



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2020 – 10:51 PM BST

PDB ID : 5YB6
Title : L-Amino acid oxidase/monooxygenase from Pseudomonas sp. AIU 813 - L-lysine complex
Authors : Im, D.; Matsui, D.; Arakawa, T.; Isobe, K.; Asano, Y.; Fushinobu, S.
Deposited on : 2017-09-03
Resolution : 2.10 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 : **FAILED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

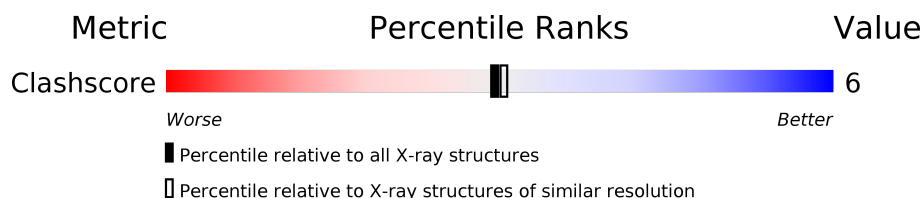
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5710 (2.10-2.10)

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 $\leq 5\%$

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	580	 85% 10% .
1	B	580	 86% 10% . .
1	C	580	 86% 9% . .
1	D	580	 86% 9% . .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 18833 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 L-amino acid oxidase/monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	556	Total	C	N	O	S	0	1	0
			4369	2785	759	802	23			
1	B	556	Total	C	N	O	S	0	0	0
			4358	2779	755	801	23			
1	C	556	Total	C	N	O	S	0	0	0
			4358	2779	755	801	23			
1	D	556	Total	C	N	O	S	0	0	0
			4358	2779	755	801	23			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP W6JQJ6
A	-18	GLY	-	expression tag	UNP W6JQJ6
A	-17	SER	-	expression tag	UNP W6JQJ6
A	-16	SER	-	expression tag	UNP W6JQJ6
A	-15	HIS	-	expression tag	UNP W6JQJ6
A	-14	HIS	-	expression tag	UNP W6JQJ6
A	-13	HIS	-	expression tag	UNP W6JQJ6
A	-12	HIS	-	expression tag	UNP W6JQJ6
A	-11	HIS	-	expression tag	UNP W6JQJ6
A	-10	HIS	-	expression tag	UNP W6JQJ6
A	-9	SER	-	expression tag	UNP W6JQJ6
A	-8	SER	-	expression tag	UNP W6JQJ6
A	-7	GLY	-	expression tag	UNP W6JQJ6
A	-6	LEU	-	expression tag	UNP W6JQJ6
A	-5	VAL	-	expression tag	UNP W6JQJ6
A	-4	PRO	-	expression tag	UNP W6JQJ6
A	-3	ARG	-	expression tag	UNP W6JQJ6
A	-2	GLY	-	expression tag	UNP W6JQJ6
A	-1	SER	-	expression tag	UNP W6JQJ6
A	0	HIS	-	expression tag	UNP W6JQJ6
A	473	PHE	SER	conflict	UNP W6JQJ6

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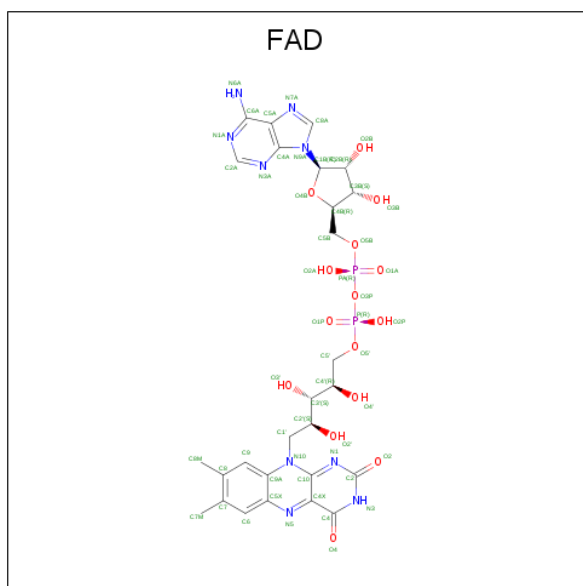
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	expression tag	UNP W6JQJ6
B	-18	GLY	-	expression tag	UNP W6JQJ6
B	-17	SER	-	expression tag	UNP W6JQJ6
B	-16	SER	-	expression tag	UNP W6JQJ6
B	-15	HIS	-	expression tag	UNP W6JQJ6
B	-14	HIS	-	expression tag	UNP W6JQJ6
B	-13	HIS	-	expression tag	UNP W6JQJ6
B	-12	HIS	-	expression tag	UNP W6JQJ6
B	-11	HIS	-	expression tag	UNP W6JQJ6
B	-10	HIS	-	expression tag	UNP W6JQJ6
B	-9	SER	-	expression tag	UNP W6JQJ6
B	-8	SER	-	expression tag	UNP W6JQJ6
B	-7	GLY	-	expression tag	UNP W6JQJ6
B	-6	LEU	-	expression tag	UNP W6JQJ6
B	-5	VAL	-	expression tag	UNP W6JQJ6
B	-4	PRO	-	expression tag	UNP W6JQJ6
B	-3	ARG	-	expression tag	UNP W6JQJ6
B	-2	GLY	-	expression tag	UNP W6JQJ6
B	-1	SER	-	expression tag	UNP W6JQJ6
B	0	HIS	-	expression tag	UNP W6JQJ6
B	473	PHE	SER	conflict	UNP W6JQJ6
C	-19	MET	-	expression tag	UNP W6JQJ6
C	-18	GLY	-	expression tag	UNP W6JQJ6
C	-17	SER	-	expression tag	UNP W6JQJ6
C	-16	SER	-	expression tag	UNP W6JQJ6
C	-15	HIS	-	expression tag	UNP W6JQJ6
C	-14	HIS	-	expression tag	UNP W6JQJ6
C	-13	HIS	-	expression tag	UNP W6JQJ6
C	-12	HIS	-	expression tag	UNP W6JQJ6
C	-11	HIS	-	expression tag	UNP W6JQJ6
C	-10	HIS	-	expression tag	UNP W6JQJ6
C	-9	SER	-	expression tag	UNP W6JQJ6
C	-8	SER	-	expression tag	UNP W6JQJ6
C	-7	GLY	-	expression tag	UNP W6JQJ6
C	-6	LEU	-	expression tag	UNP W6JQJ6
C	-5	VAL	-	expression tag	UNP W6JQJ6
C	-4	PRO	-	expression tag	UNP W6JQJ6
C	-3	ARG	-	expression tag	UNP W6JQJ6
C	-2	GLY	-	expression tag	UNP W6JQJ6
C	-1	SER	-	expression tag	UNP W6JQJ6
C	0	HIS	-	expression tag	UNP W6JQJ6
C	473	PHE	SER	conflict	UNP W6JQJ6

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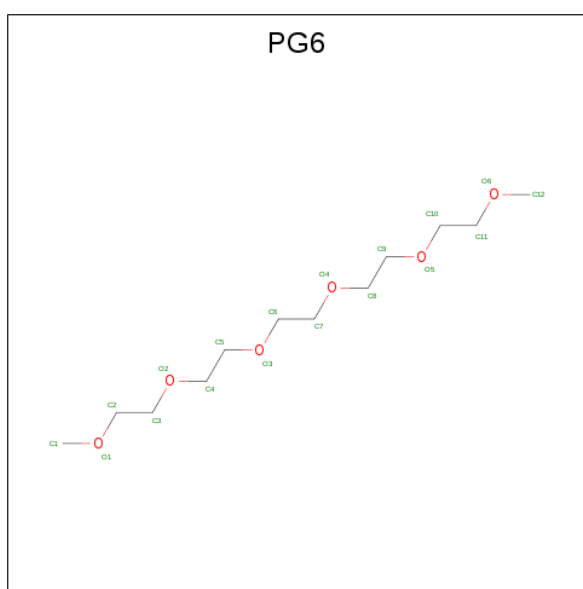
Chain	Residue	Modelled	Actual	Comment	Reference
D	-19	MET	-	expression tag	UNP W6JQJ6
D	-18	GLY	-	expression tag	UNP W6JQJ6
D	-17	SER	-	expression tag	UNP W6JQJ6
D	-16	SER	-	expression tag	UNP W6JQJ6
D	-15	HIS	-	expression tag	UNP W6JQJ6
D	-14	HIS	-	expression tag	UNP W6JQJ6
D	-13	HIS	-	expression tag	UNP W6JQJ6
D	-12	HIS	-	expression tag	UNP W6JQJ6
D	-11	HIS	-	expression tag	UNP W6JQJ6
D	-10	HIS	-	expression tag	UNP W6JQJ6
D	-9	SER	-	expression tag	UNP W6JQJ6
D	-8	SER	-	expression tag	UNP W6JQJ6
D	-7	GLY	-	expression tag	UNP W6JQJ6
D	-6	LEU	-	expression tag	UNP W6JQJ6
D	-5	VAL	-	expression tag	UNP W6JQJ6
D	-4	PRO	-	expression tag	UNP W6JQJ6
D	-3	ARG	-	expression tag	UNP W6JQJ6
D	-2	GLY	-	expression tag	UNP W6JQJ6
D	-1	SER	-	expression tag	UNP W6JQJ6
D	0	HIS	-	expression tag	UNP W6JQJ6
D	473	PHE	SER	conflict	UNP W6JQJ6

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



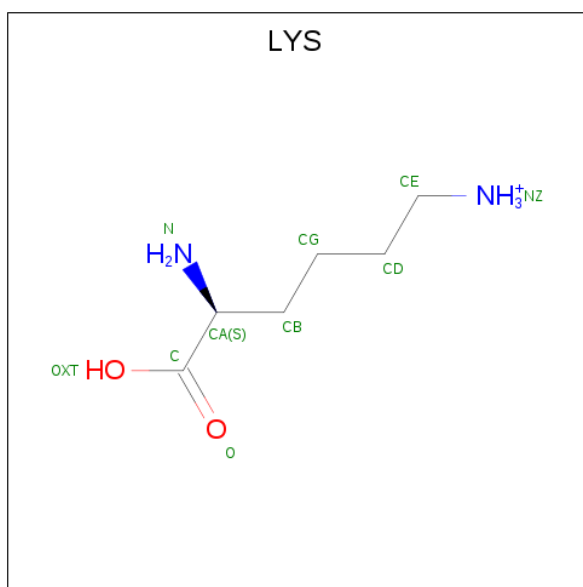
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is 1-(2-METHOXY-ETHOXY)-2-{2-[2-(2-METHOXY-ETHOXY)-ETHOXY]-ETHANE (three-letter code: PG6) (formula: C₁₂H₂₆O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			18	12	6		
3	B	1	Total	C	O	0	0
			18	12	6		
3	C	1	Total	C	O	0	0
			18	12	6		
3	D	1	Total	C	O	0	0
			18	12	6		

- Molecule 4 is LYSINE (three-letter code: LYS) (formula: C₆H₁₅N₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			10	6	2	2		
4	A	1	Total	C	N	O	0	0
			10	6	2	2		
4	B	1	Total	C	N	O	0	0
			10	6	2	2		
4	B	1	Total	C	N	O	0	0
			10	6	2	2		
4	C	1	Total	C	N	O	0	0
			10	6	2	2		
4	C	1	Total	C	N	O	0	0
			10	6	2	2		
4	D	1	Total	C	N	O	0	0
			10	6	2	2		
4	D	1	Total	C	N	O	0	0
			10	6	2	2		

- Molecule 5 is water.

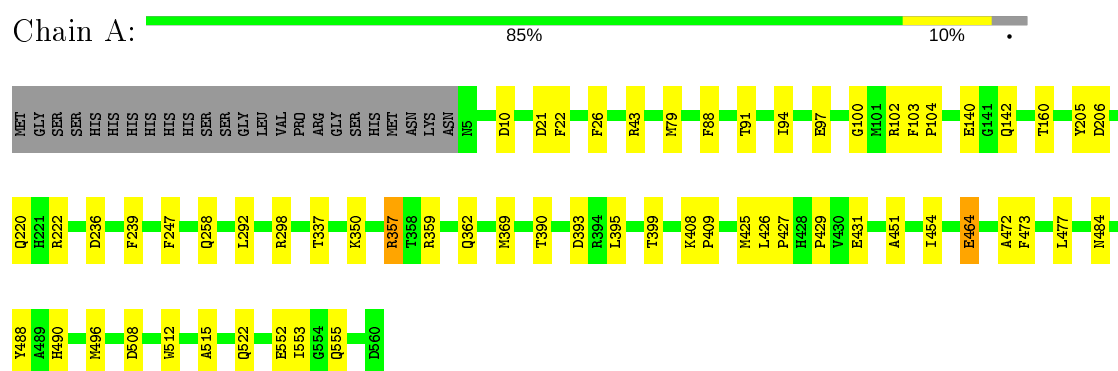
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	272	Total	O	0	0
			272	272		
5	B	260	Total	O	0	0
			260	260		
5	C	236	Total	O	0	0
			236	236		
5	D	258	Total	O	0	0
			258	258		

3 Residue-property plots

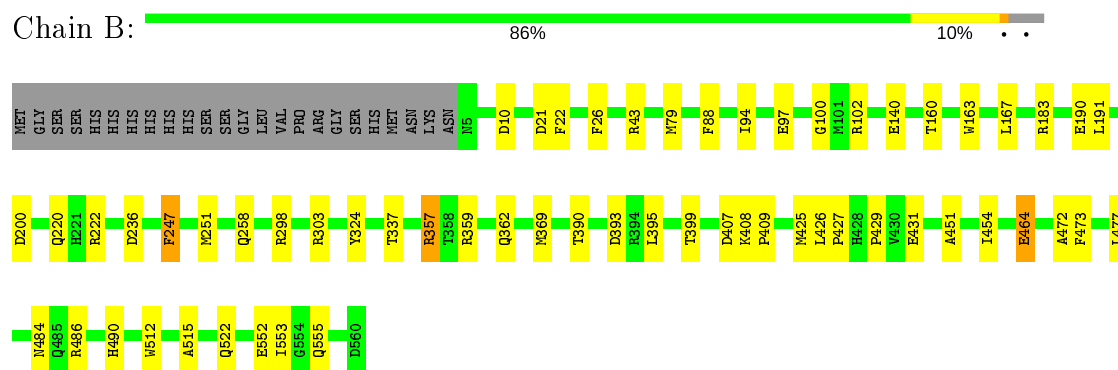
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS failed to run properly.

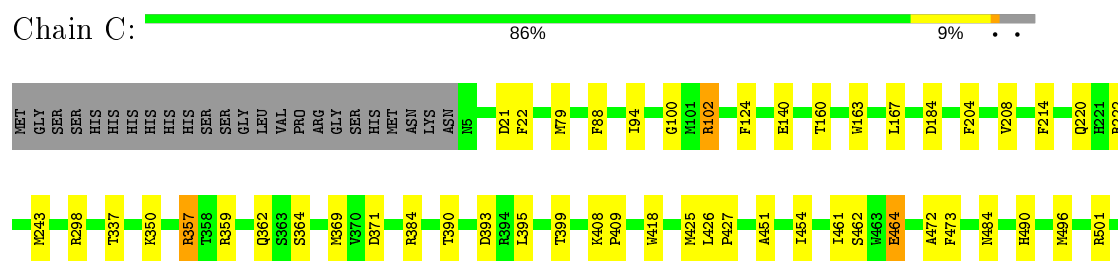
- Molecule 1: L-amino acid oxidase/monooxygenase



- Molecule 1: L-amino acid oxidase/monooxygenase

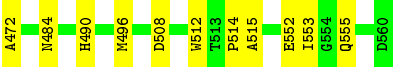
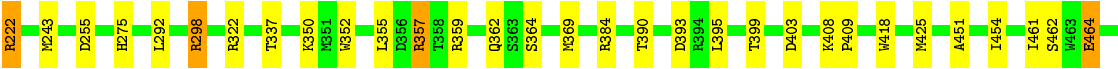
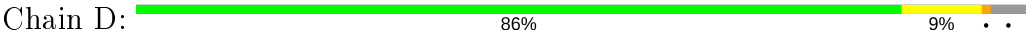


- Molecule 1: L-amino acid oxidase/monooxygenase





- Molecule 1: L-amino acid oxidase/monooxygenase



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	97.07Å 132.29Å 100.96Å 90.00° 108.67° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10	Depositor
% Data completeness (in resolution range)	99.3 (50.00-2.10)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.234 , 0.283	Depositor
Wilson B-factor (Å ²)	17.5	Xtriage
Anisotropy	0.216	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.117 for l,-k,h	Xtriage
Total number of atoms	18833	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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: PG6, 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	0.90	0/4494	0.95	19/6108 (0.3%)
1	B	0.89	1/4483 (0.0%)	0.96	16/6094 (0.3%)
1	C	0.86	1/4483 (0.0%)	0.95	16/6094 (0.3%)
1	D	0.88	1/4483 (0.0%)	0.95	17/6094 (0.3%)
All	All	0.88	3/17943 (0.0%)	0.95	68/24390 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	364	SER	CB-OG	-6.80	1.33	1.42
1	C	364	SER	CB-OG	-5.81	1.34	1.42
1	B	324	TYR	CE1-CZ	-5.14	1.31	1.38

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	357	ARG	NE-CZ-NH2	-12.37	114.11	120.30
1	B	357	ARG	NE-CZ-NH2	-11.96	114.32	120.30
1	D	357	ARG	NE-CZ-NH2	-11.55	114.53	120.30
1	A	298	ARG	NE-CZ-NH2	-11.39	114.61	120.30
1	C	357	ARG	NE-CZ-NH2	-11.38	114.61	120.30
1	B	298	ARG	NE-CZ-NH2	-11.11	114.74	120.30
1	A	222	ARG	NE-CZ-NH2	-10.56	115.02	120.30
1	B	357	ARG	NE-CZ-NH1	10.43	125.52	120.30
1	A	357	ARG	NE-CZ-NH1	10.30	125.45	120.30
1	A	222	ARG	NE-CZ-NH1	10.04	125.32	120.30
1	A	298	ARG	NE-CZ-NH1	9.90	125.25	120.30
1	B	222	ARG	NE-CZ-NH1	9.87	125.24	120.30
1	B	298	ARG	NE-CZ-NH1	9.67	125.13	120.30
1	B	236	ASP	CB-CG-OD1	9.57	126.91	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	222	ARG	NE-CZ-NH1	9.35	124.97	120.30
1	D	222	ARG	NE-CZ-NH1	9.24	124.92	120.30
1	D	222	ARG	NE-CZ-NH2	-9.19	115.70	120.30
1	C	222	ARG	NE-CZ-NH2	-9.11	115.74	120.30
1	B	222	ARG	NE-CZ-NH2	-8.84	115.88	120.30
1	D	384	ARG	NE-CZ-NH1	8.78	124.69	120.30
1	D	298	ARG	NE-CZ-NH1	8.66	124.63	120.30
1	C	357	ARG	NE-CZ-NH1	8.64	124.62	120.30
1	D	357	ARG	NE-CZ-NH1	8.54	124.57	120.30
1	C	298	ARG	NE-CZ-NH2	-8.35	116.12	120.30
1	D	298	ARG	NE-CZ-NH2	-8.07	116.27	120.30
1	B	79	MET	CG-SD-CE	-7.76	87.78	100.20
1	C	371	ASP	CB-CG-OD2	-7.75	111.33	118.30
1	A	508	ASP	CB-CG-OD2	-7.71	111.36	118.30
1	A	236	ASP	CB-CG-OD1	7.71	125.24	118.30
1	D	384	ARG	NE-CZ-NH2	-7.52	116.54	120.30
1	C	298	ARG	NE-CZ-NH1	7.32	123.96	120.30
1	A	79	MET	CG-SD-CE	-7.12	88.81	100.20
1	C	384	ARG	NE-CZ-NH1	6.70	123.65	120.30
1	A	43	ARG	NE-CZ-NH2	6.38	123.49	120.30
1	C	79	MET	CG-SD-CE	-6.35	90.05	100.20
1	D	496	MET	CG-SD-CE	-6.34	90.05	100.20
1	B	43	ARG	NE-CZ-NH2	6.26	123.43	120.30
1	C	496	MET	CG-SD-CE	-6.17	90.33	100.20
1	C	464	GLU	CB-CA-C	-6.09	98.21	110.40
1	D	206	ASP	CB-CG-OD1	6.03	123.73	118.30
1	A	10	ASP	CB-CG-OD1	5.96	123.66	118.30
1	D	464	GLU	CB-CA-C	-5.88	98.63	110.40
1	A	247	PHE	CB-CG-CD2	-5.87	116.69	120.80
1	A	464	GLU	CB-CA-C	-5.85	98.70	110.40
1	B	10	ASP	CB-CG-OD1	5.79	123.51	118.30
1	A	496	MET	CG-SD-CE	-5.59	91.25	100.20
1	A	298	ARG	CG-CD-NE	-5.55	100.14	111.80
1	D	102	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	B	464	GLU	CB-CA-C	-5.43	99.54	110.40
1	A	292	LEU	CB-CG-CD2	5.42	120.22	111.00
1	D	403	ASP	CB-CG-OD1	5.40	123.16	118.30
1	C	359	ARG	CG-CD-NE	5.35	123.03	111.80
1	C	102	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	C	501	ARG	NE-CZ-NH2	-5.31	117.65	120.30
1	D	359	ARG	CG-CD-NE	5.30	122.94	111.80
1	C	184	ASP	CB-CG-OD1	5.26	123.03	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	292	LEU	CB-CG-CD1	5.25	119.93	111.00
1	B	303	ARG	NE-CZ-NH2	-5.25	117.67	120.30
1	D	508	ASP	CB-CG-OD2	-5.24	113.59	118.30
1	A	508	ASP	CB-CG-OD1	5.23	123.00	118.30
1	B	486	ARG	NE-CZ-NH1	-5.21	117.70	120.30
1	A	206	ASP	CB-CG-OD1	5.20	122.98	118.30
1	B	247	PHE	CB-CG-CD2	-5.20	117.16	120.80
1	B	298	ARG	CG-CD-NE	-5.16	100.96	111.80
1	B	200	ASP	CB-CG-OD1	5.12	122.91	118.30
1	C	384	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	A	357	ARG	CG-CD-NE	-5.07	101.16	111.80
1	D	355	LEU	CB-CG-CD2	5.04	119.57	111.00

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	4369	0	4223	51	0
1	B	4358	0	4211	56	0
1	C	4358	0	4211	47	0
1	D	4358	0	4211	55	0
2	A	53	0	31	3	0
2	B	53	0	31	4	0
2	C	53	0	31	2	0
2	D	53	0	31	2	0
3	A	18	0	26	3	0
3	B	18	0	26	2	0
3	C	18	0	26	2	0
3	D	18	0	26	2	0
4	A	20	0	24	1	0
4	B	20	0	24	3	0
4	C	20	0	24	2	0
4	D	20	0	24	3	0
5	A	272	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	260	0	0	10	0
5	C	236	0	0	4	0
5	D	258	0	0	8	0
All	All	18833	0	17180	205	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 6.

All (205) 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:555:GLN:N	1:A:555:GLN:OE1	1.75	1.20
1:D:555:GLN:OE1	1:D:555:GLN:N	1.75	1.18
1:C:555:GLN:N	1:C:555:GLN:OE1	1.80	1.15
1:B:555:GLN:OE1	1:B:555:GLN:N	1.80	1.14
1:D:220:GLN:HE22	3:D:602:PG6:H92	1.20	1.03
1:D:160:THR:HG22	5:D:950:HOH:O	1.63	0.95
1:B:22:PHE:HB2	1:B:555:GLN:HE22	1.34	0.92
1:B:22:PHE:HB2	1:B:555:GLN:NE2	1.91	0.85
1:A:22:PHE:HB2	1:A:555:GLN:HE22	1.43	0.83
1:D:362:GLN:HG3	1:D:464:GLU:HG3	1.60	0.83
1:D:220:GLN:NE2	3:D:602:PG6:H92	1.92	0.83
1:C:22:PHE:HB2	1:C:555:GLN:HE22	1.44	0.81
1:B:362:GLN:HG3	1:B:464:GLU:CG	2.11	0.80
1:C:362:GLN:HG3	1:C:464:GLU:HG3	1.61	0.80
1:D:22:PHE:HB2	1:D:555:GLN:HE22	1.46	0.80
1:C:94:ILE:HG21	1:C:369:MET:HE2	1.63	0.79
1:A:22:PHE:HB2	1:A:555:GLN:NE2	1.97	0.78
1:A:362:GLN:HG3	1:A:464:GLU:CG	2.13	0.78
1:A:362:GLN:HG3	1:A:464:GLU:HG3	1.65	0.76
1:B:362:GLN:HG3	1:B:464:GLU:HG3	1.66	0.76
1:C:512:TRP:CZ2	1:C:555:GLN:HG2	2.20	0.76
1:C:94:ILE:HG21	1:C:369:MET:CE	2.15	0.76
1:D:275:HIS:HD2	5:D:939:HOH:O	1.69	0.76
1:D:362:GLN:HG3	1:D:464:GLU:CG	2.16	0.76
1:A:512:TRP:CZ2	1:A:555:GLN:HG2	2.22	0.75
1:B:512:TRP:CZ2	1:B:555:GLN:HG2	2.22	0.75
1:B:191:LEU:HG	5:B:843:HOH:O	1.86	0.74
1:C:362:GLN:HG3	1:C:464:GLU:CG	2.16	0.74
1:B:357:ARG:NH2	1:D:393:ASP:O	2.21	0.74
1:D:94:ILE:HG21	1:D:369:MET:HE2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:555:GLN:CD	1:D:555:GLN:H	1.89	0.74
1:D:512:TRP:CZ2	1:D:555:GLN:HG2	2.22	0.73
1:D:88:PHE:HB2	1:D:369:MET:HE1	1.70	0.73
1:C:22:PHE:HB2	1:C:555:GLN:NE2	2.02	0.73
1:C:88:PHE:HB2	1:C:369:MET:HE1	1.69	0.73
4:B:603:LYS:HE2	5:B:898:HOH:O	1.87	0.72
1:C:512:TRP:HZ2	1:C:555:GLN:HG2	1.54	0.72
1:C:160:THR:HG22	5:C:927:HOH:O	1.88	0.71
1:D:555:GLN:CD	1:D:555:GLN:N	2.44	0.71
1:D:94:ILE:HG21	1:D:369:MET:CE	2.19	0.71
1:D:22:PHE:HB2	1:D:555:GLN:NE2	2.05	0.70
1:D:512:TRP:HZ2	1:D:555:GLN:HG2	1.55	0.69
1:B:337:THR:HG1	4:B:604:LYS:N	1.91	0.69
1:C:555:GLN:N	1:C:555:GLN:CD	2.46	0.68
1:B:395:LEU:HD13	1:B:425:MET:HE1	1.75	0.68
1:A:393:ASP:O	1:C:357:ARG:NH2	2.27	0.67
1:B:512:TRP:HZ2	1:B:555:GLN:HG2	1.60	0.67
1:B:555:GLN:CD	1:B:555:GLN:N	2.48	0.67
1:B:393:ASP:O	1:D:357:ARG:NH2	2.27	0.66
1:B:94:ILE:HG21	1:B:369:MET:HE2	1.77	0.66
1:A:512:TRP:HZ2	1:A:555:GLN:HG2	1.59	0.66
1:A:337:THR:HG1	4:A:604:LYS:N	1.95	0.65
1:A:88:PHE:HB2	1:A:369:MET:HE1	1.79	0.65
1:A:94:ILE:HG21	1:A:369:MET:CE	2.27	0.64
1:D:514:PRO:O	1:D:515:ALA:HB3	1.97	0.64
1:D:337:THR:HG1	4:D:604:LYS:N	1.96	0.63
1:B:94:ILE:HG21	1:B:369:MET:CE	2.29	0.63
1:A:555:GLN:N	1:A:555:GLN:CD	2.49	0.63
1:B:362:GLN:HG3	1:B:464:GLU:HG2	1.80	0.62
1:A:357:ARG:NH2	1:C:393:ASP:O	2.32	0.62
1:D:395:LEU:HD13	1:D:425:MET:CE	2.30	0.62
1:C:395:LEU:HD13	1:C:425:MET:CE	2.30	0.62
1:A:94:ILE:HG21	1:A:369:MET:HE2	1.82	0.61
1:A:395:LEU:HD13	1:A:425:MET:HE1	1.83	0.61
1:C:337:THR:HG1	4:C:604:LYS:N	2.00	0.60
1:C:514:PRO:O	1:C:515:ALA:HB3	2.02	0.60
1:B:359:ARG:NH1	1:B:477:LEU:HD13	2.17	0.59
1:A:359:ARG:NH1	1:A:477:LEU:HD13	2.17	0.59
1:A:21:ASP:HB3	1:A:555:GLN:HG3	1.83	0.59
1:D:222:ARG:NH2	5:D:704:HOH:O	2.36	0.59
1:B:100:GLY:HA2	2:B:601:FAD:C4X	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:395:LEU:HD13	1:D:425:MET:HE1	1.85	0.58
1:B:160:THR:HG22	5:B:949:HOH:O	2.04	0.56
3:C:602:PG6:H52	5:C:887:HOH:O	2.04	0.56
1:B:102:ARG:HD2	1:B:258:GLN:OE1	2.06	0.56
1:A:362:GLN:HG3	1:A:464:GLU:HG2	1.85	0.56
1:B:21:ASP:HB3	1:B:555:GLN:HG3	1.87	0.56
1:A:102:ARG:HD2	1:A:258:GLN:OE1	2.06	0.56
1:D:472:ALA:HB1	2:D:601:FAD:HM83	1.88	0.56
1:B:140:GLU:OE1	1:D:350:LYS:HD3	2.06	0.55
1:A:160:THR:HG22	5:A:956:HOH:O	2.06	0.54
1:B:88:PHE:HB2	1:B:369:MET:HE1	1.88	0.54
1:B:362:GLN:CG	1:B:464:GLU:HG2	2.38	0.54
1:A:362:GLN:CG	1:A:464:GLU:CG	2.86	0.53
1:C:552:GLU:HG3	1:C:553:ILE:HG23	1.89	0.53
1:A:100:GLY:HA2	2:A:601:FAD:C4X	2.39	0.53
1:A:140:GLU:OE1	1:C:350:LYS:HD3	2.08	0.53
1:D:322:ARG:HD2	5:D:737:HOH:O	2.08	0.53
1:A:472:ALA:HB1	2:A:601:FAD:HM83	1.89	0.53
1:B:395:LEU:HD13	1:B:425:MET:CE	2.39	0.53
1:A:395:LEU:HD13	1:A:425:MET:CE	2.38	0.53
1:A:142:GLN:NE2	3:A:602:PG6:H52	2.24	0.53
1:C:395:LEU:HD13	1:C:425:MET:HE1	1.89	0.53
1:C:490:HIS:HE1	5:C:765:HOH:O	1.92	0.53
1:B:484:ASN:HD21	1:B:512:TRP:HA	1.74	0.53
1:A:362:GLN:CG	1:A:464:GLU:HG2	2.39	0.52
1:D:298:ARG:NH1	5:D:711:HOH:O	2.42	0.52
1:D:94:ILE:CG2	1:D:369:MET:CE	2.88	0.52
1:B:183:ARG:NH1	5:B:707:HOH:O	2.43	0.52
1:B:190:GLU:HB3	5:B:843:HOH:O	2.10	0.52
1:B:425:MET:CE	5:B:883:HOH:O	2.58	0.52
1:C:94:ILE:CG2	1:C:369:MET:CE	2.87	0.51
1:C:362:GLN:CG	1:C:464:GLU:CG	2.87	0.51
1:C:21:ASP:HB3	1:C:555:GLN:HG3	1.93	0.51
1:D:408:LYS:HB3	1:D:409:PRO:HD2	1.93	0.51
1:D:484:ASN:HD21	1:D:512:TRP:HA	1.76	0.51
1:A:552:GLU:HG3	1:A:553:ILE:HG23	1.92	0.51
1:B:552:GLU:HG3	1:B:553:ILE:HG23	1.92	0.50
1:D:512:TRP:CZ2	1:D:555:GLN:CG	2.92	0.50
1:C:512:TRP:CZ2	1:C:555:GLN:CG	2.94	0.50
1:D:418:TRP:CZ2	4:D:603:LYS:HG2	2.47	0.50
1:C:484:ASN:HB3	1:C:512:TRP:CZ3	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:21:ASP:HB3	1:D:555:GLN:HG3	1.94	0.50
1:D:100:GLY:HA2	2:D:601:FAD:C4X	2.42	0.50
1:C:408:LYS:HB3	1:C:409:PRO:HD2	1.94	0.49
1:B:220:GLN:HE22	3:B:602:PG6:H42	1.77	0.49
1:B:220:GLN:HE22	3:B:602:PG6:C4	2.26	0.49
1:B:362:GLN:CG	1:B:464:GLU:CG	2.86	0.49
1:B:247:PHE:HA	5:B:915:HOH:O	2.13	0.49
1:D:362:GLN:CG	1:D:464:GLU:CG	2.88	0.49
1:D:514:PRO:O	1:D:515:ALA:CB	2.61	0.48
1:A:26:PHE:CD1	1:A:522:GLN:HG2	2.49	0.48
1:A:484:ASN:HD21	1:A:512:TRP:HA	1.78	0.48
1:C:484:ASN:HD21	1:C:512:TRP:HA	1.77	0.48
1:A:512:TRP:CZ2	1:A:555:GLN:CG	2.97	0.48
1:A:220:GLN:NE2	3:A:602:PG6:H61	2.29	0.48
1:B:472:ALA:HB1	2:B:601:FAD:HM83	1.95	0.47
1:C:451:ALA:HA	1:C:454:ILE:HD12	1.96	0.47
1:D:552:GLU:CG	1:D:553:ILE:HG23	2.44	0.47
1:C:362:GLN:HG3	1:C:464:GLU:HG2	1.95	0.47
1:C:552:GLU:CG	1:C:553:ILE:HG23	2.44	0.47
1:D:362:GLN:HG3	1:D:464:GLU:HG2	1.94	0.47
1:B:425:MET:HE3	5:B:883:HOH:O	2.14	0.47
1:D:552:GLU:HG3	1:D:553:ILE:HG23	1.96	0.47
1:C:390:THR:HB	1:C:399:THR:HB	1.97	0.47
1:B:484:ASN:HB3	1:B:512:TRP:CZ3	2.50	0.47
1:B:100:GLY:HA2	2:B:601:FAD:N5	2.30	0.47
1:C:362:GLN:CG	1:C:464:GLU:HG2	2.45	0.47
1:C:461:ILE:HG13	1:C:462:SER:N	2.30	0.47
1:A:408:LYS:HB3	1:A:409:PRO:HD2	1.97	0.46
1:B:473:PHE:CG	1:B:515:ALA:HB2	2.51	0.46
1:B:512:TRP:CZ2	1:B:555:GLN:CG	2.97	0.45
1:D:362:GLN:CG	1:D:464:GLU:HG2	2.46	0.45
1:B:390:THR:HB	1:B:399:THR:HB	1.98	0.45
1:D:461:ILE:HG13	1:D:462:SER:N	2.31	0.45
1:A:484:ASN:HB3	1:A:512:TRP:CZ3	2.52	0.45
1:B:26:PHE:CD1	1:B:522:GLN:HG2	2.51	0.45
1:B:408:LYS:HB3	1:B:409:PRO:HD2	1.98	0.45
1:B:429:PRO:HB2	1:B:431:GLU:OE1	2.17	0.45
1:A:94:ILE:CG2	1:A:369:MET:CE	2.94	0.45
1:C:490:HIS:HD2	5:C:890:HOH:O	1.98	0.45
1:C:418:TRP:CZ2	4:C:603:LYS:HG2	2.51	0.45
1:B:451:ALA:HA	1:B:454:ILE:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:TRP:CZ2	1:C:167:LEU:HD11	2.52	0.45
1:A:390:THR:HB	1:A:399:THR:HB	1.97	0.44
1:C:204:PHE:HA	1:C:243:MET:SD	2.58	0.44
1:D:390:THR:HB	1:D:399:THR:HB	1.99	0.44
1:D:204:PHE:HA	1:D:243:MET:SD	2.58	0.44
1:C:472:ALA:HB1	2:C:601:FAD:HM83	1.99	0.44
1:C:100:GLY:HA2	2:C:601:FAD:C4X	2.48	0.44
1:D:199:TRP:O	1:D:200:ASP:C	2.56	0.44
1:A:425:MET:CE	5:A:911:HOH:O	2.66	0.44
1:A:490:HIS:HE1	5:A:743:HOH:O	2.01	0.44
1:A:426:LEU:HB3	1:A:427:PRO:HD3	2.00	0.43
1:A:103:PHE:HA	1:A:104:PRO:HD2	1.93	0.43
1:B:552:GLU:CG	1:B:553:ILE:HG23	2.48	0.43
1:A:473:PHE:CG	1:A:515:ALA:HB2	2.54	0.43
1:A:490:HIS:HD2	5:A:908:HOH:O	2.00	0.43
1:B:251:MET:CE	5:B:915:HOH:O	2.66	0.43
1:D:451:ALA:HA	1:D:454:ILE:HD12	2.01	0.43
1:B:472:ALA:O	2:B:601:FAD:HM81	2.19	0.42
1:A:205:TYR:HB2	1:A:239:PHE:HB3	2.01	0.42
1:B:407:ASP:OD1	1:B:408:LYS:HG3	2.20	0.42
1:B:97:GLU:HA	1:B:97:GLU:OE1	2.19	0.42
1:C:514:PRO:O	1:C:515:ALA:CB	2.65	0.42
1:D:255:ASP:HB2	5:D:803:HOH:O	2.19	0.42
1:A:552:GLU:CG	1:A:553:ILE:HG23	2.49	0.42
1:D:163:TRP:CZ2	1:D:167:LEU:HD11	2.55	0.42
1:B:426:LEU:HB3	1:B:427:PRO:HD3	2.02	0.42
1:A:429:PRO:HB2	1:A:431:GLU:OE1	2.19	0.42
1:B:163:TRP:CZ2	1:B:167:LEU:HD11	2.54	0.42
1:D:275:HIS:CD2	5:D:939:HOH:O	2.56	0.42
1:B:94:ILE:CG2	1:B:369:MET:CE	2.95	0.42
1:B:490:HIS:HE1	5:B:727:HOH:O	2.02	0.42
1:A:97:GLU:HA	1:A:97:GLU:OE1	2.20	0.42
1:B:357:ARG:HD3	1:B:357:ARG:HA	1.81	0.41
1:A:451:ALA:HA	1:A:454:ILE:HD12	2.02	0.41
3:A:602:PG6:H11	5:A:803:HOH:O	2.20	0.41
1:D:490:HIS:HD2	5:D:911:HOH:O	2.02	0.41
1:D:102:ARG:HB3	1:D:124:PHE:CD1	2.55	0.41
1:A:350:LYS:HD3	1:C:140:GLU:OE1	2.20	0.41
1:D:352:TRP:HB3	4:D:604:LYS:HD3	2.03	0.41
1:A:472:ALA:O	2:A:601:FAD:HM81	2.21	0.41
1:B:515:ALA:HB1	4:B:603:LYS:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:484:ASN:HB3	1:D:512:TRP:CZ3	2.54	0.41
1:C:208:VAL:O	1:C:214:PHE:HB2	2.21	0.41
1:D:208:VAL:O	1:D:214:PHE:HB2	2.21	0.41
1:C:473:PHE:CG	1:C:515:ALA:HB2	2.56	0.41
1:C:220:GLN:NE2	3:C:602:PG6:H71	2.36	0.41
1:A:91:THR:HG21	1:A:369:MET:CE	2.51	0.40
1:C:426:LEU:HB3	1:C:427:PRO:HD3	2.03	0.40
1:D:22:PHE:O	1:D:24:PHE:N	2.49	0.40
1:A:488:TYR:CE2	1:A:555:GLN:NE2	2.89	0.40
1:C:102:ARG:HB3	1:C:124:PHE:CD1	2.56	0.40
1:D:357:ARG:HD3	1:D:357:ARG:HA	1.88	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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

16 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	PG6	A	602	-	17,17,17	0.52	0	16,16,16	1.05	0
2	FAD	A	601	-	51,58,58	2.10	9 (17%)	60,89,89	2.18	16 (26%)
4	LYS	B	603	-	5,9,9	0.49	0	4,10,10	0.71	0
2	FAD	C	601	-	51,58,58	2.04	12 (23%)	60,89,89	2.20	21 (35%)
4	LYS	A	603	-	5,9,9	0.78	0	4,10,10	0.76	0
3	PG6	D	602	-	17,17,17	0.95	0	16,16,16	1.22	1 (6%)
2	FAD	B	601	-	51,58,58	2.23	9 (17%)	60,89,89	1.92	14 (23%)
2	FAD	D	601	-	51,58,58	1.93	7 (13%)	60,89,89	2.22	18 (30%)
4	LYS	D	603	-	5,9,9	0.45	0	4,10,10	0.55	0
3	PG6	C	602	-	17,17,17	0.47	0	16,16,16	0.50	0
3	PG6	B	602	-	17,17,17	0.50	0	16,16,16	0.79	0
4	LYS	D	604	-	5,9,9	0.89	0	4,10,10	1.17	0
4	LYS	A	604	-	5,9,9	0.96	0	4,10,10	0.83	0
4	LYS	B	604	-	5,9,9	0.97	0	4,10,10	0.51	0
4	LYS	C	604	-	5,9,9	0.93	0	4,10,10	1.06	0
4	LYS	C	603	-	5,9,9	0.79	0	4,10,10	0.62	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
3	PG6	A	602	-	-	5/15/15/15	-
2	FAD	A	601	-	-	6/30/50/50	0/6/6/6
4	LYS	B	603	-	-	1/5/9/9	-
2	FAD	C	601	-	-	8/30/50/50	0/6/6/6
4	LYS	A	603	-	-	1/5/9/9	-
3	PG6	D	602	-	-	7/15/15/15	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	B	601	-	-	6/30/50/50	0/6/6/6
2	FAD	D	601	-	-	9/30/50/50	0/6/6/6
4	LYS	D	603	-	-	0/5/9/9	-
3	PG6	C	602	-	-	6/15/15/15	-
3	PG6	B	602	-	-	7/15/15/15	-
4	LYS	D	604	-	-	0/5/9/9	-
4	LYS	A	604	-	-	0/5/9/9	-
4	LYS	B	604	-	-	1/5/9/9	-
4	LYS	C	604	-	-	0/5/9/9	-
4	LYS	C	603	-	-	0/5/9/9	-

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	FAD	C4X-C10	12.08	1.50	1.38
2	A	601	FAD	C4X-C10	11.17	1.50	1.38
2	D	601	FAD	C4X-C10	10.17	1.49	1.38
2	C	601	FAD	C4X-C10	9.85	1.48	1.38
2	A	601	FAD	C10-N1	3.68	1.38	1.33
2	B	601	FAD	C5X-N5	3.68	1.41	1.35
2	C	601	FAD	C9A-C5X	3.63	1.49	1.42
2	C	601	FAD	C8-C7	3.60	1.49	1.40
2	B	601	FAD	C9A-C5X	3.55	1.49	1.42
2	A	601	FAD	C5X-N5	3.46	1.41	1.35
2	B	601	FAD	C10-N1	3.37	1.37	1.33
2	D	601	FAD	C9A-C5X	3.34	1.49	1.42
2	D	601	FAD	C8-C7	3.14	1.48	1.40
2	C	601	FAD	C5A-C4A	3.04	1.49	1.40
2	B	601	FAD	C4-C4X	2.96	1.46	1.41
2	A	601	FAD	C9A-C5X	2.95	1.48	1.42
2	A	601	FAD	C4A-N3A	2.93	1.39	1.35
2	C	601	FAD	O4'-C4'	2.68	1.49	1.43
2	B	601	FAD	C8-C7	2.67	1.47	1.40
2	C	601	FAD	C1'-N10	-2.66	1.45	1.48
2	C	601	FAD	C4-C4X	2.59	1.45	1.41
2	D	601	FAD	C8A-N7A	2.57	1.39	1.34
2	C	601	FAD	O4B-C4B	-2.54	1.39	1.45
2	D	601	FAD	C2B-C1B	-2.53	1.49	1.53
2	A	601	FAD	C4-C4X	2.51	1.45	1.41
2	B	601	FAD	C1'-N10	-2.41	1.45	1.48
2	A	601	FAD	C8-C7	2.41	1.46	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	FAD	C9A-N10	2.38	1.41	1.38
2	C	601	FAD	C9A-N10	2.33	1.41	1.38
2	A	601	FAD	C2A-N1A	2.33	1.38	1.33
2	B	601	FAD	C2A-N3A	2.33	1.35	1.32
2	B	601	FAD	C5A-C4A	2.32	1.47	1.40
2	D	601	FAD	C5A-C4A	2.23	1.46	1.40
2	C	601	FAD	C8A-N7A	2.09	1.38	1.34
2	C	601	FAD	C4A-N3A	-2.09	1.32	1.35
2	A	601	FAD	C5A-C4A	2.06	1.46	1.40
2	C	601	FAD	C2A-N3A	2.05	1.35	1.32

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	FAD	C4-N3-C2	9.68	123.31	115.14
2	C	601	FAD	C4-N3-C2	8.02	121.92	115.14
2	D	601	FAD	C4-N3-C2	7.72	121.66	115.14
2	B	601	FAD	C4-N3-C2	6.99	121.05	115.14
2	D	601	FAD	C1'-N10-C9A	6.33	123.27	118.29
2	A	601	FAD	C5'-C4'-C3'	-5.33	101.90	112.20
2	B	601	FAD	C5'-C4'-C3'	-4.97	102.60	112.20
2	D	601	FAD	C5X-C9A-N10	4.71	121.13	117.72
2	C	601	FAD	C1'-N10-C9A	4.59	121.91	118.29
2	A	601	FAD	N3A-C2A-N1A	-4.30	121.96	128.68
2	C	601	FAD	C4X-C4-N3	-4.24	117.64	123.43
2	C	601	FAD	C10-C4X-N5	4.16	124.13	121.26
2	D	601	FAD	C4X-C4-N3	-4.11	117.81	123.43
2	D	601	FAD	C1B-N9A-C4A	-3.96	119.68	126.64
2	A	601	FAD	C10-C4X-N5	3.89	123.95	121.26
2	D	601	FAD	C9A-N10-C10	-3.88	116.83	121.91
2	B	601	FAD	C4A-C5A-N7A	-3.76	105.48	109.40
2	D	601	FAD	C10-C4X-N5	3.75	123.85	121.26
2	B	601	FAD	N3A-C2A-N1A	-3.64	122.99	128.68
2	B	601	FAD	C10-C4X-N5	3.55	123.72	121.26
2	C	601	FAD	C5'-C4'-C3'	-3.54	105.37	112.20
2	D	601	FAD	N3A-C2A-N1A	-3.49	123.22	128.68
2	B	601	FAD	C1'-N10-C9A	3.35	120.93	118.29
2	A	601	FAD	C4-C4X-C10	-3.35	117.73	119.95
2	C	601	FAD	N3A-C2A-N1A	-3.34	123.46	128.68
2	C	601	FAD	C5X-C9A-N10	3.23	120.06	117.72
2	A	601	FAD	C4X-C4-N3	-3.23	119.02	123.43
2	A	601	FAD	C4A-C5A-N7A	-3.19	106.07	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	FAD	O4'-C4'-C3'	3.17	116.81	109.10
2	C	601	FAD	C4A-C5A-N7A	-3.09	106.18	109.40
2	A	601	FAD	O4'-C4'-C3'	3.09	116.60	109.10
2	B	601	FAD	O4'-C4'-C3'	3.06	116.54	109.10
2	C	601	FAD	C9A-N10-C10	-3.06	117.90	121.91
2	C	601	FAD	O4B-C4B-C3B	2.95	110.96	105.11
2	B	601	FAD	O2'-C2'-C3'	2.94	116.24	109.10
2	A	601	FAD	O5'-C5'-C4'	-2.91	101.60	109.36
2	C	601	FAD	C6-C5X-C9A	2.89	122.84	119.05
2	D	601	FAD	O2'-C2'-C3'	2.78	115.86	109.10
2	B	601	FAD	C4X-C4-N3	-2.73	119.70	123.43
2	C	601	FAD	C1B-N9A-C4A	-2.73	121.85	126.64
2	C	601	FAD	C2A-N1A-C6A	2.68	123.33	118.75
2	A	601	FAD	O4B-C1B-C2B	-2.68	103.02	106.93
2	A	601	FAD	C1'-N10-C9A	2.67	120.39	118.29
2	A	601	FAD	O2'-C2'-C3'	2.65	115.53	109.10
2	D	601	FAD	O4B-C4B-C3B	2.62	110.30	105.11
2	B	601	FAD	C4-C4X-C10	-2.60	118.23	119.95
2	C	601	FAD	C6-C5X-N5	-2.59	116.20	119.05
2	B	601	FAD	O5'-C5'-C4'	-2.57	102.51	109.36
2	C	601	FAD	O2A-PA-O1A	2.54	124.80	112.24
2	B	601	FAD	O4B-C1B-C2B	-2.48	103.30	106.93
2	D	601	FAD	C4X-N5-C5X	2.48	119.25	116.77
2	D	601	FAD	C6-C5X-C9A	2.45	122.27	119.05
3	D	602	PG6	O5-C9-C8	2.42	121.29	110.39
2	D	601	FAD	C4-C4X-C10	-2.41	118.36	119.95
2	C	601	FAD	C4X-C10-N10	-2.40	117.84	120.30
2	C	601	FAD	O2'-C2'-C3'	2.38	114.89	109.10
2	B	601	FAD	C9A-N10-C10	-2.36	118.82	121.91
2	D	601	FAD	C4A-C5A-N7A	-2.35	106.95	109.40
2	D	601	FAD	O4'-C4'-C3'	2.33	114.77	109.10
2	D	601	FAD	O2A-PA-O1A	2.27	123.48	112.24
2	C	601	FAD	C4X-N5-C5X	2.27	119.04	116.77
2	A	601	FAD	C1'-N10-C10	2.24	120.42	118.41
2	C	601	FAD	C4-C4X-C10	-2.21	118.49	119.95
2	A	601	FAD	C4X-C10-N10	-2.21	118.03	120.30
2	D	601	FAD	C2A-N1A-C6A	2.21	122.53	118.75
2	B	601	FAD	O3'-C3'-C4'	-2.20	103.49	108.81
2	A	601	FAD	C9A-N10-C10	-2.15	119.09	121.91
2	A	601	FAD	C2A-N1A-C6A	2.11	122.37	118.75
2	D	601	FAD	C5'-C4'-C3'	-2.07	108.21	112.20
2	C	601	FAD	C7-C6-C5X	-2.01	118.37	121.22

There are no chirality outliers.

All (57) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	FAD	PA-O3P-P-O5'
2	C	601	FAD	C5B-O5B-PA-O2A
2	B	601	FAD	PA-O3P-P-O5'
2	D	601	FAD	C5B-O5B-PA-O2A
3	D	602	PG6	C7-C6-O3-C5
2	C	601	FAD	C2'-C3'-C4'-O4'
2	B	601	FAD	C2'-C3'-C4'-O4'
2	D	601	FAD	C2'-C3'-C4'-O4'
3	D	602	PG6	O1-C2-C3-O2
2	D	601	FAD	C2'-C3'-C4'-C5'
3	D	602	PG6	O4-C8-C9-O5
3	C	602	PG6	O5-C10-C11-O6
3	C	602	PG6	O2-C4-C5-O3
3	A	602	PG6	O3-C6-C7-O4
2	C	601	FAD	O3'-C3'-C4'-O4'
2	B	601	FAD	O3'-C3'-C4'-O4'
2	A	601	FAD	C2'-C3'-C4'-O4'
3	B	602	PG6	O2-C4-C5-O3
2	A	601	FAD	O3'-C3'-C4'-C5'
2	B	601	FAD	O3'-C3'-C4'-C5'
2	D	601	FAD	O3'-C3'-C4'-C5'
2	A	601	FAD	C2'-C3'-C4'-C5'
2	C	601	FAD	C2'-C3'-C4'-C5'
2	B	601	FAD	C2'-C3'-C4'-C5'
4	B	603	LYS	CE-CD-CG-CB
4	B	604	LYS	CE-CD-CG-CB
2	A	601	FAD	O3'-C3'-C4'-O4'
3	A	602	PG6	O4-C8-C9-O5
3	B	602	PG6	O1-C2-C3-O2
2	D	601	FAD	O3'-C3'-C4'-O4'
3	B	602	PG6	C3-C2-O1-C1
3	C	602	PG6	O3-C6-C7-O4
2	C	601	FAD	PA-O3P-P-O5'
2	D	601	FAD	PA-O3P-P-O5'
3	A	602	PG6	C7-C6-O3-C5
3	C	602	PG6	C6-C7-O4-C8
2	C	601	FAD	C5B-O5B-PA-O3P
2	D	601	FAD	C5B-O5B-PA-O3P
2	C	601	FAD	O3'-C3'-C4'-C5'
3	C	602	PG6	C7-C6-O3-C5

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Mol	Chain	Res	Type	Atoms
3	B	602	PG6	O4-C8-C9-O5
3	D	602	PG6	C4-C5-O3-C6
3	A	602	PG6	C5-C4-O2-C3
3	B	602	PG6	C8-C9-O5-C10
2	D	601	FAD	O4B-C4B-C5B-O5B
3	C	602	PG6	C8-C9-O5-C10
2	A	601	FAD	O4B-C4B-C5B-O5B
3	B	602	PG6	C10-C11-O6-C12
3	D	602	PG6	O2-C4-C5-O3
3	B	602	PG6	O5-C10-C11-O6
2	C	601	FAD	O4B-C4B-C5B-O5B
2	B	601	FAD	O4B-C4B-C5B-O5B
3	A	602	PG6	C4-C5-O3-C6
2	D	601	FAD	C5B-O5B-PA-O1A
3	D	602	PG6	C6-C7-O4-C8
4	A	603	LYS	CE-CD-CG-CB
3	D	602	PG6	O3-C6-C7-O4

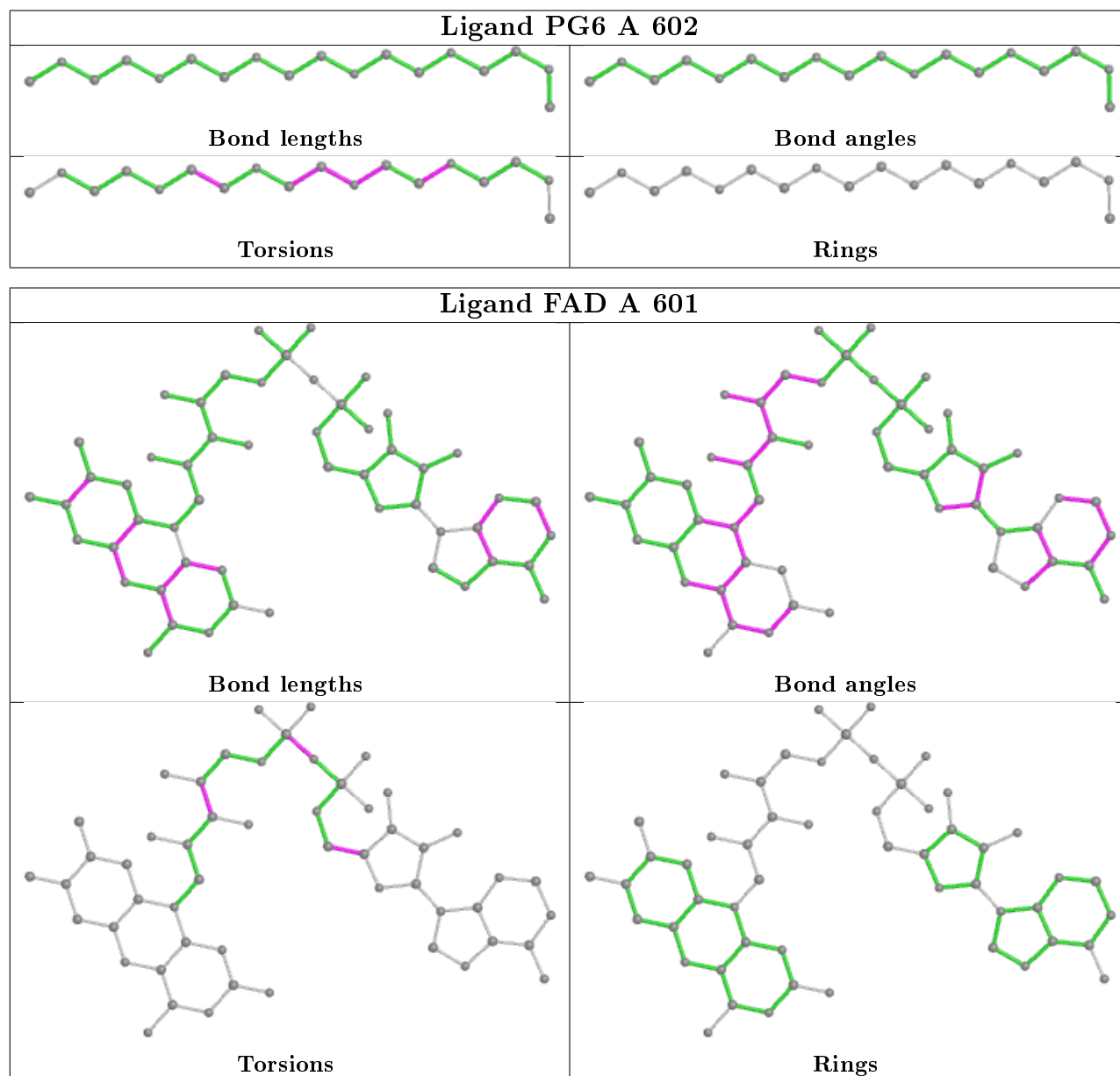
There are no ring outliers.

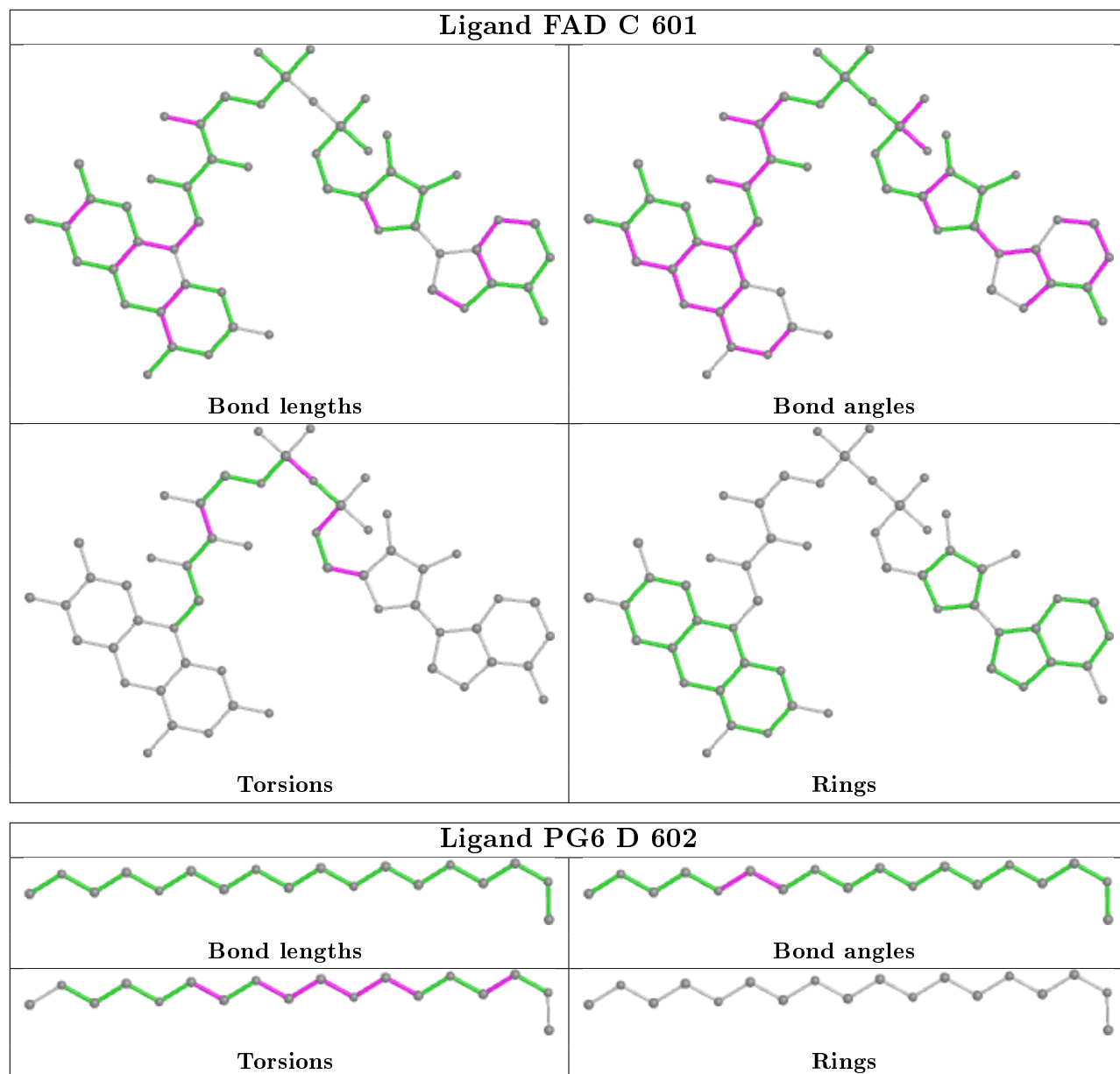
15 monomers are involved in 29 short contacts:

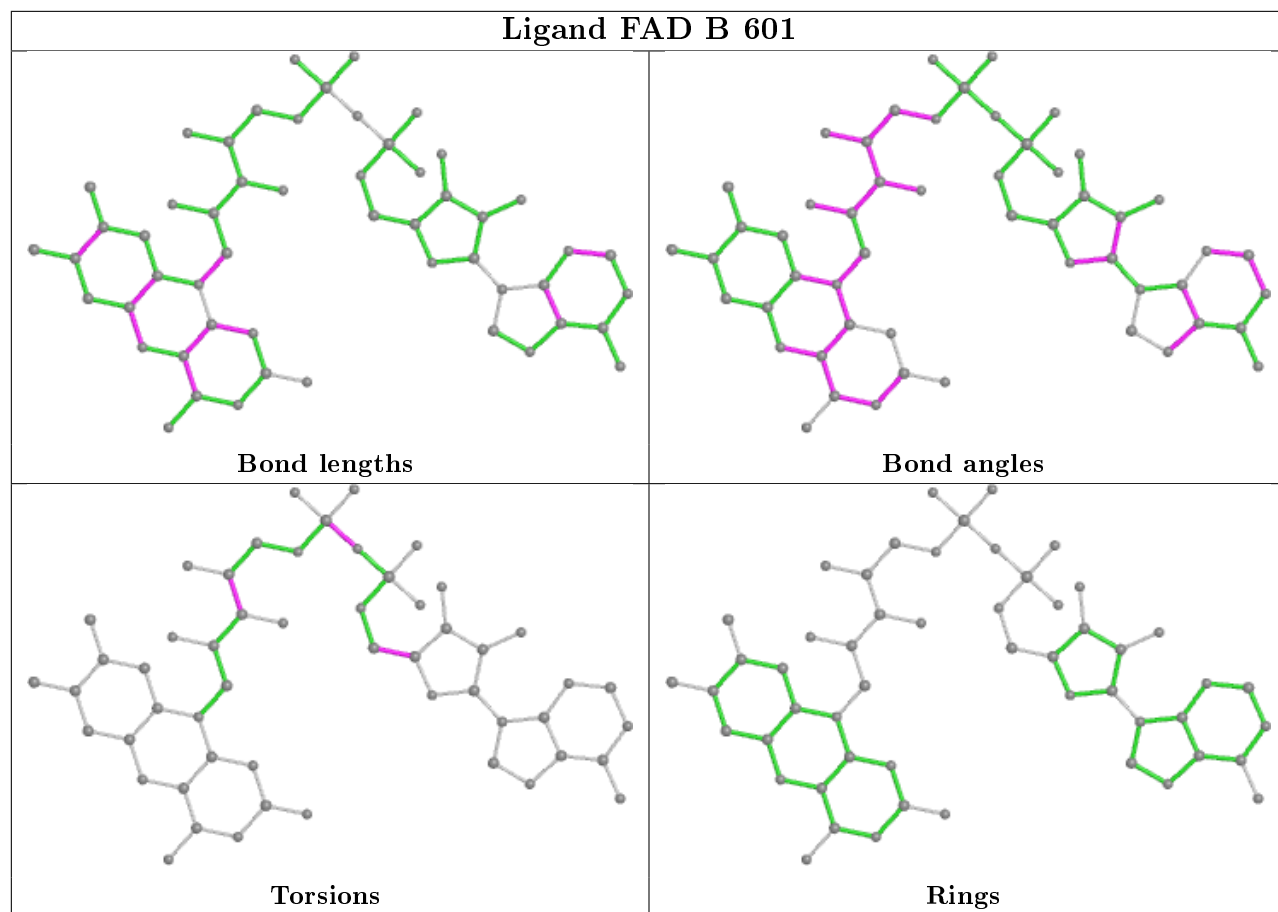
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	PG6	3	0
2	A	601	FAD	3	0
4	B	603	LYS	2	0
2	C	601	FAD	2	0
3	D	602	PG6	2	0
2	B	601	FAD	4	0
2	D	601	FAD	2	0
4	D	603	LYS	1	0
3	C	602	PG6	2	0
3	B	602	PG6	2	0
4	D	604	LYS	2	0
4	A	604	LYS	1	0
4	B	604	LYS	1	0
4	C	604	LYS	1	0
4	C	603	LYS	1	0

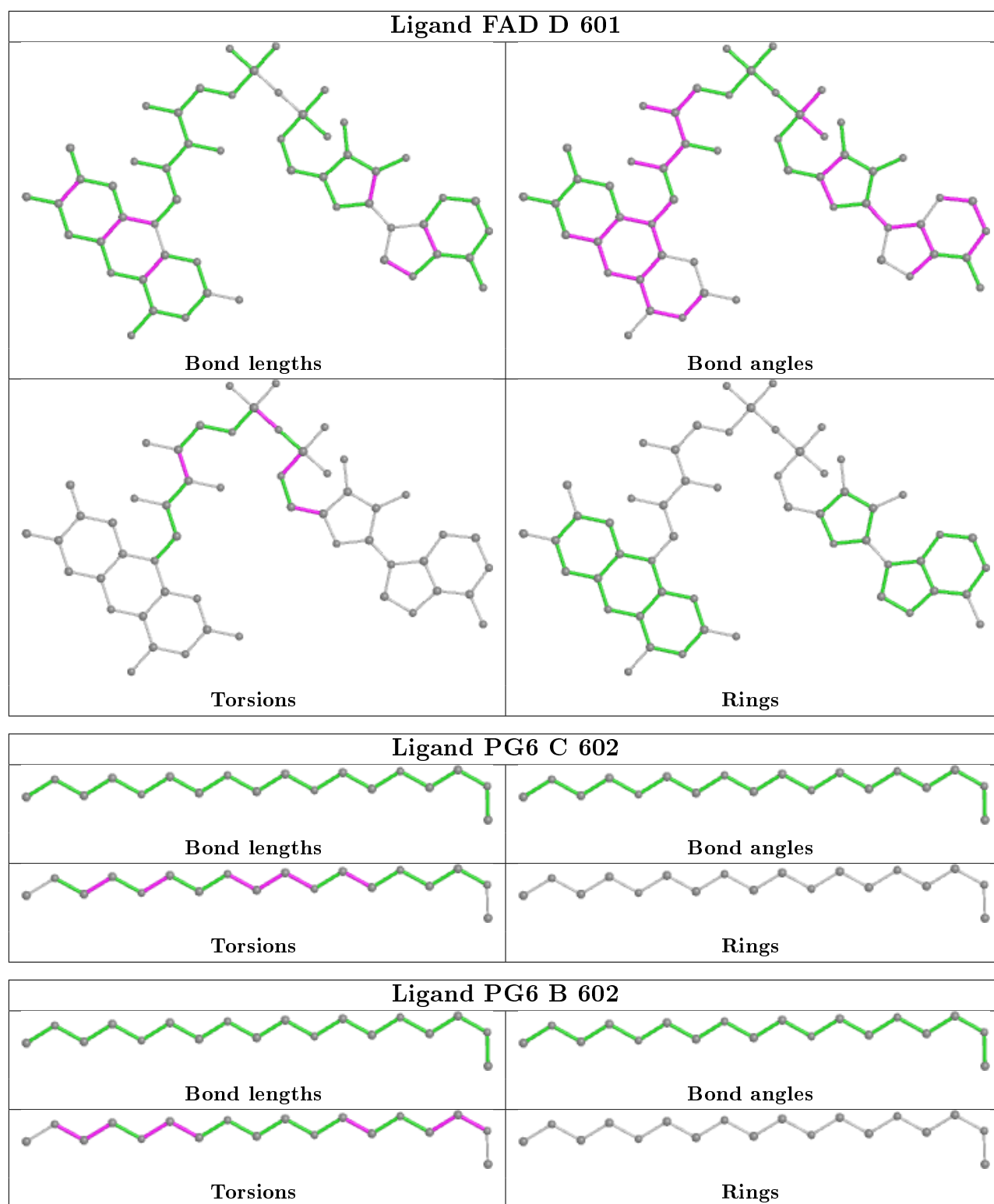
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section is therefore empty.

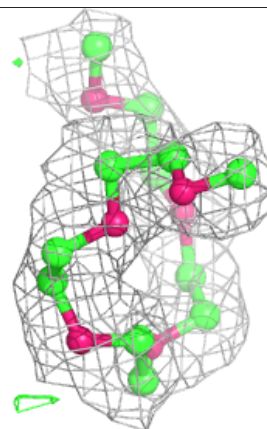
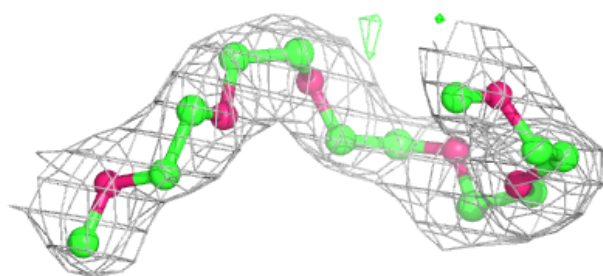
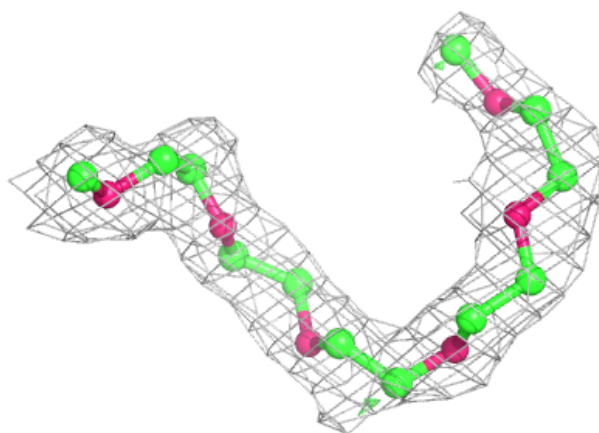
6.4 Ligands ⓘ

EDS failed to run properly - this section is therefore empty.

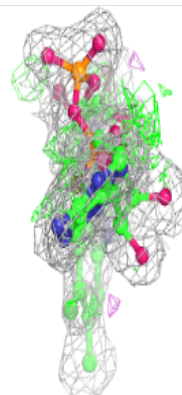
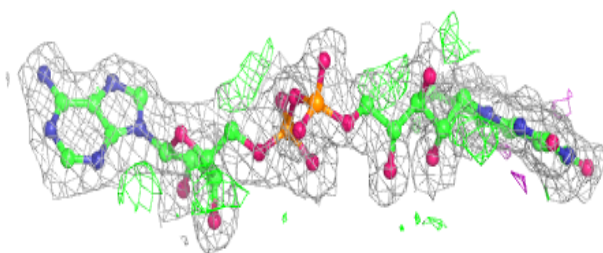
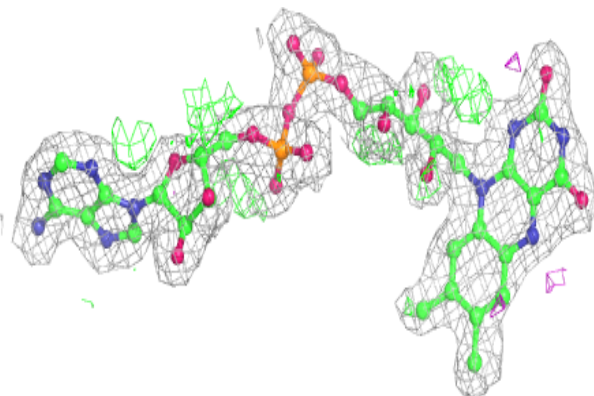
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PG6 A 602:

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

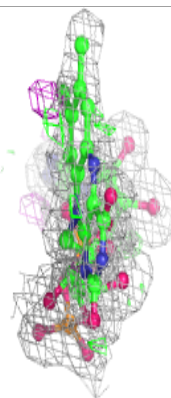
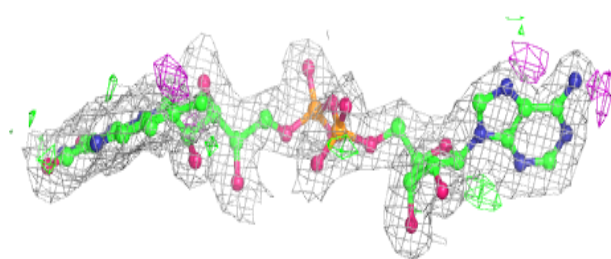
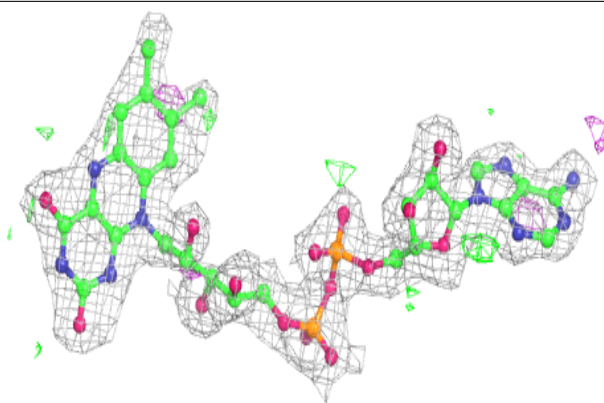
**Electron density around FAD A 601:**

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

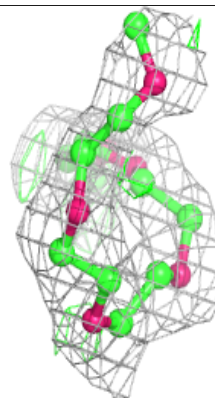
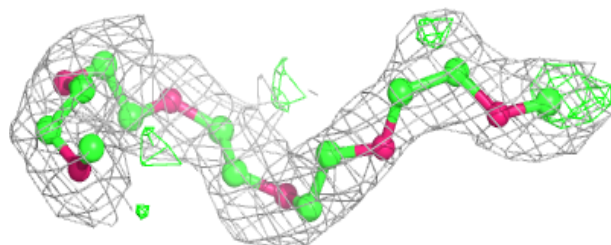
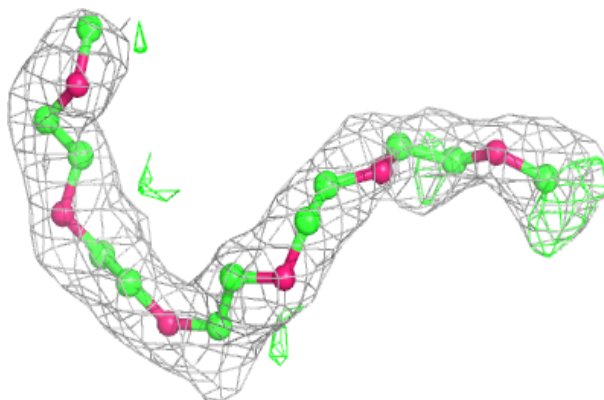


Electron density around FAD C 601:

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

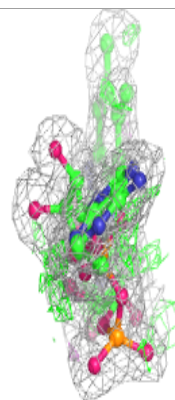
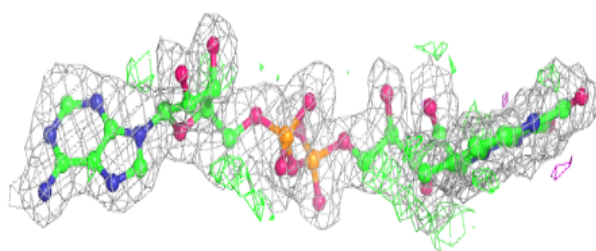
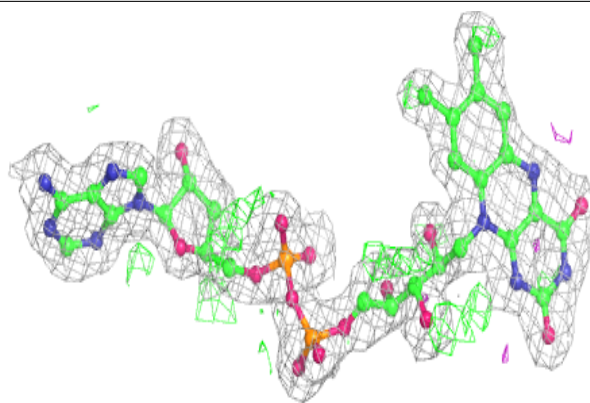
**Electron density around PG6 D 602:**

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

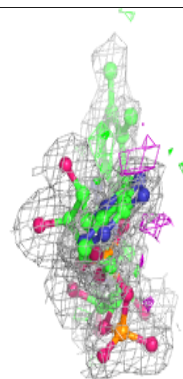
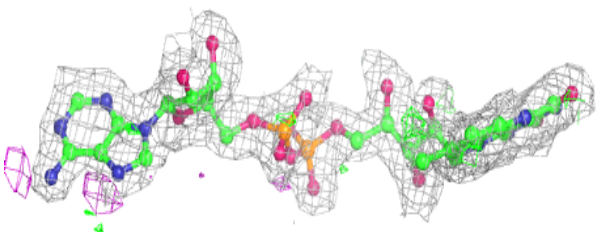
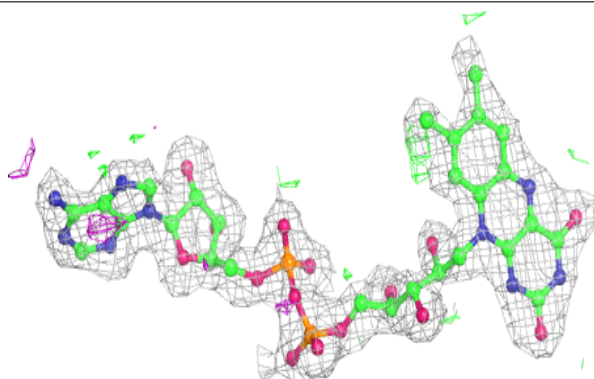


Electron density around FAD B 601:

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

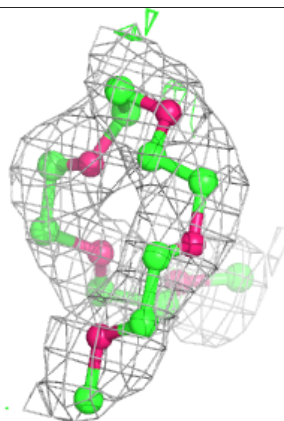
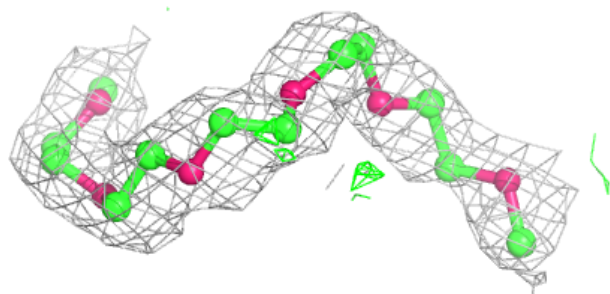
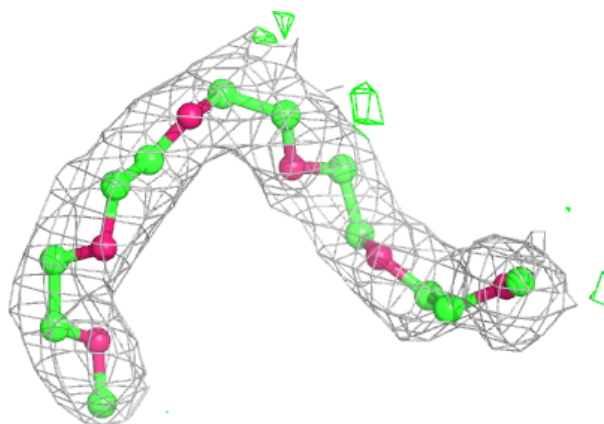
**Electron density around FAD D 601:**

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

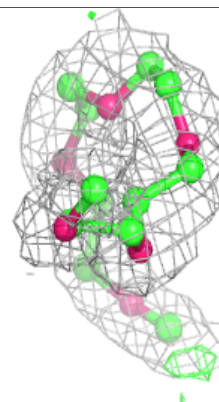
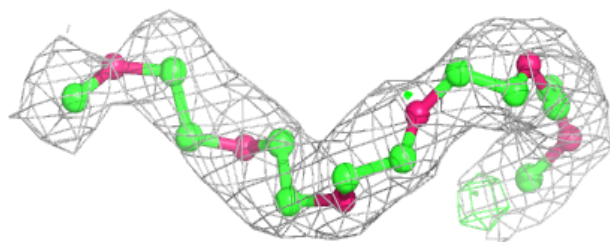
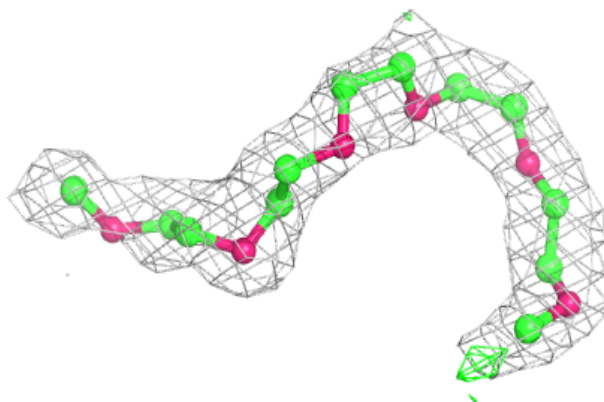


Electron density around PG6 C 602:

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

**Electron density around PG6 B 602:**

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



6.5 Other polymers

EDS failed to run properly - this section is therefore empty.