



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 05:09 pm BST

PDB ID : 1QNF
Title : STRUCTURE OF PHOTOLYASE
Authors : Miki, K.; Kitadokoro, K.
Deposited on : 1997-07-04
Resolution : 1.80 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

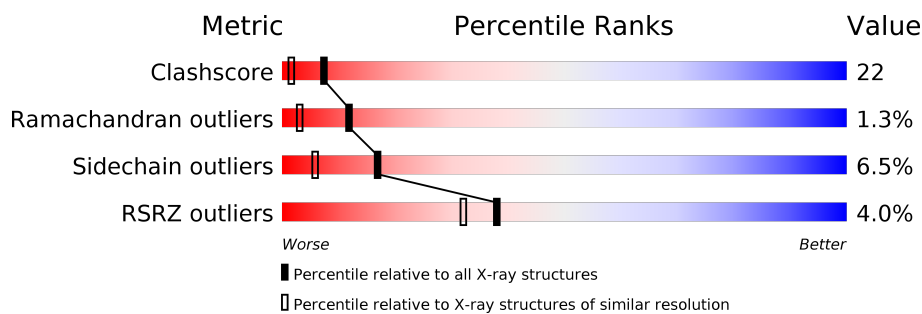
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 1.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	484	

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
2	FAD	A	485	X	-	-	-
3	HDF	A	486	-	X	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4269 atoms, of which 240 are hydrogens and 0 are deuteriums.

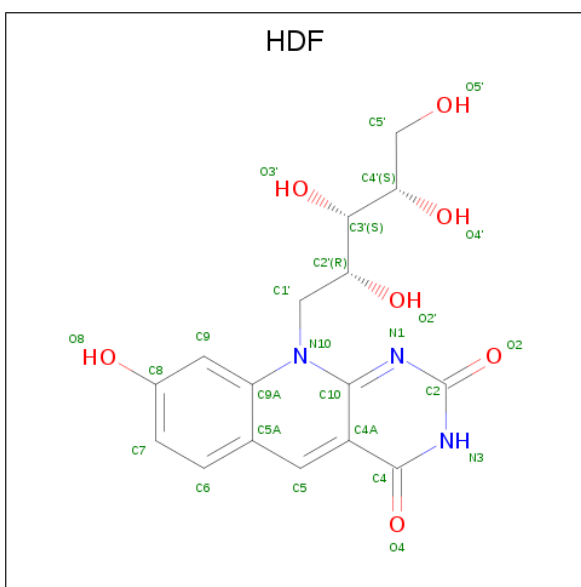
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PHOTOLYASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	475	Total	C	H	N	O	S	1	0	0
			4029	2419	240	679	680	11			

- 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
3	A	1	Total	C	N	O	0	0
			26	16	3	7		

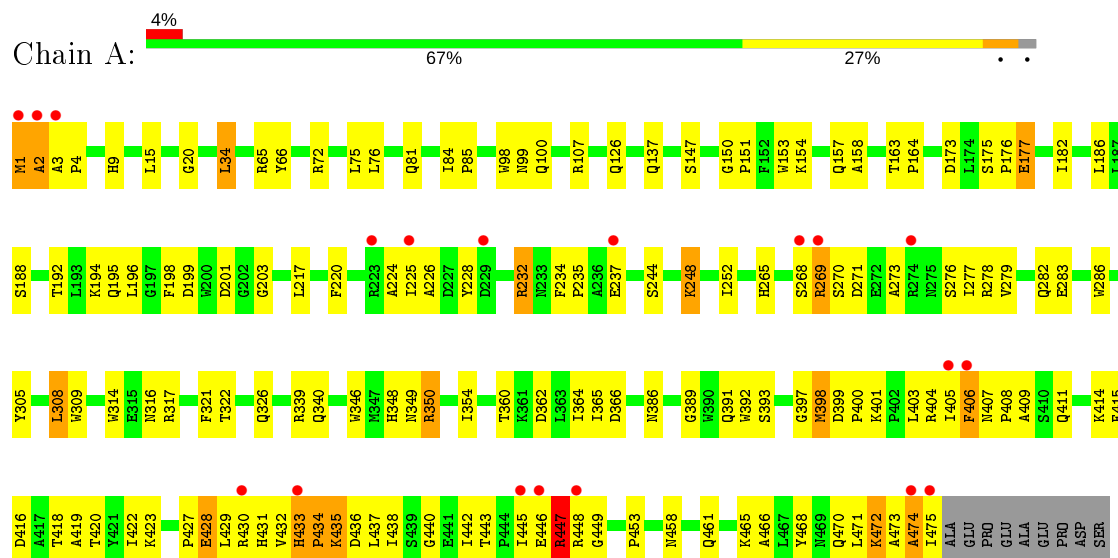
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	161	Total O 161 161	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: PHOTOLYASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	91.17Å 91.17Å 135.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 1.80 46.71 – 1.80	Depositor EDS
% Data completeness (in resolution range)	82.4 (6.00-1.80) 83.5 (46.71-1.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 1.81Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.197 , 0.239 0.202 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	17.1	Xtriage
Anisotropy	0.323	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 67.2	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	0.95	EDS
Total number of atoms	4269	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HDF, 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	0.47	0/3898	0.67	1/5312 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	447	ARG	N-CA-C	-6.81	92.61	111.00

There are no chirality outliers.

There are no planarity outliers.

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	3789	240	3705	167	0
2	A	53	0	31	6	0
3	A	26	0	16	1	0
4	A	161	0	0	20	0
All	All	4029	240	3752	170	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 22.

All (170) 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:269:ARG:H	1:A:269:ARG:CD	1.57	1.16
1:A:269:ARG:H	1:A:269:ARG:HD3	1.09	1.15
1:A:350:ARG:HG2	1:A:350:ARG:HH11	0.96	1.10
1:A:435:LYS:HD3	1:A:435:LYS:H	1.13	1.06
1:A:405:ILE:HD12	1:A:465:LYS:HE2	1.38	1.05
1:A:435:LYS:N	1:A:435:LYS:HD3	1.73	1.00
1:A:269:ARG:N	1:A:269:ARG:HD3	1.78	0.94
1:A:350:ARG:NH1	1:A:350:ARG:HG2	1.71	0.90
1:A:322:THR:O	1:A:326:GLN:HG3	1.71	0.89
1:A:445:ILE:HD12	1:A:446:GLU:N	1.86	0.89
1:A:443:THR:OG1	1:A:446:GLU:HG2	1.72	0.88
1:A:147:SER:HB2	1:A:398:MET:HE2	1.56	0.88
1:A:81:GLN:N	1:A:81:GLN:OE1	2.07	0.87
1:A:435:LYS:CD	1:A:435:LYS:H	1.85	0.87
1:A:199:ASP:HB2	4:A:561:HOH:O	1.75	0.85
1:A:269:ARG:N	1:A:269:ARG:CD	2.31	0.83
1:A:192:THR:OG1	1:A:195:GLN:HG3	1.79	0.82
1:A:433:HIS:CD2	1:A:433:HIS:H	1.95	0.82
1:A:442:ILE:HG22	1:A:447:ARG:HB3	1.60	0.82
1:A:137:GLN:NE2	4:A:532:HOH:O	2.14	0.80
1:A:350:ARG:CG	1:A:350:ARG:HH11	1.86	0.79
1:A:348:HIS:HD2	1:A:350:ARG:H	1.28	0.78
1:A:232:ARG:HG3	1:A:232:ARG:HH11	1.48	0.77
1:A:269:ARG:H	1:A:269:ARG:HD2	1.47	0.77
1:A:163:THR:HG23	1:A:164:PRO:HD2	1.66	0.76
1:A:81:GLN:NE2	4:A:510:HOH:O	2.17	0.76
1:A:473:ALA:O	1:A:474:ALA:HB2	1.87	0.75
1:A:316:ASN:HD21	1:A:366:ASP:H	1.36	0.74
1:A:445:ILE:HD12	1:A:446:GLU:HG2	1.68	0.74
1:A:199:ASP:N	4:A:559:HOH:O	1.99	0.73
1:A:442:ILE:CG2	1:A:447:ARG:CB	2.67	0.72
1:A:147:SER:HB2	1:A:398:MET:CE	2.21	0.70
1:A:445:ILE:HD12	1:A:446:GLU:H	1.54	0.70
1:A:461:GLN:HG2	1:A:465:LYS:HE3	1.72	0.70
1:A:416:ASP:OD2	1:A:422:ILE:HG13	1.92	0.69
1:A:432:VAL:HG12	1:A:433:HIS:N	2.07	0.69
1:A:461:GLN:O	1:A:465:LYS:HG3	1.92	0.69
1:A:433:HIS:O	1:A:436:ASP:N	2.24	0.69
1:A:442:ILE:HG22	1:A:447:ARG:CB	2.22	0.69
1:A:286:TRP:CD2	4:A:583:HOH:O	2.46	0.68
1:A:433:HIS:CD2	1:A:433:HIS:N	2.60	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:ILE:HG21	1:A:447:ARG:HB2	1.74	0.67
1:A:269:ARG:NH1	1:A:270:SER:HB3	2.09	0.67
1:A:348:HIS:CD2	1:A:350:ARG:H	2.09	0.67
1:A:442:ILE:CG2	1:A:447:ARG:HB2	2.24	0.66
1:A:34:LEU:HD11	1:A:84:ILE:HD12	1.79	0.65
1:A:1:MET:O	1:A:2:ALA:HB3	1.97	0.65
1:A:228:TYR:HE2	1:A:279:VAL:HG12	1.61	0.64
1:A:9:HIS:HE1	1:A:66:TYR:OH	1.80	0.64
1:A:3:ALA:HB1	1:A:4:PRO:HD2	1.79	0.64
1:A:473:ALA:O	1:A:474:ALA:CB	2.45	0.64
1:A:228:TYR:CE2	1:A:279:VAL:HG12	2.33	0.64
1:A:354:ILE:HG23	1:A:406:PHE:HE2	1.62	0.63
1:A:244:SER:HB3	2:A:485:FAD:H5'1	1.80	0.63
1:A:350:ARG:HE	1:A:411:GLN:HE22	1.47	0.62
1:A:443:THR:OG1	1:A:446:GLU:CG	2.47	0.62
1:A:265:HIS:HB2	1:A:277:ILE:HG21	1.82	0.62
1:A:158:ALA:HB3	4:A:540:HOH:O	2.01	0.60
1:A:228:TYR:O	1:A:232:ARG:HD3	2.02	0.59
1:A:461:GLN:CG	1:A:465:LYS:HE3	2.31	0.59
1:A:269:ARG:HD3	1:A:270:SER:H	1.67	0.59
1:A:232:ARG:NH1	1:A:232:ARG:HG3	2.15	0.58
1:A:445:ILE:CD1	1:A:446:GLU:HG2	2.34	0.58
1:A:386:ASN:HD22	2:A:485:FAD:H6	1.70	0.57
1:A:72:ARG:NH2	1:A:173:ASP:OD2	2.30	0.56
1:A:316:ASN:ND2	1:A:366:ASP:H	2.00	0.56
1:A:407:ASN:OD1	1:A:409:ALA:HB3	2.06	0.56
1:A:406:PHE:CZ	1:A:408:PRO:HG3	2.41	0.56
1:A:453:PRO:HD3	4:A:628:HOH:O	2.06	0.56
1:A:34:LEU:HD11	1:A:84:ILE:CD1	2.36	0.55
1:A:350:ARG:NH1	1:A:350:ARG:CG	2.52	0.55
1:A:432:VAL:CG1	1:A:433:HIS:N	2.70	0.55
1:A:427:PRO:C	1:A:429:LEU:H	2.07	0.55
1:A:447:ARG:C	1:A:448:ARG:HG2	2.26	0.55
1:A:442:ILE:HG21	1:A:447:ARG:CB	2.35	0.55
1:A:471:LEU:O	1:A:473:ALA:N	2.39	0.55
1:A:468:TYR:OH	1:A:472:LYS:HE3	2.07	0.55
1:A:427:PRO:O	1:A:429:LEU:N	2.39	0.54
1:A:399:ASP:N	1:A:400:PRO:HD3	2.22	0.54
1:A:147:SER:CB	1:A:398:MET:CE	2.86	0.54
1:A:406:PHE:C	1:A:406:PHE:CD1	2.81	0.54
1:A:305:TYR:HB3	1:A:397:GLY:HA2	1.89	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:TRP:CE3	1:A:393:SER:N	2.77	0.53
1:A:286:TRP:CE3	4:A:583:HOH:O	2.61	0.53
1:A:406:PHE:O	1:A:406:PHE:CD1	2.62	0.53
1:A:423:LYS:HE3	1:A:437:LEU:CD1	2.39	0.53
1:A:432:VAL:HG12	1:A:433:HIS:H	1.74	0.53
1:A:443:THR:HG1	1:A:446:GLU:HG2	1.73	0.53
1:A:340:GLN:HG2	1:A:346:TRP:O	2.09	0.52
1:A:434:PRO:O	1:A:438:ILE:HD13	2.09	0.52
1:A:268:SER:OG	1:A:273:ALA:HB3	2.11	0.51
1:A:163:THR:HG23	1:A:164:PRO:CD	2.38	0.51
1:A:203:GLY:N	4:A:563:HOH:O	2.25	0.50
1:A:151:PRO:HA	1:A:154:LYS:HD2	1.93	0.50
1:A:269:ARG:HD3	1:A:270:SER:N	2.27	0.50
1:A:225:ILE:CG2	1:A:226:ALA:N	2.74	0.50
1:A:153:TRP:CH2	1:A:282:GLN:HG2	2.47	0.50
1:A:228:TYR:OH	1:A:283:GLU:HG3	2.12	0.49
1:A:468:TYR:CZ	1:A:472:LYS:HE3	2.47	0.49
1:A:308:LEU:HD13	1:A:309:TRP:H	1.78	0.49
1:A:427:PRO:C	1:A:429:LEU:N	2.66	0.48
1:A:432:VAL:CG1	1:A:433:HIS:H	2.26	0.48
1:A:217:LEU:HD22	1:A:252:ILE:HD11	1.95	0.48
1:A:339:ARG:NH2	1:A:428:GLU:OE2	2.39	0.48
1:A:72:ARG:HH21	1:A:173:ASP:CG	2.15	0.48
1:A:349:ASN:HB2	2:A:485:FAD:O2'	2.14	0.47
1:A:147:SER:CB	1:A:398:MET:HE2	2.34	0.47
1:A:234:PHE:HB2	1:A:237:GLU:CG	2.45	0.47
1:A:195:GLN:NE2	4:A:557:HOH:O	2.37	0.47
1:A:364:ILE:HG22	1:A:364:ILE:O	2.15	0.47
1:A:438:ILE:N	1:A:438:ILE:CD1	2.77	0.47
1:A:438:ILE:HD12	1:A:438:ILE:N	2.31	0.46
1:A:220:PHE:CD1	1:A:224:ALA:HB3	2.50	0.46
1:A:321:PHE:HB2	1:A:365:ILE:HD13	1.97	0.46
1:A:400:PRO:O	1:A:401:LYS:HG3	2.16	0.46
1:A:308:LEU:H	1:A:308:LEU:CD1	2.29	0.46
1:A:431:HIS:CE1	1:A:448:ARG:NH1	2.84	0.46
1:A:471:LEU:C	1:A:473:ALA:N	2.69	0.45
1:A:126:GLN:NE2	4:A:525:HOH:O	2.33	0.45
1:A:423:LYS:HE3	1:A:437:LEU:HD11	1.97	0.45
1:A:286:TRP:CE2	4:A:583:HOH:O	2.69	0.45
1:A:317:ARG:HD2	4:A:596:HOH:O	2.15	0.45
1:A:339:ARG:HH22	1:A:428:GLU:CD	2.20	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:O	1:A:2:ALA:CB	2.61	0.45
1:A:348:HIS:HE1	4:A:574:HOH:O	1.99	0.45
1:A:20:GLY:H	1:A:99:ASN:HD21	1.64	0.45
1:A:176:PRO:HD2	1:A:177:GLU:OE2	2.16	0.44
1:A:414:LYS:HD2	1:A:415:PHE:CZ	2.52	0.44
1:A:15:LEU:HD22	1:A:65:ARG:HB3	1.99	0.44
1:A:440:GLY:HA3	4:A:627:HOH:O	2.18	0.44
1:A:177:GLU:CD	1:A:177:GLU:H	2.20	0.44
1:A:420:THR:HG23	4:A:624:HOH:O	2.17	0.44
1:A:195:GLN:HG2	4:A:557:HOH:O	2.18	0.44
1:A:234:PHE:HB2	1:A:237:GLU:HG3	2.00	0.43
1:A:269:ARG:N	1:A:269:ARG:HD2	2.19	0.43
1:A:269:ARG:HH11	1:A:270:SER:H	1.66	0.43
1:A:175:SER:OG	1:A:177:GLU:HG2	2.19	0.43
1:A:198:PHE:HA	4:A:559:HOH:O	2.18	0.43
1:A:466:ALA:O	1:A:470:GLN:HG3	2.18	0.43
1:A:65:ARG:HG3	4:A:569:HOH:O	2.17	0.43
1:A:248:LYS:C	1:A:248:LYS:HD3	2.38	0.43
1:A:349:ASN:ND2	2:A:485:FAD:O2'	2.48	0.43
1:A:308:LEU:CD1	1:A:308:LEU:N	2.82	0.42
1:A:420:THR:CG2	4:A:624:HOH:O	2.66	0.42
1:A:98:TRP:HE1	1:A:126:GLN:HE21	1.66	0.42
1:A:228:TYR:O	1:A:232:ARG:CD	2.66	0.42
1:A:475:ILE:O	1:A:475:ILE:HG23	2.20	0.42
1:A:234:PHE:HA	1:A:235:PRO:HD2	1.58	0.42
1:A:224:ALA:O	1:A:225:ILE:C	2.58	0.42
1:A:232:ARG:NH1	1:A:232:ARG:CG	2.81	0.42
1:A:100:GLN:HE21	1:A:107:ARG:HH12	1.68	0.42
1:A:75:LEU:C	1:A:76:LEU:HD12	2.40	0.42
1:A:225:ILE:O	1:A:276:SER:HB3	2.20	0.42
1:A:433:HIS:HE2	1:A:446:GLU:CD	2.24	0.42
1:A:150:GLY:O	1:A:154:LYS:HD2	2.19	0.41
1:A:433:HIS:O	1:A:434:PRO:C	2.58	0.41
1:A:443:THR:OG1	1:A:445:ILE:CD1	2.68	0.41
1:A:428:GLU:OE1	1:A:428:GLU:N	2.39	0.41
2:A:485:FAD:H9	2:A:485:FAD:H1'2	1.72	0.41
1:A:84:ILE:HB	1:A:85:PRO:HD3	2.02	0.41
1:A:225:ILE:HG23	1:A:226:ALA:N	2.35	0.41
1:A:418:THR:O	1:A:419:ALA:HB3	2.21	0.41
1:A:434:PRO:HB2	1:A:435:LYS:HD3	2.02	0.41
2:A:485:FAD:H3'	2:A:485:FAD:N1	2.36	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:TRP:CE3	1:A:393:SER:CA	3.04	0.41
3:A:486:HDF:O3'	3:A:486:HDF:N1	2.40	0.41
1:A:314:TRP:CH2	1:A:360:THR:HG23	2.56	0.41
1:A:389:GLY:O	1:A:392:TRP:HB3	2.21	0.41
1:A:194:LYS:HE3	1:A:194:LYS:HB2	1.73	0.40
1:A:182:ILE:HD12	1:A:186:LEU:HD11	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	473/484 (98%)	446 (94%)	21 (4%)	6 (1%)	12 3

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	449	GLY
1	A	474	ALA
1	A	2	ALA
1	A	428	GLU
1	A	472	LYS
1	A	434	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	386/393 (98%)	361 (94%)	25 (6%)	17 6

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

Mol	Chain	Res	Type
1	A	1	MET
1	A	34	LEU
1	A	157	GLN
1	A	177	GLU
1	A	188	SER
1	A	196	LEU
1	A	201	ASP
1	A	232	ARG
1	A	248	LYS
1	A	269	ARG
1	A	271	ASP
1	A	278	ARG
1	A	308	LEU
1	A	350	ARG
1	A	362	ASP
1	A	391	GLN
1	A	398	MET
1	A	403	LEU
1	A	404	ARG
1	A	406	PHE
1	A	430	ARG
1	A	433	HIS
1	A	435	LYS
1	A	447	ARG
1	A	458	ASN

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	9	HIS
1	A	30	GLN
1	A	43	GLN
1	A	99	ASN
1	A	100	GLN
1	A	112	GLN
1	A	126	GLN
1	A	130	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	137	GLN
1	A	231	GLN
1	A	310	GLN
1	A	316	ASN
1	A	348	HIS
1	A	349	ASN
1	A	386	ASN
1	A	387	ASN
1	A	391	GLN
1	A	411	GLN
1	A	433	HIS
1	A	463	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](#)

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	HDF	A	486	-	25,28,28	5.32	12 (48%)	29,41,41	3.93	18 (62%)
2	FAD	A	485	-	51,58,58	2.40	9 (17%)	60,89,89	2.83	12 (20%)

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	HDF	A	486	-	-	9/14/14/14	0/3/3/3
2	FAD	A	485	-	2/2/9/9	10/30/50/50	0/6/6/6

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	485	FAD	C1'-N10	-14.17	1.33	1.48
3	A	486	HDF	C5-C4A	-11.93	1.36	1.53
3	A	486	HDF	C9-C8	-9.19	1.35	1.51
3	A	486	HDF	C9-C9A	-8.83	1.34	1.53
3	A	486	HDF	C5A-C9A	-8.23	1.37	1.53
3	A	486	HDF	C6-C5A	-8.08	1.33	1.53
3	A	486	HDF	C5-C5A	-7.70	1.35	1.53
3	A	486	HDF	C7-C6	-7.17	1.35	1.52
3	A	486	HDF	C10-N1	-6.57	1.38	1.46
3	A	486	HDF	C7-C8	-6.17	1.36	1.51
3	A	486	HDF	C9A-N10	-6.12	1.37	1.48
3	A	486	HDF	C4A-C4	-5.34	1.43	1.51
2	A	485	FAD	C6-C5X	-4.32	1.35	1.41
2	A	485	FAD	C4-N3	3.17	1.38	1.33
2	A	485	FAD	C9-C9A	-3.02	1.34	1.40
2	A	485	FAD	C9A-C5X	-2.90	1.36	1.42
2	A	485	FAD	C10-N1	2.86	1.36	1.33
2	A	485	FAD	O4B-C1B	2.82	1.45	1.41
2	A	485	FAD	C4X-N5	2.51	1.36	1.33
3	A	486	HDF	O8-C8	-2.12	1.37	1.43
2	A	485	FAD	C8A-N7A	-2.02	1.31	1.34

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	485	FAD	C4-N3-C2	12.72	125.88	115.14
3	A	486	HDF	C5-C4A-C10	9.20	119.18	107.74
3	A	486	HDF	C9-C8-C7	9.06	121.37	110.55
2	A	485	FAD	C4-C4X-C10	7.70	125.05	119.95
2	A	485	FAD	C4X-C4-N3	-7.58	113.07	123.43
3	A	486	HDF	C5-C5A-C9A	6.98	119.62	110.04
2	A	485	FAD	C5X-C9A-N10	6.06	122.10	117.72

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	486	HDF	C4'-C3'-C2'	5.98	125.81	113.36
2	A	485	FAD	C1'-N10-C9A	5.46	122.59	118.29
2	A	485	FAD	C4-C4X-N5	-4.98	112.90	118.60
3	A	486	HDF	C1'-C2'-C3'	4.93	123.55	109.79
3	A	486	HDF	C5'-C4'-C3'	4.82	122.86	112.41
3	A	486	HDF	O8-C8-C9	4.62	119.05	109.85
3	A	486	HDF	C6-C5A-C9A	4.33	121.56	109.73
3	A	486	HDF	C6-C7-C8	4.18	118.75	111.61
2	A	485	FAD	O2'-C2'-C3'	4.02	118.88	109.10
2	A	485	FAD	C9A-N10-C10	-3.83	116.89	121.91
3	A	486	HDF	O8-C8-C7	3.56	119.23	110.16
2	A	485	FAD	O3'-C3'-C2'	3.44	117.11	108.81
3	A	486	HDF	C7-C6-C5A	3.38	119.84	112.24
3	A	486	HDF	C5-C5A-C6	3.36	118.81	112.66
3	A	486	HDF	O4-C4-C4A	3.29	127.68	122.04
3	A	486	HDF	O3'-C3'-C2'	3.10	116.29	108.81
2	A	485	FAD	C1'-C2'-C3'	3.06	118.33	109.79
3	A	486	HDF	C4A-C5-C5A	2.93	119.69	109.93
3	A	486	HDF	O2'-C2'-C3'	2.78	115.86	109.10
2	A	485	FAD	O4'-C4'-C3'	2.26	114.59	109.10
3	A	486	HDF	C9-C9A-N10	2.19	117.94	113.83
3	A	486	HDF	C5-C4A-C4	2.14	115.47	111.13
2	A	485	FAD	C4'-C3'-C2'	2.05	117.62	113.36

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	485	FAD	C4'
2	A	485	FAD	C2'

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	486	HDF	C1'-C2'-C3'-O3'
3	A	486	HDF	C1'-C2'-C3'-C4'
3	A	486	HDF	O2'-C2'-C3'-O3'
3	A	486	HDF	O2'-C2'-C3'-C4'
3	A	486	HDF	C2'-C3'-C4'-O4'
3	A	486	HDF	O3'-C3'-C4'-O4'
3	A	486	HDF	O3'-C3'-C4'-C5'
2	A	485	FAD	N10-C1'-C2'-O2'
2	A	485	FAD	C1'-C2'-C3'-O3'

Continued on next page...

Continued from previous page...

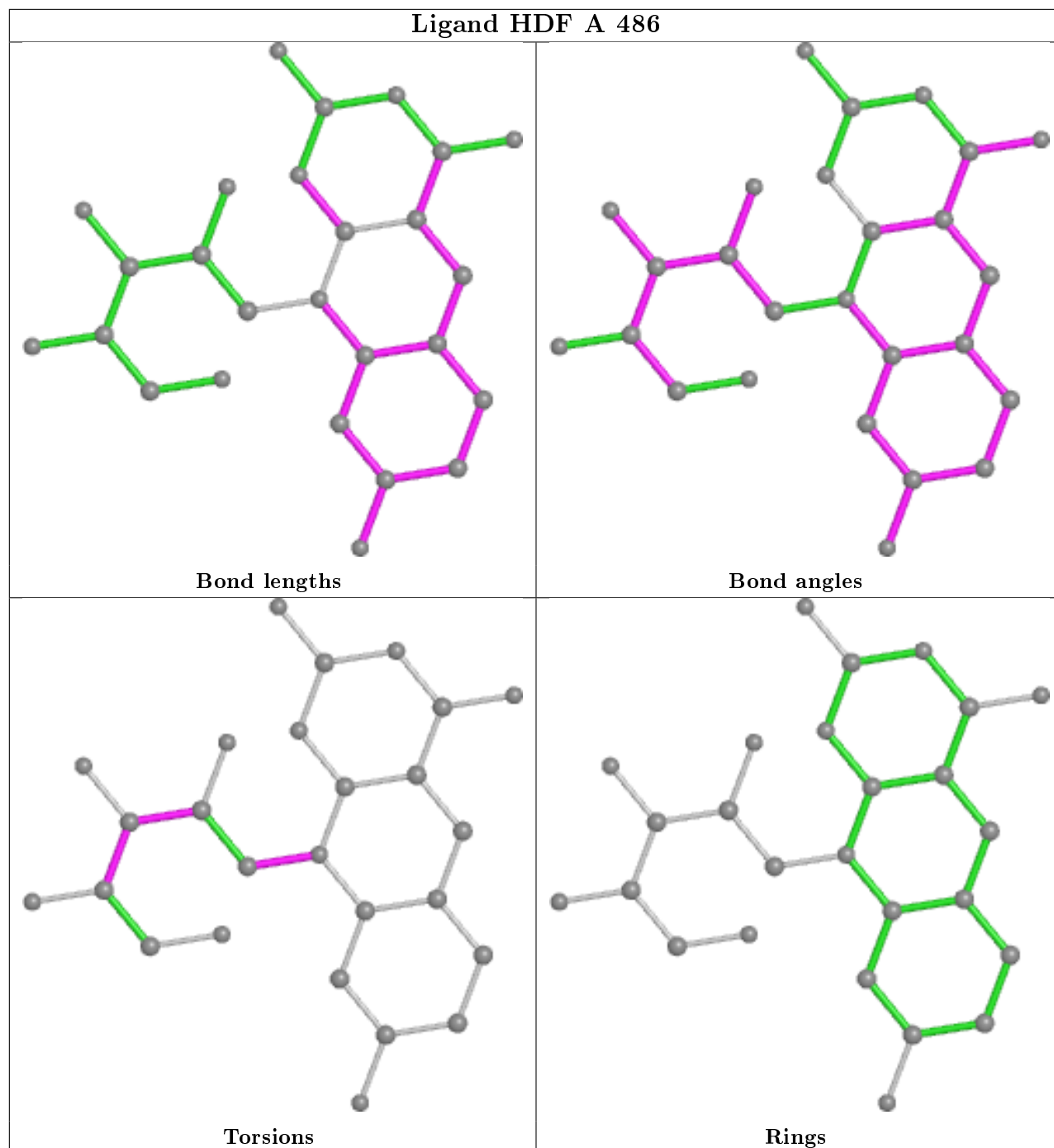
Mol	Chain	Res	Type	Atoms
2	A	485	FAD	O2'-C2'-C3'-O3'
2	A	485	FAD	O3'-C3'-C4'-O4'
2	A	485	FAD	O3'-C3'-C4'-C5'
2	A	485	FAD	O2'-C2'-C3'-C4'
2	A	485	FAD	C2'-C3'-C4'-O4'
3	A	486	HDF	C2'-C3'-C4'-C5'
2	A	485	FAD	C2'-C3'-C4'-C5'
2	A	485	FAD	N10-C1'-C2'-C3'
3	A	486	HDF	C2'-C1'-N10-C9A
2	A	485	FAD	C5B-O5B-PA-O3P

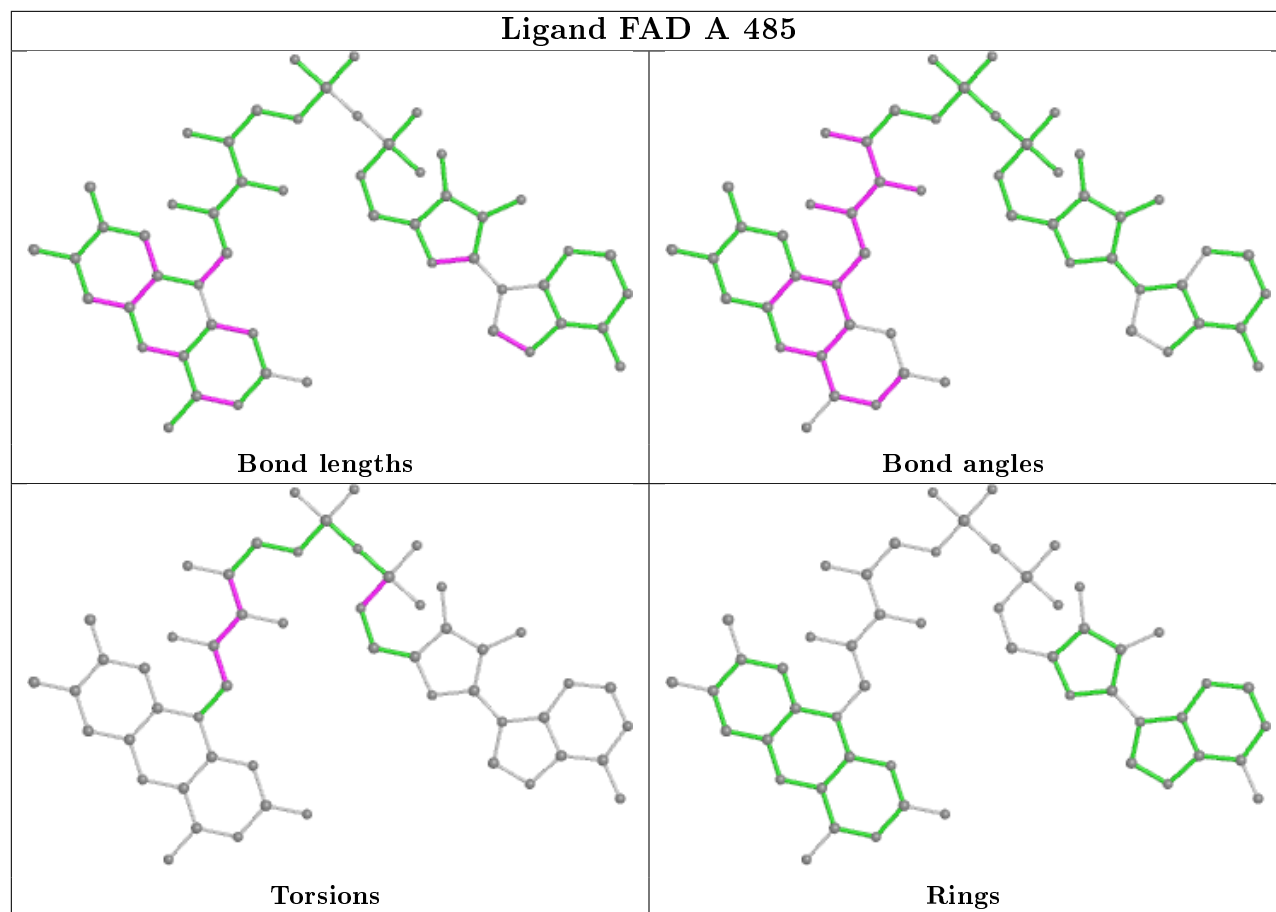
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	486	HDF	1	0
2	A	485	FAD	6	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	475/484 (98%)	-0.07	19 (4%) 38 32	9, 24, 59, 80	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	475	ILE	14.4
1	A	2	ALA	7.1
1	A	1	MET	6.3
1	A	406	PHE	3.7
1	A	445	ILE	3.4
1	A	433	HIS	3.1
1	A	223	ARG	2.8
1	A	268	SER	2.7
1	A	448	ARG	2.7
1	A	274	ARG	2.6
1	A	225	ILE	2.6
1	A	405	ILE	2.5
1	A	446	GLU	2.5
1	A	3	ALA	2.5
1	A	269	ARG	2.4
1	A	430	ARG	2.3
1	A	229	ASP	2.2
1	A	474	ALA	2.1
1	A	237	GLU	2.1

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

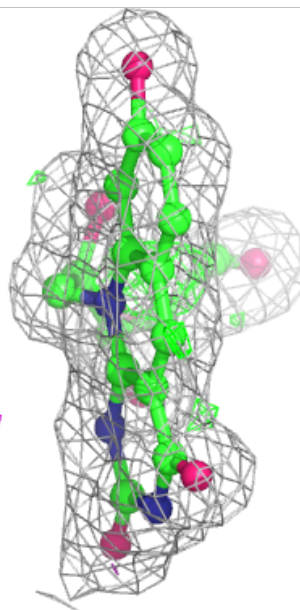
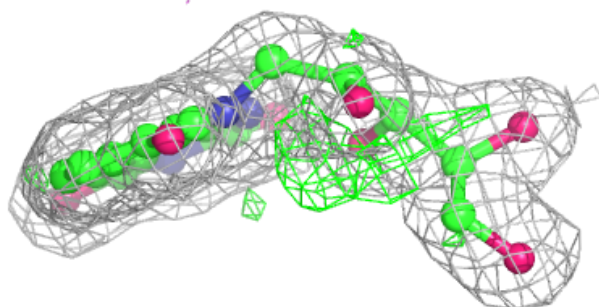
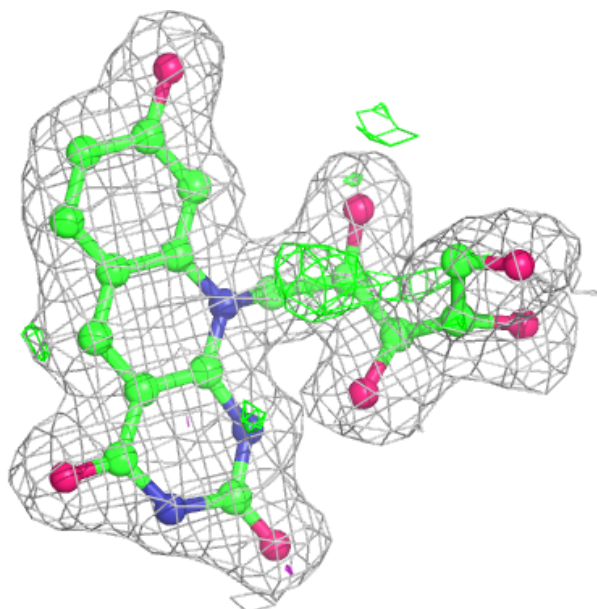
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

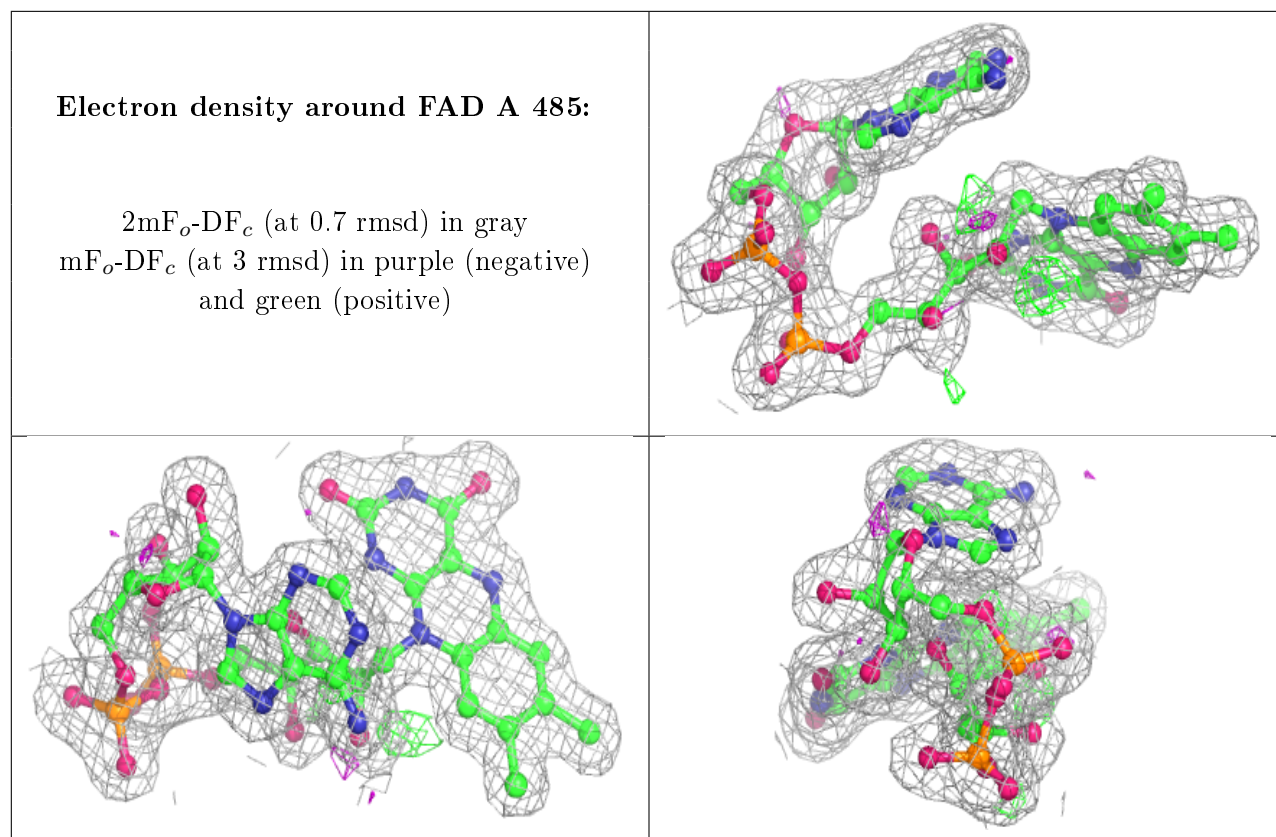
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	HDF	A	486	26/26	0.96	0.10	10,13,17,20	0
2	FAD	A	485	53/53	0.98	0.07	12,18,22,23	0

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 HDF A 486:

$2mF_o-DF_c$ (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.