



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:52 AM UTC

PDB ID : 2Y7J / pdb_00002y7j
Title : Structure of human phosphorylase kinase, gamma 2
Authors : Muniz, J.R.C.; Shrestha, A.; Savitsky, P.; Wang, J.; Rellos, P.; Fedorov, O.; Burgess-Brown, N.; Brenner, B.; Berridge, G.; Elkins, J.M.; Krojer, T.; Vollmar, M.; Che, K.H.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.M.; Weigelt, J.; Bountra, C.; Knapp, S.
Deposited on : 2011-01-31
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](#) ①) 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

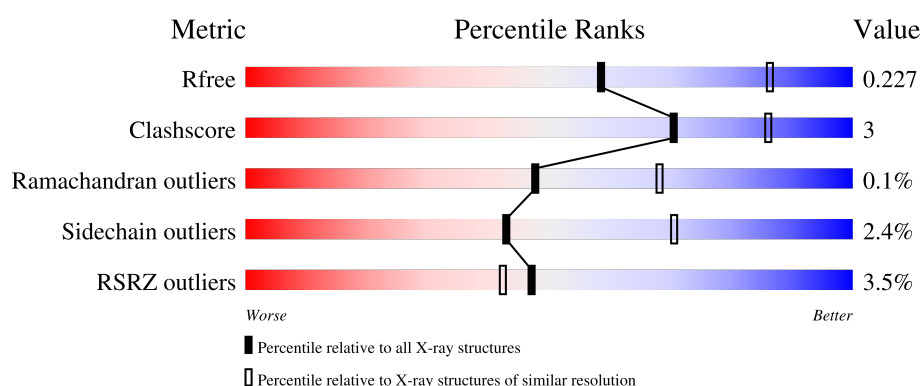
1 Overall quality at a glance

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	365	2% 71% 6% 22%
1	B	365	3% 69% 7% 23%
1	C	365	2% 68% 10% 22%
1	D	365	4% 70% 7% 23%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9378 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 PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN, TESTIS/LIVER ISOFORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	S	0	2	0
			2285	1457	399	415	14			
1	B	281	Total	C	N	O	S	0	2	0
			2226	1415	383	415	13			
1	C	284	Total	C	N	O	S	0	0	0
			2258	1442	387	415	14			
1	D	281	Total	C	N	O	S	0	0	0
			2210	1411	382	403	14			

There are 308 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-71	MET	-	expression tag	UNP P15735
A	-70	HIS	-	expression tag	UNP P15735
A	-69	HIS	-	expression tag	UNP P15735
A	-68	HIS	-	expression tag	UNP P15735
A	-67	HIS	-	expression tag	UNP P15735
A	-66	HIS	-	expression tag	UNP P15735
A	-65	HIS	-	expression tag	UNP P15735
A	-64	SER	-	expression tag	UNP P15735
A	-63	SER	-	expression tag	UNP P15735
A	-62	GLY	-	expression tag	UNP P15735
A	-61	VAL	-	expression tag	UNP P15735
A	-60	ASP	-	expression tag	UNP P15735
A	-59	ASN	-	expression tag	UNP P15735
A	-58	LYS	-	expression tag	UNP P15735
A	-57	PHE	-	expression tag	UNP P15735
A	-56	ASN	-	expression tag	UNP P15735
A	-55	LYS	-	expression tag	UNP P15735
A	-54	GLU	-	expression tag	UNP P15735
A	-53	ARG	-	expression tag	UNP P15735
A	-52	ARG	-	expression tag	UNP P15735

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-51	ARG	-	expression tag	UNP P15735
A	-50	ALA	-	expression tag	UNP P15735
A	-49	ARG	-	expression tag	UNP P15735
A	-48	ARG	-	expression tag	UNP P15735
A	-47	GLU	-	expression tag	UNP P15735
A	-46	ILE	-	expression tag	UNP P15735
A	-45	ARG	-	expression tag	UNP P15735
A	-44	HIS	-	expression tag	UNP P15735
A	-43	LEU	-	expression tag	UNP P15735
A	-42	PRO	-	expression tag	UNP P15735
A	-41	ASN	-	expression tag	UNP P15735
A	-40	LEU	-	expression tag	UNP P15735
A	-39	ASN	-	expression tag	UNP P15735
A	-38	ARG	-	expression tag	UNP P15735
A	-37	GLU	-	expression tag	UNP P15735
A	-36	GLN	-	expression tag	UNP P15735
A	-35	ARG	-	expression tag	UNP P15735
A	-34	ARG	-	expression tag	UNP P15735
A	-33	ALA	-	expression tag	UNP P15735
A	-32	PHE	-	expression tag	UNP P15735
A	-31	ILE	-	expression tag	UNP P15735
A	-30	ARG	-	expression tag	UNP P15735
A	-29	SER	-	expression tag	UNP P15735
A	-28	LEU	-	expression tag	UNP P15735
A	-27	ARG	-	expression tag	UNP P15735
A	-26	ASP	-	expression tag	UNP P15735
A	-25	ASP	-	expression tag	UNP P15735
A	-24	PRO	-	expression tag	UNP P15735
A	-23	SER	-	expression tag	UNP P15735
A	-22	GLN	-	expression tag	UNP P15735
A	-21	SER	-	expression tag	UNP P15735
A	-20	ALA	-	expression tag	UNP P15735
A	-19	ASN	-	expression tag	UNP P15735
A	-18	LEU	-	expression tag	UNP P15735
A	-17	LEU	-	expression tag	UNP P15735
A	-16	ALA	-	expression tag	UNP P15735
A	-15	GLU	-	expression tag	UNP P15735
A	-14	ALA	-	expression tag	UNP P15735
A	-13	LYS	-	expression tag	UNP P15735
A	-12	LYS	-	expression tag	UNP P15735
A	-11	LEU	-	expression tag	UNP P15735
A	-10	ASN	-	expression tag	UNP P15735

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	ASP	-	expression tag	UNP P15735
A	-8	ALA	-	expression tag	UNP P15735
A	-7	GLN	-	expression tag	UNP P15735
A	-6	PRO	-	expression tag	UNP P15735
A	-5	LYS	-	expression tag	UNP P15735
A	-4	GLY	-	expression tag	UNP P15735
A	-3	THR	-	expression tag	UNP P15735
A	-2	GLU	-	expression tag	UNP P15735
A	-1	ASN	-	expression tag	UNP P15735
A	0	LEU	-	expression tag	UNP P15735
A	1	TYR	-	expression tag	UNP P15735
A	2	PHE	-	expression tag	UNP P15735
A	3	GLN	-	expression tag	UNP P15735
A	4	SER	-	expression tag	UNP P15735
A	5	MET	-	expression tag	UNP P15735
B	-71	MET	-	expression tag	UNP P15735
B	-70	HIS	-	expression tag	UNP P15735
B	-69	HIS	-	expression tag	UNP P15735
B	-68	HIS	-	expression tag	UNP P15735
B	-67	HIS	-	expression tag	UNP P15735
B	-66	HIS	-	expression tag	UNP P15735
B	-65	HIS	-	expression tag	UNP P15735
B	-64	SER	-	expression tag	UNP P15735
B	-63	SER	-	expression tag	UNP P15735
B	-62	GLY	-	expression tag	UNP P15735
B	-61	VAL	-	expression tag	UNP P15735
B	-60	ASP	-	expression tag	UNP P15735
B	-59	ASN	-	expression tag	UNP P15735
B	-58	LYS	-	expression tag	UNP P15735
B	-57	PHE	-	expression tag	UNP P15735
B	-56	ASN	-	expression tag	UNP P15735
B	-55	LYS	-	expression tag	UNP P15735
B	-54	GLU	-	expression tag	UNP P15735
B	-53	ARG	-	expression tag	UNP P15735
B	-52	ARG	-	expression tag	UNP P15735
B	-51	ARG	-	expression tag	UNP P15735
B	-50	ALA	-	expression tag	UNP P15735
B	-49	ARG	-	expression tag	UNP P15735
B	-48	ARG	-	expression tag	UNP P15735
B	-47	GLU	-	expression tag	UNP P15735
B	-46	ILE	-	expression tag	UNP P15735
B	-45	ARG	-	expression tag	UNP P15735

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-44	HIS	-	expression tag	UNP P15735
B	-43	LEU	-	expression tag	UNP P15735
B	-42	PRO	-	expression tag	UNP P15735
B	-41	ASN	-	expression tag	UNP P15735
B	-40	LEU	-	expression tag	UNP P15735
B	-39	ASN	-	expression tag	UNP P15735
B	-38	ARG	-	expression tag	UNP P15735
B	-37	GLU	-	expression tag	UNP P15735
B	-36	GLN	-	expression tag	UNP P15735
B	-35	ARG	-	expression tag	UNP P15735
B	-34	ARG	-	expression tag	UNP P15735
B	-33	ALA	-	expression tag	UNP P15735
B	-32	PHE	-	expression tag	UNP P15735
B	-31	ILE	-	expression tag	UNP P15735
B	-30	ARG	-	expression tag	UNP P15735
B	-29	SER	-	expression tag	UNP P15735
B	-28	LEU	-	expression tag	UNP P15735
B	-27	ARG	-	expression tag	UNP P15735
B	-26	ASP	-	expression tag	UNP P15735
B	-25	ASP	-	expression tag	UNP P15735
B	-24	PRO	-	expression tag	UNP P15735
B	-23	SER	-	expression tag	UNP P15735
B	-22	GLN	-	expression tag	UNP P15735
B	-21	SER	-	expression tag	UNP P15735
B	-20	ALA	-	expression tag	UNP P15735
B	-19	ASN	-	expression tag	UNP P15735
B	-18	LEU	-	expression tag	UNP P15735
B	-17	LEU	-	expression tag	UNP P15735
B	-16	ALA	-	expression tag	UNP P15735
B	-15	GLU	-	expression tag	UNP P15735
B	-14	ALA	-	expression tag	UNP P15735
B	-13	LYS	-	expression tag	UNP P15735
B	-12	LYS	-	expression tag	UNP P15735
B	-11	LEU	-	expression tag	UNP P15735
B	-10	ASN	-	expression tag	UNP P15735
B	-9	ASP	-	expression tag	UNP P15735
B	-8	ALA	-	expression tag	UNP P15735
B	-7	GLN	-	expression tag	UNP P15735
B	-6	PRO	-	expression tag	UNP P15735
B	-5	LYS	-	expression tag	UNP P15735
B	-4	GLY	-	expression tag	UNP P15735
B	-3	THR	-	expression tag	UNP P15735

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLU	-	expression tag	UNP P15735
B	-1	ASN	-	expression tag	UNP P15735
B	0	LEU	-	expression tag	UNP P15735
B	1	TYR	-	expression tag	UNP P15735
B	2	PHE	-	expression tag	UNP P15735
B	3	GLN	-	expression tag	UNP P15735
B	4	SER	-	expression tag	UNP P15735
B	5	MET	-	expression tag	UNP P15735
C	-71	MET	-	expression tag	UNP P15735
C	-70	HIS	-	expression tag	UNP P15735
C	-69	HIS	-	expression tag	UNP P15735
C	-68	HIS	-	expression tag	UNP P15735
C	-67	HIS	-	expression tag	UNP P15735
C	-66	HIS	-	expression tag	UNP P15735
C	-65	HIS	-	expression tag	UNP P15735
C	-64	SER	-	expression tag	UNP P15735
C	-63	SER	-	expression tag	UNP P15735
C	-62	GLY	-	expression tag	UNP P15735
C	-61	VAL	-	expression tag	UNP P15735
C	-60	ASP	-	expression tag	UNP P15735
C	-59	ASN	-	expression tag	UNP P15735
C	-58	LYS	-	expression tag	UNP P15735
C	-57	PHE	-	expression tag	UNP P15735
C	-56	ASN	-	expression tag	UNP P15735
C	-55	LYS	-	expression tag	UNP P15735
C	-54	GLU	-	expression tag	UNP P15735
C	-53	ARG	-	expression tag	UNP P15735
C	-52	ARG	-	expression tag	UNP P15735
C	-51	ARG	-	expression tag	UNP P15735
C	-50	ALA	-	expression tag	UNP P15735
C	-49	ARG	-	expression tag	UNP P15735
C	-48	ARG	-	expression tag	UNP P15735
C	-47	GLU	-	expression tag	UNP P15735
C	-46	ILE	-	expression tag	UNP P15735
C	-45	ARG	-	expression tag	UNP P15735
C	-44	HIS	-	expression tag	UNP P15735
C	-43	LEU	-	expression tag	UNP P15735
C	-42	PRO	-	expression tag	UNP P15735
C	-41	ASN	-	expression tag	UNP P15735
C	-40	LEU	-	expression tag	UNP P15735
C	-39	ASN	-	expression tag	UNP P15735
C	-38	ARG	-	expression tag	UNP P15735

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-37	GLU	-	expression tag	UNP P15735
C	-36	GLN	-	expression tag	UNP P15735
C	-35	ARG	-	expression tag	UNP P15735
C	-34	ARG	-	expression tag	UNP P15735
C	-33	ALA	-	expression tag	UNP P15735
C	-32	PHE	-	expression tag	UNP P15735
C	-31	ILE	-	expression tag	UNP P15735
C	-30	ARG	-	expression tag	UNP P15735
C	-29	SER	-	expression tag	UNP P15735
C	-28	LEU	-	expression tag	UNP P15735
C	-27	ARG	-	expression tag	UNP P15735
C	-26	ASP	-	expression tag	UNP P15735
C	-25	ASP	-	expression tag	UNP P15735
C	-24	PRO	-	expression tag	UNP P15735
C	-23	SER	-	expression tag	UNP P15735
C	-22	GLN	-	expression tag	UNP P15735
C	-21	SER	-	expression tag	UNP P15735
C	-20	ALA	-	expression tag	UNP P15735
C	-19	ASN	-	expression tag	UNP P15735
C	-18	LEU	-	expression tag	UNP P15735
C	-17	LEU	-	expression tag	UNP P15735
C	-16	ALA	-	expression tag	UNP P15735
C	-15	GLU	-	expression tag	UNP P15735
C	-14	ALA	-	expression tag	UNP P15735
C	-13	LYS	-	expression tag	UNP P15735
C	-12	LYS	-	expression tag	UNP P15735
C	-11	LEU	-	expression tag	UNP P15735
C	-10	ASN	-	expression tag	UNP P15735
C	-9	ASP	-	expression tag	UNP P15735
C	-8	ALA	-	expression tag	UNP P15735
C	-7	GLN	-	expression tag	UNP P15735
C	-6	PRO	-	expression tag	UNP P15735
C	-5	LYS	-	expression tag	UNP P15735
C	-4	GLY	-	expression tag	UNP P15735
C	-3	THR	-	expression tag	UNP P15735
C	-2	GLU	-	expression tag	UNP P15735
C	-1	ASN	-	expression tag	UNP P15735
C	0	LEU	-	expression tag	UNP P15735
C	1	TYR	-	expression tag	UNP P15735
C	2	PHE	-	expression tag	UNP P15735
C	3	GLN	-	expression tag	UNP P15735
C	4	SER	-	expression tag	UNP P15735

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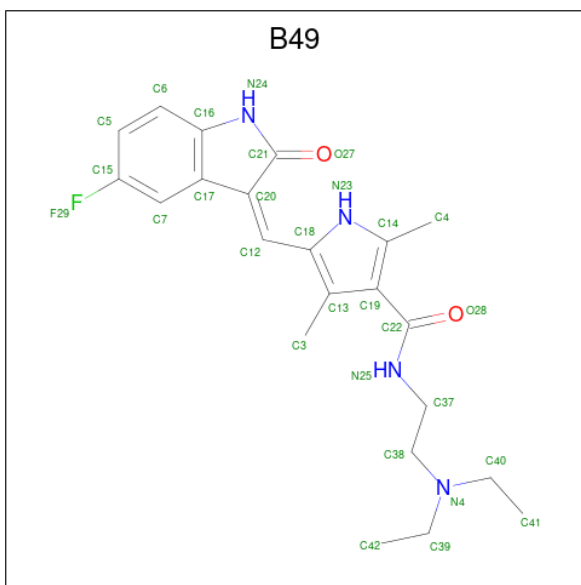
Chain	Residue	Modelled	Actual	Comment	Reference
C	5	MET	-	expression tag	UNP P15735
D	-71	MET	-	expression tag	UNP P15735
D	-70	HIS	-	expression tag	UNP P15735
D	-69	HIS	-	expression tag	UNP P15735
D	-68	HIS	-	expression tag	UNP P15735
D	-67	HIS	-	expression tag	UNP P15735
D	-66	HIS	-	expression tag	UNP P15735
D	-65	HIS	-	expression tag	UNP P15735
D	-64	SER	-	expression tag	UNP P15735
D	-63	SER	-	expression tag	UNP P15735
D	-62	GLY	-	expression tag	UNP P15735
D	-61	VAL	-	expression tag	UNP P15735
D	-60	ASP	-	expression tag	UNP P15735
D	-59	ASN	-	expression tag	UNP P15735
D	-58	LYS	-	expression tag	UNP P15735
D	-57	PHE	-	expression tag	UNP P15735
D	-56	ASN	-	expression tag	UNP P15735
D	-55	LYS	-	expression tag	UNP P15735
D	-54	GLU	-	expression tag	UNP P15735
D	-53	ARG	-	expression tag	UNP P15735
D	-52	ARG	-	expression tag	UNP P15735
D	-51	ARG	-	expression tag	UNP P15735
D	-50	ALA	-	expression tag	UNP P15735
D	-49	ARG	-	expression tag	UNP P15735
D	-48	ARG	-	expression tag	UNP P15735
D	-47	GLU	-	expression tag	UNP P15735
D	-46	ILE	-	expression tag	UNP P15735
D	-45	ARG	-	expression tag	UNP P15735
D	-44	HIS	-	expression tag	UNP P15735
D	-43	LEU	-	expression tag	UNP P15735
D	-42	PRO	-	expression tag	UNP P15735
D	-41	ASN	-	expression tag	UNP P15735
D	-40	LEU	-	expression tag	UNP P15735
D	-39	ASN	-	expression tag	UNP P15735
D	-38	ARG	-	expression tag	UNP P15735
D	-37	GLU	-	expression tag	UNP P15735
D	-36	GLN	-	expression tag	UNP P15735
D	-35	ARG	-	expression tag	UNP P15735
D	-34	ARG	-	expression tag	UNP P15735
D	-33	ALA	-	expression tag	UNP P15735
D	-32	PHE	-	expression tag	UNP P15735
D	-31	ILE	-	expression tag	UNP P15735

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-30	ARG	-	expression tag	UNP P15735
D	-29	SER	-	expression tag	UNP P15735
D	-28	LEU	-	expression tag	UNP P15735
D	-27	ARG	-	expression tag	UNP P15735
D	-26	ASP	-	expression tag	UNP P15735
D	-25	ASP	-	expression tag	UNP P15735
D	-24	PRO	-	expression tag	UNP P15735
D	-23	SER	-	expression tag	UNP P15735
D	-22	GLN	-	expression tag	UNP P15735
D	-21	SER	-	expression tag	UNP P15735
D	-20	ALA	-	expression tag	UNP P15735
D	-19	ASN	-	expression tag	UNP P15735
D	-18	LEU	-	expression tag	UNP P15735
D	-17	LEU	-	expression tag	UNP P15735
D	-16	ALA	-	expression tag	UNP P15735
D	-15	GLU	-	expression tag	UNP P15735
D	-14	ALA	-	expression tag	UNP P15735
D	-13	LYS	-	expression tag	UNP P15735
D	-12	LYS	-	expression tag	UNP P15735
D	-11	LEU	-	expression tag	UNP P15735
D	-10	ASN	-	expression tag	UNP P15735
D	-9	ASP	-	expression tag	UNP P15735
D	-8	ALA	-	expression tag	UNP P15735
D	-7	GLN	-	expression tag	UNP P15735
D	-6	PRO	-	expression tag	UNP P15735
D	-5	LYS	-	expression tag	UNP P15735
D	-4	GLY	-	expression tag	UNP P15735
D	-3	THR	-	expression tag	UNP P15735
D	-2	GLU	-	expression tag	UNP P15735
D	-1	ASN	-	expression tag	UNP P15735
D	0	LEU	-	expression tag	UNP P15735
D	1	TYR	-	expression tag	UNP P15735
D	2	PHE	-	expression tag	UNP P15735
D	3	GLN	-	expression tag	UNP P15735
D	4	SER	-	expression tag	UNP P15735
D	5	MET	-	expression tag	UNP P15735

- Molecule 2 is N-[2-(diethylamino)ethyl]-5-[(Z)-(5-fluoro-2-oxo-1,2-dihydro-3H-indol-3-ylidene)methyl]-2,4-dimethyl-1H-pyrrole-3-carboxamide (CCD ID: B49) (formula: C₂₂H₂₇FN₄O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			29	22	1	4	2		
2	B	1	Total	C	F	N	O	0	0
			29	22	1	4	2		
2	C	1	Total	C	F	N	O	0	0
			29	22	1	4	2		
2	D	1	Total	C	F	N	O	0	0
			29	22	1	4	2		

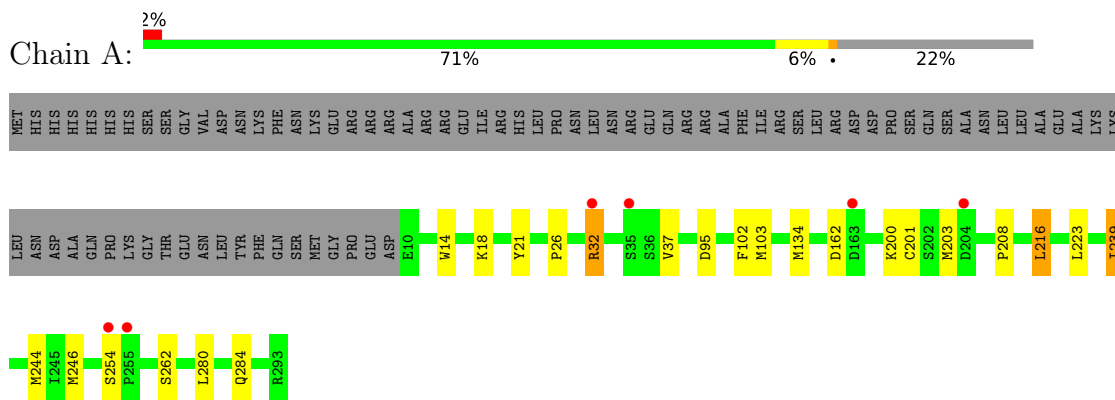
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	91	Total	O	0	0
			91	91		
3	B	60	Total	O	0	0
			60	60		
3	C	76	Total	O	0	0
			76	76		
3	D	56	Total	O	0	0
			56	56		

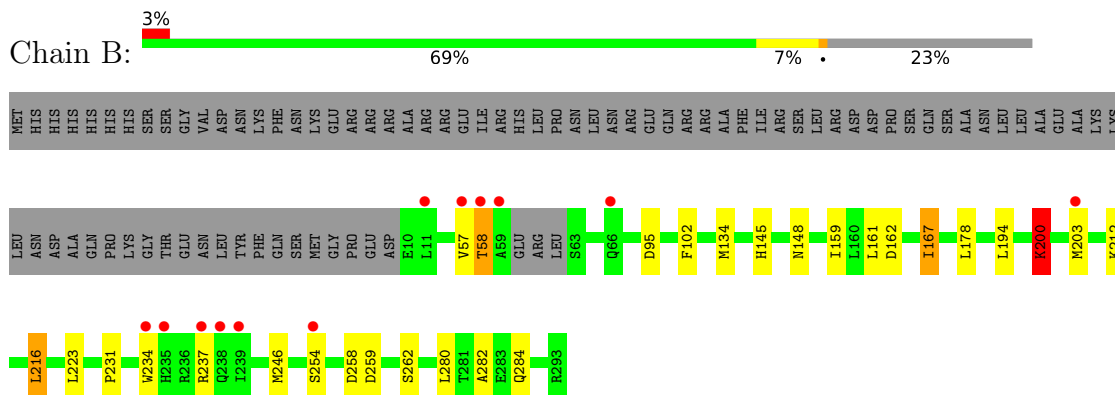
3 Residue-property plots

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.

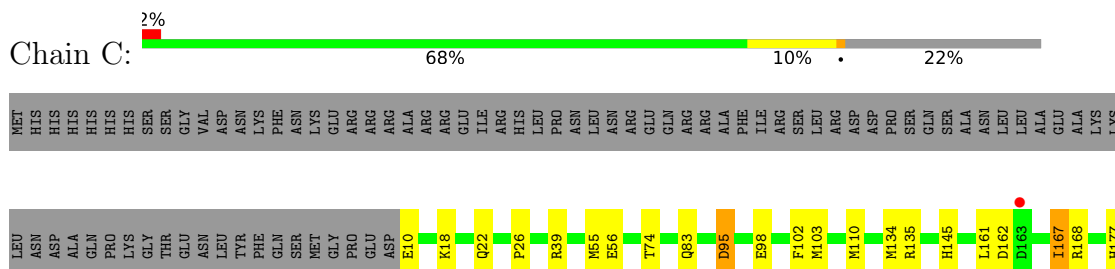
● Molecule 1: PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN, TESTIS/LIVER ISOFORM



● Molecule 1: PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN, TESTIS/LIVER ISOFORM

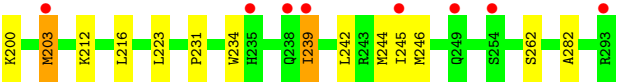
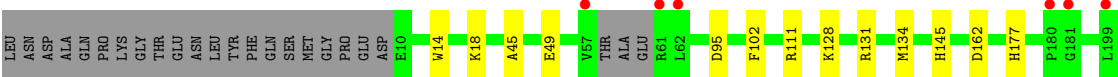
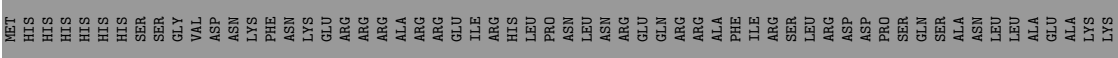


● Molecule 1: PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN, TESTIS/LIVER ISOFORM





● Molecule 1: PHOSPHORYLASE B KINASE GAMMA CATALYTIC CHAIN, TESTIS/LIVER ISOFORM



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.79Å 91.42Å 164.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.14 – 2.50 61.14 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (61.14-2.50) 99.4 (61.14-2.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.182 , 0.216 0.190 , 0.227	Depositor DCC
R_{free} test set	2343 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	42.7	Xtriage
Anisotropy	0.253	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 63.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9378	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 3.10% 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: B49

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	0.88	1/2339 (0.0%)	1.31	5/3166 (0.2%)
1	B	0.83	0/2278	1.32	9/3086 (0.3%)
1	C	0.85	0/2311	1.32	9/3130 (0.3%)
1	D	0.84	0/2262	1.29	4/3065 (0.1%)
All	All	0.85	1/9190 (0.0%)	1.31	27/12447 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	244	MET	SD-CE	6.12	1.94	1.79

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	95	ASP	CA-CB-CG	8.20	120.80	112.60
1	C	162	ASP	CA-CB-CG	7.66	120.26	112.60
1	B	200	LYS	CA-C-N	6.15	129.03	120.29
1	B	200	LYS	C-N-CA	6.15	129.03	120.29
1	D	162	ASP	CA-CB-CG	6.03	118.63	112.60
1	B	162	ASP	CA-CB-CG	6.01	118.61	112.60
1	B	259	ASP	CA-CB-CG	5.51	118.11	112.60
1	A	216	LEU	CD1-CG-CD2	5.45	122.78	110.80
1	B	262	SER	CA-C-N	5.44	127.52	120.44
1	B	262	SER	C-N-CA	5.44	127.52	120.44
1	B	102	PHE	CA-CB-CG	5.38	119.18	113.80
1	C	95	ASP	CA-CB-CG	5.33	117.93	112.60
1	A	262	SER	CA-C-N	5.25	127.27	120.44
1	A	262	SER	C-N-CA	5.25	127.27	120.44
1	C	262	SER	CA-C-N	5.24	127.30	120.28
1	C	262	SER	C-N-CA	5.24	127.30	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	102	PHE	N-CA-C	5.18	117.55	109.52
1	A	162	ASP	CA-CB-CG	5.08	117.68	112.60
1	D	262	SER	CA-C-N	5.07	127.04	120.44
1	D	262	SER	C-N-CA	5.07	127.04	120.44
1	C	56	GLU	CA-C-N	5.06	128.46	120.47
1	C	56	GLU	C-N-CA	5.06	128.46	120.47
1	C	237	ARG	CA-C-N	5.06	127.31	120.38
1	C	237	ARG	C-N-CA	5.06	127.31	120.38
1	C	247	GLU	CB-CG-CD	5.02	121.14	112.60
1	B	237	ARG	CA-C-N	5.01	126.99	120.28
1	B	237	ARG	C-N-CA	5.01	126.99	120.28

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	2285	0	2235	14	1
1	B	2226	0	2126	21	0
1	C	2258	0	2202	19	0
1	D	2210	0	2126	21	1
2	A	29	0	27	1	0
2	B	29	0	27	2	0
2	C	29	0	27	0	0
2	D	29	0	27	0	0
3	A	91	0	0	0	0
3	B	60	0	0	0	0
3	C	76	0	0	1	0
3	D	56	0	0	1	0
All	All	9378	0	8797	61	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 3.

All (61) 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:B:203:MET:HE3	1:D:203:MET:SD	2.02	0.99
1:B:159:ILE:HG22	1:B:167:ILE:HD12	1.59	0.85
1:B:194:LEU:HD11	1:D:239:ILE:HG12	1.62	0.80
1:B:159:ILE:CG2	1:B:167:ILE:HD12	2.18	0.74
1:B:246:MET:SD	1:D:203:MET:HG3	2.30	0.71
1:A:203:MET:HB2	1:C:246:MET:HE1	1.73	0.70
1:B:280:LEU:HD22	1:B:284:GLN:HB3	1.74	0.69
1:C:98:GLU:HG2	1:C:103:MET:SD	2.35	0.67
1:B:203:MET:HG3	1:D:203:MET:HB2	1.79	0.64
1:B:134:MET:HG3	1:B:223:LEU:HD13	1.79	0.64
1:C:134:MET:HG3	1:C:223:LEU:HD13	1.81	0.61
1:A:134:MET:HG3	1:A:223:LEU:HD13	1.80	0.61
2:B:1294:B49:H14	2:B:1294:B49:H23	1.83	0.60
1:D:134:MET:HG3	1:D:223:LEU:HD13	1.82	0.60
1:C:241:MET:HA	1:C:244:MET:HE2	1.84	0.59
1:B:203:MET:HA	1:D:246:MET:HE1	1.86	0.58
1:A:203:MET:HB2	1:C:246:MET:CE	2.35	0.56
1:B:200:LYS:HD2	1:B:246:MET:HE3	1.87	0.56
1:B:203:MET:SD	1:D:246:MET:SD	3.04	0.55
1:D:145:HIS:CE1	1:D:212:LYS:HB2	2.42	0.55
1:A:32[B]:ARG:HG2	1:A:37:VAL:HG23	1.90	0.53
1:B:203:MET:HG3	1:D:203:MET:CB	2.39	0.53
1:B:161:LEU:HD23	1:B:167:ILE:HD13	1.91	0.53
1:A:18:LYS:HG3	1:D:14:TRP:CE3	2.45	0.52
1:B:58:THR:HG23	1:C:39:ARG:HH22	1.73	0.52
2:A:1294:B49:H3B	2:A:1294:B49:HN25	1.75	0.52
1:B:145:HIS:CE1	1:B:212:LYS:HB2	2.45	0.52
1:B:216:LEU:HD21	1:B:282:ALA:HA	1.93	0.51
1:C:110:MET:HE2	1:C:168:ARG:HB2	1.93	0.51
1:B:194:LEU:CD1	1:D:239:ILE:HG12	2.38	0.50
1:A:280:LEU:HD22	1:A:284:GLN:HB3	1.93	0.50
1:D:49:GLU:OE1	1:D:111:ARG:NH1	2.38	0.50
1:D:242:LEU:HA	1:D:245:ILE:HD12	1.93	0.49
1:C:74:THR:HB	1:C:103:MET:HE2	1.95	0.48
1:C:83:GLN:HE22	1:C:177:HIS:HE1	1.60	0.47
1:A:14:TRP:CE3	1:D:18:LYS:HG3	2.50	0.47
1:A:14:TRP:HE3	1:D:18:LYS:HG3	1.81	0.46
1:C:26:PRO:HG2	3:C:2015:HOH:O	2.14	0.46
1:D:200:LYS:HG3	1:D:246:MET:HE3	1.97	0.46
1:C:18:LYS:O	1:C:22:GLN:HB2	2.15	0.46
1:A:21:TYR:HE1	1:A:26:PRO:HG3	1.81	0.46
1:D:128:LYS:HA	1:D:131:ARG:HH12	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:LYS:HG3	1:D:14:TRP:HE3	1.80	0.46
1:C:200:LYS:CG	1:C:246:MET:HE3	2.46	0.45
1:A:200:LYS:HG3	1:A:246:MET:HE3	1.99	0.44
1:D:128:LYS:HA	1:D:131:ARG:NH1	2.32	0.44
2:B:1294:B49:H23	2:B:1294:B49:C37	2.48	0.44
1:B:161:LEU:HD23	1:B:167:ILE:CD1	2.47	0.43
1:B:254:SER:O	1:B:258:ASP:CG	2.61	0.43
1:C:135:ARG:NH2	1:C:291:PHE:O	2.52	0.43
1:C:145:HIS:CE1	1:C:212:LYS:HB2	2.54	0.43
1:A:239:ILE:HD11	1:C:202:SER:HB2	2.00	0.43
1:C:197:GLU:O	1:C:201:CYS:HB2	2.20	0.42
1:A:239:ILE:HD12	1:C:203:MET:HG3	2.00	0.42
1:C:161:LEU:HD23	1:C:167:ILE:HG22	2.01	0.41
1:B:148:ASN:HB3	1:B:178:LEU:O	2.20	0.41
1:D:231:PRO:HB2	3:D:2051:HOH:O	2.20	0.41
1:A:200:LYS:CG	1:A:246:MET:HE3	2.50	0.41
1:C:55:MET:HB2	1:C:103:MET:HB2	2.00	0.41
1:B:231:PRO:HG2	1:B:234:TRP:HB2	2.02	0.41
1:D:216:LEU:HD21	1:D:282:ALA:HA	2.02	0.41

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:A:208:PRO:O	1:D:45:ALA:O[3_445]	2.11	0.09

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	284/365 (78%)	278 (98%)	6 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	279/365 (76%)	267 (96%)	11 (4%)	1 (0%)	30	49
1	C	282/365 (77%)	274 (97%)	8 (3%)	0	100	100
1	D	277/365 (76%)	270 (98%)	7 (2%)	0	100	100
All	All	1122/1460 (77%)	1089 (97%)	32 (3%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	58	THR

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	244/325 (75%)	236 (97%)	8 (3%)	33	61
1	B	234/325 (72%)	229 (98%)	5 (2%)	47	74
1	C	241/325 (74%)	236 (98%)	5 (2%)	47	74
1	D	231/325 (71%)	225 (97%)	6 (3%)	40	68
All	All	950/1300 (73%)	926 (98%)	24 (2%)	43	69

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32[A]	ARG
1	A	32[B]	ARG
1	A	102	PHE
1	A	103	MET
1	A	201	CYS
1	A	216	LEU
1	A	239	ILE
1	A	254	SER
1	B	57	VAL
1	B	95	ASP

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Mol	Chain	Res	Type
1	B	167	ILE
1	B	200	LYS
1	B	216	LEU
1	C	10	GLU
1	C	95	ASP
1	C	102	PHE
1	C	167	ILE
1	C	280	LEU
1	D	95	ASP
1	D	177	HIS
1	D	203	MET
1	D	234	TRP
1	D	239	ILE
1	D	244	MET

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

Mol	Chain	Res	Type
1	A	79	HIS
1	A	251	GLN
1	B	79	HIS
1	B	251	GLN
1	C	177	HIS
1	D	251	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

4 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	B49	C	1294	-	31,31,31	3.91	19 (61%)	42,44,44	3.50	18 (42%)
2	B49	B	1294	-	31,31,31	3.97	22 (70%)	42,44,44	4.08	17 (40%)
2	B49	A	1294	-	31,31,31	3.24	17 (54%)	42,44,44	3.32	17 (40%)
2	B49	D	1294	-	31,31,31	3.41	16 (51%)	42,44,44	3.31	17 (40%)

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	B49	C	1294	-	-	6/18/30/30	0/3/3/3
2	B49	B	1294	-	-	3/18/30/30	0/3/3/3
2	B49	A	1294	-	-	4/18/30/30	0/3/3/3
2	B49	D	1294	-	-	5/18/30/30	0/3/3/3

All (74) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1294	B49	C6-C16	9.67	1.55	1.39
2	C	1294	B49	C12-C18	9.16	1.61	1.40
2	B	1294	B49	C12-C18	9.08	1.61	1.40
2	C	1294	B49	C6-C16	8.52	1.53	1.39
2	A	1294	B49	C6-C16	8.16	1.52	1.39
2	D	1294	B49	C12-C18	7.81	1.58	1.40
2	C	1294	B49	C5-C15	7.45	1.51	1.37
2	A	1294	B49	C12-C18	7.42	1.57	1.40
2	D	1294	B49	C6-C16	7.19	1.51	1.39
2	C	1294	B49	C21-N24	6.49	1.42	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1294	B49	C5-C15	6.31	1.49	1.37
2	D	1294	B49	C5-C15	6.15	1.49	1.37
2	D	1294	B49	C21-N24	6.11	1.42	1.36
2	A	1294	B49	C5-C15	5.76	1.48	1.37
2	B	1294	B49	C21-N24	5.74	1.42	1.36
2	B	1294	B49	C16-N24	5.68	1.49	1.38
2	C	1294	B49	C19-C14	5.60	1.49	1.39
2	B	1294	B49	C20-C21	-5.60	1.42	1.50
2	C	1294	B49	C17-C16	5.11	1.47	1.41
2	B	1294	B49	C37-N25	-5.10	1.34	1.46
2	D	1294	B49	C12-C20	5.05	1.43	1.35
2	B	1294	B49	C7-C15	4.95	1.45	1.37
2	D	1294	B49	C7-C17	4.88	1.47	1.39
2	A	1294	B49	F29-C15	-4.44	1.25	1.36
2	D	1294	B49	C19-C14	4.31	1.47	1.39
2	A	1294	B49	C20-C21	-4.28	1.44	1.50
2	C	1294	B49	F29-C15	-4.08	1.26	1.36
2	A	1294	B49	C19-C14	3.99	1.46	1.39
2	C	1294	B49	C7-C15	3.96	1.44	1.37
2	C	1294	B49	C40-N4	3.77	1.67	1.48
2	C	1294	B49	C20-C21	-3.77	1.45	1.50
2	D	1294	B49	C16-N24	3.74	1.45	1.38
2	B	1294	B49	C22-N25	-3.65	1.27	1.33
2	B	1294	B49	C40-N4	3.63	1.66	1.48
2	C	1294	B49	C38-N4	3.62	1.55	1.47
2	D	1294	B49	C37-N25	-3.52	1.38	1.46
2	A	1294	B49	C21-N24	3.48	1.39	1.36
2	A	1294	B49	C40-N4	3.48	1.65	1.48
2	B	1294	B49	C12-C20	3.43	1.41	1.35
2	A	1294	B49	C17-C16	3.42	1.45	1.41
2	C	1294	B49	C37-N25	-3.40	1.38	1.46
2	D	1294	B49	C7-C15	3.31	1.43	1.37
2	C	1294	B49	C3-C13	3.22	1.57	1.50
2	B	1294	B49	C19-C14	3.18	1.45	1.39
2	D	1294	B49	C40-N4	3.16	1.64	1.48
2	D	1294	B49	C17-C16	3.09	1.45	1.41
2	D	1294	B49	F29-C15	-3.07	1.28	1.36
2	A	1294	B49	C37-N25	-3.06	1.39	1.46
2	C	1294	B49	O27-C21	-3.04	1.17	1.23
2	A	1294	B49	C12-C20	3.03	1.40	1.35
2	B	1294	B49	C7-C17	2.96	1.44	1.39
2	D	1294	B49	C14-N23	-2.96	1.28	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1294	B49	C38-N4	2.94	1.54	1.47
2	B	1294	B49	O28-C22	-2.83	1.18	1.23
2	D	1294	B49	C20-C21	-2.79	1.46	1.50
2	A	1294	B49	C17-C20	-2.73	1.40	1.45
2	A	1294	B49	O27-C21	-2.68	1.18	1.23
2	C	1294	B49	C4-C14	-2.65	1.45	1.49
2	C	1294	B49	C16-N24	2.63	1.43	1.38
2	B	1294	B49	C14-N23	-2.63	1.29	1.37
2	A	1294	B49	C16-N24	2.61	1.43	1.38
2	B	1294	B49	C17-C16	2.52	1.44	1.41
2	C	1294	B49	C14-N23	-2.40	1.30	1.37
2	C	1294	B49	O28-C22	-2.38	1.19	1.23
2	B	1294	B49	C6-C5	-2.35	1.35	1.38
2	B	1294	B49	C17-C20	-2.35	1.41	1.45
2	B	1294	B49	C39-N4	2.34	1.59	1.48
2	B	1294	B49	C4-C14	-2.22	1.46	1.49
2	C	1294	B49	C18-C13	2.14	1.46	1.41
2	A	1294	B49	C18-N23	-2.08	1.34	1.37
2	B	1294	B49	O27-C21	-2.07	1.19	1.23
2	A	1294	B49	C42-C39	2.06	1.61	1.50
2	D	1294	B49	C39-N4	2.01	1.58	1.48
2	A	1294	B49	C7-C15	2.01	1.41	1.37

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1294	B49	C16-N24-C21	-16.66	101.06	111.35
2	B	1294	B49	C20-C21-N24	14.14	114.66	106.91
2	C	1294	B49	C16-N24-C21	-13.39	103.08	111.35
2	C	1294	B49	C20-C21-N24	13.13	114.11	106.91
2	D	1294	B49	C16-N24-C21	-12.90	103.39	111.35
2	A	1294	B49	C20-C21-N24	12.34	113.67	106.91
2	A	1294	B49	C16-N24-C21	-12.23	103.80	111.35
2	D	1294	B49	C20-C21-N24	10.63	112.73	106.91
2	D	1294	B49	C6-C16-C17	-5.24	117.12	122.19
2	B	1294	B49	O28-C22-C19	5.23	129.37	121.53
2	B	1294	B49	C19-C22-N25	-5.21	109.40	117.66
2	B	1294	B49	C3-C13-C18	-4.59	118.95	125.62
2	C	1294	B49	C38-C37-N25	4.53	120.31	111.56
2	C	1294	B49	O27-C21-C20	-4.23	122.40	127.70
2	D	1294	B49	C6-C5-C15	4.22	122.71	118.38
2	A	1294	B49	C38-C37-N25	-4.20	103.45	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1294	B49	C6-C16-C17	-4.11	118.21	122.19
2	B	1294	B49	C6-C16-C17	-4.02	118.30	122.19
2	B	1294	B49	C3-C13-C19	3.90	137.98	125.67
2	D	1294	B49	C7-C17-C16	3.78	123.07	119.39
2	B	1294	B49	O27-C21-C20	-3.68	123.08	127.70
2	C	1294	B49	C37-N25-C22	3.57	130.29	122.47
2	A	1294	B49	C37-C38-N4	3.46	121.31	112.84
2	B	1294	B49	C6-C5-C15	3.40	121.87	118.38
2	D	1294	B49	C3-C13-C18	-3.37	120.72	125.62
2	A	1294	B49	C3-C13-C18	-3.37	120.73	125.62
2	B	1294	B49	F29-C15-C7	3.22	122.85	118.28
2	A	1294	B49	O27-C21-C20	-3.03	123.89	127.70
2	D	1294	B49	F29-C15-C7	3.03	122.59	118.28
2	D	1294	B49	C5-C15-C7	-3.00	119.28	123.23
2	D	1294	B49	C3-C13-C19	2.98	135.08	125.67
2	A	1294	B49	C3-C13-C19	2.97	135.04	125.67
2	C	1294	B49	C19-C22-N25	-2.92	113.02	117.66
2	D	1294	B49	O27-C21-N24	-2.86	121.75	126.30
2	D	1294	B49	C7-C17-C20	-2.77	129.26	133.77
2	C	1294	B49	C3-C13-C19	2.73	134.29	125.67
2	C	1294	B49	C37-C38-N4	2.62	119.25	112.84
2	C	1294	B49	O28-C22-C19	2.61	125.44	121.53
2	D	1294	B49	C20-C12-C18	-2.59	125.12	133.34
2	C	1294	B49	C41-C40-N4	2.57	131.24	114.41
2	B	1294	B49	O27-C21-N24	-2.55	122.23	126.30
2	A	1294	B49	C7-C17-C16	2.53	121.86	119.39
2	A	1294	B49	O27-C21-N24	-2.47	122.37	126.30
2	A	1294	B49	C16-C17-C20	2.46	108.20	106.62
2	B	1294	B49	C41-C40-N4	2.45	130.47	114.41
2	D	1294	B49	C17-C16-N24	2.43	110.97	108.23
2	B	1294	B49	C19-C13-C18	-2.41	103.05	106.73
2	D	1294	B49	C19-C22-N25	-2.40	113.86	117.66
2	B	1294	B49	C18-N23-C14	2.37	111.82	110.31
2	C	1294	B49	C3-C13-C18	-2.36	122.19	125.62
2	A	1294	B49	C7-C17-C20	-2.35	129.94	133.77
2	C	1294	B49	C6-C16-C17	-2.35	119.92	122.19
2	A	1294	B49	C41-C40-N4	2.33	129.71	114.41
2	B	1294	B49	C5-C15-C7	-2.33	120.16	123.23
2	B	1294	B49	C7-C17-C16	2.30	121.63	119.39
2	A	1294	B49	C19-C22-N25	-2.25	114.09	117.66
2	C	1294	B49	C18-N23-C14	2.19	111.71	110.31
2	A	1294	B49	O28-C22-C19	2.16	124.77	121.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1294	B49	C16-C17-C20	2.14	108.00	106.62
2	C	1294	B49	C42-C39-N4	2.14	128.41	114.41
2	C	1294	B49	C19-C13-C18	-2.10	103.52	106.73
2	D	1294	B49	C17-C20-C12	-2.09	121.70	133.19
2	A	1294	B49	C18-N23-C14	2.09	111.64	110.31
2	A	1294	B49	C40-N4-C39	2.08	124.10	111.98
2	C	1294	B49	F29-C15-C7	2.08	121.24	118.28
2	B	1294	B49	C17-C16-N24	2.07	110.56	108.23
2	C	1294	B49	C7-C17-C16	2.06	121.39	119.39
2	D	1294	B49	C13-C18-N23	2.03	110.20	107.43
2	D	1294	B49	C40-N4-C39	2.02	123.72	111.98

There are no chirality outliers.

All (18) torsion outliers are listed below:

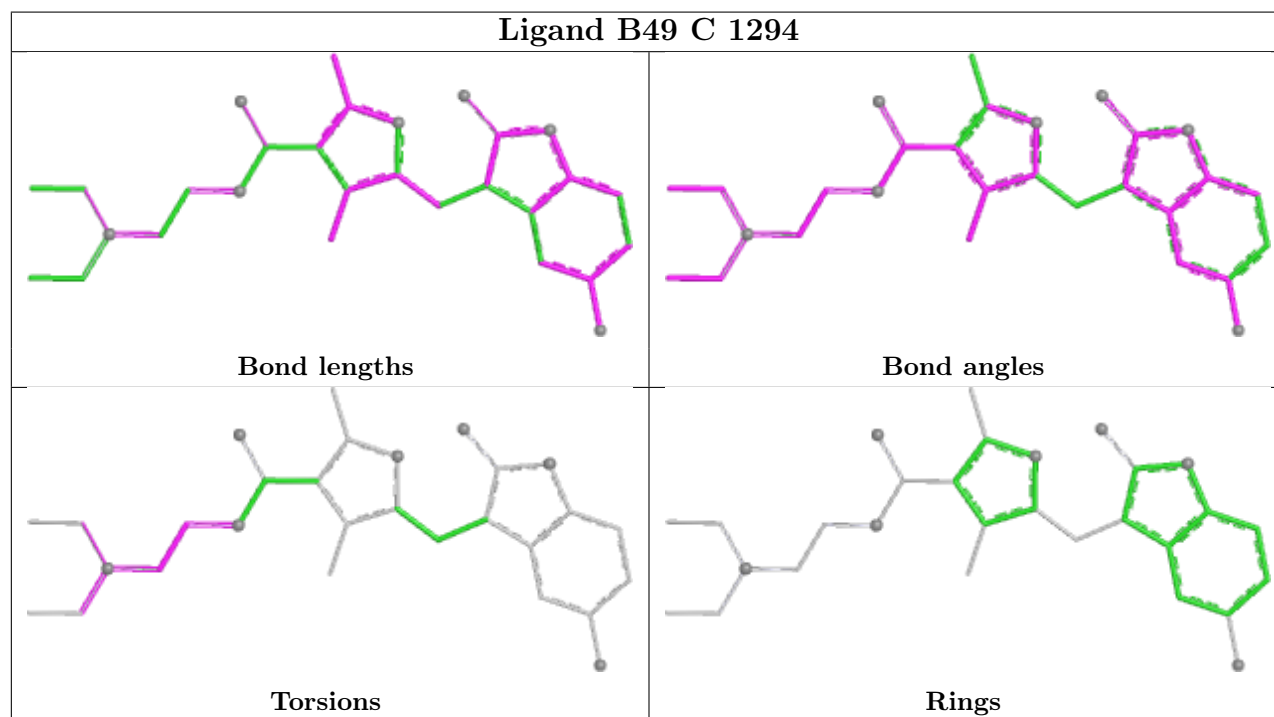
Mol	Chain	Res	Type	Atoms
2	C	1294	B49	N25-C37-C38-N4
2	B	1294	B49	C37-C38-N4-C40
2	D	1294	B49	C37-C38-N4-C40
2	C	1294	B49	C38-C37-N25-C22
2	D	1294	B49	N25-C37-C38-N4
2	A	1294	B49	N25-C37-C38-N4
2	A	1294	B49	C42-C39-N4-C38
2	C	1294	B49	C37-C38-N4-C40
2	C	1294	B49	C42-C39-N4-C38
2	C	1294	B49	C41-C40-N4-C38
2	D	1294	B49	C42-C39-N4-C40
2	C	1294	B49	C42-C39-N4-C40
2	B	1294	B49	C41-C40-N4-C38
2	B	1294	B49	N25-C37-C38-N4
2	A	1294	B49	C41-C40-N4-C38
2	A	1294	B49	C41-C40-N4-C39
2	D	1294	B49	C37-C38-N4-C39
2	D	1294	B49	C42-C39-N4-C38

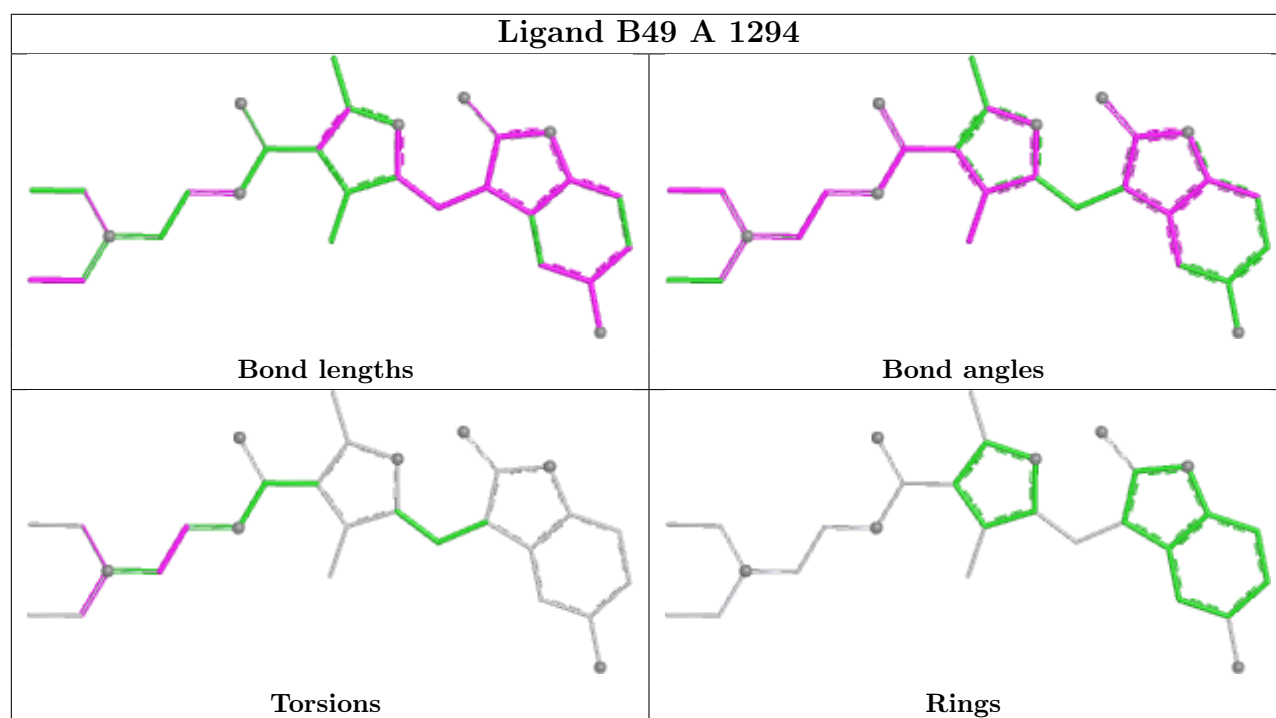
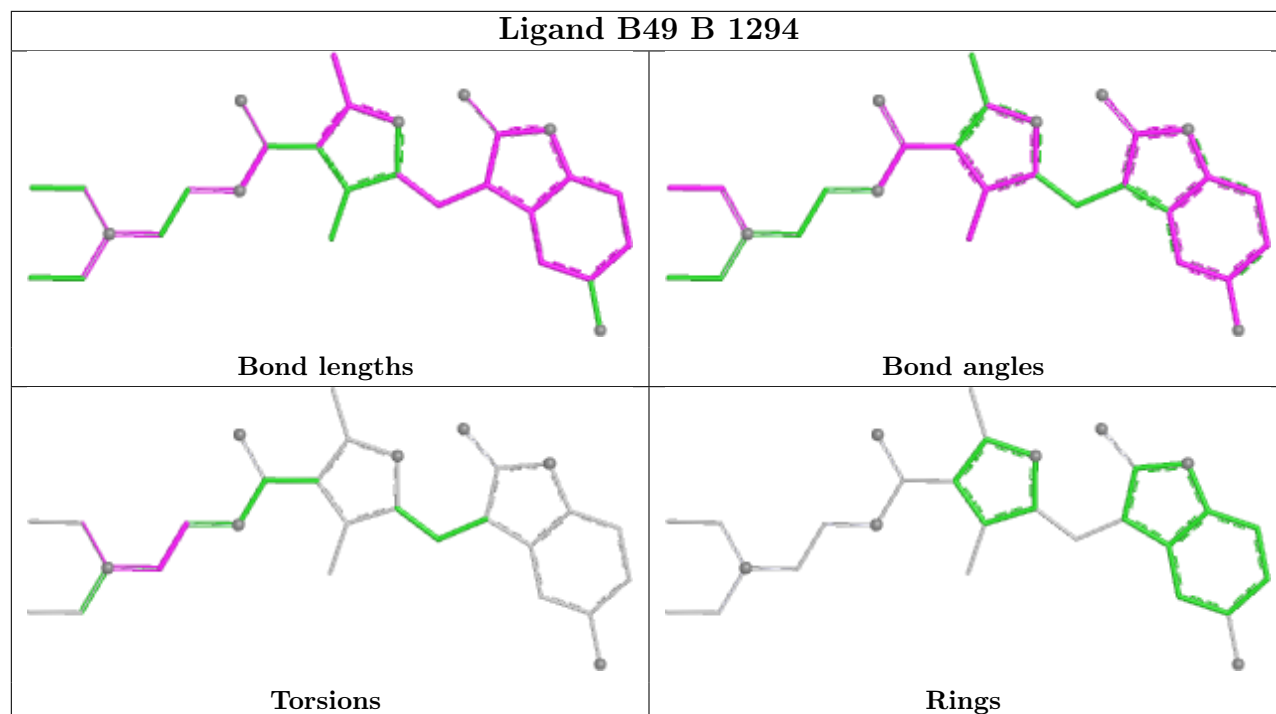
There are no ring outliers.

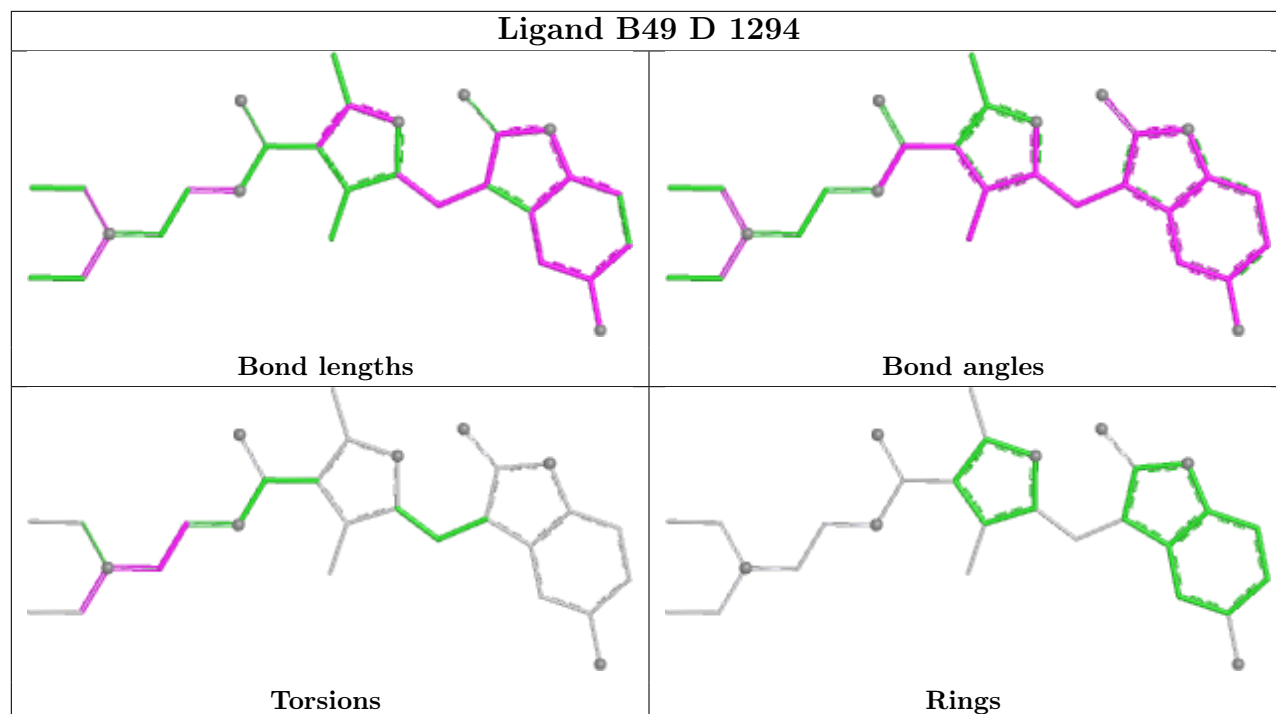
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1294	B49	2	0
2	A	1294	B49	1	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	284/365 (77%)	-0.15	6 (2%) 63 59	20, 42, 73, 102	2 (0%)
1	B	281/365 (76%)	0.11	12 (4%) 40 35	19, 50, 85, 118	2 (0%)
1	C	284/365 (77%)	-0.11	7 (2%) 58 54	27, 47, 74, 99	0
1	D	281/365 (76%)	0.19	14 (4%) 34 30	28, 53, 97, 123	0
All	All	1130/1460 (77%)	0.01	39 (3%) 47 42	19, 48, 85, 123	4 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	57	VAL	6.0
1	B	59	ALA	5.4
1	D	57	VAL	5.3
1	B	239	ILE	4.8
1	D	239	ILE	3.9
1	D	254	SER	3.8
1	B	237	ARG	3.7
1	D	293	ARG	3.6
1	D	180	PRO	3.6
1	D	61	ARG	3.5
1	C	256	GLU	3.5
1	B	238	GLN	3.4
1	C	255	PRO	3.4
1	C	293	ARG	3.1
1	D	235	HIS	3.1
1	D	181	GLY	3.0
1	B	58	THR	2.9
1	B	235	HIS	2.9
1	A	204	ASP	2.9
1	D	62	LEU	2.7
1	B	254	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	203	MET	2.5
1	A	254	SER	2.5
1	C	163	ASP	2.4
1	A	32[A]	ARG	2.3
1	C	254	SER	2.3
1	A	255	PRO	2.3
1	D	203	MET	2.2
1	B	11	LEU	2.2
1	C	258	ASP	2.2
1	B	234	TRP	2.2
1	C	251	GLN	2.1
1	A	163	ASP	2.1
1	D	199	LEU	2.1
1	D	245	ILE	2.1
1	D	238	GLN	2.1
1	D	249	GLN	2.1
1	A	35	SER	2.1
1	B	66	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

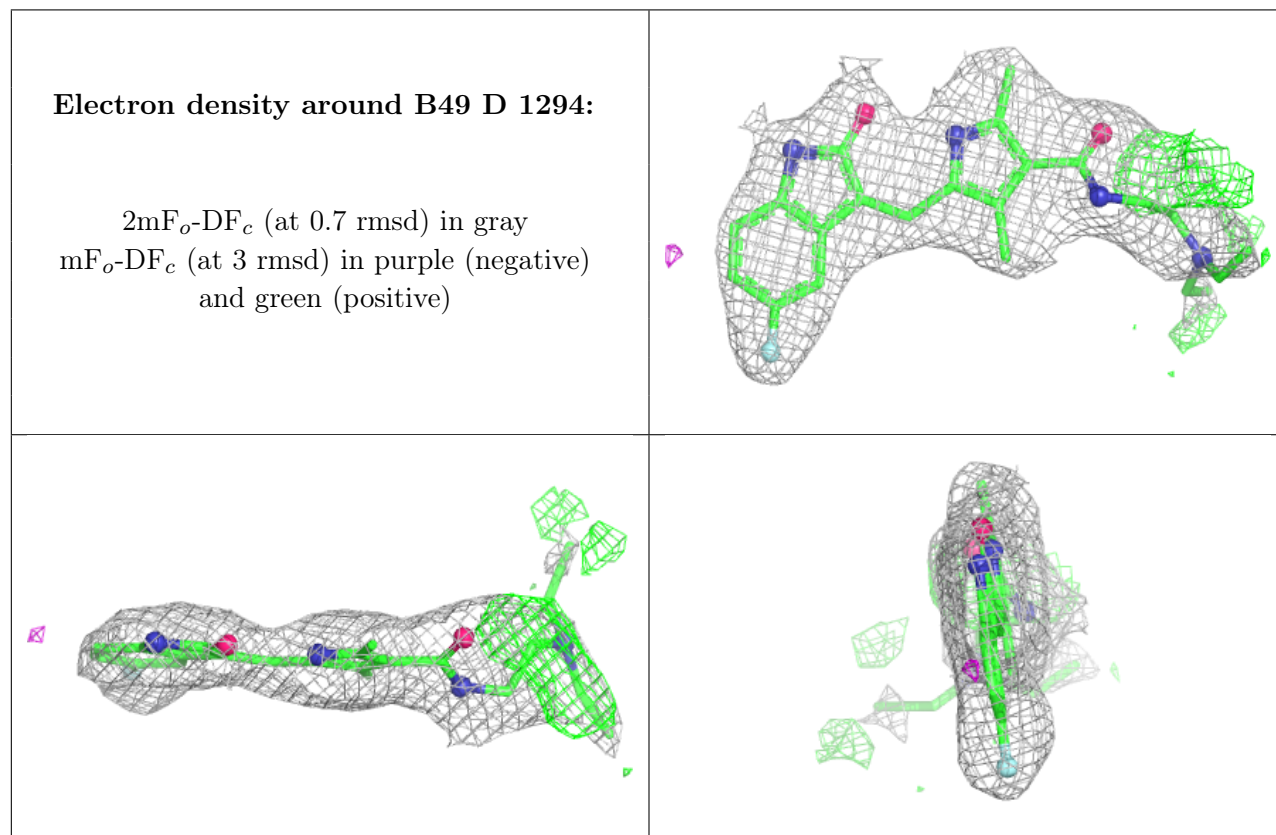
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

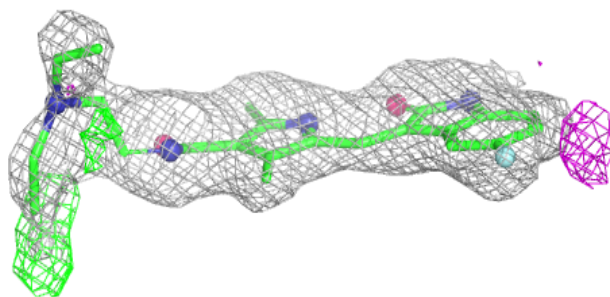
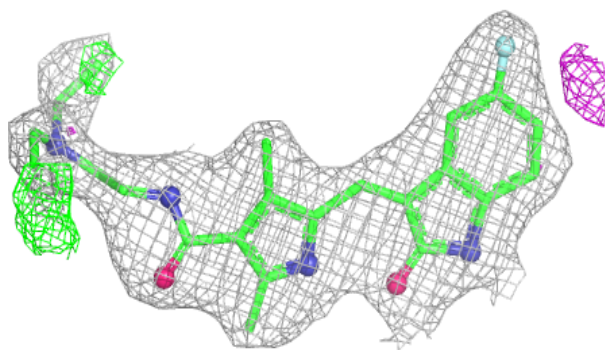
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	B49	D	1294	29/29	0.89	0.13	36,42,76,77	0
2	B49	B	1294	29/29	0.92	0.10	27,34,57,59	0
2	B49	C	1294	29/29	0.92	0.11	32,41,71,73	0
2	B49	A	1294	29/29	0.92	0.11	23,32,67,68	0

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.

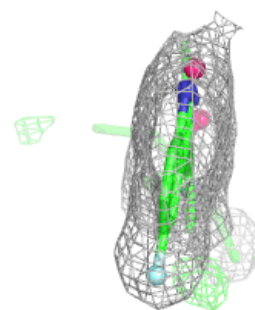
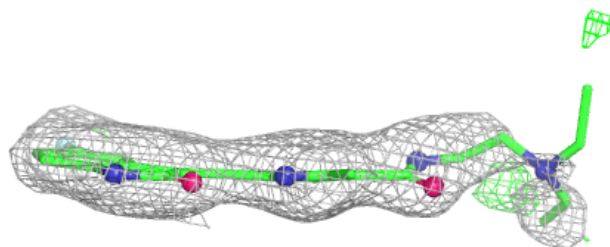
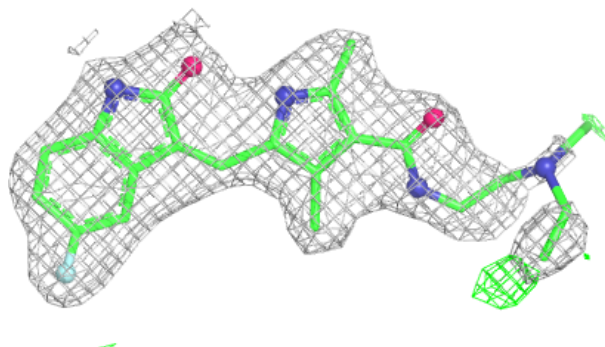


Electron density around B49 B 1294:

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

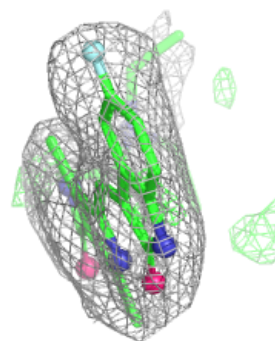
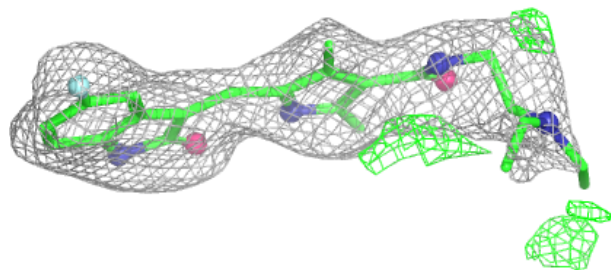
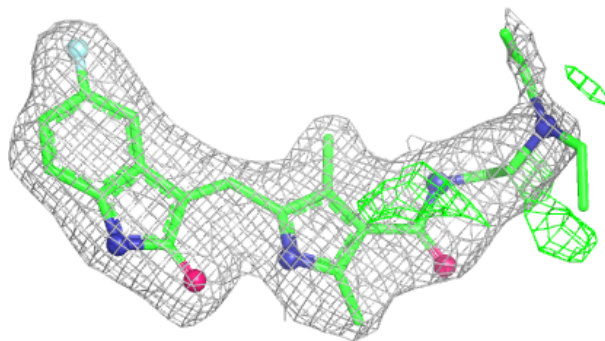
**Electron density around B49 C 1294:**

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



Electron density around B49 A 1294:

$2mF_o-DF_c$ (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.