



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 23, 2019 – 10:59 AM EDT

PDB ID : 6AC1  
Title : Rat Xanthine oxidoreductase, NADH bound form  
Authors : Okamoto, K.; Kawaguchi, Y.  
Deposited on : 2018-07-24  
Resolution : 1.77 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : 2.4  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

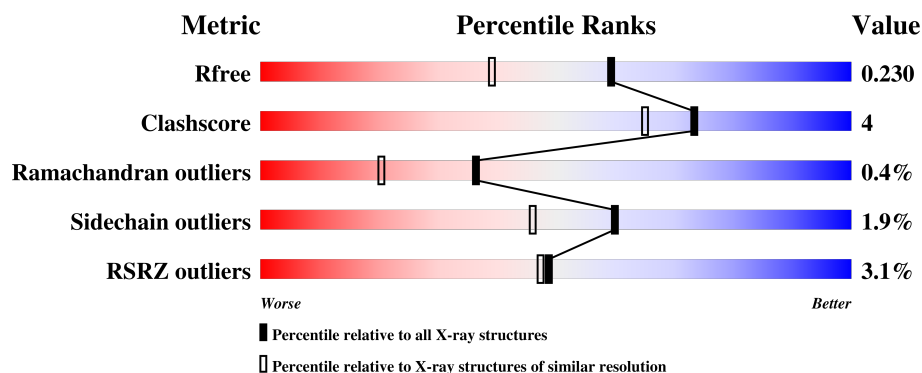
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


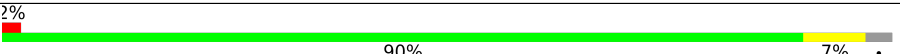
The reported resolution of this entry is 1.77 Å.

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))
$R_{free}$	111664	7886 (1.80-1.76)
Clashscore	122126	8858 (1.80-1.76)
Ramachandran outliers	120053	8764 (1.80-1.76)
Sidechain outliers	120020	8763 (1.80-1.76)
RSRZ outliers	108989	7741 (1.80-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	1331	 4% 90% 7% . .
1	B	1331	 2% 90% 7% .

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
2	URC	B	3003	-	X	-	-
4	FES	B	3001	-	-	X	-

## 2 Entry composition [i](#)

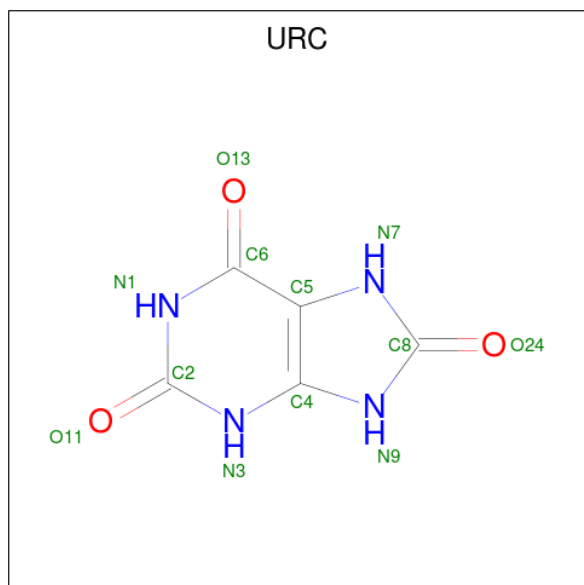
There are 7 unique types of molecules in this entry. The entry contains 21345 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Xanthine dehydrogenase/oxidase.

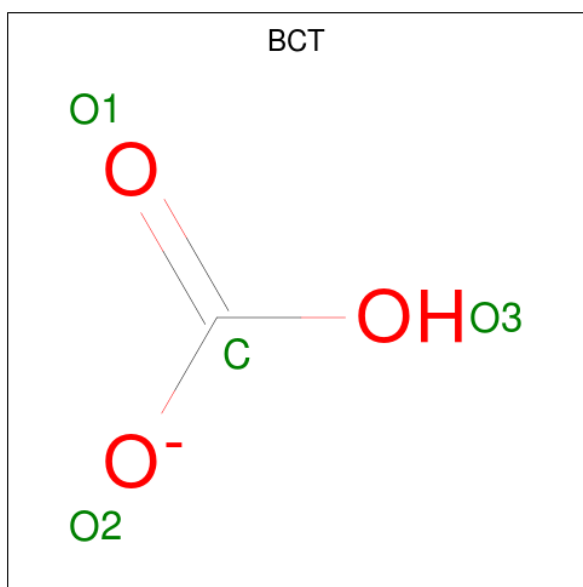
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1297	Total	C	N	O	S	0	0	0
			10033	6359	1727	1882	65			
1	B	1291	Total	C	N	O	S	0	0	0
			9971	6320	1716	1871	64			

- Molecule 2 is URIC ACID (three-letter code: URC) (formula:  $C_5H_4N_4O_3$ ).



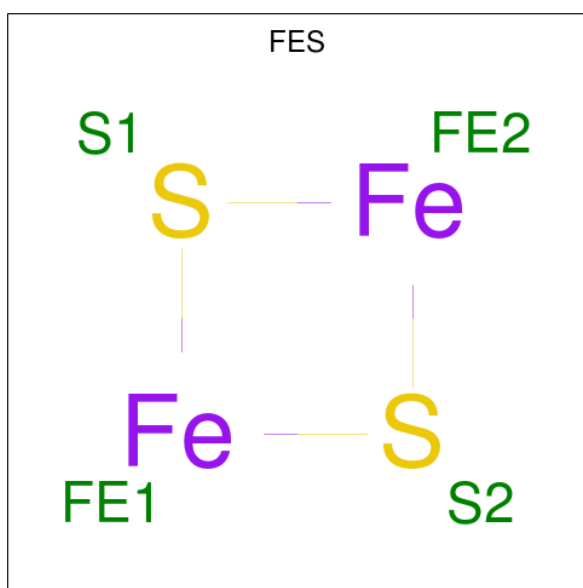
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			12	5	4	3		
2	B	1	Total	C	N	O	0	0
			12	5	4	3		

- Molecule 3 is BICARBONATE ION (three-letter code: BCT) (formula:  $CHO_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	1	3		
3	B	1	Total	C	O	0	0
			4	1	3		

- Molecule 4 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe<sub>2</sub>S<sub>2</sub>).



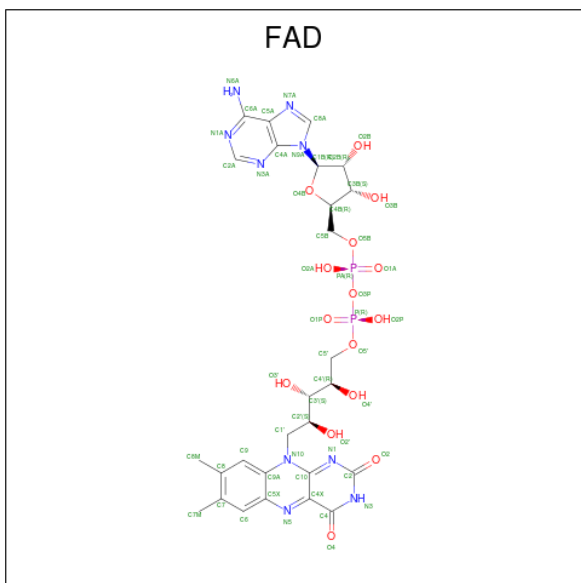
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			4	2	2		
4	A	1	Total	Fe	S	0	0
			4	2	2		

*Continued on next page...*

Continued from previous page...

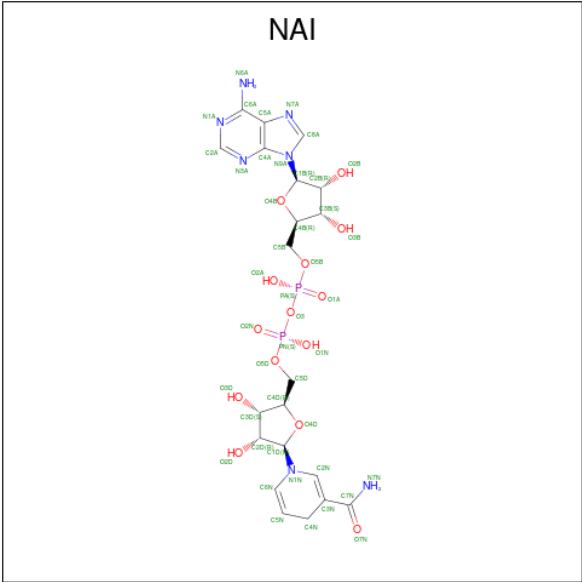
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total 4	Fe 2	S 2	0	0
4	B	1	Total 4	Fe 2	S 2	0	0

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$ ).



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

- Molecule 6 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula:  $C_{21}H_{29}N_7O_{14}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
6	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

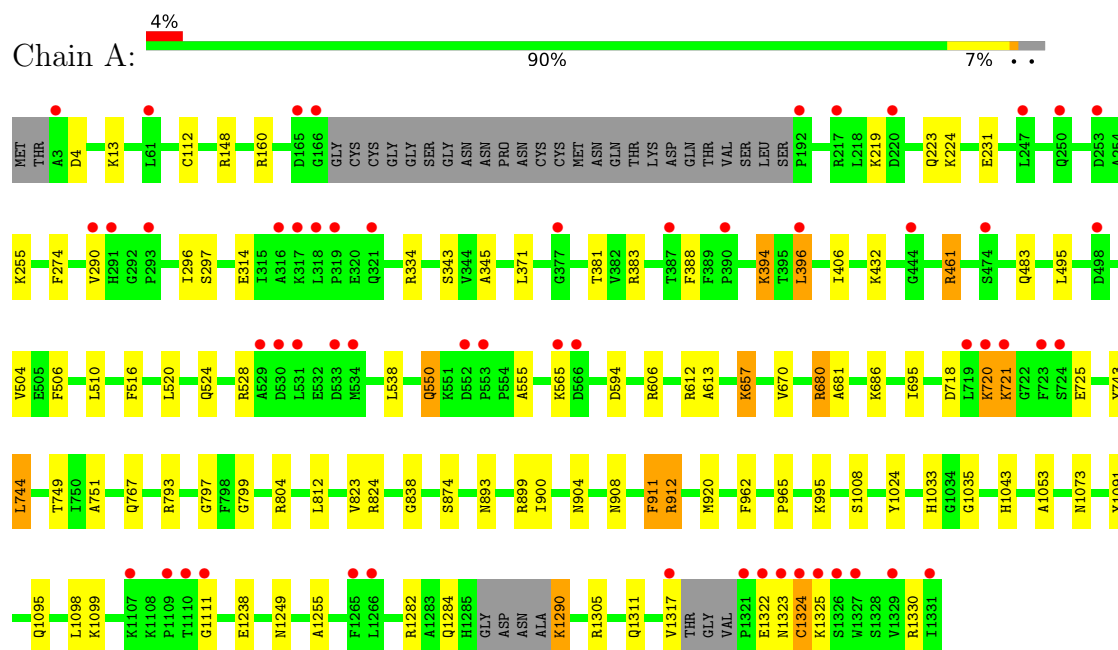
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	486	Total	O	0	0
			486	486		
7	B	613	Total	O	0	0
			613	613		

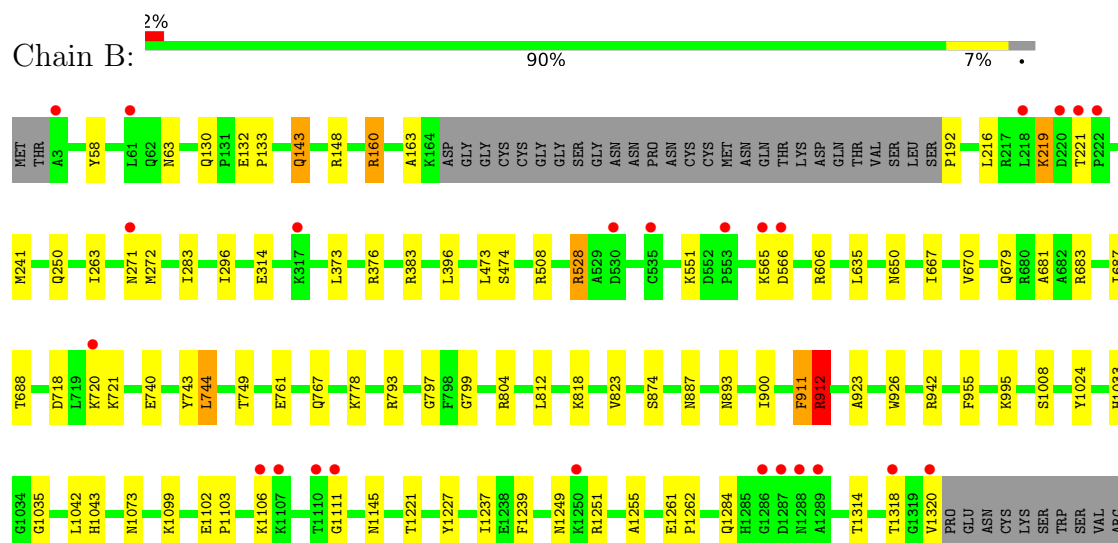
### 3 Residue-property plots

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: Xanthine dehydrogenase/oxidase



#### • Molecule 1: Xanthine dehydrogenase/oxidase





ILE

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.80Å 137.55Å 222.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.19 – 1.77 32.17 – 1.77	Depositor EDS
% Data completeness (in resolution range)	99.3 (32.19-1.77) 99.3 (32.17-1.77)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.44 (at 1.77Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, $R_{free}$	0.188 , 0.222 0.196 , 0.230	Depositor DCC
$R_{free}$ test set	14638 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.2	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 47.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	21345	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% 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: BCT, NAI, FES, FAD, URC

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	0.60	0/10244	0.73	2/13857 (0.0%)
1	B	0.64	2/10181 (0.0%)	0.79	5/13777 (0.0%)
All	All	0.62	2/20425 (0.0%)	0.76	7/27634 (0.0%)

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	10
1	B	0	9
All	All	0	19

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	740	GLU	CD-OE1	5.76	1.31	1.25
1	B	761	GLU	CD-OE1	5.37	1.31	1.25

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	793	ARG	NE-CZ-NH1	19.54	130.07	120.30
1	B	793	ARG	NE-CZ-NH2	-19.28	110.66	120.30
1	A	793	ARG	NE-CZ-NH2	-7.39	116.60	120.30
1	A	606	ARG	NE-CZ-NH1	-5.68	117.46	120.30
1	B	528	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	B	793	ARG	CD-NE-CZ	5.05	130.67	123.60
1	B	160	ARG	NE-CZ-NH1	5.03	122.81	120.30

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1305	ARG	Sidechain
1	A	1330	ARG	Sidechain
1	A	148	ARG	Sidechain
1	A	160	ARG	Sidechain
1	A	334	ARG	Sidechain
1	A	461	ARG	Sidechain
1	A	528	ARG	Sidechain
1	A	612	ARG	Sidechain
1	A	680	ARG	Sidechain
1	A	804	ARG	Sidechain
1	B	1251	ARG	Sidechain
1	B	148	ARG	Sidechain
1	B	160	ARG	Sidechain
1	B	376	ARG	Sidechain
1	B	383	ARG	Sidechain
1	B	528	ARG	Sidechain
1	B	804	ARG	Sidechain
1	B	912	ARG	Sidechain
1	B	942	ARG	Sidechain

## 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	10033	0	10041	74	0
1	B	9971	0	9982	69	0
2	A	12	0	4	0	0
2	B	12	0	4	0	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
4	A	8	0	0	1	0
4	B	8	0	0	2	0
5	A	53	0	31	3	0
5	B	53	0	31	2	0
6	A	44	0	27	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	44	0	27	1	0
7	A	486	0	0	0	0
7	B	613	0	0	4	0
All	All	21345	0	20147	144	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 4.

All (144) 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:812:LEU:HB2	7:B:3633:HOH:O	0.92	1.07
1:B:749:THR:HG22	1:B:812:LEU:HD23	1.39	1.04
1:B:718:ASP:H	1:B:893:ASN:HD22	1.16	0.93
1:B:1318:THR:HG21	1:B:1320:VAL:HG22	1.55	0.86
1:A:720:LYS:HA	1:A:720:LYS:CE	2.04	0.85
1:A:720:LYS:HA	1:A:720:LYS:HE3	1.60	0.84
1:A:695:ILE:H	1:A:904:ASN:HD22	1.28	0.80
1:B:130:GLN:HE21	1:B:132:GLU:H	1.30	0.78
1:A:812:LEU:HD21	1:A:823:VAL:O	1.85	0.77
1:B:143:GLN:NE2	7:B:3101:HOH:O	2.21	0.73
1:B:192:PRO:HD2	7:B:3518:HOH:O	1.89	0.73
1:B:241:MET:HE2	1:B:283:ILE:HG21	1.71	0.72
1:B:271:ASN:OD1	1:B:683:ARG:NH1	2.21	0.71
1:A:995:LYS:NZ	1:A:1284:GLN:HE21	1.87	0.71
1:A:812:LEU:HD11	1:A:824:ARG:CA	2.19	0.71
1:B:1318:THR:CG2	1:B:1320:VAL:HG22	2.21	0.69
1:B:718:ASP:H	1:B:893:ASN:ND2	1.90	0.69
1:A:1323:ASN:HA	1:A:1324:CYS:HB3	1.76	0.67
1:B:1221:THR:HG22	1:B:1227:TYR:HB2	1.78	0.66
1:B:812:LEU:HD11	1:B:823:VAL:C	2.17	0.66
1:A:1033:HIS:HE1	1:A:1043:HIS:HD2	1.43	0.65
1:A:718:ASP:H	1:A:893:ASN:HD22	1.45	0.65
1:A:290:VAL:CG2	1:A:297:SER:HB2	2.28	0.64
1:A:1024:TYR:HA	1:B:1073:ASN:HD21	1.63	0.64
1:A:1323:ASN:HA	1:A:1324:CYS:CB	2.28	0.64
1:A:767:GLN:HE22	1:A:799:GLY:H	1.44	0.64
1:B:749:THR:CG2	1:B:812:LEU:HD23	2.23	0.64
1:B:812:LEU:HD11	1:B:823:VAL:HB	1.80	0.63
1:B:749:THR:O	1:B:812:LEU:HD22	1.97	0.63
1:A:483:GLN:HE22	1:A:1311:GLN:HE22	1.45	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:838:GLY:H	1:A:908:ASN:HD22	1.48	0.62
1:A:995:LYS:HZ1	1:A:1284:GLN:HE21	1.48	0.61
1:A:388:PHE:HA	1:A:396:LEU:HD13	1.83	0.61
1:B:688:THR:HG23	7:B:3303:HOH:O	2.01	0.61
1:A:495:LEU:HB2	1:A:504:VAL:HG13	1.83	0.60
1:A:695:ILE:H	1:A:904:ASN:ND2	1.99	0.60
1:B:606:ARG:HD3	1:B:679:GLN:HA	1.83	0.60
1:A:1033:HIS:CE1	1:A:1043:HIS:HD2	2.21	0.59
1:B:744:LEU:HD13	4:B:3001:FES:S1	2.43	0.58
1:A:1073:ASN:HD21	1:B:1024:TYR:HA	1.67	0.58
1:A:1033:HIS:HD2	1:A:1035:GLY:H	1.49	0.58
1:A:751:ALA:HB3	1:A:812:LEU:HD23	1.85	0.58
1:B:749:THR:O	1:B:812:LEU:CD2	2.52	0.58
1:B:995:LYS:NZ	1:B:1284:GLN:HE21	2.01	0.57
1:A:812:LEU:HD11	1:A:824:ARG:HA	1.85	0.57
1:B:767:GLN:HE22	1:B:799:GLY:H	1.53	0.56
1:A:1053:ALA:O	1:A:1098:LEU:HD11	2.06	0.56
1:B:812:LEU:CD1	1:B:823:VAL:HB	2.36	0.56
1:A:290:VAL:HG23	1:A:297:SER:HB2	1.88	0.56
1:B:812:LEU:HD11	1:B:823:VAL:CB	2.35	0.56
1:A:718:ASP:H	1:A:893:ASN:ND2	2.04	0.55
1:B:1102:GLU:HG2	1:B:1103:PRO:HD3	1.90	0.54
1:A:396:LEU:HD23	1:A:396:LEU:C	2.29	0.54
1:A:720:LYS:HA	1:A:720:LYS:HE2	1.88	0.53
1:A:751:ALA:CB	1:A:812:LEU:HD23	2.39	0.53
1:B:1033:HIS:HD1	1:B:1035:GLY:H	1.55	0.53
1:A:670:VAL:HG11	1:A:681:ALA:HB3	1.91	0.52
5:A:1505:FAD:C4X	6:A:1506:NAI:C5N	2.87	0.52
1:A:371:LEU:HD21	1:A:406:ILE:HD12	1.92	0.52
1:B:812:LEU:HD21	1:B:823:VAL:O	2.09	0.52
1:B:216:LEU:O	1:B:219:LYS:CG	2.58	0.52
1:B:1249:ASN:O	1:B:1255:ALA:HA	2.10	0.51
1:A:231:GLU:OE2	1:A:680:ARG:NH1	2.43	0.51
1:A:1033:HIS:CE1	1:A:1043:HIS:CD2	2.99	0.51
1:B:271:ASN:CG	1:B:683:ARG:HH11	2.13	0.51
1:A:749:THR:HG22	1:A:812:LEU:HD22	1.93	0.51
1:A:516:PHE:CZ	1:A:520:LEU:HD11	2.46	0.51
1:A:874:SER:HB3	1:A:900:ILE:HG21	1.94	0.50
1:A:1033:HIS:CD2	1:A:1035:GLY:H	2.28	0.50
1:A:751:ALA:H	1:A:812:LEU:HD21	1.76	0.50
1:B:1318:THR:HG22	1:B:1320:VAL:HG13	1.95	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:LEU:O	1:B:219:LYS:HG2	2.11	0.49
1:A:1033:HIS:HE1	1:A:1043:HIS:CD2	2.28	0.49
1:B:1033:HIS:NE2	1:B:1043:HIS:HD2	2.11	0.49
1:A:555:ALA:HB3	1:A:1238:GLU:HG2	1.94	0.49
1:B:130:GLN:NE2	1:B:132:GLU:H	2.06	0.48
5:A:1505:FAD:C4X	6:A:1506:NAI:C6N	2.92	0.48
1:B:812:LEU:CD1	1:B:823:VAL:HG12	2.43	0.48
1:A:995:LYS:HZ3	1:A:1284:GLN:HE21	1.60	0.47
1:B:900:ILE:N	1:B:900:ILE:HD12	2.30	0.47
1:A:721:LYS:HE2	1:A:725:GLU:OE2	2.15	0.47
1:B:670:VAL:HG11	1:B:681:ALA:HB3	1.96	0.46
1:B:1314:THR:O	1:B:1318:THR:HB	2.15	0.46
1:A:751:ALA:CB	1:A:812:LEU:CD2	2.94	0.46
5:B:3005:FAD:C4X	6:B:3006:NAI:C5N	2.94	0.46
1:B:263:ILE:HD11	5:B:3005:FAD:H3B	1.98	0.46
1:B:874:SER:HB3	1:B:900:ILE:HG21	1.98	0.46
1:B:955:PHE:HA	1:B:1145:ASN:OD1	2.17	0.45
1:B:635:LEU:HD21	1:B:818:LYS:HD3	1.97	0.45
1:A:920:MET:HE3	1:A:920:MET:HB2	1.87	0.45
1:A:911:PHE:O	1:A:912:ARG:C	2.54	0.45
1:A:812:LEU:HD11	1:A:824:ARG:C	2.37	0.45
1:B:995:LYS:NZ	1:B:1284:GLN:NE2	2.64	0.45
1:A:1091:TYR:O	1:A:1095:GLN:HG2	2.16	0.45
1:A:296:ILE:CD1	1:A:314:GLU:HG3	2.46	0.45
1:B:1318:THR:HG21	1:B:1320:VAL:CG2	2.36	0.45
1:B:812:LEU:HD11	1:B:823:VAL:O	2.16	0.45
1:B:923:ALA:HA	1:B:926:TRP:NE1	2.32	0.45
1:A:900:ILE:N	1:A:900:ILE:HD12	2.33	0.44
1:B:911:PHE:O	1:B:912:ARG:C	2.55	0.44
1:B:650:ASN:OD1	1:B:778:LYS:NZ	2.50	0.44
1:A:255:LYS:HE2	1:A:274:PHE:CE1	2.53	0.43
1:A:962:PHE:CE2	1:A:965:PRO:HD3	2.53	0.43
1:B:272:MET:HA	1:B:272:MET:CE	2.48	0.43
1:A:555:ALA:O	1:A:1238:GLU:HA	2.19	0.43
1:A:720:LYS:CA	1:A:720:LYS:HE3	2.40	0.43
1:B:744:LEU:CD1	4:B:3001:FES:S1	3.06	0.43
1:A:613:ALA:O	1:A:904:ASN:HB3	2.19	0.43
1:A:657:LYS:HA	1:A:657:LYS:HD3	1.78	0.43
1:B:1261:GLU:N	1:B:1262:PRO:CD	2.82	0.43
1:B:58:TYR:OH	1:B:63:ASN:HA	2.19	0.43
1:B:667:ILE:CD1	1:B:687:ILE:HD13	2.49	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1249:ASN:O	1:A:1255:ALA:HA	2.19	0.42
1:B:130:GLN:HE21	1:B:132:GLU:N	2.07	0.42
1:B:216:LEU:O	1:B:219:LYS:HG3	2.20	0.42
1:B:812:LEU:CD1	1:B:823:VAL:CG1	2.97	0.42
1:A:749:THR:O	1:A:812:LEU:HD13	2.19	0.42
1:A:290:VAL:HG22	1:A:297:SER:HB2	2.00	0.42
1:A:550:GLN:HE21	1:A:550:GLN:CA	2.33	0.42
1:B:508:ARG:HH11	1:B:508:ARG:HD3	1.69	0.42
1:A:555:ALA:HB3	1:A:1238:GLU:CG	2.50	0.42
1:B:1035:GLY:HA3	1:B:1042:LEU:HD21	2.02	0.42
1:B:718:ASP:N	1:B:893:ASN:HD22	1.99	0.42
1:B:1033:HIS:NE2	1:B:1043:HIS:CD2	2.88	0.41
1:B:271:ASN:CG	1:B:683:ARG:HD3	2.40	0.41
1:A:1323:ASN:CA	1:A:1324:CYS:CB	2.97	0.41
1:A:751:ALA:HB3	1:A:812:LEU:CD2	2.49	0.41
1:A:1322:GLU:HA	1:A:1323:ASN:HA	1.94	0.41
1:A:550:GLN:HA	1:A:550:GLN:HE21	1.86	0.41
1:A:524:GLN:HG3	1:A:538:LEU:HD22	2.03	0.41
1:B:133:PRO:O	1:B:163:ALA:HA	2.21	0.41
1:B:296:ILE:CD1	1:B:314:GLU:HG3	2.50	0.41
1:A:394:LYS:HE3	1:A:394:LYS:HA	2.03	0.41
1:A:506:PHE:CZ	1:A:510:LEU:HD11	2.56	0.41
1:A:345:ALA:HB1	5:A:1505:FAD:H4'	2.03	0.41
1:A:594:ASP:OD1	1:A:824:ARG:HD3	2.21	0.41
1:A:1282:ARG:NH2	1:A:1290:LYS:HB3	2.36	0.40
1:A:744:LEU:HD13	4:A:1504:FES:S1	2.61	0.40
1:A:388:PHE:CD1	1:A:396:LEU:HD22	2.56	0.40
1:B:1221:THR:CG2	1:B:1227:TYR:HB2	2.48	0.40
1:B:551:LYS:HD2	1:B:1237:ILE:HD11	2.02	0.40
1:A:767:GLN:HE22	1:A:799:GLY:N	2.14	0.40
1:B:566:ASP:N	1:B:566:ASP:OD1	2.50	0.40
1:B:473:LEU:O	1:B:474:SER:HB2	2.21	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	1289/1331 (97%)	1243 (96%)	40 (3%)	6 (0%)	31	15
1	B	1287/1331 (97%)	1253 (97%)	29 (2%)	5 (0%)	36	20
All	All	2576/2662 (97%)	2496 (97%)	69 (3%)	11 (0%)	36	20

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1008	SER
1	A	1324	CYS
1	B	1008	SER
1	B	912	ARG
1	A	4	ASP
1	A	797	GLY
1	A	912	ARG
1	B	797	GLY
1	A	1111	GLY
1	B	887	ASN
1	B	1111	GLY

### 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	1097/1124 (98%)	1071 (98%)	26 (2%)	52	35
1	B	1089/1124 (97%)	1074 (99%)	15 (1%)	69	59
All	All	2186/2248 (97%)	2145 (98%)	41 (2%)	60	46

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	112	CYS
1	A	219	LYS
1	A	223	GLN
1	A	224	LYS
1	A	343	SER
1	A	381	THR
1	A	383	ARG
1	A	394	LYS
1	A	396	LEU
1	A	432	LYS
1	A	461	ARG
1	A	550	GLN
1	A	565	LYS
1	A	657	LYS
1	A	686	LYS
1	A	720	LYS
1	A	721	LYS
1	A	743	TYR
1	A	744	LEU
1	A	899	ARG
1	A	911	PHE
1	A	1099	LYS
1	A	1290	LYS
1	A	1317	VAL
1	A	1325	LYS
1	B	143	GLN
1	B	219	LYS
1	B	221	THR
1	B	250	GLN
1	B	373	LEU
1	B	396	LEU
1	B	565	LYS
1	B	720	LYS
1	B	721	LYS
1	B	743	TYR
1	B	744	LEU
1	B	911	PHE
1	B	1099	LYS
1	B	1106	LYS
1	B	1239	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	ASN
1	A	145	ASN
1	A	271	ASN
1	A	350	ASN
1	A	550	GLN
1	A	767	GLN
1	A	893	ASN
1	A	904	ASN
1	A	908	ASN
1	A	956	ASN
1	A	1016	GLN
1	A	1033	HIS
1	A	1043	HIS
1	A	1073	ASN
1	A	1194	GLN
1	A	1284	GLN
1	A	1285	HIS
1	A	1311	GLN
1	B	62	GLN
1	B	130	GLN
1	B	143	GLN
1	B	145	ASN
1	B	350	ASN
1	B	585	GLN
1	B	767	GLN
1	B	893	ASN
1	B	956	ASN
1	B	1016	GLN
1	B	1043	HIS
1	B	1073	ASN
1	B	1194	GLN
1	B	1284	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates 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
2	URC	A	1501	-	13,13,13	4.16	5 (38%)	13,19,19	4.21	7 (53%)
3	BCT	A	1502	-	0,3,3	0.00	-	0,3,3	0.00	-
4	FES	A	1503	1	0,4,4	0.00	-	-	-	-
4	FES	A	1504	1	0,4,4	0.00	-	-	-	-
5	FAD	A	1505	-	50,58,58	1.81	8 (16%)	58,89,89	2.43	17 (29%)
6	NAI	A	1506	-	41,48,48	1.21	5 (12%)	45,73,73	1.29	5 (11%)
4	FES	B	3001	1	0,4,4	0.00	-	-	-	-
4	FES	B	3002	1	0,4,4	0.00	-	-	-	-
2	URC	B	3003	-	13,13,13	4.22	6 (46%)	13,19,19	5.32	8 (61%)
3	BCT	B	3004	-	0,3,3	0.00	-	0,3,3	0.00	-
5	FAD	B	3005	-	50,58,58	1.85	9 (18%)	58,89,89	2.33	11 (18%)
6	NAI	B	3006	-	41,48,48	1.07	2 (4%)	45,73,73	1.12	3 (6%)

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	URC	A	1501	-	-	-	0/2/2/2
4	FES	A	1503	1	-	-	0/1/1/1
4	FES	A	1504	1	-	-	0/1/1/1
5	FAD	A	1505	-	-	7/30/50/50	0/6/6/6
6	NAI	A	1506	-	-	4/25/72/72	0/5/5/5
4	FES	B	3001	1	-	-	0/1/1/1

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FES	B	3002	1	-	-	0/1/1/1
2	URC	B	3003	-	-	-	0/2/2/2
5	FAD	B	3005	-	-	3/30/50/50	0/6/6/6
6	NAI	B	3006	-	-	4/25/72/72	0/5/5/5

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3003	URC	C4-N3	-10.41	1.34	1.46
2	A	1501	URC	C4-N3	-9.88	1.35	1.46
5	A	1505	FAD	C4X-C10	9.37	1.48	1.38
5	B	3005	FAD	C4X-C10	8.09	1.47	1.38
2	A	1501	URC	C4-N9	-7.97	1.35	1.44
2	B	3003	URC	C4-N9	-7.78	1.35	1.44
2	A	1501	URC	C5-N7	-5.22	1.35	1.45
2	B	3003	URC	C5-N7	-4.80	1.36	1.45
5	B	3005	FAD	C9A-C5X	4.08	1.50	1.42
2	A	1501	URC	O13-C6	4.07	1.31	1.23
5	B	3005	FAD	C4-C4X	3.96	1.48	1.41
2	B	3003	URC	O13-C6	3.88	1.31	1.23
6	A	1506	NAI	C6N-C5N	3.81	1.40	1.33
2	A	1501	URC	O24-C8	3.50	1.30	1.23
5	B	3005	FAD	C6-C5X	-3.18	1.36	1.41
2	B	3003	URC	O24-C8	3.08	1.29	1.23
6	B	3006	NAI	C6N-C5N	3.01	1.38	1.33
6	B	3006	NAI	C5A-C4A	2.96	1.47	1.40
5	A	1505	FAD	C4-C4X	2.87	1.46	1.41
6	A	1506	NAI	C5A-C4A	2.84	1.46	1.40
5	B	3005	FAD	C8-C7	2.83	1.48	1.40
5	B	3005	FAD	C9A-N10	2.75	1.42	1.38
6	A	1506	NAI	O4B-C1B	2.73	1.45	1.41
5	B	3005	FAD	C10-N1	2.71	1.36	1.33
2	B	3003	URC	O11-C2	2.57	1.28	1.23
5	A	1505	FAD	O4B-C1B	2.57	1.44	1.41
5	A	1505	FAD	C5A-C4A	2.53	1.46	1.40
6	A	1506	NAI	C7N-C3N	2.51	1.54	1.48
5	A	1505	FAD	C9A-N10	2.49	1.41	1.38
6	A	1506	NAI	C2A-N3A	2.24	1.35	1.32
5	A	1505	FAD	C8-C7	2.24	1.46	1.40
5	A	1505	FAD	C6-C5X	-2.11	1.38	1.41
5	A	1505	FAD	C9A-C5X	2.11	1.46	1.42
5	B	3005	FAD	O3'-C3'	2.10	1.47	1.43

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	3005	FAD	C6-C7	2.01	1.42	1.37

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3003	URC	C5-C4-N9	11.65	108.03	102.64
5	A	1505	FAD	C4-N3-C2	11.34	124.71	115.14
5	B	3005	FAD	C4-N3-C2	11.31	124.69	115.14
2	B	3003	URC	C4-N9-C8	-10.79	105.56	112.89
2	A	1501	URC	C4-N9-C8	-8.44	107.16	112.89
5	A	1505	FAD	C4-C4X-C10	-8.09	113.97	119.95
2	A	1501	URC	C5-C4-N9	7.44	106.08	102.64
2	B	3003	URC	N7-C8-N9	7.02	114.31	108.82
2	A	1501	URC	N7-C8-N9	5.86	113.40	108.82
5	B	3005	FAD	C4X-C4-N3	-5.25	116.16	123.47
2	A	1501	URC	C4-C5-N7	5.16	106.44	101.30
2	B	3003	URC	N1-C2-N3	4.85	121.34	116.13
2	A	1501	URC	N1-C2-N3	4.80	121.29	116.13
5	B	3005	FAD	C4-C4X-C10	-4.74	116.45	119.95
5	B	3005	FAD	C4X-N5-C5X	4.69	121.59	116.77
2	B	3003	URC	C4-C5-N7	4.44	105.72	101.30
5	B	3005	FAD	N3A-C2A-N1A	-4.10	122.07	128.68
6	A	1506	NAI	N3A-C2A-N1A	-3.88	122.43	128.68
5	A	1505	FAD	C4-C4X-N5	3.83	122.81	118.59
6	B	3006	NAI	N3A-C2A-N1A	-3.80	122.56	128.68
5	B	3005	FAD	C1'-N10-C9A	3.77	121.59	118.31
5	A	1505	FAD	C4X-C4-N3	-3.73	118.28	123.47
5	A	1505	FAD	N6A-C6A-N1A	2.98	124.75	118.57
5	A	1505	FAD	C2A-N1A-C6A	2.84	123.69	118.77
5	A	1505	FAD	C5'-C4'-C3'	2.72	117.56	112.17
5	A	1505	FAD	C5X-C9A-N10	2.66	119.75	117.71
5	B	3005	FAD	C1B-N9A-C4A	-2.66	122.04	126.64
5	A	1505	FAD	C4X-C10-N10	-2.65	117.58	120.30
2	A	1501	URC	C6-N1-C2	-2.55	122.84	126.25
5	A	1505	FAD	C10-C4X-N5	2.53	123.11	121.25
2	B	3003	URC	O11-C2-N3	-2.51	117.82	122.94
5	B	3005	FAD	C5X-C9A-N10	2.47	119.60	117.71
5	A	1505	FAD	O2'-C2'-C1'	2.46	115.51	109.53
5	B	3005	FAD	C9A-N10-C10	-2.46	118.56	121.77
2	B	3003	URC	O24-C8-N7	-2.44	122.62	125.93
2	B	3003	URC	O24-C8-N9	-2.42	122.65	125.93
5	A	1505	FAD	C1'-N10-C9A	2.36	120.37	118.31

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1506	NAI	C5A-C6A-N6A	-2.36	116.68	120.38
5	A	1505	FAD	C5A-C6A-N1A	-2.34	114.82	120.31
5	B	3005	FAD	C4-C4X-N5	2.33	121.16	118.59
5	A	1505	FAD	C1B-N9A-C4A	-2.30	122.67	126.64
5	A	1505	FAD	C4X-N5-C5X	2.28	119.11	116.77
5	B	3005	FAD	C9A-C5X-N5	-2.22	119.26	122.34
6	A	1506	NAI	N6A-C6A-N1A	2.21	123.15	118.57
6	A	1506	NAI	O4D-C4D-C3D	-2.17	100.86	105.14
2	A	1501	URC	O24-C8-N9	-2.15	123.02	125.93
6	B	3006	NAI	C4B-O4B-C1B	2.12	112.04	109.83
6	A	1506	NAI	C3N-C7N-N7N	2.12	121.43	117.67
5	A	1505	FAD	O4'-C4'-C3'	-2.11	103.97	109.11
6	B	3006	NAI	C4A-C5A-N7A	-2.08	107.23	109.40
5	A	1505	FAD	C2B-C3B-C4B	2.08	106.58	102.60

There are no chirality outliers.

All (18) torsion outliers are listed below:

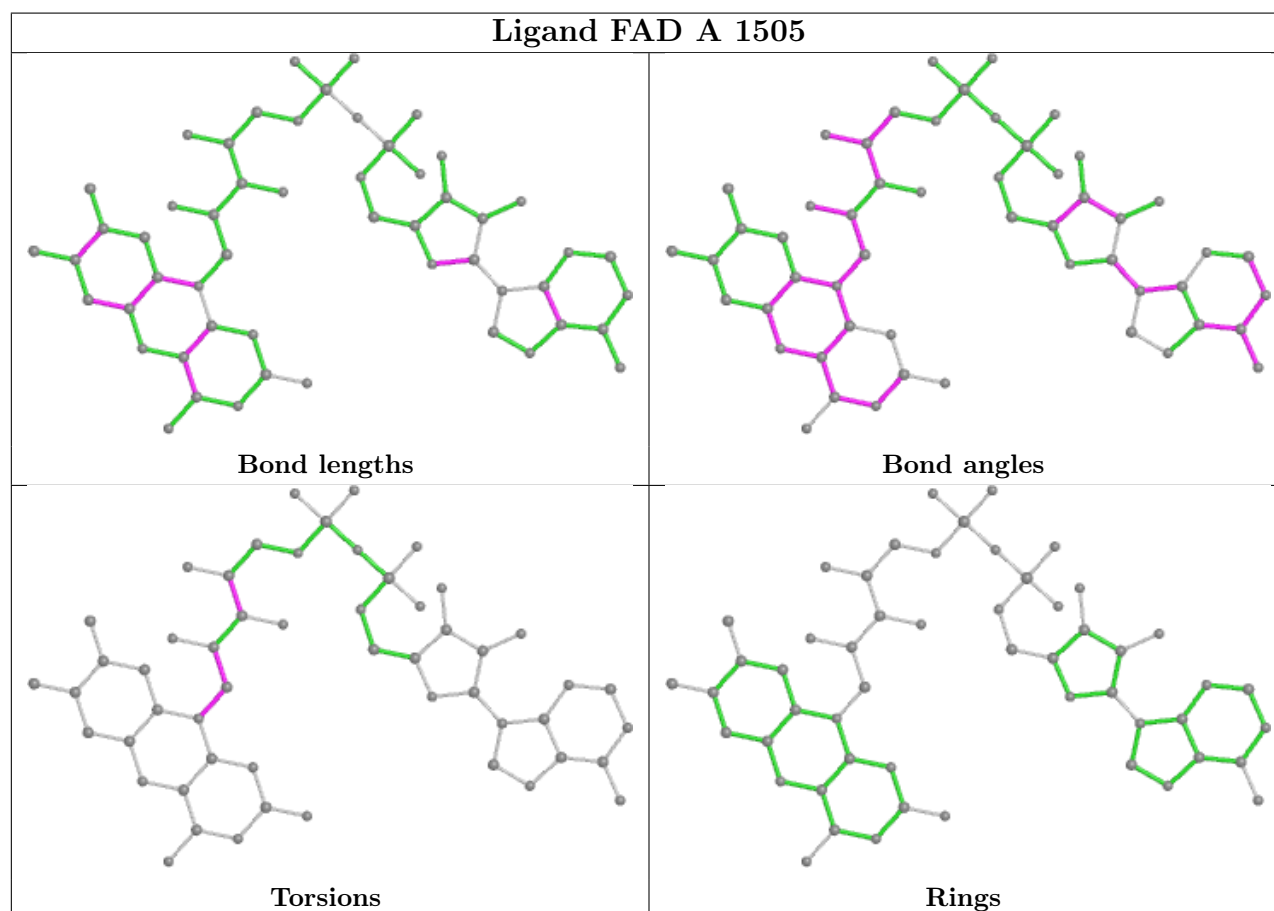
Mol	Chain	Res	Type	Atoms
5	B	3005	FAD	N10-C1'-C2'-O2'
5	A	1505	FAD	C2'-C1'-N10-C10
5	A	1505	FAD	N10-C1'-C2'-O2'
5	A	1505	FAD	N10-C1'-C2'-C3'
6	A	1506	NAI	C2D-C1D-N1N-C6N
5	A	1505	FAD	C2'-C3'-C4'-O4'
5	A	1505	FAD	C2'-C3'-C4'-C5'
6	B	3006	NAI	C2D-C1D-N1N-C6N
6	A	1506	NAI	O4D-C1D-N1N-C6N
6	B	3006	NAI	O4D-C1D-N1N-C6N
5	B	3005	FAD	N10-C1'-C2'-C3'
5	A	1505	FAD	O3'-C3'-C4'-O4'
6	B	3006	NAI	O4D-C4D-C5D-O5D
6	A	1506	NAI	O4D-C4D-C5D-O5D
5	A	1505	FAD	O3'-C3'-C4'-C5'
6	B	3006	NAI	C2N-C3N-C7N-N7N
6	A	1506	NAI	C2N-C3N-C7N-N7N
5	B	3005	FAD	C2'-C3'-C4'-C5'

There are no ring outliers.

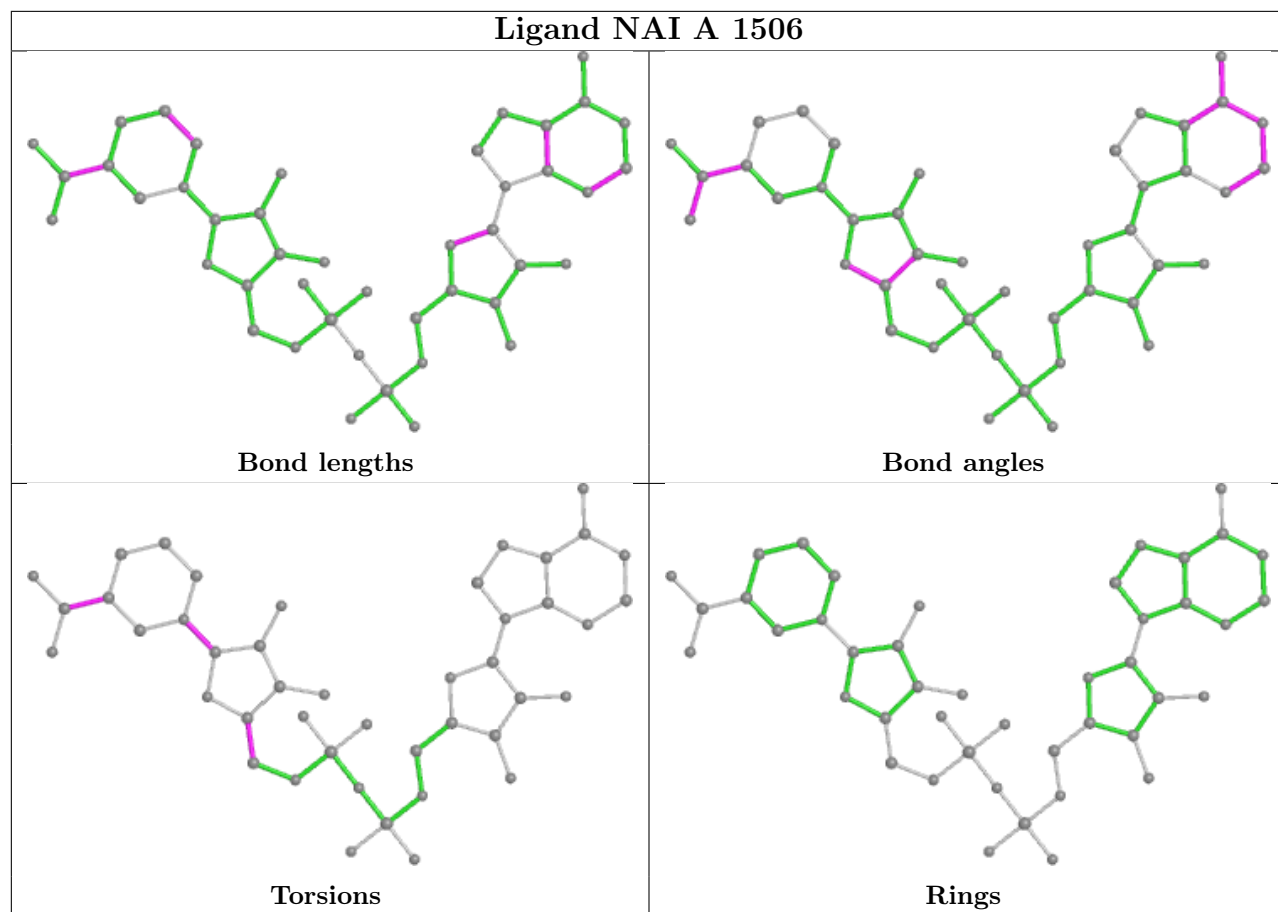
6 monomers are involved in 8 short contacts:

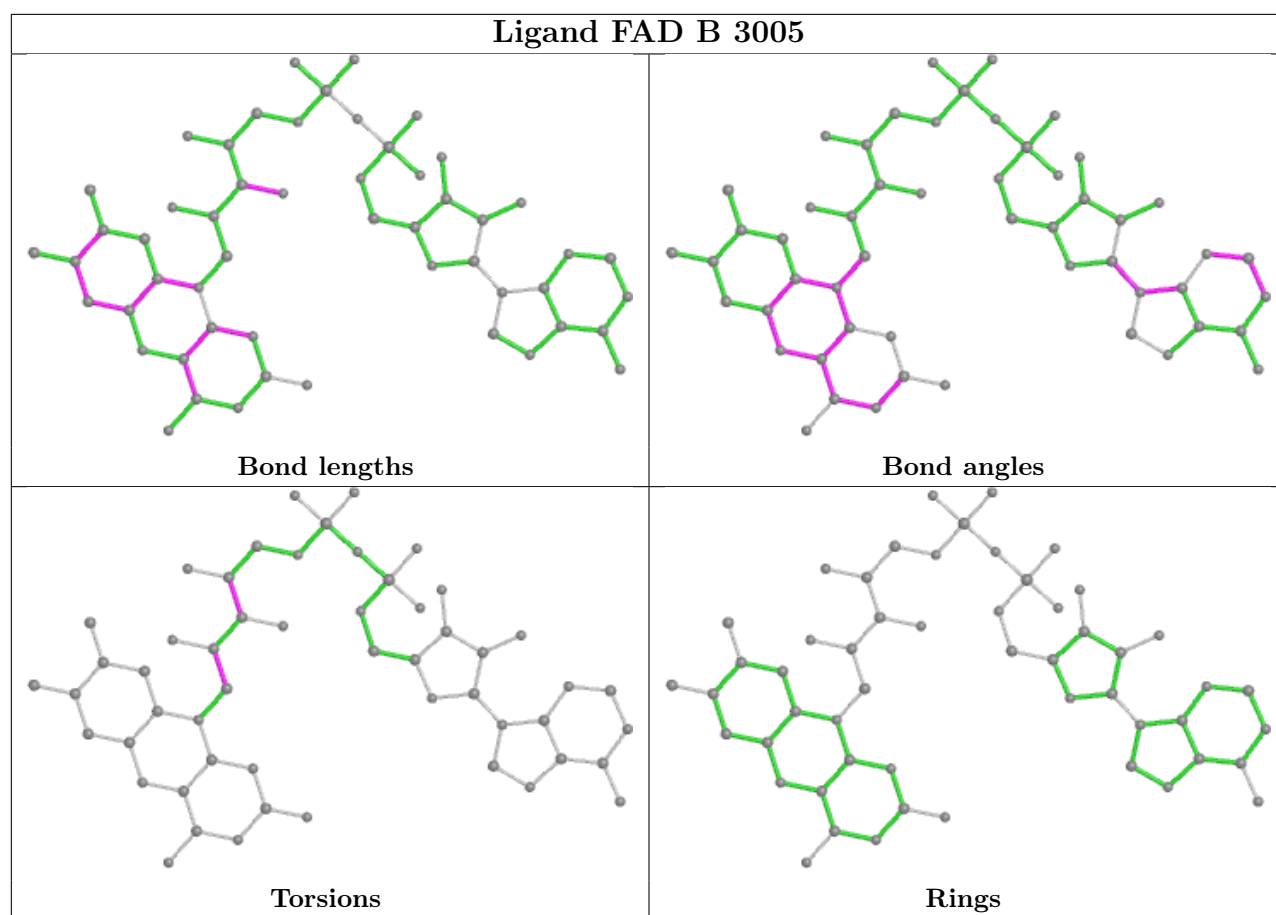
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1504	FES	1	0
5	A	1505	FAD	3	0
6	A	1506	NAI	2	0
4	B	3001	FES	2	0
5	B	3005	FAD	2	0
6	B	3006	NAI	1	0

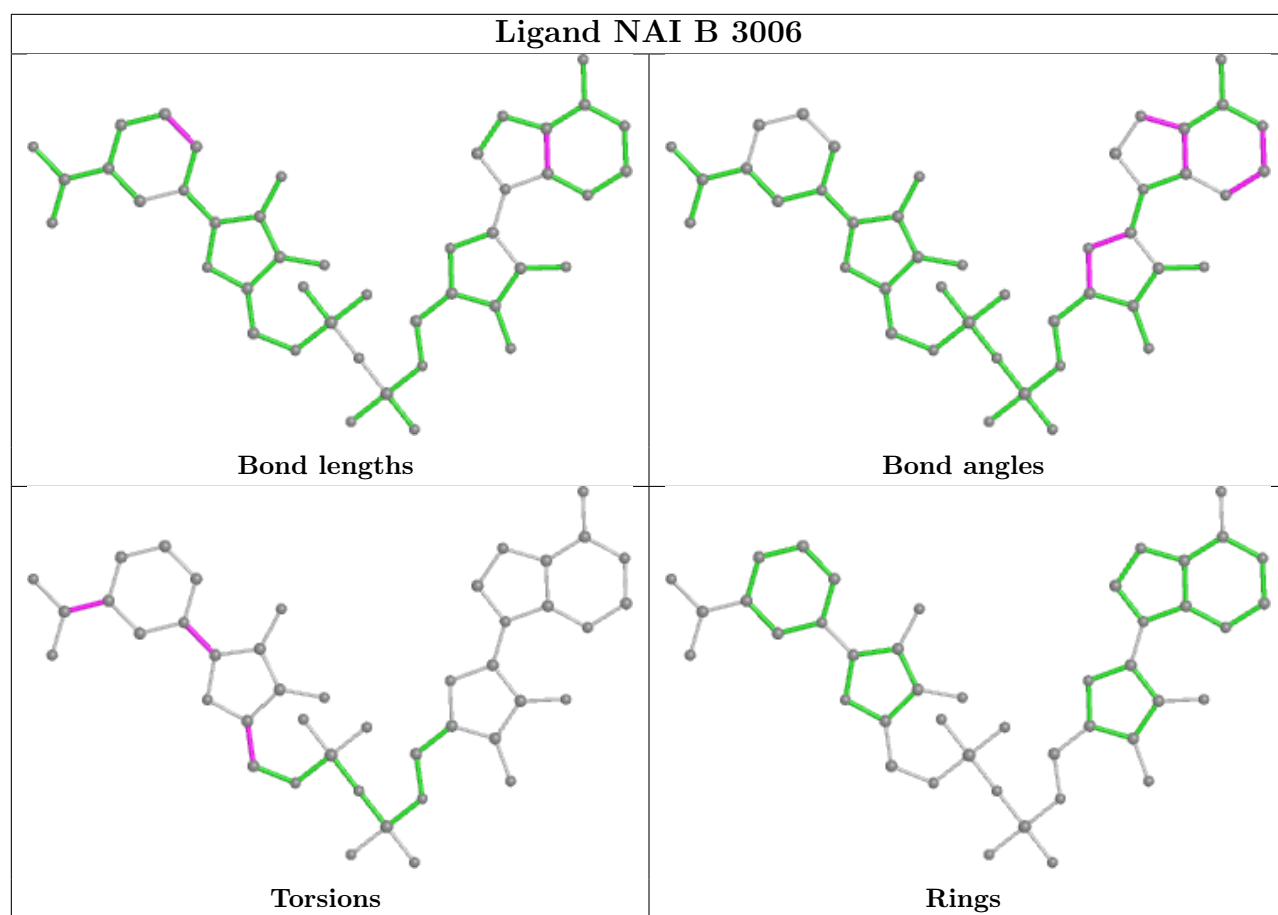
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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, 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	1297/1331 (97%)	0.07	55 (4%) 36 34	15, 25, 49, 88	0
1	B	1291/1331 (96%)	-0.09	25 (1%) 66 66	14, 21, 40, 73	0
All	All	2588/2662 (97%)	-0.01	80 (3%) 49 47	14, 23, 46, 88	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1289	ALA	8.3
1	A	1324	CYS	8.1
1	A	1323	ASN	7.4
1	A	1325	LYS	6.9
1	A	1322	GLU	5.3
1	A	1317	VAL	5.2
1	A	1111	GLY	5.0
1	B	221	THR	4.7
1	A	166	GLY	4.5
1	A	1321	PRO	4.3
1	A	566	ASP	3.9
1	B	1286	GLY	3.8
1	A	1327	TRP	3.8
1	A	3	ALA	3.7
1	B	1111	GLY	3.7
1	A	290	VAL	3.7
1	A	192	PRO	3.7
1	A	553	PRO	3.6
1	B	565	LYS	3.5
1	A	316	ALA	3.5
1	A	1110	THR	3.4
1	A	565	LYS	3.4
1	B	1110	THR	3.2
1	B	1288	ASN	3.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	247	LEU	3.2
1	A	396	LEU	3.2
1	A	1107	LYS	3.1
1	A	530	ASP	3.1
1	A	531	LEU	3.0
1	B	220	ASP	3.0
1	B	553	PRO	3.0
1	A	1326	SER	2.9
1	B	530	ASP	2.8
1	A	719	LEU	2.8
1	A	534	MET	2.8
1	A	318	LEU	2.7
1	A	390	PRO	2.7
1	B	535	CYS	2.7
1	A	1331	ILE	2.7
1	A	723	PHE	2.7
1	A	293	PRO	2.7
1	B	1287	ASP	2.7
1	A	317	LYS	2.5
1	A	721	LYS	2.5
1	A	220	ASP	2.5
1	A	61	LEU	2.5
1	B	1106	LYS	2.5
1	B	1320	VAL	2.5
1	A	387	THR	2.5
1	A	291	HIS	2.4
1	A	498	ASP	2.4
1	A	529	ALA	2.4
1	A	1266	LEU	2.4
1	A	321	GLN	2.4
1	A	1329	VAL	2.3
1	B	218	LEU	2.3
1	B	3	ALA	2.3
1	B	1250	LYS	2.3
1	A	720	LYS	2.3
1	A	1265	PHE	2.3
1	A	250	GLN	2.3
1	A	724	SER	2.2
1	B	222	PRO	2.2
1	A	444	GLY	2.2
1	A	165	ASP	2.2
1	A	533	ASP	2.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	1107	LYS	2.2
1	A	319	PRO	2.2
1	A	1109	PRO	2.2
1	A	253	ASP	2.2
1	B	61	LEU	2.1
1	B	566	ASP	2.1
1	A	377	GLY	2.1
1	A	552	ASP	2.1
1	B	1318	THR	2.1
1	A	474	SER	2.1
1	B	317	LYS	2.0
1	B	271	ASN	2.0
1	A	217	ARG	2.0
1	B	720	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 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.

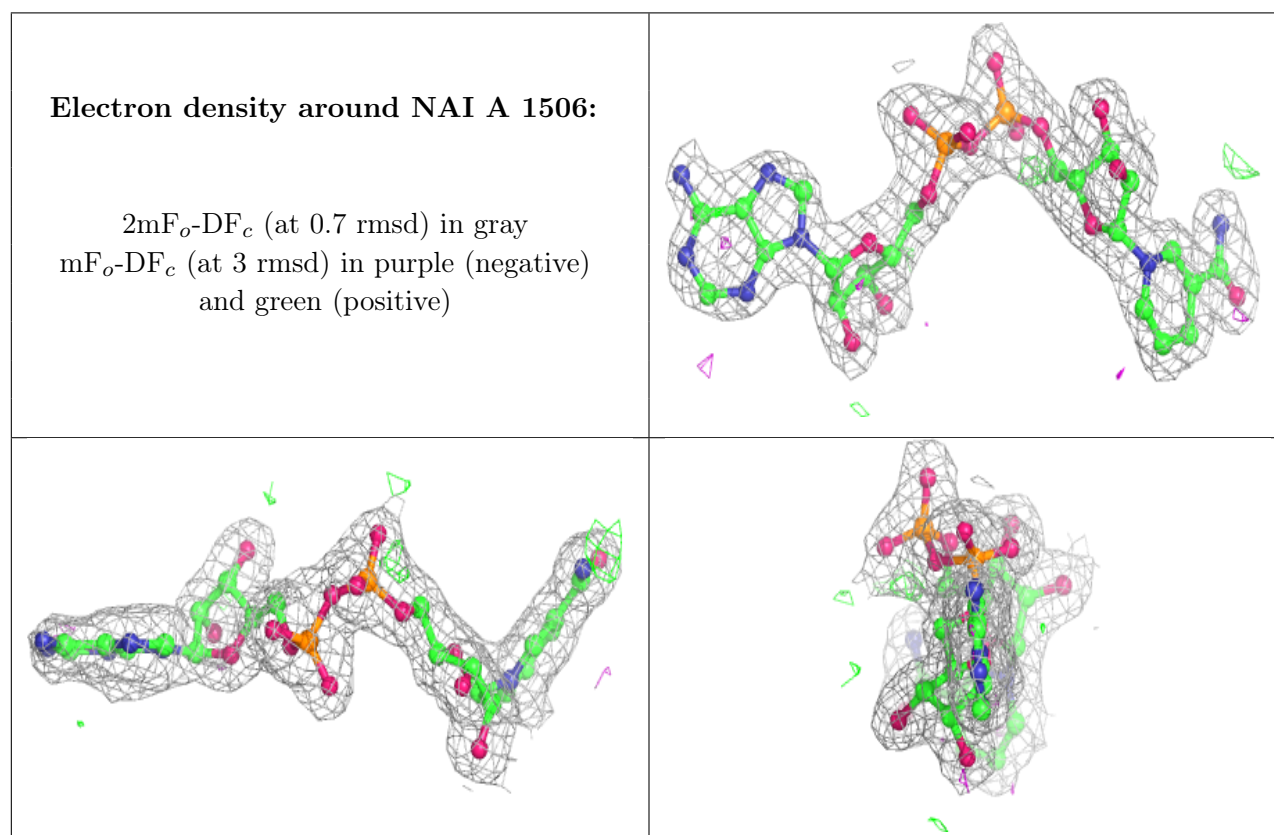
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	NAI	A	1506	44/44	0.94	0.10	26,33,41,47	0
6	NAI	B	3006	44/44	0.96	0.09	19,23,26,32	0
2	URC	A	1501	12/12	0.97	0.07	18,20,22,23	0
5	FAD	A	1505	53/53	0.97	0.08	21,24,29,32	0
3	BCT	A	1502	4/4	0.98	0.07	22,24,25,27	0
4	FES	B	3001	4/4	0.98	0.05	25,28,31,33	0
4	FES	A	1504	4/4	0.98	0.04	26,29,32,32	0
5	FAD	B	3005	53/53	0.98	0.08	16,18,20,21	0
3	BCT	B	3004	4/4	0.99	0.08	18,19,21,22	0

*Continued on next page...*

*Continued from previous page...*

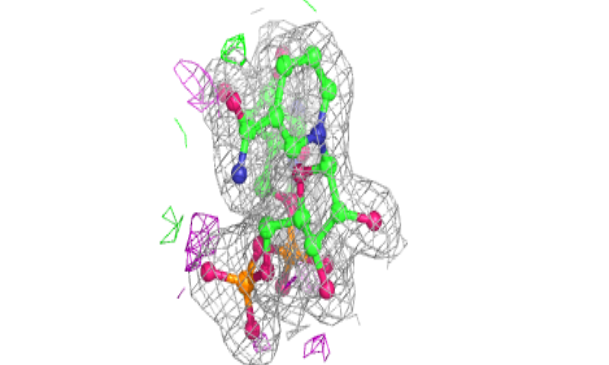
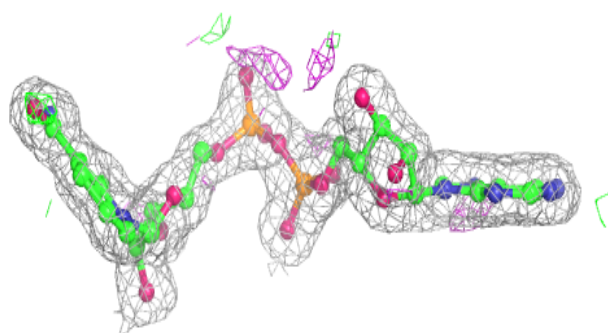
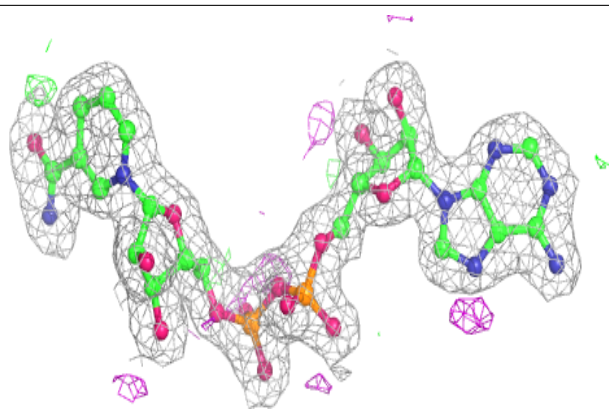
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	URC	B	3003	12/12	0.99	0.06	17,19,21,21	0
4	FES	A	1503	4/4	1.00	0.05	18,18,18,18	0
4	FES	B	3002	4/4	1.00	0.04	16,16,16,17	0

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.

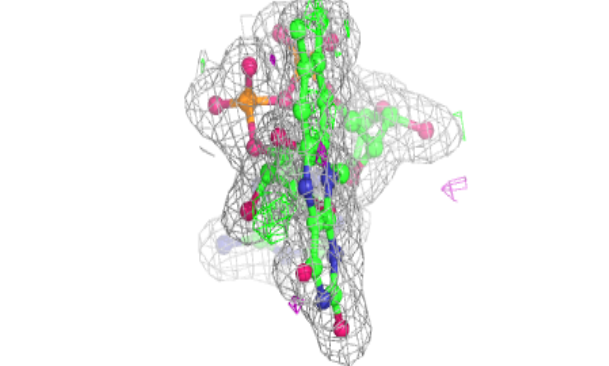
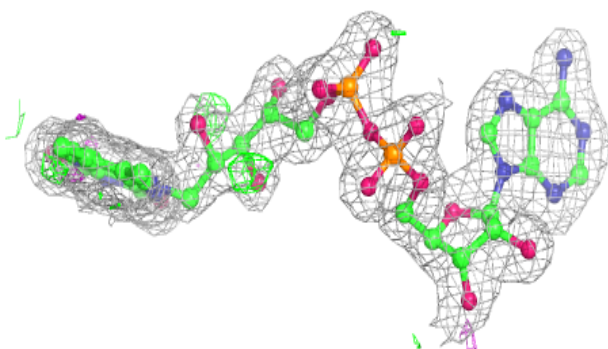
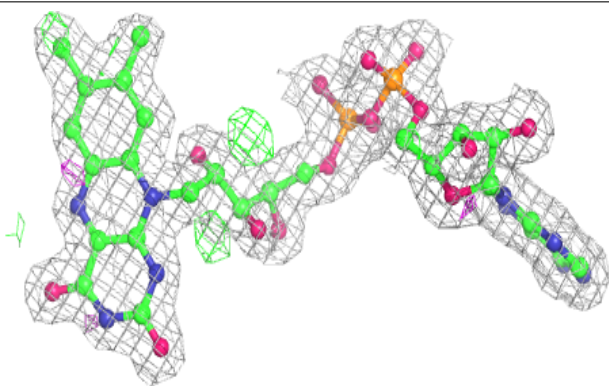


**Electron density around NAI B 3006:**

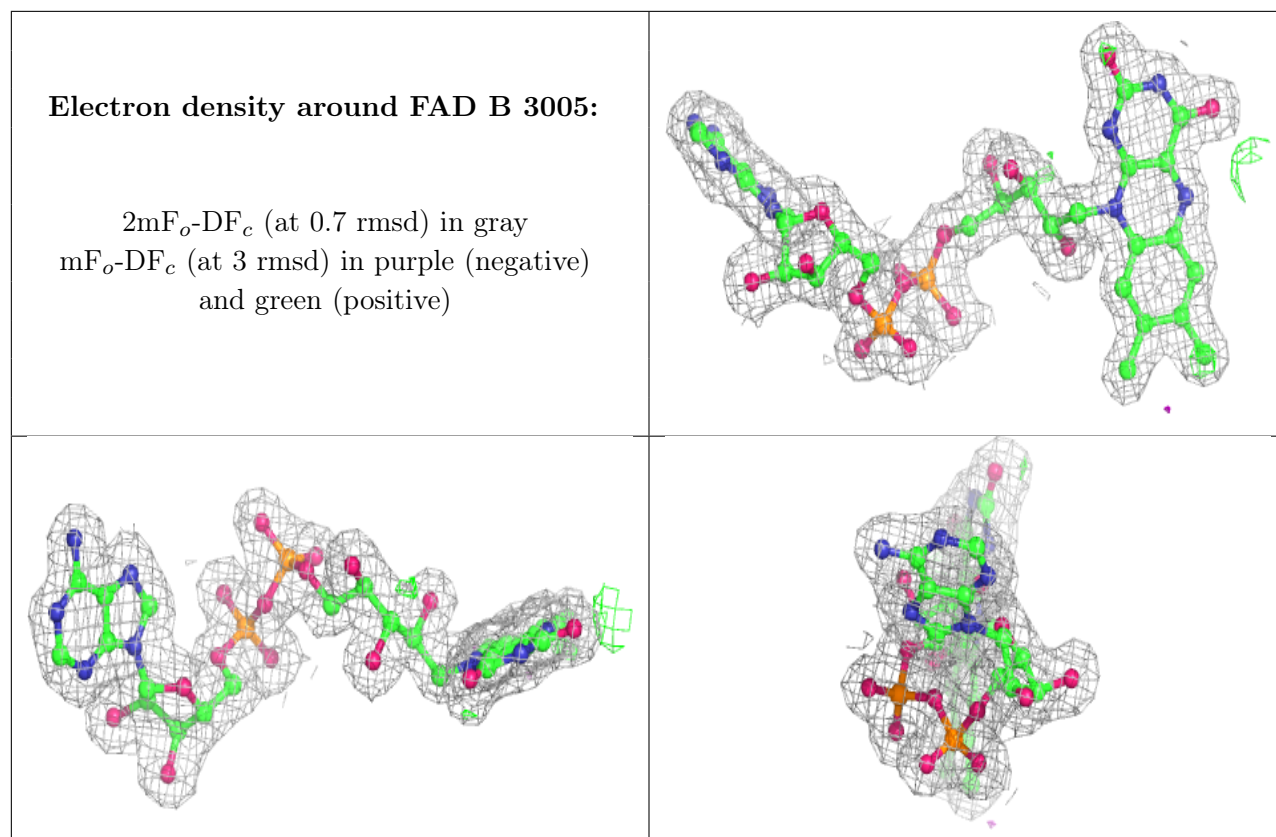
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around FAD A 1505:**

$2mF_o-DF_c$  (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.