



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:30 PM UTC

PDB ID : 4EWH / pdb_00004ewh
Title : Co-crystal structure of ACK1 with inhibitor
Authors : Liu, J.; Walker, N.; Wang, Z.
Deposited on : 2012-04-27
Resolution : 2.50 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

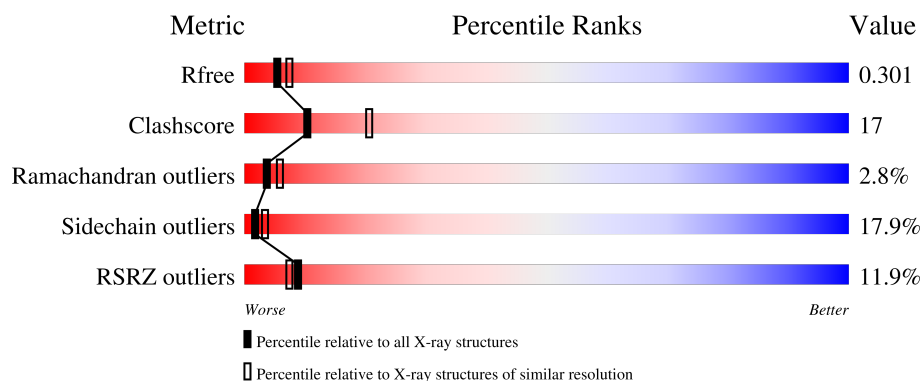
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	275	12% 61% 29% 10%
1	B	275	12% 58% 31% 11%

2 Entry composition [i](#)

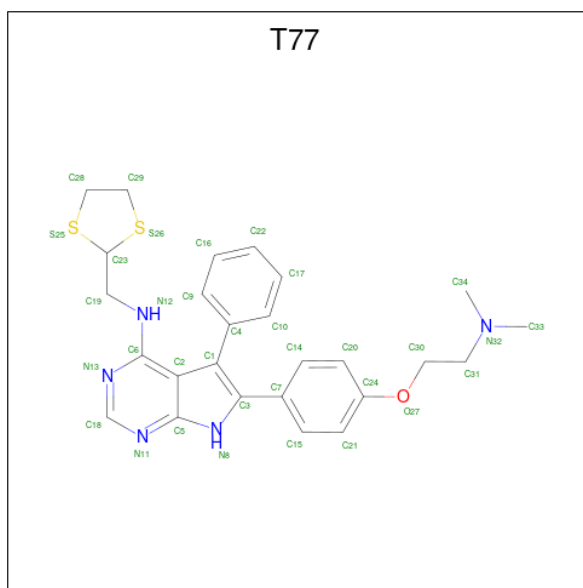
There are 3 unique types of molecules in this entry. The entry contains 4502 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Activated CDC42 kinase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	274	Total	C	N	O	P	S	0	0	0
			2202	1401	390	395	1	15			
1	A	275	Total	C	N	O	P	S	0	0	0
			2209	1405	391	397	1	15			

- Molecule 2 is 6-{4-[2-(dimethylamino)ethoxy]phenyl}-N-(1,3-dithiolan-2-ylmethyl)-5-phenyl-7H-pyrrolo[2,3-d]pyrimidin-4-amine (CCD ID: T77) (formula: C₂₆H₂₉N₅OS₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			34	26	5	1	2		
2	A	1	Total	C	N	O	S	0	0
			34	26	5	1	2		

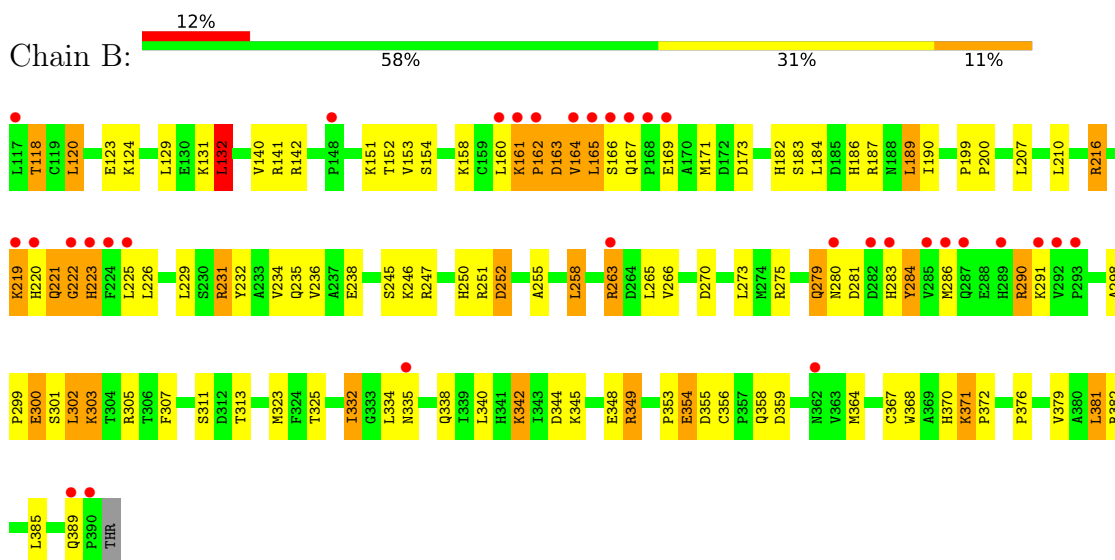
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	16	Total 16	O 16	0	0
3	A	7	Total 7	O 7	0	0

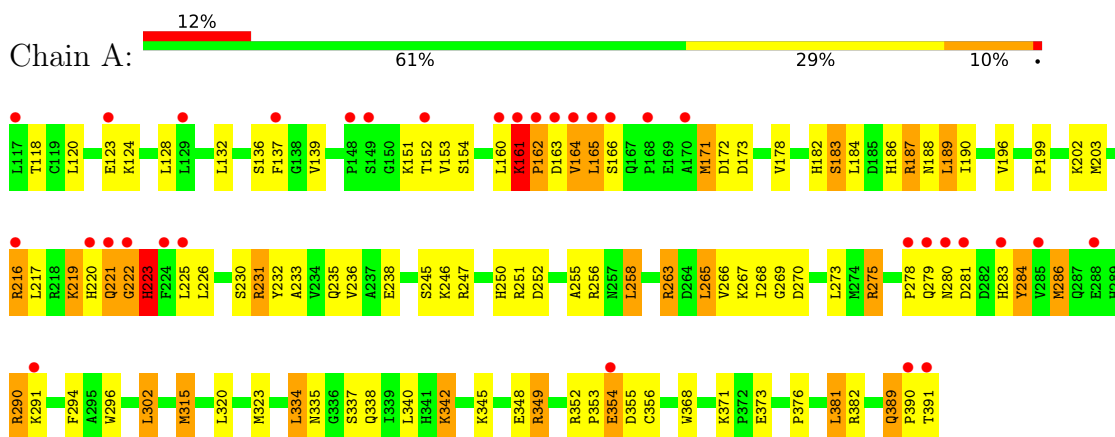
3 Residue-property plots

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: Activated CDC42 kinase 1



• Molecule 1: Activated CDC42 kinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	201.20Å 42.48Å 71.03Å 90.00° 95.29° 90.00°	Depositor
Resolution (Å)	100.00 – 2.50 100.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (100.00-2.50) 99.7 (100.00-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.256 , 0.313 (Not available) , 0.301	Depositor DCC
R_{free} test set	1083 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	47.1	Xtriage
Anisotropy	0.510	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 33.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4502	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.60% 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: T77, PTR

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	1.15	5/2245 (0.2%)	1.23	9/3038 (0.3%)
1	B	1.17	3/2238 (0.1%)	1.29	9/3028 (0.3%)
All	All	1.16	8/4483 (0.2%)	1.26	18/6066 (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
1	A	0	1
1	B	0	2
All	All	0	3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	323	MET	SD-CE	-7.95	1.59	1.79
1	A	315	MET	SD-CE	-7.29	1.61	1.79
1	A	286	MET	SD-CE	-6.49	1.63	1.79
1	A	203	MET	SD-CE	-6.45	1.63	1.79
1	B	234	VAL	CA-CB	5.92	1.60	1.54
1	B	332	ILE	CA-CB	5.52	1.59	1.54
1	A	323	MET	SD-CE	-5.44	1.66	1.79
1	A	178	VAL	CA-CB	5.06	1.59	1.54

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	129	LEU	N-CA-C	7.65	115.05	108.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	166	SER	N-CA-C	7.26	122.24	112.88
1	A	166	SER	N-CA-C	6.53	122.05	113.30
1	B	132	LEU	N-CA-C	-6.26	105.77	113.41
1	A	294	PHE	N-CA-C	6.17	118.81	111.71
1	B	311	SER	N-CA-C	-6.01	105.77	113.23
1	A	389	GLN	CA-C-N	5.94	127.27	119.84
1	A	389	GLN	C-N-CA	5.94	127.27	119.84
1	B	385	LEU	N-CA-C	5.77	117.64	111.36
1	A	268	ILE	N-CA-C	-5.54	101.53	108.84
1	A	172	ASP	N-CA-C	5.47	116.93	111.07
1	A	161	LYS	N-CA-C	5.42	121.79	109.81
1	A	223	HIS	N-CA-C	5.25	121.99	110.80
1	B	325	THR	N-CA-C	-5.24	106.12	112.88
1	B	313	THR	OG1-CB-CG2	-5.17	98.95	109.30
1	A	231	ARG	N-CA-C	-5.16	105.72	112.23
1	B	252	ASP	N-CA-CB	-5.02	105.77	111.79
1	B	223	HIS	N-CA-C	5.01	121.48	110.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	389	GLN	Peptide
1	B	163	ASP	Peptide
1	B	389	GLN	Peptide

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	2209	0	2202	70	1
1	B	2202	0	2195	79	1
2	A	34	0	29	4	0
2	B	34	0	29	5	0
3	A	7	0	0	0	0
3	B	16	0	0	1	0
All	All	4502	0	4455	152	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 17.

All (152) 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:235:GLN:HE21	1:A:266:VAL:HG12	1.34	0.92
1:A:186:HIS:HD2	1:A:188:ASN:H	1.17	0.92
1:B:235:GLN:NE2	1:B:266:VAL:HG12	1.87	0.89
1:B:216:ARG:CG	1:B:216:ARG:HH11	1.87	0.88
1:B:235:GLN:HE21	1:B:266:VAL:HG12	1.37	0.86
1:A:118:THR:HG21	1:A:182:HIS:CD2	2.14	0.83
1:A:235:GLN:NE2	1:A:266:VAL:HG12	1.93	0.83
1:B:118:THR:HG21	1:B:182:HIS:CD2	2.15	0.80
1:A:251:ARG:NH1	1:A:284:PTR:HE2	1.95	0.80
1:B:216:ARG:HH11	1:B:216:ARG:HG2	1.48	0.78
1:A:186:HIS:CD2	1:A:188:ASN:H	2.01	0.78
1:B:251:ARG:NH1	1:B:286:MET:HE2	2.02	0.75
1:A:250:HIS:HD2	1:A:252:ASP:H	1.34	0.75
1:A:335:ASN:H	1:A:338:GLN:HE21	1.33	0.75
1:B:160:LEU:HG	1:B:162:PRO:HD3	1.70	0.74
1:A:118:THR:HG21	1:A:182:HIS:HD2	1.54	0.73
1:B:342:LYS:HE2	1:B:348:GLU:OE2	1.90	0.72
1:B:299:PRO:O	1:B:300:GLU:C	2.33	0.71
1:A:232:TYR:O	1:A:236:VAL:HG23	1.90	0.71
1:A:251:ARG:HH12	1:A:284:PTR:HE2	1.52	0.71
1:A:160:LEU:HG	1:A:162:PRO:HD3	1.74	0.70
1:B:349:ARG:NH1	1:B:368:TRP:O	2.25	0.70
1:A:161:LYS:N	1:A:162:PRO:HD3	2.08	0.69
1:A:186:HIS:HB3	1:A:189:LEU:HD22	1.73	0.69
1:B:161:LYS:N	1:B:162:PRO:HD3	2.07	0.68
1:A:182:HIS:O	1:A:183:SER:CB	2.41	0.68
1:A:216:ARG:CG	1:A:216:ARG:HH11	2.07	0.67
1:B:250:HIS:HE1	1:B:270:ASP:O	1.77	0.67
1:A:279:GLN:NE2	1:A:279:GLN:HA	2.09	0.67
1:A:349:ARG:NH1	1:A:368:TRP:O	2.28	0.67
1:A:163:ASP:C	1:A:165:LEU:H	2.00	0.67
1:B:216:ARG:HG2	1:B:216:ARG:NH1	2.11	0.66
1:A:247:ARG:NH1	1:A:278:PRO:O	2.23	0.66
1:B:118:THR:HG21	1:B:182:HIS:HD2	1.60	0.65
1:B:279:GLN:NE2	1:B:279:GLN:HA	2.09	0.65
1:B:376:PRO:HB2	1:B:381:LEU:HD13	1.77	0.65
1:B:171:MET:CE	1:A:171:MET:CE	2.73	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:335:ASN:H	1:B:338:GLN:HE21	1.43	0.64
1:B:186:HIS:HB3	1:B:189:LEU:HD22	1.80	0.63
1:B:163:ASP:C	1:B:165:LEU:H	2.07	0.62
1:A:163:ASP:C	1:A:165:LEU:N	2.57	0.62
1:A:250:HIS:CD2	1:A:252:ASP:H	2.16	0.62
1:B:302:LEU:HB3	1:B:340:LEU:HD13	1.82	0.61
1:A:221:GLN:O	1:A:222:GLY:C	2.43	0.61
1:B:171:MET:HE2	1:A:171:MET:CE	2.29	0.61
2:B:401:T77:C4	2:B:401:T77:H15	2.30	0.61
1:B:160:LEU:HG	1:B:162:PRO:CD	2.30	0.61
1:A:216:ARG:HH11	1:A:216:ARG:HG3	1.66	0.60
2:B:401:T77:H15	2:B:401:T77:C9	2.32	0.60
2:A:401:T77:C4	2:A:401:T77:H15	2.31	0.60
1:A:160:LEU:HG	1:A:162:PRO:CD	2.31	0.59
1:A:182:HIS:O	1:A:183:SER:HB3	2.02	0.59
1:B:344:ASP:OD2	1:B:370:HIS:HE1	1.85	0.59
1:A:251:ARG:NH1	1:A:284:PTR:CE2	2.63	0.59
1:B:250:HIS:HD2	1:B:252:ASP:H	1.50	0.59
1:A:342:LYS:HE2	1:A:348:GLU:OE2	2.02	0.59
1:B:163:ASP:C	1:B:165:LEU:N	2.62	0.58
1:B:275:ARG:CZ	1:B:284:PTR:HE1	2.34	0.58
1:B:221:GLN:O	1:B:222:GLY:C	2.46	0.58
1:A:118:THR:CG2	1:A:182:HIS:CD2	2.87	0.57
1:A:246:LYS:O	1:A:247:ARG:HB2	2.03	0.57
1:B:120:LEU:HB2	1:A:118:THR:HG23	1.85	0.57
1:B:216:ARG:HH11	1:B:216:ARG:HG3	1.69	0.57
1:A:335:ASN:H	1:A:338:GLN:NE2	2.01	0.56
1:B:184:LEU:HB2	3:B:509:HOH:O	2.06	0.56
1:B:182:HIS:O	1:B:183:SER:CB	2.55	0.55
1:B:286:MET:SD	1:B:290:ARG:HG3	2.46	0.55
1:B:246:LYS:O	1:B:247:ARG:HB2	2.06	0.54
1:A:196:VAL:HB	1:A:202:LYS:HB2	1.90	0.54
1:B:251:ARG:HG2	1:B:307:PHE:CD1	2.42	0.53
1:B:303:LYS:HG3	1:B:340:LEU:HD11	1.91	0.53
1:A:235:GLN:HE21	1:A:266:VAL:CG1	2.15	0.52
1:A:219:LYS:HB3	1:A:220:HIS:CD2	2.43	0.52
1:B:250:HIS:CD2	1:B:252:ASP:H	2.27	0.52
1:A:280:ASN:O	1:A:281:ASP:HB2	2.09	0.52
1:A:216:ARG:CG	1:A:216:ARG:NH1	2.73	0.52
1:B:353:PRO:HB2	1:B:356:CYS:HB2	1.92	0.51
1:A:280:ASN:O	1:A:280:ASN:OD1	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:ARG:CG	1:B:216:ARG:NH1	2.57	0.51
1:B:229:LEU:O	1:B:232:TYR:HB2	2.11	0.50
1:A:250:HIS:HE1	1:A:270:ASP:O	1.94	0.50
1:A:265:LEU:HD13	1:A:267:LYS:HE2	1.94	0.50
1:B:335:ASN:H	1:B:338:GLN:NE2	2.10	0.50
1:A:187:ARG:O	1:A:267:LYS:HD3	2.12	0.50
1:B:354:GLU:O	1:B:355:ASP:HB2	2.11	0.50
1:B:299:PRO:O	1:B:302:LEU:N	2.46	0.49
1:B:232:TYR:O	1:B:236:VAL:HG23	2.13	0.48
1:B:275:ARG:CZ	1:B:284:PTR:CE1	2.91	0.48
1:A:376:PRO:HG2	1:A:381:LEU:CD1	2.44	0.48
1:B:255:ALA:HA	1:B:258:LEU:HD22	1.95	0.48
1:B:118:THR:CG2	1:B:182:HIS:CD2	2.92	0.48
2:A:401:T77:H15	2:A:401:T77:C9	2.44	0.47
2:A:401:T77:H1	2:A:401:T77:H11	1.48	0.47
1:B:286:MET:CG	1:B:290:ARG:HG3	2.44	0.47
1:B:171:MET:CE	1:A:171:MET:HE2	2.45	0.47
1:A:354:GLU:O	1:A:355:ASP:HB2	2.14	0.46
1:A:376:PRO:HG2	1:A:381:LEU:HD13	1.98	0.46
2:A:401:T77:C10	2:A:401:T77:H23	2.28	0.46
1:B:250:HIS:CE1	1:B:270:ASP:O	2.64	0.46
1:A:137:PHE:C	1:A:137:PHE:CD1	2.94	0.46
1:A:280:ASN:O	1:A:280:ASN:CG	2.58	0.46
1:A:173:ASP:OD2	1:A:290:ARG:NH2	2.40	0.45
1:B:371:LYS:O	1:B:372:PRO:C	2.59	0.45
1:B:280:ASN:O	1:B:280:ASN:OD1	2.34	0.45
1:B:300:GLU:O	1:B:301:SER:C	2.59	0.45
1:B:162:PRO:HD2	1:B:163:ASP:H	1.81	0.45
1:A:263:ARG:HG3	1:A:263:ARG:NH1	2.31	0.45
1:B:335:ASN:OD1	1:B:338:GLN:HG3	2.16	0.45
1:A:233:ALA:HB1	1:A:320:LEU:HD11	1.99	0.45
1:B:164:VAL:HG21	1:B:199:PRO:HB3	1.99	0.45
1:B:231:ARG:O	1:B:235:GLN:HG3	2.17	0.44
1:B:284:PTR:HE2	1:B:286:MET:HA	1.99	0.44
1:A:128:LEU:HD11	1:A:202:LYS:HE2	1.99	0.44
1:B:142:ARG:HH11	1:B:207:LEU:HD21	1.83	0.44
1:A:255:ALA:HA	1:A:258:LEU:HD22	1.99	0.44
1:A:286:MET:CG	1:A:290:ARG:HG3	2.47	0.44
2:B:401:T77:H1	2:B:401:T77:H11	1.54	0.44
1:A:275:ARG:HE	1:A:275:ARG:HB3	1.57	0.44
1:B:300:GLU:O	1:B:303:LYS:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:LYS:HB3	1:B:220:HIS:CD2	2.53	0.43
2:B:401:T77:C10	2:B:401:T77:H23	2.31	0.43
1:B:251:ARG:CZ	1:B:286:MET:HE2	2.48	0.43
1:B:290:ARG:O	1:B:305:ARG:NH2	2.51	0.43
1:B:162:PRO:HB2	1:B:167:GLN:HG3	2.01	0.43
1:B:173:ASP:OD2	1:B:290:ARG:NH2	2.42	0.43
1:B:280:ASN:O	1:B:281:ASP:HB2	2.18	0.43
1:A:163:ASP:CG	1:A:164:VAL:N	2.77	0.43
1:A:220:HIS:O	1:A:223:HIS:HB3	2.19	0.43
1:B:182:HIS:O	1:B:183:SER:HB3	2.19	0.43
1:A:160:LEU:C	1:A:162:PRO:HD3	2.43	0.43
1:A:184:LEU:N	1:A:184:LEU:HD23	2.33	0.42
1:A:296:TRP:O	1:A:315:MET:HG2	2.19	0.42
1:A:290:ARG:H	1:A:290:ARG:HG2	1.64	0.42
1:A:302:LEU:HB3	1:A:340:LEU:HD13	2.00	0.42
1:B:163:ASP:CG	1:B:164:VAL:N	2.78	0.42
1:B:263:ARG:NH1	1:B:263:ARG:HG3	2.34	0.42
1:A:190:ILE:HG12	1:A:269:GLY:HA2	2.01	0.42
1:A:164:VAL:HG21	1:A:199:PRO:HB3	2.01	0.42
1:B:132:LEU:HG	2:B:401:T77:C7	2.50	0.41
1:B:190:ILE:HD13	1:B:190:ILE:HA	1.90	0.41
1:B:171:MET:CE	1:A:171:MET:HE1	2.49	0.41
1:B:199:PRO:HA	1:B:200:PRO:HA	1.90	0.41
1:B:364:MET:O	1:B:367:CYS:HB2	2.20	0.41
1:A:334:LEU:N	1:A:334:LEU:CD1	2.83	0.41
1:A:353:PRO:HB2	1:A:356:CYS:HB2	2.03	0.41
1:B:131:LYS:HA	1:B:141:ARG:HG2	2.02	0.41
1:A:373:GLU:H	1:A:373:GLU:CD	2.29	0.41
1:B:140:VAL:HG22	1:B:158:LYS:HG2	2.03	0.41
1:B:275:ARG:HE	1:B:275:ARG:HB3	1.64	0.41
1:B:280:ASN:O	1:B:280:ASN:CG	2.64	0.40
1:A:162:PRO:HD2	1:A:163:ASP:H	1.86	0.40
1:B:298:ALA:O	1:B:299:PRO:C	2.61	0.40

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)
1:B:332:ILE:O	1:A:337:SER:OG[4_555]	2.05	0.15

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	272/275 (99%)	243 (89%)	20 (7%)	9 (3%)	3	4
1	B	271/275 (98%)	241 (89%)	24 (9%)	6 (2%)	5	9
All	All	543/550 (99%)	484 (89%)	44 (8%)	15 (3%)	4	6

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	162	PRO
1	B	223	HIS
1	A	162	PRO
1	A	223	HIS
1	A	390	PRO
1	A	221	GLN
1	A	222	GLY
1	B	221	GLN
1	B	164	VAL
1	B	222	GLY
1	A	164	VAL
1	A	217	LEU
1	A	183	SER
1	B	161	LYS
1	A	161	LYS

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	238/238 (100%)	196 (82%)	42 (18%)	2	3
1	B	237/238 (100%)	194 (82%)	43 (18%)	2	3
All	All	475/476 (100%)	390 (82%)	85 (18%)	2	3

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	118	THR
1	B	120	LEU
1	B	123	GLU
1	B	124	LYS
1	B	132	LEU
1	B	151	LYS
1	B	152	THR
1	B	153	VAL
1	B	154	SER
1	B	165	LEU
1	B	169	GLU
1	B	187	ARG
1	B	189	LEU
1	B	210	LEU
1	B	216	ARG
1	B	219	LYS
1	B	225	LEU
1	B	226	LEU
1	B	231	ARG
1	B	238	GLU
1	B	245	SER
1	B	258	LEU
1	B	263	ARG
1	B	265	LEU
1	B	273	LEU
1	B	279	GLN
1	B	283	HIS
1	B	290	ARG
1	B	291	LYS
1	B	300	GLU
1	B	302	LEU
1	B	303	LYS
1	B	334	LEU
1	B	342	LYS
1	B	345	LYS

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Mol	Chain	Res	Type
1	B	349	ARG
1	B	354	GLU
1	B	358	GLN
1	B	359	ASP
1	B	371	LYS
1	B	379	VAL
1	B	381	LEU
1	B	382	ARG
1	A	120	LEU
1	A	123	GLU
1	A	124	LYS
1	A	132	LEU
1	A	136	SER
1	A	139	VAL
1	A	151	LYS
1	A	152	THR
1	A	153	VAL
1	A	154	SER
1	A	165	LEU
1	A	171	MET
1	A	187	ARG
1	A	189	LEU
1	A	216	ARG
1	A	219	LYS
1	A	225	LEU
1	A	226	LEU
1	A	230	SER
1	A	231	ARG
1	A	238	GLU
1	A	245	SER
1	A	256	ARG
1	A	258	LEU
1	A	263	ARG
1	A	265	LEU
1	A	273	LEU
1	A	275	ARG
1	A	283	HIS
1	A	290	ARG
1	A	291	LYS
1	A	302	LEU
1	A	334	LEU
1	A	342	LYS

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Mol	Chain	Res	Type
1	A	345	LYS
1	A	349	ARG
1	A	352	ARG
1	A	354	GLU
1	A	371	LYS
1	A	381	LEU
1	A	382	ARG
1	A	391	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	182	HIS
1	B	188	ASN
1	B	220	HIS
1	B	235	GLN
1	B	250	HIS
1	B	279	GLN
1	B	287	GLN
1	B	309	HIS
1	B	338	GLN
1	B	358	GLN
1	B	370	HIS
1	A	167	GLN
1	A	182	HIS
1	A	186	HIS
1	A	188	ASN
1	A	220	HIS
1	A	235	GLN
1	A	250	HIS
1	A	279	GLN
1	A	287	GLN
1	A	338	GLN
1	A	358	GLN
1	A	370	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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$
1	PTR	A	284	1	15,16,17	2.01	4 (26%)	17,22,24	1.29	3 (17%)
1	PTR	B	284	1	15,16,17	2.16	2 (13%)	17,22,24	1.36	2 (11%)

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
1	PTR	A	284	1	-	1/10/11/13	0/1/1/1
1	PTR	B	284	1	-	2/10/11/13	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	284	PTR	P-OH	5.36	1.69	1.59
1	B	284	PTR	OH-CZ	-5.25	1.28	1.40
1	A	284	PTR	OH-CZ	-4.55	1.30	1.40
1	A	284	PTR	P-OH	4.11	1.67	1.59
1	A	284	PTR	CE1-CD1	2.52	1.42	1.38
1	A	284	PTR	P-O2P	-2.34	1.46	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	284	PTR	P-OH-CZ	3.22	135.35	123.88
1	B	284	PTR	O3P-P-OH	2.47	112.61	105.32
1	A	284	PTR	P-OH-CZ	2.41	132.48	123.88
1	A	284	PTR	O2P-P-OH	2.13	111.63	105.32
1	A	284	PTR	CE2-CZ-CE1	-2.10	117.10	120.16

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	284	PTR	O-C-CA-CB
1	B	284	PTR	C-CA-CB-CG
1	A	284	PTR	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	284	PTR	3	0
1	B	284	PTR	3	0

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	$\# Z > 2$
2	T77	B	401	-	38,38,38	2.22	7 (18%)	44,52,52	2.27	14 (31%)
2	T77	A	401	-	38,38,38	1.92	6 (15%)	44,52,52	2.75	19 (43%)

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	T77	B	401	-	-	3/17/26/26	0/5/5/5
2	T77	A	401	-	-	2/17/26/26	0/5/5/5

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	T77	C19-C23	-8.38	1.46	1.53
2	A	401	T77	C23-S26	-6.86	1.72	1.82
2	B	401	T77	C5-N11	6.41	1.44	1.35
2	A	401	T77	C5-N11	5.42	1.43	1.35
2	B	401	T77	C5-N8	-4.05	1.32	1.37
2	A	401	T77	C1-C3	3.47	1.43	1.38
2	A	401	T77	C2-C5	-3.21	1.36	1.41
2	B	401	T77	C2-C5	-3.19	1.36	1.41
2	B	401	T77	C23-S25	-2.92	1.78	1.82
2	A	401	T77	C2-C1	-2.91	1.38	1.46
2	B	401	T77	C23-S26	-2.90	1.78	1.82
2	B	401	T77	C15-C7	2.20	1.42	1.39
2	A	401	T77	C5-N8	-2.15	1.34	1.37

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	T77	C7-C3-C1	-7.77	123.57	131.65
2	B	401	T77	C7-C3-C1	-6.97	124.41	131.65
2	A	401	T77	C2-C5-N8	6.18	114.55	109.24
2	A	401	T77	C2-C5-N11	-6.11	120.12	126.64
2	A	401	T77	C16-C9-C4	4.69	124.98	120.36
2	B	401	T77	N13-C18-N11	-4.60	121.62	128.58
2	B	401	T77	C7-C3-N8	4.43	125.32	119.74
2	A	401	T77	C7-C3-N8	4.39	125.26	119.74
2	B	401	T77	C2-C5-N11	-4.33	122.02	126.64
2	B	401	T77	C33-N32-C34	3.96	119.86	109.72
2	B	401	T77	C2-C1-C3	-3.85	104.73	106.54
2	A	401	T77	C33-N32-C34	3.84	119.57	109.72
2	A	401	T77	N13-C18-N11	-3.63	123.08	128.58
2	B	401	T77	C2-C5-N8	3.62	112.36	109.24
2	A	401	T77	C2-C1-C3	-3.57	104.86	106.54
2	A	401	T77	C22-C16-C9	-3.57	115.83	120.24
2	B	401	T77	C15-C7-C3	-3.27	116.87	120.76
2	B	401	T77	C34-N32-C31	3.22	123.51	110.75
2	A	401	T77	C19-N12-C6	-3.22	117.20	123.18
2	A	401	T77	C34-N32-C31	3.04	122.79	110.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	T77	C15-C7-C3	-2.98	117.22	120.76
2	B	401	T77	C18-N13-C6	2.69	124.15	115.24
2	A	401	T77	C30-C31-N32	-2.62	107.58	114.57
2	A	401	T77	C1-C3-N8	2.62	111.12	108.78
2	B	401	T77	C30-C31-N32	-2.59	107.67	114.57
2	B	401	T77	C30-O27-C24	2.57	124.61	117.93
2	A	401	T77	C29-C28-S25	-2.49	102.38	110.01
2	A	401	T77	C4-C1-C3	2.47	131.18	126.60
2	A	401	T77	C18-N13-C6	2.36	123.07	115.24
2	A	401	T77	C2-C6-N13	-2.16	117.19	120.91
2	A	401	T77	C28-S25-C23	2.06	104.15	97.11
2	B	401	T77	C20-C14-C7	-2.04	118.61	120.80
2	B	401	T77	C4-C1-C3	2.04	130.39	126.60

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	T77	C30-C31-N32-C34
2	A	401	T77	C30-C31-N32-C34
2	A	401	T77	C23-C19-N12-C6
2	B	401	T77	C23-C19-N12-C6
2	B	401	T77	C1-C3-C7-C15

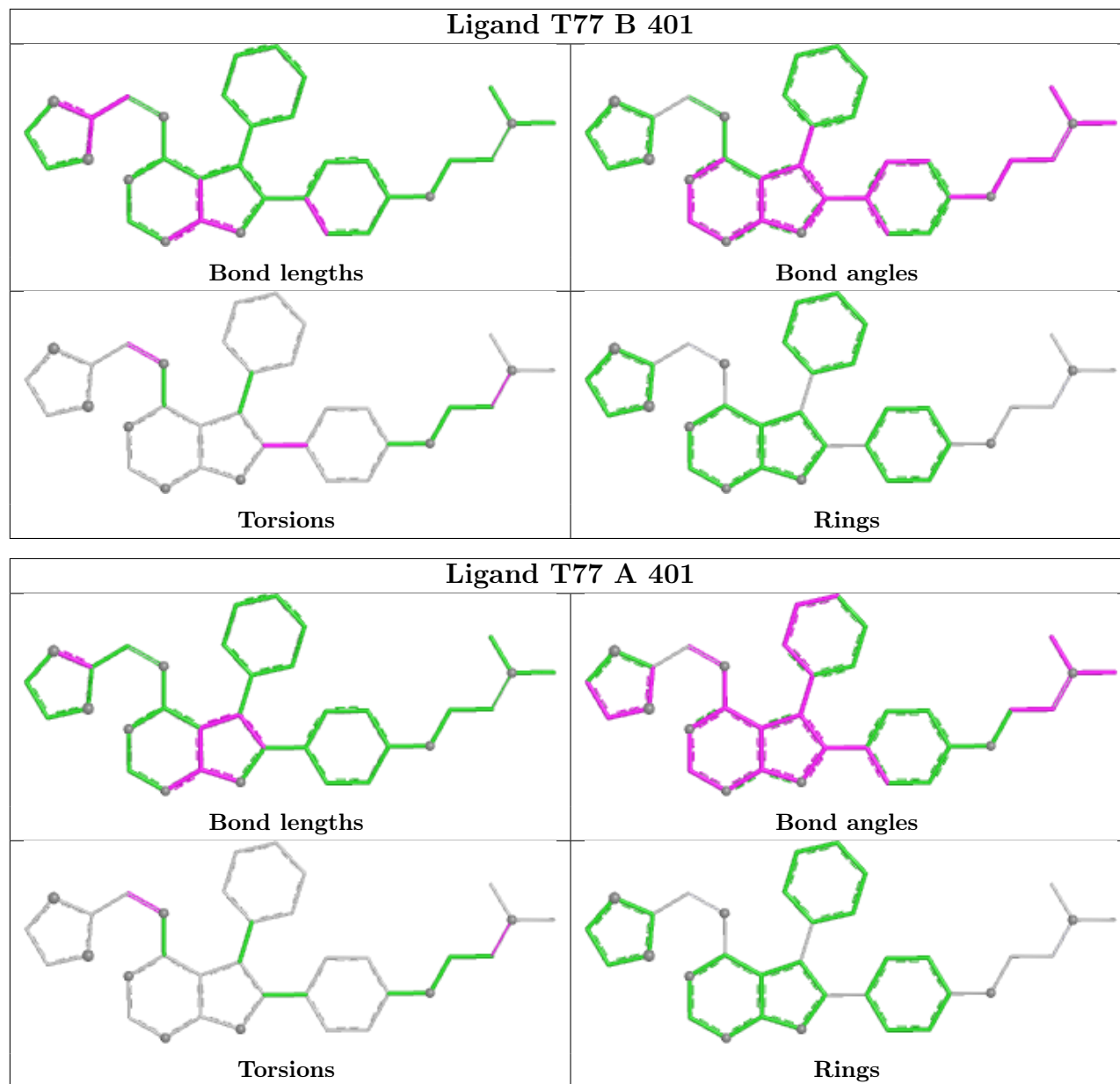
There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	T77	5	0
2	A	401	T77	4	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 [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	274/275 (99%)	0.90	33 (12%) 9 7	31, 49, 75, 93	0
1	B	273/275 (99%)	0.94	32 (11%) 9 7	30, 49, 75, 93	0
All	All	547/550 (99%)	0.92	65 (11%) 9 7	30, 49, 75, 93	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	164	VAL	6.6
1	A	164	VAL	6.6
1	B	293	PRO	6.1
1	B	165	LEU	6.0
1	A	165	LEU	5.2
1	B	390	PRO	5.2
1	B	225	LEU	5.1
1	A	162	PRO	5.0
1	A	280	ASN	4.8
1	B	292	VAL	4.2
1	A	391	THR	4.1
1	A	117	LEU	4.1
1	A	283	HIS	3.9
1	A	225	LEU	3.9
1	A	281	ASP	3.7
1	B	168	PRO	3.6
1	A	279	GLN	3.5
1	A	224	PHE	3.5
1	B	223	HIS	3.5
1	A	163	ASP	3.4
1	B	117	LEU	3.4
1	A	285	VAL	3.4
1	A	148	PRO	3.3
1	B	289	HIS	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	224	PHE	3.2
1	A	390	PRO	3.2
1	A	222	GLY	3.2
1	B	220	HIS	3.1
1	A	137	PHE	3.0
1	B	280	ASN	3.0
1	A	220	HIS	3.0
1	A	278	PRO	2.8
1	B	167	GLN	2.8
1	B	285	VAL	2.8
1	B	283	HIS	2.8
1	A	221	GLN	2.7
1	B	282	ASP	2.6
1	B	291	LYS	2.6
1	A	166	SER	2.6
1	A	288	GLU	2.5
1	B	160	LEU	2.5
1	B	162	PRO	2.5
1	B	362	ASN	2.5
1	A	216	ARG	2.5
1	A	170	ALA	2.5
1	A	152	THR	2.5
1	A	123	GLU	2.4
1	B	389	GLN	2.4
1	A	291	LYS	2.4
1	B	169	GLU	2.4
1	B	287	GLN	2.4
1	A	161	LYS	2.4
1	A	149	SER	2.3
1	B	166	SER	2.3
1	B	286	MET	2.3
1	B	263	ARG	2.3
1	A	168	PRO	2.3
1	B	148	PRO	2.2
1	A	354	GLU	2.2
1	B	161	LYS	2.2
1	B	335	ASN	2.1
1	B	219	LYS	2.1
1	A	160	LEU	2.1
1	B	222	GLY	2.1
1	A	129	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	PTR	B	284	16/17	0.78	0.17	55,63,64,65	0
1	PTR	A	284	16/17	0.87	0.19	55,62,65,65	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

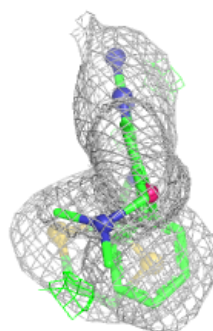
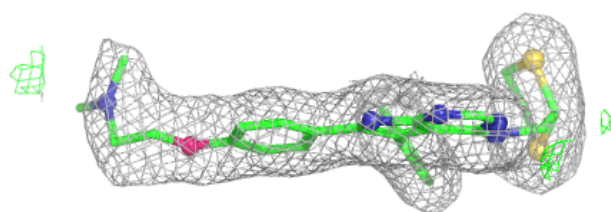
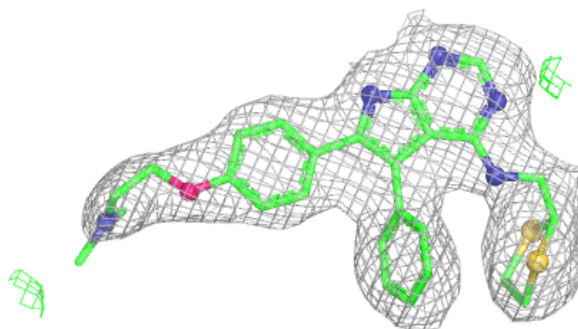
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	T77	B	401	34/34	0.94	0.09	22,34,56,60	0
2	T77	A	401	34/34	0.95	0.09	22,34,56,60	0

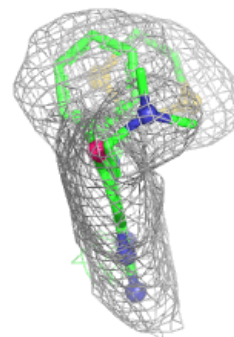
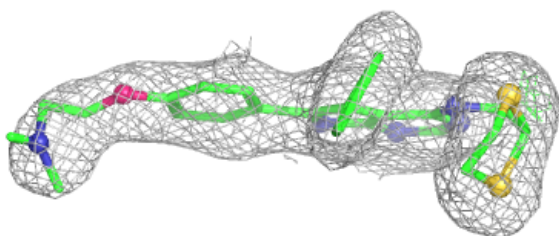
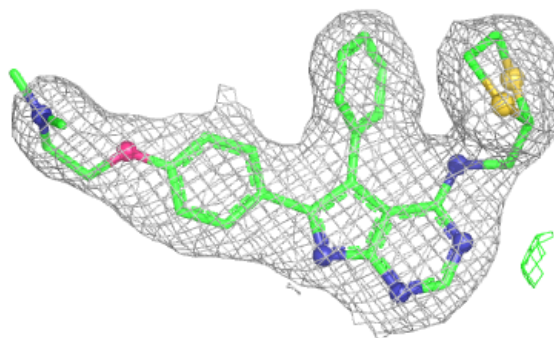
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around T77 B 401:

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

**Electron density around T77 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 [i](#)

There are no such residues in this entry.