

Full wwPDB X-ray Structure Validation Report (i)

Feb 12, 2024 – 12:56 pm GMT

PDB ID : 8CFN

Title : Crystal structure of S-adenosyl-L-homocysteine hydrolase from P. aeruginosa

in complex with F2X-Entry library fragment F03

Authors: Malecki, P.H.; Gawel, M.; Stepniewska, M.; Brzezinski, K.

Deposited on : 2023-02-03

Resolution : 1.34 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.36

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

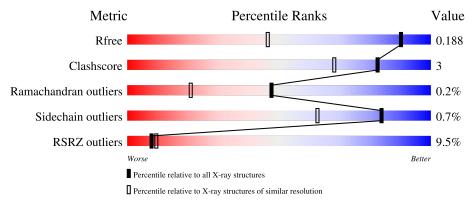
Validation Pipeline (wwPDB-VP) : 2.36

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 1.34 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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	1385 (1.36-1.32)
Clashscore	141614	1417 (1.36-1.32)
Ramachandran outliers	138981	1397 (1.36-1.32)
Sidechain outliers	138945	1397 (1.36-1.32)
RSRZ outliers	127900	1369 (1.36-1.32)

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 <=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				
			14%				
1	A	472	93%	5% •			
	~	450	5%				
1	C	472	92%	6% •			

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
4	PO4	С	512	_	-	-	X



2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 8446 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.

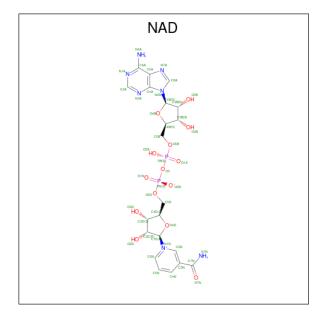
• Molecule 1 is a protein called Adenosylhomocysteinase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	462	Total 3618	C 2281	N 628	O 686	S 23	0	9	0
1	С	462	Total 3671	C 2322	N 631	O 693	S 25	0	19	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q9I685
A	-1	ASN	-	expression tag	UNP Q9I685
A	0	ALA	-	expression tag	UNP Q9I685
С	-2	SER	-	expression tag	UNP Q9I685
С	-1	ASN	-	expression tag	UNP Q9I685
С	0	ALA	-	expression tag	UNP Q9I685

• Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



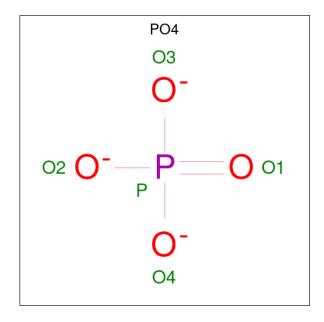


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf						
9	Λ	1	Total	С	N	О	Р	0	0					
	2 A	1	44	21	7	14	2	U						
2	C	C	C	C	C	С	1	Total	С	N	О	Р	0	0
		1	44	21	7	14	2	U						

• Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total K 1 1	0	0
3	С	1	Total K 1 1	0	0

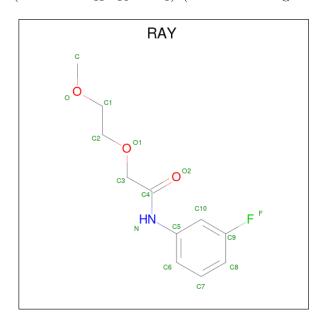
 \bullet Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O P	0	0
4	Λ	1	5 4 1	0	U
4	A	1	Total O P	0	0
4	Λ	1	5 4 1		U
4	A	1	Total O P	0	0
4	11	1	5 4 1	0	
4	\mathbf{C}	1	Total O P	0	0
4		1	5 4 1	O	U
4	\mathbf{C}	1	Total O P	0	0
4		1	5 4 1	0	0
4	\mathbf{C}	1	Total O P	0	0
T		1	5 4 1		

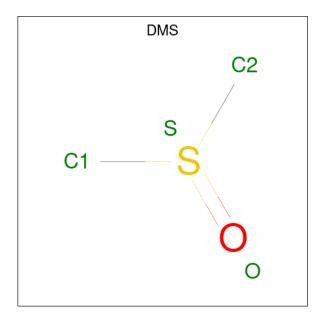


• Molecule 5 is N-(3-fluorophenyl)-2-(2-methoxyethoxy) acetamide (three-letter code: RAY) (formula: $C_{11}H_{14}FNO_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf					
5	5 A	Λ	1	Total	С	F	N	О	0	0				
)		1	16	11	1	1	3	0						
5	C	C	С	С	С	C	1	Total	С	F	N	О	0	0
9	C	1	16	11	1	1	3	0						

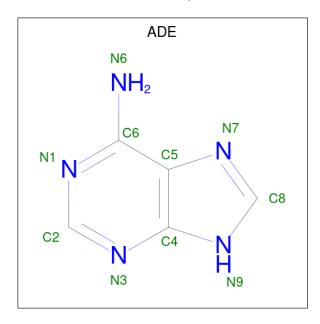
• Molecule 6 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O S 4 2 1 1	0	0
6	С	1	Total C O S 4 2 1 1	0	0
6	С	1	Total C O S 4 2 1 1	0	0
6	С	1	Total C O S 4 2 1 1	0	0

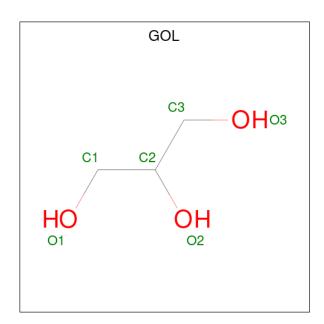
 \bullet Molecule 7 is ADENINE (three-letter code: ADE) (formula: $\mathrm{C}_5\mathrm{H}_5\mathrm{N}_5).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C N 10 5 5	0	0
7	С	1	Total C N 10 5 5	0	0

 \bullet Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $\mathrm{C_3H_8O_3}).$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	С	1	Total C O 6 3 3	0	0
8	С	1	Total C O 6 3 3	0	0

• Molecule 9 is water.

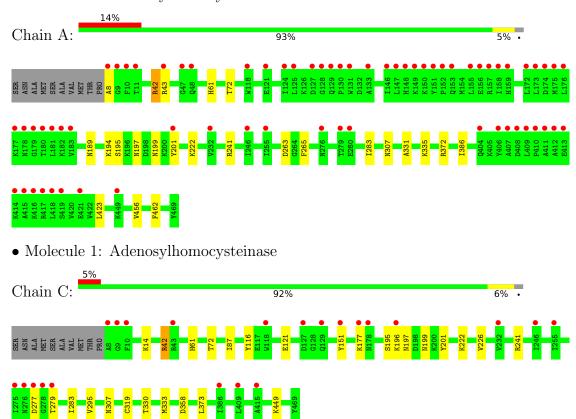
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	417	Total O 427 427	0	10
9	С	519	Total O 530 530	0	12



3 Residue-property plots (i)

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: Adenosylhomocysteinase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	142.55Å 85.31Å 111.41Å	Donogitor
a, b, c, α , β , γ	90.00° 122.52° 90.00°	Depositor
Resolution (Å)	39.46 - 1.34	Depositor
Resolution (A)	42.65 - 1.34	EDS
% Data completeness	99.2 (39.46-1.34)	Depositor
(in resolution range)	99.3 (42.65-1.34)	EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	0.98 (at 1.34Å)	Xtriage
Refinement program	PHENIX 1.19.2-4158	Depositor
D D.	0.158 , 0.188	Depositor
R, R_{free}	0.158 , 0.188	DCC
R_{free} test set	2638 reflections (1.05%)	wwPDB-VP
Wilson B-factor (Å ²)	17.8	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 54.6	EDS
L-test for twinning ²	$ < L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	8446	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.51% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ 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: K, RAY, PO4, NAD, ADE, DMS, GOL

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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.40	0/3699	0.61	0/4997	
1	С	0.42	0/3779	0.62	0/5102	
All	All	0.41	0/7478	0.62	0/10099	

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	A	3618	0	3641	17	0
1	С	3671	0	3728	18	0
2	A	44	0	26	0	0
2	С	44	0	26	2	0
3	A	1	0	0	0	0
3	С	1	0	0	0	0
4	A	15	0	0	0	0
4	С	15	0	0	1	0
5	A	16	0	0	1	0
5	С	16	0	0	0	0
6	A	4	0	6	2	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	С	12	0	18	1	0
7	A	10	0	4	0	0
7	С	10	0	4	0	0
8	С	12	0	16	2	0
9	A	427	0	0	3	0
9	С	530	0	0	8	0
All	All	8446	0	7469	38	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 3.

All (38) 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:C:373:LEU:HD22	2:C:501:NAD:N7N	2.12	0.65
1:A:241[B]:ARG:HD2	9:A:902:HOH:O	2.03	0.57
1:A:197:ASN:HA	1:A:201:TYR:HD2	1.71	0.56
1:C:241[B]:ARG:HD2	9:C:977:HOH:O	2.04	0.56
1:C:295[B]:VAL:HG12	1:C:319:CYS:SG	2.46	0.55
1:A:456:VAL:HG12	6:A:505:DMS:H23	1.89	0.54
1:C:42:ARG:HG3	1:C:72:THR:HG23	1.90	0.54
6:C:505:DMS:H23	9:C:623:HOH:O	2.09	0.53
1:A:189:ASN:HA	1:A:194:LYS:HD2	1.91	0.53
4:C:511:PO4:P	9:C:602:HOH:O	2.66	0.53
1:A:197:ASN:ND2	1:A:386:ILE:O	2.43	0.52
1:C:330:THR:HA	1:C:333[B]:MET:HE2	1.93	0.51
1:A:423:LEU:HD22	5:A:504:RAY:C7	2.41	0.50
1:C:177:LYS:HG3	9:C:943:HOH:O	2.12	0.49
1:A:195:SER:O	1:A:199:ASN:HB2	2.14	0.47
1:C:222[A]:LYS:HD3	9:C:684:HOH:O	2.14	0.47
1:A:197:ASN:HA	1:A:201:TYR:CD2	2.49	0.47
1:C:196[A]:LYS:NZ	9:C:610:HOH:O	2.48	0.46
1:C:358:ASP:OD1	8:C:509:GOL:O2	2.32	0.46
8:C:509:GOL:H12	9:C:924:HOH:O	2.16	0.46
1:A:241[B]:ARG:HD3	1:A:265:PHE:CE1	2.52	0.45
1:A:197:ASN:O	1:A:201:TYR:HB2	2.17	0.45
1:C:195:SER:O	1:C:199:ASN:HB2	2.18	0.44
1:A:283:ILE:HG13	1:A:307:ASN:HB3	2.00	0.43
1:C:197:ASN:HA	1:C:201:TYR:HD2	1.83	0.43
1:C:283:ILE:HG13	1:C:307:ASN:HB3	2.00	0.43
1:A:462:PHE:C	6:A:505:DMS:H22	2.39	0.42



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Atom-1	Atom-2	$egin{aligned} & & & & & & & & & & & & & & & & & & &$	Clash overlap (Å)
1:C:449:LYS:NZ	9:C:614:HOH:O	2.52	0.42
1:A:222:LYS:HD3	9:A:731:HOH:O	2.19	0.42
1:C:226:VAL:HG22	1:C:295[B]:VAL:CG2	2.19	0.42
1:C:121[A]:GLU:OE1	1:C:151:TYR:OH	2.49	0.42
1:A:241[B]:ARG:NH1	1:A:263:ASP:O	2.45	0.42
1:C:373:LEU:HD22	2:C:501:NAD:H71N	1.81	0.41
1:C:373:LEU:HD22 1:C:277[B]:ASP:HB2	1:C:279:THR:HG23	2.01	0.41
1:A:42:ARG:HG3	1:A:72:THR:HG23		
		2.03	0.41
1:A:8:ALA:N	9:A:609:HOH:O	2.53	0.40
1:A:331:ALA:O	1:A:335:LYS:HG3	2.21	0.40
1:C:87:ILE:HG22	1:C:116:TYR:HB2	2.03	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	Percei	ntiles
1	A	$469/472\ (99\%)$	459 (98%)	9 (2%)	1 (0%)	47	21
1	С	$479/472 \; (102\%)$	468 (98%)	10 (2%)	1 (0%)	47	21
All	All	948/944 (100%)	927 (98%)	19 (2%)	2 (0%)	47	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	61	HIS
1	С	61	HIS



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	386/385 (100%)	382 (99%)	4 (1%)	76	47	
1	С	396/385 (103%)	393 (99%)	3 (1%)	81	57	
All	All	782/770 (102%)	775 (99%)	7 (1%)	84	52	

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	ARG
1	A	43	ARG
1	A	372[A]	ARG
1	A	372[B]	ARG
1	С	14[A]	LYS
1	С	14[B]	LYS
1	С	42	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.



5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 2 are monoatomic - leaving 18 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	Во	ond leng	ths	В	ond ang	cles
WIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	RAY	A	504	-	16,16,16	1.47	3 (18%)	19,19,19	1.22	3 (15%)
2	NAD	С	501	_	42,48,48	0.56	0	50,73,73	0.77	1 (2%)
6	DMS	С	508	_	3,3,3	0.63	0	3,3,3	0.51	0
4	PO4	A	507	-	4,4,4	0.96	0	6,6,6	0.39	0
6	DMS	С	505	-	3,3,3	0.60	0	3,3,3	0.36	0
8	GOL	С	509	-	5,5,5	0.93	0	5,5,5	1.28	1 (20%)
2	NAD	A	501	-	42,48,48	0.54	0	50,73,73	0.79	1 (2%)
5	RAY	С	504	-	16,16,16	1.62	3 (18%)	19,19,19	1.84	6 (31%)
4	PO4	С	503	-	4,4,4	0.68	0	6,6,6	0.56	0
7	ADE	A	506	-	9,11,11	1.03	0	7,15,15	1.11	1 (14%)
7	ADE	С	510	-	9,11,11	0.83	0	7,15,15	1.13	1 (14%)
4	PO4	С	512	-	4,4,4	0.88	0	6,6,6	0.44	0
8	GOL	С	506	_	5,5,5	1.06	0	5,5,5	0.95	0
4	PO4	A	508	_	4,4,4	0.93	0	6,6,6	0.72	0
6	DMS	С	507	-	3,3,3	0.65	0	3,3,3	0.40	0
6	DMS	A	505	-	3,3,3	0.32	0	3,3,3	0.73	0
4	PO4	A	503	-	4,4,4	0.85	0	6,6,6	0.62	0
4	PO4	С	511	-	4,4,4	1.15	0	6,6,6	1.75	3 (50%)

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
5	RAY	A	504	-	-	2/10/10/10	0/1/1/1
2	NAD	С	501	-	-	5/26/62/62	0/5/5/5
8	GOL	С	509	-	-	2/4/4/4	-
5	RAY	С	504	-	-	8/10/10/10	0/1/1/1



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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	A	501	-	-	5/26/62/62	0/5/5/5
7	ADE	A	506	-	-	-	0/2/2/2
8	GOL	С	506	-	-	4/4/4/4	-
7	ADE	С	510	_	-	-	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
5	С	504	RAY	C4-N	5.25	1.47	1.35
5	A	504	RAY	C4-N	4.63	1.45	1.35
5	С	504	RAY	C5-N	2.48	1.46	1.41
5	A	504	RAY	O2-C4	-2.23	1.18	1.23
5	С	504	RAY	O2-C4	-2.07	1.19	1.23
5	A	504	RAY	C5-N	2.07	1.45	1.41

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{\scriptscriptstyle o})$
5	С	504	RAY	C3-C4-N	4.89	125.64	115.61
5	С	504	RAY	O2-C4-N	-3.58	117.09	123.63
5	С	504	RAY	C5-C10-C9	2.93	120.57	117.95
4	С	511	PO4	O2-P-O1	2.70	120.77	110.89
5	С	504	RAY	C8-C9-C10	-2.62	119.88	123.29
5	A	504	RAY	O1-C3-C4	-2.57	106.86	112.38
5	A	504	RAY	C5-C10-C9	2.54	120.22	117.95
4	С	511	PO4	O4-P-O1	-2.32	102.41	110.89
2	С	501	NAD	C5A-C6A-N6A	2.31	123.86	120.35
5	A	504	RAY	C8-C9-C10	-2.29	120.31	123.29
5	С	504	RAY	C5-N-C4	2.20	131.34	127.50
2	A	501	NAD	C5A-C6A-N6A	2.19	123.68	120.35
8	С	509	GOL	C3-C2-C1	-2.16	103.30	111.70
7	С	510	ADE	C5-C6-N6	2.14	123.61	120.35
4	С	511	PO4	O4-P-O3	-2.11	101.19	107.97
5	С	504	RAY	F-C9-C10	2.05	121.19	118.25
7	A	506	ADE	C5-C6-N6	2.00	123.40	120.35

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	NAD	O4D-C1D-N1N-C2N



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Mol	Chain	Res	Type	Atoms
2	A	501	NAD	O4D-C1D-N1N-C6N
2	A	501	NAD	C2D-C1D-N1N-C2N
2	A	501	NAD	C2D-C1D-N1N-C6N
2	С	501	NAD	O4D-C1D-N1N-C2N
2	С	501	NAD	O4D-C1D-N1N-C6N
2	С	501	NAD	C2D-C1D-N1N-C2N
2	С	501	NAD	C2D-C1D-N1N-C6N
5	С	504	RAY	C3-C4-N-C5
8	С	506	GOL	O1-C1-C2-O2
8	С	509	GOL	C1-C2-C3-O3
5	С	504	RAY	O2-C4-N-C5
5	С	504	RAY	C2-C1-O-C
8	С	506	GOL	O1-C1-C2-C3
8	С	506	GOL	C1-C2-C3-O3
5	С	504	RAY	O-C1-C2-O1
8	С	509	GOL	O2-C2-C3-O3
5	A	504	RAY	O-C1-C2-O1
8	С	506	GOL	O2-C2-C3-O3
5	С	504	RAY	O1-C3-C4-N
5	С	504	RAY	O1-C3-C4-O2
5	С	504	RAY	C1-C2-O1-C3
5	A	504	RAY	C4-C3-O1-C2
5	С	504	RAY	C4-C3-O1-C2
2	A	501	NAD	O4B-C4B-C5B-O5B
2	С	501	NAD	O4B-C4B-C5B-O5B

There are no ring outliers.

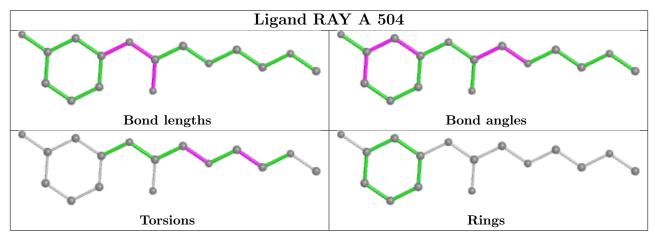
6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	504	RAY	1	0
2	С	501	NAD	2	0
6	С	505	DMS	1	0
8	С	509	GOL	2	0
6	A	505	DMS	2	0
4	С	511	PO4	1	0

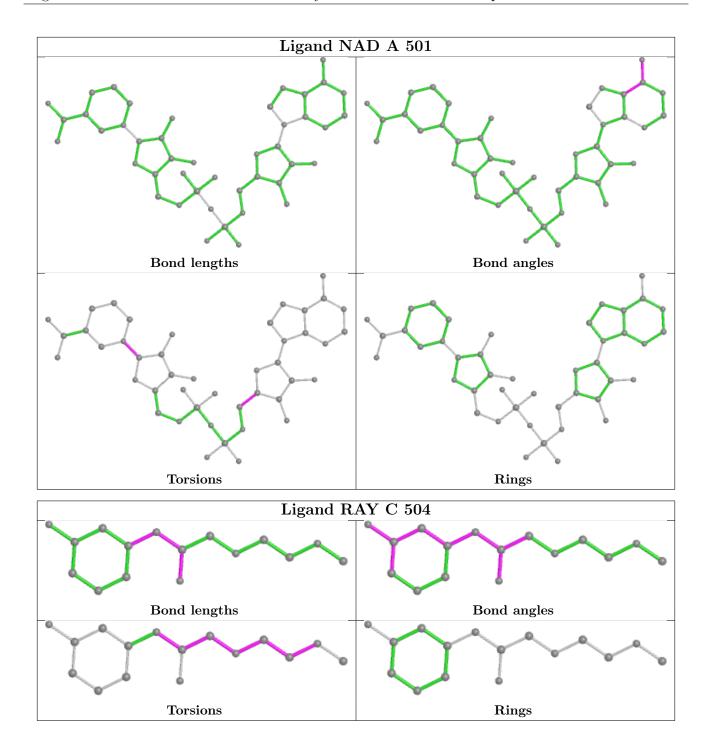
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	$OWAB(A^2)$	Q < 0.9
1	A	462/472 (97%)	0.90	66 (14%) 2 3	15, 23, 49, 80	1 (0%)
1	C	$462/472 \ (97\%)$	0.40	22 (4%) 30 36	14, 20, 35, 66	0
All	All	924/944 (97%)	0.65	88 (9%) 8 9	14, 21, 44, 80	1 (0%)

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	412	ALA	14.2
1	A	415	ALA	10.6
1	A	416	LYS	9.3
1	A	410	PRO	9.1
1	A	411	ALA	8.4
1	A	409	LEU	8.0
1	A	406	TYR	7.4
1	A	8	ALA	7.2
1	A	9	GLY	6.8
1	A	413	GLU	6.8
1	A	157	ARG	6.5
1	С	8	ALA	6.4
1	A	177	LYS	6.3
1	A	178	ASN	6.0
1	A	181	LEU	5.9
1	A	176	LEU	5.7
1	A	153	GLN	5.5
1	A	179	GLY	5.4
1	A	418	LEU	5.4
1	A	151	TYR	5.3
1	С	415	ALA	5.1
1	A	130	PRO	5.0
1	A	10	PHE	4.7
1	A	183	VAL	4.7



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Mol	Chain	Res	Type	RSRZ			
1	С	9	GLY	4.5			
1	A	414	LYS	4.5			
1	A	180	THR	4.5			
1	A	417	ARG	4.4			
1	A	407	ALA	4.2			
1	A	129	GLN	4.2			
1	A	152	PRO	4.1			
1	A	118	TRP	4.1			
1	A	146	ILE	3.9			
1	A	11	THR	3.9			
1	A	182	LYS	3.9			
1	A	43	ARG	3.9			
1	A	155	LEU	3.9			
1	С	278	GLY	3.8			
1	A	127	ASP	3.8			
1	A	158	ILE	3.8			
1	A	147	LEU	3.5			
1	С	277[A]	ASP	3.2			
1	A	279	THR	3.1			
1	A	128	GLY	3.0			
1	A	408	ASP	3.0			
1	С	279	THR	3.0			
1	A	131	TRP	2.9			
1	A	404	GLN	2.9			
1	С	127	ASP	2.9			
1	С	276[A]	ASN	2.8			
1	A	150	LYS	2.7			
1	A	156	GLU	2.7			
1	С	178	ASN	2.7			
1	A	174	ASP	2.5			
1	С	43	ARG	2.5			
1	С	177	LYS	2.5			
1	A C	419	SER	2.5			
1		196[A]	LYS	2.5			
1	A	149	LYS	2.4			
1	С	275[A]	ILE	2.4			
1	A	421	GLU	2.4			
1	A C	10	PHE	2.4			
1	С	129	GLN	2.4			
1	A	173	LEU	2.3			
1	A	255	ILE	2.3			
1	A	133	ALA	2.3			



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Mol	Chain	Res	Type	RSRZ
1	A	246	ILE	2.2
1	С	386	ILE	2.2
1	A	232	VAL	2.2
1	A	159	HIS	2.2
1	A	201	TYR	2.2
1	A	172	LEU	2.2
1	A	175	MET	2.2
1	A	449	LYS	2.2
1	A	121	GLU	2.1
1	С	255	ILE	2.1
1	A	47	GLY	2.1
1	A	125	LEU	2.1
1	С	118	TRP	2.1
1	С	151	TYR	2.1
1	С	409	LEU	2.1
1	С	232	VAL	2.1
1	A	124	ILE	2.1
1	A	280	GLU	2.0
1	A	48	GLN	2.0
1	A	148	HIS	2.0
1	С	246	ILE	2.0
1	A	276	ASN	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 monosaccharides 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
5	RAY	С	504	16/16	0.62	0.26	65,78,87,95	0

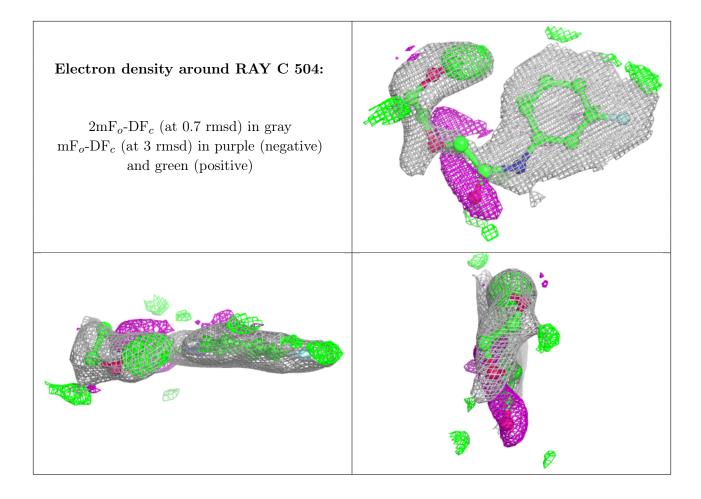


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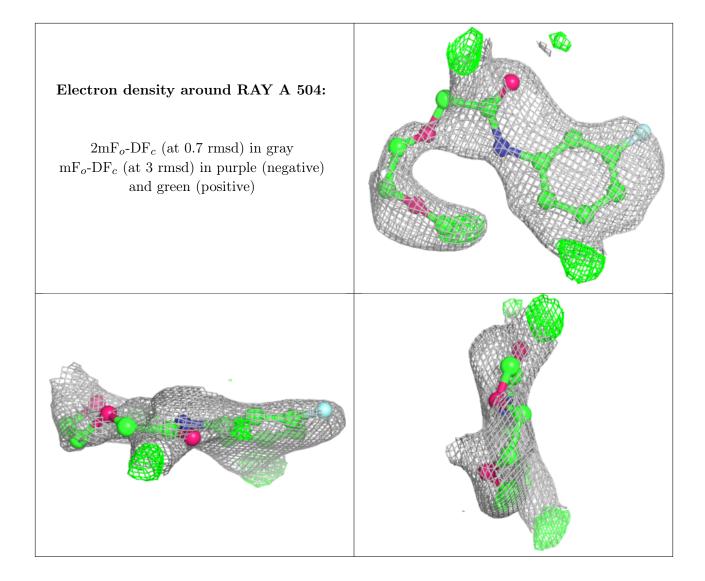
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
5	RAY	A	504	16/16	0.72	0.23	64,72,77,78	0
4	PO4	С	512	5/5	0.73	0.42	82,83,83,84	5
6	DMS	С	508	4/4	0.75	0.22	85,86,86,87	0
8	GOL	С	506	6/6	0.80	0.20	60,61,62,63	0
6	DMS	A	505	4/4	0.82	0.50	20,20,20,20	0
4	PO4	С	511	5/5	0.83	0.16	29,31,33,34	0
4	PO4	A	508	5/5	0.84	0.17	40,41,43,46	0
8	GOL	С	509	6/6	0.88	0.11	52,54,54,54	0
6	DMS	С	507	4/4	0.90	0.13	67,67,69,69	0
4	PO4	A	507	5/5	0.94	0.20	52,52,53,56	5
2	NAD	A	501	44/44	0.96	0.08	15,17,19,22	0
7	ADE	A	506	10/10	0.97	0.08	16,16,18,18	0
2	NAD	С	501	44/44	0.97	0.07	15,17,18,20	0
6	DMS	С	505	4/4	0.97	0.12	42,42,43,44	0
4	PO4	С	503	5/5	0.98	0.06	22,23,24,25	0
7	ADE	С	510	10/10	0.98	0.09	14,15,16,16	0
4	PO4	A	503	5/5	0.99	0.05	22,23,25,25	0
3	K	A	502	1/1	1.00	0.06	18,18,18,18	0
3	K	С	502	1/1	1.00	0.06	16,16,16,16	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.





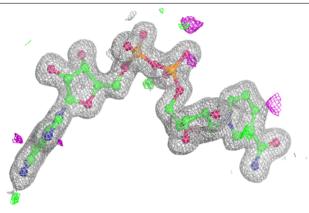


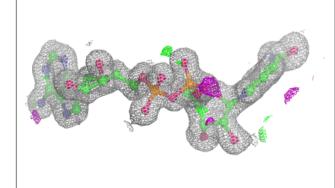


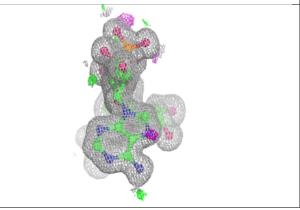


Electron density around NAD A 501:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

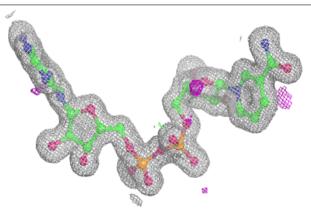


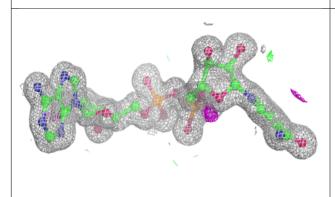


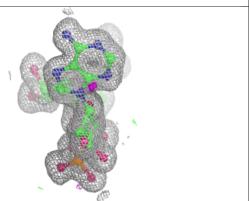


Electron density around NAD C 501:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)









6.5 Other polymers (i)

There are no such residues in this entry.

