



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:53 PM UTC

PDB ID : 7FQR / pdb_00007fqr
Title : PanDDA analysis group deposition – Crystal structure of PTP1B in complex with FMOOA000666a
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Deposited on : 2022-10-19
Resolution : 1.90 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](#) ①) 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

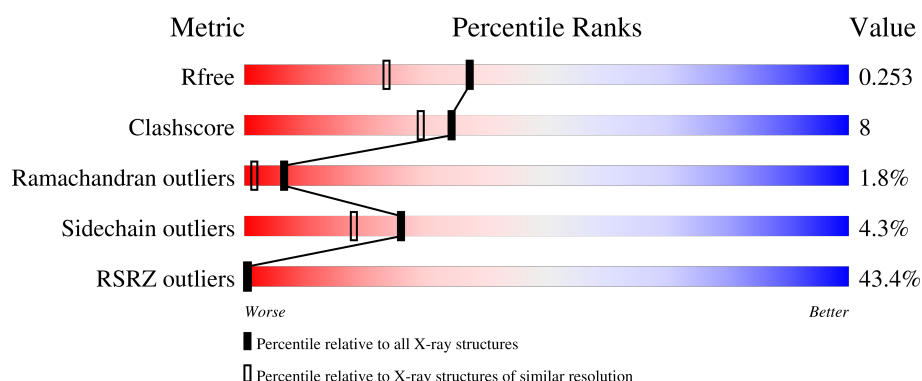
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	321	38% 71% 14% • 12%

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
3	JPD	A	702	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5163 atoms, of which 2490 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 Tyrosine-protein phosphatase non-receptor type 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	281	4931	1573	2457	424	461	16	0	22	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	SER	CYS	engineered mutation	UNP P18031
A	92	VAL	CYS	engineered mutation	UNP P18031

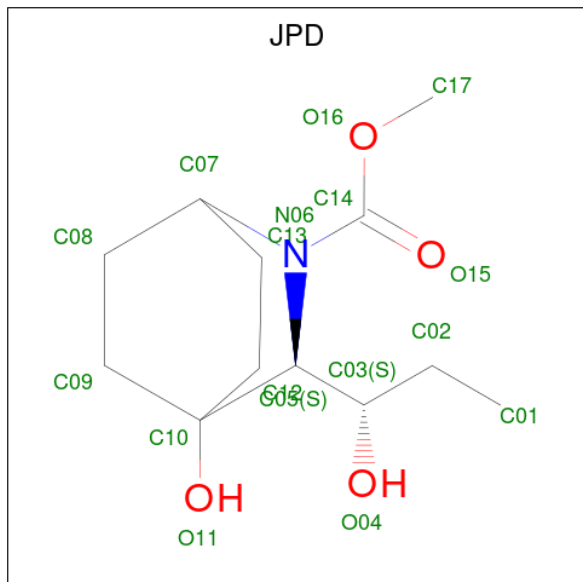
- Molecule 2 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



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

- Molecule 3 is methyl (1S,3S,4R)-4-hydroxy-3-[(1S)-1-hydroxypropyl]-2-azabicyclo[2.2.2]octa

ne-2-carboxylate (CCD ID: JPD) (formula: $C_{12}H_{21}NO_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			38	12	21	1	4		

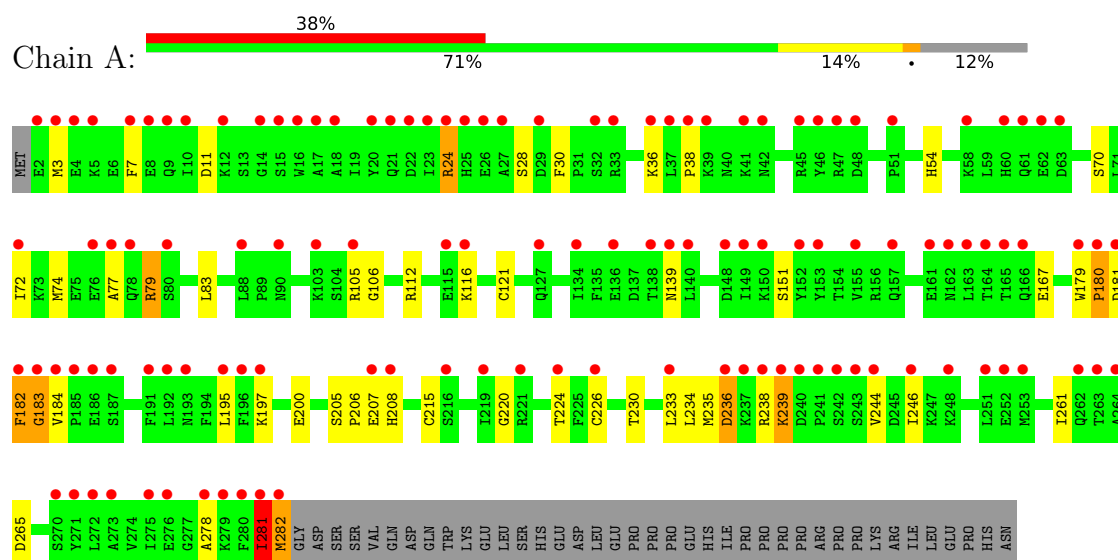
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	169	Total	O	0	10
			174	174		

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: Tyrosine-protein phosphatase non-receptor type 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	89.57Å 89.57Å 106.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.83 – 1.90 44.83 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.83-1.90) 100.0 (44.83-1.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.176 , 0.206 0.236 , 0.253	Depositor DCC
R_{free} test set	1553 reflections (3.94%)	wwPDB-VP
Wilson B-factor (Å ²)	36.5	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 74.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5163	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.15% 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: JPD, TRS

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	1.13	5/2531 (0.2%)	1.23	3/3414 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	106	GLY	C-O	7.15	1.32	1.23
1	A	70	SER	C-O	6.10	1.31	1.23
1	A	206	PRO	C-O	-6.02	1.16	1.24
1	A	195	LEU	C-O	-5.42	1.17	1.24
1	A	77	ALA	C-O	-5.41	1.17	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	236	ASP	CB-CA-C	-5.49	100.65	110.70
1	A	215	CYS	CB-CA-C	5.14	120.65	110.42
1	A	121	CYS	N-CA-CB	-5.01	102.45	110.77

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	2474	2457	2432	38	0
2	A	8	12	12	3	0
3	A	17	21	0	0	0
4	A	174	0	0	8	0
All	All	2673	2490	2444	38	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 8.

All (38) 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:236:ASP:OD1	1:A:281:ILE:HD12	1.64	0.95
1:A:181[B]:ASP:C	1:A:183[B]:GLY:H	1.92	0.78
1:A:24:ARG:NH2	4:A:803[A]:HOH:O	2.19	0.76
1:A:3:MET:CE	1:A:246[B]:ILE:HD11	2.19	0.73
1:A:116[A]:LYS:HE2	1:A:182[A]:PHE:CE2	2.27	0.70
1:A:234:LEU:O	1:A:238:ARG:HG3	1.92	0.70
1:A:179[A]:TRP:CD1	1:A:180[A]:PRO:HD2	2.28	0.68
1:A:3:MET:HE1	1:A:246[B]:ILE:HD11	1.76	0.68
1:A:79:ARG:CZ	1:A:233[B]:LEU:HD11	2.28	0.64
1:A:83:LEU:HD11	1:A:226[B]:CYS:SG	2.38	0.64
1:A:236:ASP:CG	1:A:281:ILE:HD12	2.27	0.60
1:A:278:ALA:O	1:A:282:MET:N	2.27	0.59
1:A:116[B]:LYS:HE3	1:A:181[B]:ASP:HB3	1.84	0.59
1:A:54:HIS:HB2	2:A:701:TRS:C3	2.33	0.58
1:A:54:HIS:HB2	2:A:701:TRS:H32	1.85	0.57
1:A:236:ASP:OD1	1:A:281:ILE:CD1	2.45	0.57
1:A:181[B]:ASP:O	1:A:183[B]:GLY:N	2.38	0.57
1:A:184[B]:VAL:CG2	4:A:818[B]:HOH:O	2.53	0.56
1:A:235:MET:HE1	1:A:278:ALA:HB2	1.88	0.56
1:A:167:GLU:OE1	4:A:802:HOH:O	2.17	0.56
1:A:112:ARG:NH2	1:A:181[A]:ASP:OD1	2.34	0.56
1:A:38:PRO:HD2	4:A:848:HOH:O	2.06	0.55
1:A:205:SER:HB3	1:A:207[A]:GLU:OE1	2.07	0.55
1:A:235:MET:HE1	1:A:278:ALA:CB	2.38	0.54
1:A:28:SER:HB3	1:A:30:PHE:CE2	2.43	0.52
1:A:200:GLU:HG3	4:A:821:HOH:O	2.10	0.51
1:A:220:GLY:O	1:A:224[B]:THR:HG23	2.10	0.50
1:A:181[B]:ASP:C	1:A:183[B]:GLY:N	2.59	0.50
1:A:3:MET:CE	1:A:246[B]:ILE:CD1	2.91	0.49
1:A:208:HIS:HD2	4:A:912:HOH:O	1.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184[B]:VAL:HG23	4:A:818[B]:HOH:O	2.14	0.47
1:A:74:MET:HE2	1:A:230:THR:HG21	1.98	0.46
1:A:72[B]:ILE:HD13	1:A:72[B]:ILE:N	2.32	0.44
1:A:208:HIS:HE1	4:A:917:HOH:O	1.99	0.44
1:A:54:HIS:HB2	2:A:701:TRS:H31	1.99	0.42
1:A:235:MET:O	1:A:239:LYS:N	2.52	0.42
1:A:7:PHE:O	1:A:11:ASP:HB2	2.19	0.41
1:A:36:LYS:HE2	1:A:36:LYS:HA	2.02	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	301/321 (94%)	279 (93%)	14 (5%)	8 (3%)	4 1

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	182[A]	PHE
1	A	182[B]	PHE
1	A	281	ILE
1	A	180[A]	PRO
1	A	180[B]	PRO
1	A	261	ILE
1	A	183[A]	GLY
1	A	183[B]	GLY

5.3.2 Protein sidechains ⓘ

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	276/294 (94%)	265 (96%)	11 (4%)	28	20

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ARG
1	A	79	ARG
1	A	105	ARG
1	A	139	ASN
1	A	151	SER
1	A	197	LYS
1	A	239	LYS
1	A	244	VAL
1	A	265	ASP
1	A	281	ILE
1	A	282	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	139	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	JPD	A	702	-	17,18,18	3.97	8 (47%)	19,27,27	3.25	8 (42%)
2	TRS	A	701	-	7,7,7	0.30	0	9,9,9	1.02	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
3	JPD	A	702	-	-	11/12/38/38	0/3/2/2
2	TRS	A	701	-	-	6/9/9/9	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	JPD	C03-C05	11.84	1.64	1.53
3	A	702	JPD	C05-N06	6.19	1.56	1.46
3	A	702	JPD	C14-N06	5.40	1.44	1.36
3	A	702	JPD	O16-C14	4.63	1.42	1.34
3	A	702	JPD	O11-C10	-3.22	1.39	1.44
3	A	702	JPD	C02-C03	2.73	1.60	1.52
3	A	702	JPD	C12-C10	2.39	1.56	1.53
3	A	702	JPD	C13-C07	2.06	1.57	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	JPD	C12-C10-C09	-9.76	101.96	109.70
3	A	702	JPD	O16-C14-N06	6.38	116.59	111.16
3	A	702	JPD	O16-C14-O15	-3.71	117.88	124.60
3	A	702	JPD	C08-C07-C13	-3.43	103.41	111.17
3	A	702	JPD	O11-C10-C09	2.91	114.43	108.20
3	A	702	JPD	C08-C07-N06	2.88	112.70	109.05
3	A	702	JPD	O11-C10-C12	2.68	113.94	108.20
3	A	702	JPD	C07-N06-C14	2.55	128.04	119.98

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	TRS	C1-C-C3-O3
2	A	701	TRS	C2-C-C3-O3
2	A	701	TRS	N-C-C3-O3
3	A	702	JPD	C01-C02-C03-O04
3	A	702	JPD	C01-C02-C03-C05
3	A	702	JPD	C02-C03-C05-C10
3	A	702	JPD	C02-C03-C05-N06
3	A	702	JPD	O04-C03-C05-N06
3	A	702	JPD	O15-C14-N06-C05
3	A	702	JPD	O16-C14-N06-C05
3	A	702	JPD	O15-C14-N06-C07
3	A	702	JPD	O16-C14-N06-C07
3	A	702	JPD	N06-C14-O16-C17
3	A	702	JPD	O15-C14-O16-C17
2	A	701	TRS	C3-C-C2-O2
2	A	701	TRS	N-C-C2-O2
2	A	701	TRS	C1-C-C2-O2

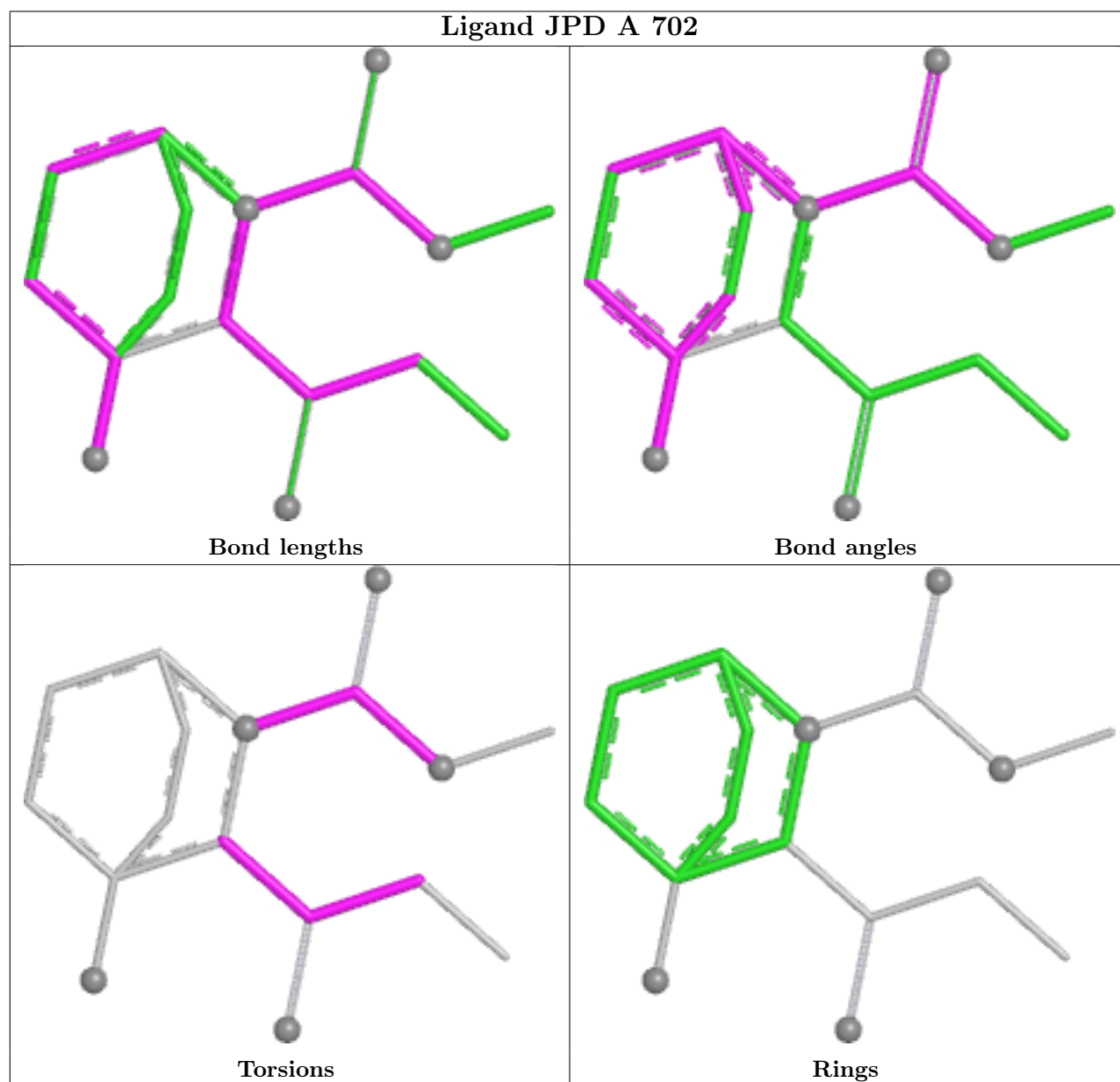
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	TRS	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 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 ⓘ

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	281/321 (87%)	3.68	122 (43%) 0 0	6, 34, 72, 114	51 (18%)

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	182[A]	PHE	25.4
1	A	280	PHE	21.1
1	A	241	PRO	20.0
1	A	181[A]	ASP	18.6
1	A	281	ILE	18.5
1	A	179[A]	TRP	18.5
1	A	196	PHE	17.7
1	A	272[A]	LEU	17.2
1	A	271	TYR	17.0
1	A	226[A]	CYS	16.4
1	A	183[A]	GLY	16.0
1	A	282	MET	15.9
1	A	192	LEU	15.6
1	A	184[A]	VAL	15.4
1	A	246[A]	ILE	15.4
1	A	185	PRO	15.3
1	A	78[A]	GLN	15.0
1	A	240	ASP	15.0
1	A	193	ASN	14.5
1	A	180[A]	PRO	14.3
1	A	243	SER	14.3
1	A	197	LYS	14.2
1	A	242	SER	14.1
1	A	224[A]	THR	14.0
1	A	279	LYS	13.6
1	A	237	LYS	13.3
1	A	152	TYR	13.2

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Mol	Chain	Res	Type	RSRZ
1	A	25[A]	HIS	13.2
1	A	72[A]	ILE	13.1
1	A	153	TYR	13.1
1	A	233[A]	LEU	12.9
1	A	238	ARG	12.7
1	A	187	SER	12.4
1	A	244	VAL	12.2
1	A	80[A]	SER	12.0
1	A	216[A]	SER	11.9
1	A	262[A]	GLN	11.5
1	A	148	ASP	11.3
1	A	207[A]	GLU	11.3
1	A	76	GLU	11.2
1	A	150	LYS	11.1
1	A	252[A]	GLU	11.0
1	A	186	GLU	10.8
1	A	116[A]	LYS	10.7
1	A	253[A]	MET	10.6
1	A	105	ARG	10.4
1	A	221	ARG	9.9
1	A	239	LYS	9.7
1	A	115	GLU	9.5
1	A	157	GLN	8.6
1	A	12	LYS	8.3
1	A	32[A]	SER	6.6
1	A	138	THR	5.2
1	A	46	TYR	4.6
1	A	3	MET	4.6
1	A	161	GLU	4.3
1	A	16	TRP	4.3
1	A	166	GLN	4.1
1	A	7	PHE	4.0
1	A	24	ARG	4.0
1	A	26	GLU	3.9
1	A	41	LYS	3.8
1	A	264	ALA	3.8
1	A	61	GLN	3.8
1	A	23	ILE	3.6
1	A	47	ARG	3.6
1	A	29	ASP	3.5
1	A	278	ALA	3.5
1	A	21	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	127	GLN	3.5
1	A	17	ALA	3.5
1	A	18	ALA	3.5
1	A	33	ARG	3.4
1	A	5	LYS	3.4
1	A	251	LEU	3.3
1	A	139	ASN	3.3
1	A	37	LEU	3.1
1	A	36	LYS	3.0
1	A	42	ASN	3.0
1	A	8	GLU	3.0
1	A	48	ASP	3.0
1	A	149	ILE	3.0
1	A	140	LEU	2.9
1	A	62	GLU	2.9
1	A	134	ILE	2.8
1	A	4	GLU	2.8
1	A	270	SER	2.8
1	A	90	ASN	2.8
1	A	164	THR	2.7
1	A	88	LEU	2.7
1	A	162	ASN	2.6
1	A	275	ILE	2.6
1	A	236	ASP	2.6
1	A	77	ALA	2.6
1	A	136	GLU	2.5
1	A	27	ALA	2.5
1	A	20	TYR	2.5
1	A	248	LYS	2.5
1	A	14	GLY	2.4
1	A	45	ARG	2.4
1	A	60	HIS	2.4
1	A	195	LEU	2.3
1	A	208	HIS	2.3
1	A	22	ASP	2.3
1	A	63	ASP	2.3
1	A	2	GLU	2.3
1	A	58	LYS	2.3
1	A	163	LEU	2.3
1	A	219	ILE	2.2
1	A	155	VAL	2.2
1	A	10	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	9	GLN	2.2
1	A	15	SER	2.2
1	A	273	ALA	2.2
1	A	191	PHE	2.1
1	A	263	THR	2.1
1	A	276	GLU	2.1
1	A	39	LYS	2.1
1	A	165	THR	2.1
1	A	51	PRO	2.0
1	A	103	LYS	2.0
1	A	38	PRO	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

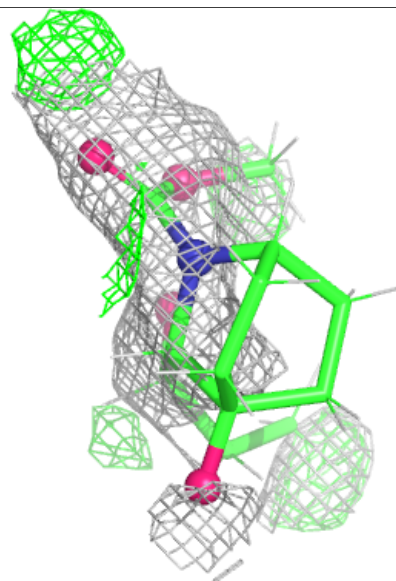
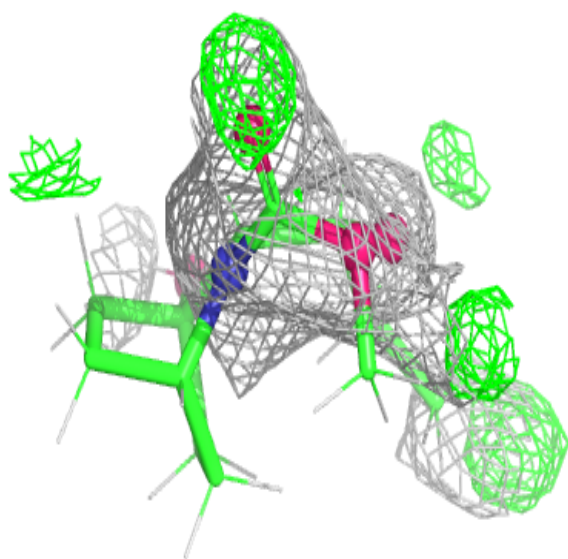
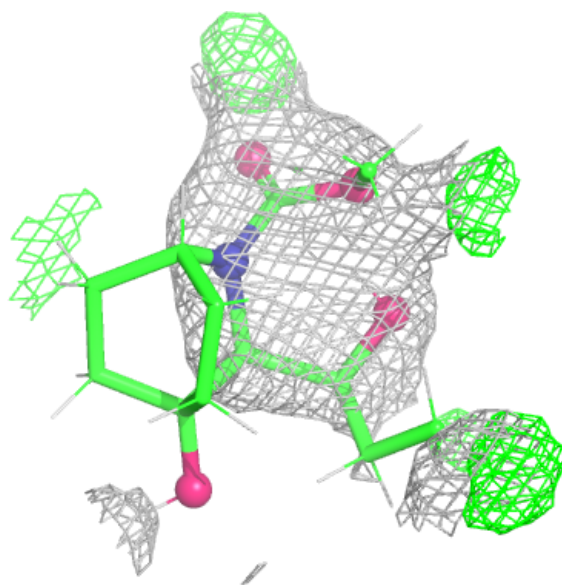
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	JPD	A	702	17/17	0.71	0.48	20,60,62,63	38
2	TRS	A	701	8/8	0.80	0.19	53,69,82,82	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 JPD A 702:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.