



Full wwPDB X-ray Structure Validation Report ⓘ

May 1, 2025 – 12:08 PM JST

PDB ID : 9LVH / pdb_00009lvh
Title : Crystal structure of the mouse RIP3 kinase domain in complexed with Tricetin
Authors : Xie, H.; Su, H.X.; Li, M.J.; Xu, Y.C.
Deposited on : 2025-02-12
Resolution : 2.38 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 Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

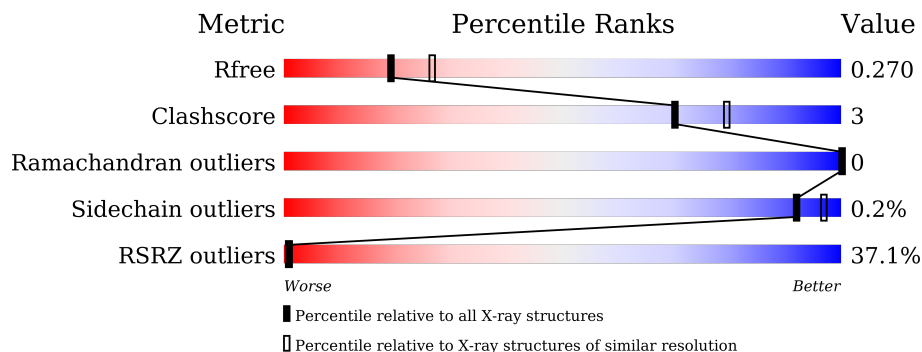
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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}	164625	6699 (2.40-2.36)
Clashscore	180529	7414 (2.40-2.36)
Ramachandran outliers	177936	7337 (2.40-2.36)
Sidechain outliers	177891	7338 (2.40-2.36)
RSRZ outliers	164620	6699 (2.40-2.36)

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	325	<div> <div>46%</div> <div> <div></div> <div>75%</div> <div>6%</div> <div>19%</div> </div> </div>
1	B	325	<div> <div>15%</div> <div> <div></div> <div>77%</div> <div>5%</div> <div>18%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4250 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 Receptor-interacting serine/threonine-protein kinase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	0	0
			2080	1342	353	377	8			
1	B	266	Total	C	N	O	S	0	0	0
			2103	1356	357	382	8			

There are 30 discrepancies between the modelled and reference sequences:

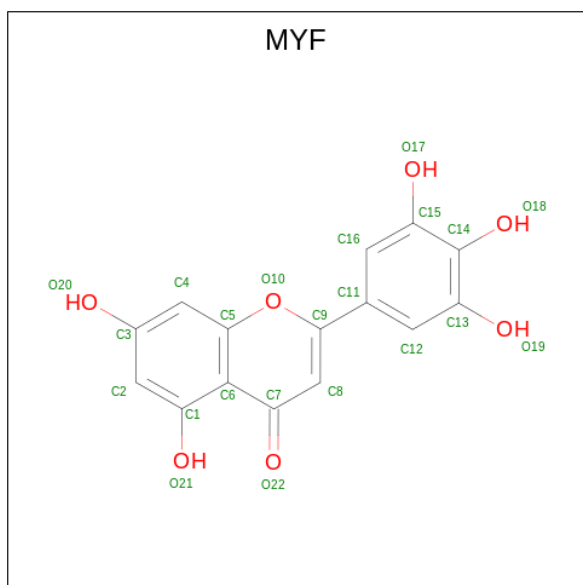
Chain	Residue	Modelled	Actual	Comment	Reference
A	111	ALA	CYS	conflict	UNP Q9QZL0
A	136	ASP	ASN	conflict	UNP Q9QZL0
A	198	LYS	ASP	conflict	UNP Q9QZL0
A	314	LEU	-	expression tag	UNP Q9QZL0
A	315	GLU	-	expression tag	UNP Q9QZL0
A	316	HIS	-	expression tag	UNP Q9QZL0
A	317	HIS	-	expression tag	UNP Q9QZL0
A	318	HIS	-	expression tag	UNP Q9QZL0
A	319	HIS	-	expression tag	UNP Q9QZL0
A	320	HIS	-	expression tag	UNP Q9QZL0
A	321	HIS	-	expression tag	UNP Q9QZL0
A	322	HIS	-	expression tag	UNP Q9QZL0
A	323	HIS	-	expression tag	UNP Q9QZL0
A	324	HIS	-	expression tag	UNP Q9QZL0
A	325	HIS	-	expression tag	UNP Q9QZL0
B	111	ALA	CYS	conflict	UNP Q9QZL0
B	136	ASP	ASN	conflict	UNP Q9QZL0
B	198	LYS	ASP	conflict	UNP Q9QZL0
B	314	LEU	-	expression tag	UNP Q9QZL0
B	315	GLU	-	expression tag	UNP Q9QZL0
B	316	HIS	-	expression tag	UNP Q9QZL0
B	317	HIS	-	expression tag	UNP Q9QZL0
B	318	HIS	-	expression tag	UNP Q9QZL0
B	319	HIS	-	expression tag	UNP Q9QZL0
B	320	HIS	-	expression tag	UNP Q9QZL0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	321	HIS	-	expression tag	UNP Q9QZL0
B	322	HIS	-	expression tag	UNP Q9QZL0
B	323	HIS	-	expression tag	UNP Q9QZL0
B	324	HIS	-	expression tag	UNP Q9QZL0
B	325	HIS	-	expression tag	UNP Q9QZL0

- Molecule 2 is 5,7-DIHYDROXY-2-(3,4,5-TRIHIDROXYPHENYL)-4H-CHROMEN-4-ONE (CCD ID: MYF) (formula: $C_{15}H_{10}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			22	15	7		
2	B	1	Total	C	O	0	0
			22	15	7		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	8	Total	O	0	0
			8	8		
3	B	15	Total	O	0	0
			15	15		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	152.42Å 51.25Å 104.91Å 90.00° 131.85° 90.00°	Depositor
Resolution (Å)	28.88 – 2.38 28.88 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.8 (28.88-2.38) 99.7 (28.88-2.38)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.250 , 0.271 0.250 , 0.270	Depositor DCC
R_{free} test set	1256 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	50.0	Xtriage
Anisotropy	0.582	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.011 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4250	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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: MYF

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	0.29	0/2128	0.51	0/2887
1	B	0.30	0/2152	0.55	0/2922
All	All	0.29	0/4280	0.53	0/5809

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 [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	2080	0	2101	15	0
1	B	2103	0	2126	14	0
2	A	22	0	8	5	0
2	B	22	0	8	4	0
3	A	8	0	0	1	0
3	B	15	0	0	0	0
All	All	4250	0	4243	28	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (28) 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:28:VAL:HG13	3:A:505:HOH:O	1.57	1.04
1:A:101:GLY:HA2	2:A:401:MYF:C12	2.07	0.84
1:B:53:VAL:HG23	1:B:58:ILE:HB	1.67	0.75
1:A:98:MET:O	2:A:401:MYF:H8	1.87	0.74
1:A:98:MET:N	2:A:401:MYF:O22	2.16	0.71
1:A:101:GLY:HA2	2:A:401:MYF:C13	2.24	0.68
1:B:294:LEU:HD12	1:B:295:VAL:HG13	1.75	0.68
1:B:55:SER:O	1:B:57:LYS:N	2.34	0.60
1:B:98:MET:N	2:B:401:MYF:O22	2.20	0.60
1:A:24:LYS:NZ	1:A:86:ASP:OD1	2.34	0.59
1:A:101:GLY:CA	2:A:401:MYF:C13	2.82	0.57
1:A:198:LYS:O	1:A:199:VAL:C	2.51	0.53
1:B:98:MET:O	2:B:401:MYF:H8	2.10	0.52
1:B:187:THR:HG22	1:B:189:ALA:H	1.75	0.52
1:B:101:GLY:HA2	2:B:401:MYF:C12	2.41	0.51
1:A:114:PRO:HB2	1:A:302:ALA:HB1	1.92	0.50
1:A:154:GLU:HG3	1:B:154:GLU:HG3	1.96	0.47
1:A:285:GLU:HB3	1:A:286:PRO:HD3	1.96	0.47
1:B:101:GLY:HA2	2:B:401:MYF:C11	2.48	0.43
1:B:294:LEU:HD12	1:B:294:LEU:C	2.44	0.43
1:A:19:ARG:HG2	1:A:83:LEU:HD23	2.00	0.43
1:A:152:ASP:CG	1:A:153:PRO:HD2	2.44	0.42
1:B:54:ASN:OD1	1:B:54:ASN:C	2.62	0.42
1:A:199:VAL:O	1:A:199:VAL:HG22	2.20	0.42
1:B:294:LEU:HD12	1:B:295:VAL:CG1	2.47	0.41
1:B:115:TRP:HB3	1:B:116:PRO:HD3	2.03	0.41
1:A:271:TRP:O	1:A:272:GLY:C	2.64	0.40
1:B:296:LYS:HA	1:B:299:VAL:HG23	2.03	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	254/325 (78%)	247 (97%)	7 (3%)	0	100	100
1	B	258/325 (79%)	254 (98%)	4 (2%)	0	100	100
All	All	512/650 (79%)	501 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	231/283 (82%)	231 (100%)	0	100	100
1	B	234/283 (83%)	233 (100%)	1 (0%)	89	95
All	All	465/566 (82%)	464 (100%)	1 (0%)	92	97

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	271	TRP

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

Mol	Chain	Res	Type
1	B	168	GLN
1	B	289	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	$\# Z > 2$
2	MYF	A	401	-	22,24,24	1.25	2 (9%)	25,36,36	1.88	4 (16%)
2	MYF	B	401	-	22,24,24	1.10	1 (4%)	25,36,36	1.48	2 (8%)

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	MYF	A	401	-	-	0/0/4/4	0/3/3/3
2	MYF	B	401	-	-	0/0/4/4	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	MYF	C12-C13	3.40	1.40	1.37
2	B	401	MYF	C8-C7	3.31	1.44	1.37
2	A	401	MYF	C8-C7	2.65	1.43	1.37

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	MYF	C6-C7-C8	-6.65	115.08	123.16
2	B	401	MYF	C6-C7-C8	-6.46	115.31	123.16
2	A	401	MYF	C15-C14-C13	4.05	122.09	119.51
2	A	401	MYF	C3-C4-C5	-2.86	116.40	120.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	MYF	C15-C16-C11	2.17	123.00	121.25
2	B	401	MYF	C3-C4-C5	-2.04	117.56	120.42

There are no chirality outliers.

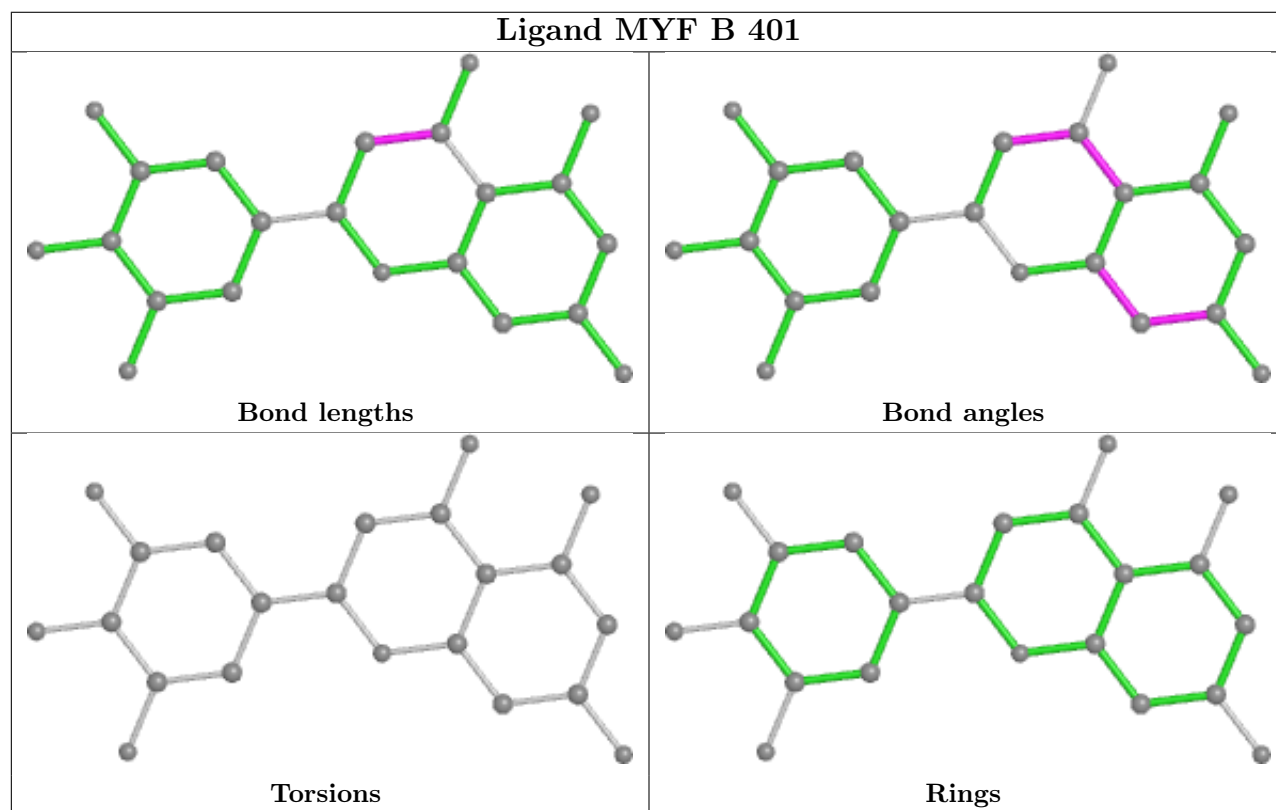
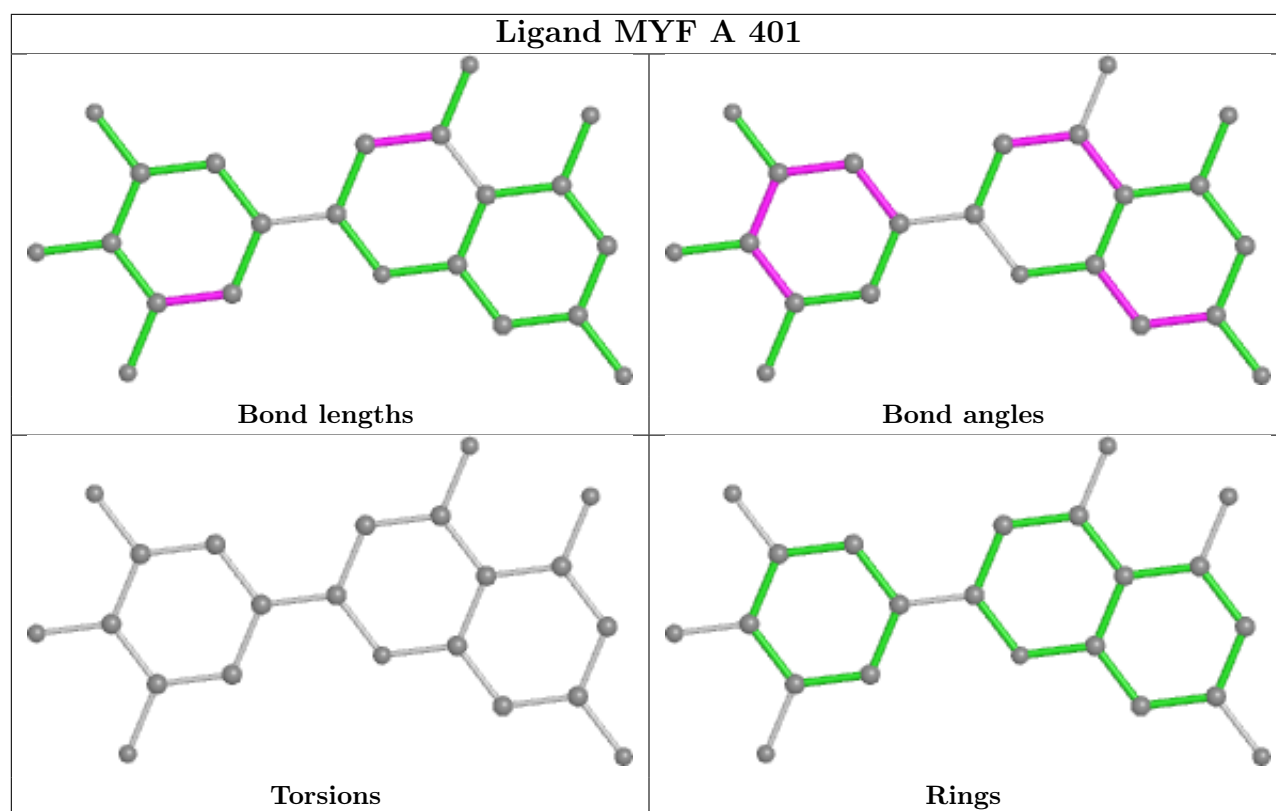
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	MYF	5	0
2	B	401	MYF	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 ⓘ

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	263/325 (80%)	2.47	148 (56%) 0 0	43, 93, 147, 334	0
1	B	266/325 (81%)	1.24	48 (18%) 4 4	41, 60, 104, 122	0
All	All	529/650 (81%)	1.85	196 (37%) 1 1	41, 73, 131, 334	0

All (196) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	281	PHE	9.9
1	A	195	LEU	8.8
1	A	196	LEU	7.6
1	A	225	ALA	7.5
1	A	247	LEU	7.2
1	A	135	LEU	6.7
1	A	201	LEU	6.5
1	B	188	LEU	6.2
1	A	199	VAL	6.2
1	A	194	GLU	6.1
1	B	227	LEU	5.8
1	A	310	LEU	5.5
1	B	187	THR	5.3
1	A	197	PHE	5.3
1	B	260	LEU	5.2
1	A	270	CYS	5.2
1	A	271	TRP	5.0
1	A	246	PRO	4.9
1	B	55	SER	4.9
1	A	306	VAL	4.7
1	A	144	LEU	4.7
1	A	210	TYR	4.7
1	A	250	LEU	4.6
1	A	193	PRO	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	198	LYS	4.5
1	B	299	VAL	4.5
1	B	160	ALA	4.5
1	A	226	GLU	4.5
1	A	312	GLN	4.5
1	A	189	ALA	4.4
1	B	261	GLU	4.4
1	A	134	SER	4.3
1	A	275	SER	4.3
1	B	201	LEU	4.3
1	A	309	TYR	4.2
1	A	282	GLN	4.2
1	B	13	ALA	4.2
1	A	260	LEU	4.2
1	A	299	VAL	4.1
1	A	71	GLU	4.1
1	B	196	LEU	4.0
1	A	243	SER	4.0
1	B	199	VAL	4.0
1	A	255	PRO	3.9
1	A	139	LEU	3.9
1	A	259	GLY	3.8
1	A	273	SER	3.8
1	A	99	GLU	3.8
1	A	13	ALA	3.8
1	A	262	LYS	3.8
1	A	269	HIS	3.8
1	B	189	ALA	3.7
1	A	32	GLY	3.7
1	A	62	VAL	3.6
1	A	167	PHE	3.6
1	A	114	PRO	3.6
1	A	263	LEU	3.6
1	A	188	LEU	3.6
1	B	200	ASN	3.5
1	A	130	CYS	3.5
1	A	274	GLN	3.5
1	A	191	LEU	3.5
1	A	215	LEU	3.5
1	B	32	GLY	3.5
1	A	20	GLU	3.5
1	B	33	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	54	ASN	3.4
1	A	249	GLU	3.4
1	A	33	PHE	3.4
1	A	294	LEU	3.4
1	A	25	LEU	3.4
1	A	204	SER	3.3
1	B	17	VAL	3.3
1	A	21	GLU	3.3
1	B	54	ASN	3.3
1	A	251	PRO	3.3
1	A	214	ILE	3.3
1	A	87	PHE	3.3
1	B	295	VAL	3.3
1	A	279	PRO	3.3
1	A	86	ASP	3.2
1	A	217	TRP	3.2
1	B	16	LEU	3.2
1	A	288	THR	3.2
1	A	190	TYR	3.2
1	A	164	LEU	3.2
1	A	29	GLY	3.2
1	A	277	ASN	3.1
1	A	19	ARG	3.1
1	A	31	GLY	3.1
1	A	142	ARG	3.1
1	B	252	PRO	3.1
1	A	107	LEU	3.1
1	A	266	LEU	3.1
1	A	209	VAL	3.1
1	A	295	VAL	3.1
1	A	253	GLY	3.1
1	A	311	SER	3.1
1	A	219	VAL	3.1
1	B	38	ARG	3.1
1	B	21	GLU	3.0
1	A	24	LYS	3.0
1	A	115	TRP	3.0
1	A	84	GLN	3.0
1	A	122	LEU	3.0
1	A	289	ASN	3.0
1	A	30	LYS	3.0
1	A	145	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	116	PRO	3.0
1	A	245	PRO	3.0
1	A	163	GLY	2.9
1	B	165	SER	2.9
1	A	224	GLU	2.9
1	A	268	ILE	2.9
1	B	311	SER	2.9
1	A	106	LEU	2.9
1	B	89	SER	2.9
1	A	203	ALA	2.9
1	A	55	SER	2.9
1	A	58	ILE	2.8
1	A	265	GLU	2.8
1	A	27	PHE	2.8
1	B	296	LYS	2.8
1	A	53	VAL	2.8
1	B	168	GLN	2.8
1	A	205	LYS	2.7
1	A	88	VAL	2.7
1	A	292	TYR	2.7
1	A	221	ALA	2.7
1	B	253	GLY	2.7
1	A	140	LEU	2.6
1	A	248	THR	2.6
1	B	297	ASP	2.6
1	A	291	VAL	2.6
1	B	166	THR	2.6
1	A	138	PRO	2.6
1	A	60	TRP	2.6
1	A	258	PRO	2.5
1	A	152	ASP	2.5
1	A	296	LYS	2.5
1	B	312	GLN	2.5
1	A	207	SER	2.5
1	A	278	ARG	2.5
1	A	208	ASP	2.5
1	A	26	GLU	2.5
1	A	290	GLU	2.5
1	A	100	ASN	2.5
1	B	43	THR	2.5
1	A	252	PRO	2.5
1	A	136	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	192	ASP	2.4
1	A	16	LEU	2.4
1	A	118	LEU	2.4
1	A	257	THR	2.4
1	B	298	LYS	2.4
1	A	146	PRO	2.4
1	A	304	SER	2.4
1	B	243	SER	2.4
1	A	64	ALA	2.4
1	A	112	PRO	2.3
1	B	110	GLU	2.3
1	A	244	ARG	2.3
1	A	168	GLN	2.3
1	B	191	LEU	2.3
1	A	137	PRO	2.3
1	B	300	ASP	2.3
1	A	272	GLY	2.3
1	B	84	GLN	2.3
1	A	150	LEU	2.3
1	A	14	VAL	2.3
1	B	143	ASP	2.3
1	B	262	LYS	2.3
1	A	307	LYS	2.2
1	A	218	ALA	2.2
1	A	213	GLY	2.2
1	B	57	LYS	2.2
1	B	310	LEU	2.2
1	A	109	PRO	2.2
1	A	300	ASP	2.2
1	A	105	GLY	2.2
1	A	63	LYS	2.2
1	A	223	ARG	2.2
1	A	121	LEU	2.2
1	A	301	ALA	2.2
1	A	59	SER	2.1
1	A	206	ALA	2.1
1	B	99	GLU	2.1
1	A	151	LEU	2.1
1	B	309	TYR	2.1
1	A	34	GLY	2.1
1	A	308	HIS	2.1
1	B	167	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	204	SER	2.0
1	A	287	LYS	2.0
1	A	90	GLY	2.0
1	B	308	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 monosaccharides in this entry.

6.4 Ligands [i](#)

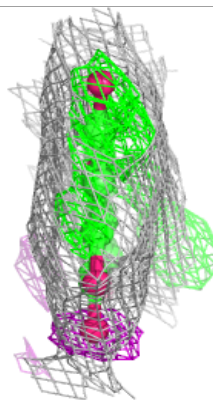
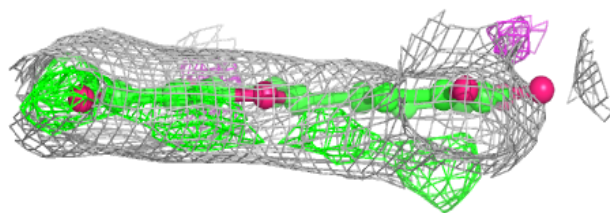
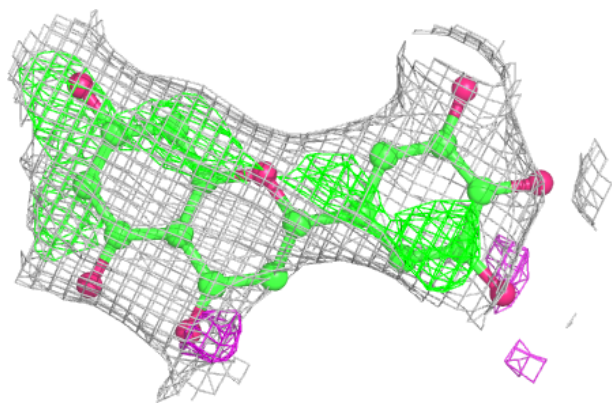
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MYF	A	401	22/22	0.69	0.27	56,105,120,125	0
2	MYF	B	401	22/22	0.75	0.23	74,88,92,94	0

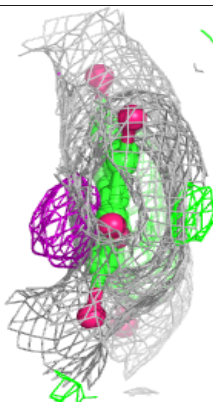
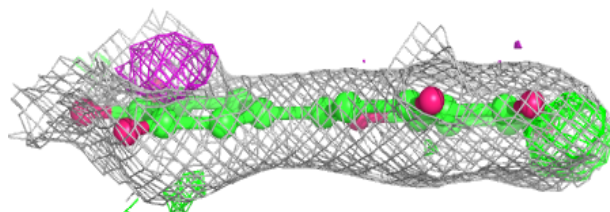
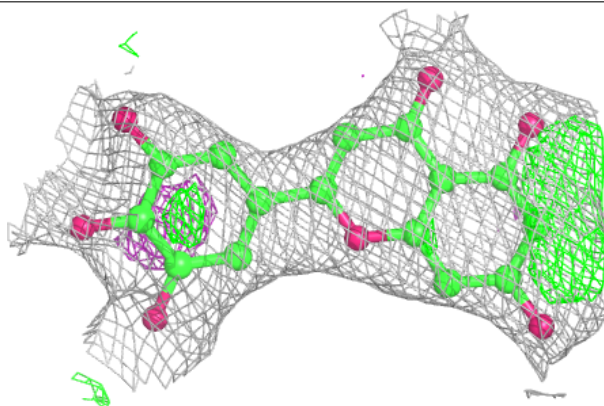
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around MYF 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)

**Electron density around MYF 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.