



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:28 AM UTC

PDB ID : 6FWA / pdb_00006fwa
Title : Crystal structure of L-tryptophan oxidase VioA from *Chromobacterium violaceum* in complex with 7-Methyl-L-Tryptophan
Authors : Lai, H.E.; Morgan, M.; Moore, S.; Freemont, P.
Deposited on : 2018-03-05
Resolution : 2.85 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

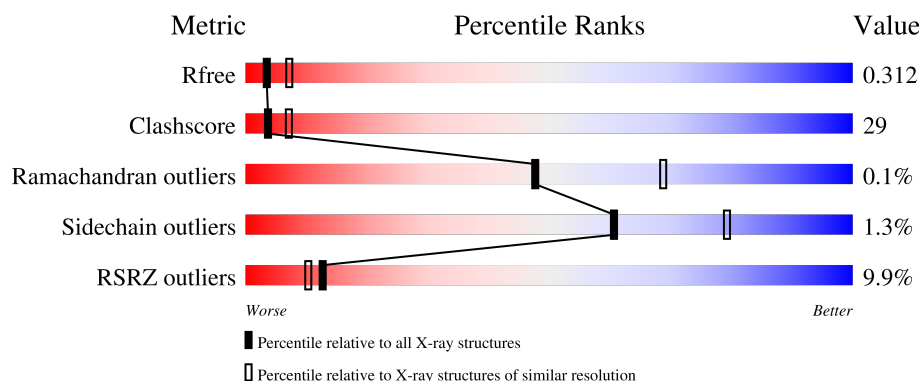
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

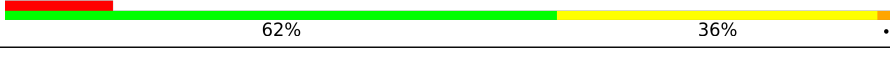
The reported resolution of this entry is 2.85 Å.

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	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	417	
1	B	417	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	E95	B	502	-	-	X	-

2 Entry composition [i](#)

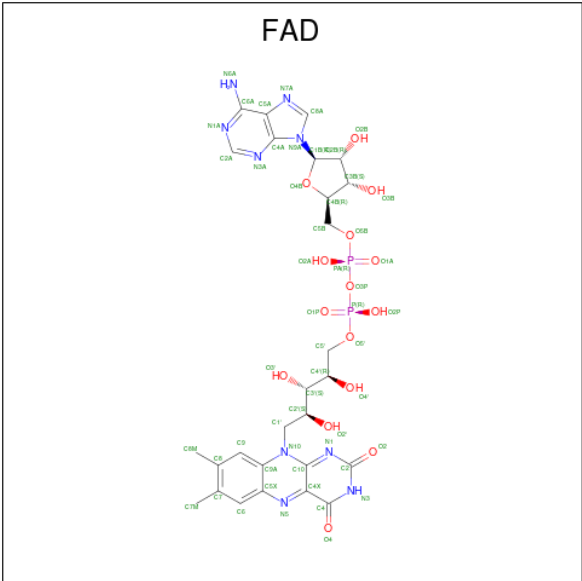
There are 5 unique types of molecules in this entry. The entry contains 6529 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Flavin-dependent L-tryptophan oxidase VioA.

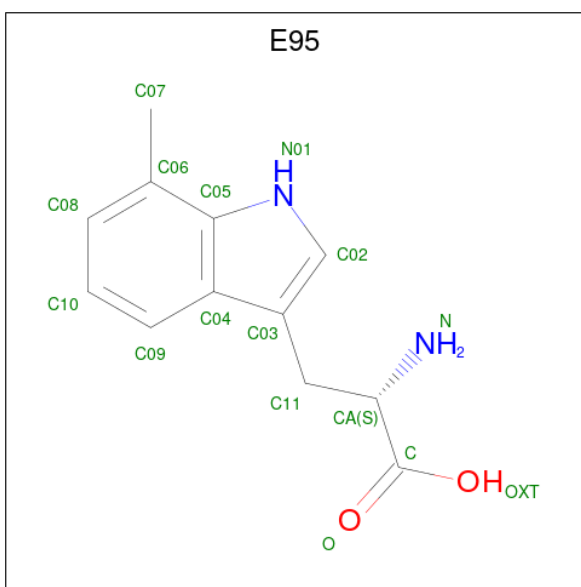
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	417	Total	C	N	O	S	0	6	0
			3156	2018	538	582	18			
1	A	415	Total	C	N	O	S	0	7	0
			3140	2012	546	565	17			

- 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	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is 7-Methyl-L-Tryptophan (CCD ID: E95) (formula: $C_{12}H_{14}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			16	12	2	2		
3	A	1	Total	C	N	O	0	0
			16	12	2	2		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		

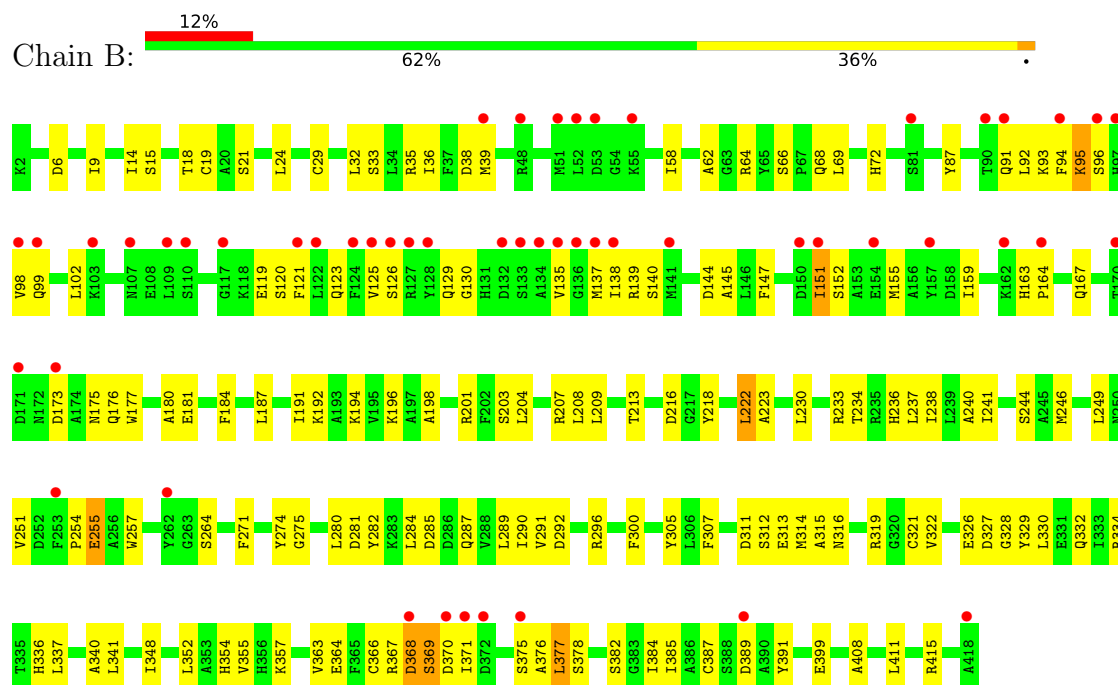
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	37	Total	O	0	0
			37	37		
5	A	56	Total	O	0	0
			56	56		

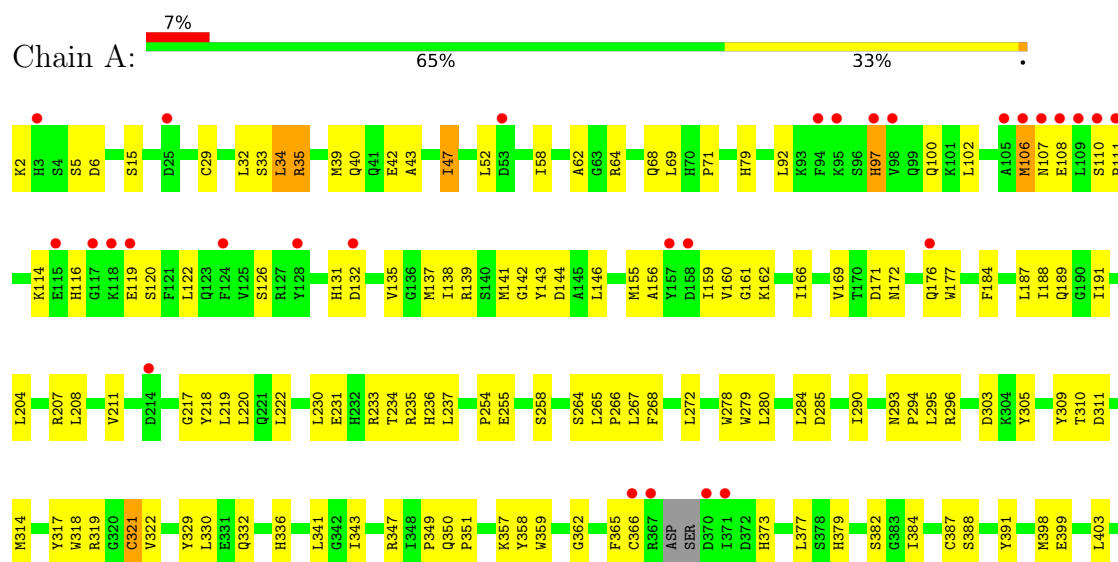
3 Residue-property plots

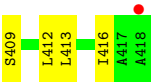
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Flavin-dependent L-tryptophan oxidase VioA



- Molecule 1: Flavin-dependent L-tryptophan oxidase VioA





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	151.34Å 172.42Å 94.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.13 – 2.85 47.13 – 2.85	Depositor EDS
% Data completeness (in resolution range)	95.3 (47.13-2.85) 96.0 (47.13-2.85)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.86Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.230 , 0.316 0.236 , 0.312	Depositor DCC
R_{free} test set	1510 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	64.0	Xtriage
Anisotropy	0.702	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 60.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6529	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, FAD, E95

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.75	2/3243 (0.1%)	0.90	6/4403 (0.1%)
1	B	0.56	0/3254	0.81	5/4419 (0.1%)
All	All	0.66	2/6497 (0.0%)	0.85	11/8822 (0.1%)

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	4
1	B	0	2
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	35	ARG	C-N	-27.67	0.98	1.33
1	A	34	LEU	C-N	-5.97	1.25	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	34	LEU	CA-C-N	21.65	153.60	122.86
1	A	34	LEU	C-N-CA	21.65	153.60	122.86
1	A	34	LEU	O-C-N	-14.00	106.19	123.27
1	A	366	CYS	N-CA-C	13.46	125.67	111.14
1	B	368	ASP	N-CA-C	-12.79	84.51	108.17
1	B	255	GLU	N-CA-C	7.42	119.36	111.28
1	B	98	VAL	N-CA-C	7.00	117.76	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	39	MET	N-CA-C	6.41	118.34	111.36
1	B	369	SER	N-CA-C	5.29	117.04	111.28
1	A	365	PHE	N-CA-C	5.24	117.16	109.24
1	A	47	ILE	N-CA-C	-5.03	100.51	107.80

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	GLU	Peptide
1	A	34	LEU	Mainchain
1	A	35	ARG	Mainchain
1	A	97	HIS	Peptide
1	B	151	ILE	Peptide
1	B	95	LYS	Mainchain

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	3140	0	2948	128	0
1	B	3156	0	2963	226	0
2	A	53	0	31	7	0
2	B	53	0	31	6	0
3	A	16	0	0	3	0
3	B	16	0	0	8	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	56	0	0	11	0
5	B	37	0	0	6	0
All	All	6529	0	5973	360	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 29.

All (360) 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:95:LYS:CD	1:B:99:GLN:HG3	1.19	1.66
1:B:145:ALA:CB	3:B:502:E95:C07	1.75	1.64
1:B:95:LYS:CE	1:B:99:GLN:HG3	1.17	1.61
1:B:91:GLN:CB	1:B:93:LYS:NZ	1.72	1.52
1:B:95:LYS:HD3	1:B:99:GLN:CG	1.32	1.51
1:B:95:LYS:HD3	1:B:99:GLN:CD	1.40	1.45
1:B:95:LYS:HE2	1:B:99:GLN:N	1.36	1.38
1:B:91:GLN:CB	1:B:93:LYS:HZ2	1.31	1.32
1:B:95:LYS:CD	1:B:99:GLN:CG	1.94	1.32
1:B:145:ALA:HB1	3:B:502:E95:C07	1.44	1.31
1:B:91:GLN:HB3	1:B:93:LYS:NZ	0.96	1.29
1:B:95:LYS:CE	1:B:99:GLN:CG	2.08	1.23
1:B:91:GLN:CG	1:B:93:LYS:HZ2	1.53	1.21
1:B:95:LYS:HG3	1:B:96:SER:O	1.38	1.21
1:A:144:ASP:OD1	1:A:296:ARG:NH1	1.76	1.19
1:B:95:LYS:CE	1:B:99:GLN:H	1.57	1.17
1:B:94:PHE:HB2	1:B:289:LEU:CD2	1.77	1.15
1:B:155:MET:SD	1:B:369:SER:CB	2.37	1.13
1:B:94:PHE:HB2	1:B:289:LEU:HD22	1.32	1.10
1:B:145:ALA:HB3	3:B:502:E95:C07	1.80	1.08
1:B:145:ALA:HB2	3:B:502:E95:C07	1.85	1.04
1:B:91:GLN:CG	1:B:93:LYS:NZ	2.17	1.01
1:B:94:PHE:CB	1:B:289:LEU:HD22	1.91	1.01
1:B:94:PHE:CB	1:B:289:LEU:CD2	2.39	1.00
1:B:94:PHE:CE2	1:B:284:LEU:CD1	2.48	0.96
1:B:91:GLN:HB3	1:B:93:LYS:HZ3	1.14	0.94
1:A:102:LEU:HD21	1:A:106:MET:HE3	1.46	0.94
1:B:94:PHE:CG	1:B:289:LEU:HD21	2.03	0.92
1:B:275:GLY:N	1:B:352:LEU:HD11	1.85	0.92
1:B:95:LYS:HE2	1:B:99:GLN:HG3	1.35	0.92
1:B:94:PHE:CE2	1:B:284:LEU:HD11	2.04	0.91
1:B:92:LEU:C	1:B:93:LYS:HD2	1.95	0.91
1:B:95:LYS:NZ	1:B:99:GLN:HG3	1.86	0.90
1:B:313:GLU:HG2	1:B:314:MET:N	1.86	0.89
1:B:95:LYS:CD	1:B:99:GLN:CD	2.36	0.88
1:B:95:LYS:HD3	1:B:99:GLN:NE2	1.91	0.86
1:B:155:MET:O	1:B:159:ILE:HG13	1.76	0.86
1:B:94:PHE:CZ	1:B:284:LEU:HD12	2.11	0.85
1:A:119:GLU:OE2	1:A:120:SER:O	1.93	0.84
1:B:94:PHE:CE2	1:B:284:LEU:HD12	2.11	0.84
1:B:274:TYR:HA	1:B:352:LEU:HD13	1.60	0.83
1:B:95:LYS:CE	1:B:99:GLN:N	2.24	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:CYS:SG	5:A:603:HOH:O	2.37	0.83
1:B:91:GLN:HB3	1:B:93:LYS:HZ1	1.01	0.83
1:B:38:ASP:HB3	1:B:204:LEU:HD23	1.61	0.82
1:B:370:ASP:O	5:B:601:HOH:O	1.98	0.82
1:B:313:GLU:HG2	1:B:314:MET:H	1.45	0.80
1:B:138:ILE:HG12	1:B:147:PHE:HE2	1.47	0.80
1:A:102:LEU:HD12	1:A:137:MET:HB3	1.64	0.79
1:A:254:PRO:O	1:A:258:SER:O	2.01	0.79
1:A:42:GLU:OE1	1:A:43:ALA:N	2.15	0.79
1:B:251:VAL:CG1	1:B:257:TRP:CZ2	2.66	0.79
1:A:122:LEU:HD23	1:A:122:LEU:O	1.82	0.79
1:B:251:VAL:CG1	1:B:257:TRP:HZ2	1.96	0.78
1:B:94:PHE:CG	1:B:289:LEU:CD2	2.65	0.78
1:B:95:LYS:NZ	1:B:99:GLN:CG	2.43	0.78
1:B:91:GLN:CD	1:B:93:LYS:NZ	2.43	0.77
1:B:332:GLN:HE22	1:B:336:HIS:CD2	2.02	0.77
1:A:332[A]:GLN:NE2	5:A:603:HOH:O	2.18	0.77
1:B:95:LYS:HE2	1:B:99:GLN:CA	2.15	0.76
1:B:274:TYR:CA	1:B:352:LEU:HD13	2.16	0.76
1:B:95:LYS:HE2	1:B:99:GLN:H	0.94	0.76
1:A:102:LEU:CD2	1:A:106:MET:HE3	2.15	0.75
1:B:95:LYS:HE2	1:B:99:GLN:CG	1.94	0.75
1:B:91:GLN:CD	1:B:93:LYS:CE	2.59	0.75
1:A:267:LEU:HD12	1:A:362:GLY:HA3	1.67	0.75
1:B:91:GLN:CD	1:B:93:LYS:HE3	2.11	0.75
1:B:68:GLN:NE2	1:B:176:GLN:OE1	2.19	0.74
1:B:91:GLN:CB	1:B:93:LYS:HZ1	1.65	0.74
1:B:144:ASP:OD2	1:B:296:ARG:NH1	2.21	0.74
1:B:91:GLN:HG2	1:B:93:LYS:HZ2	1.52	0.73
1:B:62:ALA:HA	2:B:501:FAD:N5	2.03	0.73
1:B:254:PRO:HD2	1:B:255:GLU:HG2	1.70	0.73
1:A:40:GLN:NE2	2:A:501:FAD:O2B	2.21	0.72
1:A:176:GLN:CD	1:A:177:TRP:H	1.97	0.72
1:B:94:PHE:CD1	1:B:289:LEU:HD21	2.24	0.71
1:B:93:LYS:HD2	1:B:93:LYS:N	2.06	0.70
1:B:95:LYS:HZ3	1:B:99:GLN:CG	2.04	0.70
1:B:120:SER:HA	1:B:152:SER:HA	1.73	0.69
1:A:160:VAL:HG23	1:A:166:ILE:HD12	1.73	0.69
1:B:274:TYR:HA	1:B:352:LEU:CD1	2.22	0.68
1:B:208:LEU:HA	1:B:222:LEU:HD12	1.75	0.68
1:B:357:LYS:NZ	5:B:603:HOH:O	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:GLN:HE22	1:B:336:HIS:CG	2.11	0.67
1:B:251:VAL:HG12	1:B:257:TRP:HE1	1.60	0.67
1:A:64:ARG:HH21	3:A:502:E95:C	2.08	0.66
1:B:366:CYS:SG	1:B:368:ASP:O	2.52	0.66
1:A:208:LEU:CA	1:A:222:LEU:HD23	2.26	0.66
1:A:358:TYR:HD1	5:A:629:HOH:O	1.77	0.66
1:B:138:ILE:HG12	1:B:147:PHE:CE2	2.31	0.65
1:A:62:ALA:HA	2:A:501:FAD:N5	2.12	0.65
1:B:95:LYS:CG	1:B:96:SER:O	2.30	0.65
1:A:161:GLY:C	1:A:162:LYS:HE2	2.22	0.65
1:B:35:ARG:NH1	1:B:203:SER:OG	2.30	0.64
1:A:68:GLN:OE1	1:A:176:GLN:N	2.26	0.64
1:A:97:HIS:ND1	1:A:100:GLN:HB2	2.13	0.64
1:A:295:LEU:HD23	1:A:318:TRP:CZ2	2.31	0.64
1:B:222:LEU:HD23	1:B:230:LEU:HD22	1.80	0.64
1:B:377:LEU:N	1:B:377:LEU:HD12	2.12	0.64
1:A:162:LYS:HE2	1:A:162:LYS:N	2.11	0.64
1:B:213:THR:HG21	1:B:382:SER:HB3	1.79	0.64
1:B:94:PHE:CZ	1:B:284:LEU:CD1	2.76	0.64
1:B:95:LYS:HG2	1:B:99:GLN:HB2	1.79	0.64
1:B:64:ARG:HD3	1:B:87:TYR:CZ	2.33	0.64
1:A:138:ILE:HA	1:A:141:MET:HE3	1.78	0.63
1:A:413:LEU:HA	1:A:416:ILE:HG12	1.81	0.63
1:B:144:ASP:HB3	1:B:313:GLU:OE1	1.98	0.63
1:B:377:LEU:HD11	1:B:391:TYR:CG	2.34	0.63
1:A:102:LEU:HG	1:A:106:MET:HB2	1.80	0.63
1:B:251:VAL:HG11	1:B:257:TRP:CZ2	2.33	0.63
1:A:122:LEU:HD23	1:A:122:LEU:C	2.23	0.62
1:A:208:LEU:HA	1:A:222:LEU:HD23	1.80	0.62
1:B:251:VAL:HG12	1:B:257:TRP:NE1	2.15	0.62
1:B:95:LYS:CD	1:B:99:GLN:NE2	2.59	0.62
1:B:332:GLN:NE2	1:B:336:HIS:CD2	2.68	0.62
1:B:99:GLN:NE2	1:B:290:ILE:O	2.33	0.61
1:A:294:PRO:HA	1:A:314:MET:HE2	1.82	0.61
1:B:251:VAL:HG12	1:B:251:VAL:O	2.00	0.61
1:B:95:LYS:HE2	1:B:99:GLN:CB	2.29	0.61
1:B:275:GLY:N	1:B:352:LEU:CD1	2.62	0.61
1:A:155:MET:O	1:A:159:ILE:HG13	1.99	0.61
1:B:94:PHE:CD1	1:B:289:LEU:CD2	2.84	0.61
1:B:291:VAL:HG11	1:B:340:ALA:HB1	1.81	0.60
1:A:156:ALA:O	1:A:160:VAL:HG12	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:GLU:O	1:A:120:SER:C	2.42	0.60
1:B:94:PHE:HB2	1:B:289:LEU:HD23	1.80	0.60
1:B:95:LYS:CD	1:B:99:GLN:CB	2.79	0.60
1:B:213:THR:HG22	1:B:218:TYR:CD1	2.37	0.60
1:B:326:GLU:O	1:B:330:LEU:HD12	2.02	0.60
1:A:29:CYS:HA	1:A:32:LEU:HD13	1.84	0.60
1:B:377:LEU:HD11	1:B:391:TYR:CD1	2.37	0.60
1:A:106:MET:CE	1:A:169:VAL:HG12	2.33	0.59
1:A:119:GLU:CD	1:A:120:SER:O	2.45	0.59
1:B:274:TYR:C	1:B:352:LEU:CD1	2.75	0.59
1:B:209:LEU:O	1:B:249:LEU:HD23	2.02	0.59
1:A:237:LEU:HD23	1:A:384:ILE:HD12	1.85	0.58
1:A:162:LYS:NZ	1:A:172:ASN:CB	2.66	0.58
1:A:162:LYS:HZ2	1:A:172:ASN:CG	2.10	0.58
1:B:92:LEU:HD21	1:B:290:ILE:HD13	1.85	0.58
1:A:102:LEU:HD21	1:A:106:MET:CE	2.26	0.58
1:B:95:LYS:HZ3	1:B:99:GLN:HG2	1.68	0.58
1:B:292:ASP:OD1	1:B:292:ASP:N	2.36	0.58
1:B:64:ARG:NH1	3:B:502:E95:OXT	2.37	0.58
1:B:313:GLU:O	1:B:314:MET:C	2.47	0.58
1:A:211:VAL:HG12	1:A:220:LEU:HD22	1.85	0.57
1:B:91:GLN:OE1	1:B:93:LYS:NZ	2.37	0.57
1:B:319:ARG:HH11	1:B:322:VAL:HG23	1.70	0.57
1:A:110:SER:OG	1:A:111:PRO:HD3	2.05	0.57
1:B:151:ILE:HD11	1:B:155:MET:HE2	1.86	0.57
1:B:274:TYR:C	1:B:352:LEU:HD13	2.30	0.56
1:B:94:PHE:HB3	1:B:289:LEU:HD22	1.85	0.56
1:A:357:LYS:HG2	1:A:359:TRP:NE1	2.19	0.56
1:A:357:LYS:HG2	1:A:359:TRP:CE2	2.41	0.56
1:B:91:GLN:OE1	1:B:93:LYS:CE	2.53	0.56
1:B:95:LYS:NZ	1:B:99:GLN:HG2	2.19	0.56
1:B:139:ARG:O	1:B:296:ARG:NH2	2.39	0.56
1:A:379:HIS:ND1	1:A:382:SER:OG	2.31	0.56
1:A:293:ASN:O	1:A:296:ARG:HD2	2.05	0.56
1:B:95:LYS:HG3	1:B:96:SER:C	2.24	0.55
1:B:408:ALA:HA	1:B:411:LEU:HD13	1.87	0.55
1:A:280:LEU:HD11	1:A:303:ASP:HB3	1.89	0.55
1:A:399:GLU:O	1:A:403:LEU:HG	2.06	0.55
1:A:162:LYS:NZ	1:A:172:ASN:CG	2.65	0.55
1:A:310:THR:OG1	1:A:314:MET:HB2	2.08	0.54
1:A:317:TYR:OH	1:A:332[A]:GLN:OE1	2.24	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:ASP:C	1:B:282:TYR:HD1	2.15	0.54
1:B:354:HIS:HD2	5:B:617:HOH:O	1.90	0.54
1:A:62:ALA:HA	2:A:501:FAD:C4X	2.38	0.54
1:A:268:PHE:HD2	5:A:629:HOH:O	1.91	0.54
1:B:163:HIS:NE2	3:B:502:E95:N	2.55	0.54
1:A:79[A]:HIS:NE2	5:A:602:HOH:O	2.11	0.53
1:A:144:ASP:CG	1:A:296:ARG:NH1	2.65	0.53
1:B:321[A]:CYS:SG	1:B:329:TYR:HA	2.49	0.53
1:A:314:MET:O	1:A:318:TRP:HD1	1.92	0.53
1:A:409:SER:O	1:A:413:LEU:HD12	2.08	0.53
1:A:343:ILE:HD12	1:A:347[A]:ARG:HB2	1.90	0.53
1:B:129:GLN:OE1	1:B:130:GLY:N	2.39	0.53
1:B:209:LEU:HD11	1:B:223:ALA:HB2	1.90	0.53
1:A:139:ARG:O	1:A:296:ARG:NH2	2.41	0.53
1:A:92:LEU:HD11	1:A:290:ILE:HD12	1.89	0.53
1:A:162:LYS:NZ	1:A:172:ASN:HB2	2.24	0.53
1:A:264:SER:O	1:A:265:LEU:HD22	2.09	0.53
1:A:373:HIS:ND1	1:A:373:HIS:O	2.42	0.53
1:B:58:ILE:HG22	1:B:305:TYR:CZ	2.43	0.52
1:A:236:HIS:HB3	1:A:412:LEU:HD11	1.90	0.52
1:B:237:LEU:HD12	1:B:238:ILE:N	2.24	0.52
1:B:95:LYS:HG2	1:B:99:GLN:CB	2.39	0.52
1:B:311:ASP:N	1:B:311:ASP:OD1	2.42	0.52
1:A:294:PRO:HD2	1:A:336:HIS:CD2	2.44	0.52
3:A:502:E95:N	3:A:502:E95:C02	2.73	0.52
1:A:2:LYS:N	5:A:609:HOH:O	2.41	0.52
1:B:62:ALA:HA	2:B:501:FAD:C4X	2.40	0.52
1:B:375:SER:HA	1:B:391:TYR:O	2.10	0.52
1:A:144:ASP:CG	1:A:296:ARG:HH12	2.18	0.52
1:B:209:LEU:O	1:B:249:LEU:CD2	2.58	0.52
1:B:271:PHE:HB2	1:B:355:VAL:HG13	1.90	0.52
1:B:334:ARG:NH1	1:B:348:ILE:O	2.43	0.52
1:A:413:LEU:HD12	1:A:413:LEU:H	1.74	0.51
1:B:93:LYS:N	1:B:93:LYS:CD	2.73	0.51
1:A:6:ASP:HB2	1:A:33:SER:H	1.74	0.51
1:A:267:LEU:HD23	1:A:311:ASP:HB3	1.91	0.51
1:A:272:LEU:HD23	1:A:351:PRO:HG3	1.92	0.51
1:B:280:LEU:C	1:B:282:TYR:H	2.18	0.51
1:A:106:MET:CE	1:A:169:VAL:CG1	2.89	0.51
1:B:95:LYS:HD2	1:B:96:SER:H	1.76	0.51
1:B:234:THR:HG22	1:B:236:HIS:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:502:E95:N	3:B:502:E95:C09	2.72	0.51
1:B:123:GLN:HA	1:B:126:SER:HB2	1.92	0.51
1:B:213:THR:HG21	1:B:382:SER:CB	2.40	0.51
1:B:167:GLN:NE2	1:B:173:ASP:HA	2.26	0.50
1:B:72:HIS:N	1:B:399:GLU:OE1	2.45	0.50
1:A:176:GLN:NE2	1:A:177:TRP:O	2.44	0.50
1:B:284:LEU:HD23	1:B:300:PHE:CE2	2.47	0.50
1:B:192:LYS:HE2	1:B:196:LYS:HE3	1.94	0.50
1:A:126:SER:O	1:A:126:SER:OG	2.28	0.50
1:A:106:MET:HE3	1:A:169:VAL:CG1	2.42	0.49
1:B:91:GLN:C	1:B:92:LEU:HD12	2.37	0.49
1:B:244:SER:OG	1:B:364:GLU:OE2	2.13	0.49
1:B:282:TYR:HD1	1:B:282:TYR:N	2.10	0.49
1:A:122:LEU:C	1:A:122:LEU:CD2	2.85	0.49
1:A:5:SER:O	1:A:234:THR:HA	2.12	0.49
1:A:211:VAL:HG12	1:A:220:LEU:CD2	2.43	0.49
1:B:274:TYR:CA	1:B:352:LEU:CD1	2.86	0.49
1:A:398:MET:HG3	2:A:501:FAD:H2'	1.95	0.49
1:A:236:HIS:NE2	1:A:416:ILE:HG22	2.28	0.49
1:B:251:VAL:HG13	1:B:257:TRP:HZ2	1.78	0.49
1:B:241:ILE:HG22	2:B:501:FAD:O4B	2.13	0.48
1:A:106:MET:HE3	1:A:169:VAL:HG11	1.95	0.48
1:B:236:HIS:CE1	1:B:415:ARG:HH12	2.31	0.48
1:B:385:ILE:HG21	1:B:408:ALA:HB1	1.94	0.48
1:B:282:TYR:N	1:B:282:TYR:CD1	2.81	0.48
1:B:284:LEU:HD23	1:B:300:PHE:CZ	2.49	0.48
1:A:47:ILE:HG23	1:A:184:PHE:HB2	1.96	0.48
1:A:102:LEU:CD1	1:A:137:MET:HB3	2.40	0.48
1:B:64:ARG:HG2	1:B:87:TYR:CE1	2.48	0.48
1:B:66:SER:OG	1:B:69:LEU:HB3	2.14	0.48
1:B:6:ASP:OD2	1:B:33:SER:N	2.37	0.48
1:B:119:GLU:HB3	1:B:123:GLN:HE21	1.78	0.48
1:A:58:ILE:HG22	1:A:305:TYR:CZ	2.49	0.48
1:B:332:GLN:C	1:B:332:GLN:CD	2.82	0.47
1:B:389:ASP:OD2	5:B:602:HOH:O	2.20	0.47
1:A:132:ASP:OD1	1:A:132:ASP:N	2.47	0.47
1:B:129:GLN:CD	1:B:130:GLY:H	2.21	0.47
3:A:502:E95:C07	5:A:615:HOH:O	2.62	0.47
1:B:285:ASP:O	1:B:287:GLN:HG3	2.13	0.47
1:B:91:GLN:CD	1:B:93:LYS:HZ1	2.16	0.47
1:B:95:LYS:HG3	1:B:96:SER:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:GLN:CG	1:B:93:LYS:CE	2.93	0.47
1:B:29:CYS:HA	1:B:32:LEU:HD12	1.95	0.47
1:B:68:GLN:HG3	1:B:175:ASN:HA	1.95	0.47
1:B:99:GLN:HG2	1:B:140:SER:OG	2.14	0.47
1:B:411:LEU:HD12	1:B:411:LEU:H	1.79	0.47
1:A:217:GLY:HA3	1:A:235:ARG:HA	1.97	0.47
1:A:350[B]:GLN:OE1	5:A:604:HOH:O	2.20	0.47
1:B:274:TYR:C	1:B:352:LEU:HD11	2.37	0.47
1:B:352:LEU:CD1	1:B:352:LEU:H	2.28	0.47
1:A:310:THR:OG1	1:A:311:ASP:N	2.48	0.47
3:B:502:E95:N	3:B:502:E95:C04	2.78	0.46
1:B:271:PHE:CD2	1:B:307:PHE:HB3	2.50	0.46
1:B:319:ARG:HH11	1:B:322:VAL:CG2	2.29	0.46
1:B:216:ASP:OD1	1:B:233:ARG:NH2	2.29	0.46
1:A:47:ILE:CD1	5:A:606:HOH:O	2.62	0.46
1:A:285:ASP:OD1	1:A:285:ASP:N	2.49	0.46
1:A:388:SER:HB3	1:A:391:TYR:CE1	2.50	0.46
1:B:187:LEU:O	1:B:191:ILE:HG13	2.15	0.46
1:B:208:LEU:CA	1:B:222:LEU:HD12	2.42	0.46
1:B:367:ARG:C	1:B:369:SER:N	2.73	0.46
1:B:376:ALA:C	1:B:377:LEU:HD12	2.41	0.46
1:A:330:LEU:HD23	1:A:330:LEU:HA	1.73	0.46
1:B:314:MET:HE2	1:B:314:MET:HA	1.98	0.46
1:B:181:GLU:O	1:B:181:GLU:HG2	2.16	0.46
1:A:219:LEU:HD23	1:A:233:ARG:HG3	1.98	0.46
1:A:106:MET:HE1	1:A:169:VAL:HG12	1.97	0.45
1:A:142:GLY:HA2	1:A:296:ARG:NH2	2.31	0.45
1:B:151:ILE:HG12	1:B:152:SER:H	1.80	0.45
1:B:246:MET:HE3	1:B:246:MET:HB2	1.69	0.45
1:B:15:SER:O	1:B:19:CYS:HB2	2.17	0.45
1:B:237:LEU:HG	1:B:384:ILE:HG23	1.99	0.45
1:B:246:MET:HE1	5:B:605:HOH:O	2.17	0.45
1:B:275:GLY:H	1:B:352:LEU:HD11	1.75	0.45
1:B:64:ARG:HD3	1:B:87:TYR:OH	2.15	0.45
1:B:95:LYS:CG	1:B:96:SER:N	2.80	0.45
1:B:313:GLU:O	1:B:316:ASN:N	2.50	0.45
1:B:102:LEU:HD23	1:B:137:MET:HB3	2.00	0.44
1:B:312:SER:O	1:B:315:ALA:HB3	2.17	0.44
1:B:180:ALA:HB2	1:B:184:PHE:CD1	2.52	0.44
1:B:282:TYR:HB3	1:B:284:LEU:HD13	2.00	0.44
1:B:332:GLN:NE2	1:B:336:HIS:NE2	2.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:ILE:HA	1:A:141:MET:CE	2.45	0.44
1:A:218:TYR:CE2	1:A:384:ILE:HD11	2.53	0.44
1:A:114:LYS:C	1:A:116:HIS:H	2.26	0.44
1:A:119:GLU:CD	1:A:119:GLU:C	2.86	0.44
1:B:164:PRO:HG3	1:B:177:TRP:CD2	2.53	0.43
1:B:9:ILE:HB	1:B:36:ILE:HD13	2.01	0.43
1:B:94:PHE:HE2	1:B:284:LEU:CD1	2.23	0.43
1:B:95:LYS:HE3	1:B:99:GLN:H	1.69	0.43
1:A:184:PHE:CE2	1:A:398:MET:HE1	2.52	0.43
1:B:18:THR:HG22	1:B:191:ILE:HD13	2.00	0.43
1:B:64:ARG:HD2	1:B:164:PRO:HG2	2.01	0.43
1:B:24:LEU:HD13	1:B:198:ALA:HB3	2.00	0.43
1:B:95:LYS:CG	1:B:99:GLN:HB2	2.45	0.43
1:B:327[A]:ASP:OD1	1:B:328:GLY:N	2.52	0.43
1:B:201[A]:ARG:HE	1:B:201[A]:ARG:HB2	1.67	0.43
1:A:267:LEU:HD22	1:A:309:TYR:CE1	2.54	0.43
1:A:377:LEU:HD13	1:A:391:TYR:CG	2.54	0.43
1:A:295:LEU:HD23	1:A:318:TRP:HZ2	1.79	0.43
2:A:501:FAD:H9	2:A:501:FAD:H1'1	1.83	0.43
1:B:240:ALA:HA	1:B:387:CYS:HB3	1.99	0.42
1:A:15:SER:HB3	1:A:387:CYS:SG	2.59	0.42
1:A:39:MET:HE3	2:A:501:FAD:C5A	2.49	0.42
1:A:188:ILE:HD12	1:A:189[B]:GLN:H	1.81	0.42
1:B:332:GLN:NE2	1:B:336:HIS:CE1	2.87	0.42
1:A:107:ASN:ND2	1:A:171:ASP:OD1	2.52	0.42
1:B:251:VAL:HG12	1:B:257:TRP:CE2	2.54	0.42
1:A:295:LEU:CD2	1:A:318:TRP:CZ2	3.01	0.42
1:B:135:VAL:HG12	1:B:135:VAL:O	2.19	0.42
1:A:64:ARG:HG2	2:A:501:FAD:O4	2.18	0.42
1:A:71:PRO:HD2	1:A:399:GLU:OE1	2.20	0.42
1:A:131:HIS:O	1:A:135:VAL:HG13	2.19	0.42
1:B:21:SER:HB2	1:B:194:LYS:HE2	2.01	0.42
1:B:280:LEU:CD2	1:B:285:ASP:HB3	2.50	0.42
1:A:204:LEU:HD23	1:A:204:LEU:HA	1.83	0.42
1:A:143:TYR:HB2	1:A:146:LEU:HD13	2.02	0.41
1:A:69:LEU:C	1:A:71:PRO:HD3	2.45	0.41
1:A:187:LEU:O	1:A:191:ILE:HD12	2.19	0.41
1:B:14:ILE:O	1:B:18:THR:HG23	2.20	0.41
1:B:123:GLN:N	1:B:123:GLN:OE1	2.54	0.41
1:B:282:TYR:CE2	1:B:341:LEU:HD23	2.55	0.41
1:B:352:LEU:HD12	1:B:352:LEU:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:PHE:O	1:B:125:VAL:HG23	2.20	0.41
1:B:207:ARG:O	1:B:222:LEU:HA	2.20	0.41
1:A:102:LEU:HB2	1:A:137:MET:HG2	2.01	0.41
1:A:319:ARG:HB2	1:A:358:TYR:CD1	2.55	0.41
1:A:341:LEU:HA	1:A:341:LEU:HD23	1.83	0.41
1:B:280:LEU:C	1:B:282:TYR:N	2.78	0.41
1:B:415:ARG:O	1:B:415:ARG:HG2	2.21	0.41
1:A:230:LEU:HD12	1:A:231:GLU:H	1.85	0.41
1:A:296:ARG:NH2	5:A:601:HOH:O	2.06	0.41
1:B:62:ALA:HA	2:B:501:FAD:C5X	2.51	0.41
1:B:159:ILE:HG23	1:B:163:HIS:HE1	1.85	0.41
2:B:501:FAD:HM71	2:B:501:FAD:HM83	1.86	0.41
1:B:135:VAL:HA	1:B:138:ILE:CG2	2.51	0.41
1:B:201[B]:ARG:HD2	5:B:604:HOH:O	2.20	0.41
1:B:213:THR:HG22	1:B:218:TYR:HD1	1.79	0.41
1:B:264:SER:HA	1:B:363:VAL:O	2.21	0.41
1:B:352:LEU:H	1:B:352:LEU:HD12	1.86	0.41
1:B:377:LEU:N	1:B:377:LEU:CD1	2.83	0.41
1:A:162:LYS:HZ1	1:A:172:ASN:HB2	1.84	0.41
1:A:266:PRO:HA	1:A:359:TRP:O	2.20	0.41
1:A:268:PHE:HB2	5:A:629:HOH:O	2.21	0.41
1:B:389:ASP:OD1	2:B:501:FAD:H5'2	2.21	0.41
1:B:95:LYS:CG	1:B:99:GLN:CB	2.99	0.40
1:B:337:LEU:HD23	1:B:337:LEU:HA	1.98	0.40
1:A:161:GLY:CA	1:A:162:LYS:HE2	2.51	0.40
1:A:230:LEU:HD12	1:A:231:GLU:N	2.36	0.40
1:A:279:TRP:O	1:A:284:LEU:HB2	2.21	0.40
1:A:322:VAL:HG23	1:A:329:TYR:CD1	2.56	0.40
1:B:180:ALA:HB2	1:B:184:PHE:CE1	2.56	0.40
1:A:278:TRP:CD1	1:A:349:PRO:HG2	2.57	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	418/417 (100%)	372 (89%)	46 (11%)	0	100	100
1	B	421/417 (101%)	379 (90%)	41 (10%)	1 (0%)	43	62
All	All	839/834 (101%)	751 (90%)	87 (10%)	1 (0%)	48	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	371	ILE

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	302/340 (89%)	297 (98%)	5 (2%)	53	75
1	B	307/340 (90%)	304 (99%)	3 (1%)	68	83
All	All	609/680 (90%)	601 (99%)	8 (1%)	61	79

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	222	LEU
1	B	377	LEU
1	B	378	SER
1	A	52	LEU
1	A	106	MET
1	A	207	ARG
1	A	255	GLU
1	A	321	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	22	HIS
1	B	68	GLN
1	B	74	GLN
1	B	99	GLN
1	B	123	GLN
1	B	332	GLN
1	A	22	HIS
1	A	40	GLN
1	A	131	HIS
1	A	172	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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	E95	B	502	-	16,17,17	1.72	3 (18%)	19,24,24	1.21	2 (10%)
3	E95	A	502	-	16,17,17	1.73	4 (25%)	19,24,24	1.09	1 (5%)
2	FAD	A	501	-	58,58,58	4.15	21 (36%)	85,89,89	3.36	25 (29%)
2	FAD	B	501	4	58,58,58	4.10	20 (34%)	85,89,89	3.34	21 (24%)

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	E95	B	502	-	-	8/8/8/8	0/2/2/2
3	E95	A	502	-	-	5/8/8/8	0/2/2/2
2	FAD	A	501	-	-	3/34/50/50	0/6/6/6
2	FAD	B	501	4	-	3/34/50/50	0/6/6/6

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	FAD	C5A-C4A	13.97	1.64	1.39
2	A	501	FAD	C5A-C4A	13.80	1.63	1.39
2	A	501	FAD	C8A-N7A	-11.96	1.08	1.31
2	B	501	FAD	C8A-N7A	-11.79	1.09	1.31
2	B	501	FAD	C4A-N9A	11.71	1.62	1.37
2	A	501	FAD	C4A-N9A	10.51	1.59	1.37
2	A	501	FAD	C5A-N7A	-10.48	1.19	1.39
2	B	501	FAD	C5A-N7A	-10.01	1.20	1.39
2	A	501	FAD	C8A-N9A	-9.47	1.21	1.37
2	B	501	FAD	C8A-N9A	-9.04	1.22	1.37
2	B	501	FAD	C2A-N3A	-8.42	1.19	1.33
2	A	501	FAD	C2A-N3A	-8.13	1.19	1.33
2	A	501	FAD	C4A-N3A	-7.75	1.19	1.34
2	B	501	FAD	C4A-N3A	-6.65	1.22	1.34
2	A	501	FAD	C5A-C6A	6.65	1.59	1.41
2	B	501	FAD	C5A-C6A	6.49	1.59	1.41
2	A	501	FAD	C2A-N1A	-6.33	1.22	1.33
2	B	501	FAD	C2A-N1A	-5.50	1.24	1.33
2	A	501	FAD	C2-N1	4.84	1.47	1.36
2	B	501	FAD	C2-N1	4.83	1.47	1.36
2	A	501	FAD	C5X-N5	4.62	1.47	1.39
2	B	501	FAD	C5X-N5	3.95	1.46	1.39
3	B	502	E95	C02-N01	-3.81	1.31	1.37
3	A	502	E95	C02-N01	-3.63	1.31	1.37
3	A	502	E95	C04-C05	-3.42	1.37	1.41
3	B	502	E95	C04-C05	-3.33	1.37	1.41
2	B	501	FAD	C6A-N1A	3.10	1.44	1.35
2	A	501	FAD	C6A-N6A	3.07	1.42	1.34
2	A	501	FAD	C6A-N1A	2.99	1.44	1.35
2	A	501	FAD	C1B-N9A	-2.89	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	FAD	C6A-N6A	2.87	1.41	1.34
2	A	501	FAD	O4B-C1B	2.77	1.48	1.42
3	A	502	E95	C05-N01	-2.73	1.33	1.37
3	B	502	E95	C05-N01	-2.64	1.33	1.37
2	B	501	FAD	C2B-C3B	-2.58	1.46	1.53
2	B	501	FAD	C3B-C4B	-2.55	1.46	1.53
2	B	501	FAD	O2-C2	-2.53	1.19	1.24
2	A	501	FAD	O2'-C2'	-2.43	1.38	1.43
2	A	501	FAD	C2B-C1B	-2.42	1.45	1.53
2	B	501	FAD	O4B-C1B	2.42	1.47	1.42
2	B	501	FAD	O2'-C2'	-2.33	1.38	1.43
2	A	501	FAD	C3B-C4B	-2.33	1.47	1.53
3	A	502	E95	C04-C03	-2.28	1.40	1.44
2	B	501	FAD	O4B-C4B	2.27	1.50	1.45
2	A	501	FAD	C2-N3	2.21	1.43	1.39
2	B	501	FAD	C4X-C10	2.18	1.50	1.44
2	A	501	FAD	C2B-C3B	-2.13	1.47	1.53
2	A	501	FAD	C4X-C10	2.08	1.50	1.44

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	FAD	N3A-C4A-N9A	14.13	151.21	127.17
2	B	501	FAD	N3A-C4A-N9A	13.24	149.69	127.17
2	B	501	FAD	C5A-C4A-N9A	-12.49	92.20	105.81
2	B	501	FAD	C5A-N7A-C8A	12.32	122.81	103.45
2	A	501	FAD	C5A-N7A-C8A	12.11	122.48	103.45
2	A	501	FAD	C5A-C4A-N9A	-11.86	92.89	105.81
2	B	501	FAD	C6A-C5A-N7A	9.58	150.56	132.09
2	A	501	FAD	C6A-C5A-N7A	9.34	150.09	132.09
2	A	501	FAD	C4A-C5A-N7A	-8.16	101.25	110.58
2	A	501	FAD	C5A-C4A-N3A	-7.85	115.91	126.72
2	B	501	FAD	C4A-C5A-N7A	-7.64	101.85	110.58
2	A	501	FAD	C2A-N3A-C4A	7.51	130.17	111.83
2	B	501	FAD	C6A-C5A-C4A	-7.05	107.55	117.18
2	B	501	FAD	C2A-N3A-C4A	6.92	128.72	111.83
2	B	501	FAD	C5A-C4A-N3A	-6.31	118.03	126.72
2	A	501	FAD	C6A-C5A-C4A	-6.26	108.63	117.18
2	A	501	FAD	N9A-C8A-N7A	4.51	120.33	113.94
2	B	501	FAD	C4B-O4B-C1B	-4.49	99.56	109.47
2	B	501	FAD	N9A-C8A-N7A	4.09	119.75	113.94
2	B	501	FAD	O4B-C4B-C3B	3.38	111.86	105.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	FAD	C4-N3-C2	-3.36	119.67	125.64
2	A	501	FAD	O2-C2-N1	-3.02	116.78	121.80
2	B	501	FAD	C5'-C4'-C3'	-2.90	106.75	112.22
2	A	501	FAD	C4-N3-C2	-2.89	120.52	125.64
2	B	501	FAD	O4-C4-C4X	-2.88	118.93	126.53
2	A	501	FAD	C4B-O4B-C1B	-2.87	103.14	109.47
3	A	502	E95	C04-C05-C06	-2.80	120.31	123.28
2	B	501	FAD	O2-C2-N1	-2.80	117.14	121.80
3	B	502	E95	C04-C05-C06	-2.78	120.34	123.28
2	A	501	FAD	C4X-C10-N10	2.71	120.36	116.48
2	A	501	FAD	C4A-N9A-C8A	-2.58	103.03	105.74
2	A	501	FAD	O4-C4-C4X	-2.57	119.75	126.53
2	B	501	FAD	C5B-C4B-C3B	-2.56	105.99	115.21
2	A	501	FAD	C4-C4X-N5	2.48	121.63	118.21
2	B	501	FAD	C4X-C10-N10	2.47	120.02	116.48
2	A	501	FAD	C5X-C9A-N10	2.41	120.15	117.97
2	A	501	FAD	C10-C4X-N5	-2.36	120.00	124.81
2	A	501	FAD	O4B-C1B-N9A	-2.34	103.59	108.09
2	A	501	FAD	C5'-C4'-C3'	-2.33	107.83	112.22
2	B	501	FAD	C4A-N9A-C8A	-2.26	103.36	105.74
2	B	501	FAD	O2P-P-O3P	-2.25	101.20	107.27
2	A	501	FAD	O2-C2-N3	2.23	122.86	118.58
2	A	501	FAD	C4X-C4-N3	2.22	118.91	113.25
2	A	501	FAD	C4'-C3'-C2'	-2.15	110.00	113.57
2	A	501	FAD	C1'-C2'-C3'	-2.14	103.85	109.66
2	B	501	FAD	O2P-P-O5'	2.08	116.98	107.57
2	B	501	FAD	C4X-C4-N3	2.05	118.47	113.25
3	B	502	E95	C07-C06-C05	-2.04	118.94	121.42
2	A	501	FAD	O2A-PA-O5B	2.03	116.78	107.57

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	502	E95	C04-C03-C11-CA
3	B	502	E95	C03-C11-CA-N
3	B	502	E95	O-C-CA-N
3	A	502	E95	C03-C11-CA-N
3	B	502	E95	OXT-C-CA-N
3	B	502	E95	C02-C03-C11-CA
3	A	502	E95	OXT-C-CA-N
3	A	502	E95	O-C-CA-N

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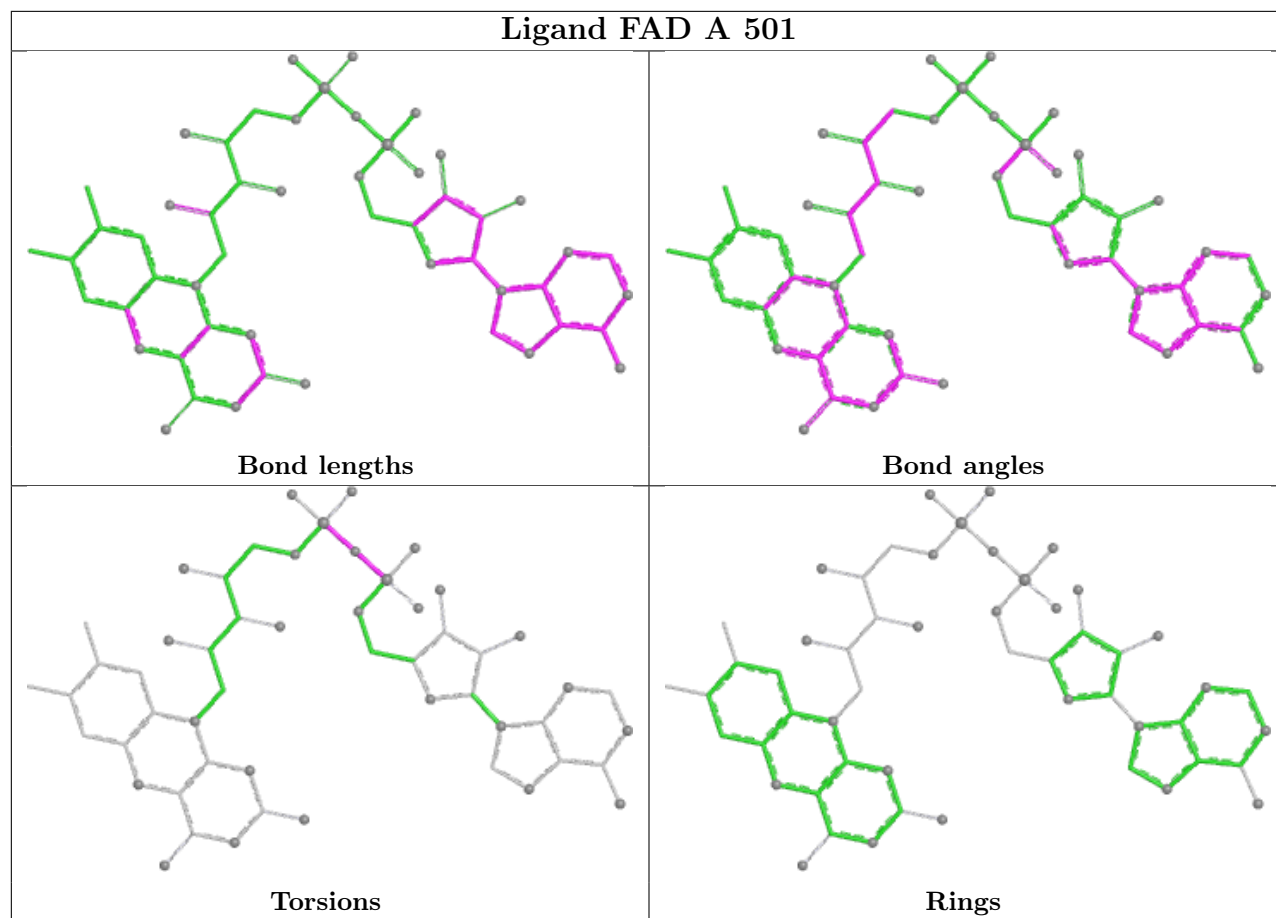
Mol	Chain	Res	Type	Atoms
2	A	501	FAD	PA-O3P-P-O5'
2	A	501	FAD	P-O3P-PA-O1A
3	B	502	E95	O-C-CA-C11
3	B	502	E95	OXT-C-CA-C11
2	B	501	FAD	C5'-O5'-P-O3P
3	B	502	E95	C03-C11-CA-C
3	A	502	E95	C04-C03-C11-CA
2	B	501	FAD	O2'-C2'-C3'-O3'
2	B	501	FAD	O4B-C4B-C5B-O5B
3	A	502	E95	C02-C03-C11-CA
2	A	501	FAD	P-O3P-PA-O2A

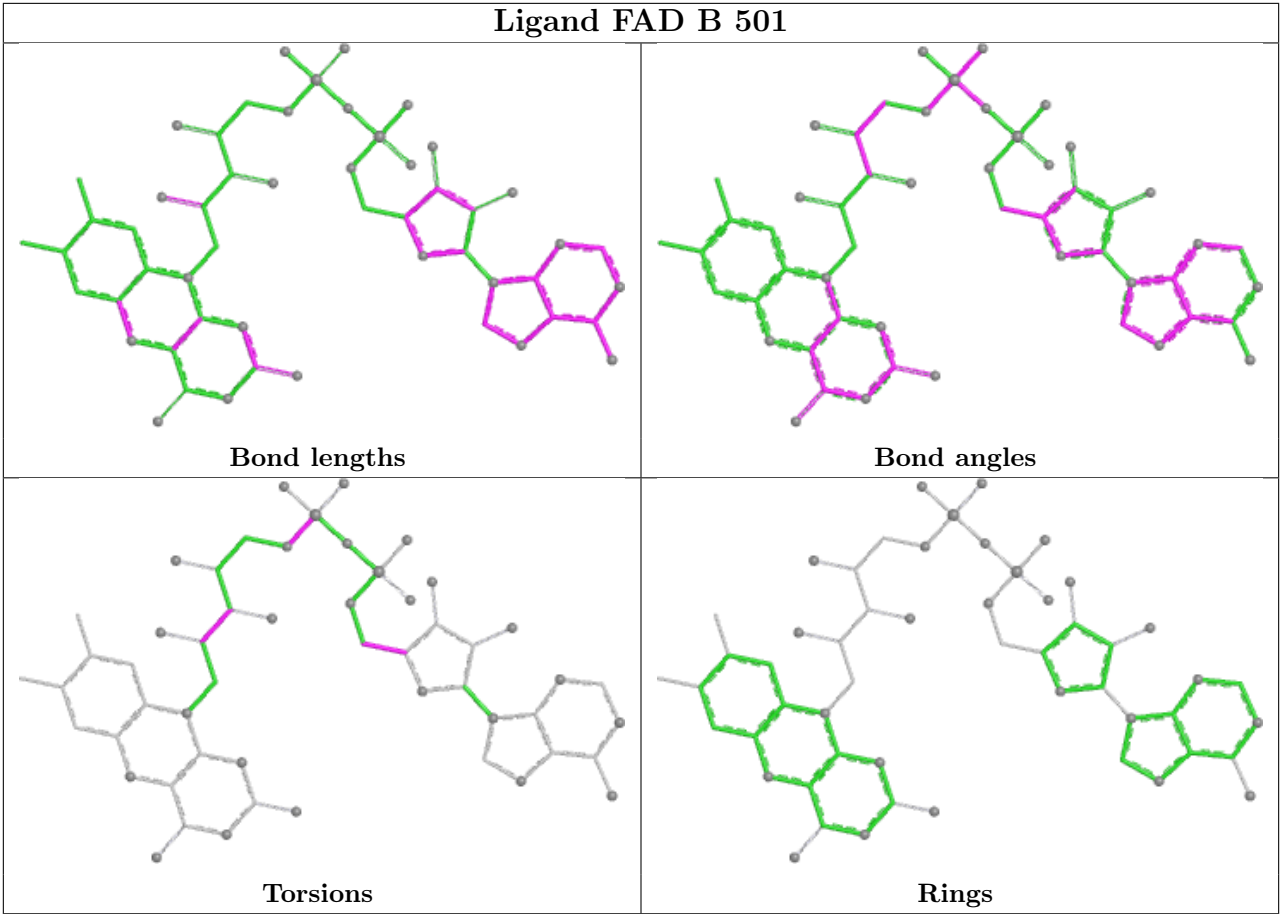
There are no ring outliers.

4 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502	E95	8	0
3	A	502	E95	3	0
2	A	501	FAD	7	0
2	B	501	FAD	6	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	35:ARG	C	36:ILE	N	0.98

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	415/417 (99%)	0.74	30 (7%) 21 16	32, 63, 116, 144	7 (1%)
1	B	417/417 (100%)	1.01	52 (12%) 8 6	36, 72, 145, 167	6 (1%)
All	All	832/834 (99%)	0.88	82 (9%) 13 10	32, 68, 137, 167	13 (1%)

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	122	LEU	5.8
1	B	98	VAL	5.4
1	B	137	MET	5.3
1	B	125	VAL	5.3
1	B	94	PHE	4.8
1	A	117	GLY	4.7
1	B	170	THR	3.9
1	B	52	LEU	3.6
1	B	162	LYS	3.6
1	A	418	ALA	3.6
1	B	128	TYR	3.6
1	B	368	ASP	3.5
1	B	372	ASP	3.5
1	A	108	GLU	3.4
1	A	128	TYR	3.3
1	B	90	THR	3.3
1	A	176	GLN	3.3
1	B	141	MET	3.2
1	A	3	HIS	3.2
1	B	151	ILE	3.2
1	A	370	ASP	3.2
1	B	99	GLN	3.2
1	B	371	ILE	3.2
1	A	106	MET	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	367	ARG	2.9
1	A	25	ASP	2.9
1	B	91	GLN	2.9
1	B	173	ASP	2.9
1	B	375	SER	2.9
1	A	109	LEU	2.9
1	A	115	GLU	2.8
1	A	111	PRO	2.8
1	B	138	ILE	2.8
1	B	135	VAL	2.7
1	B	121	PHE	2.7
1	B	127	ARG	2.7
1	A	107	ASN	2.7
1	B	150	ASP	2.7
1	B	124	PHE	2.7
1	B	132	ASP	2.7
1	B	133	SER	2.7
1	A	118	LYS	2.7
1	A	366	CYS	2.7
1	A	371	ILE	2.6
1	B	157	TYR	2.6
1	B	39	MET	2.6
1	B	107	ASN	2.6
1	B	253	PHE	2.6
1	A	94	PHE	2.5
1	A	97	HIS	2.5
1	A	132	ASP	2.5
1	B	164	PRO	2.4
1	B	262	TYR	2.4
1	B	96	SER	2.4
1	A	105	ALA	2.3
1	B	136	GLY	2.3
1	B	126	SER	2.3
1	B	97	HIS	2.3
1	B	389	ASP	2.3
1	A	95[A]	LYS	2.3
1	B	110	SER	2.3
1	A	119	GLU	2.2
1	A	110	SER	2.2
1	B	117	GLY	2.2
1	B	109	LEU	2.2
1	B	134	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	370	ASP	2.2
1	A	158	ASP	2.2
1	A	53	ASP	2.2
1	A	157	TYR	2.1
1	B	55	LYS	2.1
1	B	53	ASP	2.1
1	A	214	ASP	2.1
1	A	124	PHE	2.1
1	B	81	SER	2.1
1	B	154	GLU	2.1
1	B	48	ARG	2.1
1	B	171	ASP	2.1
1	B	418	ALA	2.1
1	B	51	MET	2.0
1	A	98	VAL	2.0
1	B	103	LYS	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](#)

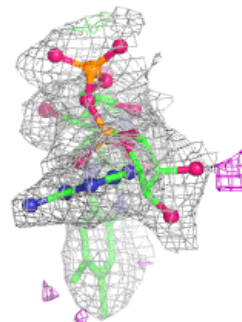
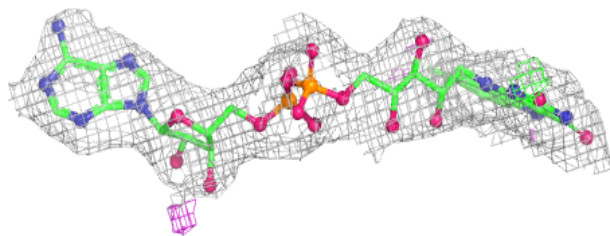
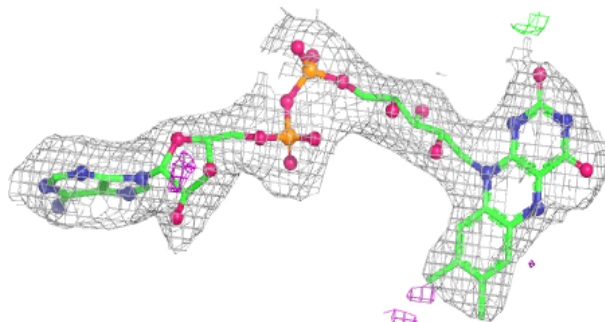
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

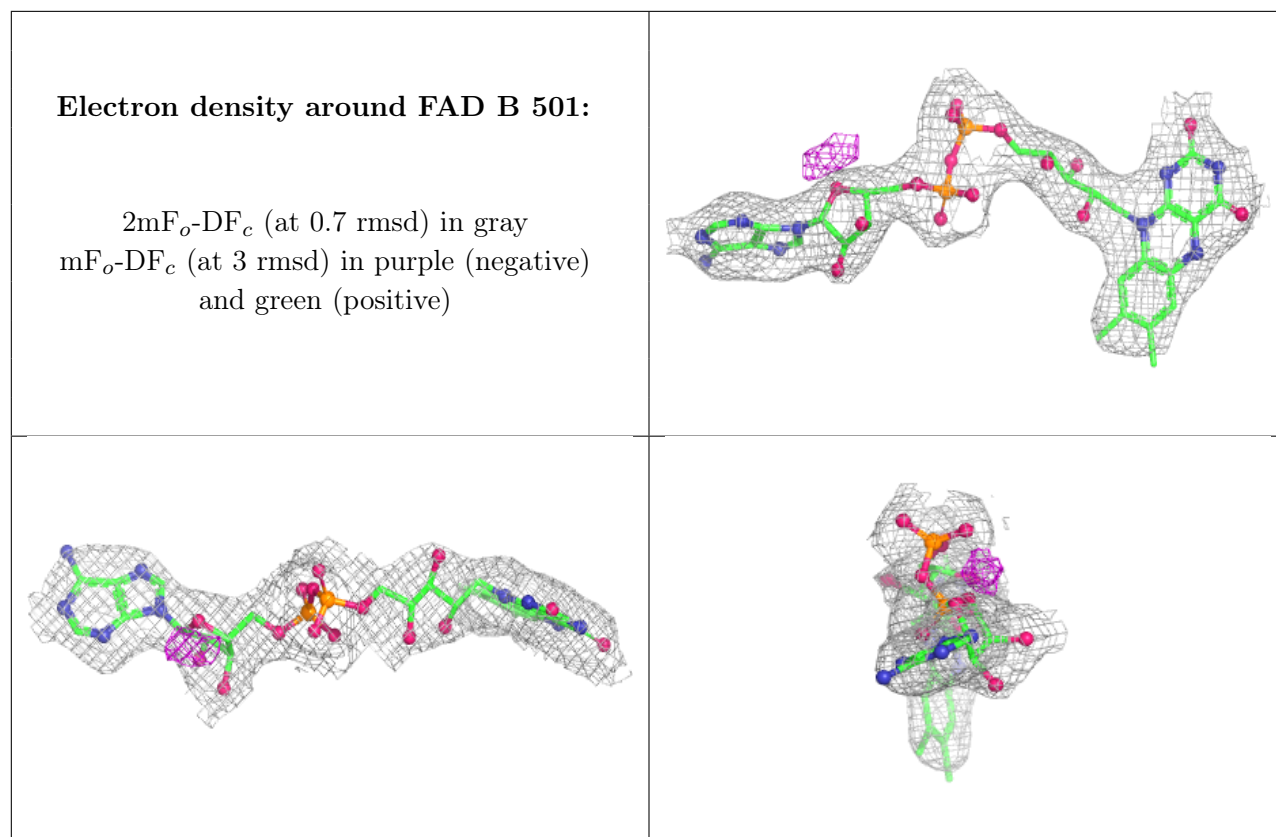
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	E95	B	502	16/16	0.64	0.27	73,85,104,104	0
3	E95	A	502	16/16	0.76	0.17	57,63,68,70	0
4	MG	A	503	1/1	0.85	0.26	59,59,59,59	0
4	MG	B	503	1/1	0.86	0.30	55,55,55,55	0
2	FAD	A	501	53/53	0.94	0.10	35,52,74,82	0
2	FAD	B	501	53/53	0.95	0.10	37,55,63,66	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 A 501:

$2mF_o-DF_c$ (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.