



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2024 – 10:07 pm GMT

PDB ID : 8PF3
Title : Crystal structure of Trypanosoma brucei trypanothione reductase in complex with 1-(3,4-dichlorobenzyl)-4-(((5-((4-fluorophenethyl)carbamoyl)furan-2-yl)methyl)(4-fluorophenyl)carbamoyl)-1-(3-phenylpropyl)piperazin-1-ium
Authors : Exertier, C.; Ilari, A.; Fiorillo, A.; Antonelli, L.
Deposited on : 2023-06-15
Resolution : 2.15 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

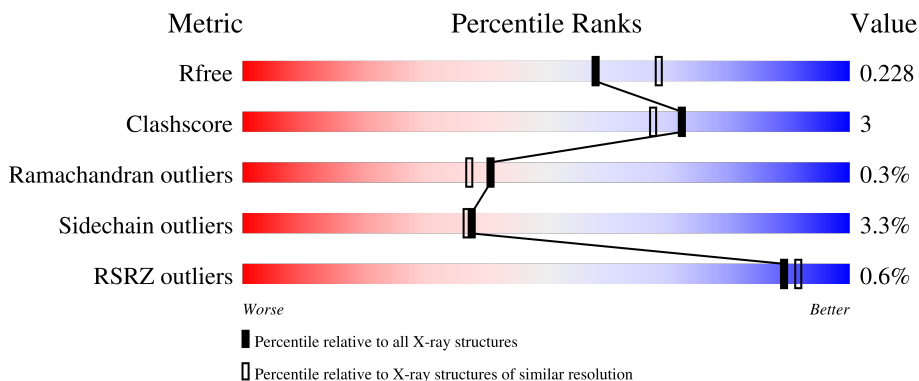
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


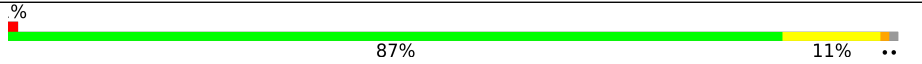
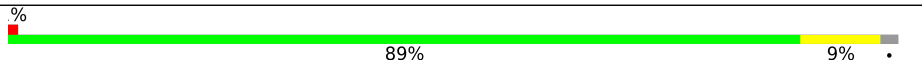

The reported resolution of this entry is 2.15 Å.

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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	495	 88% 10% ..
1	B	495	 87% 11% ..
1	C	495	 89% 9% .
1	D	495	 90% 9% .

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
3	YJ6	A	502	-	-	-	X
3	YJ6	B	502	-	-	-	X
3	YJ6	C	502	-	-	-	X
4	PEG	A	504	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16115 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 Trypanothione reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	489	3790	2412	649	708	21	0	10	0
1	B	489	3795	2419	644	712	20	6	14	0
1	C	486	3731	2377	636	699	19	5	6	0
1	D	490	3751	2388	638	705	20	0	5	0

There are 12 discrepancies between the modelled and reference sequences:

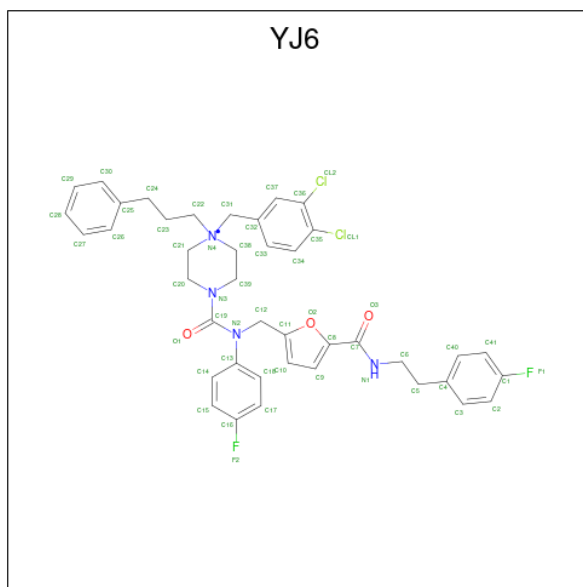
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP A0A3L6KZJ1
A	-1	SER	-	expression tag	UNP A0A3L6KZJ1
A	0	HIS	-	expression tag	UNP A0A3L6KZJ1
B	-2	GLY	-	expression tag	UNP A0A3L6KZJ1
B	-1	SER	-	expression tag	UNP A0A3L6KZJ1
B	0	HIS	-	expression tag	UNP A0A3L6KZJ1
C	-2	GLY	-	expression tag	UNP A0A3L6KZJ1
C	-1	SER	-	expression tag	UNP A0A3L6KZJ1
C	0	HIS	-	expression tag	UNP A0A3L6KZJ1
D	-2	GLY	-	expression tag	UNP A0A3L6KZJ1
D	-1	SER	-	expression tag	UNP A0A3L6KZJ1
D	0	HIS	-	expression tag	UNP A0A3L6KZJ1

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



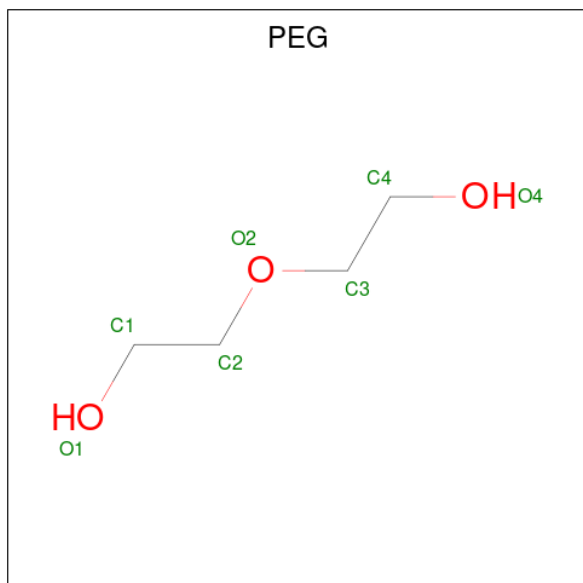
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	A	1	53	27	9	15	2	0	0
2	B	1	53	27	9	15	2	0	0
2	C	1	53	27	9	15	2	0	0
2	D	1	53	27	9	15	2	0	0

- Molecule 3 is 4-[(3,4-dichlorophenyl)methyl]-{N}-(4-fluorophenyl)-{N}-[[5-[2-(4-fluorophenyl)ethylcarbamoyl]furan-2-yl]methyl]-4-(3-phenylpropyl)-1,4¹-diazinane-1-carboxamide (three-letter code: YJ6) (formula: C₄₁H₄₁Cl₂F₂N₄O₃) (labeled as "Ligand of Interest" by depositor).



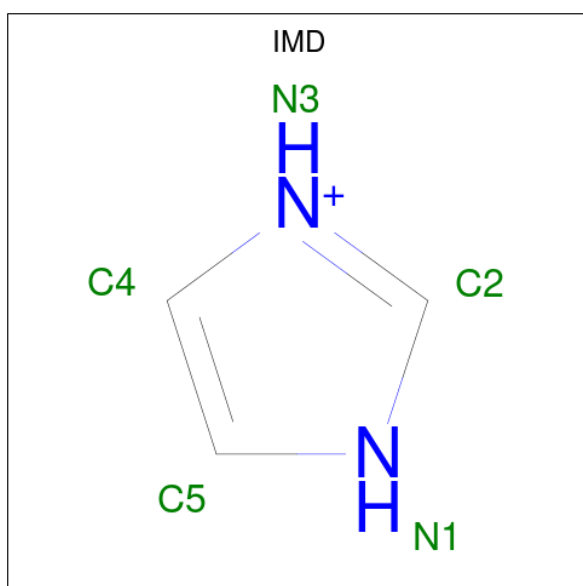
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf		
			Total	C	Cl	F	N			O	
3	A	1	Total	52	41	2	2	4	3	0	0
3	B	1	Total	52	41	2	2	4	3	0	0
3	C	1	Total	52	41	2	2	4	3	0	0
3	D	1	Total	52	41	2	2	4	3	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 7 4 3	0	0
4	A	1	Total C O 7 4 3	0	0
4	C	1	Total C O 7 4 3	0	0
4	D	1	Total C O 7 4 3	0	0

- Molecule 5 is IMIDAZOLE (three-letter code: IMD) (formula: C₃H₅N₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C N 5 3 2	0	0

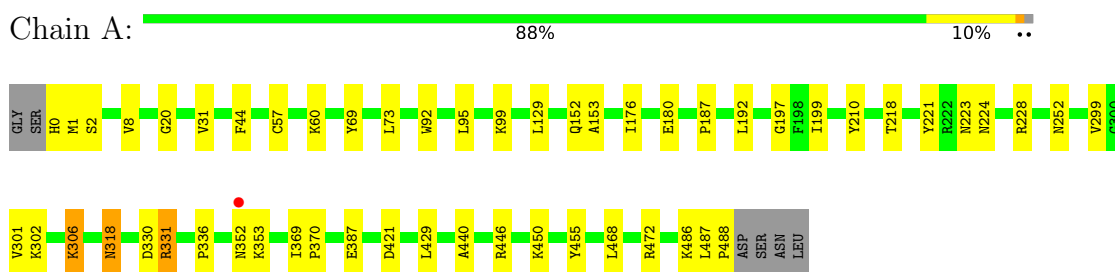
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	178	Total O 178 178	0	0
6	B	141	Total O 141 141	0	0
6	C	110	Total O 110 110	0	0
6	D	166	Total O 166 166	0	0

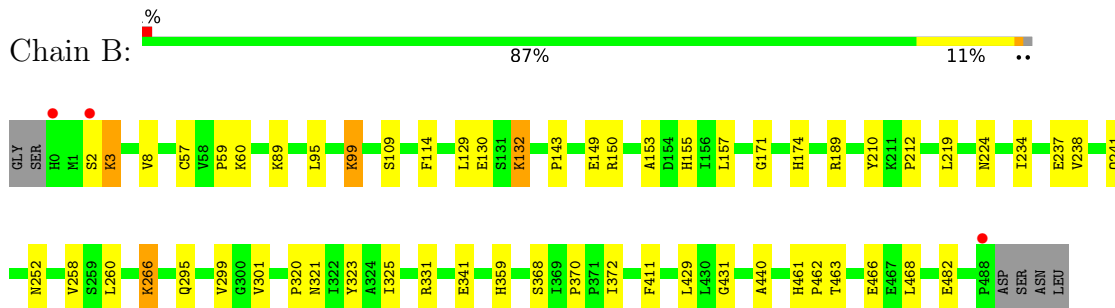
3 Residue-property plots [i](#)

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.

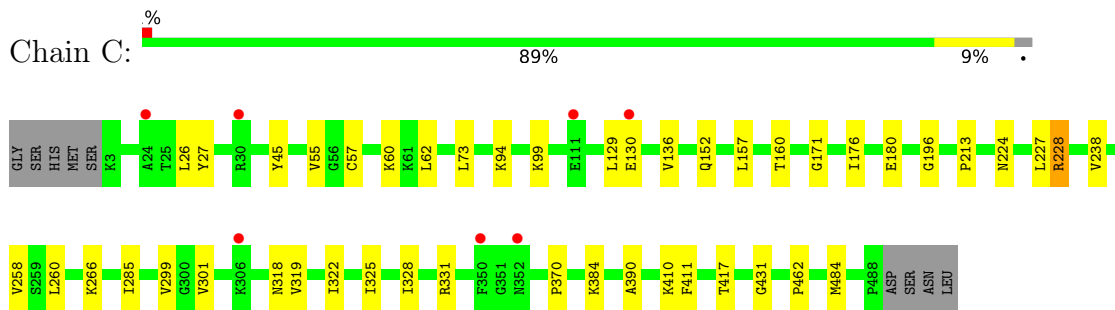
- Molecule 1: Trypanothione reductase



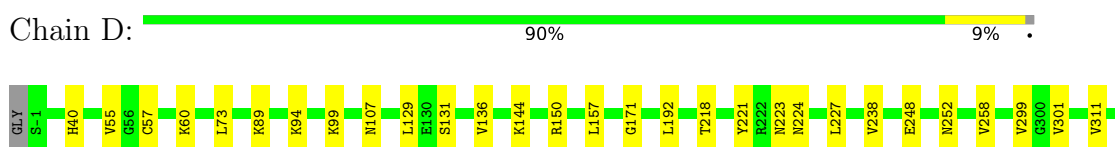
- Molecule 1: Trypanothione reductase



- Molecule 1: Trypanothione reductase



- Molecule 1: Trypanothione reductase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	100.70Å 63.74Å 170.10Å 90.00° 97.75° 90.00°	Depositor
Resolution (Å)	168.54 – 2.15 168.54 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.6 (168.54-2.15) 99.7 (168.54-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.14Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.179 , 0.224 0.186 , 0.228	Depositor DCC
R_{free} test set	5804 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	38.1	Xtrriage
Anisotropy	0.051	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 28.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16115	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.46% 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: FAD, IMD, YJ6, PEG

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	0.69	0/3891	0.85	1/5272 (0.0%)
1	B	0.69	0/3913	0.84	0/5304
1	C	0.71	0/3827	0.82	0/5188
1	D	0.70	0/3845	0.85	2/5215 (0.0%)
All	All	0.70	0/15476	0.84	3/20979 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	150	ARG	NE-CZ-NH1	-5.40	117.60	120.30
1	D	150	ARG	CB-CA-C	5.24	120.87	110.40
1	A	455	TYR	CA-CB-CG	5.13	123.15	113.40

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	3790	0	3826	36	0
1	B	3795	0	3845	29	0
1	C	3731	0	3767	19	0
1	D	3751	0	3779	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	53	0	31	0	0
2	B	53	0	31	0	0
2	C	53	0	31	0	0
2	D	53	0	31	0	0
3	A	52	0	0	3	0
3	B	52	0	0	2	0
3	C	52	0	0	3	0
3	D	52	0	0	2	0
4	A	14	0	20	9	0
4	C	7	0	10	2	0
4	D	7	0	10	0	0
5	B	5	0	5	0	0
6	A	178	0	0	6	0
6	B	141	0	0	2	0
6	C	110	0	0	2	0
6	D	166	0	0	2	0
All	All	16115	0	15386	106	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 3.

All (106) 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:199:ILE:H	4:A:504:PEG:H32	1.26	1.00
3:D:502:YJ6:C21	3:D:502:YJ6:C33	2.42	0.97
1:B:320:PRO:O	1:B:321[B]:ASN:ND2	2.03	0.89
1:A:336:PRO:HG3	3:B:502:YJ6:CL1	2.22	0.77
1:D:224[A]:ASN:HD22	1:D:252:ASN:HD21	1.32	0.77
3:C:502:YJ6:CL2	6:D:764:HOH:O	2.43	0.73
1:A:224:ASN:HD22	1:A:252:ASN:HD21	1.35	0.73
1:C:224[A]:ASN:OD1	1:C:228[A]:ARG:NH1	2.22	0.73
1:A:318:ASN:HD22	1:A:318:ASN:H	1.40	0.70
1:A:129:LEU:HD23	1:A:299:VAL:HG21	1.76	0.68
1:B:143:PRO:HB3	1:B:295[B]:GLN:HE21	1.60	0.65
1:D:94[A]:LYS:NZ	6:D:602:HOH:O	2.29	0.64
1:A:44:PHE:CE2	4:A:503:PEG:H42	2.36	0.61
1:A:197:GLY:HA3	4:A:504:PEG:H41	1.83	0.60
1:B:341:GLU:OE2	1:B:359:HIS:HE1	1.85	0.59
1:D:227:LEU:HD12	1:D:238[A]:VAL:HG11	1.84	0.59
1:A:152[B]:GLN:HG3	6:A:733:HOH:O	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:LEU:O	1:C:27:TYR:CD1	2.56	0.58
1:A:199:ILE:N	4:A:504:PEG:H32	2.08	0.58
3:B:502:YJ6:C10	3:B:502:YJ6:C13	2.82	0.58
1:B:130:GLU:OE1	1:B:150:ARG:NH2	2.36	0.57
1:C:370:PRO:HG2	6:C:622:HOH:O	2.06	0.56
1:B:299:VAL:HG23	1:B:301:VAL:HG23	1.87	0.56
1:A:331[A]:ARG:NH2	6:A:604:HOH:O	2.39	0.54
1:A:440:ALA:HB3	1:B:440:ALA:HB3	1.90	0.54
1:C:266:LYS:N	1:C:266:LYS:HD2	2.21	0.54
1:A:421:ASP:O	1:A:450:LYS:HD3	2.08	0.54
1:A:44:PHE:HE2	4:A:503:PEG:H42	1.73	0.53
1:B:171:GLY:HA3	1:B:258:VAL:O	2.09	0.52
1:D:171:GLY:HA3	1:D:258:VAL:O	2.08	0.52
1:B:224:ASN:HD22	1:B:252:ASN:HD21	1.56	0.52
1:C:157:LEU:HD11	1:C:325:ILE:HG12	1.92	0.52
1:A:302:LYS:H	1:A:318:ASN:HD21	1.58	0.52
1:A:2:SER:OG	1:A:152[A]:GLN:NE2	2.42	0.51
1:B:8:VAL:HG23	1:B:153:ALA:HB2	1.92	0.51
1:C:410:LYS:HE2	6:C:603:HOH:O	2.10	0.51
1:C:411:PHE:CD2	1:C:431:GLY:HA3	2.46	0.51
1:A:221:TYR:CE2	1:A:223:ASN:HB2	2.46	0.51
1:D:221:TYR:CE2	1:D:223:ASN:HB2	2.47	0.49
1:B:368:SER:OG	1:B:370:PRO:O	2.21	0.49
3:A:502:YJ6:C33	3:A:502:YJ6:C21	2.91	0.49
1:B:130:GLU:CD	1:B:150:ARG:HH12	2.15	0.49
1:B:157:LEU:HD11	1:B:325:ILE:HG12	1.95	0.48
1:A:92:TRP:HB3	1:A:187:PRO:HD3	1.95	0.48
3:C:502:YJ6:CL1	1:D:335:THR:CG2	2.98	0.48
1:D:238[B]:VAL:HG21	1:D:372:ILE:HD11	1.96	0.48
1:D:157:LEU:HD11	1:D:325:ILE:HG12	1.94	0.48
1:B:174:HIS:HD2	6:B:729:HOH:O	1.97	0.48
1:B:238[B]:VAL:HG21	1:B:372:ILE:HD11	1.96	0.48
1:C:62:LEU:HD22	1:D:403:ILE:HD12	1.96	0.48
1:B:234:ILE:O	1:B:238[A]:VAL:HG12	2.14	0.47
1:A:318:ASN:H	1:A:318:ASN:ND2	2.11	0.47
1:A:20:GLY:HA2	1:A:31:VAL:HG11	1.96	0.47
1:A:302:LYS:H	1:A:318:ASN:ND2	2.13	0.47
3:C:502:YJ6:CL1	1:D:335:THR:HG21	2.52	0.47
1:A:95:LEU:HD22	1:A:210:TYR:CZ	2.49	0.47
1:B:411:PHE:CD2	1:B:431:GLY:HA3	2.50	0.46
1:A:199:ILE:HB	4:A:504:PEG:H31	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:ILE:HB	1:A:180:GLU:HB2	1.98	0.46
1:A:0[A]:HIS:CD2	6:A:658:HOH:O	2.69	0.46
1:B:95:LEU:HD22	1:B:210:TYR:CZ	2.52	0.45
1:B:429:LEU:HD21	1:B:468:LEU:HD21	1.99	0.45
3:A:502:YJ6:CL1	3:A:502:YJ6:C3	3.02	0.45
1:B:59:PRO:HB3	1:B:99:LYS:HD3	1.99	0.45
1:A:299:VAL:HG23	1:A:301:VAL:HG23	1.99	0.44
1:A:369:ILE:HA	1:A:370:PRO:HA	1.86	0.44
1:C:171:GLY:HA3	1:C:258:VAL:O	2.18	0.44
1:B:461:HIS:HA	1:B:462:PRO:HA	1.79	0.44
1:A:1[A]:MET:SD	6:A:770:HOH:O	2.61	0.44
1:D:299:VAL:HG23	1:D:301:VAL:HG23	1.98	0.44
1:B:129:LEU:HD23	1:B:299:VAL:HG21	1.99	0.43
1:A:429:LEU:HD21	1:A:468:LEU:HD21	1.98	0.43
4:A:504:PEG:H22	6:A:615:HOH:O	2.19	0.43
1:C:130:GLU:HB2	1:C:136:VAL:CG2	2.49	0.43
1:B:266:LYS:N	1:B:266:LYS:HD3	2.32	0.43
1:C:285:ILE:O	4:C:503:PEG:H22	2.19	0.43
1:A:199:ILE:HB	4:A:504:PEG:C3	2.48	0.42
1:B:155:HIS:HB3	1:B:323:TYR:HE2	1.84	0.42
1:C:196:GLY:H	4:C:503:PEG:C1	2.31	0.42
1:A:69:TYR:O	1:A:73:LEU:HG	2.19	0.42
1:C:160:THR:OG1	1:C:328:ILE:HD12	2.20	0.42
1:D:470:SER:HB3	3:D:502:YJ6:C22	2.50	0.42
1:A:192:LEU:HA	1:A:218:THR:O	2.19	0.42
1:A:0[A]:HIS:N	6:A:609:HOH:O	2.51	0.42
1:A:197:GLY:HA3	4:A:504:PEG:C4	2.47	0.42
1:B:237:GLU:O	1:B:241:GLN:HG3	2.19	0.42
1:D:320:PRO:O	1:D:321:ASN:CG	2.58	0.42
1:C:176:ILE:HB	1:C:180:GLU:HB2	2.01	0.42
3:A:502:YJ6:C20	3:A:502:YJ6:C32	2.98	0.42
1:B:463:THR:O	1:B:466:GLU:HG2	2.20	0.42
1:C:227:LEU:HD12	1:C:238:VAL:HG11	2.02	0.42
1:C:390:ALA:HB3	1:C:417:THR:OG1	2.20	0.41
1:D:411:PHE:CE2	1:D:464:SER:HB3	2.55	0.41
1:C:319:VAL:HG11	1:C:322:ILE:HD12	2.03	0.41
1:D:40:HIS:H	1:D:107:ASN:HD21	1.67	0.41
1:A:8:VAL:CG2	1:A:153:ALA:HB2	2.50	0.41
1:D:311:VAL:HA	1:D:316:ARG:O	2.21	0.41
1:A:306:LYS:CE	1:A:330:ASP:OD2	2.69	0.41
1:B:219:LEU:C	1:B:219:LEU:HD23	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:299:VAL:HG23	1:C:301:VAL:HG23	2.03	0.41
1:B:189:ARG:HA	1:B:212:PRO:HD2	2.02	0.41
1:C:73:LEU:HD23	1:D:73:LEU:CD2	2.50	0.40
1:A:487:LEU:O	1:A:488:PRO:C	2.60	0.40
1:B:3:LYS:HE3	1:B:149:GLU:OE1	2.21	0.40
1:B:114:PHE:O	6:B:601:HOH:O	2.21	0.40
1:D:192:LEU:HA	1:D:218:THR:O	2.22	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	496/495 (100%)	485 (98%)	11 (2%)	0	100	100
1	B	501/495 (101%)	481 (96%)	17 (3%)	3 (1%)	25	18
1	C	490/495 (99%)	471 (96%)	17 (4%)	2 (0%)	34	29
1	D	493/495 (100%)	480 (97%)	11 (2%)	2 (0%)	34	29
All	All	1980/1980 (100%)	1917 (97%)	56 (3%)	7 (0%)	41	29

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	2[A]	SER
1	B	2[B]	SER
1	B	132	LYS
1	D	481	GLY
1	C	45	TYR
1	C	55	VAL
1	D	55	VAL

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	412/407 (101%)	397 (96%)	15 (4%)	35	33
1	B	416/407 (102%)	403 (97%)	13 (3%)	40	39
1	C	405/407 (100%)	388 (96%)	17 (4%)	30	28
1	D	408/407 (100%)	393 (96%)	15 (4%)	34	32
All	All	1641/1628 (101%)	1581 (96%)	60 (4%)	38	32

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	CYS
1	A	60	LYS
1	A	99	LYS
1	A	228[A]	ARG
1	A	228[B]	ARG
1	A	306	LYS
1	A	318	ASN
1	A	331[A]	ARG
1	A	331[B]	ARG
1	A	352	ASN
1	A	353	LYS
1	A	387	GLU
1	A	446	ARG
1	A	472	ARG
1	A	486	LYS
1	B	3	LYS
1	B	57	CYS
1	B	60	LYS
1	B	89[A]	LYS
1	B	89[B]	LYS
1	B	99	LYS
1	B	109	SER
1	B	132	LYS
1	B	260	LEU

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Mol	Chain	Res	Type
1	B	266	LYS
1	B	331[A]	ARG
1	B	331[B]	ARG
1	B	482	GLU
1	C	57	CYS
1	C	60	LYS
1	C	94[A]	LYS
1	C	94[B]	LYS
1	C	99	LYS
1	C	129	LEU
1	C	152	GLN
1	C	213	PRO
1	C	228[A]	ARG
1	C	228[B]	ARG
1	C	260	LEU
1	C	318	ASN
1	C	331[A]	ARG
1	C	331[B]	ARG
1	C	384	LYS
1	C	462	PRO
1	C	484	MET
1	D	57	CYS
1	D	60	LYS
1	D	89	LYS
1	D	99	LYS
1	D	129	LEU
1	D	131	SER
1	D	136	VAL
1	D	144	LYS
1	D	248	GLU
1	D	331	ARG
1	D	335	THR
1	D	446	ARG
1	D	455	TYR
1	D	472	ARG
1	D	485	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	223	ASN
1	A	224	ASN

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Mol	Chain	Res	Type
1	A	318	ASN
1	B	107	ASN
1	B	174	HIS
1	B	224	ASN
1	B	359	HIS
1	C	152	GLN
1	C	318	ASN
1	C	359	HIS
1	D	107	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

13 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	$\# Z > 2$
2	FAD	A	501	-	53,58,58	0.70	0	68,89,89	0.84	2 (2%)
2	FAD	D	501	-	53,58,58	0.63	0	68,89,89	0.82	2 (2%)
3	YJ6	D	502	-	54,57,57	0.70	1 (1%)	69,79,79	1.42	9 (13%)
4	PEG	A	504	-	6,6,6	0.08	0	5,5,5	0.27	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	YJ6	A	502	-	54,57,57	0.67	2 (3%)	69,79,79	1.01	6 (8%)
2	FAD	B	501	-	53,58,58	0.65	0	68,89,89	0.84	2 (2%)
3	YJ6	C	502	-	54,57,57	0.71	2 (3%)	69,79,79	1.18	6 (8%)
5	IMD	B	503	-	3,5,5	0.26	0	4,5,5	0.64	0
2	FAD	C	501	-	53,58,58	0.64	0	68,89,89	0.81	1 (1%)
4	PEG	D	503	-	6,6,6	0.19	0	5,5,5	0.16	0
3	YJ6	B	502	-	54,57,57	0.65	1 (1%)	69,79,79	1.33	6 (8%)
4	PEG	A	503	-	6,6,6	0.62	0	5,5,5	0.47	0
4	PEG	C	503	-	6,6,6	0.24	0	5,5,5	0.22	0

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
2	FAD	A	501	-	-	4/30/50/50	0/6/6/6
2	FAD	D	501	-	-	3/30/50/50	0/6/6/6
3	YJ6	D	502	-	-	11/34/50/50	0/6/6/6
4	PEG	A	504	-	-	2/4/4/4	-
3	YJ6	A	502	-	-	20/34/50/50	1/6/6/6
2	FAD	B	501	-	-	4/30/50/50	0/6/6/6
3	YJ6	C	502	-	-	14/34/50/50	0/6/6/6
5	IMD	B	503	-	-	-	0/1/1/1
2	FAD	C	501	-	-	4/30/50/50	0/6/6/6
4	PEG	D	503	-	-	1/4/4/4	-
3	YJ6	B	502	-	-	18/34/50/50	0/6/6/6
4	PEG	A	503	-	-	4/4/4/4	-
4	PEG	C	503	-	-	1/4/4/4	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	YJ6	C10-C11	-3.53	1.34	1.39
3	C	502	YJ6	C10-C11	-3.48	1.34	1.39
3	D	502	YJ6	C10-C11	-3.24	1.35	1.39
3	B	502	YJ6	C10-C11	-3.10	1.35	1.39
3	C	502	YJ6	C12-C11	-2.41	1.49	1.51
3	A	502	YJ6	C12-C11	-2.00	1.49	1.51

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	YJ6	C20-C21-N4	5.87	115.17	108.75
3	D	502	YJ6	C20-C21-N4	5.31	114.55	108.75
3	D	502	YJ6	C12-C11-C10	4.56	136.49	129.06
3	B	502	YJ6	C12-C11-C10	4.23	135.96	129.06
3	C	502	YJ6	C39-C38-N4	4.06	113.19	108.75
3	C	502	YJ6	C12-C11-C10	4.03	135.63	129.06
3	D	502	YJ6	C39-C38-N4	3.96	113.08	108.75
3	C	502	YJ6	C20-C21-N4	3.89	113.01	108.75
3	D	502	YJ6	C11-C12-N2	3.87	119.04	112.76
3	C	502	YJ6	C22-C23-C24	3.83	117.77	110.60
3	B	502	YJ6	C39-C38-N4	3.50	112.58	108.75
3	A	502	YJ6	C12-C11-C10	3.49	134.75	129.06
3	B	502	YJ6	C38-C39-N3	-3.42	107.01	111.36
3	A	502	YJ6	C11-C12-N2	3.36	118.20	112.76
2	D	501	FAD	O2P-P-O1P	3.29	128.51	112.24
3	A	502	YJ6	C39-C38-N4	3.20	112.25	108.75
3	D	502	YJ6	O1-C19-N3	-3.08	117.04	123.80
3	C	502	YJ6	C32-C31-N4	3.00	120.48	115.57
2	A	501	FAD	C5A-C6A-N6A	2.97	124.86	120.35
3	D	502	YJ6	C20-N3-C19	2.80	132.60	121.14
3	B	502	YJ6	C22-C23-C24	2.77	115.78	110.60
2	C	501	FAD	O2P-P-O1P	2.69	125.55	112.24
3	B	502	YJ6	C32-C31-N4	2.62	119.85	115.57
3	D	502	YJ6	C22-C23-C24	2.60	115.47	110.60
3	A	502	YJ6	C20-C21-N4	2.48	111.46	108.75
3	A	502	YJ6	C8-C7-N1	2.30	118.80	115.59
2	B	501	FAD	O2P-P-O1P	2.29	123.56	112.24
3	D	502	YJ6	C38-C39-N3	-2.28	108.46	111.36
3	A	502	YJ6	C22-C23-C24	2.27	114.84	110.60
2	A	501	FAD	O2A-PA-O1A	2.26	123.42	112.24
2	B	501	FAD	C5A-C6A-N6A	2.23	123.75	120.35
3	D	502	YJ6	C39-N3-C20	-2.21	108.36	112.62
3	C	502	YJ6	C38-C39-N3	-2.07	108.73	111.36
2	D	501	FAD	O2A-PA-O1A	2.02	122.25	112.24

There are no chirality outliers.

All (86) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	YJ6	O3-C7-C8-C9
3	A	502	YJ6	N3-C19-N2-C13

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Mol	Chain	Res	Type	Atoms
3	A	502	YJ6	N2-C19-N3-C20
3	A	502	YJ6	N2-C19-N3-C39
3	A	502	YJ6	O1-C19-N3-C20
3	A	502	YJ6	O1-C19-N3-C39
3	A	502	YJ6	C32-C31-N4-C21
3	A	502	YJ6	C32-C31-N4-C22
3	A	502	YJ6	C32-C31-N4-C38
3	B	502	YJ6	O3-C7-C8-C9
3	B	502	YJ6	N3-C19-N2-C13
3	B	502	YJ6	N2-C19-N3-C20
3	B	502	YJ6	N2-C19-N3-C39
3	B	502	YJ6	O1-C19-N3-C20
3	B	502	YJ6	O1-C19-N3-C39
3	B	502	YJ6	N4-C31-C32-C37
3	C	502	YJ6	O3-C7-C8-C9
3	C	502	YJ6	N3-C19-N2-C13
3	C	502	YJ6	O1-C19-N2-C13
3	C	502	YJ6	N2-C19-N3-C20
3	C	502	YJ6	N2-C19-N3-C39
3	C	502	YJ6	O1-C19-N3-C20
3	C	502	YJ6	O1-C19-N3-C39
3	D	502	YJ6	O3-C7-C8-C9
3	D	502	YJ6	N4-C31-C32-C33
3	B	502	YJ6	N4-C31-C32-C33
3	D	502	YJ6	N4-C31-C32-C37
3	C	502	YJ6	N4-C22-C23-C24
3	A	502	YJ6	N4-C22-C23-C24
3	D	502	YJ6	C32-C31-N4-C21
3	B	502	YJ6	N4-C22-C23-C24
4	A	504	PEG	C4-C3-O2-C2
4	D	503	PEG	O1-C1-C2-O2
3	D	502	YJ6	N4-C22-C23-C24
3	B	502	YJ6	C22-C23-C24-C25
4	A	503	PEG	O2-C3-C4-O4
4	A	504	PEG	O2-C3-C4-O4
3	A	502	YJ6	C23-C22-N4-C21
2	B	501	FAD	O4B-C4B-C5B-O5B
3	B	502	YJ6	C4-C5-C6-N1
3	D	502	YJ6	C32-C31-N4-C38
3	A	502	YJ6	C22-C23-C24-C25
3	C	502	YJ6	C22-C23-C24-C25
3	A	502	YJ6	C23-C22-N4-C38

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Mol	Chain	Res	Type	Atoms
3	A	502	YJ6	O1-C19-N2-C13
3	D	502	YJ6	C32-C31-N4-C22
4	C	503	PEG	O1-C1-C2-O2
3	A	502	YJ6	C23-C22-N4-C31
3	B	502	YJ6	C11-C12-N2-C13
3	C	502	YJ6	C23-C22-N4-C31
3	A	502	YJ6	N4-C31-C32-C33
3	B	502	YJ6	O1-C19-N2-C13
3	D	502	YJ6	N3-C19-N2-C13
2	A	501	FAD	PA-O3P-P-O5'
2	B	501	FAD	PA-O3P-P-O5'
2	C	501	FAD	PA-O3P-P-O5'
2	D	501	FAD	PA-O3P-P-O5'
3	D	502	YJ6	C22-C23-C24-C25
2	A	501	FAD	P-O3P-PA-O2A
2	B	501	FAD	P-O3P-PA-O2A
2	C	501	FAD	P-O3P-PA-O2A
2	D	501	FAD	P-O3P-PA-O2A
3	D	502	YJ6	O1-C19-N2-C13
3	C	502	YJ6	O1-C19-N2-C12
4	A	503	PEG	C1-C2-O2-C3
4	A	503	PEG	C4-C3-O2-C2
2	B	501	FAD	C3B-C4B-C5B-O5B
2	C	501	FAD	O4B-C4B-C5B-O5B
3	C	502	YJ6	N3-C19-N2-C12
2	A	501	FAD	P-O3P-PA-O1A
4	A	503	PEG	O1-C1-C2-O2
3	B	502	YJ6	C23-C24-C25-C30
3	A	502	YJ6	C23-C24-C25-C26
3	C	502	YJ6	C23-C22-N4-C21
3	B	502	YJ6	C23-C24-C25-C26
3	A	502	YJ6	C23-C24-C25-C30
3	B	502	YJ6	O3-C7-N1-C6
3	B	502	YJ6	C8-C7-N1-C6
2	A	501	FAD	O4B-C4B-C5B-O5B
2	C	501	FAD	P-O3P-PA-O1A
3	A	502	YJ6	C4-C5-C6-N1
3	B	502	YJ6	C11-C12-N2-C19
3	A	502	YJ6	N4-C31-C32-C37
2	D	501	FAD	O4B-C4B-C5B-O5B
3	C	502	YJ6	C23-C22-N4-C38
3	D	502	YJ6	C11-C12-N2-C13

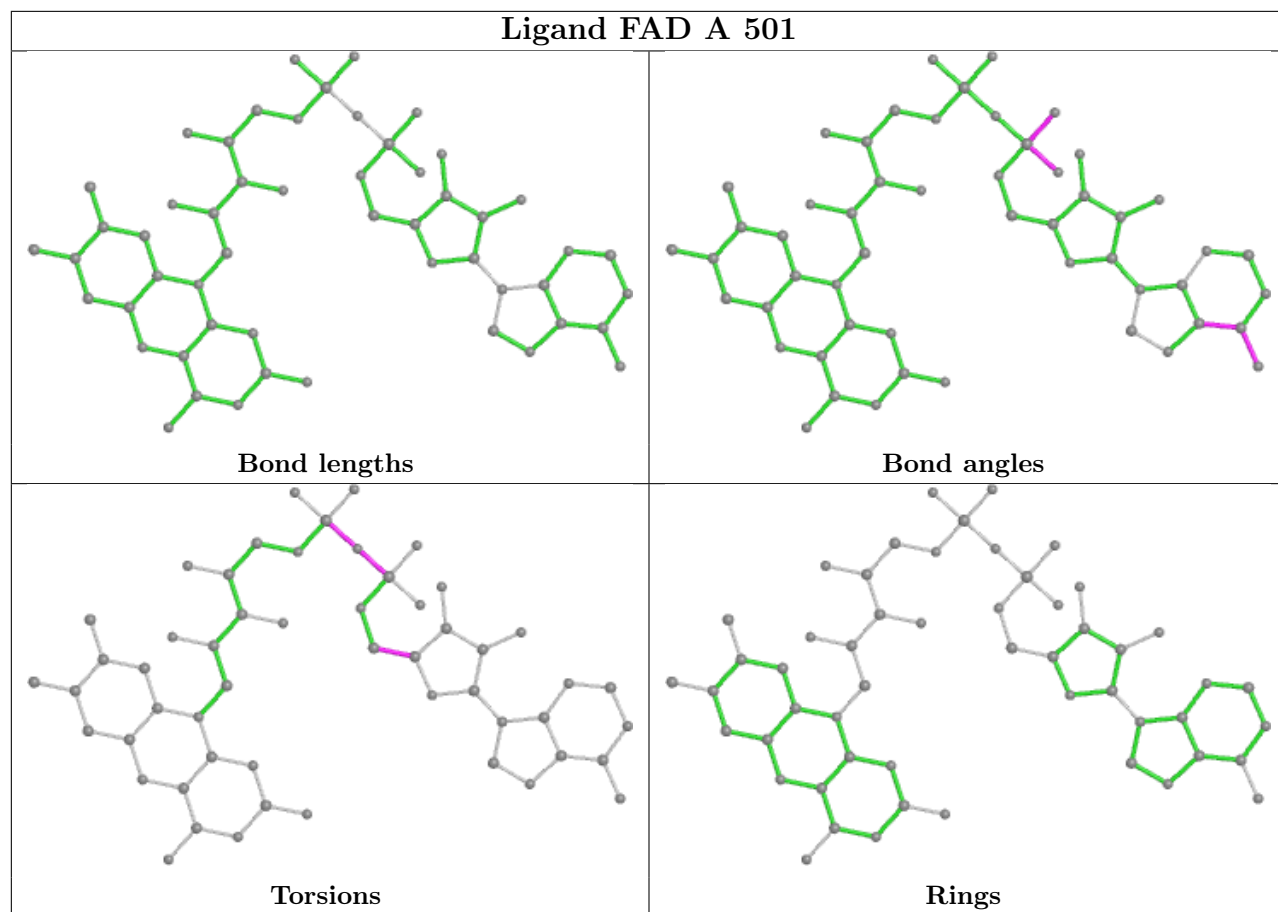
All (1) ring outliers are listed below:

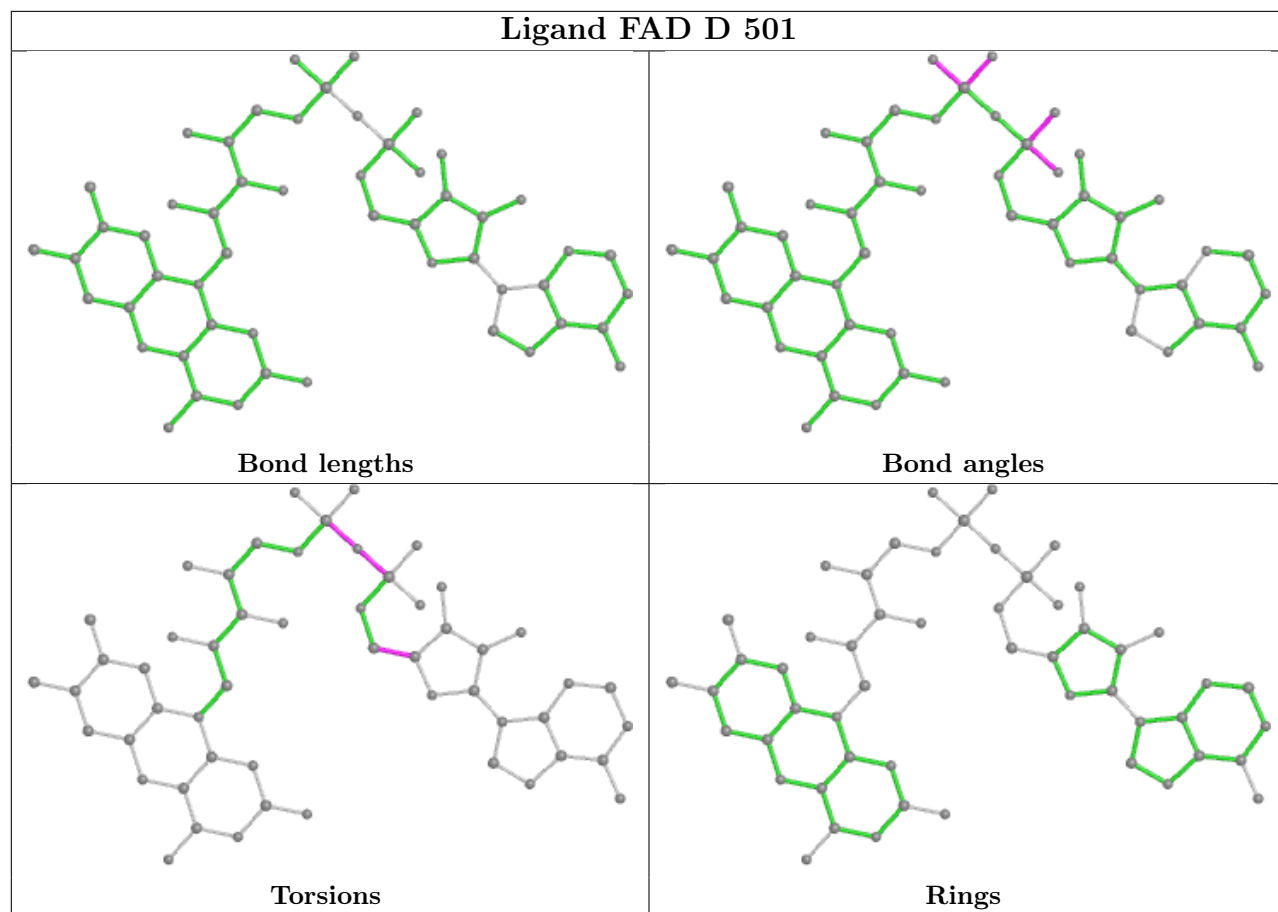
Mol	Chain	Res	Type	Atoms
3	A	502	YJ6	C20-C21-C38-C39-N3-N4

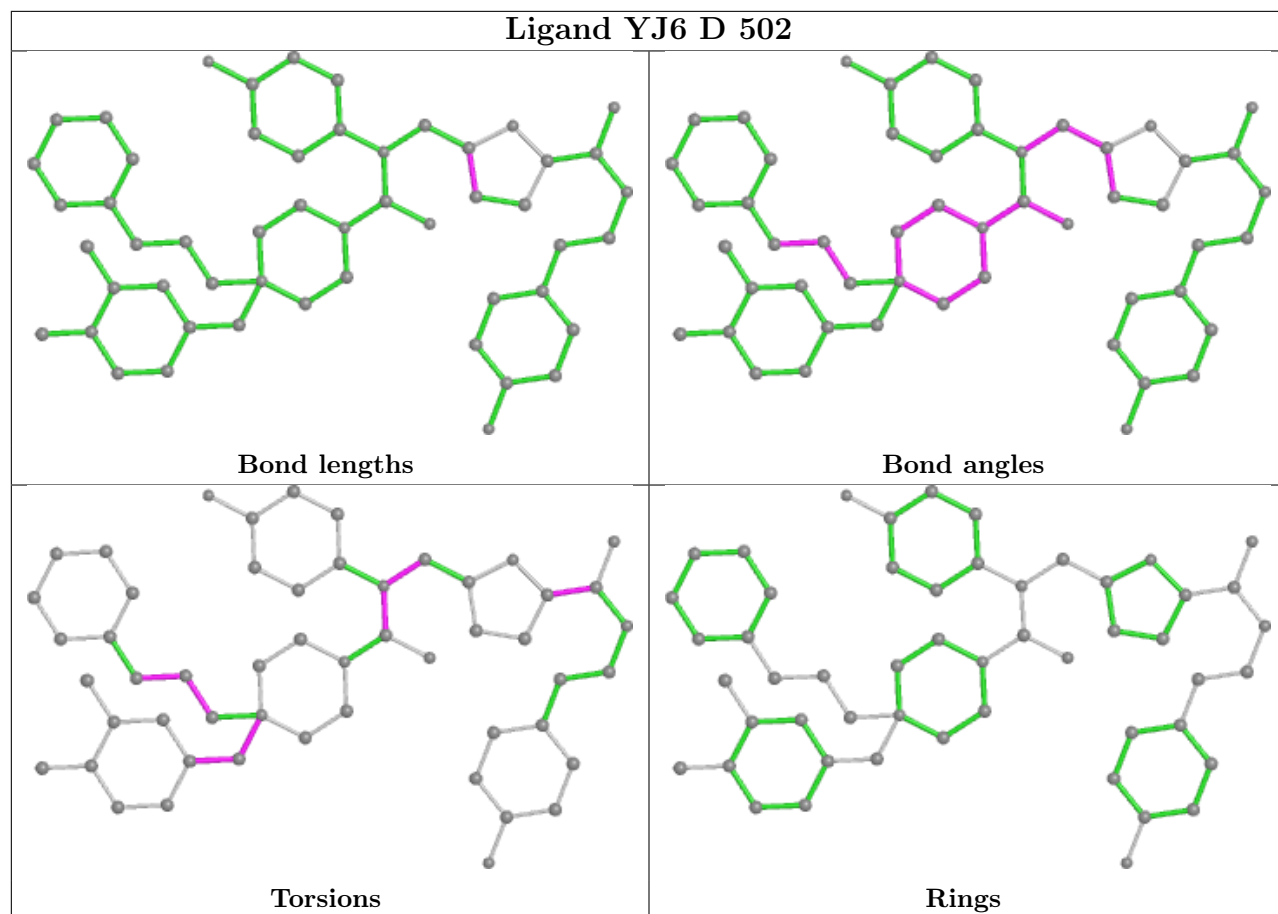
7 monomers are involved in 21 short contacts:

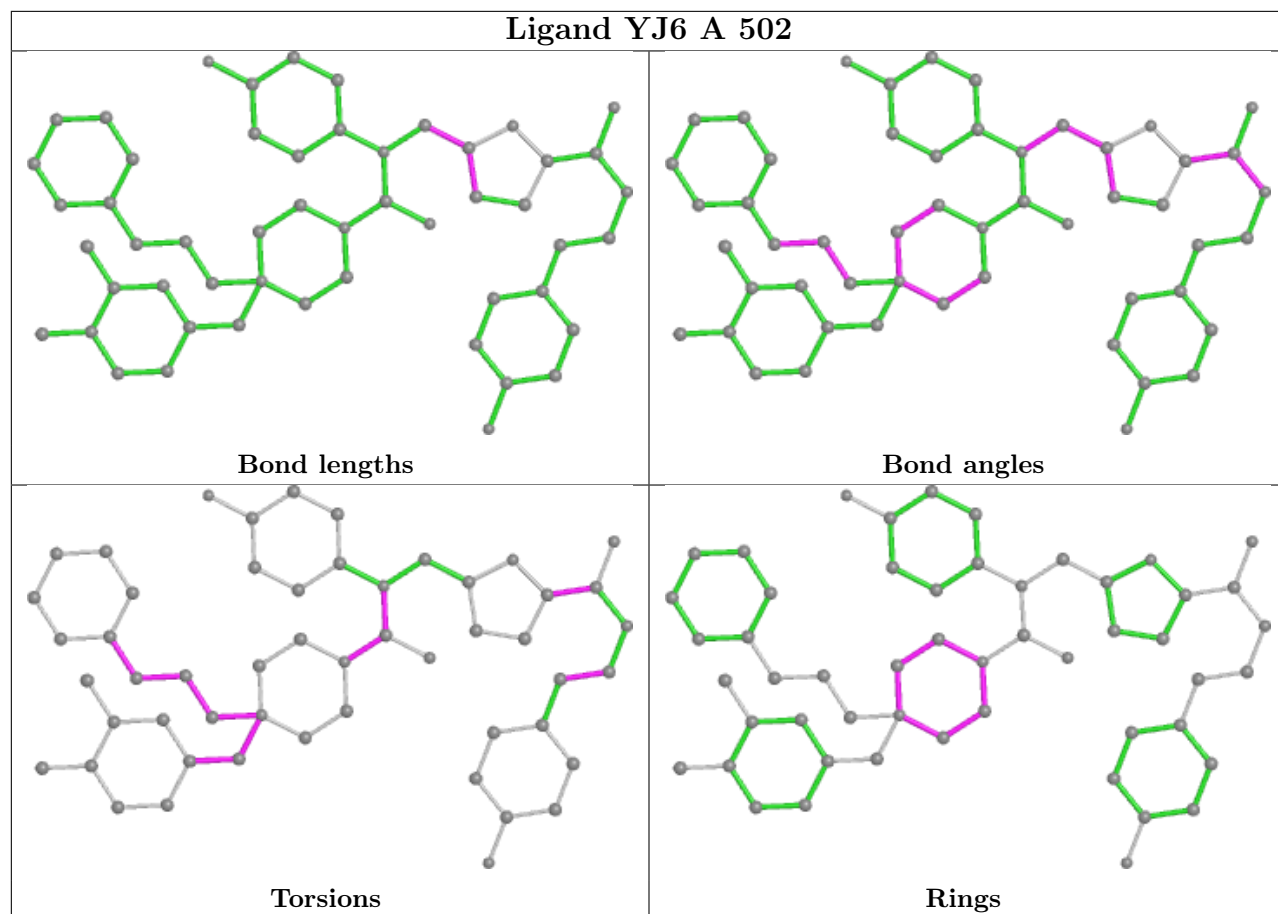
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	502	YJ6	2	0
4	A	504	PEG	7	0
3	A	502	YJ6	3	0
3	C	502	YJ6	3	0
3	B	502	YJ6	2	0
4	A	503	PEG	2	0
4	C	503	PEG	2	0

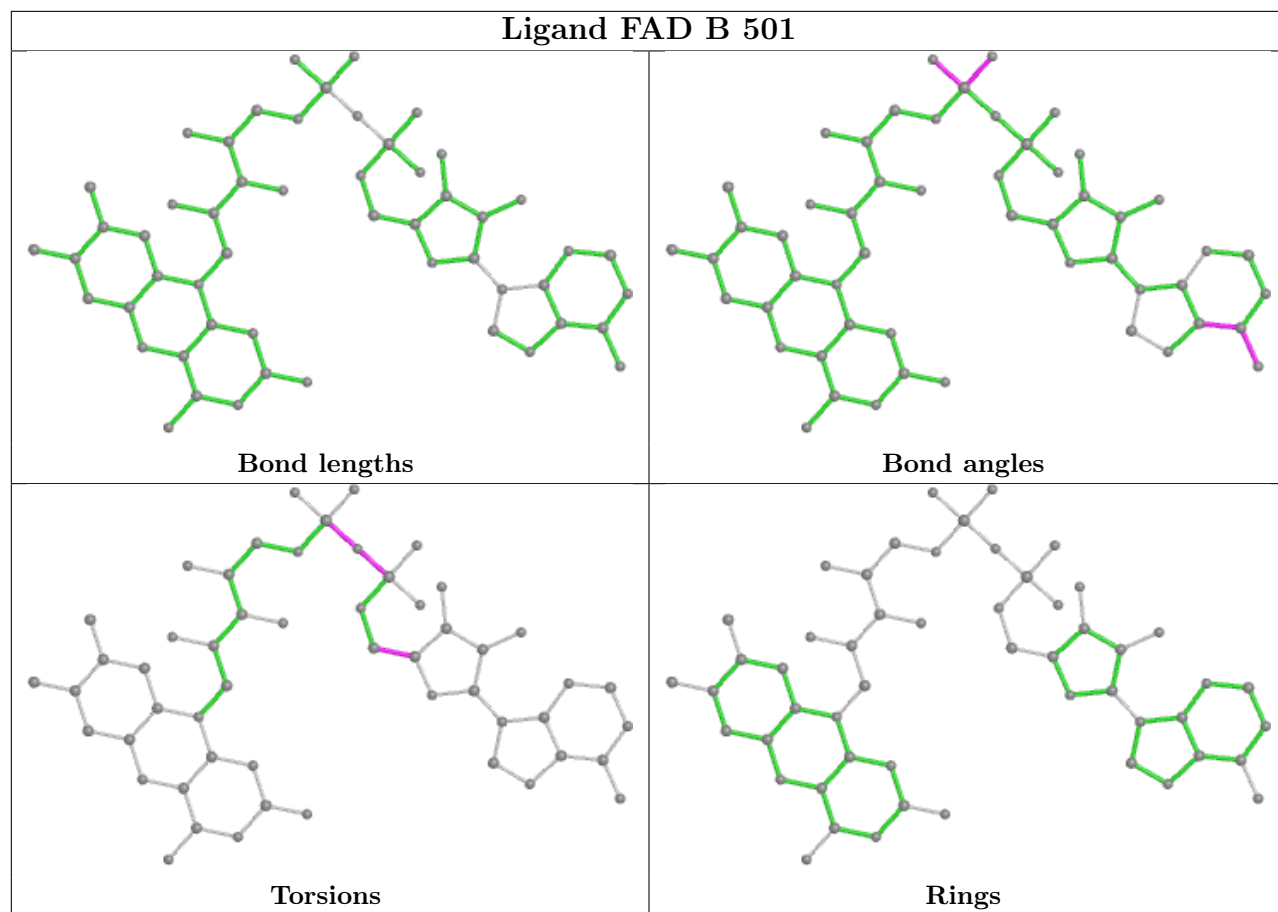
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

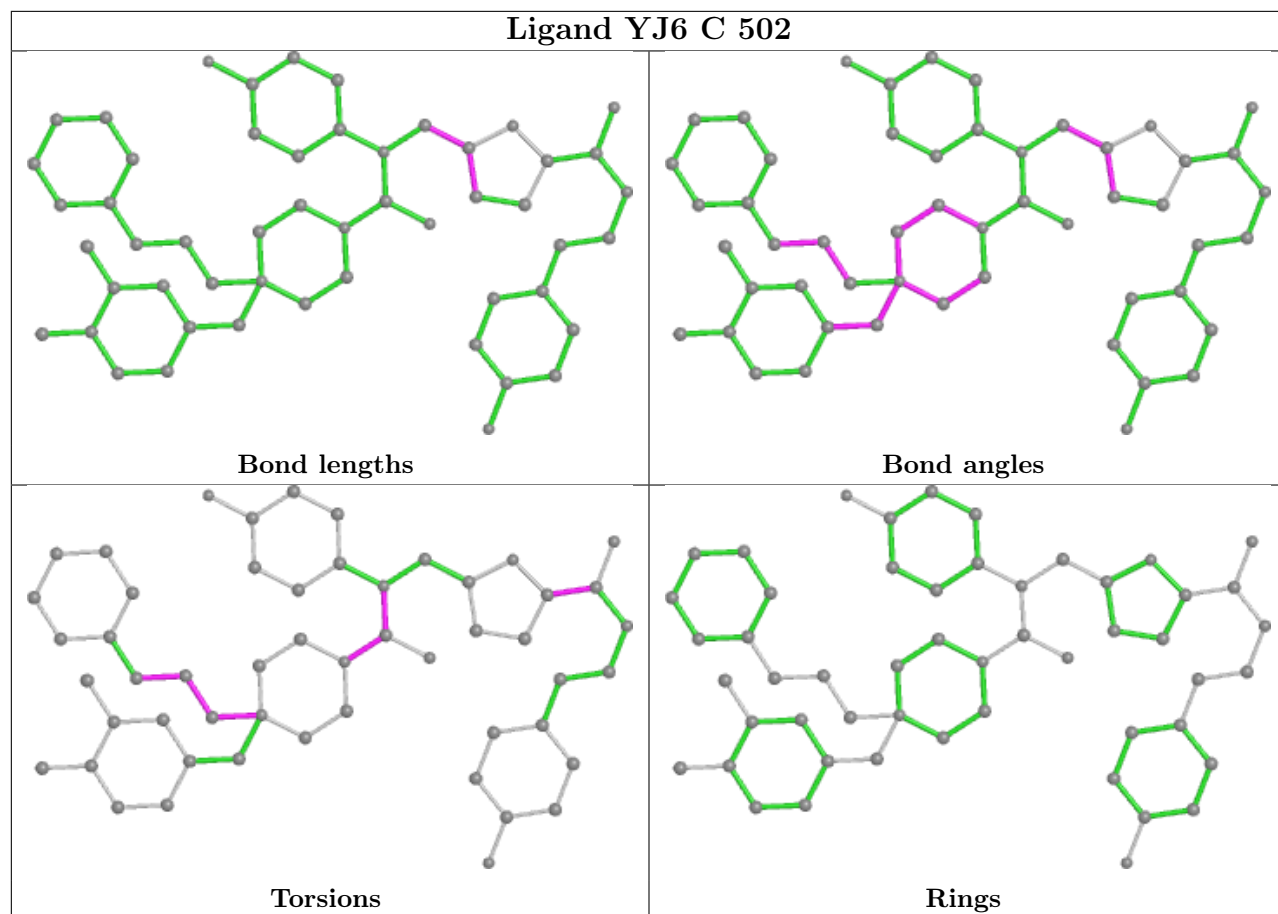


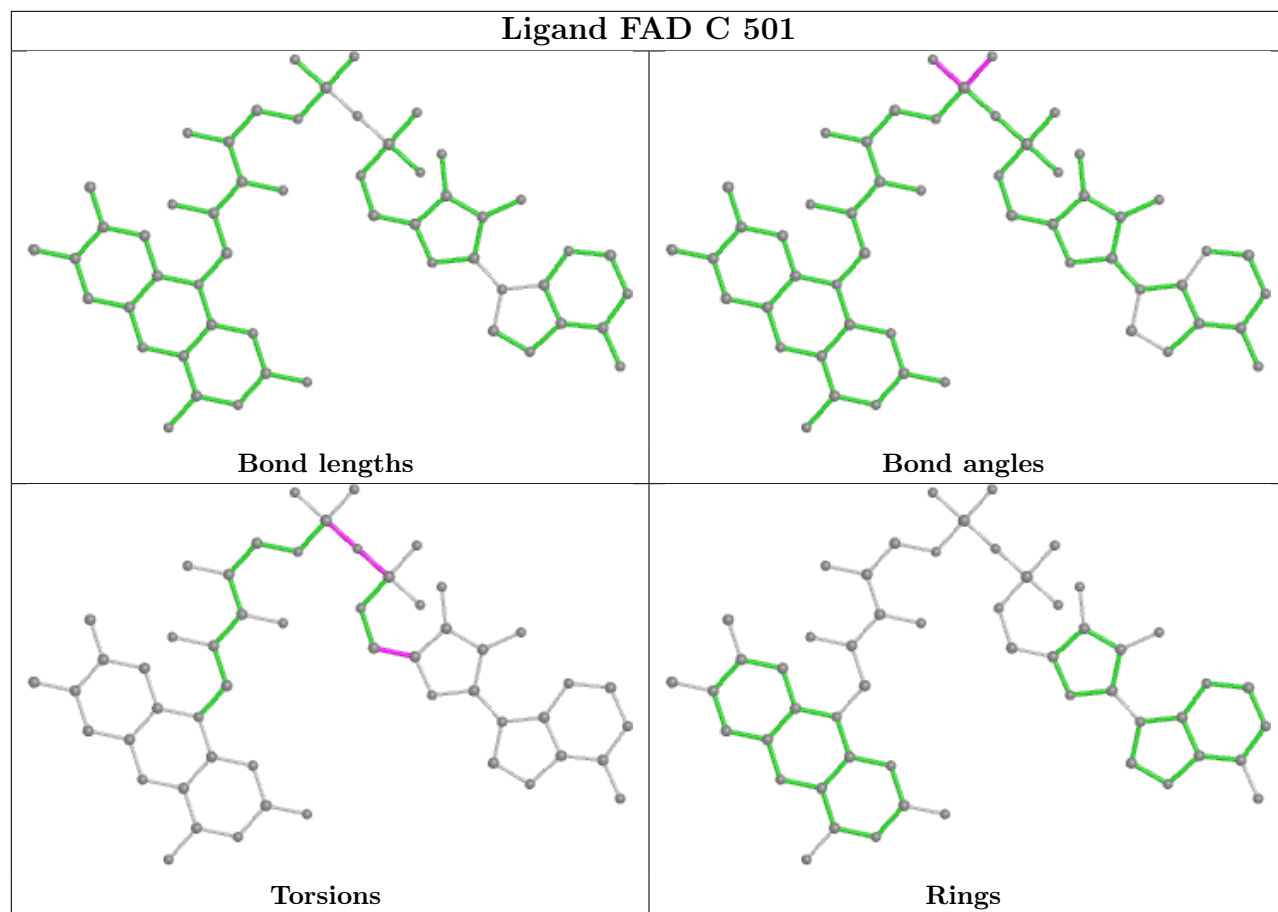


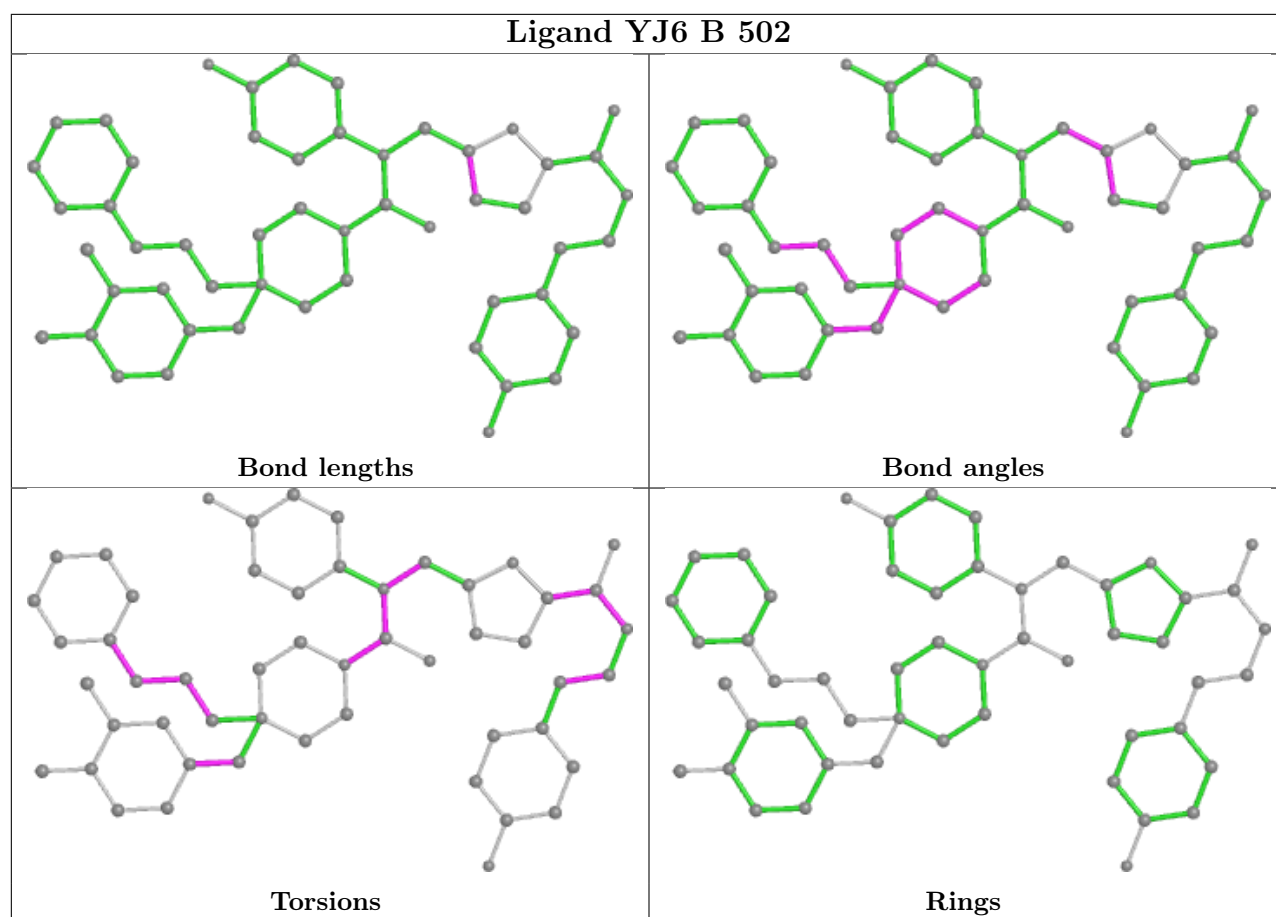












5.7 Other polymers [i](#)

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 [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	489/495 (98%)	-0.28	1 (0%) 95 96	25, 36, 56, 86	0
1	B	489/495 (98%)	-0.24	3 (0%) 89 91	27, 39, 64, 110	1 (0%)
1	C	486/495 (98%)	-0.04	7 (1%) 75 80	27, 45, 90, 123	1 (0%)
1	D	490/495 (98%)	-0.25	0 100 100	25, 39, 61, 95	0
All	All	1954/1980 (98%)	-0.21	11 (0%) 89 91	25, 39, 73, 123	2 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	352	ASN	5.6
1	C	30	ARG	4.6
1	B	0	HIS	3.5
1	B	488	PRO	3.0
1	B	2[A]	SER	2.9
1	C	24	ALA	2.7
1	C	350	PHE	2.4
1	C	130	GLU	2.3
1	C	111	GLU	2.0
1	A	352	ASN	2.0
1	C	306	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 monosaccharides in this entry.

6.4 Ligands

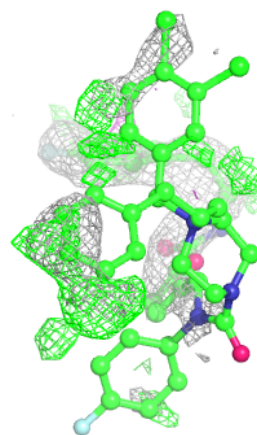
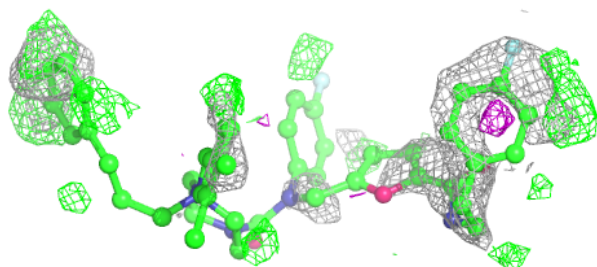
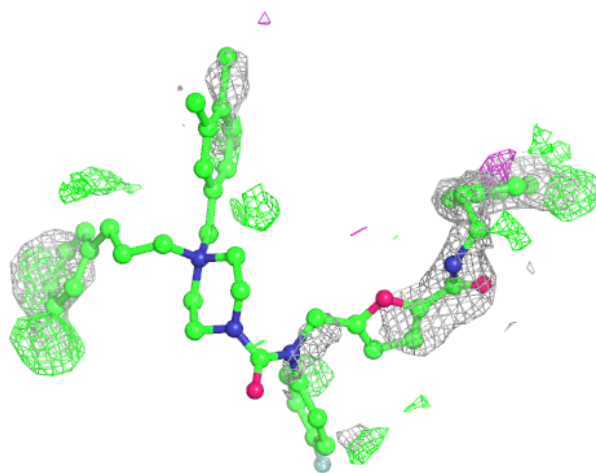
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	YJ6	B	502	52/52	0.47	0.58	53,123,156,159	52
3	YJ6	A	502	52/52	0.56	0.48	48,108,149,157	52
3	YJ6	D	502	52/52	0.66	0.40	72,155,213,222	0
5	IMD	B	503	5/5	0.66	0.24	79,82,89,90	0
3	YJ6	C	502	52/52	0.70	0.50	41,123,179,184	52
4	PEG	C	503	7/7	0.72	0.31	65,82,90,94	0
4	PEG	A	503	7/7	0.77	0.29	20,23,25,25	7
4	PEG	A	504	7/7	0.86	0.27	22,28,38,45	7
4	PEG	D	503	7/7	0.88	0.22	64,77,85,86	0
2	FAD	C	501	53/53	0.97	0.10	34,43,53,59	0
2	FAD	B	501	53/53	0.98	0.09	27,32,39,41	0
2	FAD	A	501	53/53	0.98	0.10	21,28,32,34	0
2	FAD	D	501	53/53	0.98	0.10	24,28,31,32	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.

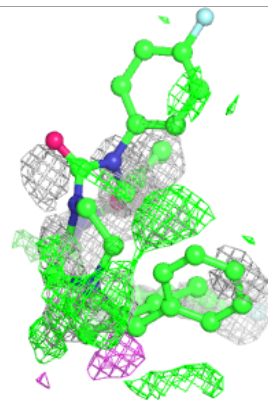
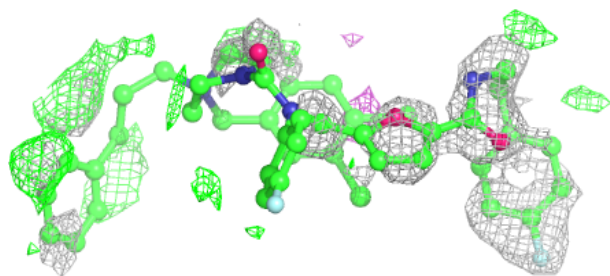
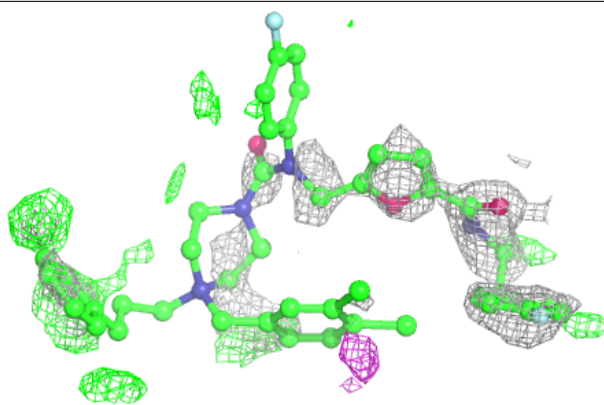
Electron density around YJ6 B 502:

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

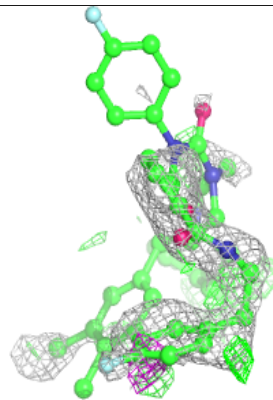
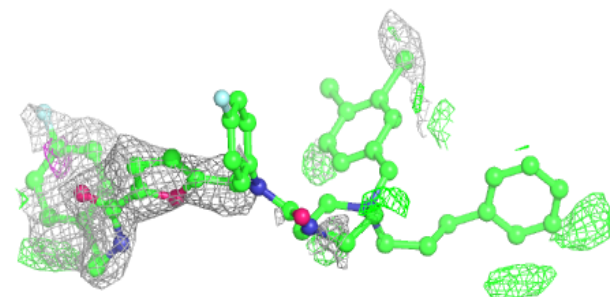
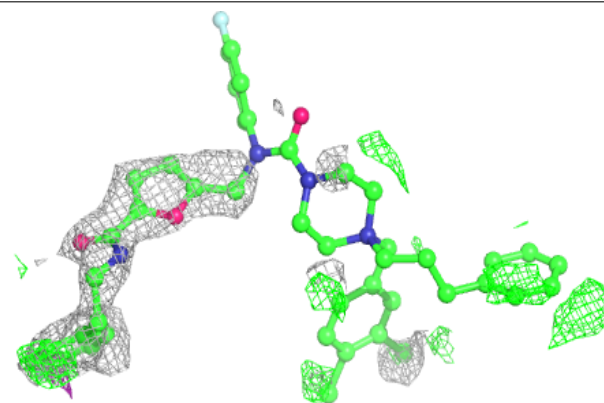


Electron density around YJ6 A 502:

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

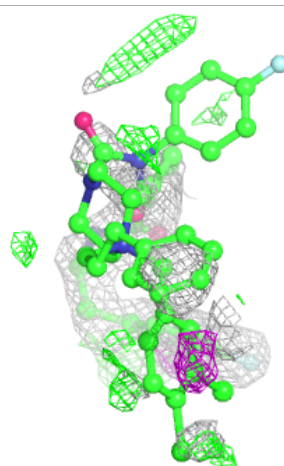
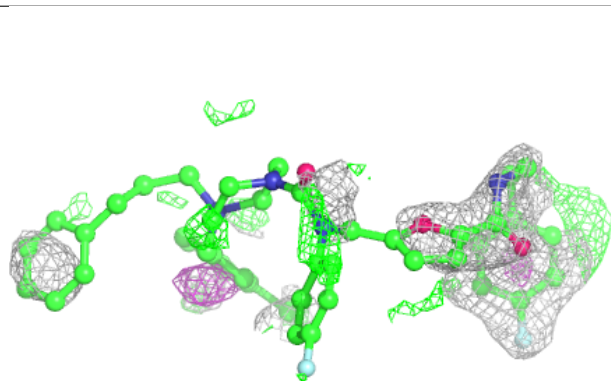
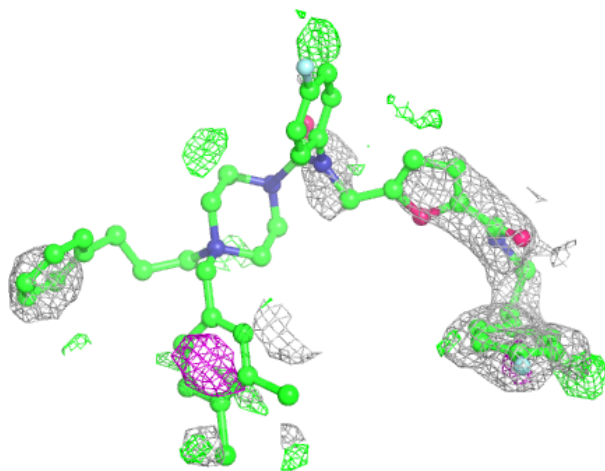
**Electron density around YJ6 D 502:**

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



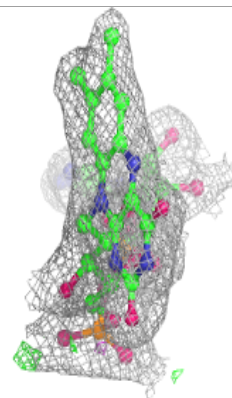
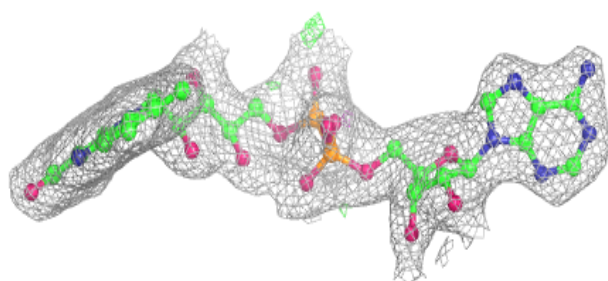
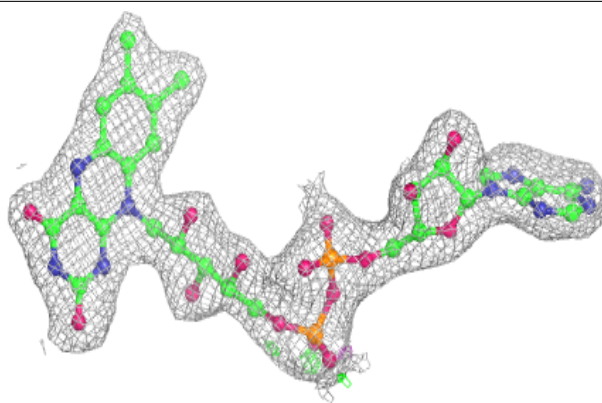
Electron density around YJ6 C 502:

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

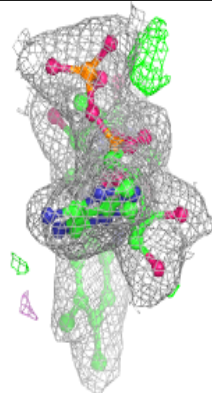
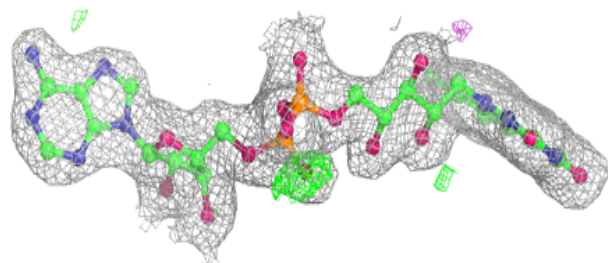
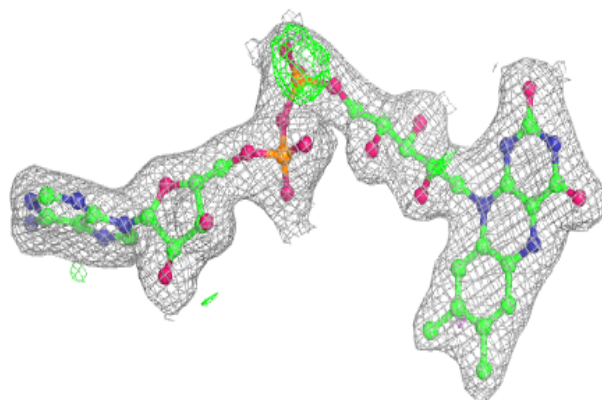


Electron density around FAD C 501:

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

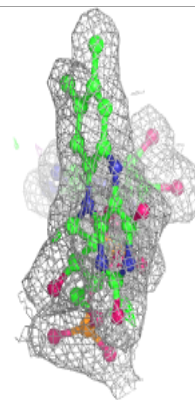
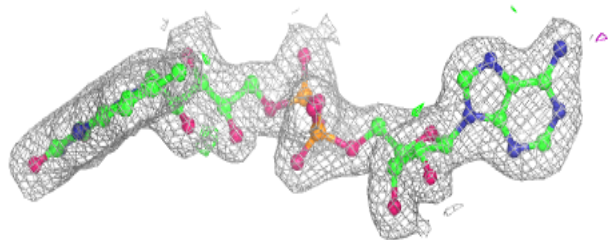
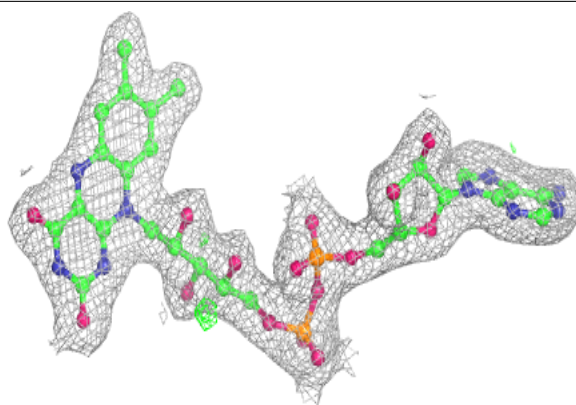
**Electron density around FAD B 501:**

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

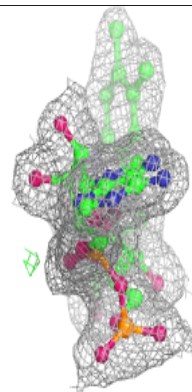
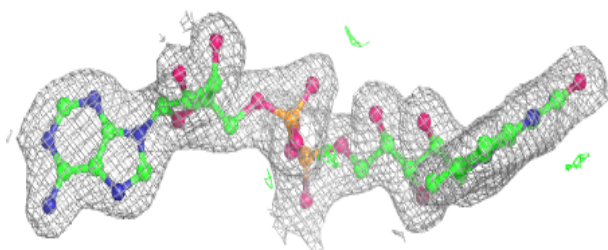
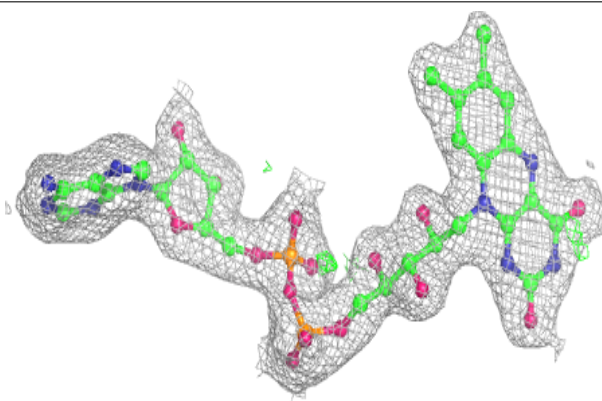


Electron density around FAD A 501:

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

**Electron density around FAD D 501:**

$2mF_o-DF_c$ (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.