



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 22, 2023 – 06:35 PM JST

PDB ID : 7X7J
Title : Ancestral L-Lys oxidase (AncLLysO-2) L-Lys binding form
Authors : Motoyama, T.; Ishida, C.; Hasebe, F.; Ito, S.; Nakano, S.
Deposited on : 2022-03-09
Resolution : 1.40 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (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

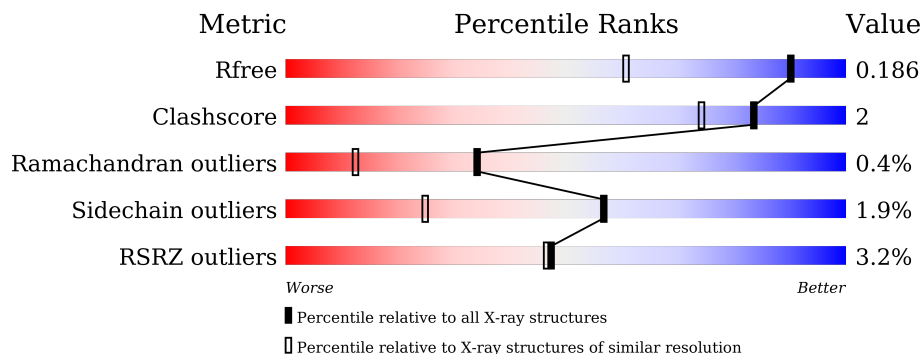
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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	593	
1	B	593	

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	LYS	A	602	-	-	-	X
3	LYS	B	602	-	-	X	X

2 Entry composition i

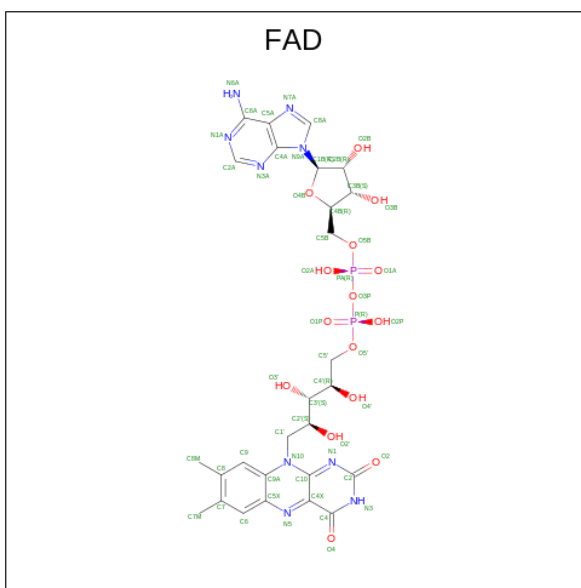
There are 4 unique types of molecules in this entry. The entry contains 10771 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FAD dependent enzyme.

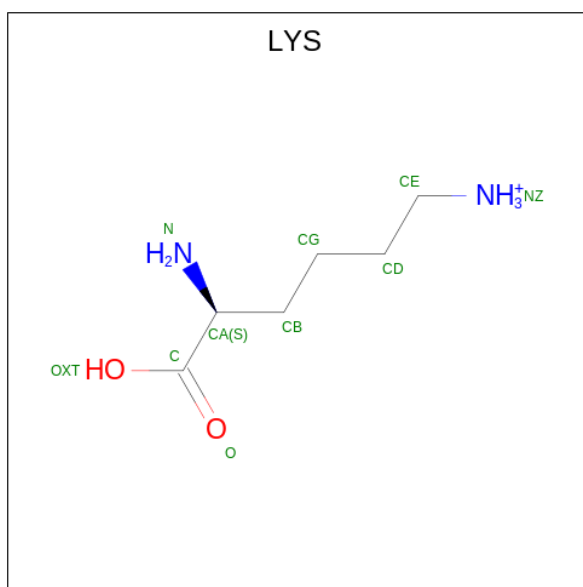
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	583	Total	C	N	O	S	0	0	0
			4512	2879	748	868	17			
1	B	583	Total	C	N	O	S	0	0	0
			4512	2879	748	868	17			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
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		

- Molecule 3 is LYSINE (three-letter code: LYS) (formula: $C_6H_{15}N_2O_2$) (labeled as "Ligand of Interest" by depositor).



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

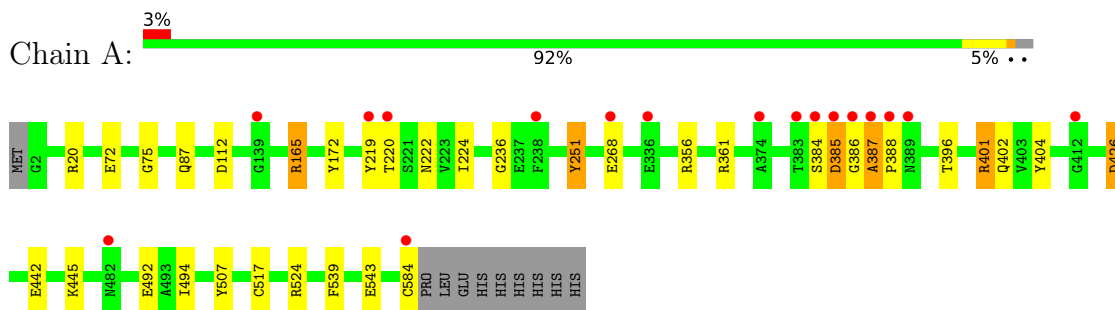
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	798	798	798	0	0
4	B	823	823	823	0	0

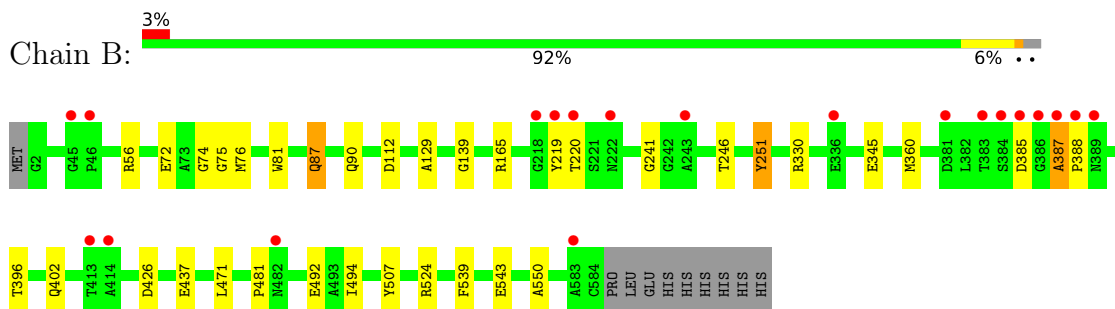
3 Residue-property plots [i](#)

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: FAD dependent enzyme



- Molecule 1: FAD dependent enzyme



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.41Å 77.40Å 93.41Å 90.00° 104.36° 90.00°	Depositor
Resolution (Å)	45.30 – 1.40 45.25 – 1.39	Depositor EDS
% Data completeness (in resolution range)	99.1 (45.30-1.40) 99.1 (45.25-1.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 1.39Å)	Xtrriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.158 , 0.183 0.162 , 0.186	Depositor DCC
R_{free} test set	10663 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	14.9	Xtrriage
Anisotropy	0.070	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10771	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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

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	0.81	3/4643 (0.1%)	0.98	10/6358 (0.2%)
1	B	0.80	4/4643 (0.1%)	0.93	4/6358 (0.1%)
All	All	0.80	7/9286 (0.1%)	0.95	14/12716 (0.1%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	543	GLU	CD-OE2	-11.16	1.13	1.25
1	A	492	GLU	CD-OE2	-7.38	1.17	1.25
1	B	72	GLU	CD-OE2	-7.10	1.17	1.25
1	B	492	GLU	CD-OE2	-7.00	1.18	1.25
1	B	437	GLU	CD-OE1	-5.67	1.19	1.25
1	A	72	GLU	CD-OE2	-5.50	1.19	1.25
1	B	139	GLY	C-O	5.33	1.32	1.23

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	TYR	CB-CG-CD2	-8.88	115.67	121.00
1	B	251	TYR	CB-CG-CD2	-7.57	116.46	121.00
1	A	251	TYR	CB-CG-CD2	-7.21	116.68	121.00
1	A	20	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	B	330	ARG	NE-CZ-NH1	-6.63	116.99	120.30
1	A	172	TYR	CB-CG-CD1	6.31	124.79	121.00
1	A	361	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	B	251	TYR	CB-CG-CD1	5.52	124.31	121.00
1	A	356	ARG	NE-CZ-NH1	-5.48	117.56	120.30
1	B	165	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	A	165	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	A	401	ARG	NE-CZ-NH1	-5.35	117.62	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	251	TYR	CB-CG-CD1	5.15	124.09	121.00
1	A	361	ARG	NE-CZ-NH2	-5.06	117.77	120.30

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	4512	0	4246	21	0
1	B	4512	0	4246	22	0
2	A	53	0	31	3	0
2	B	53	0	31	5	0
3	A	10	0	12	4	0
3	B	10	0	12	6	0
4	A	798	0	0	2	0
4	B	823	0	0	4	0
All	All	10771	0	8578	43	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 2.

All (43) 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:B:507:TYR:OH	3:B:602:LYS:HA	1.59	1.01
1:A:387:ALA:HB3	1:A:388:PRO:HD3	1.55	0.86
1:B:75:GLY:HA2	2:B:601:FAD:N5	1.94	0.81
1:B:75:GLY:HA2	2:B:601:FAD:C5X	2.13	0.78
1:A:442:GLU:OE1	1:A:445:LYS:HE2	1.89	0.73
1:A:112:ASP:HB2	1:A:385:ASP:OD1	1.89	0.72
1:A:387:ALA:CB	1:A:388:PRO:HD3	2.22	0.69
1:A:75:GLY:HA2	2:A:601:FAD:N5	2.13	0.63
1:B:75:GLY:HA2	2:B:601:FAD:C4X	2.29	0.63
1:A:75:GLY:HA2	2:A:601:FAD:C5X	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:THR:HG22	3:A:602:LYS:HB3	1.84	0.59
1:B:507:TYR:HH	3:B:602:LYS:HA	1.69	0.54
1:B:524:ARG:O	1:B:539:PHE:HA	2.07	0.54
1:A:524:ARG:O	1:A:539:PHE:HA	2.08	0.53
1:A:401:ARG:O	1:A:402:GLN:HG2	2.09	0.53
1:A:387:ALA:HB3	1:A:388:PRO:CD	2.34	0.52
1:B:345:GLU:HG2	4:B:1265:HOH:O	2.08	0.52
1:B:387:ALA:HB3	1:B:388:PRO:HD3	1.93	0.51
1:A:507:TYR:CZ	3:A:602:LYS:HD2	2.47	0.50
1:B:550:ALA:HB1	3:B:602:LYS:HD3	1.94	0.49
1:B:75:GLY:CA	2:B:601:FAD:C4X	2.91	0.49
1:B:471:LEU:HD11	1:B:481:PRO:HB3	1.93	0.49
1:A:75:GLY:HA2	2:A:601:FAD:C4X	2.45	0.47
1:A:219:TYR:HB2	1:A:404:TYR:OH	2.15	0.46
1:A:507:TYR:HH	3:A:602:LYS:N	2.13	0.46
1:B:220:THR:HB	3:B:602:LYS:HE3	1.98	0.45
1:A:387:ALA:CB	1:A:388:PRO:CD	2.93	0.45
1:B:81:TRP:HB2	1:B:90:GLN:HA	2.00	0.44
1:B:220:THR:HG22	3:B:602:LYS:HG3	1.99	0.44
1:B:76:MET:H	2:B:601:FAD:C4	2.30	0.43
1:B:129:ALA:CB	4:B:944:HOH:O	2.66	0.43
1:B:112:ASP:HB2	1:B:385:ASP:OD2	2.18	0.42
1:A:386:GLY:O	1:A:388:PRO:HD2	2.19	0.42
1:B:246:THR:CG2	4:B:738:HOH:O	2.68	0.42
1:A:426:ASP:HB3	4:A:1023:HOH:O	2.20	0.42
1:A:87:GLN:HE21	1:A:87:GLN:HB2	1.64	0.42
1:A:236:GLY:HA3	4:A:1257:HOH:O	2.19	0.41
1:B:56:ARG:O	1:B:74:GLY:HA3	2.21	0.41
1:A:222:ASN:OD1	1:A:224:ILE:HG12	2.21	0.41
1:B:220:THR:CB	3:B:602:LYS:HE3	2.51	0.41
1:B:87:GLN:NE2	1:B:241:GLY:H	2.18	0.40
1:B:246:THR:HG21	4:B:738:HOH:O	2.20	0.40
1:A:507:TYR:CE2	3:A:602:LYS:CD	3.04	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	581/593 (98%)	567 (98%)	11 (2%)	3 (0%)	29	9
1	B	581/593 (98%)	567 (98%)	12 (2%)	2 (0%)	41	18
All	All	1162/1186 (98%)	1134 (98%)	23 (2%)	5 (0%)	34	12

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	387	ALA
1	A	385	ASP
1	B	387	ALA
1	A	426	ASP
1	B	426	ASP

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	464/474 (98%)	456 (98%)	8 (2%)	60	31
1	B	464/474 (98%)	456 (98%)	8 (2%)	60	31
All	All	928/948 (98%)	912 (98%)	16 (2%)	57	31

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	165	ARG

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Mol	Chain	Res	Type
1	A	251	TYR
1	A	268	GLU
1	A	384	SER
1	A	396	THR
1	A	494	ILE
1	A	517	CYS
1	A	584	CYS
1	B	87	GLN
1	B	219	TYR
1	B	251	TYR
1	B	360	MET
1	B	396	THR
1	B	402	GLN
1	B	494	ILE
1	B	543	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	389	ASN
1	A	428	GLN
1	B	87	GLN
1	B	389	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

4 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	LYS	B	602	-	8,9,9	1.33	2 (25%)	9,10,10	1.08	1 (11%)
2	FAD	A	601	-	53,58,58	1.13	3 (5%)	68,89,89	0.87	1 (1%)
3	LYS	A	602	-	8,9,9	1.08	1 (12%)	9,10,10	1.88	2 (22%)
2	FAD	B	601	-	53,58,58	0.97	2 (3%)	68,89,89	0.97	4 (5%)

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	LYS	B	602	-	-	5/9/9/9	-
2	FAD	A	601	-	-	2/30/50/50	0/6/6/6
3	LYS	A	602	-	-	7/9/9/9	-
2	FAD	B	601	-	-	2/30/50/50	0/6/6/6

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	FAD	C1'-C2'	-4.05	1.46	1.52
2	B	601	FAD	C1'-C2'	-3.61	1.47	1.52
3	A	602	LYS	OXT-C	-2.91	1.21	1.30
2	A	601	FAD	O2'-C2'	-2.68	1.37	1.43
3	B	602	LYS	OXT-C	-2.56	1.22	1.30
3	B	602	LYS	O-C	2.24	1.28	1.22
2	B	601	FAD	P-O2P	-2.15	1.45	1.55
2	A	601	FAD	P-O2P	-2.06	1.45	1.55

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	LYS	OXT-C-O	-4.79	113.22	124.09
2	A	601	FAD	C5A-C6A-N6A	3.10	125.07	120.35
3	B	602	LYS	OXT-C-O	-2.80	117.74	124.09
2	B	601	FAD	C4-N3-C2	-2.56	120.92	125.64
2	B	601	FAD	C5A-C6A-N6A	2.52	124.18	120.35
2	B	601	FAD	O4B-C1B-C2B	-2.50	103.28	106.93
3	A	602	LYS	OXT-C-CA	2.41	121.60	113.38
2	B	601	FAD	O2P-P-O1P	2.21	123.18	112.24

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	FAD	PA-O3P-P-O5'
2	B	601	FAD	PA-O3P-P-O5'
3	A	602	LYS	O-C-CA-N
3	A	602	LYS	C-CA-CB-CG
3	B	602	LYS	O-C-CA-N
3	A	602	LYS	OXT-C-CA-N
3	B	602	LYS	OXT-C-CA-N
3	B	602	LYS	CA-CB-CG-CD
3	A	602	LYS	CG-CD-CE-NZ
3	B	602	LYS	C-CA-CB-CG
3	B	602	LYS	N-CA-CB-CG
3	A	602	LYS	O-C-CA-CB
3	A	602	LYS	CA-CB-CG-CD
3	A	602	LYS	OXT-C-CA-CB
2	A	601	FAD	O4B-C4B-C5B-O5B
2	B	601	FAD	O4B-C4B-C5B-O5B

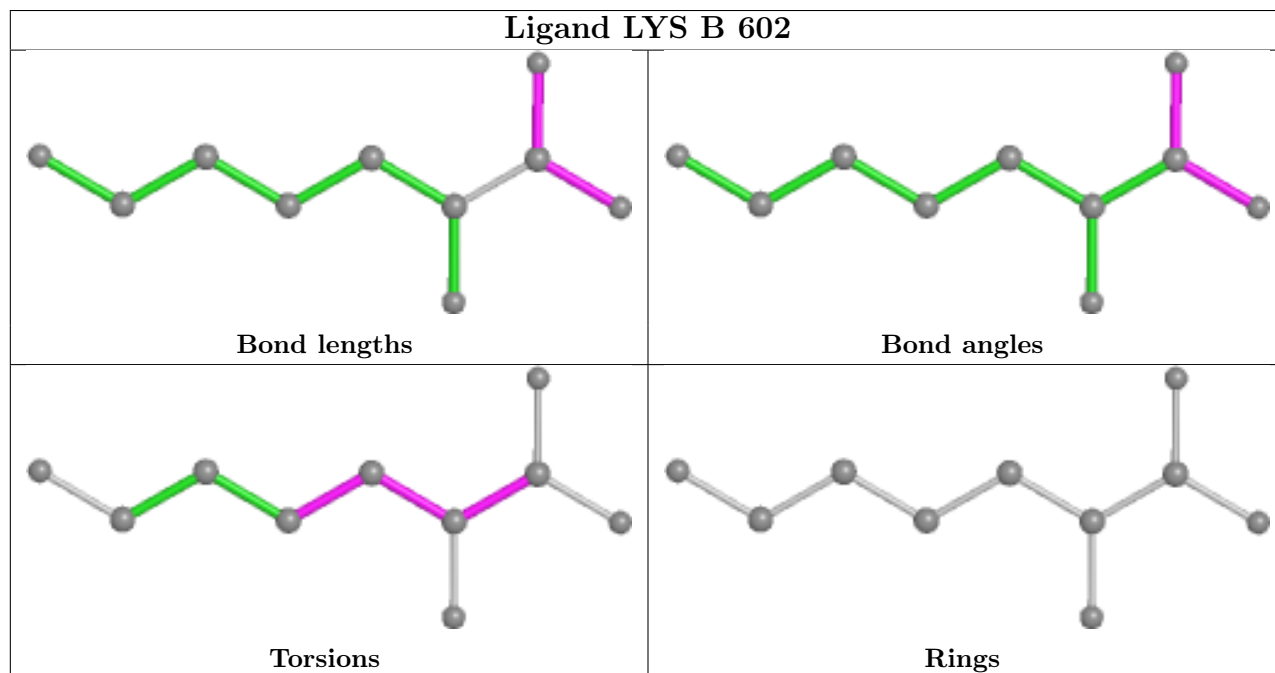
There are no ring outliers.

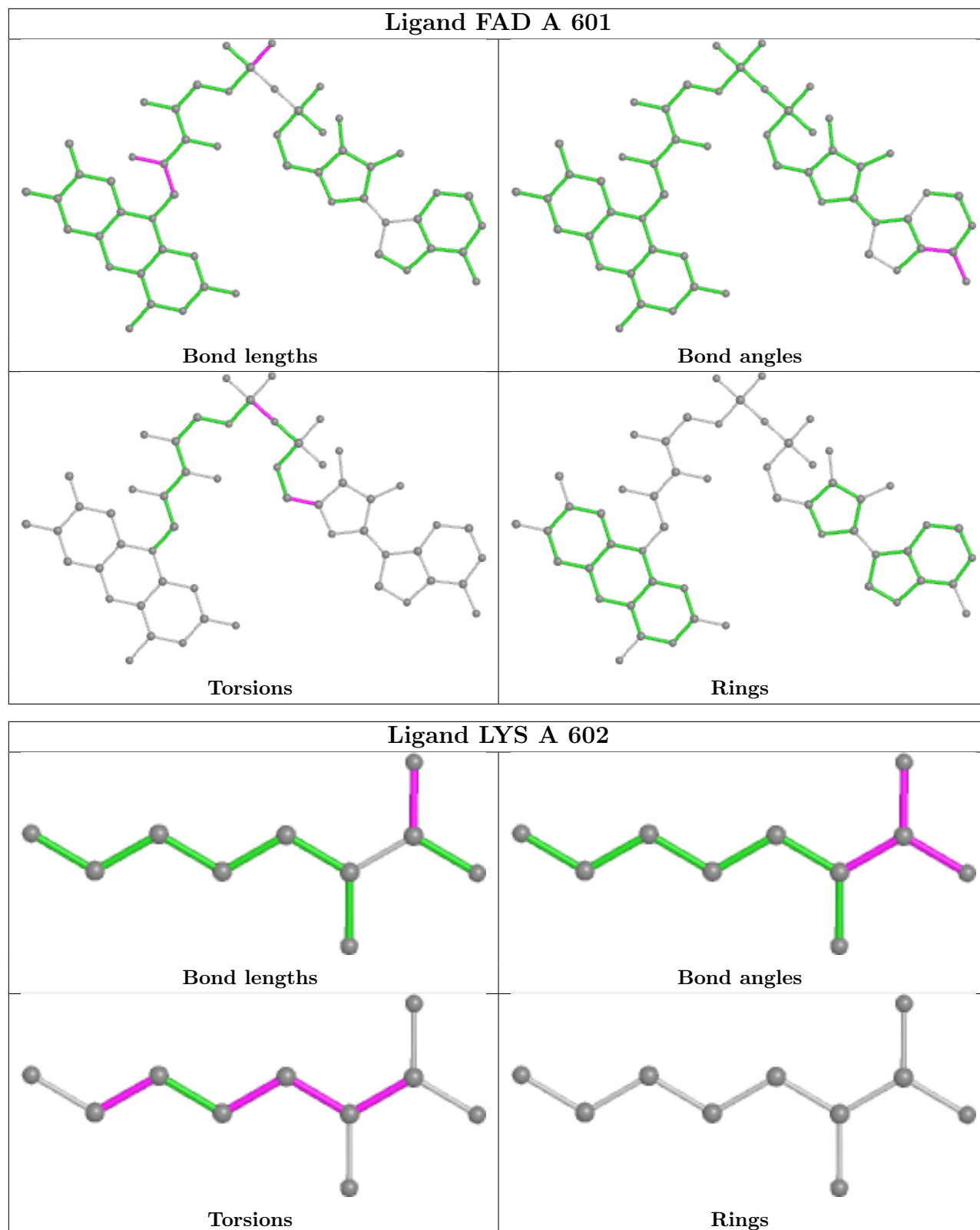
4 monomers are involved in 18 short contacts:

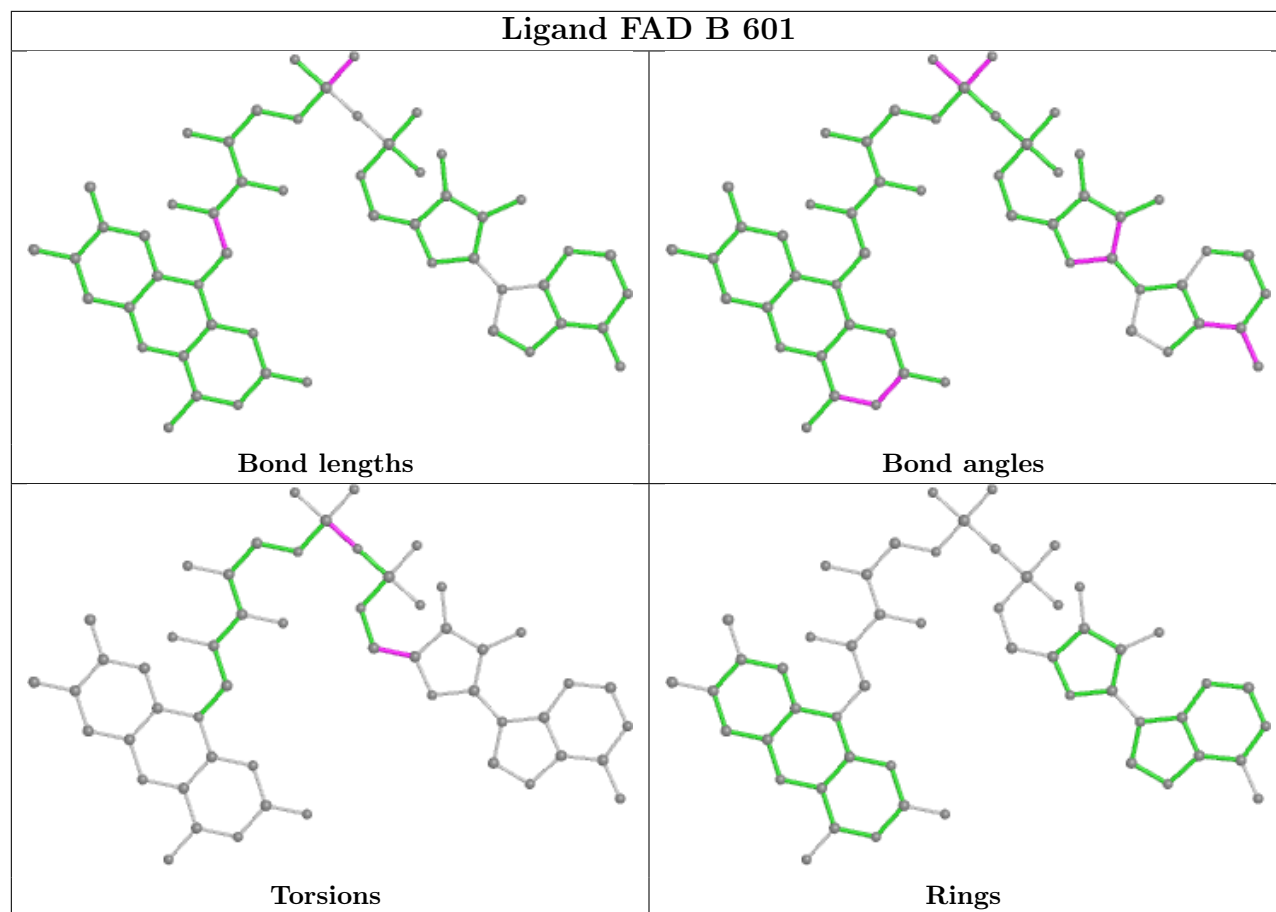
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	LYS	6	0
2	A	601	FAD	3	0
3	A	602	LYS	4	0
2	B	601	FAD	5	0

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	583/593 (98%)	0.33	17 (2%) 51 50	9, 14, 27, 106	0
1	B	583/593 (98%)	0.25	20 (3%) 45 44	9, 14, 27, 92	0
All	All	1166/1186 (98%)	0.29	37 (3%) 47 46	9, 14, 27, 106	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	386	GLY	23.2
1	B	386	GLY	23.1
1	A	219	TYR	10.8
1	B	384	SER	9.9
1	B	385	ASP	8.3
1	B	387	ALA	7.2
1	A	384	SER	6.9
1	A	385	ASP	6.1
1	B	219	TYR	6.0
1	B	388	PRO	5.6
1	A	383	THR	4.9
1	B	389	ASN	4.8
1	A	387	ALA	3.9
1	A	220	THR	3.6
1	B	383	THR	3.6
1	A	389	ASN	3.4
1	A	374	ALA	3.3
1	A	238	PHE	3.3
1	A	482	ASN	3.2
1	B	46	PRO	3.2
1	A	584	CYS	3.1
1	B	381	ASP	3.0
1	B	414	ALA	2.8
1	A	139	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	583	ALA	2.7
1	B	220	THR	2.6
1	B	413	THR	2.6
1	A	268	GLU	2.6
1	B	482	ASN	2.6
1	B	218	GLY	2.5
1	A	336	GLU	2.4
1	B	336	GLU	2.3
1	B	45	GLY	2.3
1	A	388	PRO	2.3
1	A	412	GLY	2.1
1	B	222	ASN	2.1
1	B	243	ALA	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 [i](#)

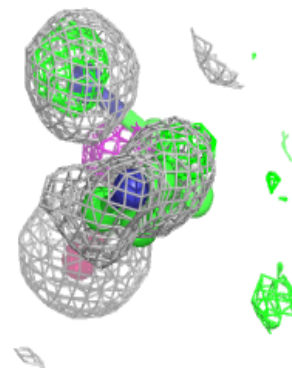
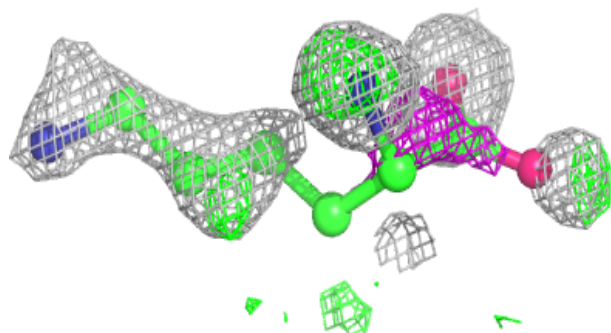
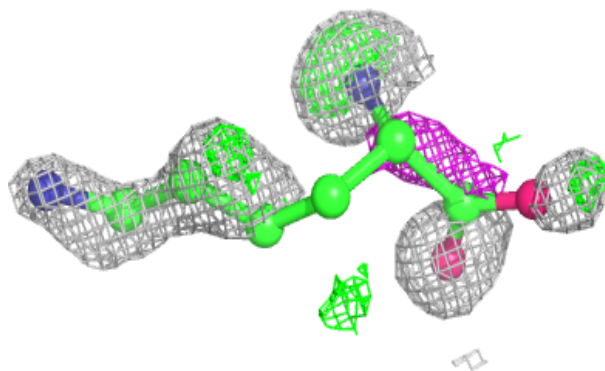
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	LYS	B	602	10/10	0.50	0.47	19,31,34,36	10
3	LYS	A	602	10/10	0.67	0.43	18,30,39,42	10
2	FAD	A	601	53/53	0.97	0.08	9,11,17,20	0
2	FAD	B	601	53/53	0.97	0.08	9,11,20,22	0

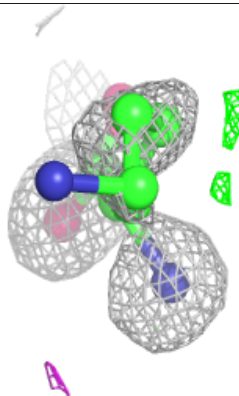
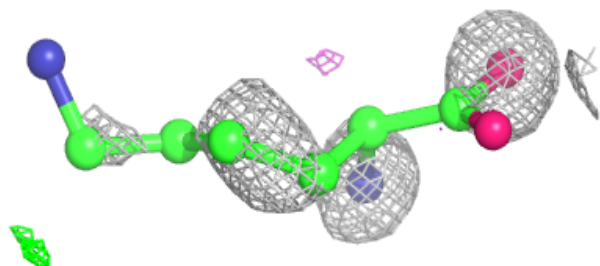
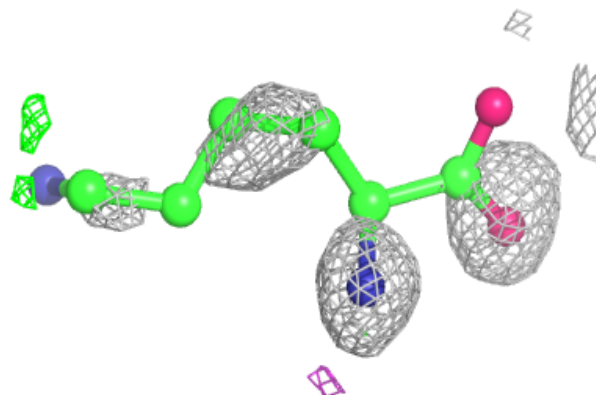
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around LYS 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)

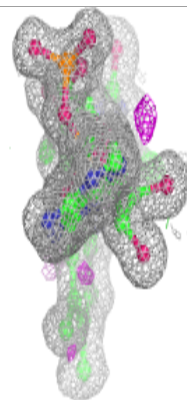
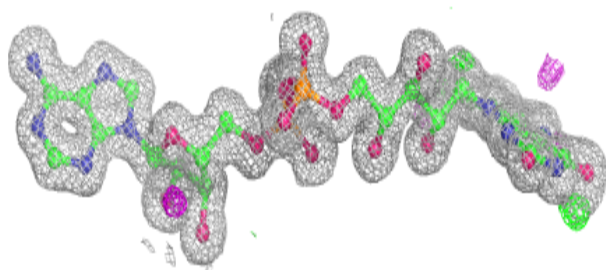
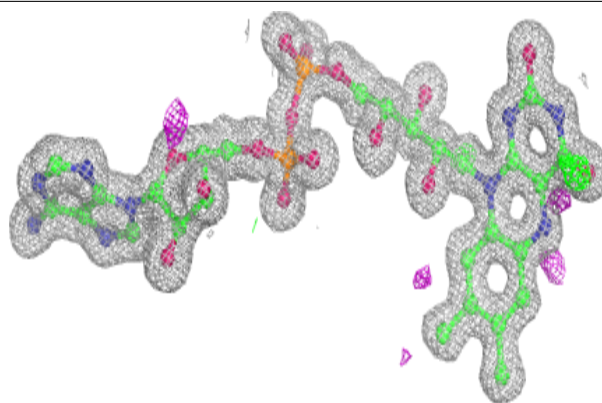
**Electron density around LYS A 602:**

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

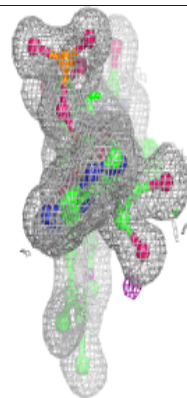
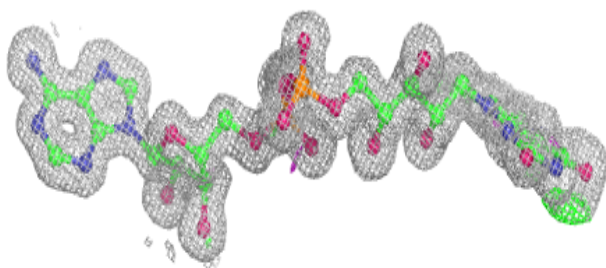
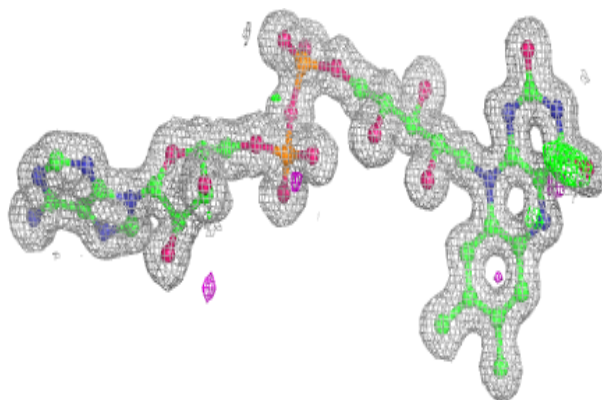


Electron density around FAD A 601:

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

**Electron density around FAD 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.