



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 05:29 AM BST

PDB ID : 5G3S
Title : The structure of the L-tryptophan oxidase VioA from *Chromobacterium violaceum* - Samarium derivative
Authors : Krausze, J.; Rabe, J.; Moser, J.
Deposited on : 2016-05-01
Resolution : 2.08 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

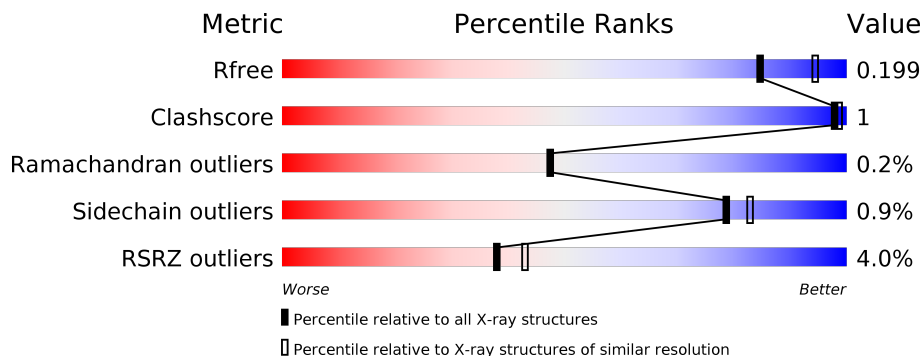
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.08 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6189 (2.10-2.06)
Clashscore	141614	6738 (2.10-2.06)
Ramachandran outliers	138981	6663 (2.10-2.06)
Sidechain outliers	138945	6664 (2.10-2.06)
RSRZ outliers	127900	6057 (2.10-2.06)

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 $\leq 5\%$. 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	423	 4% 95%
1	B	423	 4% 94%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 13097 atoms, of which 6189 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 L-TRYPTOPHAN OXIDASE VIOA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	412	6237	2030	3045	555	586	21	0	4	0
1	B	407	6220	2020	3055	550	576	19	0	4	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q9S3V1
A	-3	PRO	-	expression tag	UNP Q9S3V1
A	-2	LEU	-	expression tag	UNP Q9S3V1
A	-1	GLY	-	expression tag	UNP Q9S3V1
A	0	SER	-	expression tag	UNP Q9S3V1
A	3	GLN	HIS	engineered mutation	UNP Q9S3V1
B	-4	GLY	-	expression tag	UNP Q9S3V1
B	-3	PRO	-	expression tag	UNP Q9S3V1
B	-2	LEU	-	expression tag	UNP Q9S3V1
B	-1	GLY	-	expression tag	UNP Q9S3V1
B	0	SER	-	expression tag	UNP Q9S3V1
B	3	GLN	HIS	engineered mutation	UNP Q9S3V1

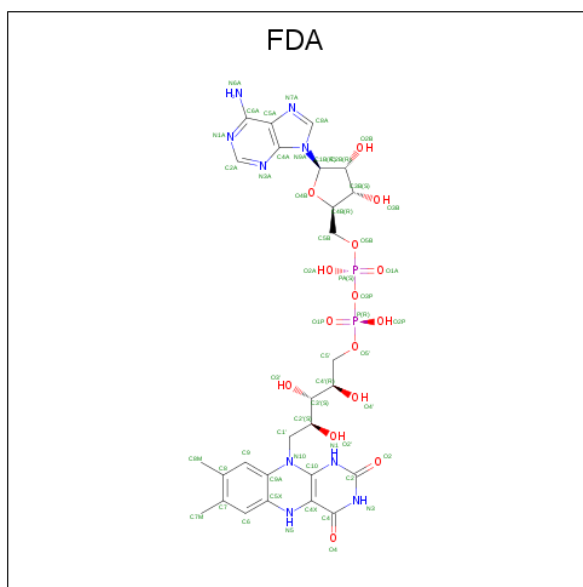
- Molecule 2 is SAMARIUM (III) ION (three-letter code: SM) (formula: Sm).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	4	Total	Sm	0	0
			4	4		
2	A	7	Total	Sm	0	0
			7	7		

- Molecule 3 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

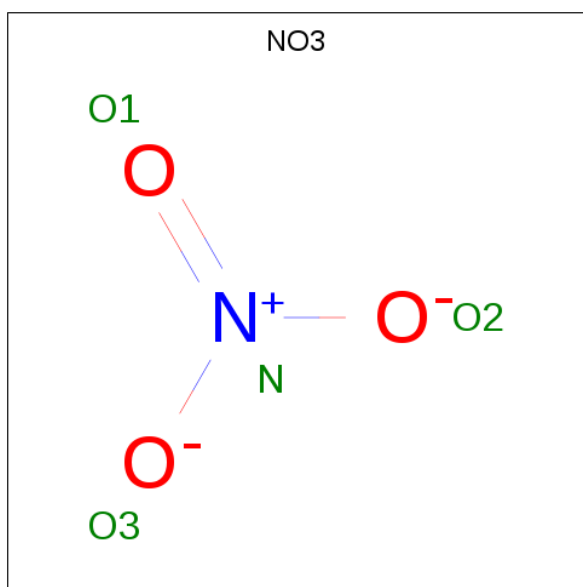
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	6	Total Hg 6 6	0	0
3	A	6	Total Hg 6 6	0	0

- Molecule 4 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (three-letter code: FDA) (formula: $C_{27}H_{35}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C H N O P 85 27 32 9 15 2	0	0
4	B	1	Total C H N O P 86 27 33 9 15 2	0	0

- Molecule 5 is NITRATE ION (three-letter code: NO3) (formula: NO_3).

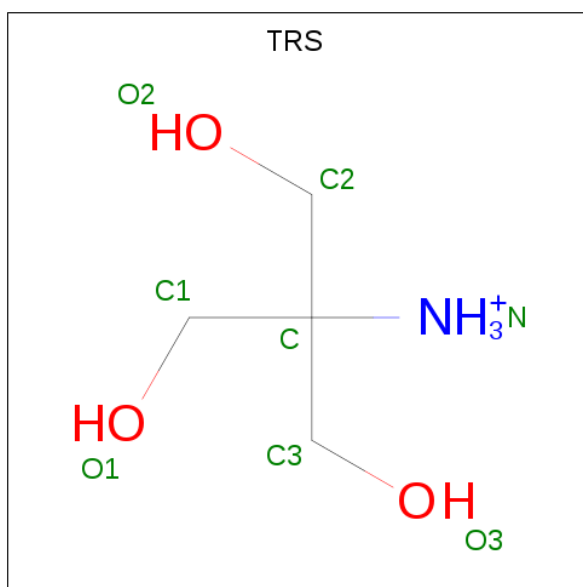


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total N O 4 1 3	0	0
5	A	1	Total N O 4 1 3	0	0
5	A	1	Total N O 4 1 3	0	0
5	B	1	Total N O 4 1 3	0	0
5	B	1	Total N O 4 1 3	0	0

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 7 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
7	A	1	20	4	12	1	3	0	0
7	B	1	20	4	12	1	3	0	0

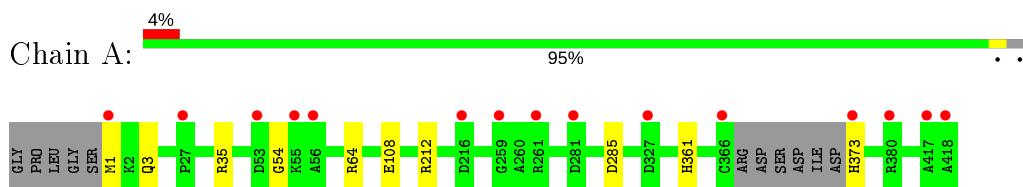
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	A	188	188	188	0	0
8	B	195	195	195	0	0

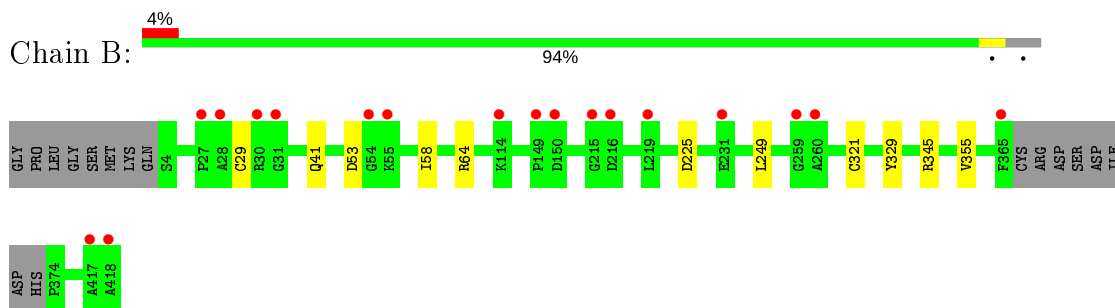
3 Residue-property plots [i](#)

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: L-TRYPTOPHAN OXIDASE VIOA



- Molecule 1: L-TRYPTOPHAN OXIDASE VIOA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.88Å 87.07Å 78.02Å 90.00° 112.95° 90.00°	Depositor
Resolution (Å)	19.98 – 2.08 19.98 – 2.08	Depositor EDS
% Data completeness (in resolution range)	98.4 (19.98-2.08) 97.7 (19.98-2.08)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.07Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.165 , 0.188 0.184 , 0.199	Depositor DCC
R_{free} test set	2482 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	23.2	Xtrriage
Anisotropy	0.644	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.021 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13097	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.98 % 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 6.2647e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FDA, CL, SM, TRS, HG, CSS, NO3

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	0.25	0/3277	0.43	0/4434
1	B	0.25	0/3249	0.42	0/4391
All	All	0.25	0/6526	0.43	0/8825

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	3192	3045	3029	4	0
1	B	3165	3055	3040	5	0
2	A	7	0	0	0	0
2	B	4	0	0	0	0
3	A	6	0	0	0	0
3	B	6	0	0	1	0
4	A	53	32	33	0	0
4	B	53	33	33	0	0
5	A	12	0	0	0	0
5	B	8	0	0	0	0
6	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	1	0	0	0	0
7	A	8	12	10	0	0
7	B	8	12	11	0	0
8	A	188	0	0	2	0
8	B	195	0	0	1	0
All	All	6908	6189	6156	9	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 1.

All (9) 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:29:CYS:SG	3:B:427:HG:HG	2.02	0.77
1:A:3:GLN:OE1	1:A:35:ARG:NH1	2.35	0.57
1:A:108:GLU:OE1	8:A:2075:HOH:O	2.20	0.49
1:B:41:GLN:NE2	1:B:225:ASP:OD2	2.40	0.49
1:B:321[A]:CYS:SG	1:B:329:TYR:HA	2.56	0.45
1:B:345:ARG:NH2	8:B:2167:HOH:O	2.48	0.44
1:A:285:ASP:N	1:A:285:ASP:OD1	2.52	0.43
1:A:361:HIS:NE2	8:A:2161:HOH:O	2.34	0.42
1:B:58:ILE:HD11	1:B:355:VAL:HG21	2.03	0.41

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	411/423 (97%)	400 (97%)	10 (2%)	1 (0%)	47	47
1	B	406/423 (96%)	399 (98%)	6 (2%)	1 (0%)	47	47
All	All	817/846 (97%)	799 (98%)	16 (2%)	2 (0%)	47	47

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	GLY
1	B	53	ASP

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	320/343 (93%)	316 (99%)	4 (1%)	69	74
1	B	318/343 (93%)	316 (99%)	2 (1%)	86	89
All	All	638/686 (93%)	632 (99%)	6 (1%)	78	83

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	64	ARG
1	A	212	ARG
1	A	373	HIS
1	B	64	ARG
1	B	249	LEU

Some 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](#)

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSS	A	395	1,3	4,6,7	1.08	0	1,6,8	0.00	0
1	CSS	B	395	1,3	4,6,7	1.11	0	1,6,8	0.03	0

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
1	CSS	A	395	1,3	-	0/1/5/7	-
1	CSS	B	395	1,3	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 35 ligands modelled in this entry, 26 are monoatomic - leaving 9 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
5	NO3	B	431	2	1,3,3	0.63	0	0,3,3	0.00	-
5	NO3	A	433	-	1,3,3	0.64	0	0,3,3	0.00	-
7	TRS	B	433	2	7,7,7	0.35	0	9,9,9	0.48	0
4	FDA	A	432	-	51,58,58	2.17	9 (17%)	60,89,89	2.23	8 (13%)
5	NO3	A	435	2	1,3,3	0.63	0	0,3,3	0.00	-
4	FDA	B	429	-	51,58,58	2.17	9 (17%)	60,89,89	2.28	8 (13%)
7	TRS	A	438	2	7,7,7	0.40	0	9,9,9	0.82	0
5	NO3	A	434	-	1,3,3	0.64	0	0,3,3	0.00	-
5	NO3	B	430	-	1,3,3	0.63	0	0,3,3	0.00	-

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	FDA	A	432	-	-	5/30/50/50	0/6/6/6
4	FDA	B	429	-	-	1/30/50/50	0/6/6/6
7	TRS	A	438	2	-	0/9/9/9	-
7	TRS	B	433	2	-	3/9/9/9	-

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	432	FDA	C10-N1	9.16	1.45	1.33
4	B	429	FDA	C10-N1	9.03	1.44	1.33
4	A	432	FDA	C4X-N5	8.37	1.45	1.33
4	B	429	FDA	C4X-N5	8.21	1.45	1.33
4	B	429	FDA	C4-C4X	4.97	1.49	1.41
4	A	432	FDA	C4-C4X	4.60	1.49	1.41
4	B	429	FDA	C8-C7	3.45	1.49	1.40
4	A	432	FDA	C8-C7	3.43	1.49	1.40
4	A	432	FDA	C9A-C5X	3.34	1.49	1.42
4	B	429	FDA	C9A-C5X	3.32	1.49	1.42
4	B	429	FDA	C2-N1	-2.50	1.33	1.38
4	A	432	FDA	C2-N1	-2.35	1.33	1.38
4	A	432	FDA	C2-N3	-2.33	1.33	1.38
4	B	429	FDA	C2-N3	-2.22	1.33	1.38
4	B	429	FDA	C5A-C4A	2.18	1.46	1.40
4	A	432	FDA	C5A-C4A	2.14	1.46	1.40
4	A	432	FDA	C2A-N3A	2.09	1.35	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	429	FDA	C2A-N3A	2.05	1.35	1.32

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	429	FDA	C4-N3-C2	11.28	124.67	115.14
4	A	432	FDA	C4-N3-C2	11.09	124.50	115.14
4	B	429	FDA	C1'-N10-C9A	8.52	125.00	118.29
4	A	432	FDA	C1'-N10-C9A	8.28	124.81	118.29
4	B	429	FDA	C4X-C4-N3	-4.80	116.86	123.43
4	A	432	FDA	C4X-C4-N3	-4.53	117.23	123.43
4	A	432	FDA	N3A-C2A-N1A	-3.69	122.91	128.68
4	B	429	FDA	N3A-C2A-N1A	-3.64	122.98	128.68
4	A	432	FDA	C1'-N10-C10	-3.14	115.60	118.41
4	B	429	FDA	C1'-N10-C10	-3.12	115.61	118.41
4	B	429	FDA	C4X-N5-C5X	3.06	119.83	116.77
4	A	432	FDA	C4X-N5-C5X	2.70	119.47	116.77
4	A	432	FDA	C4-C4X-C10	-2.64	118.20	119.95
4	A	432	FDA	P-O3P-PA	-2.52	124.18	132.83
4	B	429	FDA	C4-C4X-C10	-2.50	118.30	119.95
4	B	429	FDA	P-O3P-PA	-2.48	124.33	132.83

There are no chirality outliers.

All (9) torsion outliers are listed below:

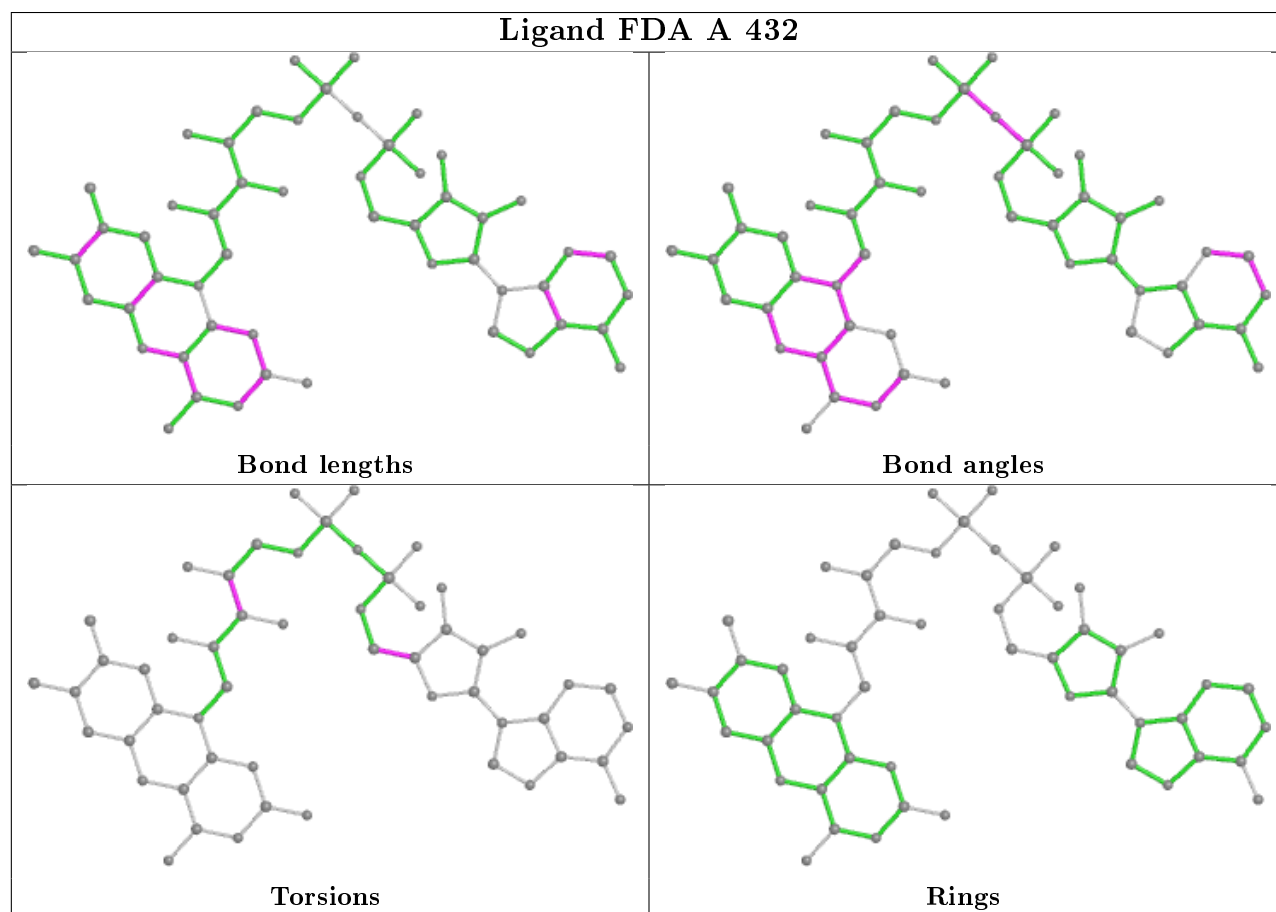
Mol	Chain	Res	Type	Atoms
7	B	433	TRS	C2-C-C3-O3
7	B	433	TRS	N-C-C3-O3
4	A	432	FDA	C2'-C3'-C4'-O4'
7	B	433	TRS	C1-C-C3-O3
4	A	432	FDA	C2'-C3'-C4'-C5'
4	A	432	FDA	O3'-C3'-C4'-C5'
4	A	432	FDA	O3'-C3'-C4'-O4'
4	B	429	FDA	O4B-C4B-C5B-O5B
4	A	432	FDA	O4B-C4B-C5B-O5B

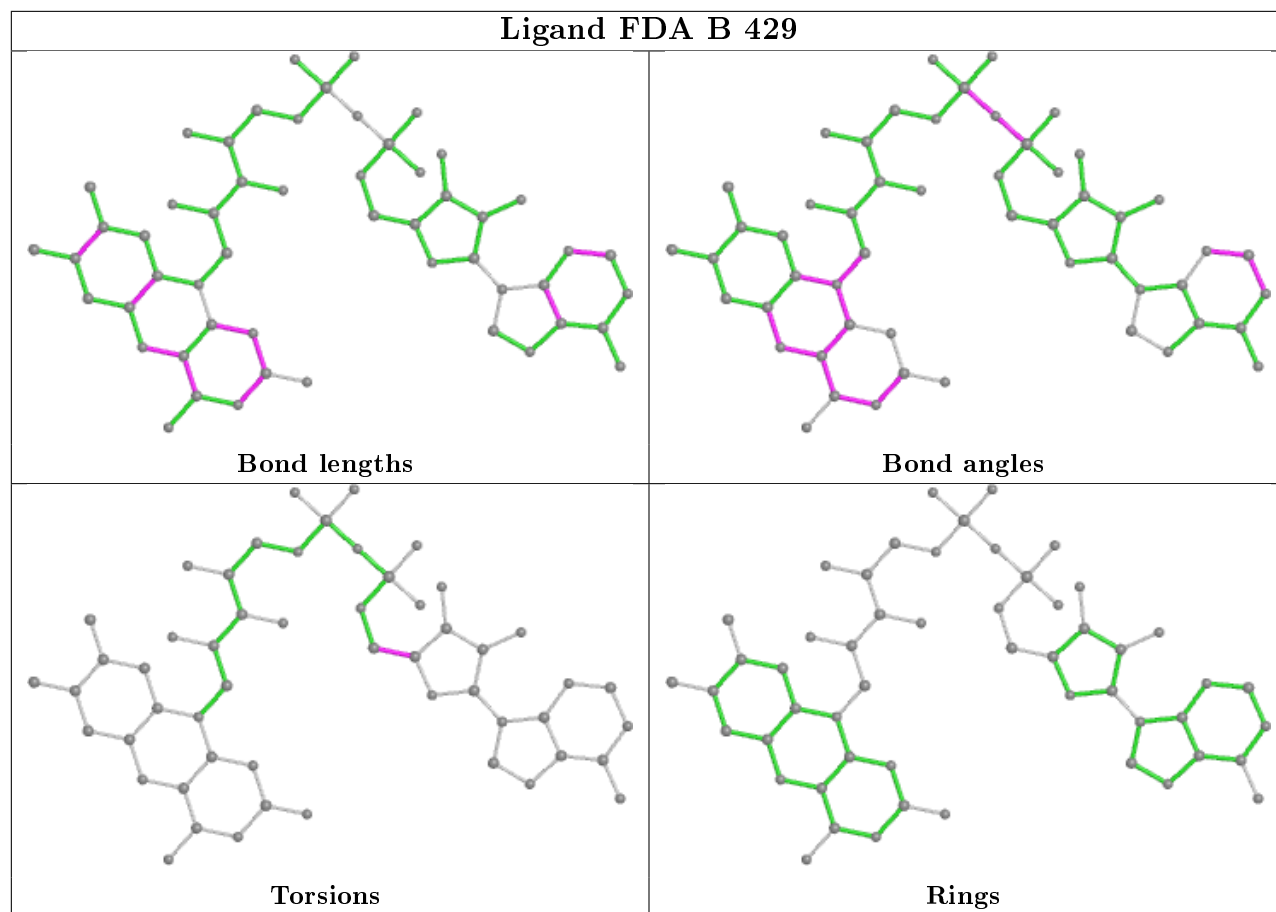
There are no ring outliers.

No monomer is involved in short contacts.

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	411/423 (97%)	0.15	15 (3%) 42 48	15, 26, 53, 89	0
1	B	406/423 (95%)	0.20	18 (4%) 34 39	14, 26, 47, 87	0
All	All	817/846 (96%)	0.17	33 (4%) 38 43	14, 26, 50, 89	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	418	ALA	5.8
1	B	55	LYS	5.4
1	A	327	ASP	4.6
1	A	55	LYS	4.3
1	B	418	ALA	4.2
1	B	27	PRO	4.1
1	B	215	GLY	3.8
1	B	150	ASP	3.7
1	B	259	GLY	3.7
1	B	417	ALA	3.6
1	B	216	ASP	3.6
1	B	30	ARG	3.1
1	A	27	PRO	3.0
1	A	366	CYS	2.9
1	B	260	ALA	2.8
1	A	281	ASP	2.8
1	A	261	ARG	2.6
1	A	417	ALA	2.6
1	B	219	LEU	2.5
1	A	216	ASP	2.5
1	A	380	ARG	2.4
1	A	56	ALA	2.3
1	A	53	ASP	2.3
1	B	114	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	31	GLY	2.2
1	B	365	PHE	2.2
1	B	231	GLU	2.1
1	B	149	PRO	2.1
1	B	28	ALA	2.1
1	A	373	HIS	2.0
1	A	1	MET	2.0
1	A	259	GLY	2.0
1	B	54	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	CSS	B	395	7/8	0.72	0.18	29,36,44,50	0
1	CSS	A	395	7/8	0.79	0.13	32,37,44,51	0

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, 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(Å ²)	Q<0.9
3	HG	A	431	1/1	0.68	0.18	133,133,133,133	1
5	NO3	B	430	4/4	0.75	0.18	52,55,55,55	0
2	SM	A	422	1/1	0.82	0.19	104,104,104,104	1
5	NO3	A	433	4/4	0.82	0.16	55,55,55,55	0
5	NO3	A	434	4/4	0.85	0.18	54,54,55,55	0
7	TRS	B	433	8/8	0.86	0.17	27,38,45,46	0
3	HG	B	428	1/1	0.87	0.10	126,126,126,126	1

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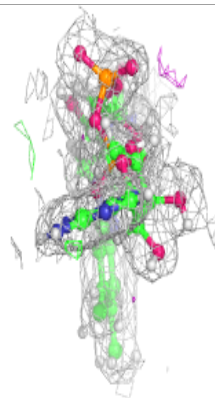
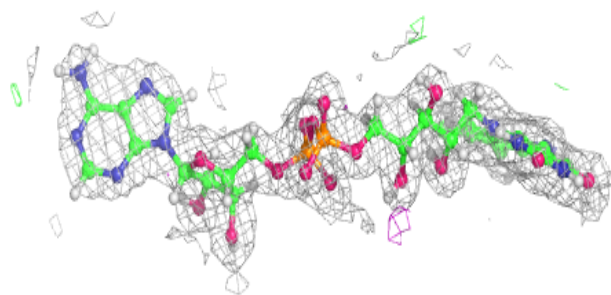
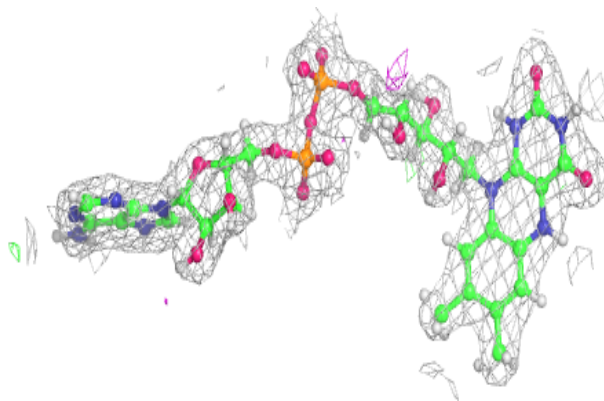
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	HG	B	426	1/1	0.88	0.13	68,68,68,68	1
2	SM	A	423	1/1	0.88	0.18	118,118,118,118	0
2	SM	B	421	1/1	0.89	0.09	105,105,105,105	1
5	NO3	A	435	4/4	0.91	0.17	26,27,27,35	0
3	HG	B	425	1/1	0.91	0.13	88,88,88,88	1
6	CL	B	432	1/1	0.92	0.09	23,23,23,23	0
7	TRS	A	438	8/8	0.92	0.13	22,30,36,37	0
5	NO3	B	431	4/4	0.93	0.15	29,29,30,36	0
2	SM	B	422	1/1	0.94	0.16	90,90,90,90	0
3	HG	A	427	1/1	0.96	0.10	82,82,82,82	1
3	HG	A	428	1/1	0.96	0.09	91,91,91,91	1
2	SM	A	425	1/1	0.97	0.18	133,133,133,133	0
2	SM	A	424	1/1	0.97	0.18	73,73,73,73	1
3	HG	B	427	1/1	0.97	0.05	25,25,25,25	1
3	HG	B	424	1/1	0.97	0.03	43,43,43,43	1
4	FDA	B	429	53/53	0.97	0.11	12,19,26,28	0
4	FDA	A	432	53/53	0.97	0.13	9,18,22,23	0
6	CL	A	436	1/1	0.98	0.09	23,23,23,23	0
2	SM	B	420	1/1	0.98	0.15	35,35,35,35	0
6	CL	A	437	1/1	0.98	0.09	42,42,42,42	0
2	SM	B	419	1/1	0.98	0.15	60,60,60,60	0
2	SM	A	419	1/1	0.99	0.15	47,47,47,47	1
3	HG	B	423	1/1	0.99	0.03	29,29,29,29	0
2	SM	A	420	1/1	1.00	0.14	34,34,34,34	0
3	HG	A	430	1/1	1.00	0.04	49,49,49,49	1
2	SM	A	421	1/1	1.00	0.12	29,29,29,29	0
3	HG	A	426	1/1	1.00	0.01	25,25,25,25	0
3	HG	A	429	1/1	1.00	0.01	21,21,21,21	1

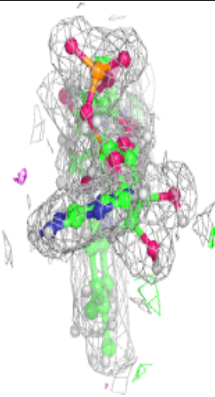
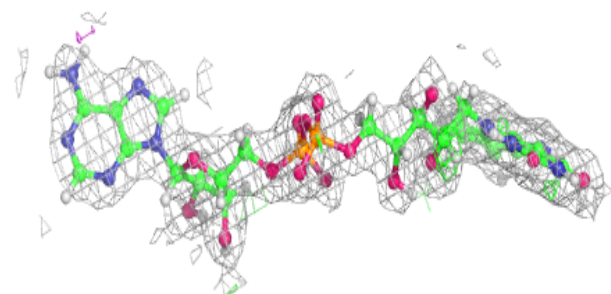
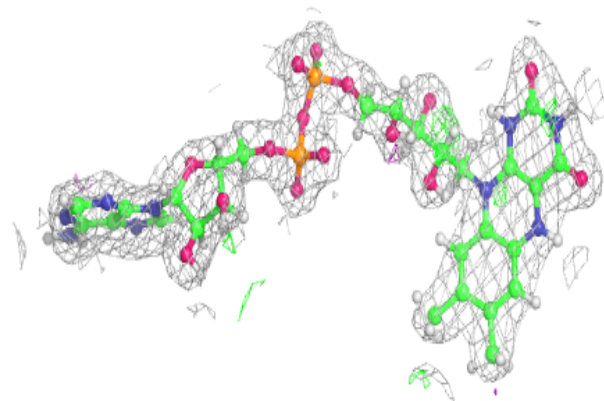
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around FDA B 429:

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

**Electron density around FDA A 432:**

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



6.5 Other polymers

There are no such residues in this entry.