



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 09:24 PM UTC

PDB ID : 5KZ7 / pdb_00005kz7
Title : Mark2 complex with 7-[(1S)-1-(4-fluorophenyl)ethyl]-5,5-dimethyl-2-(3-pyridylamino)pyrrolo[2,3-d]pyrimidin-6-one
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Deposited on : 2016-07-23
Resolution : 3.20 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

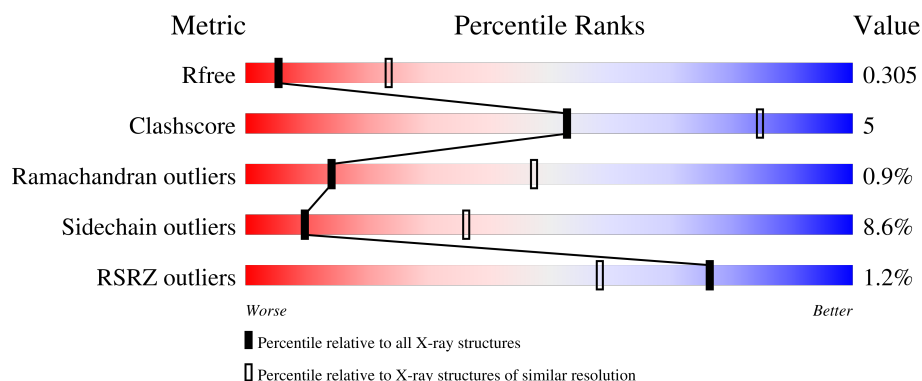
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	346	% 66% 18% • 14%
1	B	346	% 64% 18% •• 14%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4799 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 Serine/threonine-protein kinase MARK2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	0	0
			2378	1532	405	429	12			
1	B	296	Total	C	N	O	S	0	0	0
			2365	1522	405	426	12			

There are 40 discrepancies between the modelled and reference sequences:

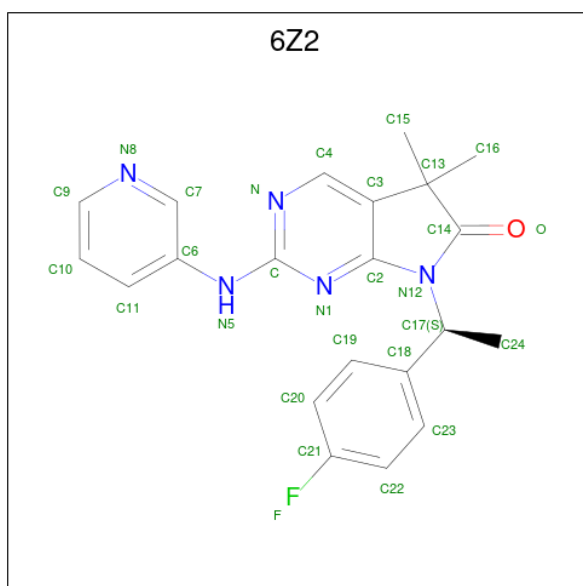
Chain	Residue	Modelled	Actual	Comment	Reference
A	19	MET	-	initiating methionine	UNP Q7KZI7
A	20	ALA	-	expression tag	UNP Q7KZI7
A	21	HIS	-	expression tag	UNP Q7KZI7
A	22	ASN	-	expression tag	UNP Q7KZI7
A	23	HIS	-	expression tag	UNP Q7KZI7
A	24	ARG	-	expression tag	UNP Q7KZI7
A	25	HIS	-	expression tag	UNP Q7KZI7
A	26	LYS	-	expression tag	UNP Q7KZI7
A	27	HIS	-	expression tag	UNP Q7KZI7
A	28	ALA	-	expression tag	UNP Q7KZI7
A	29	ASP	-	expression tag	UNP Q7KZI7
A	30	TYR	-	expression tag	UNP Q7KZI7
A	31	LYS	-	expression tag	UNP Q7KZI7
A	32	ASP	-	expression tag	UNP Q7KZI7
A	33	ASP	-	expression tag	UNP Q7KZI7
A	34	ASP	-	expression tag	UNP Q7KZI7
A	35	ASP	-	expression tag	UNP Q7KZI7
A	36	LYS	-	expression tag	UNP Q7KZI7
A	37	LYS	-	expression tag	UNP Q7KZI7
A	38	LEU	-	expression tag	UNP Q7KZI7
B	19	MET	-	initiating methionine	UNP Q7KZI7
B	20	ALA	-	expression tag	UNP Q7KZI7
B	21	HIS	-	expression tag	UNP Q7KZI7
B	22	ASN	-	expression tag	UNP Q7KZI7
B	23	HIS	-	expression tag	UNP Q7KZI7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	24	ARG	-	expression tag	UNP Q7KZI7
B	25	HIS	-	expression tag	UNP Q7KZI7
B	26	LYS	-	expression tag	UNP Q7KZI7
B	27	HIS	-	expression tag	UNP Q7KZI7
B	28	ALA	-	expression tag	UNP Q7KZI7
B	29	ASP	-	expression tag	UNP Q7KZI7
B	30	TYR	-	expression tag	UNP Q7KZI7
B	31	LYS	-	expression tag	UNP Q7KZI7
B	32	ASP	-	expression tag	UNP Q7KZI7
B	33	ASP	-	expression tag	UNP Q7KZI7
B	34	ASP	-	expression tag	UNP Q7KZI7
B	35	ASP	-	expression tag	UNP Q7KZI7
B	36	LYS	-	expression tag	UNP Q7KZI7
B	37	LYS	-	expression tag	UNP Q7KZI7
B	38	LEU	-	expression tag	UNP Q7KZI7

- Molecule 2 is 7-[(1 {S})-1-(4-fluorophenyl)ethyl]-5,5-dimethyl-2-(pyridin-3-ylamino)pyrrolo[2,3-d]pyrimidin-6-one (CCD ID: 6Z2) (formula: C₂₁H₂₀FN₅O).

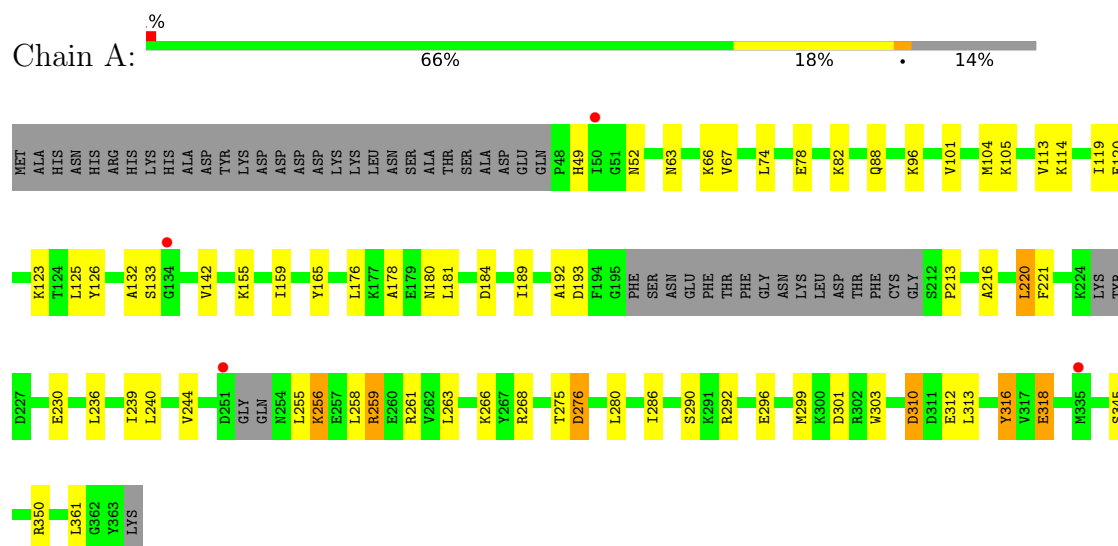


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			28	21	1	5	1		
2	B	1	Total	C	F	N	O	0	0
			28	21	1	5	1		

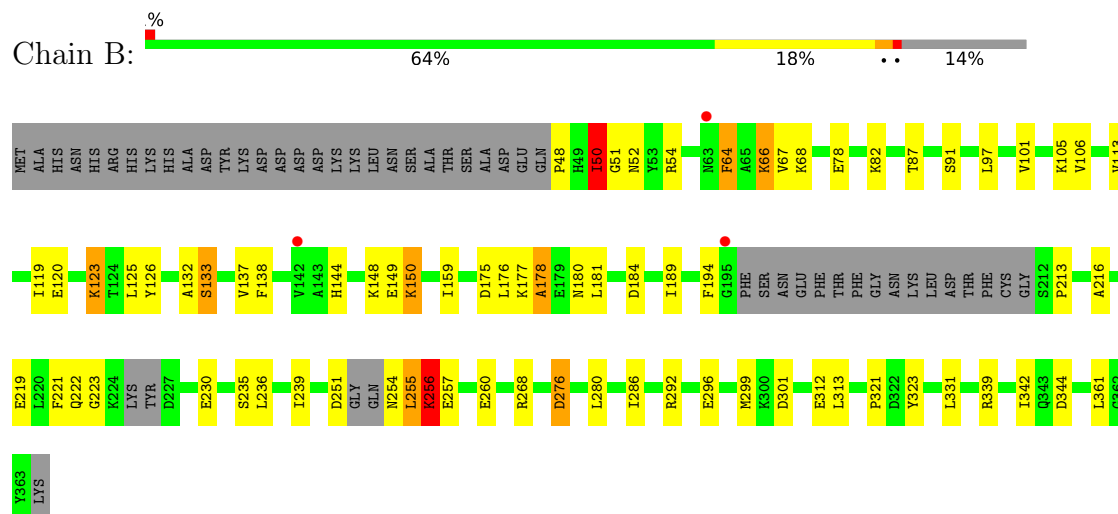
3 Residue-property plots [i](#)

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: Serine/threonine-protein kinase MARK2



- Molecule 1: Serine/threonine-protein kinase MARK2



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	119.35Å 119.35Å 98.74Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.53 – 3.20 19.53 – 3.20	Depositor EDS
% Data completeness (in resolution range)	94.9 (19.53-3.20) 94.6 (19.53-3.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 3.22Å)	Xtriage
Refinement program	BUSTER-TNT	Depositor
R, R_{free}	0.222 , 0.293 0.237 , 0.305	Depositor DCC
R_{free} test set	635 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	70.1	Xtriage
Anisotropy	0.212	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 64.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.073 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4799	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.60% 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:
6Z2

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	0.85	0/2424	1.48	16/3265 (0.5%)
1	B	0.86	0/2410	1.48	25/3250 (0.8%)
All	All	0.85	0/4834	1.48	41/6515 (0.6%)

There are no bond length outliers.

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	316	TYR	CA-C-N	8.43	131.81	120.77
1	A	316	TYR	C-N-CA	8.43	131.81	120.77
1	B	138	PHE	CA-CB-CG	7.70	121.50	113.80
1	A	132	ALA	CA-C-N	7.25	130.32	120.38
1	A	132	ALA	C-N-CA	7.25	130.32	120.38
1	A	275	THR	CA-C-N	6.96	130.47	120.79
1	A	275	THR	C-N-CA	6.96	130.47	120.79
1	B	256	LYS	N-CA-C	-6.96	103.78	111.36
1	B	256	LYS	CA-C-N	6.55	129.34	120.44
1	B	256	LYS	C-N-CA	6.55	129.34	120.44
1	B	52	ASN	CA-CB-CG	6.46	119.06	112.60
1	B	137	VAL	CA-C-N	6.38	129.66	120.79
1	B	137	VAL	C-N-CA	6.38	129.66	120.79
1	B	132	ALA	CA-C-N	6.38	128.83	120.28
1	B	132	ALA	C-N-CA	6.38	128.83	120.28
1	A	310	ASP	CA-CB-CG	6.28	118.88	112.60
1	B	175	ASP	CA-CB-CG	5.92	118.52	112.60
1	A	113	VAL	N-CA-CB	5.68	117.03	110.49
1	B	213	PRO	N-CA-C	5.67	117.62	110.70
1	A	213	PRO	N-CA-C	5.61	117.55	110.70
1	A	276	ASP	CA-CB-CG	5.56	118.16	112.60
1	A	230	GLU	CA-C-N	5.53	127.64	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	GLU	C-N-CA	5.53	127.64	120.56
1	B	180	ASN	CA-CB-CG	5.42	118.03	112.60
1	B	133	SER	N-CA-C	5.42	117.19	111.28
1	B	113	VAL	N-CA-CB	5.31	116.60	110.49
1	A	180	ASN	CA-CB-CG	5.31	117.91	112.60
1	B	344	ASP	CA-CB-CG	5.28	117.88	112.60
1	B	178	ALA	CA-C-N	5.25	127.31	120.28
1	B	178	ALA	C-N-CA	5.25	127.31	120.28
1	B	149	GLU	CA-C-N	5.19	127.24	120.28
1	B	149	GLU	C-N-CA	5.19	127.24	120.28
1	B	230	GLU	CA-C-N	5.17	127.18	120.56
1	B	230	GLU	C-N-CA	5.17	127.18	120.56
1	B	260	GLU	CA-C-N	5.06	127.06	120.28
1	B	260	GLU	C-N-CA	5.06	127.06	120.28
1	A	193	ASP	CA-C-N	5.05	130.32	122.49
1	A	193	ASP	C-N-CA	5.05	130.32	122.49
1	B	184	ASP	CA-CB-CG	5.02	117.62	112.60
1	A	184	ASP	CA-CB-CG	5.00	117.61	112.60
1	B	276	ASP	CA-CB-CG	5.00	117.61	112.60

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	2378	0	2411	24	0
1	B	2365	0	2386	27	0
2	A	28	0	0	0	0
2	B	28	0	0	0	0
All	All	4799	0	4797	48	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 5.

All (48) 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:259:ARG:HH11	1:A:263:LEU:HD11	1.43	0.83
1:B:50:ILE:HG23	1:B:51:GLY:H	1.56	0.69
1:A:119:ILE:HB	1:A:126:TYR:HB2	1.73	0.69
1:B:286:ILE:HB	1:B:292:ARG:HG2	1.75	0.68
1:A:256:LYS:HE3	1:A:256:LYS:HA	1.75	0.68
1:B:119:ILE:HB	1:B:126:TYR:HB2	1.74	0.67
1:A:296:GLU:HA	1:A:299:MET:HE3	1.78	0.66
1:B:296:GLU:HA	1:B:299:MET:HE3	1.79	0.65
1:A:220:LEU:HD11	1:B:256:LYS:HE3	1.81	0.61
1:A:259:ARG:NH1	1:A:263:LEU:HD11	2.14	0.59
1:A:165:TYR:CD1	1:A:316:TYR:HD2	2.21	0.59
1:A:178:ALA:HA	1:A:181:LEU:HD12	1.85	0.58
1:B:178:ALA:HA	1:B:181:LEU:HD12	1.83	0.58
1:A:176:LEU:HB3	1:A:239:ILE:HD11	1.87	0.57
1:B:176:LEU:HB2	1:B:235:SER:HB3	1.88	0.56
1:A:67:VAL:HG22	1:A:82:LYS:HG3	1.88	0.55
1:A:216:ALA:HB2	1:B:255:LEU:HD13	1.89	0.55
1:B:148:LYS:HB3	1:B:150:LYS:HD2	1.87	0.54
1:B:67:VAL:HG22	1:B:82:LYS:HG3	1.89	0.54
1:A:299:MET:HG2	1:A:313:LEU:HD23	1.91	0.53
1:B:87:THR:HG23	1:B:123:LYS:HB3	1.91	0.53
1:B:120:GLU:HG2	1:B:125:LEU:HD13	1.93	0.51
1:B:159:ILE:HG12	1:B:189:ILE:HG21	1.94	0.50
1:B:254:ASN:HB3	1:B:257:GLU:HB2	1.94	0.50
1:B:176:LEU:HB3	1:B:239:ILE:HD11	1.93	0.50
1:A:159:ILE:HG12	1:A:189:ILE:HG21	1.95	0.49
1:A:120:GLU:HG2	1:A:125:LEU:HD13	1.95	0.49
1:B:299:MET:HG2	1:B:313:LEU:HD23	1.95	0.49
1:B:219:GLU:HA	1:B:222:GLN:HB2	1.97	0.47
1:A:221:PHE:CD1	1:A:259:ARG:HG2	2.50	0.47
1:A:276:ASP:HB3	1:A:303:TRP:HD1	1.80	0.46
1:A:240:LEU:O	1:A:244:VAL:HG22	2.16	0.46
1:B:159:ILE:HG22	1:B:236:LEU:HD21	1.98	0.46
1:B:321:PRO:HB3	1:B:323:TYR:CE1	2.52	0.45
1:A:345:SER:HA	1:A:350:ARG:HG3	1.98	0.45
1:A:286:ILE:HB	1:A:292:ARG:HG2	1.98	0.45
1:A:52:ASN:OD1	1:A:74:LEU:HG	2.17	0.45
1:A:256:LYS:HZ1	1:B:223:GLY:HA2	1.80	0.45
1:A:280:LEU:HD13	1:A:301:ASP:CG	2.41	0.44
1:A:159:ILE:HG22	1:A:236:LEU:HD21	1.98	0.44
1:B:48:PRO:HB2	1:B:54:ARG:HG3	2.00	0.43
1:A:101:VAL:HG12	1:A:105:LYS:HE3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280:LEU:HD13	1:B:301:ASP:OD1	2.19	0.42
1:B:97:LEU:HD21	1:B:125:LEU:HD23	2.01	0.42
1:B:216:ALA:HB3	1:B:221:PHE:HE2	1.85	0.41
1:B:101:VAL:HG12	1:B:105:LYS:HE3	2.02	0.41
1:B:66:LYS:HD3	1:B:68:LYS:HE2	2.02	0.41
1:B:339:ARG:HA	1:B:342:ILE:HD12	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	288/346 (83%)	260 (90%)	26 (9%)	2 (1%)	18	52
1	B	288/346 (83%)	267 (93%)	18 (6%)	3 (1%)	12	45
All	All	576/692 (83%)	527 (92%)	44 (8%)	5 (1%)	14	47

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	192	ALA
1	B	50	ILE
1	B	194	PHE
1	A	318	GLU
1	B	64	PHE

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	257/307 (84%)	232 (90%)	25 (10%)	8	32
1	B	253/307 (82%)	234 (92%)	19 (8%)	12	42
All	All	510/614 (83%)	466 (91%)	44 (9%)	10	36

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

Mol	Chain	Res	Type
1	A	49	HIS
1	A	63	ASN
1	A	66	LYS
1	A	78	GLU
1	A	88	GLN
1	A	96	LYS
1	A	104	MET
1	A	114	LYS
1	A	123	LYS
1	A	133	SER
1	A	142	VAL
1	A	155	LYS
1	A	220	LEU
1	A	255	LEU
1	A	256	LYS
1	A	258	LEU
1	A	259	ARG
1	A	261	ARG
1	A	266	LYS
1	A	268	ARG
1	A	290	SER
1	A	310	ASP
1	A	312	GLU
1	A	318	GLU
1	A	361	LEU
1	B	50	ILE
1	B	64	PHE
1	B	66	LYS
1	B	78	GLU
1	B	91	SER
1	B	106	VAL
1	B	123	LYS
1	B	133	SER

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Mol	Chain	Res	Type
1	B	144	HIS
1	B	150	LYS
1	B	177	LYS
1	B	251	ASP
1	B	255	LEU
1	B	256	LYS
1	B	268	ARG
1	B	276	ASP
1	B	312	GLU
1	B	331	LEU
1	B	361	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	HIS
1	A	90	ASN
1	A	108	ASN
1	A	180	ASN
1	A	254	ASN
1	A	297	GLN
1	A	343	GLN
1	B	90	ASN
1	B	180	ASN
1	B	288	ASN
1	B	297	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

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	6Z2	A	401	-	31,31,31	2.91	6 (19%)	38,46,46	1.93	12 (31%)
2	6Z2	B	401	-	31,31,31	2.98	5 (16%)	38,46,46	1.83	14 (36%)

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	6Z2	A	401	-	-	0/12/32/32	0/4/4/4
2	6Z2	B	401	-	-	0/12/32/32	0/4/4/4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	6Z2	C13-C14	-10.85	1.41	1.52
2	B	401	6Z2	C13-C14	-10.18	1.41	1.52
2	B	401	6Z2	C13-C3	-8.30	1.40	1.51
2	B	401	6Z2	O-C14	7.70	1.34	1.22
2	A	401	6Z2	C13-C3	-7.41	1.41	1.51
2	A	401	6Z2	O-C14	7.04	1.33	1.22
2	B	401	6Z2	C6-N5	-2.64	1.35	1.40
2	B	401	6Z2	C2-N12	-2.50	1.34	1.38
2	A	401	6Z2	C6-N5	-2.41	1.35	1.40
2	A	401	6Z2	C22-C21	2.20	1.41	1.37
2	A	401	6Z2	C20-C21	2.02	1.41	1.37

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	6Z2	N-C-N1	-4.95	121.63	126.42
2	A	401	6Z2	C4-C3-C13	4.91	135.99	130.44
2	B	401	6Z2	C3-C13-C14	4.49	103.85	101.70
2	B	401	6Z2	C4-C3-C13	4.15	135.12	130.44
2	B	401	6Z2	N-C-N1	-3.73	122.81	126.42
2	A	401	6Z2	C3-C13-C14	3.18	103.22	101.70
2	A	401	6Z2	C3-C2-N1	-2.87	124.10	126.47
2	A	401	6Z2	C24-C17-N12	2.77	115.00	111.16
2	A	401	6Z2	C11-C6-C7	-2.74	115.12	117.78
2	A	401	6Z2	C2-N12-C14	-2.51	109.10	110.61
2	B	401	6Z2	C4-N-C	2.51	119.25	115.81
2	B	401	6Z2	C10-C11-C6	2.47	122.57	119.73
2	B	401	6Z2	C2-N12-C14	-2.42	109.16	110.61
2	B	401	6Z2	C3-C2-N1	-2.35	124.53	126.47
2	A	401	6Z2	N5-C-N	2.23	122.62	116.29
2	B	401	6Z2	N5-C-N	2.23	122.60	116.29
2	B	401	6Z2	C24-C17-N12	2.18	114.18	111.16
2	A	401	6Z2	O-C14-C13	-2.18	124.80	126.81
2	A	401	6Z2	C16-C13-C3	2.15	113.78	110.55
2	B	401	6Z2	C3-C4-N	-2.14	121.29	124.18
2	B	401	6Z2	O-C14-C13	-2.12	124.85	126.81
2	B	401	6Z2	C11-C10-C9	-2.11	115.87	118.92
2	B	401	6Z2	C11-C6-C7	-2.11	115.73	117.78
2	B	401	6Z2	C18-C17-N12	2.10	113.98	110.82
2	A	401	6Z2	C10-C11-C6	2.09	122.14	119.73
2	A	401	6Z2	C4-N-C	2.00	118.56	115.81

There are no chirality outliers.

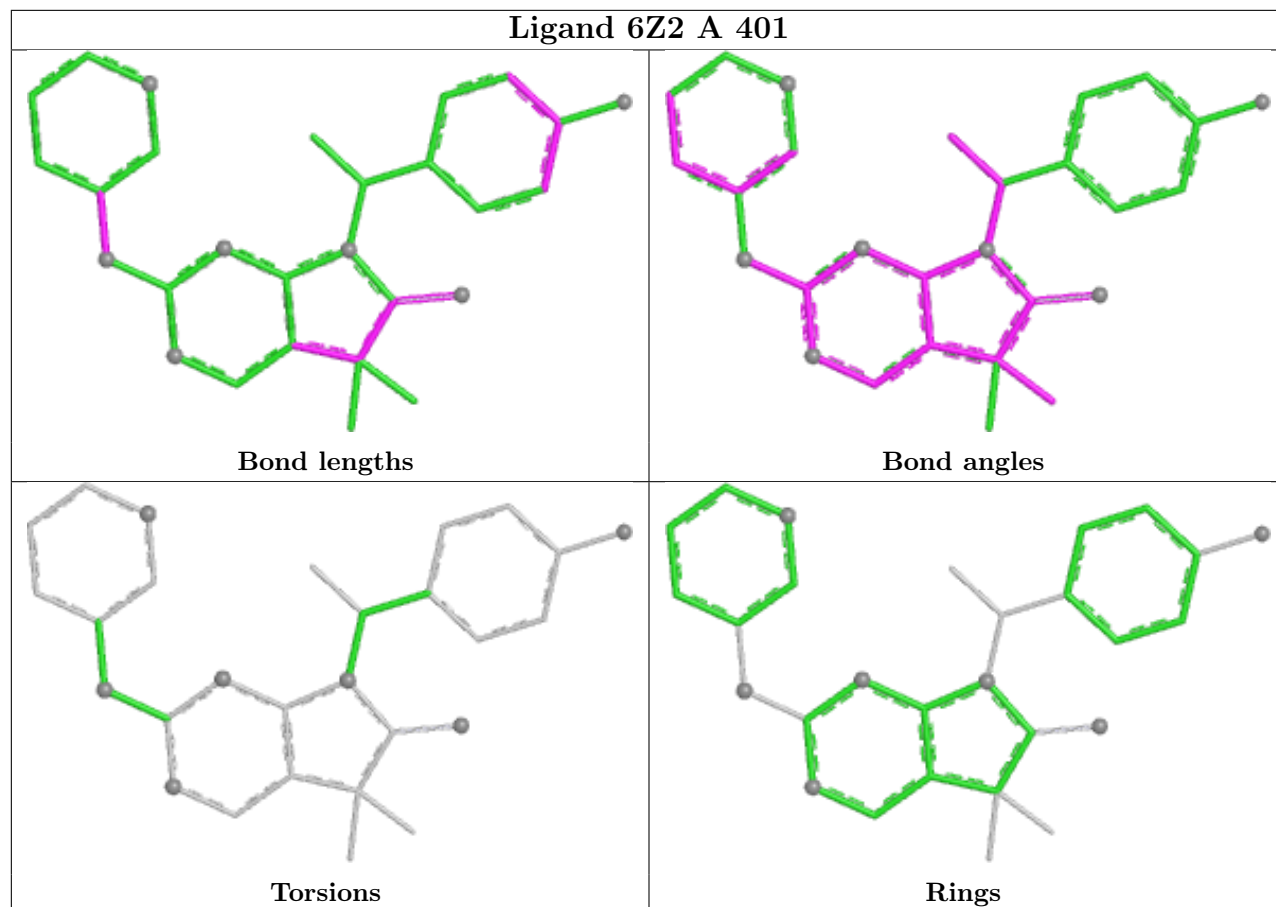
There are no torsion outliers.

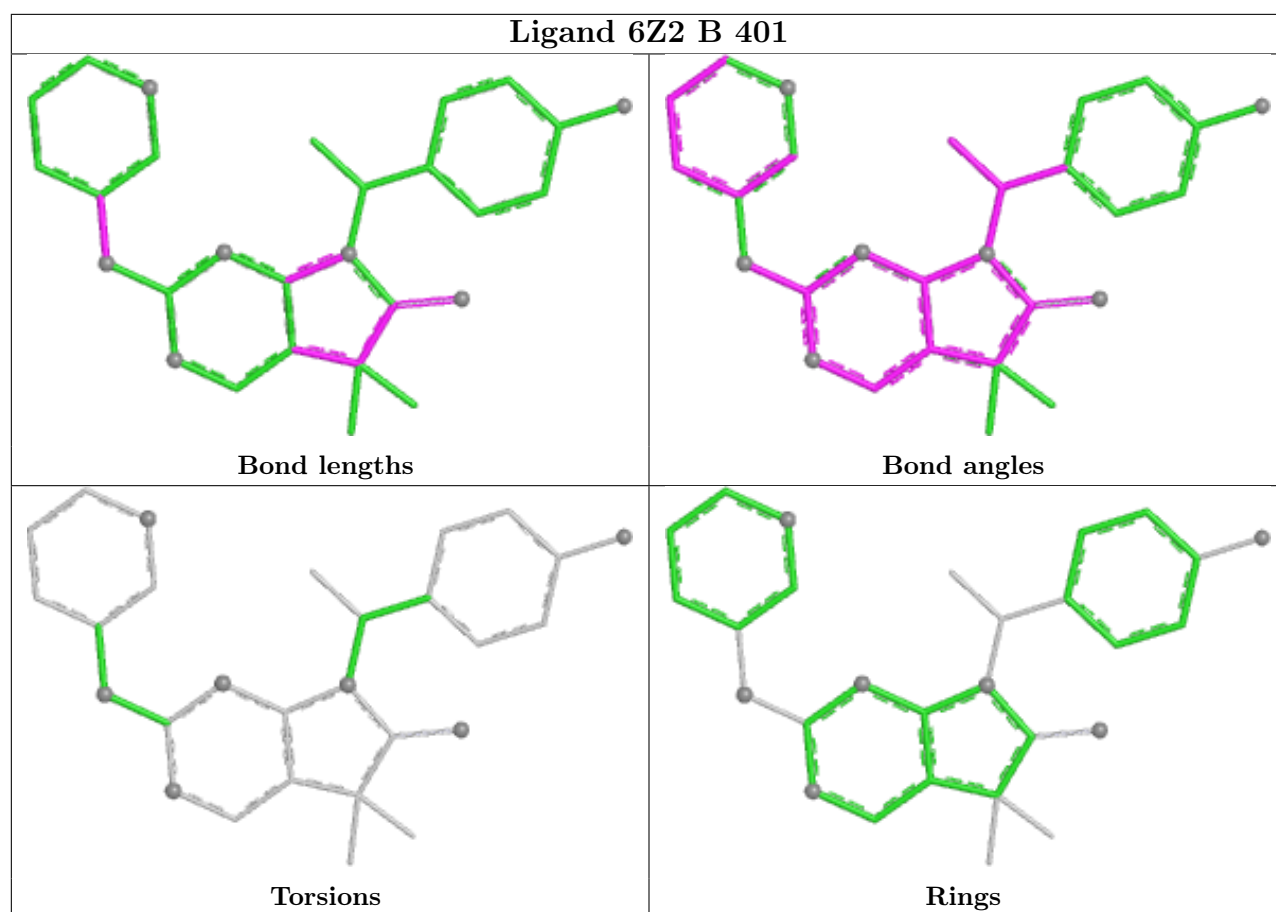
There are no ring outliers.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	296/346 (85%)	0.16	4 (1%) 73 54	40, 72, 98, 143	0
1	B	296/346 (85%)	0.02	3 (1%) 79 63	46, 69, 101, 138	0
All	All	592/692 (85%)	0.09	7 (1%) 76 58	40, 70, 99, 143	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	142	VAL	2.7
1	A	335	MET	2.6
1	A	50	ILE	2.5
1	B	195	GLY	2.3
1	A	251	ASP	2.2
1	B	63	ASN	2.1
1	A	134	GLY	2.1

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](#)

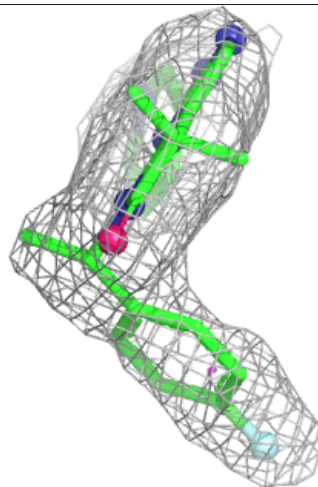
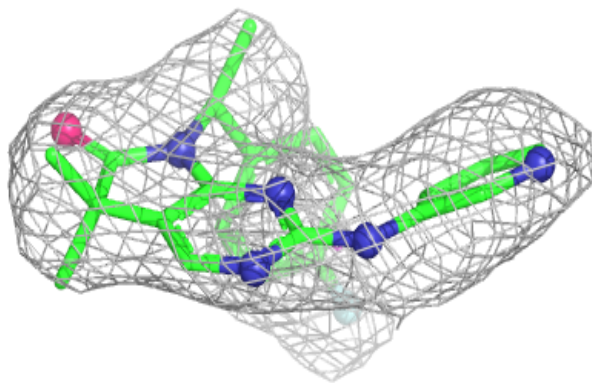
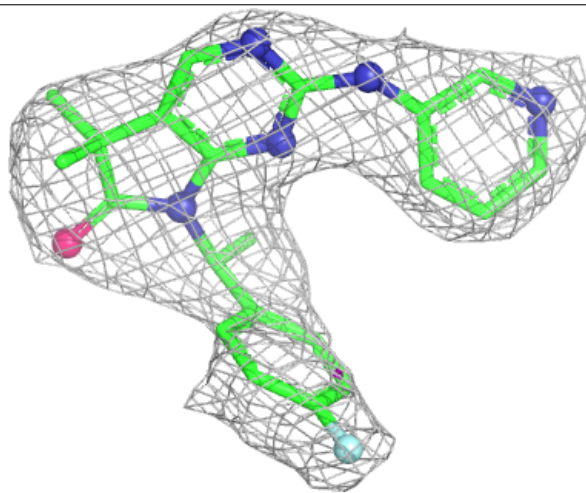
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists 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
2	6Z2	A	401	28/28	0.92	0.10	51,52,53,54	0
2	6Z2	B	401	28/28	0.94	0.10	62,63,64,64	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.

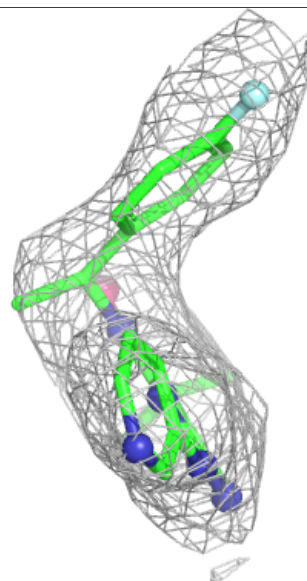
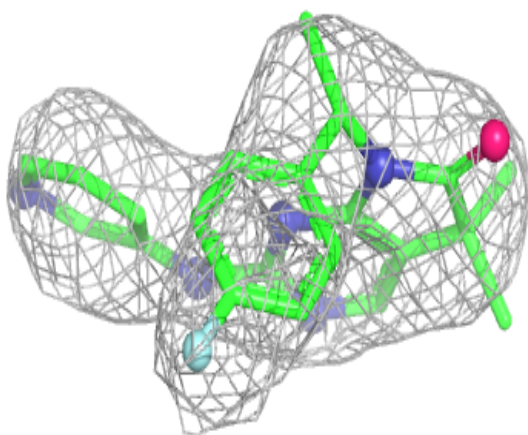
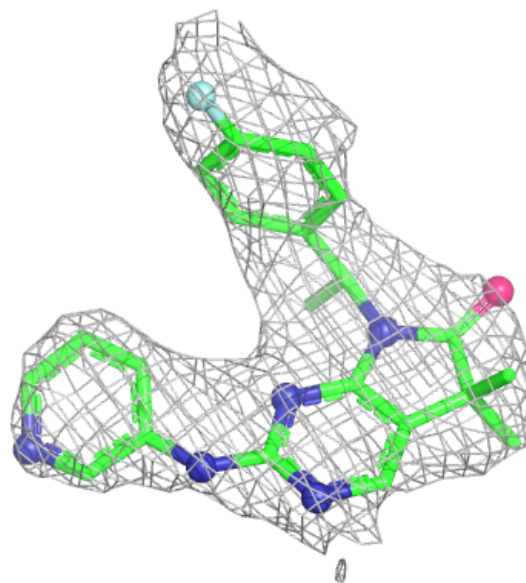
Electron density around 6Z2 A 401:

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 6Z2 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.