



# Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 08:11 am BST

PDB ID : 3ISH  
Title : Crystal structure of Helicobacter pylori thioredoxin reductase  
Authors : Sanders, D.; Obiero, J.; van Straaten, K.  
Deposited on : 2009-08-25  
Resolution : 2.43 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 : 2.11  
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) : 2.11

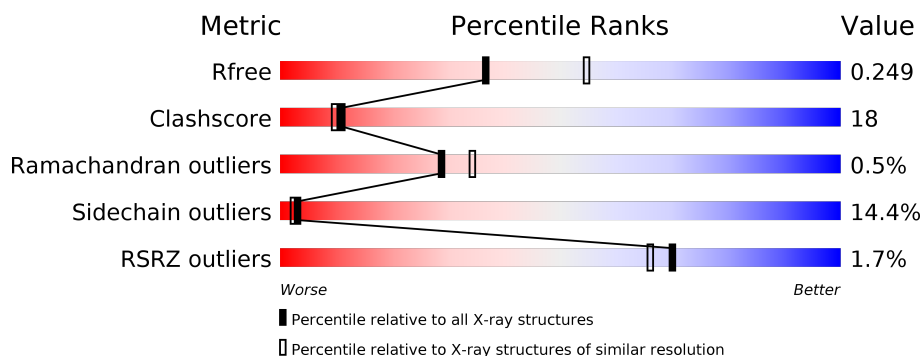
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.43 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	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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 on 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	311	<div> <div>2%</div> <div> <div></div> <div>69%</div> <div>24%</div> <div>6%</div> </div> </div>
1	B	311	<div> <div>2%</div> <div> <div></div> <div>67%</div> <div>26%</div> <div>6%</div> </div> </div>
1	C	311	<div> <div>%</div> <div> <div></div> <div>61%</div> <div>29%</div> <div>9%</div> </div> </div>

2 Entry composition ⓘ

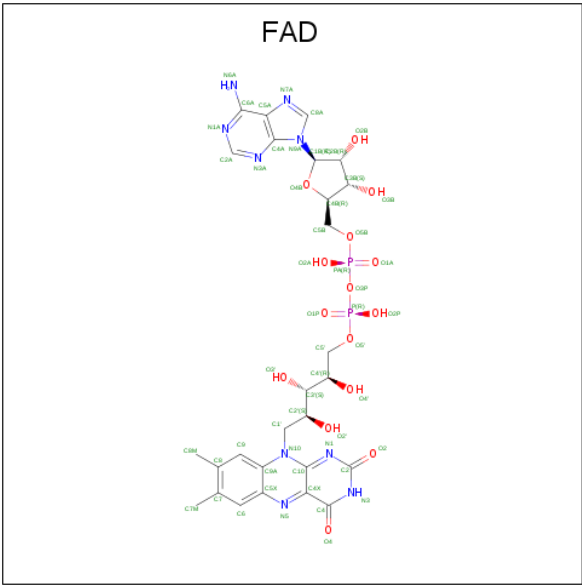
There are 3 unique types of molecules in this entry. The entry contains 7715 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Thioredoxin reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	0	0	0
			2354	1493	396	450	15			
1	B	311	Total	C	N	O	S	0	0	0
			2354	1493	396	450	15			
1	C	311	Total	C	N	O	S	0	0	0
			2353	1492	396	450	15			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



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

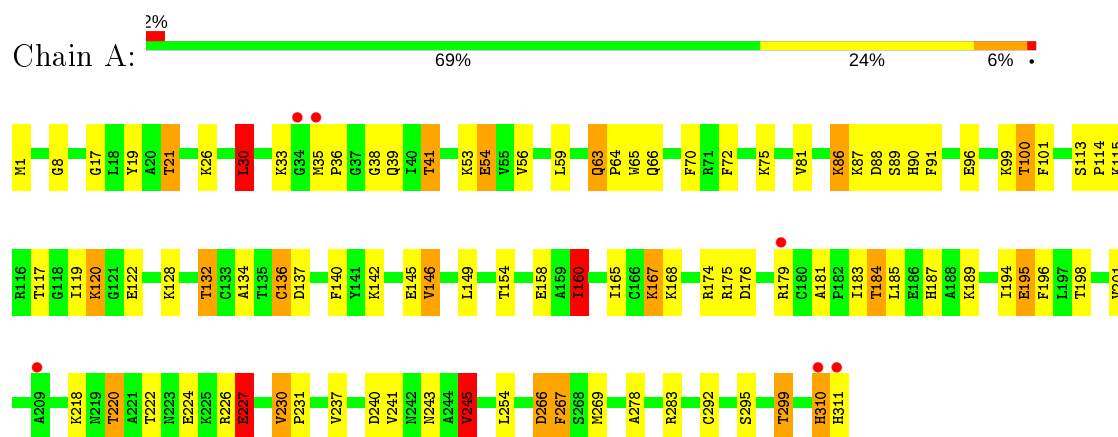
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	185	Total 185	O 185	0	0
3	B	173	Total 173	O 173	0	0
3	C	137	Total 137	O 137	0	0

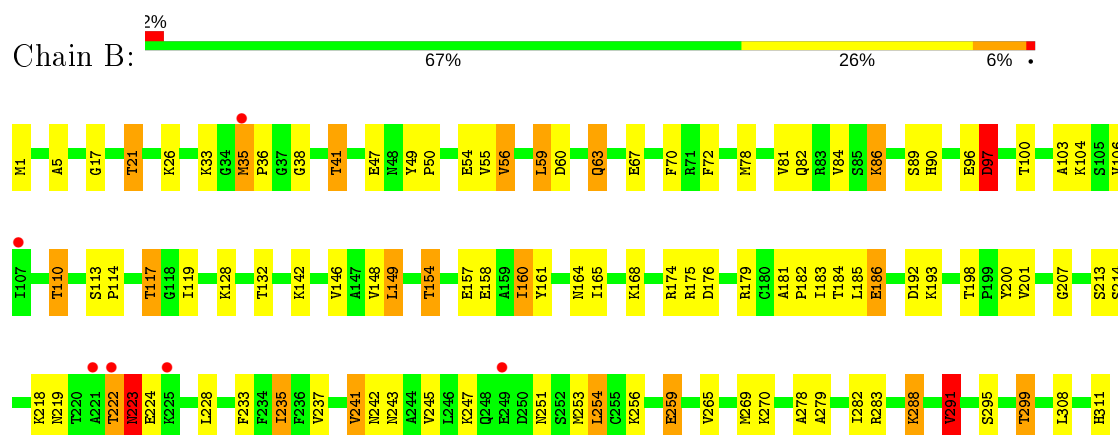
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

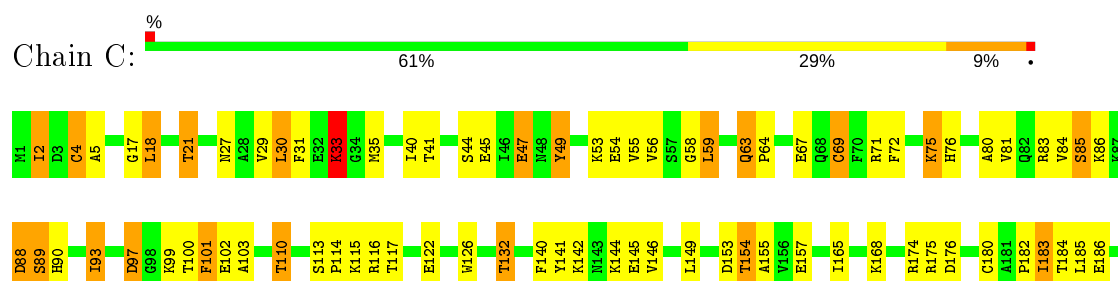
#### • Molecule 1: Thioredoxin reductase

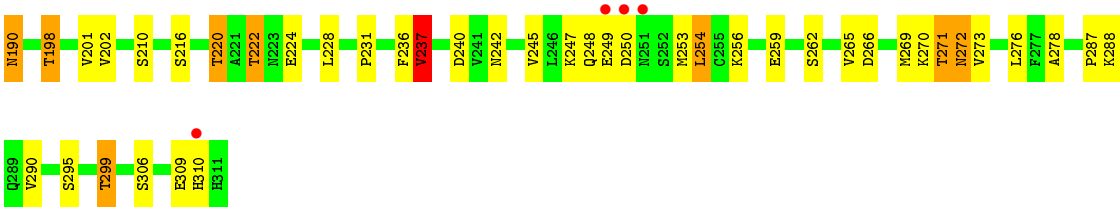


#### • Molecule 1: Thioredoxin reductase



#### • Molecule 1: Thioredoxin reductase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.40 Å 89.40 Å 279.90 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.98 – 2.43 19.98 – 2.43	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.98-2.43) 99.9 (19.98-2.43)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.58 (at 2.44 Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, $R_{free}$	0.178 , 0.252 0.181 , 0.249	Depositor DCC
$R_{free}$ test set	2490 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.7	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 46.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.047 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7715	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality

### 5.1 Standard geometry

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

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	8/2398 (0.3%)	1.13	7/3234 (0.2%)
1	B	1.20	7/2398 (0.3%)	1.14	7/3234 (0.2%)
1	C	1.27	16/2397 (0.7%)	1.11	10/3232 (0.3%)
All	All	1.23	31/7193 (0.4%)	1.13	24/9700 (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	B	0	1

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	88	ASP	CB-CG	7.18	1.66	1.51
1	C	86	LYS	CD-CE	7.17	1.69	1.51
1	C	309	GLU	CD-OE1	6.38	1.32	1.25
1	A	243	ASN	CB-CG	-6.06	1.37	1.51
1	C	86	LYS	CB-CG	5.96	1.68	1.52
1	B	186	GLU	CG-CD	5.93	1.60	1.51
1	A	195	GLU	CG-CD	5.91	1.60	1.51
1	C	86	LYS	CE-NZ	5.89	1.63	1.49
1	C	86	LYS	CG-CD	5.80	1.72	1.52
1	A	65	TRP	CB-CG	5.79	1.60	1.50
1	C	4	CYS	CB-SG	5.78	1.92	1.82
1	C	237	VAL	CB-CG1	-5.74	1.40	1.52
1	C	55	VAL	CB-CG2	5.67	1.64	1.52
1	C	309	GLU	CG-CD	5.65	1.60	1.51
1	A	19	TYR	CE1-CZ	5.60	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	47	GLU	CG-CD	5.50	1.60	1.51
1	C	69	CYS	CB-SG	5.46	1.91	1.82
1	A	136	CYS	CB-SG	5.36	1.91	1.82
1	C	49	TYR	CD2-CE2	5.30	1.47	1.39
1	C	259	GLU	CG-CD	5.28	1.59	1.51
1	B	54	GLU	CD-OE1	5.25	1.31	1.25
1	B	259	GLU	CB-CG	-5.20	1.42	1.52
1	A	245	VAL	CB-CG2	-5.20	1.42	1.52
1	A	146	VAL	CA-CB	5.19	1.65	1.54
1	A	227	GLU	CG-CD	5.17	1.59	1.51
1	B	54	GLU	CG-CD	5.14	1.59	1.51
1	C	67	GLU	CB-CG	5.13	1.61	1.52
1	C	49	TYR	CD1-CE1	5.12	1.47	1.39
1	B	243	ASN	CB-CG	-5.09	1.39	1.51
1	B	70	PHE	CE2-CZ	5.06	1.47	1.37
1	B	148	VAL	CB-CG1	5.04	1.63	1.52

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	ILE	CG1-CB-CG2	-9.37	90.79	111.40
1	A	266	ASP	CB-CG-OD1	7.47	125.02	118.30
1	C	116	ARG	NE-CZ-NH2	-7.34	116.63	120.30
1	C	272	ASN	N-CA-CB	-6.95	98.09	110.60
1	B	157	GLU	CB-CA-C	-6.80	96.80	110.40
1	C	116	ARG	NE-CZ-NH1	6.78	123.69	120.30
1	C	126	TRP	C-N-CA	-6.41	108.84	122.30
1	B	97	ASP	CB-CG-OD2	6.13	123.81	118.30
1	B	86	LYS	CD-CE-NZ	5.85	125.16	111.70
1	B	254	LEU	CB-CG-CD2	5.83	120.92	111.00
1	A	30	LEU	CA-CB-CG	5.72	128.45	115.30
1	C	59	LEU	CA-CB-CG	5.70	128.40	115.30
1	C	237	VAL	CG1-CB-CG2	5.68	119.99	110.90
1	B	291	VAL	CB-CA-C	-5.57	100.81	111.40
1	C	228	LEU	CA-CB-CG	5.47	127.88	115.30
1	B	157	GLU	CA-CB-CG	5.46	125.40	113.40
1	A	243	ASN	CB-CA-C	-5.41	99.58	110.40
1	A	160	ILE	CB-CA-C	5.31	122.22	111.60
1	A	230	VAL	C-N-CD	5.21	139.34	128.40
1	B	254	LEU	CA-CB-CG	5.20	127.26	115.30
1	C	97	ASP	CB-CG-OD1	-5.06	113.74	118.30
1	C	33	LYS	CB-CA-C	-5.03	100.33	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	VAL	CB-CA-C	-5.03	101.84	111.40
1	C	30	LEU	CA-CB-CG	5.02	126.84	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	222	THR	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	2354	0	2338	73	0
1	B	2354	0	2338	87	0
1	C	2353	0	2334	98	0
2	A	53	0	31	2	0
2	B	53	0	31	0	0
2	C	53	0	31	2	0
3	A	185	0	0	32	0
3	B	173	0	0	19	0
3	C	137	0	0	22	0
All	All	7715	0	7103	259	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 18.

All (259) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:GLN:HG2	3:A:474:HOH:O	1.49	1.10
1:B:21:THR:HG23	1:B:72:PHE:HB2	1.38	1.06
1:A:240:ASP:HB2	3:A:406:HOH:O	1.57	1.04
1:C:45:GLU:HB3	3:C:320:HOH:O	1.53	1.04
1:B:245:VAL:HB	3:B:556:HOH:O	1.56	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:ARG:HD2	3:A:467:HOH:O	1.59	1.02
1:A:176:ASP:HA	1:A:198:THR:CG2	1.90	1.02
1:C:45:GLU:HG2	3:C:410:HOH:O	1.62	0.99
1:A:269:MET:HE2	1:A:278:ALA:O	1.66	0.96
1:A:176:ASP:OD1	1:A:198:THR:HG22	1.64	0.96
1:C:271:THR:HG22	1:C:273:VAL:H	1.30	0.94
1:A:176:ASP:HA	1:A:198:THR:HG21	1.48	0.93
1:B:201:VAL:HB	3:B:537:HOH:O	1.69	0.93
1:C:153:ASP:O	1:C:157:GLU:HG2	1.69	0.92
1:B:36:PRO:HB3	3:B:390:HOH:O	1.69	0.92
1:C:2:ILE:HD13	1:C:2:ILE:C	1.92	0.89
1:B:269:MET:HE1	1:B:283:ARG:HG2	1.57	0.87
1:C:299:THR:HG21	3:C:413:HOH:O	1.73	0.86
1:B:128:LYS:CE	3:B:392:HOH:O	2.23	0.85
1:C:21:THR:CG2	1:C:72:PHE:HB2	2.07	0.85
1:C:220:THR:HG21	3:C:340:HOH:O	1.77	0.85
1:A:100:THR:HG22	3:A:463:HOH:O	1.78	0.83
1:C:222:THR:HG22	1:C:224:GLU:H	1.42	0.83
1:B:21:THR:HG21	3:B:312:HOH:O	1.77	0.82
1:C:21:THR:HG22	1:C:72:PHE:HB2	1.62	0.81
1:A:142:LYS:O	1:A:165:ILE:O	1.98	0.81
1:B:176:ASP:HA	1:B:198:THR:HG21	1.64	0.80
1:B:245:VAL:CG2	3:B:556:HOH:O	2.30	0.80
1:B:160:ILE:HG12	1:B:161:TYR:N	1.97	0.79
1:C:198:THR:HG21	3:C:371:HOH:O	1.82	0.78
1:C:21:THR:HG23	1:C:72:PHE:O	1.83	0.78
1:B:299:THR:HG21	3:B:359:HOH:O	1.82	0.78
1:A:267:PHE:HD1	3:A:447:HOH:O	1.68	0.77
1:A:269:MET:CE	1:A:278:ALA:O	2.33	0.77
1:A:184:THR:HG21	3:A:487:HOH:O	1.84	0.76
1:B:182:PRO:O	1:B:186:GLU:HG3	1.83	0.76
1:C:247:LYS:HB2	1:C:253:MET:HE1	1.69	0.74
1:C:101:PHE:CZ	3:C:545:HOH:O	2.41	0.73
1:B:117:THR:HG21	1:B:119:ILE:HD12	1.71	0.73
1:C:40:ILE:HG22	3:C:526:HOH:O	1.87	0.73
1:C:31:PHE:CE2	1:C:93:ILE:HD11	2.23	0.73
1:B:21:THR:CG2	1:B:72:PHE:HB2	2.19	0.72
1:C:2:ILE:O	1:C:2:ILE:HD13	1.89	0.72
1:A:222:THR:HG22	1:A:224:GLU:H	1.54	0.72
1:B:269:MET:CE	1:B:283:ARG:HG2	2.20	0.72
1:B:207:GLY:HA2	1:B:213:SER:OG	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:54:GLU:HB3	3:C:419:HOH:O	1.90	0.71
1:A:113:SER:HB3	3:A:343:HOH:O	1.90	0.71
1:C:154:THR:HG22	3:C:359:HOH:O	1.91	0.71
1:A:114:PRO:HG3	1:A:132:THR:HG21	1.72	0.70
1:B:1:MET:HE3	1:B:90:HIS:HB2	1.73	0.69
1:C:222:THR:HG22	1:C:224:GLU:N	2.07	0.69
1:B:84:VAL:HG23	1:B:245:VAL:HG22	1.74	0.69
1:B:128:LYS:CD	3:B:392:HOH:O	2.41	0.69
1:B:78:MET:HG2	3:B:460:HOH:O	1.91	0.68
1:B:269:MET:HE2	1:B:278:ALA:O	1.93	0.68
1:A:222:THR:HG21	3:A:458:HOH:O	1.94	0.68
1:B:117:THR:HG23	1:B:119:ILE:H	1.59	0.68
1:C:254:LEU:HD13	1:C:276:LEU:HD22	1.76	0.68
1:A:160:ILE:HG22	1:A:194:ILE:CD1	2.24	0.67
1:B:104:LYS:CE	1:B:311:HIS:O	2.43	0.67
1:C:271:THR:HG21	1:C:276:LEU:HD23	1.76	0.67
1:B:104:LYS:NZ	1:B:311:HIS:O	2.29	0.66
1:A:63:GLN:NE2	3:A:339:HOH:O	2.28	0.66
1:B:104:LYS:HE2	1:B:311:HIS:O	1.96	0.66
1:B:1:MET:HE2	1:B:104:LYS:N	2.10	0.66
1:A:175:ARG:O	1:A:198:THR:HG23	1.96	0.66
1:C:21:THR:HG21	3:C:315:HOH:O	1.93	0.66
1:A:17:GLY:O	1:A:21:THR:HB	1.96	0.65
1:C:63:GLN:HG3	1:C:64:PRO:HD3	1.77	0.65
1:A:21:THR:CG2	1:A:72:PHE:HB2	2.27	0.65
1:A:145:GLU:O	1:A:231:PRO:HD2	1.96	0.65
1:A:295:SER:O	1:A:299:THR:HG23	1.96	0.65
1:B:38:GLY:O	1:B:41:THR:HB	1.97	0.64
1:B:218:LYS:HD3	1:B:223:ASN:HB3	1.78	0.63
1:B:245:VAL:CB	3:B:556:HOH:O	2.23	0.63
1:B:219:ASN:O	1:B:223:ASN:HA	1.98	0.63
1:A:86:LYS:HD3	1:A:90:HIS:O	2.00	0.62
1:A:21:THR:HG21	3:A:314:HOH:O	1.98	0.62
1:A:299:THR:HG21	3:A:420:HOH:O	1.99	0.62
1:B:218:LYS:HB3	3:B:537:HOH:O	1.99	0.61
1:A:226:ARG:HG2	1:A:227:GLU:N	2.16	0.61
1:A:176:ASP:OD1	1:A:198:THR:CG2	2.44	0.61
1:A:160:ILE:HG22	1:A:194:ILE:HD11	1.82	0.61
1:C:44:SER:HB3	3:C:551:HOH:O	2.01	0.60
1:B:269:MET:HE2	1:B:279:ALA:HA	1.84	0.60
1:B:128:LYS:HE3	3:B:392:HOH:O	1.97	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:PHE:CD1	1:C:101:PHE:N	2.70	0.59
1:B:149:LEU:HB3	1:B:235:ILE:HG22	1.85	0.59
1:C:183:ILE:HG23	3:C:414:HOH:O	2.00	0.59
1:C:266:ASP:HB2	3:C:387:HOH:O	2.02	0.59
1:B:241:VAL:HG13	1:B:282:ILE:HD12	1.83	0.59
1:A:176:ASP:HA	1:A:198:THR:HG23	1.81	0.59
1:C:2:ILE:HD12	1:C:103:ALA:HB2	1.85	0.59
1:B:259:GLU:HB2	1:C:237:VAL:HG22	1.84	0.58
1:C:182:PRO:HD2	3:C:414:HOH:O	2.03	0.58
1:C:84:VAL:HG23	1:C:245:VAL:HG22	1.84	0.58
1:B:117:THR:CG2	1:B:119:ILE:HD12	2.34	0.58
1:A:292:CYS:HB3	3:A:536:HOH:O	2.03	0.57
1:B:117:THR:CG2	1:B:119:ILE:H	2.17	0.57
1:C:88:ASP:CG	1:C:89:SER:H	2.08	0.57
2:A:348:FAD:C7	3:A:538:HOH:O	2.52	0.57
1:A:21:THR:HG23	1:A:72:PHE:HB2	1.85	0.57
1:C:110:THR:CG2	1:C:242:ASN:O	2.53	0.57
1:B:55:VAL:O	1:B:56:VAL:HG23	2.05	0.56
1:A:310:HIS:HA	3:A:557:HOH:O	2.05	0.56
1:B:295:SER:O	1:B:299:THR:HG22	2.05	0.56
1:B:82:GLN:HB2	1:B:96:GLU:HG3	1.88	0.56
1:B:245:VAL:HG23	3:B:556:HOH:O	2.03	0.55
1:A:54:GLU:HG2	3:A:453:HOH:O	2.07	0.54
1:A:269:MET:HE1	1:A:283:ARG:HG2	1.89	0.54
1:C:142:LYS:O	1:C:165:ILE:O	2.25	0.54
1:C:306:SER:O	1:C:310:HIS:HD2	1.91	0.54
1:A:267:PHE:CD1	3:A:447:HOH:O	2.49	0.54
1:A:220:THR:HG21	3:A:357:HOH:O	2.07	0.54
1:A:38:GLY:O	1:A:41:THR:HB	2.08	0.54
1:B:175:ARG:NH2	1:B:179:ARG:NH1	2.56	0.53
1:B:17:GLY:O	1:B:21:THR:HB	2.08	0.53
1:B:1:MET:CE	1:B:90:HIS:HB2	2.38	0.53
1:B:47:GLU:HB2	1:B:55:VAL:HG22	1.91	0.53
1:B:241:VAL:HG13	1:B:282:ILE:CD1	2.37	0.53
2:C:348:FAD:HM73	3:C:339:HOH:O	2.09	0.52
1:C:71:ARG:HG2	1:C:71:ARG:O	2.09	0.52
1:B:179:ARG:HD3	3:B:462:HOH:O	2.09	0.52
1:C:254:LEU:HD13	1:C:276:LEU:CD2	2.39	0.52
1:C:310:HIS:HA	3:C:329:HOH:O	2.09	0.52
1:B:1:MET:HE2	1:B:104:LYS:CA	2.40	0.52
1:C:117:THR:OG1	1:C:122:GLU:OE2	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:247:LYS:CB	1:C:253:MET:HE1	2.38	0.52
1:C:99:LYS:HD2	3:C:555:HOH:O	2.09	0.52
1:A:311:HIS:HE1	3:A:347:HOH:O	1.92	0.52
1:B:219:ASN:HB3	3:B:535:HOH:O	2.10	0.52
1:C:271:THR:HB	1:C:276:LEU:O	2.09	0.52
1:B:50:PRO:HD2	1:B:291:VAL:HG13	1.92	0.51
1:C:31:PHE:CZ	1:C:93:ILE:HD11	2.45	0.51
1:C:33:LYS:HG2	1:C:80:ALA:CB	2.40	0.51
1:A:119:ILE:O	1:A:120:LYS:C	2.48	0.51
1:C:141:TYR:HA	1:C:144:LYS:HD2	1.93	0.51
1:C:186:GLU:O	1:C:190:ASN:HB2	2.11	0.51
1:B:175:ARG:NH2	1:B:179:ARG:HH12	2.08	0.51
1:B:247:LYS:CE	1:B:251:ASN:OD1	2.59	0.51
3:A:322:HOH:O	1:B:63:GLN:NE2	2.44	0.50
1:C:63:GLN:HG3	1:C:64:PRO:CD	2.40	0.50
1:B:247:LYS:HE3	1:B:251:ASN:OD1	2.12	0.50
1:A:1:MET:HA	3:A:462:HOH:O	2.12	0.50
1:A:117:THR:H	1:A:122:GLU:CD	2.15	0.50
1:C:85:SER:HB3	1:C:248:GLN:OE1	2.11	0.50
1:B:104:LYS:HD3	1:B:308:LEU:HD22	1.94	0.49
1:C:272:ASN:HB3	1:C:273:VAL:HG23	1.94	0.49
1:A:181:ALA:HB3	1:A:184:THR:HG23	1.93	0.49
1:C:2:ILE:CD1	1:C:103:ALA:CB	2.90	0.49
1:C:145:GLU:O	1:C:231:PRO:HD2	2.13	0.49
1:C:17:GLY:O	1:C:21:THR:HB	2.13	0.49
1:C:33:LYS:HG2	1:C:80:ALA:HB2	1.93	0.49
1:C:140:PHE:HZ	3:C:320:HOH:O	1.96	0.48
1:B:142:LYS:O	1:B:165:ILE:O	2.31	0.48
1:A:115:LYS:HE2	1:A:240:ASP:OD2	2.13	0.48
1:C:110:THR:HG23	1:C:242:ASN:O	2.14	0.48
1:B:158:GLU:HA	1:B:158:GLU:OE2	2.12	0.48
1:C:83:ARG:HH22	1:C:249:GLU:HG3	1.77	0.48
1:C:222:THR:CG2	1:C:224:GLU:OE2	2.62	0.48
1:B:200:TYR:HA	1:B:218:LYS:O	2.14	0.48
1:C:83:ARG:NH2	1:C:249:GLU:HG3	2.29	0.47
1:C:222:THR:HG23	1:C:224:GLU:CG	2.44	0.47
1:A:128:LYS:NZ	3:A:440:HOH:O	2.46	0.47
1:A:196:PHE:N	1:A:196:PHE:CD1	2.81	0.47
1:A:136:CYS:SG	2:A:348:FAD:C4X	3.03	0.47
1:A:160:ILE:HD12	1:A:160:ILE:HG21	1.58	0.47
1:C:265:VAL:HA	1:C:270:LYS:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:LYS:HD2	1:A:101:PHE:CZ	2.50	0.47
1:C:222:THR:HG21	1:C:224:GLU:OE2	2.15	0.47
1:A:36:PRO:HD3	3:A:511:HOH:O	2.15	0.46
1:B:175:ARG:HH22	1:B:179:ARG:HH12	1.63	0.46
1:B:295:SER:O	1:B:299:THR:CG2	2.63	0.46
1:A:66:GLN:O	1:A:70:PHE:HB2	2.15	0.46
1:B:288:LYS:HD3	3:B:427:HOH:O	2.14	0.46
1:A:218:LYS:HE2	3:A:550:HOH:O	2.16	0.46
1:A:26:LYS:HD2	3:A:477:HOH:O	2.15	0.46
1:C:271:THR:CG2	1:C:272:ASN:N	2.78	0.46
1:A:310:HIS:HE1	3:A:407:HOH:O	1.98	0.46
1:C:18:LEU:HB2	1:C:69:CYS:HA	1.98	0.45
1:B:56:VAL:HG13	1:B:60:ASP:HB2	1.97	0.45
1:C:176:ASP:HA	1:C:198:THR:CG2	2.46	0.45
1:A:266:ASP:HB2	3:A:442:HOH:O	2.16	0.45
1:A:86:LYS:HE3	1:A:91:PHE:CZ	2.51	0.45
1:B:35:MET:HE1	1:B:59:LEU:HD11	1.98	0.45
3:A:360:HOH:O	1:B:164:ASN:HB3	2.16	0.45
1:B:247:LYS:CA	1:B:253:MET:HE1	2.47	0.45
1:A:137:ASP:HA	1:A:140:PHE:CD1	2.52	0.45
1:C:44:SER:O	1:C:45:GLU:CG	2.65	0.45
1:A:189:LYS:CE	3:A:330:HOH:O	2.64	0.44
1:B:247:LYS:HA	1:B:253:MET:CE	2.48	0.44
1:B:97:ASP:HA	3:B:508:HOH:O	2.17	0.44
1:C:110:THR:HG23	1:C:242:ASN:HB2	1.98	0.44
1:C:27:ASN:HA	1:C:75:LYS:HZ1	1.83	0.44
1:C:142:LYS:HA	1:C:165:ILE:HG22	1.99	0.44
1:A:167:LYS:NZ	3:A:383:HOH:O	2.51	0.44
1:B:5:ALA:HB3	1:B:106:VAL:HG22	1.99	0.44
1:A:230:VAL:HG23	1:A:230:VAL:O	2.17	0.44
1:C:2:ILE:HD12	1:C:103:ALA:CB	2.48	0.44
1:C:110:THR:HG21	1:C:242:ASN:O	2.17	0.44
1:C:113:SER:HA	1:C:114:PRO:HD3	1.80	0.43
1:C:40:ILE:O	1:C:58:GLY:HA3	2.18	0.43
1:A:175:ARG:C	1:A:198:THR:HG23	2.38	0.43
1:B:110:THR:CG2	1:B:242:ASN:O	2.66	0.43
1:B:181:ALA:HA	1:B:182:PRO:HD3	1.78	0.43
1:C:114:PRO:HG2	1:C:132:THR:HG21	2.00	0.43
1:C:222:THR:HG23	1:C:224:GLU:HG3	1.99	0.43
1:A:222:THR:HG22	1:A:224:GLU:N	2.28	0.43
1:C:27:ASN:OD1	1:C:75:LYS:HE3	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:90:HIS:HD2	1:C:102:GLU:HB2	1.82	0.43
1:A:168:LYS:HE2	1:A:195:GLU:OE2	2.19	0.43
1:B:86:LYS:HE3	1:B:89:SER:HA	2.01	0.43
1:A:189:LYS:HE3	3:A:330:HOH:O	2.19	0.43
1:B:49:TYR:HA	1:B:50:PRO:HD3	1.92	0.43
1:A:187:HIS:HD2	3:A:469:HOH:O	2.02	0.42
1:C:155:ALA:HB2	1:C:236:PHE:HB2	2.01	0.42
1:A:63:GLN:N	1:A:64:PRO:HD2	2.35	0.42
1:C:157:GLU:HG3	3:C:344:HOH:O	2.19	0.42
1:C:222:THR:CG2	1:C:224:GLU:CG	2.97	0.42
1:C:29:VAL:HG22	1:C:75:LYS:HD2	2.01	0.42
1:B:128:LYS:NZ	3:B:392:HOH:O	2.50	0.42
1:C:115:LYS:HE2	1:C:240:ASP:OD1	2.20	0.42
1:A:75:LYS:HE3	3:A:478:HOH:O	2.18	0.42
1:B:182:PRO:HD3	3:C:553:HOH:O	2.19	0.42
1:C:222:THR:CG2	1:C:224:GLU:HB2	2.50	0.42
1:B:224:GLU:HB2	3:B:535:HOH:O	2.20	0.42
1:B:247:LYS:HA	1:B:253:MET:HE1	2.01	0.42
1:B:256:LYS:NZ	1:C:202:VAL:O	2.43	0.42
1:A:87:LYS:O	1:A:88:ASP:HB2	2.20	0.42
1:C:47:GLU:HB3	3:C:532:HOH:O	2.19	0.42
1:B:113:SER:HA	1:B:114:PRO:HD3	1.86	0.42
1:B:154:THR:O	1:B:158:GLU:HG2	2.20	0.42
1:C:2:ILE:HD11	1:C:5:ALA:N	2.35	0.42
1:C:176:ASP:HA	1:C:198:THR:HG21	2.02	0.41
1:C:269:MET:HB3	1:C:278:ALA:O	2.20	0.41
1:C:49:TYR:CE1	1:C:290:VAL:HG12	2.54	0.41
1:C:2:ILE:HD11	1:C:4:CYS:C	2.40	0.41
1:B:1:MET:HE3	1:B:103:ALA:C	2.41	0.41
1:A:8:GLY:O	1:A:30:LEU:HD21	2.20	0.41
1:C:81:VAL:HG12	1:C:245:VAL:HG23	2.02	0.41
1:C:2:ILE:C	1:C:2:ILE:CD1	2.70	0.41
1:B:86:LYS:HD2	1:B:90:HIS:O	2.20	0.41
1:C:222:THR:HG21	1:C:224:GLU:HB2	2.02	0.41
1:A:81:VAL:HG12	1:A:245:VAL:CG2	2.50	0.41
1:C:101:PHE:CE2	3:C:545:HOH:O	2.68	0.41
1:B:265:VAL:HA	1:B:270:LYS:O	2.21	0.41
1:A:181:ALA:HB3	1:A:184:THR:CG2	2.51	0.41
2:C:348:FAD:H1'1	2:C:348:FAD:H9	1.88	0.41
1:B:247:LYS:HE2	1:B:251:ASN:OD1	2.20	0.40
1:C:30:LEU:C	1:C:30:LEU:HD13	2.41	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:LEU:HB2	1:B:233:PHE:CE1	2.56	0.40
1:B:81:VAL:HG12	1:B:245:VAL:HG23	2.03	0.40
1:A:134:ALA:HB3	1:A:158:GLU:OE1	2.21	0.40
1:B:214:SER:HA	1:B:228:LEU:O	2.21	0.40
1:C:287:PRO:O	1:C:288:LYS:HB2	2.21	0.40
1:A:33:LYS:O	1:A:33:LYS:HG3	2.21	0.40
1:C:271:THR:HG22	1:C:273:VAL:N	2.13	0.40
1:C:295:SER:O	1:C:299:THR:HG23	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	309/311 (99%)	295 (96%)	13 (4%)	1 (0%)	41	49
1	B	309/311 (99%)	295 (96%)	12 (4%)	2 (1%)	25	29
1	C	309/311 (99%)	295 (96%)	12 (4%)	2 (1%)	25	29
All	All	927/933 (99%)	885 (96%)	37 (4%)	5 (0%)	29	34

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	33	LYS
1	B	223	ASN
1	A	35	MET
1	C	35	MET
1	B	35	MET

### 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	250/250 (100%)	217 (87%)	33 (13%)	4	3
1	B	250/250 (100%)	217 (87%)	33 (13%)	4	3
1	C	250/250 (100%)	208 (83%)	42 (17%)	2	1
All	All	750/750 (100%)	642 (86%)	108 (14%)	3	2

All (108) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	THR
1	A	30	LEU
1	A	41	THR
1	A	53	LYS
1	A	54	GLU
1	A	56	VAL
1	A	59	LEU
1	A	63	GLN
1	A	86	LYS
1	A	89	SER
1	A	96	GLU
1	A	100	THR
1	A	120	LYS
1	A	132	THR
1	A	146	VAL
1	A	149	LEU
1	A	154	THR
1	A	160	ILE
1	A	167	LYS
1	A	174	ARG
1	A	183	ILE
1	A	184	THR
1	A	185	LEU
1	A	201	VAL
1	A	220	THR
1	A	227	GLU

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Mol	Chain	Res	Type
1	A	237	VAL
1	A	241	VAL
1	A	245	VAL
1	A	254	LEU
1	A	267	PHE
1	A	299	THR
1	A	310	HIS
1	B	21	THR
1	B	26	LYS
1	B	33	LYS
1	B	41	THR
1	B	56	VAL
1	B	59	LEU
1	B	63	GLN
1	B	67	GLU
1	B	97	ASP
1	B	100	THR
1	B	110	THR
1	B	117	THR
1	B	132	THR
1	B	146	VAL
1	B	149	LEU
1	B	154	THR
1	B	160	ILE
1	B	168	LYS
1	B	174	ARG
1	B	183	ILE
1	B	184	THR
1	B	185	LEU
1	B	192	ASP
1	B	193	LYS
1	B	222	THR
1	B	223	ASN
1	B	235	ILE
1	B	237	VAL
1	B	241	VAL
1	B	254	LEU
1	B	288	LYS
1	B	291	VAL
1	B	299	THR
1	C	2	ILE
1	C	18	LEU

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Mol	Chain	Res	Type
1	C	21	THR
1	C	41	THR
1	C	53	LYS
1	C	56	VAL
1	C	59	LEU
1	C	63	GLN
1	C	75	LYS
1	C	76	HIS
1	C	85	SER
1	C	89	SER
1	C	93	ILE
1	C	97	ASP
1	C	100	THR
1	C	101	PHE
1	C	110	THR
1	C	132	THR
1	C	146	VAL
1	C	149	LEU
1	C	154	THR
1	C	168	LYS
1	C	174	ARG
1	C	175	ARG
1	C	180	CYS
1	C	183	ILE
1	C	184	THR
1	C	185	LEU
1	C	190	ASN
1	C	198	THR
1	C	201	VAL
1	C	210	SER
1	C	216	SER
1	C	220	THR
1	C	222	THR
1	C	237	VAL
1	C	250	ASP
1	C	254	LEU
1	C	256	LYS
1	C	262	SER
1	C	271	THR
1	C	299	THR

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

Mol	Chain	Res	Type
1	B	63	GLN
1	C	66	GLN
1	C	90	HIS
1	C	251	ASN
1	C	310	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

3 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	A	348	-	51,58,58	1.61	8 (15%)	60,89,89	1.96	10 (16%)
2	FAD	B	348	-	51,58,58	1.54	7 (13%)	60,89,89	2.05	9 (15%)
2	FAD	C	348	-	51,58,58	1.67	9 (17%)	60,89,89	1.72	10 (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
2	FAD	A	348	-	-	2/30/50/50	0/6/6/6
2	FAD	B	348	-	-	1/30/50/50	0/6/6/6
2	FAD	C	348	-	-	2/30/50/50	0/6/6/6

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	348	FAD	C4X-N5	4.76	1.40	1.33
2	C	348	FAD	C4-N3	4.68	1.41	1.33
2	A	348	FAD	C4X-N5	4.53	1.39	1.33
2	C	348	FAD	C4X-N5	4.29	1.39	1.33
2	B	348	FAD	C1'-N10	4.07	1.52	1.48
2	C	348	FAD	C2A-N1A	3.96	1.41	1.33
2	B	348	FAD	C4-N3	3.81	1.39	1.33
2	A	348	FAD	C4X-C10	3.73	1.42	1.38
2	C	348	FAD	C2A-N3A	3.64	1.38	1.32
2	A	348	FAD	C10-N1	3.59	1.37	1.33
2	A	348	FAD	C4-N3	3.57	1.39	1.33
2	A	348	FAD	C2A-N3A	3.56	1.37	1.32
2	A	348	FAD	C6-C5X	-3.46	1.36	1.41
2	C	348	FAD	C10-N1	3.32	1.37	1.33
2	C	348	FAD	C1'-N10	3.31	1.51	1.48
2	B	348	FAD	C2A-N3A	3.04	1.37	1.32
2	B	348	FAD	O4B-C1B	-2.95	1.37	1.41
2	B	348	FAD	C10-N1	2.86	1.36	1.33
2	C	348	FAD	C6-C5X	-2.68	1.37	1.41
2	B	348	FAD	C4X-C10	2.54	1.41	1.38
2	A	348	FAD	C1'-N10	2.54	1.50	1.48
2	A	348	FAD	C4'-C3'	-2.30	1.49	1.53
2	C	348	FAD	C5X-N5	2.30	1.39	1.35
2	C	348	FAD	C2'-C3'	-2.06	1.49	1.53

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	348	FAD	N3A-C2A-N1A	-9.46	113.89	128.68
2	A	348	FAD	C4-N3-C2	8.28	122.14	115.14
2	C	348	FAD	N3A-C2A-N1A	-7.73	116.59	128.68
2	B	348	FAD	C4-N3-C2	6.35	120.51	115.14
2	B	348	FAD	C5X-C9A-N10	5.89	121.99	117.72
2	A	348	FAD	C4X-C4-N3	-5.15	116.39	123.43
2	A	348	FAD	C1'-N10-C10	4.52	122.46	118.41
2	A	348	FAD	N3A-C2A-N1A	-4.07	122.32	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	348	FAD	C1'-N10-C10	4.01	122.00	118.41
2	A	348	FAD	C5X-C9A-N10	3.85	120.50	117.72
2	C	348	FAD	C4-N3-C2	3.83	118.38	115.14
2	B	348	FAD	C9A-N10-C10	-3.75	117.00	121.91
2	C	348	FAD	C1B-N9A-C4A	-3.44	120.60	126.64
2	A	348	FAD	O4B-C1B-C2B	-3.15	102.33	106.93
2	A	348	FAD	C4A-C5A-N7A	-3.00	106.27	109.40
2	A	348	FAD	C5'-C4'-C3'	-2.90	106.60	112.20
2	B	348	FAD	C4X-C4-N3	-2.87	119.50	123.43
2	B	348	FAD	C2A-N1A-C6A	2.76	123.47	118.75
2	C	348	FAD	C1'-N10-C10	2.64	120.78	118.41
2	A	348	FAD	C4-C4X-C10	2.63	121.69	119.95
2	B	348	FAD	C1'-N10-C9A	2.61	120.35	118.29
2	C	348	FAD	C2A-N1A-C6A	2.60	123.21	118.75
2	C	348	FAD	C2B-C3B-C4B	2.46	107.42	102.64
2	C	348	FAD	O3'-C3'-C2'	-2.42	102.96	108.81
2	C	348	FAD	C4X-C4-N3	-2.27	120.33	123.43
2	B	348	FAD	C4-C4X-C10	-2.21	118.48	119.95
2	C	348	FAD	C4X-N5-C5X	2.10	118.87	116.77
2	A	348	FAD	C9A-N10-C10	-2.09	119.17	121.91
2	C	348	FAD	N6A-C6A-N1A	2.02	122.78	118.57

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	348	FAD	PA-O3P-P-O5'
2	C	348	FAD	C3B-C4B-C5B-O5B
2	C	348	FAD	O4B-C4B-C5B-O5B
2	B	348	FAD	O4B-C4B-C5B-O5B
2	A	348	FAD	O4B-C4B-C5B-O5B

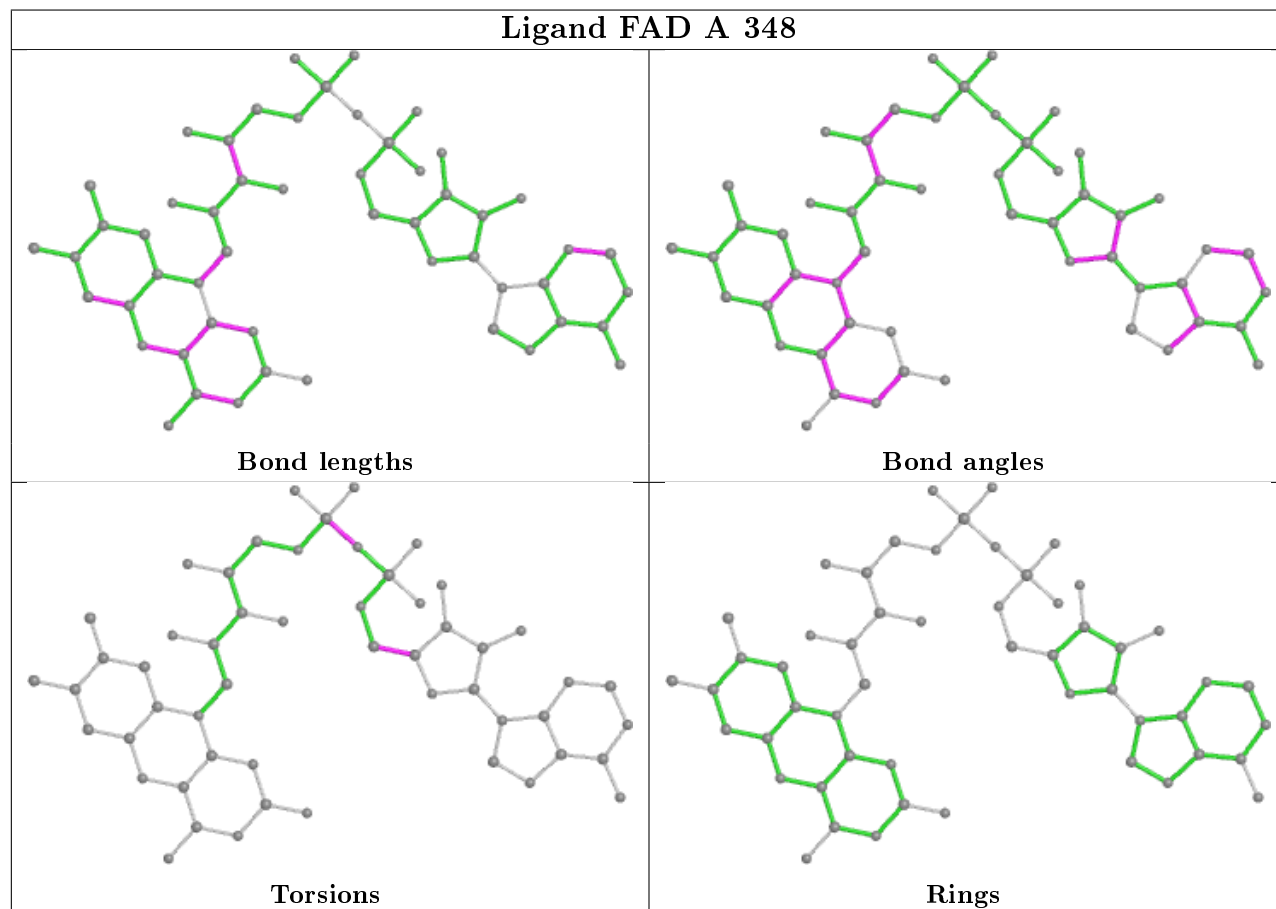
There are no ring outliers.

2 monomers are involved in 4 short contacts:

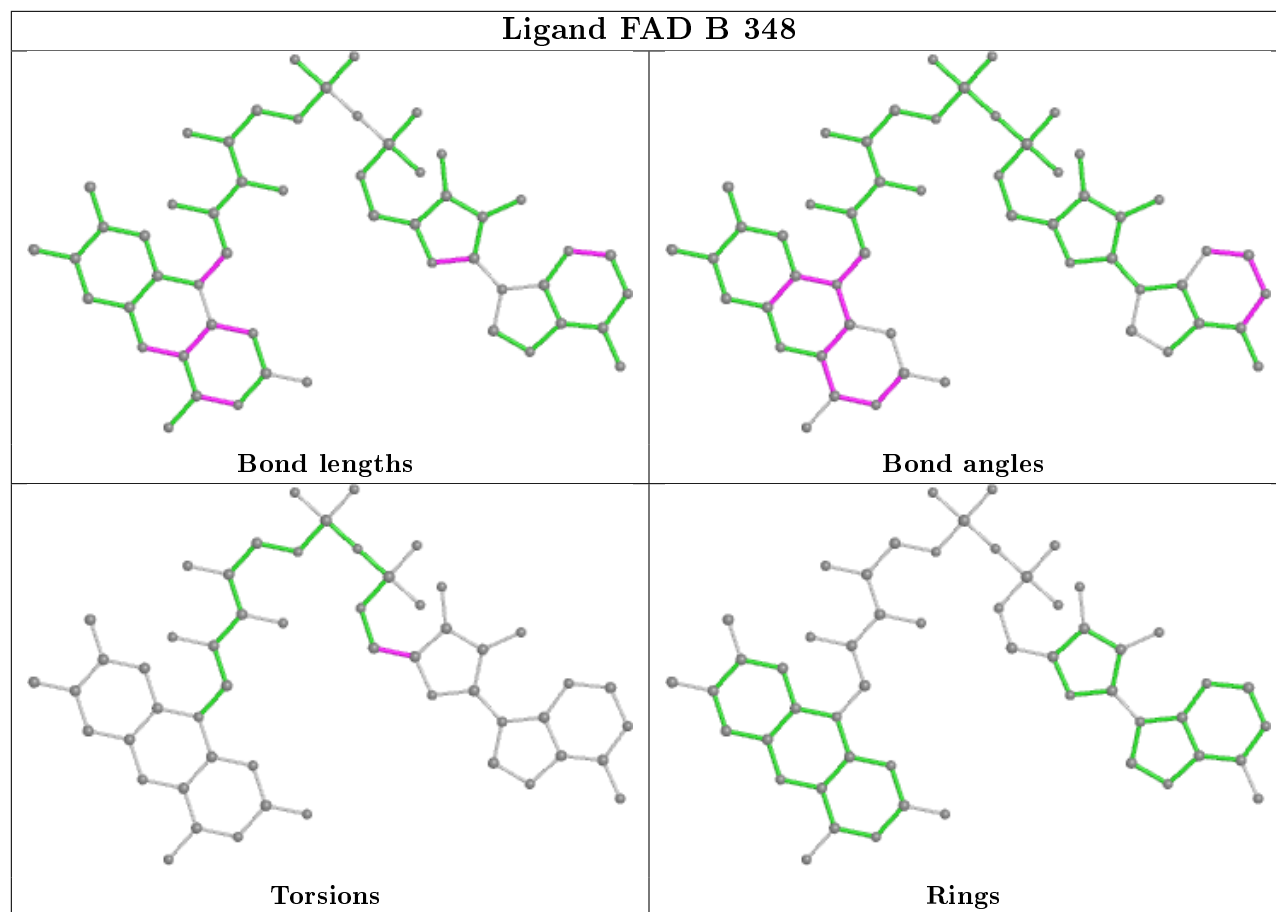
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	348	FAD	2	0
2	C	348	FAD	2	0

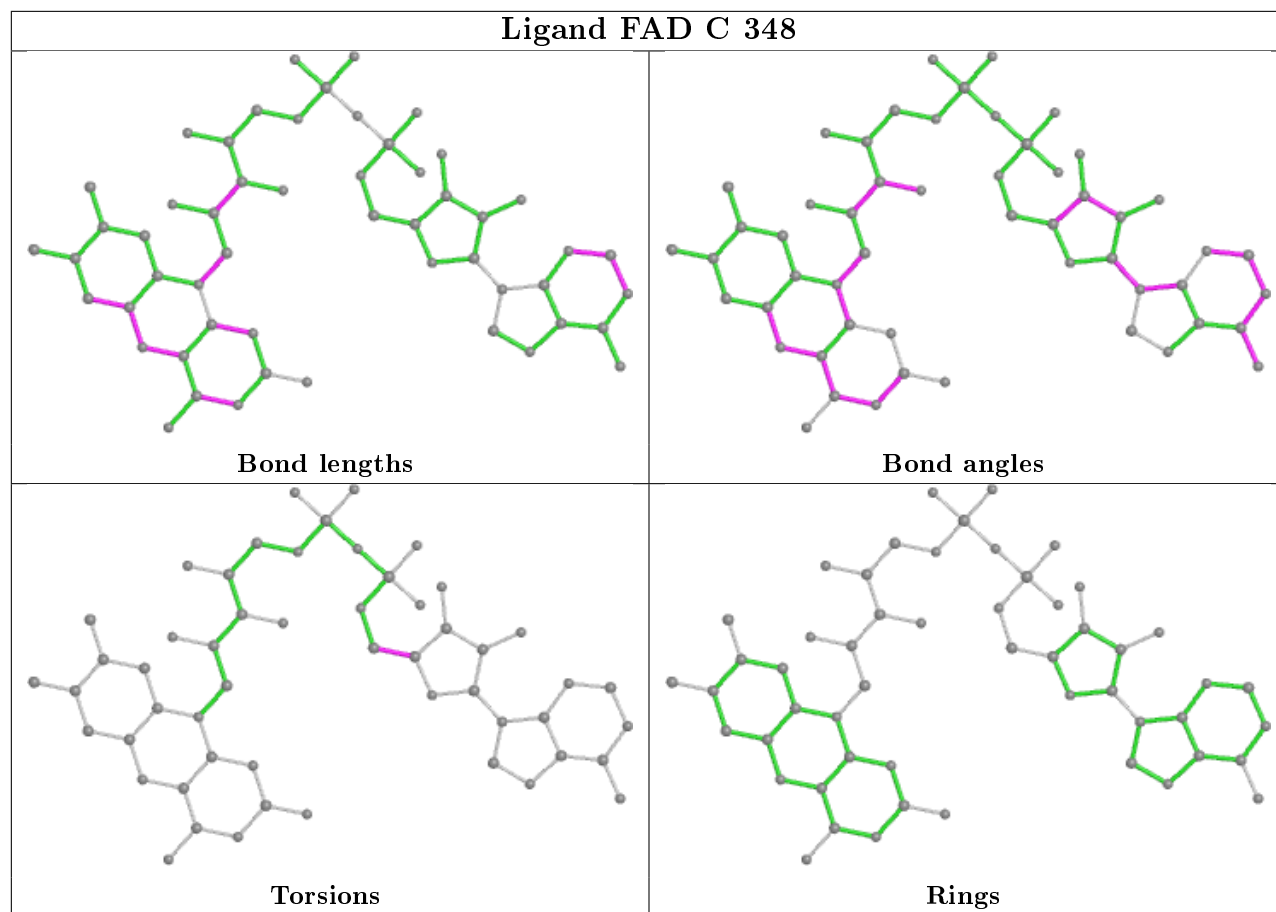
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









## 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	311/311 (100%)	-0.44	6 (1%) 66 63	22, 37, 54, 67	0
1	B	311/311 (100%)	-0.43	6 (1%) 66 63	23, 36, 57, 64	0
1	C	311/311 (100%)	-0.42	4 (1%) 77 75	23, 37, 53, 62	0
All	All	933/933 (100%)	-0.43	16 (1%) 70 66	22, 37, 55, 67	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	209	ALA	5.2
1	C	251	ASN	4.5
1	B	35	MET	4.0
1	A	35	MET	3.9
1	C	310	HIS	3.5
1	C	249	GLU	2.6
1	B	221	ALA	2.6
1	B	107	ILE	2.4
1	A	310	HIS	2.3
1	A	311	HIS	2.3
1	B	222	THR	2.2
1	A	34	GLY	2.2
1	B	249	GLU	2.1
1	B	225	LYS	2.1
1	A	179	ARG	2.0
1	C	250	ASP	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](#)

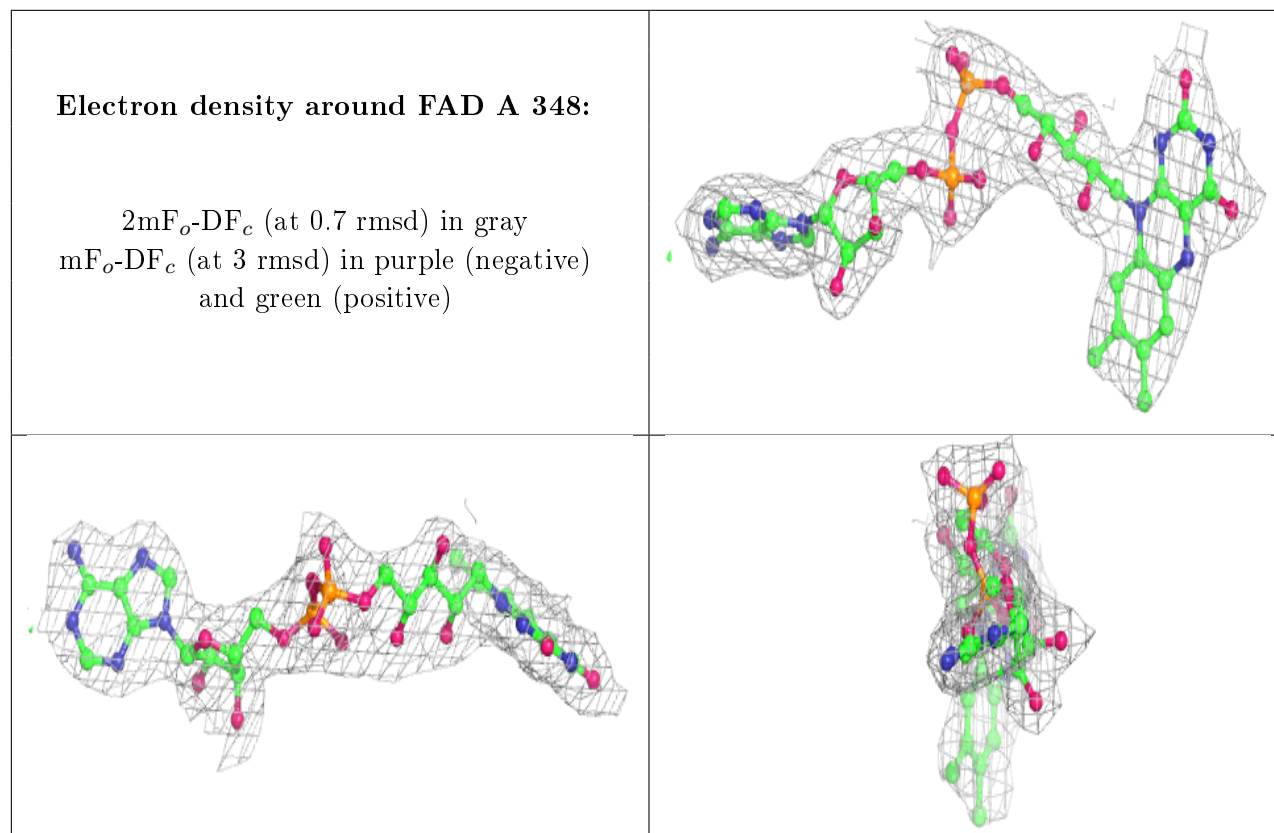
There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

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

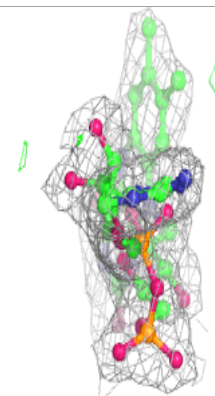
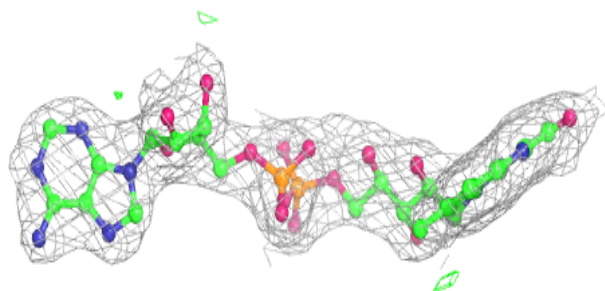
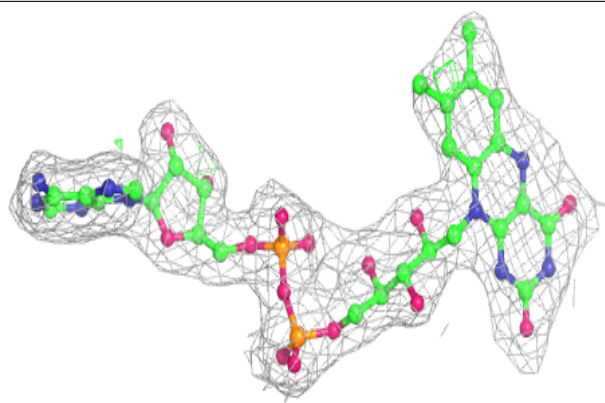
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	FAD	A	348	53/53	0.98	0.08	19,27,31,31	0
2	FAD	B	348	53/53	0.98	0.07	21,26,30,36	0
2	FAD	C	348	53/53	0.98	0.08	21,31,38,39	0

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.

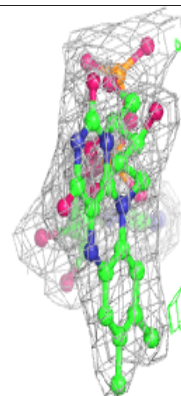
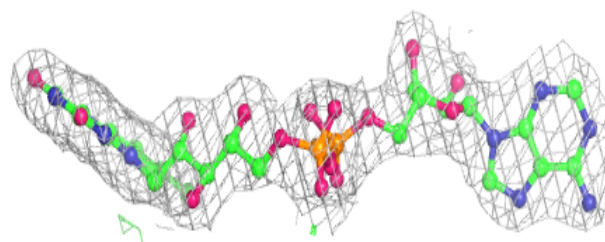
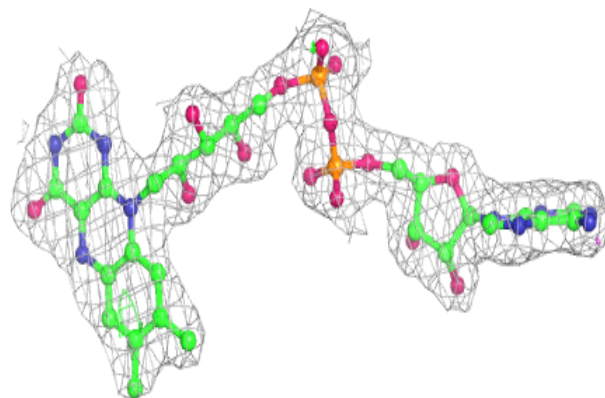


**Electron density around FAD B 348:**

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

**Electron density around FAD C 348:**

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



## 6.5 Other polymers

There are no such residues in this entry.