



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:58 PM UTC

PDB ID : 5QTJ / pdb_00005qtj
Title : T. brucei FPPS in complex with CID 47256035
Authors : Muenzker, L.; Petrick, J.K.; Schleberger, C.; Cornaciu, I.; Marquez, J.A.; Jahnke, W.
Deposited on : 2019-08-09
Resolution : 2.10 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

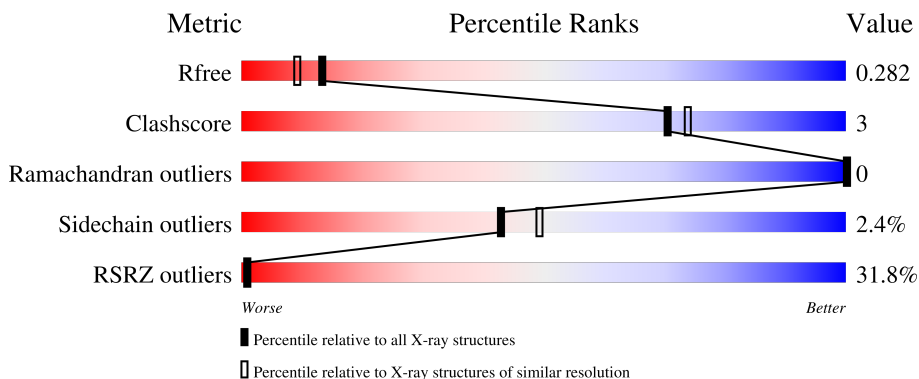
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	369	

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
2	PJS	A	401	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2753 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.

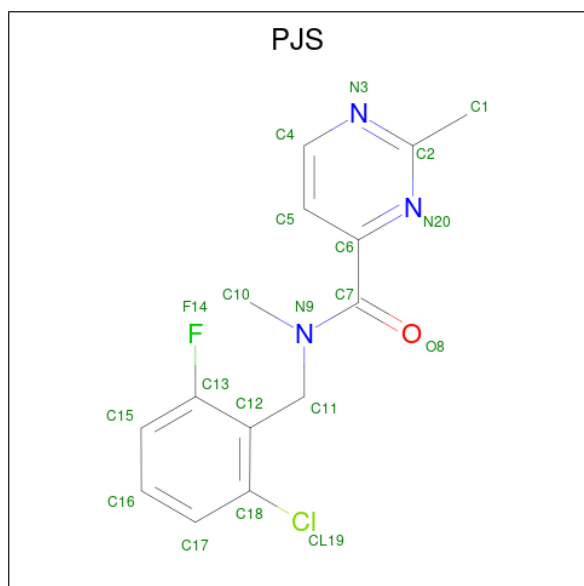
- Molecule 1 is a protein called Farnesyl pyrophosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	330	2629	1678	426	498	27	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q86C09
A	0	PRO	-	expression tag	UNP Q86C09

- Molecule 2 is N-[(2-chloro-6-fluorophenyl)methyl]-N,2-dimethylpyrimidine-4-carboxamide (CCD ID: PJS) (formula: C₁₄H₁₃ClFN₃O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	F	N	O	
2	A	1	20	14	1	1	3	1	0

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).

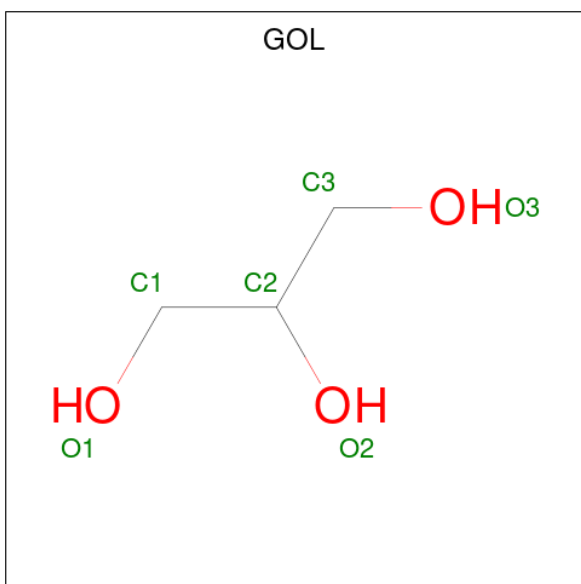


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		

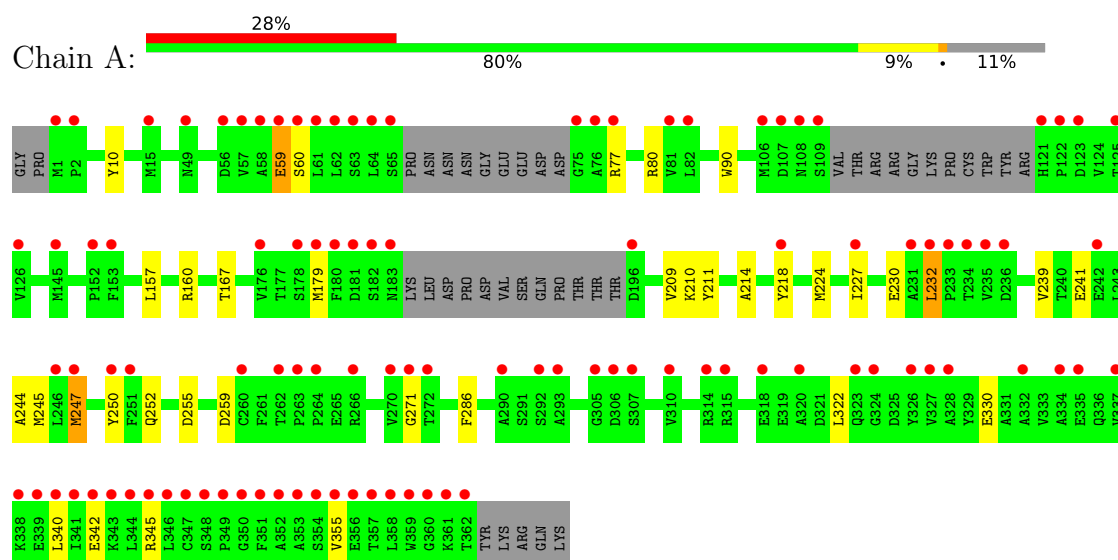
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	87	Total	O	0	0
			87	87		

3 Residue-property plots

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: Farnesyl pyrophosphate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	60.54Å 60.54Å 342.17Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	57.03 – 2.10 57.03 – 2.10	Depositor EDS
% Data completeness (in resolution range)	77.8 (57.03-2.10) 77.8 (57.03-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.240 , 0.278 0.244 , 0.282	Depositor DCC
R_{free} test set	885 reflections (3.78%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 74.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	2753	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.86% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, GOL, PJS, NA

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	0.11	0/2679	0.28	0/3619

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

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	2629	0	2584	18	0
2	A	20	0	0	0	0
3	A	10	0	0	0	0
4	A	1	0	0	0	0
5	A	6	0	8	0	0
6	A	87	0	0	0	0
All	All	2753	0	2592	18	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 (18) 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:A:167:THR:HG23	1:A:211:TYR:HD1	1.63	0.64
1:A:210:LYS:HG3	1:A:245:MET:SD	2.48	0.54
1:A:77:ARG:HG2	1:A:80:ARG:HH21	1.77	0.50
1:A:209:VAL:HG22	1:A:252:GLN:HG2	1.93	0.50
1:A:160:ARG:HD2	1:A:227:ILE:HD11	1.95	0.48
1:A:10:TYR:HB2	1:A:90:TRP:CZ2	2.49	0.48
1:A:157:LEU:HD11	1:A:224:MET:HE2	1.96	0.48
1:A:239:VAL:HG13	1:A:340:LEU:HD22	1.95	0.48
1:A:214:ALA:HA	1:A:218:TYR:HD2	1.79	0.47
1:A:167:THR:HG23	1:A:211:TYR:CD1	2.46	0.46
1:A:286:PHE:HB2	1:A:322:LEU:HD11	1.97	0.46
1:A:244:ALA:HA	1:A:247:MET:HE2	1.99	0.45
1:A:241:GLU:O	1:A:245:MET:HG2	2.18	0.42
1:A:342:GLU:CD	1:A:345:ARG:HE	2.27	0.42
1:A:59:GLU:OE1	1:A:60:SER:OG	2.31	0.42
1:A:259:ASP:O	1:A:271:GLY:HA3	2.20	0.42
1:A:250:TYR:CE2	1:A:330:GLU:HB3	2.55	0.41
1:A:227:ILE:HG12	1:A:232:LEU:HD12	2.04	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	322/369 (87%)	316 (98%)	6 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	286/322 (89%)	279 (98%)	7 (2%)	43	49

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

Mol	Chain	Res	Type
1	A	59	GLU
1	A	179	MET
1	A	230	GLU
1	A	232	LEU
1	A	247	MET
1	A	255	ASP
1	A	355	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	A	254	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\# Z > 2$
3	PO4	A	404	-	4,4,4	0.95	0	6,6,6	0.46	0
2	PJS	A	401	-	21,21,21	0.79	0	27,29,29	2.06	9 (33%)
5	GOL	A	405	-	5,5,5	0.92	0	5,5,5	1.12	1 (20%)
3	PO4	A	402	-	4,4,4	0.96	0	6,6,6	0.45	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
2	PJS	A	401	-	-	1/12/12/12	0/2/2/2
5	GOL	A	405	-	-	2/4/4/4	-

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	PJS	C6-N20-C2	4.86	122.29	116.70
2	A	401	PJS	C5-C6-N20	-4.20	118.02	122.92
2	A	401	PJS	C5-C4-N3	-3.14	120.13	123.97
2	A	401	PJS	N3-C2-N20	-3.10	120.37	125.53
2	A	401	PJS	C4-C5-C6	3.07	118.90	117.02
2	A	401	PJS	C1-C2-N3	2.65	120.02	117.20
2	A	401	PJS	F14-C13-C12	2.30	120.52	117.64
2	A	401	PJS	C18-C12-C13	2.15	118.61	115.20
2	A	401	PJS	O8-C7-C6	-2.14	115.03	118.90
5	A	405	GOL	C3-C2-C1	-2.05	104.28	111.80

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	PJS	C12-C11-N9-C7
5	A	405	GOL	O2-C2-C3-O3

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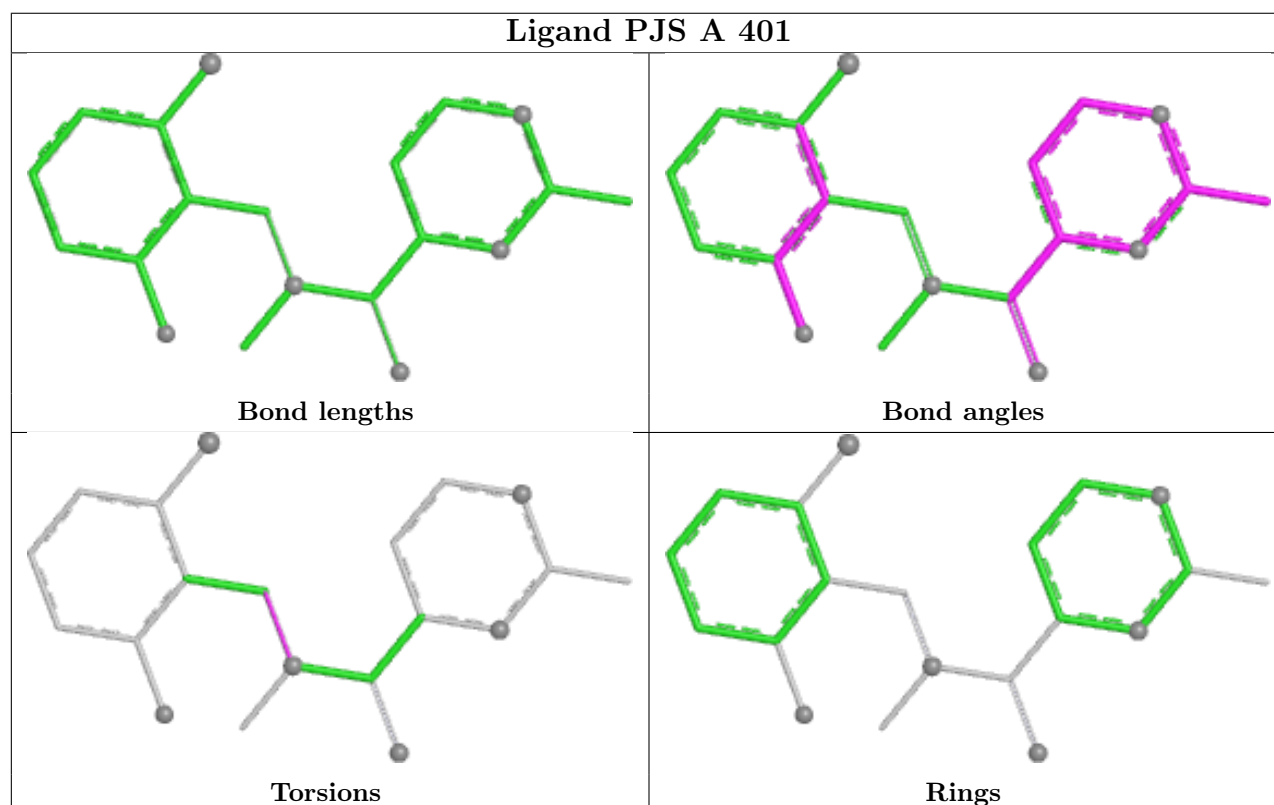
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Mol	Chain	Res	Type	Atoms
5	A	405	GOL	C1-C2-C3-O3

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	330/369 (89%)	2.10	105 (31%) 1 1	16, 51, 101, 139	13 (3%)

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	358	LEU	23.4
1	A	355	VAL	23.0
1	A	362	THR	23.0
1	A	357	THR	21.7
1	A	359	TRP	20.4
1	A	251	PHE	20.0
1	A	353	ALA	19.6
1	A	361	LYS	17.9
1	A	354	SER	17.8
1	A	218	TYR	16.8
1	A	360	GLY	16.2
1	A	356	GLU	14.1
1	A	247	MET	13.7
1	A	64	LEU	7.7
1	A	350	GLY	6.1
1	A	346	LEU	6.1
1	A	62	LEU	5.8
1	A	61	LEU	5.4
1	A	344	LEU	5.4
1	A	60	SER	5.1
1	A	75	GLY	5.1
1	A	81	VAL	4.7
1	A	352	ALA	4.5
1	A	56	ASP	4.5
1	A	342	GLU	4.4
1	A	233	PRO	4.4
1	A	196	ASP	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	293	ALA	4.2
1	A	63	SER	4.2
1	A	122	PRO	4.2
1	A	349	PRO	4.2
1	A	179	MET	3.9
1	A	351	PHE	3.9
1	A	337	VAL	3.8
1	A	180	PHE	3.8
1	A	338	LYS	3.8
1	A	1	MET	3.8
1	A	292	SER	3.7
1	A	106	MET	3.7
1	A	345	ARG	3.7
1	A	341	ILE	3.6
1	A	65	SER	3.6
1	A	59	GLU	3.6
1	A	82	LEU	3.6
1	A	232	LEU	3.5
1	A	58	ALA	3.5
1	A	182	SER	3.5
1	A	235	VAL	3.4
1	A	109	SER	3.4
1	A	123	ASP	3.3
1	A	234	THR	3.3
1	A	183	ASN	3.3
1	A	242	GLU	3.2
1	A	227	ILE	3.1
1	A	307	SER	3.1
1	A	77	ARG	3.1
1	A	318	GLU	3.0
1	A	324	GLY	3.0
1	A	305	GLY	3.0
1	A	181	ASP	2.9
1	A	347	CYS	2.9
1	A	272	THR	2.9
1	A	49	ASN	2.9
1	A	343	LYS	2.9
1	A	348	SER	2.9
1	A	328	ALA	2.8
1	A	340	LEU	2.8
1	A	314	ARG	2.8
1	A	152	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	335	GLU	2.7
1	A	250	TYR	2.7
1	A	246	LEU	2.7
1	A	264	PRO	2.7
1	A	121	HIS	2.7
1	A	306	ASP	2.7
1	A	320	ALA	2.6
1	A	339	GLU	2.6
1	A	76	ALA	2.6
1	A	231	ALA	2.6
1	A	236	ASP	2.6
1	A	153	PHE	2.5
1	A	15	MET	2.5
1	A	263	PRO	2.5
1	A	315	ARG	2.5
1	A	57	VAL	2.5
1	A	126	VAL	2.5
1	A	107	ASP	2.4
1	A	176	VAL	2.4
1	A	327	VAL	2.4
1	A	310	VAL	2.4
1	A	290	ALA	2.4
1	A	125	THR	2.4
1	A	271	GLY	2.3
1	A	334	ALA	2.3
1	A	262	THR	2.3
1	A	145	MET	2.3
1	A	323	GLN	2.2
1	A	178	SER	2.2
1	A	2	PRO	2.2
1	A	270	VAL	2.2
1	A	260	CYS	2.1
1	A	332	ALA	2.1
1	A	108	ASN	2.1
1	A	326	TYR	2.1
1	A	266	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

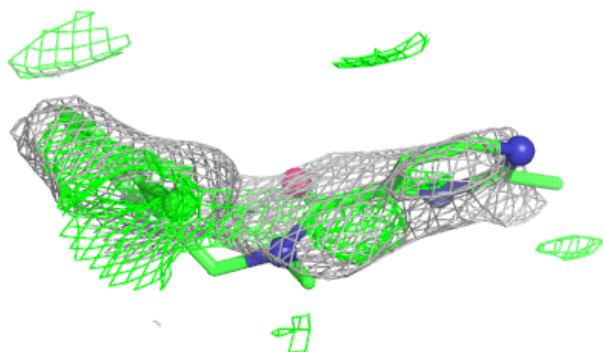
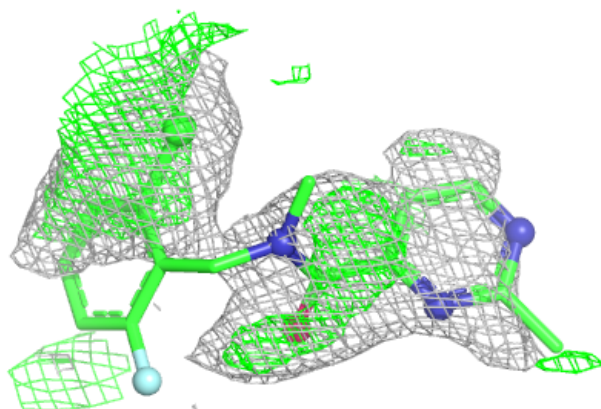
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PJS	A	401	20/20	0.76	0.52	42,53,56,59	20
3	PO4	A	404	5/5	0.76	0.22	106,107,108,110	0
3	PO4	A	402	5/5	0.78	0.19	114,116,118,123	0
5	GOL	A	405	6/6	0.78	0.17	56,63,67,68	0
4	NA	A	403	1/1	0.95	0.15	55,55,55,55	0

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

Electron density around PJS A 401:

$2mF_o-DF_c$ (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.