



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2021 – 10:57 PM EDT

PDB ID : 3K4C  
Title : Pyranose 2-oxidase H167A/T169G mutant  
Authors : Divne, C.; Tan, T.C.  
Deposited on : 2009-10-05  
Resolution : 1.70 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.

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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 : 2.23.2  
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) : 2.23.2

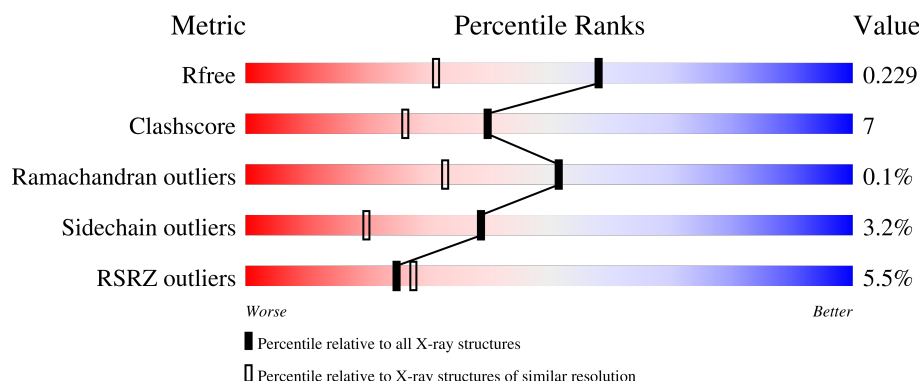
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	623	<div> <div>3%</div> <div>80%</div> <div>11%</div> <div>8%</div> </div>
1	B	623	<div> <div>3%</div> <div>78%</div> <div>12%</div> <div>8%</div> </div>
1	C	623	<div> <div>4%</div> <div>81%</div> <div>10%</div> <div>8%</div> </div>
1	D	623	<div> <div>11%</div> <div>75%</div> <div>15%</div> <div>8%</div> </div>

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
4	MES	C	901	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 20305 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 Pyranose 2-oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	576	Total	C	N	O	S	0	0	0
			4534	2863	775	871	25			
1	B	576	Total	C	N	O	S	0	0	0
			4534	2863	775	871	25			
1	C	575	Total	C	N	O	S	0	0	0
			4525	2858	774	869	24			
1	D	574	Total	C	N	O	S	0	0	0
			4518	2854	773	867	24			

There are 8 discrepancies between the modelled and reference sequences:

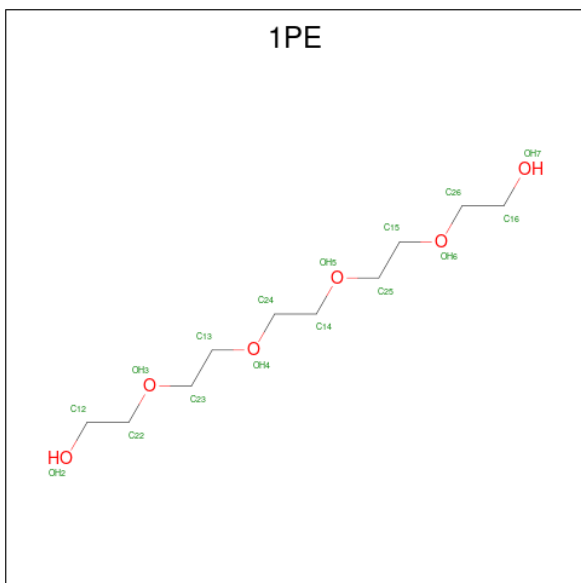
Chain	Residue	Modelled	Actual	Comment	Reference
A	167	ALA	HIS	engineered mutation	UNP Q7ZA32
A	169	GLY	THR	engineered mutation	UNP Q7ZA32
B	167	ALA	HIS	engineered mutation	UNP Q7ZA32
B	169	GLY	THR	engineered mutation	UNP Q7ZA32
C	167	ALA	HIS	engineered mutation	UNP Q7ZA32
C	169	GLY	THR	engineered mutation	UNP Q7ZA32
D	167	ALA	HIS	engineered mutation	UNP Q7ZA32
D	169	GLY	THR	engineered mutation	UNP Q7ZA32

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



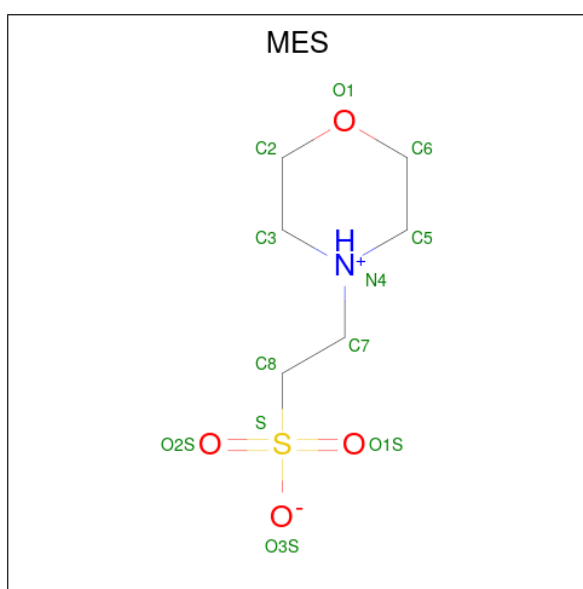
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	B	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	C	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	D	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 3 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula:  $\text{C}_{10}\text{H}_{22}\text{O}_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			14	9	5		
3	A	1	Total	C	O	0	0
			12	8	4		
3	B	1	Total	C	O	0	0
			16	10	6		
3	D	1	Total	C	O	0	0
			16	10	6		

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	498	Total	O	0	0
			498	498		
5	B	554	Total	O	0	0
			554	554		
5	C	504	Total	O	0	0
			504	504		

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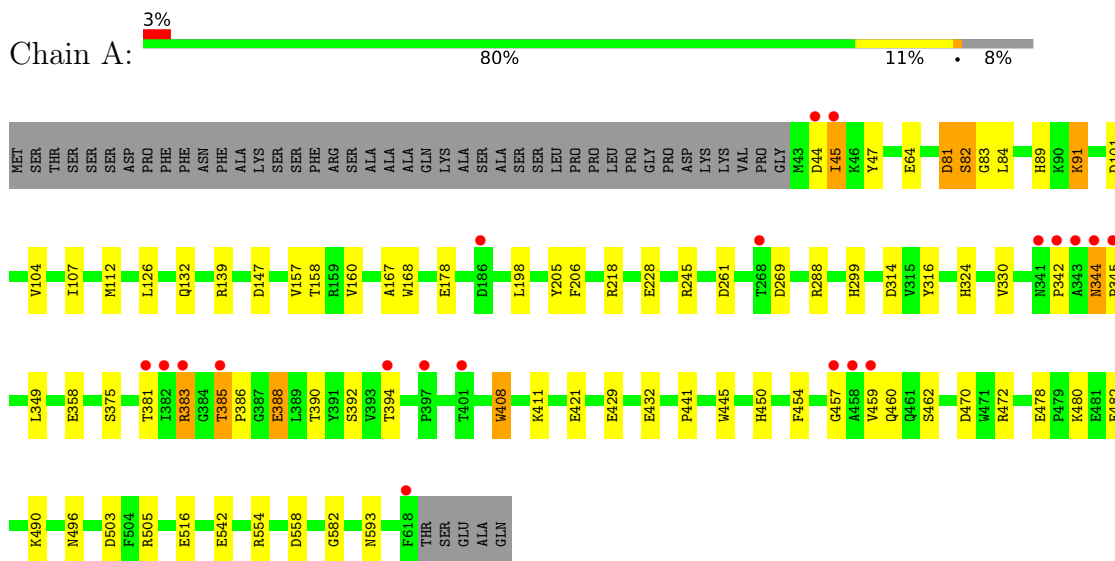
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	344	Total 344	O 344	0	0

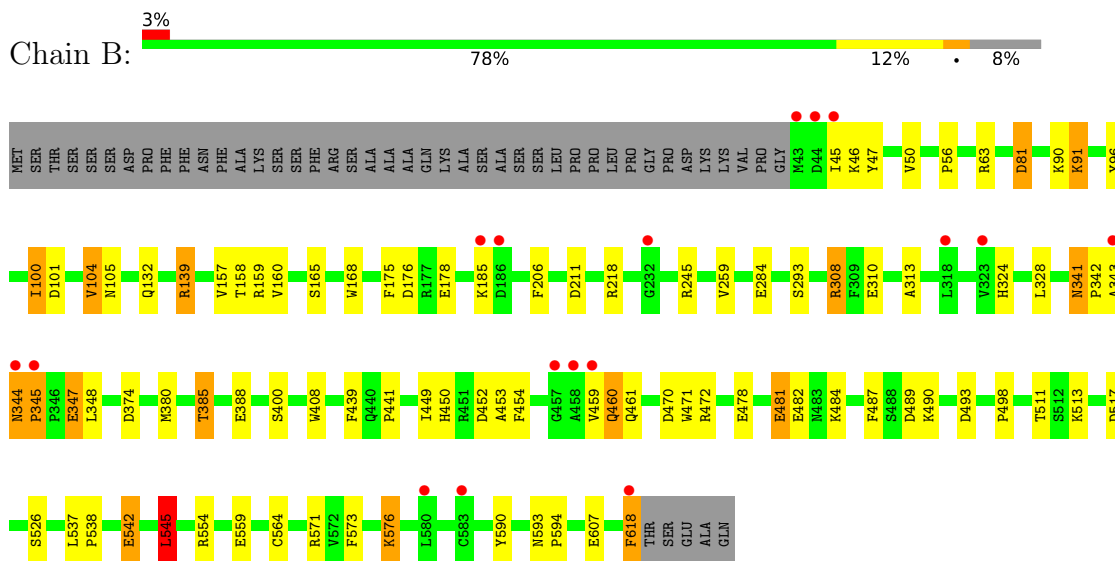
### 3 Residue-property plots [i](#)

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: Pyranose 2-oxidase

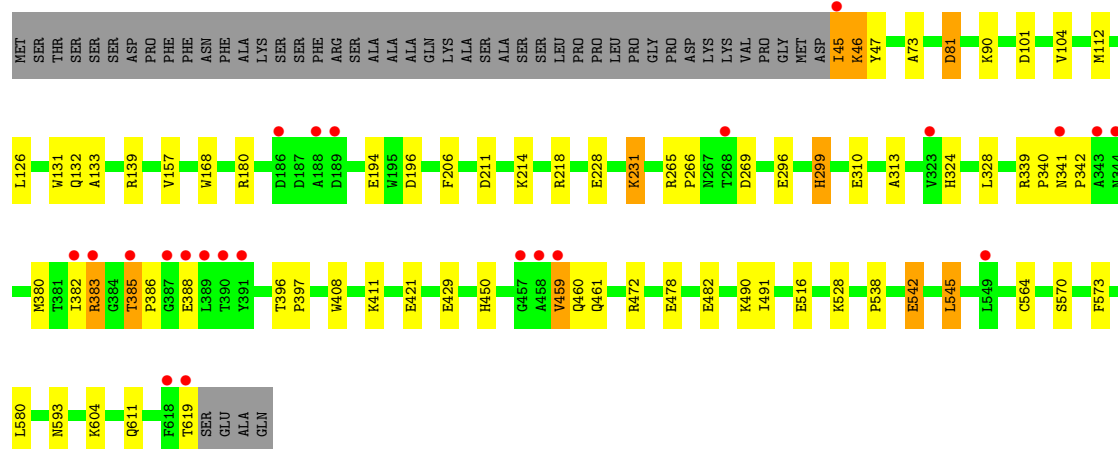
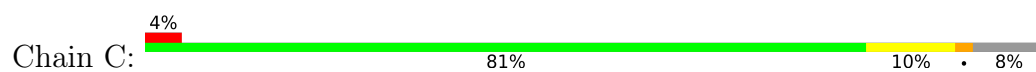


#### • Molecule 1: Pyranose 2-oxidase

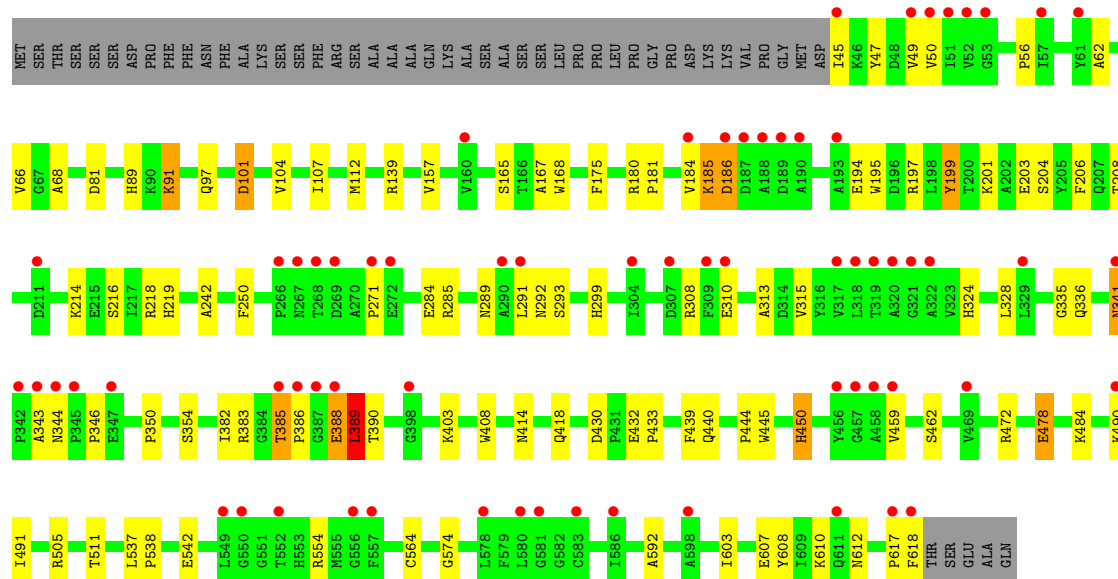
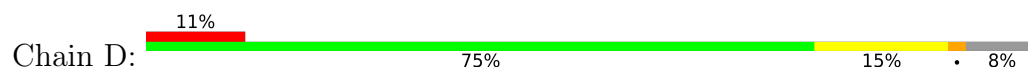


#### • Molecule 1: Pyranose 2-oxidase





• Molecule 1: Pyranose 2-oxidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.21Å 102.96Å 137.12Å 90.00° 90.82° 90.00°	Depositor
Resolution (Å)	29.30 – 1.70 29.29 – 1.70	Depositor EDS
% Data completeness (in resolution range)	96.8 (29.30-1.70) 96.8 (29.29-1.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.5	Depositor
R, $R_{free}$	0.180 , 0.216 0.198 , 0.229	Depositor DCC
$R_{free}$ test set	3027 reflections (1.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.8	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 46.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for -k,-h,-l 0.008 for k,h,-l 0.022 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20305	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 1PE, MES, 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	1.23	16/4649 (0.3%)	1.08	17/6320 (0.3%)
1	B	1.20	7/4649 (0.2%)	1.15	23/6320 (0.4%)
1	C	1.09	9/4640 (0.2%)	1.01	10/6309 (0.2%)
1	D	0.96	2/4633 (0.0%)	0.94	5/6299 (0.1%)
All	All	1.13	34/18571 (0.2%)	1.05	55/25248 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	D	0	1
All	All	0	3

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	82	SER	CB-OG	12.12	1.58	1.42
1	B	542	GLU	CD-OE1	8.97	1.35	1.25
1	A	82	SER	N-CA	8.77	1.63	1.46
1	B	481	GLU	CG-CD	8.40	1.64	1.51
1	A	542	GLU	CD-OE1	8.05	1.34	1.25
1	A	82	SER	CA-CB	7.04	1.63	1.52
1	C	542	GLU	CD-OE1	6.70	1.33	1.25
1	B	81	ASP	CB-CG	-6.40	1.38	1.51
1	A	316	TYR	CD1-CE1	6.26	1.48	1.39
1	A	383	ARG	CG-CD	6.24	1.67	1.51
1	D	542	GLU	CD-OE1	6.08	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	542	GLU	CD-OE2	6.08	1.32	1.25
1	C	542	GLU	CG-CD	6.05	1.61	1.51
1	A	542	GLU	CG-CD	5.91	1.60	1.51
1	A	91	LYS	CB-CG	-5.84	1.36	1.52
1	D	478	GLU	CD-OE1	5.79	1.32	1.25
1	C	296	GLU	CG-CD	5.76	1.60	1.51
1	A	228	GLU	CG-CD	5.60	1.60	1.51
1	A	421	GLU	CB-CG	5.56	1.62	1.52
1	B	559	GLU	CD-OE2	-5.54	1.19	1.25
1	C	542	GLU	CD-OE2	5.52	1.31	1.25
1	B	482	GLU	CD-OE1	5.49	1.31	1.25
1	A	516	GLU	CG-CD	5.49	1.60	1.51
1	B	104	VAL	CB-CG1	-5.41	1.41	1.52
1	A	358	GLU	CD-OE1	5.39	1.31	1.25
1	C	482	GLU	CD-OE2	5.38	1.31	1.25
1	C	482	GLU	CD-OE1	5.37	1.31	1.25
1	C	478	GLU	CD-OE2	5.27	1.31	1.25
1	A	330	VAL	CB-CG1	-5.11	1.42	1.52
1	C	194	GLU	CB-CG	-5.08	1.42	1.52
1	A	582	GLY	N-CA	-5.05	1.38	1.46
1	A	482	GLU	CG-CD	5.04	1.59	1.51
1	C	482	GLU	CG-CD	5.01	1.59	1.51
1	A	83	GLY	N-CA	5.00	1.53	1.46

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	139	ARG	NE-CZ-NH2	-19.20	110.70	120.30
1	B	139	ARG	NE-CZ-NH1	17.86	129.23	120.30
1	B	81	ASP	CB-CG-OD1	-16.86	103.13	118.30
1	C	139	ARG	NE-CZ-NH2	-16.04	112.28	120.30
1	C	139	ARG	NE-CZ-NH1	13.35	126.97	120.30
1	A	139	ARG	NE-CZ-NH1	12.41	126.51	120.30
1	D	139	ARG	NE-CZ-NH2	-10.43	115.09	120.30
1	C	81	ASP	CB-CG-OD1	-10.38	108.96	118.30
1	A	139	ARG	NE-CZ-NH2	-10.13	115.23	120.30
1	B	81	ASP	CB-CG-OD2	9.54	126.88	118.30
1	D	389	LEU	CB-CG-CD1	-9.35	95.10	111.00
1	B	308	ARG	NE-CZ-NH2	-9.12	115.74	120.30
1	A	314	ASP	CB-CG-OD1	8.59	126.03	118.30
1	B	211	ASP	CB-CG-OD2	-8.47	110.67	118.30
1	B	211	ASP	CB-CG-OD1	8.43	125.89	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	314	ASP	CB-CG-OD2	-8.15	110.96	118.30
1	C	180	ARG	NE-CZ-NH1	-7.40	116.60	120.30
1	B	159	ARG	NE-CZ-NH1	7.05	123.82	120.30
1	B	175	PHE	CB-CG-CD1	6.89	125.62	120.80
1	A	503	ASP	CB-CG-OD1	6.84	124.45	118.30
1	D	139	ARG	NE-CZ-NH1	6.84	123.72	120.30
1	B	374	ASP	CB-CG-OD1	6.74	124.37	118.30
1	A	261	ASP	CB-CG-OD1	6.67	124.30	118.30
1	A	554	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	A	349	LEU	CB-CG-CD2	6.34	121.78	111.00
1	D	180	ARG	NE-CZ-NH1	-6.34	117.13	120.30
1	B	175	PHE	CB-CG-CD2	-6.29	116.40	120.80
1	A	470	ASP	CB-CG-OD2	-6.22	112.70	118.30
1	C	81	ASP	CB-CG-OD2	6.06	123.75	118.30
1	A	147	ASP	CB-CG-OD1	6.02	123.72	118.30
1	B	139	ARG	CD-NE-CZ	5.99	131.98	123.60
1	B	545	LEU	CB-CG-CD1	5.93	121.09	111.00
1	B	470	ASP	CB-CG-OD1	5.91	123.62	118.30
1	B	245	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	81	ASP	CB-CG-OD2	5.78	123.50	118.30
1	B	374	ASP	CB-CG-OD2	-5.77	113.11	118.30
1	C	139	ARG	CG-CD-NE	-5.66	99.92	111.80
1	B	176	ASP	CB-CG-OD2	5.51	123.26	118.30
1	C	380	MET	CG-SD-CE	-5.51	91.38	100.20
1	B	91	LYS	CA-CB-CG	5.43	125.35	113.40
1	B	571	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	B	96	TYR	CB-CG-CD2	5.37	124.22	121.00
1	C	516	GLU	OE1-CD-OE2	-5.32	116.91	123.30
1	A	288	ARG	NE-CZ-NH2	-5.32	117.64	120.30
1	A	503	ASP	CB-CG-OD2	-5.30	113.53	118.30
1	A	245	ARG	NE-CZ-NH1	5.29	122.95	120.30
1	A	82	SER	CA-CB-OG	5.29	125.49	111.20
1	B	380	MET	CG-SD-CE	-5.29	91.74	100.20
1	B	481	GLU	OE1-CD-OE2	-5.25	117.00	123.30
1	A	261	ASP	CB-CG-OD2	-5.24	113.59	118.30
1	C	545	LEU	CB-CG-CD1	5.20	119.84	111.00
1	D	389	LEU	CA-CB-CG	-5.19	103.36	115.30
1	C	211	ASP	CB-CG-OD1	5.16	122.94	118.30
1	B	554	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	A	198	LEU	CB-CG-CD2	5.01	119.51	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	81	ASP	Peptide
1	B	449	ILE	Peptide
1	D	388	GLU	Peptide

## 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	4534	0	4382	47	0
1	B	4534	0	4382	61	0
1	C	4525	0	4376	70	0
1	D	4518	0	4369	85	0
2	A	53	0	31	0	0
2	B	53	0	31	0	0
2	C	53	0	29	0	0
2	D	53	0	28	1	0
3	A	26	0	31	0	0
3	B	16	0	22	0	0
3	D	16	0	22	0	0
4	B	12	0	12	3	0
4	C	12	0	12	13	0
5	A	498	0	0	15	0
5	B	554	0	0	10	0
5	C	504	0	0	13	0
5	D	344	0	0	12	0
All	All	20305	0	17727	264	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 7.

All (264) 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:C:133:ALA:CB	4:C:901:MES:H71	1.40	1.50
1:C:299:HIS:CE1	1:C:310:GLU:HG2	1.60	1.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:383:ARG:HB2	1:C:383:ARG:NH1	1.45	1.31
1:C:383:ARG:HH11	1:C:383:ARG:CB	1.47	1.25
1:C:133:ALA:CB	4:C:901:MES:C7	2.20	1.18
1:A:45:ILE:H	1:A:45:ILE:HD12	1.01	1.13
1:C:133:ALA:HB2	4:C:901:MES:H71	1.18	1.12
1:C:133:ALA:HB3	4:C:901:MES:H71	1.15	1.11
1:C:101:ASP:O	1:C:104:VAL:HG12	1.50	1.07
1:C:133:ALA:HB2	4:C:901:MES:O1S	1.56	1.04
1:C:133:ALA:HB3	4:C:901:MES:C7	1.86	1.02
1:D:45:ILE:HA	5:D:2497:HOH:O	1.61	0.99
1:A:45:ILE:H	1:A:45:ILE:CD1	1.78	0.94
1:B:576:LYS:HD3	1:B:576:LYS:N	1.79	0.94
1:D:101:ASP:O	1:D:104:VAL:HG12	1.68	0.94
1:A:45:ILE:HD12	1:A:45:ILE:N	1.81	0.94
1:D:343:ALA:O	1:D:344:ASN:ND2	2.00	0.93
1:C:133:ALA:HB2	4:C:901:MES:C7	1.92	0.90
1:C:383:ARG:HB2	1:C:383:ARG:HH11	0.73	0.90
1:C:299:HIS:CE1	1:C:310:GLU:CG	2.54	0.89
1:C:490:LYS:HD3	1:C:491:ILE:HD13	1.55	0.88
1:B:347:GLU:HG3	1:B:348:LEU:HG	1.55	0.87
1:B:343:ALA:O	1:B:344:ASN:ND2	2.08	0.87
1:C:126:LEU:CD1	1:C:132:GLN:HG3	2.05	0.86
1:D:185:LYS:HD3	5:D:2678:HOH:O	1.75	0.85
1:B:101:ASP:O	1:B:104:VAL:HG12	1.77	0.85
1:D:285:ARG:HA	1:D:328:LEU:HD11	1.58	0.85
1:D:341:ASN:HD21	1:D:343:ALA:HB3	1.43	0.83
1:C:126:LEU:HD12	1:C:132:GLN:HG3	1.62	0.82
1:B:618:PHE:C	1:B:618:PHE:HD1	1.83	0.81
1:C:411:LYS:HE3	5:C:2449:HOH:O	1.79	0.81
1:D:343:ALA:C	1:D:344:ASN:HD22	1.84	0.81
1:A:101:ASP:OD2	1:A:459:VAL:HG13	1.82	0.80
1:A:84:LEU:HD23	5:B:2054:HOH:O	1.81	0.79
1:B:618:PHE:C	1:B:618:PHE:CD1	2.55	0.79
1:A:383:ARG:HB3	1:A:392:SER:HB3	1.65	0.78
1:D:185:LYS:H	1:D:185:LYS:HD2	1.49	0.77
1:B:385:THR:HG23	1:B:388:GLU:OE1	1.85	0.77
1:D:185:LYS:H	1:D:185:LYS:CD	1.95	0.77
1:D:341:ASN:HD22	1:D:343:ALA:H	1.36	0.73
1:B:450:HIS:CE1	1:B:472:ARG:HH11	2.07	0.73
1:D:341:ASN:ND2	1:D:343:ALA:H	1.86	0.73
1:B:341:ASN:C	1:B:341:ASN:HD22	1.92	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:608:TYR:CZ	1:D:612:ASN:OD1	2.42	0.72
1:A:450:HIS:HD2	5:A:1424:HOH:O	1.72	0.71
1:A:82:SER:HB2	5:A:1477:HOH:O	1.92	0.70
1:A:505:ARG:HD3	5:A:1785:HOH:O	1.92	0.70
1:D:157:VAL:HG21	1:D:324:HIS:HE1	1.56	0.69
1:B:450:HIS:HD2	5:B:1237:HOH:O	1.75	0.69
1:D:341:ASN:HD22	1:D:341:ASN:C	1.96	0.69
1:D:459:VAL:HG12	1:D:459:VAL:O	1.92	0.69
1:D:505:ARG:NH2	5:D:2273:HOH:O	2.25	0.68
1:D:285:ARG:HA	1:D:328:LEU:CD1	2.24	0.68
1:C:101:ASP:O	1:C:104:VAL:CG1	2.35	0.67
1:C:126:LEU:CD1	1:C:132:GLN:CG	2.72	0.67
1:A:157:VAL:HG21	1:A:324:HIS:HE1	1.60	0.66
1:B:450:HIS:HE1	1:B:472:ARG:HH11	1.42	0.66
1:A:344:ASN:HD22	1:A:345:PRO:HD2	1.60	0.65
1:B:489:ASP:O	1:B:490:LYS:HD2	1.96	0.65
1:D:617:PRO:O	1:D:618:PHE:C	2.35	0.65
1:D:389:LEU:HD12	1:D:389:LEU:C	2.00	0.65
1:D:308:ARG:HG3	1:D:308:ARG:HH11	1.62	0.65
1:C:132:GLN:OE1	4:C:901:MES:H31	1.97	0.64
1:A:132:GLN:HG2	5:A:2468:HOH:O	1.98	0.63
1:B:459:VAL:HG12	1:B:461:GLN:NE2	2.14	0.63
1:B:478:GLU:HG3	1:B:511:THR:OG1	2.00	0.62
1:B:459:VAL:HG22	5:B:2672:HOH:O	1.98	0.62
1:B:459:VAL:CG2	5:B:2672:HOH:O	2.48	0.62
1:D:389:LEU:HD12	1:D:389:LEU:O	1.99	0.61
1:D:450:HIS:HD2	5:D:2499:HOH:O	1.84	0.60
1:C:450:HIS:CE1	1:C:472:ARG:HH11	2.19	0.60
1:D:185:LYS:HD2	1:D:185:LYS:N	2.16	0.60
1:B:81:ASP:OD2	1:B:90:LYS:NZ	2.34	0.60
1:D:45:ILE:CA	5:D:2497:HOH:O	2.34	0.59
1:A:383:ARG:HD2	1:A:390:THR:O	2.02	0.59
1:B:308:ARG:HD2	5:B:2220:HOH:O	2.03	0.59
1:D:444:PRO:HD2	1:D:445:TRP:CZ3	2.38	0.59
1:D:291:LEU:O	1:D:292:ASN:HB2	2.03	0.58
1:D:382:ILE:HD13	5:D:2622:HOH:O	2.03	0.58
1:A:101:ASP:HB3	1:A:459:VAL:HG22	1.85	0.57
1:D:62:ALA:O	1:D:66:VAL:HG23	2.05	0.57
1:D:459:VAL:O	1:D:459:VAL:CG1	2.52	0.57
1:B:50:VAL:HG13	1:B:313:ALA:HB2	1.86	0.57
1:B:63:ARG:HD2	1:B:259:VAL:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:GLN:OE1	4:B:901:MES:H31	2.04	0.57
1:C:133:ALA:CB	4:C:901:MES:H72	2.28	0.56
1:C:450:HIS:HE1	1:C:472:ARG:HD2	1.70	0.56
1:D:414:ASN:O	1:D:418:GLN:HG3	2.06	0.56
1:A:457:GLY:HA2	5:A:2149:HOH:O	2.06	0.56
1:C:126:LEU:HD13	1:C:132:GLN:CG	2.35	0.56
1:D:478:GLU:HG3	1:D:511:THR:OG1	2.06	0.55
1:A:385:THR:O	1:A:388:GLU:HB2	2.06	0.55
1:B:542:GLU:HB2	1:B:545:LEU:HD22	1.88	0.55
1:C:382:ILE:HD13	5:C:2150:HOH:O	2.07	0.55
1:B:293:SER:O	1:B:576:LYS:HE2	2.06	0.55
1:C:131:TRP:O	1:C:132:GLN:HG2	2.06	0.55
1:B:100:ILE:HD13	1:B:100:ILE:O	2.07	0.55
1:D:308:ARG:HH11	1:D:308:ARG:CG	2.20	0.55
1:A:344:ASN:HD22	1:A:345:PRO:CD	2.20	0.54
1:C:604:LYS:NZ	5:C:1648:HOH:O	2.26	0.54
1:C:157:VAL:HG21	1:C:324:HIS:HE1	1.72	0.54
1:B:178:GLU:OE1	1:B:439:PHE:HE1	1.90	0.54
1:C:299:HIS:ND1	1:C:310:GLU:HG2	2.12	0.54
1:C:385:THR:OG1	1:C:388:GLU:CD	2.45	0.54
1:C:542:GLU:HB2	1:C:545:LEU:HD22	1.89	0.54
1:A:385:THR:HG22	1:A:386:PRO:HD2	1.89	0.54
1:A:411:LYS:HD3	5:A:2592:HOH:O	2.08	0.54
1:B:100:ILE:CD1	1:B:453:ALA:HB2	2.38	0.54
1:C:450:HIS:HD2	5:C:1651:HOH:O	1.89	0.54
1:B:342:PRO:C	1:B:344:ASN:H	2.11	0.54
1:C:47:TYR:O	1:C:313:ALA:HA	2.08	0.53
1:C:528:LYS:NZ	5:C:2436:HOH:O	2.40	0.53
1:A:104:VAL:HG13	1:A:454:PHE:O	2.07	0.53
1:C:383:ARG:NH1	1:C:383:ARG:CB	2.30	0.53
1:D:450:HIS:CE1	1:D:472:ARG:HH11	2.25	0.53
1:B:493:ASP:OD2	5:B:1303:HOH:O	2.19	0.53
1:C:328:LEU:C	1:C:328:LEU:HD23	2.28	0.53
1:B:284:GLU:OE1	1:B:308:ARG:NH2	2.42	0.52
1:A:450:HIS:CE1	1:A:472:ARG:HH11	2.27	0.52
1:A:478:GLU:CD	1:A:480:LYS:HE2	2.30	0.52
1:A:381:THR:HB	1:A:394:THR:OG1	2.09	0.52
1:D:216:SER:HB3	1:D:219:HIS:HB3	1.91	0.52
1:D:432:GLU:HB2	1:D:433:PRO:HD2	1.92	0.52
1:A:101:ASP:HB3	1:A:459:VAL:CG2	2.40	0.52
1:A:478:GLU:HG2	1:A:480:LYS:HE2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:ALA:HB2	4:C:901:MES:C8	2.40	0.52
1:C:429:GLU:HG2	5:C:2850:HOH:O	2.09	0.52
1:B:100:ILE:HD11	1:B:453:ALA:HB2	1.92	0.52
1:D:185:LYS:O	1:D:186:ASP:C	2.46	0.52
1:B:341:ASN:C	1:B:341:ASN:ND2	2.63	0.51
1:D:335:GLY:O	1:D:346:PRO:HB3	2.10	0.51
1:D:50:VAL:HG23	1:D:50:VAL:O	2.11	0.51
1:A:178:GLU:OE1	1:A:441:PRO:HG3	2.11	0.51
1:B:538:PRO:HG2	1:C:538:PRO:HG2	1.92	0.51
1:D:385:THR:HG22	1:D:386:PRO:HD2	1.92	0.51
1:A:101:ASP:OD2	5:A:2823:HOH:O	2.19	0.51
1:C:132:GLN:OE1	4:C:901:MES:C3	2.59	0.51
1:D:285:ARG:CA	1:D:328:LEU:HD11	2.38	0.51
1:C:126:LEU:HD13	1:C:132:GLN:HG3	1.92	0.50
1:D:341:ASN:HD21	1:D:343:ALA:CB	2.20	0.50
1:D:341:ASN:ND2	1:D:343:ALA:HB3	2.18	0.50
1:A:558:ASP:OD2	5:A:2726:HOH:O	2.19	0.49
1:C:490:LYS:HD3	1:C:491:ILE:CD1	2.37	0.49
1:D:603:ILE:O	1:D:607:GLU:HG3	2.11	0.49
1:D:346:PRO:HG2	1:D:350:PRO:HA	1.94	0.49
1:D:289:ASN:OD1	1:D:292:ASN:N	2.46	0.49
1:C:450:HIS:HE1	1:C:472:ARG:HH11	1.60	0.49
1:D:81:ASP:HB2	5:D:2214:HOH:O	2.13	0.49
1:D:181:PRO:HG2	1:D:195:TRP:HZ2	1.78	0.49
1:C:81:ASP:OD2	1:C:90:LYS:NZ	2.44	0.48
1:C:133:ALA:HB2	4:C:901:MES:S	2.52	0.48
1:C:460:GLN:HB2	5:C:1928:HOH:O	2.13	0.48
1:D:385:THR:O	1:D:388:GLU:HG3	2.13	0.48
1:B:178:GLU:HB2	5:B:1867:HOH:O	2.13	0.48
1:B:459:VAL:HG12	1:B:461:GLN:HE22	1.78	0.48
1:C:81:ASP:OD1	1:C:81:ASP:N	2.47	0.48
1:D:308:ARG:CG	1:D:308:ARG:NH1	2.77	0.48
1:C:46:LYS:HG3	1:C:47:TYR:N	2.26	0.48
1:D:341:ASN:ND2	1:D:341:ASN:C	2.67	0.48
1:B:81:ASP:OD1	1:B:81:ASP:C	2.47	0.47
1:D:194:GLU:OE1	5:D:2796:HOH:O	2.20	0.47
1:A:460:GLN:HB2	5:A:1838:HOH:O	2.14	0.47
1:D:389:LEU:HD12	1:D:389:LEU:HA	1.16	0.47
1:C:385:THR:O	1:C:386:PRO:C	2.50	0.47
1:B:47:TYR:O	1:B:313:ALA:HA	2.15	0.47
1:A:505:ARG:HD2	5:A:2693:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:ASP:OD2	1:C:459:VAL:HG23	2.15	0.47
1:D:184:VAL:HG13	5:D:2678:HOH:O	2.15	0.47
1:D:199:TYR:O	1:D:203:GLU:HG3	2.14	0.47
1:B:91:LYS:NZ	1:B:452:ASP:OD1	2.46	0.46
1:B:537:LEU:HB3	1:B:538:PRO:HD2	1.97	0.46
1:A:82:SER:HB3	5:A:2308:HOH:O	2.16	0.46
1:A:158:THR:HG22	1:A:160:VAL:HG22	1.97	0.46
1:D:450:HIS:HE1	1:D:472:ARG:HH11	1.62	0.46
1:C:564:CYS:HG	1:C:573:PHE:HE2	1.64	0.46
1:A:44:ASP:HB2	1:A:47:TYR:CZ	2.51	0.45
1:C:231:LYS:HB2	1:C:231:LYS:HE2	1.48	0.45
1:D:89:HIS:CE1	1:D:91:LYS:HB3	2.50	0.45
1:B:81:ASP:OD1	1:B:81:ASP:N	2.45	0.45
1:C:450:HIS:CE1	1:C:472:ARG:HD2	2.51	0.45
1:D:385:THR:OG1	1:D:388:GLU:OE1	2.20	0.45
1:D:439:PHE:C	1:D:440:GLN:HG2	2.37	0.45
1:B:104:VAL:HG13	1:B:105:ASN:N	2.32	0.45
1:C:196:ASP:OD1	5:C:2646:HOH:O	2.21	0.45
1:D:47:TYR:O	1:D:313:ALA:HA	2.17	0.45
1:D:218:ARG:HD2	5:D:1256:HOH:O	2.16	0.45
1:A:126:LEU:HD12	1:A:132:GLN:HG3	1.99	0.44
1:A:342:PRO:C	1:A:344:ASN:N	2.71	0.44
1:B:450:HIS:HE1	1:B:472:ARG:HD2	1.83	0.44
1:B:481:GLU:OE2	1:B:484:LYS:NZ	2.48	0.44
1:C:459:VAL:HG13	1:C:461:GLN:NE2	2.32	0.44
5:C:2186:HOH:O	1:D:462:SER:HB2	2.17	0.44
1:C:570:SER:HB3	1:C:580:LEU:O	2.18	0.44
1:D:56:PRO:HD3	1:D:165:SER:HB3	1.99	0.44
1:D:208:THR:HA	1:D:242:ALA:HA	1.99	0.44
1:A:89:HIS:CE1	1:A:91:LYS:HB2	2.53	0.44
1:C:341:ASN:HA	1:C:342:PRO:HD2	1.90	0.44
1:A:450:HIS:HE1	1:A:472:ARG:HH11	1.64	0.44
1:C:214:LYS:O	5:C:2277:HOH:O	2.21	0.44
1:C:460:GLN:OE1	5:C:1928:HOH:O	2.21	0.44
1:D:107:ILE:HG12	1:D:167:ALA:HB1	1.99	0.44
1:B:607:GLU:HG3	5:B:2890:HOH:O	2.17	0.44
1:D:490:LYS:HG3	1:D:491:ILE:HD13	2.00	0.44
1:A:478:GLU:CG	1:A:480:LYS:HE2	2.48	0.44
1:D:45:ILE:N	5:D:2497:HOH:O	2.50	0.43
1:C:265:ARG:HA	1:C:266:PRO:C	2.38	0.43
4:C:901:MES:H51	4:C:901:MES:H82	1.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:343:ALA:C	1:D:344:ASN:ND2	2.55	0.43
1:D:68:ALA:HB2	1:D:610:LYS:NZ	2.33	0.43
1:B:218:ARG:HD2	5:B:1188:HOH:O	2.18	0.43
1:A:64:GLU:OE2	1:A:205:TYR:OH	2.29	0.43
1:D:197:ARG:NH2	1:D:607:GLU:OE1	2.47	0.43
1:A:432:GLU:H	1:A:432:GLU:CD	2.20	0.43
1:C:339:ARG:HA	1:C:340:PRO:HD3	1.85	0.43
1:B:139:ARG:HD3	4:B:901:MES:O2S	2.19	0.42
1:B:158:THR:HG22	1:B:160:VAL:HG22	2.01	0.42
1:C:228:GLU:HG3	1:C:231:LYS:NZ	2.33	0.42
1:A:505:ARG:NH1	5:A:2693:HOH:O	2.29	0.42
1:D:554:ARG:O	1:D:564:CYS:HB2	2.19	0.42
1:A:462:SER:OG	4:B:901:MES:H61	2.20	0.42
1:B:157:VAL:HG21	1:B:324:HIS:HE1	1.83	0.42
1:B:487:PHE:HB3	1:B:498:PRO:HB2	2.01	0.42
1:B:564:CYS:HG	1:B:573:PHE:HE2	1.67	0.42
1:C:218:ARG:HD2	5:C:1133:HOH:O	2.20	0.42
1:B:104:VAL:HG23	1:B:454:PHE:O	2.20	0.42
1:B:513:LYS:NZ	1:B:517:ASP:OD2	2.53	0.42
1:C:45:ILE:HB	1:C:46:LYS:H	1.20	0.42
1:C:396:THR:HA	1:C:397:PRO:HD3	1.90	0.42
1:C:385:THR:N	1:C:388:GLU:OE1	2.47	0.42
1:A:450:HIS:HE1	1:A:472:ARG:HD2	1.85	0.42
1:C:383:ARG:NH1	1:C:383:ARG:CG	2.83	0.42
1:D:201:LYS:HD3	1:D:603:ILE:HG21	2.01	0.42
1:D:299:HIS:CD2	1:D:310:GLU:HG2	2.55	0.42
1:A:218:ARG:HD2	5:A:1396:HOH:O	2.20	0.41
1:A:375:SER:HA	5:A:2923:HOH:O	2.19	0.41
1:B:471:TRP:CH2	1:B:526:SER:HA	2.55	0.41
1:D:175:PHE:CE1	1:D:592:ALA:HB3	2.55	0.41
1:D:293:SER:HA	1:D:574:GLY:O	2.20	0.41
1:B:328:LEU:HD23	1:B:328:LEU:C	2.40	0.41
1:D:284:GLU:O	1:D:285:ARG:HB3	2.21	0.41
1:B:56:PRO:HD3	1:B:165:SER:HB3	2.03	0.41
1:B:590:TYR:CE2	1:B:594:PRO:HB3	2.55	0.41
1:D:299:HIS:NE2	1:D:310:GLU:CD	2.74	0.41
1:B:344:ASN:O	1:B:345:PRO:C	2.58	0.41
1:C:611:GLN:HG2	5:C:2779:HOH:O	2.21	0.41
1:D:385:THR:H	1:D:388:GLU:CD	2.24	0.41
1:B:385:THR:CG2	1:B:388:GLU:OE1	2.62	0.41
1:B:460:GLN:HB2	5:B:2241:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ILE:HG12	1:A:167:ALA:HB1	2.02	0.41
5:A:2721:HOH:O	1:B:461:GLN:HB3	2.20	0.41
1:B:185:LYS:H	1:B:185:LYS:HG2	1.68	0.41
1:C:101:ASP:CG	1:C:459:VAL:HG23	2.40	0.41
1:D:97:GLN:HG3	1:D:250:PHE:CE2	2.56	0.41
1:D:336:GLN:NE2	1:D:344:ASN:O	2.53	0.41
1:D:390:THR:HB	5:D:2845:HOH:O	2.20	0.41
1:D:537:LEU:HB3	1:D:538:PRO:HD2	2.02	0.41
1:D:608:TYR:CD1	1:D:608:TYR:C	2.94	0.41
1:D:218:ARG:HG3	1:D:430:ASP:OD2	2.20	0.41
1:A:408:TRP:CD1	1:A:408:TRP:C	2.95	0.40
1:D:354:SER:OG	1:D:484:LYS:NZ	2.53	0.40
1:B:576:LYS:N	1:B:576:LYS:CD	2.65	0.40
1:D:49:VAL:HG22	1:D:315:VAL:HB	2.03	0.40
1:C:47:TYR:CD2	1:C:73:ALA:HB2	2.56	0.40
2:D:801:FAD:H9	2:D:801:FAD:H1'1	1.87	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	574/623 (92%)	559 (97%)	15 (3%)	0	100	100
1	B	574/623 (92%)	557 (97%)	16 (3%)	1 (0%)	47	30
1	C	573/623 (92%)	558 (97%)	15 (3%)	0	100	100
1	D	572/623 (92%)	551 (96%)	19 (3%)	2 (0%)	41	24
All	All	2293/2492 (92%)	2225 (97%)	65 (3%)	3 (0%)	51	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	389	LEU
1	D	186	ASP
1	B	345	PRO

### 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	502/540 (93%)	487 (97%)	15 (3%)	41	22
1	B	502/540 (93%)	484 (96%)	18 (4%)	35	16
1	C	501/540 (93%)	486 (97%)	15 (3%)	41	22
1	D	500/540 (93%)	484 (97%)	16 (3%)	39	20
All	All	2005/2160 (93%)	1941 (97%)	64 (3%)	39	20

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ILE
1	A	112	MET
1	A	168	TRP
1	A	206	PHE
1	A	269	ASP
1	A	299	HIS
1	A	344	ASN
1	A	385	THR
1	A	388	GLU
1	A	408	TRP
1	A	429	GLU
1	A	445	TRP
1	A	490	LYS
1	A	496	ASN
1	A	593	ASN
1	B	45	ILE
1	B	46	LYS
1	B	100	ILE
1	B	168	TRP

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Mol	Chain	Res	Type
1	B	206	PHE
1	B	310	GLU
1	B	341	ASN
1	B	344	ASN
1	B	347	GLU
1	B	385	THR
1	B	400	SER
1	B	408	TRP
1	B	441	PRO
1	B	460	GLN
1	B	545	LEU
1	B	576	LYS
1	B	593	ASN
1	B	618	PHE
1	C	45	ILE
1	C	46	LYS
1	C	112	MET
1	C	168	TRP
1	C	206	PHE
1	C	231	LYS
1	C	269	ASP
1	C	299	HIS
1	C	383	ARG
1	C	385	THR
1	C	408	TRP
1	C	421	GLU
1	C	459	VAL
1	C	593	ASN
1	C	619	THR
1	D	91	LYS
1	D	101	ASP
1	D	112	MET
1	D	168	TRP
1	D	185	LYS
1	D	199	TYR
1	D	204	SER
1	D	206	PHE
1	D	214	LYS
1	D	271	PRO
1	D	341	ASN
1	D	383	ARG
1	D	385	THR

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Mol	Chain	Res	Type
1	D	403	LYS
1	D	408	TRP
1	D	450	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	263	GLN
1	A	299	HIS
1	A	324	HIS
1	A	341	ASN
1	A	344	ASN
1	A	450	HIS
1	B	341	ASN
1	B	450	HIS
1	B	461	GLN
1	B	611	GLN
1	C	224	ASN
1	C	263	GLN
1	C	299	HIS
1	C	341	ASN
1	C	344	ASN
1	C	450	HIS
1	C	461	GLN
1	D	132	GLN
1	D	207	GLN
1	D	324	HIS
1	D	341	ASN
1	D	344	ASN
1	D	450	HIS
1	D	612	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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



## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	FAD	C	801	-	51,58,58	1.49	12 (23%)	60,89,89	2.59	18 (30%)
4	MES	B	901	-	12,12,12	2.41	3 (25%)	14,16,16	5.06	7 (50%)
3	1PE	B	902	-	15,15,15	0.61	0	14,14,14	0.26	0
2	FAD	D	801	-	51,58,58	1.94	15 (29%)	60,89,89	3.69	20 (33%)
3	1PE	A	904	-	13,13,15	0.73	0	12,12,14	0.35	0
2	FAD	B	801	-	51,58,58	1.94	15 (29%)	60,89,89	2.52	12 (20%)
3	1PE	A	905	-	11,11,15	0.82	0	10,10,14	0.54	0
2	FAD	A	801	-	51,58,58	1.68	9 (17%)	60,89,89	2.51	21 (35%)
3	1PE	D	903	-	15,15,15	0.70	0	14,14,14	0.48	0
4	MES	C	901	-	12,12,12	2.03	1 (8%)	14,16,16	4.75	11 (78%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	C	801	-	-	3/30/50/50	0/6/6/6
4	MES	B	901	-	-	2/6/14/14	0/1/1/1
3	1PE	B	902	-	-	1/13/13/13	-
2	FAD	D	801	-	-	3/30/50/50	0/6/6/6
3	1PE	A	904	-	-	2/11/11/13	-
2	FAD	B	801	-	-	1/30/50/50	0/6/6/6
3	1PE	A	905	-	-	2/9/9/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	A	801	-	-	3/30/50/50	0/6/6/6
3	1PE	D	903	-	-	2/13/13/13	-
4	MES	C	901	-	-	2/6/14/14	0/1/1/1

All (55) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	901	MES	C8-S	-7.69	1.66	1.77
4	C	901	MES	C8-S	-6.52	1.68	1.77
2	D	801	FAD	C10-N1	6.05	1.41	1.33
2	B	801	FAD	C4X-C10	5.73	1.44	1.38
2	B	801	FAD	C1'-N10	5.30	1.53	1.48
2	A	801	FAD	C4A-N3A	-5.15	1.28	1.35
2	B	801	FAD	C4A-N3A	-4.14	1.29	1.35
2	D	801	FAD	C6-C5X	4.11	1.48	1.41
2	A	801	FAD	C4X-C10	3.86	1.42	1.38
2	B	801	FAD	O4B-C1B	3.71	1.46	1.41
2	A	801	FAD	C8M-C8	3.66	1.58	1.51
2	B	801	FAD	C10-N1	3.62	1.37	1.33
2	A	801	FAD	C4X-N5	3.62	1.38	1.33
2	C	801	FAD	C2B-C1B	-3.45	1.48	1.53
2	B	801	FAD	C2B-C1B	-3.10	1.49	1.53
2	D	801	FAD	C4-N3	3.05	1.38	1.33
2	B	801	FAD	C4-C4X	3.01	1.46	1.41
2	D	801	FAD	C2-N3	-2.99	1.32	1.38
2	D	801	FAD	C4-C4X	2.92	1.46	1.41
2	B	801	FAD	C5A-C4A	-2.89	1.33	1.40
2	A	801	FAD	C2A-N3A	2.88	1.36	1.32
2	C	801	FAD	C4'-C3'	2.86	1.58	1.53
2	D	801	FAD	O4B-C4B	-2.85	1.38	1.45
2	A	801	FAD	C4-N3	2.76	1.37	1.33
2	C	801	FAD	O3B-C3B	-2.73	1.36	1.43
2	D	801	FAD	O2B-C2B	-2.72	1.36	1.43
2	D	801	FAD	C2B-C3B	-2.72	1.45	1.53
2	A	801	FAD	C2A-N1A	-2.67	1.28	1.33
2	C	801	FAD	C10-N1	2.58	1.36	1.33
2	B	801	FAD	C4-N3	2.52	1.37	1.33
2	D	801	FAD	C5'-C4'	2.49	1.55	1.51
2	B	801	FAD	O3B-C3B	-2.45	1.37	1.43
2	C	801	FAD	C4-C4X	2.42	1.45	1.41
2	B	801	FAD	C8M-C8	2.41	1.55	1.51
2	D	801	FAD	O3B-C3B	-2.38	1.37	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	FAD	C2A-N3A	2.37	1.35	1.32
2	D	801	FAD	C1'-N10	-2.34	1.45	1.48
2	D	801	FAD	C2A-N3A	2.32	1.35	1.32
2	C	801	FAD	C9-C8	2.32	1.43	1.37
2	C	801	FAD	O4B-C4B	-2.29	1.39	1.45
2	A	801	FAD	C9-C9A	2.29	1.45	1.40
2	D	801	FAD	C2-N1	-2.26	1.33	1.38
4	B	901	MES	O2S-S	2.25	1.51	1.45
2	C	801	FAD	C2A-N1A	2.23	1.38	1.33
2	C	801	FAD	PA-O2A	-2.22	1.44	1.55
2	D	801	FAD	C4X-C10	2.21	1.41	1.38
2	B	801	FAD	C2-N1	-2.21	1.33	1.38
2	A	801	FAD	C3B-C4B	-2.13	1.47	1.53
2	C	801	FAD	C2-N1	-2.10	1.34	1.38
2	C	801	FAD	O5B-C5B	-2.10	1.36	1.44
2	B	801	FAD	O4B-C4B	-2.09	1.40	1.45
2	B	801	FAD	C2-N3	-2.08	1.34	1.38
4	B	901	MES	O1S-S	2.07	1.51	1.45
2	D	801	FAD	C9A-N10	2.07	1.41	1.38
2	C	801	FAD	C4X-N5	2.01	1.36	1.33

All (89) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	FAD	C4-C4X-C10	-18.69	107.58	119.95
4	C	901	MES	O3S-S-C8	-12.71	85.21	105.77
2	B	801	FAD	C4-C4X-C10	-12.28	111.82	119.95
4	B	901	MES	O2S-S-C8	-11.13	93.51	106.92
2	D	801	FAD	C4-C4X-N5	11.11	131.30	118.60
4	B	901	MES	O3S-S-C8	-10.88	88.17	105.77
2	A	801	FAD	C4-N3-C2	9.23	122.93	115.14
2	D	801	FAD	C4-N3-C2	-9.21	107.36	115.14
2	D	801	FAD	C4X-C4-N3	7.91	134.25	123.43
2	C	801	FAD	C4-C4X-C10	-7.27	115.14	119.95
2	B	801	FAD	C1'-N10-C9A	7.13	123.91	118.29
2	C	801	FAD	C1'-N10-C9A	7.03	123.83	118.29
2	C	801	FAD	C4-N3-C2	6.93	121.00	115.14
4	B	901	MES	C5-N4-C3	6.82	124.18	108.83
2	A	801	FAD	C4-C4X-C10	-6.41	115.71	119.95
4	C	901	MES	C5-N4-C3	6.14	122.64	108.83
2	C	801	FAD	C4-C4X-N5	6.01	125.46	118.60
2	A	801	FAD	C1'-N10-C9A	5.81	122.86	118.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	FAD	C4-C4X-N5	5.64	125.04	118.60
2	C	801	FAD	C5A-C6A-N6A	5.45	128.64	120.35
4	C	901	MES	O1S-S-C8	-5.35	100.47	106.92
4	B	901	MES	O3S-S-O2S	4.93	123.32	111.27
4	C	901	MES	O1-C2-C3	-4.79	101.25	111.80
2	C	801	FAD	N3A-C2A-N1A	-4.79	121.20	128.68
2	A	801	FAD	C5A-C6A-N1A	-4.54	110.06	120.35
2	C	801	FAD	C1'-N10-C10	-4.52	114.36	118.41
4	B	901	MES	O1S-S-C8	-4.44	101.56	106.92
2	A	801	FAD	C2A-N1A-C6A	4.30	126.11	118.75
2	B	801	FAD	O4B-C1B-C2B	4.19	113.05	106.93
2	B	801	FAD	N3A-C2A-N1A	-4.08	122.31	128.68
2	B	801	FAD	C5A-C6A-N6A	4.05	126.51	120.35
2	D	801	FAD	O4B-C4B-C5B	4.04	122.68	109.37
2	D	801	FAD	O2A-PA-O1A	4.04	132.22	112.24
2	A	801	FAD	C4-C4X-N5	3.98	123.15	118.60
2	C	801	FAD	O2'-C2'-C3'	3.94	118.69	109.10
2	A	801	FAD	N6A-C6A-N1A	3.81	126.47	118.57
2	D	801	FAD	O2B-C2B-C3B	3.76	124.00	111.82
2	A	801	FAD	C4A-C5A-N7A	-3.72	105.52	109.40
4	C	901	MES	O2S-S-C8	-3.71	102.45	106.92
2	B	801	FAD	C2B-C3B-C4B	3.65	109.74	102.64
2	A	801	FAD	N3A-C2A-N1A	-3.51	123.19	128.68
2	D	801	FAD	C7-C6-C5X	-3.49	116.28	121.22
2	D	801	FAD	C1'-N10-C9A	3.48	121.03	118.29
4	C	901	MES	C7-N4-C5	3.47	120.10	111.23
2	D	801	FAD	N3A-C2A-N1A	-3.38	123.39	128.68
2	C	801	FAD	C4X-N5-C5X	3.38	120.14	116.77
2	D	801	FAD	C5B-C4B-C3B	3.13	126.92	115.18
2	C	801	FAD	O2B-C2B-C3B	3.12	121.92	111.82
2	A	801	FAD	O3B-C3B-C4B	3.12	120.07	111.05
4	C	901	MES	C2-C3-N4	3.10	114.80	110.10
4	C	901	MES	O3S-S-O1S	3.06	118.76	111.27
2	C	801	FAD	C10-C4X-N5	-3.03	119.16	121.26
2	A	801	FAD	C4X-C4-N3	-3.02	119.31	123.43
2	D	801	FAD	O5'-P-O1P	-2.95	97.54	109.07
2	B	801	FAD	C9A-N10-C10	-2.92	118.09	121.91
2	D	801	FAD	O2B-C2B-C1B	2.91	121.59	110.85
2	A	801	FAD	C7M-C7-C6	-2.86	113.49	120.34
2	B	801	FAD	C10-C4X-N5	2.71	123.13	121.26
2	C	801	FAD	O4B-C4B-C3B	2.68	110.41	105.11
2	C	801	FAD	O2B-C2B-C1B	2.67	120.72	110.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	FAD	C4X-N5-C5X	2.67	119.44	116.77
2	D	801	FAD	O5B-PA-O1A	-2.62	98.84	109.07
2	B	801	FAD	C5X-C9A-N10	2.60	119.60	117.72
4	B	901	MES	C7-N4-C3	2.58	117.83	111.23
2	D	801	FAD	C5A-C6A-N6A	2.57	124.26	120.35
2	A	801	FAD	C6-C5X-N5	-2.56	116.23	119.05
2	A	801	FAD	O4'-C4'-C3'	2.53	115.26	109.10
4	B	901	MES	C7-N4-C5	2.52	117.67	111.23
2	C	801	FAD	C3B-C2B-C1B	2.50	104.74	100.98
2	B	801	FAD	O3B-C3B-C4B	2.48	118.22	111.05
4	C	901	MES	O3S-S-O2S	2.48	117.33	111.27
2	C	801	FAD	N6A-C6A-N1A	-2.46	113.48	118.57
2	D	801	FAD	C4X-C10-N10	-2.45	117.78	120.30
2	B	801	FAD	O2B-C2B-C3B	2.34	119.38	111.82
2	C	801	FAD	C4X-C4-N3	-2.25	120.35	123.43
2	C	801	FAD	O4B-C1B-C2B	2.22	110.17	106.93
2	A	801	FAD	O2B-C2B-C3B	2.21	118.96	111.82
2	A	801	FAD	C5X-C9A-N10	2.18	119.29	117.72
2	D	801	FAD	C7M-C7-C6	-2.17	115.14	120.34
2	D	801	FAD	C9A-N10-C10	-2.17	119.06	121.91
2	A	801	FAD	C4X-C10-N10	-2.13	118.11	120.30
4	C	901	MES	C7-N4-C3	2.12	116.65	111.23
2	A	801	FAD	C7-C6-C5X	-2.11	118.23	121.22
2	D	801	FAD	O3B-C3B-C4B	2.10	117.11	111.05
2	C	801	FAD	O3B-C3B-C4B	2.05	116.97	111.05
4	C	901	MES	C6-O1-C2	-2.04	103.08	109.89
2	A	801	FAD	O2B-C2B-C1B	2.03	118.36	110.85
2	A	801	FAD	C2B-C3B-C4B	2.01	106.54	102.64
2	A	801	FAD	C5A-C6A-N6A	2.01	123.40	120.35

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	801	FAD	PA-O3P-P-O5'
2	D	801	FAD	PA-O3P-P-O5'
4	B	901	MES	C8-C7-N4-C5
4	B	901	MES	N4-C7-C8-S
4	C	901	MES	C8-C7-N4-C5
4	C	901	MES	N4-C7-C8-S
2	D	801	FAD	O4B-C4B-C5B-O5B
3	A	905	1PE	OH6-C15-C25-OH5

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Mol	Chain	Res	Type	Atoms
3	D	903	1PE	OH5-C14-C24-OH4
2	A	801	FAD	PA-O3P-P-O5'
3	D	903	1PE	OH7-C16-C26-OH6
3	A	904	1PE	OH6-C15-C25-OH5
3	A	905	1PE	OH5-C14-C24-OH4
3	B	902	1PE	OH5-C14-C24-OH4
2	B	801	FAD	O4B-C4B-C5B-O5B
2	A	801	FAD	P-O3P-PA-O2A
2	C	801	FAD	P-O3P-PA-O2A
2	D	801	FAD	P-O3P-PA-O2A
2	A	801	FAD	O4B-C4B-C5B-O5B
2	C	801	FAD	O4B-C4B-C5B-O5B
3	A	904	1PE	OH7-C16-C26-OH6

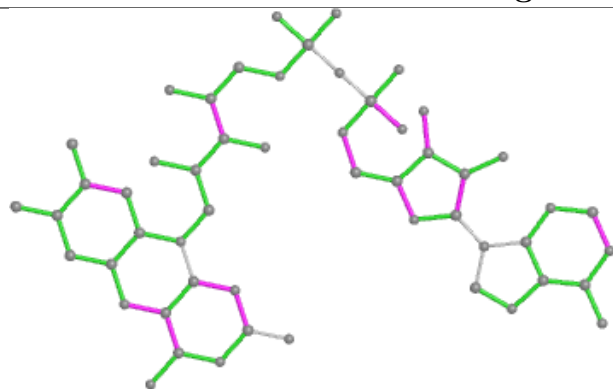
There are no ring outliers.

3 monomers are involved in 17 short contacts:

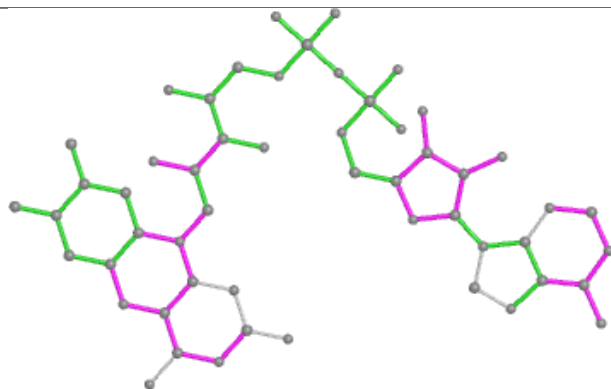
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	901	MES	3	0
2	D	801	FAD	1	0
4	C	901	MES	13	0

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.

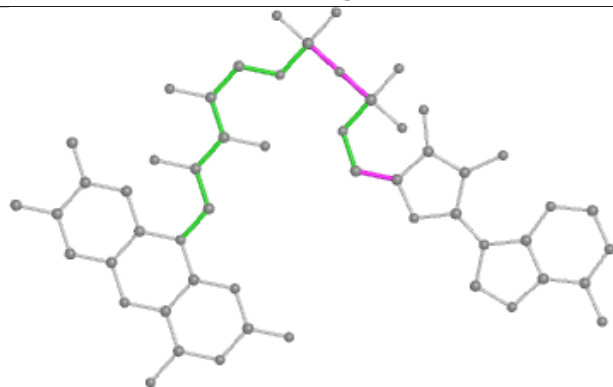
## Ligand FAD C 801



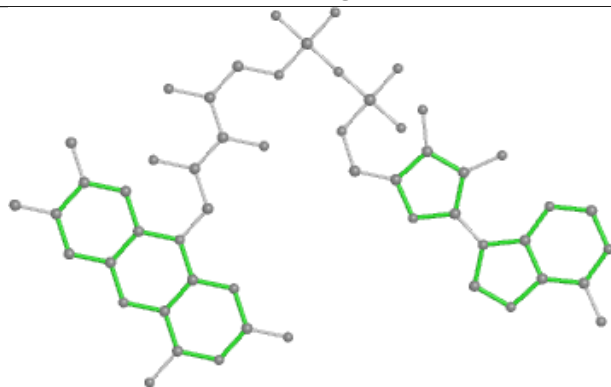
Bond lengths



Bond angles

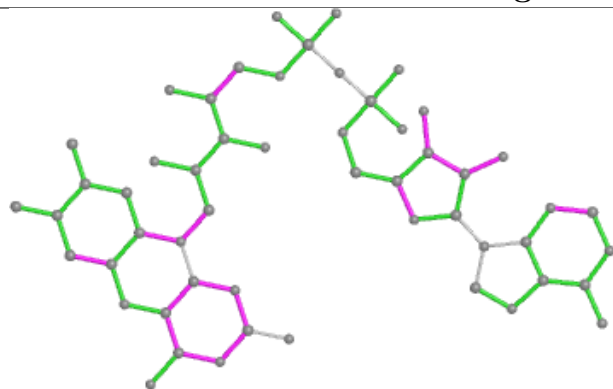


Torsions

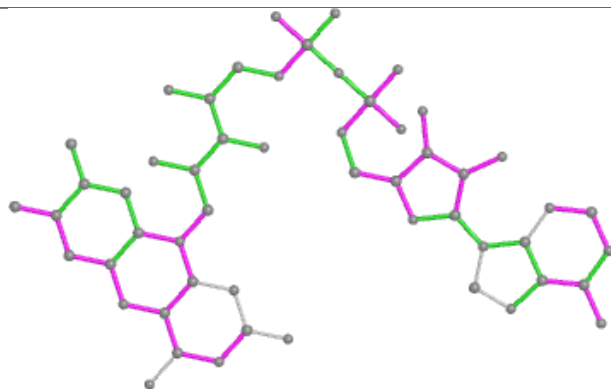


Rings

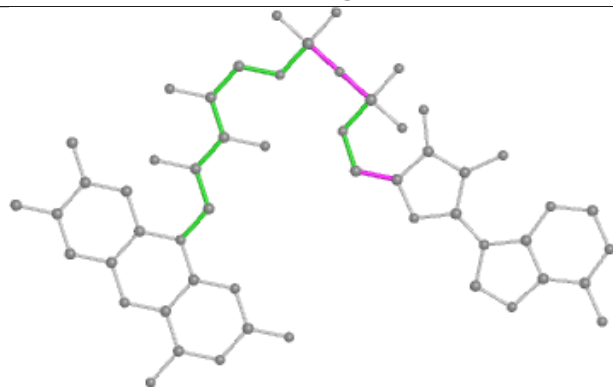
## Ligand FAD D 801



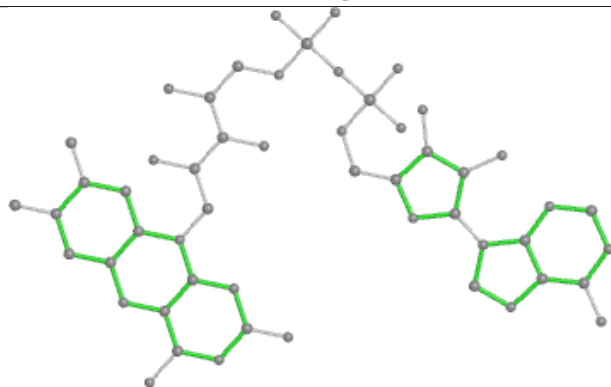
Bond lengths



Bond angles



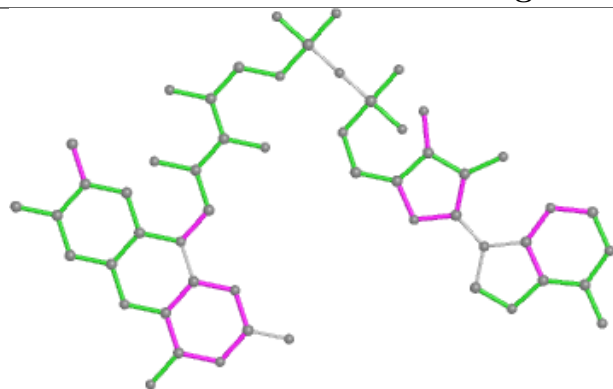
Torsions



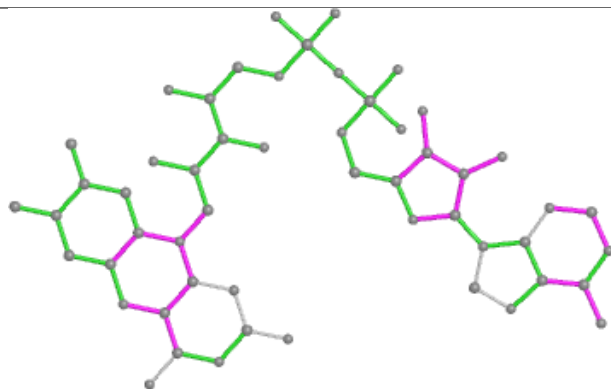
Rings



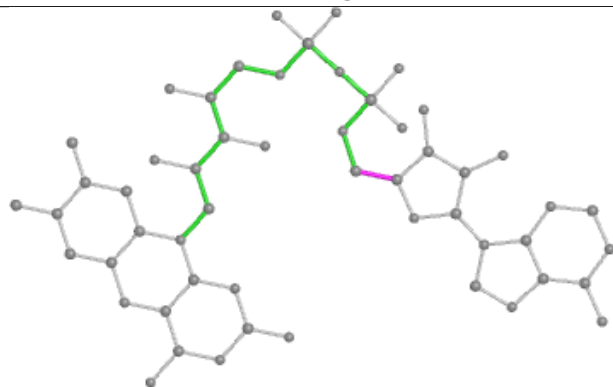
## Ligand FAD B 801



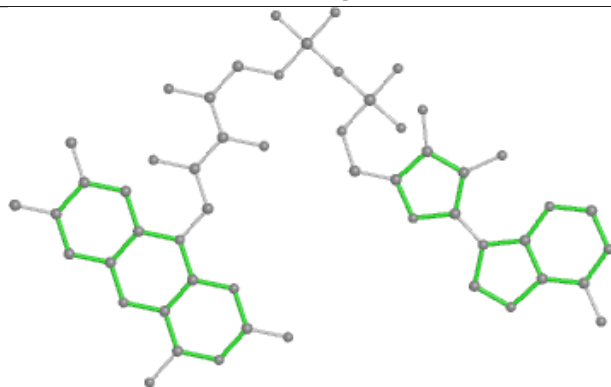
Bond lengths



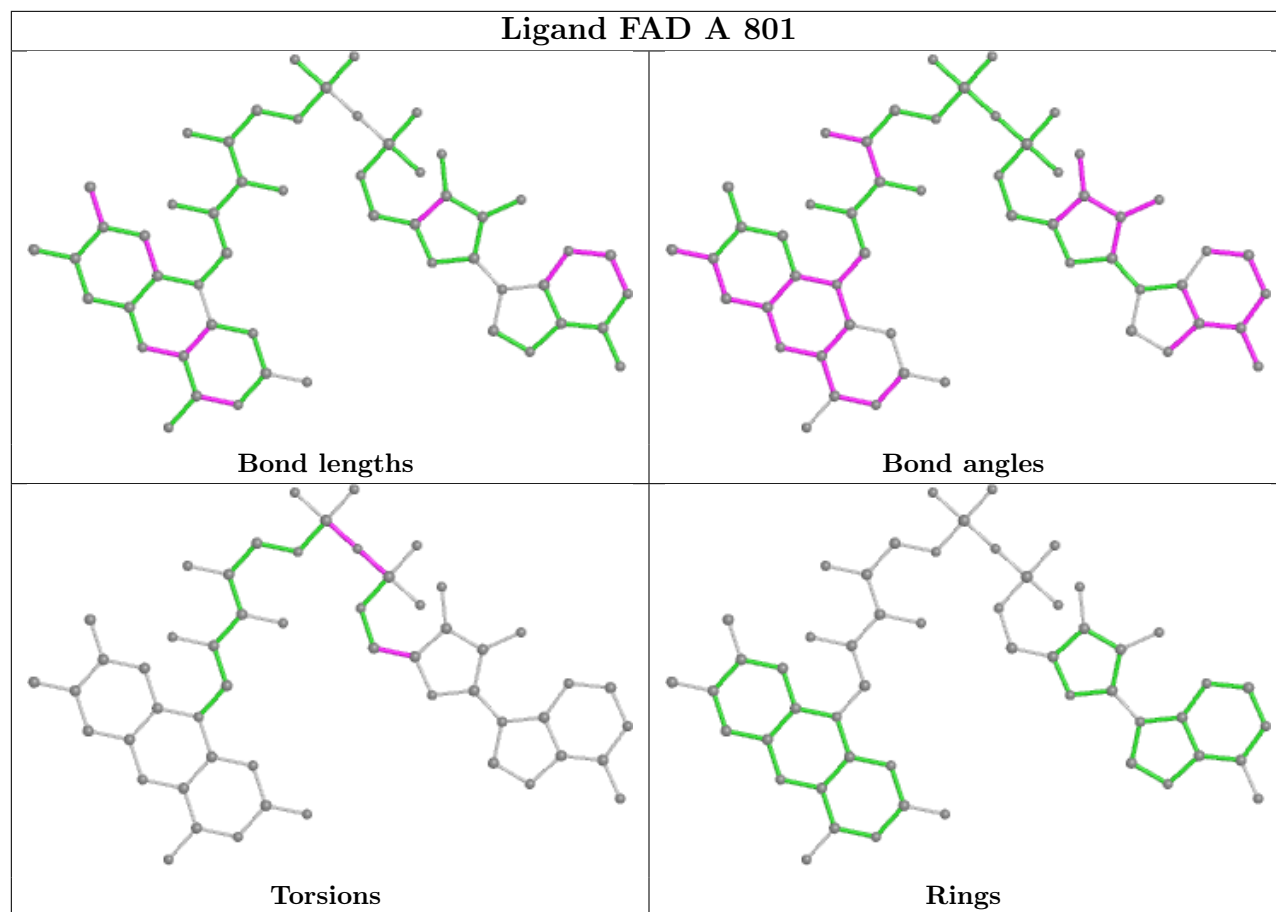
Bond angles



Torsions



Rings



## 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	576/623 (92%)	0.08	20 (3%) 44 49	4, 10, 24, 40	0
1	B	576/623 (92%)	0.03	17 (2%) 50 54	4, 10, 22, 45	0
1	C	575/623 (92%)	0.15	23 (4%) 38 42	6, 13, 28, 39	0
1	D	574/623 (92%)	0.61	67 (11%) 4 5	3, 14, 24, 40	0
All	All	2301/2492 (92%)	0.22	127 (5%) 25 27	3, 12, 25, 45	0

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	459	VAL	8.2
1	C	389	LEU	7.9
1	D	618	PHE	7.8
1	A	459	VAL	7.1
1	C	619	THR	6.4
1	A	344	ASN	5.8
1	D	343	ALA	5.8
1	B	458	ALA	5.7
1	C	390	THR	5.7
1	A	381	THR	5.3
1	D	345	PRO	5.1
1	D	184	VAL	5.1
1	D	617	PRO	5.0
1	B	45	ILE	5.0
1	C	343	ALA	4.9
1	D	45	ILE	4.8
1	A	343	ALA	4.8
1	A	345	PRO	4.8
1	D	458	ALA	4.8
1	A	457	GLY	4.4
1	C	45	ILE	4.4

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Mol	Chain	Res	Type	RSRZ
1	C	383	ARG	4.4
1	D	385	THR	4.3
1	D	51	ILE	4.3
1	D	268	THR	4.3
1	B	345	PRO	4.2
1	C	382	ILE	4.1
1	C	458	ALA	4.1
1	B	44	ASP	4.1
1	D	269	ASP	4.0
1	D	290	ALA	4.0
1	B	459	VAL	3.9
1	C	388	GLU	3.9
1	A	458	ALA	3.9
1	D	186	ASP	3.9
1	A	401	THR	3.9
1	D	187	ASP	3.8
1	C	188	ALA	3.7
1	A	45	ILE	3.7
1	D	190	ALA	3.7
1	B	618	PHE	3.7
1	D	57	ILE	3.7
1	D	318	LEU	3.6
1	C	344	ASN	3.6
1	D	344	ASN	3.5
1	B	185	LYS	3.5
1	C	618	PHE	3.4
1	D	549	LEU	3.4
1	D	52	VAL	3.4
1	D	342	PRO	3.4
1	D	457	GLY	3.3
1	D	557	PHE	3.3
1	D	580	LEU	3.3
1	B	344	ASN	3.3
1	B	343	ALA	3.2
1	B	43	MET	3.2
1	D	309	PHE	3.2
1	D	321	GLY	3.2
1	D	317	VAL	3.0
1	D	611	GLN	3.0
1	D	322	ALA	3.0
1	D	50	VAL	2.9
1	A	342	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	271	PRO	2.9
1	A	385	THR	2.9
1	C	385	THR	2.8
1	C	189	ASP	2.7
1	D	398	GLY	2.7
1	A	383	ARG	2.7
1	C	459	VAL	2.7
1	D	272	GLU	2.7
1	D	341	ASN	2.7
1	D	583	CYS	2.7
1	D	53	GLY	2.6
1	D	320	ALA	2.6
1	D	586	ILE	2.6
1	B	318	LEU	2.6
1	D	188	ALA	2.6
1	D	193	ALA	2.6
1	D	598	ALA	2.6
1	A	394	THR	2.6
1	B	232	GLY	2.5
1	D	189	ASP	2.5
1	A	186	ASP	2.5
1	A	618	PHE	2.5
1	B	186	ASP	2.5
1	D	319	THR	2.5
1	D	347	GLU	2.5
1	C	186	ASP	2.5
1	D	490	LYS	2.5
1	B	457	GLY	2.5
1	A	341	ASN	2.4
1	D	304	ILE	2.4
1	B	583	CYS	2.4
1	D	267	ASN	2.4
1	D	329	LEU	2.4
1	A	268	THR	2.4
1	A	397	PRO	2.3
1	B	580	LEU	2.3
1	D	291	LEU	2.3
1	C	391	TYR	2.3
1	C	268	THR	2.3
1	D	578	LEU	2.3
1	A	382	ILE	2.3
1	C	387	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	552	THR	2.2
1	D	266	PRO	2.2
1	D	61	TYR	2.2
1	C	457	GLY	2.2
1	D	581	GLY	2.1
1	D	310	GLU	2.1
1	D	388	GLU	2.1
1	D	387	GLY	2.1
1	D	307	ASP	2.1
1	D	386	PRO	2.1
1	D	556	GLY	2.1
1	C	341	ASN	2.1
1	D	456	TYR	2.1
1	B	323	VAL	2.1
1	D	49	VAL	2.1
1	D	160	VAL	2.1
1	C	549	LEU	2.1
1	C	323	VAL	2.0
1	D	469	VAL	2.0
1	D	211	ASP	2.0
1	A	44	ASP	2.0
1	D	550	GLY	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, 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(Å <sup>2</sup> )	Q<0.9
3	1PE	A	905	12/16	0.86	0.12	29,31,36,38	0

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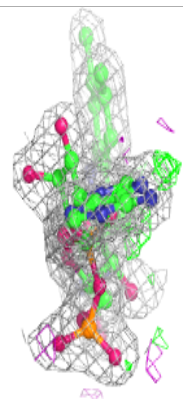
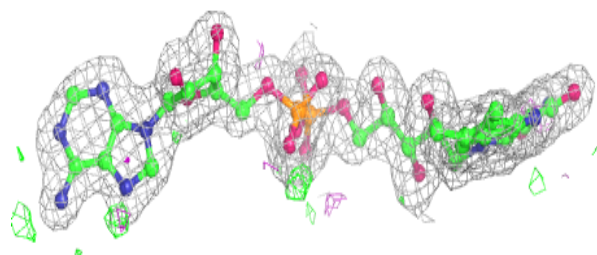
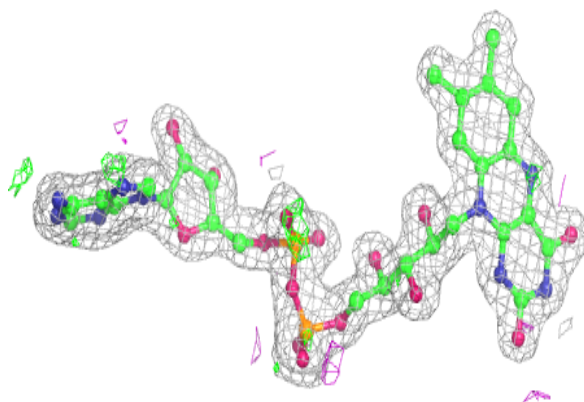
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	1PE	D	903	16/16	0.86	0.14	37,45,51,55	0
3	1PE	B	902	16/16	0.88	0.13	35,38,48,55	0
3	1PE	A	904	14/16	0.89	0.11	30,35,39,42	0
4	MES	C	901	12/12	0.95	0.12	26,30,32,33	0
2	FAD	D	801	53/53	0.96	0.12	19,24,29,31	0
4	MES	B	901	12/12	0.97	0.10	24,28,31,31	0
2	FAD	B	801	53/53	0.98	0.11	10,12,15,18	0
2	FAD	C	801	53/53	0.98	0.10	13,17,21,23	0
2	FAD	A	801	53/53	0.98	0.10	8,12,16,19	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.

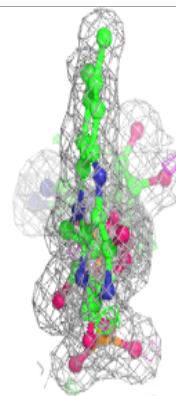
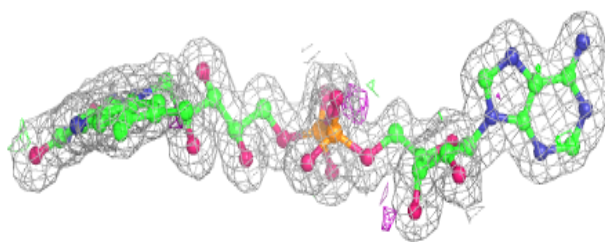
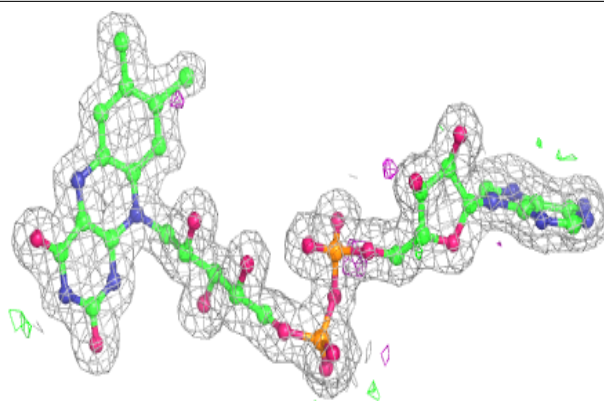
**Electron density around FAD D 801:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

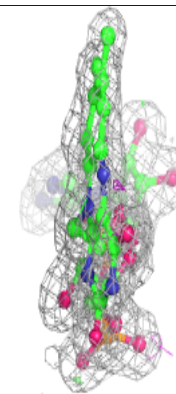
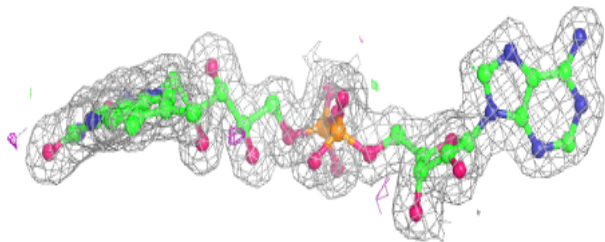
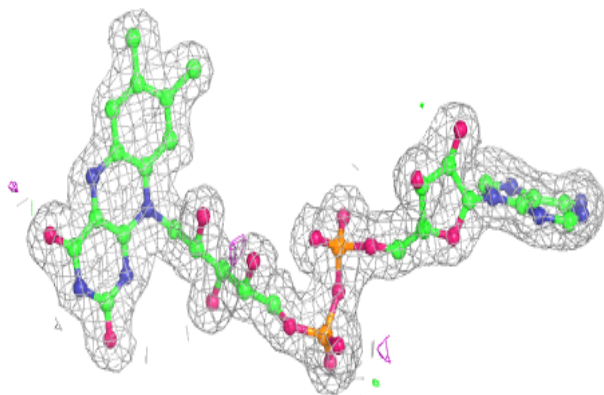


**Electron density around FAD B 801:**

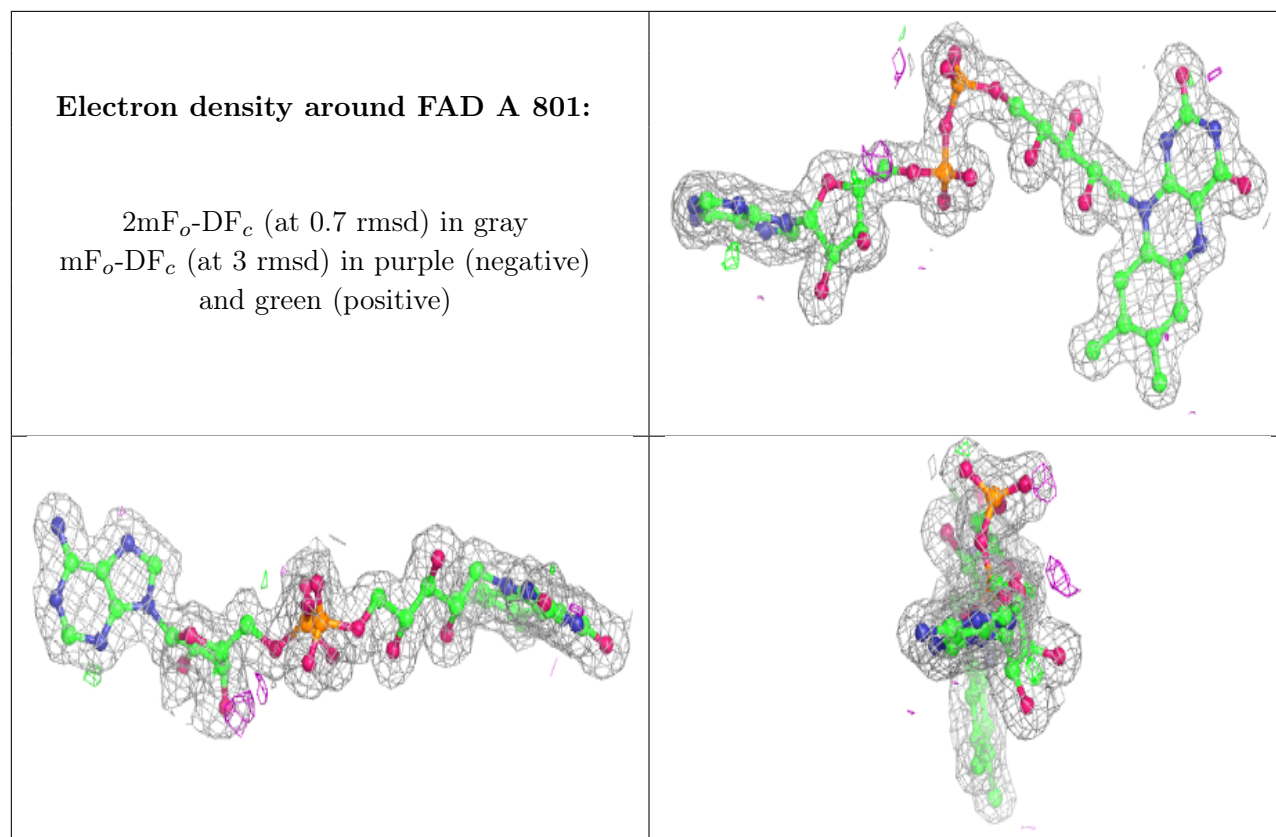
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around FAD C 801:**

$2mF_o-DF_c$  (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.