wwPDB EM Validation Summary Report

Aug 23, 2026 – 12:46 AM JST

PDB ID	:	9XIR / pdb_00009xir
EMDB ID	:	EMD-66913
Title	:	Structure of dodecameric TpkB bound to AMP-PNP from Thermus thermophilus
Authors	:	Torri, M.; Kanno, R.; Mizoguchi, A.; Humbel, B.; Tani, K.; Masui, R.
Deposited on	:	2025-11-03
Resolution	:	3.20 Å(reported)

This is a wwPDB EM Validation Summary 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/EMValidationReportHelp
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:

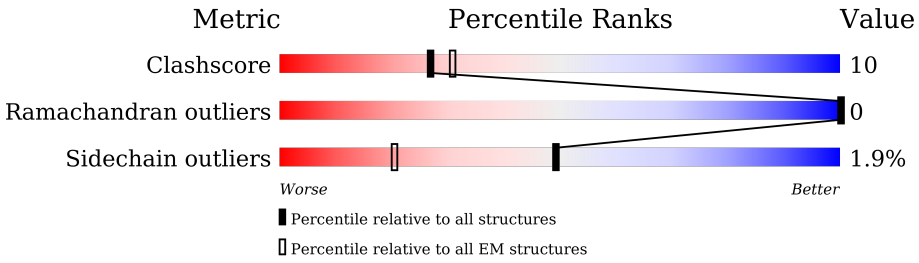
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

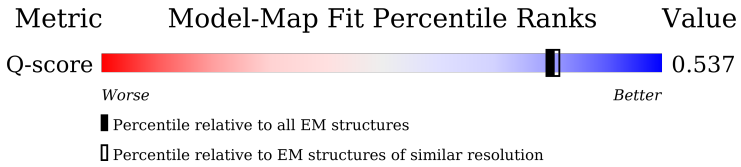
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	692	7% 56% 18% · 25%
1	B	692	7% 57% 17% · 25%
1	C	692	7% 57% 17% · 25%
1	D	692	7% 57% 17% · 25%

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Mol	Chain	Length	Quality of chain
1	E	692	8% 56% 18% 25%
1	F	692	7% 57% 17% 25%
1	G	692	7% 56% 18% 25%
1	H	692	7% 57% 17% 25%
1	I	692	7% 57% 17% 25%
1	J	692	7% 56% 18% 25%
1	K	692	7% 56% 18% 25%
1	L	692	7% 56% 17% 25%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 50652 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 protein kinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	B	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	C	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	D	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	E	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	F	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	G	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	H	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	I	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	J	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	K	516	Total 4190	C 2669	N 743	O 763	S 15	5	0
1	L	516	Total 4190	C 2669	N 743	O 763	S 15	5	0

There are 288 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MET	-	initiating methionine	UNP Q5SK09
A	-22	GLY	-	expression tag	UNP Q5SK09
A	-21	SER	-	expression tag	UNP Q5SK09
A	-20	SER	-	expression tag	UNP Q5SK09
A	-19	HIS	-	expression tag	UNP Q5SK09
A	-18	HIS	-	expression tag	UNP Q5SK09

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	HIS	-	expression tag	UNP Q5SK09
A	-16	HIS	-	expression tag	UNP Q5SK09
A	-15	HIS	-	expression tag	UNP Q5SK09
A	-14	HIS	-	expression tag	UNP Q5SK09
A	-13	SER	-	expression tag	UNP Q5SK09
A	-12	SER	-	expression tag	UNP Q5SK09
A	-11	GLY	-	expression tag	UNP Q5SK09
A	-10	GLU	-	expression tag	UNP Q5SK09
A	-9	ASN	-	expression tag	UNP Q5SK09
A	-8	LEU	-	expression tag	UNP Q5SK09
A	-7	TYR	-	expression tag	UNP Q5SK09
A	-6	PHE	-	expression tag	UNP Q5SK09
A	-5	GLN	-	expression tag	UNP Q5SK09
A	-4	GLY	-	expression tag	UNP Q5SK09
A	-3	GLY	-	expression tag	UNP Q5SK09
A	-2	LEU	-	expression tag	UNP Q5SK09
A	-1	ASN	-	expression tag	UNP Q5SK09
A	0	HIS	-	expression tag	UNP Q5SK09
B	-23	MET	-	initiating methionine	UNP Q5SK09
B	-22	GLY	-	expression tag	UNP Q5SK09
B	-21	SER	-	expression tag	UNP Q5SK09
B	-20	SER	-	expression tag	UNP Q5SK09
B	-19	HIS	-	expression tag	UNP Q5SK09
B	-18	HIS	-	expression tag	UNP Q5SK09
B	-17	HIS	-	expression tag	UNP Q5SK09
B	-16	HIS	-	expression tag	UNP Q5SK09
B	-15	HIS	-	expression tag	UNP Q5SK09
B	-14	HIS	-	expression tag	UNP Q5SK09
B	-13	SER	-	expression tag	UNP Q5SK09
B	-12	SER	-	expression tag	UNP Q5SK09
B	-11	GLY	-	expression tag	UNP Q5SK09
B	-10	GLU	-	expression tag	UNP Q5SK09
B	-9	ASN	-	expression tag	UNP Q5SK09
B	-8	LEU	-	expression tag	UNP Q5SK09
B	-7	TYR	-	expression tag	UNP Q5SK09
B	-6	PHE	-	expression tag	UNP Q5SK09
B	-5	GLN	-	expression tag	UNP Q5SK09
B	-4	GLY	-	expression tag	UNP Q5SK09
B	-3	GLY	-	expression tag	UNP Q5SK09
B	-2	LEU	-	expression tag	UNP Q5SK09
B	-1	ASN	-	expression tag	UNP Q5SK09
B	0	HIS	-	expression tag	UNP Q5SK09

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-23	MET	-	initiating methionine	UNP Q5SK09
C	-22	GLY	-	expression tag	UNP Q5SK09
C	-21	SER	-	expression tag	UNP Q5SK09
C	-20	SER	-	expression tag	UNP Q5SK09
C	-19	HIS	-	expression tag	UNP Q5SK09
C	-18	HIS	-	expression tag	UNP Q5SK09
C	-17	HIS	-	expression tag	UNP Q5SK09
C	-16	HIS	-	expression tag	UNP Q5SK09
C	-15	HIS	-	expression tag	UNP Q5SK09
C	-14	HIS	-	expression tag	UNP Q5SK09
C	-13	SER	-	expression tag	UNP Q5SK09
C	-12	SER	-	expression tag	UNP Q5SK09
C	-11	GLY	-	expression tag	UNP Q5SK09
C	-10	GLU	-	expression tag	UNP Q5SK09
C	-9	ASN	-	expression tag	UNP Q5SK09
C	-8	LEU	-	expression tag	UNP Q5SK09
C	-7	TYR	-	expression tag	UNP Q5SK09
C	-6	PHE	-	expression tag	UNP Q5SK09
C	-5	GLN	-	expression tag	UNP Q5SK09
C	-4	GLY	-	expression tag	UNP Q5SK09
C	-3	GLY	-	expression tag	UNP Q5SK09
C	-2	LEU	-	expression tag	UNP Q5SK09
C	-1	ASN	-	expression tag	UNP Q5SK09
C	0	HIS	-	expression tag	UNP Q5SK09
D	-23	MET	-	initiating methionine	UNP Q5SK09
D	-22	GLY	-	expression tag	UNP Q5SK09
D	-21	SER	-	expression tag	UNP Q5SK09
D	-20	SER	-	expression tag	UNP Q5SK09
D	-19	HIS	-	expression tag	UNP Q5SK09
D	-18	HIS	-	expression tag	UNP Q5SK09
D	-17	HIS	-	expression tag	UNP Q5SK09
D	-16	HIS	-	expression tag	UNP Q5SK09
D	-15	HIS	-	expression tag	UNP Q5SK09
D	-14	HIS	-	expression tag	UNP Q5SK09
D	-13	SER	-	expression tag	UNP Q5SK09
D	-12	SER	-	expression tag	UNP Q5SK09
D	-11	GLY	-	expression tag	UNP Q5SK09
D	-10	GLU	-	expression tag	UNP Q5SK09
D	-9	ASN	-	expression tag	UNP Q5SK09
D	-8	LEU	-	expression tag	UNP Q5SK09
D	-7	TYR	-	expression tag	UNP Q5SK09
D	-6	PHE	-	expression tag	UNP Q5SK09

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	GLN	-	expression tag	UNP Q5SK09
D	-4	GLY	-	expression tag	UNP Q5SK09
D	-3	GLY	-	expression tag	UNP Q5SK09
D	-2	LEU	-	expression tag	UNP Q5SK09
D	-1	ASN	-	expression tag	UNP Q5SK09
D	0	HIS	-	expression tag	UNP Q5SK09
E	-23	MET	-	initiating methionine	UNP Q5SK09
E	-22	GLY	-	expression tag	UNP Q5SK09
E	-21	SER	-	expression tag	UNP Q5SK09
E	-20	SER	-	expression tag	UNP Q5SK09
E	-19	HIS	-	expression tag	UNP Q5SK09
E	-18	HIS	-	expression tag	UNP Q5SK09
E	-17	HIS	-	expression tag	UNP Q5SK09
E	-16	HIS	-	expression tag	UNP Q5SK09
E	-15	HIS	-	expression tag	UNP Q5SK09
E	-14	HIS	-	expression tag	UNP Q5SK09
E	-13	SER	-	expression tag	UNP Q5SK09
E	-12	SER	-	expression tag	UNP Q5SK09
E	-11	GLY	-	expression tag	UNP Q5SK09
E	-10	GLU	-	expression tag	UNP Q5SK09
E	-9	ASN	-	expression tag	UNP Q5SK09
E	-8	LEU	-	expression tag	UNP Q5SK09
E	-7	TYR	-	expression tag	UNP Q5SK09
E	-6	PHE	-	expression tag	UNP Q5SK09
E	-5	GLN	-	expression tag	UNP Q5SK09
E	-4	GLY	-	expression tag	UNP Q5SK09
E	-3	GLY	-	expression tag	UNP Q5SK09
E	-2	LEU	-	expression tag	UNP Q5SK09
E	-1	ASN	-	expression tag	UNP Q5SK09
E	0	HIS	-	expression tag	UNP Q5SK09
F	-23	MET	-	initiating methionine	UNP Q5SK09
F	-22	GLY	-	expression tag	UNP Q5SK09
F	-21	SER	-	expression tag	UNP Q5SK09
F	-20	SER	-	expression tag	UNP Q5SK09
F	-19	HIS	-	expression tag	UNP Q5SK09
F	-18	HIS	-	expression tag	UNP Q5SK09
F	-17	HIS	-	expression tag	UNP Q5SK09
F	-16	HIS	-	expression tag	UNP Q5SK09
F	-15	HIS	-	expression tag	UNP Q5SK09
F	-14	HIS	-	expression tag	UNP Q5SK09
F	-13	SER	-	expression tag	UNP Q5SK09
F	-12	SER	-	expression tag	UNP Q5SK09

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-11	GLY	-	expression tag	UNP Q5SK09
F	-10	GLU	-	expression tag	UNP Q5SK09
F	-9	ASN	-	expression tag	UNP Q5SK09
F	-8	LEU	-	expression tag	UNP Q5SK09
F	-7	TYR	-	expression tag	UNP Q5SK09
F	-6	PHE	-	expression tag	UNP Q5SK09
F	-5	GLN	-	expression tag	UNP Q5SK09
F	-4	GLY	-	expression tag	UNP Q5SK09
F	-3	GLY	-	expression tag	UNP Q5SK09
F	-2	LEU	-	expression tag	UNP Q5SK09
F	-1	ASN	-	expression tag	UNP Q5SK09
F	0	HIS	-	expression tag	UNP Q5SK09
G	-23	MET	-	initiating methionine	UNP Q5SK09
G	-22	GLY	-	expression tag	UNP Q5SK09
G	-21	SER	-	expression tag	UNP Q5SK09
G	-20	SER	-	expression tag	UNP Q5SK09
G	-19	HIS	-	expression tag	UNP Q5SK09
G	-18	HIS	-	expression tag	UNP Q5SK09
G	-17	HIS	-	expression tag	UNP Q5SK09
G	-16	HIS	-	expression tag	UNP Q5SK09
G	-15	HIS	-	expression tag	UNP Q5SK09
G	-14	HIS	-	expression tag	UNP Q5SK09
G	-13	SER	-	expression tag	UNP Q5SK09
G	-12	SER	-	expression tag	UNP Q5SK09
G	-11	GLY	-	expression tag	UNP Q5SK09
G	-10	GLU	-	expression tag	UNP Q5SK09
G	-9	ASN	-	expression tag	UNP Q5SK09
G	-8	LEU	-	expression tag	UNP Q5SK09
G	-7	TYR	-	expression tag	UNP Q5SK09
G	-6	PHE	-	expression tag	UNP Q5SK09
G	-5	GLN	-	expression tag	UNP Q5SK09
G	-4	GLY	-	expression tag	UNP Q5SK09
G	-3	GLY	-	expression tag	UNP Q5SK09
G	-2	LEU	-	expression tag	UNP Q5SK09
G	-1	ASN	-	expression tag	UNP Q5SK09
G	0	HIS	-	expression tag	UNP Q5SK09
H	-23	MET	-	initiating methionine	UNP Q5SK09
H	-22	GLY	-	expression tag	UNP Q5SK09
H	-21	SER	-	expression tag	UNP Q5SK09
H	-20	SER	-	expression tag	UNP Q5SK09
H	-19	HIS	-	expression tag	UNP Q5SK09
H	-18	HIS	-	expression tag	UNP Q5SK09

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-17	HIS	-	expression tag	UNP Q5SK09
H	-16	HIS	-	expression tag	UNP Q5SK09
H	-15	HIS	-	expression tag	UNP Q5SK09
H	-14	HIS	-	expression tag	UNP Q5SK09
H	-13	SER	-	expression tag	UNP Q5SK09
H	-12	SER	-	expression tag	UNP Q5SK09
H	-11	GLY	-	expression tag	UNP Q5SK09
H	-10	GLU	-	expression tag	UNP Q5SK09
H	-9	ASN	-	expression tag	UNP Q5SK09
H	-8	LEU	-	expression tag	UNP Q5SK09
H	-7	TYR	-	expression tag	UNP Q5SK09
H	-6	PHE	-	expression tag	UNP Q5SK09
H	-5	GLN	-	expression tag	UNP Q5SK09
H	-4	GLY	-	expression tag	UNP Q5SK09
H	-3	GLY	-	expression tag	UNP Q5SK09
H	-2	LEU	-	expression tag	UNP Q5SK09
H	-1	ASN	-	expression tag	UNP Q5SK09
H	0	HIS	-	expression tag	UNP Q5SK09
I	-23	MET	-	initiating methionine	UNP Q5SK09
I	-22	GLY	-	expression tag	UNP Q5SK09
I	-21	SER	-	expression tag	UNP Q5SK09
I	-20	SER	-	expression tag	UNP Q5SK09
I	-19	HIS	-	expression tag	UNP Q5SK09
I	-18	HIS	-	expression tag	UNP Q5SK09
I	-17	HIS	-	expression tag	UNP Q5SK09
I	-16	HIS	-	expression tag	UNP Q5SK09
I	-15	HIS	-	expression tag	UNP Q5SK09
I	-14	HIS	-	expression tag	UNP Q5SK09
I	-13	SER	-	expression tag	UNP Q5SK09
I	-12	SER	-	expression tag	UNP Q5SK09
I	-11	GLY	-	expression tag	UNP Q5SK09
I	-10	GLU	-	expression tag	UNP Q5SK09
I	-9	ASN	-	expression tag	UNP Q5SK09
I	-8	LEU	-	expression tag	UNP Q5SK09
I	-7	TYR	-	expression tag	UNP Q5SK09
I	-6	PHE	-	expression tag	UNP Q5SK09
I	-5	GLN	-	expression tag	UNP Q5SK09
I	-4	GLY	-	expression tag	UNP Q5SK09
I	-3	GLY	-	expression tag	UNP Q5SK09
I	-2	LEU	-	expression tag	UNP Q5SK09
I	-1	ASN	-	expression tag	UNP Q5SK09
I	0	HIS	-	expression tag	UNP Q5SK09

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-23	MET	-	initiating methionine	UNP Q5SK09
J	-22	GLY	-	expression tag	UNP Q5SK09
J	-21	SER	-	expression tag	UNP Q5SK09
J	-20	SER	-	expression tag	UNP Q5SK09
J	-19	HIS	-	expression tag	UNP Q5SK09
J	-18	HIS	-	expression tag	UNP Q5SK09
J	-17	HIS	-	expression tag	UNP Q5SK09
J	-16	HIS	-	expression tag	UNP Q5SK09
J	-15	HIS	-	expression tag	UNP Q5SK09
J	-14	HIS	-	expression tag	UNP Q5SK09
J	-13	SER	-	expression tag	UNP Q5SK09
J	-12	SER	-	expression tag	UNP Q5SK09
J	-11	GLY	-	expression tag	UNP Q5SK09
J	-10	GLU	-	expression tag	UNP Q5SK09
J	-9	ASN	-	expression tag	UNP Q5SK09
J	-8	LEU	-	expression tag	UNP Q5SK09
J	-7	TYR	-	expression tag	UNP Q5SK09
J	-6	PHE	-	expression tag	UNP Q5SK09
J	-5	GLN	-	expression tag	UNP Q5SK09
J	-4	GLY	-	expression tag	UNP Q5SK09
J	-3	GLY	-	expression tag	UNP Q5SK09
J	-2	LEU	-	expression tag	UNP Q5SK09
J	-1	ASN	-	expression tag	UNP Q5SK09
J	0	HIS	-	expression tag	UNP Q5SK09
K	-23	MET	-	initiating methionine	UNP Q5SK09
K	-22	GLY	-	expression tag	UNP Q5SK09
K	-21	SER	-	expression tag	UNP Q5SK09
K	-20	SER	-	expression tag	UNP Q5SK09
K	-19	HIS	-	expression tag	UNP Q5SK09
K	-18	HIS	-	expression tag	UNP Q5SK09
K	-17	HIS	-	expression tag	UNP Q5SK09
K	-16	HIS	-	expression tag	UNP Q5SK09
K	-15	HIS	-	expression tag	UNP Q5SK09
K	-14	HIS	-	expression tag	UNP Q5SK09
K	-13	SER	-	expression tag	UNP Q5SK09
K	-12	SER	-	expression tag	UNP Q5SK09
K	-11	GLY	-	expression tag	UNP Q5SK09
K	-10	GLU	-	expression tag	UNP Q5SK09
K	-9	ASN	-	expression tag	UNP Q5SK09
K	-8	LEU	-	expression tag	UNP Q5SK09
K	-7	TYR	-	expression tag	UNP Q5SK09
K	-6	PHE	-	expression tag	UNP Q5SK09

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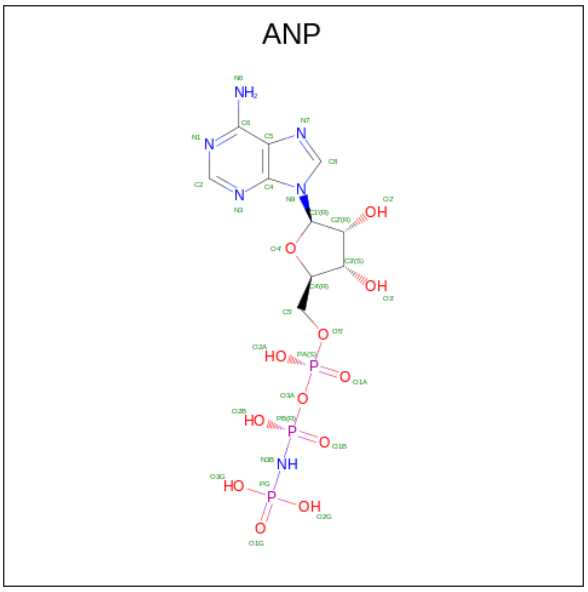
Chain	Residue	Modelled	Actual	Comment	Reference
K	-5	GLN	-	expression tag	UNP Q5SK09
K	-4	GLY	-	expression tag	UNP Q5SK09
K	-3	GLY	-	expression tag	UNP Q5SK09
K	-2	LEU	-	expression tag	UNP Q5SK09
K	-1	ASN	-	expression tag	UNP Q5SK09
K	0	HIS	-	expression tag	UNP Q5SK09
L	-23	MET	-	initiating methionine	UNP Q5SK09
L	-22	GLY	-	expression tag	UNP Q5SK09
L	-21	SER	-	expression tag	UNP Q5SK09
L	-20	SER	-	expression tag	UNP Q5SK09
L	-19	HIS	-	expression tag	UNP Q5SK09
L	-18	HIS	-	expression tag	UNP Q5SK09
L	-17	HIS	-	expression tag	UNP Q5SK09
L	-16	HIS	-	expression tag	UNP Q5SK09
L	-15	HIS	-	expression tag	UNP Q5SK09
L	-14	HIS	-	expression tag	UNP Q5SK09
L	-13	SER	-	expression tag	UNP Q5SK09
L	-12	SER	-	expression tag	UNP Q5SK09
L	-11	GLY	-	expression tag	UNP Q5SK09
L	-10	GLU	-	expression tag	UNP Q5SK09
L	-9	ASN	-	expression tag	UNP Q5SK09
L	-8	LEU	-	expression tag	UNP Q5SK09
L	-7	TYR	-	expression tag	UNP Q5SK09
L	-6	PHE	-	expression tag	UNP Q5SK09
L	-5	GLN	-	expression tag	UNP Q5SK09
L	-4	GLY	-	expression tag	UNP Q5SK09
L	-3	GLY	-	expression tag	UNP Q5SK09
L	-2	LEU	-	expression tag	UNP Q5SK09
L	-1	ASN	-	expression tag	UNP Q5SK09
L	0	HIS	-	expression tag	UNP Q5SK09

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$) (labeled as "Ligand of Interest" by depositor).

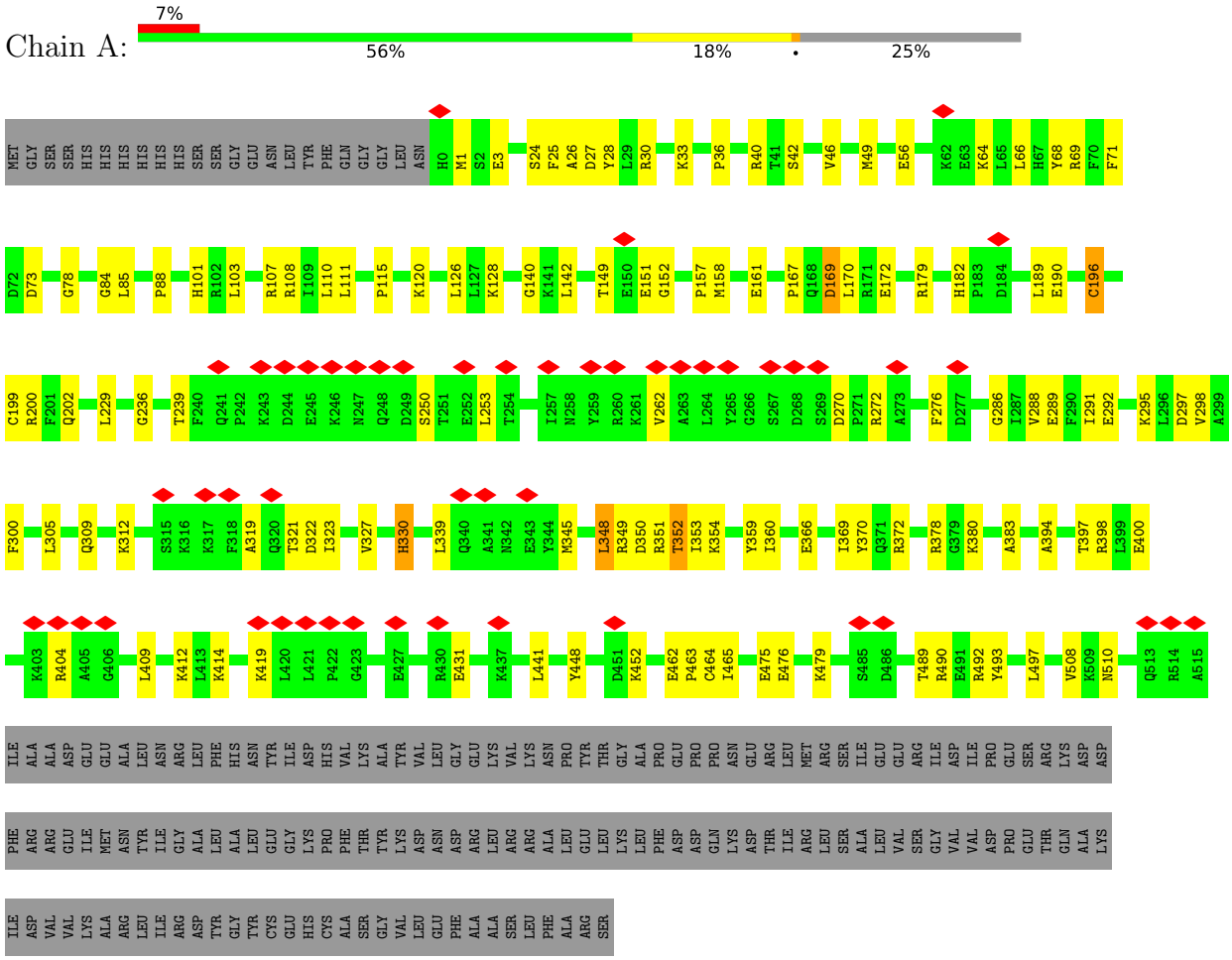


Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	B	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	C	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	D	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	E	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	F	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	G	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	H	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	I	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	J	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	K	1	Total	C	N	O	P	0
			31	10	6	12	3	
2	L	1	Total	C	N	O	P	0
			31	10	6	12	3	

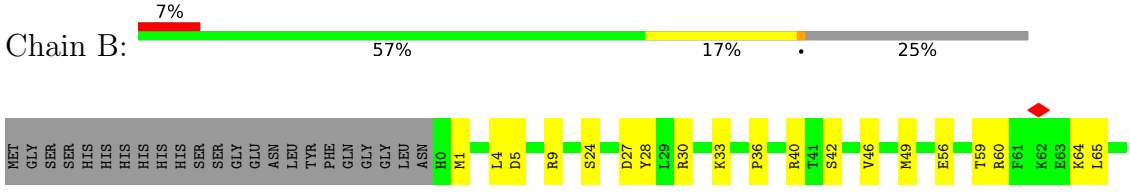
3 Residue-property plots (i)

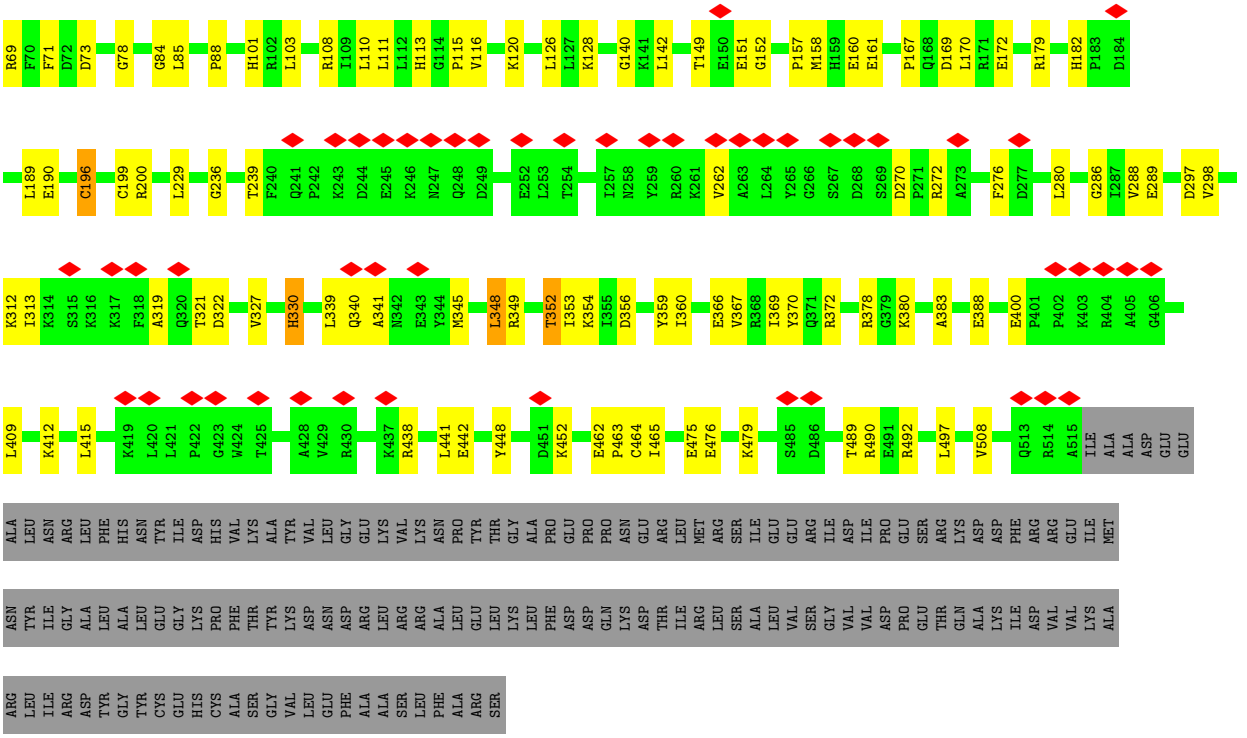
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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 protein kinase



• Molecule 1: Serine protein kinase

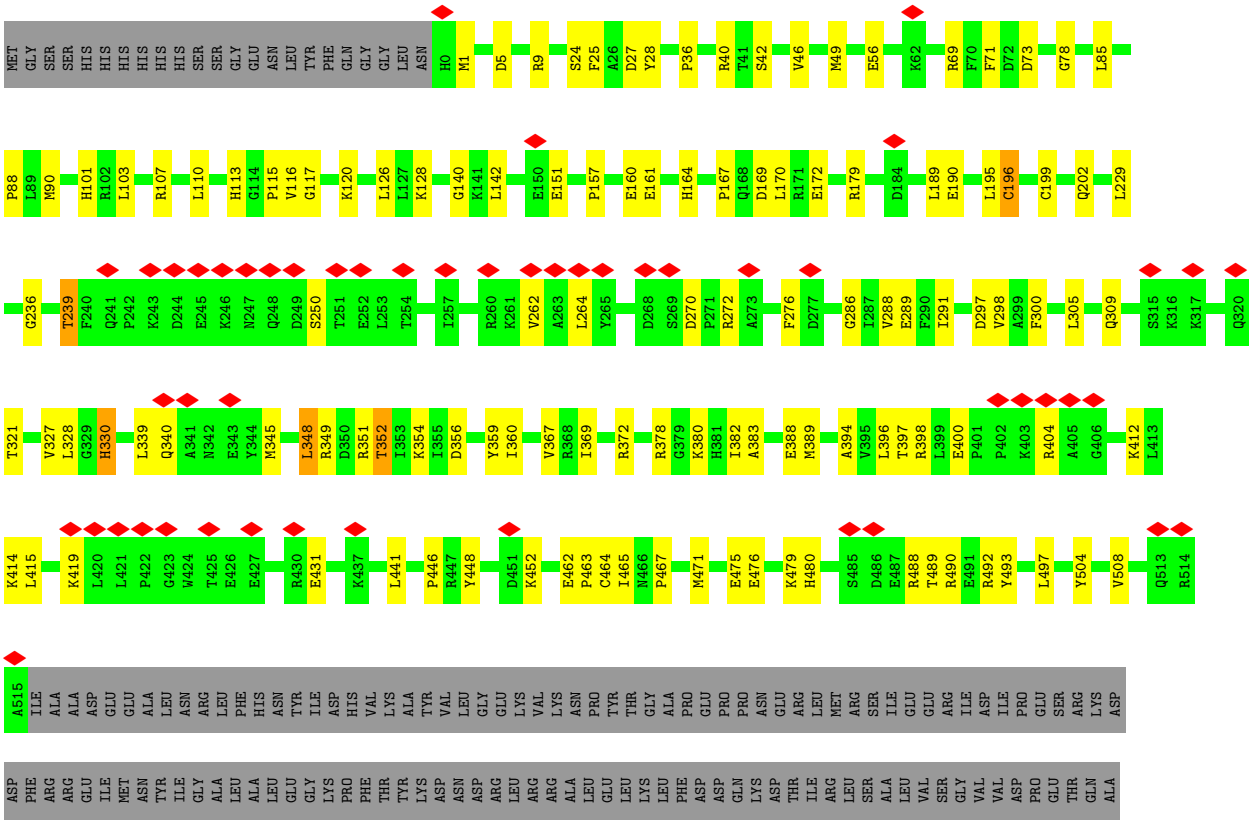




• Molecule 1: Serine protein kinase

Chain C:



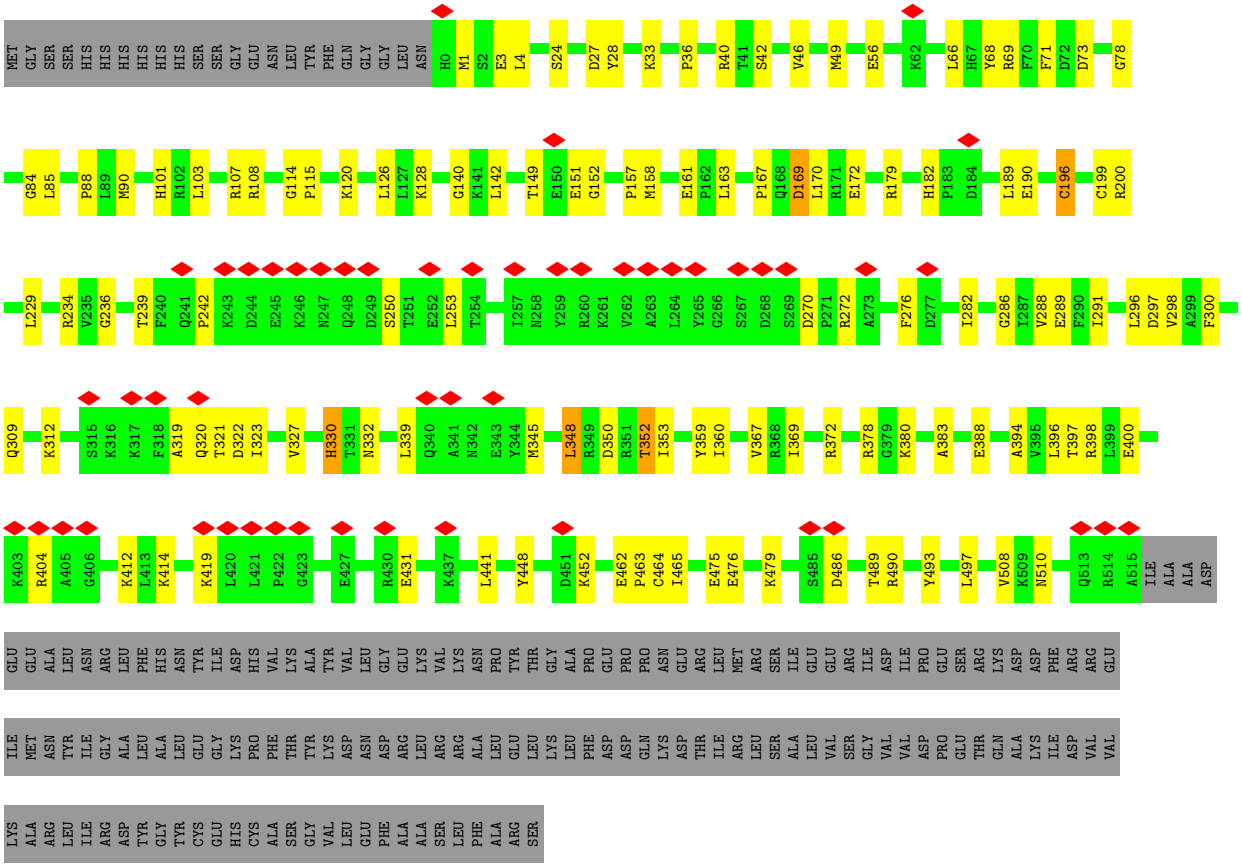




• Molecule 1: Serine protein kinase

Chain D:

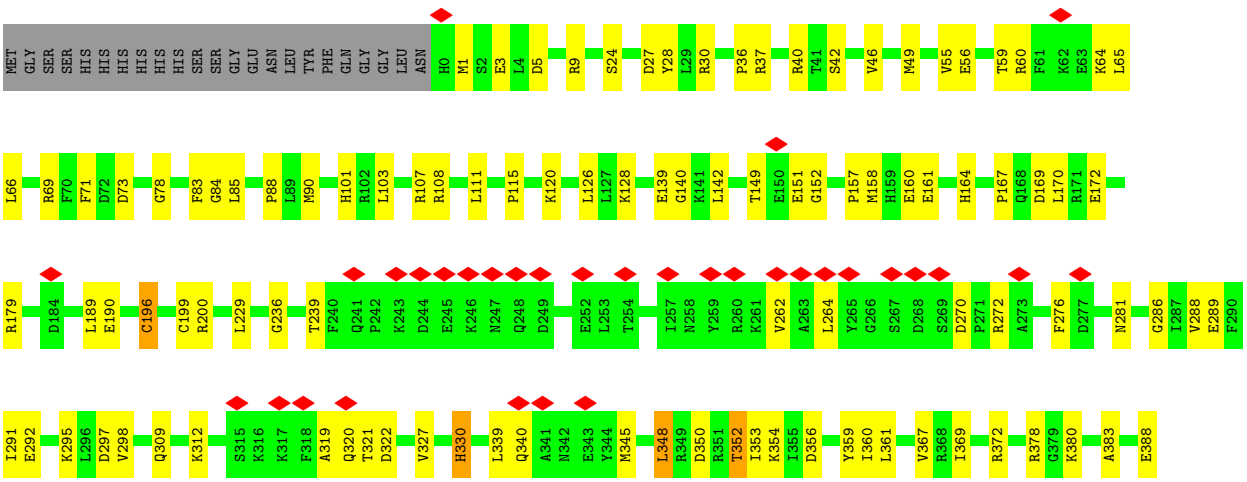


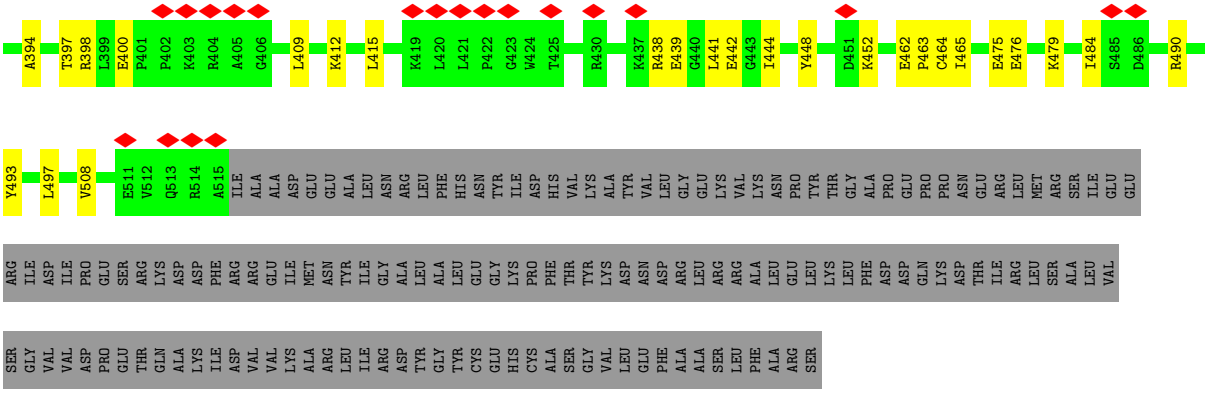


• Molecule 1: Serine protein kinase

Chain E:



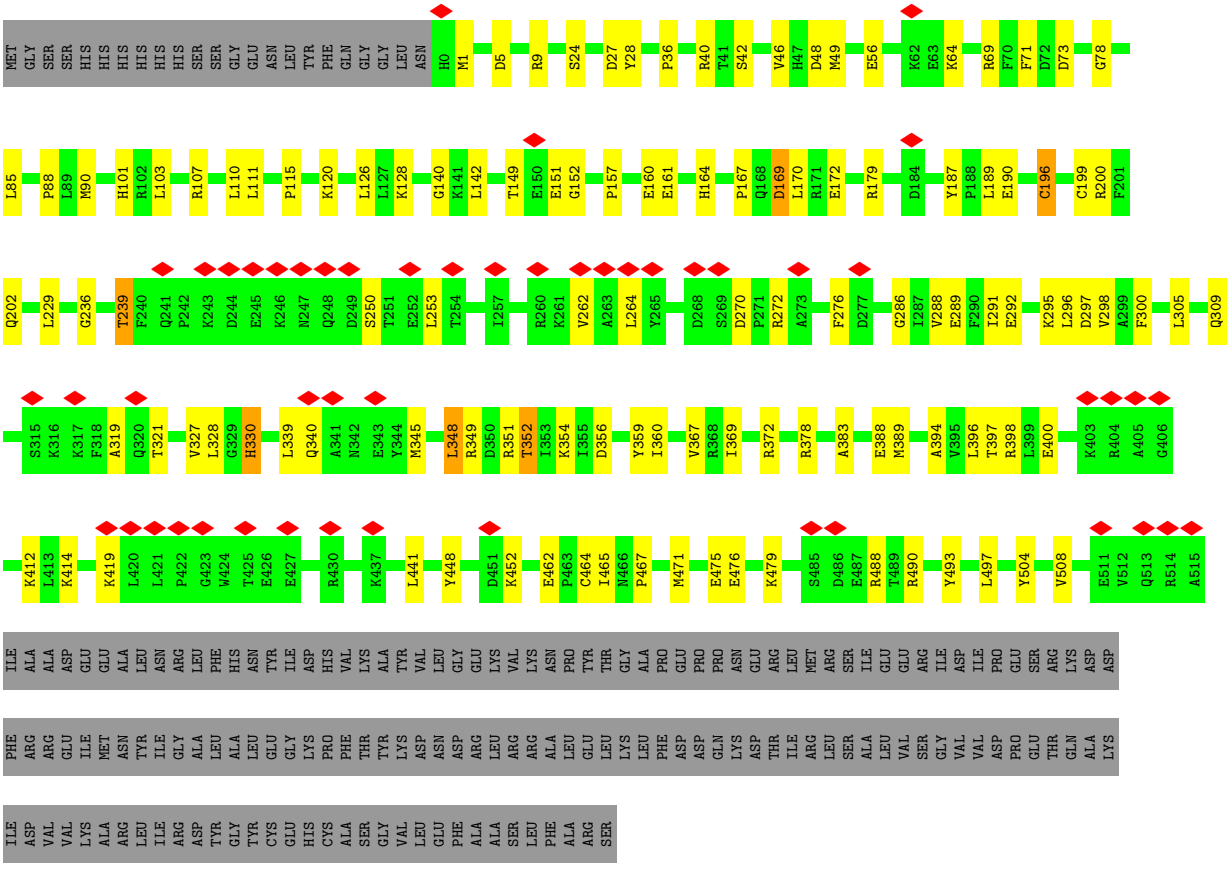




• Molecule 1: Serine protein kinase

Chain F:

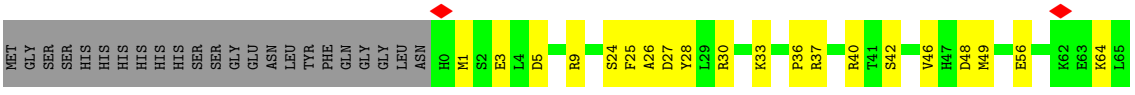


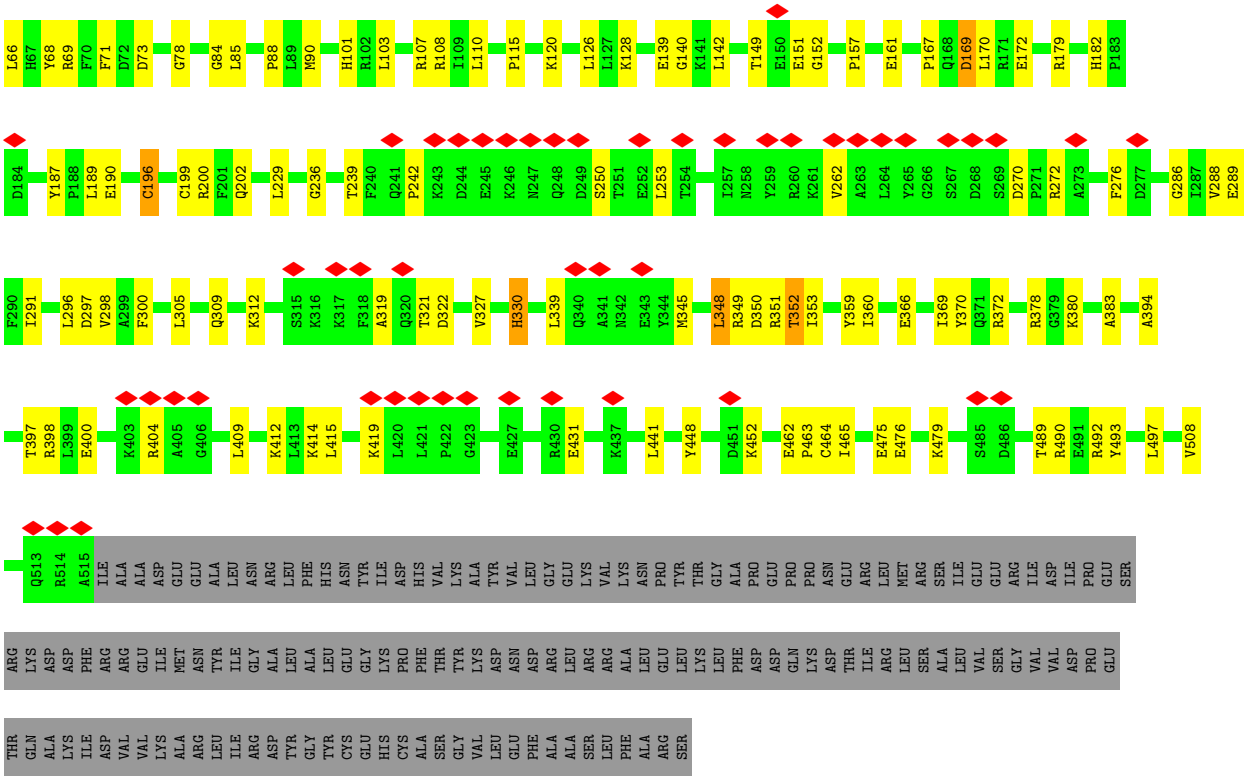


• Molecule 1: Serine protein kinase

Chain G:



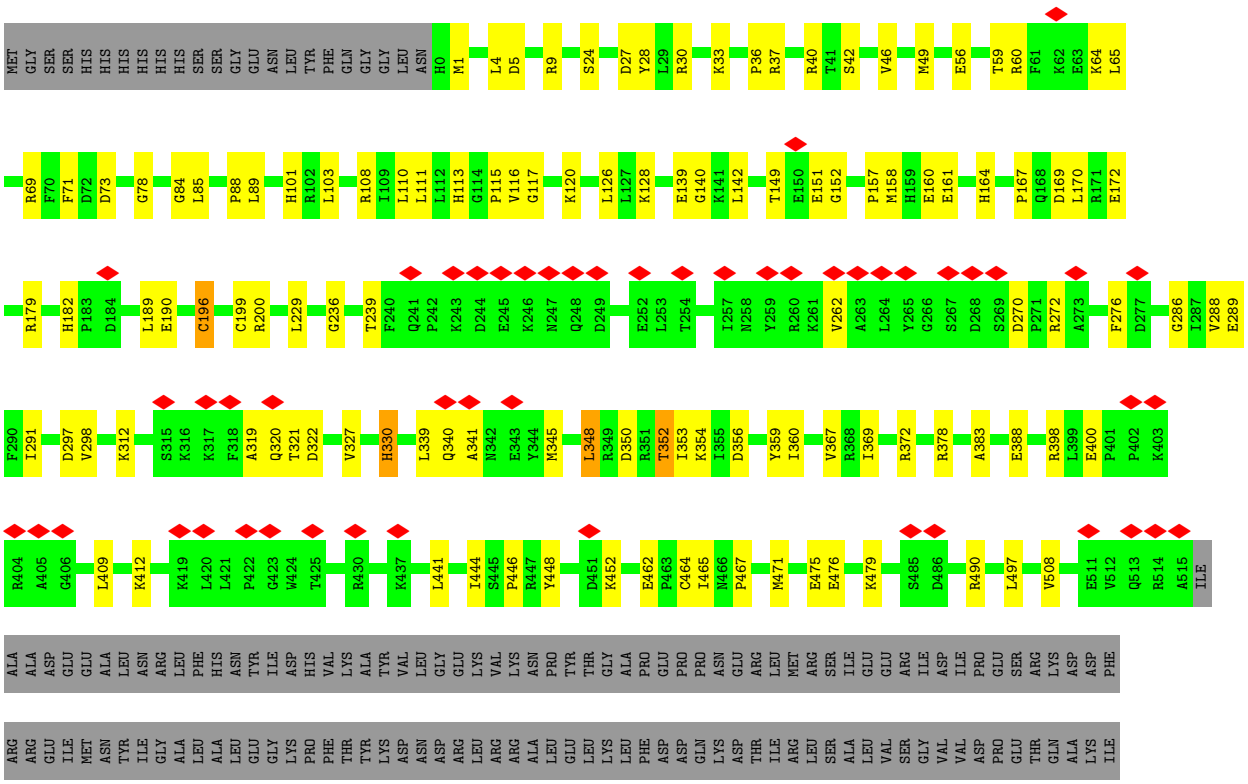




• Molecule 1: Serine protein kinase

Chain H:



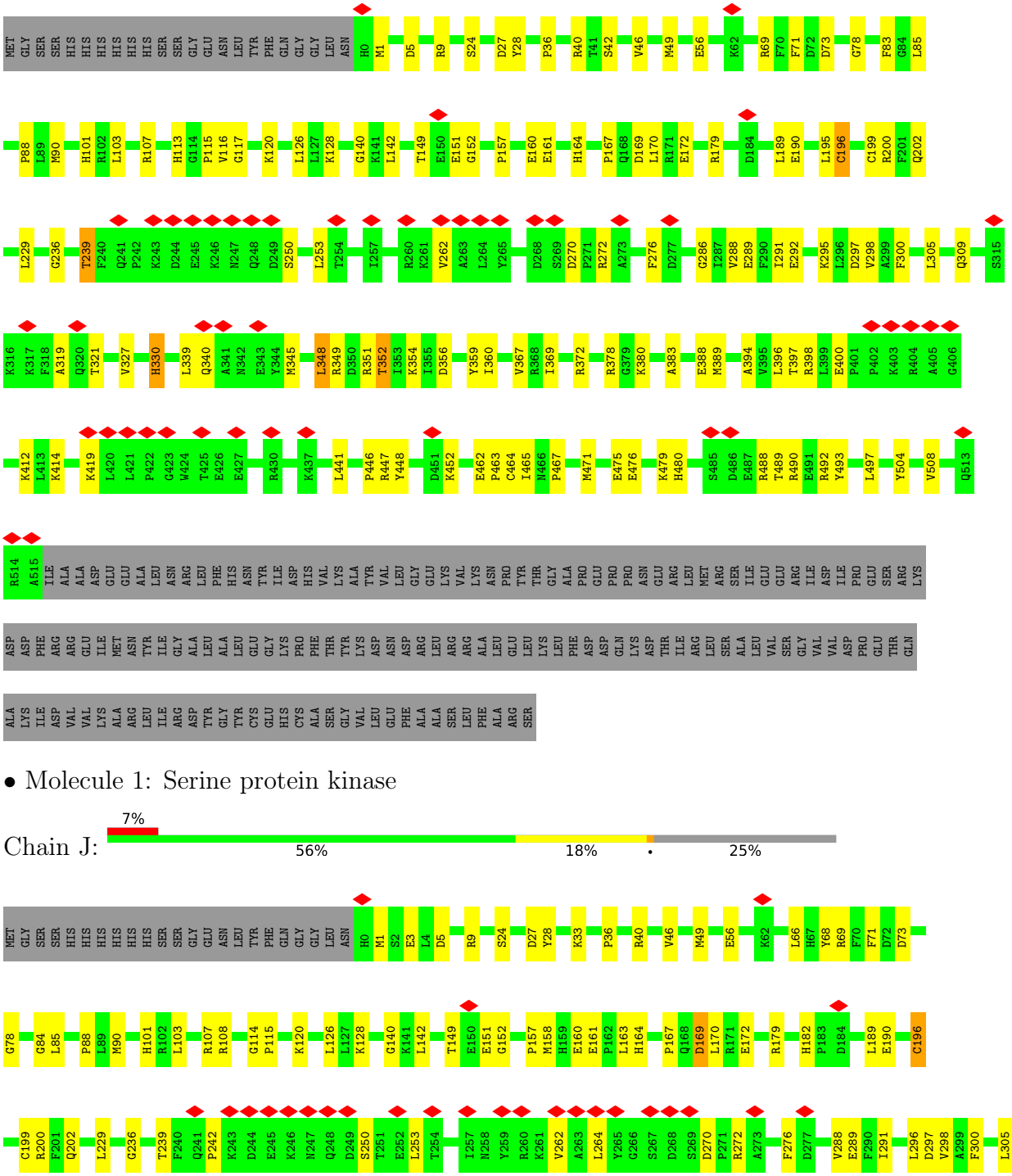




• Molecule 1: Serine protein kinase

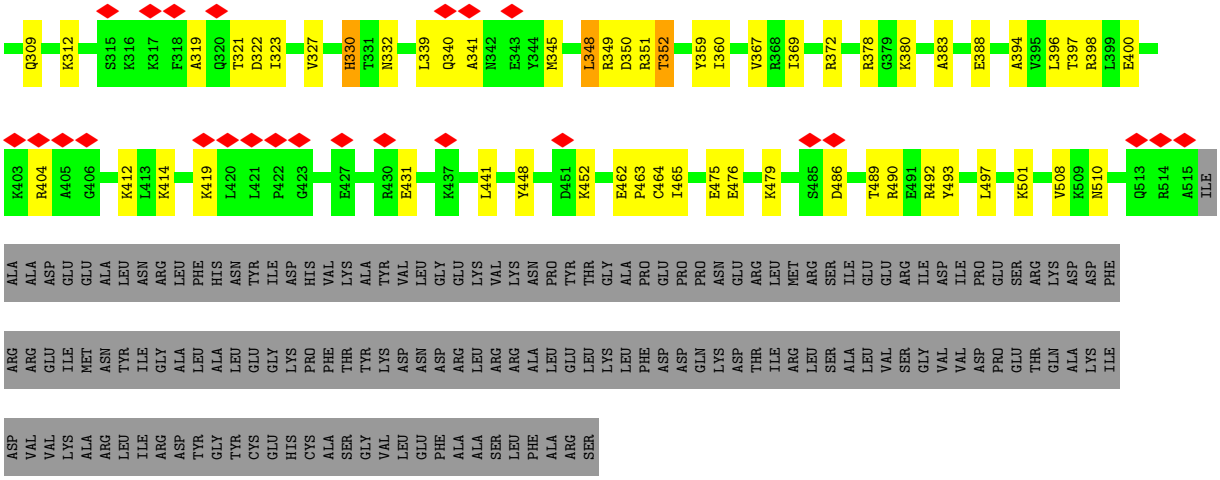
Chain I:





• Molecule 1: Serine protein kinase

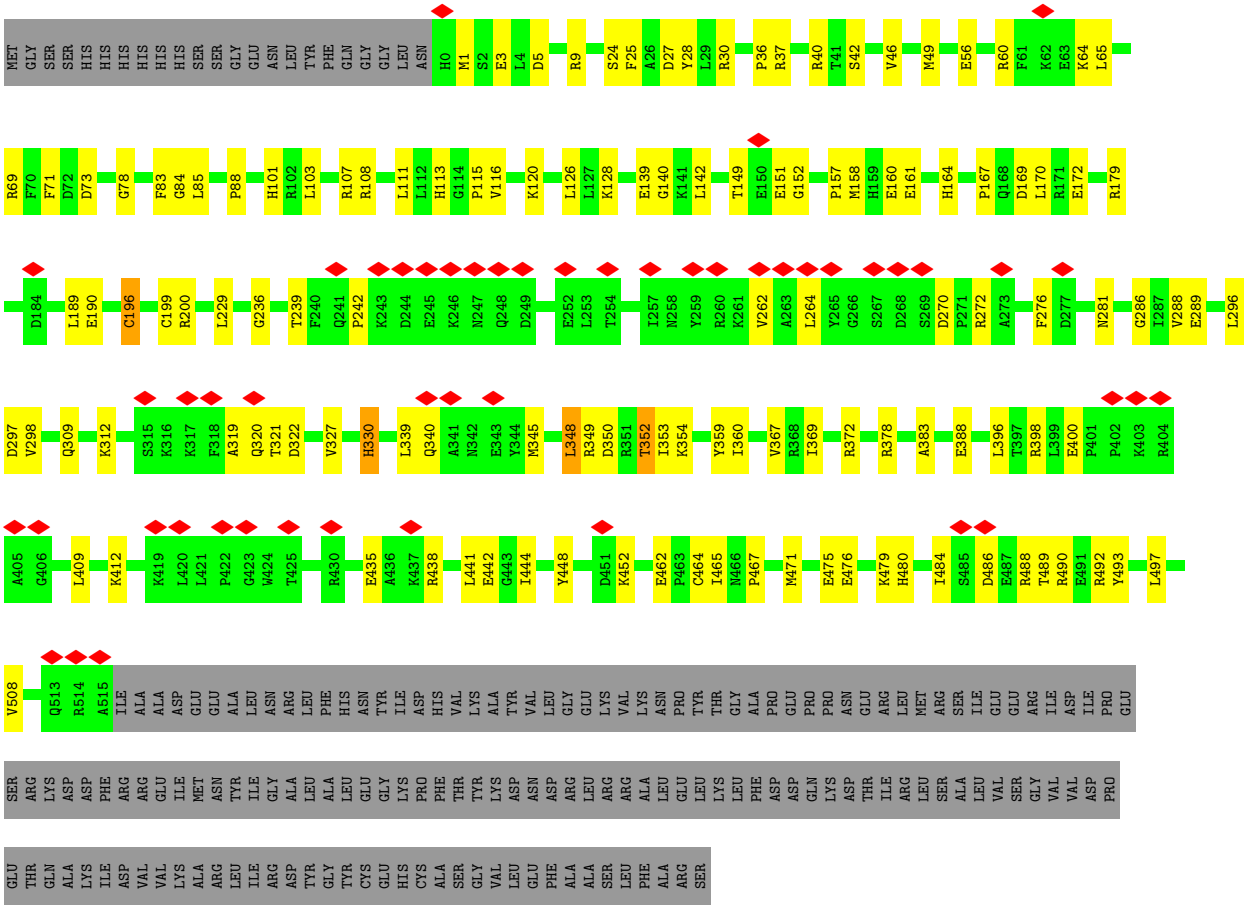
Chain J:



• Molecule 1: Serine protein kinase

Chain K:

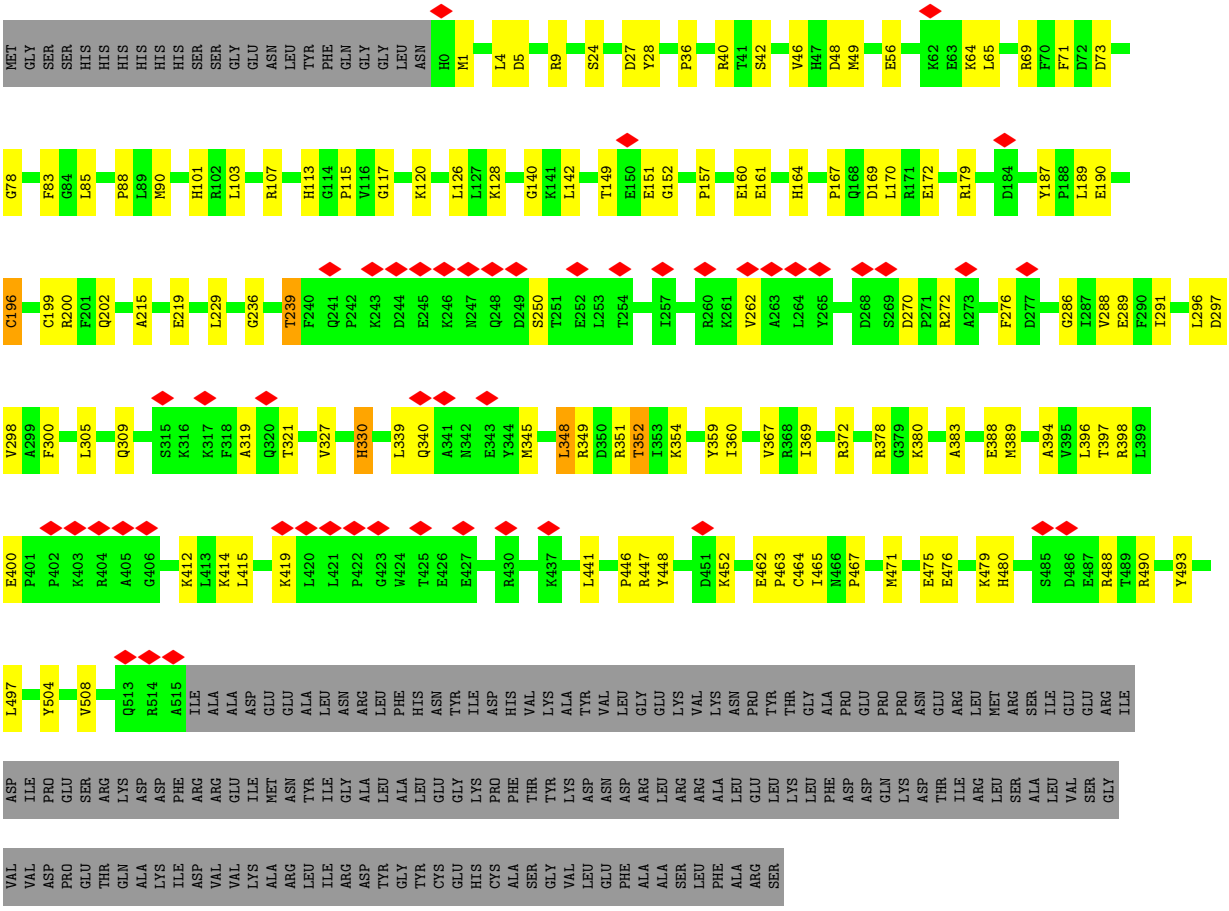




• Molecule 1: Serine protein kinase

Chain L:




MET GLY SER SER HIS HIS HIS HIS HIS SER SER GLY GLU ASN LEU TYR PHE GLN GLY GLY LEU ASN
HO M1 L4 D5 R9 S24 D27 Y28 P36 R40 T41 S42 V46 H47 D48 M49 E56 K62 E63 K64 L65 R69 F70 F71 D72 D73
G78 F83 G84 L85 P88 L89 M90 H101 R102 L103 R107 H113 G114 P115 V116 G117 K120 L126 L127 K128 G140 K141 L142 T149 E150 E151 G152 P157 E160 E161 H164 P167 Q168 D169 L170 R171 E172 R179 D184 Y187 P188 L189 E190
C196 C199 R200 F201 Q202 A215 E219 L229 G236 T239 F240 Q241 P242 K243 D244 E245 K246 N247 Q248 D249 S250 T251 E252 L253 T254 T257 R260 K261 V262 A263 L264 Y265 D268 S269 D270 P271 R272 A273 F276 D277 G286 I287 V288 E289 F290 I291 L296 D297
V298 A299 F300 L305 Q309 S315 K316 K317 F318 A319 Q320 T321 V327 H330 L339 Q340 A341 N342 E343 Y344 M345 L348 R349 D350 R351 T352 I353 K354 Y359 I360 V367 R368 I369 R372 R378 G379 K380 A383 E388 M389 A394 V395 L396 T397 R398 L399
E400 P401 P402 K403 R404 A405 G406 K412 L413 K414 L415 K419 L420 L421 P422 G423 W424 T425 E426 E427 R430 K437 L441 P446 R447 Y448 D451 K452 E462 P463 C464 I465 N466 P467 M471 E475 E476 K479 H480 S485 D486 E487 R488 T489 R490 Y493
L497 Y504 V508 Q513 R514 A515 ILE ALA ALA ASP GLU GLU ALA LEU ASN ARG LEU PHE HIS ASN TYR ILE ASP HIS VAL LYS ALA TYR VAL LEU GLY GLU LYS VAL LYS ASN PRO TYR THR GLY ALA PRO GLU PRO PRO ASN GLU ARG LEU MET ARG SER ILE GLU GLU ARG ILE
ASP ILE PRO GLU SER ARG LYS ASP ASP PHE ARG ARG GLU ILE MET ASN TYR ILE GLY ALA LEU ALA LEU GLU GLY LYS PRO PHE THR TYR LYS ASP ASN ASP ARG LEU ARG ARG ALA LEU GLU LEU LYS LEU PHE ASP ASP GLN LYS ASP THR ILE ARG LEU SER ALA LEU VAL SER GLY
VAL VAL ASP PRO GLU THR GLN ALA LYS ILE ASP VAL VAL LYS ALA ARG LEU ILE ARG ASP TYR GLY TYR CYS GLU HIS CYS ALA SER GLY VAL LEU GLU PHE ALA ALA SER LEU PHE ALA ARG SER

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D6	Depositor
Number of particles used	16347	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	1.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.111	Depositor
Minimum map value	-0.062	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	410.0, 410.0, 410.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.15	0/4293	0.32	1/5795 (0.0%)
1	B	0.15	0/4293	0.31	1/5795 (0.0%)
1	C	0.15	0/4293	0.32	1/5795 (0.0%)
1	D	0.15	0/4293	0.31	1/5795 (0.0%)
1	E	0.15	0/4293	0.31	1/5795 (0.0%)
1	F	0.15	0/4293	0.32	1/5795 (0.0%)
1	G	0.15	0/4293	0.31	1/5795 (0.0%)
1	H	0.15	0/4293	0.31	1/5795 (0.0%)
1	I	0.15	0/4293	0.32	1/5795 (0.0%)
1	J	0.15	0/4293	0.31	1/5795 (0.0%)
1	K	0.15	0/4293	0.31	1/5795 (0.0%)
1	L	0.15	0/4293	0.32	1/5795 (0.0%)
All	All	0.15	0/51516	0.32	12/69540 (0.0%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	196	CYS	CA-CB-SG	7.42	131.45	114.40
1	G	196	CYS	CA-CB-SG	7.33	131.26	114.40
1	A	196	CYS	CA-CB-SG	7.32	131.24	114.40
1	D	196	CYS	CA-CB-SG	7.29	131.17	114.40
1	J	196	CYS	CA-CB-SG	7.26	131.10	114.40

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	4190	0	4193	84	0
1	B	4190	0	4193	82	0
1	C	4190	0	4193	90	0
1	D	4190	0	4193	79	0
1	E	4190	0	4193	87	0
1	F	4190	0	4193	85	0
1	G	4190	0	4193	84	0
1	H	4190	0	4193	88	0
1	I	4190	0	4193	91	0
1	J	4190	0	4193	86	0
1	K	4190	0	4193	96	0
1	L	4190	0	4193	94	0
2	A	31	0	13	3	0
2	B	31	0	13	4	0
2	C	31	0	13	2	0
2	D	31	0	13	3	0
2	E	31	0	13	5	0
2	F	31	0	13	3	0
2	G	31	0	13	3	0
2	H	31	0	13	4	0
2	I	31	0	13	6	0
2	J	31	0	13	3	0
2	K	31	0	13	5	0
2	L	31	0	13	6	0
All	All	50652	0	50472	1003	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 10.

The worst 5 of 1003 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:K:340:GLN:HA	1:K:345:MET:HG3	1.71	0.73
1:G:475:GLU:HG3	1:G:497:LEU:HD23	1.71	0.71
1:E:340:GLN:HA	1:E:345:MET:HG3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:475:GLU:HG3	1:J:497:LEU:HD23	1.72	0.70
1:D:56:GLU:OE2	1:D:69:ARG:NH1	2.26	0.69

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 PDB entries followed by that with respect to all EM entries.

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	519/692 (75%)	499 (96%)	20 (4%)	0	100	100
1	B	519/692 (75%)	499 (96%)	20 (4%)	0	100	100
1	C	519/692 (75%)	496 (96%)	23 (4%)	0	100	100
1	D	519/692 (75%)	499 (96%)	20 (4%)	0	100	100
1	E	519/692 (75%)	499 (96%)	20 (4%)	0	100	100
1	F	519/692 (75%)	497 (96%)	22 (4%)	0	100	100
1	G	519/692 (75%)	497 (96%)	22 (4%)	0	100	100
1	H	519/692 (75%)	499 (96%)	20 (4%)	0	100	100
1	I	519/692 (75%)	495 (95%)	24 (5%)	0	100	100
1	J	519/692 (75%)	498 (96%)	21 (4%)	0	100	100
1	K	519/692 (75%)	498 (96%)	21 (4%)	0	100	100
1	L	519/692 (75%)	498 (96%)	21 (4%)	0	100	100
All	All	6228/8304 (75%)	5974 (96%)	254 (4%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	441/600 (74%)	431 (98%)	10 (2%)	44	70
1	B	441/600 (74%)	431 (98%)	10 (2%)	44	70
1	C	441/600 (74%)	429 (97%)	12 (3%)	39	68
1	D	441/600 (74%)	432 (98%)	9 (2%)	48	72
1	E	441/600 (74%)	430 (98%)	11 (2%)	42	69
1	F	441/600 (74%)	429 (97%)	12 (3%)	39	68
1	G	441/600 (74%)	430 (98%)	11 (2%)	42	69
1	H	441/600 (74%)	432 (98%)	9 (2%)	48	72
1	I	441/600 (74%)	431 (98%)	10 (2%)	44	70
1	J	441/600 (74%)	430 (98%)	11 (2%)	42	69
1	K	441/600 (74%)	431 (98%)	10 (2%)	44	70
1	L	441/600 (74%)	430 (98%)	11 (2%)	42	69
All	All	5292/7200 (74%)	5166 (98%)	126 (2%)	49	70

5 of 126 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	330[A]	HIS
1	K	339	LEU
1	G	348[B]	LEU
1	K	330[B]	HIS
1	L	330[A]	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	241	GLN
1	K	309	GLN
1	L	241	GLN
1	E	320	GLN

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Mol	Chain	Res	Type
1	E	309	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 (i)

12 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	ANP	J	701	-	32,33,33	1.06	5 (15%)	44,52,52	0.97	1 (2%)
2	ANP	G	701	-	32,33,33	1.08	5 (15%)	44,52,52	0.97	1 (2%)
2	ANP	K	701	-	32,33,33	1.07	5 (15%)	44,52,52	0.97	1 (2%)
2	ANP	H	701	-	32,33,33	1.07	5 (15%)	44,52,52	0.97	1 (2%)
2	ANP	I	701	-	32,33,33	1.06	5 (15%)	44,52,52	0.97	1 (2%)
2	ANP	B	701	-	32,33,33	1.06	5 (15%)	44,52,52	0.97	1 (2%)
2	ANP	A	701	-	32,33,33	1.06	5 (15%)	44,52,52	0.97	1 (2%)
2	ANP	F	701	-	32,33,33	1.06	5 (15%)	44,52,52	0.98	1 (2%)
2	ANP	L	701	-	32,33,33	1.07	5 (15%)	44,52,52	0.97	1 (2%)
2	ANP	C	701	-	32,33,33	1.07	5 (15%)	44,52,52	0.98	1 (2%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	ANP	D	701	-	32,33,33	1.06	5 (15%)	44,52,52	0.98	1 (2%)
2	ANP	E	701	-	32,33,33	1.06	5 (15%)	44,52,52	0.97	1 (2%)

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	ANP	J	701	-	-	3/18/38/38	0/3/3/3
2	ANP	G	701	-	-	3/18/38/38	0/3/3/3
2	ANP	K	701	-	-	3/18/38/38	0/3/3/3
2	ANP	H	701	-	-	3/18/38/38	0/3/3/3
2	ANP	I	701	-	-	3/18/38/38	0/3/3/3
2	ANP	B	701	-	-	3/18/38/38	0/3/3/3
2	ANP	A	701	-	-	3/18/38/38	0/3/3/3
2	ANP	F	701	-	-	3/18/38/38	0/3/3/3
2	ANP	L	701	-	-	3/18/38/38	0/3/3/3
2	ANP	C	701	-	-	3/18/38/38	0/3/3/3
2	ANP	D	701	-	-	3/18/38/38	0/3/3/3
2	ANP	E	701	-	-	3/18/38/38	0/3/3/3

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	701	ANP	PG-O1G	3.26	1.51	1.46
2	C	701	ANP	PG-O1G	3.25	1.51	1.46
2	K	701	ANP	PG-O1G	3.24	1.51	1.46
2	B	701	ANP	PG-O1G	3.24	1.51	1.46
2	H	701	ANP	PG-O1G	3.23	1.51	1.46

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	I	701	ANP	O2B-PB-O1B	4.11	118.53	109.92
2	D	701	ANP	O2B-PB-O1B	4.10	118.53	109.92
2	L	701	ANP	O2B-PB-O1B	4.10	118.52	109.92
2	C	701	ANP	O2B-PB-O1B	4.10	118.52	109.92
2	B	701	ANP	O2B-PB-O1B	4.09	118.50	109.92

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	ANP	PB-N3B-PG-O1G
2	A	701	ANP	PG-N3B-PB-O1B
2	A	701	ANP	PG-N3B-PB-O3A
2	B	701	ANP	PB-N3B-PG-O1G
2	B	701	ANP	PG-N3B-PB-O1B

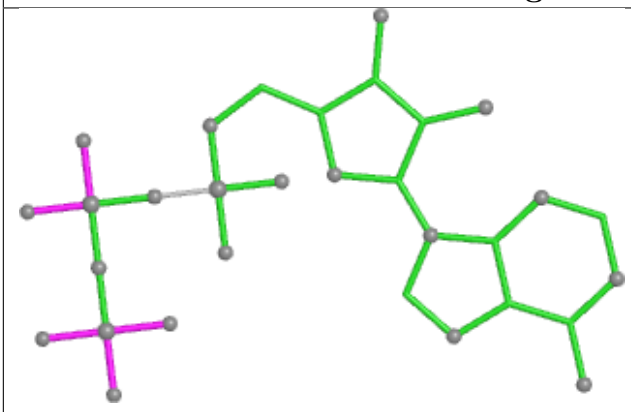
There are no ring outliers.

12 monomers are involved in 47 short contacts:

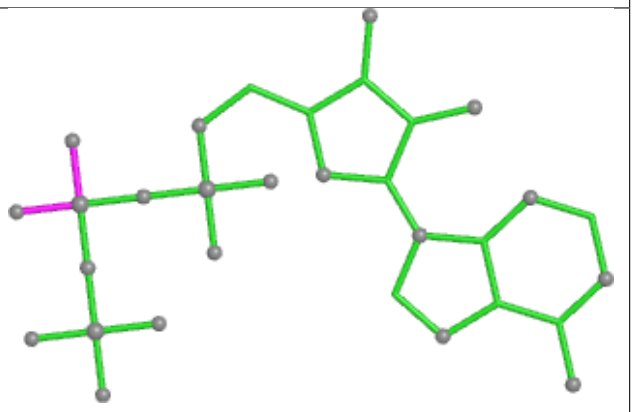
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	701	ANP	3	0
2	G	701	ANP	3	0
2	K	701	ANP	5	0
2	H	701	ANP	4	0
2	I	701	ANP	6	0
2	B	701	ANP	4	0
2	A	701	ANP	3	0
2	F	701	ANP	3	0
2	L	701	ANP	6	0
2	C	701	ANP	2	0
2	D	701	ANP	3	0
2	E	701	ANP	5	0

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 then 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.

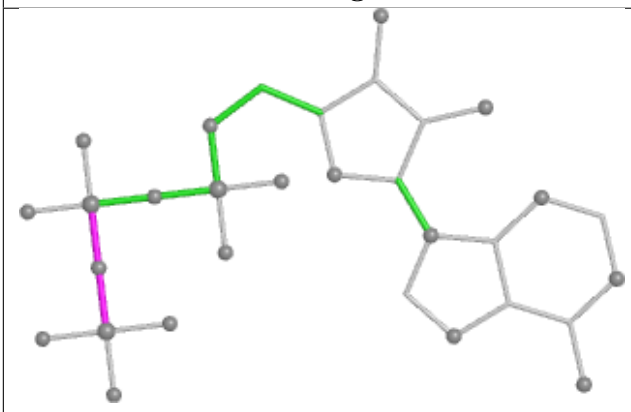
Ligand ANP J 701



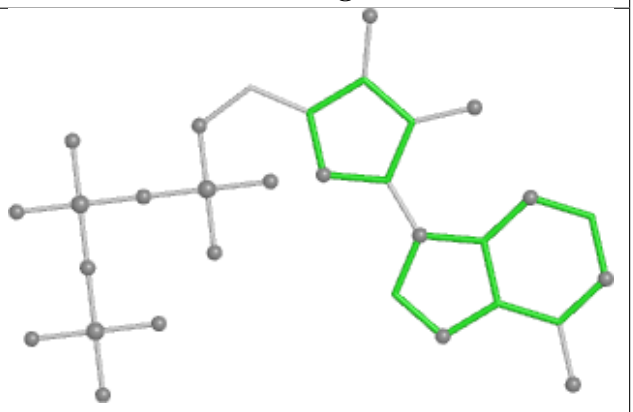
Bond lengths



Bond angles

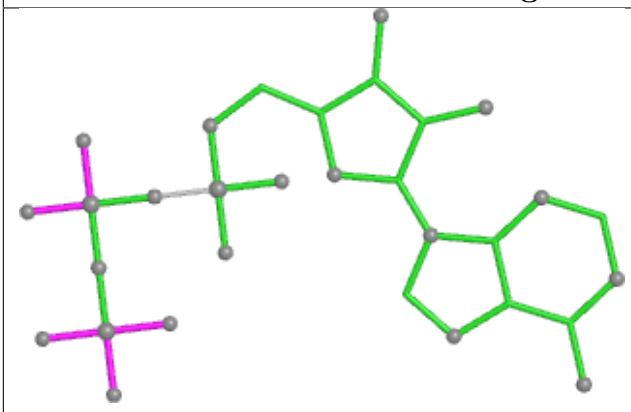


Torsions

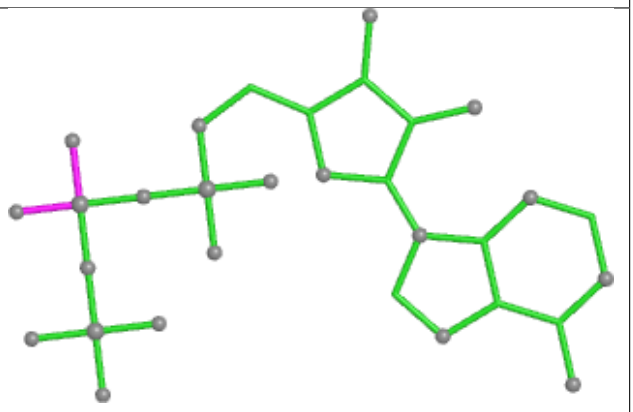


Rings

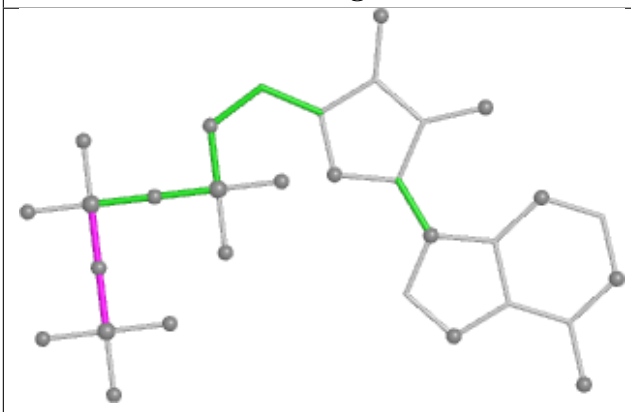
Ligand ANP G 701



Bond lengths



Bond angles



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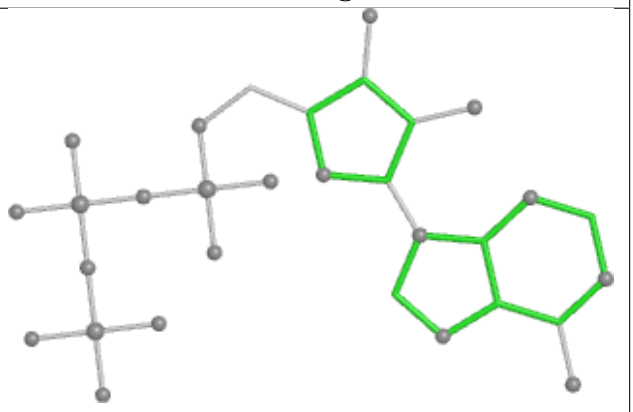
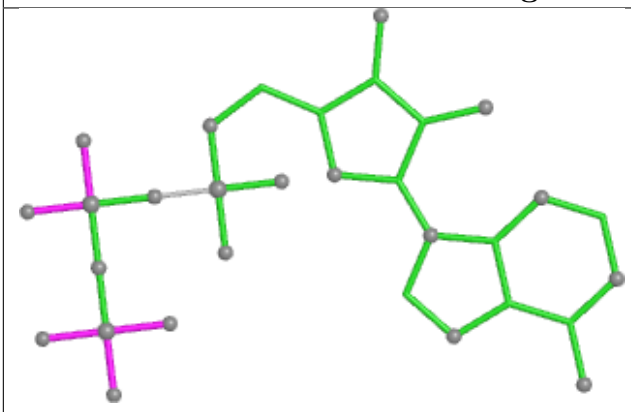
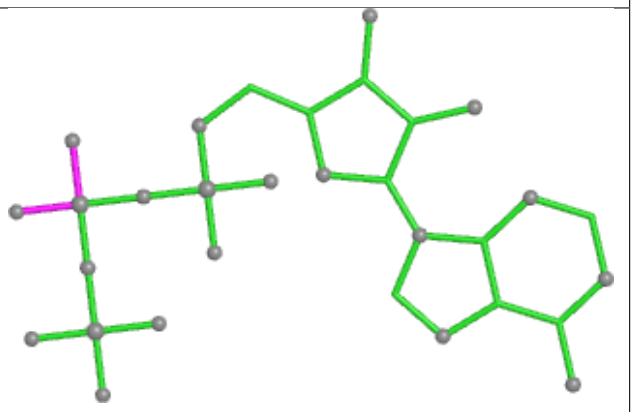


Rings

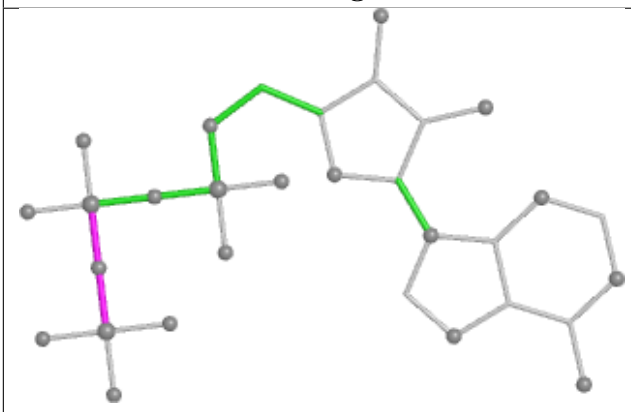
Ligand ANP K 701



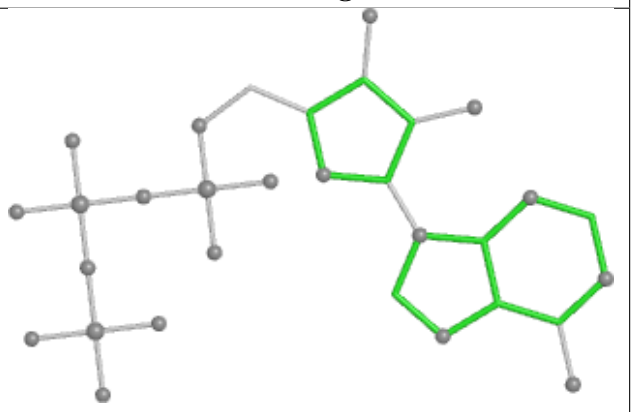
Bond lengths



Bond angles

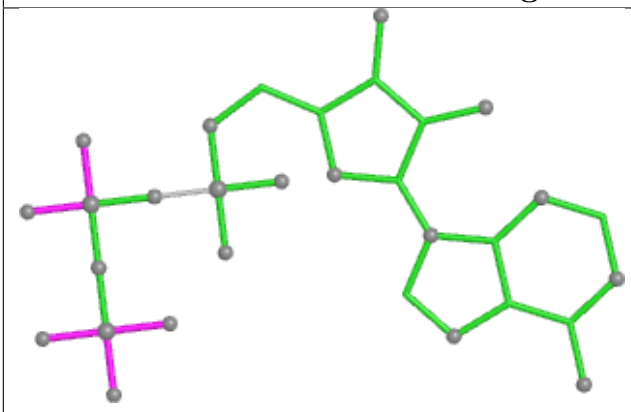


Torsions

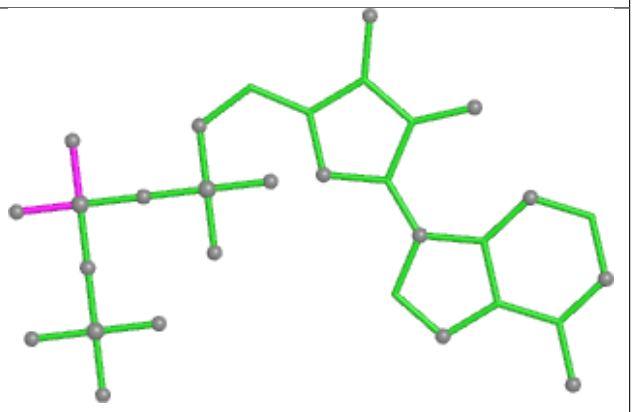


Rings

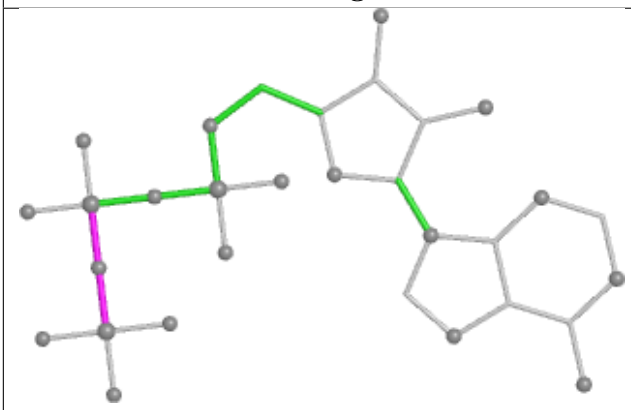
Ligand ANP H 701



Bond lengths



Bond angles



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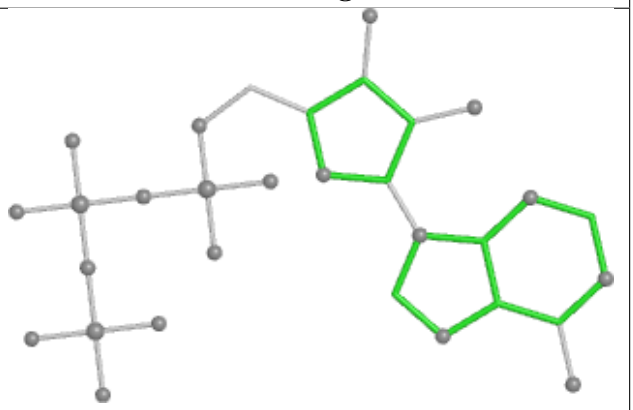
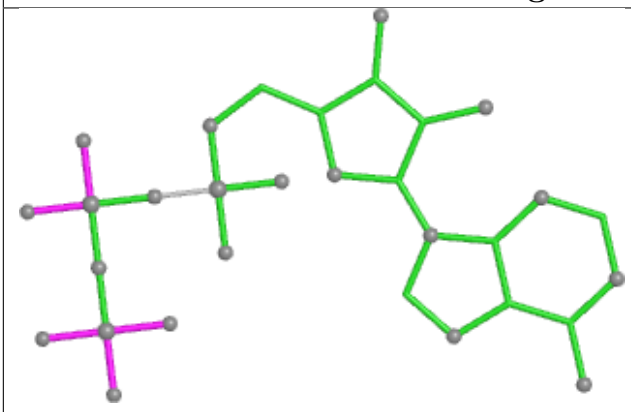


Rings

Ligand ANP I 701



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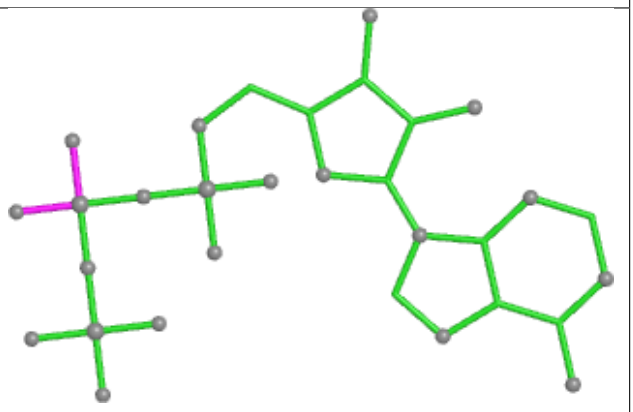
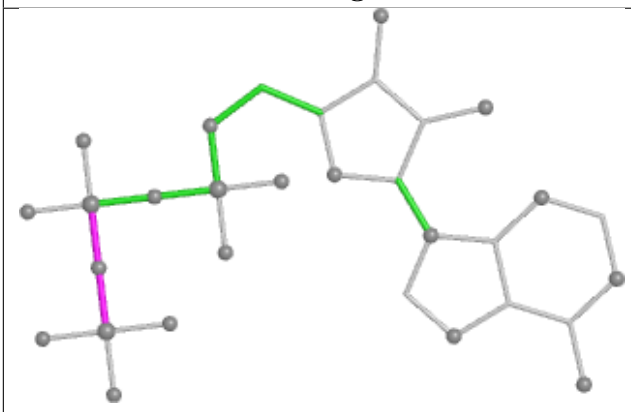


Bond angles



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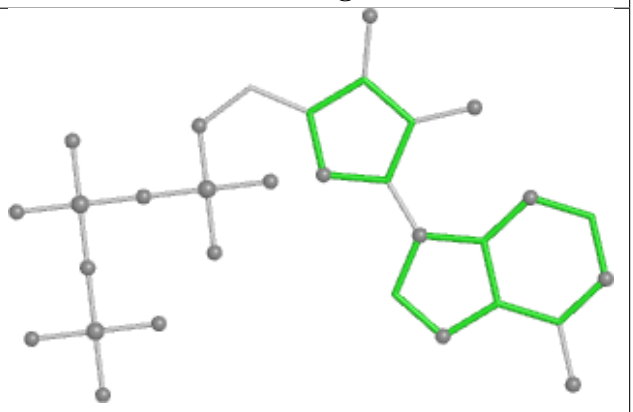
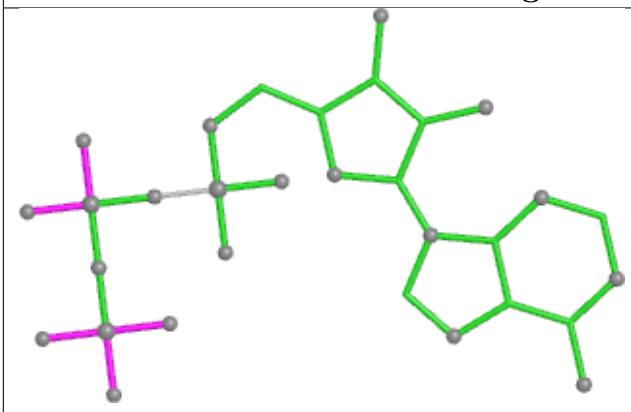


Rings

Ligand ANP B 701



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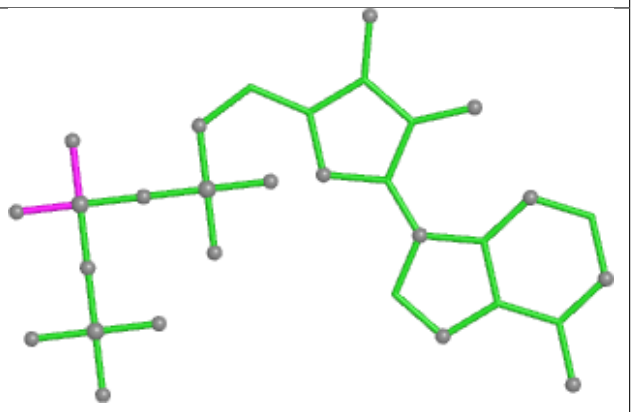
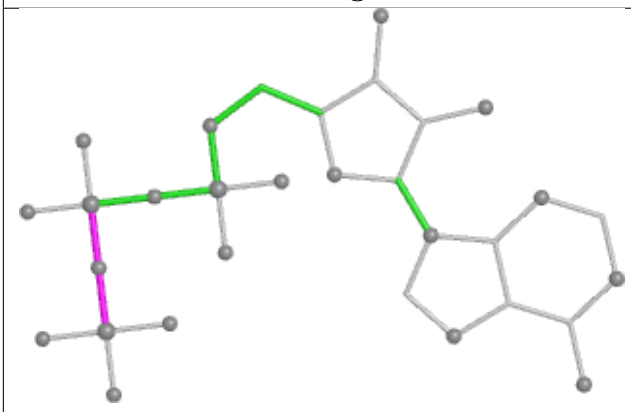
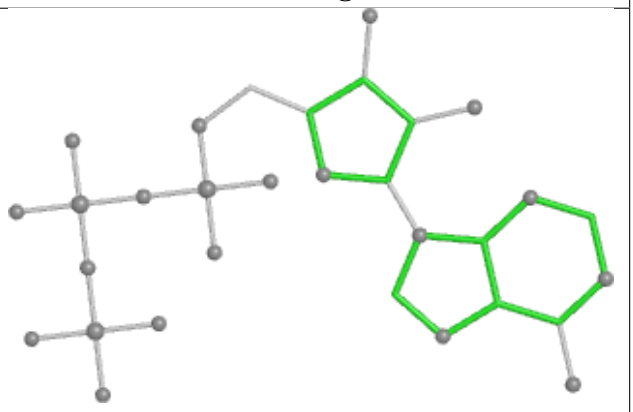


Bond angles

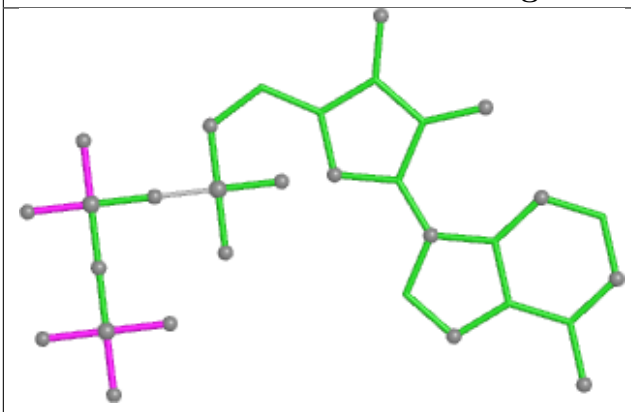


Torsions



Rings

Ligand ANP A 701



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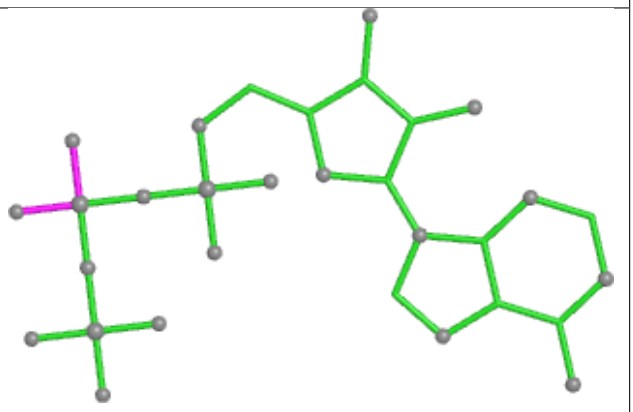
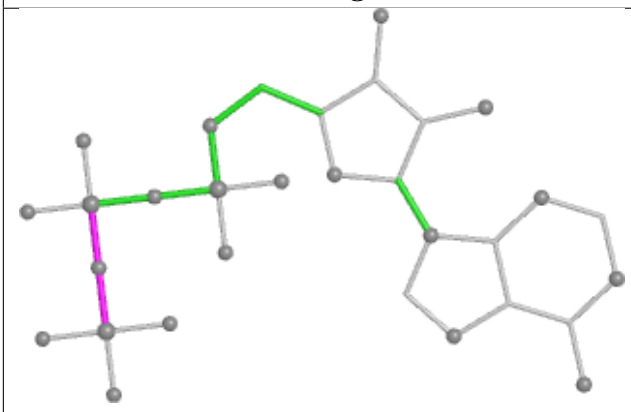


Bond angles



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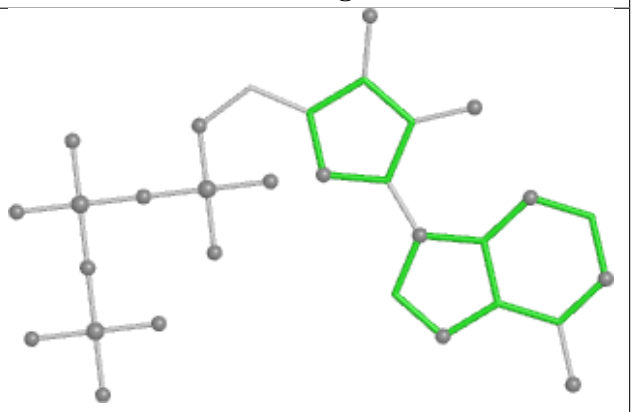
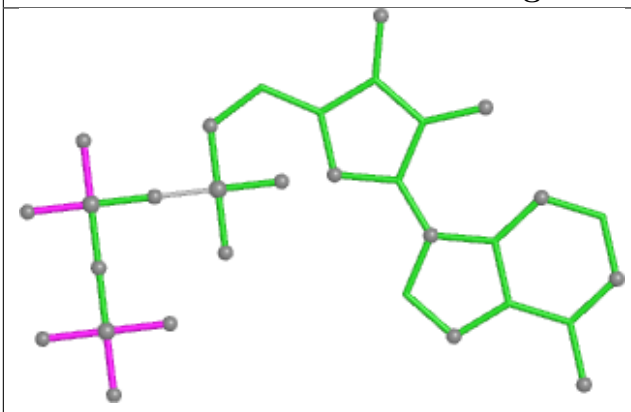


Rings

Ligand ANP F 701



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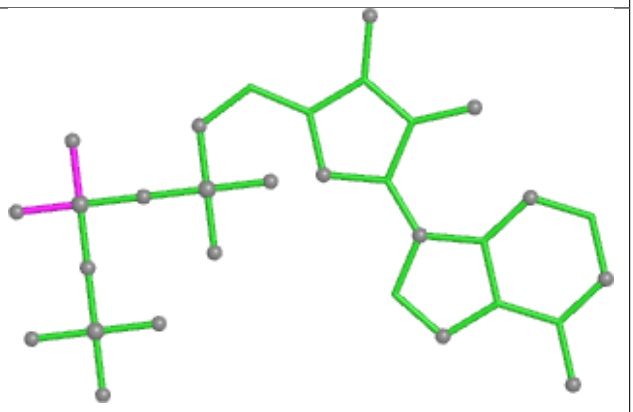

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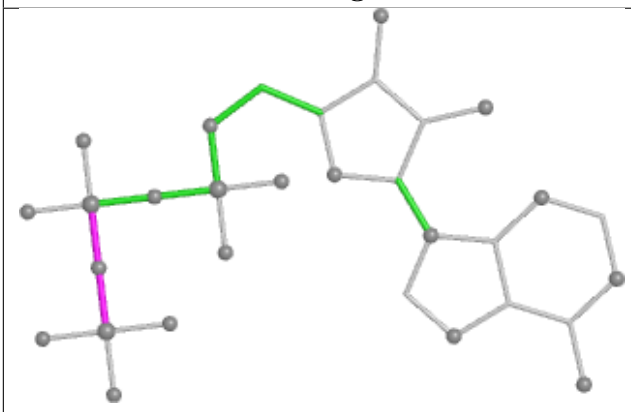
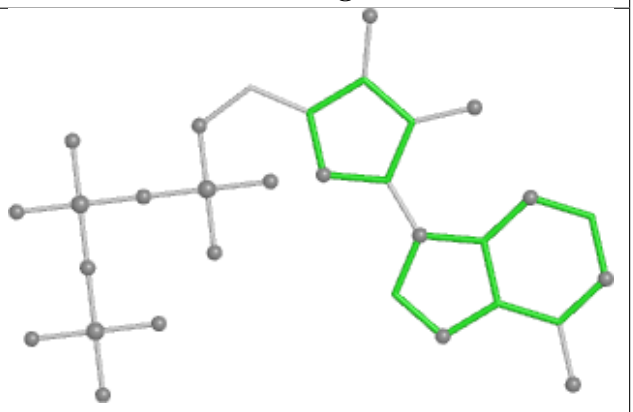
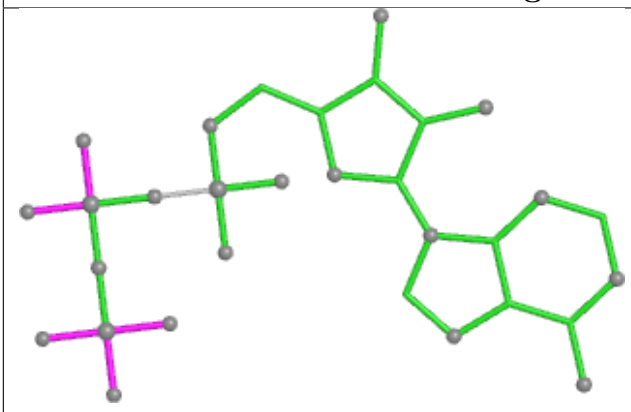


Torsions



Rings

Ligand ANP L 701



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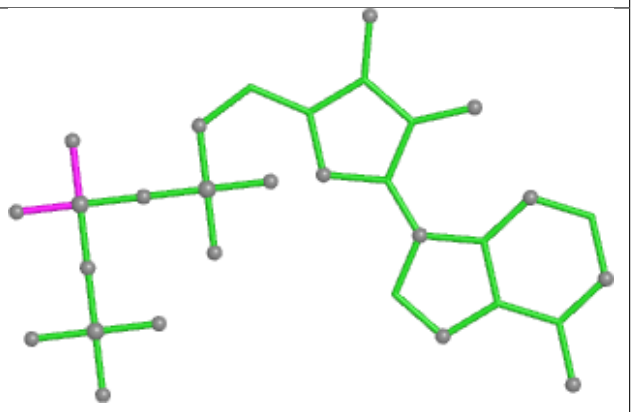
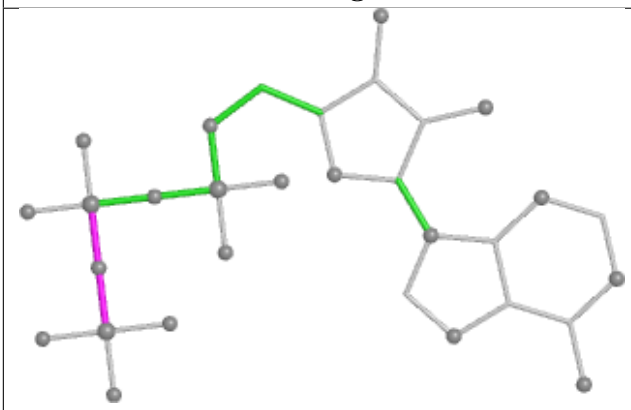
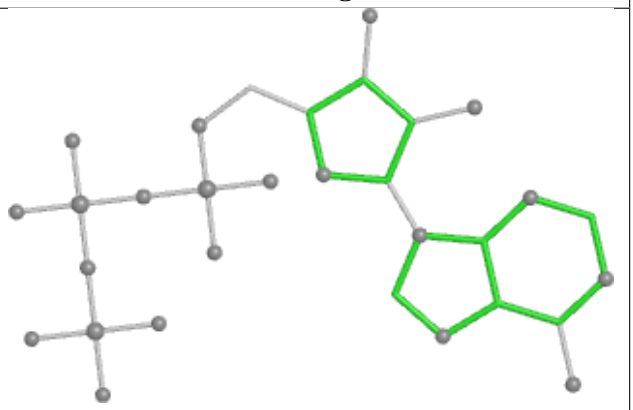


Bond angles

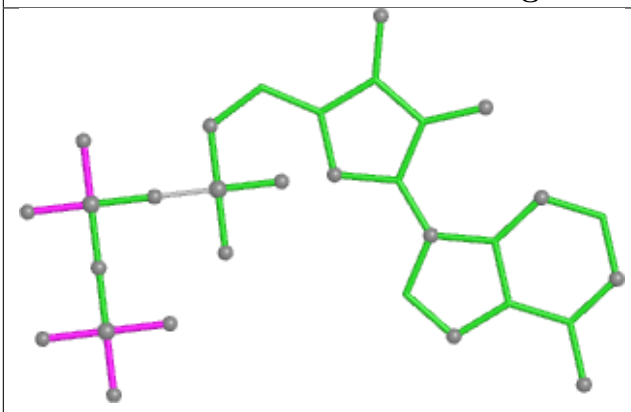


Torsions



Rings

Ligand ANP C 701



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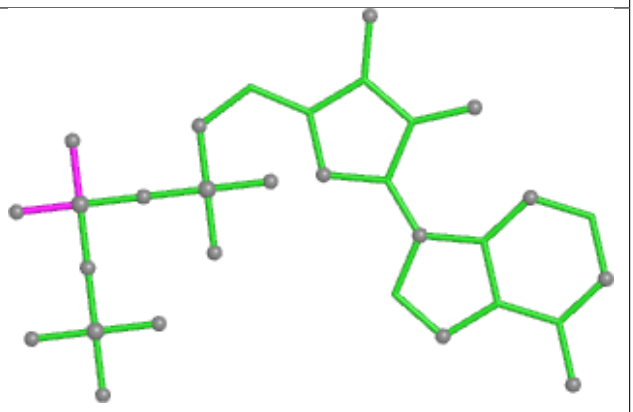
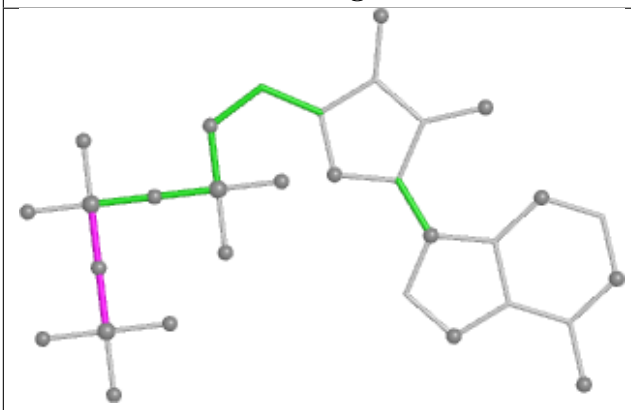


Bond angles



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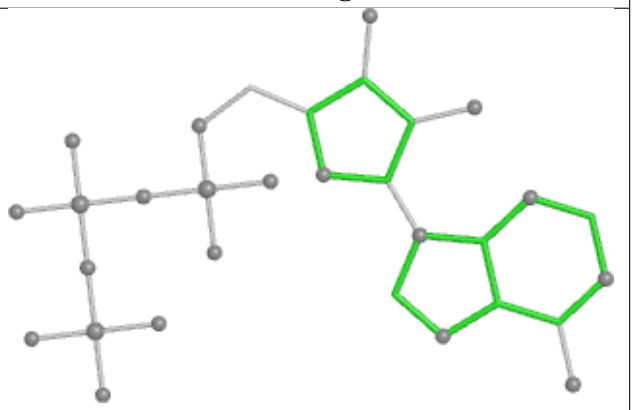
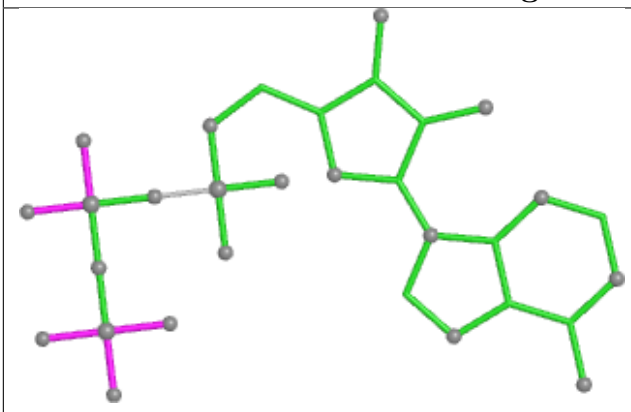


Rings

Ligand ANP D 701



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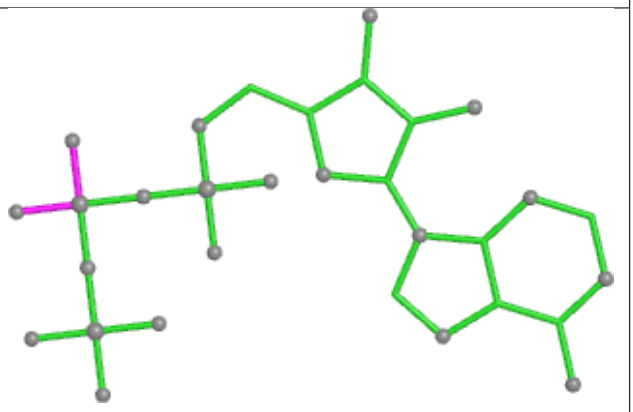
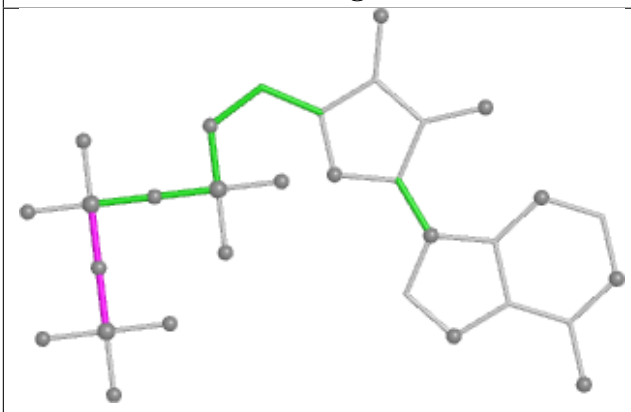


Bond angles



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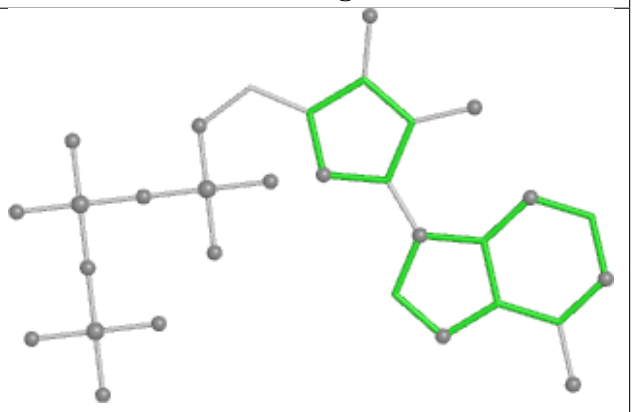
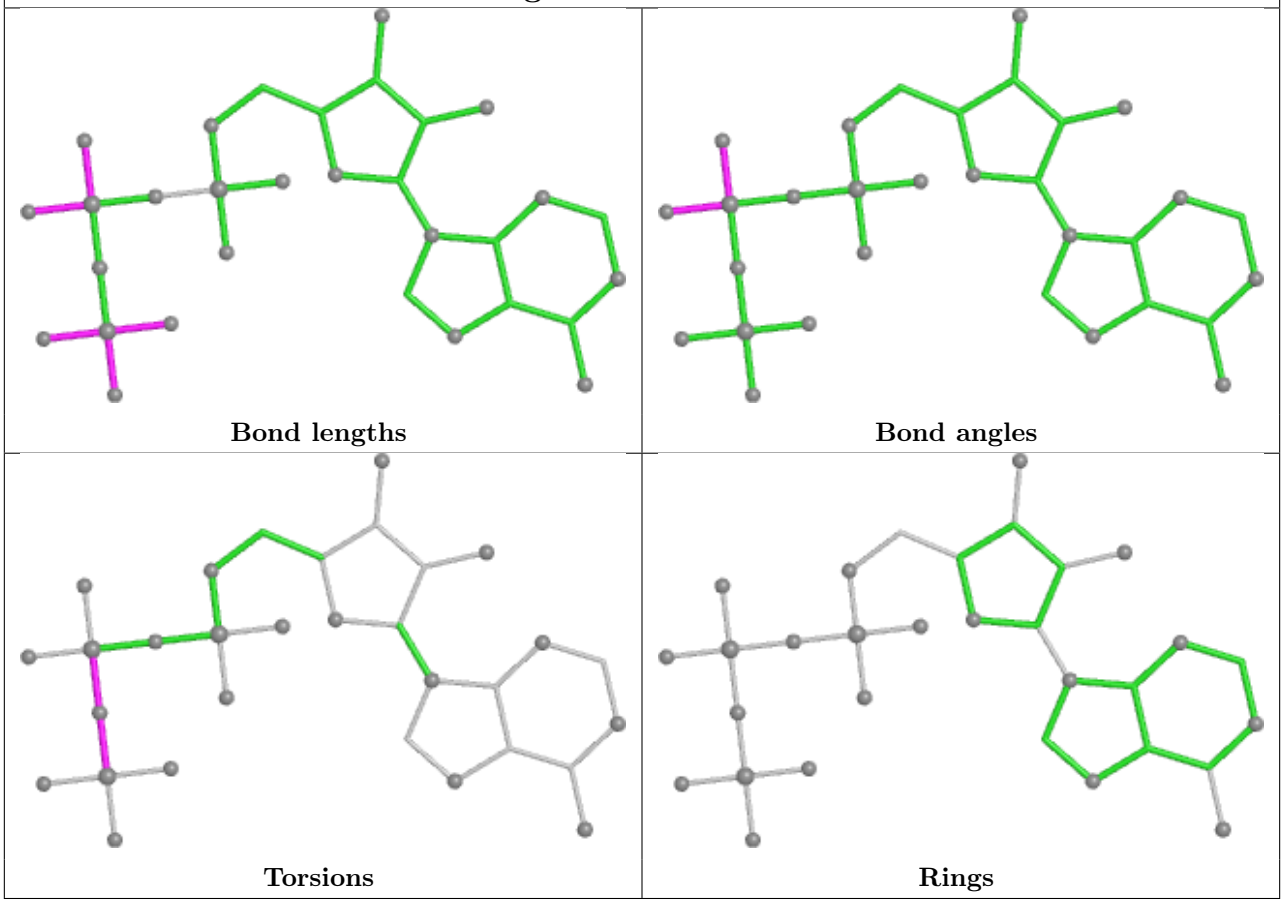


Rings

Ligand ANP E 701



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.

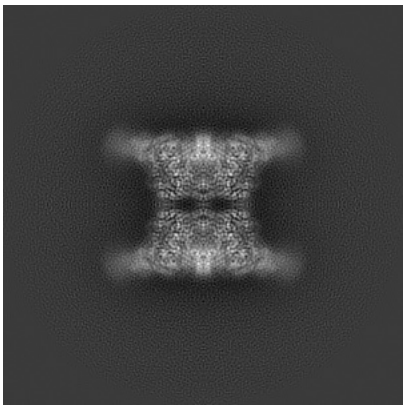
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-66913. These allow visual inspection of the internal detail of the map and identification of artifacts.

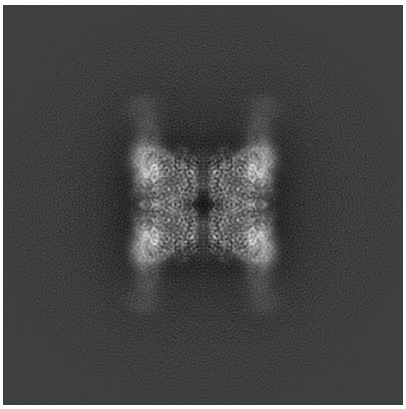
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

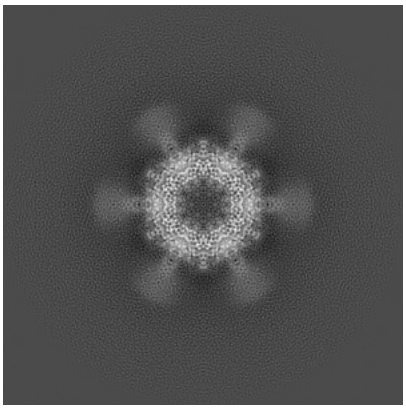
6.1.1 Primary map



X

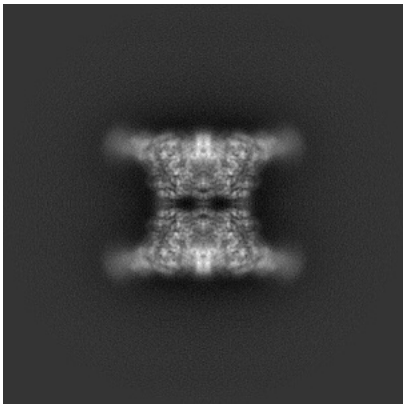


Y

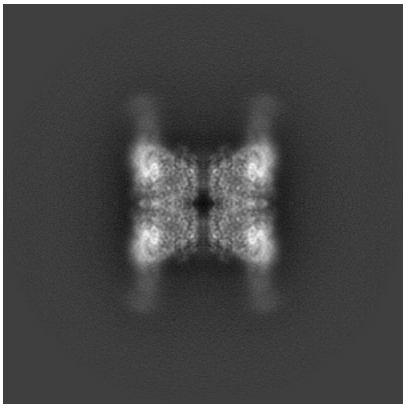


Z

6.1.2 Raw map



X



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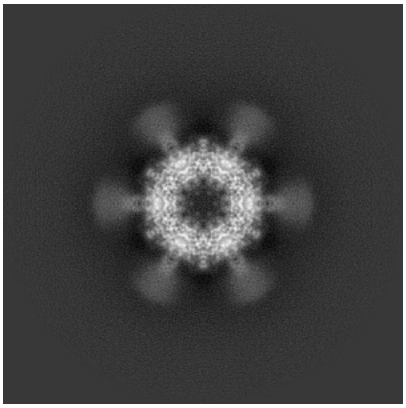
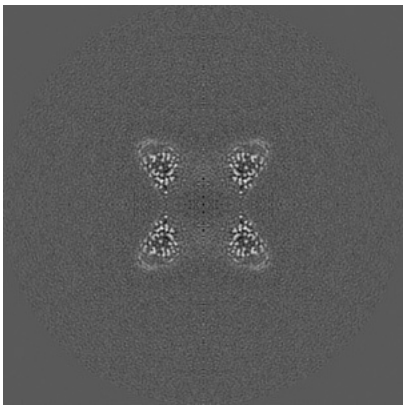


Z

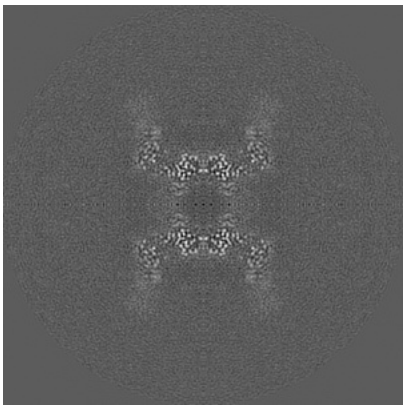
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

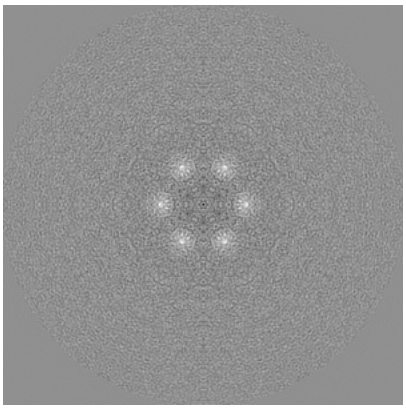
6.2.1 Primary map



X Index: 250

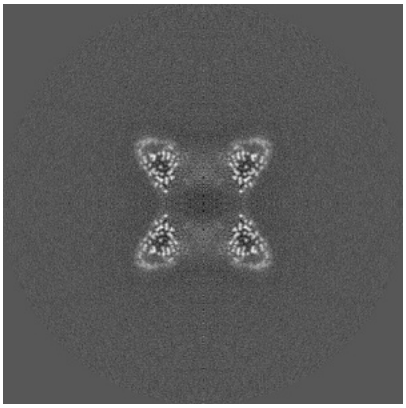


Y Index: 250

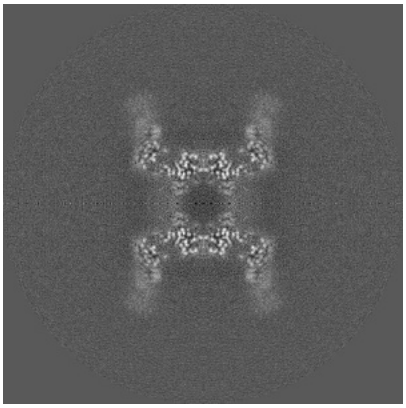


Z Index: 250

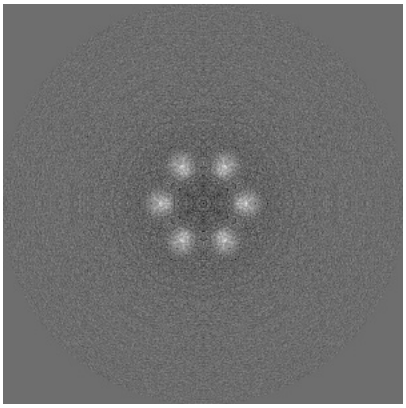
6.2.2 Raw map



X Index: 250



Y Index: 250

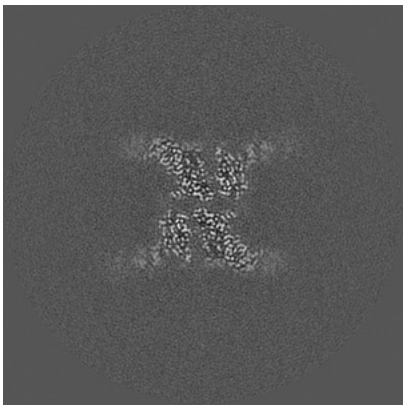


Z Index: 250

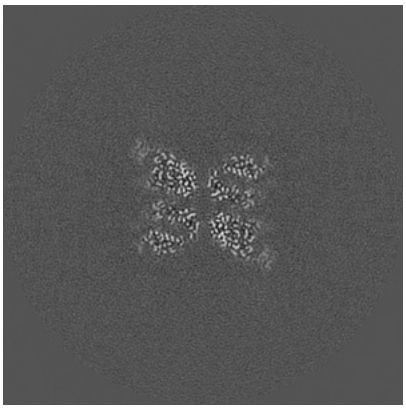
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

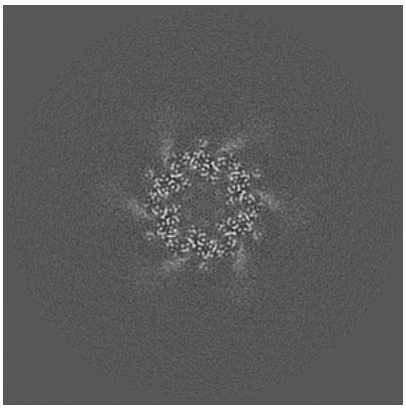
6.3.1 Primary map



X Index: 210

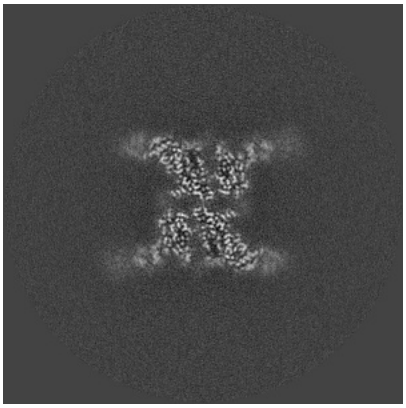


Y Index: 282

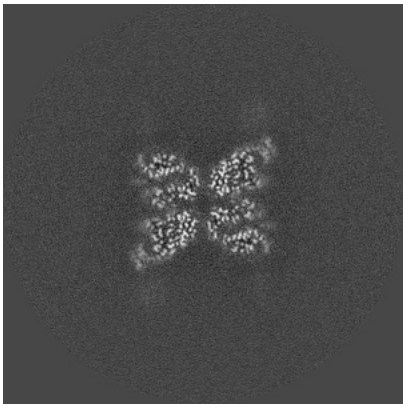


Z Index: 308

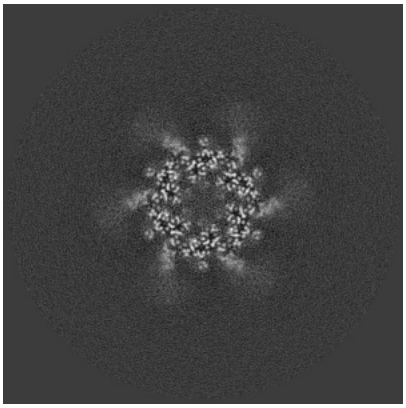
6.3.2 Raw map



X Index: 210



Y Index: 218

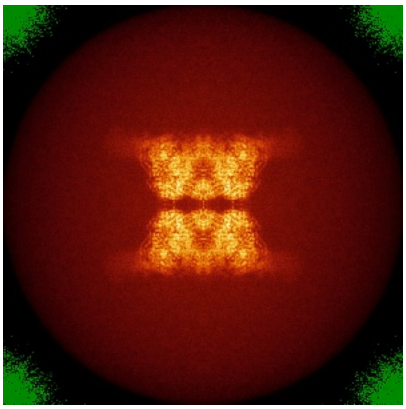


Z Index: 192

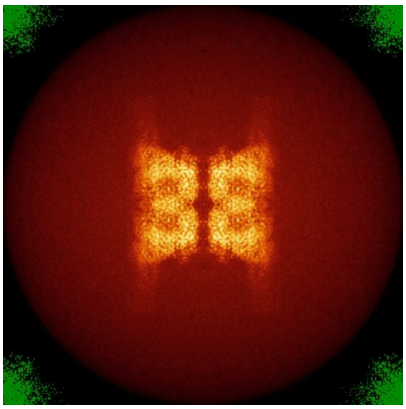
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

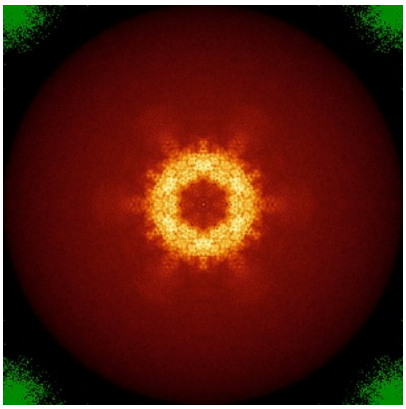
6.4.1 Primary map



X

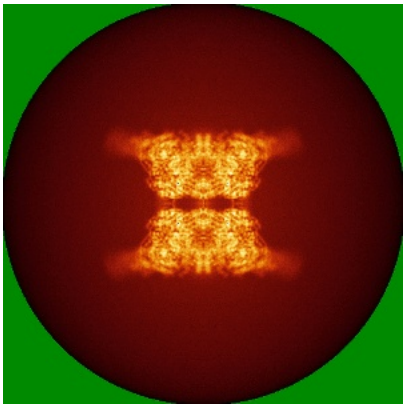


Y

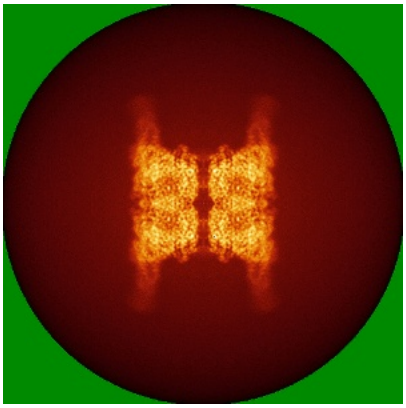


Z

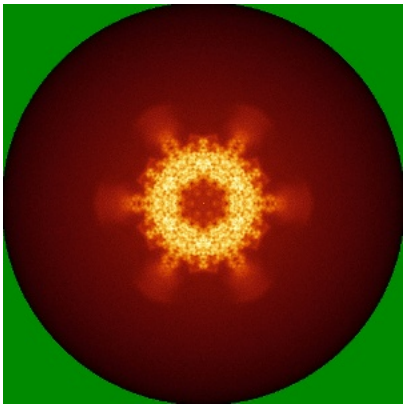
6.4.2 Raw map



X



Y

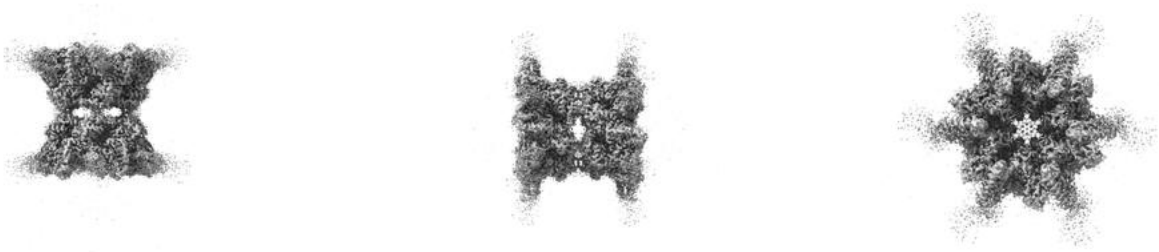


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

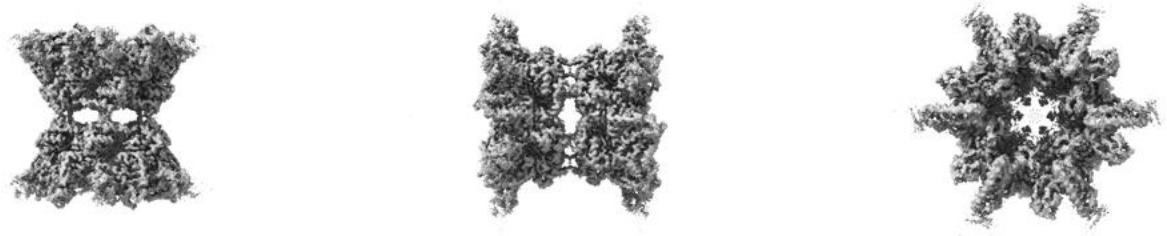
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

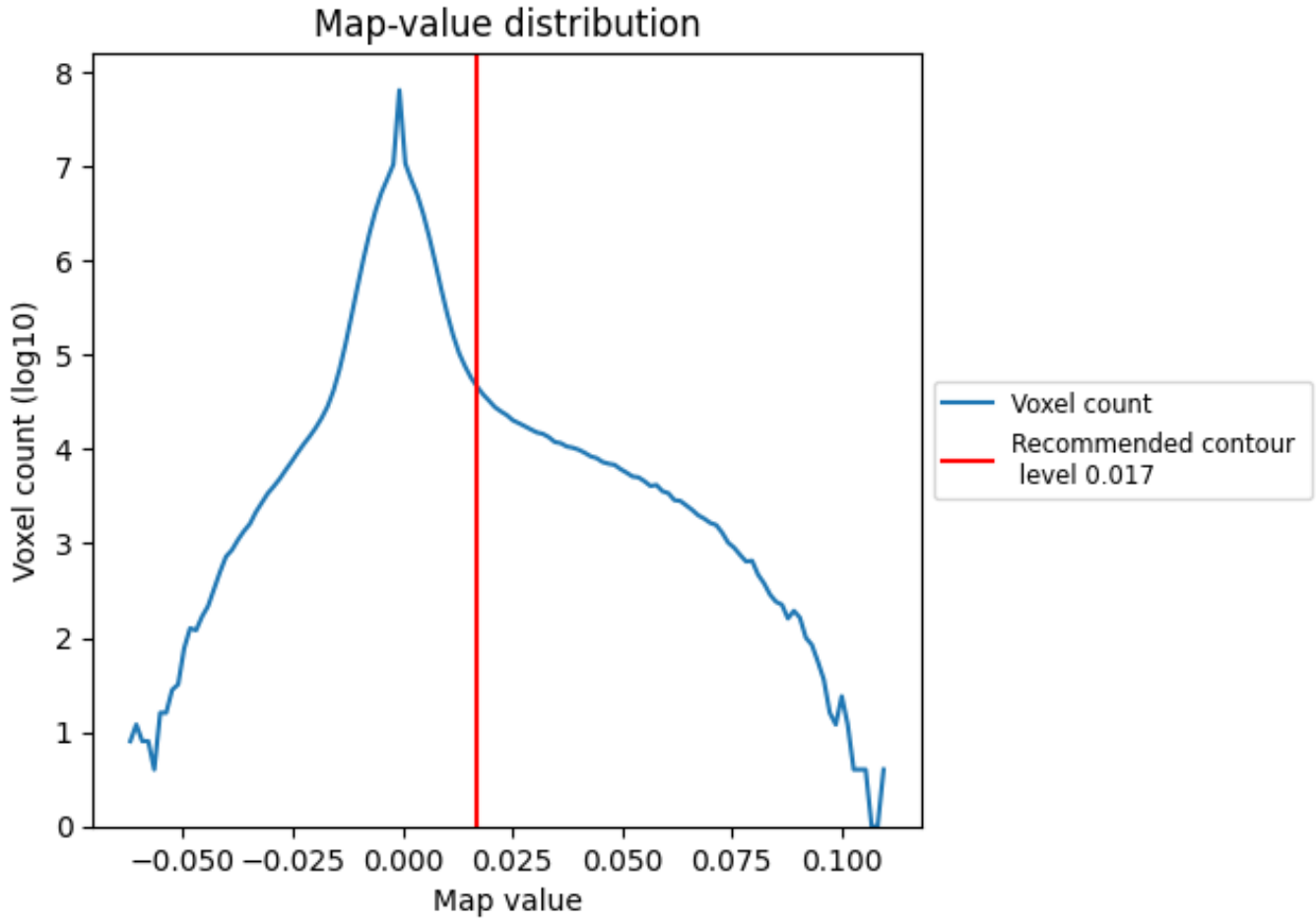
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

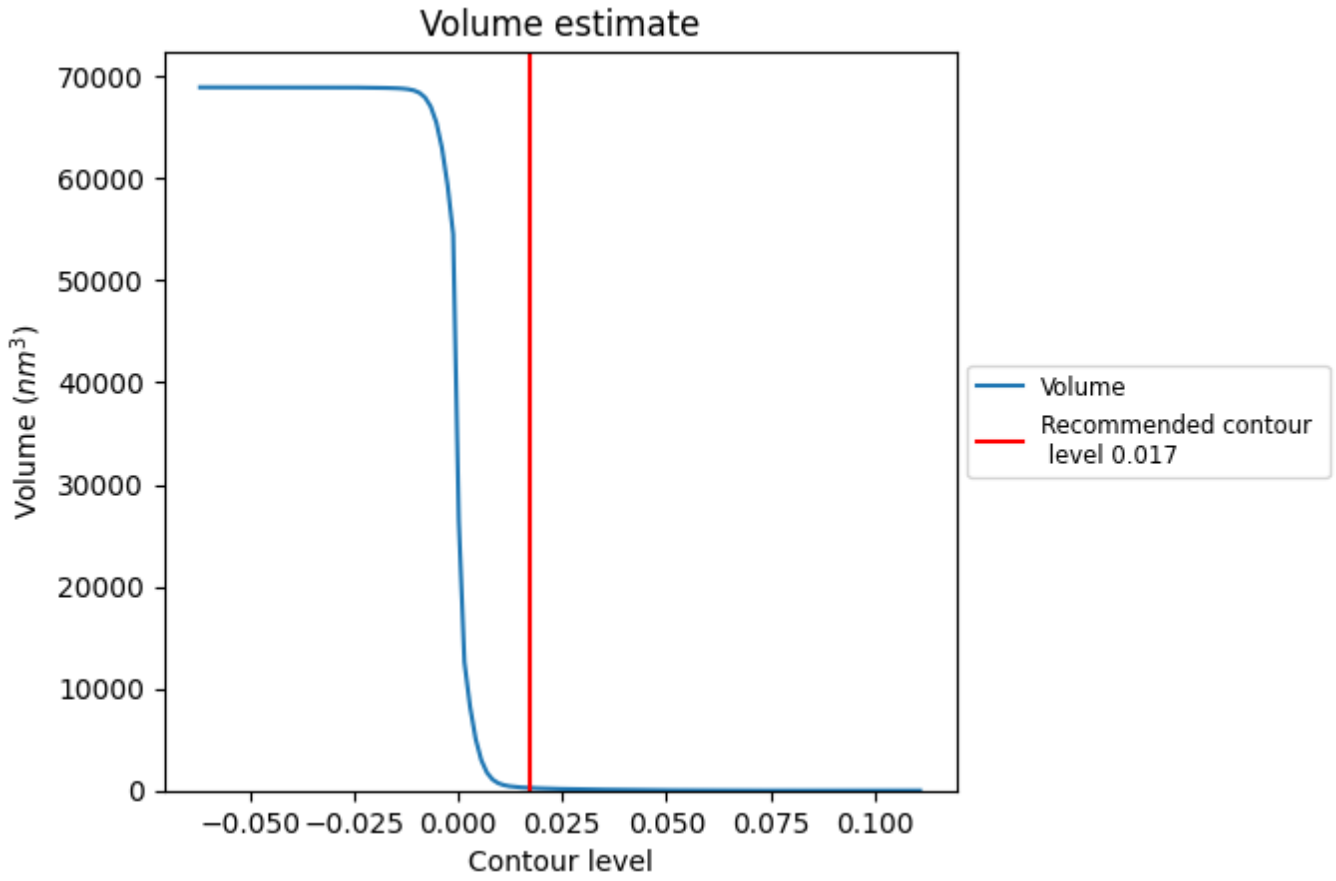
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

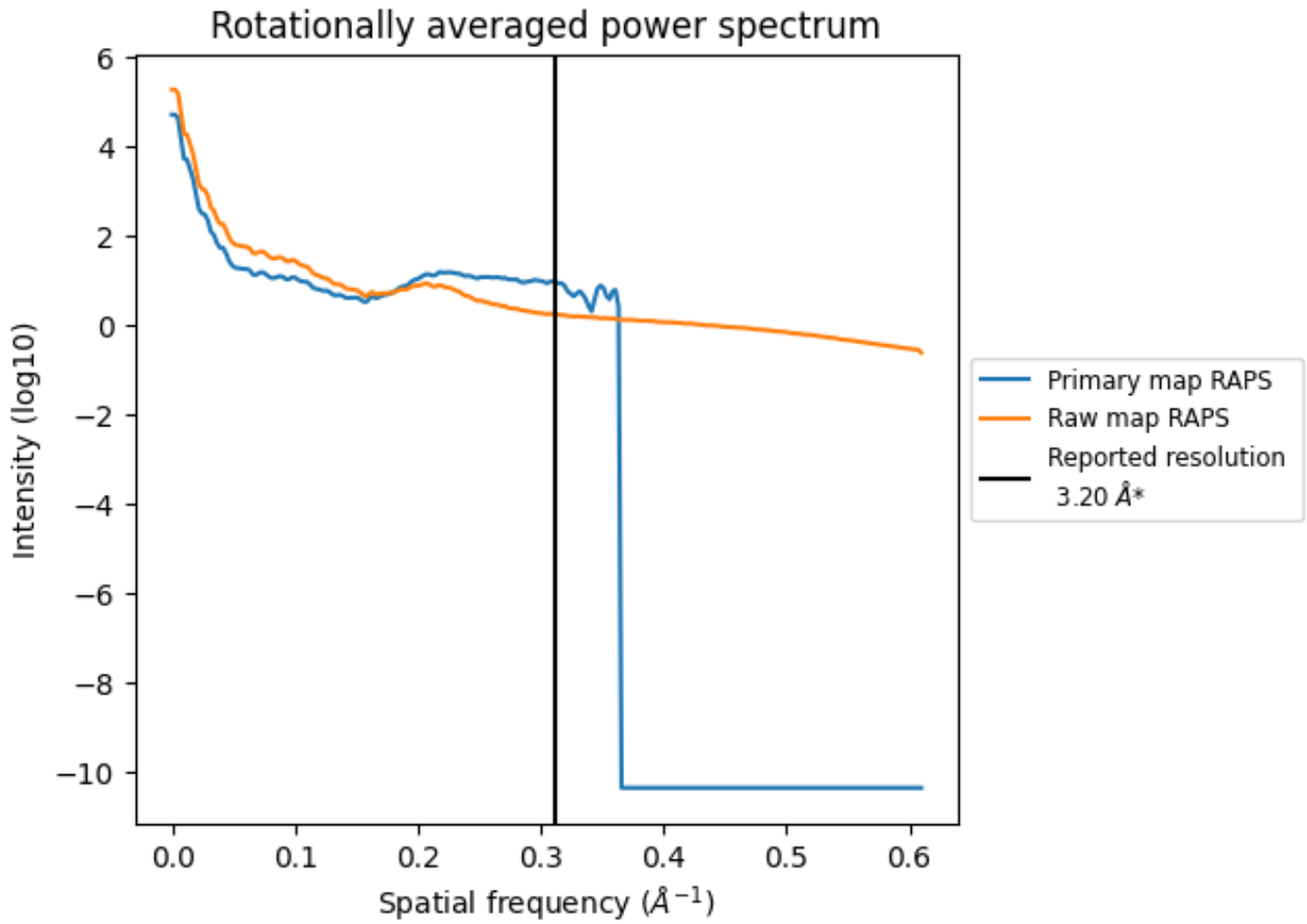
7.2 Volume estimate (i)



The volume at the recommended contour level is 263 nm^3; this corresponds to an approximate mass of 238 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

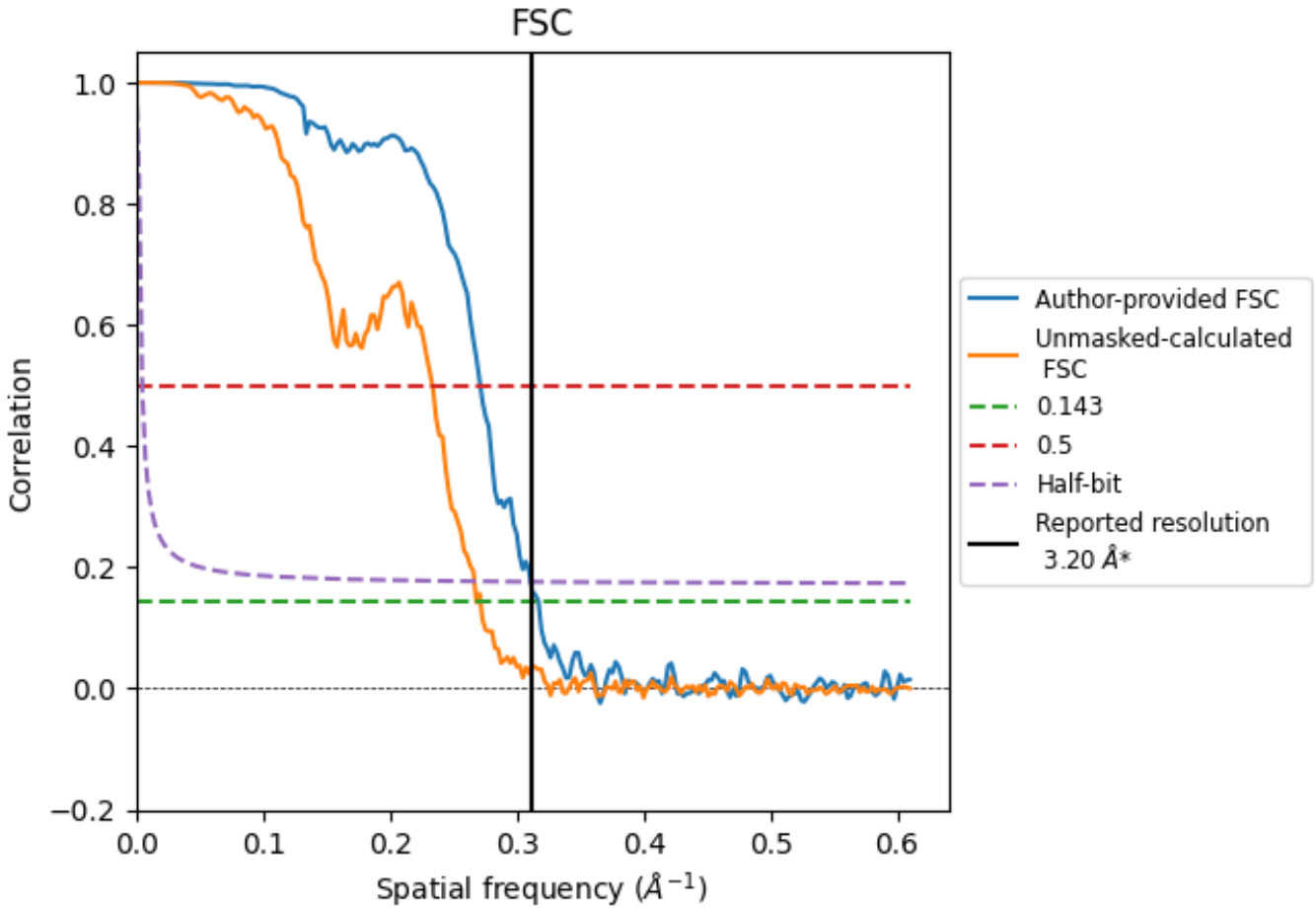


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8.2 Resolution estimates (i)

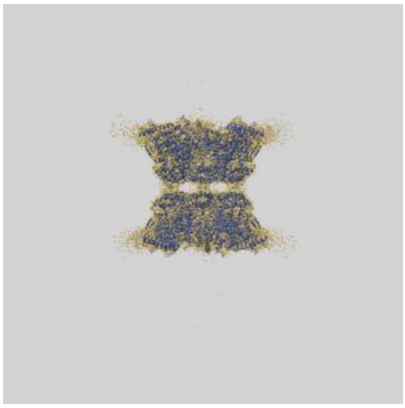
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.15	3.69	3.22
Unmasked-calculated*	3.73	4.28	3.75

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.73 differs from the reported value 3.2 by more than 10 %

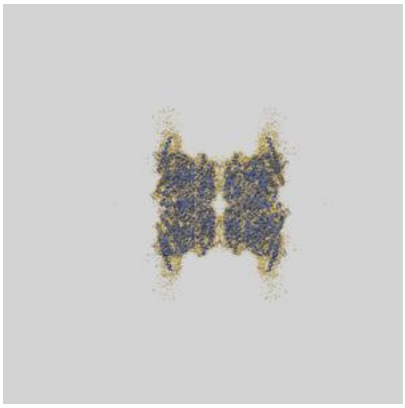
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-66913 and PDB model 9XIR. Per-residue inclusion information can be found in section 3 on page 13.

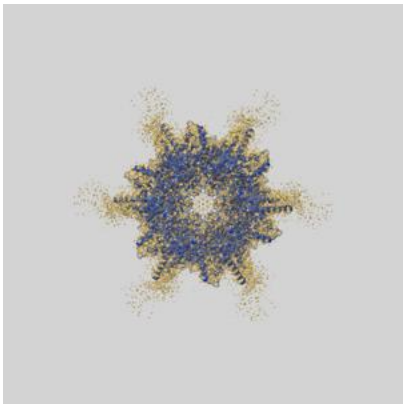
9.1 Map-model overlay



X



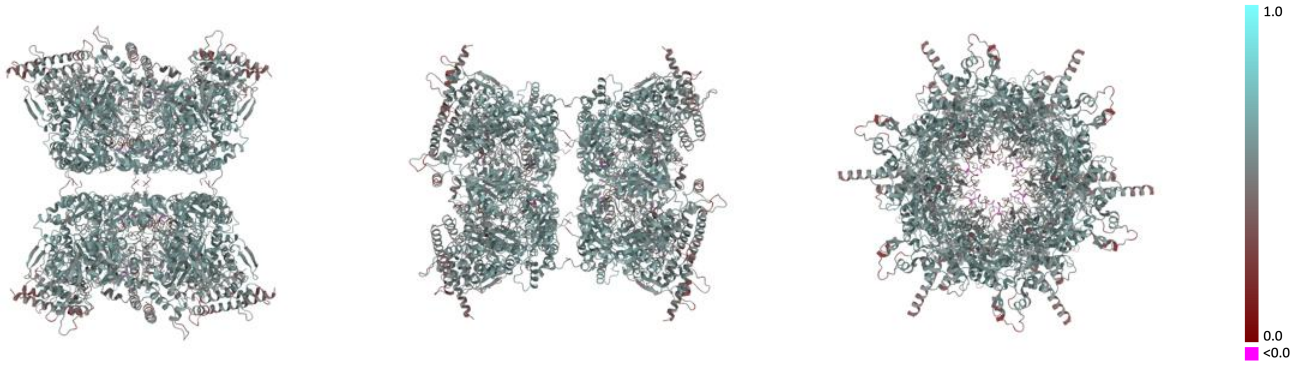
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

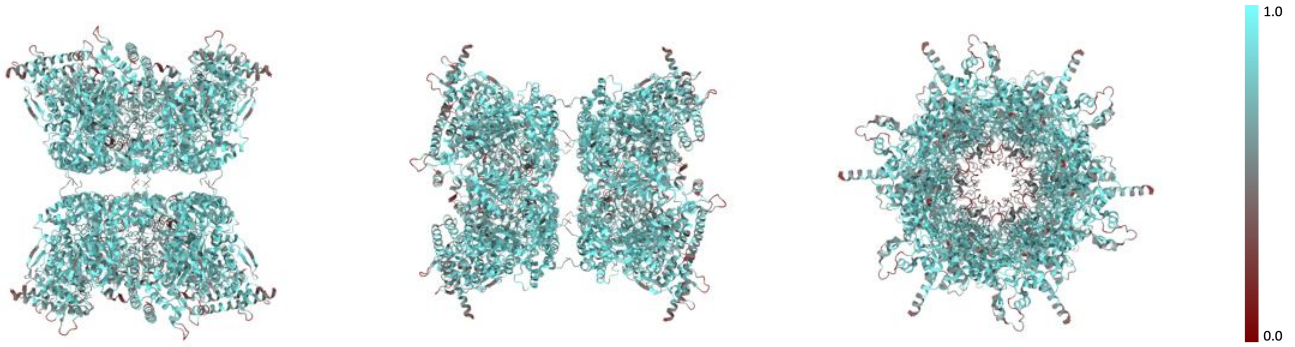
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

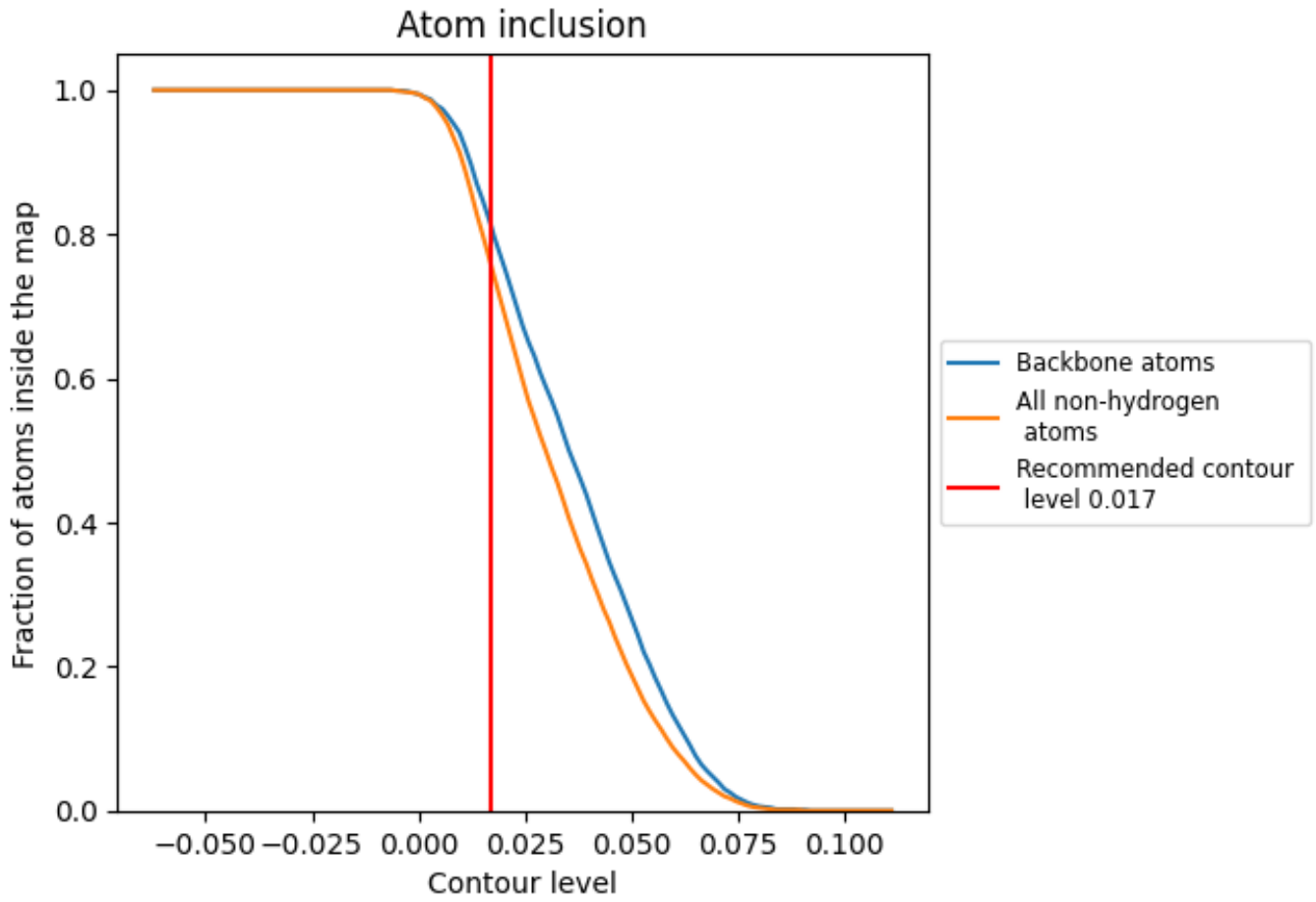
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.017).

9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7570	0.5370
A	0.7560	0.5350
B	0.7580	0.5370
C	0.7550	0.5370
D	0.7560	0.5370
E	0.7590	0.5360
F	0.7570	0.5360
G	0.7560	0.5360
H	0.7580	0.5370
I	0.7560	0.5380
J	0.7560	0.5370
K	0.7570	0.5370
L	0.7560	0.5360

