



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:28 PM UTC

PDB ID : 1SG0 / pdb_00001sg0
Title : Crystal structure analysis of QR2 in complex with resveratrol
Authors : Buryanovskyy, L.; Fu, Y.; Boyd, M.; Ma, Y.; Tsieh, T.C.; Wu, J.M.; Zhang, Z.
Deposited on : 2004-02-22
Resolution : 1.50 Å(reported)

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

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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

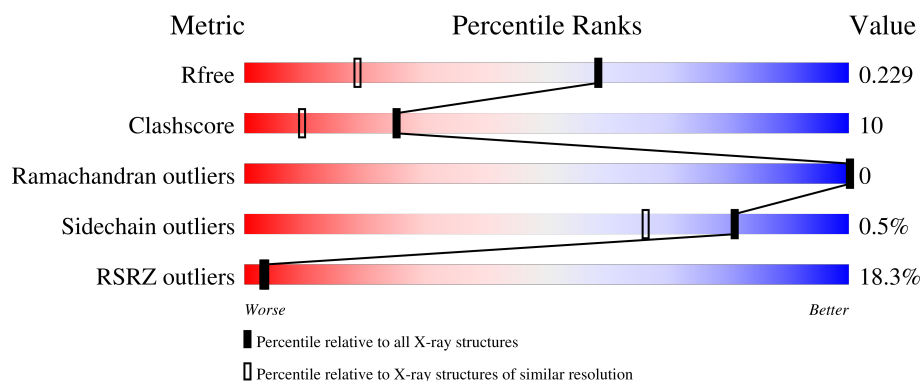
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	230	25% 79% 20% .
1	B	230	12% 81% 18% .

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4143 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.

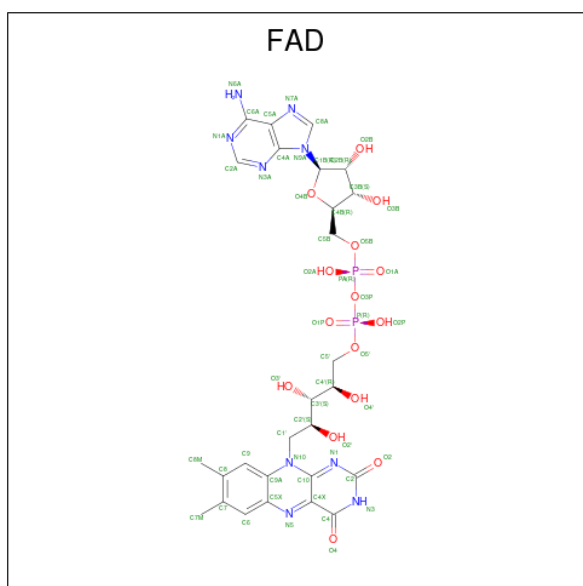
- Molecule 1 is a protein called NRH dehydrogenase [quinone] 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1824	1174	304	338	8			
1	B	230	Total	C	N	O	S	0	0	0
			1824	1174	304	338	8			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

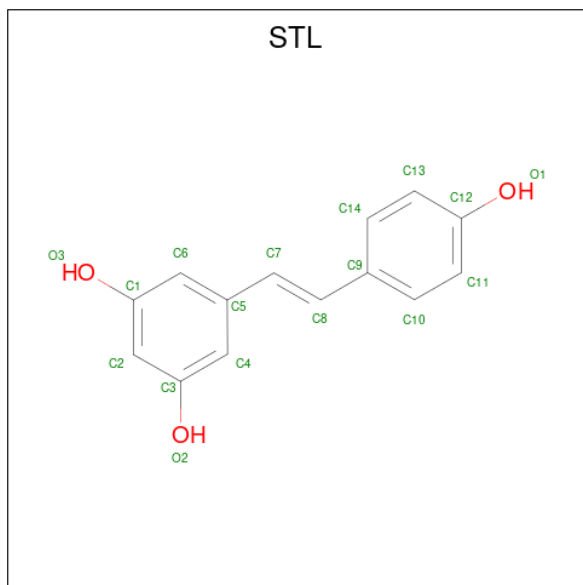
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

- Molecule 4 is RESVERATROL (CCD ID: STL) (formula: $C_{14}H_{12}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			17	14	3		
4	B	1	Total	C	O	0	0
			17	14	3		

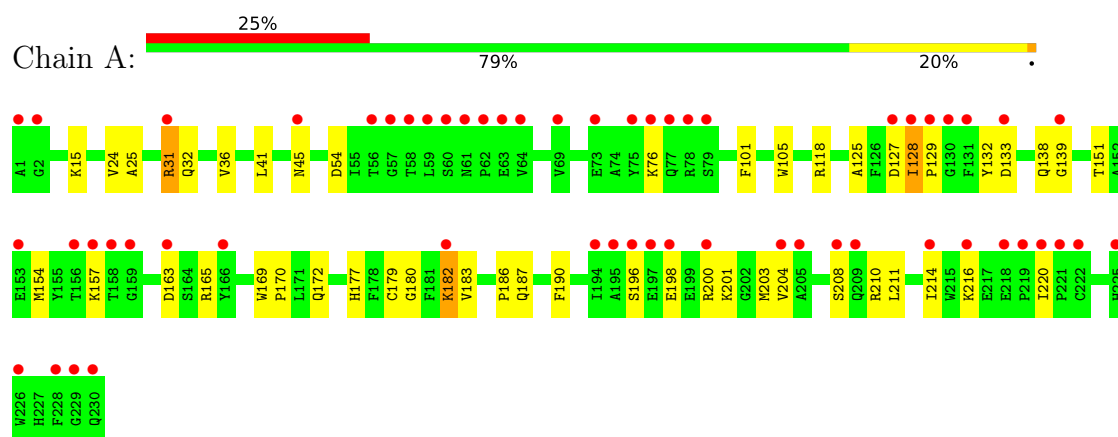
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	163	Total	O	0	0
			163	163		
5	B	190	Total	O	0	0
			190	190		

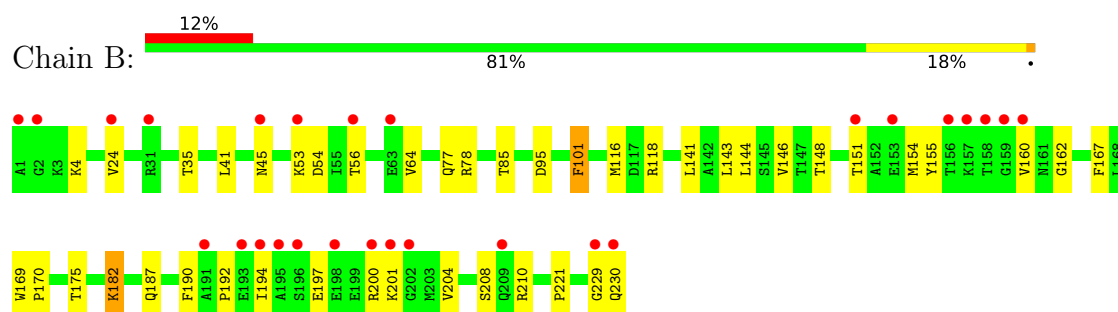
3 Residue-property plots

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: NRH dehydrogenase [quinone] 2



• Molecule 1: NRH dehydrogenase [quinone] 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.33Å 106.37Å 56.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.43 – 1.50 28.43 – 1.50	Depositor EDS
% Data completeness (in resolution range)	94.2 (28.43-1.50) 94.5 (28.43-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.97 (at 1.50Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.214 , 0.234 0.210 , 0.229	Depositor DCC
R_{free} test set	7744 reflections (9.59%)	wwPDB-VP
Wilson B-factor (Å ²)	11.2	Xtriage
Anisotropy	0.677	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 48.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4143	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.78% 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: FAD, ZN, STL

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	0.34	0/1874	0.86	4/2542 (0.2%)
1	B	0.34	0/1874	0.88	6/2542 (0.2%)
All	All	0.34	0/3748	0.87	10/5084 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	101	PHE	N-CA-C	8.22	115.62	108.22
1	A	101	PHE	N-CA-C	7.83	115.27	108.22
1	B	182	LYS	N-CA-C	-7.67	96.72	109.46
1	A	182	LYS	N-CA-C	-7.08	97.70	108.96
1	A	36	VAL	N-CA-C	5.68	116.06	108.11
1	B	95	ASP	N-CA-C	-5.56	106.63	113.41
1	A	41	LEU	N-CA-C	5.45	117.65	111.11
1	B	41	LEU	N-CA-C	5.43	117.63	111.11
1	B	190	PHE	N-CA-C	5.28	117.88	109.96
1	B	221	PRO	N-CA-C	-5.21	101.74	112.47

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1824	0	1779	44	0
1	B	1824	0	1779	30	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	53	0	31	0	0
3	B	53	0	31	0	0
4	A	17	0	10	0	0
4	B	17	0	10	1	0
5	A	163	0	0	3	0
5	B	190	0	0	3	0
All	All	4143	0	3640	72	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 10.

All (72) 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:128:ILE:HG23	1:A:129:PRO:HD3	1.27	1.08
1:A:31:ARG:HH11	1:A:31:ARG:HB3	1.20	1.07
1:A:211:LEU:HA	1:A:214:ILE:HG23	1.55	0.85
1:B:116:MET:HE2	1:B:175:THR:HG21	1.62	0.79
1:B:45:ASN:HB3	5:B:583:HOH:O	1.84	0.76
1:A:211:LEU:HA	1:A:214:ILE:CG2	2.20	0.71
1:A:128:ILE:CG2	1:A:129:PRO:HD3	2.15	0.67
1:B:24:VAL:CG1	1:B:208:SER:HB3	2.23	0.67
1:A:187:GLN:HE21	1:A:210:ARG:HH11	1.43	0.66
1:A:31:ARG:HH11	1:A:31:ARG:CB	2.04	0.65
1:A:105:TRP:CZ2	4:B:502:STL:H14	2.34	0.63
1:A:169:TRP:HB3	1:A:170:PRO:HD3	1.82	0.62
1:A:31:ARG:HB3	1:A:31:ARG:NH1	2.04	0.61
1:B:187:GLN:HE21	1:B:210:ARG:HH11	1.47	0.61
1:A:157:LYS:HB2	5:A:631:HOH:O	2.03	0.58
1:A:139:GLY:H	1:A:182:LYS:NZ	2.01	0.57
1:A:132:TYR:CE2	1:B:160:VAL:HG22	2.42	0.55
1:A:190:PHE:H	1:A:203:MET:HE1	1.72	0.55
1:B:24:VAL:HG21	1:B:204:VAL:CG1	2.38	0.54
1:A:31:ARG:HH12	1:A:32:GLN:HG3	1.73	0.53
1:A:190:PHE:N	1:A:203:MET:HE1	2.23	0.53
1:B:24:VAL:HG11	1:B:208:SER:HB3	1.91	0.53
1:A:151:THR:HG23	1:A:154:MET:HE3	1.91	0.52
1:B:169:TRP:HB3	1:B:170:PRO:HD3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:LEU:C	1:B:143:LEU:HD23	2.35	0.51
1:B:54:ASP:OD2	1:B:118:ARG:HD2	2.11	0.51
1:A:211:LEU:HD23	1:A:214:ILE:HG21	1.92	0.51
1:A:24:VAL:CG1	1:A:208:SER:HB3	2.41	0.50
1:B:229:GLY:O	1:B:230:GLN:HB3	2.12	0.49
1:A:201:LYS:O	1:A:204:VAL:HG22	2.13	0.49
1:A:172:GLN:HE22	1:A:186:PRO:HD3	1.78	0.48
1:A:187:GLN:NE2	1:A:210:ARG:HH11	2.11	0.48
1:A:216:LYS:N	1:A:216:LYS:HD2	2.30	0.47
1:A:211:LEU:CA	1:A:214:ILE:HG23	2.38	0.47
1:B:197:GLU:HA	1:B:200:ARG:HH21	1.80	0.47
1:B:101:PHE:CZ	1:B:146:VAL:HG22	2.50	0.46
1:A:163:ASP:OD2	1:A:165:ARG:HB2	2.15	0.46
1:A:128:ILE:HD12	1:A:128:ILE:O	2.14	0.46
1:A:138:GLN:HA	1:A:180:GLY:O	2.15	0.46
1:A:157:LYS:NZ	1:A:157:LYS:HB3	2.31	0.46
1:A:24:VAL:HG11	1:A:208:SER:HB3	1.97	0.46
1:B:24:VAL:HG13	1:B:208:SER:HB3	1.96	0.46
1:A:25:ALA:HA	1:A:211:LEU:CD1	2.47	0.44
1:B:4:LYS:HG2	1:B:35:THR:HB	1.98	0.44
1:B:230:GLN:HE21	1:B:230:GLN:HA	1.82	0.44
1:B:141:LEU:HD23	1:B:182:LYS:HB2	1.98	0.44
1:A:76:LYS:HB2	1:A:76:LYS:NZ	2.33	0.44
1:B:53:LYS:HB2	1:B:53:LYS:NZ	2.31	0.44
1:B:143:LEU:HD23	1:B:144:LEU:N	2.32	0.44
1:B:151:THR:HG23	1:B:154:MET:HE3	1.99	0.44
1:A:151:THR:OG1	1:A:154:MET:HE3	2.17	0.44
1:B:151:THR:OG1	1:B:154:MET:HE3	2.18	0.44
1:A:54:ASP:OD2	1:A:118:ARG:HD2	2.18	0.43
1:A:132:TYR:HA	1:A:177:HIS:O	2.19	0.43
1:A:45:ASN:HB3	5:A:632:HOH:O	2.19	0.42
1:B:85:THR:HG21	5:B:548:HOH:O	2.19	0.42
1:B:194:ILE:HG13	5:B:557:HOH:O	2.20	0.42
1:A:198:GLU:CD	1:A:198:GLU:H	2.28	0.42
1:A:127:ASP:HB3	1:A:129:PRO:HD2	2.02	0.42
1:A:25:ALA:HA	1:A:211:LEU:HD13	2.02	0.41
1:A:76:LYS:HB2	1:A:76:LYS:HZ2	1.85	0.41
1:A:125:ALA:HB1	1:A:179:CYS:SG	2.61	0.41
1:A:196:SER:O	1:A:200:ARG:HG3	2.20	0.41
1:B:77:GLN:O	1:B:78:ARG:HB2	2.20	0.41
1:B:155:TYR:HA	1:B:162:GLY:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:197:GLU:HG3	1:B:201:LYS:HE3	2.03	0.41
1:A:133:ASP:HB2	5:A:597:HOH:O	2.21	0.41
1:A:15:LYS:HD2	1:B:64:VAL:HG22	2.03	0.41
1:B:167:PHE:CD1	1:B:167:PHE:C	2.99	0.41
1:A:183:VAL:O	1:A:220:ILE:HG12	2.21	0.40
1:B:56:THR:HG22	1:B:56:THR:O	2.20	0.40
1:B:148:THR:O	1:B:192:PRO:HD2	2.21	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	228/230 (99%)	215 (94%)	13 (6%)	0	100	100
1	B	228/230 (99%)	217 (95%)	11 (5%)	0	100	100
All	All	456/460 (99%)	432 (95%)	24 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	194/194 (100%)	192 (99%)	2 (1%)	68	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	194/194 (100%)	194 (100%)	0	100	100
All	All	388/388 (100%)	386 (100%)	2 (0%)	81	66

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	ARG
1	A	128	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	GLN
1	A	187	GLN
1	A	212	GLN
1	B	161	ASN
1	B	187	GLN
1	B	230	GLN

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
4	STL	B	502	-	18,18,18	2.47	11 (61%)	24,24,24	0.51	0
3	FAD	B	433	-	58,58,58	1.83	9 (15%)	85,89,89	2.29	10 (11%)
4	STL	A	501	-	18,18,18	2.48	13 (72%)	24,24,24	0.50	0
3	FAD	A	434	-	58,58,58	1.78	10 (17%)	85,89,89	2.28	12 (14%)

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
4	STL	B	502	-	-	0/5/5/5	0/2/2/2
3	FAD	B	433	-	-	8/34/50/50	0/6/6/6
4	STL	A	501	-	-	0/5/5/5	0/2/2/2
3	FAD	A	434	-	-	8/34/50/50	0/6/6/6

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	433	FAD	PA-O3P	7.46	1.67	1.59
3	A	434	FAD	PA-O3P	7.28	1.67	1.59
3	B	433	FAD	P-O3P	5.41	1.65	1.59
3	A	434	FAD	P-O3P	5.23	1.65	1.59
3	B	433	FAD	C4X-N5	4.21	1.39	1.30
3	A	434	FAD	C4X-N5	4.09	1.39	1.30
3	B	433	FAD	C5'-C4'	4.01	1.57	1.51
3	A	434	FAD	C5'-C4'	4.01	1.57	1.51
4	B	502	STL	C6-C1	3.59	1.44	1.39
4	B	502	STL	C11-C10	3.54	1.44	1.38
4	A	501	STL	C4-C3	3.44	1.44	1.39
4	B	502	STL	C4-C3	3.39	1.44	1.39
4	A	501	STL	C2-C1	3.30	1.44	1.39
4	B	502	STL	C6-C5	3.30	1.45	1.39
4	A	501	STL	C6-C1	3.30	1.44	1.39
4	A	501	STL	C14-C13	3.26	1.44	1.38
4	B	502	STL	C2-C1	3.20	1.43	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	501	STL	C2-C3	3.11	1.43	1.39
4	B	502	STL	C2-C3	3.09	1.43	1.39
4	A	501	STL	C6-C5	3.09	1.45	1.39
4	A	501	STL	C11-C10	3.05	1.43	1.38
4	B	502	STL	C11-C12	2.86	1.44	1.39
4	B	502	STL	C10-C9	2.81	1.45	1.39
4	A	501	STL	C10-C9	2.79	1.45	1.39
4	A	501	STL	C13-C12	2.75	1.44	1.39
3	A	434	FAD	C5B-C4B	-2.73	1.43	1.51
4	B	502	STL	C14-C13	2.72	1.43	1.38
3	B	433	FAD	C10-N1	2.63	1.38	1.33
3	B	433	FAD	C5B-C4B	-2.63	1.43	1.51
3	A	434	FAD	C9A-C5X	2.58	1.45	1.41
3	A	434	FAD	C10-N1	2.55	1.38	1.33
4	A	501	STL	C11-C12	2.53	1.43	1.39
3	A	434	FAD	C2A-N1A	2.44	1.38	1.33
3	B	433	FAD	C2A-N1A	2.44	1.38	1.33
3	B	433	FAD	C9A-C5X	2.43	1.45	1.41
3	B	433	FAD	C9A-N10	2.31	1.45	1.41
4	B	502	STL	C13-C12	2.30	1.43	1.39
4	A	501	STL	C4-C5	2.20	1.43	1.39
3	A	434	FAD	C9A-N10	2.20	1.45	1.41
4	A	501	STL	C14-C9	2.19	1.43	1.39
4	B	502	STL	C4-C5	2.17	1.43	1.39
4	A	501	STL	C8-C7	2.06	1.41	1.31
3	A	434	FAD	C9-C9A	2.05	1.43	1.39

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	433	FAD	O3P-PA-O1A	-10.74	78.40	110.70
3	A	434	FAD	O3P-PA-O1A	-10.71	78.48	110.70
3	B	433	FAD	O2P-P-O3P	-10.64	78.52	107.27
3	A	434	FAD	O2P-P-O3P	-10.60	78.63	107.27
3	B	433	FAD	O2A-PA-O3P	-7.66	86.56	107.27
3	A	434	FAD	O2A-PA-O3P	-7.45	87.12	107.27
3	A	434	FAD	O3P-P-O1P	-7.12	89.27	110.70
3	B	433	FAD	O3P-P-O1P	-6.99	89.68	110.70
3	B	433	FAD	O2A-PA-O1A	4.82	134.88	112.44
3	A	434	FAD	O2A-PA-O1A	4.71	134.35	112.44
3	B	433	FAD	O2P-P-O5'	2.59	119.31	107.57
3	A	434	FAD	O2P-P-O5'	2.53	119.04	107.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	434	FAD	O2P-P-O1P	2.40	123.59	112.44
3	B	433	FAD	O2P-P-O1P	2.32	123.23	112.44
3	B	433	FAD	C9A-C5X-N5	-2.32	120.00	122.45
3	A	434	FAD	C9A-C5X-N5	-2.26	120.05	122.45
3	A	434	FAD	O4B-C1B-C2B	-2.16	102.00	106.62
3	A	434	FAD	N3A-C2A-N1A	-2.14	125.35	128.58
3	A	434	FAD	C4X-C10-N10	2.13	119.53	116.48
3	B	433	FAD	N3A-C2A-N1A	-2.13	125.36	128.58
3	B	433	FAD	O4B-C1B-C2B	-2.11	102.11	106.62
3	A	434	FAD	O3'-C3'-C4'	-2.03	104.33	108.93

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	434	FAD	C5B-O5B-PA-O1A
3	A	434	FAD	C4'-C5'-O5'-P
3	A	434	FAD	C5'-O5'-P-O2P
3	B	433	FAD	C5B-O5B-PA-O1A
3	B	433	FAD	C4'-C5'-O5'-P
3	B	433	FAD	C5'-O5'-P-O2P
3	A	434	FAD	O3'-C3'-C4'-C5'
3	B	433	FAD	O3'-C3'-C4'-C5'
3	A	434	FAD	C2'-C3'-C4'-C5'
3	B	433	FAD	C2'-C3'-C4'-C5'
3	A	434	FAD	C2B-C1B-N9A-C8A
3	A	434	FAD	C2'-C3'-C4'-O4'
3	B	433	FAD	C2'-C3'-C4'-O4'
3	B	433	FAD	O3'-C3'-C4'-O4'
3	A	434	FAD	O3'-C3'-C4'-O4'
3	B	433	FAD	C2B-C1B-N9A-C8A

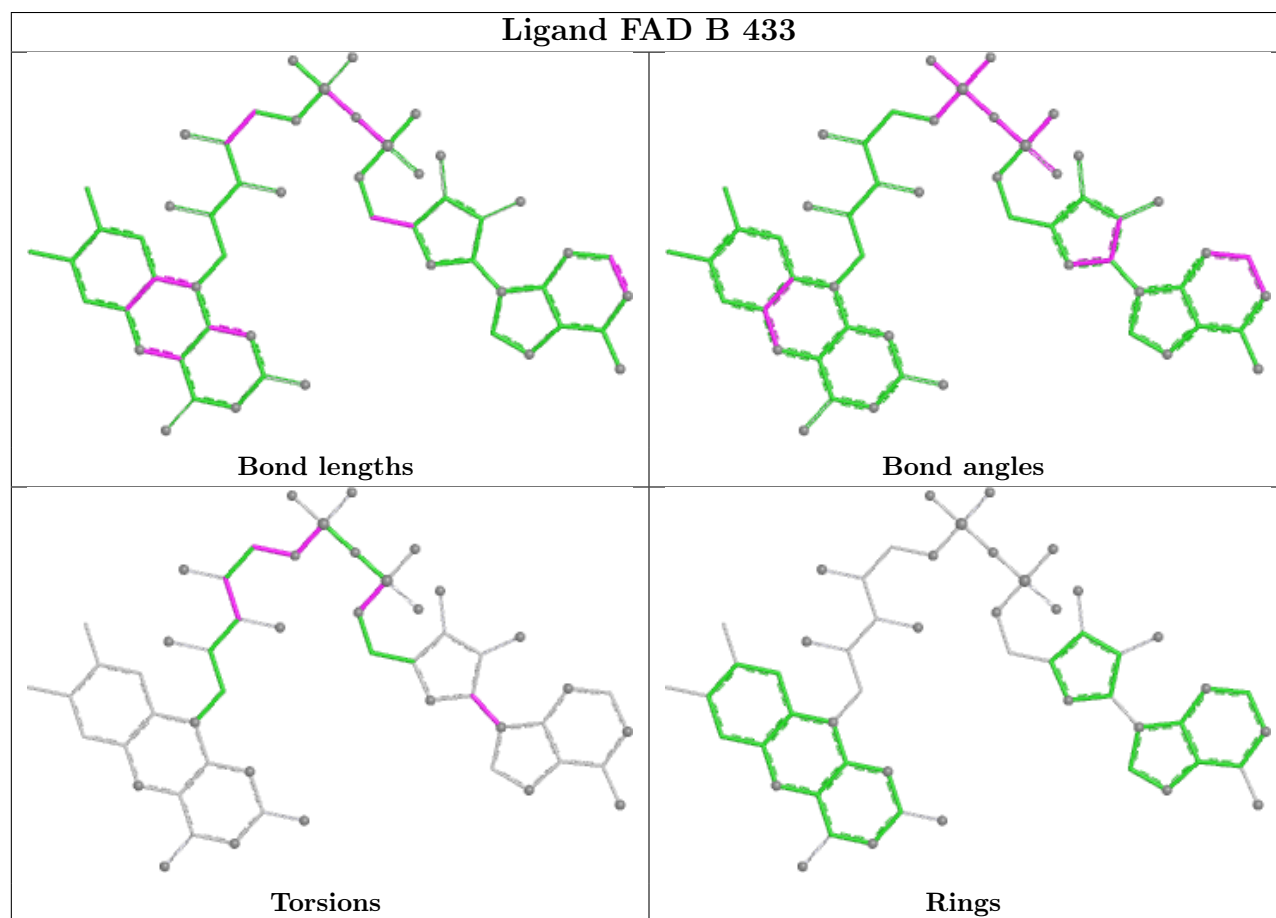
There are no ring outliers.

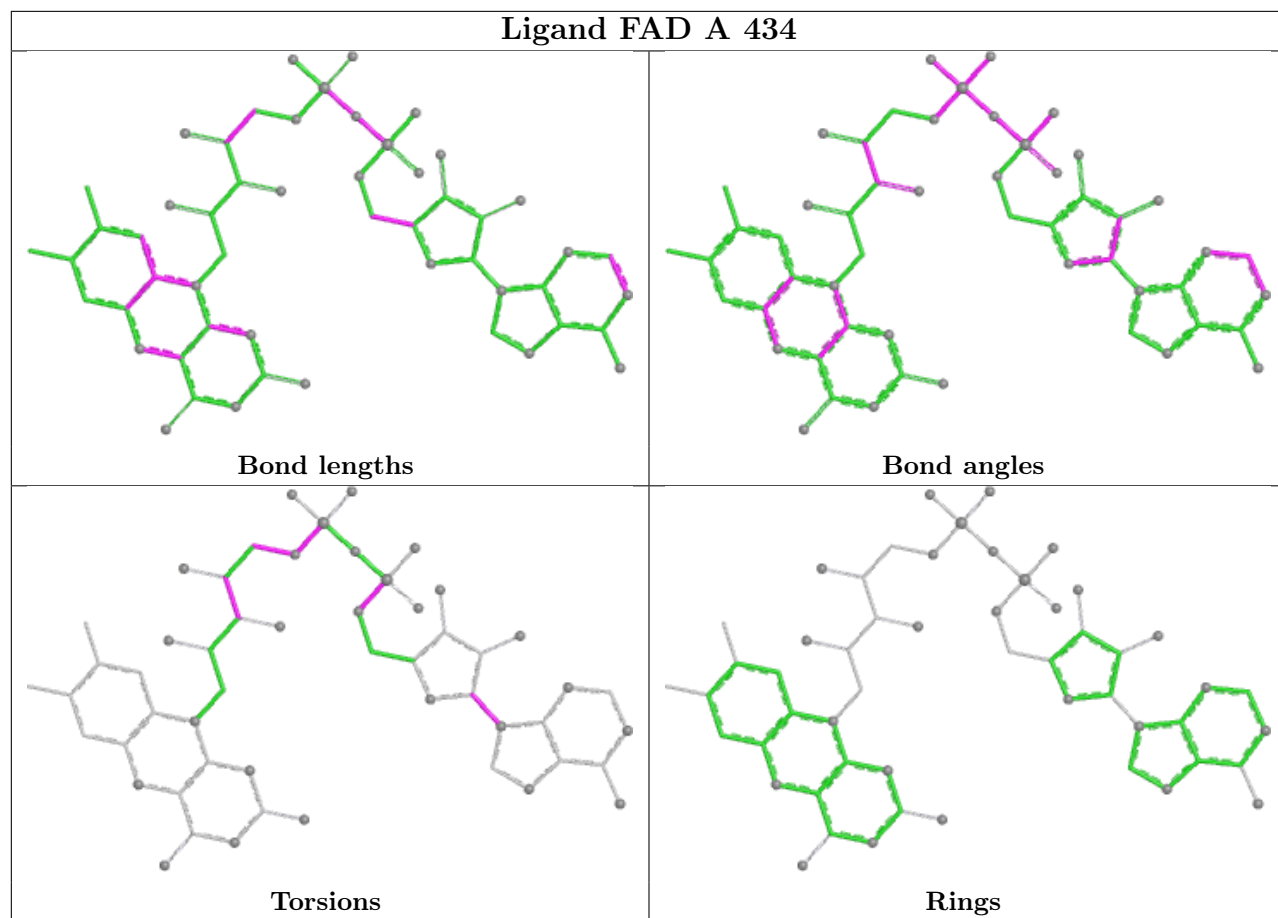
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	502	STL	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, 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	230/230 (100%)	1.14	57 (24%) 2 2	6, 15, 33, 48	0
1	B	230/230 (100%)	0.66	27 (11%) 9 9	6, 13, 29, 43	0
All	All	460/460 (100%)	0.90	84 (18%) 3 3	6, 14, 31, 48	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	ALA	12.6
1	A	128	ILE	11.1
1	A	1	ALA	8.5
1	A	129	PRO	8.4
1	B	230	GLN	7.7
1	A	194	ILE	5.3
1	A	58	THR	5.0
1	A	230	GLN	4.8
1	A	158	THR	4.5
1	A	59	LEU	4.3
1	A	229	GLY	4.3
1	B	198	GLU	4.3
1	A	62	PRO	4.2
1	A	197	GLU	4.2
1	A	57	GLY	4.1
1	A	195	ALA	4.0
1	B	45	ASN	4.0
1	B	194	ILE	4.0
1	A	60	SER	3.9
1	A	153	GLU	3.9
1	A	225	HIS	3.8
1	A	198	GLU	3.7
1	A	63	GLU	3.7
1	B	157	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	45	ASN	3.5
1	A	200	ARG	3.5
1	B	63	GLU	3.4
1	A	228	PHE	3.4
1	B	158	THR	3.4
1	A	216	LYS	3.3
1	A	64	VAL	3.3
1	A	204	VAL	3.3
1	B	160	VAL	3.3
1	B	195	ALA	3.3
1	A	196	SER	3.2
1	B	200	ARG	3.2
1	A	159	GLY	3.2
1	A	61	ASN	3.2
1	B	196	SER	3.2
1	A	131	PHE	3.1
1	A	214	ILE	3.1
1	A	79	SER	3.1
1	A	78	ARG	3.1
1	B	159	GLY	3.1
1	A	156	THR	3.0
1	B	229	GLY	3.0
1	B	2	GLY	2.8
1	A	2	GLY	2.8
1	A	221	PRO	2.7
1	B	56	THR	2.7
1	A	219	PRO	2.7
1	A	56	THR	2.6
1	B	209	GLN	2.6
1	A	220	ILE	2.6
1	B	191	ALA	2.6
1	A	76	LYS	2.6
1	A	73	GLU	2.6
1	A	133	ASP	2.6
1	A	208	SER	2.6
1	A	205	ALA	2.5
1	A	226	TRP	2.5
1	A	182	LYS	2.5
1	A	157	LYS	2.5
1	B	53	LYS	2.5
1	A	209	GLN	2.5
1	A	127	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	31	ARG	2.4
1	B	153	GLU	2.4
1	B	24	VAL	2.4
1	A	218	GLU	2.4
1	B	202	GLY	2.4
1	A	31	ARG	2.3
1	A	77	GLN	2.3
1	B	151	THR	2.2
1	A	130	GLY	2.2
1	A	69	VAL	2.2
1	A	222	CYS	2.2
1	B	156	THR	2.2
1	A	163	ASP	2.2
1	B	201	LYS	2.2
1	A	75	TYR	2.1
1	A	139	GLY	2.1
1	B	193	GLU	2.0
1	A	166	TYR	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.

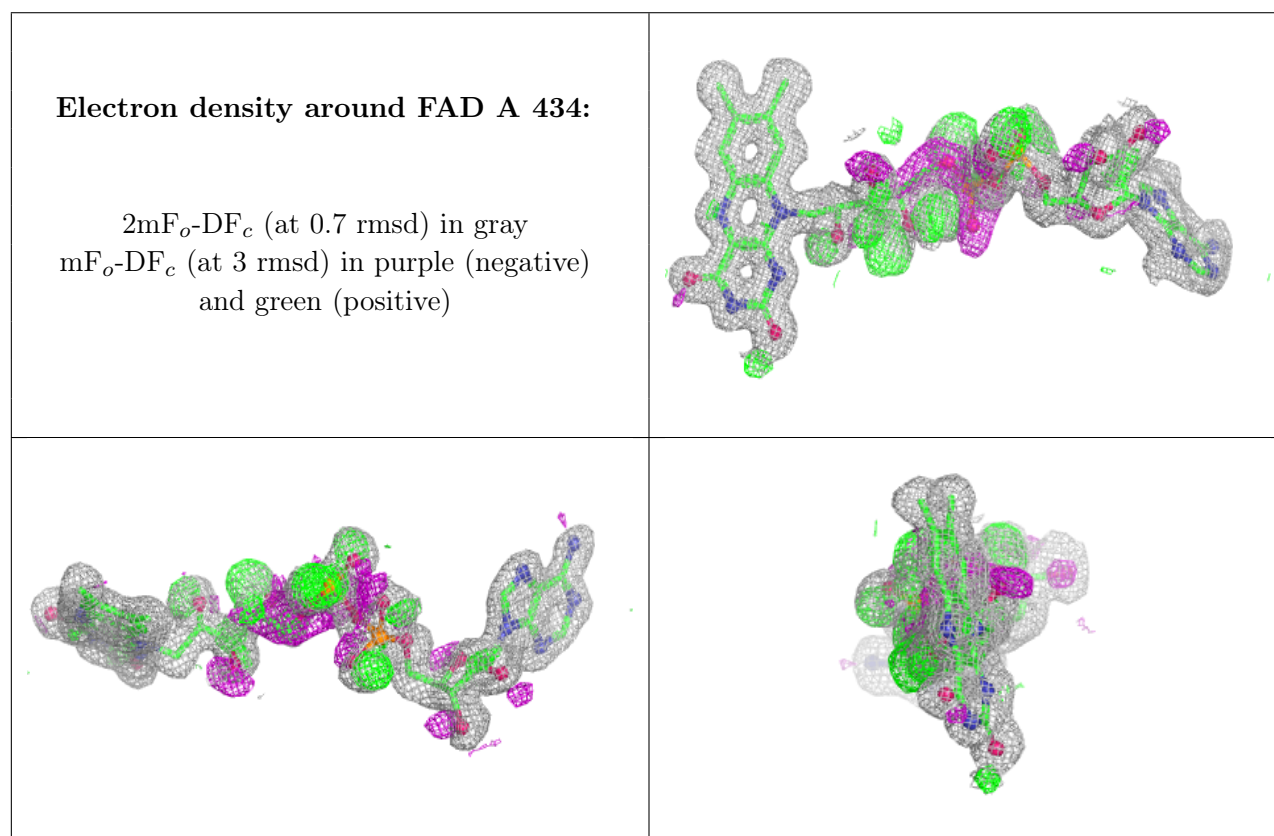
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	STL	A	501	17/17	0.75	0.23	16,22,33,34	0
4	STL	B	502	17/17	0.81	0.17	13,14,17,18	0
3	FAD	A	434	53/53	0.83	0.15	7,18,25,28	0
3	FAD	B	433	53/53	0.85	0.15	8,21,25,29	0
2	ZN	A	231	1/1	0.96	0.06	15,15,15,15	0

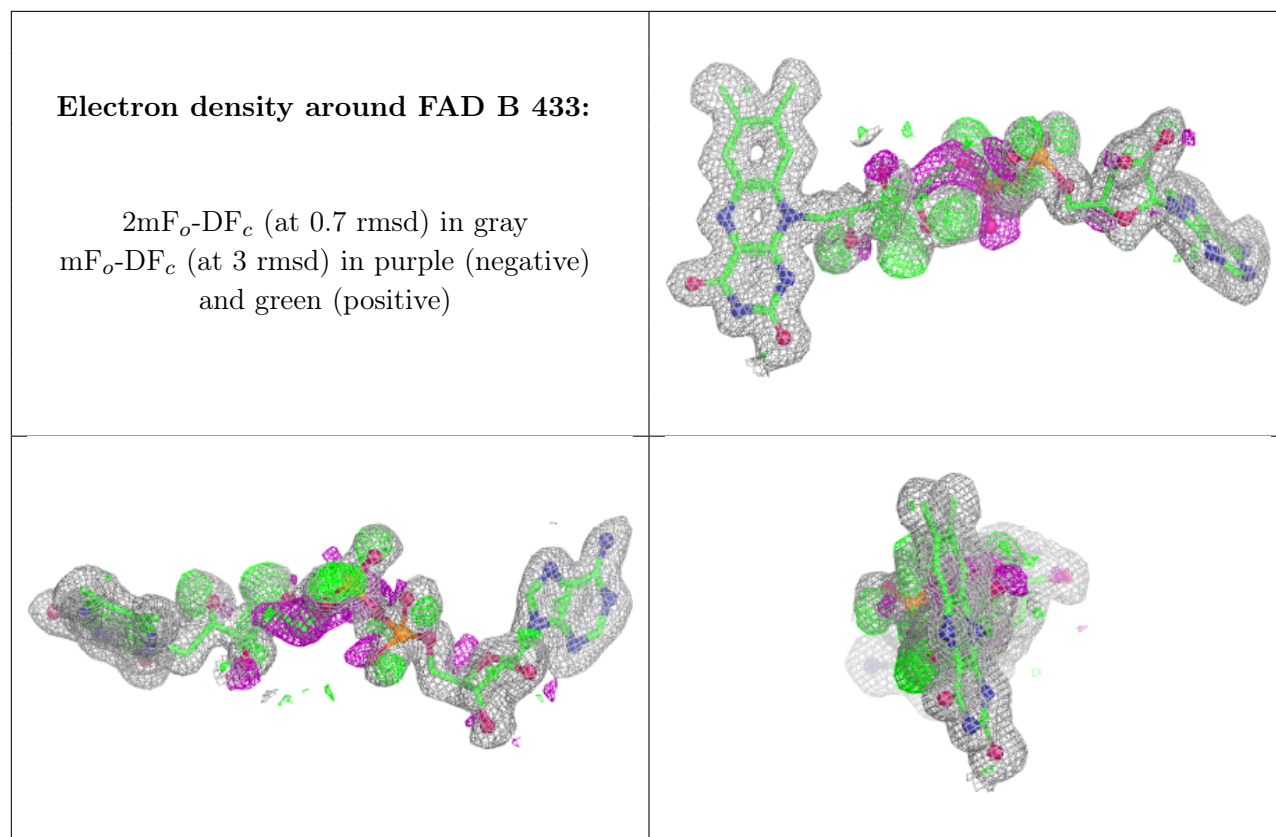
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	B	232	1/1	0.98	0.03	13,13,13,13	0

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.





6.5 Other polymers [i](#)

There are no such residues in this entry.