Full wwPDB EM Validation Report (i)

May 25, 2024 – 02:00 PM EDT

PDB ID	:	7RGI
EMDB ID	:	EMD-24450
Title	:	HUMAN RETINAL VARIANT IMPDH1(546) TREATED WITH GTP, ATP, IMP, NAD+; INTERFACE-CENTERED
Authors	:	Burrell, A.L.; Kollman, J.M.
Deposited on	:	2021-07-15
Resolution	:	3.60 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp
with specific help available everywhere you see the (i) 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:

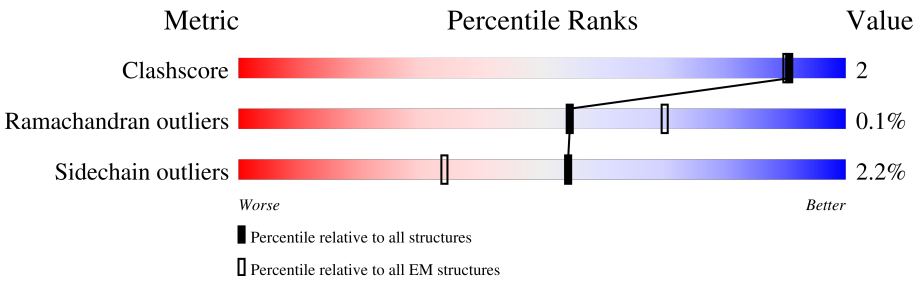
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 3.60 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	546	12% 63% • 35%
1	B	546	11% 60% 5% 35%
1	C	546	11% 61% • 35%
1	D	546	12% 61% 5% 35%
1	E	546	11% 60% 5% 35%
1	F	546	11% 60% 5% 35%
1	G	546	11% 60% 6% 35%
1	H	546	11% 59% 6% 35%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 44008 atoms, of which 22048 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 Inosine-5'-monophosphate dehydrogenase 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	357	5397	1691	2719	460	509	18	0	0
1	B	357	5397	1691	2719	460	509	18	0	0
1	C	357	5397	1691	2719	460	509	18	0	0
1	D	357	5397	1691	2719	460	509	18	0	0
1	E	357	5397	1691	2719	460	509	18	0	0
1	F	357	5397	1691	2719	460	509	18	0	0
1	G	357	5397	1691	2719	460	509	18	0	0
1	H	357	5397	1691	2719	460	509	18	0	0

There are 296 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	510	THR	-	expression tag	UNP P20839
A	511	PHE	-	expression tag	UNP P20839
A	512	LEU	-	expression tag	UNP P20839
A	513	PRO	-	expression tag	UNP P20839
A	514	PHE	-	expression tag	UNP P20839
A	515	THR	-	expression tag	UNP P20839
A	516	LYS	-	expression tag	UNP P20839
A	517	SER	-	expression tag	UNP P20839
A	518	GLY	-	expression tag	UNP P20839
A	519	CYS	-	expression tag	UNP P20839
A	520	THR	-	expression tag	UNP P20839
A	521	GLU	-	expression tag	UNP P20839
A	522	ASP	-	expression tag	UNP P20839
A	523	SER	-	expression tag	UNP P20839

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Chain	Residue	Modelled	Actual	Comment	Reference
A	524	GLY	-	expression tag	UNP P20839
A	525	GLY	-	expression tag	UNP P20839
A	526	GLY	-	expression tag	UNP P20839
A	527	ARG	-	expression tag	UNP P20839
A	528	GLY	-	expression tag	UNP P20839
A	529	GLY	-	expression tag	UNP P20839
A	530	GLY	-	expression tag	UNP P20839
A	531	GLY	-	expression tag	UNP P20839
A	532	ASP	-	expression tag	UNP P20839
A	533	ALA	-	expression tag	UNP P20839
A	534	PRO	-	expression tag	UNP P20839
A	535	GLN	-	expression tag	UNP P20839
A	536	CYS	-	expression tag	UNP P20839
A	537	PRO	-	expression tag	UNP P20839
A	538	LEU	-	expression tag	UNP P20839
A	539	LEU	-	expression tag	UNP P20839
A	540	GLY	-	expression tag	UNP P20839
A	541	THR	-	expression tag	UNP P20839
A	542	ALA	-	expression tag	UNP P20839
A	543	SER	-	expression tag	UNP P20839
A	544	LEU	-	expression tag	UNP P20839
A	545	HIS	-	expression tag	UNP P20839
A	546	ASN	-	expression tag	UNP P20839
B	510	THR	-	expression tag	UNP P20839
B	511	PHE	-	expression tag	UNP P20839
B	512	LEU	-	expression tag	UNP P20839
B	513	PRO	-	expression tag	UNP P20839
B	514	PHE	-	expression tag	UNP P20839
B	515	THR	-	expression tag	UNP P20839
B	516	LYS	-	expression tag	UNP P20839
B	517	SER	-	expression tag	UNP P20839
B	518	GLY	-	expression tag	UNP P20839
B	519	CYS	-	expression tag	UNP P20839
B	520	THR	-	expression tag	UNP P20839
B	521	GLU	-	expression tag	UNP P20839
B	522	ASP	-	expression tag	UNP P20839
B	523	SER	-	expression tag	UNP P20839
B	524	GLY	-	expression tag	UNP P20839
B	525	GLY	-	expression tag	UNP P20839
B	526	GLY	-	expression tag	UNP P20839
B	527	ARG	-	expression tag	UNP P20839
B	528	GLY	-	expression tag	UNP P20839

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Chain	Residue	Modelled	Actual	Comment	Reference
B	529	GLY	-	expression tag	UNP P20839
B	530	GLY	-	expression tag	UNP P20839
B	531	GLY	-	expression tag	UNP P20839
B	532	ASP	-	expression tag	UNP P20839
B	533	ALA	-	expression tag	UNP P20839
B	534	PRO	-	expression tag	UNP P20839
B	535	GLN	-	expression tag	UNP P20839
B	536	CYS	-	expression tag	UNP P20839
B	537	PRO	-	expression tag	UNP P20839
B	538	LEU	-	expression tag	UNP P20839
B	539	LEU	-	expression tag	UNP P20839
B	540	GLY	-	expression tag	UNP P20839
B	541	THR	-	expression tag	UNP P20839
B	542	ALA	-	expression tag	UNP P20839
B	543	SER	-	expression tag	UNP P20839
B	544	LEU	-	expression tag	UNP P20839
B	545	HIS	-	expression tag	UNP P20839
B	546	ASN	-	expression tag	UNP P20839
C	510	THR	-	expression tag	UNP P20839
C	511	PHE	-	expression tag	UNP P20839
C	512	LEU	-	expression tag	UNP P20839
C	513	PRO	-	expression tag	UNP P20839
C	514	PHE	-	expression tag	UNP P20839
C	515	THR	-	expression tag	UNP P20839
C	516	LYS	-	expression tag	UNP P20839
C	517	SER	-	expression tag	UNP P20839
C	518	GLY	-	expression tag	UNP P20839
C	519	CYS	-	expression tag	UNP P20839
C	520	THR	-	expression tag	UNP P20839
C	521	GLU	-	expression tag	UNP P20839
C	522	ASP	-	expression tag	UNP P20839
C	523	SER	-	expression tag	UNP P20839
C	524	GLY	-	expression tag	UNP P20839
C	525	GLY	-	expression tag	UNP P20839
C	526	GLY	-	expression tag	UNP P20839
C	527	ARG	-	expression tag	UNP P20839
C	528	GLY	-	expression tag	UNP P20839
C	529	GLY	-	expression tag	UNP P20839
C	530	GLY	-	expression tag	UNP P20839
C	531	GLY	-	expression tag	UNP P20839
C	532	ASP	-	expression tag	UNP P20839
C	533	ALA	-	expression tag	UNP P20839

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Chain	Residue	Modelled	Actual	Comment	Reference
C	534	PRO	-	expression tag	UNP P20839
C	535	GLN	-	expression tag	UNP P20839
C	536	CYS	-	expression tag	UNP P20839
C	537	PRO	-	expression tag	UNP P20839
C	538	LEU	-	expression tag	UNP P20839
C	539	LEU	-	expression tag	UNP P20839
C	540	GLY	-	expression tag	UNP P20839
C	541	THR	-	expression tag	UNP P20839
C	542	ALA	-	expression tag	UNP P20839
C	543	SER	-	expression tag	UNP P20839
C	544	LEU	-	expression tag	UNP P20839
C	545	HIS	-	expression tag	UNP P20839
C	546	ASN	-	expression tag	UNP P20839
D	510	THR	-	expression tag	UNP P20839
D	511	PHE	-	expression tag	UNP P20839
D	512	LEU	-	expression tag	UNP P20839
D	513	PRO	-	expression tag	UNP P20839
D	514	PHE	-	expression tag	UNP P20839
D	515	THR	-	expression tag	UNP P20839
D	516	LYS	-	expression tag	UNP P20839
D	517	SER	-	expression tag	UNP P20839
D	518	GLY	-	expression tag	UNP P20839
D	519	CYS	-	expression tag	UNP P20839
D	520	THR	-	expression tag	UNP P20839
D	521	GLU	-	expression tag	UNP P20839
D	522	ASP	-	expression tag	UNP P20839
D	523	SER	-	expression tag	UNP P20839
D	524	GLY	-	expression tag	UNP P20839
D	525	GLY	-	expression tag	UNP P20839
D	526	GLY	-	expression tag	UNP P20839
D	527	ARG	-	expression tag	UNP P20839
D	528	GLY	-	expression tag	UNP P20839
D	529	GLY	-	expression tag	UNP P20839
D	530	GLY	-	expression tag	UNP P20839
D	531	GLY	-	expression tag	UNP P20839
D	532	ASP	-	expression tag	UNP P20839
D	533	ALA	-	expression tag	UNP P20839
D	534	PRO	-	expression tag	UNP P20839
D	535	GLN	-	expression tag	UNP P20839
D	536	CYS	-	expression tag	UNP P20839
D	537	PRO	-	expression tag	UNP P20839
D	538	LEU	-	expression tag	UNP P20839

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Chain	Residue	Modelled	Actual	Comment	Reference
D	539	LEU	-	expression tag	UNP P20839
D	540	GLY	-	expression tag	UNP P20839
D	541	THR	-	expression tag	UNP P20839
D	542	ALA	-	expression tag	UNP P20839
D	543	SER	-	expression tag	UNP P20839
D	544	LEU	-	expression tag	UNP P20839
D	545	HIS	-	expression tag	UNP P20839
D	546	ASN	-	expression tag	UNP P20839
E	510	THR	-	expression tag	UNP P20839
E	511	PHE	-	expression tag	UNP P20839
E	512	LEU	-	expression tag	UNP P20839
E	513	PRO	-	expression tag	UNP P20839
E	514	PHE	-	expression tag	UNP P20839
E	515	THR	-	expression tag	UNP P20839
E	516	LYS	-	expression tag	UNP P20839
E	517	SER	-	expression tag	UNP P20839
E	518	GLY	-	expression tag	UNP P20839
E	519	CYS	-	expression tag	UNP P20839
E	520	THR	-	expression tag	UNP P20839
E	521	GLU	-	expression tag	UNP P20839
E	522	ASP	-	expression tag	UNP P20839
E	523	SER	-	expression tag	UNP P20839
E	524	GLY	-	expression tag	UNP P20839
E	525	GLY	-	expression tag	UNP P20839
E	526	GLY	-	expression tag	UNP P20839
E	527	ARG	-	expression tag	UNP P20839
E	528	GLY	-	expression tag	UNP P20839
E	529	GLY	-	expression tag	UNP P20839
E	530	GLY	-	expression tag	UNP P20839
E	531	GLY	-	expression tag	UNP P20839
E	532	ASP	-	expression tag	UNP P20839
E	533	ALA	-	expression tag	UNP P20839
E	534	PRO	-	expression tag	UNP P20839
E	535	GLN	-	expression tag	UNP P20839
E	536	CYS	-	expression tag	UNP P20839
E	537	PRO	-	expression tag	UNP P20839
E	538	LEU	-	expression tag	UNP P20839
E	539	LEU	-	expression tag	UNP P20839
E	540	GLY	-	expression tag	UNP P20839
E	541	THR	-	expression tag	UNP P20839
E	542	ALA	-	expression tag	UNP P20839
E	543	SER	-	expression tag	UNP P20839

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Chain	Residue	Modelled	Actual	Comment	Reference
E	544	LEU	-	expression tag	UNP P20839
E	545	HIS	-	expression tag	UNP P20839
E	546	ASN	-	expression tag	UNP P20839
F	510	THR	-	expression tag	UNP P20839
F	511	PHE	-	expression tag	UNP P20839
F	512	LEU	-	expression tag	UNP P20839
F	513	PRO	-	expression tag	UNP P20839
F	514	PHE	-	expression tag	UNP P20839
F	515	THR	-	expression tag	UNP P20839
F	516	LYS	-	expression tag	UNP P20839
F	517	SER	-	expression tag	UNP P20839
F	518	GLY	-	expression tag	UNP P20839
F	519	CYS	-	expression tag	UNP P20839
F	520	THR	-	expression tag	UNP P20839
F	521	GLU	-	expression tag	UNP P20839
F	522	ASP	-	expression tag	UNP P20839
F	523	SER	-	expression tag	UNP P20839
F	524	GLY	-	expression tag	UNP P20839
F	525	GLY	-	expression tag	UNP P20839
F	526	GLY	-	expression tag	UNP P20839
F	527	ARG	-	expression tag	UNP P20839
F	528	GLY	-	expression tag	UNP P20839
F	529	GLY	-	expression tag	UNP P20839
F	530	GLY	-	expression tag	UNP P20839
F	531	GLY	-	expression tag	UNP P20839
F	532	ASP	-	expression tag	UNP P20839
F	533	ALA	-	expression tag	UNP P20839
F	534	PRO	-	expression tag	UNP P20839
F	535	GLN	-	expression tag	UNP P20839
F	536	CYS	-	expression tag	UNP P20839
F	537	PRO	-	expression tag	UNP P20839
F	538	LEU	-	expression tag	UNP P20839
F	539	LEU	-	expression tag	UNP P20839
F	540	GLY	-	expression tag	UNP P20839
F	541	THR	-	expression tag	UNP P20839
F	542	ALA	-	expression tag	UNP P20839
F	543	SER	-	expression tag	UNP P20839
F	544	LEU	-	expression tag	UNP P20839
F	545	HIS	-	expression tag	UNP P20839
F	546	ASN	-	expression tag	UNP P20839
G	510	THR	-	expression tag	UNP P20839
G	511	PHE	-	expression tag	UNP P20839

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Chain	Residue	Modelled	Actual	Comment	Reference
G	512	LEU	-	expression tag	UNP P20839
G	513	PRO	-	expression tag	UNP P20839
G	514	PHE	-	expression tag	UNP P20839
G	515	THR	-	expression tag	UNP P20839
G	516	LYS	-	expression tag	UNP P20839
G	517	SER	-	expression tag	UNP P20839
G	518	GLY	-	expression tag	UNP P20839
G	519	CYS	-	expression tag	UNP P20839
G	520	THR	-	expression tag	UNP P20839
G	521	GLU	-	expression tag	UNP P20839
G	522	ASP	-	expression tag	UNP P20839
G	523	SER	-	expression tag	UNP P20839
G	524	GLY	-	expression tag	UNP P20839
G	525	GLY	-	expression tag	UNP P20839
G	526	GLY	-	expression tag	UNP P20839
G	527	ARG	-	expression tag	UNP P20839
G	528	GLY	-	expression tag	UNP P20839
G	529	GLY	-	expression tag	UNP P20839
G	530	GLY	-	expression tag	UNP P20839
G	531	GLY	-	expression tag	UNP P20839
G	532	ASP	-	expression tag	UNP P20839
G	533	ALA	-	expression tag	UNP P20839
G	534	PRO	-	expression tag	UNP P20839
G	535	GLN	-	expression tag	UNP P20839
G	536	CYS	-	expression tag	UNP P20839
G	537	PRO	-	expression tag	UNP P20839
G	538	LEU	-	expression tag	UNP P20839
G	539	LEU	-	expression tag	UNP P20839
G	540	GLY	-	expression tag	UNP P20839
G	541	THR	-	expression tag	UNP P20839
G	542	ALA	-	expression tag	UNP P20839
G	543	SER	-	expression tag	UNP P20839
G	544	LEU	-	expression tag	UNP P20839
G	545	HIS	-	expression tag	UNP P20839
G	546	ASN	-	expression tag	UNP P20839
H	510	THR	-	expression tag	UNP P20839
H	511	PHE	-	expression tag	UNP P20839
H	512	LEU	-	expression tag	UNP P20839
H	513	PRO	-	expression tag	UNP P20839
H	514	PHE	-	expression tag	UNP P20839
H	515	THR	-	expression tag	UNP P20839
H	516	LYS	-	expression tag	UNP P20839

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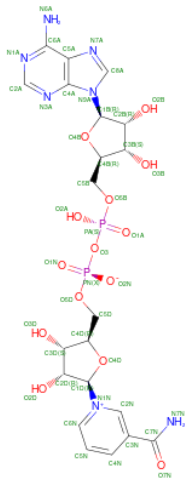
Chain	Residue	Modelled	Actual	Comment	Reference
H	517	SER	-	expression tag	UNP P20839
H	518	GLY	-	expression tag	UNP P20839
H	519	CYS	-	expression tag	UNP P20839
H	520	THR	-	expression tag	UNP P20839
H	521	GLU	-	expression tag	UNP P20839
H	522	ASP	-	expression tag	UNP P20839
H	523	SER	-	expression tag	UNP P20839
H	524	GLY	-	expression tag	UNP P20839
H	525	GLY	-	expression tag	UNP P20839
H	526	GLY	-	expression tag	UNP P20839
H	527	ARG	-	expression tag	UNP P20839
H	528	GLY	-	expression tag	UNP P20839
H	529	GLY	-	expression tag	UNP P20839
H	530	GLY	-	expression tag	UNP P20839
H	531	GLY	-	expression tag	UNP P20839
H	532	ASP	-	expression tag	UNP P20839
H	533	ALA	-	expression tag	UNP P20839
H	534	PRO	-	expression tag	UNP P20839
H	535	GLN	-	expression tag	UNP P20839
H	536	CYS	-	expression tag	UNP P20839
H	537	PRO	-	expression tag	UNP P20839
H	538	LEU	-	expression tag	UNP P20839
H	539	LEU	-	expression tag	UNP P20839
H	540	GLY	-	expression tag	UNP P20839
H	541	THR	-	expression tag	UNP P20839
H	542	ALA	-	expression tag	UNP P20839
H	543	SER	-	expression tag	UNP P20839
H	544	LEU	-	expression tag	UNP P20839
H	545	HIS	-	expression tag	UNP P20839
H	546	ASN	-	expression tag	UNP P20839

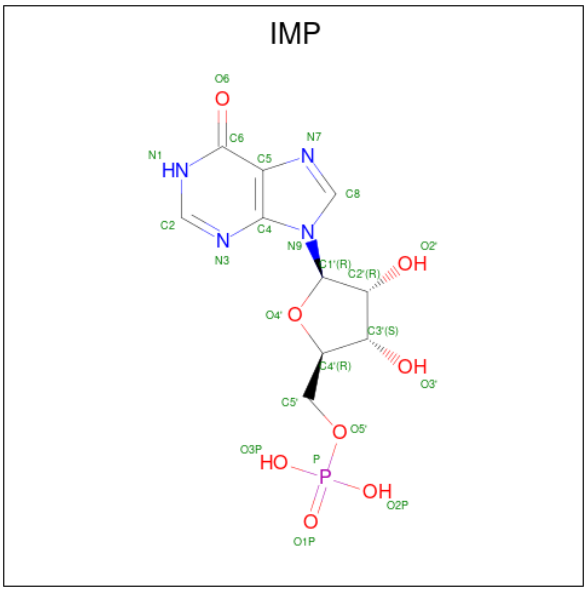
- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).

NAD



Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
2	A	1	70	21	26	7	14	2	0
2	B	1	70	21	26	7	14	2	0
2	C	1	70	21	26	7	14	2	0
2	D	1	70	21	26	7	14	2	0
2	E	1	70	21	26	7	14	2	0
2	F	1	70	21	26	7	14	2	0
2	G	1	70	21	26	7	14	2	0
2	H	1	70	21	26	7	14	2	0

- Molecule 3 is INOSINIC ACID (three-letter code: IMP) (formula: $C_{10}H_{13}N_4O_8P$) (labeled as "Ligand of Interest" by depositor).



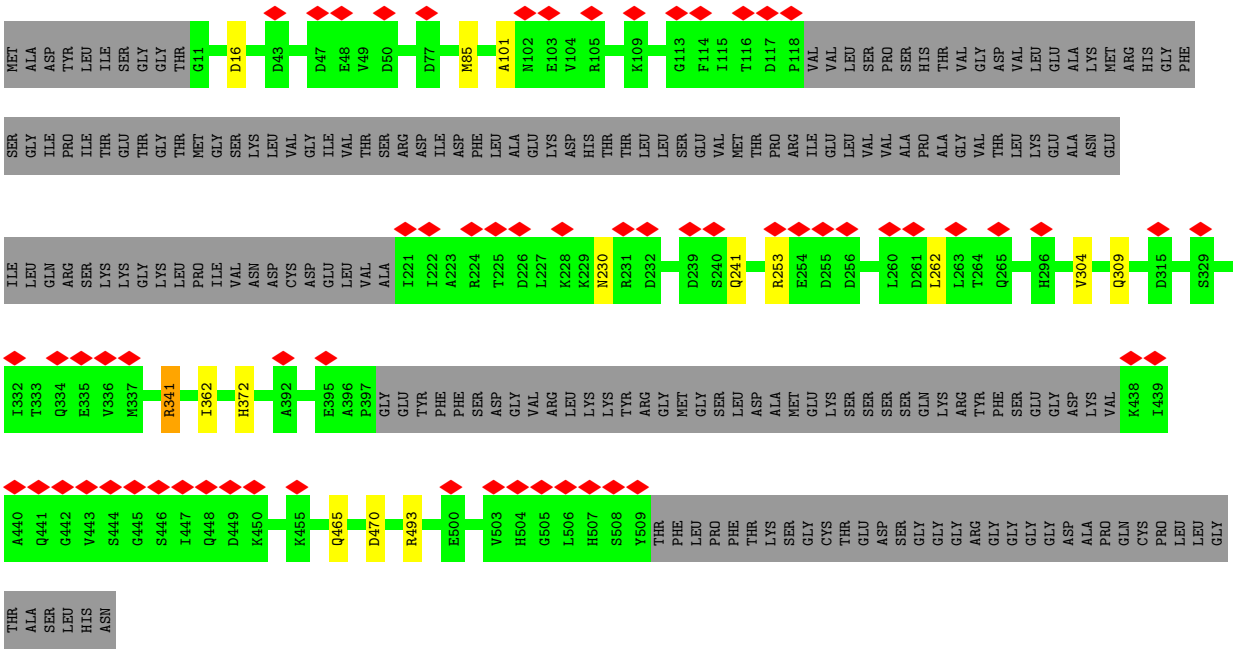
Mol	Chain	Residues	Atoms						AltConf
3	A	1	Total	C	H	N	O	P	0
			34	10	11	4	8	1	
3	B	1	Total	C	H	N	O	P	0
			34	10	11	4	8	1	
3	C	1	Total	C	H	N	O	P	0
			34	10	11	4	8	1	
3	D	1	Total	C	H	N	O	P	0
			34	10	11	4	8	1	
3	E	1	Total	C	H	N	O	P	0
			34	10	11	4	8	1	
3	F	1	Total	C	H	N	O	P	0
			34	10	11	4	8	1	
3	G	1	Total	C	H	N	O	P	0
			34	10	11	4	8	1	
3	H	1	Total	C	H	N	O	P	0
			34	10	11	4	8	1	

3 Residue-property plots (i)

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

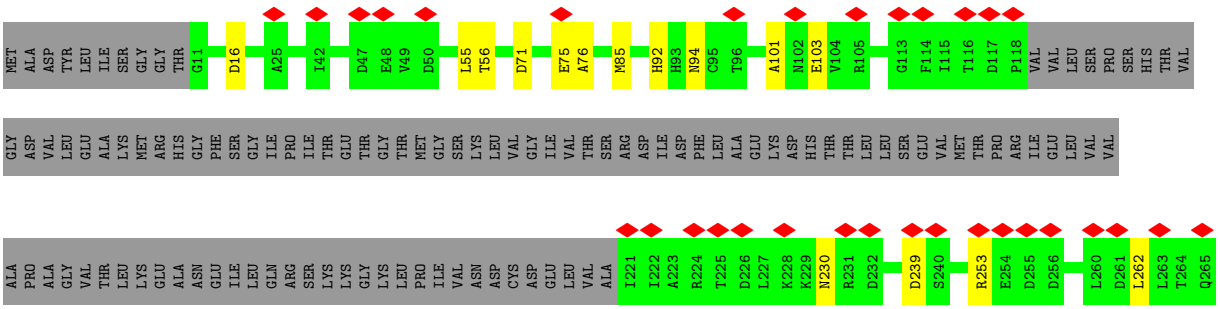
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 1

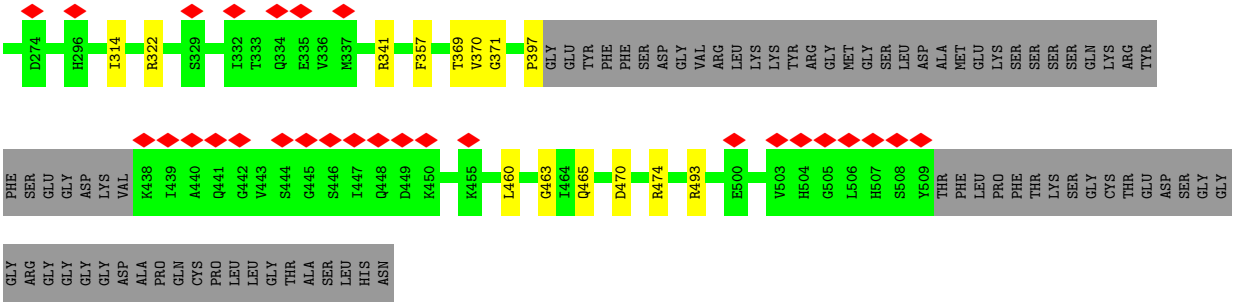
Chain A:



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 1

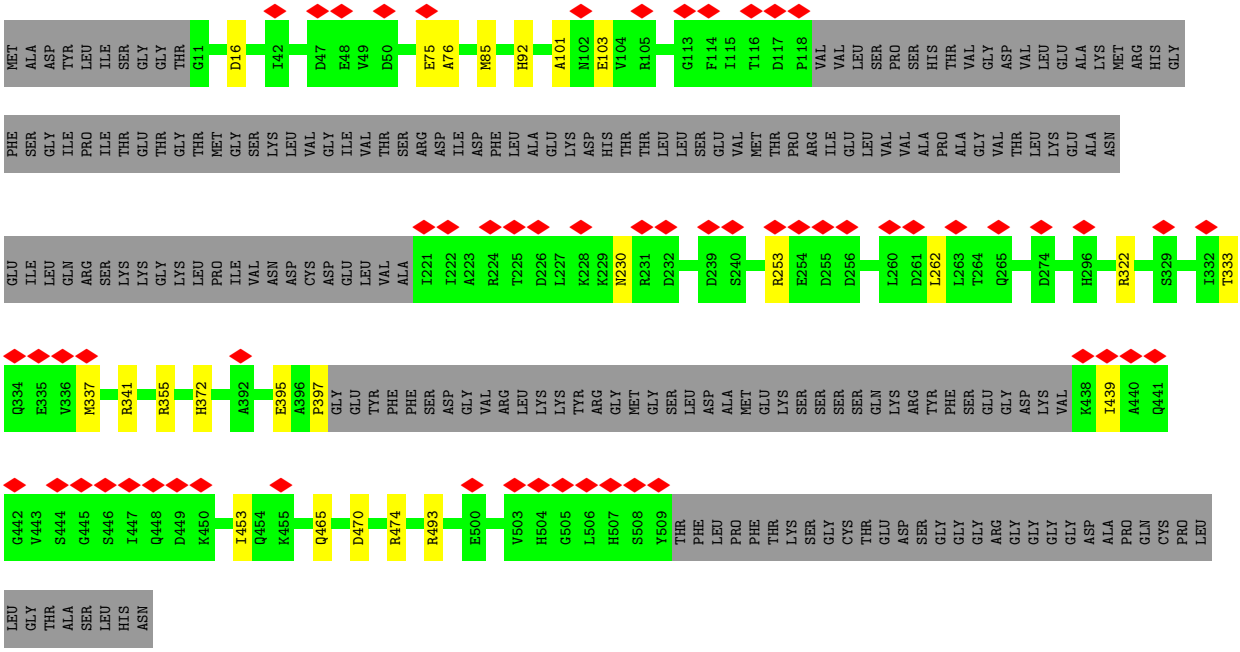
Chain B:





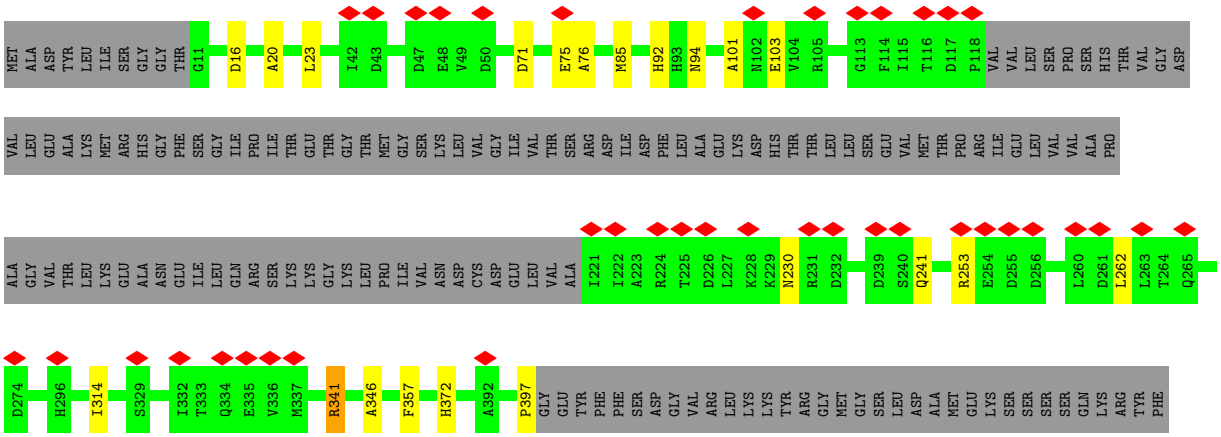
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 1

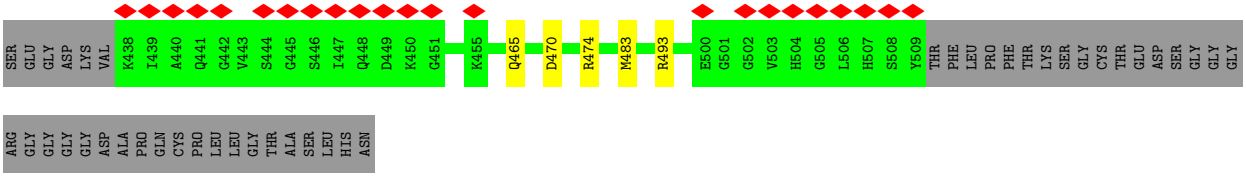
Chain C:



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 1

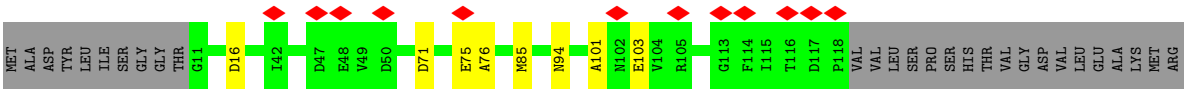
Chain D:

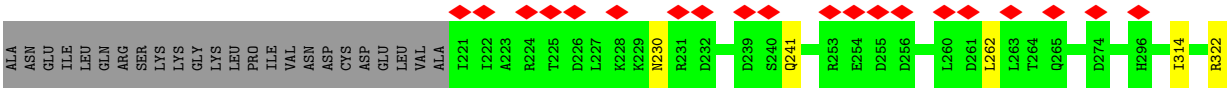


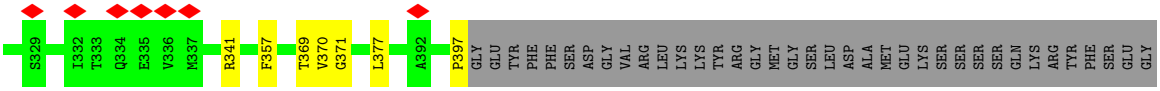


• Molecule 1: Inosine-5'-monophosphate dehydrogenase 1

Chain E:

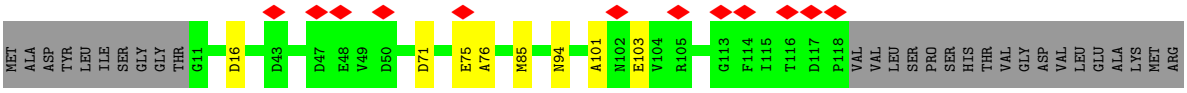


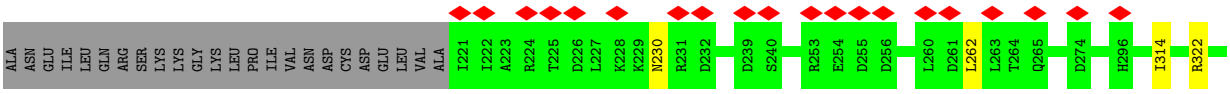


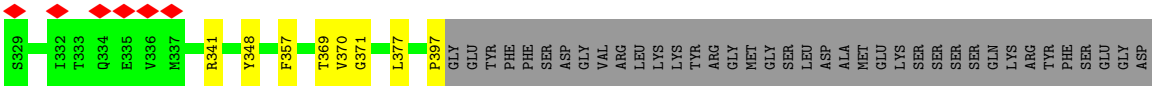


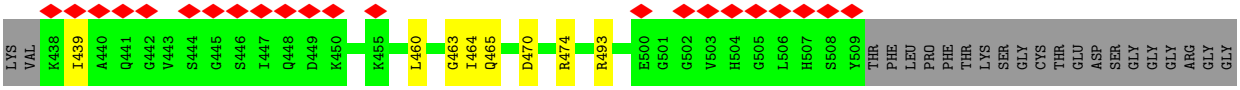
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 1

Chain F:



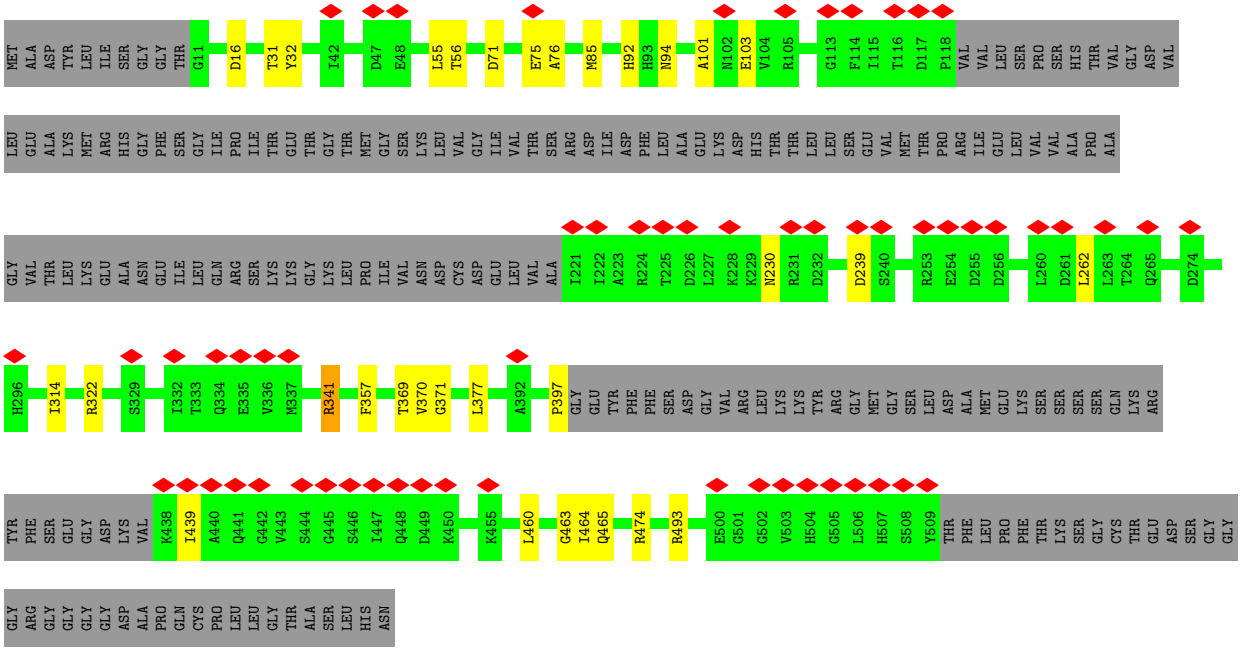






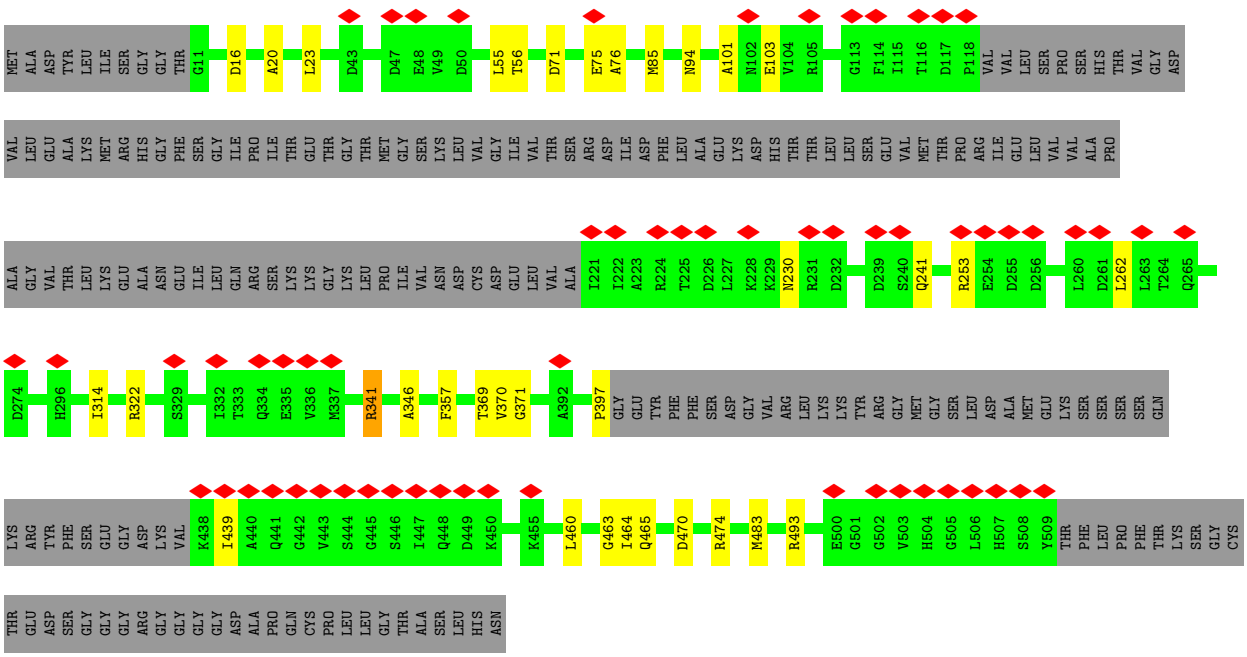
• Molecule 1: Inosine-5'-monophosphate dehydrogenase 1

Chain G:



• Molecule 1: Inosine-5'-monophosphate dehydrogenase 1

Chain H:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66449	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	10.358	Depositor
Minimum map value	-7.982	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.198	Depositor
Recommended contour level	1.57	Depositor
Map size (Å)	371.19998, 371.19998, 371.19998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.54	0/2718	0.92	3/3670 (0.1%)
1	B	0.53	0/2718	0.89	5/3670 (0.1%)
1	C	0.55	0/2718	0.94	6/3670 (0.2%)
1	D	0.54	0/2718	0.90	5/3670 (0.1%)
1	E	0.53	0/2718	0.87	4/3670 (0.1%)
1	F	0.54	0/2718	0.88	4/3670 (0.1%)
1	G	0.54	0/2718	0.88	4/3670 (0.1%)
1	H	0.53	0/2718	0.86	6/3670 (0.2%)
All	All	0.54	0/21744	0.89	37/29360 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	F	0	1
1	G	0	1
All	All	0	3

There are no bond length outliers.

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	341	ARG	NE-CZ-NH1	10.69	125.64	120.30
1	D	341	ARG	NE-CZ-NH1	10.09	125.34	120.30
1	H	341	ARG	NE-CZ-NH1	9.53	125.07	120.30
1	E	341	ARG	NE-CZ-NH1	9.42	125.01	120.30
1	B	341	ARG	NE-CZ-NH1	9.41	125.01	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	341	ARG	NE-CZ-NH1	9.33	124.97	120.30
1	C	341	ARG	NE-CZ-NH1	9.18	124.89	120.30
1	G	341	ARG	NE-CZ-NH1	9.14	124.87	120.30
1	B	474	ARG	NE-CZ-NH2	6.95	123.78	120.30
1	C	355	ARG	NE-CZ-NH2	6.90	123.75	120.30
1	D	474	ARG	NE-CZ-NH2	6.87	123.74	120.30
1	G	322	ARG	NE-CZ-NH1	6.84	123.72	120.30
1	H	474	ARG	NE-CZ-NH2	6.84	123.72	120.30
1	F	322	ARG	NE-CZ-NH1	6.83	123.72	120.30
1	C	474	ARG	NE-CZ-NH2	6.76	123.68	120.30
1	G	493	ARG	NE-CZ-NH1	6.65	123.62	120.30
1	H	493	ARG	NE-CZ-NH1	6.65	123.62	120.30
1	D	493	ARG	NE-CZ-NH1	6.56	123.58	120.30
1	F	493	ARG	NE-CZ-NH1	6.55	123.57	120.30
1	E	474	ARG	NE-CZ-NH2	6.47	123.54	120.30
1	F	474	ARG	NE-CZ-NH2	6.33	123.46	120.30
1	B	322	ARG	NE-CZ-NH1	6.29	123.45	120.30
1	H	322	ARG	NE-CZ-NH1	6.20	123.40	120.30
1	E	493	ARG	NE-CZ-NH1	6.14	123.37	120.30
1	C	322	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	E	322	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	A	493	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	B	493	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	C	493	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	H	23	LEU	CA-CB-CG	5.39	127.70	115.30
1	D	23	LEU	CA-CB-CG	5.38	127.66	115.30
1	A	253	ARG	NE-CZ-NH2	5.29	122.94	120.30
1	G	474	ARG	NE-CZ-NH2	5.21	122.91	120.30
1	B	253	ARG	NE-CZ-NH2	5.11	122.86	120.30
1	D	253	ARG	NE-CZ-NH2	5.11	122.85	120.30
1	C	253	ARG	NE-CZ-NH2	5.08	122.84	120.30
1	H	253	ARG	NE-CZ-NH2	5.07	122.83	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	341	ARG	Sidechain
1	F	348	TYR	Sidechain
1	G	341	ARG	Sidechain

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	2678	2719	2715	2	0
1	B	2678	2719	2715	10	0
1	C	2678	2719	2715	5	0
1	D	2678	2719	2715	8	0
1	E	2678	2719	2715	11	0
1	F	2678	2719	2715	11	0
1	G	2678	2719	2715	13	0
1	H	2678	2719	2715	14	0
2	A	44	26	26	0	0
2	B	44	26	26	0	0
2	C	44	26	26	0	0
2	D	44	26	26	0	0
2	E	44	26	26	0	0
2	F	44	26	26	0	0
2	G	44	26	26	0	0
2	H	44	26	26	0	0
3	A	23	11	11	0	0
3	B	23	11	11	0	0
3	C	23	11	11	0	0
3	D	23	11	11	0	0
3	E	23	11	11	0	0
3	F	23	11	11	0	0
3	G	23	11	11	0	0
3	H	23	11	11	0	0
All	All	21960	22048	22016	69	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 2.

All (69) 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:D:75:GLU:HB2	1:D:397:PRO:HG3	1.73	0.70
1:H:75:GLU:HB2	1:H:397:PRO:HG3	1.73	0.70
1:B:75:GLU:HB2	1:B:397:PRO:HG3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:75:GLU:HB2	1:F:397:PRO:HG3	1.73	0.70
1:E:75:GLU:HB2	1:E:397:PRO:HG3	1.73	0.69
1:C:75:GLU:HB2	1:C:397:PRO:HG3	1.73	0.69
1:G:75:GLU:HB2	1:G:397:PRO:HG3	1.73	0.69
1:F:377:LEU:HD12	1:F:464:ILE:HD11	1.92	0.52
1:B:71:ASP:OD2	1:B:94:ASN:ND2	2.43	0.52
1:F:71:ASP:OD2	1:F:94:ASN:ND2	2.43	0.51
1:B:370:VAL:HG22	1:B:460:LEU:HD23	1.94	0.50
1:D:314:ILE:HD13	1:D:357:PHE:HD2	1.76	0.50
1:F:370:VAL:HG22	1:F:460:LEU:HD23	1.94	0.50
1:E:314:ILE:HD13	1:E:357:PHE:HD2	1.76	0.50
1:H:314:ILE:HD13	1:H:357:PHE:HD2	1.77	0.49
1:E:71:ASP:OD2	1:E:94:ASN:ND2	2.43	0.49
1:G:370:VAL:HG22	1:G:460:LEU:HD23	1.94	0.49
1:G:314:ILE:HD13	1:G:357:PHE:HD2	1.76	0.49
1:E:370:VAL:HG22	1:E:460:LEU:HD23	1.94	0.49
1:F:314:ILE:HD13	1:F:357:PHE:HD2	1.76	0.49
1:H:370:VAL:HG22	1:H:460:LEU:HD23	1.94	0.49
1:B:314:ILE:HD13	1:B:357:PHE:HD2	1.76	0.49
1:D:71:ASP:OD2	1:D:94:ASN:ND2	2.43	0.47
1:H:71:ASP:OD2	1:H:94:ASN:ND2	2.43	0.47
1:G:369:THR:HG23	1:G:371:GLY:H	1.80	0.47
1:B:55:LEU:HD23	1:B:56:THR:HG23	1.97	0.46
1:G:71:ASP:OD2	1:G:94:ASN:ND2	2.43	0.46
1:G:55:LEU:HD23	1:G:56:THR:HG23	1.98	0.45
1:F:369:THR:HG23	1:F:371:GLY:H	1.81	0.45
1:B:369:THR:HG23	1:B:371:GLY:H	1.82	0.44
1:B:101:ALA:HB2	1:B:262:LEU:HB3	2.00	0.44
1:F:101:ALA:HB2	1:F:262:LEU:HB3	2.00	0.44
1:H:55:LEU:HD23	1:H:56:THR:HG23	1.99	0.44
1:C:101:ALA:HB2	1:C:262:LEU:HB3	2.00	0.44
1:G:101:ALA:HB2	1:G:262:LEU:HB3	2.00	0.44
1:H:369:THR:HG23	1:H:371:GLY:H	1.83	0.44
1:D:101:ALA:HB2	1:D:262:LEU:HB3	2.00	0.44
1:E:369:THR:HG23	1:E:371:GLY:H	1.81	0.44
1:H:101:ALA:HB2	1:H:262:LEU:HB3	2.00	0.44
1:A:101:ALA:HB2	1:A:262:LEU:HB3	2.00	0.43
1:C:333:THR:HG23	1:C:337:MET:SD	2.59	0.43
1:E:101:ALA:HB2	1:E:262:LEU:HB3	2.00	0.43
1:H:341:ARG:HG2	1:H:346:ALA:HB2	2.01	0.43
1:G:31:THR:HG22	1:G:32:TYR:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:76:ALA:HA	1:C:103:GLU:OE2	2.19	0.42
1:H:464:ILE:HD13	1:H:464:ILE:HG21	1.82	0.42
1:F:463:GLY:HA2	1:G:439:ILE:HD13	2.02	0.42
1:G:76:ALA:HA	1:G:103:GLU:OE2	2.19	0.42
1:B:463:GLY:HA2	1:C:439:ILE:HD13	2.02	0.42
1:D:341:ARG:HG2	1:D:346:ALA:HB2	2.00	0.42
1:F:76:ALA:HA	1:F:103:GLU:OE2	2.19	0.42
1:B:76:ALA:HA	1:B:103:GLU:OE2	2.19	0.42
1:D:314:ILE:HG21	1:D:357:PHE:CD2	2.55	0.42
1:H:314:ILE:HG21	1:H:357:PHE:CD2	2.55	0.42
1:E:314:ILE:HG21	1:E:357:PHE:CD2	2.55	0.41
1:G:463:GLY:HA2	1:H:439:ILE:HD13	2.02	0.41
1:E:439:ILE:HD13	1:H:463:GLY:HA2	2.02	0.41
1:A:304:VAL:HA	1:A:309:GLN:HE21	1.85	0.41
1:B:314:ILE:HG21	1:B:357:PHE:CD2	2.55	0.41
1:E:377:LEU:HD12	1:E:464:ILE:HD11	2.03	0.41
1:G:377:LEU:HD12	1:G:464:ILE:HD11	2.02	0.41
1:D:76:ALA:HA	1:D:103:GLU:OE2	2.19	0.41
1:F:314:ILE:HG21	1:F:357:PHE:CD2	2.55	0.41
1:H:76:ALA:HA	1:H:103:GLU:OE2	2.20	0.41
1:E:463:GLY:HA2	1:F:439:ILE:HD13	2.02	0.41
1:G:314:ILE:HG21	1:G:357:PHE:CD2	2.55	0.41
1:E:76:ALA:HA	1:E:103:GLU:OE2	2.19	0.41
1:D:20:ALA:HB1	1:D:483:MET:CE	2.51	0.40
1:H:20:ALA:HB1	1:H:483:MET:CE	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	351/546 (64%)	332 (95%)	18 (5%)	1 (0%)	41 75

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	351/546 (64%)	328 (93%)	23 (7%)	0	100	100
1	C	351/546 (64%)	330 (94%)	21 (6%)	0	100	100
1	D	351/546 (64%)	330 (94%)	20 (6%)	1 (0%)	41	75
1	E	351/546 (64%)	330 (94%)	20 (6%)	1 (0%)	41	75
1	F	351/546 (64%)	331 (94%)	20 (6%)	0	100	100
1	G	351/546 (64%)	328 (93%)	23 (7%)	0	100	100
1	H	351/546 (64%)	324 (92%)	26 (7%)	1 (0%)	41	75
All	All	2808/4368 (64%)	2633 (94%)	171 (6%)	4 (0%)	54	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	241	GLN
1	H	241	GLN
1	A	241	GLN
1	E	241	GLN

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	285/440 (65%)	278 (98%)	7 (2%)	47	75
1	B	285/440 (65%)	278 (98%)	7 (2%)	47	75
1	C	285/440 (65%)	276 (97%)	9 (3%)	39	70
1	D	285/440 (65%)	278 (98%)	7 (2%)	47	75
1	E	285/440 (65%)	280 (98%)	5 (2%)	59	81
1	F	285/440 (65%)	280 (98%)	5 (2%)	59	81
1	G	285/440 (65%)	279 (98%)	6 (2%)	53	78
1	H	285/440 (65%)	280 (98%)	5 (2%)	59	81
All	All	2280/3520 (65%)	2229 (98%)	51 (2%)	54	77

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	ASP
1	A	85	MET
1	A	230	ASN
1	A	362	ILE
1	A	372	HIS
1	A	465	GLN
1	A	470	ASP
1	B	16	ASP
1	B	85	MET
1	B	92	HIS
1	B	230	ASN
1	B	239	ASP
1	B	465	GLN
1	B	470	ASP
1	C	16	ASP
1	C	85	MET
1	C	92	HIS
1	C	230	ASN
1	C	372	HIS
1	C	395	GLU
1	C	453	ILE
1	C	465	GLN
1	C	470	ASP
1	D	16	ASP
1	D	85	MET
1	D	92	HIS
1	D	230	ASN
1	D	372	HIS
1	D	465	GLN
1	D	470	ASP
1	E	16	ASP
1	E	85	MET
1	E	230	ASN
1	E	465	GLN
1	E	470	ASP
1	F	16	ASP
1	F	85	MET
1	F	230	ASN
1	F	465	GLN
1	F	470	ASP
1	G	16	ASP
1	G	85	MET

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Mol	Chain	Res	Type
1	G	92	HIS
1	G	230	ASN
1	G	239	ASP
1	G	465	GLN
1	H	16	ASP
1	H	85	MET
1	H	230	ASN
1	H	465	GLN
1	H	470	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

16 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	$\#\|Z\| > 2$
3	IMP	E	601	-	21,25,25	1.25	3 (14%)	24,38,38	1.05	2 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	IMP	F	601	-	21,25,25	1.21	3 (14%)	24,38,38	0.93	1 (4%)
3	IMP	B	601	-	21,25,25	1.21	3 (14%)	24,38,38	0.94	1 (4%)
2	NAD	E	600	-	42,48,48	1.30	2 (4%)	50,73,73	1.26	4 (8%)
3	IMP	A	601	-	21,25,25	1.07	2 (9%)	24,38,38	1.15	1 (4%)
2	NAD	B	600	-	42,48,48	1.31	1 (2%)	50,73,73	1.29	4 (8%)
3	IMP	C	601	-	21,25,25	1.16	3 (14%)	24,38,38	0.92	0
3	IMP	D	601	-	21,25,25	1.17	3 (14%)	24,38,38	0.90	0
2	NAD	D	600	-	42,48,48	1.29	1 (2%)	50,73,73	1.17	3 (6%)
3	IMP	G	601	-	21,25,25	1.26	3 (14%)	24,38,38	1.03	2 (8%)
2	NAD	G	600	-	42,48,48	1.30	2 (4%)	50,73,73	1.23	4 (8%)
2	NAD	H	600	-	42,48,48	1.30	2 (4%)	50,73,73	1.26	4 (8%)
2	NAD	C	600	-	42,48,48	1.29	2 (4%)	50,73,73	1.27	5 (10%)
2	NAD	A	600	-	42,48,48	1.27	2 (4%)	50,73,73	1.23	4 (8%)
2	NAD	F	600	-	42,48,48	1.29	1 (2%)	50,73,73	1.29	5 (10%)
3	IMP	H	601	-	21,25,25	1.26	3 (14%)	24,38,38	1.06	2 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	IMP	E	601	-	-	3/6/26/26	0/3/3/3
3	IMP	F	601	-	-	0/6/26/26	0/3/3/3
3	IMP	B	601	-	-	0/6/26/26	0/3/3/3
2	NAD	E	600	-	-	5/26/62/62	0/5/5/5
3	IMP	A	601	-	-	1/6/26/26	0/3/3/3
2	NAD	B	600	-	-	4/26/62/62	0/5/5/5
3	IMP	C	601	-	-	1/6/26/26	0/3/3/3
3	IMP	D	601	-	-	1/6/26/26	0/3/3/3
2	NAD	D	600	-	-	4/26/62/62	0/5/5/5
3	IMP	G	601	-	-	3/6/26/26	0/3/3/3
2	NAD	G	600	-	-	4/26/62/62	0/5/5/5
2	NAD	H	600	-	-	4/26/62/62	0/5/5/5
2	NAD	C	600	-	-	4/26/62/62	0/5/5/5
2	NAD	A	600	-	-	5/26/62/62	0/5/5/5
2	NAD	F	600	-	-	1/26/62/62	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	IMP	H	601	-	-	3/6/26/26	0/3/3/3

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600	NAD	C3N-C7N	-6.44	1.40	1.50
2	E	600	NAD	C3N-C7N	-6.36	1.41	1.50
2	H	600	NAD	C3N-C7N	-6.31	1.41	1.50
2	D	600	NAD	C3N-C7N	-6.29	1.41	1.50
2	G	600	NAD	C3N-C7N	-6.27	1.41	1.50
2	C	600	NAD	C3N-C7N	-6.25	1.41	1.50
2	A	600	NAD	C3N-C7N	-6.24	1.41	1.50
2	F	600	NAD	C3N-C7N	-6.16	1.41	1.50
3	G	601	IMP	O4'-C1'	2.79	1.45	1.41
3	H	601	IMP	O4'-C1'	2.69	1.44	1.41
3	E	601	IMP	O4'-C1'	2.67	1.44	1.41
3	C	601	IMP	C5-C4	-2.64	1.36	1.43
3	B	601	IMP	O4'-C1'	2.58	1.44	1.41
3	F	601	IMP	C5-C4	-2.58	1.36	1.43
3	G	601	IMP	C5-C4	-2.57	1.36	1.43
3	H	601	IMP	C5-C4	-2.56	1.36	1.43
3	B	601	IMP	C5-C4	-2.56	1.36	1.43
3	D	601	IMP	C5-C4	-2.56	1.36	1.43
3	E	601	IMP	C5-C4	-2.54	1.36	1.43
3	A	601	IMP	C5-C4	-2.47	1.36	1.43
3	H	601	IMP	C2-N3	2.42	1.34	1.29
3	G	601	IMP	C2-N3	2.39	1.34	1.29
3	E	601	IMP	C2-N3	2.37	1.34	1.29
3	C	601	IMP	C2-N3	2.37	1.34	1.29
3	F	601	IMP	O4'-C1'	2.35	1.44	1.41
3	D	601	IMP	O4'-C1'	2.33	1.44	1.41
3	A	601	IMP	C2-N3	2.30	1.34	1.29
3	F	601	IMP	C2-N3	2.30	1.34	1.29
3	B	601	IMP	C2-N3	2.28	1.34	1.29
2	G	600	NAD	C8A-N7A	-2.26	1.30	1.34
3	D	601	IMP	C2-N3	2.24	1.33	1.29
2	C	600	NAD	C8A-N7A	-2.12	1.30	1.34
2	E	600	NAD	C8A-N7A	-2.09	1.31	1.34
2	A	600	NAD	C8A-N7A	-2.08	1.31	1.34
2	H	600	NAD	C8A-N7A	-2.06	1.31	1.34
3	C	601	IMP	O4'-C1'	2.02	1.43	1.41

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	600	NAD	PN-O3-PA	-4.95	115.83	132.83
2	C	600	NAD	PN-O3-PA	-4.90	116.03	132.83
2	G	600	NAD	PN-O3-PA	-4.89	116.04	132.83
2	H	600	NAD	PN-O3-PA	-4.88	116.08	132.83
2	A	600	NAD	PN-O3-PA	-4.84	116.23	132.83
2	E	600	NAD	PN-O3-PA	-4.77	116.45	132.83
2	F	600	NAD	PN-O3-PA	-4.67	116.80	132.83
3	A	601	IMP	O4'-C1'-C2'	-4.17	100.83	106.93
2	D	600	NAD	C5A-C6A-N6A	3.93	126.32	120.35
2	F	600	NAD	C5A-C6A-N6A	3.84	126.19	120.35
2	C	600	NAD	C5A-C6A-N6A	3.79	126.11	120.35
2	D	600	NAD	PN-O3-PA	-3.79	119.82	132.83
2	E	600	NAD	C5A-C6A-N6A	3.75	126.05	120.35
2	B	600	NAD	C5A-C6A-N6A	3.74	126.03	120.35
2	H	600	NAD	C5A-C6A-N6A	3.50	125.67	120.35
2	G	600	NAD	C5A-C6A-N6A	3.38	125.48	120.35
2	A	600	NAD	C5A-C6A-N6A	3.19	125.20	120.35
2	D	600	NAD	N6A-C6A-N1A	-2.94	112.48	118.57
3	E	601	IMP	O4'-C4'-C3'	-2.91	99.35	105.11
2	F	600	NAD	N6A-C6A-N1A	-2.87	112.61	118.57
3	H	601	IMP	O4'-C4'-C3'	-2.84	99.50	105.11
2	E	600	NAD	N6A-C6A-N1A	-2.79	112.78	118.57
2	C	600	NAD	N6A-C6A-N1A	-2.78	112.80	118.57
3	G	601	IMP	O4'-C4'-C3'	-2.77	99.63	105.11
2	B	600	NAD	N6A-C6A-N1A	-2.74	112.88	118.57
2	F	600	NAD	C6N-N1N-C2N	-2.71	119.50	121.97
2	H	600	NAD	N6A-C6A-N1A	-2.61	113.15	118.57
2	A	600	NAD	N6A-C6A-N1A	-2.45	113.48	118.57
2	B	600	NAD	C6N-N1N-C2N	-2.44	119.75	121.97
2	G	600	NAD	N6A-C6A-N1A	-2.44	113.52	118.57
3	F	601	IMP	O4'-C4'-C3'	-2.36	100.45	105.11
2	H	600	NAD	C6N-N1N-C2N	-2.29	119.89	121.97
3	B	601	IMP	O4'-C4'-C3'	-2.29	100.59	105.11
2	G	600	NAD	C6N-N1N-C2N	-2.24	119.93	121.97
3	H	601	IMP	O2P-P-O5'	2.24	112.68	106.73
2	E	600	NAD	C6N-N1N-C2N	-2.23	119.94	121.97
3	E	601	IMP	O2P-P-O5'	2.14	112.43	106.73
3	G	601	IMP	O2P-P-O5'	2.13	112.41	106.73
2	F	600	NAD	O7N-C7N-C3N	2.13	122.18	119.63
2	C	600	NAD	C6N-N1N-C2N	-2.09	120.07	121.97
2	A	600	NAD	O7N-C7N-C3N	2.09	122.13	119.63
2	C	600	NAD	O7N-C7N-N7N	-2.05	119.66	122.58

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	600	NAD	PA-O3-PN-O5D
2	A	600	NAD	C5D-O5D-PN-O3
2	A	600	NAD	C5D-O5D-PN-O1N
2	B	600	NAD	C5D-O5D-PN-O1N
2	C	600	NAD	C5D-O5D-PN-O1N
2	E	600	NAD	C5D-O5D-PN-O3
2	F	600	NAD	PA-O3-PN-O5D
2	G	600	NAD	C5D-O5D-PN-O1N
2	H	600	NAD	C5D-O5D-PN-O1N
3	E	601	IMP	C3'-C4'-C5'-O5'
3	G	601	IMP	C3'-C4'-C5'-O5'
3	H	601	IMP	C3'-C4'-C5'-O5'
3	E	601	IMP	O4'-C4'-C5'-O5'
3	G	601	IMP	O4'-C4'-C5'-O5'
3	H	601	IMP	O4'-C4'-C5'-O5'
2	D	600	NAD	C2N-C3N-C7N-O7N
2	E	600	NAD	O4D-C4D-C5D-O5D
2	D	600	NAD	C4N-C3N-C7N-O7N
2	B	600	NAD	C4D-C5D-O5D-PN
2	C	600	NAD	C4D-C5D-O5D-PN
2	H	600	NAD	C4D-C5D-O5D-PN
2	G	600	NAD	C4D-C5D-O5D-PN
3	G	601	IMP	C4'-C5'-O5'-P
2	D	600	NAD	C2N-C3N-C7N-N7N
2	E	600	NAD	PA-O3-PN-O5D
2	C	600	NAD	C5D-O5D-PN-O3
2	G	600	NAD	C5D-O5D-PN-O3
2	D	600	NAD	C4N-C3N-C7N-N7N
2	A	600	NAD	C4D-C5D-O5D-PN
3	E	601	IMP	C4'-C5'-O5'-P
3	H	601	IMP	C4'-C5'-O5'-P
2	E	600	NAD	C5D-O5D-PN-O1N
2	E	600	NAD	C3D-C4D-C5D-O5D
2	G	600	NAD	O4D-C4D-C5D-O5D
2	B	600	NAD	O4D-C4D-C5D-O5D
2	C	600	NAD	O4D-C4D-C5D-O5D
2	H	600	NAD	O4D-C4D-C5D-O5D
2	B	600	NAD	C5D-O5D-PN-O3
2	H	600	NAD	C5D-O5D-PN-O3
2	A	600	NAD	O4D-C4D-C5D-O5D

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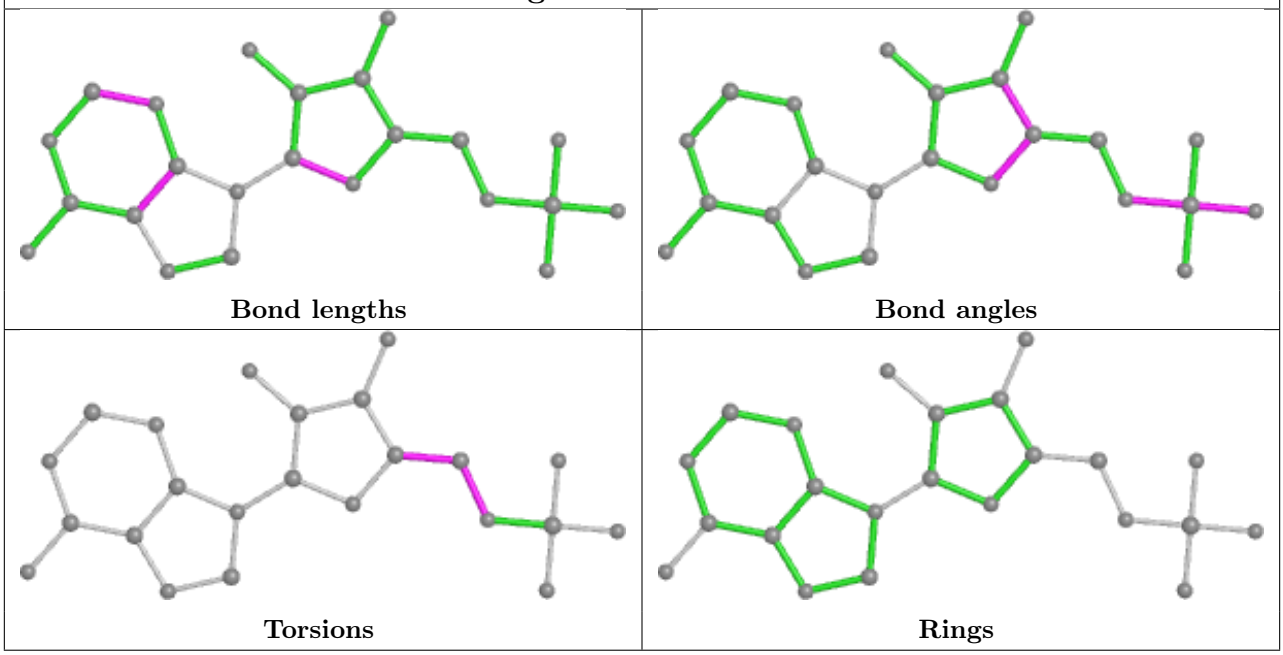
Mol	Chain	Res	Type	Atoms
3	A	601	IMP	O4'-C4'-C5'-O5'
3	C	601	IMP	O4'-C4'-C5'-O5'
3	D	601	IMP	O4'-C4'-C5'-O5'

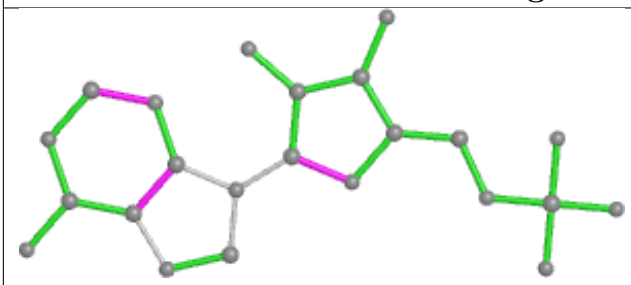
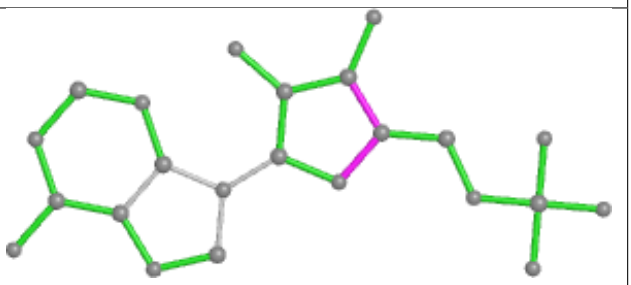
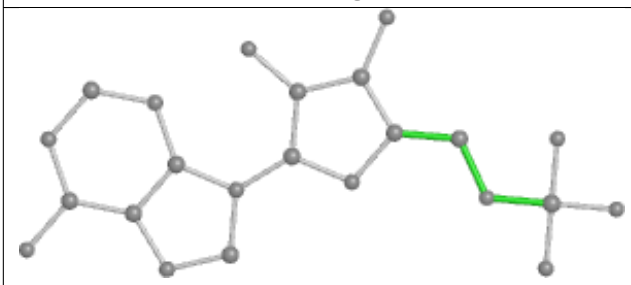
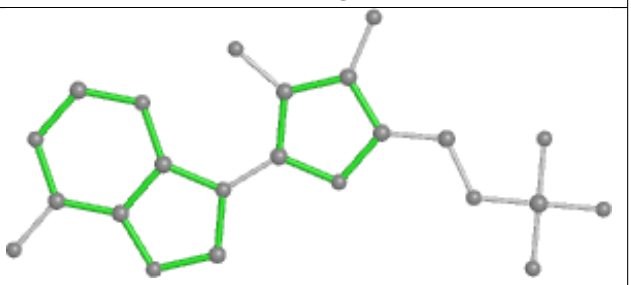
There are no ring outliers.

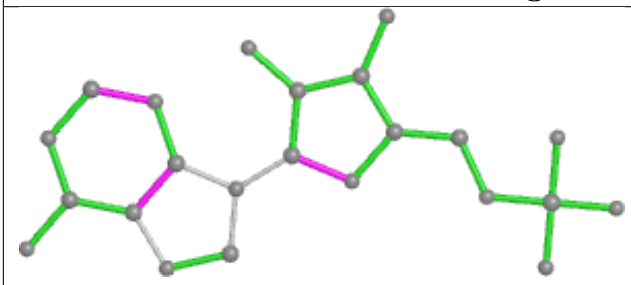
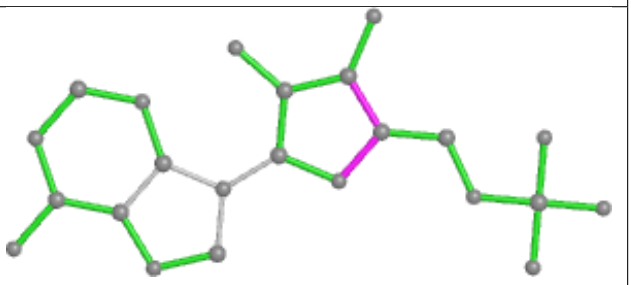
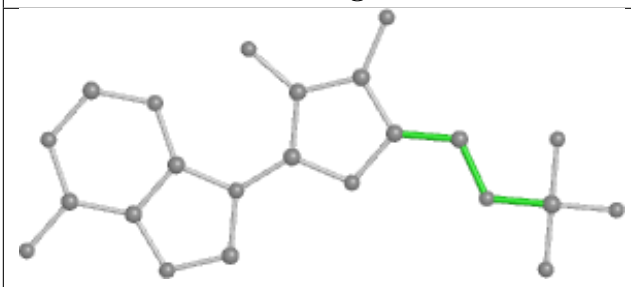
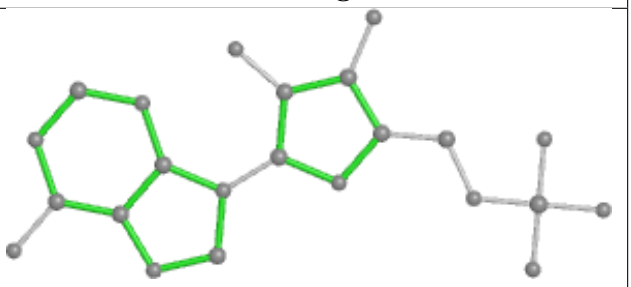
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

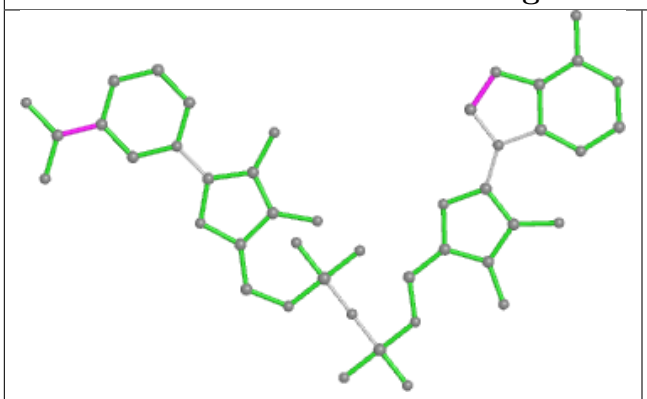
Ligand IMP E 601



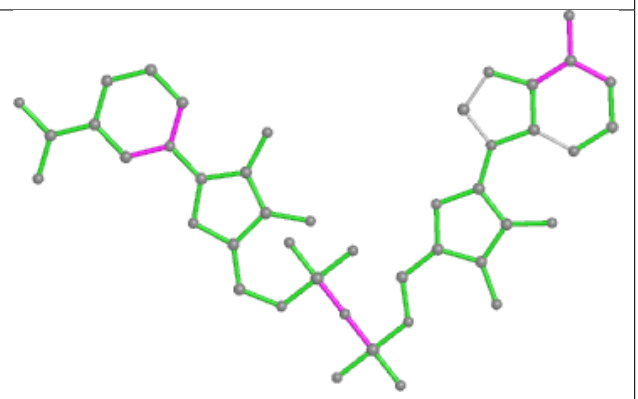
Ligand IMP F 601	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand IMP B 601	
 Bond lengths	 Bond angles
 Torsions	 Rings

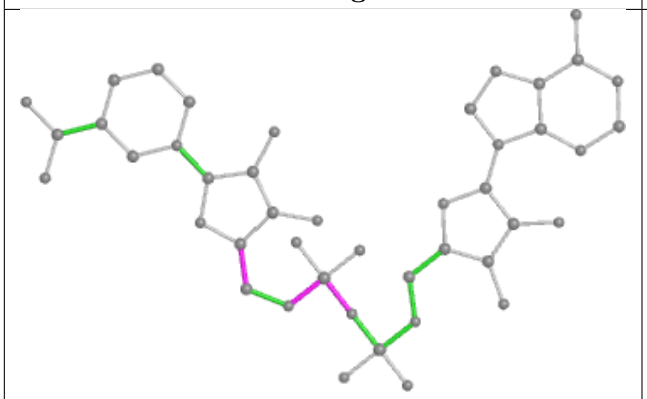
Ligand NAD E 600



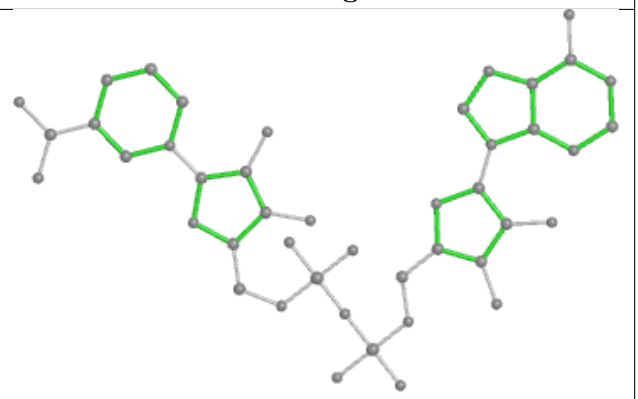
Bond lengths



Bond angles

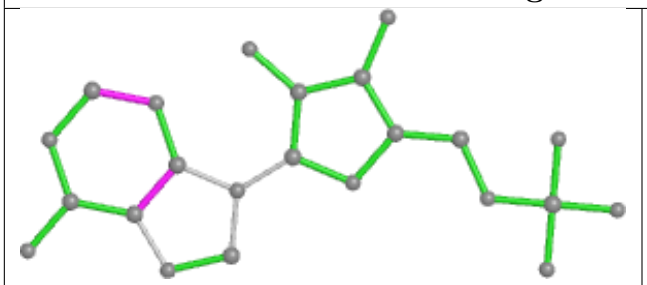


Torsions

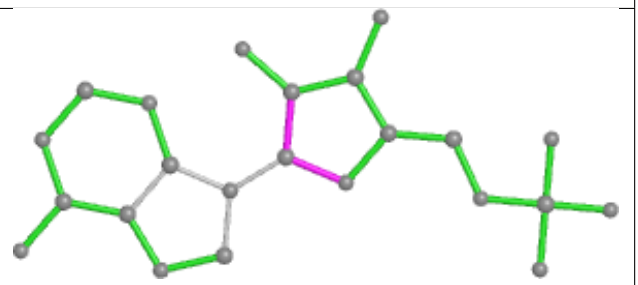


Rings

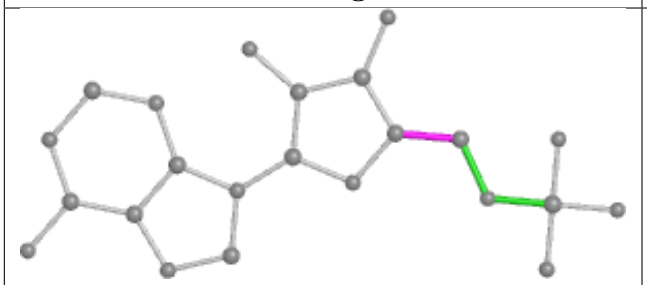
Ligand IMP A 601



Bond lengths



Bond angles



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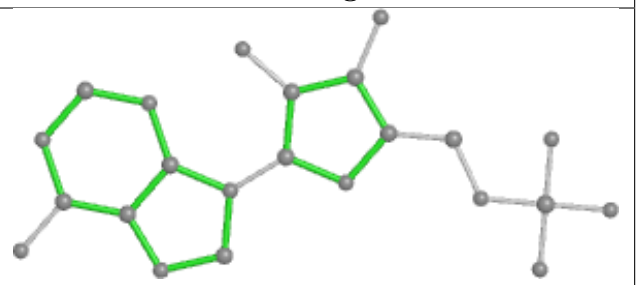
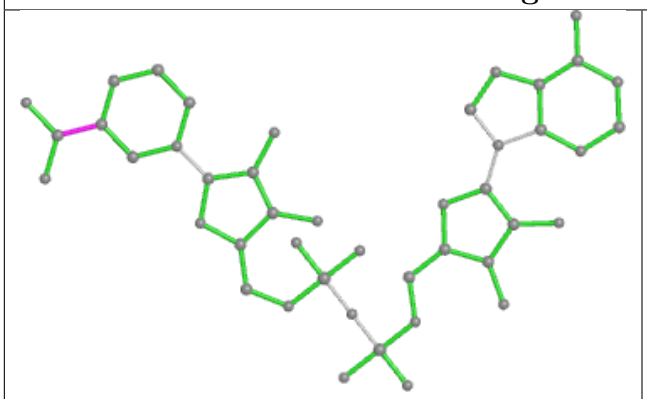


Rings

Ligand NAD B 600



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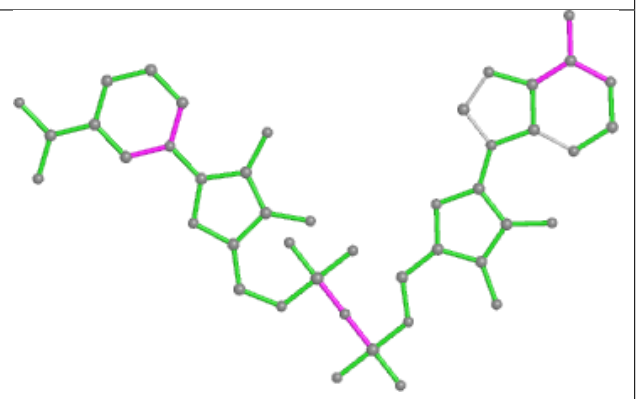
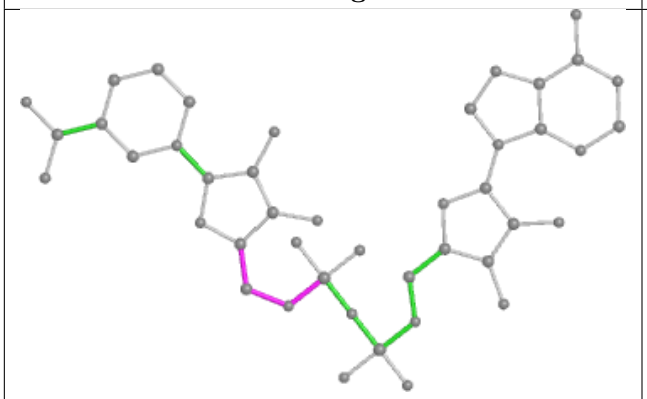
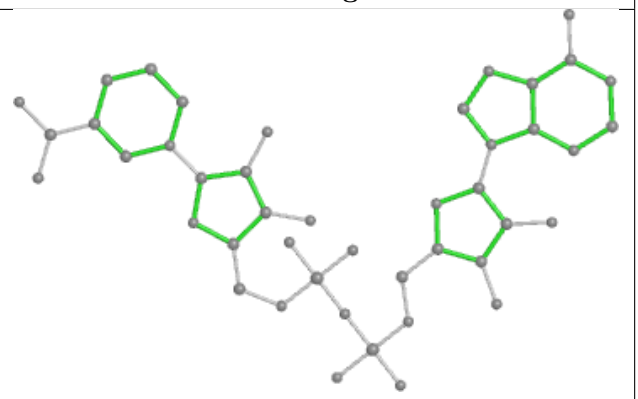


Bond angles

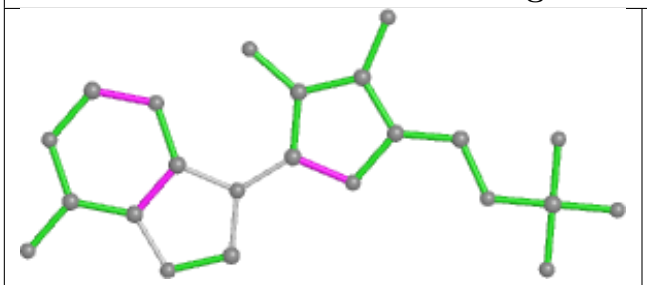


Torsions



Rings

Ligand IMP C 601



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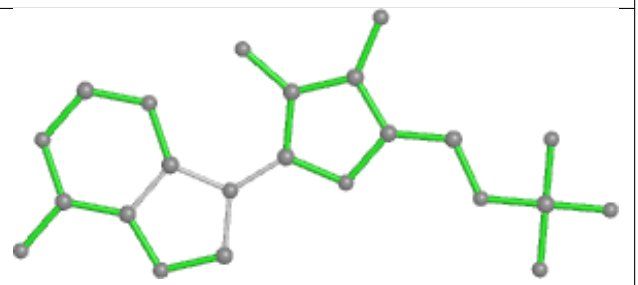
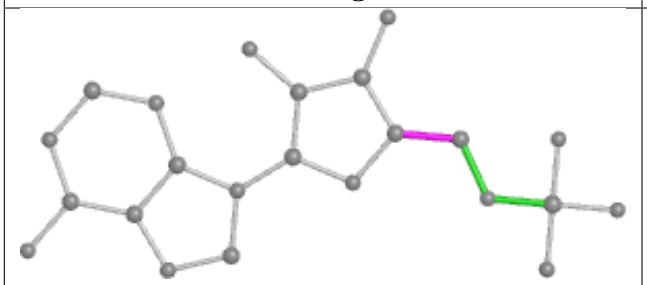


Bond angles



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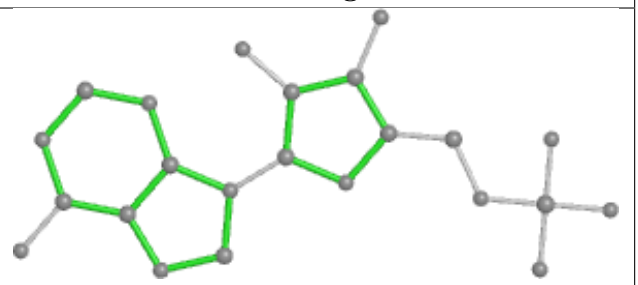
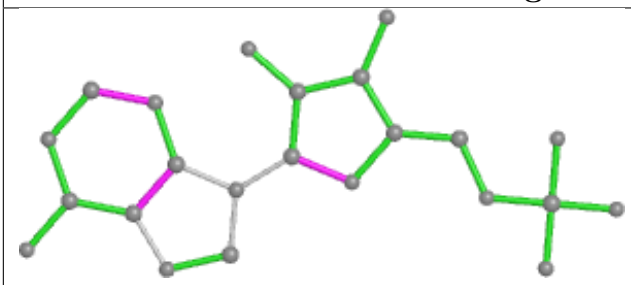
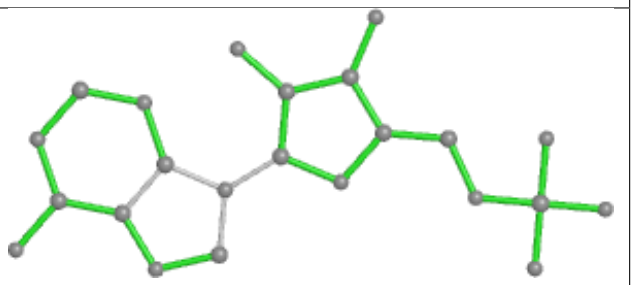


Rings

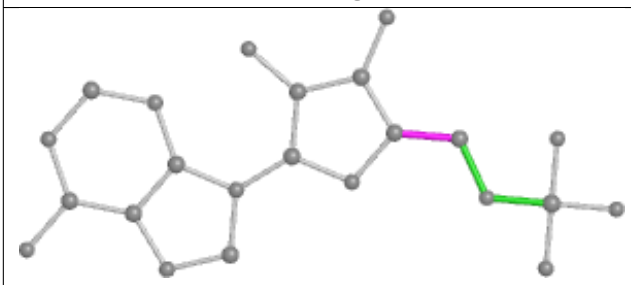
Ligand IMP D 601



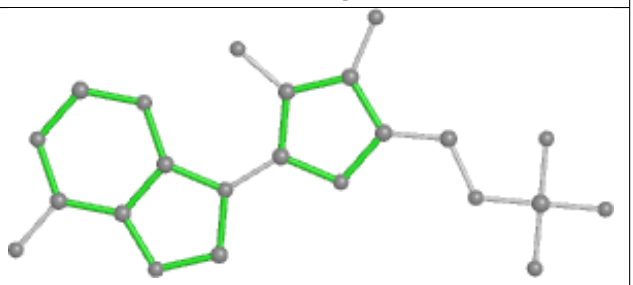
Bond lengths



Bond angles

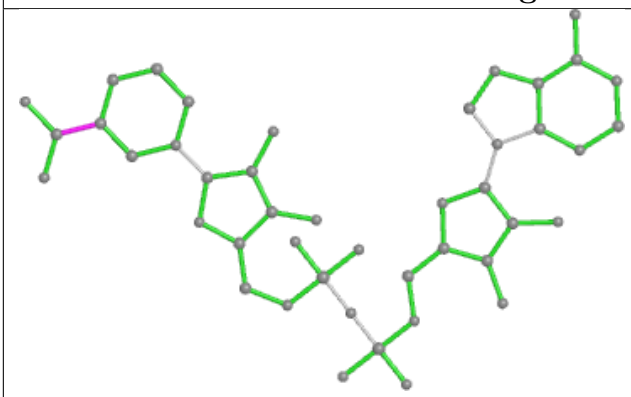


Torsions



Rings

Ligand NAD D 600



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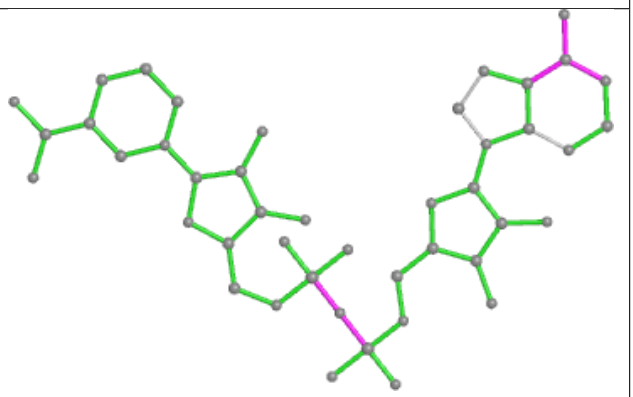
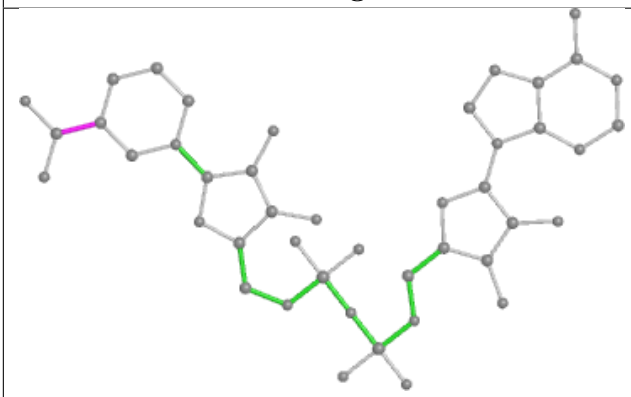


Bond angles



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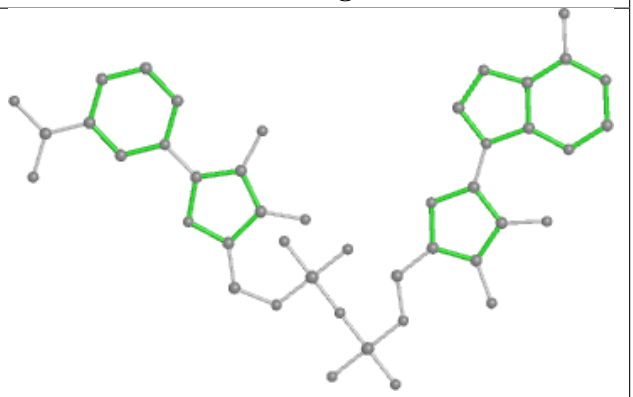
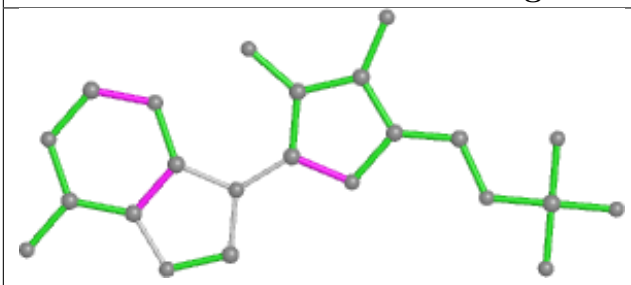


Rings

Ligand IMP G 601



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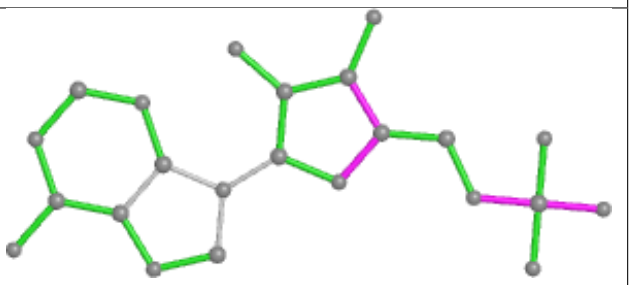
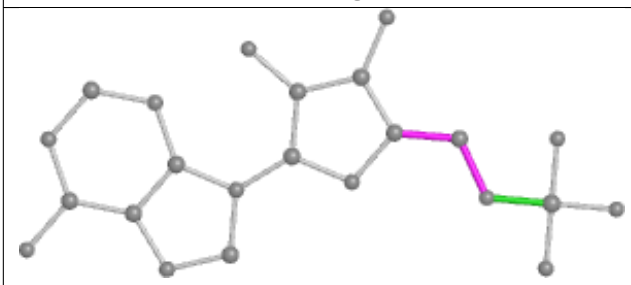


Bond angles



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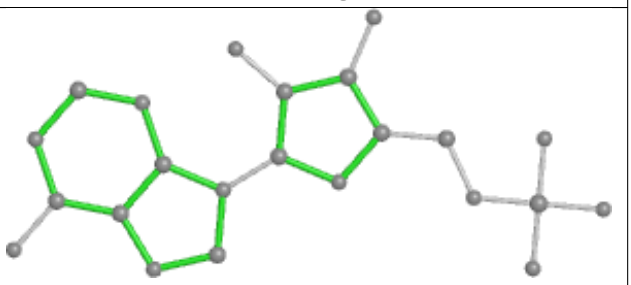
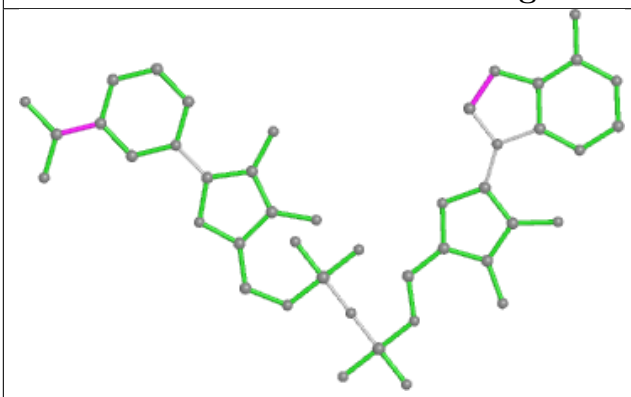


Rings

Ligand NAD G 600



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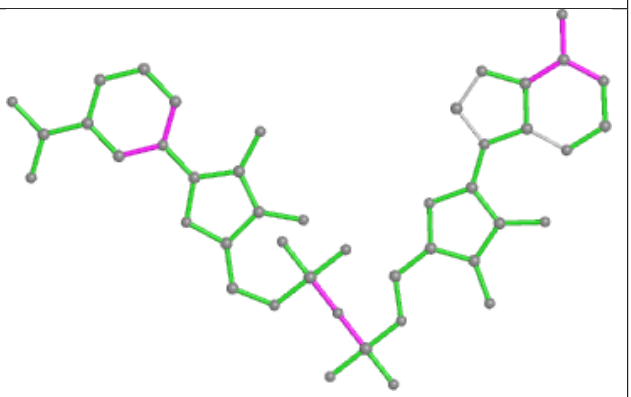

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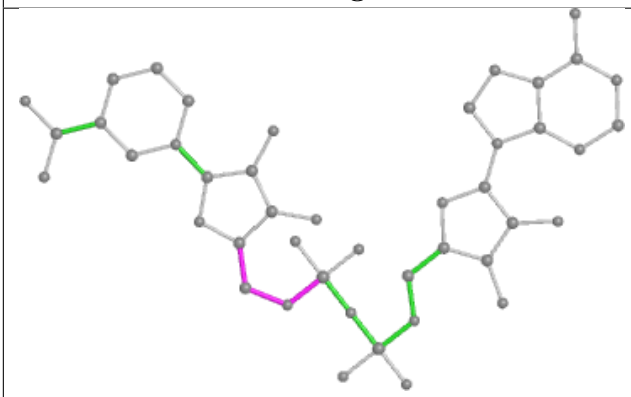
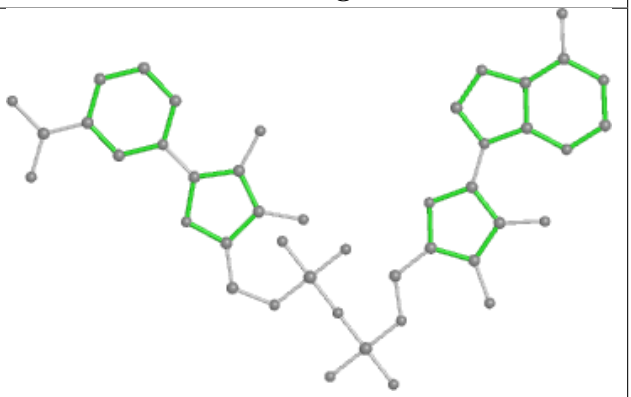
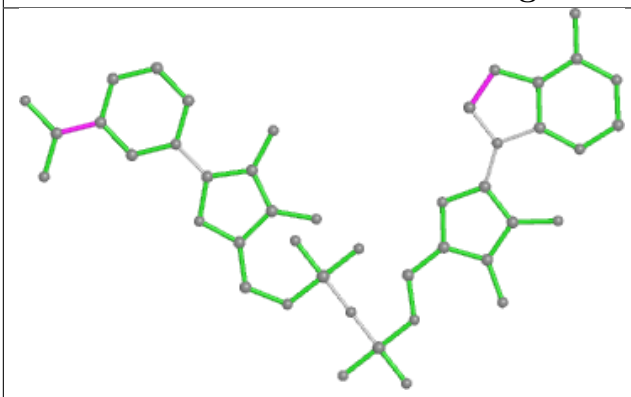
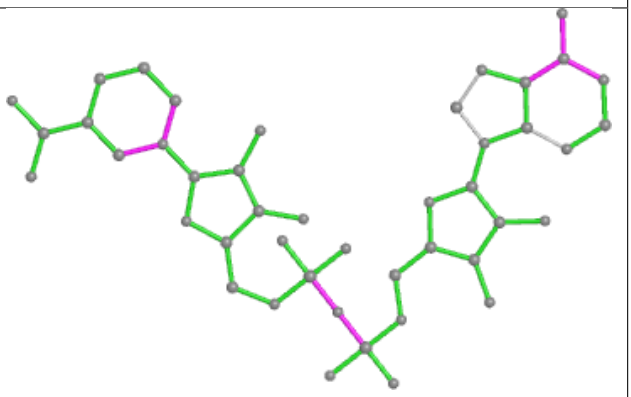
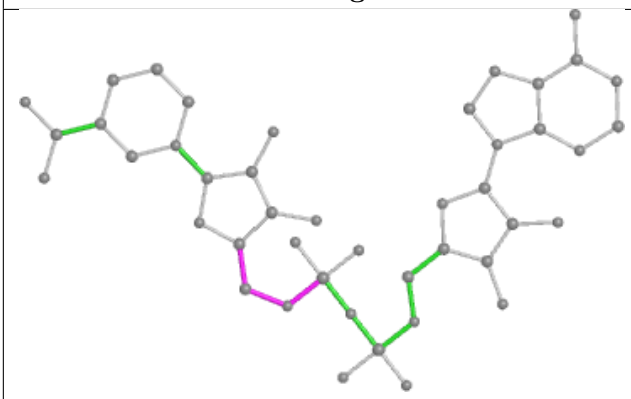
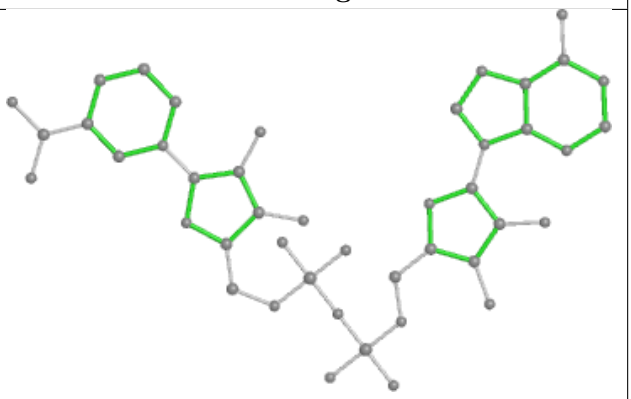
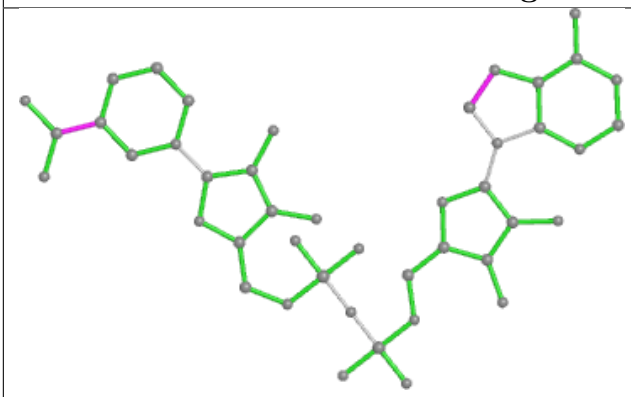
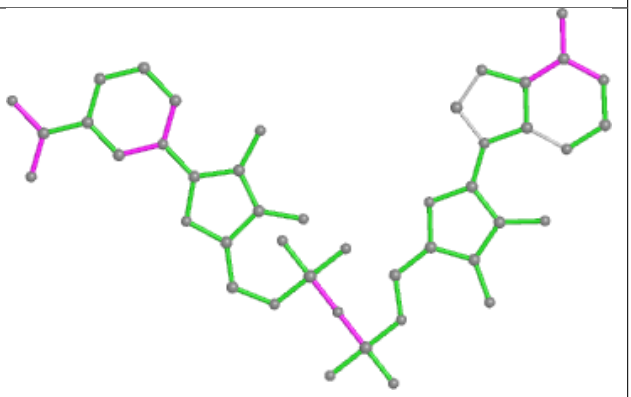
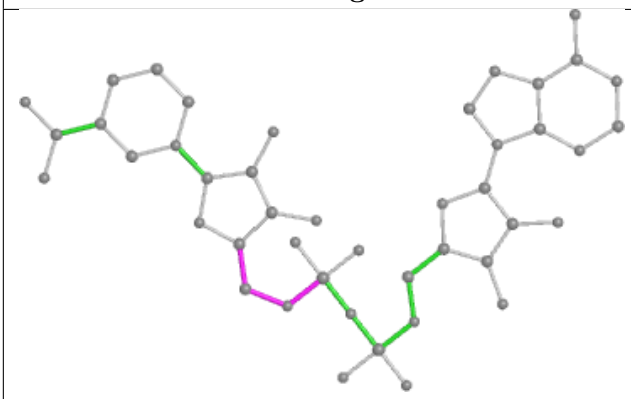
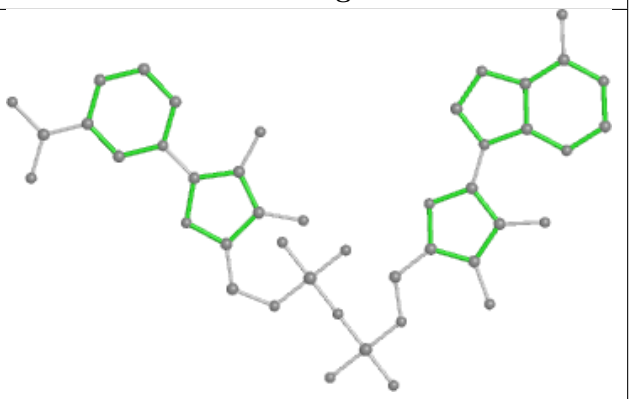


Torsions



Rings

Ligand NAD H 600	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand NAD C 600	
 Bond lengths	 Bond angles
 Torsions	 Rings

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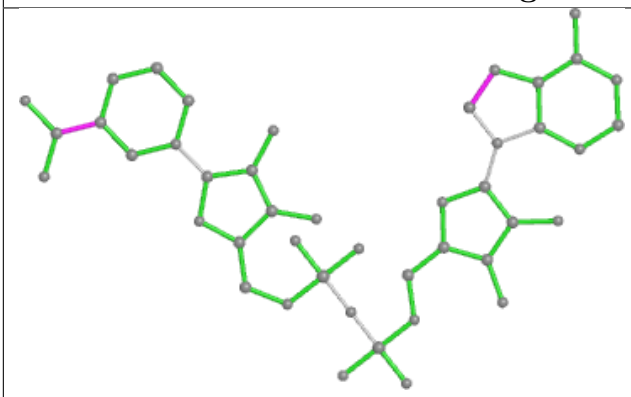
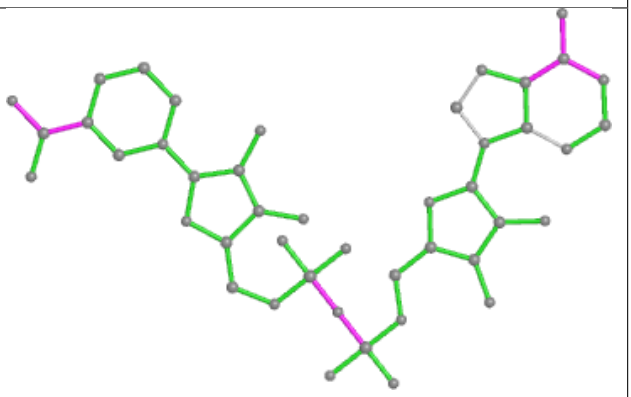
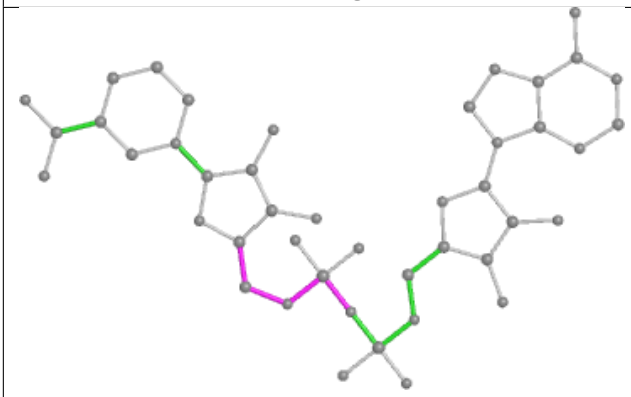
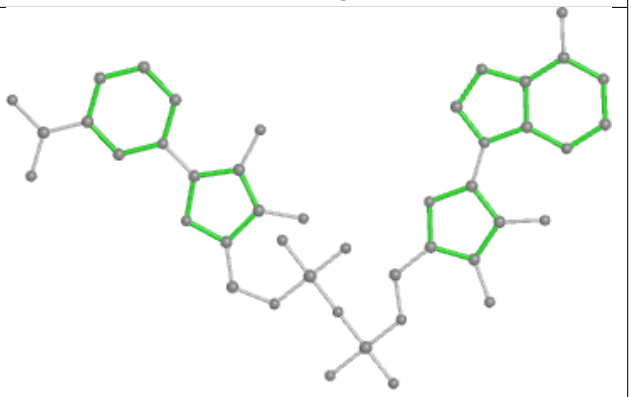
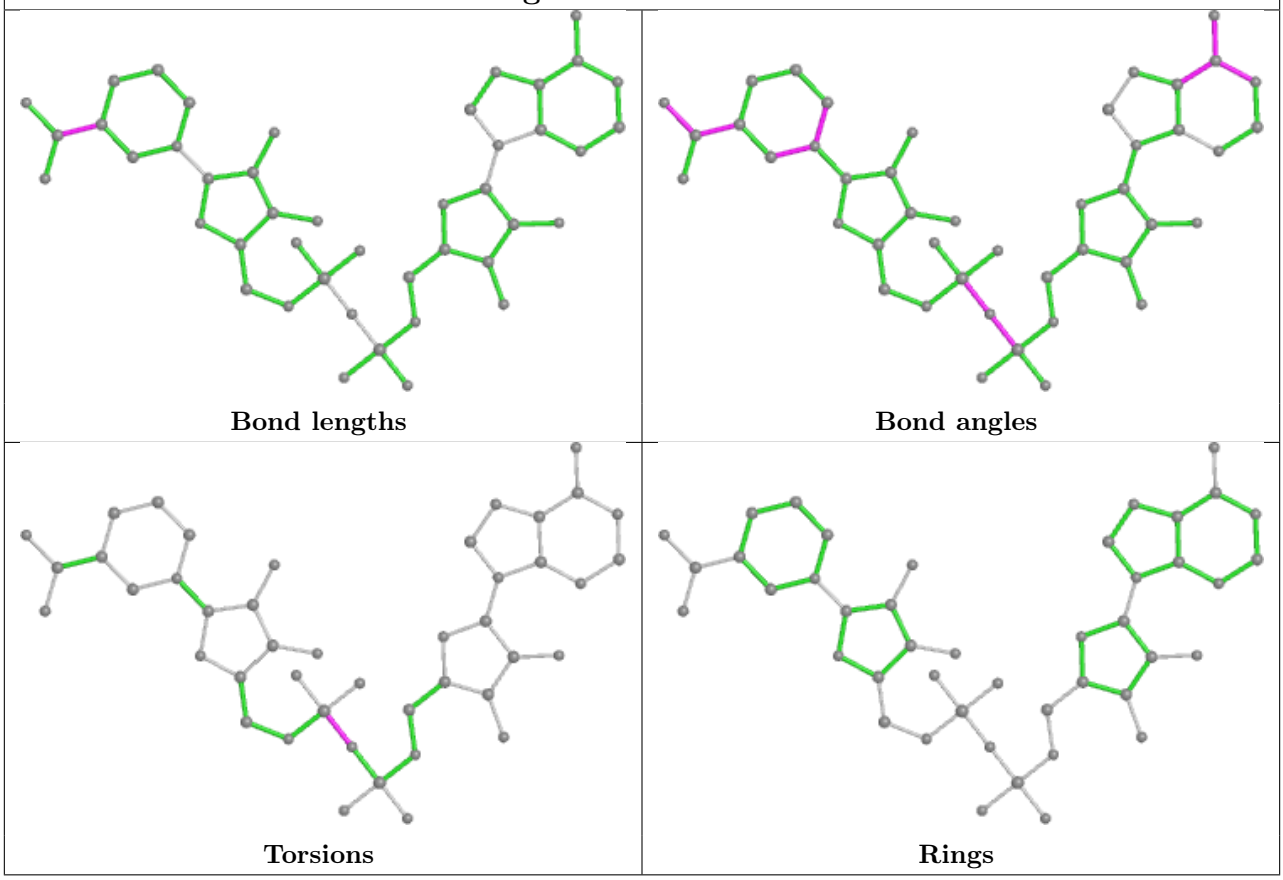
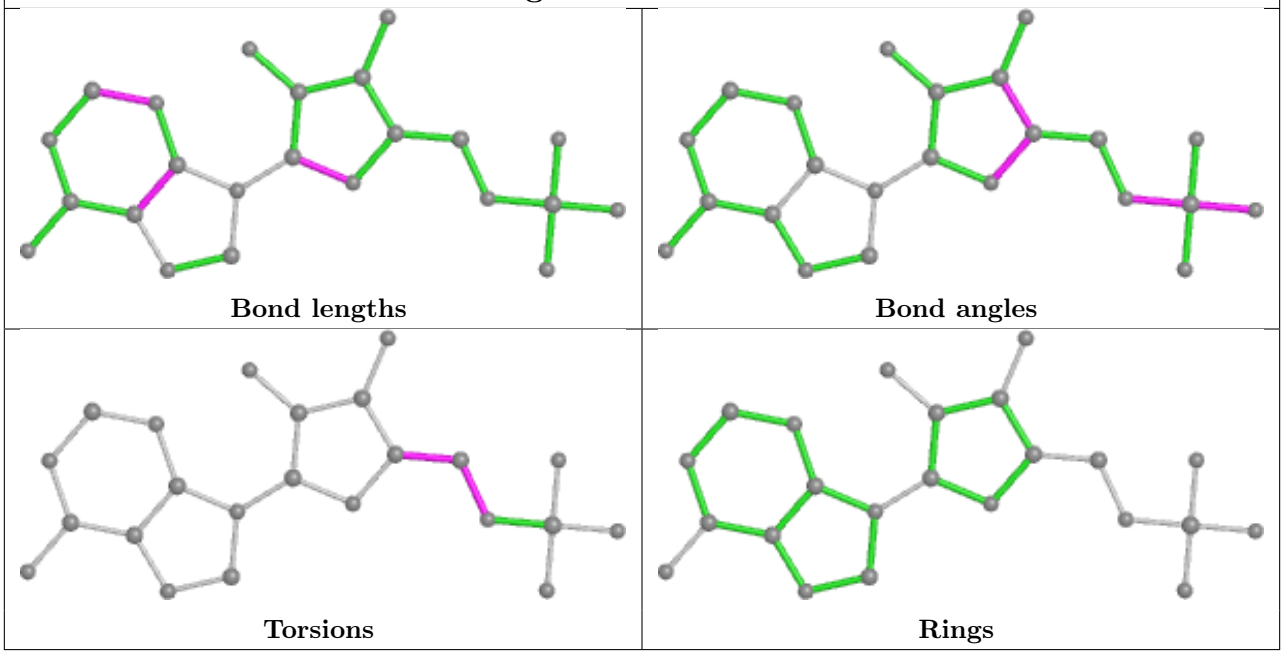
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand NAD F 600



Ligand IMP H 601



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.

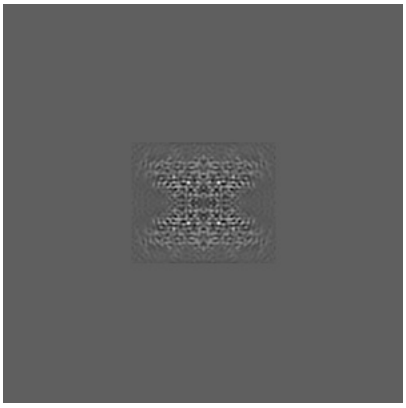
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-24450. These allow visual inspection of the internal detail of the map and identification of artifacts.

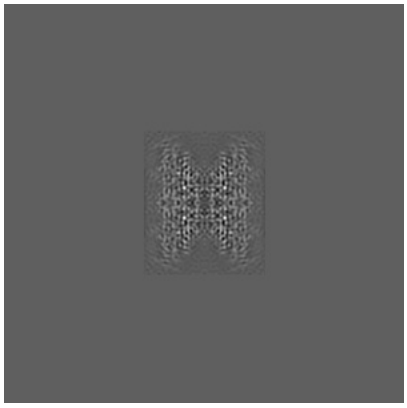
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

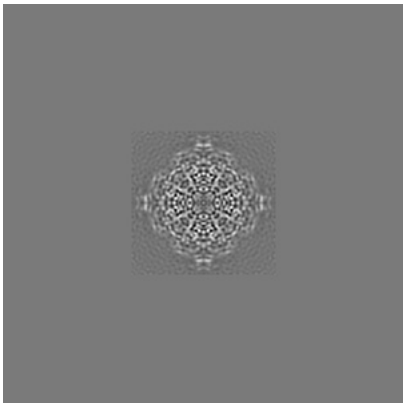
6.1.1 Primary map



X



Y

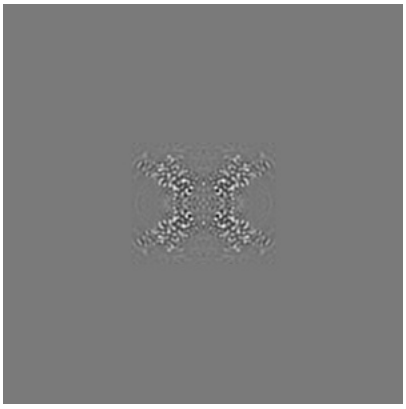


Z

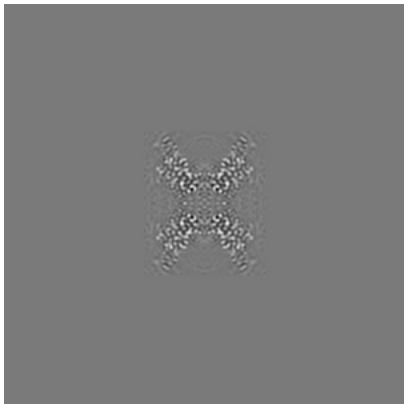
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

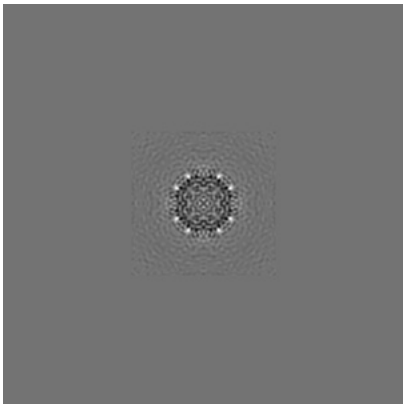
6.2.1 Primary map



X Index: 160



Y Index: 160

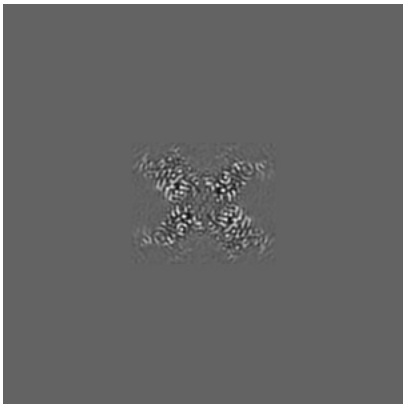


Z Index: 160

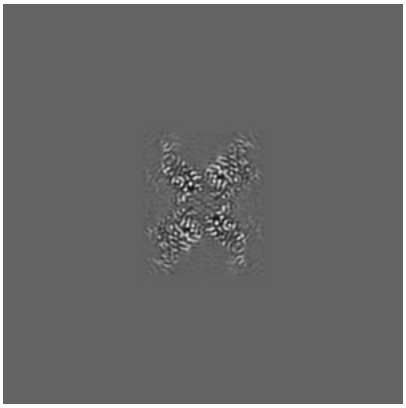
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 165



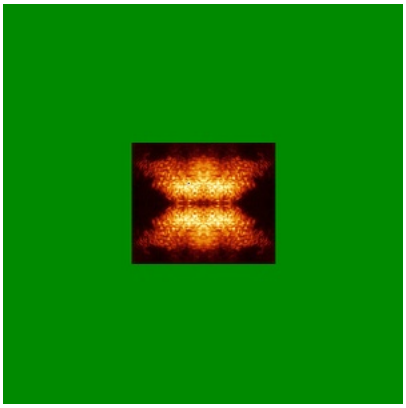
Y Index: 165

Z Index: 144

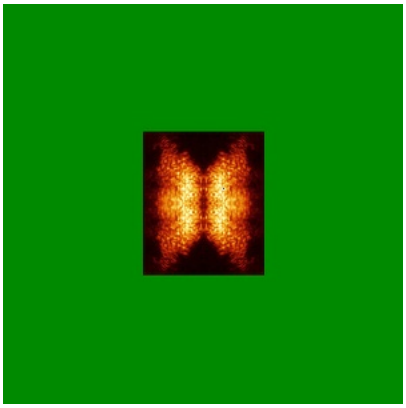
The images above show the largest variance slices of the map in three orthogonal directions.

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

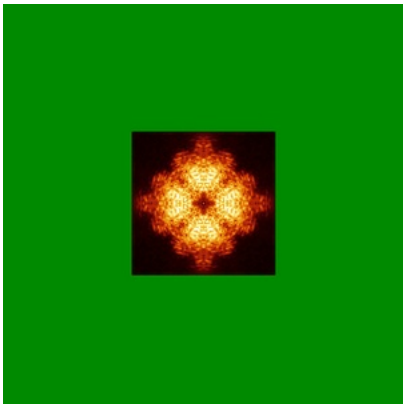
6.4.1 Primary map



X



Y



Z

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 1.57. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

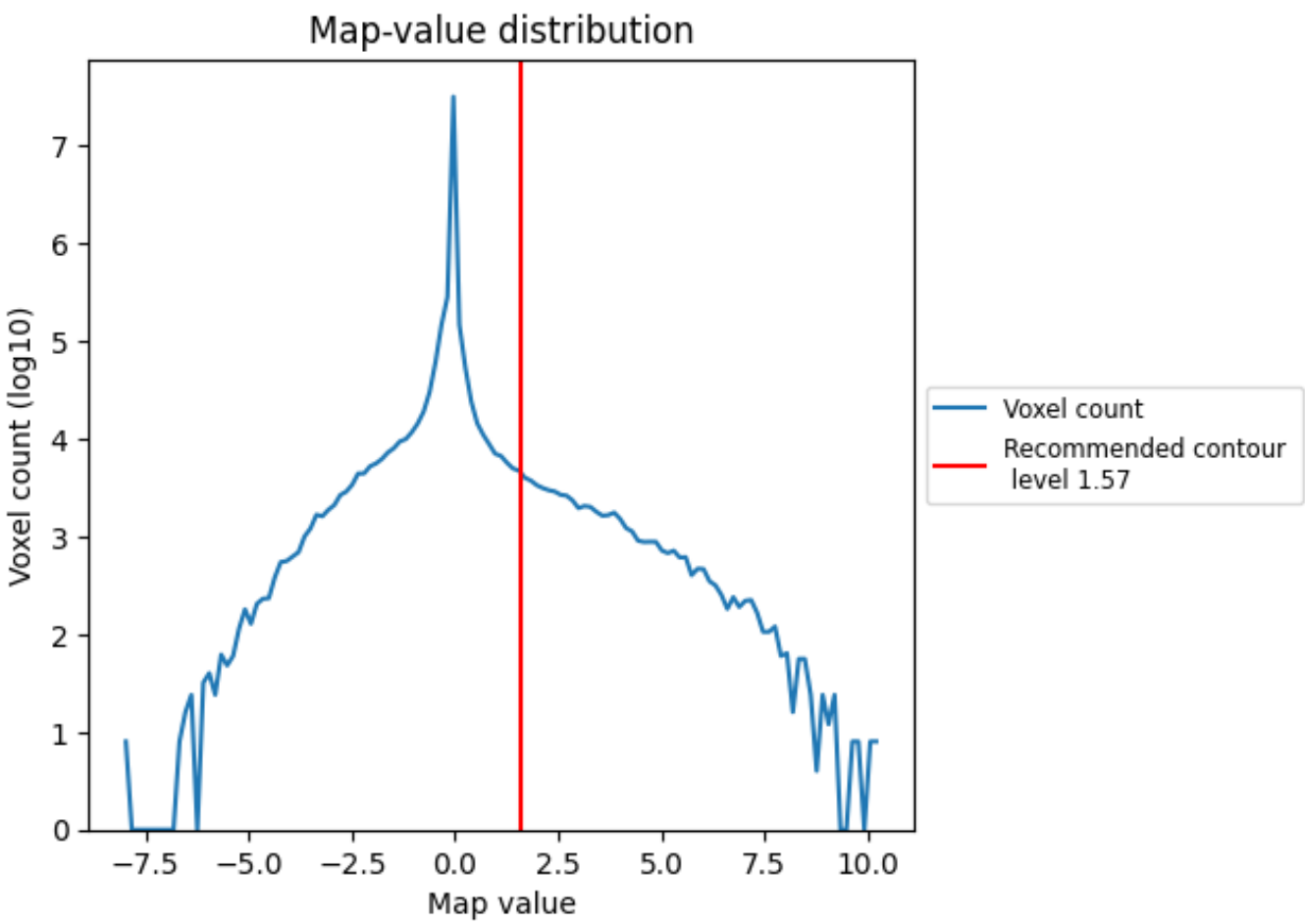
6.6 Mask visualisation (i)

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

7 Map analysis (i)

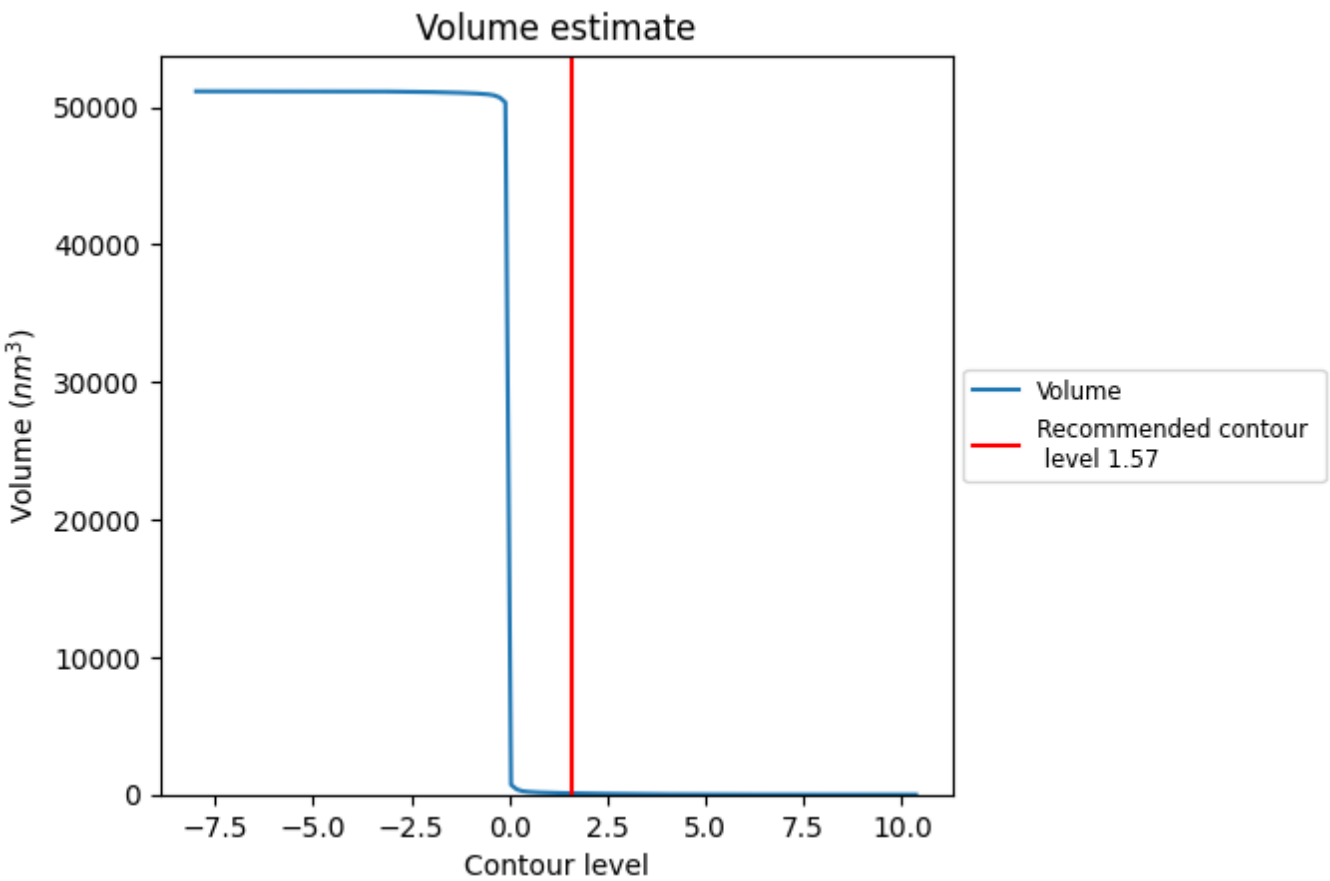
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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.

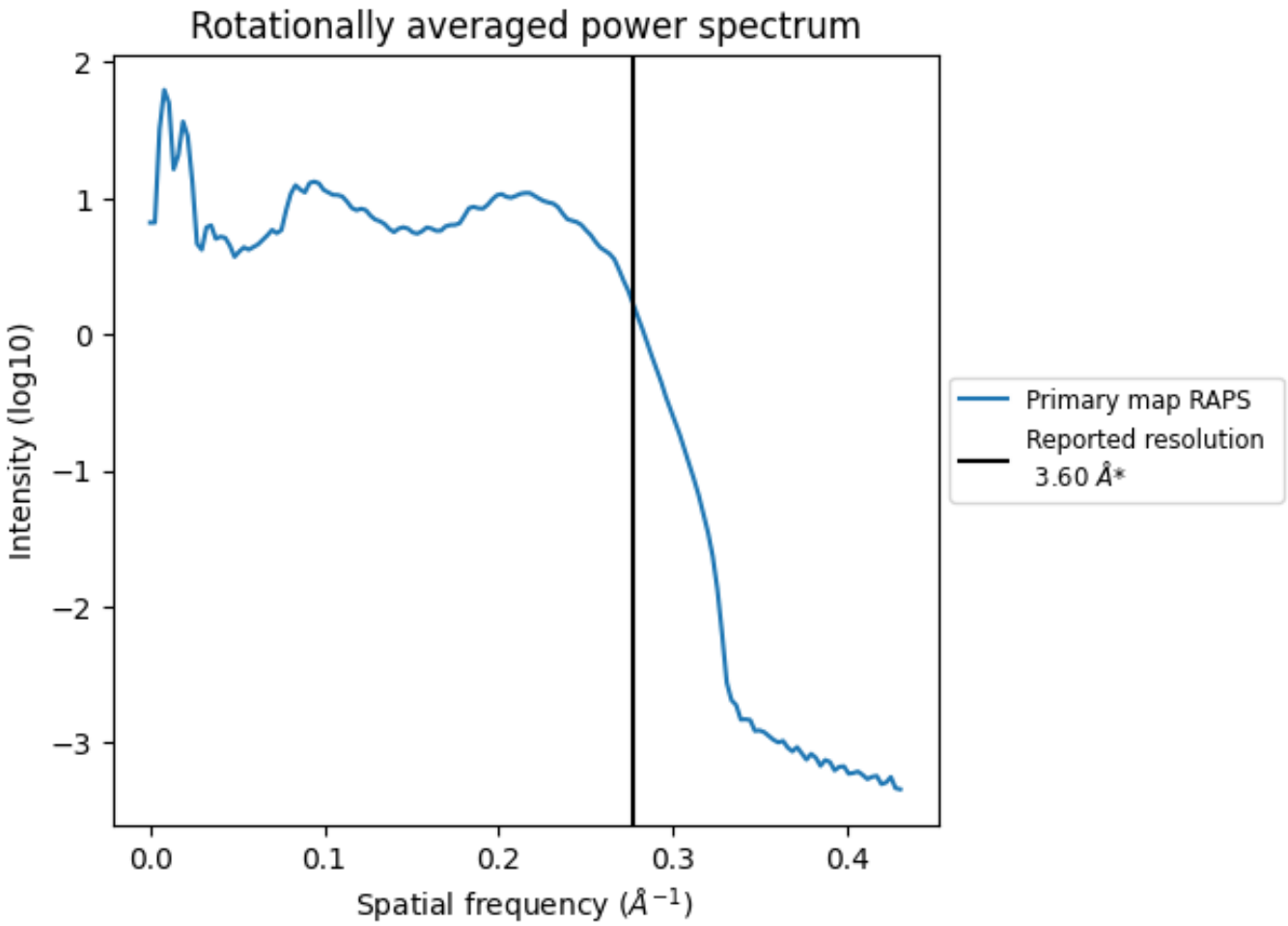
7.2 Volume estimate (i)



The volume at the recommended contour level is 93 nm^3; this corresponds to an approximate mass of 84 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 0.278 Å^{-1}

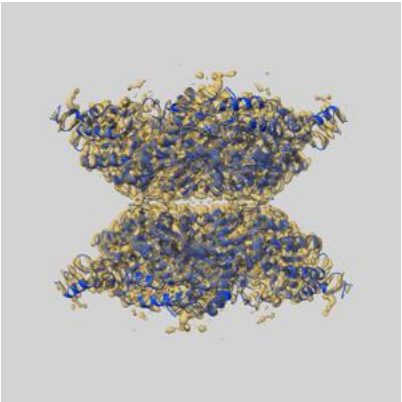
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

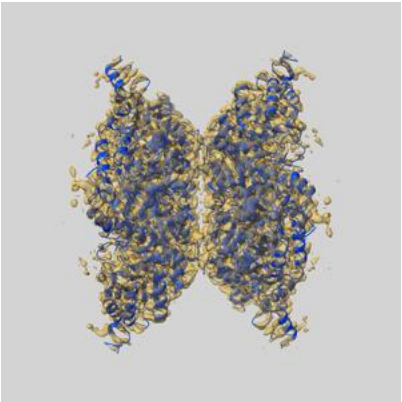
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-24450 and PDB model 7RGI. Per-residue inclusion information can be found in section 3 on page 13.

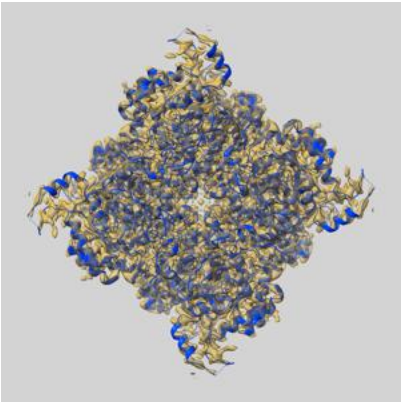
9.1 Map-model overlay (i)



X



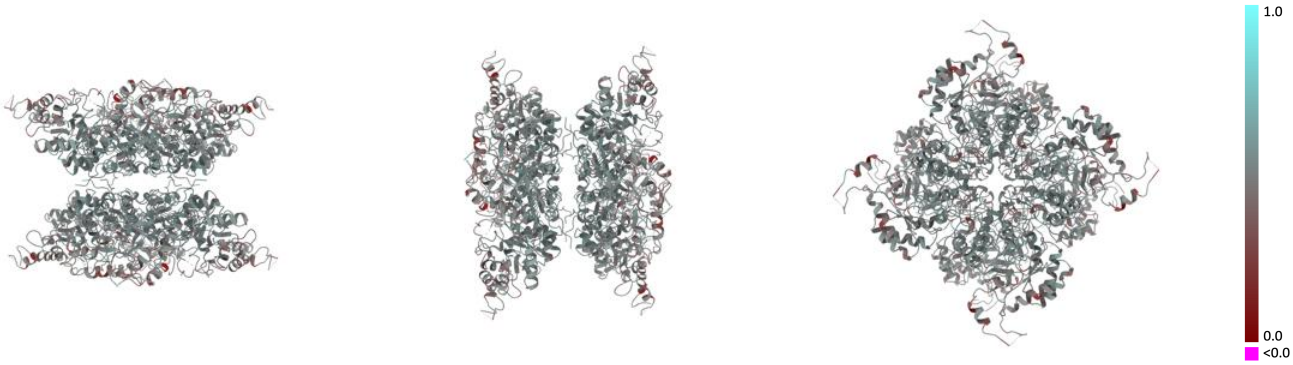
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.57 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.

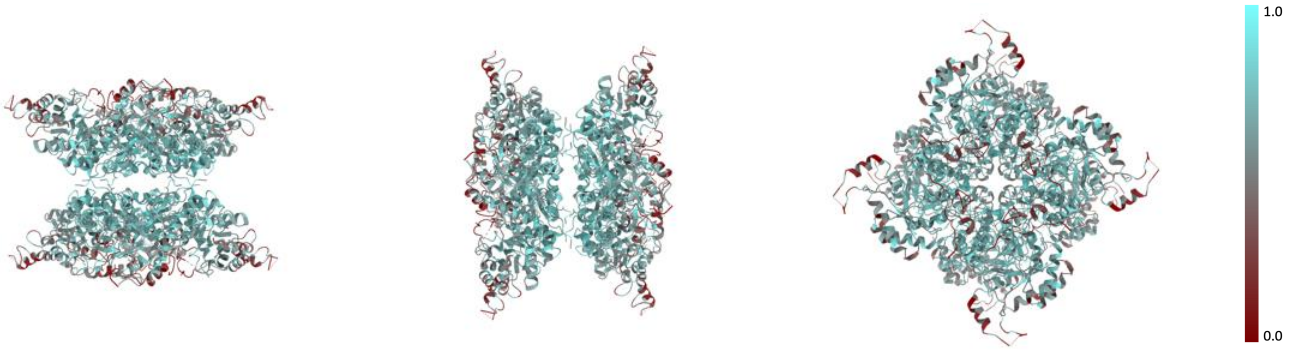
9.2 Q-score mapped to coordinate model (i)



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.

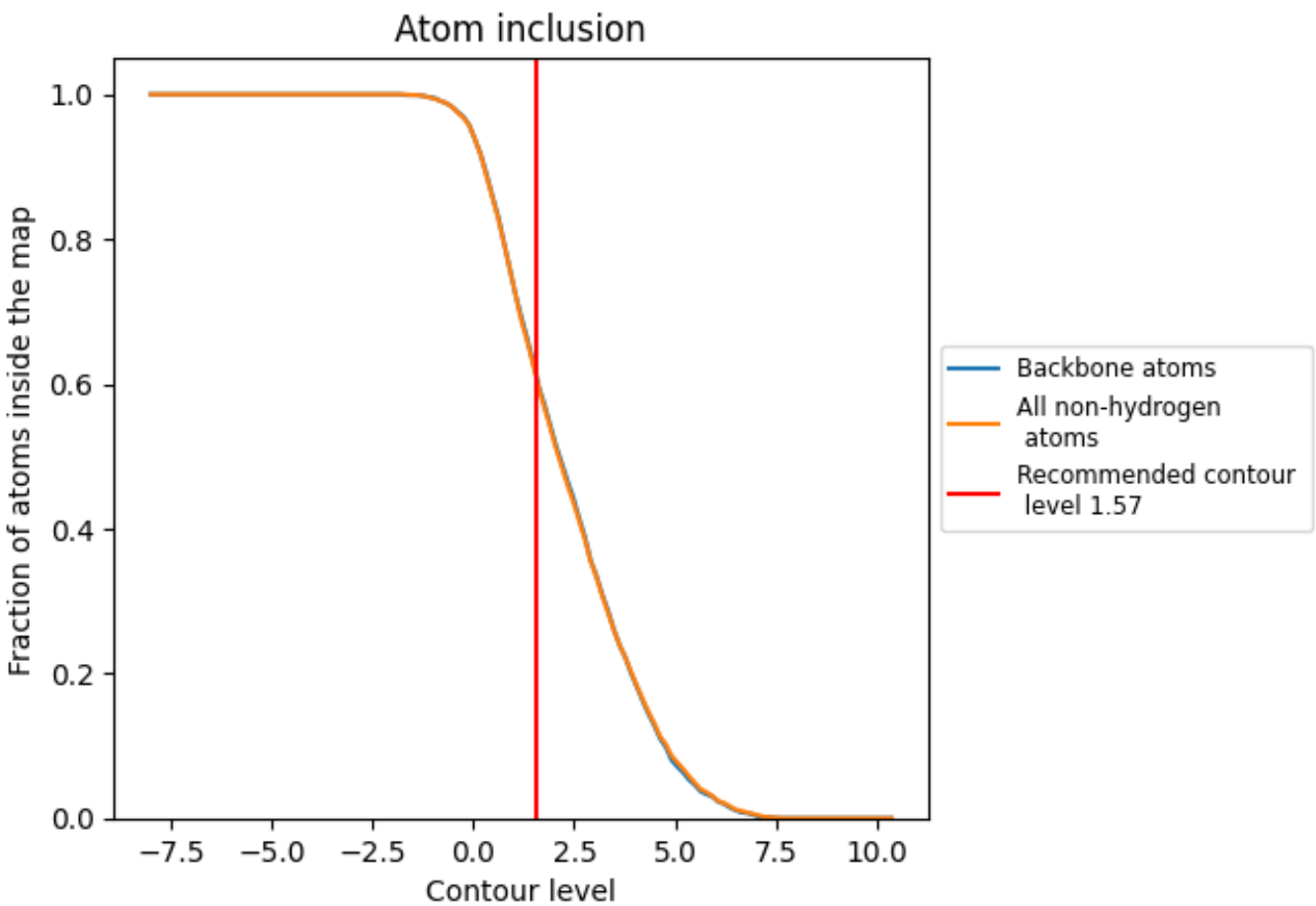
9.3 Atom inclusion mapped to coordinate model (i)



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 (1.57).

9.4 Atom inclusion (i)



At the recommended contour level, 61% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (1.57) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6070	0.4910
A	0.6060	0.4910
B	0.6110	0.4910
C	0.6100	0.4900
D	0.6040	0.4890
E	0.6110	0.4910
F	0.6090	0.4910
G	0.6110	0.4910
H	0.6110	0.4910