



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2021 – 06:12 PM EDT

PDB ID : 2GHL
Title : Mutant Mus Musculus P38 Kinase Domain in Complex with Inhibitor PG-874743
Authors : Walter, R.L.; Mekel, M.J.; Evdokimov, A.G.; Pokross, M.E.; Brugel, T.A.
Deposited on : 2006-03-27
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.23.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

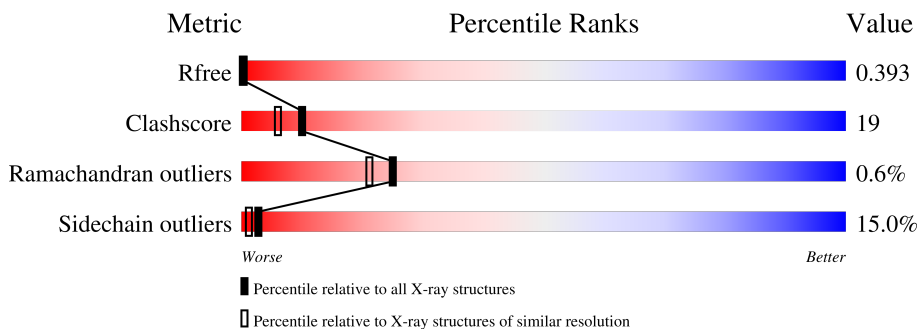
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

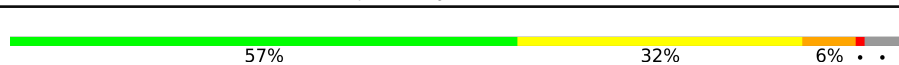
The reported resolution of this entry is 2.10 Å.

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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	348	 57% 32% 6% . .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3031 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.

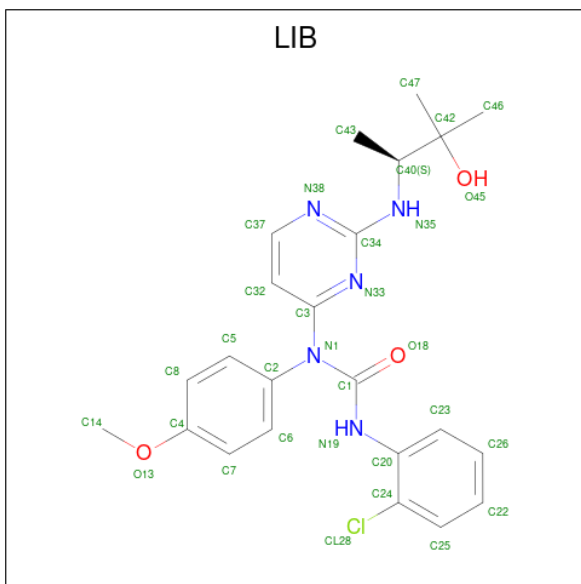
- Molecule 1 is a protein called Mitogen-activated protein kinase 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	334	2689	1726	460	492	11	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	180	ALA	THR	engineered mutation	UNP P47811
A	182	PHE	TYR	engineered mutation	UNP P47811

- Molecule 2 is 3-(2-CHLOROPHENYL)-1-(2-{{(1S)-2-HYDROXY-1,2-DIMETHYLPROPYL}AMINO}PYRIMIDIN-4-YL)-1-(4-METHOXYPHENYL)UREA (three-letter code: LIB) (formula: C₂₃H₂₆ClN₅O₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
2	A	1	32	23	1	5	3	0	0

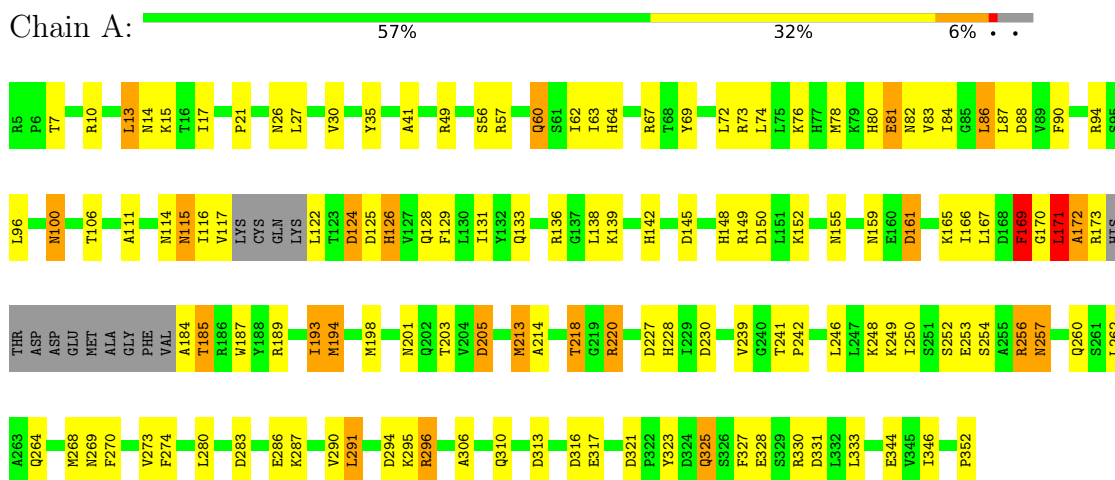
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	310	Total 310	O 310	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: Mitogen-activated protein kinase 14



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.26Å 74.43Å 76.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.45 – 2.10 34.17 – 2.32	Depositor EDS
% Data completeness (in resolution range)	(Not available) (53.45-2.10) 81.0 (34.17-2.32)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.31Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.199 , 0.301 0.405 , 0.393	Depositor DCC
R_{free} test set	745 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	46.2	Xtrriage
Anisotropy	0.353	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 29.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.020 for -h,l,k	Xtrriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	3031	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.67% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: LIB

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	0.76	2/2752 (0.1%)	0.93	12/3737 (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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	213	MET	SD-CE	-6.08	1.43	1.77
1	A	69	TYR	C-N	-5.26	1.22	1.34

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	296	ARG	NE-CZ-NH2	-7.48	116.56	120.30
1	A	331	ASP	CB-CG-OD2	7.04	124.64	118.30
1	A	296	ARG	NE-CZ-NH1	6.36	123.48	120.30
1	A	321	ASP	CB-CG-OD2	5.80	123.52	118.30
1	A	313	ASP	CB-CG-OD2	5.69	123.42	118.30
1	A	205	ASP	CB-CG-OD2	5.68	123.41	118.30
1	A	124	ASP	CB-CG-OD2	5.62	123.35	118.30
1	A	145	ASP	CB-CG-OD2	5.59	123.33	118.30
1	A	227	ASP	CB-CG-OD2	5.38	123.14	118.30
1	A	230	ASP	CB-CG-OD2	5.15	122.94	118.30
1	A	161	ASP	N-CA-CB	-5.11	101.41	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	283	ASP	CB-CG-OD2	5.10	122.89	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	171	LEU	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2689	0	2676	101	0
2	A	32	0	26	4	0
3	A	310	0	0	35	0
All	All	3031	0	2702	103	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 19.

All (103) 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:172:ALA:O	1:A:173:ARG:CB	2.18	0.89
1:A:161:ASP:HB3	3:A:666:HOH:O	1.78	0.83
1:A:81:GLU:H	1:A:81:GLU:CD	1.88	0.78
1:A:159:ASN:HB2	3:A:666:HOH:O	1.86	0.75
1:A:111:ALA:HB1	1:A:115:ASN:ND2	2.01	0.75
1:A:149:ARG:NH1	1:A:172:ALA:H	1.85	0.73
1:A:125:ASP:HB3	3:A:641:HOH:O	1.88	0.73
1:A:122:LEU:HD22	3:A:620:HOH:O	1.88	0.73
1:A:78:MET:HG3	1:A:169:PHE:CE1	2.24	0.72
1:A:167:LEU:HB2	3:A:705:HOH:O	1.88	0.72
1:A:166:ILE:O	1:A:169:PHE:HE2	1.73	0.71
1:A:352:PRO:C	3:A:660:HOH:O	2.29	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:THR:HG22	1:A:220:ARG:H	1.57	0.70
1:A:193:ILE:C	1:A:193:ILE:HD13	2.15	0.68
1:A:81:GLU:HG2	3:A:695:HOH:O	1.94	0.67
1:A:60:GLN:HG2	3:A:559:HOH:O	1.95	0.67
1:A:148:HIS:HD2	1:A:150:ASP:H	1.44	0.65
1:A:126:HIS:CD2	3:A:620:HOH:O	2.49	0.65
1:A:166:ILE:HG22	1:A:169:PHE:HD2	1.61	0.65
1:A:116:ILE:HG23	1:A:122:LEU:HD21	1.80	0.64
1:A:87:LEU:HG	1:A:106:THR:HA	1.80	0.64
1:A:149:ARG:NH1	1:A:172:ALA:N	2.46	0.63
1:A:131:ILE:HG21	1:A:213:MET:HE3	1.79	0.63
1:A:139:LYS:NZ	1:A:317:GLU:O	2.29	0.63
1:A:250:ILE:O	1:A:256:ARG:NH1	2.32	0.63
1:A:290:VAL:HG12	3:A:424:HOH:O	1.97	0.63
1:A:152:LYS:HZ2	1:A:185:THR:HG1	1.47	0.63
1:A:78:MET:HG3	1:A:169:PHE:HE1	1.63	0.61
1:A:242:PRO:HB3	1:A:246:LEU:HD23	1.84	0.60
1:A:100:ASN:ND2	3:A:634:HOH:O	2.24	0.59
2:A:401:LIB:C26	3:A:635:HOH:O	2.49	0.59
1:A:76:LYS:NZ	1:A:344:GLU:O	2.33	0.59
1:A:172:ALA:HB2	3:A:648:HOH:O	2.01	0.59
1:A:193:ILE:HD13	1:A:194:MET:N	2.18	0.58
1:A:57:ARG:HD3	1:A:60:GLN:NE2	2.19	0.58
1:A:131:ILE:HG13	1:A:213:MET:HE2	1.86	0.57
1:A:214:ALA:O	1:A:218:THR:HB	2.06	0.56
1:A:142:HIS:HD2	3:A:406:HOH:O	1.88	0.56
1:A:171:LEU:N	1:A:172:ALA:O	2.39	0.56
1:A:84:ILE:HD12	1:A:165:LYS:HB3	1.87	0.55
1:A:171:LEU:HD11	1:A:327:PHE:CZ	2.40	0.55
1:A:74:LEU:CD2	1:A:170:GLY:HA3	2.36	0.55
1:A:310:GLN:HG2	3:A:562:HOH:O	2.06	0.54
1:A:155:ASN:CB	3:A:705:HOH:O	2.55	0.54
1:A:249:LYS:NZ	1:A:294:ASP:OD2	2.36	0.54
1:A:83:VAL:HG13	1:A:169:PHE:CE2	2.44	0.53
1:A:184:ALA:HB3	1:A:187:TRP:CE2	2.43	0.53
1:A:290:VAL:O	1:A:296:ARG:HD3	2.09	0.53
1:A:316:ASP:OD1	3:A:661:HOH:O	2.18	0.53
1:A:260:GLN:C	3:A:673:HOH:O	2.46	0.53
1:A:290:VAL:O	1:A:296:ARG:CD	2.57	0.53
1:A:30:VAL:HG12	2:A:401:LIB:CL28	2.46	0.53
1:A:273:VAL:HG23	1:A:274:PHE:CD1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:HIS:CD2	1:A:82:ASN:H	2.28	0.52
1:A:155:ASN:ND2	3:A:705:HOH:O	2.42	0.52
1:A:27:LEU:HD22	1:A:41:ALA:HB2	1.92	0.52
1:A:189:ARG:HD2	3:A:552:HOH:O	2.10	0.52
1:A:124:ASP:OD2	1:A:128:GLN:NE2	2.40	0.51
1:A:81:GLU:OE1	1:A:136:ARG:NH1	2.44	0.50
1:A:74:LEU:HD21	1:A:170:GLY:HA3	1.92	0.50
1:A:287:LYS:CD	3:A:420:HOH:O	2.59	0.50
1:A:280:LEU:CD2	1:A:306:ALA:HB3	2.41	0.50
1:A:253:GLU:O	1:A:257:ASN:HB2	2.12	0.50
1:A:239:VAL:HG21	1:A:291:LEU:HD13	1.94	0.49
1:A:201:ASN:OD1	1:A:203:THR:HG23	2.11	0.49
1:A:280:LEU:HD21	1:A:306:ALA:HB3	1.94	0.49
1:A:35:TYR:HB3	3:A:653:HOH:O	2.12	0.49
1:A:116:ILE:CG2	1:A:122:LEU:HD21	2.43	0.49
1:A:73:ARG:CZ	3:A:703:HOH:O	2.61	0.49
1:A:270:PHE:HA	1:A:273:VAL:HG22	1.95	0.48
1:A:325:GLN:NE2	3:A:707:HOH:O	2.47	0.48
1:A:106:THR:HB	2:A:401:LIB:H142	1.95	0.48
1:A:86:LEU:HD22	1:A:88:ASP:O	2.14	0.47
1:A:218:THR:CG2	1:A:220:ARG:HG3	2.44	0.47
1:A:268:MET:HE2	3:A:702:HOH:O	2.13	0.47
1:A:122:LEU:HD13	3:A:620:HOH:O	2.13	0.47
1:A:269:ASN:ND2	3:A:658:HOH:O	2.47	0.47
1:A:83:VAL:CG1	1:A:169:PHE:CZ	2.98	0.46
1:A:131:ILE:HG21	1:A:213:MET:CE	2.43	0.46
1:A:13:LEU:C	3:A:662:HOH:O	2.55	0.46
1:A:148:HIS:CE1	1:A:169:PHE:HA	2.51	0.45
1:A:142:HIS:HE1	1:A:205:ASP:OD1	2.00	0.45
1:A:218:THR:HG21	3:A:543:HOH:O	2.16	0.45
1:A:73:ARG:NH2	3:A:703:HOH:O	2.50	0.45
1:A:189:ARG:HE	1:A:193:ILE:HD11	1.81	0.45
2:A:401:LIB:N33	2:A:401:LIB:N19	2.59	0.45
1:A:21:PRO:HD3	1:A:90:PHE:CE1	2.53	0.44
1:A:171:LEU:HD12	1:A:328:GLU:OE2	2.18	0.44
1:A:148:HIS:ND1	1:A:169:PHE:HA	2.33	0.43
1:A:193:ILE:C	1:A:193:ILE:CD1	2.83	0.43
1:A:323:TYR:CD2	1:A:325:GLN:HG2	2.55	0.42
1:A:155:ASN:CG	3:A:705:HOH:O	2.57	0.42
1:A:149:ARG:HH12	1:A:172:ALA:N	2.16	0.42
1:A:167:LEU:O	3:A:705:HOH:O	2.22	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:ARG:NH2	3:A:653:HOH:O	2.53	0.42
1:A:14:ASN:O	1:A:15:LYS:HB2	2.19	0.41
1:A:155:ASN:HD22	1:A:155:ASN:HA	1.65	0.41
1:A:56:SER:HB3	3:A:692:HOH:O	2.21	0.41
1:A:161:ASP:CB	3:A:666:HOH:O	2.53	0.41
1:A:170:GLY:HA2	1:A:171:LEU:HA	1.83	0.41
1:A:129:PHE:O	1:A:133:GLN:HG3	2.21	0.40
1:A:148:HIS:HE1	1:A:167:LEU:O	2.03	0.40
1:A:241:THR:HB	1:A:242:PRO:HD2	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	328/348 (94%)	303 (92%)	23 (7%)	2 (1%)	25 21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	169	PHE
1	A	172	ALA

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	293/306 (96%)	249 (85%)	44 (15%)	3 1

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	10	ARG
1	A	13	LEU
1	A	17	ILE
1	A	26	ASN
1	A	49	ARG
1	A	60	GLN
1	A	62	ILE
1	A	63	ILE
1	A	64	HIS
1	A	72	LEU
1	A	81	GLU
1	A	86	LEU
1	A	94	ARG
1	A	96	LEU
1	A	100	ASN
1	A	114	ASN
1	A	115	ASN
1	A	117	VAL
1	A	126	HIS
1	A	138	LEU
1	A	169	PHE
1	A	171	LEU
1	A	185	THR
1	A	193	ILE
1	A	194	MET
1	A	198	MET
1	A	218	THR
1	A	220	ARG
1	A	228	HIS
1	A	248	LYS
1	A	252	SER
1	A	254	SER
1	A	256	ARG
1	A	257	ASN
1	A	262	LEU
1	A	264	GLN
1	A	286	GLU

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Mol	Chain	Res	Type
1	A	291	LEU
1	A	295	LYS
1	A	325	GLN
1	A	330	ARG
1	A	333	LEU
1	A	346	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	HIS
1	A	80	HIS
1	A	107	HIS
1	A	114	ASN
1	A	115	ASN
1	A	142	HIS
1	A	148	HIS
1	A	155	ASN
1	A	257	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	LIB	A	401	-	32,34,34	1.09	2 (6%)	43,48,48	1.94	8 (18%)

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	LIB	A	401	-	-	2/28/28/28	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	LIB	C2-N1	-3.37	1.39	1.44
2	A	401	LIB	C1-N19	-2.52	1.32	1.37

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	LIB	N38-C34-N33	-6.32	120.56	126.55
2	A	401	LIB	C37-N38-C34	5.46	120.29	115.45
2	A	401	LIB	C32-C3-N33	-3.87	117.22	123.53
2	A	401	LIB	N35-C34-N33	3.78	122.86	117.18
2	A	401	LIB	N19-C1-N1	3.48	118.88	114.78
2	A	401	LIB	C32-C37-N38	-3.24	119.93	123.96
2	A	401	LIB	C34-N33-C3	2.20	121.91	114.64
2	A	401	LIB	C2-N1-C3	-2.10	114.23	118.80

There are no chirality outliers.

All (2) torsion outliers are listed below:

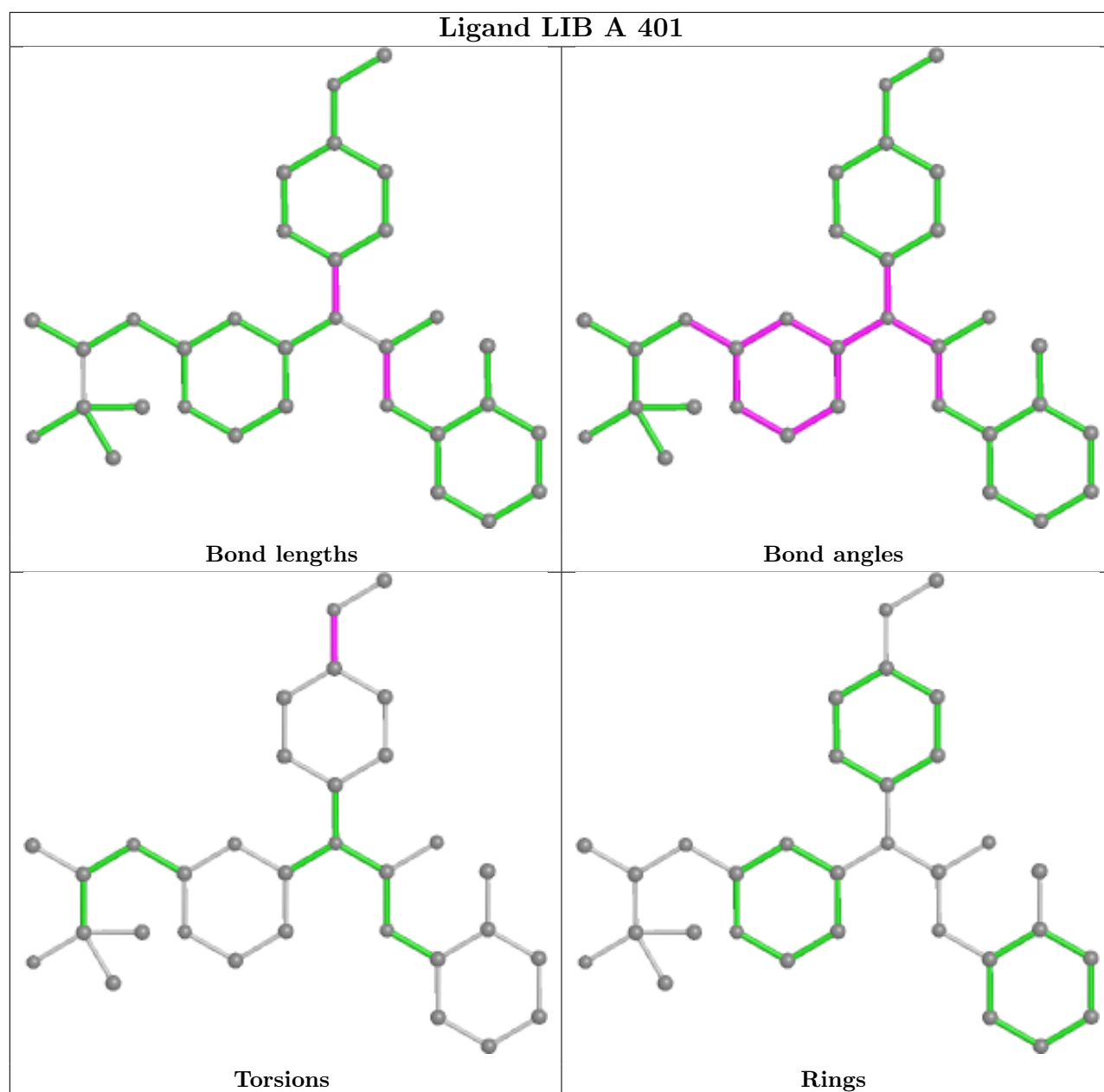
Mol	Chain	Res	Type	Atoms
2	A	401	LIB	C8-C4-O13-C14
2	A	401	LIB	C7-C4-O13-C14

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	LIB	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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

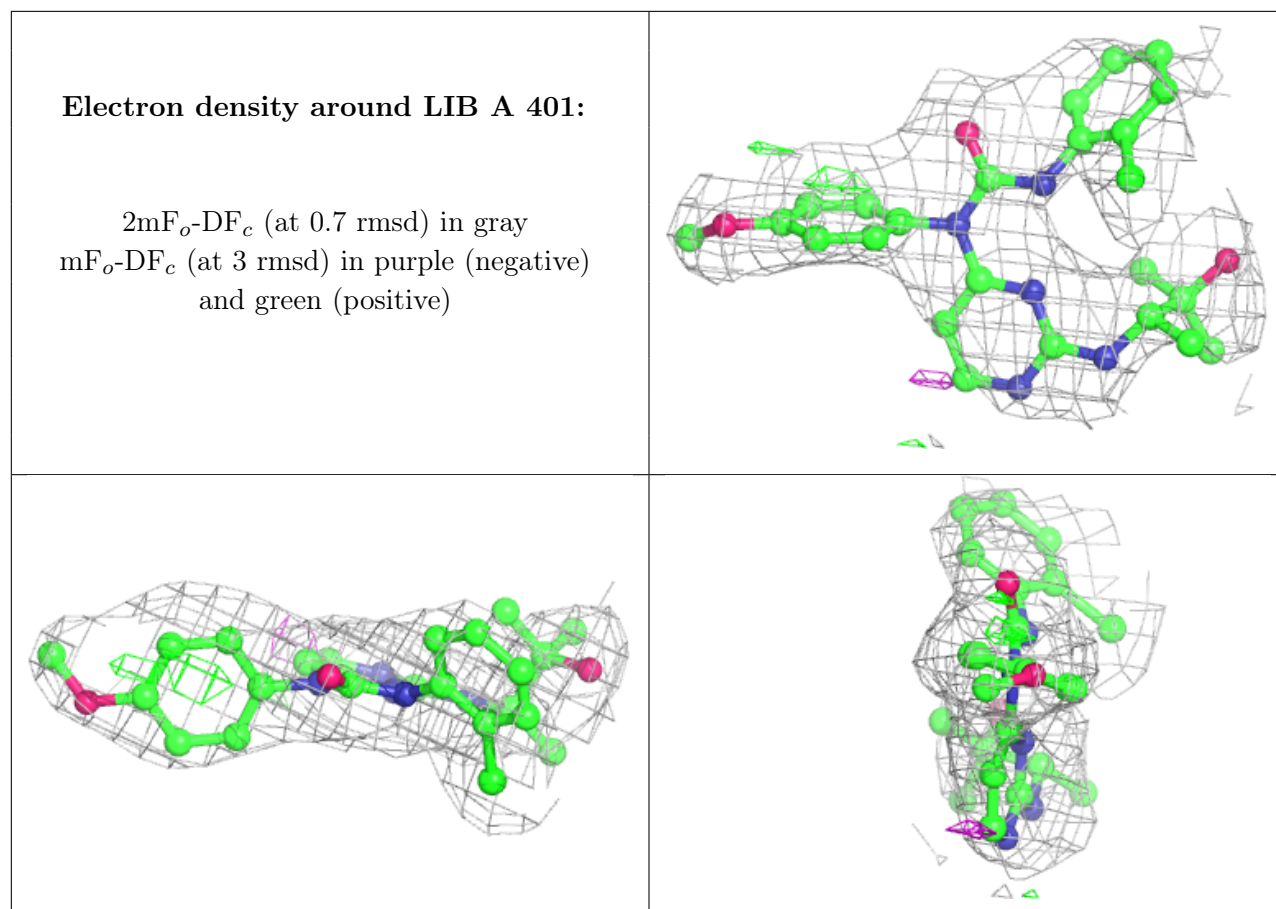
6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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



6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.