

Full wwPDB X-ray Structure Validation Report (i)

May 14, 2020 – 01:26 pm BST

:	5NAE
:	Pseudomonas fluorescens kynurenine 3-monooxygenase (KMO) in complex
	with $3-\{5-chloro-2-oxo-6-[(1R)-1-(pyridin-2-yl)ethoxy]-2,3-dihydro-1,3-$
	benzoxazol-3-yl}propanoic acid
:	Rowland, P.
:	2017-02-27
:	1.76 Å(reported)
	:

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

We welcome your comments at *validation@mail.wwpdb.org* A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

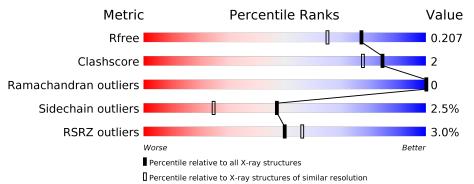
Xtriage (Phenix) EDS buster-report Percentile statistics Refmac CCP4 Ideal geometry (proteins) Ideal geometry (DNA, RNA)	: : : : : :	 1.8.5 (274361), CSD as541be (2020) 1.13 2.11 1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove) Engh & Huber (2001) Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R_{free}	130704	$2340 \ (1.76-1.76)$
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437(1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 >=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 <=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	А	461	89%	8%	·
1	В	461	^{2%} 91%	7%	·



5NAE

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7985 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.

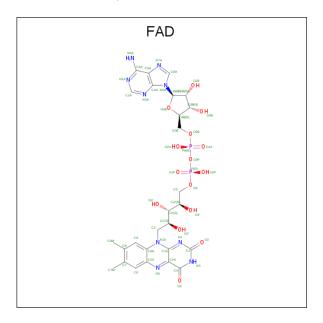
• Molecule 1 is a protein called Kynurenine 3-monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	448	Total 3474	C 2176	11	O 638	S 17	0	1	0
1	В	451		C 2192	Ν	Ο	S 17	0	2	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	252	SER	CYS	engineered mutation	UNP Q84HF5
А	461	SER	CYS	engineered mutation	UNP Q84HF5
В	252	SER	CYS	engineered mutation	UNP Q84HF5
В	461	SER	CYS	engineered mutation	UNP Q84HF5

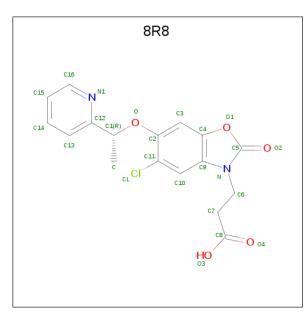
• Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
0	Λ	1	Total	С	Ν	Ο	Р	0	0
	А	L	53	27	9	15	2	0	0
0	р	1	Total	С	Ν	Ο	Р	0	0
	D		53	27	9	15	2	U	

• Molecule 3 is 3-[5-chloranyl-2-oxidanylidene-6-[(1 {R})-1-pyridin-2-ylethoxy]-1,3-benzoxazol -3-yl]propanoic acid (three-letter code: 8R8) (formula: $C_{17}H_{15}ClN_2O_5$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	Δ	1	Total	С	Cl	Ν	Ο	0	0	
0	А	L	25	17	1	2	5	0	0	
9	D	1	Total	С	Cl	Ν	Ο	0	0	
0	D	L	25	17	1	2	5	0	0	

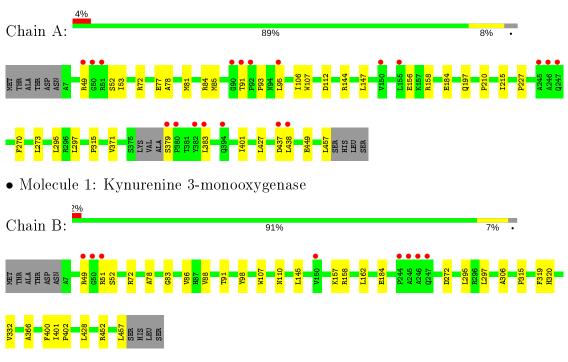
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	386	Total O 386 386	0	0
4	В	471	Total O 471 471	0	0



3 Residue-property plots (i)

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: Kynurenine 3-monooxygenase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	69.13Å 52.39 Å 137.59 Å	Depositor
a, b, c, α , β , γ	90.00° 104.74° 90.00°	Depositor
Resolution (Å)	66.53 - 1.76	Depositor
Resolution (A)	66.53 - 1.76	EDS
% Data completeness	$97.6\ (66.53-1.76)$	Depositor
(in resolution range)	$98.0\ (66.53 ext{-}1.76)$	EDS
R _{merge}	0.06	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.24 ~({\rm at}~1.76{\rm \AA})$	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
D D .	0.177 , 0.206	Depositor
R, R_{free}	0.181 , 0.207	DCC
R_{free} test set	3657 reflections $(3.95%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	24.0	Xtriage
Anisotropy	0.348	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34 , 50.4	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.017 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7985	wwPDB-VP
Average B, all atoms $(Å^2)$	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 29.07 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6510e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 8R8, 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	Mol Chain		lengths	Bond	angles
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.49	0/3552	0.61	0/4825
1	В	0.53	0/3580	0.61	0/4864
All	All	0.51	0/7132	0.61	0/9689

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	А	3474	0	3432	17	0
1	В	3498	0	3465	15	0
2	А	53	0	31	1	0
2	В	53	0	31	0	0
3	А	25	0	0	0	0
3	В	25	0	0	0	0
4	А	386	0	0	2	0
4	В	471	0	0	3	0
All	All	7985	0	6959	32	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 2.



Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:184:GLU:HG2	1:B:297:LEU:HD22	1.67	0.76
1:A:427:LEU:HD11	1:A:449:GLU:HB3	1.67	0.76
1:A:84:ARG:O	1:A:95:LEU:O	2.10	0.69
1:A:184:GLU:HG2	1:A:295:LEU:HD11	1.75	0.69
1:B:86:VAL:HG12	1:B:88:VAL:HG23	1.79	0.64
1:A:53:ILE:HG23	2:A:501:FAD:HM72	1.83	0.61
1:A:295:LEU:HB3	1:A:315:PRO:HD2	1.86	0.57
1:B:295:LEU:HB3	1:B:315:PRO:HD2	1.89	0.55
1:A:184:GLU:HG3	1:A:297:LEU:CD2	2.41	0.51
1:B:452:ARG:HD3	4:B:981:HOH:O	2.10	0.51
1:A:81:MET:HB2	1:A:106:ILE:HG13	1.96	0.48
1:B:332:VAL:HG21	4:B:606:HOH:O	2.14	0.48
1:B:401:ILE:HD12	1:B:457:LEU:HD12	1.96	0.47
1:B:83:GLY:HA2	1:B:98:TYR:CD2	2.49	0.47
1:B:402:PRO:HG3	4:B:862:HOH:O	2.13	0.47
1:A:184:GLU:CG	1:A:295:LEU:HD11	2.43	0.47
1:A:85:MET:SD	1:A:93:PRO:HB2	2.55	0.47
1:A:78:ALA:HB1	1:A:107:TRP:HB3	1.95	0.46
1:B:400:PHE:HZ	1:B:428:LEU:HD11	1.81	0.45
1:A:371:VAL:HG13	4:A:621:HOH:O	2.16	0.44
1:B:78:ALA:HB1	1:B:107:TRP:HB3	1.99	0.44
1:A:84:ARG:HG3	1:A:215:ILE:HD12	1.99	0.44
1:A:401:ILE:HD12	1:A:457:LEU:HD12	2.00	0.43
1:A:197:GLN:HG2	4:A:857:HOH:O	2.19	0.43
1:B:52:SER:HB3	1:B:110:ASN:HD21	1.83	0.42
1:B:319:PHE:HB2	1:B:366:ALA:O	2.20	0.42
1:B:145:LEU:HD11	1:B:157:LYS:HB2	2.02	0.41
1:A:210:PRO:O	1:A:227:PRO:HG3	2.20	0.41
1:B:162:LEU:O	1:B:306:ALA:HA	2.21	0.41
1:A:144:ARG:NH2	1:A:156:GLU:HB3	2.35	0.41
1:B:320:HIS:HB2	1:B:366:ALA:HA	2.02	0.40
1:A:270:PHE:HB3	1:A:273:LEU:HB3	2.03	0.40

All (32) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	Percen	tiles
1	А	445/461~(96%)	438~(98%)	7(2%)	0	100	100
1	В	451/461 (98%)	443 (98%)	8 (2%)	0	100	100
All	All	896/922~(97%)	881 (98%)	15~(2%)	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	А	362/372~(97%)	350~(97%)	12 (3%)	38 15
1	В	365/372~(98%)	359~(98%)	6~(2%)	62 45
All	All	727/744~(98%)	709~(98%)	18 (2%)	47 25

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	49	ARG
1	А	52	SER
1	А	72	ARG
1	А	77	GLU
1	А	91	THR
1	А	112	ASP
1	А	147	LEU
1	А	158	ARG

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Mol	Chain	Res	Type
1	А	379	SER
1	А	383	LEU
1	А	437	ASP
1	А	438	LEU
1	В	49	ARG
1	В	51	ARG
1	В	72	ARG
1	В	91	THR
1	В	158	ARG
1	В	272	ASP

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Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	54	ASN
1	В	269	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

4 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	Tune	Chain	Res	Link	Bo	ond leng	\mathbf{ths}	В	ond ang	les
	Type	Cham	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	8R8	А	502	-	$18,\!27,\!27$	0.85	1 (5%)	$20,\!38,\!38$	0.54	0
3	8R8	В	502	-	18,27,27	0.79	0	$20,\!38,\!38$	0.80	1(5%)
2	FAD	А	501	-	51, 58, 58	1.41	5 (9%)	$60,\!89,\!89$	2.12	<mark>6 (10%)</mark>
2	FAD	В	501	-	51, 58, 58	1.40	5 (9%)	60,89,89	2.16	6(10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	8R8	А	502	-	-	4/11/13/13	0/3/3/3
3	8R8	В	502	-	-	5/11/13/13	0/3/3/3
2	FAD	А	501	-	-	1/30/50/50	0/6/6/6
2	FAD	В	501	-	-	1/30/50/50	0/6/6/6

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(Å)
2	А	501	FAD	C4X-C10	7.26	1.46	1.38
2	В	501	FAD	C4X-C10	6.81	1.45	1.38
2	А	501	FAD	C4-N3	3.58	1.39	1.33
2	В	501	FAD	C4-N3	3.31	1.38	1.33
2	В	501	FAD	C4-C4X	3.25	1.47	1.41
2	В	501	FAD	C9A-N10	3.23	1.42	1.38
2	А	501	FAD	C9A-N10	2.74	1.42	1.38
2	А	501	FAD	C4-C4X	2.43	1.45	1.41
2	А	501	FAD	C5X-N5	2.28	1.39	1.35
2	В	501	FAD	C5X-N5	2.22	1.39	1.35
3	А	502	8R8	C3-C2	2.11	1.40	1.36

All (11) bond length outliers are listed below:

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\mathbf{Ideal}(^{o})$
2	В	501	FAD	C4-N3-C2	12.47	125.67	115.14
2	А	501	FAD	C4-N3-C2	12.31	125.54	115.14
2	А	501	FAD	C4X-C4-N3	-6.70	114.27	123.43
2	В	501	FAD	C4X-C4-N3	-6.49	114.55	123.43
2	В	501	FAD	C10-C4X-N5	4.54	124.40	121.26
2	А	501	FAD	C10-C4X-N5	4.07	124.07	121.26
2	В	501	FAD	C4-C4X-C10	-4.03	117.28	119.95

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Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	501	FAD	C4-C4X-C10	-3.68	117.52	119.95
2	В	501	FAD	C4X-C10-N10	-3.67	116.53	120.30
2	А	501	FAD	C4X-C10-N10	-3.47	116.74	120.30
2	В	501	FAD	C5A-C6A-N6A	2.17	123.65	120.35
2	А	501	FAD	C5A-C6A-N6A	2.14	123.61	120.35
3	В	502	8R8	C2-C3-C4	-2.01	117.69	120.06

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There are no chirality outliers.

Mol	Chain	Res	Type	Atoms
3	А	502	8R8	C-C1-O-C2
3	А	502	8R8	C12-C1-O-C2
3	В	502	8R8	O-C1-C12-N1
3	А	502	8R8	C-C1-C12-C13
3	В	502	8R8	O-C1-C12-C13
3	В	502	8R8	C-C1-C12-C13
3	В	502	8R8	C-C1-O-C2
3	В	502	8R8	C12-C1-O-C2
3	А	502	8R8	O-C1-C12-C13
2	А	501	FAD	O4B-C4B-C5B-O5B
2	В	501	FAD	O4B-C4B-C5B-O5B

All (11) torsion outliers are listed below:

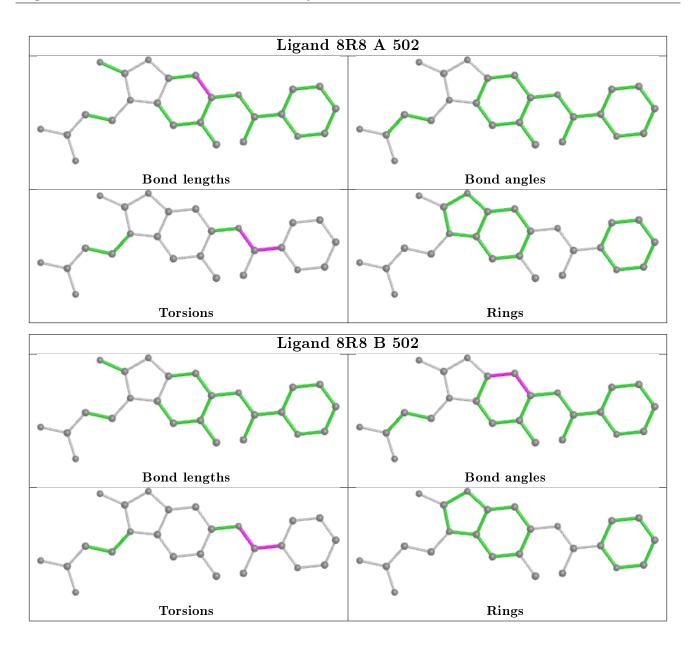
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	501	FAD	1	0

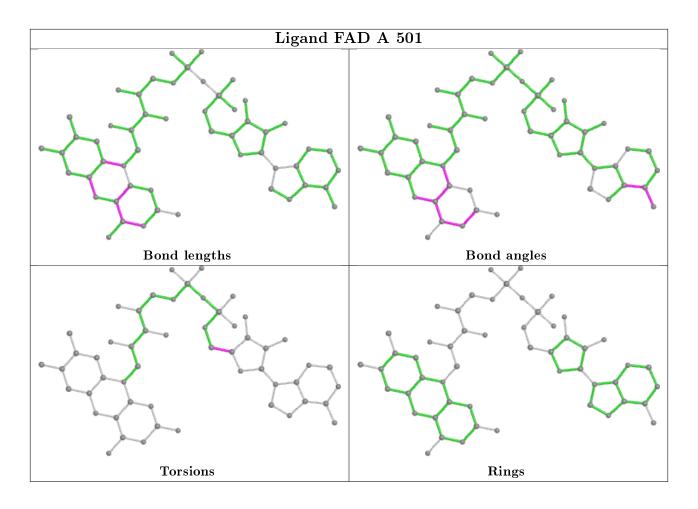
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.



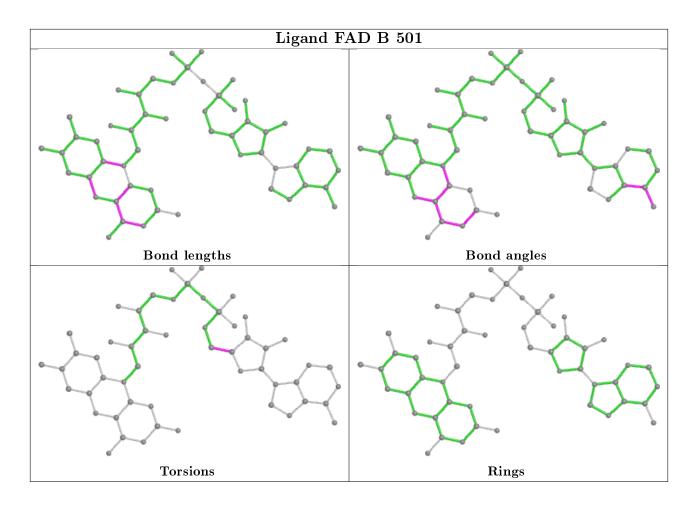












5.7 Other polymers (i)

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^{th} 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	А	448/461~(97%)	0.02	19 (4%) 36 42	24, 39, 65, 93	0
1	В	$451/461 \ (97\%)$	-0.32	8 (1%) 68 76	15, 26, 49, 89	0
All	All	899/922~(97%)	-0.15	27 (3%) 50 56	15, 33, 60, 93	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	50	GLY	6.8
1	В	246	ALA	5.7
1	А	246	ALA	5.3
1	В	50	GLY	4.8
1	В	245	ALA	4.2
1	А	379	SER	4.2
1	А	90	GLY	4.0
1	А	245	ALA	3.8
1	А	380	PRO	3.8
1	А	382	TYR	3.6
1	В	150	VAL	3.6
1	А	49	ARG	3.5
1	А	91	THR	3.4
1	А	95	LEU	3.3
1	В	244	PRO	3.3
1	В	247	GLN	3.3
1	А	92	PRO	3.0
1	А	51	ARG	2.8
1	А	437	ASP	2.6
1	В	49	ARG	2.5
1	В	51	ARG	2.5
1	А	438	LEU	2.3
1	А	150	VAL	2.3
1	А	383	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	А	247	GLN	2.1
1	А	394	GLN	2.1
1	А	155	LEU	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.

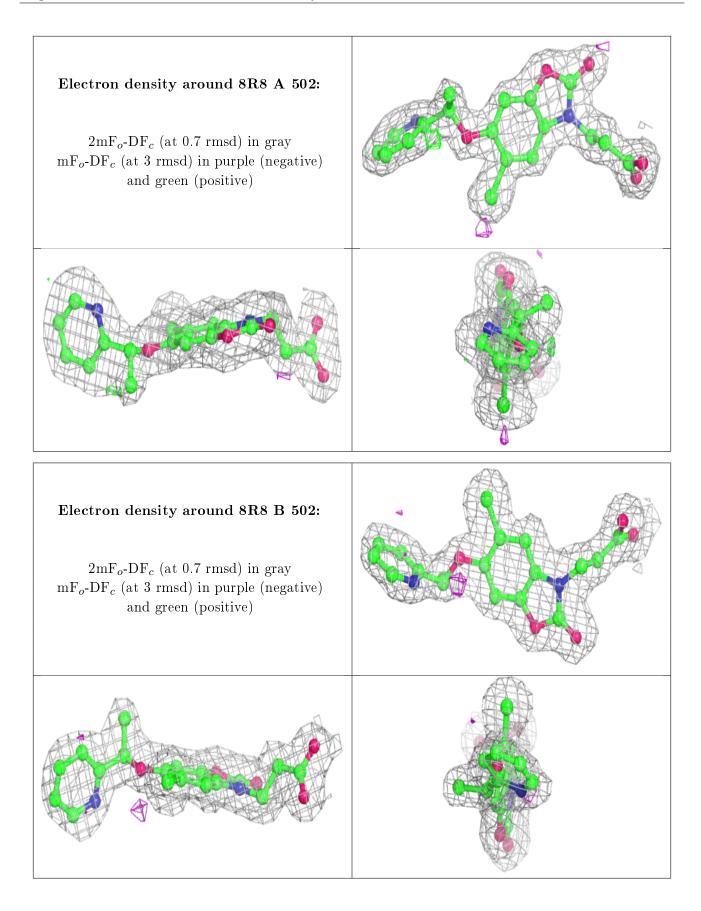
6.4 Ligands (i)

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^{th} 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.

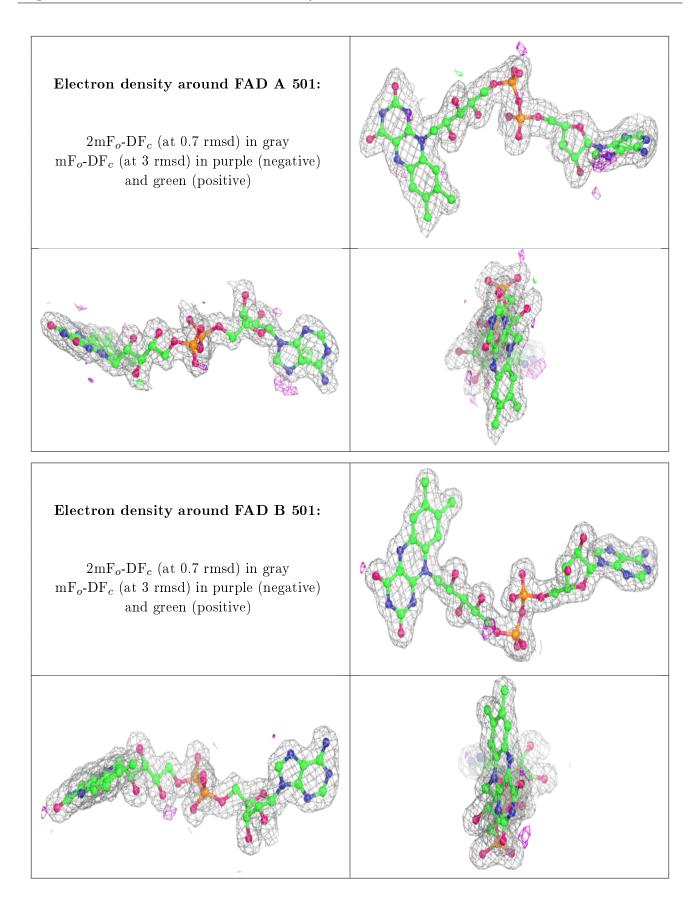
Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B} ext{-factors}({ m \AA}^2)$	$Q{<}0.9$
3	8R8	А	502	25/25	0.96	0.07	$28,\!31,\!34,\!36$	0
3	8R8	В	502	25/25	0.97	0.07	21,24,32,34	0
2	FAD	А	501	53/53	0.98	0.08	$25,\!29,\!33,\!34$	0
2	FAD	В	501	53/53	0.99	0.07	15,18,22,25	0

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.

