



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 19, 2022 – 03:43 PM JST

PDB ID : 7WJV
Title : Crystal structure of human liver FBPase complexed with an covalent inhibitor
Authors : Cao, H.; Huang, Y.; Ren, Y.; Wan, J.
Deposited on : 2022-01-08
Resolution : 1.72 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 types of validation reports are described at <http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : ?? (??), CSD ??CSD?? (????)
Xtriage (Phenix) : 1.13
EDS : 2.29
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) : 2.29

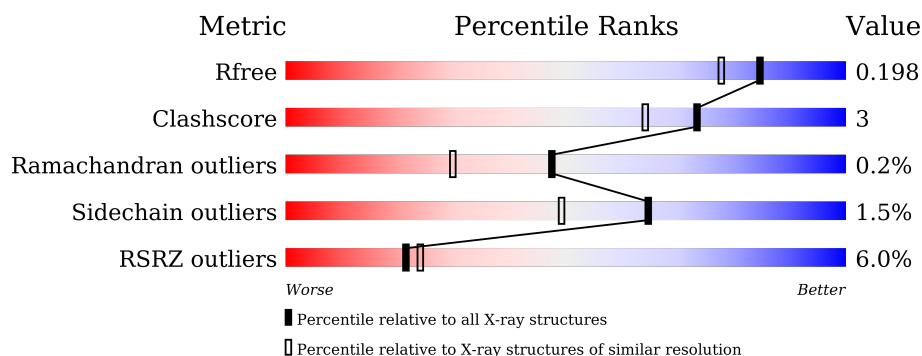
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.72 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	5722 (1.74-1.70)
Clashscore	141614	6152 (1.74-1.70)
Ramachandran outliers	138981	6051 (1.74-1.70)
Sidechain outliers	138945	6051 (1.74-1.70)
RSRZ outliers	127900	5629 (1.74-1.70)

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 $\leq 5\%$. 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	348	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>8% • 7%</div> </div> </div>
1	B	348	<div> <div>4%</div> <div> <div></div> <div>88%</div> <div>5% 6%</div> </div> </div>
1	C	348	<div> <div>8%</div> <div> <div></div> <div>86%</div> <div>7% • 6%</div> </div> </div>
1	D	348	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>7% • 8%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	LSA	A	402	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 11179 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 Fructose-1,6-bisphosphatase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	S	0	1	0
			2471	1572	416	466	17			
1	B	327	Total	C	N	O	S	0	0	0
			2485	1581	417	470	17			
1	C	326	Total	C	N	O	S	0	1	0
			2488	1583	419	469	17			
1	D	320	Total	C	N	O	S	0	0	0
			2443	1556	409	461	17			

There are 40 discrepancies between the modelled and reference sequences:

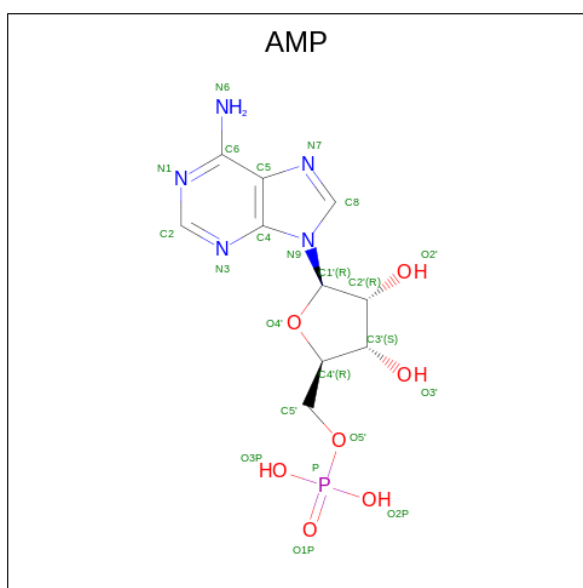
Chain	Residue	Modelled	Actual	Comment	Reference
A	338	LEU	-	expression tag	UNP Q2TU34
A	339	GLU	-	expression tag	UNP Q2TU34
A	340	HIS	-	expression tag	UNP Q2TU34
A	341	HIS	-	expression tag	UNP Q2TU34
A	342	HIS	-	expression tag	UNP Q2TU34
A	343	HIS	-	expression tag	UNP Q2TU34
A	344	HIS	-	expression tag	UNP Q2TU34
A	345	HIS	-	expression tag	UNP Q2TU34
A	346	HIS	-	expression tag	UNP Q2TU34
A	347	HIS	-	expression tag	UNP Q2TU34
B	338	LEU	-	expression tag	UNP Q2TU34
B	339	GLU	-	expression tag	UNP Q2TU34
B	340	HIS	-	expression tag	UNP Q2TU34
B	341	HIS	-	expression tag	UNP Q2TU34
B	342	HIS	-	expression tag	UNP Q2TU34
B	343	HIS	-	expression tag	UNP Q2TU34
B	344	HIS	-	expression tag	UNP Q2TU34
B	345	HIS	-	expression tag	UNP Q2TU34
B	346	HIS	-	expression tag	UNP Q2TU34
B	347	HIS	-	expression tag	UNP Q2TU34
C	338	LEU	-	expression tag	UNP Q2TU34

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Chain	Residue	Modelled	Actual	Comment	Reference
C	339	GLU	-	expression tag	UNP Q2TU34
C	340	HIS	-	expression tag	UNP Q2TU34
C	341	HIS	-	expression tag	UNP Q2TU34
C	342	HIS	-	expression tag	UNP Q2TU34
C	343	HIS	-	expression tag	UNP Q2TU34
C	344	HIS	-	expression tag	UNP Q2TU34
C	345	HIS	-	expression tag	UNP Q2TU34
C	346	HIS	-	expression tag	UNP Q2TU34
C	347	HIS	-	expression tag	UNP Q2TU34
D	338	LEU	-	expression tag	UNP Q2TU34
D	339	GLU	-	expression tag	UNP Q2TU34
D	340	HIS	-	expression tag	UNP Q2TU34
D	341	HIS	-	expression tag	UNP Q2TU34
D	342	HIS	-	expression tag	UNP Q2TU34
D	343	HIS	-	expression tag	UNP Q2TU34
D	344	HIS	-	expression tag	UNP Q2TU34
D	345	HIS	-	expression tag	UNP Q2TU34
D	346	HIS	-	expression tag	UNP Q2TU34
D	347	HIS	-	expression tag	UNP Q2TU34

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).



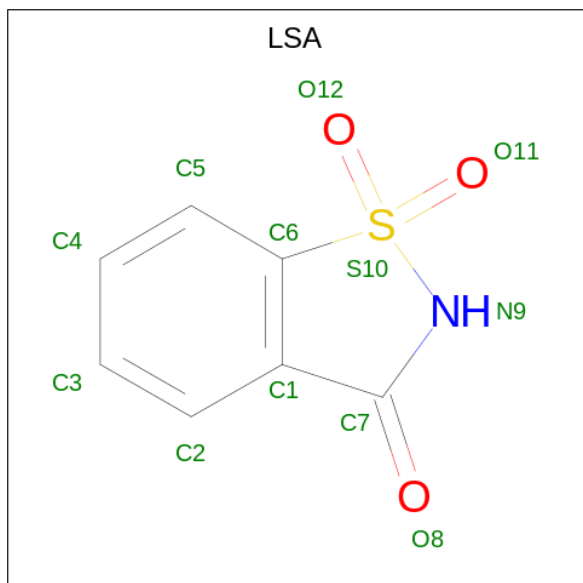
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 3 is 1,2-BENZISOTHIAZOL-3(2H)-ONE 1,1-DIOXIDE (three-letter code: LSA) (formula: $C_7H_5NO_3S$).

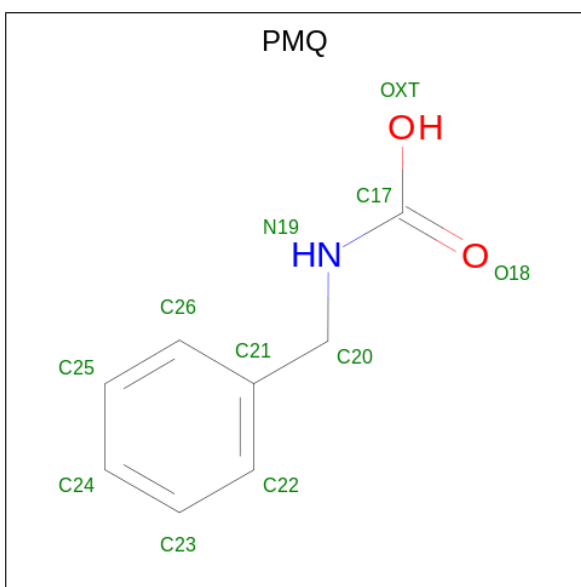


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			12	7	1	3	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

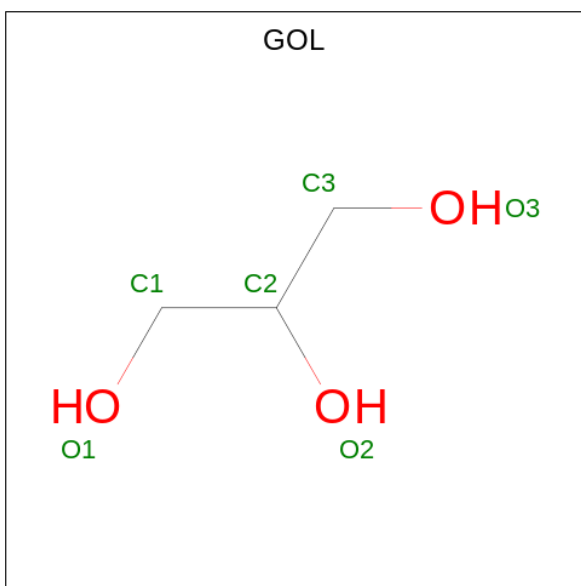
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		

- Molecule 5 is benzylcarbamic acid (three-letter code: PMQ) (formula: $C_8H_9NO_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			10	8	1	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	C	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		

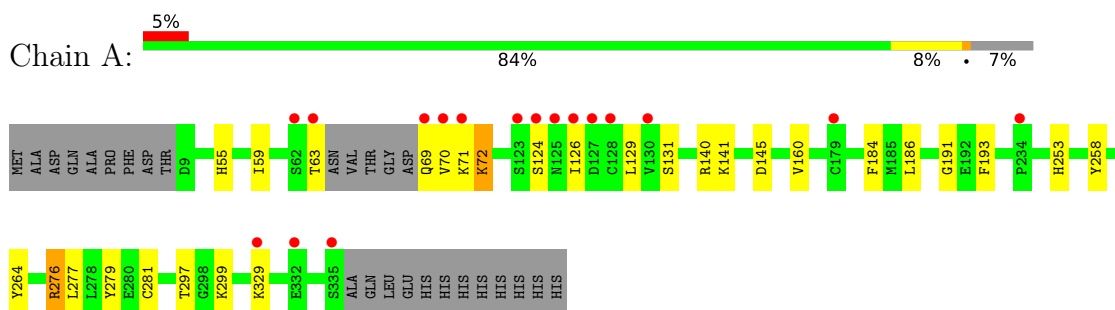
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	291	Total 291	O 291	0	0
7	B	328	Total 328	O 328	0	0
7	C	270	Total 270	O 270	0	0
7	D	269	Total 269	O 269	0	0

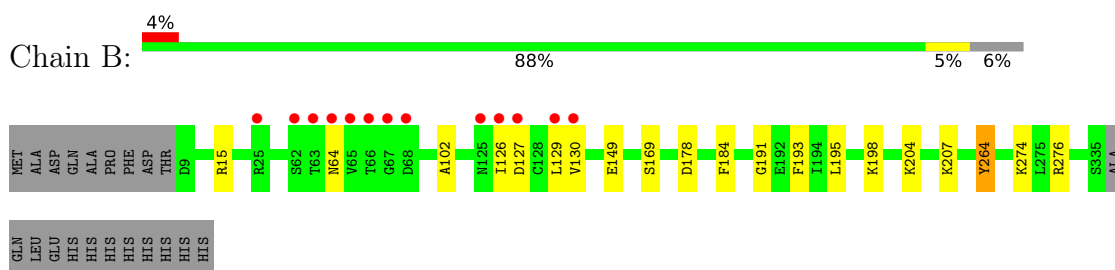
3 Residue-property plots [i](#)

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.

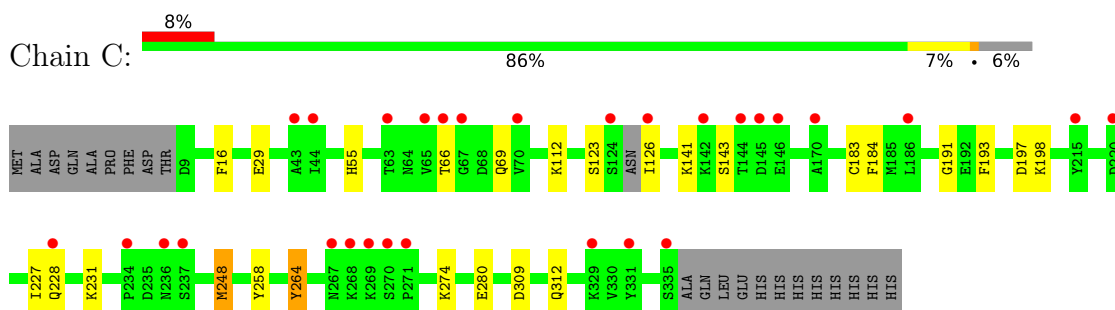
• Molecule 1: Fructose-1,6-bisphosphatase 1



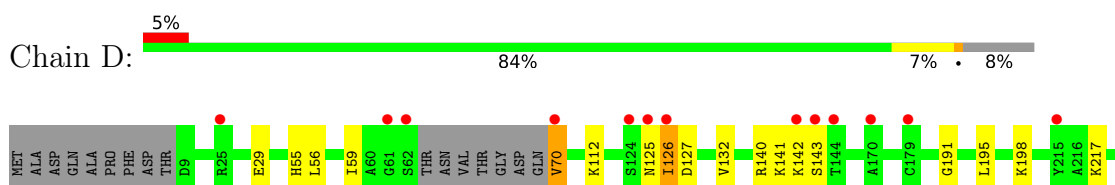
• Molecule 1: Fructose-1,6-bisphosphatase 1



• Molecule 1: Fructose-1,6-bisphosphatase 1



• Molecule 1: Fructose-1,6-bisphosphatase 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.64Å 83.62Å 278.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.45 – 1.72 46.45 – 1.72	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.45-1.72) 99.8 (46.45-1.72)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 1.73Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.174 , 0.198 0.173 , 0.198	Depositor DCC
R_{free} test set	2000 reflections (1.20%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11179	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% of the height of the origin peak. No significant pseudotranslation is detected.*

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: PMQ, LSA, GOL, AMP, MG

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	0.38	0/2514	0.57	0/3395
1	B	0.36	0/2529	0.56	0/3416
1	C	0.34	0/2534	0.54	0/3423
1	D	0.38	0/2486	0.56	0/3358
All	All	0.37	0/10063	0.56	0/13592

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	2471	0	2514	25	0
1	B	2485	0	2527	19	0
1	C	2488	0	2529	16	0
1	D	2443	0	2485	14	0
2	A	23	0	12	0	0
2	B	23	0	12	0	0
2	C	23	0	12	0	0
2	D	23	0	12	0	0
3	A	12	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	B	10	0	8	5	0
6	B	6	0	8	0	0
6	C	6	0	8	0	0
6	D	6	0	8	0	0
7	A	291	0	0	5	0
7	B	328	0	0	1	0
7	C	270	0	0	3	0
7	D	269	0	0	3	0
All	All	11179	0	10140	66	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 (66) 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:127:ASP:HA	5:B:501:PMQ:H23	1.52	0.90
1:B:102:ALA:HB3	1:B:149:GLU:HG2	1.71	0.72
1:C:198:LYS:NZ	7:C:502:HOH:O	2.28	0.64
1:B:102:ALA:CB	1:B:149:GLU:HG2	2.29	0.63
1:C:264:TYR:CZ	1:C:274:LYS:HD3	2.34	0.62
1:A:140:ARG:NH2	7:A:502:HOH:O	2.31	0.62
1:A:140:ARG:HG3	1:A:160:VAL:HG21	1.81	0.61
1:B:129:LEU:HB2	5:B:501:PMQ:HN19	1.66	0.60
1:D:56:LEU:HD21	1:D:70:VAL:HB	1.83	0.59
1:A:191:GLY:HA3	1:C:191:GLY:HA3	1.87	0.55
1:B:191:GLY:HA3	1:D:191:GLY:HA3	1.88	0.54
1:B:129:LEU:H	5:B:501:PMQ:C22	2.18	0.54
1:C:248:MET:HE1	1:C:280:GLU:HB3	1.91	0.53
1:A:70:VAL:HG22	1:A:126:ILE:CG2	2.39	0.53
1:A:71:LYS:NZ	7:A:501:HOH:O	2.30	0.52
1:C:55:HIS:NE2	7:C:503:HOH:O	2.33	0.51
1:A:297:THR:OG1	1:A:299:LYS:HG2	2.10	0.51
1:D:195:LEU:HD21	1:D:198:LYS:HG2	1.92	0.51
1:A:141:LYS:NZ	7:A:509:HOH:O	2.45	0.49
1:C:16:PHE:HE2	1:C:198:LYS:HE2	1.76	0.49
1:A:276[A]:ARG:HG2	1:A:279:TYR:OH	2.12	0.49
1:C:183:CYS:HB2	1:C:197:ASP:HB2	1.95	0.49
1:A:70:VAL:HG22	1:A:126:ILE:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:126:ILE:HD12	1:D:132:VAL:HG11	1.94	0.48
1:C:29:GLU:OE2	1:C:112:LYS:HG2	2.13	0.48
1:C:258:TYR:OH	1:D:127:ASP:HB2	2.14	0.48
1:D:277:LEU:HA	1:D:281:CYS:HB2	1.97	0.46
1:D:277:LEU:HD23	1:D:307:PRO:HB3	1.98	0.46
1:C:66:THR:CB	1:C:69:GLN:HG3	2.46	0.46
1:A:253:HIS:CD2	5:B:501:PMQ:H25	2.50	0.46
1:B:184:PHE:HB3	1:B:193:PHE:HB3	1.98	0.46
1:C:123:SER:HA	1:C:126:ILE:HB	1.97	0.46
1:A:129:LEU:O	1:B:169:SER:N	2.37	0.45
1:A:253:HIS:CD2	1:B:129:LEU:HD23	2.51	0.45
1:B:264:TYR:CZ	1:B:274:LYS:HD3	2.52	0.45
1:A:258:TYR:CD2	1:B:126:ILE:HD11	2.52	0.45
1:C:228:GLN:NE2	7:C:501:HOH:O	2.20	0.44
1:B:207:LYS:NZ	7:B:608:HOH:O	2.50	0.44
1:D:309:ASP:HB3	1:D:312:GLN:HB3	2.00	0.44
1:B:204:LYS:CA	1:B:204:LYS:HE2	2.47	0.44
1:A:72:LYS:HD3	7:A:739:HOH:O	2.18	0.43
1:A:258:TYR:CE1	1:B:126:ILE:HG13	2.52	0.43
1:B:129:LEU:HB2	5:B:501:PMQ:N19	2.32	0.43
1:D:29:GLU:OE1	1:D:112:LYS:HG2	2.19	0.43
1:B:204:LYS:HE2	1:B:204:LYS:HA	1.99	0.43
1:C:141:LYS:HE2	1:C:143:SER:OG	2.19	0.43
1:A:131:SER:OG	1:B:130:VAL:HG13	2.18	0.43
1:A:277:LEU:HA	1:A:281:CYS:HB2	2.01	0.43
1:C:227:ILE:HG22	1:C:231:LYS:HD2	2.01	0.43
1:B:195:LEU:HD21	1:B:198:LYS:HG2	2.01	0.42
1:C:184:PHE:HB3	1:C:193:PHE:HB3	2.01	0.42
1:A:141:LYS:NZ	1:A:145:ASP:O	2.39	0.42
1:A:184:PHE:HB3	1:A:193:PHE:HB3	2.00	0.42
1:D:55:HIS:HA	1:D:59:ILE:HG22	2.02	0.42
1:A:71:LYS:HA	1:A:71:LYS:HD3	1.81	0.41
1:A:186:LEU:HB2	1:A:193:PHE:CE1	2.56	0.41
1:D:272:ASN:HA	7:D:507:HOH:O	2.20	0.41
1:B:15:ARG:HD3	7:D:503:HOH:O	2.20	0.41
1:C:309:ASP:HB3	1:C:312:GLN:HB3	2.02	0.41
1:D:140:ARG:O	1:D:142:LYS:HD3	2.21	0.41
1:A:329:LYS:HA	1:A:329:LYS:HD2	1.88	0.41
1:A:55:HIS:HA	1:A:59:ILE:HG22	2.03	0.40
1:D:126:ILE:HA	7:D:506:HOH:O	2.20	0.40
1:D:141:LYS:NZ	1:D:143:SER:HB2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ILE:HG21	1:A:126:ILE:HD13	1.81	0.40
1:A:299:LYS:HE2	7:A:738:HOH:O	2.20	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	Percentiles	
1	A	319/348 (92%)	312 (98%)	6 (2%)	1 (0%)	41	24
1	B	325/348 (93%)	319 (98%)	5 (2%)	1 (0%)	41	24
1	C	323/348 (93%)	317 (98%)	6 (2%)	0	100	100
1	D	316/348 (91%)	310 (98%)	6 (2%)	0	100	100
All	All	1283/1392 (92%)	1258 (98%)	23 (2%)	2 (0%)	47	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	SER
1	B	64	ASN

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	269/291 (92%)	263 (98%)	6 (2%)	52	33
1	B	270/291 (93%)	267 (99%)	3 (1%)	73	62
1	C	270/291 (93%)	268 (99%)	2 (1%)	84	76
1	D	266/291 (91%)	260 (98%)	6 (2%)	50	31
All	All	1075/1164 (92%)	1058 (98%)	17 (2%)	65	47

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	THR
1	A	69	GLN
1	A	72	LYS
1	A	264	TYR
1	A	276[A]	ARG
1	A	276[B]	ARG
1	B	178	ASP
1	B	264	TYR
1	B	276	ARG
1	C	248	MET
1	C	264	TYR
1	D	70	VAL
1	D	125	ASN
1	D	126	ILE
1	D	217	LYS
1	D	264	TYR
1	D	269	LYS

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

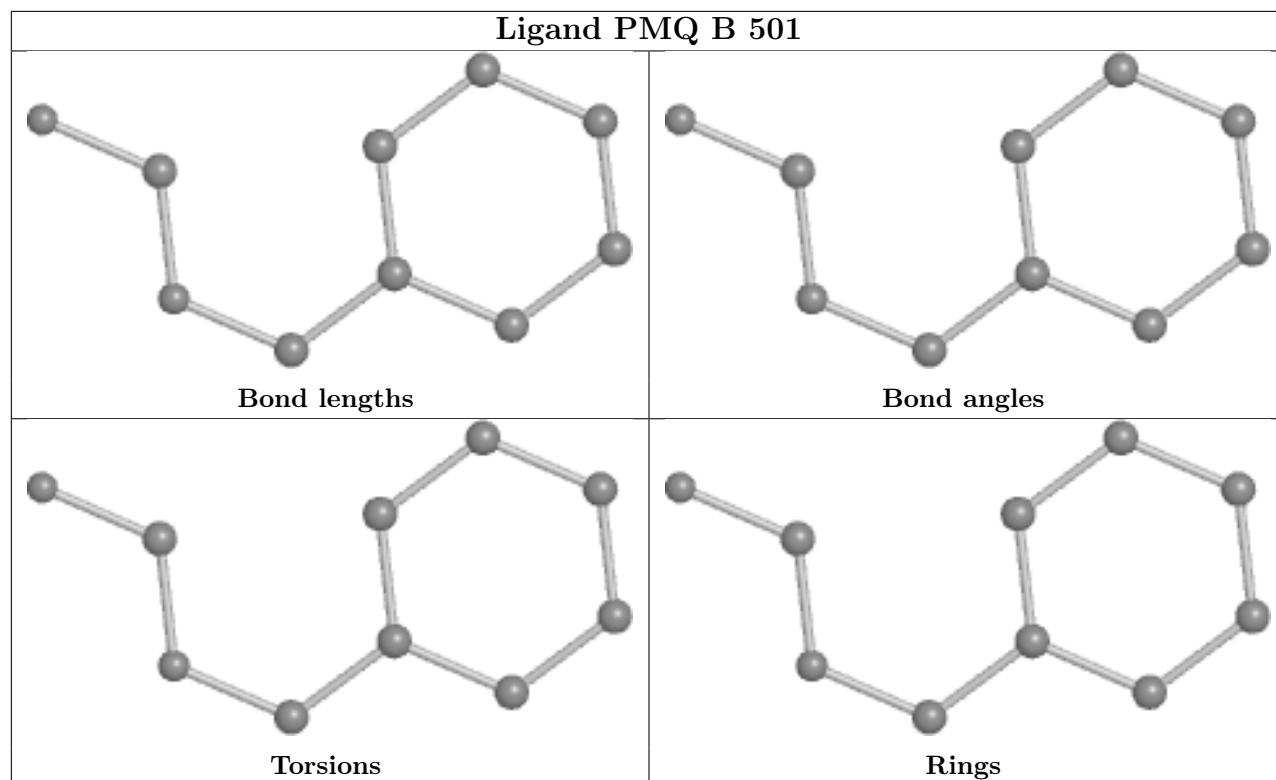
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	322/348 (92%)	0.19	17 (5%) 26 29	12, 20, 38, 57	0
1	B	327/348 (93%)	0.16	13 (3%) 38 42	12, 18, 36, 57	0
1	C	326/348 (93%)	0.51	29 (8%) 9 11	13, 22, 45, 57	0
1	D	320/348 (91%)	0.24	19 (5%) 22 24	13, 19, 41, 55	0
All	All	1295/1392 (93%)	0.28	78 (6%) 21 24	12, 20, 41, 57	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	66	THR	9.1
1	C	66	THR	8.8
1	A	63	THR	7.6
1	B	67	GLY	7.5
1	D	269	LYS	6.8
1	B	63	THR	6.5
1	C	65	VAL	6.3
1	A	62	SER	6.2
1	D	125	ASN	6.2
1	D	70	VAL	6.2
1	C	144	THR	6.1
1	D	126	ILE	5.6
1	A	70	VAL	5.5
1	B	65	VAL	5.4
1	A	124	SER	5.3
1	A	128	CYS	5.0
1	B	62	SER	4.9
1	A	125	ASN	4.9
1	D	144	THR	4.4
1	C	269	LYS	4.3
1	A	126	ILE	4.2

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Mol	Chain	Res	Type	RSRZ
1	C	268	LYS	4.1
1	C	236	ASN	4.1
1	D	124	SER	4.0
1	C	234	PRO	3.9
1	C	335	SER	3.9
1	D	266	ALA	3.8
1	C	126	ILE	3.8
1	B	125	ASN	3.8
1	A	335	SER	3.7
1	A	71	LYS	3.6
1	C	67	GLY	3.5
1	D	268	LYS	3.5
1	D	62	SER	3.4
1	A	69	GLN	3.1
1	C	63	THR	3.1
1	D	142	LYS	3.1
1	C	220	ASP	3.1
1	C	329	LYS	3.0
1	D	215	TYR	3.0
1	B	64	ASN	3.0
1	B	127	ASP	3.0
1	A	332	GLU	2.9
1	A	127	ASP	2.8
1	B	129	LEU	2.8
1	C	124	SER	2.8
1	D	267	ASN	2.8
1	A	130	VAL	2.7
1	C	267	ASN	2.7
1	D	61	GLY	2.6
1	A	329	LYS	2.6
1	C	145	ASP	2.6
1	A	179	CYS	2.6
1	C	215	TYR	2.5
1	B	25	ARG	2.5
1	D	271	PRO	2.5
1	D	236	ASN	2.5
1	B	126	ILE	2.5
1	C	70	VAL	2.5
1	C	146	GLU	2.4
1	C	142	LYS	2.4
1	D	143	SER	2.4
1	C	186	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	234	PRO	2.4
1	C	271	PRO	2.3
1	C	228	GLN	2.3
1	C	170	ALA	2.3
1	D	179	CYS	2.3
1	B	68	ASP	2.3
1	C	270	SER	2.2
1	C	331	TYR	2.2
1	B	130	VAL	2.2
1	C	237	SER	2.2
1	C	44	ILE	2.1
1	D	170	ALA	2.1
1	A	123	SER	2.1
1	D	25	ARG	2.0
1	C	43	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, 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.

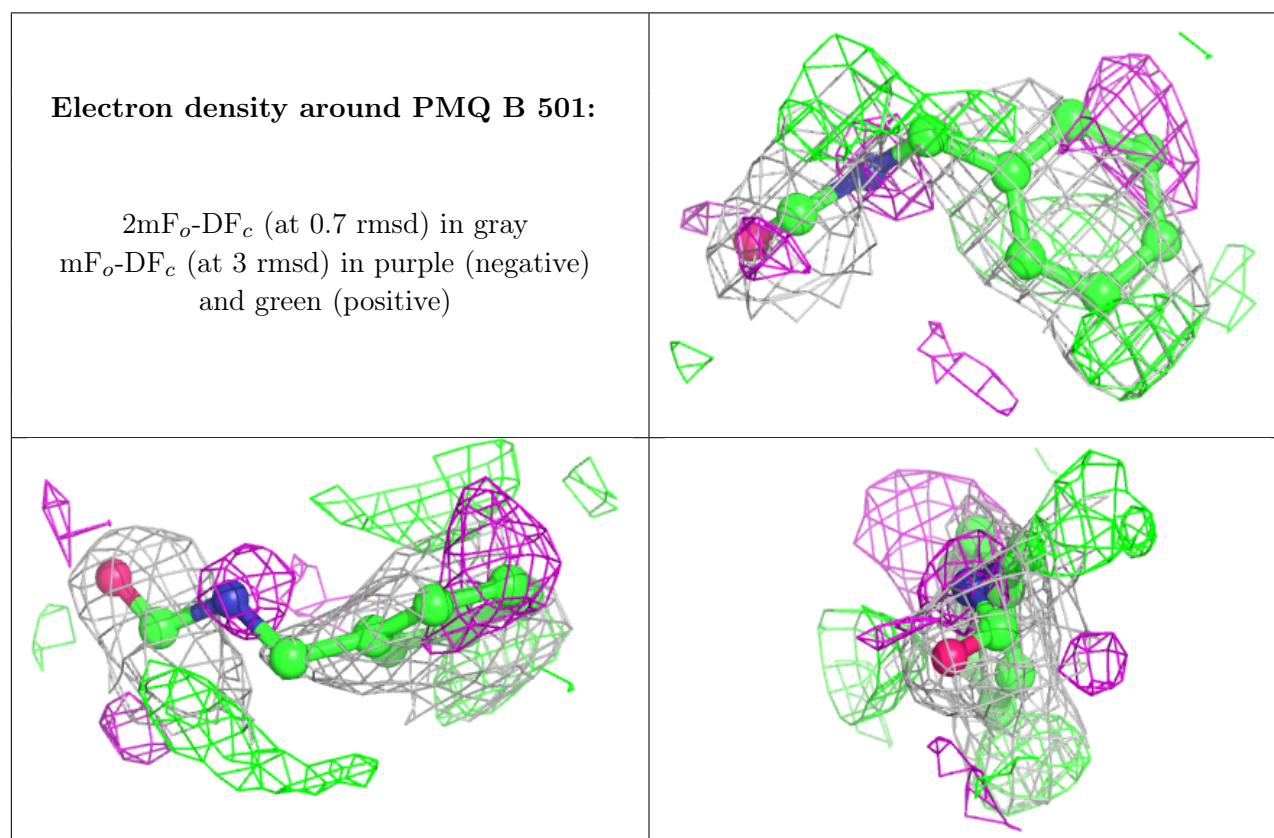
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	LSA	A	402	12/12	0.66	0.50	43,53,63,76	0
5	PMQ	B	501	10/11	0.70	0.33	37,41,44,53	0
6	GOL	C	402	6/6	0.83	0.29	26,36,40,43	0
6	GOL	D	402	6/6	0.84	0.20	23,39,46,46	0
6	GOL	B	503	6/6	0.94	0.15	21,26,28,31	0
2	AMP	C	401	23/23	0.96	0.08	17,21,23,25	0
2	AMP	A	401	23/23	0.97	0.07	16,18,21,23	0
2	AMP	B	502	23/23	0.97	0.07	14,17,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	AMP	D	401	23/23	0.98	0.07	15,18,20,24	0
4	MG	A	403	1/1	0.98	0.08	21,21,21,21	0
4	MG	B	504	1/1	0.99	0.09	15,15,15,15	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.