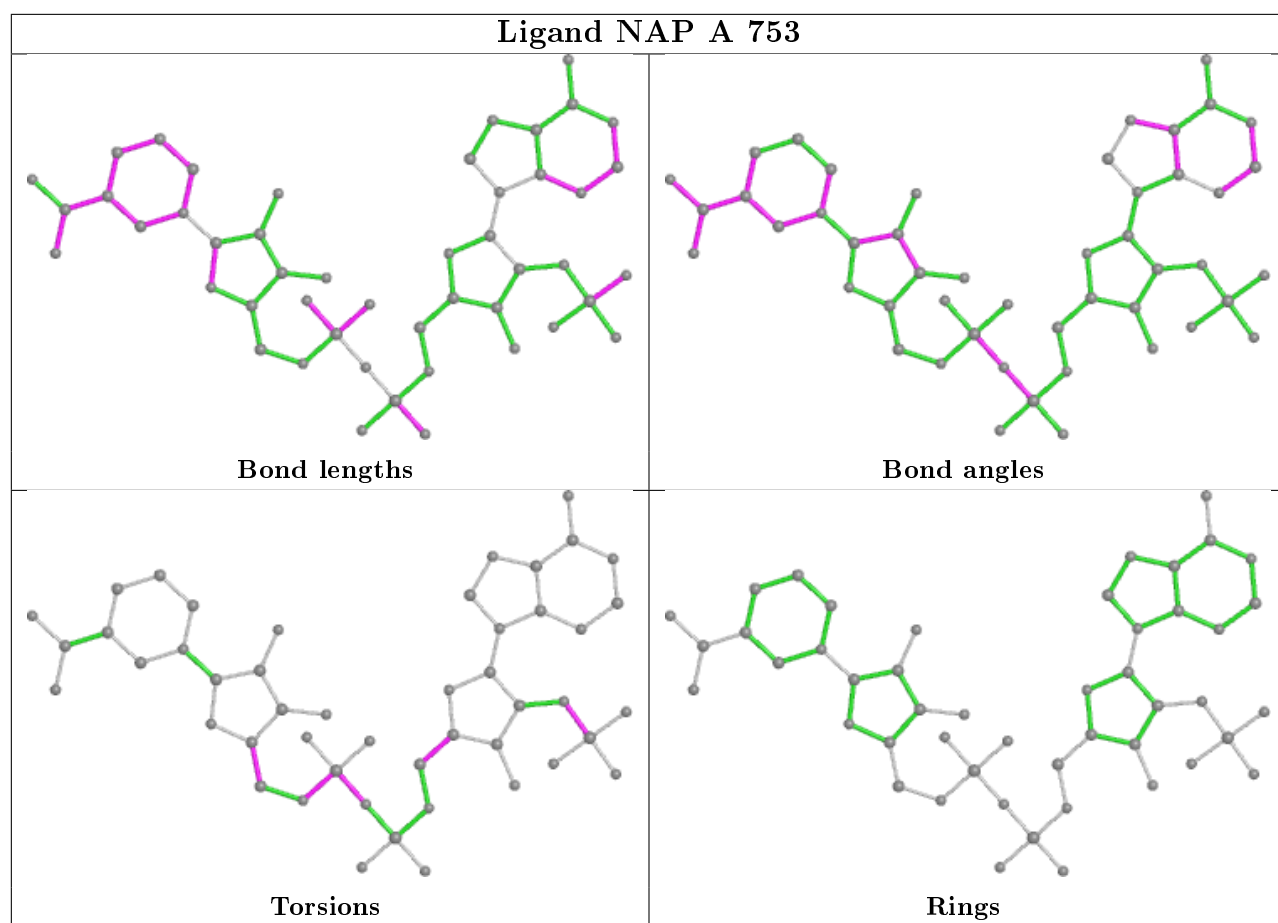
1 monomer is involved in 4 short contacts:

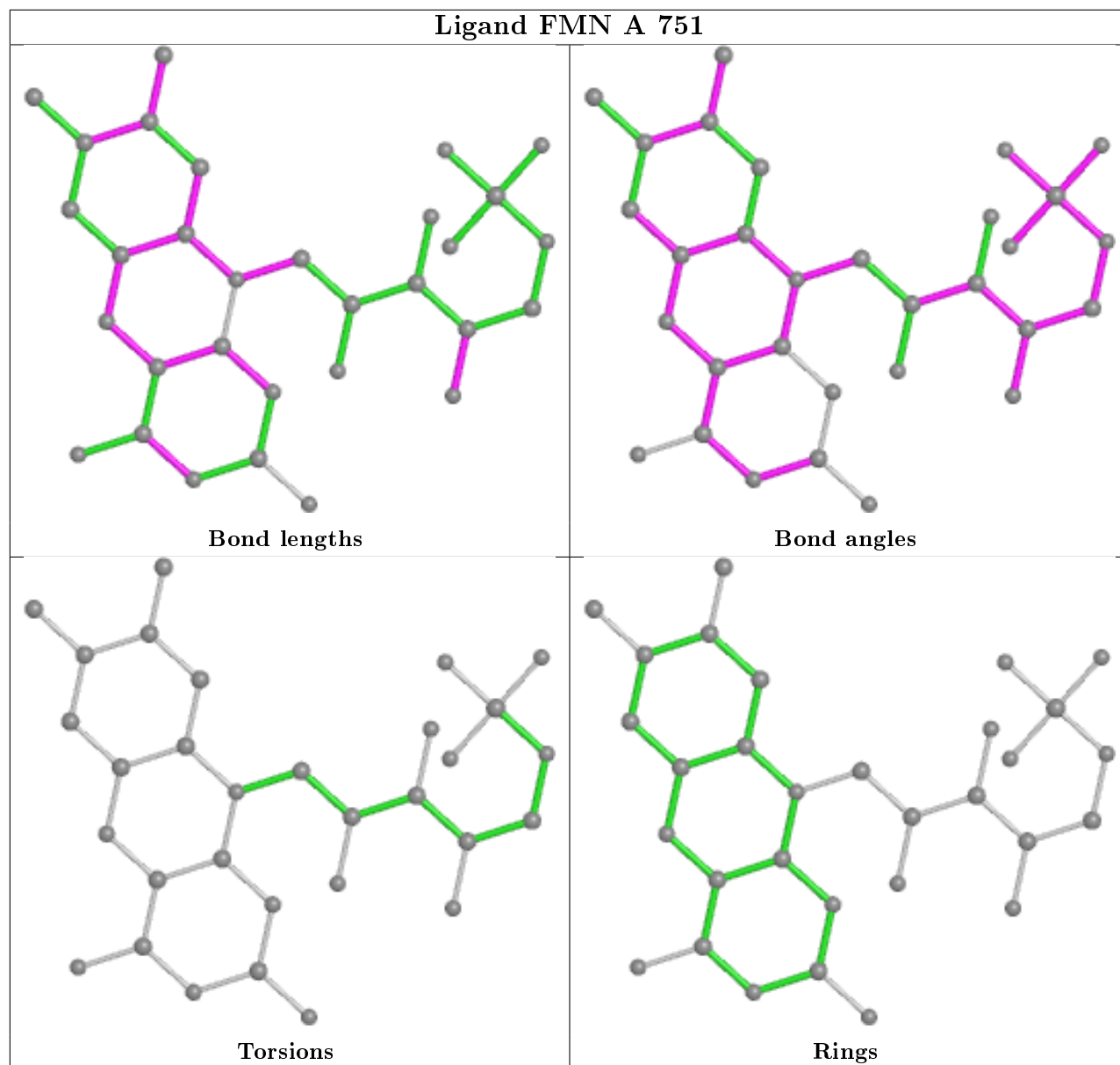
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	753	NAP	4	0

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 [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, 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	607/622 (97%)	-0.22	12 (1%) 65 68	22, 38, 59, 84	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	238	GLU	4.2
1	A	251	GLU	3.9
1	A	240	SER	3.6
1	A	600	ALA	3.3
1	A	500	ALA	3.2
1	A	239	GLU	3.2
1	A	506	ARG	2.8
1	A	241	SER	2.7
1	A	254	ASP	2.5
1	A	252	ASP	2.4
1	A	242	ILE	2.2
1	A	554	GLY	2.1

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.

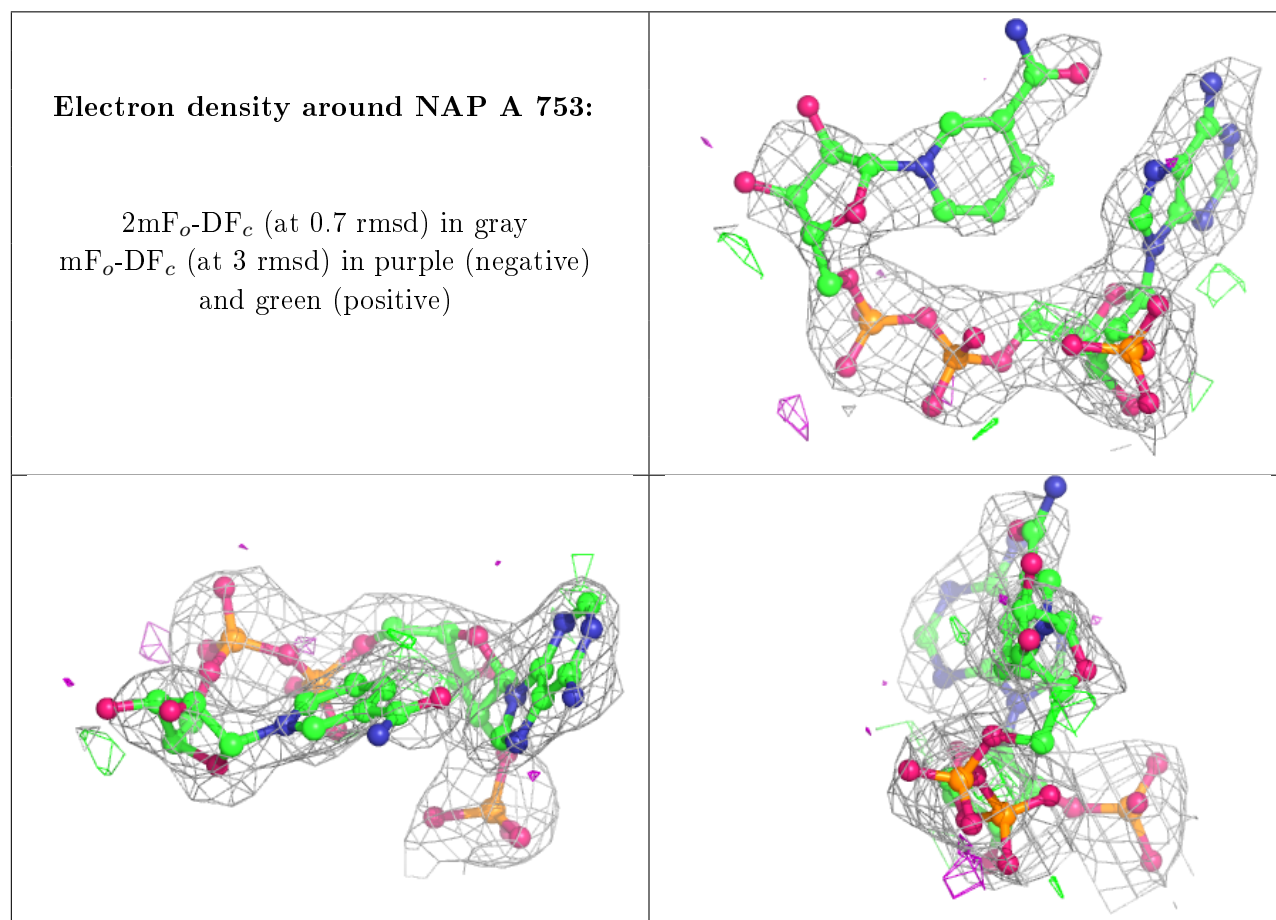
6.4 Ligands [i](#)

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, 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.

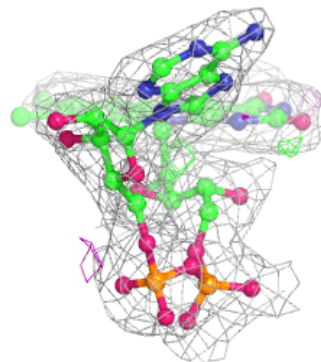
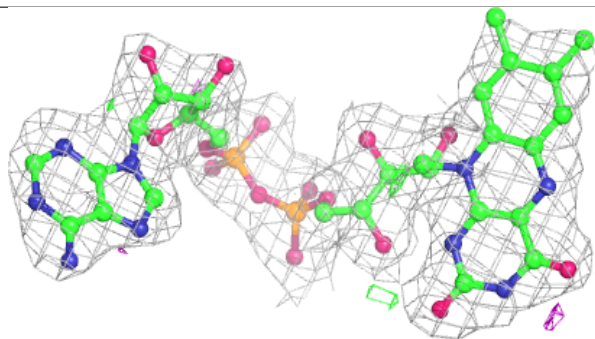
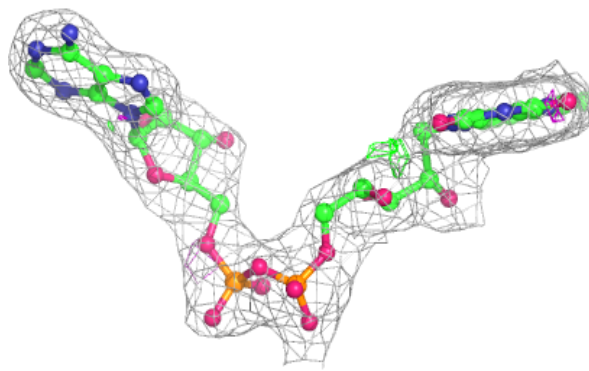
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAP	A	753	48/48	0.92	0.19	36,50,67,69	0
3	FAD	A	752	53/53	0.94	0.14	24,28,33,37	0
2	FMN	A	751	31/31	0.96	0.14	23,28,32,33	0

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.



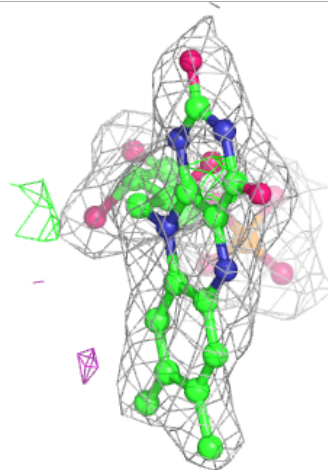
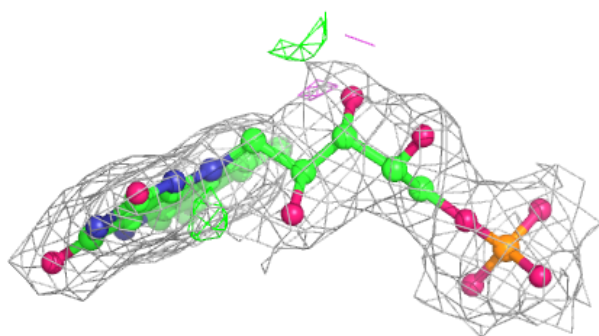
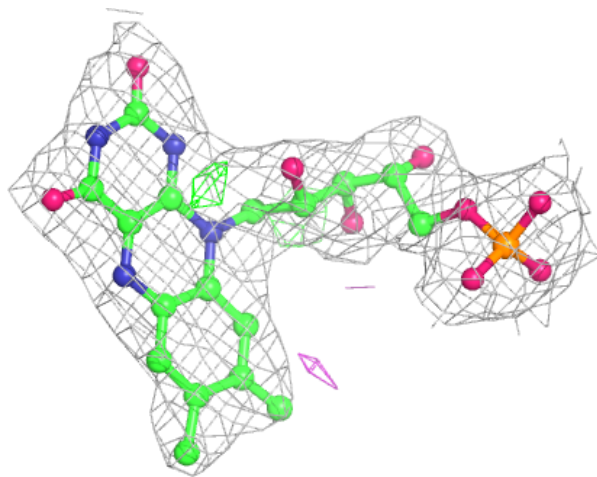
Electron density around FAD A 752:

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



Electron density around FMN A 751:

$2mF_o-DF_c$ (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.