

Full wwPDB X-ray Structure Validation Report (i)

Dec 2, 2023 - 01:32 pm GMT

PDB ID	:	1V1M
Title	:	CROSSTALK BETWEEN COFACTOR BINDING AND THE PHOSPHO-
		RYLATION LOOP CONFORMATION IN THE BCKD MACHINE
Authors	:	Li, J.; Wynn, R.M.; Machius, M.; Chuang, J.L.; Karthikeyan, S.; Tomchick,
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Deposited on	:	2004-04-20
Resolution	:	2.00 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 (i)) were used in the production of this report:

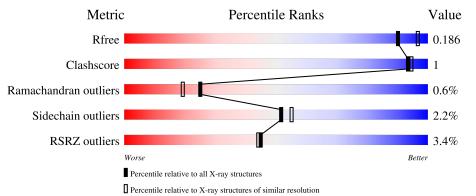
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as 541 be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.00 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	А	400	4% 84% 88%	• 7%
2	В	342	^{2%} 93%	5% •



1V1M

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 6268 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 2-OXOISOVALERATE DEHYDROGENASE ALPHA SUB-UNIT.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	372	Total 3000	C 1896	N 534	0 554	S 16	0	3	0

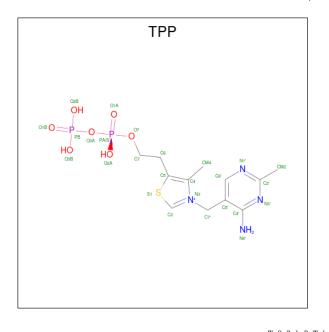
There is a discrepancy between the modelled and reference sequences:

Chai	n Residue	Modelled	Actual	Comment	Reference
A	295	ALA	ASP	engineered mutation	UNP P12694

• Molecule 2 is a protein called 2-OXOISOVALERATE DEHYDROGENASE BETA SUB-UNIT.

Mol	Chain	Residues		At	\mathbf{oms}			ZeroOcc	AltConf	Trace
2	В	336	Total 2636	C 1699	N 435	O 487	S 15	0	2	0

• Molecule 3 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: $C_{12}H_{19}N_4O_7P_2S$).



Mol	Chain	Residues		Α	ton	ıs			ZeroOcc	AltConf
3	А	1	Total 26	C 12	N 4	0 7	Р 2	S 1	0	0

• Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	2	Total Cl 2 2	0	0
4	В	1	Total Cl 1 1	0	0

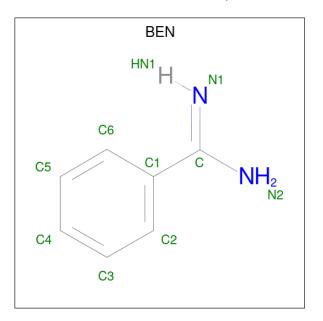
• Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	Total K 1 1	0	0
5	В	1	Total K 1 1	0	0

• Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	Total Mn 1 1	0	0

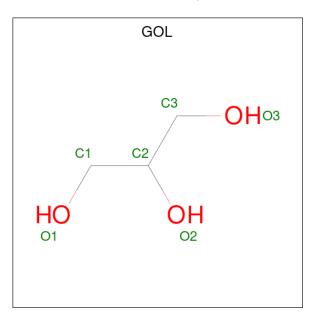
• Molecule 7 is BENZAMIDINE (three-letter code: BEN) (formula: $C_7H_8N_2$).





\mathbf{N}	lol	Chain	Residues	Atoms			ZeroOcc	AltConf
	7	А	1	Total 9	$\begin{array}{c} \mathrm{C} \\ 7 \end{array}$	N 2	0	0

• Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
8	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
8	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0

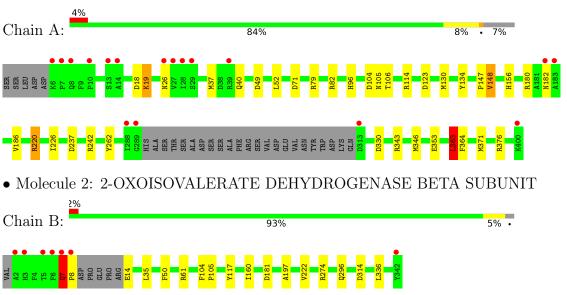
• Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	А	321	Total O 321 321	0	0
9	В	252	Total O 252 252	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: 2-OXOISOVALERATE DEHYDROGENASE ALPHA SUBUNIT



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	145.29Å 145.29 Å 69.17 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.87 - 2.00	Depositor
Resolution (A)	36.32 - 2.00	EDS
% Data completeness	$95.5\ (28.87-2.00)$	Depositor
(in resolution range)	95.5(36.32 - 2.00)	EDS
R _{merge}	0.12	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.07 (at 2.00 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
D D.	0.129 , 0.170	Depositor
R, R_{free}	0.150 , 0.186	DCC
R_{free} test set	1535 reflections (2.83%)	wwPDB-VP
Wilson B-factor $(Å^2)$	16.6	Xtriage
Anisotropy	0.423	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39, 64.2	EDS
L-test for twinning ²	$< L > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6268	wwPDB-VP
Average B, all atoms $(Å^2)$	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.84% of the height of the origin peak. No significant pseudotranslation is detected.

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: CL, MN, TPP, GOL, K, BEN

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	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.97	2/3073~(0.1%)	0.95	15/4151~(0.4%)
2	В	0.90	0/2705	0.88	6/3675~(0.2%)
All	All	0.94	2/5778~(0.0%)	0.92	21/7826~(0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	В	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	130	MET	CG-SD	-5.68	1.66	1.81
1	А	346	MET	CG-SD	5.17	1.94	1.81

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	В	61	ARG	NE-CZ-NH1	7.96	124.28	120.30
1	А	82	ARG	NE-CZ-NH2	-7.83	116.39	120.30
1	А	123	ASP	CB-CG-OD1	7.58	125.13	118.30
1	А	363	LEU	CA-CB-CG	7.50	132.56	115.30
1	А	104	ASP	CB-CG-OD2	7.48	125.03	118.30
1	А	18	ASP	CB-CG-OD2	6.39	124.05	118.30
1	А	180	ARG	NE-CZ-NH1	6.32	123.46	120.30
2	В	61	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	А	330	ASP	CB-CG-OD1	5.97	123.67	118.30

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$Ideal(^{o})$	
1	А	71	ASP	CB-CG-OD1	5.92	123.62	118.30	
1	А	79	ARG	NE-CZ-NH1	5.90	123.25	120.30	
1	А	37	MET	CG-SD-CE	-5.65	91.16	100.20	
1	А	82	ARG	NE-CZ-NH1	5.59	123.09	120.30	
1	А	371	MET	CG-SD-CE	-5.57	91.29	100.20	
1	А	237	ASP	CB-CG-OD1	5.53	123.28	118.30	
1	А	49	ASP	CB-CG-OD1	5.35	123.12	118.30	
2	В	274	ARG	NE-CZ-NH1	5.32	122.96	120.30	
2	В	181	ASP	CB-CG-OD1	5.25	123.03	118.30	
1	А	220	ARG	NE-CZ-NH1	5.19	122.89	120.30	
2	В	160	ILE	CG1-CB-CG2	5.11	122.65	111.40	

CB-CG-OD2

There are no chirality outliers.

В

All (1) planarity outliers are listed below:

314

ASP

Mol	Chain	Res	Type	Group
2	В	7	GLN	Peptide

Too-close contacts (i) 5.2

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.

5.03

122.83

118.30

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	3000	0	2913	12	0
2	В	2636	0	2588	3	0
3	А	26	0	16	1	0
4	А	2	0	0	1	0
4	В	1	0	0	0	0
5	А	1	0	0	0	0
5	В	1	0	0	0	0
6	А	1	0	0	0	0
7	А	9	0	7	0	0
8	В	18	0	24	0	0
9	А	321	0	0	4	1
9	В	252	0	0	0	1
All	All	6268	0	5548	16	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 1.

All (16) 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)
3:A:1401:TPP:H2	4:A:1402:CL:CL	2.27	0.71
1:A:363:LEU:HD22	1:A:364:PHE:CE2	2.36	0.60
1:A:19:LYS:NZ	9:A:2009:HOH:O	2.37	0.57
1:A:105:ASN:ND2	9:A:2099:HOH:O	2.32	0.52
1:A:242:ARG:HD3	9:A:2215:HOH:O	2.12	0.49
1:A:363:LEU:HD22	1:A:364:PHE:CZ	2.47	0.49
1:A:134:TYR:CE2	1:A:353:GLU:HG2	2.48	0.48
1:A:376:ARG:NH1	9:A:2293:HOH:O	2.49	0.46
1:A:52:LEU:HD21	1:A:262:TYR:CZ	2.52	0.44
1:A:363:LEU:HD22	1:A:364:PHE:CD2	2.52	0.44
2:B:222:VAL:HG11	2:B:336:LEU:HD11	2.00	0.43
1:A:96:HIS:CE1	1:A:114:ARG:O	2.72	0.43
2:B:104:PHE:N	2:B:105:PRO:CD	2.83	0.42
1:A:147:PRO:O	1:A:148:VAL:HG22	2.21	0.41
1:A:106:THR:HA	1:A:156:HIS:CD2	2.56	0.41
2:B:7:GLN:CB	2:B:8:PRO:HD3	2.51	0.41

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	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2073:HOH:O	9:B:2024:HOH:O[1_554]	2.16	0.04

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	А	371/400~(93%)	362~(98%)	7 (2%)	2~(0%)	29 23	

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	Chain Analysed Favoured Allowed Outliers Percentiles										
IVIOI	Chain	Analyseu	ravoureu	Allowed	Outliers	Fercentine	38				
2	В	334/342~(98%)	323~(97%)	9~(3%)	2(1%)	25 19					
All	All	705/742~(95%)	685 (97%)	16 (2%)	4 (1%)	25 19					

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All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
2	В	7	GLN	
2	В	197	ALA	
1	А	226	ILE	
1	А	148	VAL	

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	312/334~(93%)	304~(97%)	8 (3%)	46 48
2	В	285/289~(99%)	280~(98%)	5(2%)	59 63
All	All	597/623~(96%)	584 (98%)	13 (2%)	52 55

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	19	LYS
1	А	26	ASN
1	А	40	GLN
1	А	182	ASN
1	А	186	VAL
1	А	220	ARG
1	А	343	ARG
1	А	363	LEU
2	В	14	GLU
2	В	35	LEU
2	В	50	PHE
2	В	117	TYR

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Mol	Chain	Res	Type
2	В	296	GLN

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such side chains are listed below:

Mol	Chain	Res	Type	
1	А	24	GLN	
1	А	40	GLN	
1	А	361	ASN	
2	В	296	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 6 are monoatomic - leaving 5 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	Turne	Chain	in Res Link		Link Bond lengths			Bond angles		
IVIOI	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
8	GOL	В	2344	-	$5,\!5,\!5$	0.45	0	$5,\!5,\!5$	0.45	0
8	GOL	В	2345	-	$5,\!5,\!5$	0.33	0	$5,\!5,\!5$	0.84	0
3	TPP	А	1401	6	22,27,27	2.25	5 (22%)	29,40,40	2.45	9 (31%)



Mol	Type	Chain	Res	Link Bond lengths			Bond angles			
1VIOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
8	GOL	В	2346	-	$5,\!5,\!5$	0.27	0	$5,\!5,\!5$	0.81	0
7	BEN	А	1406	-	$9,\!9,\!9$	1.32	1 (11%)	$7,\!11,\!11$	1.15	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	\mathbf{Res}	Link	Chirals	Torsions	Rings
8	GOL	В	2344	-	-	0/4/4/4	-
8	GOL	В	2345	-	-	2/4/4/4	-
3	TPP	А	1401	6	-	0/16/17/17	0/2/2/2
8	GOL	В	2346	-	-	2/4/4/4	-
7	BEN	А	1406	-	-	0/4/4/4	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	А	1401	TPP	C6-C5	-6.18	1.48	1.50
3	А	1401	TPP	C2-N3	5.90	1.48	1.36
7	А	1406	BEN	C1-C	-3.53	1.40	1.47
3	А	1401	TPP	C4-N3	-3.08	1.37	1.39
3	А	1401	TPP	PB-O1B	2.76	1.59	1.50
3	А	1401	TPP	C7'-C5'	2.28	1.56	1.51

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	1401	TPP	C6-C5-C4	5.99	132.24	127.43
3	А	1401	TPP	C7'-N3-C2	-5.96	114.58	125.35
3	А	1401	TPP	CM2-C2'-N1'	5.17	122.82	117.14
3	А	1401	TPP	C5-C4-N3	4.07	115.72	107.57
3	А	1401	TPP	N1'-C2'-N3'	-3.89	118.85	125.54
3	А	1401	TPP	C6'-N1'-C2'	3.11	121.25	115.96
3	А	1401	TPP	C5'-C7'-N3	-2.60	108.94	113.28
3	А	1401	TPP	CM4-C4-C5	-2.58	121.95	127.60
3	А	1401	TPP	C2'-N3'-C4'	2.52	122.01	118.08

There are no chirality outliers.

All (4) torsion outliers are listed below:



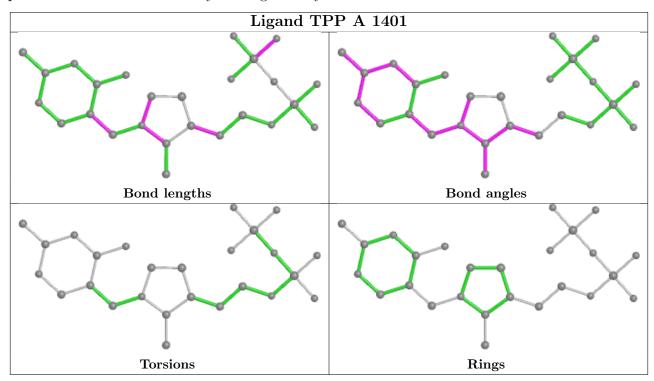
Mol	Chain	Res	Type	Atoms
8	В	2345	GOL	C1-C2-C3-O3
8	В	2346	GOL	O1-C1-C2-O2
8	В	2346	GOL	O1-C1-C2-C3
8	В	2345	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

[Mol	Chain	\mathbf{Res}	Type	Clashes	Symm-Clashes
	3	А	1401	TPP	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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	372/400~(93%)	-0.35	17 (4%) 32 31	5, 15, 37, 53	0
2	В	336/342~(98%)	-0.60	7 (2%) 63 62	6, 12, 31, 64	0
All	All	708/742~(95%)	-0.47	24 (3%) 45 44	5, 13, 35, 64	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	289	GLY	7.3
1	А	28	ILE	5.9
1	А	6	LYS	4.3
2	В	5	THR	4.0
2	В	8	PRO	3.8
1	А	8	GLN	3.8
1	А	26	ASN	3.8
1	А	7	PRO	3.7
1	А	313	ASP	3.2
1	А	400	LYS	3.1
1	А	183	ALA	3.1
1	А	288	ILE	3.1
2	В	7	GLN	3.0
1	А	182	ASN	2.9
1	А	14	ALA	2.6
2	В	3	HIS	2.5
1	А	10	PRO	2.4
1	А	27	VAL	2.3
1	А	29	SER	2.2
2	В	6	PHE	2.2
1	А	13	SER	2.1
1	А	39	ARG	2.1
2	В	342	TYR	2.1
2	В	2	ALA	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.

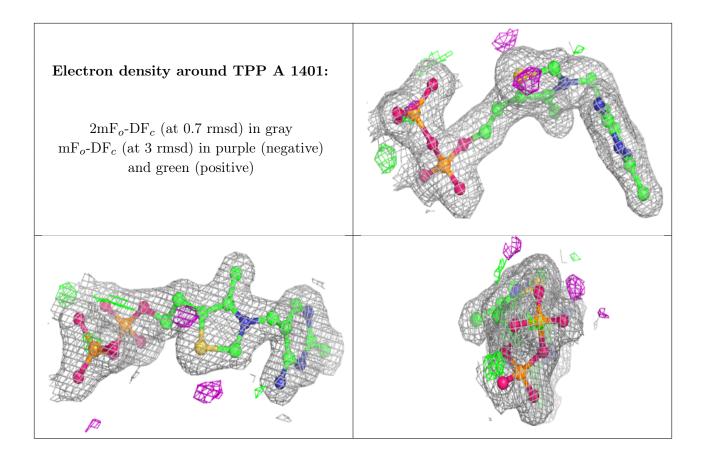
6.4 Ligands (i)

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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	$Q{<}0.9$
8	GOL	В	2345	6/6	0.81	0.30	31,46,48,54	0
7	BEN	А	1406	9/9	0.86	0.25	47,51,55,57	0
4	CL	В	2343	1/1	0.89	0.14	$65,\!65,\!65,\!65$	0
4	CL	А	1403	1/1	0.91	0.10	44,44,44,44	0
8	GOL	В	2346	6/6	0.91	0.14	32,43,44,46	0
4	CL	А	1402	1/1	0.98	0.20	37,37,37,37	0
3	TPP	А	1401	26/26	0.99	0.10	7,12,13,16	0
8	GOL	В	2344	6/6	0.99	0.14	12,14,15,16	0
5	Κ	В	2347	1/1	1.00	0.04	24,24,24,24	0
6	MN	А	1405	1/1	1.00	0.08	13,13,13,13	0
5	Κ	А	1404	1/1	1.00	0.07	19,19,19,19	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.

