

wwPDB X-ray Structure Validation Summary Report (i)

Jan 3, 2024 – 12:33 pm GMT

PDB ID : 5G5G

Title : Escherichia coli Periplasmic Aldehyde Oxidase

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Deposited on : 2016-05-25

Resolution : 1.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

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

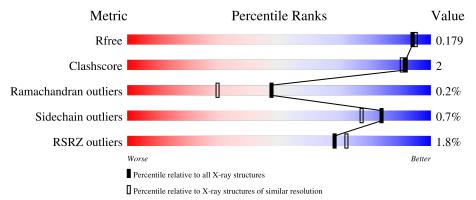
Validation Pipeline (wwPDB-VP) : 2.36

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 1.70 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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						
1	A	229	73% • 24%						
2	В	318	94%	5% •					
3	С	732	95%	•					

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
6	CL	A	1229	-	-	X	-
7	ACT	В	1321	-	-	X	-
9	SF4	В	320	-	-	X	-



2 Entry composition (i)

There are 13 unique types of molecules in this entry. The entry contains 10479 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 PUTATIVE XANTHINE DEHYDROGENASE YAGT IRON-SULFUR-BINDING SUBUNIT.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	175	Total 1341	C 820	N 239	O 269	S 13	0	7	0

• Molecule 2 is a protein called PUTATIVE XANTHINE DEHYDROGENASE YAGR MOLYBDENUM-BINDING SU SUBUNIT.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	316	Total 2400	C 1509	N 439	O 444	S 8	0	4	0

• Molecule 3 is a protein called PUTATIVE XANTHINE DEHYDROGENASE YAGS FAD-BINDING SUBUNIT.

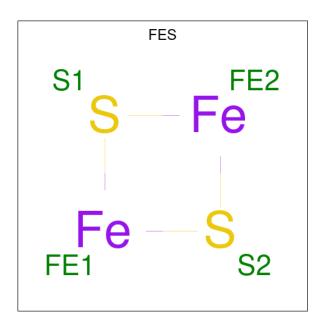
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
3	С	731	Total 5569	C 3477	N 989	O 1076	S 27	0	14	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	88	VAL	ALA	cloning artifact	UNP P77489
С	391	GLY	ASP	cloning artifact	UNP P77489

• Molecule 4 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).





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

• Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

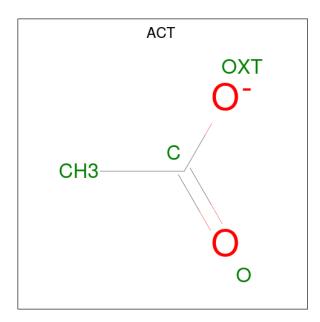
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total I 2 2	0	0
5	В	2	Total I 2 2	0	0
5	С	3	Total I 3 3	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	3	Total Cl 3 3	0	0
6	В	4	Total Cl 4 4	0	0
6	С	5	Total Cl 5 5	0	0

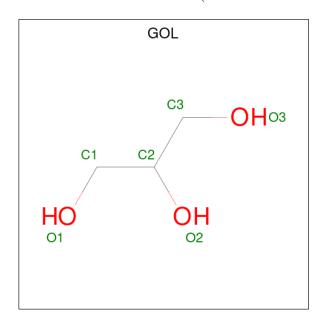
 \bullet Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: $\mathrm{C_2H_3O_2}).$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	В	1	Total C O 4 2 2	0	0
7	С	1	Total C O 4 2 2	0	0
7	С	1	Total C O 4 2 2	0	0

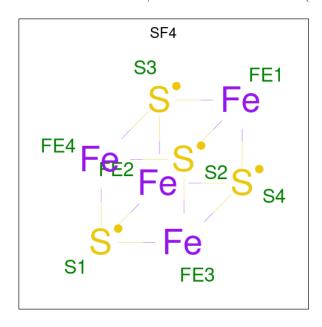
 \bullet Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $\mathrm{C_3H_8O_3}).$





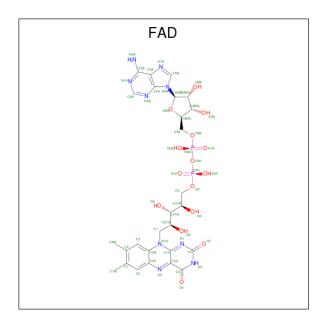
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 6 3 3	0	0
8	A	1	Total C O 6 3 3	0	0
8	В	1	Total C O 6 3 3	0	0
8	В	1	Total C O 6 3 3	0	0
8	С	1	Total C O 6 3 3	0	0
8	С	1	Total C O 6 3 3	0	0

• Molecule 9 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



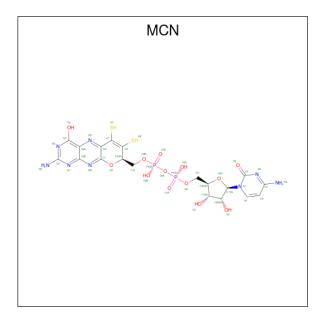
M	ol	Chain	Residues	Atoms			ZeroOcc	AltConf
()	В	1	Total	Fe	S	0	0
				8	4	4		





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
10	В	1	Total 53	C 27			P 2	0	0

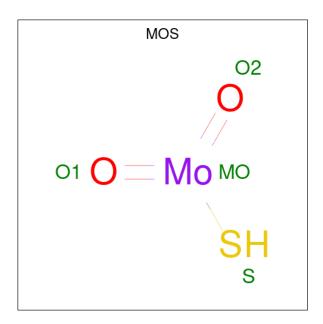
 \bullet Molecule 11 is PTERIN CYTOSINE DINUCLEOTIDE (three-letter code: MCN) (formula: $C_{19}H_{22}N_8O_{13}P_2S_2).$



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
11	С	1	Total 44		N 8		P 2	S 2	0	0

 \bullet Molecule 12 is DIOXOTHIOMOLYBDENUM(VI) ION (three-letter code: MOS) (formula: HMoO2S).





Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf
19	С	1	Total	Мо	О	S	0	0
12		1	4	1	2	1		U

• Molecule 13 is water.

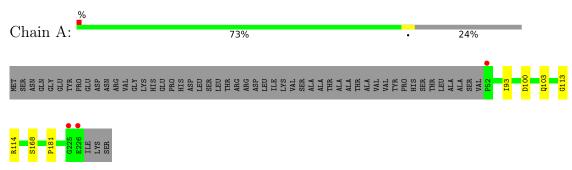
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	175	Total O 175 175	0	0
13	В	248	Total O 248 248	0	0
13	С	558	Total O 558 558	0	0



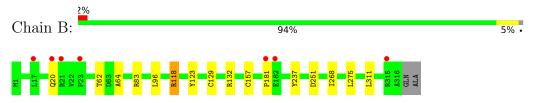
3 Residue-property plots (i)

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.

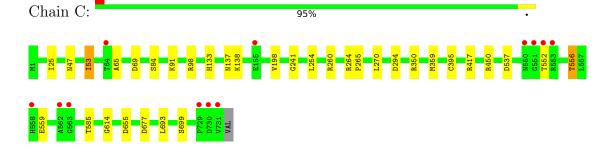
• Molecule 1: PUTATIVE XANTHINE DEHYDROGENASE YAGT IRON-SULFUR-BINDING SUBUNIT



• Molecule 2: PUTATIVE XANTHINE DEHYDROGENASE YAGR MOLYBDENUM-BINDING SU SUBUNIT



• Molecule 3: PUTATIVE XANTHINE DEHYDROGENASE YAGS FAD-BINDING SUBUNIT





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	109.68Å 78.34Å 151.91Å	Donositor
a, b, c, α , β , γ	90.00° 99.69° 90.00°	Depositor
Resolution (Å)	48.32 - 1.70	Depositor
Resolution (A)	48.32 - 1.70	EDS
% Data completeness	98.5 (48.32-1.70)	Depositor
(in resolution range)	98.5 (48.32-1.70)	EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.95 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
P. P.	0.138 , 0.167	Depositor
R, R_{free}	0.153 , 0.179	DCC
R_{free} test set	6835 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	16.0	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38 , 48.1	EDS
L-test for twinning ²	$ < L >=0.46, < L^2>=0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10479	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.92% 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: CL, IOD, MCN, ACT, CSD, MOS, FES, GOL, FAD, SF4

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	Bo	nd lengths	Bond angles		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	0.72	0/1364	0.82	2/1850 (0.1%)	
2	В	0.70	0/2447	0.84	8/3327 (0.2%)	
3	С	0.77	$1/5693 \ (0.0\%)$	0.88	9/7730 (0.1%)	
All	All	0.75	1/9504 (0.0%)	0.86	19/12907 (0.1%)	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
3	С	84	SER	CB-OG	-6.53	1.33	1.42

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	114	ARG	NE-CZ-NH2	-8.36	116.12	120.30
3	С	417	ARG	NE-CZ-NH1	8.24	124.42	120.30
3	С	450	ARG	NE-CZ-NH1	7.27	123.94	120.30
2	В	118[A]	ARG	NE-CZ-NH2	-6.98	116.81	120.30
2	В	118[B]	ARG	NE-CZ-NH2	-6.98	116.81	120.30

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	1341	0	1319	4	0
2	В	2400	0	2449	13	0
3	С	5569	0	5522	14	0
4	A	8	0	0	0	0
5	A	2	0	0	0	0
5	В	2	0	0	0	0
5	С	3	0	0	1	0
6	A	3	0	0	3	0
6	В	4	0	0	0	0
6	С	5	0	0	0	0
7	A	4	0	3	0	0
7	В	4	0	3	3	0
7	С	8	0	6	0	0
8	A	12	0	16	1	0
8	В	12	0	16	1	0
8	С	12	0	16	1	0
9	В	8	0	0	3	0
10	В	53	0	31	0	0
11	С	44	0	16	0	0
12	С	4	0	0	0	0
13	A	175	0	0	0	1
13	В	248	0	0	0	0
13	С	558	0	0	0	1
All	All	10479	0	9397	30	1

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.

The worst 5 of 30 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	$\operatorname{distance}\ (ext{Å})$	$overlap(ext{Å})$
2:B:129:CYS:HG	9:B:320:SF4:FE2	0.63	0.91
1:A:103:GLN:OE1	6:A:1229:CL:CL	2.30	0.86
3:C:53[A]:ILE:HD11	3:C:254:LEU:HD12	1.73	0.70
2:B:157:CYS:HG	9:B:320:SF4:FE4	1.11	0.68
3:C:25:ILE:HD12	8:C:1742:GOL:H31	1.79	0.65

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.



Atom-1	1100111 1		Clash overlap (Å)
13:A:2030:HOH:O	13:C:2076:HOH:O[3_445]	2.18	0.02

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	Perce	ntiles
1	A	180/229 (79%)	177 (98%)	3 (2%)	0	100	100
2	В	318/318 (100%)	315 (99%)	3 (1%)	0	100	100
3	С	742/732 (101%)	727 (98%)	13 (2%)	2 (0%)	41	24
All	All	1240/1279 (97%)	1219 (98%)	19 (2%)	2 (0%)	47	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	С	241	GLY
3	С	350	ARG

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	Perce	ntiles
1	A	148/186 (80%)	146 (99%)	2 (1%)	67	53
2	В	247/244 (101%)	246 (100%)	1 (0%)	91	87
3	С	578/565 (102%)	573 (99%)	5 (1%)	78	70
All	All	973/995 (98%)	965 (99%)	8 (1%)	84	74



	c	\circ	• 1	• , 1		•	. 1 1 .		1 1	1 1
Э	Oİ.	8	residues	with a	ı non-rotan	neric s	ıdechaın	are	listed	below:

Mol	Chain	Res	Type
3	С	556	THR
3	С	552	THR
3	С	53[B]	ILE
3	С	53[A]	ILE
3	С	91	LYS

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)

1 non-standard protein/DNA/RNA residue is 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	В	ond leng	${ m gths}$	F	Bond an	gles
	Туре	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
3	CSD	С	395	3	3,7,8	0.74	0	1,8,10	6.34	1 (100%)

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.

\mathbf{Mol}	\mathbf{Type}	Chain	Res	Link	Chirals	Torsions	Rings
3	CSD	С	395	3	-	1/2/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
3	С	395	CSD	OD1-SG-CB	-6.34	93.47	105.54

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	С	395	CSD	CA-CB-SG-OD1

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, 19 are monoatomic - leaving 16 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	В	Bond lengths			Bond angles		
IVIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
8	GOL	A	1233	-	5,5,5	0.32	0	5,5,5	0.84	0	
8	GOL	С	1741	-	5,5,5	0.54	0	5,5,5	0.69	0	
7	ACT	С	1739	-	3,3,3	0.78	0	3,3,3	0.73	0	
8	GOL	A	1232	-	5,5,5	0.47	0	5,5,5	0.93	0	
7	ACT	В	1321	-	3,3,3	0.92	0	3,3,3	1.08	0	
7	ACT	A	1231	-	3,3,3	0.79	0	3,3,3	0.69	0	
7	ACT	С	1740	-	3,3,3	0.88	0	3,3,3	0.34	0	
8	GOL	С	1742	-	5,5,5	0.41	0	5,5,5	1.11	0	
10	FAD	В	321	-	53,58,58	3.62	22 (41%)	68,89,89	3.46	31 (45%)	
11	MCN	С	921	12	41,48,48	4.54	18 (43%)	49,74,74	4.00	25 (51%)	
8	GOL	В	1322	-	5,5,5	0.54	0	5,5,5	0.39	0	
4	FES	A	230	1	0,4,4	-	-	-			



Mol	Tuno	Chain	Res	Link	В	ond leng	gths	В	ond ang	gles
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
4	FES	A	231	1	0,4,4	-	-	-		
9	SF4	В	320	2	0,12,12	-	-	-		
8	GOL	В	1323	-	5,5,5	0.38	0	5,5,5	0.40	0
12	MOS	С	922	11	0,3,3	-	-	-		

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
8	GOL	A	1233	-	-	2/4/4/4	-
8	GOL	С	1741	-	-	0/4/4/4	-
8	GOL	A	1232	-	-	3/4/4/4	-
8	GOL	С	1742	-	-	2/4/4/4	-
10	FAD	В	321	-	-	0/30/50/50	0/6/6/6
11	MCN	С	921	12	-	2/22/54/54	0/5/5/5
8	GOL	В	1322	-	-	1/4/4/4	-
4	FES	A	230	1	-	-	0/1/1/1
4	FES	A	231	1	-	-	0/1/1/1
9	SF4	В	320	2	-	-	0/6/5/5
8	GOL	В	1323	-	-	0/4/4/4	-

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(A)
11	С	921	MCN	C6'-N5'	16.37	1.56	1.32
10	В	321	FAD	C2A-N3A	12.35	1.52	1.32
11	С	921	MCN	C6'-C7	11.59	1.60	1.43
11	С	921	MCN	C4A-C4B	9.48	1.57	1.40
10	В	321	FAD	C4X-N5	9.13	1.48	1.30

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
10	В	321	FAD	C2A-N1A-C6A	11.84	139.01	118.75
10	В	321	FAD	N3A-C2A-N1A	-11.42	110.83	128.68
11	С	921	MCN	N1'-C2'-N3'	-9.64	114.37	127.22
11	С	921	MCN	C4B-C4A-N5'	-9.54	110.90	122.41
10	В	321	FAD	C4A-C5A-N7A	8.89	118.67	109.40



There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1232	GOL	O1-C1-C2-C3
8	A	1233	GOL	O1-C1-C2-C3
8	A	1232	GOL	O1-C1-C2-O2
8	A	1233	GOL	O1-C1-C2-O2
11	С	921	MCN	C3'-C4D-C5'-O5'

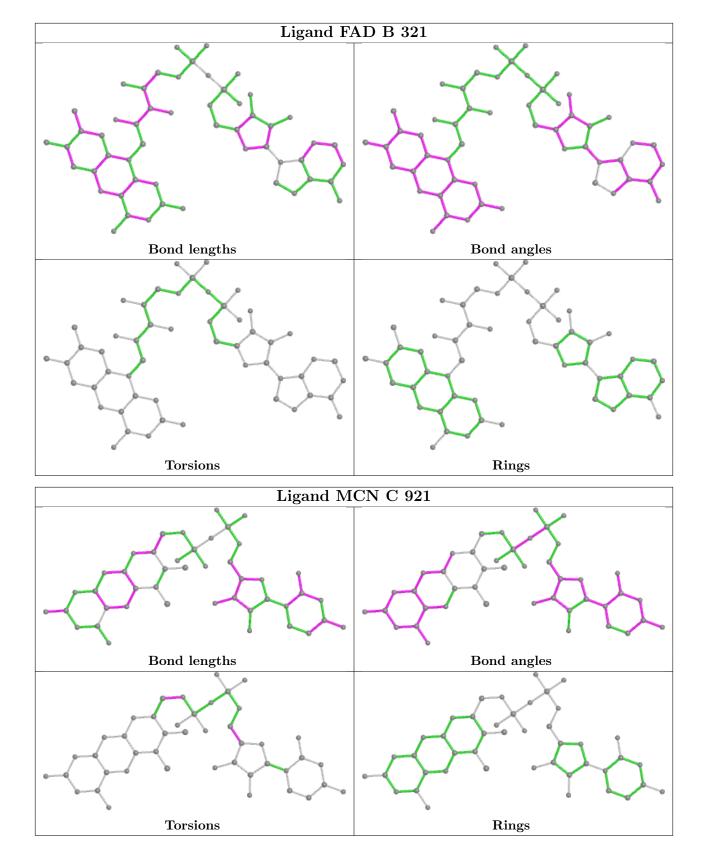
There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	1232	GOL	1	0
7	В	1321	ACT	3	0
8	С	1742	GOL	1	0
8	В	1322	GOL	1	0
9	В	320	SF4	3	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>	# RSRZ > 2	$OWAB(Å^2)$	Q<0.9
1	A	175/229 (76%)	-0.26	3 (1%) 70 74	10, 16, 31, 60	0
2	В	316/318 (99%)	-0.19	7 (2%) 62 66	11, 21, 36, 62	0
3	С	730/732 (99%)	-0.31	12 (1%) 72 76	10, 17, 35, 61	0
All	All	1221/1279 (95%)	-0.27	22 (1%) 68 72	10, 17, 35, 62	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	С	731	VAL	4.3
3	С	562	ALA	3.8
3	С	551	GLY	3.8
1	A	52	PRO	3.8
3	С	730	ASP	3.6

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, 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
3	CSD	С	395	8/9	0.97	0.10	17,20,26,27	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.



6.4 Ligands (i)

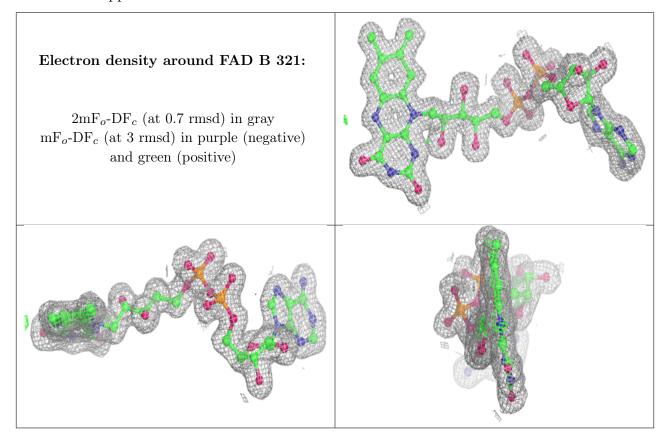
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\operatorname{B-factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
8	GOL	A	1233	6/6	0.74	0.18	35,40,42,46	0
8	GOL	С	1742	6/6	0.81	0.14	34,39,41,43	0
7	ACT	С	1739	4/4	0.82	0.17	53,53,58,58	0
9	SF4	В	320	8/8	0.84	0.15	15,17,19,20	0
8	GOL	С	1741	6/6	0.86	0.13	28,39,43,43	0
8	GOL	A	1232	6/6	0.88	0.13	26,31,32,40	0
7	ACT	В	1321	4/4	0.90	0.18	20,23,34,38	0
6	CL	A	1230	1/1	0.90	0.07	43,43,43,43	0
8	GOL	В	1322	6/6	0.90	0.19	39,41,43,45	0
6	CL	С	1737	1/1	0.91	0.11	36,36,36,36	0
7	ACT	A	1231	4/4	0.91	0.09	27,33,34,36	0
6	CL	В	4000	1/1	0.93	0.08	29,29,29,29	0
7	ACT	С	1740	4/4	0.93	0.08	34,37,38,39	0
5	IOD	A	3000	1/1	0.94	0.06	30,30,30,30	1
8	GOL	В	1323	6/6	0.94	0.14	21,37,40,42	0
4	FES	A	230	4/4	0.94	0.11	10,10,11,11	0
6	CL	В	1319	1/1	0.94	0.07	39,39,39,39	0
6	CL	В	1320	1/1	0.94	0.06	37,37,37,37	0
6	CL	С	1735	1/1	0.96	0.06	24,24,24,24	0
6	CL	С	4000	1/1	0.97	0.10	26,26,26,26	0
6	CL	A	1229	1/1	0.97	0.10	27,27,27,27	0
5	IOD	В	3000	1/1	0.98	0.04	30,30,30,30	1
6	CL	С	1736	1/1	0.98	0.05	37,37,37,37	0
5	IOD	В	1317	1/1	0.98	0.04	28,28,28,28	1
10	FAD	В	321	53/53	0.98	0.07	10,12,14,14	0
6	CL	В	1318	1/1	0.99	0.06	25,25,25,25	0
6	CL	A	1228	1/1	0.99	0.04	29,29,29,29	0
5	IOD	С	1732	1/1	0.99	0.04	23,23,23,23	1
5	IOD	С	1734	1/1	0.99	0.04	27,27,27,27	1
11	MCN	С	921	44/44	0.99	0.07	9,10,11,11	0
12	MOS	С	922	4/4	0.99	0.08	12,12,14,14	1
6	CL	С	1738	1/1	1.00	0.04	33,33,33,33	0
5	IOD	С	1733	1/1	1.00	0.03	25,25,25,25	1
4	FES	A	231	4/4	1.00	0.06	9,9,10,10	0
5	IOD	A	1227	1/1	1.00	0.05	13,13,13,13	1

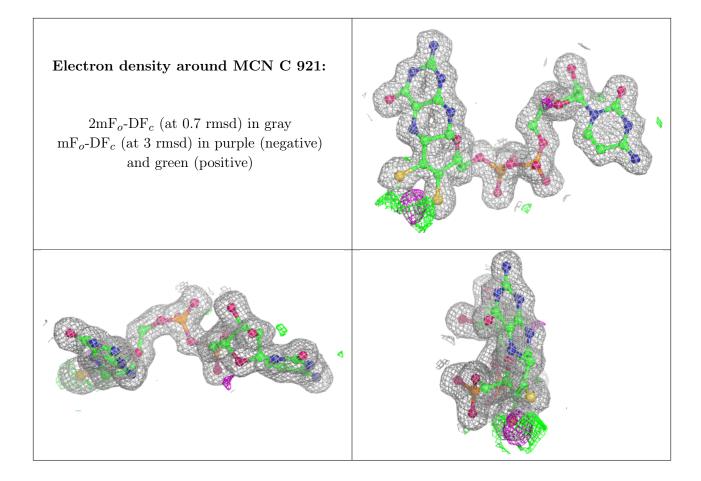
The following is a graphical depiction of the model fit to experimental electron density of all



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.







6.5 Other polymers (i)

There are no such residues in this entry.

