



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 07:22 AM UTC

PDB ID : 5YB7 / pdb_00005yb7
Title : L-Amino acid oxidase/monooxygenase from Pseudomonas sp. AIU 813 -
L-ornithine complex
Authors : Im, D.; Matsui, D.; Arakawa, T.; Isobe, K.; Asano, Y.; Fushinobu, S.
Deposited on : 2017-09-03
Resolution : 2.00 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 : 4-5-2 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

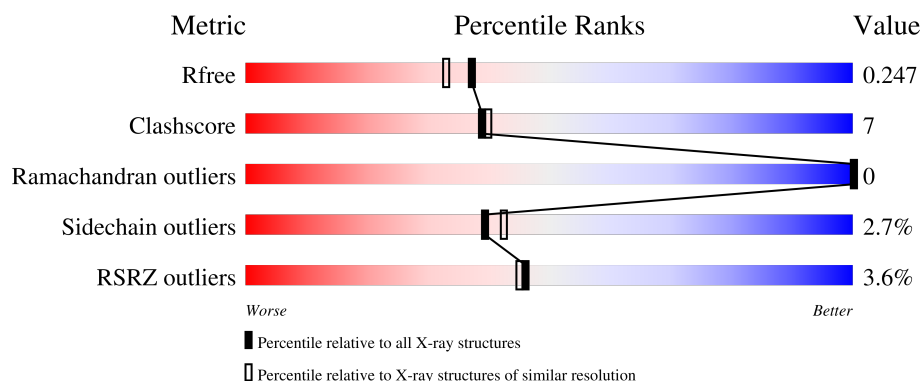
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

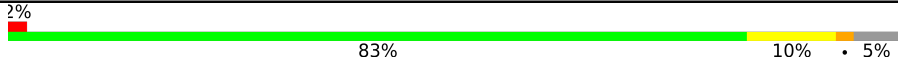
The reported resolution of this entry is 2.00 Å.

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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	580	
1	B	580	
1	C	580	
1	D	580	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 18307 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called L-amino acid oxidase/monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	549	Total	C	N	O	S	0	0	0
			4305	2749	742	791	23			
1	B	549	Total	C	N	O	S	0	0	0
			4305	2749	742	791	23			
1	C	549	Total	C	N	O	S	0	0	0
			4305	2749	742	791	23			
1	D	549	Total	C	N	O	S	0	1	0
			4316	2758	743	792	23			

There are 84 discrepancies between the modelled and reference sequences:

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

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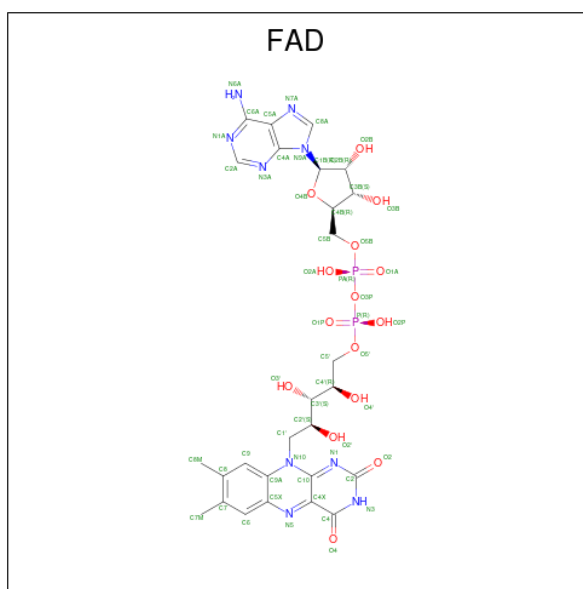
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	expression tag	UNP W6JQJ6
B	-18	GLY	-	expression tag	UNP W6JQJ6
B	-17	SER	-	expression tag	UNP W6JQJ6
B	-16	SER	-	expression tag	UNP W6JQJ6
B	-15	HIS	-	expression tag	UNP W6JQJ6
B	-14	HIS	-	expression tag	UNP W6JQJ6
B	-13	HIS	-	expression tag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

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

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



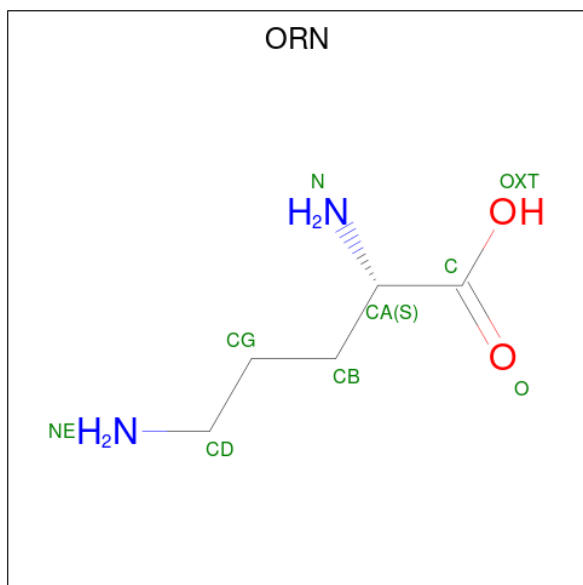
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

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

- Molecule 3 is L-ornithine (CCD ID: ORN) (formula: $C_5H_{12}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	5	2	2		
3	A	1	Total	C	N	O	0	0
			9	5	2	2		
3	B	1	Total	C	N	O	0	0
			9	5	2	2		
3	B	1	Total	C	N	O	0	0
			9	5	2	2		
3	C	1	Total	C	N	O	0	0
			9	5	2	2		
3	C	1	Total	C	N	O	0	0
			9	5	2	2		
3	D	1	Total	C	N	O	0	0
			9	5	2	2		
3	D	1	Total	C	N	O	0	0
			9	5	2	2		

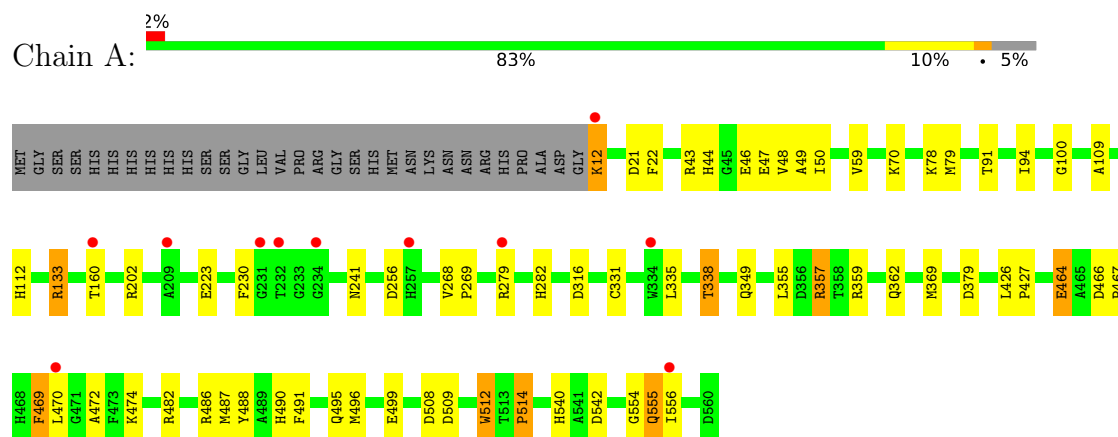
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	244	Total 244	O 244	0	0
4	B	266	Total 266	O 266	0	0
4	C	152	Total 152	O 152	0	0
4	D	130	Total 130	O 130	0	0

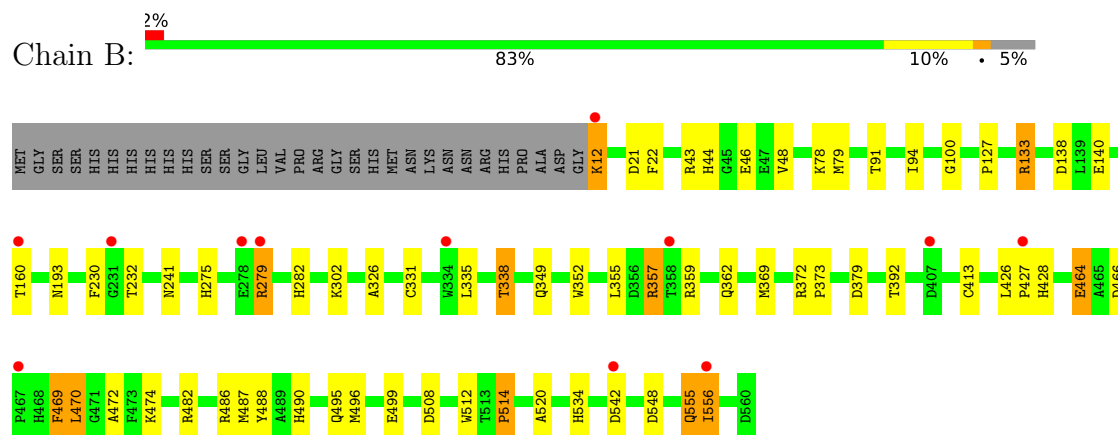
3 Residue-property plots

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.

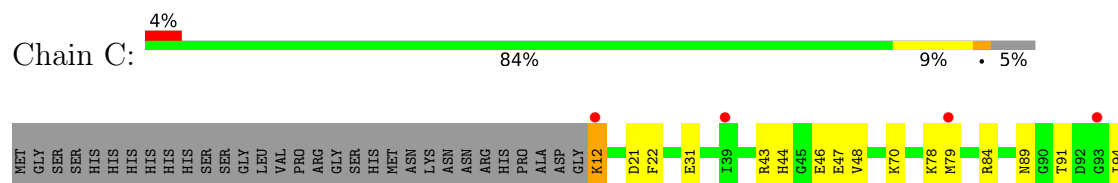
- Molecule 1: L-amino acid oxidase/monooxygenase

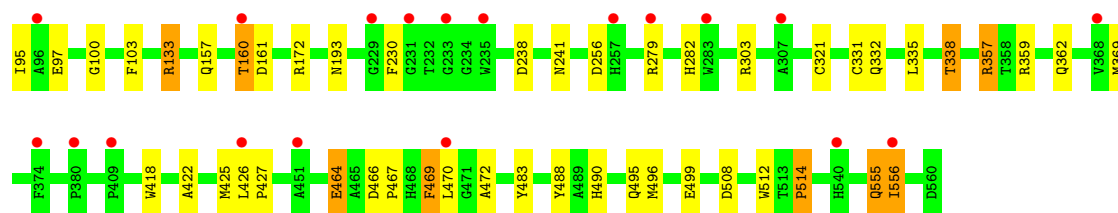


- Molecule 1: L-amino acid oxidase/monooxygenase

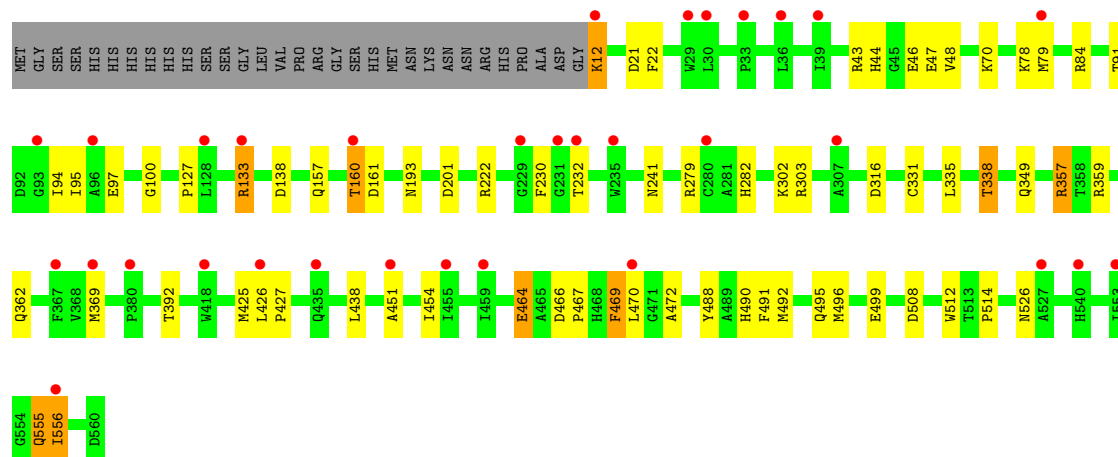
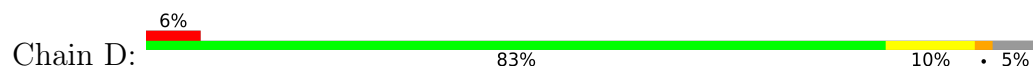


- Molecule 1: L-amino acid oxidase/monooxygenase





● Molecule 1: L-amino acid oxidase/monooxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	94.60Å 132.90Å 101.90Å 90.00° 111.50° 90.00°	Depositor
Resolution (Å)	94.81 – 2.00 94.81 – 2.00	Depositor EDS
% Data completeness (in resolution range)	93.0 (94.81-2.00) 93.0 (94.81-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.49 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.198 , 0.240 0.204 , 0.247	Depositor DCC
R_{free} test set	2015 reflections (1.28%)	wwPDB-VP
Wilson B-factor (Å ²)	29.5	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 33.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18307	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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: ORN, 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	7/4428 (0.2%)	1.08	9/6019 (0.1%)
1	B	1.21	5/4428 (0.1%)	1.07	12/6019 (0.2%)
1	C	1.03	1/4428 (0.0%)	1.02	11/6019 (0.2%)
1	D	1.02	1/4440 (0.0%)	1.02	7/6035 (0.1%)
All	All	1.13	14/17724 (0.1%)	1.05	39/24092 (0.2%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	59	VAL	C-O	6.51	1.31	1.24
1	B	520	ALA	C-O	-5.95	1.17	1.24
1	B	413	CYS	N-CA	-5.94	1.39	1.46
1	A	554	GLY	C-O	-5.77	1.17	1.23
1	B	326	ALA	C-O	-5.70	1.16	1.23
1	A	512	TRP	N-CA	-5.52	1.38	1.46
1	C	422	ALA	C-O	-5.44	1.17	1.24
1	A	491	PHE	N-CA	5.31	1.53	1.46
1	B	548	ASP	C-O	-5.31	1.17	1.24
1	A	50	ILE	C-O	-5.23	1.18	1.24
1	A	49	ALA	C-O	5.18	1.30	1.23
1	B	534	HIS	C-O	-5.11	1.17	1.24
1	D	438	LEU	C-O	-5.09	1.18	1.24
1	A	202	ARG	CA-C	5.05	1.58	1.52

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	469	PHE	CA-C-N	-7.09	112.66	122.87
1	A	469	PHE	C-N-CA	-7.09	112.66	122.87
1	B	496	MET	CG-SD-CE	-6.96	85.59	100.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	496	MET	CG-SD-CE	-6.43	86.75	100.90
1	B	469	PHE	N-CA-C	-6.42	99.29	109.23
1	A	469	PHE	N-CA-C	-6.33	99.04	108.99
1	C	464	GLU	CB-CA-C	-6.21	98.42	110.46
1	C	160	THR	CB-CA-C	-6.02	101.18	110.81
1	D	464	GLU	CB-CA-C	-5.95	98.91	110.46
1	D	469	PHE	N-CA-C	-5.89	100.09	109.23
1	B	469	PHE	CA-C-N	-5.84	112.83	123.34
1	B	469	PHE	C-N-CA	-5.84	112.83	123.34
1	A	464	GLU	CB-CA-C	-5.83	99.14	110.46
1	C	103	PHE	CB-CA-C	5.75	115.86	110.17
1	C	89	ASN	CB-CA-C	-5.58	102.94	109.80
1	A	514	PRO	CA-C-N	-5.56	113.59	122.66
1	A	514	PRO	C-N-CA	-5.56	113.59	122.66
1	D	160	THR	CB-CA-C	-5.54	101.94	110.81
1	D	496	MET	CG-SD-CE	-5.43	88.95	100.90
1	B	464	GLU	CB-CA-C	-5.40	99.99	110.46
1	B	514	PRO	N-CA-C	5.35	121.72	113.75
1	C	469	PHE	N-CA-C	-5.35	99.60	108.75
1	B	12	LYS	CA-CB-CG	-5.32	103.45	114.10
1	C	469	PHE	CA-C-N	-5.32	111.38	121.54
1	C	469	PHE	C-N-CA	-5.32	111.38	121.54
1	C	514	PRO	CA-C-N	-5.25	114.10	122.66
1	C	514	PRO	C-N-CA	-5.25	114.10	122.66
1	A	12	LYS	CA-CB-CG	-5.21	103.67	114.10
1	D	12	LYS	CA-CB-CG	-5.17	103.75	114.10
1	C	12	LYS	CA-CB-CG	-5.14	103.83	114.10
1	B	514	PRO	CA-C-N	-5.12	114.32	122.66
1	B	514	PRO	C-N-CA	-5.12	114.32	122.66
1	C	496	MET	CG-SD-CE	-5.12	89.65	100.90
1	A	514	PRO	N-CA-C	5.10	121.34	113.75
1	B	470	LEU	N-CA-C	-5.08	104.34	110.44
1	D	469	PHE	CA-C-N	-5.07	111.85	121.54
1	D	469	PHE	C-N-CA	-5.07	111.85	121.54
1	B	428	HIS	N-CA-C	5.04	116.42	110.07
1	B	534	HIS	N-CA-C	-5.02	106.00	111.82

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	4305	0	4166	55	1
1	B	4305	0	4166	64	1
1	C	4305	0	4166	57	0
1	D	4316	0	4174	61	0
2	A	53	0	31	3	0
2	B	53	0	31	4	0
2	C	53	0	31	4	0
2	D	53	0	31	3	0
3	A	18	0	22	1	0
3	B	18	0	22	2	0
3	C	18	0	22	2	0
3	D	18	0	22	1	0
4	A	244	0	0	2	0
4	B	266	0	0	10	0
4	C	152	0	0	8	0
4	D	130	0	0	8	0
All	All	18307	0	16884	233	1

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 (233) 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:555:GLN:OE1	1:B:555:GLN:N	1.61	1.31
1:C:555:GLN:OE1	1:C:555:GLN:N	1.63	1.26
1:D:555:GLN:OE1	1:D:555:GLN:N	1.69	1.25
1:A:555:GLN:OE1	1:A:555:GLN:N	1.69	1.25
1:A:555:GLN:H	1:A:555:GLN:CD	1.58	1.09
1:C:555:GLN:H	1:C:555:GLN:CD	1.58	1.07
1:B:555:GLN:H	1:B:555:GLN:CD	1.62	1.07
1:D:555:GLN:H	1:D:555:GLN:CD	1.63	1.04
1:C:22:PHE:HB2	1:C:555:GLN:NE2	1.76	1.01
1:C:466:ASP:O	1:C:469:PHE:O	1.81	0.98
1:A:22:PHE:HB2	1:A:555:GLN:NE2	1.80	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:22:PHE:HB2	1:D:555:GLN:NE2	1.81	0.95
1:A:466:ASP:O	1:A:469:PHE:O	1.85	0.95
1:A:94:ILE:HG21	1:A:369:MET:CE	1.97	0.94
1:D:466:ASP:O	1:D:469:PHE:O	1.86	0.94
1:B:466:ASP:O	1:B:469:PHE:O	1.85	0.94
1:B:94:ILE:HG21	1:B:369:MET:CE	1.99	0.91
1:B:279:ARG:NH2	4:B:701:HOH:O	1.97	0.89
1:B:22:PHE:HB2	1:B:555:GLN:NE2	1.89	0.87
1:B:555:GLN:N	1:B:555:GLN:CD	2.25	0.86
1:B:508:ASP:OD2	1:B:514:PRO:O	1.93	0.85
1:A:508:ASP:OD2	1:A:514:PRO:O	1.94	0.85
1:A:94:ILE:HG21	1:A:369:MET:HE2	1.59	0.83
1:B:302:LYS:HE3	4:B:705:HOH:O	1.80	0.82
1:D:302:LYS:HE3	4:D:1514:HOH:O	1.79	0.81
1:D:508:ASP:OD2	1:D:514:PRO:O	1.99	0.81
1:B:94:ILE:HG21	1:B:369:MET:HE2	1.62	0.81
1:C:94:ILE:HG21	1:C:369:MET:CE	2.11	0.80
1:C:508:ASP:OD2	1:C:514:PRO:O	2.02	0.78
1:D:91:THR:HG21	1:D:369:MET:HE1	1.66	0.78
1:D:94:ILE:HG21	1:D:369:MET:CE	2.14	0.77
1:C:555:GLN:N	1:C:555:GLN:CD	2.24	0.77
1:A:91:THR:HG21	1:A:369:MET:HE1	1.67	0.76
1:C:91:THR:HG21	1:C:369:MET:HE1	1.66	0.76
1:B:91:THR:HG21	1:B:369:MET:HE1	1.69	0.75
1:D:555:GLN:N	1:D:555:GLN:CD	2.27	0.74
1:C:321:CYS:SG	4:C:809:HOH:O	2.45	0.74
1:A:241:ASN:OD1	1:A:359:ARG:NH2	2.24	0.71
1:B:241:ASN:OD1	1:B:359:ARG:NH2	2.25	0.70
1:B:362:GLN:HG3	1:B:464:GLU:CG	2.22	0.70
1:A:362:GLN:HG3	1:A:464:GLU:CG	2.22	0.69
1:B:362:GLN:CG	1:B:464:GLU:HG2	2.23	0.69
1:C:94:ILE:HG21	1:C:369:MET:HE2	1.75	0.69
1:D:241:ASN:OD1	1:D:359:ARG:NH2	2.25	0.69
1:C:241:ASN:OD1	1:C:359:ARG:NH2	2.28	0.67
1:B:94:ILE:CG2	1:B:369:MET:CE	2.73	0.67
1:D:94:ILE:HG21	1:D:369:MET:HE2	1.77	0.67
1:A:555:GLN:N	1:A:555:GLN:CD	2.26	0.66
1:A:94:ILE:CG2	1:A:369:MET:CE	2.72	0.66
1:B:362:GLN:HG3	1:B:464:GLU:HG2	1.77	0.65
1:A:362:GLN:CG	1:A:464:GLU:HG2	2.27	0.65
1:C:362:GLN:HG3	1:C:464:GLU:CG	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:362:GLN:HG3	1:A:464:GLU:HG3	1.80	0.63
1:C:362:GLN:CG	1:C:464:GLU:HG2	2.28	0.63
1:B:302:LYS:CE	4:B:705:HOH:O	2.43	0.63
1:C:472:ALA:HB1	2:C:601:FAD:HM82	1.82	0.62
1:D:472:ALA:HB1	2:D:601:FAD:HM82	1.81	0.62
1:D:362:GLN:HG3	1:D:464:GLU:CG	2.30	0.62
1:A:349:GLN:HE22	3:A:603:ORN:HE2	1.49	0.61
1:D:490:HIS:HD2	4:D:1613:HOH:O	1.84	0.59
1:D:84:ARG:HD3	4:D:1626:HOH:O	2.03	0.59
1:D:362:GLN:CG	1:D:464:GLU:HG2	2.32	0.59
1:A:362:GLN:HG3	1:A:464:GLU:HG2	1.83	0.59
1:D:362:GLN:HG3	1:D:464:GLU:HG3	1.85	0.58
1:A:512:TRP:CZ2	1:A:555:GLN:HG2	2.38	0.58
1:D:22:PHE:HB2	1:D:555:GLN:HE21	1.68	0.58
1:A:426:LEU:HD21	1:C:426:LEU:HD21	1.86	0.57
1:A:512:TRP:HZ2	1:A:555:GLN:HG2	1.69	0.57
1:D:512:TRP:HZ2	1:D:555:GLN:HG2	1.70	0.57
1:D:491[B]:PHE:CD1	1:D:526:ASN:O	2.58	0.57
1:B:362:GLN:HG3	1:B:464:GLU:HG3	1.87	0.56
1:D:302:LYS:CE	4:D:1514:HOH:O	2.47	0.56
1:A:362:GLN:CG	1:A:464:GLU:CG	2.83	0.55
1:D:512:TRP:CZ2	1:D:555:GLN:HG2	2.41	0.55
1:C:362:GLN:HG3	1:C:464:GLU:HG2	1.86	0.55
1:B:362:GLN:CG	1:B:464:GLU:CG	2.84	0.55
1:C:362:GLN:HG3	1:C:464:GLU:HG3	1.88	0.54
1:D:94:ILE:CG2	1:D:369:MET:CE	2.86	0.54
1:D:43:ARG:HD2	1:D:46:GLU:OE2	2.07	0.54
1:A:22:PHE:HB2	1:A:555:GLN:HE22	1.71	0.54
1:B:302:LYS:NZ	4:B:705:HOH:O	2.37	0.54
1:C:43:ARG:HD2	1:C:46:GLU:OE2	2.08	0.54
1:A:335:LEU:HA	1:A:338:THR:HG22	1.91	0.53
1:A:472:ALA:O	2:A:601:FAD:HM81	2.09	0.53
1:C:22:PHE:HB2	1:C:555:GLN:HE22	1.68	0.53
1:C:94:ILE:CG2	1:C:369:MET:CE	2.84	0.53
1:C:426:LEU:HB3	1:C:427:PRO:HD3	1.90	0.53
1:C:512:TRP:HZ2	1:C:555:GLN:HG2	1.73	0.53
1:D:491[B]:PHE:CE2	1:D:526:ASN:HB3	2.44	0.53
1:C:512:TRP:CZ2	1:C:555:GLN:HG2	2.43	0.53
1:D:491[A]:PHE:CE1	1:D:492:MET:SD	3.01	0.52
1:D:349:GLN:HE22	3:D:603:ORN:HE2	1.57	0.52
1:D:362:GLN:CG	1:D:464:GLU:CG	2.87	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:426:LEU:HB3	1:D:427:PRO:HD3	1.91	0.52
1:C:488:TYR:CE2	1:C:555:GLN:NE2	2.78	0.52
1:B:488:TYR:CE2	1:B:555:GLN:NE2	2.78	0.52
1:D:22:PHE:HB2	1:D:555:GLN:HE22	1.73	0.52
1:D:303:ARG:CZ	4:D:1590:HOH:O	2.58	0.52
1:B:349:GLN:HE22	3:B:603:ORN:HE2	1.58	0.51
1:A:338:THR:HG21	1:A:470:LEU:HD11	1.92	0.51
1:B:426:LEU:HB3	1:B:427:PRO:HD3	1.93	0.50
1:C:21:ASP:HB3	1:C:555:GLN:HG3	1.94	0.50
1:B:335:LEU:HA	1:B:338:THR:HG22	1.91	0.50
1:C:362:GLN:CG	1:C:464:GLU:CG	2.87	0.50
1:D:222:ARG:NH2	4:D:1507:HOH:O	2.43	0.50
1:C:84:ARG:HD3	4:C:848:HOH:O	2.11	0.50
1:B:100:GLY:HA2	2:B:601:FAD:N5	2.26	0.50
1:B:512:TRP:CZ2	1:B:555:GLN:HG2	2.46	0.50
1:C:157:GLN:NE2	1:C:161:ASP:OD1	2.42	0.50
1:A:488:TYR:CE2	1:A:555:GLN:NE2	2.80	0.50
1:C:22:PHE:HB2	1:C:555:GLN:HE21	1.69	0.50
1:A:426:LEU:HB3	1:A:427:PRO:HD3	1.94	0.49
1:B:160:THR:OG1	1:B:230:PHE:HB2	2.12	0.49
1:C:490:HIS:HD2	4:C:825:HOH:O	1.94	0.49
1:C:172:ARG:HD3	4:C:769:HOH:O	2.11	0.49
1:A:490:HIS:HE1	4:A:705:HOH:O	1.94	0.49
1:A:22:PHE:HB2	1:A:555:GLN:HE21	1.71	0.49
1:C:418:TRP:CZ2	3:C:602:ORN:HD2	2.47	0.49
1:D:100:GLY:HA2	2:D:601:FAD:N5	2.28	0.49
1:D:335:LEU:HA	1:D:338:THR:HG22	1.93	0.49
1:B:94:ILE:HG21	1:B:369:MET:HE3	1.91	0.49
1:B:472:ALA:O	2:B:601:FAD:HM81	2.12	0.49
1:D:338:THR:HG21	1:D:470:LEU:HD11	1.95	0.48
1:D:362:GLN:HG3	1:D:464:GLU:HG2	1.93	0.48
1:A:94:ILE:HG21	1:A:369:MET:HE3	1.91	0.48
1:A:21:ASP:HB3	1:A:555:GLN:HG3	1.95	0.48
1:A:357:ARG:HH11	1:A:357:ARG:HA	1.78	0.48
1:A:490:HIS:HD2	4:A:853:HOH:O	1.97	0.48
1:A:542:ASP:OD1	1:A:542:ASP:N	2.46	0.48
1:B:490:HIS:HD2	4:B:870:HOH:O	1.96	0.48
1:C:160:THR:OG1	1:C:230:PHE:HB2	2.13	0.48
1:B:426:LEU:HD21	1:D:426:LEU:HD21	1.94	0.48
1:D:100:GLY:HA2	2:D:601:FAD:C5X	2.44	0.48
1:C:335:LEU:HA	1:C:338:THR:HG22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:ARG:O	1:A:486:ARG:HG3	2.14	0.48
1:B:357:ARG:HA	1:B:357:ARG:HH11	1.77	0.48
1:A:160:THR:OG1	1:A:230:PHE:HB2	2.14	0.47
1:D:157:GLN:NE2	1:D:161:ASP:OD1	2.46	0.47
1:C:357:ARG:HA	1:C:357:ARG:HH11	1.80	0.47
1:B:43:ARG:HD2	1:B:46:GLU:OE2	2.14	0.47
1:D:160:THR:OG1	1:D:230:PHE:HB2	2.14	0.47
1:B:21:ASP:HB3	1:B:555:GLN:HG3	1.96	0.47
1:B:279:ARG:NH1	4:B:709:HOH:O	2.42	0.47
1:B:512:TRP:HZ2	1:B:555:GLN:HG2	1.79	0.47
1:B:22:PHE:HB2	1:B:555:GLN:HE21	1.77	0.47
1:B:193:ASN:CG	1:B:556:ILE:HD13	2.40	0.47
1:D:21:ASP:HB3	1:D:555:GLN:HG3	1.97	0.47
1:C:466:ASP:OD1	1:C:467:PRO:HD2	2.15	0.46
1:D:331:CYS:HB2	1:D:335:LEU:HD12	1.96	0.46
1:B:140:GLU:HA	1:D:349:GLN:HE21	1.80	0.46
1:C:100:GLY:HA2	2:C:601:FAD:N5	2.29	0.46
1:B:338:THR:HG21	1:B:470:LEU:HD11	1.97	0.46
1:B:474:LYS:HB3	1:B:514:PRO:HB3	1.97	0.46
1:C:338:THR:HG21	1:C:470:LEU:HD11	1.98	0.46
1:D:488:TYR:CE2	1:D:555:GLN:NE2	2.84	0.46
1:B:275:HIS:HD2	4:B:954:HOH:O	1.98	0.46
1:B:133:ARG:HH11	1:B:133:ARG:HB3	1.81	0.46
1:B:355:LEU:HD23	1:B:487:MET:HE3	1.97	0.46
1:A:43:ARG:HD2	1:A:46:GLU:OE2	2.15	0.45
1:A:335:LEU:HD23	1:A:338:THR:HG22	1.97	0.45
1:A:379:ASP:C	1:A:379:ASP:OD1	2.59	0.45
1:D:44:HIS:HB3	1:D:282:HIS:CG	2.52	0.45
1:C:193:ASN:CG	1:C:556:ILE:HD13	2.42	0.45
1:B:335:LEU:HD23	1:B:338:THR:HG22	1.98	0.45
1:D:316:ASP:C	1:D:316:ASP:OD1	2.60	0.45
1:A:100:GLY:HA2	2:A:601:FAD:N5	2.32	0.45
1:B:193:ASN:ND2	1:B:556:ILE:CD1	2.80	0.45
1:C:44:HIS:HB3	1:C:282:HIS:CG	2.52	0.45
1:C:238:ASP:OD2	3:C:602:ORN:NE	2.45	0.45
1:D:47:GLU:HA	1:D:70:LYS:O	2.17	0.45
1:B:490:HIS:HE1	4:B:710:HOH:O	1.99	0.44
1:C:490:HIS:HE1	4:C:714:HOH:O	1.99	0.44
1:D:466:ASP:OD1	1:D:467:PRO:HD2	2.17	0.44
1:D:193:ASN:CG	1:D:556:ILE:HD13	2.43	0.44
1:A:47:GLU:HA	1:A:70:LYS:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:482:ARG:O	1:B:486:ARG:HG3	2.17	0.44
1:A:133:ARG:HH11	1:A:133:ARG:HB3	1.83	0.44
1:A:474:LYS:HB3	1:A:514:PRO:HB3	1.98	0.44
1:D:451:ALA:HA	1:D:454:ILE:HD12	1.99	0.44
1:B:94:ILE:CG2	1:B:369:MET:HE3	2.47	0.44
1:C:100:GLY:HA2	2:C:601:FAD:C5X	2.48	0.44
1:A:509:ASP:N	1:A:509:ASP:OD1	2.51	0.43
1:C:472:ALA:O	2:C:601:FAD:HM82	2.18	0.43
1:D:357:ARG:HH11	1:D:357:ARG:HA	1.83	0.43
1:C:425:MET:O	1:C:426:LEU:C	2.60	0.43
1:A:335:LEU:HD23	1:A:338:THR:CG2	2.48	0.43
1:B:44:HIS:HB3	1:B:282:HIS:CG	2.52	0.43
1:B:279:ARG:CZ	4:B:701:HOH:O	2.52	0.43
1:A:316:ASP:OD1	1:A:316:ASP:C	2.62	0.43
1:C:97:GLU:HA	1:C:97:GLU:OE1	2.18	0.43
1:D:133:ARG:HB3	1:D:133:ARG:HH11	1.84	0.43
1:A:466:ASP:OD1	1:A:467:PRO:HD2	2.19	0.43
1:B:362:GLN:HG2	1:B:464:GLU:HG2	2.00	0.43
1:C:47:GLU:HA	1:C:70:LYS:O	2.19	0.43
1:B:372:ARG:HB2	1:B:373:PRO:HD2	2.01	0.43
1:C:303:ARG:CZ	4:C:812:HOH:O	2.67	0.42
1:D:127:PRO:HG2	1:D:232:THR:HA	2.01	0.42
1:A:223:GLU:OE2	1:C:483:TYR:OH	2.31	0.42
1:B:335:LEU:HD23	1:B:338:THR:CG2	2.50	0.42
1:A:331:CYS:HB2	1:A:335:LEU:HD12	2.01	0.42
1:C:332:GLN:NE2	4:C:702:HOH:O	2.38	0.42
1:D:138:ASP:O	1:D:392:THR:HA	2.19	0.42
1:C:256:ASP:OD1	1:C:256:ASP:N	2.53	0.42
1:A:109:ALA:O	1:A:112:HIS:HB3	2.19	0.42
1:C:331:CYS:HB2	1:C:335:LEU:HD12	2.01	0.42
1:A:44:HIS:HB3	1:A:282:HIS:CG	2.55	0.42
1:B:127:PRO:HG2	1:B:232:THR:HA	2.02	0.42
1:A:100:GLY:HA2	2:A:601:FAD:C5X	2.50	0.41
1:A:362:GLN:HG2	1:A:464:GLU:HG2	2.01	0.41
1:A:355:LEU:HD23	1:A:487:MET:HE3	2.02	0.41
1:D:302:LYS:NZ	4:D:1514:HOH:O	2.51	0.41
1:D:362:GLN:HG2	1:D:464:GLU:HG2	2.02	0.41
1:D:95:ILE:HD12	1:D:95:ILE:C	2.44	0.41
1:B:542:ASP:OD1	1:B:542:ASP:N	2.46	0.41
1:B:279:ARG:NH1	4:B:701:HOH:O	2.54	0.41
1:B:472:ALA:HB1	2:B:601:FAD:HM83	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:PHE:HB2	1:B:555:GLN:HE22	1.79	0.41
1:B:379:ASP:C	1:B:379:ASP:OD1	2.64	0.41
1:C:94:ILE:HG21	1:C:369:MET:HE3	1.97	0.41
1:D:201:ASP:HB2	4:D:1543:HOH:O	2.20	0.41
1:A:256:ASP:OD1	1:A:256:ASP:N	2.54	0.41
1:C:31:GLU:CG	4:C:708:HOH:O	2.68	0.41
1:C:362:GLN:HG2	1:C:464:GLU:HG2	2.03	0.41
1:D:425:MET:O	1:D:426:LEU:C	2.63	0.41
1:D:426:LEU:HB3	1:D:427:PRO:CD	2.51	0.41
1:B:100:GLY:HA2	2:B:601:FAD:C4X	2.50	0.41
1:B:352:TRP:HB3	3:B:603:ORN:HD2	2.03	0.40
1:B:331:CYS:HB2	1:B:335:LEU:HD12	2.02	0.40
1:A:268:VAL:HB	1:A:269:PRO:CD	2.52	0.40
1:C:95:ILE:C	1:C:95:ILE:HD12	2.46	0.40
1:D:97:GLU:OE1	1:D:97:GLU:HA	2.21	0.40
1:B:138:ASP:O	1:B:392:THR:HA	2.22	0.40
1:C:133:ARG:HB3	1:C:133:ARG:HH11	1.86	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:HIS:CD2	1:B:279:ARG:NH2[2_556]	1.90	0.30

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	547/580 (94%)	535 (98%)	12 (2%)	0	100	100
1	B	547/580 (94%)	536 (98%)	11 (2%)	0	100	100
1	C	547/580 (94%)	533 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	548/580 (94%)	534 (97%)	14 (3%)	0	100	100
All	All	2189/2320 (94%)	2138 (98%)	51 (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	448/474 (94%)	436 (97%)	12 (3%)	39	42
1	B	448/474 (94%)	436 (97%)	12 (3%)	39	42
1	C	448/474 (94%)	436 (97%)	12 (3%)	39	42
1	D	449/474 (95%)	437 (97%)	12 (3%)	39	42
All	All	1793/1896 (95%)	1745 (97%)	48 (3%)	39	42

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LYS
1	A	48	VAL
1	A	78	LYS
1	A	79	MET
1	A	133	ARG
1	A	279	ARG
1	A	338	THR
1	A	357	ARG
1	A	495	GLN
1	A	499	GLU
1	A	555	GLN
1	A	556	ILE
1	B	12	LYS
1	B	48	VAL
1	B	78	LYS
1	B	79	MET

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Mol	Chain	Res	Type
1	B	133	ARG
1	B	279	ARG
1	B	338	THR
1	B	357	ARG
1	B	495	GLN
1	B	499	GLU
1	B	555	GLN
1	B	556	ILE
1	C	12	LYS
1	C	48	VAL
1	C	78	LYS
1	C	79	MET
1	C	133	ARG
1	C	279	ARG
1	C	338	THR
1	C	357	ARG
1	C	495	GLN
1	C	499	GLU
1	C	555	GLN
1	C	556	ILE
1	D	12	LYS
1	D	48	VAL
1	D	78	LYS
1	D	79	MET
1	D	133	ARG
1	D	279	ARG
1	D	338	THR
1	D	357	ARG
1	D	495	GLN
1	D	499	GLU
1	D	555	GLN
1	D	556	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	257	HIS
1	A	275	HIS
1	A	332	GLN
1	A	339	GLN
1	A	349	GLN
1	A	484	ASN

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Mol	Chain	Res	Type
1	A	490	HIS
1	B	86	GLN
1	B	275	HIS
1	B	349	GLN
1	B	484	ASN
1	B	490	HIS
1	B	500	GLN
1	C	86	GLN
1	C	275	HIS
1	C	339	GLN
1	C	349	GLN
1	C	435	GLN
1	C	484	ASN
1	C	490	HIS
1	C	540	HIS
1	D	86	GLN
1	D	275	HIS
1	D	339	GLN
1	D	349	GLN
1	D	428	HIS
1	D	484	ASN
1	D	490	HIS

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](#)

12 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	ORN	D	603	-	7,8,8	1.17	1 (14%)	6,9,9	1.43	1 (16%)
2	FAD	B	601	-	58,58,58	1.64	11 (18%)	85,89,89	1.98	23 (27%)
2	FAD	D	601	-	58,58,58	1.92	8 (13%)	85,89,89	2.10	27 (31%)
2	FAD	C	601	-	58,58,58	2.01	11 (18%)	85,89,89	2.03	25 (29%)
3	ORN	A	603	-	7,8,8	0.58	0	6,9,9	0.95	0
3	ORN	D	602	-	7,8,8	0.99	1 (14%)	6,9,9	1.52	1 (16%)
3	ORN	B	603	-	7,8,8	1.05	1 (14%)	6,9,9	1.14	0
3	ORN	C	602	-	7,8,8	0.98	1 (14%)	6,9,9	1.69	1 (16%)
2	FAD	A	601	-	58,58,58	1.80	12 (20%)	85,89,89	1.90	23 (27%)
3	ORN	A	602	-	7,8,8	0.73	0	6,9,9	1.65	1 (16%)
3	ORN	C	603	-	7,8,8	1.51	1 (14%)	6,9,9	2.52	1 (16%)
3	ORN	B	602	-	7,8,8	0.70	0	6,9,9	1.24	1 (16%)

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	ORN	D	603	-	-	0/8/8/8	-
2	FAD	B	601	-	-	1/34/50/50	0/6/6/6
2	FAD	D	601	-	-	8/34/50/50	0/6/6/6
2	FAD	C	601	-	-	3/34/50/50	0/6/6/6
3	ORN	A	603	-	-	1/8/8/8	-
3	ORN	D	602	-	-	2/8/8/8	-
3	ORN	B	603	-	-	0/8/8/8	-
3	ORN	C	602	-	-	5/8/8/8	-
2	FAD	A	601	-	-	3/34/50/50	0/6/6/6
3	ORN	A	602	-	-	0/8/8/8	-
3	ORN	C	603	-	-	0/8/8/8	-
3	ORN	B	602	-	-	4/8/8/8	-

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	FAD	P-O3P	7.36	1.67	1.59
2	D	601	FAD	P-O3P	6.83	1.66	1.59
2	D	601	FAD	C9A-C5X	6.21	1.51	1.41
2	C	601	FAD	PA-O3P	6.15	1.66	1.59
2	C	601	FAD	C9A-C5X	5.83	1.50	1.41
2	D	601	FAD	C5A-C4A	5.60	1.49	1.39
2	A	601	FAD	C5A-C4A	5.34	1.48	1.39
2	C	601	FAD	C5A-C4A	4.93	1.47	1.39
2	A	601	FAD	PA-O3P	4.62	1.64	1.59
2	A	601	FAD	C9A-C5X	4.46	1.48	1.41
2	B	601	FAD	P-O3P	4.45	1.64	1.59
2	D	601	FAD	PA-O3P	4.43	1.64	1.59
2	B	601	FAD	C9A-C5X	3.99	1.47	1.41
2	A	601	FAD	C1'-C2'	-3.95	1.47	1.52
3	C	603	ORN	OXT-C	-3.81	1.18	1.30
2	C	601	FAD	C8-C7	3.67	1.49	1.40
2	D	601	FAD	C8-C7	3.63	1.49	1.40
2	B	601	FAD	C4-N3	-3.43	1.32	1.38
2	B	601	FAD	C5A-C4A	3.42	1.45	1.39
2	A	601	FAD	C4-N3	-3.36	1.32	1.38
2	B	601	FAD	C1'-C2'	-3.29	1.48	1.52
2	D	601	FAD	C5A-C6A	3.23	1.50	1.41
2	B	601	FAD	C4X-N5	3.10	1.37	1.30
2	A	601	FAD	C2A-N1A	3.05	1.39	1.33
3	D	603	ORN	OXT-C	-2.91	1.21	1.30
2	A	601	FAD	C5X-N5	-2.79	1.34	1.39
2	A	601	FAD	C6-C7	-2.72	1.35	1.39
2	B	601	FAD	C8A-N7A	2.66	1.36	1.31
2	C	601	FAD	C5A-C6A	2.62	1.48	1.41
3	D	602	ORN	OXT-C	-2.55	1.22	1.30
3	C	602	ORN	OXT-C	-2.54	1.22	1.30
2	D	601	FAD	C2A-N1A	2.54	1.38	1.33
2	A	601	FAD	C10-N1	2.39	1.38	1.33
2	A	601	FAD	C4X-N5	2.38	1.35	1.30
2	C	601	FAD	C5X-N5	-2.33	1.35	1.39
2	C	601	FAD	C4X-N5	2.30	1.35	1.30
2	B	601	FAD	C8-C7	2.26	1.46	1.40
2	B	601	FAD	C9-C8	-2.23	1.36	1.39
2	C	601	FAD	C4A-N9A	-2.17	1.33	1.37
2	D	601	FAD	C10-N10	2.13	1.41	1.37
2	B	601	FAD	C10-N1	2.12	1.37	1.33
2	C	601	FAD	O2'-C2'	-2.10	1.38	1.43
2	A	601	FAD	C5A-N7A	-2.09	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	FAD	C8A-N7A	2.04	1.35	1.31
2	B	601	FAD	O2'-C2'	-2.02	1.39	1.43
3	B	603	ORN	O-C	2.01	1.28	1.22
2	A	601	FAD	P-O3P	2.00	1.61	1.59

All (104) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	FAD	N3A-C2A-N1A	-5.98	119.53	128.58
2	C	601	FAD	C5A-C4A-N3A	-5.64	118.94	126.72
2	D	601	FAD	C5A-C4A-N3A	-5.40	119.28	126.72
2	B	601	FAD	N3A-C4A-N9A	5.21	136.02	127.17
3	C	603	ORN	OXT-C-O	-5.19	112.31	124.08
2	A	601	FAD	N3A-C4A-N9A	5.06	135.78	127.17
2	D	601	FAD	O4B-C4B-C5B	5.00	125.34	109.33
2	B	601	FAD	C5A-C4A-N3A	-4.92	119.95	126.72
2	B	601	FAD	C4A-N9A-C8A	4.71	110.69	105.74
2	A	601	FAD	C5A-C4A-N3A	-4.67	120.28	126.72
2	C	601	FAD	N3A-C4A-N9A	4.62	135.02	127.17
2	A	601	FAD	N3A-C2A-N1A	-4.58	121.65	128.58
2	B	601	FAD	C2A-N3A-C4A	4.56	122.97	111.83
2	D	601	FAD	N3A-C4A-N9A	4.50	134.82	127.17
2	D	601	FAD	C4B-O4B-C1B	-4.50	99.54	109.47
2	A	601	FAD	C5'-C4'-C3'	-4.47	103.78	112.22
2	C	601	FAD	O3P-PA-O1A	-4.29	97.81	110.70
2	C	601	FAD	O2P-P-O3P	-4.14	96.09	107.27
2	D	601	FAD	O4-C4-C4X	-4.14	115.62	126.53
2	A	601	FAD	C4A-N9A-C8A	4.04	109.98	105.74
2	D	601	FAD	O2-C2-N1	-4.01	115.14	121.80
2	C	601	FAD	N3A-C2A-N1A	-3.88	122.71	128.58
2	B	601	FAD	C5'-C4'-C3'	-3.85	104.95	112.22
2	D	601	FAD	O2P-P-O1P	3.84	130.31	112.44
3	C	602	ORN	OXT-C-O	-3.82	115.40	124.08
2	C	601	FAD	O4-C4-C4X	-3.81	116.48	126.53
2	D	601	FAD	C4A-C5A-N7A	-3.79	106.25	110.58
2	C	601	FAD	C2A-N3A-C4A	3.76	121.01	111.83
2	D	601	FAD	O4B-C1B-C2B	-3.73	98.62	106.62
2	C	601	FAD	C4A-C5A-N7A	-3.68	106.38	110.58
2	B	601	FAD	O4-C4-C4X	-3.63	116.96	126.53
2	B	601	FAD	C5X-C9A-N10	3.60	121.22	117.97
3	A	602	ORN	OXT-C-O	-3.56	116.01	124.08
2	C	601	FAD	C4A-N9A-C8A	3.51	109.43	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	FAD	C1'-N10-C9A	3.43	127.30	120.63
2	A	601	FAD	O2-C2-N1	-3.41	116.14	121.80
2	D	601	FAD	C2A-N3A-C4A	3.36	120.04	111.83
2	C	601	FAD	O2-C2-N1	-3.34	116.26	121.80
2	D	601	FAD	O5B-C5B-C4B	3.33	120.32	108.99
2	A	601	FAD	C8M-C8-C7	-3.32	113.98	120.76
2	C	601	FAD	O4-C4-N3	3.29	126.29	120.11
3	D	603	ORN	OXT-C-O	-3.27	116.67	124.08
2	C	601	FAD	O2A-PA-O3P	3.25	116.07	107.27
2	A	601	FAD	C2A-N1A-C6A	3.25	124.07	118.73
2	A	601	FAD	O4-C4-C4X	-3.25	117.96	126.53
2	D	601	FAD	O2A-PA-O1A	3.17	127.17	112.44
2	D	601	FAD	O2P-P-O3P	-3.16	98.73	107.27
2	C	601	FAD	C9A-C5X-N5	-3.16	119.10	122.45
2	B	601	FAD	C9-C8-C7	3.10	124.24	119.69
2	A	601	FAD	C2A-N3A-C4A	3.04	119.25	111.83
2	D	601	FAD	O4B-C1B-N9A	3.01	113.87	108.09
2	C	601	FAD	O2A-PA-O1A	2.95	126.15	112.44
2	D	601	FAD	O4-C4-N3	2.95	125.65	120.11
3	D	602	ORN	OXT-C-O	-2.94	117.40	124.08
2	D	601	FAD	C4A-N9A-C8A	2.94	108.82	105.74
2	D	601	FAD	N3A-C2A-N1A	-2.93	124.14	128.58
2	A	601	FAD	O3P-P-O1P	-2.92	101.93	110.70
2	D	601	FAD	C5'-C4'-C3'	-2.86	106.83	112.22
2	C	601	FAD	C5X-C9A-N10	2.83	120.53	117.97
2	D	601	FAD	O2B-C2B-C1B	2.83	119.85	110.10
2	A	601	FAD	C9-C8-C7	2.81	123.81	119.69
2	C	601	FAD	O2P-P-O1P	2.80	125.49	112.44
2	D	601	FAD	C5A-N7A-C8A	2.77	107.80	103.45
2	D	601	FAD	O2A-PA-O3P	-2.72	99.91	107.27
2	A	601	FAD	C5A-N7A-C8A	2.71	107.70	103.45
2	B	601	FAD	N9A-C8A-N7A	-2.68	110.14	113.94
2	A	601	FAD	O2P-P-O1P	2.68	124.90	112.44
2	C	601	FAD	C8M-C8-C9	-2.67	114.87	119.57
2	B	601	FAD	C5A-C6A-N6A	-2.61	116.83	123.29
2	C	601	FAD	C5A-N7A-C8A	2.55	107.45	103.45
2	C	601	FAD	C2A-N1A-C6A	2.55	122.91	118.73
2	B	601	FAD	O4'-C4'-C3'	2.54	115.20	109.25
2	B	601	FAD	C9A-C5X-N5	-2.54	119.76	122.45
2	C	601	FAD	O4B-C1B-C2B	-2.50	101.27	106.62
2	A	601	FAD	O4'-C4'-C3'	2.49	115.08	109.25
2	A	601	FAD	N9A-C8A-N7A	-2.45	110.46	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	FAD	C4A-C5A-N7A	-2.42	107.82	110.58
2	B	601	FAD	C8M-C8-C7	-2.41	115.83	120.76
2	A	601	FAD	N6A-C6A-N1A	2.37	123.66	118.38
3	B	602	ORN	OXT-C-O	-2.36	118.73	124.08
2	B	601	FAD	O2P-P-O1P	2.35	123.39	112.44
2	B	601	FAD	O2A-PA-O1A	2.35	123.39	112.44
2	A	601	FAD	C1'-C2'-C3'	-2.34	103.32	109.66
2	B	601	FAD	C7M-C7-C6	2.33	123.67	119.57
2	B	601	FAD	O4-C4-N3	2.29	124.42	120.11
2	C	601	FAD	N9A-C8A-N7A	-2.28	110.71	113.94
2	A	601	FAD	O5B-PA-O1A	-2.27	99.95	108.94
2	B	601	FAD	C2A-N1A-C6A	2.21	122.37	118.73
2	C	601	FAD	C1'-C2'-C3'	-2.21	103.67	109.66
2	D	601	FAD	C9A-C5X-N5	-2.19	120.13	122.45
2	D	601	FAD	C4X-C4-N3	2.15	118.72	113.25
2	D	601	FAD	C4X-C10-N1	-2.14	119.33	124.59
2	A	601	FAD	C4X-C4-N3	2.13	118.69	113.25
2	D	601	FAD	C10-N1-C2	2.13	121.47	116.85
2	D	601	FAD	C4-N3-C2	-2.12	121.87	125.64
2	B	601	FAD	C4X-C4-N3	2.11	118.62	113.25
2	C	601	FAD	C6-C5X-C9A	2.09	121.92	119.05
2	A	601	FAD	C1'-N10-C9A	2.07	124.66	120.63
2	B	601	FAD	N6A-C6A-N1A	2.07	122.98	118.38
2	A	601	FAD	C4B-O4B-C1B	-2.07	104.90	109.47
2	B	601	FAD	C6-C7-C8	-2.07	116.66	119.69
2	D	601	FAD	O2-C2-N3	2.03	122.47	118.58
2	C	601	FAD	C9-C8-C7	2.02	122.66	119.69
2	C	601	FAD	C5'-C4'-C3'	-2.01	108.42	112.22

There are no chirality outliers.

All (27) 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'
2	C	601	FAD	C5B-O5B-PA-O1A
2	D	601	FAD	C5B-O5B-PA-O1A
2	D	601	FAD	C5B-O5B-PA-O2A
2	D	601	FAD	C5B-O5B-PA-O3P
3	B	602	ORN	C-CA-CB-CG
3	D	602	ORN	N-CA-CB-CG
3	D	602	ORN	C-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
2	D	601	FAD	C2'-C3'-C4'-O4'
2	C	601	FAD	PA-O3P-P-O5'
3	B	602	ORN	N-CA-CB-CG
3	C	602	ORN	CA-CB-CG-CD
2	D	601	FAD	O3'-C3'-C4'-O4'
2	D	601	FAD	C2'-C3'-C4'-C5'
3	B	602	ORN	NE-CD-CG-CB
3	C	602	ORN	NE-CD-CG-CB
2	A	601	FAD	O4B-C4B-C5B-O5B
2	A	601	FAD	C2B-C1B-N9A-C8A
2	D	601	FAD	C3B-C4B-C5B-O5B
2	C	601	FAD	C2B-C1B-N9A-C8A
3	C	602	ORN	N-CA-CB-CG
2	D	601	FAD	C4B-C5B-O5B-PA
3	A	603	ORN	OXT-C-CA-N
3	B	602	ORN	OXT-C-CA-N
3	C	602	ORN	O-C-CA-N
3	C	602	ORN	OXT-C-CA-N

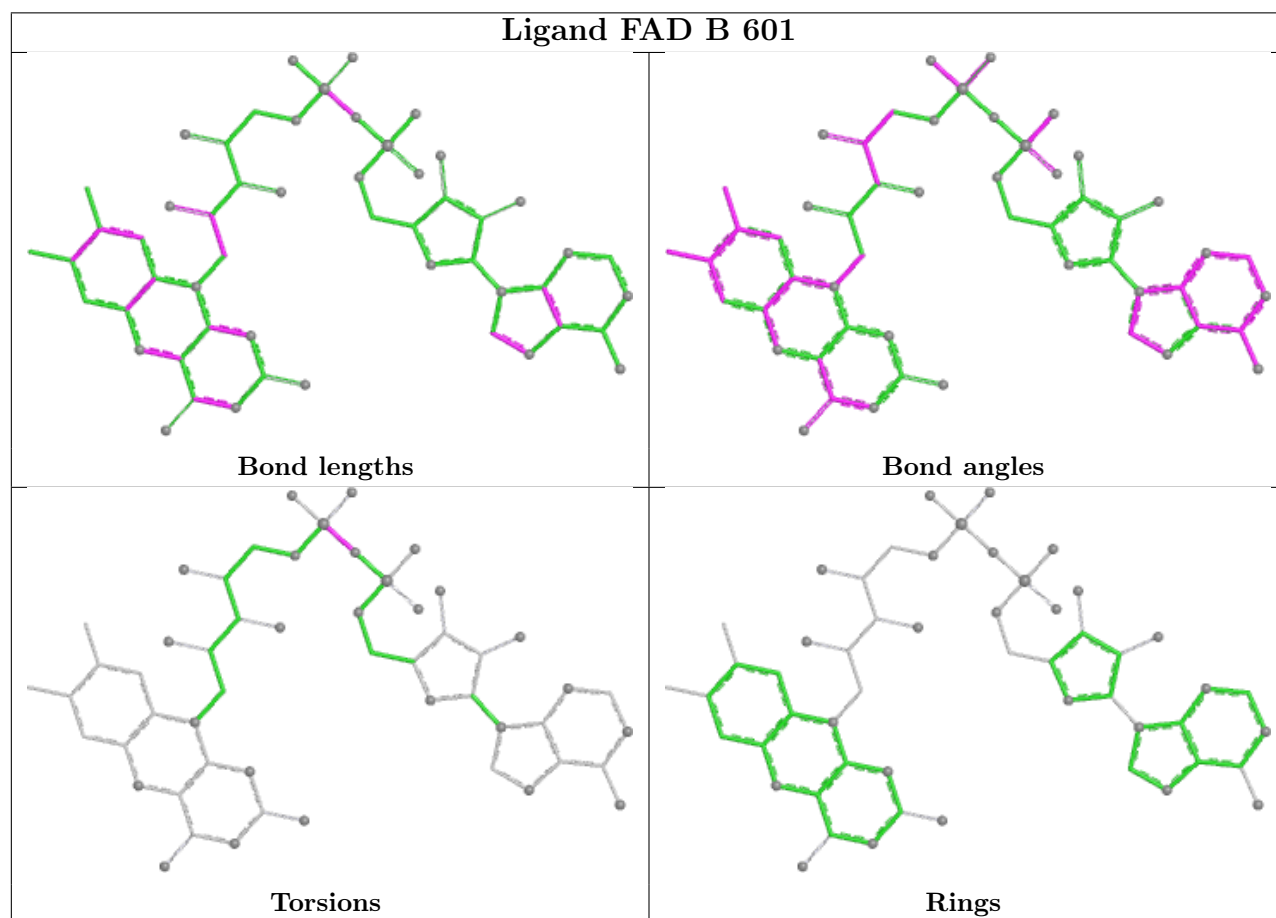
There are no ring outliers.

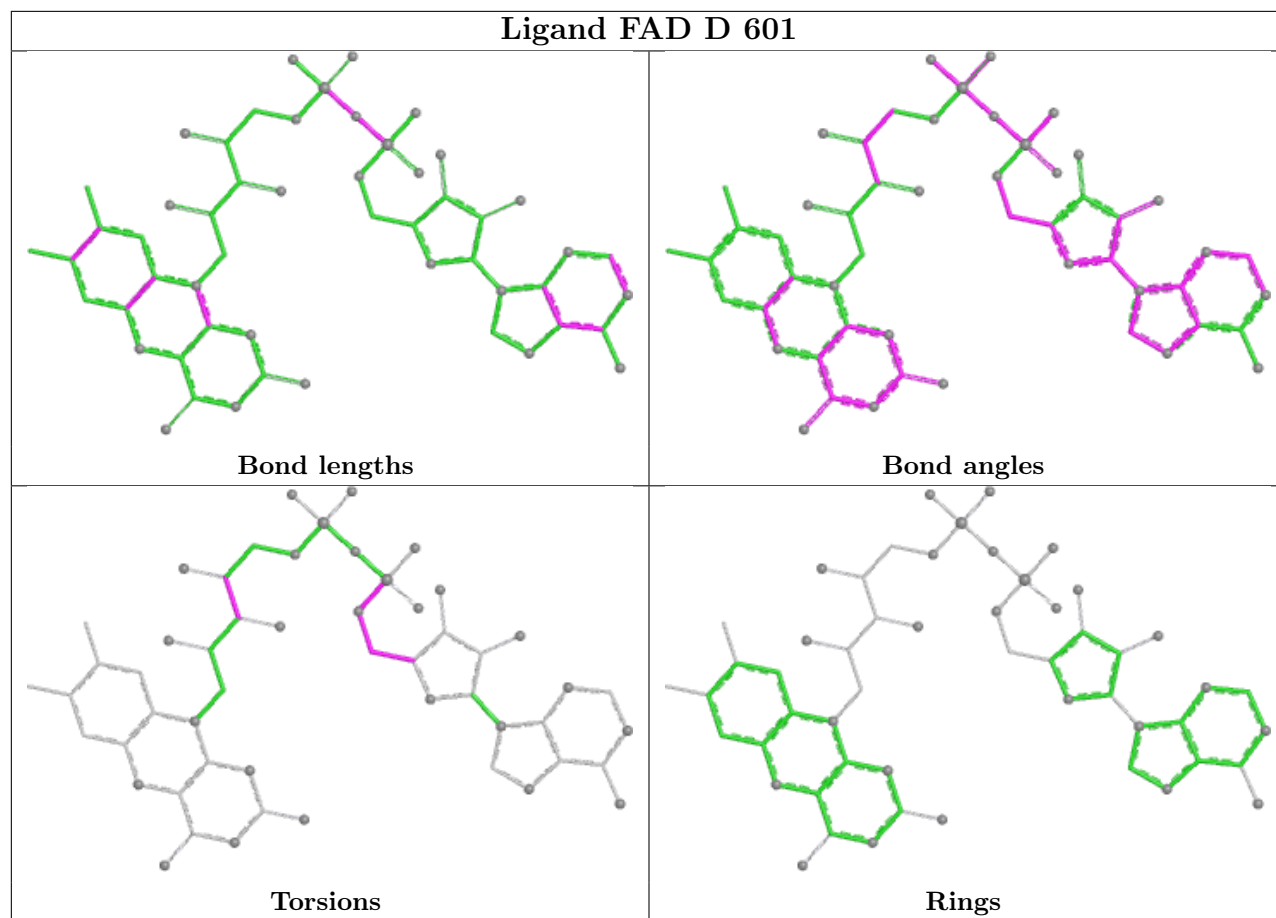
8 monomers are involved in 20 short contacts:

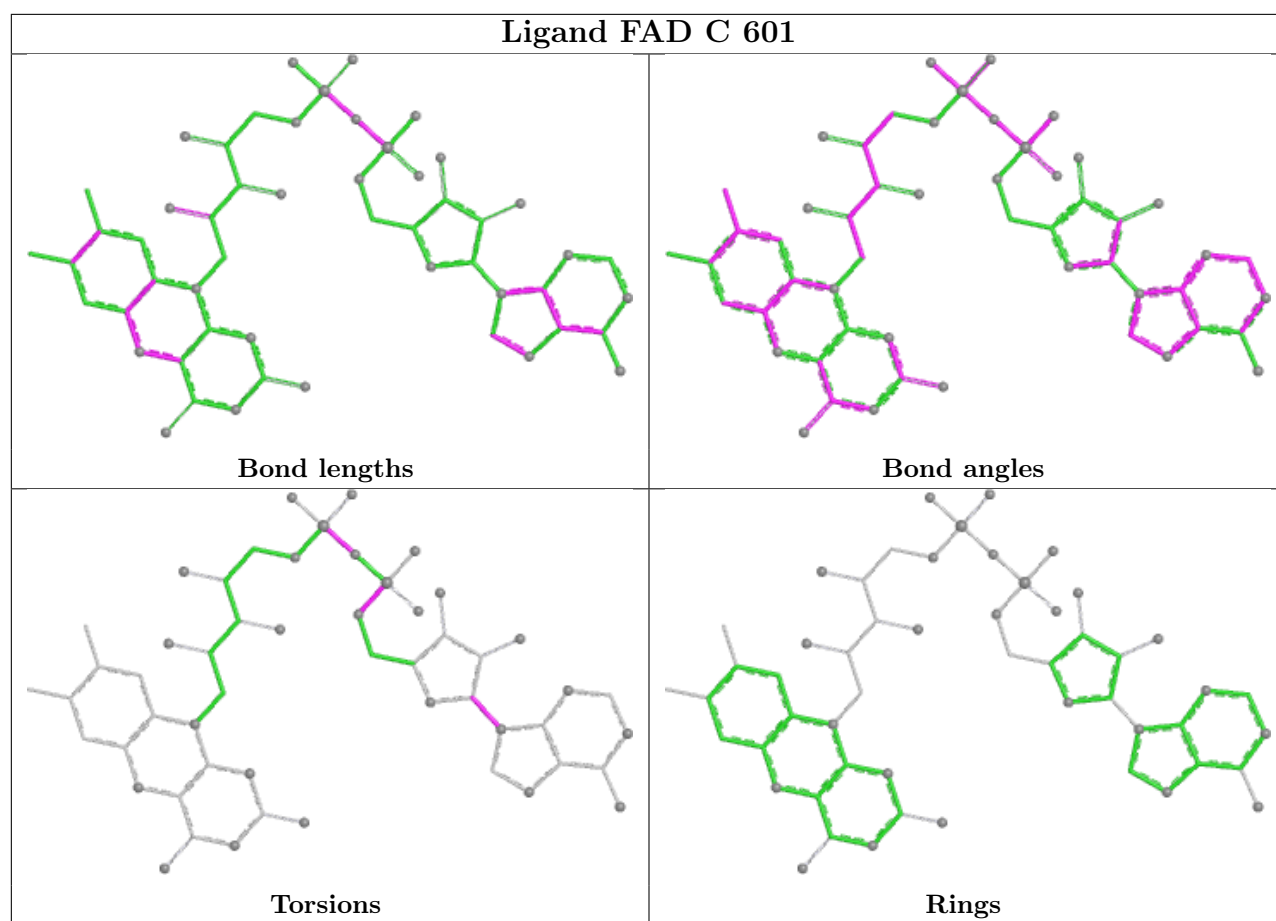
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	603	ORN	1	0
2	B	601	FAD	4	0
2	D	601	FAD	3	0
2	C	601	FAD	4	0
3	A	603	ORN	1	0
3	B	603	ORN	2	0
3	C	602	ORN	2	0
2	A	601	FAD	3	0

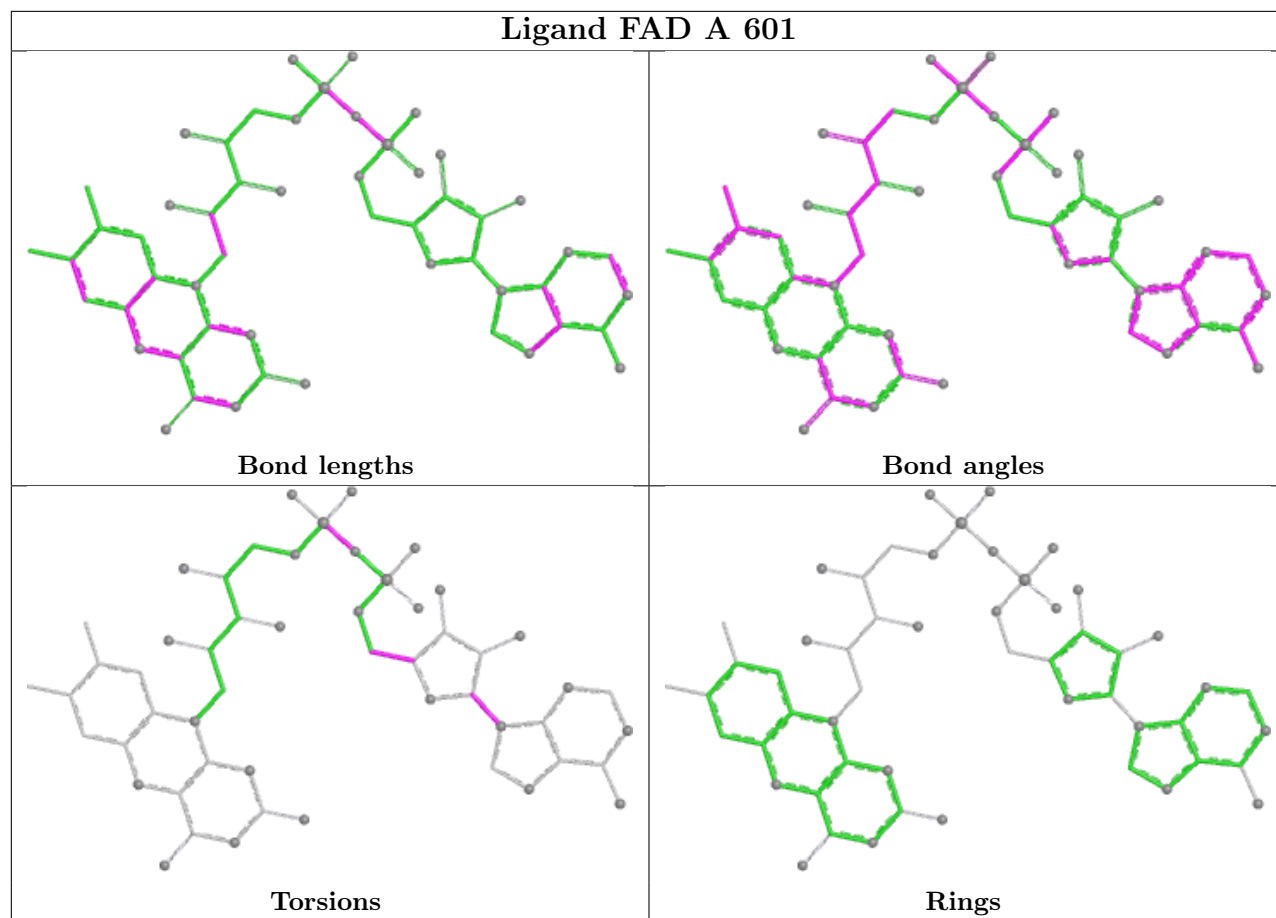
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	549/580 (94%)	-0.01	11 (2%) 65 64	17, 29, 46, 88	0
1	B	549/580 (94%)	0.01	12 (2%) 62 61	17, 30, 48, 77	0
1	C	549/580 (94%)	0.54	23 (4%) 40 39	25, 38, 59, 102	0
1	D	549/580 (94%)	0.70	32 (5%) 29 27	17, 40, 60, 96	1 (0%)
All	All	2196/2320 (94%)	0.31	78 (3%) 46 45	17, 35, 56, 102	1 (0%)

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	160	THR	4.2
1	A	160	THR	3.8
1	D	39	ILE	3.3
1	D	96	ALA	3.3
1	D	556	ILE	3.3
1	D	30	LEU	3.3
1	A	12	LYS	3.3
1	B	12	LYS	3.2
1	B	231	GLY	3.1
1	C	380	PRO	3.1
1	D	307	ALA	3.0
1	D	229	GLY	3.0
1	D	160	THR	3.0
1	C	96	ALA	3.0
1	C	39	ILE	2.8
1	C	374	PHE	2.7
1	D	93	GLY	2.7
1	D	380	PRO	2.7
1	D	232	THR	2.6
1	C	426	LEU	2.6
1	C	540	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	235	TRP	2.6
1	C	79	MET	2.6
1	D	367	PHE	2.5
1	A	334	TRP	2.5
1	D	231	GLY	2.5
1	C	160	THR	2.5
1	C	470	LEU	2.5
1	D	79	MET	2.5
1	B	334	TRP	2.5
1	C	283	TRP	2.5
1	B	542	ASP	2.4
1	C	556	ILE	2.4
1	D	12	LYS	2.4
1	D	470	LEU	2.4
1	C	229	GLY	2.4
1	B	407	ASP	2.4
1	D	459	ILE	2.4
1	C	451	ALA	2.3
1	B	556	ILE	2.3
1	C	368	VAL	2.3
1	D	29	TRP	2.3
1	D	235	TRP	2.3
1	D	527	ALA	2.3
1	A	556	ILE	2.2
1	A	231	GLY	2.2
1	B	278	GLU	2.2
1	B	427	PRO	2.2
1	D	540	HIS	2.2
1	A	234	GLY	2.1
1	B	467	PRO	2.1
1	C	257	HIS	2.1
1	D	133	ARG	2.1
1	A	209	ALA	2.1
1	A	470	LEU	2.1
1	A	232	THR	2.1
1	B	279	ARG	2.1
1	C	93	GLY	2.1
1	C	279	ARG	2.1
1	D	455	ILE	2.1
1	D	451	ALA	2.1
1	D	128	LEU	2.1
1	D	435	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	409	PRO	2.1
1	C	233	GLY	2.1
1	C	12	LYS	2.1
1	D	418	TRP	2.1
1	C	307	ALA	2.1
1	D	369	MET	2.0
1	D	36	LEU	2.0
1	A	257	HIS	2.0
1	D	553	ILE	2.0
1	D	426	LEU	2.0
1	A	279	ARG	2.0
1	D	280	CYS	2.0
1	B	358	THR	2.0
1	D	33	PRO	2.0
1	C	231	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 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, 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.

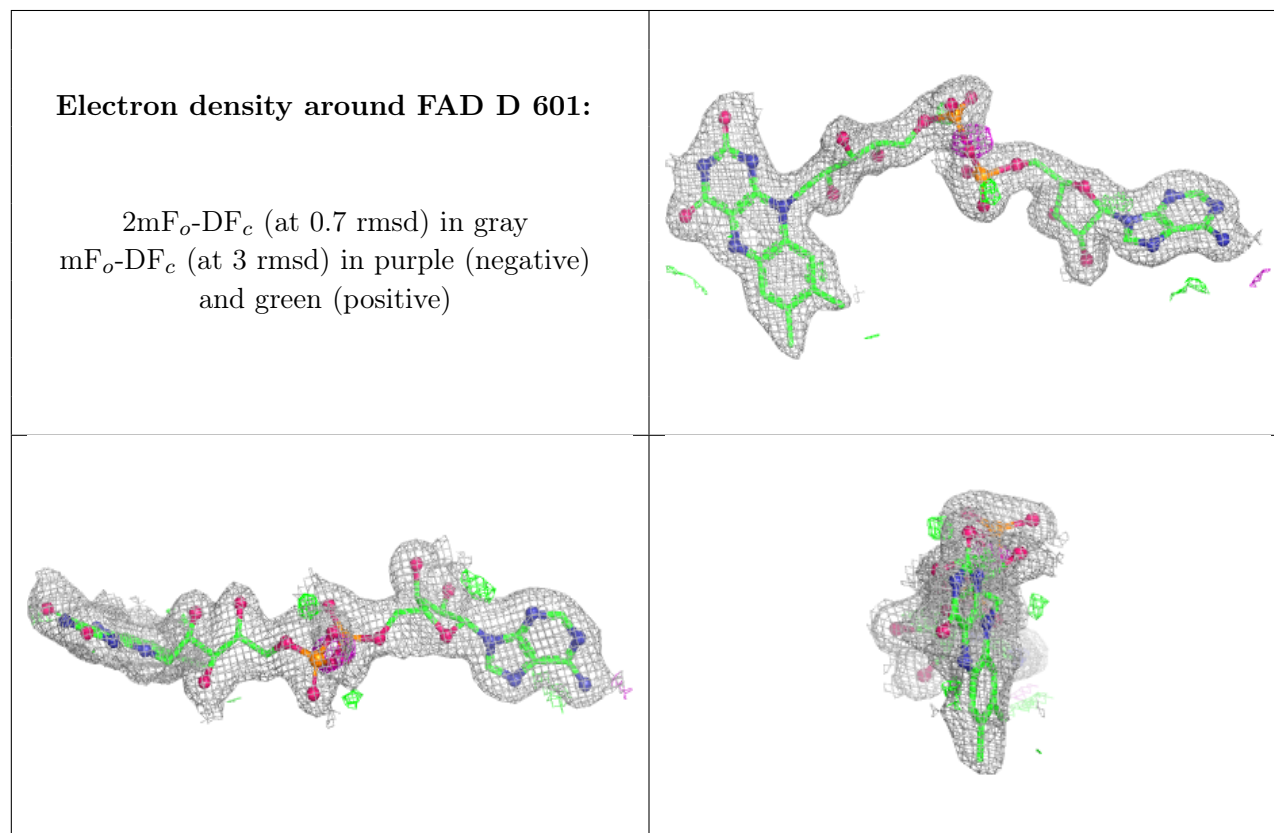
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ORN	D	602	9/9	0.79	0.16	45,51,57,58	0
3	ORN	C	602	9/9	0.86	0.13	42,49,54,55	0
3	ORN	A	602	9/9	0.87	0.16	39,45,58,68	0
3	ORN	B	602	9/9	0.89	0.13	40,48,51,55	0
3	ORN	C	603	9/9	0.90	0.11	27,30,33,35	0
3	ORN	B	603	9/9	0.91	0.09	32,36,38,39	0
3	ORN	A	603	9/9	0.92	0.08	31,34,39,39	0
3	ORN	D	603	9/9	0.92	0.08	28,29,32,33	0

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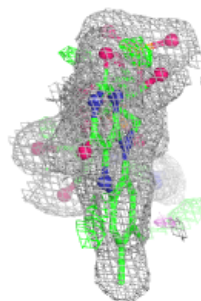
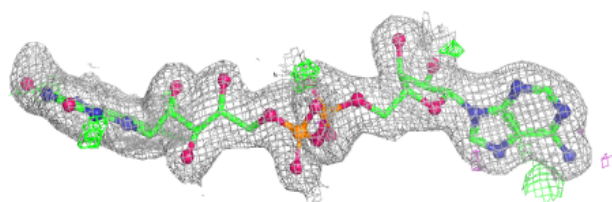
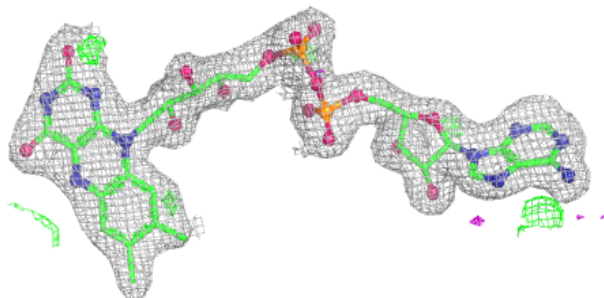
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	FAD	D	601	53/53	0.95	0.08	27,33,45,51	0
2	FAD	C	601	53/53	0.96	0.07	27,33,45,54	0
2	FAD	A	601	53/53	0.96	0.06	18,23,27,31	0
2	FAD	B	601	53/53	0.97	0.06	16,21,27,33	0

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.

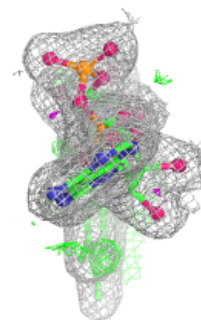
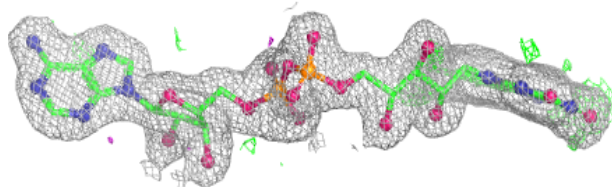
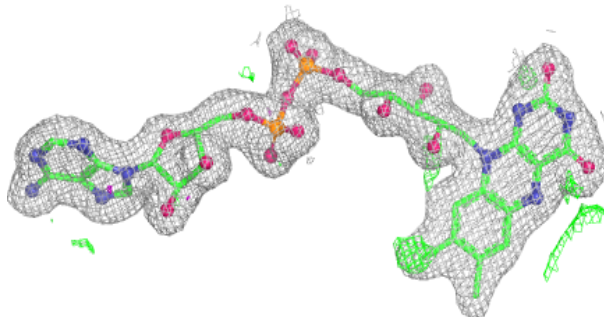


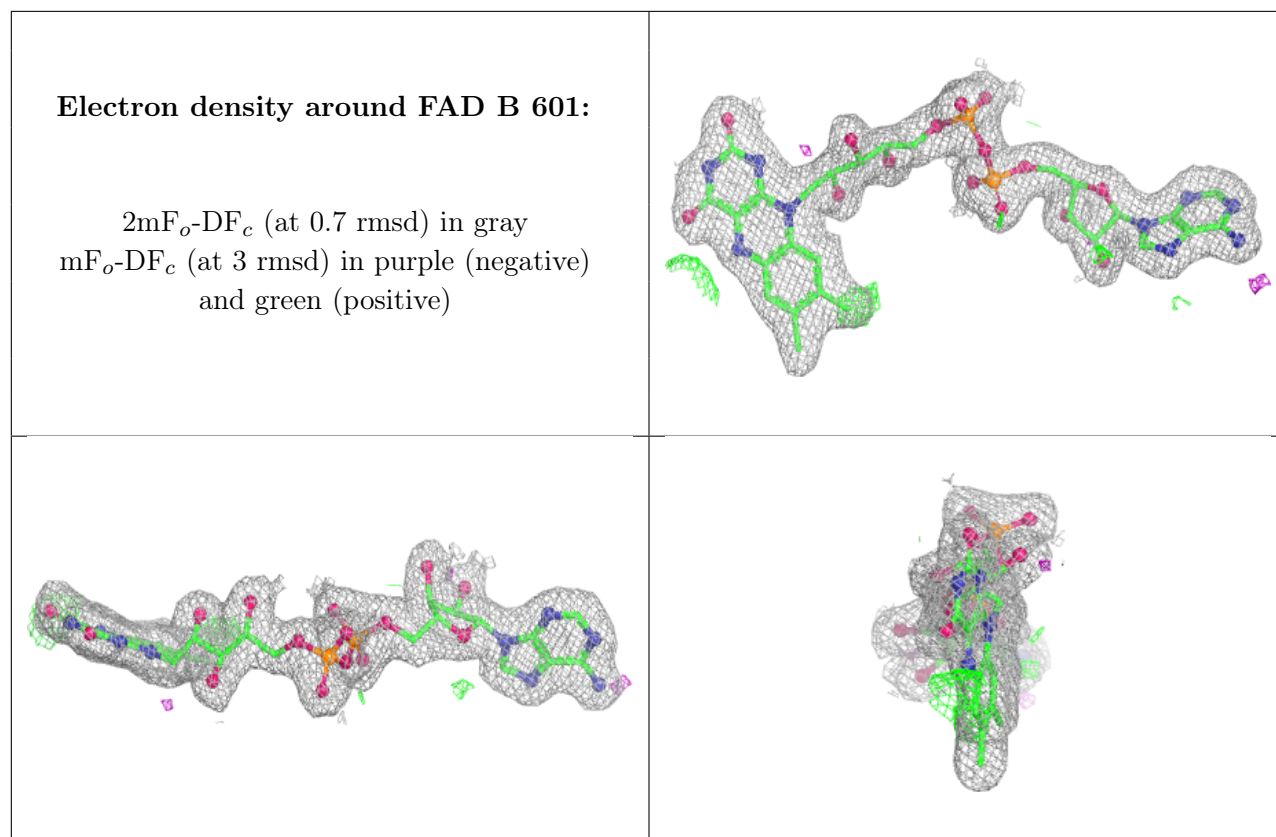
Electron density around FAD C 601:

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

**Electron density around 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.