



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:27 PM UTC

PDB ID : 9GP0 / pdb\_00009gp0  
Title : 4-allyl syringol oxidase from *Streptomyces cavernae*: complex with Vanillyl alcohol  
Authors : Mattevi, A.; Alvigini, L.  
Deposited on : 2024-09-06  
Resolution : 1.75 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](mailto: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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

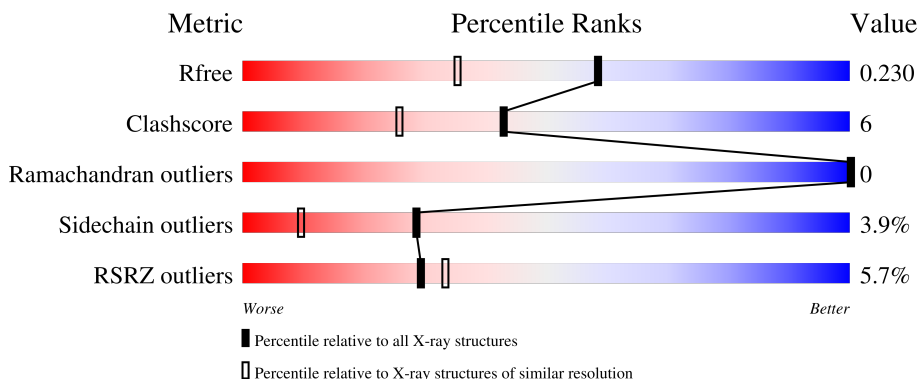
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 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))
$R_{free}$	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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  $\geq 3$ , 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	554	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>• 5%</div> </div> </div>
1	B	554	<div> <div>6%</div> <div> <div></div> <div>84%</div> <div>9%</div> <div>• 5%</div> </div> </div>

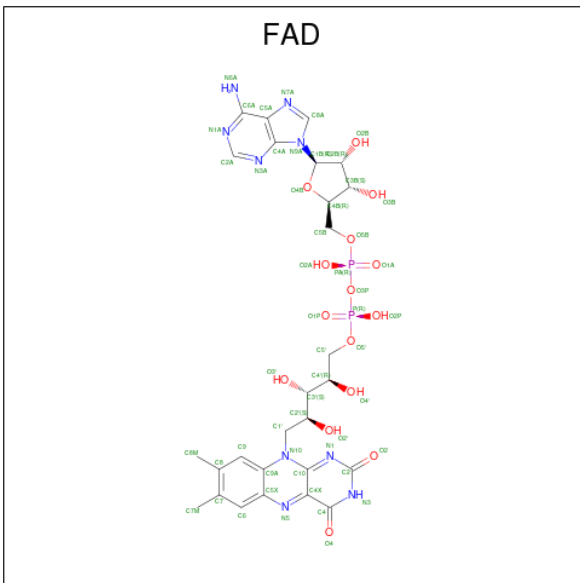


In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 4-allyl syringol oxidase from *Streptomyces cavernae*.

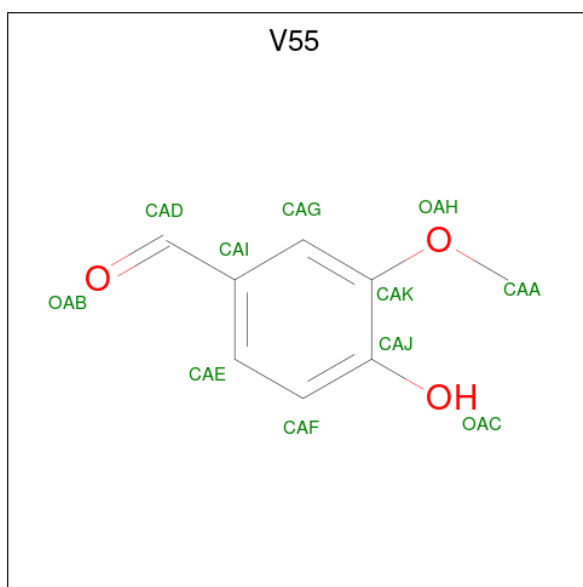
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total 4069	C 2579	N 705	O 763	S 22	0	0	0
1	B	524	Total 4069	C 2579	N 705	O 763	S 22	0	0	0

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



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

- Molecule 3 is 4-hydroxy-3-methoxybenzaldehyde (CCD ID: V55) (formula:  $\text{C}_8\text{H}_8\text{O}_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	8	3		
3	B	1	Total	C	O	0	0
			11	8	3		

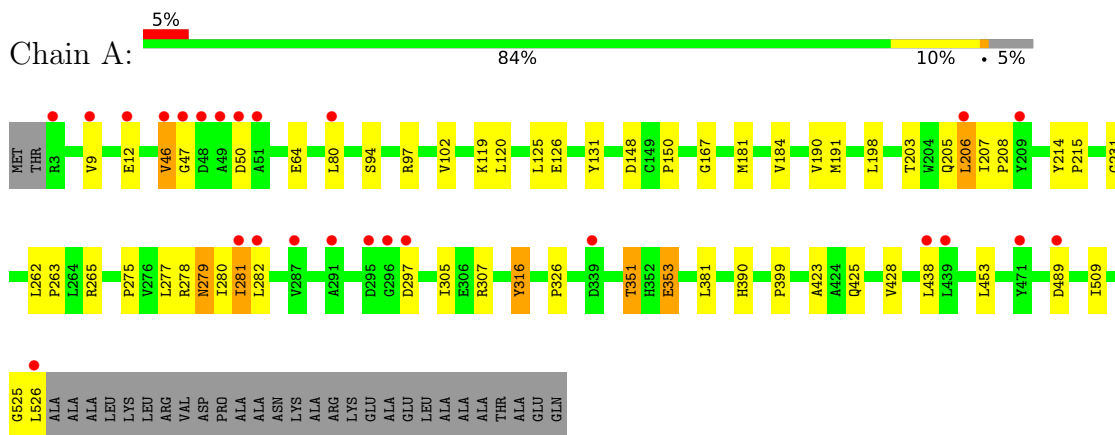
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	318	Total	O	0	0
			318	318		
4	B	240	Total	O	0	0
			240	240		

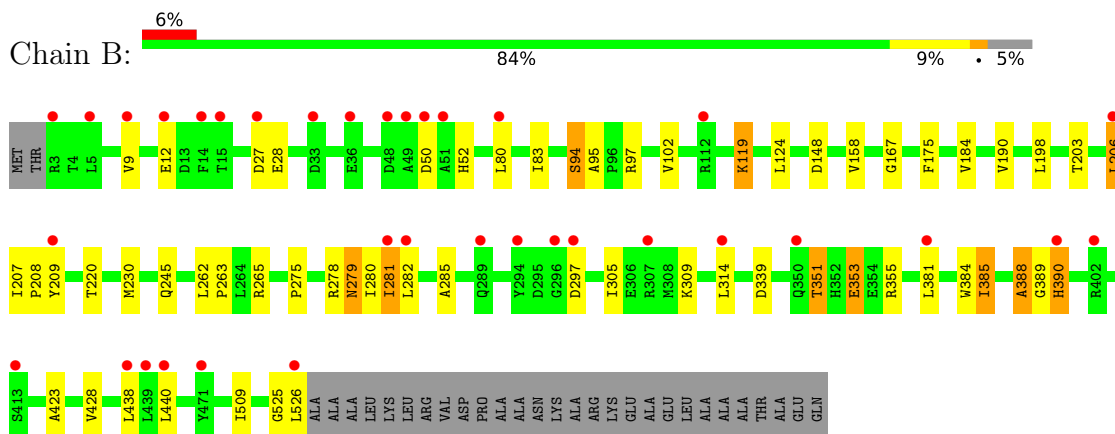
### 3 Residue-property plots

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 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: 4-allyl syringol oxidase from *Streptomyces cavernae*



- Molecule 1: 4-allyl syringol oxidase from *Streptomyces cavernae*



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.42Å 83.42Å 298.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	72.24 – 1.75 72.24 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.0 (72.24-1.75) 98.9 (72.24-1.75)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.33 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.194 , 0.227 0.201 , 0.230	Depositor DCC
$R_{free}$ test set	5790 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.8	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 22.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.098 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8824	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: FAD, V55

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	1.06	3/4172 (0.1%)	1.28	7/5672 (0.1%)
1	B	1.04	1/4172 (0.0%)	1.26	5/5672 (0.1%)
All	All	1.05	4/8344 (0.0%)	1.27	12/11344 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	209	TYR	C-O	5.69	1.30	1.24
1	A	126	GLU	CA-C	5.39	1.59	1.52
1	A	316	TYR	C-O	-5.21	1.18	1.24
1	A	181	MET	CB-CG	-5.10	1.37	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	388	ALA	N-CA-C	5.89	118.77	110.23
1	A	64	GLU	CB-CG-CD	5.80	122.46	112.60
1	B	95	ALA	N-CA-C	5.80	116.96	109.65
1	A	125	LEU	N-CA-C	5.61	118.36	109.50
1	B	124	LEU	N-CA-C	-5.37	100.15	108.90
1	A	215	PRO	N-CA-C	5.35	123.49	112.47
1	B	385	ILE	N-CA-C	-5.33	102.99	109.01
1	A	316	TYR	N-CA-C	-5.23	105.66	111.36
1	A	181	MET	CG-SD-CE	-5.20	89.46	100.90
1	A	326	PRO	N-CA-CB	5.15	106.07	103.19
1	B	389	GLY	N-CA-C	-5.11	103.64	111.10
1	A	214	TYR	CB-CA-C	5.02	115.85	110.08

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	4069	0	3958	50	0
1	B	4069	0	3958	49	0
2	A	53	0	30	5	0
2	B	53	0	31	2	0
3	A	11	0	8	0	0
3	B	11	0	7	3	0
4	A	318	0	0	10	0
4	B	240	0	0	9	0
All	All	8824	0	7992	100	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 (100) 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:390:HIS:NE2	2:A:601:FAD:C8M	1.70	1.52
1:A:206:LEU:HB3	4:A:986:HOH:O	1.32	1.24
1:B:526:LEU:HD12	4:B:905:HOH:O	1.38	1.23
1:A:489:ASP:HB3	4:A:927:HOH:O	1.47	1.12
1:A:526:LEU:HD12	4:A:970:HOH:O	1.52	1.08
1:A:97:ARG:NH1	1:A:526:LEU:HD11	1.68	1.07
1:A:97:ARG:HH12	1:A:526:LEU:HD11	1.13	1.05
1:B:97:ARG:HH22	1:B:526:LEU:HD21	1.27	0.98
1:A:489:ASP:HB3	4:A:943:HOH:O	1.63	0.96
1:B:97:ARG:NH1	1:B:526:LEU:HD11	1.81	0.96
1:A:97:ARG:HH22	1:A:526:LEU:HD21	1.28	0.95
1:B:97:ARG:HH12	1:B:526:LEU:HD11	1.34	0.92
1:A:206:LEU:HD23	4:A:986:HOH:O	1.69	0.92
1:A:47:GLY:HA2	4:A:780:HOH:O	1.76	0.85
1:A:184:VAL:HG22	1:A:190:VAL:HG12	1.59	0.84
1:B:339:ASP:HB2	4:B:915:HOH:O	1.79	0.82
1:A:390:HIS:CD2	2:A:601:FAD:C8M	2.65	0.80
1:B:27:ASP:HB2	4:B:848:HOH:O	1.83	0.79
1:A:80:LEU:HD11	1:A:509:ILE:CD1	2.18	0.74

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:184:VAL:HG22	1:B:190:VAL:HG12	1.70	0.73
1:A:206:LEU:CD2	4:A:986:HOH:O	2.33	0.72
1:B:97:ARG:NH2	1:B:526:LEU:HD21	2.02	0.72
1:A:281:ILE:HG22	1:A:423:ALA:HB2	1.71	0.71
1:A:97:ARG:NH2	1:A:526:LEU:HD21	2.06	0.69
1:A:278:ARG:HB3	1:A:282:LEU:HD21	1.74	0.69
1:A:80:LEU:HD11	1:A:509:ILE:HD13	1.73	0.69
1:B:80:LEU:HD11	1:B:509:ILE:HD13	1.75	0.69
1:A:525:GLY:O	1:A:526:LEU:HB2	1.92	0.69
1:B:80:LEU:HD11	1:B:509:ILE:CD1	2.24	0.67
1:B:278:ARG:HB3	1:B:282:LEU:HD21	1.75	0.67
1:A:184:VAL:HG22	1:A:190:VAL:CG1	2.24	0.67
1:B:203:THR:HB	1:B:206:LEU:HD11	1.77	0.66
1:B:525:GLY:O	1:B:526:LEU:HB2	1.97	0.65
1:B:280:ILE:HD13	1:B:309:LYS:HG2	1.79	0.65
1:A:97:ARG:HH12	1:A:526:LEU:CD1	2.02	0.62
1:A:351:THR:HG22	1:A:353:GLU:H	1.64	0.62
1:A:203:THR:HB	1:A:206:LEU:HD11	1.82	0.61
1:B:184:VAL:HG22	1:B:190:VAL:CG1	2.31	0.61
1:A:275:PRO:HG2	1:A:428:VAL:HG22	1.84	0.60
1:B:351:THR:HG22	1:B:353:GLU:H	1.65	0.60
1:A:390:HIS:CE1	2:A:601:FAD:C8M	2.75	0.55
1:B:390:HIS:HE1	3:B:602:V55:CAA	2.21	0.54
1:A:46:VAL:HG13	1:A:453:LEU:HB2	1.87	0.54
1:A:390:HIS:NE2	2:A:601:FAD:C8	2.63	0.53
1:B:385:ILE:HG13	1:B:388:ALA:HB2	1.91	0.53
1:B:281:ILE:HG22	1:B:423:ALA:HB2	1.91	0.53
1:B:278:ARG:CB	1:B:282:LEU:HD21	2.39	0.53
1:B:52:HIS:CE1	4:B:916:HOH:O	2.62	0.52
1:A:281:ILE:HG22	1:A:423:ALA:CB	2.39	0.52
1:A:489:ASP:CB	4:A:943:HOH:O	2.40	0.51
1:B:207:ILE:HD12	1:B:208:PRO:HD2	1.93	0.51
1:A:278:ARG:CB	1:A:282:LEU:HD21	2.38	0.51
1:A:307:ARG:HD2	4:A:987:HOH:O	2.10	0.50
1:B:280:ILE:HG21	1:B:305:ILE:HG23	1.94	0.50
1:B:279:ASN:O	1:B:282:LEU:HD23	2.12	0.50
1:A:203:THR:CB	1:A:206:LEU:HD11	2.41	0.49
1:B:52:HIS:HE1	4:B:916:HOH:O	1.94	0.49
1:B:203:THR:CB	1:B:206:LEU:HD11	2.41	0.49
1:A:265:ARG:HG2	1:A:428:VAL:HG23	1.95	0.49
1:A:280:ILE:HG21	1:A:305:ILE:HG23	1.96	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:ASN:O	1:A:282:LEU:HD23	2.13	0.48
1:B:281:ILE:CD1	4:B:912:HOH:O	2.60	0.48
1:A:281:ILE:CG2	1:A:423:ALA:HB2	2.39	0.48
1:A:80:LEU:CD1	1:A:509:ILE:HD13	2.41	0.47
1:A:148:ASP:OD1	1:A:167:GLY:HA3	2.15	0.47
1:A:206:LEU:CB	4:A:986:HOH:O	2.16	0.47
1:B:390:HIS:CE1	3:B:602:V55:CAA	2.97	0.46
1:A:207:ILE:HD12	1:A:208:PRO:HD2	1.98	0.46
1:B:148:ASP:OD1	1:B:167:GLY:HA3	2.16	0.46
1:B:80:LEU:CD1	1:B:509:ILE:HD13	2.43	0.46
1:B:28:GLU:HB3	4:B:904:HOH:O	2.15	0.45
1:B:275:PRO:HG2	1:B:428:VAL:HG22	1.98	0.45
1:B:390:HIS:HE1	3:B:602:V55:HAA1	1.81	0.45
1:B:97:ARG:HH12	1:B:526:LEU:CD1	2.17	0.45
1:B:245:GLN:OE1	1:B:355:ARG:NH1	2.49	0.45
1:B:281:ILE:HD12	4:B:912:HOH:O	2.16	0.45
1:A:205:GLN:HG3	1:A:231:GLY:HA3	1.99	0.44
2:B:601:FAD:O5B	2:B:601:FAD:H8A	2.17	0.44
1:A:80:LEU:HD12	1:A:80:LEU:O	2.18	0.44
1:A:262:LEU:HB3	1:A:263:PRO:HD3	1.99	0.44
1:A:120:LEU:HD23	1:B:262:LEU:HD21	2.00	0.43
1:A:277:LEU:O	1:A:425:GLN:HA	2.18	0.43
1:B:278:ARG:CA	1:B:282:LEU:HD21	2.49	0.43
1:B:278:ARG:HB3	1:B:282:LEU:CD2	2.47	0.43
1:A:278:ARG:CA	1:A:282:LEU:HD21	2.48	0.43
1:A:80:LEU:HA	1:A:102:VAL:O	2.19	0.42
2:A:601:FAD:O5B	2:A:601:FAD:H8A	2.20	0.42
1:B:158:VAL:HG22	1:B:230:MET:HB3	2.01	0.42
1:B:390:HIS:NE2	2:B:601:FAD:HM83	2.35	0.42
1:B:265:ARG:HG2	1:B:428:VAL:HG23	2.01	0.42
1:B:80:LEU:HA	1:B:102:VAL:O	2.19	0.42
1:B:262:LEU:HB3	1:B:263:PRO:HD3	2.02	0.41
1:B:281:ILE:HG22	1:B:423:ALA:CB	2.50	0.41
1:A:262:LEU:HD13	1:A:399:PRO:CG	2.51	0.41
1:B:119:LYS:NZ	4:B:712:HOH:O	2.52	0.41
1:B:175:PHE:CD1	1:B:220:THR:HG21	2.55	0.41
1:A:131:TYR:CZ	1:A:150:PRO:HD3	2.55	0.41
1:A:279:ASN:HA	1:A:316:TYR:O	2.21	0.41
1:B:285:ALA:HA	1:B:384:TRP:CE3	2.56	0.40
1:B:83:ILE:HG21	1:B:94:SER:HB3	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	522/554 (94%)	512 (98%)	10 (2%)	0	100	100
1	B	522/554 (94%)	509 (98%)	13 (2%)	0	100	100
All	All	1044/1108 (94%)	1021 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

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	424/444 (96%)	408 (96%)	16 (4%)	29	10
1	B	424/444 (96%)	407 (96%)	17 (4%)	28	9
All	All	848/888 (96%)	815 (96%)	33 (4%)	28	9

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	VAL
1	A	12	GLU
1	A	46	VAL
1	A	50	ASP
1	A	94	SER
1	A	119	LYS
1	A	191	MET
1	A	198	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	206	LEU
1	A	279	ASN
1	A	281	ILE
1	A	297	ASP
1	A	351	THR
1	A	353	GLU
1	A	381	LEU
1	A	438	LEU
1	B	9	VAL
1	B	12	GLU
1	B	50	ASP
1	B	94	SER
1	B	119	LYS
1	B	198	LEU
1	B	206	LEU
1	B	279	ASN
1	B	281	ILE
1	B	297	ASP
1	B	314	LEU
1	B	351	THR
1	B	353	GLU
1	B	381	LEU
1	B	390	HIS
1	B	438	LEU
1	B	440	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	HIS
1	A	74	ASN
1	A	250	ASN
1	A	289	GLN
1	A	343	GLN
1	A	350	GLN
1	A	506	ASN
1	B	52	HIS
1	B	74	ASN
1	B	289	GLN
1	B	343	GLN
1	B	350	GLN
1	B	390	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	506	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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	V55	B	602	-	11,11,11	2.04	2 (18%)	14,14,14	1.70	3 (21%)
3	V55	A	602	-	11,11,11	2.22	2 (18%)	14,14,14	1.85	4 (28%)
2	FAD	A	601	-	58,58,58	0.67	1 (1%)	85,89,89	0.66	0
2	FAD	B	601	-	58,58,58	0.57	0	85,89,89	0.77	2 (2%)

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	V55	B	602	-	-	2/4/4/4	0/1/1/1
3	V55	A	602	-	-	2/4/4/4	0/1/1/1
2	FAD	A	601	-	-	4/34/50/50	0/6/6/6
2	FAD	B	601	-	-	3/34/50/50	0/6/6/6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	V55	OAB-CAD	6.43	1.44	1.21
3	B	602	V55	OAB-CAD	5.70	1.41	1.21
3	A	602	V55	CAI-CAD	-3.25	1.38	1.47
3	B	602	V55	CAI-CAD	-3.16	1.38	1.47
2	A	601	FAD	C2-N1	-2.06	1.32	1.36

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	V55	OAB-CAD-CAI	-3.97	111.11	124.56
3	B	602	V55	OAB-CAD-CAI	-3.62	112.31	124.56
3	A	602	V55	CAE-CAF-CAJ	-3.30	117.20	120.50
3	B	602	V55	CAA-OAH-CAK	-3.19	112.84	117.51
3	B	602	V55	CAE-CAF-CAJ	-2.54	117.96	120.50
3	A	602	V55	CAF-CAJ-CAK	2.32	122.18	119.55
3	A	602	V55	CAE-CAI-CAG	2.32	121.64	118.72
2	B	601	FAD	C4-N3-C2	-2.27	121.61	125.64
2	B	601	FAD	O3P-P-O1P	-2.05	104.54	110.70

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	V55	OAB-CAD-CAI-CAG
3	A	602	V55	OAB-CAD-CAI-CAE
2	B	601	FAD	O4'-C4'-C5'-O5'
2	A	601	FAD	C3'-C4'-C5'-O5'
2	B	601	FAD	C3'-C4'-C5'-O5'
2	B	601	FAD	C4'-C5'-O5'-P
3	B	602	V55	OAB-CAD-CAI-CAG
2	A	601	FAD	O4'-C4'-C5'-O5'
2	A	601	FAD	C4'-C5'-O5'-P
3	B	602	V55	OAB-CAD-CAI-CAE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
2	A	601	FAD	C2'-C3'-C4'-O4'

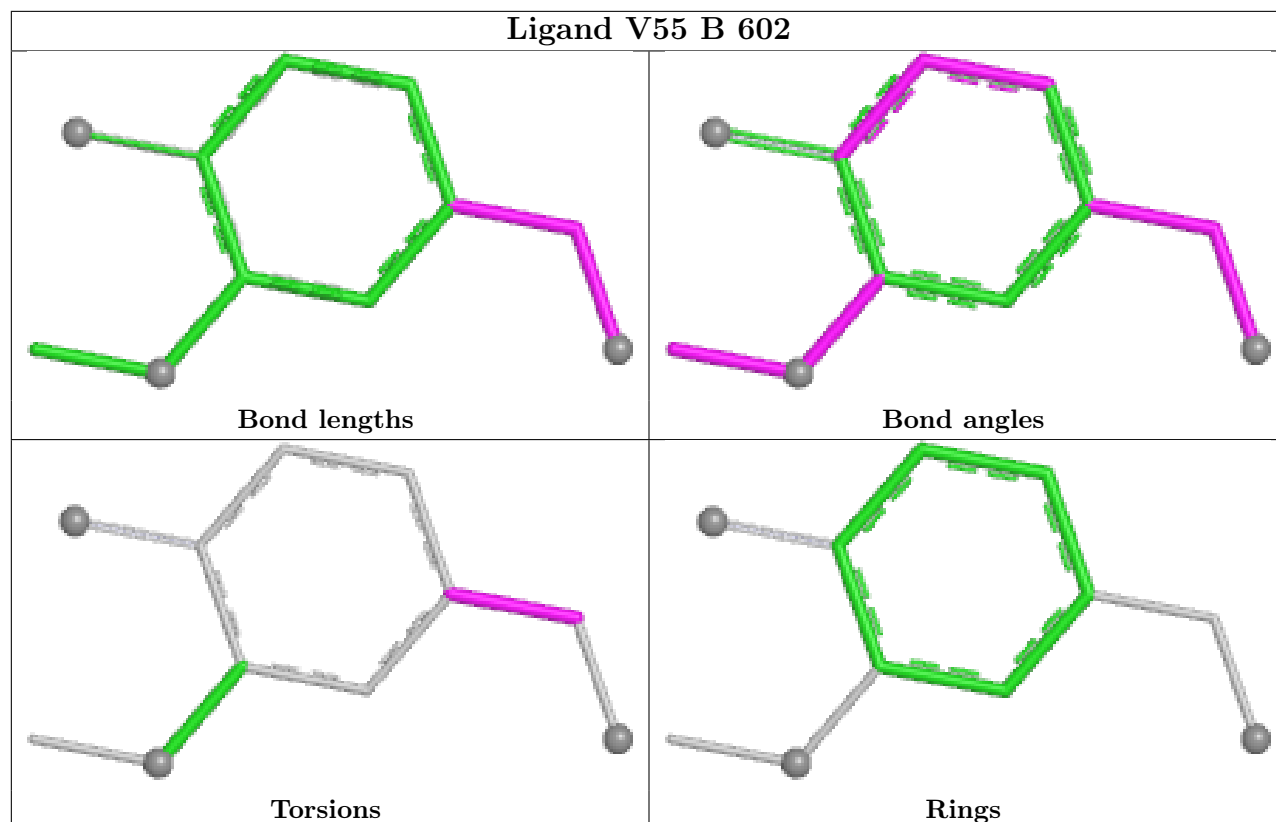
There are no ring outliers.

3 monomers are involved in 10 short contacts:

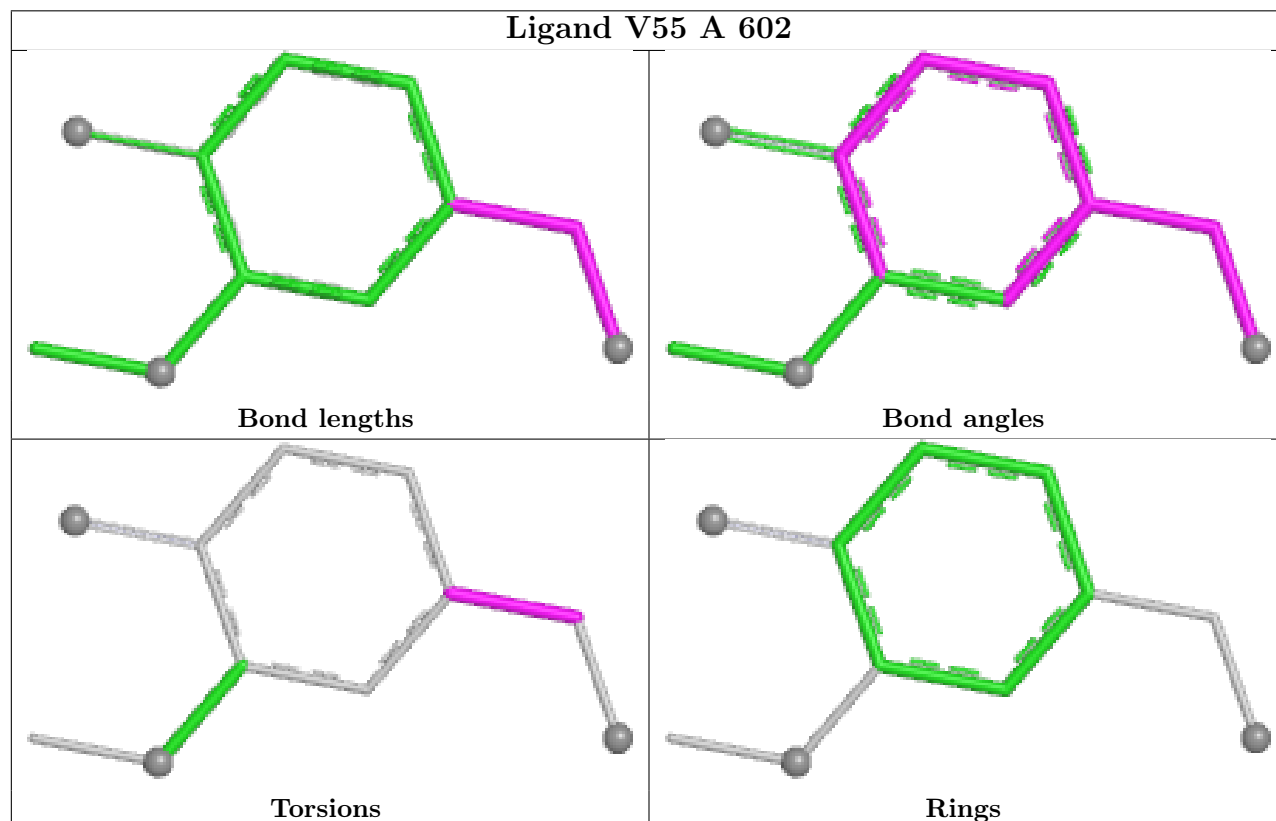
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	V55	3	0
2	A	601	FAD	5	0
2	B	601	FAD	2	0

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.

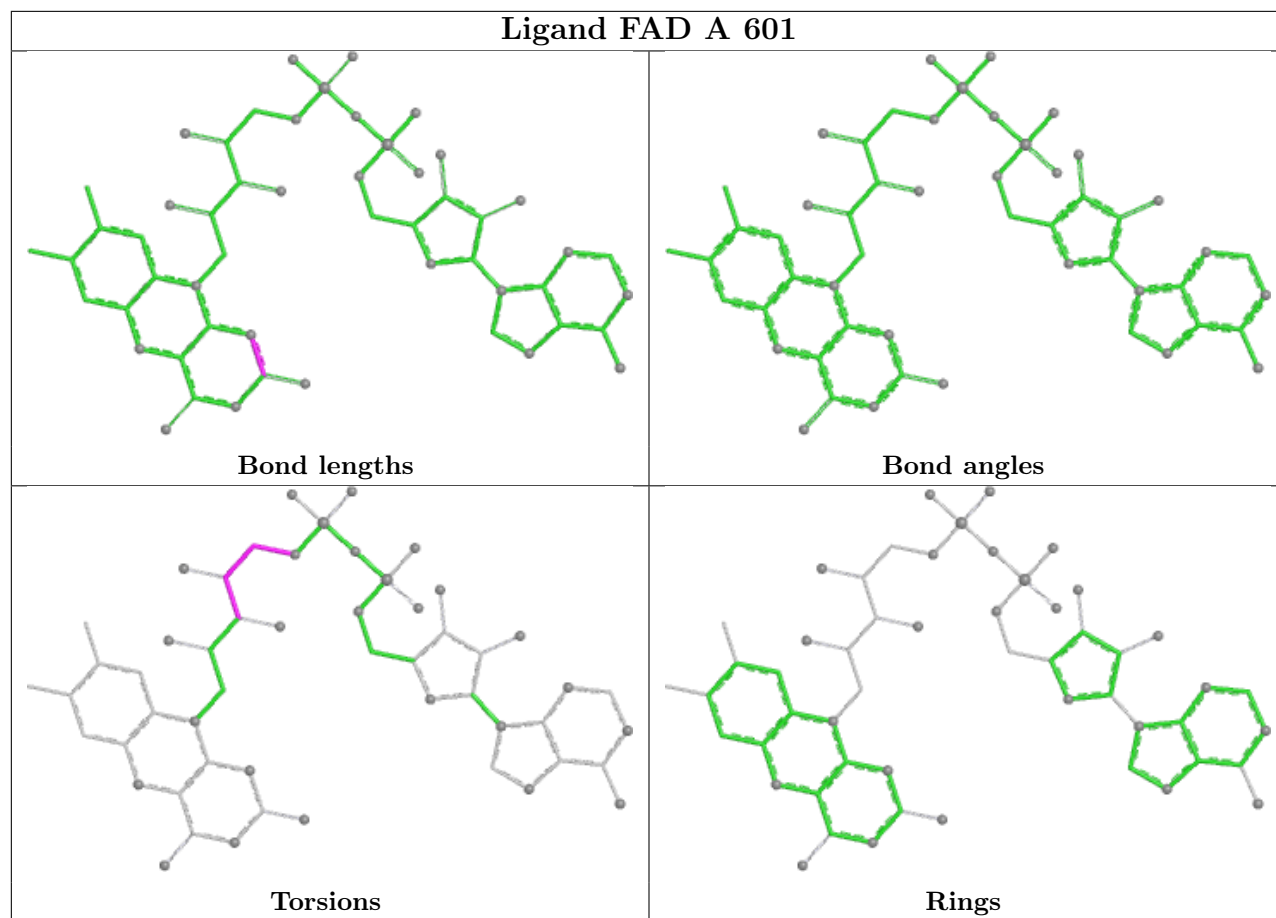
## Ligand V55 B 602

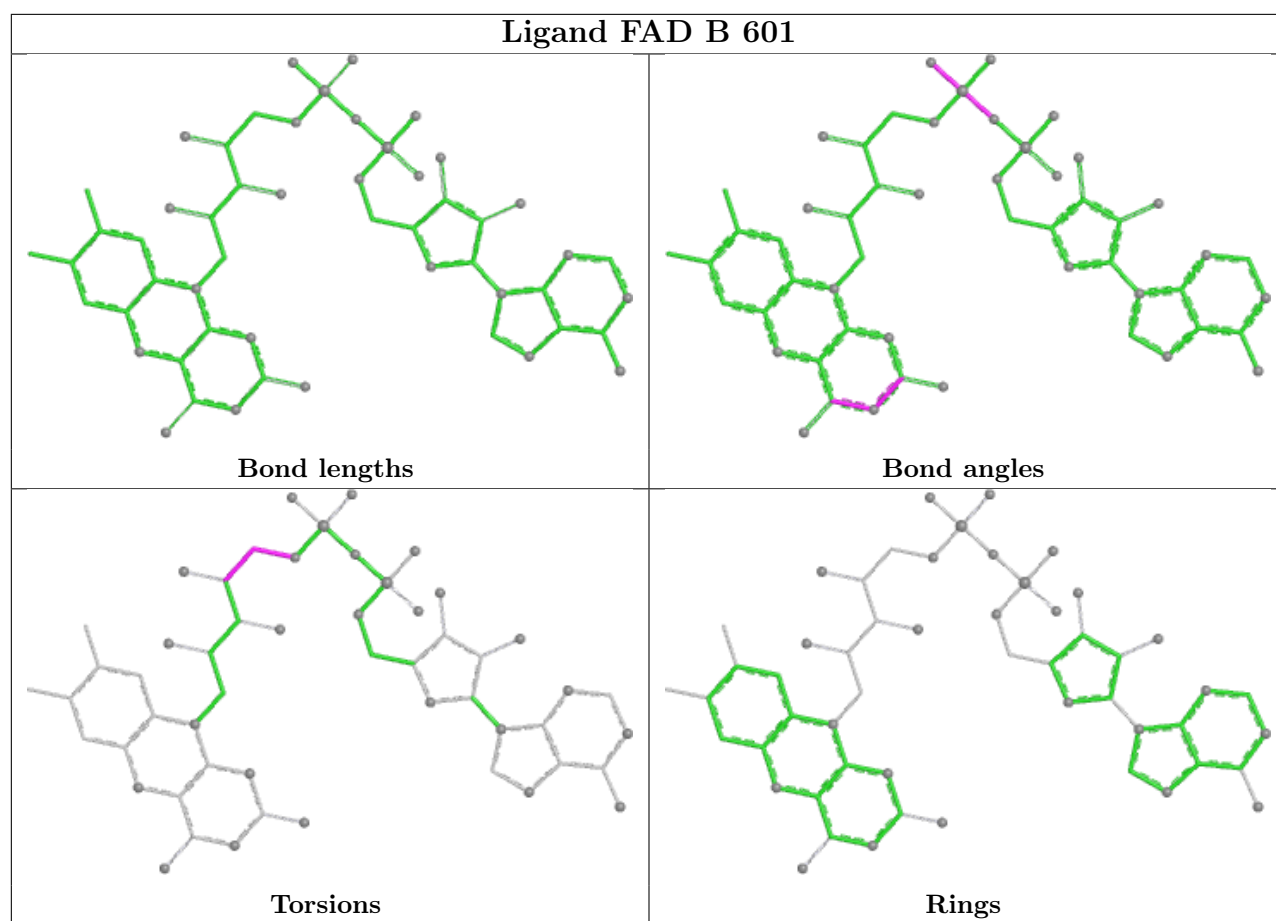


## Ligand V55 A 602









## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	524/554 (94%)	0.22	25 (4%) 35 41	18, 27, 46, 67	0
1	B	524/554 (94%)	0.52	35 (6%) 24 28	20, 31, 51, 70	0
All	All	1048/1108 (94%)	0.37	60 (5%) 29 33	18, 29, 49, 70	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	51	ALA	5.1
1	A	282	LEU	4.5
1	B	471	TYR	4.5
1	B	526	LEU	4.5
1	B	51	ALA	4.4
1	A	46	VAL	4.3
1	A	471	TYR	4.3
1	A	526	LEU	4.2
1	A	439	LEU	3.8
1	B	80	LEU	3.8
1	B	206	LEU	3.4
1	B	282	LEU	3.4
1	A	49	ALA	3.3
1	B	296	GLY	3.3
1	B	5	LEU	3.3
1	B	381	LEU	3.3
1	B	297	ASP	3.3
1	A	80	LEU	3.2
1	B	438	LEU	3.2
1	A	296	GLY	3.2
1	B	49	ALA	3.2
1	B	9	VAL	3.2
1	A	438	LEU	3.0
1	B	50	ASP	3.0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	307	ARG	3.0
1	A	50	ASP	2.9
1	A	489	ASP	2.9
1	B	350	GLN	2.9
1	A	339	ASP	2.8
1	B	33	ASP	2.8
1	B	294	TYR	2.7
1	A	297	ASP	2.6
1	B	439	LEU	2.5
1	A	48	ASP	2.5
1	B	209	TYR	2.5
1	B	112	ARG	2.5
1	B	402	ARG	2.5
1	B	413	SER	2.4
1	B	27	ASP	2.4
1	B	390	HIS	2.4
1	A	47	GLY	2.4
1	B	3	ARG	2.4
1	B	281	ILE	2.3
1	B	12	GLU	2.3
1	B	440	LEU	2.3
1	A	12	GLU	2.3
1	A	291	ALA	2.2
1	B	14	PHE	2.2
1	A	281	ILE	2.2
1	B	314	LEU	2.2
1	B	15	THR	2.2
1	A	206	LEU	2.2
1	A	3	ARG	2.2
1	A	287	VAL	2.1
1	B	36	GLU	2.1
1	B	289	GLN	2.1
1	A	209	TYR	2.1
1	A	9	VAL	2.1
1	B	48	ASP	2.1
1	A	295	ASP	2.1

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

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

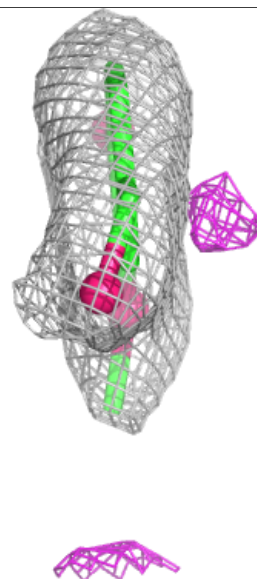
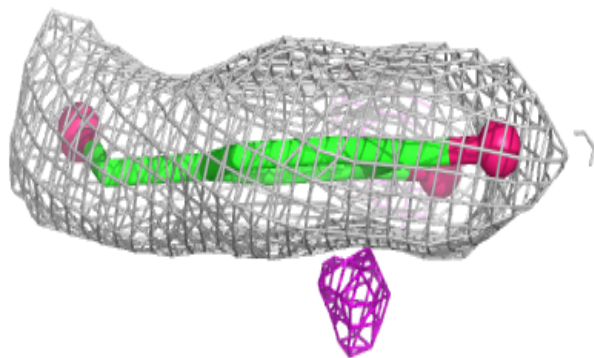
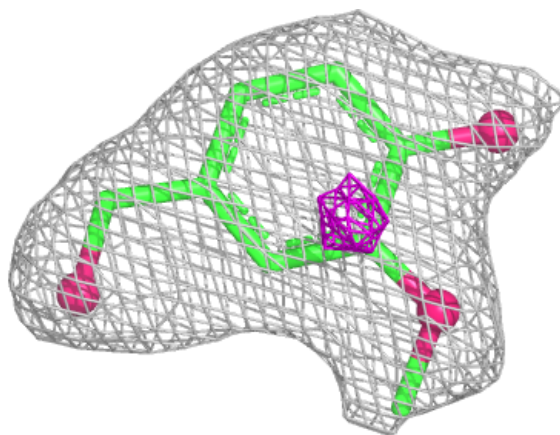
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	V55	B	602	11/11	0.90	0.12	48,51,58,61	0
3	V55	A	602	11/11	0.92	0.11	34,43,50,52	0
2	FAD	B	601	53/53	0.96	0.07	24,27,34,40	0
2	FAD	A	601	53/53	0.98	0.05	16,21,27,32	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.

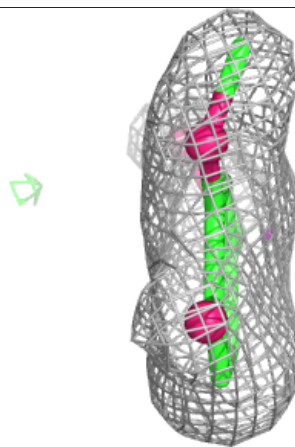
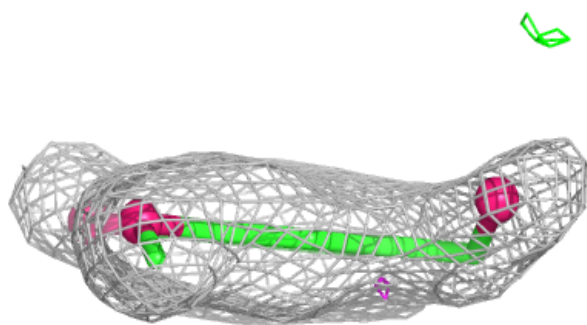
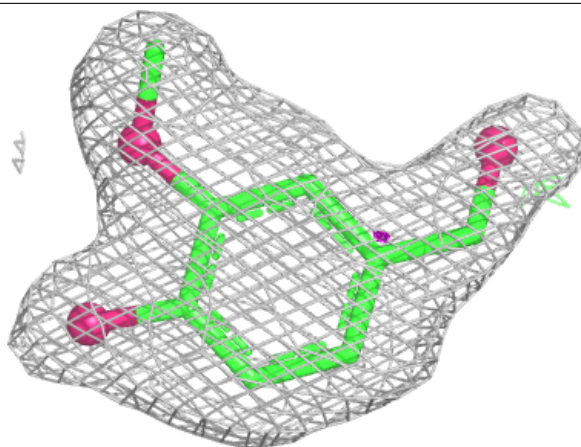
**Electron density around V55 B 602:**

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

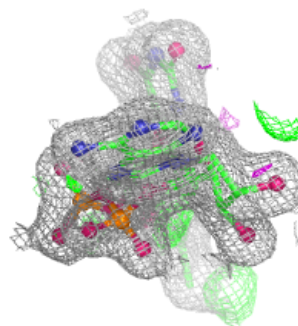
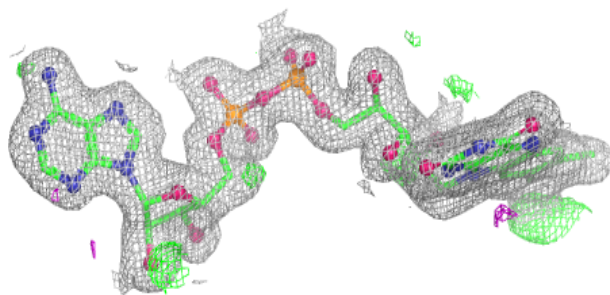
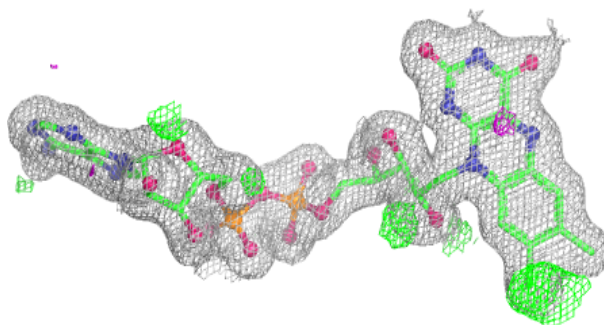


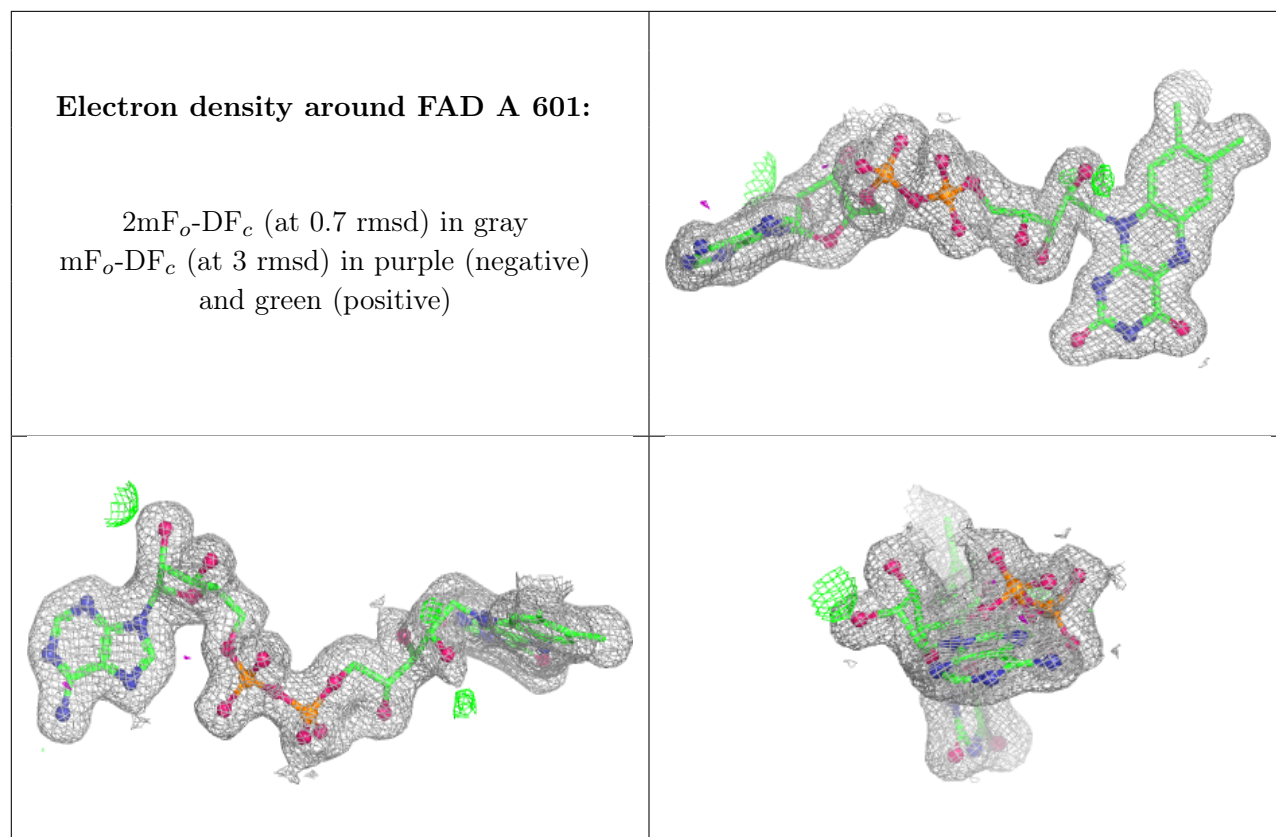
**Electron density around V55 A 602:**

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

**Electron density around FAD 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.