



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:19 PM UTC

PDB ID : 7FTT / pdb_00007ftt
Title : Crystal Structure of human cyclic GMP-AMP synthase in complex with 5-bromo-N-[[2-fluoro-5-(1-methylpyrazol-4-yl)phenyl]methyl]-2-hydroxybenzamide
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Deposited on : 2023-02-08
Resolution : 2.23 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

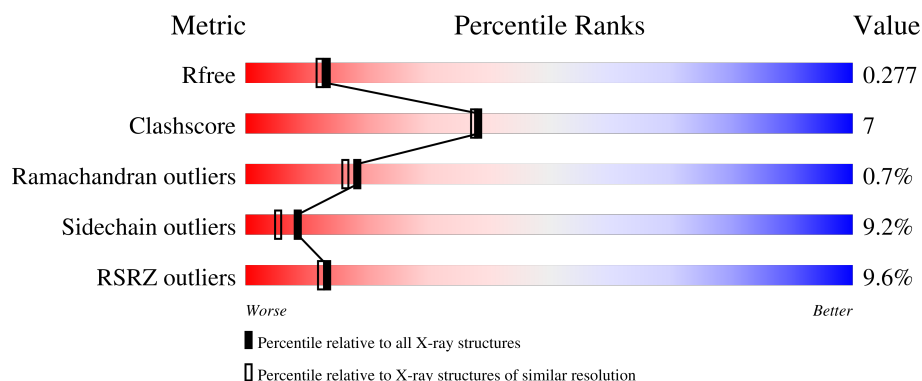
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	362	7% 72% 19% • 5%
1	B	362	11% 73% 22% • •

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5761 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.

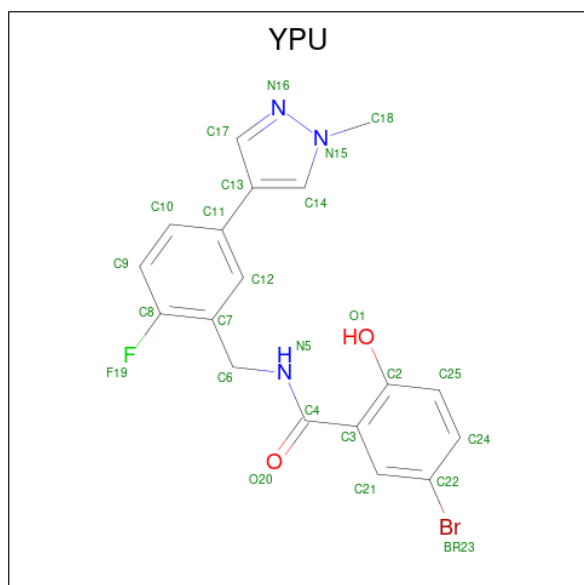
- Molecule 1 is a protein called Cyclic GMP-AMP synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	0	0	0
			2838	1819	488	516	15			
1	B	348	Total	C	N	O	S	0	0	0
			2865	1833	493	524	15			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is 5-bromo-N-{[(5P)-2-fluoro-5-(1-methyl-1H-pyrazol-4-yl)phenyl]methyl}-2-hydroxybenzamide (CCD ID: YPU) (formula: C₁₈H₁₅BrFN₃O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	Br	C	F	N	O	0	0
			25	1	18	1	3	2		
3	B	1	Total	Br	C	F	N	O	0	0
			25	1	18	1	3	2		

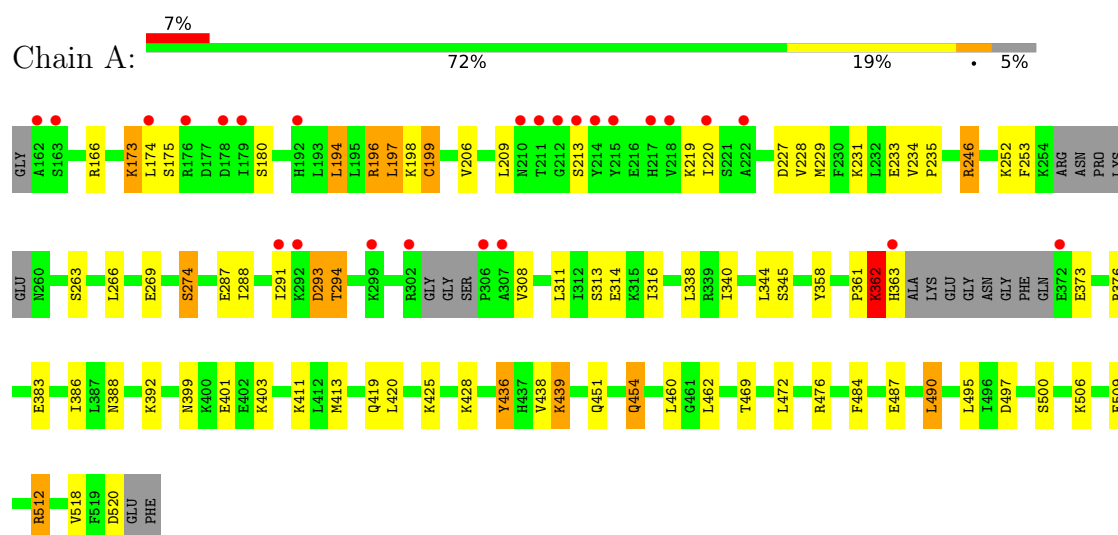
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	O	0	0
			3	3		
4	B	3	Total	O	0	0
			3	3		

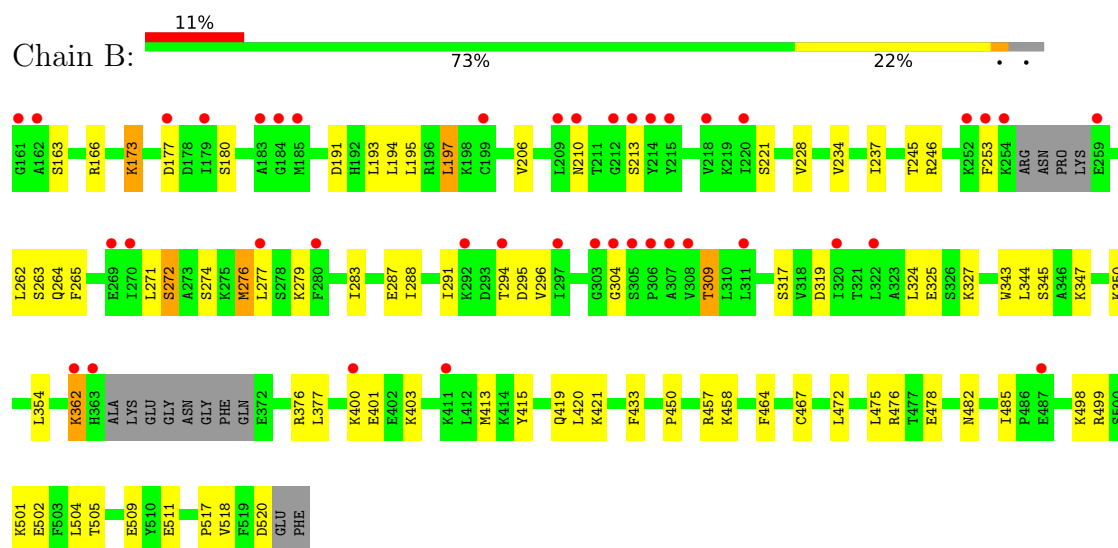
3 Residue-property plots [i](#)

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: Cyclic GMP-AMP synthase



• Molecule 1: Cyclic GMP-AMP synthase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	218.77Å 46.23Å 89.75Å 90.00° 110.39° 90.00°	Depositor
Resolution (Å)	56.15 – 2.23 56.15 – 2.23	Depositor EDS
% Data completeness (in resolution range)	63.4 (56.15-2.23) 60.9 (56.15-2.23)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.55 (at 2.22Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.209 , 0.287 (Not available) , 0.277	Depositor DCC
R_{free} test set	1232 reflections (2.98%)	wwPDB-VP
Wilson B-factor (Å ²)	42.8	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 38.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5761	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 7.57% 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: YPU, ZN

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	0.41	0/2892	0.61	0/3875
1	B	0.37	0/2920	0.56	0/3914
All	All	0.39	0/5812	0.59	0/7789

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	2838	0	2889	43	0
1	B	2865	0	2909	38	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	25	0	0	0	0
3	B	25	0	0	0	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
All	All	5761	0	5798	80	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 7.

All (80) 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:476:ARG:NH2	1:A:509:GLU:OE2	2.01	0.92
1:A:469:THR:OG1	1:A:512:ARG:NH2	2.11	0.83
1:B:400:LYS:HA	1:B:403:LYS:HE2	1.69	0.73
1:A:313:SER:OG	1:A:314:GLU:N	2.16	0.72
1:A:413:MET:HB3	1:A:438:VAL:CG1	2.22	0.70
1:B:234:VAL:HB	1:B:237:ILE:HD11	1.76	0.68
1:B:271:LEU:HD21	1:B:276:MET:HE1	1.78	0.65
1:A:197:LEU:HB3	1:A:206:VAL:HG11	1.78	0.65
1:B:309:THR:OG1	1:B:319:ASP:OD1	2.18	0.61
1:B:288:ILE:HG23	1:B:296:VAL:HB	1.82	0.61
1:B:475:LEU:HD23	1:B:501:LYS:HG2	1.84	0.58
1:B:279:LYS:O	1:B:283:ILE:HG13	2.04	0.57
1:B:287:GLU:O	1:B:291:ILE:HG12	2.05	0.56
1:A:388:ASN:O	1:B:347:LYS:HE2	2.06	0.56
1:A:291:ILE:HG22	1:A:294:THR:H	1.69	0.56
1:B:210:ASN:HB2	1:B:213:SER:OG	2.07	0.55
1:B:325:GLU:OE1	1:B:327:LYS:NZ	2.38	0.55
1:B:362:LYS:HA	1:B:362:LYS:HE2	1.90	0.54
1:B:511:GLU:OE1	1:B:517:PRO:HD2	2.08	0.54
1:A:209:LEU:HD11	1:A:358:TYR:CZ	2.42	0.54
1:B:482:ASN:HB3	1:B:485:ILE:O	2.10	0.52
1:A:413:MET:HB3	1:A:438:VAL:HG11	1.92	0.52
1:A:291:ILE:HG21	1:A:294:THR:HG23	1.91	0.51
1:A:383:GLU:OE2	1:A:439:LYS:HG2	2.11	0.51
1:B:350:LYS:O	1:B:354:LEU:HG	2.11	0.51
1:B:498:LYS:HE3	1:B:502:GLU:OE2	2.11	0.51
1:A:209:LEU:HD22	1:A:229:MET:SD	2.51	0.50
1:B:421:LYS:NZ	1:B:433:PHE:O	2.35	0.50
1:B:253:PHE:HE1	1:B:271:LEU:HB2	1.77	0.50
1:A:419:GLN:HB3	1:A:518:VAL:HG22	1.94	0.50
1:B:191:ASP:O	1:B:195:LEU:HG	2.12	0.49
1:B:173:LYS:HD3	1:B:177:ASP:OD2	2.11	0.49
1:A:338:LEU:HD13	1:A:484:PHE:CE1	2.47	0.49
1:A:344:LEU:HD11	1:A:386:ILE:HG23	1.94	0.49
1:A:311:LEU:HD12	1:A:316:ILE:O	2.13	0.49
1:A:246:ARG:HD2	1:A:487:GLU:HB2	1.95	0.48
1:A:274:SER:OG	1:A:373:GLU:OE2	2.30	0.48
1:A:436:TYR:OH	1:A:490:LEU:HD22	2.13	0.48
1:A:194:LEU:O	1:A:198:LYS:HG3	2.14	0.48
1:A:451:GLN:HB2	1:A:454:GLN:CG	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:SER:O	1:A:213:SER:OG	2.27	0.47
1:A:313:SER:HG	1:A:314:GLU:N	2.11	0.47
1:B:193:LEU:O	1:B:197:LEU:HB2	2.13	0.47
1:A:233:GLU:HG3	1:A:234:VAL:N	2.29	0.47
1:A:291:ILE:HG23	1:A:293:ASP:OD2	2.15	0.47
1:B:413:MET:HE2	1:B:467:CYS:HB3	1.96	0.46
1:A:451:GLN:HB2	1:A:454:GLN:HG3	1.97	0.46
1:A:497:ASP:OD1	1:A:497:ASP:N	2.49	0.46
1:A:361:PRO:O	1:A:362:LYS:HB2	2.15	0.46
1:B:413:MET:HG2	1:B:464:PHE:HE1	1.81	0.45
1:A:196:ARG:HG2	1:A:287:GLU:HB2	1.97	0.45
1:B:197:LEU:HB3	1:B:206:VAL:HG11	1.99	0.44
1:B:221:SER:HB3	1:B:415:TYR:HE1	1.82	0.44
1:A:392:LYS:HB2	1:A:392:LYS:HE2	1.85	0.44
1:B:245:THR:O	1:B:246:ARG:HB2	2.18	0.44
1:B:475:LEU:HD21	1:B:504:LEU:HD23	1.99	0.44
1:B:221:SER:HB3	1:B:415:TYR:CE1	2.52	0.43
1:B:344:LEU:HD23	1:B:344:LEU:HA	1.74	0.43
1:B:419:GLN:HB3	1:B:518:VAL:HG22	2.00	0.43
1:A:233:GLU:HG2	1:A:235:PRO:HD3	1.99	0.43
1:A:196:ARG:O	1:A:199:CYS:HB2	2.19	0.43
1:A:173:LYS:C	1:A:175:SER:H	2.26	0.43
1:A:344:LEU:HD23	1:A:344:LEU:HA	1.80	0.43
1:A:206:VAL:HA	1:A:231:LYS:O	2.18	0.43
1:A:451:GLN:O	1:A:454:GLN:HG3	2.19	0.43
1:A:252:LYS:NZ	1:A:269:GLU:OE1	2.36	0.42
1:B:476:ARG:NH2	1:B:509:GLU:OE2	2.30	0.42
1:A:399:ASN:O	1:A:403:LYS:HG2	2.20	0.42
1:A:495:LEU:HD23	1:A:495:LEU:HA	1.88	0.42
1:B:420:LEU:HD23	1:B:420:LEU:HA	1.86	0.42
1:B:265:PHE:O	1:B:272:SER:HB3	2.20	0.42
1:B:166:ARG:NH2	1:B:457:ARG:HG3	2.35	0.42
1:B:472:LEU:HD22	1:B:505:THR:HG23	2.02	0.41
1:A:472:LEU:HD23	1:A:472:LEU:HA	1.85	0.41
1:B:343:TRP:HB2	1:B:450:PRO:HB3	2.03	0.41
1:A:338:LEU:O	1:A:340:ILE:N	2.53	0.40
1:A:253:PHE:CE2	1:A:266:LEU:HD21	2.56	0.40
1:A:420:LEU:HD23	1:A:420:LEU:HA	1.87	0.40
1:B:377:LEU:HA	1:B:377:LEU:HD23	1.87	0.40
1:B:478:GLU:HG2	1:B:501:LYS:NZ	2.37	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	335/362 (92%)	314 (94%)	18 (5%)	3 (1%)	14	11
1	B	342/362 (94%)	323 (94%)	17 (5%)	2 (1%)	21	20
All	All	677/724 (94%)	637 (94%)	35 (5%)	5 (1%)	18	16

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	345	SER
1	A	362	LYS
1	B	345	SER
1	B	304	GLY
1	A	174	LEU

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	321/334 (96%)	286 (89%)	35 (11%)	6	3
1	B	323/334 (97%)	299 (93%)	24 (7%)	13	10
All	All	644/668 (96%)	585 (91%)	59 (9%)	8	5

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	ARG

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Mol	Chain	Res	Type
1	A	173	LYS
1	A	180	SER
1	A	194	LEU
1	A	196	ARG
1	A	197	LEU
1	A	199	CYS
1	A	219	LYS
1	A	220	ILE
1	A	227	ASP
1	A	228	VAL
1	A	246	ARG
1	A	263	SER
1	A	274	SER
1	A	288	ILE
1	A	293	ASP
1	A	294	THR
1	A	308	VAL
1	A	362	LYS
1	A	363	HIS
1	A	376	ARG
1	A	401	GLU
1	A	411	LYS
1	A	425	LYS
1	A	428	LYS
1	A	436	TYR
1	A	439	LYS
1	A	454	GLN
1	A	460	LEU
1	A	462	LEU
1	A	490	LEU
1	A	500	SER
1	A	506	LYS
1	A	512	ARG
1	A	520	ASP
1	B	163	SER
1	B	173	LYS
1	B	180	SER
1	B	194	LEU
1	B	197	LEU
1	B	228	VAL
1	B	262	LEU
1	B	263	SER

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Mol	Chain	Res	Type
1	B	264	GLN
1	B	272	SER
1	B	274	SER
1	B	276	MET
1	B	277	LEU
1	B	294	THR
1	B	295	ASP
1	B	309	THR
1	B	317	SER
1	B	324	LEU
1	B	362	LYS
1	B	376	ARG
1	B	401	GLU
1	B	458	LYS
1	B	499	ARG
1	B	520	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	264	GLN
1	A	419	GLN
1	B	264	GLN
1	B	429	HIS
1	B	507	GLN
1	B	514	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	YPU	A	602	-	27,27,27	0.20	0	37,38,38	0.60	1 (2%)
3	YPU	B	602	-	27,27,27	0.25	0	37,38,38	0.57	1 (2%)

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	YPU	A	602	-	-	0/13/13/13	0/3/3/3
3	YPU	B	602	-	-	0/13/13/13	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	YPU	C7-C6-N5	-2.13	108.85	113.15
3	B	602	YPU	C7-C6-N5	-2.03	109.05	113.15

There are no chirality outliers.

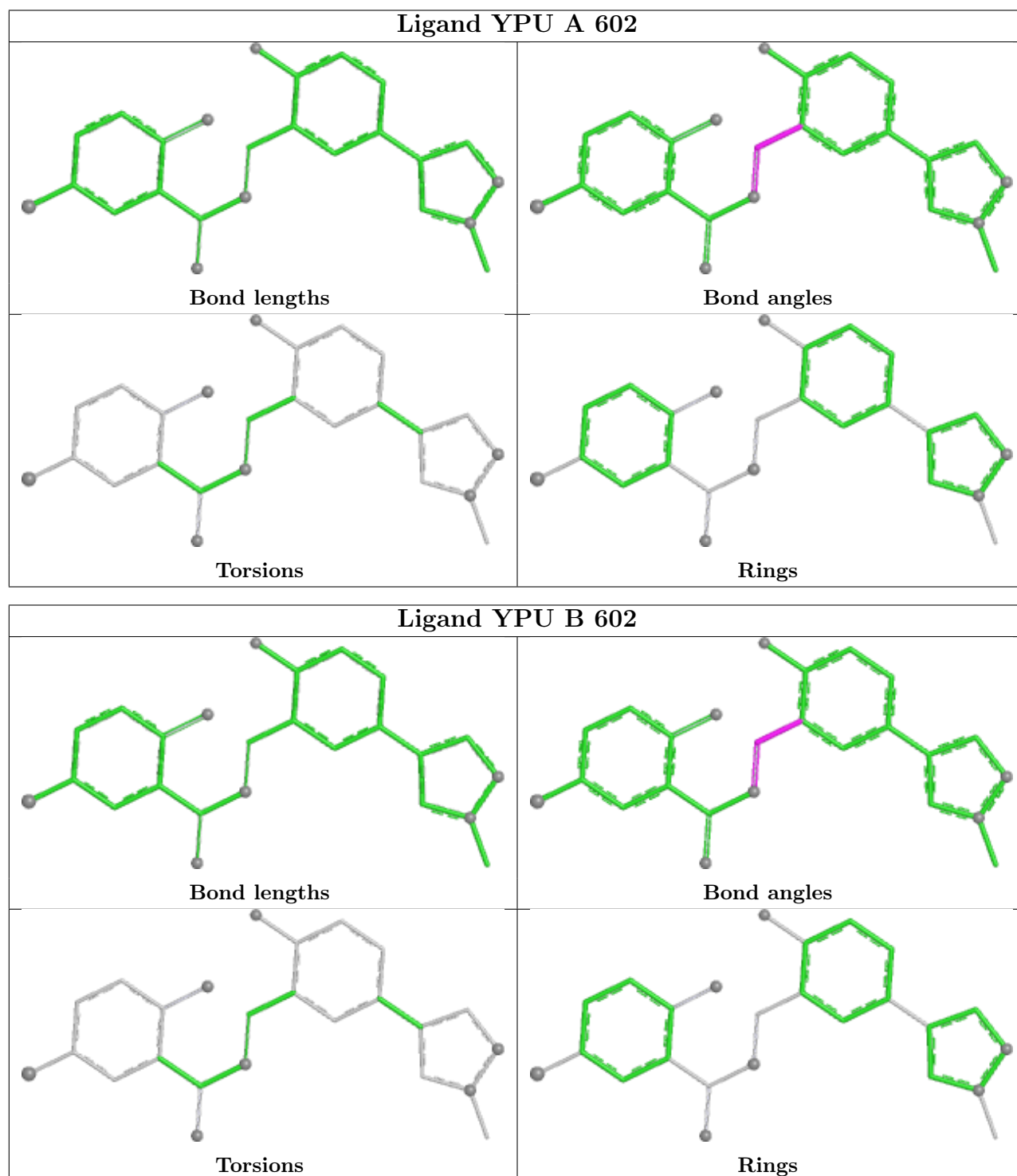
There are no torsion outliers.

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	343/362 (94%)	0.29	25 (7%) 21 19	21, 48, 92, 157	0
1	B	348/362 (96%)	0.56	41 (11%) 9 8	25, 56, 120, 175	0
All	All	691/724 (95%)	0.43	66 (9%) 13 12	21, 51, 110, 175	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	304	GLY	7.6
1	B	218	VAL	5.6
1	B	322	LEU	4.9
1	A	218	VAL	4.8
1	B	305	SER	4.4
1	B	215	TYR	4.3
1	A	213	SER	4.0
1	B	306	PRO	3.9
1	B	212	GLY	3.9
1	B	214	TYR	3.8
1	A	215	TYR	3.8
1	A	363	HIS	3.6
1	B	213	SER	3.5
1	A	212	GLY	3.5
1	A	179	ILE	3.4
1	B	303	GLY	3.3
1	B	259	GLU	3.3
1	A	291	ILE	3.3
1	B	179	ILE	3.3
1	B	161	GLY	3.2
1	B	184	GLY	3.2
1	A	302	ARG	3.1
1	A	306	PRO	3.1
1	B	280	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	308	VAL	3.0
1	A	178	ASP	3.0
1	B	363	HIS	2.9
1	B	220	ILE	2.9
1	A	220	ILE	2.9
1	B	199	CYS	2.8
1	B	400	LYS	2.8
1	A	162	ALA	2.8
1	B	162	ALA	2.7
1	B	253	PHE	2.7
1	B	294	THR	2.6
1	B	411	LYS	2.6
1	B	210	ASN	2.5
1	B	297	ILE	2.5
1	B	311	LEU	2.5
1	B	183	ALA	2.5
1	A	211	THR	2.5
1	B	209	LEU	2.4
1	B	185	MET	2.4
1	B	252	LYS	2.4
1	A	174	LEU	2.4
1	A	292	LYS	2.4
1	B	277	LEU	2.3
1	B	270	ILE	2.3
1	B	292	LYS	2.3
1	B	320	ILE	2.2
1	A	176	ARG	2.2
1	B	269	GLU	2.2
1	A	299	LYS	2.2
1	B	362	LYS	2.2
1	A	372	GLU	2.2
1	A	163	SER	2.1
1	A	214	TYR	2.1
1	B	487	GLU	2.1
1	B	177	ASP	2.1
1	A	307	ALA	2.1
1	A	210	ASN	2.1
1	A	222	ALA	2.0
1	B	254	LYS	2.0
1	B	307	ALA	2.0
1	A	192	HIS	2.0
1	A	217	HIS	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](#)

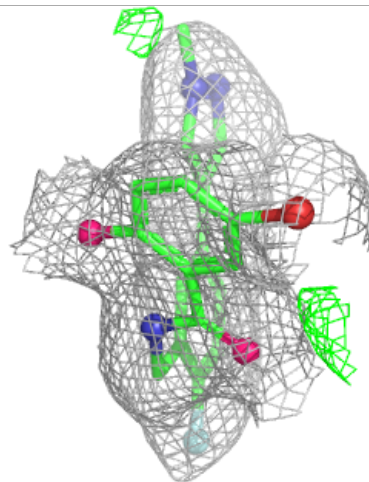
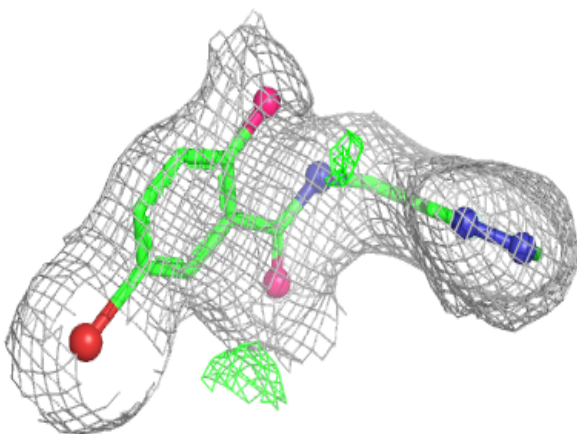
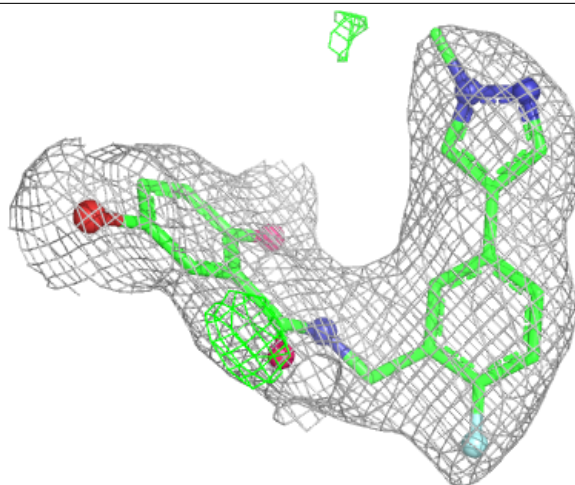
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	YPU	B	602	25/25	0.97	0.08	27,41,59,62	0
3	YPU	A	602	25/25	0.98	0.07	23,37,49,55	0
2	ZN	A	601	1/1	1.00	0.02	41,41,41,41	0
2	ZN	B	601	1/1	1.00	0.02	43,43,43,43	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.

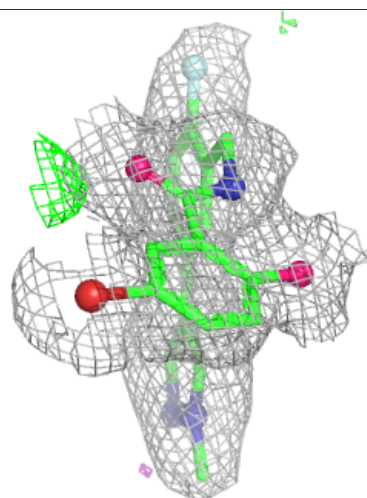
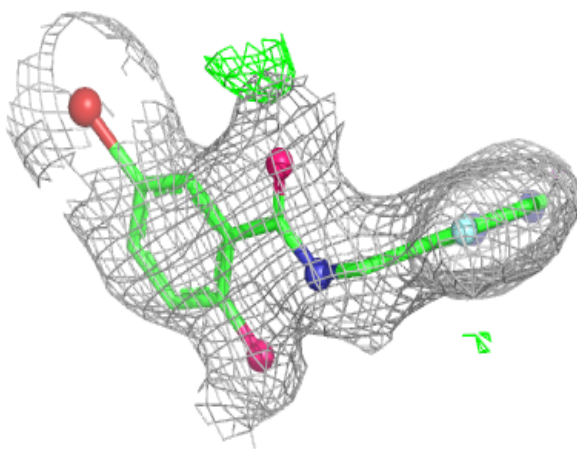
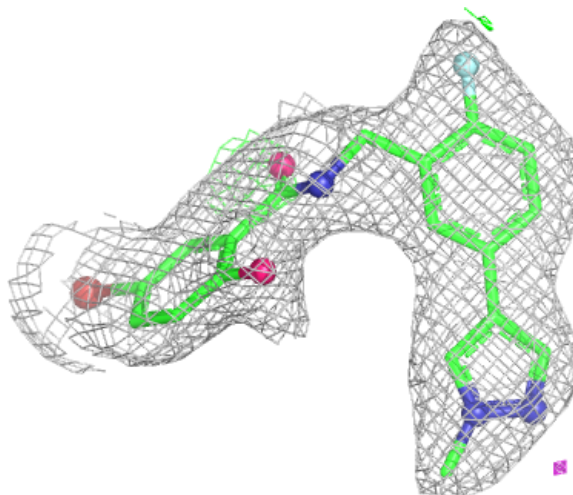
Electron density around YPU B 602:

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



Electron density around YPU A 602:

$2mF_o-DF_c$ (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.