



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 03:48 PM UTC

PDB ID : 6GVS / pdb_00006gvs
Title : Engineered glycolyl-CoA reductase comprising 8 mutations with bound NADP+
Authors : Zarzycki, J.; Trudeau, D.; Scheffen, M.; Erb, T.J.; Tawfik, D.S.
Deposited on : 2018-06-21
Resolution : 2.58 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

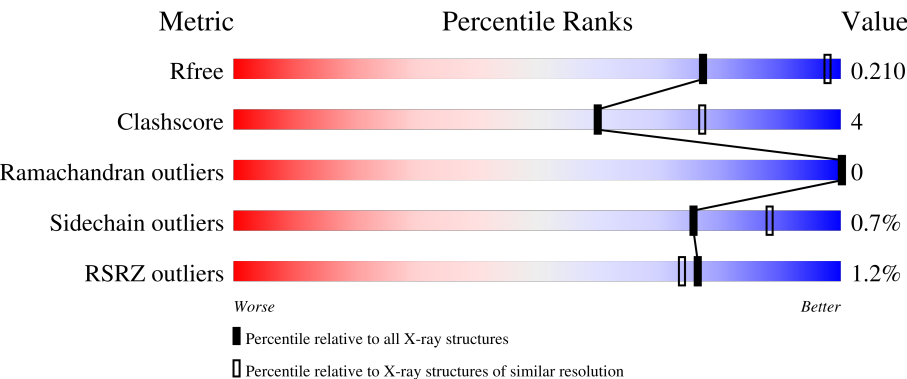
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	522	75%8%16%
1	B	522	% 76%7%16%
1	C	522	% 78%6%16%
1	D	522	% 74%10%16%
1	E	522	% 76%8%16%

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Mol	Chain	Length	Quality of chain
1	F	522	3% 72% 11% • 16%
1	G	522	% 78% 5% • 16%
1	H	522	77% 7% 16%
1	I	522	2% 79% 6% 16%
1	J	522	76% 8% 16%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 33944 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Aldehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	441	Total	C	N	O	S	0	0	0
			3299	2072	572	633	22			
1	B	440	Total	C	N	O	S	0	0	0
			3294	2069	571	632	22			
1	C	441	Total	C	N	O	S	0	0	0
			3299	2072	572	633	22			
1	D	440	Total	C	N	O	S	0	0	0
			3294	2069	571	632	22			
1	E	441	Total	C	N	O	S	0	0	0
			3299	2072	572	633	22			
1	F	441	Total	C	N	O	S	0	0	0
			3299	2072	572	633	22			
1	G	440	Total	C	N	O	S	0	0	0
			3294	2069	571	632	22			
1	H	441	Total	C	N	O	S	0	0	0
			3299	2072	572	633	22			
1	I	441	Total	C	N	O	S	0	0	0
			3299	2072	572	633	22			
1	J	440	Total	C	N	O	S	0	0	0
			3294	2069	571	632	22			

There are 660 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q21A49
A	2	ALA	-	expression tag	UNP Q21A49
A	3	HIS	-	expression tag	UNP Q21A49
A	4	HIS	-	expression tag	UNP Q21A49
A	5	HIS	-	expression tag	UNP Q21A49
A	6	HIS	-	expression tag	UNP Q21A49
A	7	HIS	-	expression tag	UNP Q21A49
A	8	HIS	-	expression tag	UNP Q21A49
A	9	VAL	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
A	10	GLY	-	expression tag	UNP Q21A49
A	11	THR	-	expression tag	UNP Q21A49
A	12	ASN	-	expression tag	UNP Q21A49
A	13	ASP	-	expression tag	UNP Q21A49
A	14	ALA	-	expression tag	UNP Q21A49
A	15	ASN	-	expression tag	UNP Q21A49
A	16	ILE	-	expression tag	UNP Q21A49
A	17	ALA	-	expression tag	UNP Q21A49
A	18	ASP	-	expression tag	UNP Q21A49
A	19	VAL	-	expression tag	UNP Q21A49
A	20	VAL	-	expression tag	UNP Q21A49
A	21	THR	-	expression tag	UNP Q21A49
A	22	LYS	-	expression tag	UNP Q21A49
A	23	VAL	-	expression tag	UNP Q21A49
A	24	LEU	-	expression tag	UNP Q21A49
A	25	GLY	-	expression tag	UNP Q21A49
A	26	GLU	-	expression tag	UNP Q21A49
A	27	TYR	-	expression tag	UNP Q21A49
A	28	GLY	-	expression tag	UNP Q21A49
A	29	ALA	-	expression tag	UNP Q21A49
A	30	PRO	-	expression tag	UNP Q21A49
A	31	GLY	-	expression tag	UNP Q21A49
A	32	ALA	-	expression tag	UNP Q21A49
A	33	VAL	-	expression tag	UNP Q21A49
A	34	SER	-	expression tag	UNP Q21A49
A	35	VAL	-	expression tag	UNP Q21A49
A	36	ALA	-	expression tag	UNP Q21A49
A	37	ALA	-	expression tag	UNP Q21A49
A	38	LEU	-	expression tag	UNP Q21A49
A	39	THR	-	expression tag	UNP Q21A49
A	40	ALA	-	expression tag	UNP Q21A49
A	41	LYS	-	expression tag	UNP Q21A49
A	42	SER	-	expression tag	UNP Q21A49
A	43	PRO	-	expression tag	UNP Q21A49
A	44	ASP	-	expression tag	UNP Q21A49
A	45	GLY	-	expression tag	UNP Q21A49
A	46	LYS	-	expression tag	UNP Q21A49
A	47	SER	-	expression tag	UNP Q21A49
A	48	ASN	-	expression tag	UNP Q21A49
A	49	SER	-	expression tag	UNP Q21A49
A	50	SER	-	expression tag	UNP Q21A49
A	51	ALA	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
A	52	ASP	-	expression tag	UNP Q21A49
A	53	ALA	-	expression tag	UNP Q21A49
A	54	ASP	-	expression tag	UNP Q21A49
A	55	VAL	-	expression tag	UNP Q21A49
A	56	VAL	-	expression tag	UNP Q21A49
A	57	ALA	-	expression tag	UNP Q21A49
A	58	ARG	-	expression tag	UNP Q21A49
A	222	GLY	PRO	engineered mutation	UNP Q21A49
A	257	ARG	ILE	engineered mutation	UNP Q21A49
A	261	LEU	ASN	engineered mutation	UNP Q21A49
A	280	LEU	ILE	engineered mutation	UNP Q21A49
A	326	ILE	LEU	engineered mutation	UNP Q21A49
A	327	THR	PRO	engineered mutation	UNP Q21A49
A	329	THR	VAL	engineered mutation	UNP Q21A49
A	481	HIS	LEU	engineered mutation	UNP Q21A49
B	1	MET	-	initiating methionine	UNP Q21A49
B	2	ALA	-	expression tag	UNP Q21A49
B	3	HIS	-	expression tag	UNP Q21A49
B	4	HIS	-	expression tag	UNP Q21A49
B	5	HIS	-	expression tag	UNP Q21A49
B	6	HIS	-	expression tag	UNP Q21A49
B	7	HIS	-	expression tag	UNP Q21A49
B	8	HIS	-	expression tag	UNP Q21A49
B	9	VAL	-	expression tag	UNP Q21A49
B	10	GLY	-	expression tag	UNP Q21A49
B	11	THR	-	expression tag	UNP Q21A49
B	12	ASN	-	expression tag	UNP Q21A49
B	13	ASP	-	expression tag	UNP Q21A49
B	14	ALA	-	expression tag	UNP Q21A49
B	15	ASN	-	expression tag	UNP Q21A49
B	16	ILE	-	expression tag	UNP Q21A49
B	17	ALA	-	expression tag	UNP Q21A49
B	18	ASP	-	expression tag	UNP Q21A49
B	19	VAL	-	expression tag	UNP Q21A49
B	20	VAL	-	expression tag	UNP Q21A49
B	21	THR	-	expression tag	UNP Q21A49
B	22	LYS	-	expression tag	UNP Q21A49
B	23	VAL	-	expression tag	UNP Q21A49
B	24	LEU	-	expression tag	UNP Q21A49
B	25	GLY	-	expression tag	UNP Q21A49
B	26	GLU	-	expression tag	UNP Q21A49
B	27	TYR	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
B	28	GLY	-	expression tag	UNP Q21A49
B	29	ALA	-	expression tag	UNP Q21A49
B	30	PRO	-	expression tag	UNP Q21A49
B	31	GLY	-	expression tag	UNP Q21A49
B	32	ALA	-	expression tag	UNP Q21A49
B	33	VAL	-	expression tag	UNP Q21A49
B	34	SER	-	expression tag	UNP Q21A49
B	35	VAL	-	expression tag	UNP Q21A49
B	36	ALA	-	expression tag	UNP Q21A49
B	37	ALA	-	expression tag	UNP Q21A49
B	38	LEU	-	expression tag	UNP Q21A49
B	39	THR	-	expression tag	UNP Q21A49
B	40	ALA	-	expression tag	UNP Q21A49
B	41	LYS	-	expression tag	UNP Q21A49
B	42	SER	-	expression tag	UNP Q21A49
B	43	PRO	-	expression tag	UNP Q21A49
B	44	ASP	-	expression tag	UNP Q21A49
B	45	GLY	-	expression tag	UNP Q21A49
B	46	LYS	-	expression tag	UNP Q21A49
B	47	SER	-	expression tag	UNP Q21A49
B	48	ASN	-	expression tag	UNP Q21A49
B	49	SER	-	expression tag	UNP Q21A49
B	50	SER	-	expression tag	UNP Q21A49
B	51	ALA	-	expression tag	UNP Q21A49
B	52	ASP	-	expression tag	UNP Q21A49
B	53	ALA	-	expression tag	UNP Q21A49
B	54	ASP	-	expression tag	UNP Q21A49
B	55	VAL	-	expression tag	UNP Q21A49
B	56	VAL	-	expression tag	UNP Q21A49
B	57	ALA	-	expression tag	UNP Q21A49
B	58	ARG	-	expression tag	UNP Q21A49
B	222	GLY	PRO	engineered mutation	UNP Q21A49
B	257	ARG	ILE	engineered mutation	UNP Q21A49
B	261	LEU	ASN	engineered mutation	UNP Q21A49
B	280	LEU	ILE	engineered mutation	UNP Q21A49
B	326	ILE	LEU	engineered mutation	UNP Q21A49
B	327	THR	PRO	engineered mutation	UNP Q21A49
B	329	THR	VAL	engineered mutation	UNP Q21A49
B	481	HIS	LEU	engineered mutation	UNP Q21A49
C	1	MET	-	initiating methionine	UNP Q21A49
C	2	ALA	-	expression tag	UNP Q21A49
C	3	HIS	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
C	4	HIS	-	expression tag	UNP Q21A49
C	5	HIS	-	expression tag	UNP Q21A49
C	6	HIS	-	expression tag	UNP Q21A49
C	7	HIS	-	expression tag	UNP Q21A49
C	8	HIS	-	expression tag	UNP Q21A49
C	9	VAL	-	expression tag	UNP Q21A49
C	10	GLY	-	expression tag	UNP Q21A49
C	11	THR	-	expression tag	UNP Q21A49
C	12	ASN	-	expression tag	UNP Q21A49
C	13	ASP	-	expression tag	UNP Q21A49
C	14	ALA	-	expression tag	UNP Q21A49
C	15	ASN	-	expression tag	UNP Q21A49
C	16	ILE	-	expression tag	UNP Q21A49
C	17	ALA	-	expression tag	UNP Q21A49
C	18	ASP	-	expression tag	UNP Q21A49
C	19	VAL	-	expression tag	UNP Q21A49
C	20	VAL	-	expression tag	UNP Q21A49
C	21	THR	-	expression tag	UNP Q21A49
C	22	LYS	-	expression tag	UNP Q21A49
C	23	VAL	-	expression tag	UNP Q21A49
C	24	LEU	-	expression tag	UNP Q21A49
C	25	GLY	-	expression tag	UNP Q21A49
C	26	GLU	-	expression tag	UNP Q21A49
C	27	TYR	-	expression tag	UNP Q21A49
C	28	GLY	-	expression tag	UNP Q21A49
C	29	ALA	-	expression tag	UNP Q21A49
C	30	PRO	-	expression tag	UNP Q21A49
C	31	GLY	-	expression tag	UNP Q21A49
C	32	ALA	-	expression tag	UNP Q21A49
C	33	VAL	-	expression tag	UNP Q21A49
C	34	SER	-	expression tag	UNP Q21A49
C	35	VAL	-	expression tag	UNP Q21A49
C	36	ALA	-	expression tag	UNP Q21A49
C	37	ALA	-	expression tag	UNP Q21A49
C	38	LEU	-	expression tag	UNP Q21A49
C	39	THR	-	expression tag	UNP Q21A49
C	40	ALA	-	expression tag	UNP Q21A49
C	41	LYS	-	expression tag	UNP Q21A49
C	42	SER	-	expression tag	UNP Q21A49
C	43	PRO	-	expression tag	UNP Q21A49
C	44	ASP	-	expression tag	UNP Q21A49
C	45	GLY	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
C	46	LYS	-	expression tag	UNP Q21A49
C	47	SER	-	expression tag	UNP Q21A49
C	48	ASN	-	expression tag	UNP Q21A49
C	49	SER	-	expression tag	UNP Q21A49
C	50	SER	-	expression tag	UNP Q21A49
C	51	ALA	-	expression tag	UNP Q21A49
C	52	ASP	-	expression tag	UNP Q21A49
C	53	ALA	-	expression tag	UNP Q21A49
C	54	ASP	-	expression tag	UNP Q21A49
C	55	VAL	-	expression tag	UNP Q21A49
C	56	VAL	-	expression tag	UNP Q21A49
C	57	ALA	-	expression tag	UNP Q21A49
C	58	ARG	-	expression tag	UNP Q21A49
C	222	GLY	PRO	engineered mutation	UNP Q21A49
C	257	ARG	ILE	engineered mutation	UNP Q21A49
C	261	LEU	ASN	engineered mutation	UNP Q21A49
C	280	LEU	ILE	engineered mutation	UNP Q21A49
C	326	ILE	LEU	engineered mutation	UNP Q21A49
C	327	THR	PRO	engineered mutation	UNP Q21A49
C	329	THR	VAL	engineered mutation	UNP Q21A49
C	481	HIS	LEU	engineered mutation	UNP Q21A49
D	1	MET	-	initiating methionine	UNP Q21A49
D	2	ALA	-	expression tag	UNP Q21A49
D	3	HIS	-	expression tag	UNP Q21A49
D	4	HIS	-	expression tag	UNP Q21A49
D	5	HIS	-	expression tag	UNP Q21A49
D	6	HIS	-	expression tag	UNP Q21A49
D	7	HIS	-	expression tag	UNP Q21A49
D	8	HIS	-	expression tag	UNP Q21A49
D	9	VAL	-	expression tag	UNP Q21A49
D	10	GLY	-	expression tag	UNP Q21A49
D	11	THR	-	expression tag	UNP Q21A49
D	12	ASN	-	expression tag	UNP Q21A49
D	13	ASP	-	expression tag	UNP Q21A49
D	14	ALA	-	expression tag	UNP Q21A49
D	15	ASN	-	expression tag	UNP Q21A49
D	16	ILE	-	expression tag	UNP Q21A49
D	17	ALA	-	expression tag	UNP Q21A49
D	18	ASP	-	expression tag	UNP Q21A49
D	19	VAL	-	expression tag	UNP Q21A49
D	20	VAL	-	expression tag	UNP Q21A49
D	21	THR	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
D	22	LYS	-	expression tag	UNP Q21A49
D	23	VAL	-	expression tag	UNP Q21A49
D	24	LEU	-	expression tag	UNP Q21A49
D	25	GLY	-	expression tag	UNP Q21A49
D	26	GLU	-	expression tag	UNP Q21A49
D	27	TYR	-	expression tag	UNP Q21A49
D	28	GLY	-	expression tag	UNP Q21A49
D	29	ALA	-	expression tag	UNP Q21A49
D	30	PRO	-	expression tag	UNP Q21A49
D	31	GLY	-	expression tag	UNP Q21A49
D	32	ALA	-	expression tag	UNP Q21A49
D	33	VAL	-	expression tag	UNP Q21A49
D	34	SER	-	expression tag	UNP Q21A49
D	35	VAL	-	expression tag	UNP Q21A49
D	36	ALA	-	expression tag	UNP Q21A49
D	37	ALA	-	expression tag	UNP Q21A49
D	38	LEU	-	expression tag	UNP Q21A49
D	39	THR	-	expression tag	UNP Q21A49
D	40	ALA	-	expression tag	UNP Q21A49
D	41	LYS	-	expression tag	UNP Q21A49
D	42	SER	-	expression tag	UNP Q21A49
D	43	PRO	-	expression tag	UNP Q21A49
D	44	ASP	-	expression tag	UNP Q21A49
D	45	GLY	-	expression tag	UNP Q21A49
D	46	LYS	-	expression tag	UNP Q21A49
D	47	SER	-	expression tag	UNP Q21A49
D	48	ASN	-	expression tag	UNP Q21A49
D	49	SER	-	expression tag	UNP Q21A49
D	50	SER	-	expression tag	UNP Q21A49
D	51	ALA	-	expression tag	UNP Q21A49
D	52	ASP	-	expression tag	UNP Q21A49
D	53	ALA	-	expression tag	UNP Q21A49
D	54	ASP	-	expression tag	UNP Q21A49
D	55	VAL	-	expression tag	UNP Q21A49
D	56	VAL	-	expression tag	UNP Q21A49
D	57	ALA	-	expression tag	UNP Q21A49
D	58	ARG	-	expression tag	UNP Q21A49
D	222	GLY	PRO	engineered mutation	UNP Q21A49
D	257	ARG	ILE	engineered mutation	UNP Q21A49
D	261	LEU	ASN	engineered mutation	UNP Q21A49
D	280	LEU	ILE	engineered mutation	UNP Q21A49
D	326	ILE	LEU	engineered mutation	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
D	327	THR	PRO	engineered mutation	UNP Q21A49
D	329	THR	VAL	engineered mutation	UNP Q21A49
D	481	HIS	LEU	engineered mutation	UNP Q21A49
E	1	MET	-	initiating methionine	UNP Q21A49
E	2	ALA	-	expression tag	UNP Q21A49
E	3	HIS	-	expression tag	UNP Q21A49
E	4	HIS	-	expression tag	UNP Q21A49
E	5	HIS	-	expression tag	UNP Q21A49
E	6	HIS	-	expression tag	UNP Q21A49
E	7	HIS	-	expression tag	UNP Q21A49
E	8	HIS	-	expression tag	UNP Q21A49
E	9	VAL	-	expression tag	UNP Q21A49
E	10	GLY	-	expression tag	UNP Q21A49
E	11	THR	-	expression tag	UNP Q21A49
E	12	ASN	-	expression tag	UNP Q21A49
E	13	ASP	-	expression tag	UNP Q21A49
E	14	ALA	-	expression tag	UNP Q21A49
E	15	ASN	-	expression tag	UNP Q21A49
E	16	ILE	-	expression tag	UNP Q21A49
E	17	ALA	-	expression tag	UNP Q21A49
E	18	ASP	-	expression tag	UNP Q21A49
E	19	VAL	-	expression tag	UNP Q21A49
E	20	VAL	-	expression tag	UNP Q21A49
E	21	THR	-	expression tag	UNP Q21A49
E	22	LYS	-	expression tag	UNP Q21A49
E	23	VAL	-	expression tag	UNP Q21A49
E	24	LEU	-	expression tag	UNP Q21A49
E	25	GLY	-	expression tag	UNP Q21A49
E	26	GLU	-	expression tag	UNP Q21A49
E	27	TYR	-	expression tag	UNP Q21A49
E	28	GLY	-	expression tag	UNP Q21A49
E	29	ALA	-	expression tag	UNP Q21A49
E	30	PRO	-	expression tag	UNP Q21A49
E	31	GLY	-	expression tag	UNP Q21A49
E	32	ALA	-	expression tag	UNP Q21A49
E	33	VAL	-	expression tag	UNP Q21A49
E	34	SER	-	expression tag	UNP Q21A49
E	35	VAL	-	expression tag	UNP Q21A49
E	36	ALA	-	expression tag	UNP Q21A49
E	37	ALA	-	expression tag	UNP Q21A49
E	38	LEU	-	expression tag	UNP Q21A49
E	39	THR	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
E	40	ALA	-	expression tag	UNP Q21A49
E	41	LYS	-	expression tag	UNP Q21A49
E	42	SER	-	expression tag	UNP Q21A49
E	43	PRO	-	expression tag	UNP Q21A49
E	44	ASP	-	expression tag	UNP Q21A49
E	45	GLY	-	expression tag	UNP Q21A49
E	46	LYS	-	expression tag	UNP Q21A49
E	47	SER	-	expression tag	UNP Q21A49
E	48	ASN	-	expression tag	UNP Q21A49
E	49	SER	-	expression tag	UNP Q21A49
E	50	SER	-	expression tag	UNP Q21A49
E	51	ALA	-	expression tag	UNP Q21A49
E	52	ASP	-	expression tag	UNP Q21A49
E	53	ALA	-	expression tag	UNP Q21A49
E	54	ASP	-	expression tag	UNP Q21A49
E	55	VAL	-	expression tag	UNP Q21A49
E	56	VAL	-	expression tag	UNP Q21A49
E	57	ALA	-	expression tag	UNP Q21A49
E	58	ARG	-	expression tag	UNP Q21A49
E	222	GLY	PRO	engineered mutation	UNP Q21A49
E	257	ARG	ILE	engineered mutation	UNP Q21A49
E	261	LEU	ASN	engineered mutation	UNP Q21A49
E	280	LEU	ILE	engineered mutation	UNP Q21A49
E	326	ILE	LEU	engineered mutation	UNP Q21A49
E	327	THR	PRO	engineered mutation	UNP Q21A49
E	329	THR	VAL	engineered mutation	UNP Q21A49
E	481	HIS	LEU	engineered mutation	UNP Q21A49
F	1	MET	-	initiating methionine	UNP Q21A49
F	2	ALA	-	expression tag	UNP Q21A49
F	3	HIS	-	expression tag	UNP Q21A49
F	4	HIS	-	expression tag	UNP Q21A49
F	5	HIS	-	expression tag	UNP Q21A49
F	6	HIS	-	expression tag	UNP Q21A49
F	7	HIS	-	expression tag	UNP Q21A49
F	8	HIS	-	expression tag	UNP Q21A49
F	9	VAL	-	expression tag	UNP Q21A49
F	10	GLY	-	expression tag	UNP Q21A49
F	11	THR	-	expression tag	UNP Q21A49
F	12	ASN	-	expression tag	UNP Q21A49
F	13	ASP	-	expression tag	UNP Q21A49
F	14	ALA	-	expression tag	UNP Q21A49
F	15	ASN	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
F	16	ILE	-	expression tag	UNP Q21A49
F	17	ALA	-	expression tag	UNP Q21A49
F	18	ASP	-	expression tag	UNP Q21A49
F	19	VAL	-	expression tag	UNP Q21A49
F	20	VAL	-	expression tag	UNP Q21A49
F	21	THR	-	expression tag	UNP Q21A49
F	22	LYS	-	expression tag	UNP Q21A49
F	23	VAL	-	expression tag	UNP Q21A49
F	24	LEU	-	expression tag	UNP Q21A49
F	25	GLY	-	expression tag	UNP Q21A49
F	26	GLU	-	expression tag	UNP Q21A49
F	27	TYR	-	expression tag	UNP Q21A49
F	28	GLY	-	expression tag	UNP Q21A49
F	29	ALA	-	expression tag	UNP Q21A49
F	30	PRO	-	expression tag	UNP Q21A49
F	31	GLY	-	expression tag	UNP Q21A49
F	32	ALA	-	expression tag	UNP Q21A49
F	33	VAL	-	expression tag	UNP Q21A49
F	34	SER	-	expression tag	UNP Q21A49
F	35	VAL	-	expression tag	UNP Q21A49
F	36	ALA	-	expression tag	UNP Q21A49
F	37	ALA	-	expression tag	UNP Q21A49
F	38	LEU	-	expression tag	UNP Q21A49
F	39	THR	-	expression tag	UNP Q21A49
F	40	ALA	-	expression tag	UNP Q21A49
F	41	LYS	-	expression tag	UNP Q21A49
F	42	SER	-	expression tag	UNP Q21A49
F	43	PRO	-	expression tag	UNP Q21A49
F	44	ASP	-	expression tag	UNP Q21A49
F	45	GLY	-	expression tag	UNP Q21A49
F	46	LYS	-	expression tag	UNP Q21A49
F	47	SER	-	expression tag	UNP Q21A49
F	48	ASN	-	expression tag	UNP Q21A49
F	49	SER	-	expression tag	UNP Q21A49
F	50	SER	-	expression tag	UNP Q21A49
F	51	ALA	-	expression tag	UNP Q21A49
F	52	ASP	-	expression tag	UNP Q21A49
F	53	ALA	-	expression tag	UNP Q21A49
F	54	ASP	-	expression tag	UNP Q21A49
F	55	VAL	-	expression tag	UNP Q21A49
F	56	VAL	-	expression tag	UNP Q21A49
F	57	ALA	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
F	58	ARG	-	expression tag	UNP Q21A49
F	222	GLY	PRO	engineered mutation	UNP Q21A49
F	257	ARG	ILE	engineered mutation	UNP Q21A49
F	261	LEU	ASN	engineered mutation	UNP Q21A49
F	280	LEU	ILE	engineered mutation	UNP Q21A49
F	326	ILE	LEU	engineered mutation	UNP Q21A49
F	327	THR	PRO	engineered mutation	UNP Q21A49
F	329	THR	VAL	engineered mutation	UNP Q21A49
F	481	HIS	LEU	engineered mutation	UNP Q21A49
G	1	MET	-	initiating methionine	UNP Q21A49
G	2	ALA	-	expression tag	UNP Q21A49
G	3	HIS	-	expression tag	UNP Q21A49
G	4	HIS	-	expression tag	UNP Q21A49
G	5	HIS	-	expression tag	UNP Q21A49
G	6	HIS	-	expression tag	UNP Q21A49
G	7	HIS	-	expression tag	UNP Q21A49
G	8	HIS	-	expression tag	UNP Q21A49
G	9	VAL	-	expression tag	UNP Q21A49
G	10	GLY	-	expression tag	UNP Q21A49
G	11	THR	-	expression tag	UNP Q21A49
G	12	ASN	-	expression tag	UNP Q21A49
G	13	ASP	-	expression tag	UNP Q21A49
G	14	ALA	-	expression tag	UNP Q21A49
G	15	ASN	-	expression tag	UNP Q21A49
G	16	ILE	-	expression tag	UNP Q21A49
G	17	ALA	-	expression tag	UNP Q21A49
G	18	ASP	-	expression tag	UNP Q21A49
G	19	VAL	-	expression tag	UNP Q21A49
G	20	VAL	-	expression tag	UNP Q21A49
G	21	THR	-	expression tag	UNP Q21A49
G	22	LYS	-	expression tag	UNP Q21A49
G	23	VAL	-	expression tag	UNP Q21A49
G	24	LEU	-	expression tag	UNP Q21A49
G	25	GLY	-	expression tag	UNP Q21A49
G	26	GLU	-	expression tag	UNP Q21A49
G	27	TYR	-	expression tag	UNP Q21A49
G	28	GLY	-	expression tag	UNP Q21A49
G	29	ALA	-	expression tag	UNP Q21A49
G	30	PRO	-	expression tag	UNP Q21A49
G	31	GLY	-	expression tag	UNP Q21A49
G	32	ALA	-	expression tag	UNP Q21A49
G	33	VAL	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
G	34	SER	-	expression tag	UNP Q21A49
G	35	VAL	-	expression tag	UNP Q21A49
G	36	ALA	-	expression tag	UNP Q21A49
G	37	ALA	-	expression tag	UNP Q21A49
G	38	LEU	-	expression tag	UNP Q21A49
G	39	THR	-	expression tag	UNP Q21A49
G	40	ALA	-	expression tag	UNP Q21A49
G	41	LYS	-	expression tag	UNP Q21A49
G	42	SER	-	expression tag	UNP Q21A49
G	43	PRO	-	expression tag	UNP Q21A49
G	44	ASP	-	expression tag	UNP Q21A49
G	45	GLY	-	expression tag	UNP Q21A49
G	46	LYS	-	expression tag	UNP Q21A49
G	47	SER	-	expression tag	UNP Q21A49
G	48	ASN	-	expression tag	UNP Q21A49
G	49	SER	-	expression tag	UNP Q21A49
G	50	SER	-	expression tag	UNP Q21A49
G	51	ALA	-	expression tag	UNP Q21A49
G	52	ASP	-	expression tag	UNP Q21A49
G	53	ALA	-	expression tag	UNP Q21A49
G	54	ASP	-	expression tag	UNP Q21A49
G	55	VAL	-	expression tag	UNP Q21A49
G	56	VAL	-	expression tag	UNP Q21A49
G	57	ALA	-	expression tag	UNP Q21A49
G	58	ARG	-	expression tag	UNP Q21A49
G	222	GLY	PRO	engineered mutation	UNP Q21A49
G	257	ARG	ILE	engineered mutation	UNP Q21A49
G	261	LEU	ASN	engineered mutation	UNP Q21A49
G	280	LEU	ILE	engineered mutation	UNP Q21A49
G	326	ILE	LEU	engineered mutation	UNP Q21A49
G	327	THR	PRO	engineered mutation	UNP Q21A49
G	329	THR	VAL	engineered mutation	UNP Q21A49
G	481	HIS	LEU	engineered mutation	UNP Q21A49
H	1	MET	-	initiating methionine	UNP Q21A49
H	2	ALA	-	expression tag	UNP Q21A49
H	3	HIS	-	expression tag	UNP Q21A49
H	4	HIS	-	expression tag	UNP Q21A49
H	5	HIS	-	expression tag	UNP Q21A49
H	6	HIS	-	expression tag	UNP Q21A49
H	7	HIS	-	expression tag	UNP Q21A49
H	8	HIS	-	expression tag	UNP Q21A49
H	9	VAL	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
H	10	GLY	-	expression tag	UNP Q21A49
H	11	THR	-	expression tag	UNP Q21A49
H	12	ASN	-	expression tag	UNP Q21A49
H	13	ASP	-	expression tag	UNP Q21A49
H	14	ALA	-	expression tag	UNP Q21A49
H	15	ASN	-	expression tag	UNP Q21A49
H	16	ILE	-	expression tag	UNP Q21A49
H	17	ALA	-	expression tag	UNP Q21A49
H	18	ASP	-	expression tag	UNP Q21A49
H	19	VAL	-	expression tag	UNP Q21A49
H	20	VAL	-	expression tag	UNP Q21A49
H	21	THR	-	expression tag	UNP Q21A49
H	22	LYS	-	expression tag	UNP Q21A49
H	23	VAL	-	expression tag	UNP Q21A49
H	24	LEU	-	expression tag	UNP Q21A49
H	25	GLY	-	expression tag	UNP Q21A49
H	26	GLU	-	expression tag	UNP Q21A49
H	27	TYR	-	expression tag	UNP Q21A49
H	28	GLY	-	expression tag	UNP Q21A49
H	29	ALA	-	expression tag	UNP Q21A49
H	30	PRO	-	expression tag	UNP Q21A49
H	31	GLY	-	expression tag	UNP Q21A49
H	32	ALA	-	expression tag	UNP Q21A49
H	33	VAL	-	expression tag	UNP Q21A49
H	34	SER	-	expression tag	UNP Q21A49
H	35	VAL	-	expression tag	UNP Q21A49
H	36	ALA	-	expression tag	UNP Q21A49
H	37	ALA	-	expression tag	UNP Q21A49
H	38	LEU	-	expression tag	UNP Q21A49
H	39	THR	-	expression tag	UNP Q21A49
H	40	ALA	-	expression tag	UNP Q21A49
H	41	LYS	-	expression tag	UNP Q21A49
H	42	SER	-	expression tag	UNP Q21A49
H	43	PRO	-	expression tag	UNP Q21A49
H	44	ASP	-	expression tag	UNP Q21A49
H	45	GLY	-	expression tag	UNP Q21A49
H	46	LYS	-	expression tag	UNP Q21A49
H	47	SER	-	expression tag	UNP Q21A49
H	48	ASN	-	expression tag	UNP Q21A49
H	49	SER	-	expression tag	UNP Q21A49
H	50	SER	-	expression tag	UNP Q21A49
H	51	ALA	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
H	52	ASP	-	expression tag	UNP Q21A49
H	53	ALA	-	expression tag	UNP Q21A49
H	54	ASP	-	expression tag	UNP Q21A49
H	55	VAL	-	expression tag	UNP Q21A49
H	56	VAL	-	expression tag	UNP Q21A49
H	57	ALA	-	expression tag	UNP Q21A49
H	58	ARG	-	expression tag	UNP Q21A49
H	222	GLY	PRO	engineered mutation	UNP Q21A49
H	257	ARG	ILE	engineered mutation	UNP Q21A49
H	261	LEU	ASN	engineered mutation	UNP Q21A49
H	280	LEU	ILE	engineered mutation	UNP Q21A49
H	326	ILE	LEU	engineered mutation	UNP Q21A49
H	327	THR	PRO	engineered mutation	UNP Q21A49
H	329	THR	VAL	engineered mutation	UNP Q21A49
H	481	HIS	LEU	engineered mutation	UNP Q21A49
I	1	MET	-	initiating methionine	UNP Q21A49
I	2	ALA	-	expression tag	UNP Q21A49
I	3	HIS	-	expression tag	UNP Q21A49
I	4	HIS	-	expression tag	UNP Q21A49
I	5	HIS	-	expression tag	UNP Q21A49
I	6	HIS	-	expression tag	UNP Q21A49
I	7	HIS	-	expression tag	UNP Q21A49
I	8	HIS	-	expression tag	UNP Q21A49
I	9	VAL	-	expression tag	UNP Q21A49
I	10	GLY	-	expression tag	UNP Q21A49
I	11	THR	-	expression tag	UNP Q21A49
I	12	ASN	-	expression tag	UNP Q21A49
I	13	ASP	-	expression tag	UNP Q21A49
I	14	ALA	-	expression tag	UNP Q21A49
I	15	ASN	-	expression tag	UNP Q21A49
I	16	ILE	-	expression tag	UNP Q21A49
I	17	ALA	-	expression tag	UNP Q21A49
I	18	ASP	-	expression tag	UNP Q21A49
I	19	VAL	-	expression tag	UNP Q21A49
I	20	VAL	-	expression tag	UNP Q21A49
I	21	THR	-	expression tag	UNP Q21A49
I	22	LYS	-	expression tag	UNP Q21A49
I	23	VAL	-	expression tag	UNP Q21A49
I	24	LEU	-	expression tag	UNP Q21A49
I	25	GLY	-	expression tag	UNP Q21A49
I	26	GLU	-	expression tag	UNP Q21A49
I	27	TYR	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
I	28	GLY	-	expression tag	UNP Q21A49
I	29	ALA	-	expression tag	UNP Q21A49
I	30	PRO	-	expression tag	UNP Q21A49
I	31	GLY	-	expression tag	UNP Q21A49
I	32	ALA	-	expression tag	UNP Q21A49
I	33	VAL	-	expression tag	UNP Q21A49
I	34	SER	-	expression tag	UNP Q21A49
I	35	VAL	-	expression tag	UNP Q21A49
I	36	ALA	-	expression tag	UNP Q21A49
I	37	ALA	-	expression tag	UNP Q21A49
I	38	LEU	-	expression tag	UNP Q21A49
I	39	THR	-	expression tag	UNP Q21A49
I	40	ALA	-	expression tag	UNP Q21A49
I	41	LYS	-	expression tag	UNP Q21A49
I	42	SER	-	expression tag	UNP Q21A49
I	43	PRO	-	expression tag	UNP Q21A49
I	44	ASP	-	expression tag	UNP Q21A49
I	45	GLY	-	expression tag	UNP Q21A49
I	46	LYS	-	expression tag	UNP Q21A49
I	47	SER	-	expression tag	UNP Q21A49
I	48	ASN	-	expression tag	UNP Q21A49
I	49	SER	-	expression tag	UNP Q21A49
I	50	SER	-	expression tag	UNP Q21A49
I	51	ALA	-	expression tag	UNP Q21A49
I	52	ASP	-	expression tag	UNP Q21A49
I	53	ALA	-	expression tag	UNP Q21A49
I	54	ASP	-	expression tag	UNP Q21A49
I	55	VAL	-	expression tag	UNP Q21A49
I	56	VAL	-	expression tag	UNP Q21A49
I	57	ALA	-	expression tag	UNP Q21A49
I	58	ARG	-	expression tag	UNP Q21A49
I	222	GLY	PRO	engineered mutation	UNP Q21A49
I	257	ARG	ILE	engineered mutation	UNP Q21A49
I	261	LEU	ASN	engineered mutation	UNP Q21A49
I	280	LEU	ILE	engineered mutation	UNP Q21A49
I	326	ILE	LEU	engineered mutation	UNP Q21A49
I	327	THR	PRO	engineered mutation	UNP Q21A49
I	329	THR	VAL	engineered mutation	UNP Q21A49
I	481	HIS	LEU	engineered mutation	UNP Q21A49
J	1	MET	-	initiating methionine	UNP Q21A49
J	2	ALA	-	expression tag	UNP Q21A49
J	3	HIS	-	expression tag	UNP Q21A49

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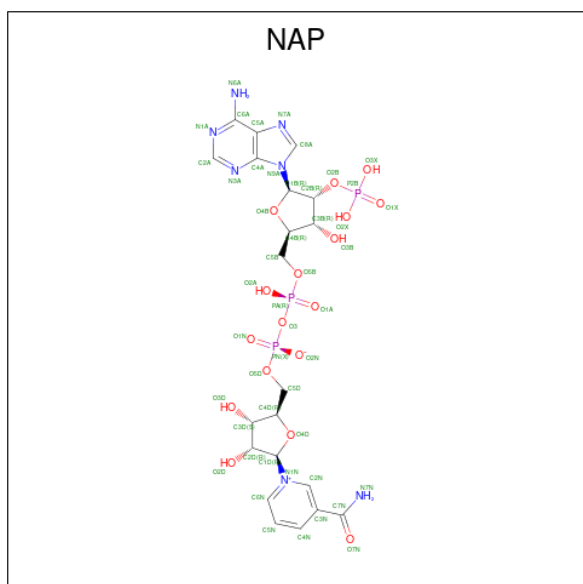
Chain	Residue	Modelled	Actual	Comment	Reference
J	4	HIS	-	expression tag	UNP Q21A49
J	5	HIS	-	expression tag	UNP Q21A49
J	6	HIS	-	expression tag	UNP Q21A49
J	7	HIS	-	expression tag	UNP Q21A49
J	8	HIS	-	expression tag	UNP Q21A49
J	9	VAL	-	expression tag	UNP Q21A49
J	10	GLY	-	expression tag	UNP Q21A49
J	11	THR	-	expression tag	UNP Q21A49
J	12	ASN	-	expression tag	UNP Q21A49
J	13	ASP	-	expression tag	UNP Q21A49
J	14	ALA	-	expression tag	UNP Q21A49
J	15	ASN	-	expression tag	UNP Q21A49
J	16	ILE	-	expression tag	UNP Q21A49
J	17	ALA	-	expression tag	UNP Q21A49
J	18	ASP	-	expression tag	UNP Q21A49
J	19	VAL	-	expression tag	UNP Q21A49
J	20	VAL	-	expression tag	UNP Q21A49
J	21	THR	-	expression tag	UNP Q21A49
J	22	LYS	-	expression tag	UNP Q21A49
J	23	VAL	-	expression tag	UNP Q21A49
J	24	LEU	-	expression tag	UNP Q21A49
J	25	GLY	-	expression tag	UNP Q21A49
J	26	GLU	-	expression tag	UNP Q21A49
J	27	TYR	-	expression tag	UNP Q21A49
J	28	GLY	-	expression tag	UNP Q21A49
J	29	ALA	-	expression tag	UNP Q21A49
J	30	PRO	-	expression tag	UNP Q21A49
J	31	GLY	-	expression tag	UNP Q21A49
J	32	ALA	-	expression tag	UNP Q21A49
J	33	VAL	-	expression tag	UNP Q21A49
J	34	SER	-	expression tag	UNP Q21A49
J	35	VAL	-	expression tag	UNP Q21A49
J	36	ALA	-	expression tag	UNP Q21A49
J	37	ALA	-	expression tag	UNP Q21A49
J	38	LEU	-	expression tag	UNP Q21A49
J	39	THR	-	expression tag	UNP Q21A49
J	40	ALA	-	expression tag	UNP Q21A49
J	41	LYS	-	expression tag	UNP Q21A49
J	42	SER	-	expression tag	UNP Q21A49
J	43	PRO	-	expression tag	UNP Q21A49
J	44	ASP	-	expression tag	UNP Q21A49
J	45	GLY	-	expression tag	UNP Q21A49

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Chain	Residue	Modelled	Actual	Comment	Reference
J	46	LYS	-	expression tag	UNP Q21A49
J	47	SER	-	expression tag	UNP Q21A49
J	48	ASN	-	expression tag	UNP Q21A49
J	49	SER	-	expression tag	UNP Q21A49
J	50	SER	-	expression tag	UNP Q21A49
J	51	ALA	-	expression tag	UNP Q21A49
J	52	ASP	-	expression tag	UNP Q21A49
J	53	ALA	-	expression tag	UNP Q21A49
J	54	ASP	-	expression tag	UNP Q21A49
J	55	VAL	-	expression tag	UNP Q21A49
J	56	VAL	-	expression tag	UNP Q21A49
J	57	ALA	-	expression tag	UNP Q21A49
J	58	ARG	-	expression tag	UNP Q21A49
J	222	GLY	PRO	engineered mutation	UNP Q21A49
J	257	ARG	ILE	engineered mutation	UNP Q21A49
J	261	LEU	ASN	engineered mutation	UNP Q21A49
J	280	LEU	ILE	engineered mutation	UNP Q21A49
J	326	ILE	LEU	engineered mutation	UNP Q21A49
J	327	THR	PRO	engineered mutation	UNP Q21A49
J	329	THR	VAL	engineered mutation	UNP Q21A49
J	481	HIS	LEU	engineered mutation	UNP Q21A49

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			38	16	2	17	3		
2	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	F	1	Total	C	N	O	P	0	0
			38	16	2	17	3		
2	G	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	H	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	I	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	J	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	K	0	0
			1	1		
3	B	1	Total	K	0	0
			1	1		
3	C	1	Total	K	0	0
			1	1		
3	D	1	Total	K	0	0
			1	1		
3	E	1	Total	K	0	0
			1	1		
3	F	1	Total	K	0	0
			1	1		
3	G	1	Total	K	0	0
			1	1		
3	H	1	Total	K	0	0
			1	1		
3	I	1	Total	K	0	0
			1	1		
3	J	1	Total	K	0	0
			1	1		

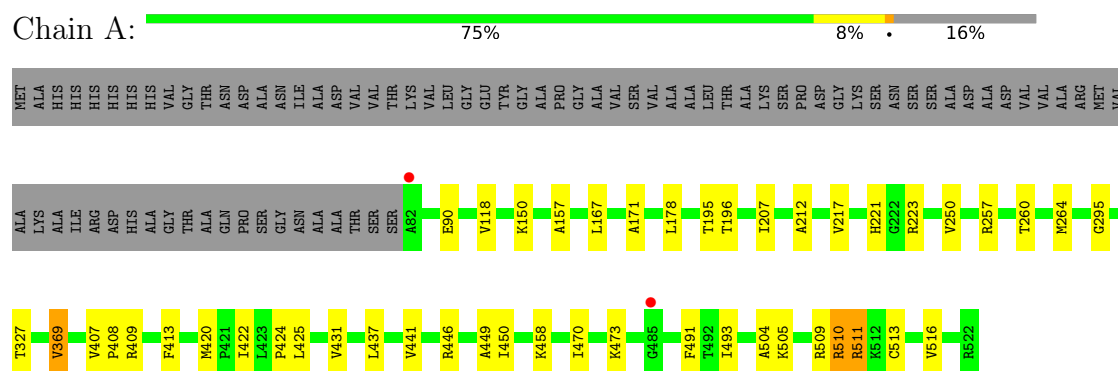
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	64	Total O 64 64	0	0
4	B	46	Total O 46 46	0	0
4	C	36	Total O 36 36	0	0
4	D	29	Total O 29 29	0	0
4	E	51	Total O 51 51	0	0
4	F	24	Total O 24 24	0	0
4	G	79	Total O 79 79	0	0
4	H	53	Total O 53 53	0	0
4	I	71	Total O 71 71	0	0
4	J	51	Total O 51 51	0	0

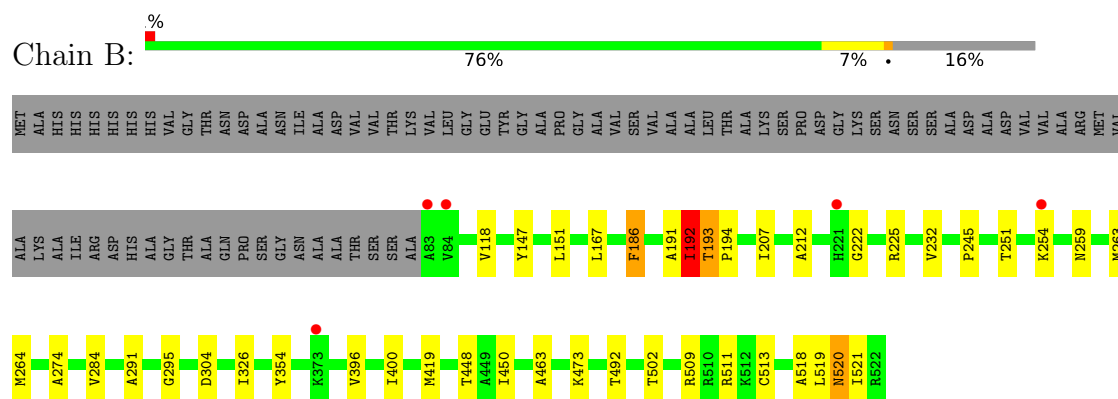
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

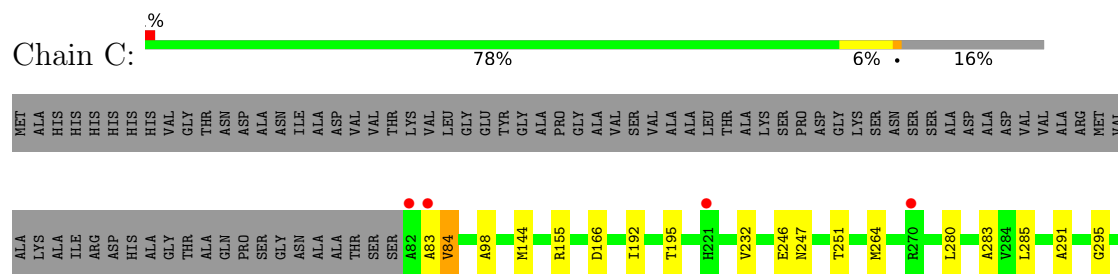
• Molecule 1: Aldehyde dehydrogenase



• Molecule 1: Aldehyde dehydrogenase

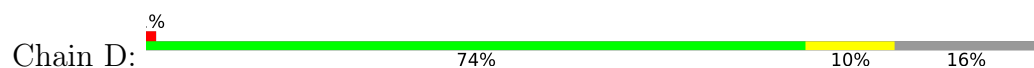


• Molecule 1: Aldehyde dehydrogenase

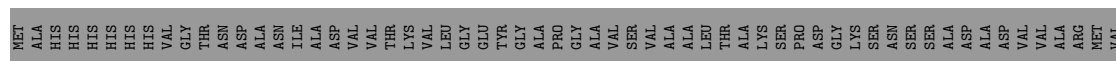
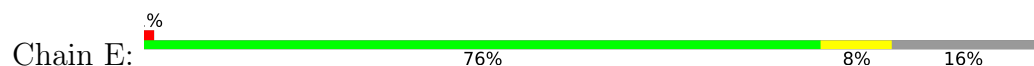




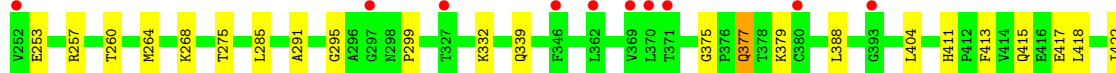
- Molecule 1: Aldehyde dehydrogenase



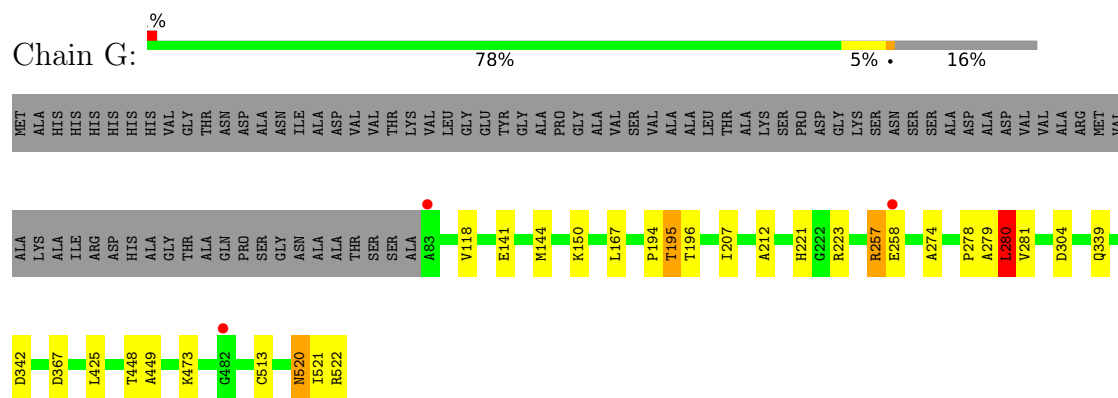
- Molecule 1: Aldehyde dehydrogenase



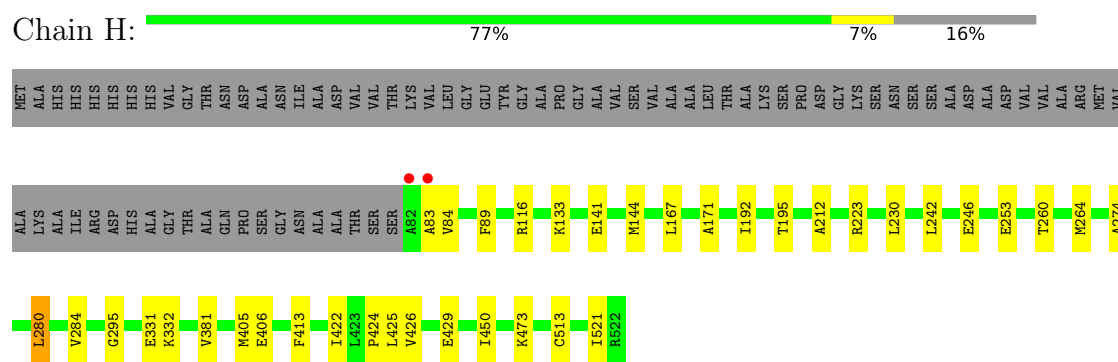
- Molecule 1: Aldehyde dehydrogenase



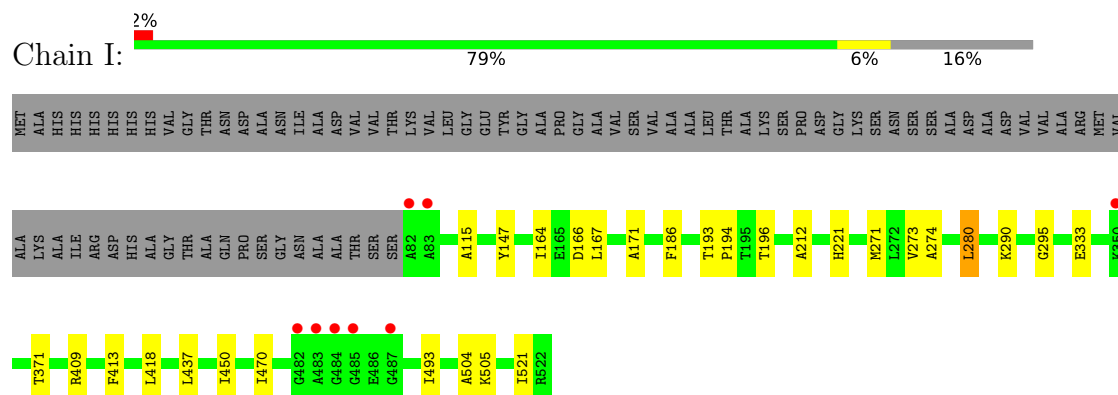
- Molecule 1: Aldehyde dehydrogenase



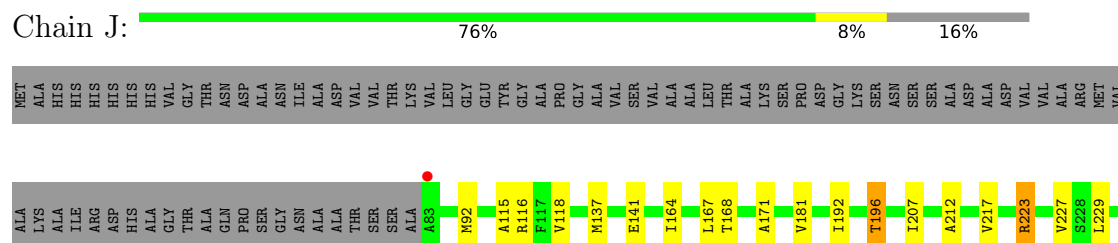
- Molecule 1: Aldehyde dehydrogenase



- Molecule 1: Aldehyde dehydrogenase



- Molecule 1: Aldehyde dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	362.20Å 123.18Å 165.10Å 90.00° 109.25° 90.00°	Depositor
Resolution (Å)	39.13 – 2.58 39.13 – 2.58	Depositor EDS
% Data completeness (in resolution range)	96.8 (39.13-2.58) 85.0 (39.13-2.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.71 (at 2.58Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.192 , 0.210 0.192 , 0.210	Depositor DCC
R_{free} test set	1963 reflections (0.91%)	wwPDB-VP
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.489	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	33944	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.58	4/3345 (0.1%)	0.40	2/4533 (0.0%)
1	B	0.53	3/3340 (0.1%)	0.47	3/4526 (0.1%)
1	C	0.32	1/3345 (0.0%)	0.37	1/4533 (0.0%)
1	D	0.51	0/3340	0.38	2/4526 (0.0%)
1	E	0.43	1/3345 (0.0%)	0.41	5/4533 (0.1%)
1	F	0.65	4/3345 (0.1%)	0.48	5/4533 (0.1%)
1	G	0.58	6/3340 (0.2%)	0.41	1/4526 (0.0%)
1	H	0.39	2/3345 (0.1%)	0.38	2/4533 (0.0%)
1	I	0.47	2/3345 (0.1%)	0.44	5/4533 (0.1%)
1	J	0.59	2/3340 (0.1%)	0.41	0/4526
All	All	0.51	25/33430 (0.1%)	0.42	26/45302 (0.1%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	281	VAL	C-O	-6.46	1.16	1.24
1	H	406	GLU	C-O	-6.15	1.16	1.24
1	G	195	THR	C-O	-6.03	1.16	1.24
1	B	192	ILE	C-O	-6.02	1.17	1.24
1	G	279	ALA	C-O	-5.82	1.17	1.24
1	I	273	VAL	C-O	-5.82	1.17	1.24
1	G	194	PRO	C-O	-5.77	1.16	1.23
1	A	504	ALA	C-O	-5.76	1.16	1.24
1	A	509	ARG	C-O	-5.75	1.16	1.23
1	B	191	ALA	C-O	-5.75	1.17	1.24
1	G	280	LEU	C-O	-5.59	1.17	1.24
1	E	338	ALA	C-O	-5.47	1.17	1.24
1	C	521	ILE	CA-C	-5.41	1.47	1.53
1	A	510	ARG	C-O	-5.41	1.17	1.24
1	F	509	ARG	C-O	-5.38	1.17	1.23
1	F	511	ARG	C-O	-5.38	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	448	THR	C-O	-5.35	1.17	1.23
1	H	426	VAL	C-O	-5.25	1.18	1.24
1	F	521	ILE	C-O	-5.16	1.18	1.24
1	I	194	PRO	C-O	-5.14	1.17	1.23
1	J	252	VAL	C-O	-5.13	1.18	1.24
1	A	511	ARG	C-O	-5.12	1.17	1.23
1	G	278	PRO	C-O	-5.08	1.17	1.24
1	J	254	LYS	C-O	-5.08	1.18	1.24
1	F	510	ARG	C-O	-5.03	1.17	1.24

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	193	THR	CA-C-N	11.14	130.90	119.76
1	B	193	THR	C-N-CA	11.14	130.90	119.76
1	F	415	GLN	N-CA-C	8.74	121.96	111.82
1	I	196	THR	N-CA-C	8.36	120.16	111.14
1	E	521	ILE	N-CA-C	7.60	118.68	111.91
1	C	83	ALA	N-CA-C	7.55	120.49	110.53
1	E	265	ALA	N-CA-C	7.08	119.08	111.36
1	B	225	ARG	N-CA-C	6.97	118.53	111.07
1	E	338	ALA	N-CA-C	6.83	118.72	111.28
1	I	147	TYR	N-CA-C	6.82	118.71	111.28
1	F	184	SER	CA-C-N	6.77	126.69	119.85
1	F	184	SER	C-N-CA	6.77	126.69	119.85
1	H	83	ALA	N-CA-C	6.71	120.21	110.28
1	H	429	GLU	N-CA-C	6.69	118.66	111.36
1	I	521	ILE	N-CA-C	6.17	117.40	111.91
1	A	516	VAL	N-CA-C	5.97	116.77	108.89
1	I	193	THR	CA-C-N	5.70	125.90	120.31
1	I	193	THR	C-N-CA	5.70	125.90	120.31
1	G	521	ILE	N-CA-C	5.41	117.40	111.77
1	D	338	ALA	N-CA-C	5.32	117.08	111.28
1	F	375	GLY	CA-C-N	5.29	125.19	119.85
1	F	375	GLY	C-N-CA	5.29	125.19	119.85
1	A	369	VAL	N-CA-C	5.23	120.23	113.07
1	E	85	SER	N-CA-C	5.12	117.72	110.50
1	D	223	ARG	N-CA-C	5.05	117.52	111.71
1	E	521	ILE	CB-CA-C	-5.01	106.43	112.19

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3299	0	3384	30	0
1	B	3294	0	3379	33	0
1	C	3299	0	3384	22	0
1	D	3294	0	3379	40	0
1	E	3299	0	3384	24	0
1	F	3299	0	3384	49	0
1	G	3294	0	3379	27	0
1	H	3299	0	3384	24	0
1	I	3299	0	3384	17	0
1	J	3294	0	3379	30	0
2	A	48	0	23	2	0
2	B	48	0	23	3	0
2	C	48	0	23	3	0
2	D	38	0	18	3	0
2	E	48	0	23	0	0
2	F	38	0	18	5	0
2	G	48	0	23	1	0
2	H	48	0	23	5	0
2	I	48	0	23	2	0
2	J	48	0	23	7	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
4	A	64	0	0	5	0
4	B	46	0	0	2	0
4	C	36	0	0	2	0
4	D	29	0	0	1	0
4	E	51	0	0	5	0
4	F	24	0	0	3	0
4	G	79	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	53	0	0	1	0
4	I	71	0	0	2	0
4	J	51	0	0	2	0
All	All	33944	0	34040	292	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 4.

All (292) 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:G:473:LYS:NZ	1:H:513:CYS:SG	2.48	0.85
1:C:513:CYS:SG	1:D:473:LYS:NZ	2.50	0.83
2:J:601:NAP:H8A	2:J:601:NAP:H52A	1.60	0.82
2:C:601:NAP:H2B	2:C:601:NAP:N3A	1.96	0.78
2:B:601:NAP:H51A	2:B:601:NAP:O1N	1.85	0.77
1:J:223:ARG:NH1	1:J:378:THR:HG21	2.02	0.75
1:C:195:THR:N	2:C:601:NAP:O1N	2.21	0.73
2:J:601:NAP:O2X	2:J:601:NAP:O3B	2.07	0.71
1:E:473:LYS:NZ	1:F:513:CYS:SG	2.57	0.71
1:A:513:CYS:SG	1:B:473:LYS:NZ	2.57	0.70
2:H:601:NAP:H52A	2:H:601:NAP:H8A	1.73	0.70
1:B:518:ALA:O	1:B:519:LEU:HB2	1.92	0.70
2:D:601:NAP:H51N	2:D:601:NAP:O1A	1.91	0.70
1:E:473:LYS:NZ	4:E:702:HOH:O	2.26	0.69
1:F:428:VAL:HG12	1:F:429:GLU:N	2.10	0.67
1:G:257:ARG:CG	1:G:257:ARG:HH21	2.08	0.66
1:G:258:GLU:OE2	1:G:258:GLU:N	2.25	0.66
1:B:284:VAL:HG12	1:B:291:ALA:HB1	1.77	0.66
1:A:510:ARG:HG3	4:A:738:HOH:O	1.96	0.66
1:B:354:TYR:HB2	1:B:400:ILE:HD13	1.76	0.66
1:F:428:VAL:HG12	1:F:429:GLU:H	1.62	0.65
1:C:473:LYS:NZ	1:D:513:CYS:SG	2.63	0.63
1:G:513:CYS:SG	1:H:473:LYS:NZ	2.66	0.63
1:J:223:ARG:HH11	1:J:378:THR:HG21	1.63	0.62
1:F:339:GLN:N	4:F:701:HOH:O	2.20	0.62
1:D:195:THR:HG21	1:D:223:ARG:HB3	1.80	0.62
1:E:217:VAL:HG22	1:E:250:VAL:CG2	2.29	0.62
1:F:225:ARG:NH2	1:F:253:GLU:O	2.33	0.62
1:B:520:ASN:OD1	1:B:520:ASN:N	2.17	0.61
1:F:133:LYS:NZ	1:F:137:MET:HE3	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:217:VAL:HG22	1:J:250:VAL:CG2	2.30	0.61
1:A:473:LYS:NZ	1:B:513:CYS:SG	2.61	0.61
1:J:116:ARG:NH2	1:J:242:LEU:O	2.34	0.61
1:J:223:ARG:HH11	1:J:378:THR:CG2	2.14	0.61
1:I:504:ALA:N	4:I:706:HOH:O	2.32	0.61
1:F:413:PHE:HB3	1:F:424:PRO:HG3	1.83	0.60
1:G:274:ALA:HB1	1:G:280:LEU:HD13	1.83	0.60
1:B:274:ALA:HB2	1:B:284:VAL:HG21	1.82	0.60
1:C:295:GLY:O	2:C:601:NAP:H2N	2.01	0.60
1:J:137:MET:HE2	1:J:227:VAL:HA	1.83	0.60
1:F:285:LEU:HD23	1:F:291:ALA:HB3	1.85	0.59
1:A:195:THR:HG21	1:A:223:ARG:HD3	1.85	0.59
1:D:147:TYR:CE2	1:D:151:LEU:HD11	2.37	0.58
1:E:264:MET:HE1	1:E:283:ALA:HB1	1.84	0.58
1:C:285:LEU:HD23	1:C:291:ALA:HB3	1.84	0.58
1:F:388:LEU:HD13	1:F:422:ILE:HD11	1.85	0.58
1:H:521:ILE:HD12	1:H:521:ILE:O	2.04	0.58
1:B:118:VAL:HG13	1:B:207:ILE:HG23	1.86	0.58
1:F:195:THR:N	2:F:601:NAP:O1N	2.33	0.58
1:J:168:THR:OG1	4:J:701:HOH:O	2.17	0.58
1:C:84:VAL:HG23	1:C:246:GLU:HG2	1.85	0.57
1:F:521:ILE:HG13	4:F:709:HOH:O	2.04	0.57
1:E:332:LYS:HE2	4:E:705:HOH:O	2.03	0.57
1:F:428:VAL:HG11	1:F:433:ASP:CB	2.33	0.57
4:E:702:HOH:O	1:F:513:CYS:SG	2.58	0.57
1:B:492:THR:HG1	1:B:502:THR:HG1	1.50	0.57
1:I:274:ALA:HB1	1:I:280:LEU:HD13	1.87	0.57
1:A:413:PHE:HB3	1:A:424:PRO:HG3	1.88	0.56
1:D:195:THR:N	2:D:601:NAP:O1N	2.39	0.56
1:B:193:THR:HB	1:B:194:PRO:HD2	1.88	0.56
1:F:435:ILE:HD12	1:F:462:MET:HB2	1.88	0.55
1:D:196:THR:HG23	1:D:326:ILE:HB	1.88	0.55
1:F:428:VAL:HG11	1:F:433:ASP:HB3	1.87	0.55
1:J:196:THR:HG23	1:J:326:ILE:HB	1.88	0.55
1:J:92:MET:HE3	1:J:263:MET:HB2	1.87	0.55
1:H:116:ARG:NH2	1:H:242:LEU:O	2.38	0.55
1:J:181:VAL:HG11	1:J:510:ARG:NH1	2.22	0.55
1:F:184:SER:OG	1:G:522:ARG:OXT	2.23	0.55
2:H:601:NAP:H8A	2:H:601:NAP:C5B	2.36	0.55
1:F:157:ALA:HB2	1:F:491:PHE:HE2	1.72	0.55
1:D:521:ILE:C	1:D:521:ILE:HD12	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:260:THR:HG22	1:F:264:MET:HE3	1.88	0.54
1:G:342:ASP:CG	4:G:711:HOH:O	2.51	0.54
1:A:221:HIS:CD2	2:A:601:NAP:H3B	2.43	0.54
1:J:118:VAL:HG13	1:J:207:ILE:HG23	1.90	0.54
2:D:601:NAP:H51N	2:D:601:NAP:PA	2.48	0.53
1:D:428:VAL:HG21	1:D:434:ALA:HB2	1.90	0.53
1:H:260:THR:CG2	1:H:264:MET:HE3	2.39	0.53
1:A:446:ARG:NE	4:A:701:HOH:O	2.20	0.53
1:E:332:LYS:CE	4:E:705:HOH:O	2.57	0.53
1:H:260:THR:HG22	1:H:264:MET:HE3	1.90	0.53
1:E:167:LEU:HD11	1:E:212:ALA:HA	1.91	0.53
1:B:167:LEU:HD11	1:B:212:ALA:HA	1.91	0.52
1:B:295:GLY:O	2:B:601:NAP:H2N	2.09	0.52
1:D:420:MET:O	1:D:422:ILE:N	2.39	0.52
2:H:601:NAP:H52A	2:H:601:NAP:C8A	2.37	0.52
1:I:409:ARG:HE	1:I:437:LEU:HD13	1.74	0.52
1:A:437:LEU:O	1:A:441:VAL:HG12	2.10	0.52
1:B:147:TYR:CE2	1:B:151:LEU:HD11	2.45	0.52
1:J:354:TYR:HB2	1:J:400:ILE:HD12	1.92	0.52
1:E:137:MET:HE2	1:E:227:VAL:HA	1.91	0.52
1:A:409:ARG:HE	1:A:437:LEU:HD13	1.74	0.52
1:H:274:ALA:HB1	1:H:280:LEU:HD13	1.91	0.51
1:H:195:THR:N	2:H:601:NAP:O1N	2.39	0.51
1:H:133:LYS:HE3	1:H:230:LEU:HD21	1.92	0.51
1:E:405:MET:HE1	1:E:422:ILE:HG23	1.93	0.51
1:F:153:LYS:HE2	1:F:197:ASN:OD1	2.11	0.51
1:I:450:ILE:N	1:I:450:ILE:HD12	2.26	0.51
1:J:229:LEU:CD2	1:J:253:GLU:OE1	2.58	0.51
1:A:178:LEU:HD22	1:D:180:LEU:HD11	1.92	0.51
1:B:192:ILE:HD13	1:B:263:MET:HE1	1.93	0.51
1:C:425:LEU:C	1:C:425:LEU:HD23	2.36	0.51
1:F:515:MET:HG2	1:F:519:LEU:HD12	1.92	0.51
1:G:221:HIS:ND1	2:G:601:NAP:H3B	2.26	0.50
1:I:470:ILE:HD12	1:I:493:ILE:HD13	1.94	0.50
1:J:167:LEU:HD11	1:J:212:ALA:HA	1.93	0.50
1:E:520:ASN:OD1	1:E:520:ASN:N	2.44	0.50
1:F:101:LEU:O	1:F:105:GLN:HG3	2.12	0.50
1:H:331:GLU:HG3	1:H:450:ILE:HD13	1.94	0.50
1:J:141:GLU:HG2	1:J:223:ARG:O	2.12	0.50
2:J:601:NAP:H8A	2:J:601:NAP:H3B	1.93	0.50
1:D:92:MET:HE3	1:D:259:ASN:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:167:LEU:HD11	1:F:212:ALA:HA	1.94	0.50
1:C:354:TYR:HB2	1:C:400:ILE:HD12	1.94	0.49
1:J:229:LEU:HD21	1:J:253:GLU:OE1	2.12	0.49
1:F:428:VAL:CG1	1:F:433:ASP:CB	2.90	0.49
1:E:311:LYS:NZ	1:E:315:ASP:OD2	2.45	0.49
2:J:601:NAP:H52A	2:J:601:NAP:C8A	2.38	0.49
1:H:167:LEU:HD11	1:H:212:ALA:HA	1.94	0.49
1:B:284:VAL:CG1	1:B:291:ALA:HB1	2.41	0.49
1:B:264:MET:HE3	1:B:284:VAL:HA	1.93	0.49
4:B:704:HOH:O	1:C:521:ILE:HG13	2.11	0.49
1:B:492:THR:OG1	1:B:502:THR:OG1	2.25	0.48
1:B:186:PHE:CE2	1:B:509:ARG:HG2	2.47	0.48
1:I:115:ALA:HB2	1:I:164:ILE:HD13	1.94	0.48
1:A:425:LEU:HD23	1:A:425:LEU:C	2.38	0.48
1:E:513:CYS:SG	1:F:473:LYS:NZ	2.77	0.48
1:D:223:ARG:O	1:D:223:ARG:HG3	2.13	0.48
1:F:450:ILE:N	1:F:450:ILE:HD12	2.28	0.48
1:A:327:THR:CB	4:A:705:HOH:O	2.60	0.48
1:C:457:ARG:O	4:C:701:HOH:O	2.20	0.48
1:A:450:ILE:N	1:A:450:ILE:HD12	2.28	0.48
1:D:167:LEU:HD11	1:D:212:ALA:HA	1.96	0.48
1:H:521:ILE:HD12	1:H:521:ILE:C	2.37	0.48
1:I:295:GLY:O	2:I:601:NAP:H2N	2.14	0.48
1:B:232:VAL:HG11	1:B:251:THR:HG22	1.96	0.48
1:F:157:ALA:HB2	1:F:491:PHE:CE2	2.49	0.48
1:G:257:ARG:HH21	1:G:257:ARG:HG2	1.78	0.48
1:I:166:ASP:O	1:I:505:LYS:HE2	2.14	0.48
1:I:221:HIS:CD2	2:I:601:NAP:H3B	2.48	0.48
1:B:254:LYS:O	1:B:259:ASN:ND2	2.47	0.47
1:G:257:ARG:CG	1:G:257:ARG:NH2	2.73	0.47
1:G:522:ARG:NE	4:G:710:HOH:O	2.45	0.47
1:F:377:GLN:HG3	1:F:379:LYS:H	1.78	0.47
1:F:428:VAL:CG1	1:F:433:ASP:HB2	2.44	0.47
1:E:192:ILE:HD13	1:E:280:LEU:HD11	1.97	0.47
1:A:167:LEU:HD11	1:A:212:ALA:HA	1.96	0.47
1:D:418:LEU:HD22	1:D:420:MET:CE	2.45	0.47
1:J:274:ALA:HB2	1:J:284:VAL:HG11	1.96	0.47
1:J:299:PRO:HD2	1:J:332:LYS:HD2	1.96	0.47
1:I:171:ALA:HB2	1:J:171:ALA:HB2	1.97	0.47
1:D:119:GLN:OE1	4:D:701:HOH:O	2.20	0.47
1:A:150:LYS:NZ	1:A:196:THR:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:258:GLU:N	1:G:258:GLU:CD	2.72	0.47
1:C:155:ARG:NE	4:C:705:HOH:O	2.31	0.46
1:A:217:VAL:HG22	1:A:250:VAL:CG2	2.45	0.46
1:B:245:PRO:O	4:B:701:HOH:O	2.20	0.46
1:G:144:MET:HE1	1:G:195:THR:HB	1.98	0.46
1:B:396:VAL:HB	1:B:400:ILE:HD12	1.98	0.46
1:D:497:THR:OG1	1:D:499:GLU:OE1	2.30	0.46
1:H:425:LEU:C	1:H:425:LEU:HD23	2.40	0.46
1:I:470:ILE:CD1	1:I:493:ILE:HD13	2.45	0.46
1:G:257:ARG:HG2	1:G:257:ARG:NH2	2.30	0.46
1:D:223:ARG:HE	1:D:223:ARG:HB2	1.59	0.46
1:D:311:LYS:NZ	1:D:315:ASP:OD2	2.43	0.46
1:B:521:ILE:HG21	1:D:463:ALA:HB3	1.97	0.45
1:G:141:GLU:HG2	1:G:223:ARG:O	2.16	0.45
1:J:253:GLU:OE1	1:J:253:GLU:HA	2.15	0.45
1:D:101:LEU:HD13	1:D:101:LEU:O	2.16	0.45
1:F:295:GLY:O	2:F:601:NAP:H2N	2.16	0.45
1:A:157:ALA:HB2	1:A:491:PHE:CE2	2.51	0.45
1:C:192:ILE:HD13	1:C:280:LEU:HD11	1.98	0.45
1:F:413:PHE:CD1	1:F:418:LEU:HD11	2.52	0.45
1:H:405:MET:HE1	1:H:422:ILE:HG23	1.99	0.45
1:B:192:ILE:HD13	1:B:192:ILE:N	2.31	0.45
2:J:601:NAP:H3B	2:J:601:NAP:C8A	2.47	0.45
1:A:327:THR:HB	4:A:705:HOH:O	2.16	0.45
1:B:511:ARG:NH2	1:C:521:ILE:O	2.50	0.45
1:I:186:PHE:CZ	1:I:271:MET:HE3	2.51	0.45
1:D:449:ALA:CB	1:D:466:ILE:HD13	2.47	0.44
1:G:342:ASP:CB	4:G:711:HOH:O	2.64	0.44
1:J:440:GLU:OE2	4:J:702:HOH:O	2.21	0.44
1:C:264:MET:HE1	1:C:283:ALA:HB1	2.00	0.44
1:E:331:GLU:HG3	1:E:450:ILE:HD13	1.99	0.44
1:H:332:LYS:NZ	4:H:710:HOH:O	2.51	0.44
1:J:192:ILE:HD13	1:J:280:LEU:HD11	1.99	0.44
1:B:519:LEU:HD23	1:B:519:LEU:HA	1.72	0.44
1:F:425:LEU:HD23	1:F:425:LEU:C	2.42	0.44
2:F:601:NAP:O2A	4:F:702:HOH:O	2.21	0.44
1:G:339:GLN:HG2	4:G:708:HOH:O	2.17	0.44
1:J:196:THR:HG21	1:J:326:ILE:O	2.18	0.44
1:F:260:THR:CG2	1:F:264:MET:HE3	2.47	0.44
1:F:428:VAL:CG1	1:F:429:GLU:N	2.79	0.44
1:I:167:LEU:HD11	1:I:212:ALA:HA	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:MET:C	1:A:422:ILE:H	2.25	0.44
1:B:222:GLY:N	2:B:601:NAP:O2X	2.51	0.44
1:F:428:VAL:CG1	1:F:433:ASP:HB3	2.47	0.44
1:A:407:VAL:HB	1:A:408:PRO:HD2	1.99	0.44
1:F:134:MET:HE1	1:F:230:LEU:HG	1.99	0.44
1:A:295:GLY:O	2:A:601:NAP:H2N	2.18	0.44
1:D:117:PHE:N	1:D:117:PHE:CD1	2.82	0.44
1:J:137:MET:HE2	1:J:227:VAL:CA	2.47	0.44
1:A:470:ILE:CD1	1:A:493:ILE:HD13	2.48	0.43
1:D:360:ALA:O	1:D:364:GLN:HG3	2.19	0.43
1:G:167:LEU:HD11	1:G:212:ALA:HA	1.99	0.43
1:G:195:THR:OG1	1:G:221:HIS:ND1	2.51	0.43
1:J:470:ILE:HD12	1:J:493:ILE:HD13	1.99	0.43
1:C:144:MET:HE2	1:C:195:THR:HG22	2.00	0.43
1:G:367:ASP:OD2	4:G:701:HOH:O	2.20	0.43
1:C:466:ILE:HG12	1:C:468:THR:HG23	2.00	0.43
1:I:186:PHE:CE2	1:I:271:MET:HE3	2.53	0.43
1:J:376:PRO:HD3	1:J:416:GLU:HG3	2.00	0.43
2:J:601:NAP:C8A	2:J:601:NAP:C3B	2.96	0.43
1:B:521:ILE:H	1:B:521:ILE:HG13	1.69	0.43
1:D:365:LEU:O	1:D:369:VAL:HG22	2.19	0.43
1:J:296:ALA:HB2	2:J:601:NAP:O3D	2.19	0.43
1:B:450:ILE:HD12	1:B:450:ILE:N	2.34	0.43
1:E:497:THR:OG1	1:E:499:GLU:OE1	2.34	0.43
1:H:141:GLU:HG2	1:H:223:ARG:O	2.19	0.43
1:G:520:ASN:OD1	1:G:520:ASN:N	2.42	0.42
1:F:299:PRO:HD2	1:F:332:LYS:CG	2.50	0.42
1:D:195:THR:HG23	1:D:221:HIS:HB2	1.99	0.42
1:F:466:ILE:HG12	1:F:468:THR:HG23	2.00	0.42
1:F:428:VAL:CG1	1:F:429:GLU:H	2.31	0.42
1:F:449:ALA:CB	1:F:466:ILE:HD13	2.50	0.42
1:A:260:THR:O	1:A:264:MET:HG3	2.20	0.42
1:D:413:PHE:CD1	1:D:418:LEU:HD11	2.54	0.42
1:E:171:ALA:HB2	1:H:171:ALA:HB2	2.01	0.42
4:A:708:HOH:O	1:D:521:ILE:HG13	2.19	0.42
1:B:304:ASP:OD1	1:B:304:ASP:C	2.63	0.42
1:C:413:PHE:HB3	1:C:424:PRO:HG3	2.01	0.42
1:E:272:LEU:O	1:E:291:ALA:HA	2.20	0.42
1:E:406:GLU:OE1	4:E:701:HOH:O	2.21	0.42
1:A:171:ALA:HB2	1:D:171:ALA:HB2	2.02	0.42
1:A:449:ALA:C	1:A:450:ILE:HD12	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:326:ILE:HA	1:B:419:MET:HE2	2.02	0.42
1:C:232:VAL:HG11	1:C:251:THR:HG22	2.02	0.42
1:D:86:ASP:OD2	1:D:233:ARG:NE	2.46	0.42
1:D:449:ALA:HB2	1:D:466:ILE:HD13	2.01	0.42
1:F:223:ARG:HD2	2:F:601:NAP:C1B	2.49	0.42
1:D:272:LEU:HD13	1:D:284:VAL:HG23	2.02	0.42
1:F:133:LYS:NZ	1:F:137:MET:HB2	2.35	0.41
1:F:499:GLU:N	1:F:499:GLU:OE1	2.53	0.41
1:A:90:GLU:HG2	1:I:371:THR:HG21	2.02	0.41
1:A:118:VAL:HG13	1:A:207:ILE:HG23	2.02	0.41
1:D:521:ILE:HD12	1:D:521:ILE:O	2.19	0.41
1:E:144:MET:HE2	1:E:195:THR:HG22	2.01	0.41
1:G:118:VAL:HG13	1:G:207:ILE:HG23	2.02	0.41
1:H:413:PHE:HB3	1:H:424:PRO:HG3	2.02	0.41
1:D:195:THR:CG2	1:D:223:ARG:HB3	2.50	0.41
1:E:271:MET:HE2	1:E:292:ILE:HG13	2.01	0.41
1:F:411:HIS:ND1	1:F:413:PHE:HB2	2.35	0.41
1:H:89:PHE:O	1:H:253:GLU:N	2.53	0.41
1:C:166:ASP:HB3	1:C:504:ALA:HB3	2.02	0.41
1:F:332:LYS:HE2	1:F:417:GLU:HG3	2.03	0.41
1:G:339:GLN:O	4:G:702:HOH:O	2.22	0.41
1:H:192:ILE:HD13	1:H:280:LEU:HD21	2.01	0.41
1:I:413:PHE:CD1	1:I:418:LEU:HD11	2.55	0.41
1:E:144:MET:CE	1:E:195:THR:HG22	2.51	0.41
1:F:97:GLU:OE1	1:F:268:LYS:NZ	2.45	0.41
1:D:275:THR:HA	1:D:294:ALA:HB3	2.02	0.41
1:E:413:PHE:CD1	1:E:418:LEU:HD11	2.56	0.41
1:J:115:ALA:HB2	1:J:164:ILE:HD13	2.02	0.41
1:E:459:LEU:HD13	1:F:515:MET:HE1	2.01	0.41
1:H:84:VAL:HA	1:H:246:GLU:OE2	2.21	0.41
1:J:326:ILE:HA	1:J:419:MET:HE2	2.02	0.41
1:A:431:VAL:HG11	1:A:458:LYS:HD2	2.02	0.41
1:C:98:ALA:HB1	1:C:247:ASN:ND2	2.36	0.41
1:C:379:LYS:HE3	1:C:379:LYS:HB3	1.62	0.41
1:D:225:ARG:O	1:D:229:LEU:HD13	2.20	0.41
1:D:334:ILE:HD11	1:D:423:LEU:HD21	2.02	0.41
2:F:601:NAP:P2B	2:F:601:NAP:O3B	2.79	0.41
1:G:304:ASP:OD1	1:G:304:ASP:C	2.63	0.41
1:G:425:LEU:HD23	1:G:425:LEU:C	2.46	0.41
1:A:178:LEU:CD2	1:D:180:LEU:HD11	2.51	0.41
1:E:225:ARG:CD	1:E:255:PRO:HD2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:450:ILE:HD12	1:J:450:ILE:N	2.36	0.41
1:F:194:PRO:HD3	1:F:275:THR:HB	2.03	0.40
1:F:450:ILE:HG22	1:F:451:MET:N	2.36	0.40
1:H:274:ALA:HB2	1:H:284:VAL:HG11	2.03	0.40
1:I:290:LYS:NZ	4:I:711:HOH:O	2.54	0.40
1:C:377:GLN:HG3	1:C:379:LYS:HB2	2.03	0.40
1:F:200:GLU:H	1:F:200:GLU:CD	2.29	0.40
1:G:150:LYS:NZ	1:G:196:THR:O	2.53	0.40
1:G:448:THR:HG22	1:G:449:ALA:N	2.37	0.40
1:H:144:MET:HE2	1:H:381:VAL:HB	2.03	0.40
1:D:103:GLN:HE22	1:D:107:LEU:HD21	1.86	0.40
1:A:511:ARG:NH2	1:B:463:ALA:O	2.53	0.40
1:B:193:THR:HA	1:B:194:PRO:HD3	1.93	0.40
1:D:203:VAL:HG23	1:D:231:LEU:HD21	2.03	0.40
1:D:369:VAL:HB	1:D:420:MET:HE1	2.03	0.40
1:H:295:GLY:O	2:H:601:NAP:H2N	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	439/522 (84%)	432 (98%)	7 (2%)	0	100	100
1	B	438/522 (84%)	426 (97%)	12 (3%)	0	100	100
1	C	439/522 (84%)	427 (97%)	12 (3%)	0	100	100
1	D	438/522 (84%)	430 (98%)	8 (2%)	0	100	100
1	E	439/522 (84%)	431 (98%)	8 (2%)	0	100	100
1	F	439/522 (84%)	429 (98%)	10 (2%)	0	100	100
1	G	438/522 (84%)	430 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	439/522 (84%)	430 (98%)	9 (2%)	0	100	100
1	I	439/522 (84%)	429 (98%)	10 (2%)	0	100	100
1	J	438/522 (84%)	425 (97%)	13 (3%)	0	100	100
All	All	4386/5220 (84%)	4289 (98%)	97 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	357/414 (86%)	354 (99%)	3 (1%)	73	87
1	B	357/414 (86%)	354 (99%)	3 (1%)	73	87
1	C	357/414 (86%)	355 (99%)	2 (1%)	78	89
1	D	357/414 (86%)	355 (99%)	2 (1%)	78	89
1	E	357/414 (86%)	353 (99%)	4 (1%)	65	83
1	F	357/414 (86%)	353 (99%)	4 (1%)	65	83
1	G	357/414 (86%)	354 (99%)	3 (1%)	73	87
1	H	357/414 (86%)	356 (100%)	1 (0%)	86	94
1	I	357/414 (86%)	355 (99%)	2 (1%)	78	89
1	J	357/414 (86%)	355 (99%)	2 (1%)	78	89
All	All	3570/4140 (86%)	3544 (99%)	26 (1%)	76	88

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	257	ARG
1	A	369	VAL
1	A	505	LYS
1	B	186	PHE
1	B	192	ILE

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Mol	Chain	Res	Type
1	B	520	ASN
1	C	84	VAL
1	C	379	LYS
1	D	118	VAL
1	D	223	ARG
1	E	84	VAL
1	E	186	PHE
1	E	339	GLN
1	E	520	ASN
1	F	257	ARG
1	F	377	GLN
1	F	404	LEU
1	F	510	ARG
1	G	257	ARG
1	G	280	LEU
1	G	520	ASN
1	H	280	LEU
1	I	280	LEU
1	I	333	GLU
1	J	196	THR
1	J	223	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	221	HIS
1	A	366	GLN
1	A	445	ASN
1	C	146	ASN
1	C	445	ASN
1	D	103	GLN
1	D	443	HIS
1	E	128	GLN
1	E	221	HIS
1	E	364	GLN
1	G	339	GLN
1	G	351	ASN
1	H	146	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 for Mogul analysis.

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	NAP	D	601	-	38,40,52	4.13	12 (31%)	49,61,80	1.52	5 (10%)
2	NAP	A	601	-	50,52,52	3.69	22 (44%)	71,80,80	2.02	19 (26%)
2	NAP	H	601	-	50,52,52	3.57	19 (38%)	71,80,80	1.99	18 (25%)
2	NAP	J	601	-	50,52,52	3.60	20 (40%)	71,80,80	1.99	19 (26%)
2	NAP	C	601	-	50,52,52	3.56	19 (38%)	71,80,80	1.83	17 (23%)
2	NAP	B	601	-	50,52,52	3.52	18 (36%)	71,80,80	1.88	17 (23%)
2	NAP	E	601	-	50,52,52	3.67	20 (40%)	71,80,80	1.97	19 (26%)
2	NAP	I	601	-	50,52,52	3.74	22 (44%)	71,80,80	2.18	23 (32%)
2	NAP	F	601	-	38,40,52	4.32	15 (39%)	49,61,80	1.44	7 (14%)
2	NAP	G	601	-	50,52,52	3.75	19 (38%)	71,80,80	2.18	26 (36%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAP	D	601	-	-	6/31/60/67	0/3/3/5
2	NAP	A	601	-	-	6/35/67/67	0/5/5/5
2	NAP	H	601	-	-	13/35/67/67	0/5/5/5
2	NAP	J	601	-	-	12/35/67/67	0/5/5/5
2	NAP	C	601	-	-	8/35/67/67	0/5/5/5
2	NAP	B	601	-	-	5/35/67/67	0/5/5/5
2	NAP	E	601	-	-	11/35/67/67	0/5/5/5
2	NAP	I	601	-	-	3/35/67/67	0/5/5/5
2	NAP	F	601	-	-	13/31/60/67	0/3/3/5
2	NAP	G	601	-	-	9/35/67/67	0/5/5/5

All (186) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	601	NAP	O4D-C1D	14.61	1.60	1.40
2	G	601	NAP	O4D-C1D	14.43	1.59	1.40
2	J	601	NAP	O4D-C1D	13.76	1.59	1.40
2	A	601	NAP	O4D-C1D	13.75	1.58	1.40
2	D	601	NAP	O4D-C1D	13.66	1.58	1.40
2	I	601	NAP	O4D-C1D	13.55	1.58	1.40
2	C	601	NAP	O4D-C1D	13.47	1.58	1.40
2	E	601	NAP	O4D-C1D	13.46	1.58	1.40
2	H	601	NAP	O4D-C1D	12.89	1.57	1.40
2	B	601	NAP	O4D-C1D	12.60	1.57	1.40
2	F	601	NAP	C1B-C2B	-12.06	1.29	1.52
2	D	601	NAP	C1B-C2B	-11.62	1.30	1.52
2	I	601	NAP	C2B-C1B	-10.21	1.28	1.53
2	H	601	NAP	C2B-C1B	-9.96	1.28	1.53
2	B	601	NAP	C2B-C1B	-9.67	1.29	1.53
2	G	601	NAP	C2B-C1B	-9.51	1.29	1.53
2	J	601	NAP	C2B-C1B	-9.47	1.29	1.53
2	C	601	NAP	C2B-C1B	-9.36	1.30	1.53
2	A	601	NAP	C2B-C1B	-9.26	1.30	1.53
2	E	601	NAP	C2B-C1B	-9.18	1.30	1.53
2	E	601	NAP	O4B-C1B	8.79	1.62	1.42
2	F	601	NAP	O4B-C1B	8.36	1.61	1.43
2	D	601	NAP	O4B-C4B	-8.33	1.30	1.44
2	H	601	NAP	O4B-C1B	8.32	1.61	1.42
2	F	601	NAP	O4B-C4B	-8.28	1.30	1.44
2	G	601	NAP	O4D-C4D	-8.23	1.26	1.45
2	C	601	NAP	O4B-C1B	8.06	1.60	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	NAP	O4D-C4D	-8.06	1.27	1.45
2	D	601	NAP	O4B-C1B	8.06	1.61	1.43
2	B	601	NAP	O4B-C1B	7.92	1.60	1.42
2	G	601	NAP	O4B-C1B	7.86	1.60	1.42
2	J	601	NAP	O4B-C1B	7.77	1.60	1.42
2	A	601	NAP	O4D-C4D	-7.63	1.28	1.45
2	A	601	NAP	O4B-C1B	7.50	1.59	1.42
2	I	601	NAP	O4D-C4D	-7.41	1.28	1.45
2	I	601	NAP	O4B-C4B	-7.40	1.28	1.45
2	E	601	NAP	O4D-C4D	-7.31	1.28	1.45
2	C	601	NAP	O4D-C4D	-7.29	1.28	1.45
2	I	601	NAP	O4B-C1B	7.22	1.58	1.42
2	H	601	NAP	O4D-C4D	-7.22	1.28	1.45
2	D	601	NAP	O4D-C4D	-7.19	1.29	1.45
2	J	601	NAP	O4D-C4D	-7.18	1.29	1.45
2	F	601	NAP	O4D-C4D	-7.16	1.29	1.45
2	A	601	NAP	O4B-C4B	-7.11	1.29	1.45
2	H	601	NAP	O4B-C4B	-6.59	1.30	1.45
2	J	601	NAP	O4B-C4B	-6.54	1.30	1.45
2	B	601	NAP	O4B-C4B	-6.49	1.30	1.45
2	G	601	NAP	O4B-C4B	-6.22	1.31	1.45
2	E	601	NAP	O4B-C4B	-6.20	1.31	1.45
2	C	601	NAP	O4B-C4B	-6.08	1.31	1.45
2	F	601	NAP	C7N-N7N	5.76	1.43	1.33
2	I	601	NAP	C7N-N7N	5.54	1.43	1.33
2	I	601	NAP	O7N-C7N	-5.35	1.14	1.24
2	H	601	NAP	C7N-N7N	5.33	1.42	1.33
2	J	601	NAP	C7N-N7N	5.31	1.42	1.33
2	G	601	NAP	O7N-C7N	-5.28	1.14	1.24
2	A	601	NAP	C7N-N7N	5.21	1.42	1.33
2	D	601	NAP	C7N-N7N	5.21	1.42	1.33
2	G	601	NAP	C4N-C3N	-5.20	1.31	1.39
2	E	601	NAP	O7N-C7N	-5.17	1.14	1.24
2	C	601	NAP	C7N-N7N	5.17	1.42	1.33
2	A	601	NAP	O7N-C7N	-4.80	1.15	1.24
2	E	601	NAP	C7N-N7N	4.78	1.41	1.33
2	E	601	NAP	C4N-C3N	-4.77	1.32	1.39
2	J	601	NAP	O7N-C7N	-4.69	1.15	1.24
2	B	601	NAP	O7N-C7N	-4.67	1.15	1.24
2	J	601	NAP	C6A-N6A	4.66	1.46	1.34
2	B	601	NAP	C7N-N7N	4.54	1.41	1.33
2	D	601	NAP	O7N-C7N	-4.53	1.15	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	601	NAP	C7N-N7N	4.53	1.41	1.33
2	F	601	NAP	O7N-C7N	-4.47	1.15	1.24
2	C	601	NAP	O7N-C7N	-4.45	1.15	1.24
2	J	601	NAP	C4N-C3N	-4.44	1.32	1.39
2	H	601	NAP	O7N-C7N	-4.43	1.15	1.24
2	A	601	NAP	C5A-N7A	-4.40	1.31	1.39
2	A	601	NAP	C4N-C3N	-4.39	1.32	1.39
2	G	601	NAP	O3D-C3D	-4.38	1.32	1.43
2	F	601	NAP	C4N-C3N	-4.35	1.32	1.39
2	G	601	NAP	C5N-C4N	-4.35	1.31	1.38
2	A	601	NAP	C5A-C4A	-4.28	1.31	1.39
2	E	601	NAP	C5A-C4A	-4.23	1.31	1.39
2	C	601	NAP	C4N-C3N	-4.22	1.33	1.39
2	I	601	NAP	O3D-C3D	-4.21	1.32	1.43
2	A	601	NAP	O3D-C3D	-4.20	1.32	1.43
2	B	601	NAP	C6A-N6A	4.19	1.44	1.34
2	H	601	NAP	O3D-C3D	-4.18	1.32	1.43
2	G	601	NAP	C6A-N6A	4.16	1.44	1.34
2	C	601	NAP	C6A-N6A	4.16	1.44	1.34
2	E	601	NAP	O3D-C3D	-4.07	1.32	1.43
2	F	601	NAP	O3D-C3D	-4.05	1.32	1.43
2	H	601	NAP	C6A-N6A	4.05	1.44	1.34
2	H	601	NAP	C4N-C3N	-4.03	1.33	1.39
2	I	601	NAP	C5A-N7A	-4.00	1.31	1.39
2	E	601	NAP	C5N-C4N	-3.97	1.32	1.38
2	I	601	NAP	C6A-N6A	3.94	1.44	1.34
2	C	601	NAP	C5A-C4A	-3.88	1.32	1.39
2	F	601	NAP	C5N-C4N	-3.87	1.32	1.38
2	G	601	NAP	C5A-C4A	-3.86	1.32	1.39
2	I	601	NAP	C5N-C4N	-3.85	1.32	1.38
2	B	601	NAP	O3D-C3D	-3.85	1.33	1.43
2	J	601	NAP	C5N-C4N	-3.84	1.32	1.38
2	I	601	NAP	C4N-C3N	-3.82	1.33	1.39
2	I	601	NAP	C5A-C4A	-3.78	1.32	1.39
2	B	601	NAP	C4N-C3N	-3.76	1.33	1.39
2	J	601	NAP	O3D-C3D	-3.68	1.33	1.43
2	C	601	NAP	O3D-C3D	-3.65	1.33	1.43
2	C	601	NAP	C5A-N7A	-3.64	1.32	1.39
2	H	601	NAP	C5A-C4A	-3.63	1.32	1.39
2	A	601	NAP	C8A-N9A	-3.60	1.31	1.37
2	D	601	NAP	C5N-C4N	-3.59	1.32	1.38
2	D	601	NAP	O3D-C3D	-3.58	1.34	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	601	NAP	O3B-C3B	-3.57	1.34	1.43
2	E	601	NAP	C6A-N6A	3.55	1.43	1.34
2	A	601	NAP	C5N-C4N	-3.52	1.32	1.38
2	D	601	NAP	PN-O3	-3.49	1.55	1.59
2	B	601	NAP	C5A-C4A	-3.46	1.32	1.39
2	E	601	NAP	C5A-N7A	-3.45	1.32	1.39
2	H	601	NAP	C5N-C4N	-3.44	1.33	1.38
2	I	601	NAP	C8A-N9A	-3.36	1.31	1.37
2	D	601	NAP	C4N-C3N	-3.36	1.34	1.39
2	A	601	NAP	O3B-C3B	-3.34	1.34	1.43
2	G	601	NAP	C5A-N7A	-3.33	1.33	1.39
2	B	601	NAP	O3B-C3B	-3.31	1.34	1.43
2	B	601	NAP	C5N-C4N	-3.29	1.33	1.38
2	C	601	NAP	C5N-C4N	-3.26	1.33	1.38
2	A	601	NAP	C6A-N6A	3.26	1.42	1.34
2	I	601	NAP	O3B-C3B	-3.26	1.34	1.43
2	E	601	NAP	PA-O3	3.24	1.63	1.59
2	D	601	NAP	O3B-C3B	-3.17	1.35	1.43
2	E	601	NAP	O3B-C3B	-3.16	1.35	1.43
2	H	601	NAP	C5A-N7A	-3.12	1.33	1.39
2	F	601	NAP	O3B-C3B	-3.12	1.35	1.43
2	E	601	NAP	P2B-O2B	3.04	1.64	1.59
2	J	601	NAP	C5A-C4A	-3.04	1.33	1.39
2	C	601	NAP	C8A-N9A	-3.02	1.32	1.37
2	C	601	NAP	O3B-C3B	-3.01	1.35	1.43
2	J	601	NAP	P2B-O2B	2.96	1.64	1.59
2	H	601	NAP	O3B-C3B	-2.95	1.35	1.43
2	E	601	NAP	C8A-N9A	-2.94	1.32	1.37
2	H	601	NAP	C8A-N9A	-2.92	1.32	1.37
2	J	601	NAP	C5A-N7A	-2.92	1.33	1.39
2	G	601	NAP	C8A-N9A	-2.87	1.32	1.37
2	B	601	NAP	C5A-N7A	-2.84	1.33	1.39
2	J	601	NAP	O3B-C3B	-2.84	1.35	1.43
2	E	601	NAP	C4A-N9A	-2.83	1.31	1.37
2	B	601	NAP	C8A-N9A	-2.79	1.32	1.37
2	J	601	NAP	C2N-N1N	-2.65	1.32	1.35
2	I	601	NAP	C2N-N1N	-2.57	1.32	1.35
2	F	601	NAP	P2B-O2B	2.56	1.64	1.59
2	C	601	NAP	PN-O2N	-2.55	1.43	1.55
2	I	601	NAP	PN-O2N	-2.51	1.43	1.55
2	A	601	NAP	P2B-O2X	-2.49	1.45	1.54
2	A	601	NAP	PN-O2N	-2.48	1.43	1.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	601	NAP	C8A-N9A	-2.44	1.33	1.37
2	H	601	NAP	C4A-N9A	-2.40	1.32	1.37
2	E	601	NAP	C2N-N1N	-2.37	1.32	1.35
2	A	601	NAP	C6A-N1A	-2.36	1.29	1.35
2	A	601	NAP	PA-O2A	-2.34	1.44	1.55
2	A	601	NAP	C2N-N1N	-2.33	1.32	1.35
2	I	601	NAP	C4A-N9A	-2.32	1.32	1.37
2	G	601	NAP	C2N-N1N	-2.31	1.32	1.35
2	B	601	NAP	PN-O2N	-2.31	1.44	1.55
2	I	601	NAP	PA-O2A	-2.30	1.44	1.55
2	G	601	NAP	PA-O3	2.30	1.62	1.59
2	B	601	NAP	C2N-N1N	-2.27	1.32	1.35
2	I	601	NAP	P2B-O3X	-2.27	1.46	1.54
2	I	601	NAP	P2B-O2X	-2.22	1.46	1.54
2	J	601	NAP	PN-O2N	-2.21	1.45	1.55
2	H	601	NAP	O5D-C5D	-2.19	1.36	1.44
2	C	601	NAP	C4A-N9A	-2.18	1.33	1.37
2	C	601	NAP	O5D-C5D	-2.18	1.36	1.44
2	J	601	NAP	C2N-C3N	-2.16	1.35	1.39
2	J	601	NAP	O5D-C5D	-2.15	1.36	1.44
2	G	601	NAP	PN-O1N	-2.14	1.43	1.50
2	A	601	NAP	P2B-O3X	-2.14	1.46	1.54
2	H	601	NAP	C2N-N1N	-2.13	1.32	1.35
2	G	601	NAP	O5D-C5D	-2.12	1.36	1.44
2	F	601	NAP	O5D-C5D	-2.10	1.36	1.44
2	F	601	NAP	C2N-N1N	-2.07	1.32	1.35
2	A	601	NAP	C5A-C6A	-2.06	1.35	1.41
2	C	601	NAP	O5B-C5B	-2.06	1.36	1.44
2	E	601	NAP	O5D-C5D	-2.06	1.36	1.44
2	I	601	NAP	C6A-N1A	-2.05	1.30	1.35
2	H	601	NAP	PN-O2N	-2.03	1.45	1.55
2	B	601	NAP	C4A-N9A	-2.02	1.33	1.37
2	F	601	NAP	PN-O2N	-2.00	1.46	1.55

All (170) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	601	NAP	C4D-O4D-C1D	-7.07	103.45	109.92
2	G	601	NAP	C5A-C4A-N3A	-6.52	117.74	126.72
2	H	601	NAP	N3A-C2A-N1A	-6.19	119.21	128.58
2	E	601	NAP	N3A-C2A-N1A	-6.13	119.30	128.58
2	C	601	NAP	N3A-C2A-N1A	-6.05	119.42	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	NAP	N3A-C2A-N1A	-5.85	119.73	128.58
2	A	601	NAP	C5A-C4A-N3A	-5.83	118.69	126.72
2	I	601	NAP	C3N-C7N-N7N	5.76	124.84	117.74
2	J	601	NAP	N3A-C2A-N1A	-5.71	119.94	128.58
2	A	601	NAP	N3A-C2A-N1A	-5.70	119.95	128.58
2	I	601	NAP	C5A-C4A-N3A	-5.66	118.92	126.72
2	C	601	NAP	C5A-C4A-N3A	-5.65	118.94	126.72
2	I	601	NAP	O4B-C1B-C2B	-5.45	97.20	106.59
2	I	601	NAP	N3A-C2A-N1A	-5.37	120.45	128.58
2	G	601	NAP	N3A-C2A-N1A	-5.34	120.50	128.58
2	E	601	NAP	C4A-N9A-C1B	-5.30	114.23	126.63
2	J	601	NAP	C5A-C4A-N3A	-5.21	119.54	126.72
2	B	601	NAP	C5A-C4A-N3A	-5.13	119.65	126.72
2	A	601	NAP	O4B-C1B-C2B	-5.11	97.80	106.59
2	H	601	NAP	C4A-N9A-C1B	-5.00	114.93	126.63
2	E	601	NAP	C1B-N9A-C8A	4.71	137.55	127.09
2	I	601	NAP	P2B-O2B-C2B	-4.65	111.02	123.43
2	G	601	NAP	C3N-C7N-N7N	4.64	123.45	117.74
2	H	601	NAP	C5A-C4A-N3A	-4.64	120.33	126.72
2	E	601	NAP	N9A-C8A-N7A	-4.50	107.55	113.94
2	E	601	NAP	C5A-C4A-N3A	-4.49	120.54	126.72
2	G	601	NAP	C4D-O4D-C1D	-4.43	105.87	109.92
2	H	601	NAP	C1B-N9A-C8A	4.42	136.91	127.09
2	J	601	NAP	C4D-O4D-C1D	-4.37	105.92	109.92
2	B	601	NAP	C4A-N9A-C1B	-4.32	116.53	126.63
2	J	601	NAP	N6A-C6A-N1A	-4.29	108.82	118.38
2	A	601	NAP	O7N-C7N-N7N	-4.28	116.43	122.62
2	H	601	NAP	N9A-C8A-N7A	-4.28	107.86	113.94
2	I	601	NAP	C4D-O4D-C1D	-4.27	106.02	109.92
2	B	601	NAP	N9A-C8A-N7A	-4.26	107.89	113.94
2	A	601	NAP	C3N-C7N-N7N	4.24	122.96	117.74
2	G	601	NAP	O7N-C7N-N7N	-4.23	116.51	122.62
2	B	601	NAP	C4D-O4D-C1D	-4.13	106.15	109.92
2	G	601	NAP	C2A-N3A-C4A	3.94	121.46	111.83
2	H	601	NAP	N6A-C6A-N1A	-3.93	109.62	118.38
2	G	601	NAP	O4B-C1B-C2B	-3.93	99.83	106.59
2	G	601	NAP	N3A-C4A-N9A	3.87	133.74	127.17
2	H	601	NAP	O2A-PA-O3	3.86	117.72	107.27
2	J	601	NAP	N9A-C8A-N7A	-3.81	108.53	113.94
2	J	601	NAP	C4A-N9A-C1B	-3.78	117.80	126.63
2	J	601	NAP	C1B-N9A-C8A	3.77	135.46	127.09
2	B	601	NAP	C1B-N9A-C8A	3.73	135.37	127.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	NAP	C2A-N3A-C4A	3.73	120.93	111.83
2	I	601	NAP	N6A-C6A-N1A	-3.70	110.14	118.38
2	A	601	NAP	P2B-O2B-C2B	-3.69	113.58	123.43
2	I	601	NAP	C2A-N3A-C4A	3.69	120.84	111.83
2	B	601	NAP	C2A-N3A-C4A	3.67	120.79	111.83
2	E	601	NAP	N6A-C6A-N1A	-3.67	110.21	118.38
2	A	601	NAP	N9A-C8A-N7A	-3.66	108.75	113.94
2	E	601	NAP	C4D-O4D-C1D	-3.64	106.60	109.92
2	B	601	NAP	N6A-C6A-N1A	-3.63	110.29	118.38
2	I	601	NAP	O4B-C1B-N9A	-3.63	101.11	108.09
2	A	601	NAP	N3A-C4A-N9A	3.61	133.31	127.17
2	J	601	NAP	C2A-N3A-C4A	3.61	120.64	111.83
2	A	601	NAP	C6N-N1N-C2N	-3.61	118.81	121.88
2	A	601	NAP	C2A-N3A-C4A	3.58	120.58	111.83
2	E	601	NAP	C2A-N3A-C4A	3.55	120.50	111.83
2	H	601	NAP	C2A-N3A-C4A	3.49	120.35	111.83
2	F	601	NAP	C6N-N1N-C2N	-3.48	118.92	121.88
2	J	601	NAP	C5A-C4A-N9A	3.45	109.57	105.81
2	C	601	NAP	N9A-C8A-N7A	-3.44	109.05	113.94
2	C	601	NAP	N3A-C4A-N9A	3.43	133.00	127.17
2	J	601	NAP	C5A-C6A-N6A	3.42	131.76	123.29
2	J	601	NAP	C4A-C5A-N7A	-3.42	106.67	110.58
2	G	601	NAP	N9A-C8A-N7A	-3.41	109.10	113.94
2	F	601	NAP	C4D-O4D-C1D	-3.38	106.83	109.92
2	E	601	NAP	C3N-C7N-N7N	3.35	121.86	117.74
2	A	601	NAP	N6A-C6A-N1A	-3.32	110.98	118.38
2	G	601	NAP	O4B-C1B-N9A	-3.30	101.76	108.09
2	G	601	NAP	P2B-O2B-C2B	-3.29	114.64	123.43
2	C	601	NAP	P2B-O2B-C2B	-3.24	114.78	123.43
2	J	601	NAP	C3N-C7N-N7N	3.23	121.72	117.74
2	E	601	NAP	C6N-N1N-C2N	-3.21	119.15	121.88
2	J	601	NAP	C5A-N7A-C8A	3.20	108.49	103.45
2	C	601	NAP	C5B-C4B-C3B	-3.17	103.80	115.21
2	I	601	NAP	N9A-C8A-N7A	-3.14	109.48	113.94
2	H	601	NAP	C4D-O4D-C1D	-3.11	107.08	109.92
2	I	601	NAP	O7N-C7N-N7N	-3.06	118.19	122.62
2	I	601	NAP	C5A-C4A-N9A	3.05	109.13	105.81
2	H	601	NAP	C5A-N7A-C8A	3.05	108.24	103.45
2	A	601	NAP	C5A-N7A-C8A	3.03	108.21	103.45
2	G	601	NAP	N6A-C6A-N1A	-3.02	111.64	118.38
2	C	601	NAP	N6A-C6A-N1A	-2.93	111.86	118.38
2	B	601	NAP	C5A-N7A-C8A	2.92	108.04	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	NAP	N3A-C4A-N9A	2.84	132.00	127.17
2	F	601	NAP	O3-PA-O1A	-2.84	102.17	110.70
2	G	601	NAP	C5A-N7A-C8A	2.82	107.88	103.45
2	I	601	NAP	N3A-C4A-N9A	2.81	131.94	127.17
2	F	601	NAP	O2A-PA-O3	2.79	114.82	107.27
2	H	601	NAP	C4A-C5A-N7A	-2.75	107.44	110.58
2	D	601	NAP	C6N-N1N-C2N	-2.74	119.54	121.88
2	I	601	NAP	C1B-N9A-C8A	2.73	133.15	127.09
2	E	601	NAP	C5A-N7A-C8A	2.68	107.66	103.45
2	H	601	NAP	C5A-C6A-N6A	2.68	129.91	123.29
2	D	601	NAP	C2N-C3N-C4N	2.67	121.36	118.26
2	J	601	NAP	C2N-C3N-C4N	2.65	121.33	118.26
2	F	601	NAP	C3N-C7N-N7N	2.62	120.97	117.74
2	G	601	NAP	C6A-C5A-C4A	2.62	120.75	117.18
2	I	601	NAP	O2N-PN-O3	2.61	114.32	107.27
2	I	601	NAP	C4A-N9A-C1B	-2.59	120.56	126.63
2	J	601	NAP	C5B-C4B-C3B	-2.59	105.89	115.21
2	B	601	NAP	C4A-C5A-N7A	-2.59	107.62	110.58
2	I	601	NAP	C5A-C6A-N6A	2.58	129.68	123.29
2	G	601	NAP	C6N-N1N-C2N	-2.56	119.70	121.88
2	E	601	NAP	O7N-C7N-N7N	-2.56	118.91	122.62
2	B	601	NAP	O7N-C7N-N7N	-2.55	118.94	122.62
2	C	601	NAP	C2N-C3N-C4N	2.54	121.21	118.26
2	F	601	NAP	C2N-C3N-C4N	2.54	121.21	118.26
2	I	601	NAP	C5D-C4D-C3D	-2.50	106.20	115.21
2	C	601	NAP	C6A-C5A-C4A	2.49	120.58	117.18
2	G	601	NAP	C5A-C4A-N9A	2.48	108.52	105.81
2	C	601	NAP	C4A-N9A-C1B	-2.48	120.83	126.63
2	A	601	NAP	O2N-PN-O3	2.48	113.97	107.27
2	G	601	NAP	C5B-C4B-C3B	-2.46	106.36	115.21
2	G	601	NAP	C2N-N1N-C1D	2.46	124.55	119.13
2	B	601	NAP	O7N-C7N-C3N	2.45	122.60	119.60
2	E	601	NAP	P2B-O2B-C2B	-2.45	116.89	123.43
2	I	601	NAP	C5A-N7A-C8A	2.45	107.30	103.45
2	E	601	NAP	C5A-C4A-N9A	2.44	108.47	105.81
2	H	601	NAP	O4B-C1B-N9A	2.43	112.76	108.09
2	J	601	NAP	P2B-O2B-C2B	-2.43	116.95	123.43
2	I	601	NAP	C4A-C5A-N7A	-2.43	107.81	110.58
2	H	601	NAP	N3A-C4A-N9A	2.41	131.27	127.17
2	J	601	NAP	C2B-C1B-N9A	-2.41	109.79	113.75
2	C	601	NAP	C5A-N7A-C8A	2.40	107.23	103.45
2	G	601	NAP	C4N-C3N-C7N	-2.38	114.59	121.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	601	NAP	C5A-C4A-N9A	2.36	108.38	105.81
2	E	601	NAP	C4A-N9A-C8A	2.35	108.21	105.74
2	B	601	NAP	C5A-C4A-N9A	2.33	108.35	105.81
2	G	601	NAP	O3X-P2B-O2B	2.30	114.80	105.85
2	C	601	NAP	C6N-N1N-C2N	-2.28	119.94	121.88
2	G	601	NAP	C3B-C2B-C1B	2.28	107.17	102.81
2	G	601	NAP	C4A-C5A-N7A	-2.25	108.01	110.58
2	A	601	NAP	C4A-N9A-C1B	-2.25	121.37	126.63
2	E	601	NAP	N3A-C4A-N9A	2.25	131.00	127.17
2	F	601	NAP	C5D-C4D-C3D	-2.25	107.11	115.21
2	A	601	NAP	C6A-C5A-C4A	2.25	120.25	117.18
2	B	601	NAP	C4A-N9A-C8A	2.24	108.09	105.74
2	C	601	NAP	O4B-C1B-C2B	-2.24	102.73	106.59
2	C	601	NAP	C1B-N9A-C8A	2.23	132.05	127.09
2	H	601	NAP	O2B-C2B-C1B	-2.23	102.21	110.05
2	G	601	NAP	C5D-C4D-C3D	-2.22	107.21	115.21
2	H	601	NAP	C4A-N9A-C8A	2.21	108.06	105.74
2	B	601	NAP	C5A-C6A-N6A	2.19	128.72	123.29
2	J	601	NAP	N3A-C4A-N9A	2.19	130.88	127.17
2	E	601	NAP	C4A-C5A-N7A	-2.16	108.11	110.58
2	A	601	NAP	C4A-C5A-N7A	-2.16	108.12	110.58
2	I	601	NAP	O7N-C7N-C3N	-2.15	116.97	119.60
2	D	601	NAP	O4B-C4B-C3B	-2.14	102.66	104.63
2	B	601	NAP	C2B-C1B-N9A	-2.12	110.27	113.75
2	I	601	NAP	C6A-C5A-C4A	2.11	120.06	117.18
2	G	601	NAP	C4A-N9A-C1B	-2.10	121.72	126.63
2	G	601	NAP	C1B-N9A-C8A	2.10	131.75	127.09
2	C	601	NAP	C3N-C7N-N7N	2.08	120.31	117.74
2	A	601	NAP	C1B-N9A-C8A	2.08	131.71	127.09
2	E	601	NAP	C5A-C6A-N6A	2.07	128.41	123.29
2	C	601	NAP	C5A-C4A-N9A	2.07	108.06	105.81
2	A	601	NAP	C5A-C6A-N6A	2.07	128.41	123.29
2	D	601	NAP	P2B-O2B-C2B	-2.06	118.01	123.54
2	E	601	NAP	C2N-C3N-C4N	2.04	120.64	118.26
2	I	601	NAP	O2A-PA-O3	2.04	112.78	107.27
2	G	601	NAP	C6N-N1N-C1D	-2.03	115.74	119.73
2	H	601	NAP	C5D-C4D-C3D	-2.02	107.94	115.21
2	A	601	NAP	C5A-C4A-N9A	2.01	108.00	105.81
2	J	601	NAP	C6A-C5A-C4A	2.00	119.91	117.18

There are no chirality outliers.

All (86) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	NAP	C5D-O5D-PN-O2N
2	A	601	NAP	O4D-C1D-N1N-C6N
2	C	601	NAP	C5D-O5D-PN-O3
2	C	601	NAP	C5D-O5D-PN-O1N
2	C	601	NAP	C5D-O5D-PN-O2N
2	D	601	NAP	C1B-C2B-O2B-P2B
2	D	601	NAP	O4D-C4D-C5D-O5D
2	D	601	NAP	C3D-C4D-C5D-O5D
2	F	601	NAP	C5B-O5B-PA-O1A
2	F	601	NAP	C5B-O5B-PA-O2A
2	F	601	NAP	C5B-O5B-PA-O3
2	F	601	NAP	O4B-C4B-C5B-O5B
2	F	601	NAP	C3B-C2B-O2B-P2B
2	G	601	NAP	C5B-O5B-PA-O2A
2	H	601	NAP	C5B-O5B-PA-O1A
2	H	601	NAP	C5B-O5B-PA-O2A
2	H	601	NAP	C5B-O5B-PA-O3
2	H	601	NAP	C5D-O5D-PN-O3
2	H	601	NAP	C5D-O5D-PN-O2N
2	H	601	NAP	O4D-C4D-C5D-O5D
2	J	601	NAP	C5B-O5B-PA-O1A
2	J	601	NAP	C5B-O5B-PA-O2A
2	J	601	NAP	C5B-O5B-PA-O3
2	J	601	NAP	O4D-C1D-N1N-C6N
2	B	601	NAP	C3B-C4B-C5B-O5B
2	E	601	NAP	C3D-C4D-C5D-O5D
2	F	601	NAP	C3B-C4B-C5B-O5B
2	F	601	NAP	O4D-C4D-C5D-O5D
2	F	601	NAP	C3D-C4D-C5D-O5D
2	G	601	NAP	C3D-C4D-C5D-O5D
2	H	601	NAP	C3D-C4D-C5D-O5D
2	J	601	NAP	C3B-C4B-C5B-O5B
2	A	601	NAP	O4D-C4D-C5D-O5D
2	A	601	NAP	C3D-C4D-C5D-O5D
2	B	601	NAP	O4D-C4D-C5D-O5D
2	E	601	NAP	O4B-C4B-C5B-O5B
2	E	601	NAP	C3B-C4B-C5B-O5B
2	E	601	NAP	O4D-C4D-C5D-O5D
2	G	601	NAP	O4D-C4D-C5D-O5D
2	A	601	NAP	C4D-C5D-O5D-PN
2	B	601	NAP	C3D-C4D-C5D-O5D
2	I	601	NAP	C3D-C4D-C5D-O5D
2	B	601	NAP	O4B-C4B-C5B-O5B

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Mol	Chain	Res	Type	Atoms
2	J	601	NAP	O4B-C4B-C5B-O5B
2	B	601	NAP	C2B-O2B-P2B-O1X
2	G	601	NAP	C2B-O2B-P2B-O1X
2	E	601	NAP	C2B-C1B-N9A-C8A
2	D	601	NAP	PA-O3-PN-O1N
2	C	601	NAP	PA-O3-PN-O5D
2	J	601	NAP	PA-O3-PN-O5D
2	H	601	NAP	C3B-C4B-C5B-O5B
2	F	601	NAP	PN-O3-PA-O2A
2	H	601	NAP	PA-O3-PN-O1N
2	J	601	NAP	PN-O3-PA-O1A
2	F	601	NAP	C4D-C5D-O5D-PN
2	D	601	NAP	C5B-O5B-PA-O1A
2	E	601	NAP	C5B-O5B-PA-O2A
2	G	601	NAP	C5B-O5B-PA-O1A
2	G	601	NAP	C5B-O5B-PA-O3
2	G	601	NAP	C4D-C5D-O5D-PN
2	I	601	NAP	C4D-C5D-O5D-PN
2	E	601	NAP	PA-O3-PN-O2N
2	H	601	NAP	PN-O3-PA-O2A
2	C	601	NAP	C2B-C1B-N9A-C4A
2	E	601	NAP	C2B-C1B-N9A-C4A
2	C	601	NAP	C2B-C1B-N9A-C8A
2	C	601	NAP	C2B-O2B-P2B-O3X
2	G	601	NAP	O4B-C4B-C5B-O5B
2	J	601	NAP	C3B-C2B-O2B-P2B
2	J	601	NAP	C1B-C2B-O2B-P2B
2	A	601	NAP	O4D-C1D-N1N-C2N
2	J	601	NAP	O4D-C1D-N1N-C2N
2	E	601	NAP	C4D-C5D-O5D-PN
2	H	601	NAP	C4D-C5D-O5D-PN
2	C	601	NAP	C4B-C5B-O5B-PA
2	I	601	NAP	O4D-C4D-C5D-O5D
2	H	601	NAP	O4B-C4B-C5B-O5B
2	E	601	NAP	PA-O3-PN-O1N
2	F	601	NAP	PA-O3-PN-O2N
2	G	601	NAP	PA-O3-PN-O2N
2	E	601	NAP	O4B-C1B-N9A-C8A
2	F	601	NAP	C1B-C2B-O2B-P2B
2	D	601	NAP	PN-O3-PA-O2A
2	F	601	NAP	PA-O3-PN-O1N
2	H	601	NAP	PN-O3-PA-O1A

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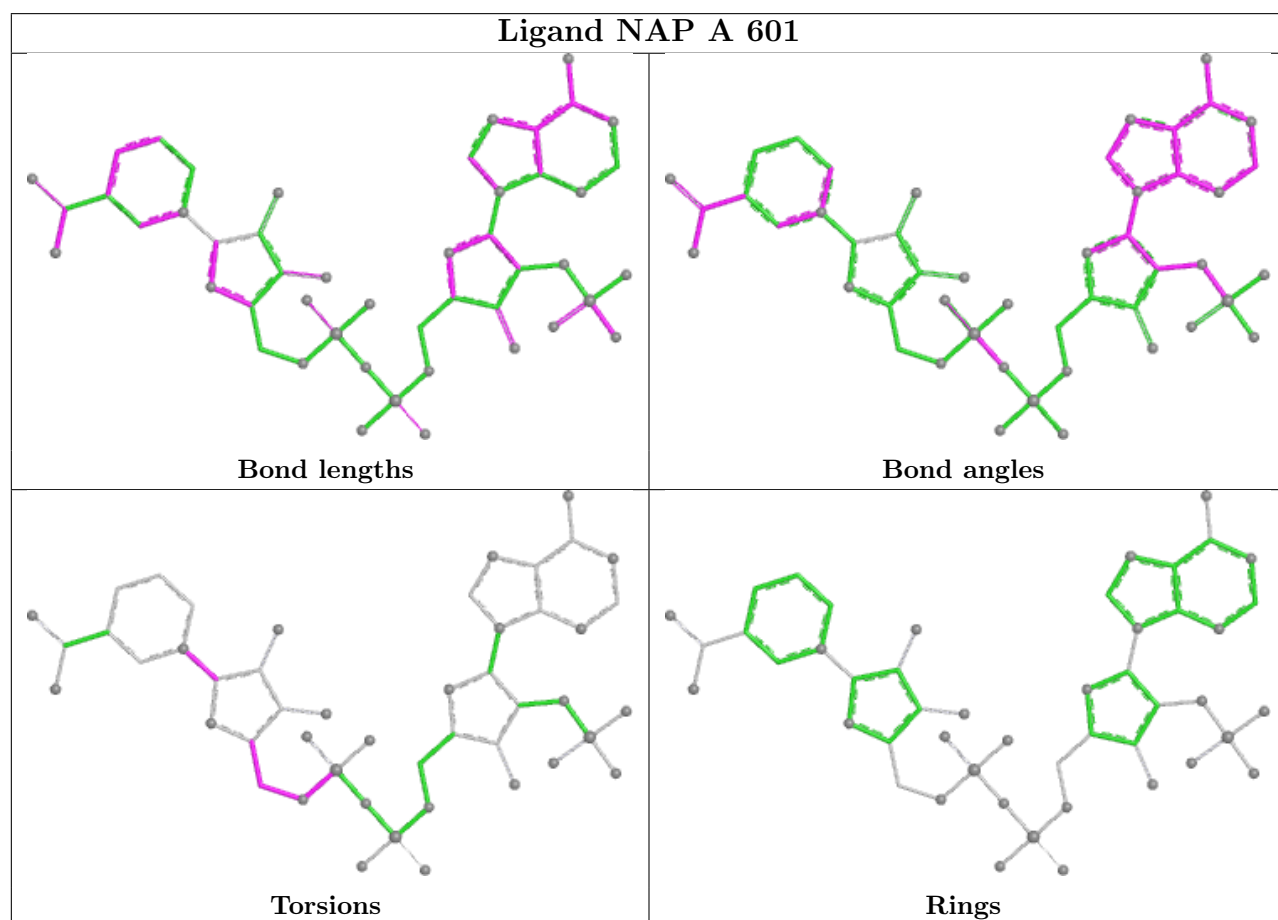
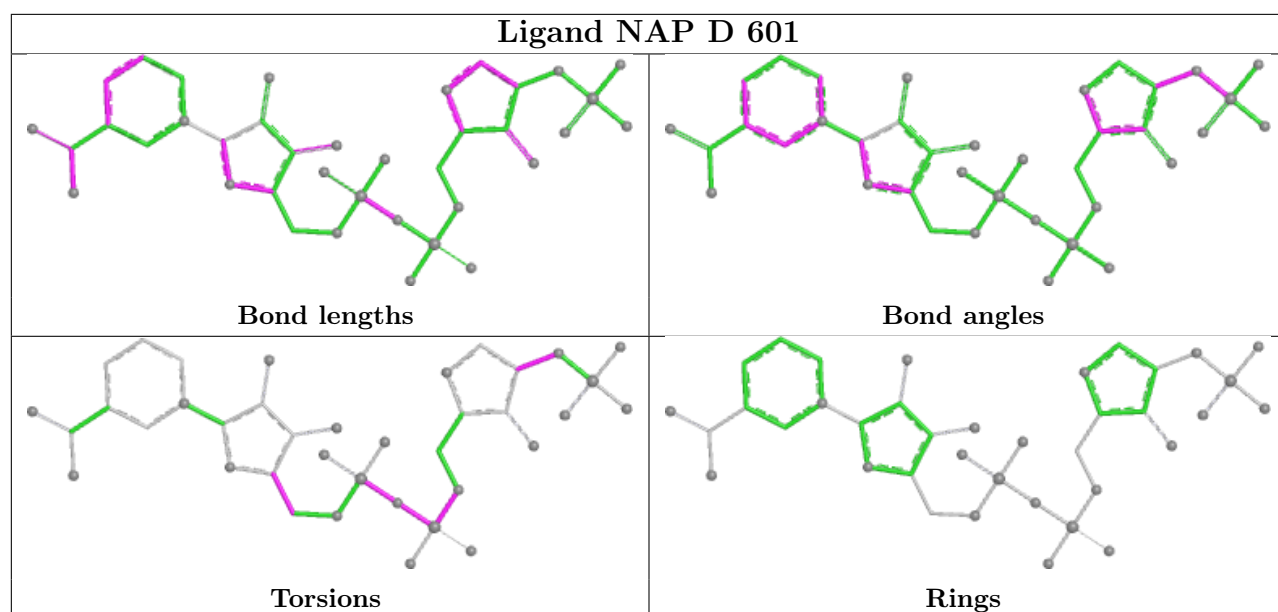
Mol	Chain	Res	Type	Atoms
2	J	601	NAP	PN-O3-PA-O2A

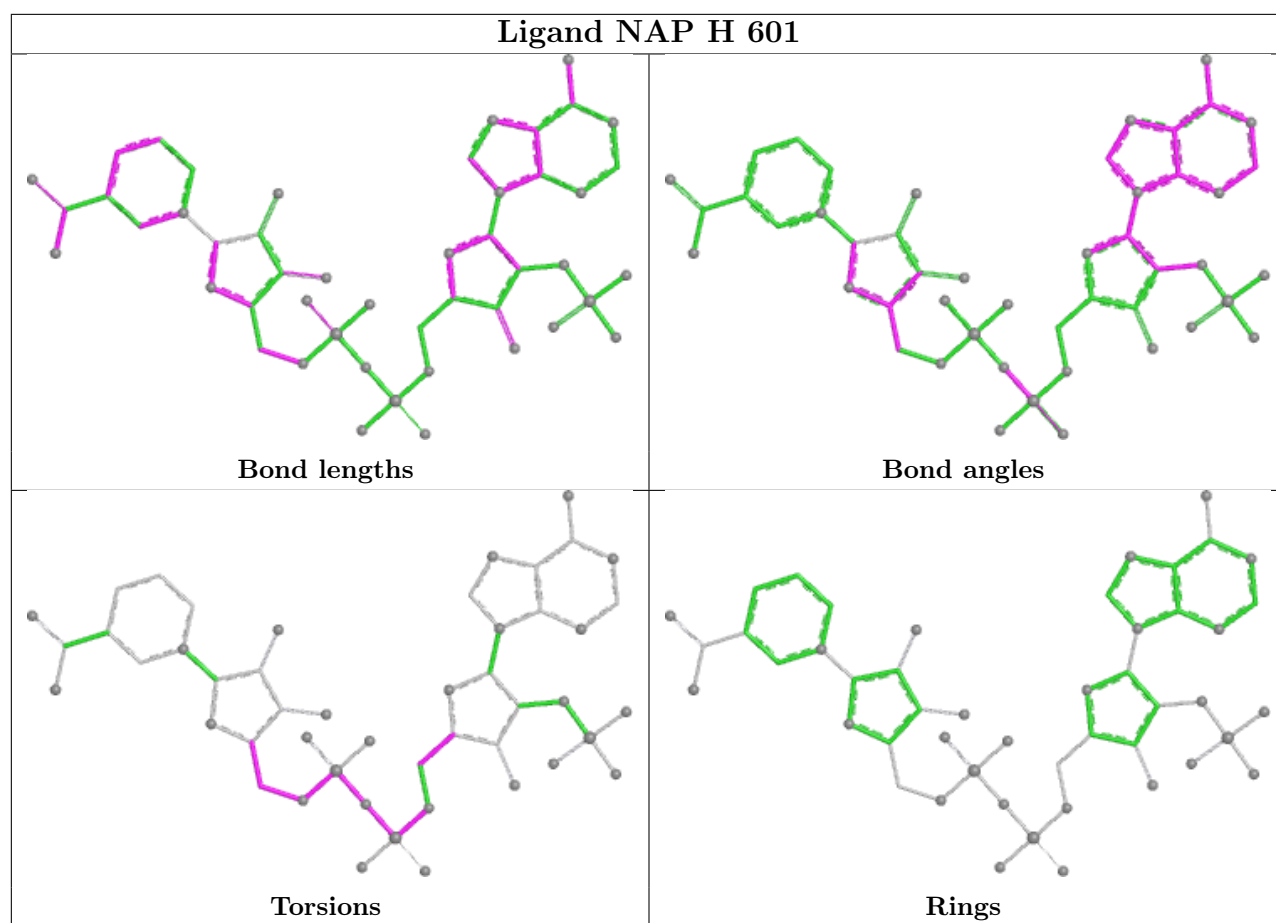
There are no ring outliers.

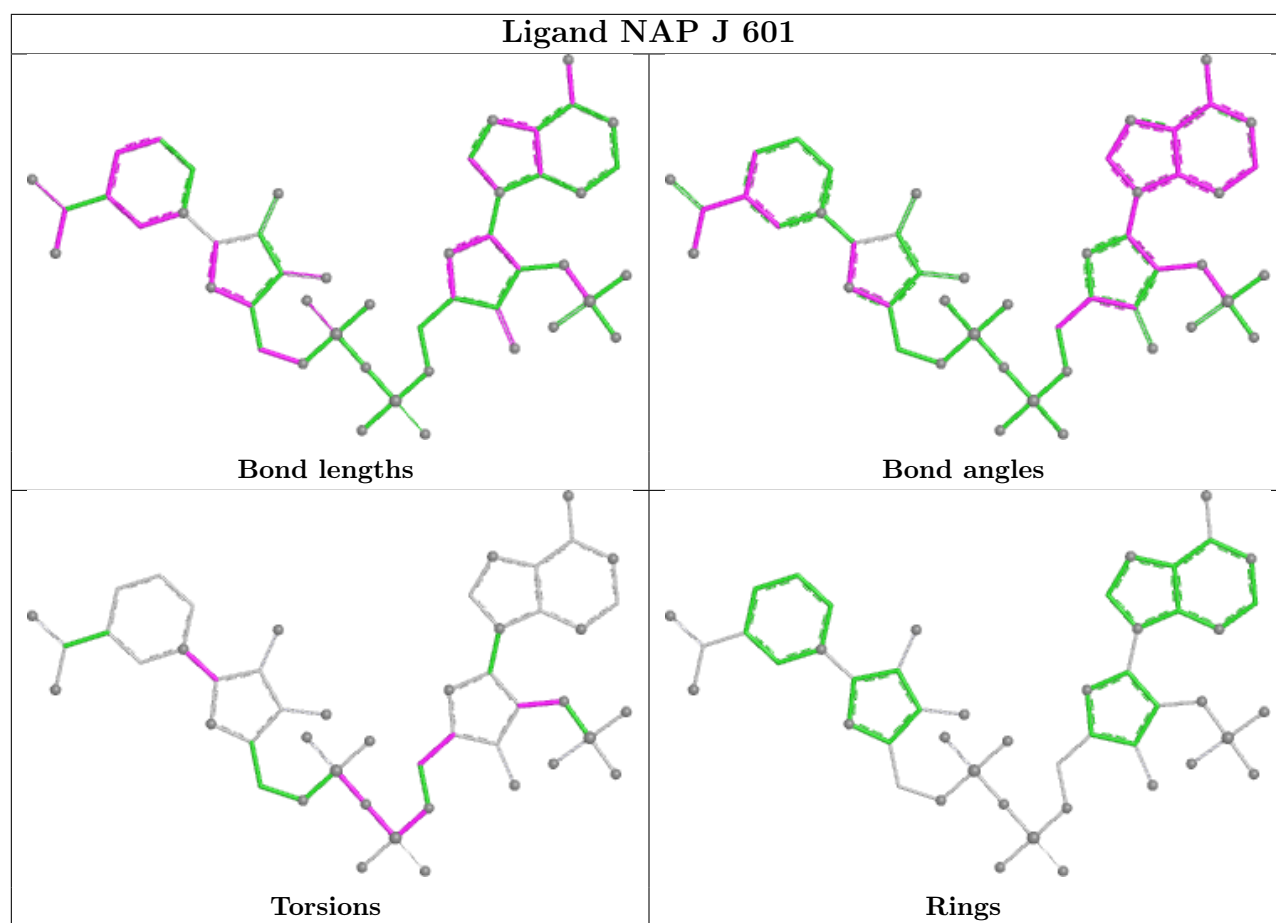
9 monomers are involved in 31 short contacts:

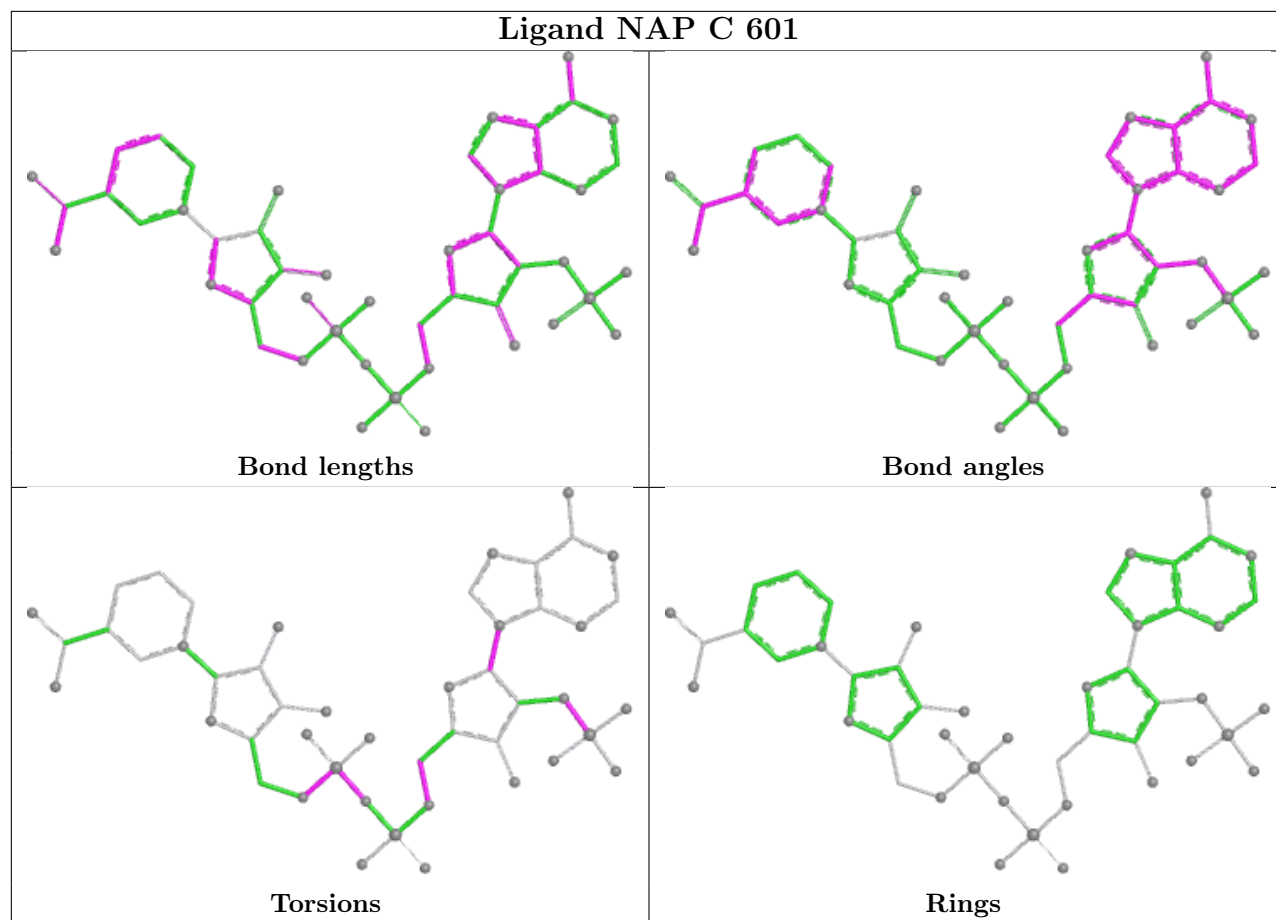
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	601	NAP	3	0
2	A	601	NAP	2	0
2	H	601	NAP	5	0
2	J	601	NAP	7	0
2	C	601	NAP	3	0
2	B	601	NAP	3	0
2	I	601	NAP	2	0
2	F	601	NAP	5	0
2	G	601	NAP	1	0

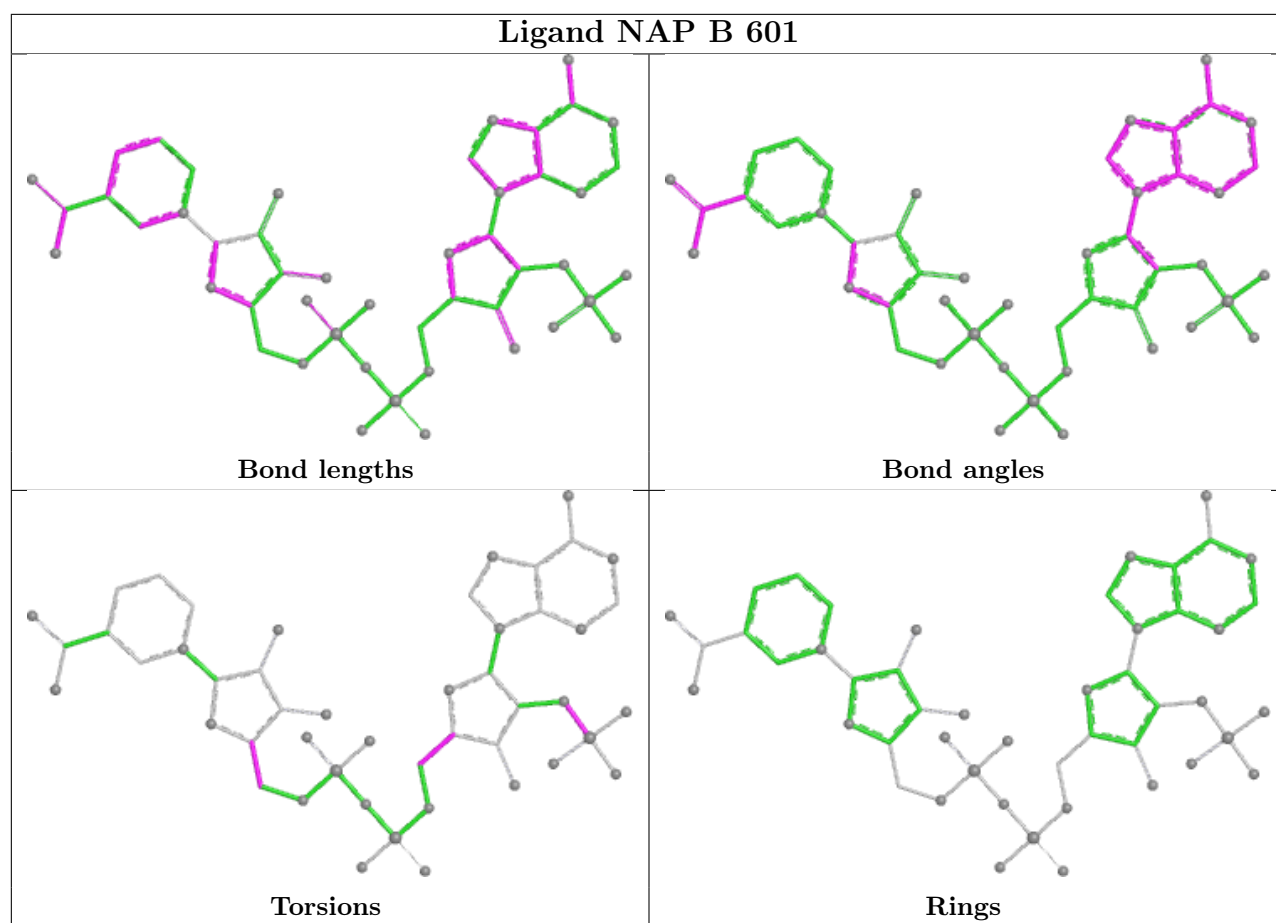
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

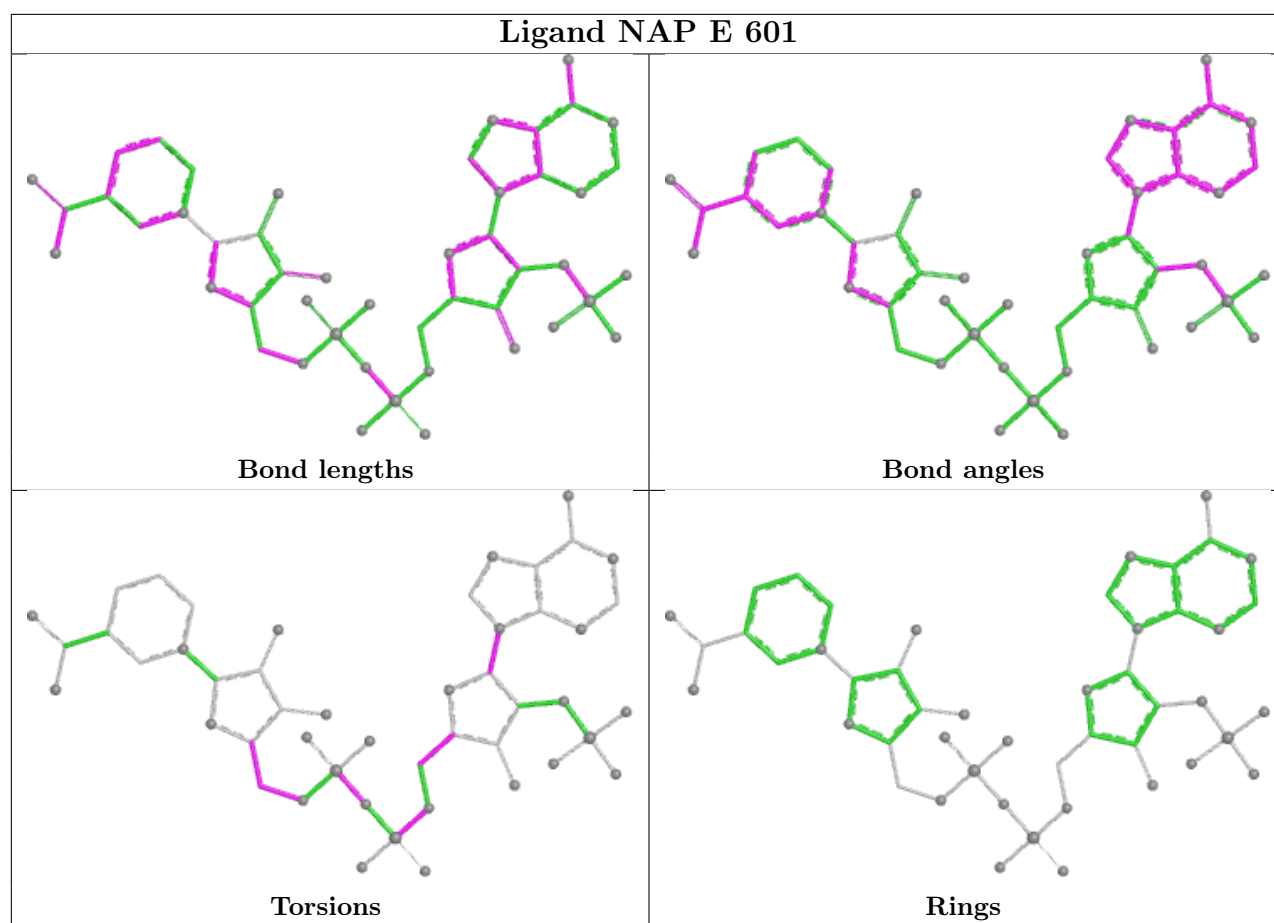




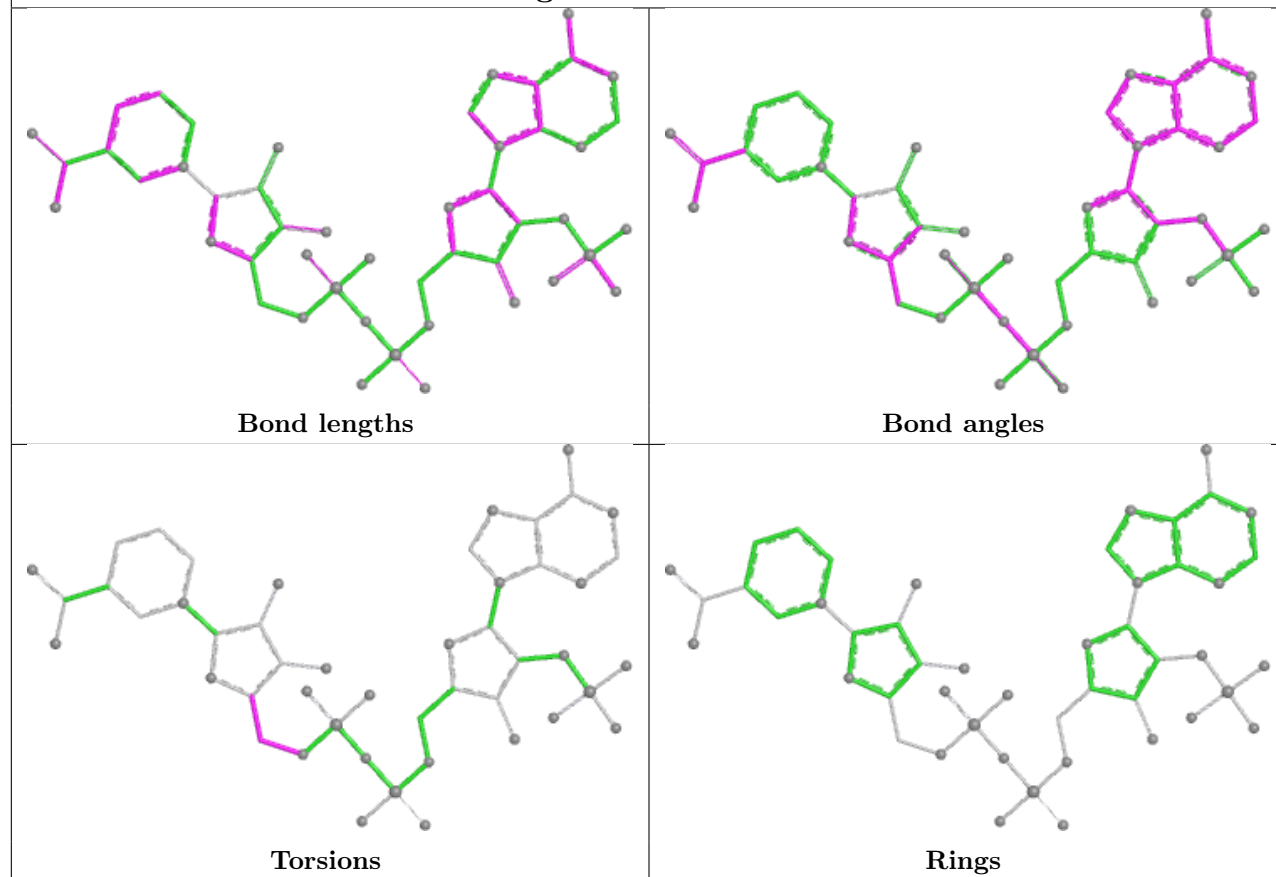




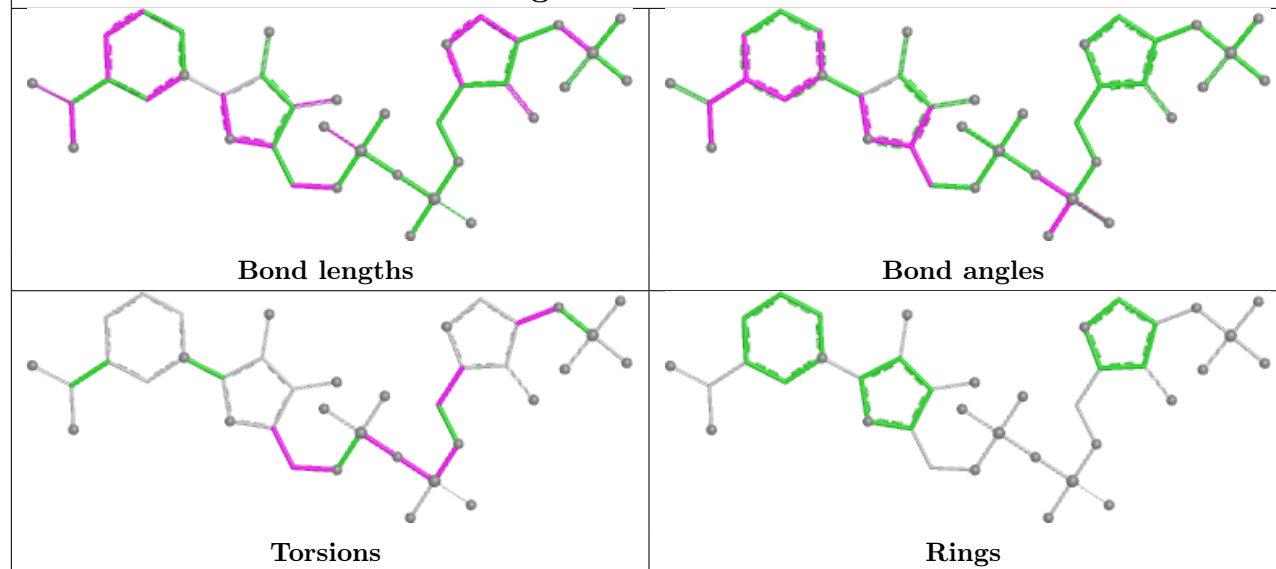


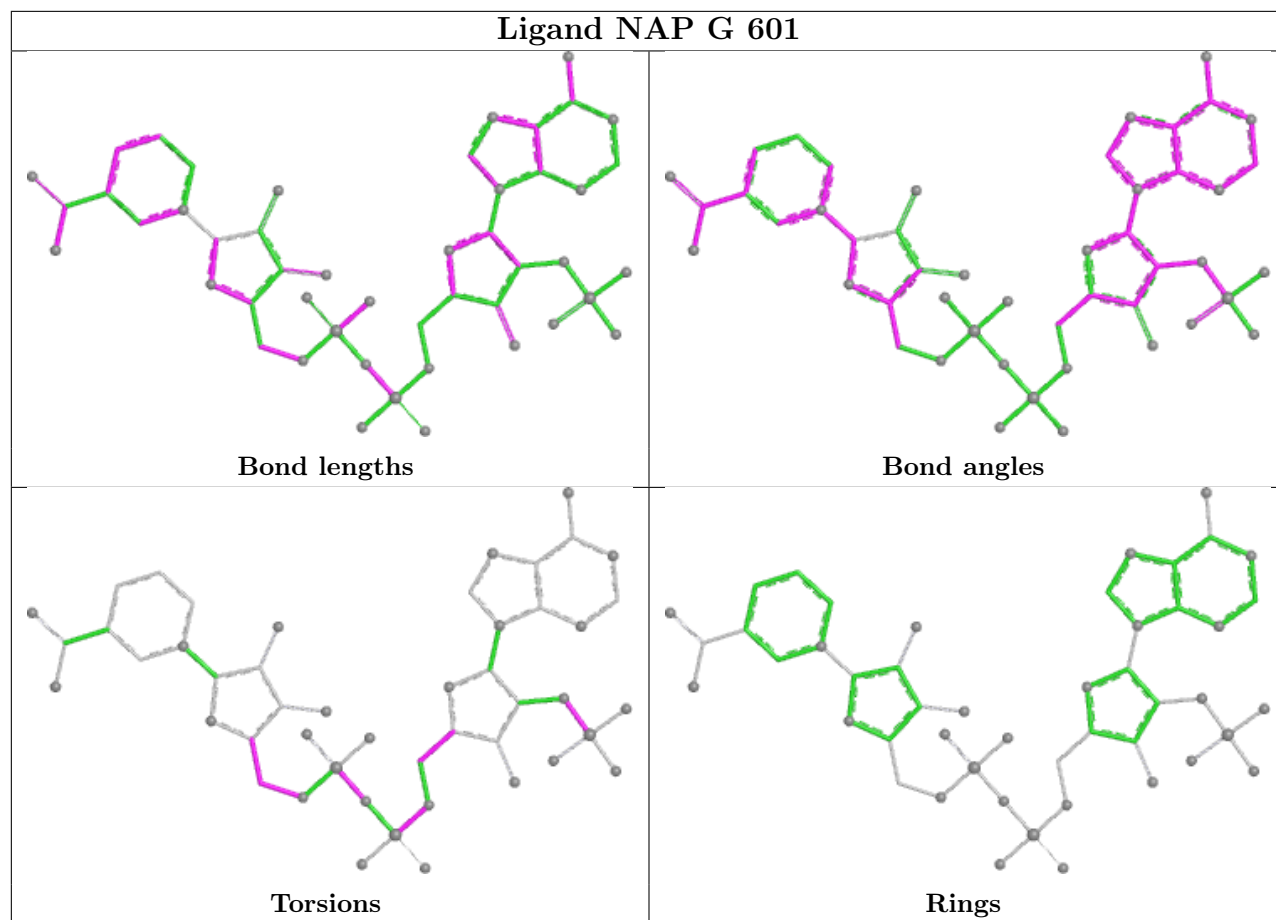


Ligand NAP I 601



Ligand NAP F 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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	441/522 (84%)	0.10	2 (0%) 87 86	38, 53, 75, 109	0
1	B	440/522 (84%)	0.22	5 (1%) 78 75	40, 57, 82, 106	0
1	C	441/522 (84%)	0.25	6 (1%) 73 70	40, 57, 79, 116	0
1	D	440/522 (84%)	0.41	4 (0%) 81 79	40, 63, 85, 116	0
1	E	441/522 (84%)	0.18	7 (1%) 70 67	38, 54, 75, 117	0
1	F	441/522 (84%)	0.61	15 (3%) 48 43	37, 66, 91, 119	0
1	G	440/522 (84%)	-0.05	3 (0%) 84 82	34, 49, 67, 105	0
1	H	441/522 (84%)	0.06	2 (0%) 87 86	36, 51, 72, 110	0
1	I	441/522 (84%)	0.05	8 (1%) 67 64	36, 50, 69, 107	0
1	J	440/522 (84%)	0.12	2 (0%) 87 86	37, 55, 77, 95	0
All	All	4406/5220 (84%)	0.20	54 (1%) 76 74	34, 55, 80, 119	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	82	ALA	5.2
1	D	83	ALA	5.0
1	E	83	ALA	4.5
1	E	82	ALA	4.3
1	H	82	ALA	4.3
1	I	82	ALA	4.2
1	C	82	ALA	3.7
1	E	485	GLY	3.6
1	G	482	GLY	3.6
1	C	373	LYS	3.3
1	F	82	ALA	3.3
1	G	83	ALA	3.0
1	E	84	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	327	THR	3.0
1	C	83	ALA	3.0
1	J	83	ALA	2.9
1	I	482	GLY	2.9
1	D	84	VAL	2.9
1	E	221	HIS	2.8
1	F	83	ALA	2.8
1	B	83	ALA	2.8
1	A	485	GLY	2.8
1	C	221	HIS	2.7
1	H	83	ALA	2.6
1	F	221	HIS	2.6
1	F	483	ALA	2.5
1	F	371	THR	2.5
1	F	252	VAL	2.4
1	B	373	LYS	2.3
1	B	221	HIS	2.3
1	I	484	GLY	2.3
1	I	485	GLY	2.3
1	I	83	ALA	2.2
1	F	346	PHE	2.2
1	I	350	LYS	2.2
1	I	487	GLY	2.2
1	F	482	GLY	2.2
1	D	287	THR	2.2
1	F	393	GLY	2.2
1	I	483	ALA	2.1
1	F	380	CYS	2.1
1	F	297	GLY	2.1
1	E	482	GLY	2.1
1	F	370	LEU	2.1
1	G	258	GLU	2.1
1	C	379	LYS	2.1
1	F	369	VAL	2.1
1	C	270	ARG	2.1
1	F	362	LEU	2.1
1	E	94	ALA	2.0
1	B	254	LYS	2.0
1	D	221	HIS	2.0
1	B	84	VAL	2.0
1	J	481	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

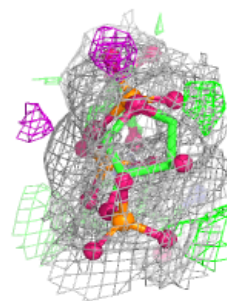
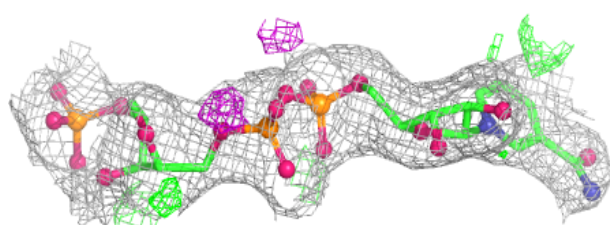
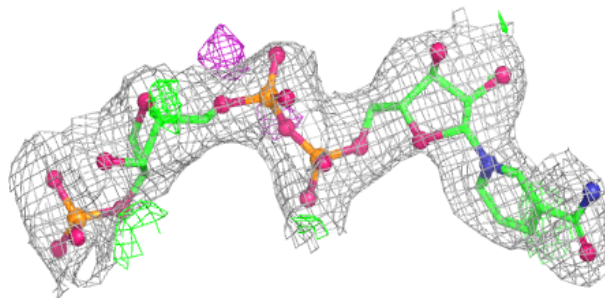
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAP	F	601	38/48	0.83	0.16	64,93,140,142	0
2	NAP	E	601	48/48	0.86	0.14	35,106,156,159	0
2	NAP	D	601	38/48	0.86	0.14	46,88,121,122	0
2	NAP	H	601	48/48	0.86	0.15	50,87,108,112	48
2	NAP	J	601	48/48	0.86	0.14	46,91,111,117	48
2	NAP	C	601	48/48	0.87	0.15	52,95,122,124	48
2	NAP	B	601	48/48	0.89	0.13	35,99,134,138	0
2	NAP	G	601	48/48	0.90	0.15	35,84,131,132	0
2	NAP	A	601	48/48	0.92	0.12	48,72,96,101	0
3	K	E	602	1/1	0.92	0.10	60,60,60,60	0
2	NAP	I	601	48/48	0.93	0.11	39,65,84,88	0
3	K	D	602	1/1	0.94	0.08	76,76,76,76	0
3	K	C	602	1/1	0.94	0.08	67,67,67,67	0
3	K	A	602	1/1	0.95	0.06	63,63,63,63	0
3	K	F	602	1/1	0.95	0.05	70,70,70,70	0
3	K	J	602	1/1	0.95	0.09	64,64,64,64	0
3	K	H	602	1/1	0.96	0.05	58,58,58,58	0
3	K	I	602	1/1	0.96	0.09	58,58,58,58	0
3	K	B	602	1/1	0.96	0.05	64,64,64,64	0
3	K	G	602	1/1	0.97	0.05	51,51,51,51	0

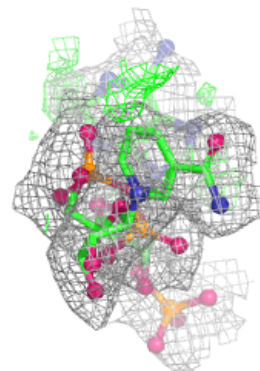
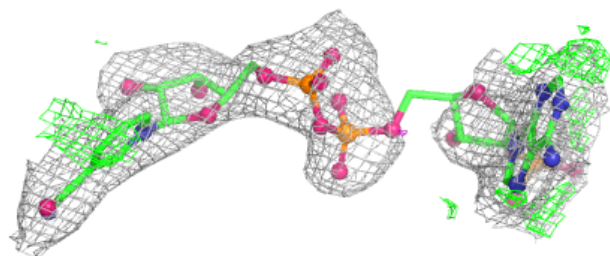
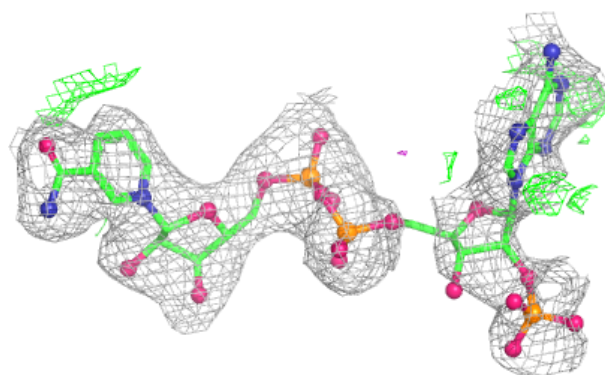
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAP F 601:

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

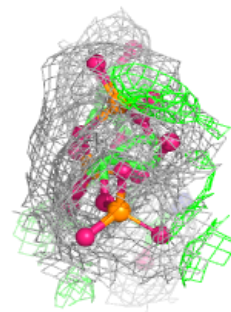
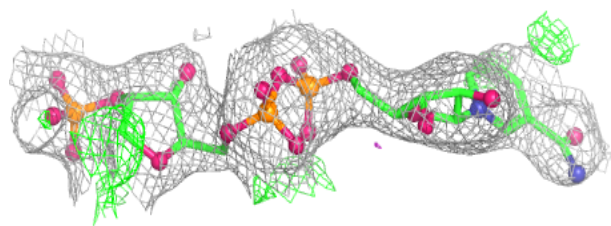
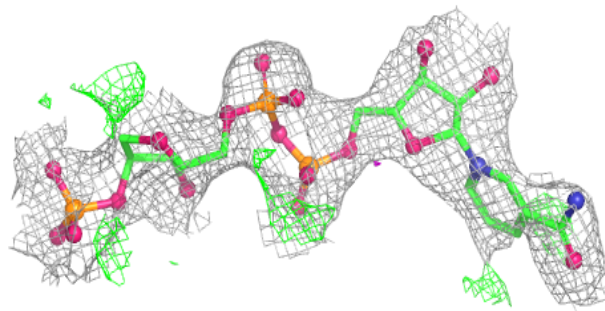
**Electron density around NAP E 601:**

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

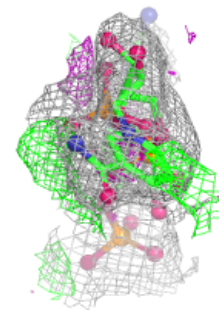
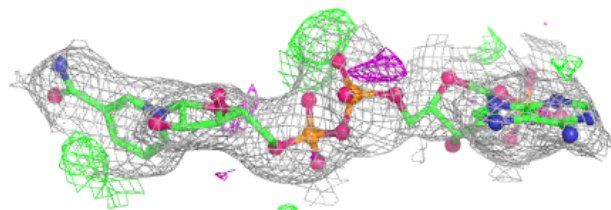
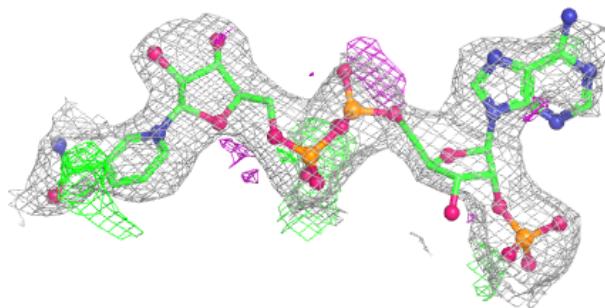


Electron density around NAP D 601:

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

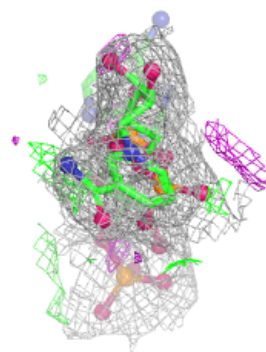
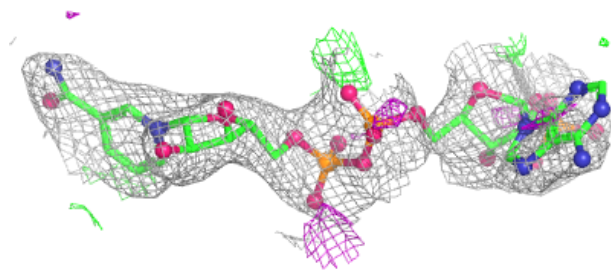
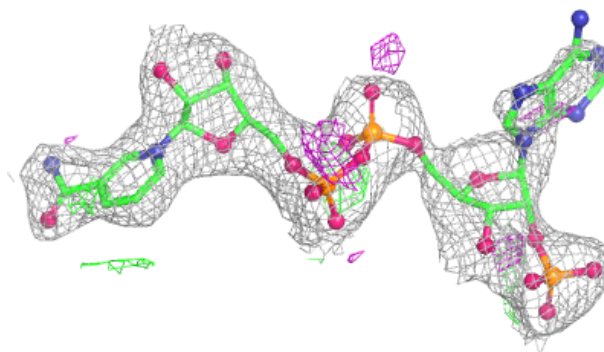
**Electron density around NAP H 601:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

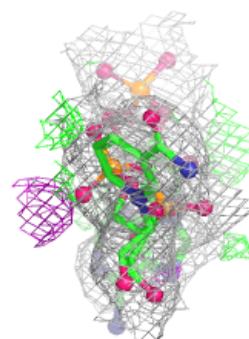
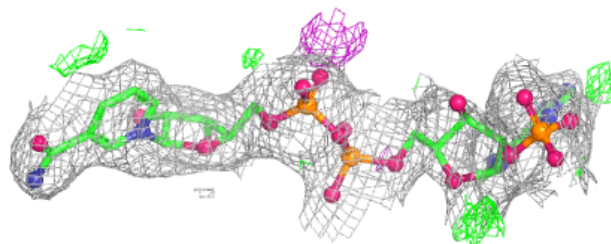
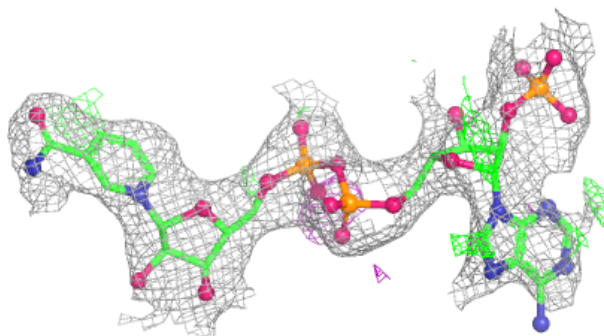


Electron density around NAP J 601:

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

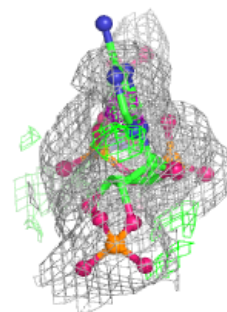
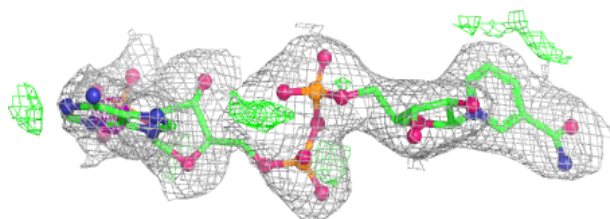
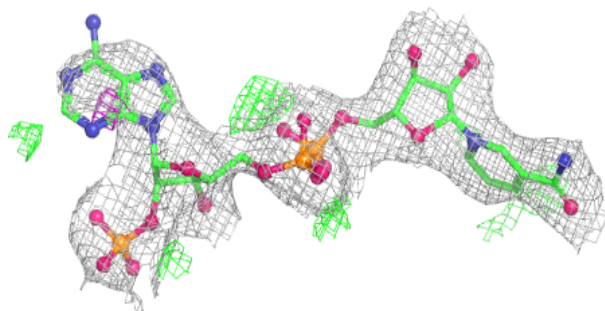
**Electron density around NAP C 601:**

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

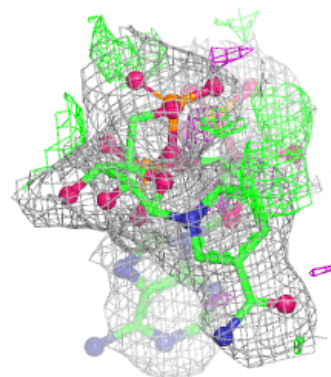
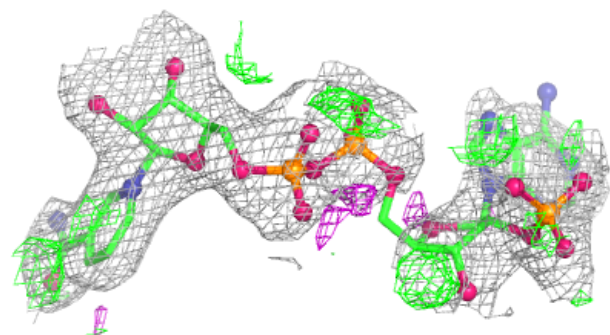
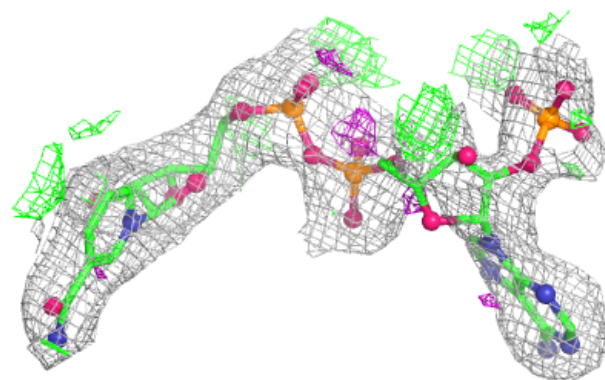


Electron density around NAP B 601:

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

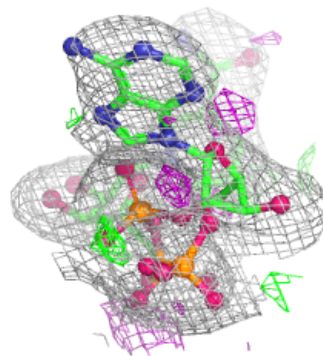
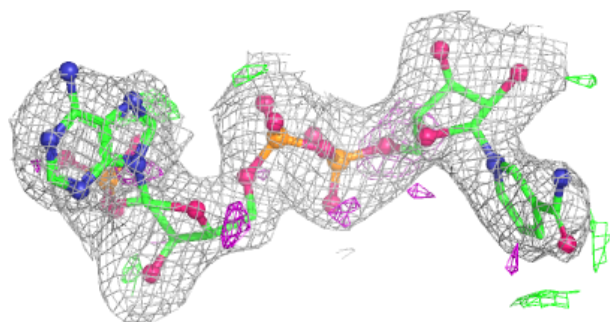
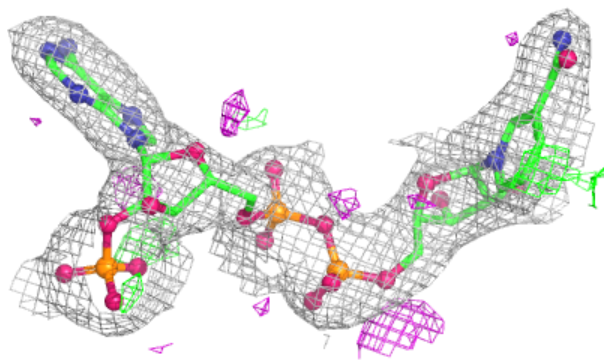
**Electron density around NAP G 601:**

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

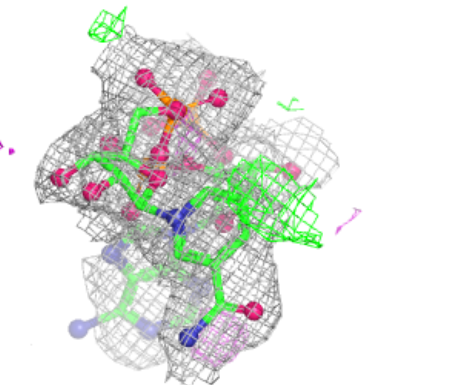
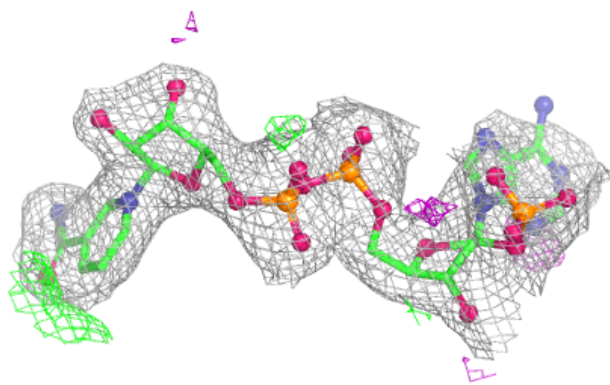
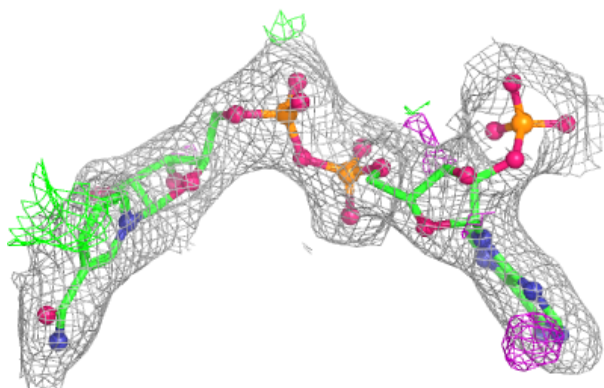


Electron density around NAP A 601:

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

**Electron density around NAP I 601:**

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



6.5 Other polymers ⓘ

There are no such residues in this entry.