



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 23, 2024 – 06:04 AM EDT

PDB ID : 6GVS  
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](mailto: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>.

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

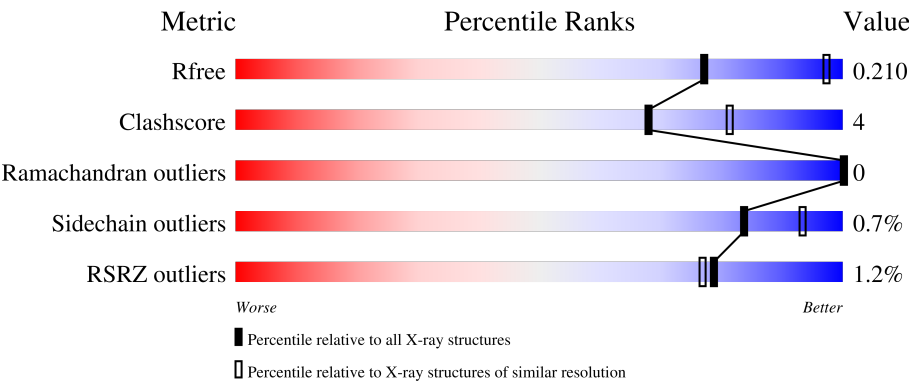
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

# 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 <sub>free</sub>	130704	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614 (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  $\geq 3$ , 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	<div><div></div><div>77%7%16%</div></div>
1	B	522	<div><div>%</div><div>77%7%16%</div></div>
1	C	522	<div><div>%</div><div>79%6%16%</div></div>
1	D	522	<div><div>2%</div><div>75%9%16%</div></div>
1	E	522	<div><div>%</div><div>79%5%16%</div></div>

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Mol	Chain	Length	Quality of chain
1	F	522	<div><div><div></div><div></div><div></div></div><div>4%75%9%16%</div></div>
1	G	522	<div><div><div></div><div></div><div></div></div><div>80%•16%</div></div>
1	H	522	<div><div><div></div><div></div><div></div></div><div>79%5%16%</div></div>
1	I	522	<div><div><div></div><div></div><div></div></div><div>80%•16%</div></div>
1	J	522	<div><div><div></div><div></div><div></div></div><div>%77%7%16%</div></div>

## 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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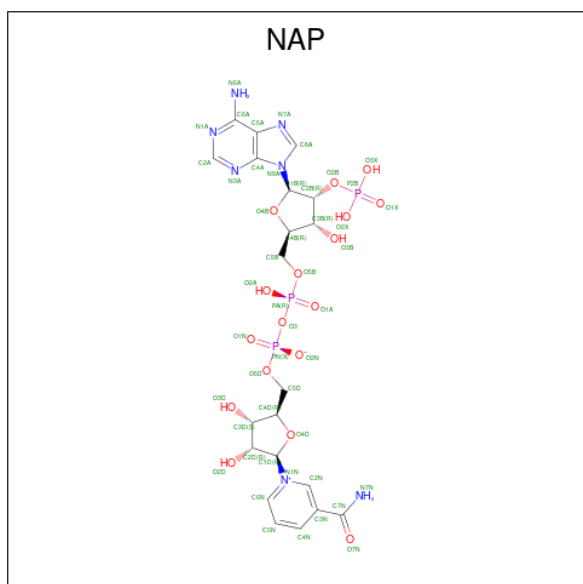
Chain	Residue	Modelled	Actual	Comment	Reference
J	4	HIS	-	expression tag	UNP Q21A49
J	5	HIS	-	expression tag	UNP Q21A49
J	6	HIS	-	expression tag	UNP Q21A49
J	7	HIS	-	expression tag	UNP Q21A49
J	8	HIS	-	expression tag	UNP Q21A49
J	9	VAL	-	expression tag	UNP Q21A49
J	10	GLY	-	expression tag	UNP Q21A49
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 (three-letter code: 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 (three-letter code: 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		

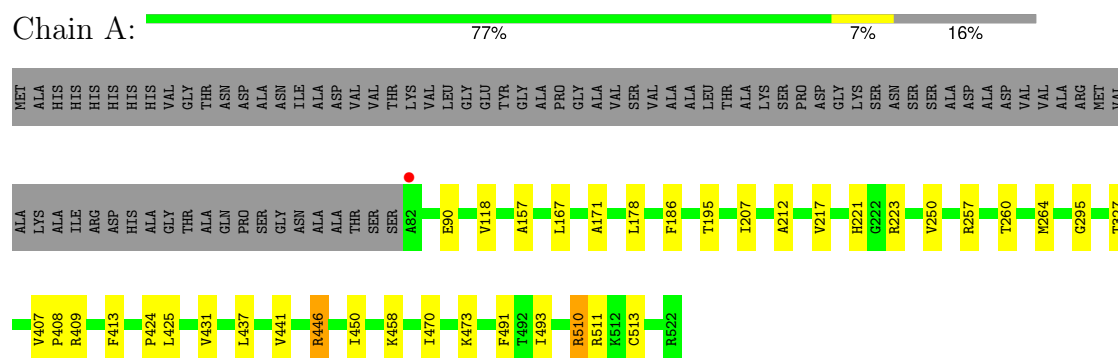
- Molecule 4 is water.

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

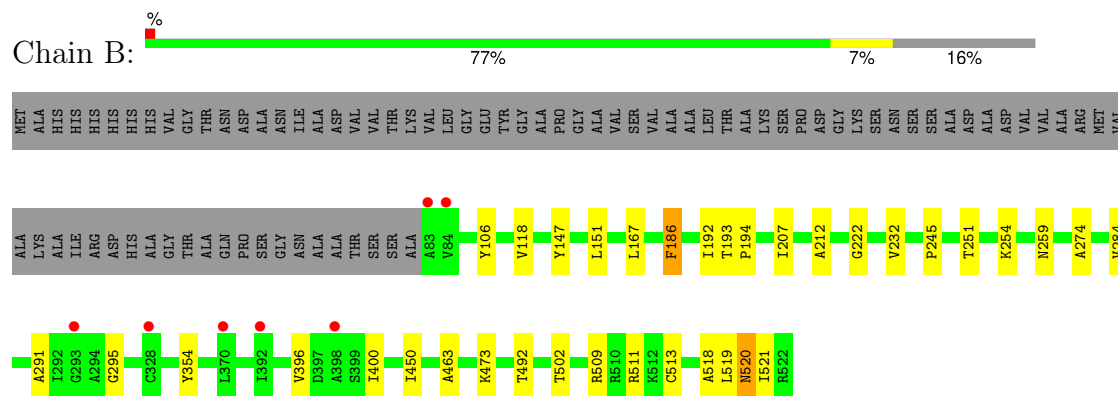
### 3 Residue-property plots [i](#)

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

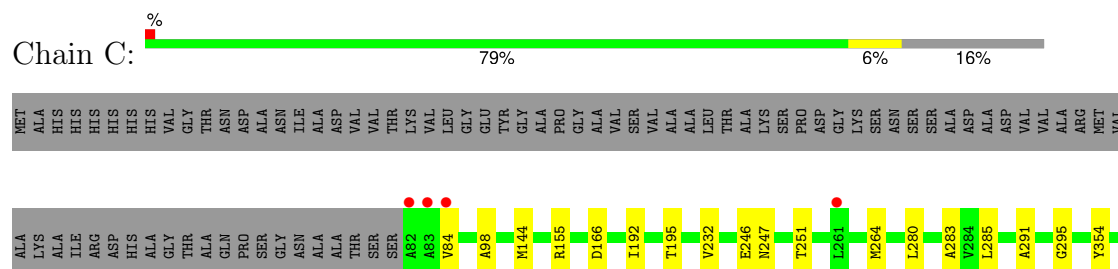
#### • Molecule 1: Aldehyde dehydrogenase

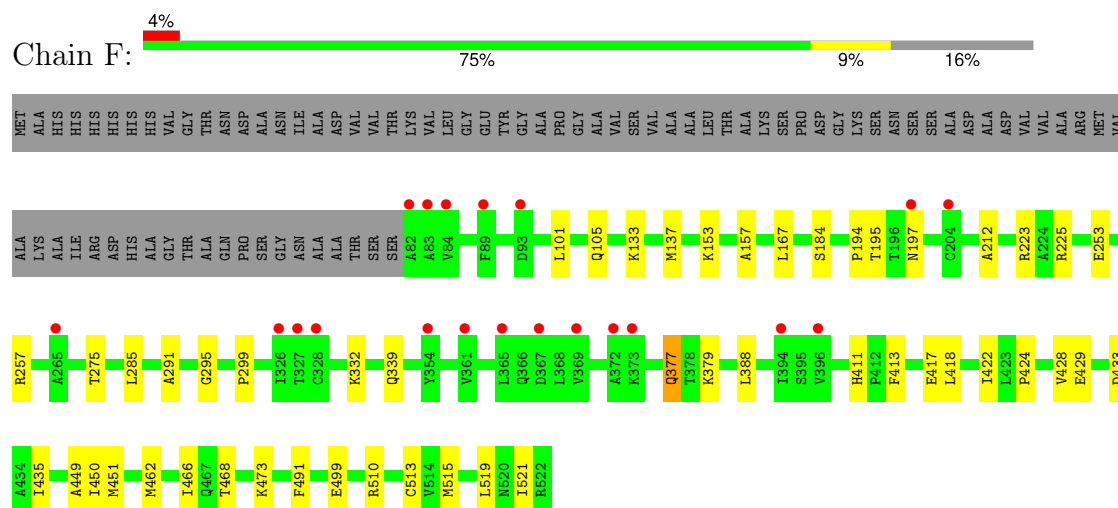
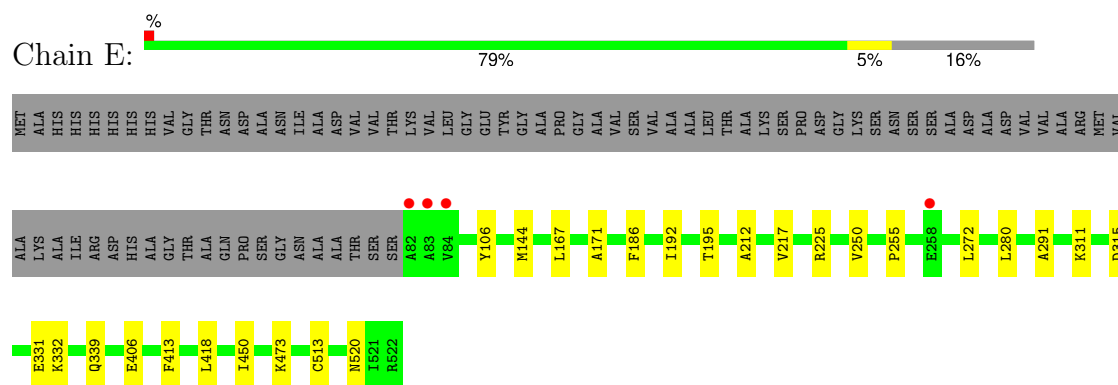
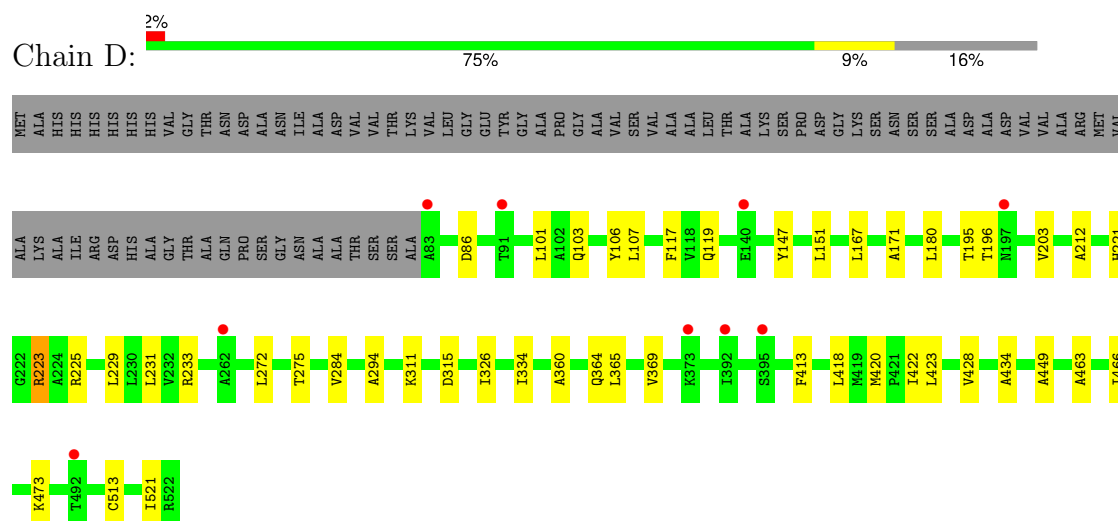


#### • Molecule 1: Aldehyde dehydrogenase



#### • Molecule 1: Aldehyde dehydrogenase

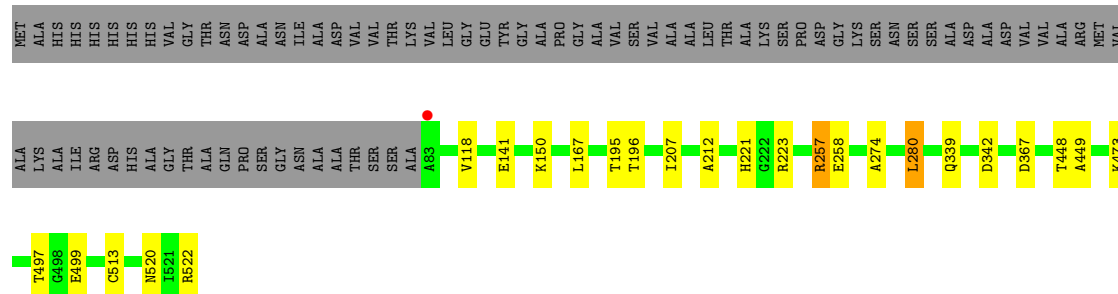






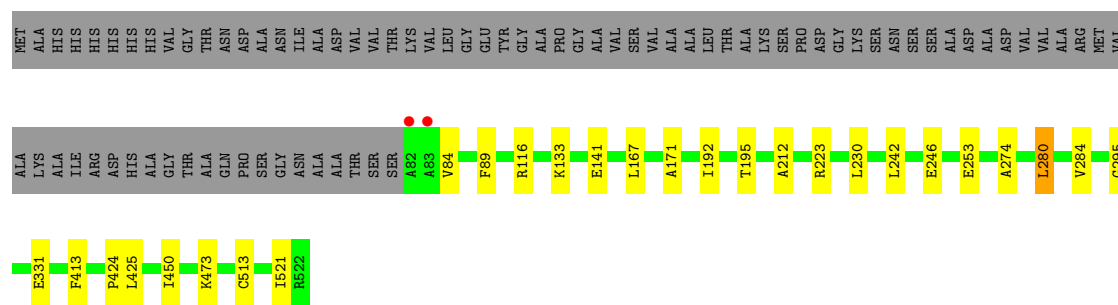
- Molecule 1: Aldehyde dehydrogenase

Chain G:



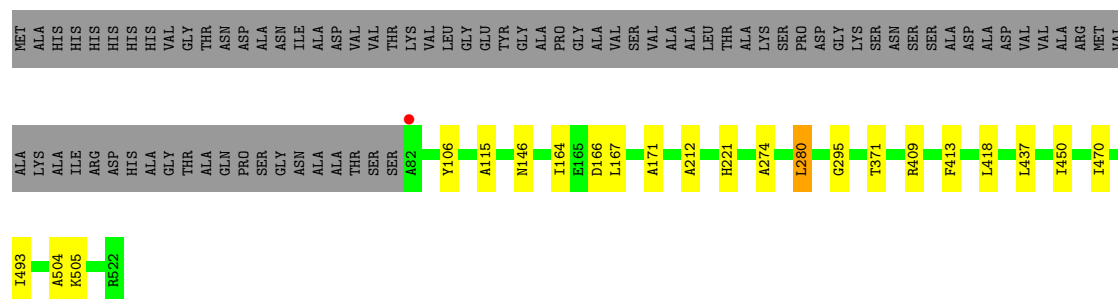
- Molecule 1: Aldehyde dehydrogenase

Chain H:



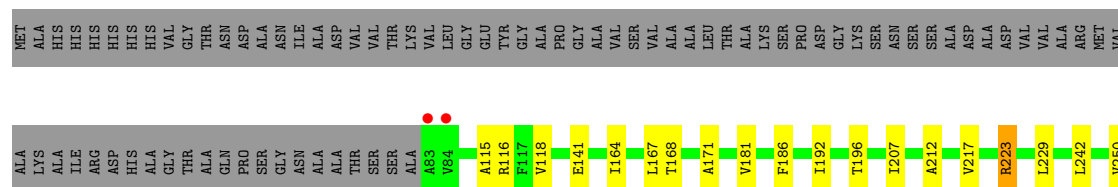
- Molecule 1: Aldehyde dehydrogenase

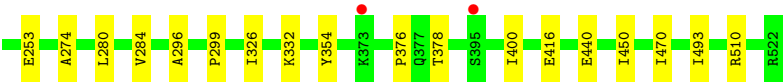
Chain I:



- Molecule 1: Aldehyde dehydrogenase

Chain J:





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	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 (0.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.2	Xtriage
Anisotropy	0.489	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 34.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	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 <sup>2</sup> )	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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.47	0/3345	0.48	0/4533
1	B	0.43	0/3340	0.47	0/4526
1	C	0.34	0/3345	0.46	0/4533
1	D	0.44	0/3340	0.46	0/4526
1	E	0.37	0/3345	0.47	0/4533
1	F	0.53	0/3345	0.49	0/4533
1	G	0.47	0/3340	0.48	0/4526
1	H	0.38	0/3345	0.47	0/4533
1	I	0.43	0/3345	0.47	0/4533
1	J	0.46	0/3340	0.47	0/4526
All	All	0.43	0/33430	0.47	0/45302

There are no bond length outliers.

There are no bond angle outliers.

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	27	0
1	B	3294	0	3379	28	0
1	C	3299	0	3384	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3294	0	3379	38	0
1	E	3299	0	3384	18	0
1	F	3299	0	3384	41	0
1	G	3294	0	3379	25	0
1	H	3299	0	3384	19	0
1	I	3299	0	3384	14	0
1	J	3294	0	3379	26	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
4	H	53	0	0	0	0
4	I	71	0	0	1	0
4	J	51	0	0	2	0
All	All	33944	0	34040	255	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 (255) 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
1:A:513:CYS:SG	1:B:473:LYS:NZ	2.57	0.72
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
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:C:473:LYS:NZ	1:D:513:CYS:SG	2.63	0.65
1:F:428:VAL:HG12	1:F:429:GLU:H	1.62	0.65
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: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: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:C:285:LEU:HD23	1:C:291:ALA:HB3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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
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:A:221:HIS:CD2	2:A:601:NAP:H3B	2.43	0.54
1:F:184:SER:OG	1:G:522:ARG:OXT	2.23	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: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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:133:LYS:HE3	1:H:230:LEU:HD21	1.92	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: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:B:492:THR:HG1	1:B:502:THR:HG1	1.50	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: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:D:521:ILE:C	1:D:521:ILE:HD12	2.33	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
4:B:704:HOH:O	1:C:521:ILE:HG13	2.11	0.49
1:G:342:ASP:CG	4:G:711:HOH:O	2.51	0.49
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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:C:264:MET:HE1	1:C:283:ALA:HB1	1.98	0.46
1:B:396:VAL:HB	1:B:400:ILE:HD12	1.98	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:C:425:LEU:C	1:C:425:LEU:HD23	2.36	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:E:144:MET:HE2	1:E:195:THR:HG22	1.97	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: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: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:A:425:LEU:HD23	1:A:425:LEU:C	2.38	0.44
1:E:331:GLU:HG3	1:E:450:ILE:HD13	1.99	0.44
1:J:192:ILE:HD13	1:J:280:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:519:LEU:HD23	1:B:519:LEU:HA	1.72	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: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
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: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:A:470:ILE:CD1	1:A:493:ILE:HD13	2.48	0.43
1:H:521:ILE:HD12	1:H:521:ILE:C	2.37	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: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: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: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:G:497:THR:OG1	1:G:499:GLU:OE1	2.35	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:C:144:MET:HE2	1:C:195:THR:HG22	2.01	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ALA:HB2	1:D:171:ALA:HB2	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:G:258:GLU:N	1:G:258:GLU:CD	2.72	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: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: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:H:425:LEU:C	1:H:425:LEU:HD23	2.40	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: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:H:84:VAL:HA	1:H:246:GLU:OE2	2.21	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: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
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:C:377:GLN:HG3	1:C:379:LYS:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:369:VAL:HB	1:D:420:MET:HE1	2.03	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: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:H:295:GLY:O	2:H:601:NAP:H2N	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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
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%)	353 (99%)	4 (1%)	73	88
1	B	357/414 (86%)	354 (99%)	3 (1%)	81	92
1	C	357/414 (86%)	356 (100%)	1 (0%)	92	97
1	D	357/414 (86%)	355 (99%)	2 (1%)	86	94
1	E	357/414 (86%)	354 (99%)	3 (1%)	81	92
1	F	357/414 (86%)	354 (99%)	3 (1%)	81	92
1	G	357/414 (86%)	355 (99%)	2 (1%)	86	94
1	H	357/414 (86%)	356 (100%)	1 (0%)	92	97
1	I	357/414 (86%)	354 (99%)	3 (1%)	81	92
1	J	357/414 (86%)	355 (99%)	2 (1%)	86	94
All	All	3570/4140 (86%)	3546 (99%)	24 (1%)	84	93

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

Mol	Chain	Res	Type
1	A	186	PHE
1	A	257	ARG
1	A	446	ARG
1	A	510	ARG
1	B	106	TYR
1	B	186	PHE
1	B	520	ASN
1	C	379	LYS
1	D	106	TYR
1	D	223	ARG
1	E	106	TYR
1	E	186	PHE
1	E	339	GLN
1	F	257	ARG
1	F	377	GLN
1	F	510	ARG

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Mol	Chain	Res	Type
1	G	257	ARG
1	G	280	LEU
1	H	280	LEU
1	I	106	TYR
1	I	146	ASN
1	I	280	LEU
1	J	186	PHE
1	J	223	ARG

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](#)

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	B	601	-	46,52,52	3.78	14 (30%)	61,80,80	1.85	8 (13%)
2	NAP	H	601	-	46,52,52	3.84	15 (32%)	61,80,80	2.06	10 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAP	I	601	-	46,52,52	3.88	19 (41%)	61,80,80	2.24	14 (22%)
2	NAP	J	601	-	46,52,52	3.85	17 (36%)	61,80,80	2.02	11 (18%)
2	NAP	E	601	-	46,52,52	4.02	16 (34%)	61,80,80	1.95	11 (18%)
2	NAP	D	601	-	38,40,52	4.13	12 (31%)	49,61,80	1.52	5 (10%)
2	NAP	G	601	-	46,52,52	4.01	16 (34%)	61,80,80	2.11	18 (29%)
2	NAP	F	601	-	38,40,52	4.32	15 (39%)	49,61,80	1.44	7 (14%)
2	NAP	A	601	-	46,52,52	3.89	19 (41%)	61,80,80	1.96	11 (18%)
2	NAP	C	601	-	46,52,52	3.82	17 (36%)	61,80,80	1.76	11 (18%)

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	B	601	-	-	5/31/67/67	0/5/5/5
2	NAP	H	601	-	-	13/31/67/67	0/5/5/5
2	NAP	I	601	-	-	3/31/67/67	0/5/5/5
2	NAP	J	601	-	-	12/31/67/67	0/5/5/5
2	NAP	E	601	-	-	8/31/67/67	0/5/5/5
2	NAP	D	601	-	-	6/31/60/67	0/3/3/5
2	NAP	G	601	-	-	9/31/67/67	0/5/5/5
2	NAP	F	601	-	-	13/31/60/67	0/3/3/5
2	NAP	A	601	-	-	6/31/67/67	0/5/5/5
2	NAP	C	601	-	-	6/31/67/67	0/5/5/5

All (160) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	601	NAP	O4B-C1B	16.32	1.62	1.40
2	H	601	NAP	O4B-C1B	15.49	1.61	1.40
2	C	601	NAP	O4B-C1B	15.04	1.60	1.40
2	B	601	NAP	O4B-C1B	14.79	1.60	1.40
2	G	601	NAP	O4B-C1B	14.69	1.60	1.40
2	F	601	NAP	O4D-C1D	14.61	1.60	1.40
2	J	601	NAP	O4B-C1B	14.53	1.60	1.40
2	G	601	NAP	O4D-C1D	14.43	1.59	1.40
2	A	601	NAP	O4B-C1B	14.05	1.59	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
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	O4B-C1B	13.57	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	F	601	NAP	O4B-C1B	8.36	1.61	1.43
2	D	601	NAP	O4B-C4B	-8.33	1.30	1.44
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	B	601	NAP	O4D-C4D	-8.06	1.27	1.45
2	D	601	NAP	O4B-C1B	8.06	1.61	1.43
2	A	601	NAP	O4D-C4D	-7.63	1.28	1.45
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	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

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
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	B	601	NAP	C7N-N7N	4.54	1.41	1.33
2	D	601	NAP	O7N-C7N	-4.53	1.15	1.24
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	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	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	H	601	NAP	O3D-C3D	-4.18	1.32	1.43
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	C4N-C3N	-4.03	1.33	1.39
2	E	601	NAP	C5N-C4N	-3.97	1.32	1.38
2	F	601	NAP	C5N-C4N	-3.87	1.32	1.38
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	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	D	601	NAP	C5N-C4N	-3.59	1.32	1.38
2	D	601	NAP	O3D-C3D	-3.58	1.34	1.43
2	G	601	NAP	O3B-C3B	-3.57	1.34	1.43
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	H	601	NAP	C5N-C4N	-3.44	1.33	1.38
2	J	601	NAP	C6A-N6A	3.36	1.46	1.34
2	D	601	NAP	C4N-C3N	-3.36	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	NAP	O3B-C3B	-3.34	1.34	1.43
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	I	601	NAP	O3B-C3B	-3.26	1.34	1.43
2	E	601	NAP	PA-O3	3.24	1.63	1.59
2	I	601	NAP	C4A-N3A	-3.18	1.31	1.35
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	F	601	NAP	O3B-C3B	-3.12	1.35	1.43
2	B	601	NAP	C1B-N9A	-3.08	1.42	1.49
2	E	601	NAP	P2B-O2B	3.04	1.64	1.59
2	B	601	NAP	C6A-N6A	3.03	1.44	1.34
2	C	601	NAP	O3B-C3B	-3.01	1.35	1.43
2	G	601	NAP	C6A-N6A	3.00	1.44	1.34
2	C	601	NAP	C6A-N6A	3.00	1.44	1.34
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	I	601	NAP	C1B-N9A	-2.93	1.42	1.49
2	H	601	NAP	C6A-N6A	2.92	1.44	1.34
2	I	601	NAP	C6A-N6A	2.85	1.44	1.34
2	J	601	NAP	O3B-C3B	-2.84	1.35	1.43
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	E	601	NAP	C6A-N6A	2.57	1.43	1.34
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	E	601	NAP	C1B-N9A	-2.54	1.43	1.49
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
2	A	601	NAP	C1B-N9A	-2.46	1.43	1.49
2	A	601	NAP	C5A-N7A	-2.45	1.31	1.39
2	H	601	NAP	C1B-N9A	-2.44	1.43	1.49
2	E	601	NAP	C2N-N1N	-2.37	1.32	1.35
2	A	601	NAP	C6A-N6A	2.36	1.42	1.34
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	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

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	NAP	C2A-N3A	2.29	1.35	1.32
2	C	601	NAP	C1B-N9A	-2.28	1.44	1.49
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	C5A-N7A	-2.25	1.31	1.39
2	J	601	NAP	C1B-N9A	-2.22	1.44	1.49
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	A	601	NAP	C6A-C5A	-2.19	1.35	1.43
2	H	601	NAP	O5D-C5D	-2.19	1.36	1.44
2	C	601	NAP	O5D-C5D	-2.18	1.36	1.44
2	G	601	NAP	C1B-N9A	-2.17	1.44	1.49
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	C	601	NAP	C5A-N7A	-2.06	1.32	1.39
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	H	601	NAP	PN-O2N	-2.03	1.45	1.55
2	F	601	NAP	PN-O2N	-2.00	1.46	1.55

All (106) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	601	NAP	C5A-C6A-N6A	7.51	131.76	120.31
2	D	601	NAP	C4D-O4D-C1D	-7.07	103.45	109.92
2	E	601	NAP	C1B-N9A-C4A	-7.06	114.23	126.64
2	H	601	NAP	N3A-C2A-N1A	-6.97	119.21	128.67
2	E	601	NAP	N3A-C2A-N1A	-6.90	119.30	128.67
2	C	601	NAP	N3A-C2A-N1A	-6.82	119.42	128.67
2	H	601	NAP	C1B-N9A-C4A	-6.66	114.93	126.64
2	B	601	NAP	N3A-C2A-N1A	-6.59	119.73	128.67
2	J	601	NAP	N3A-C2A-N1A	-6.43	119.94	128.67
2	A	601	NAP	N3A-C2A-N1A	-6.42	119.95	128.67
2	H	601	NAP	C5A-C6A-N6A	6.30	129.91	120.31
2	I	601	NAP	C5A-C6A-N6A	6.15	129.68	120.31
2	I	601	NAP	N3A-C2A-N1A	-6.06	120.45	128.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	601	NAP	N3A-C2A-N1A	-6.02	120.50	128.67
2	I	601	NAP	C3N-C7N-N7N	5.76	124.84	117.74
2	I	601	NAP	O4B-C1B-N9A	-5.75	101.11	108.75
2	B	601	NAP	C1B-N9A-C4A	-5.75	116.53	126.64
2	B	601	NAP	C5A-C6A-N6A	5.52	128.72	120.31
2	I	601	NAP	O4B-C1B-C2B	-5.51	97.20	106.61
2	E	601	NAP	C5A-C6A-N6A	5.32	128.41	120.31
2	A	601	NAP	C5A-C6A-N6A	5.31	128.41	120.31
2	G	601	NAP	O4B-C1B-N9A	-5.27	101.76	108.75
2	A	601	NAP	O4B-C1B-C2B	-5.17	97.80	106.61
2	J	601	NAP	C1B-N9A-C4A	-5.03	117.80	126.64
2	C	601	NAP	C5A-C6A-N6A	4.75	127.55	120.31
2	H	601	NAP	C4B-O4B-C1B	-4.70	105.62	109.92
2	G	601	NAP	C5A-C6A-N6A	4.70	127.46	120.31
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	J	601	NAP	N6A-C6A-N1A	-4.45	108.82	118.33
2	G	601	NAP	C4D-O4D-C1D	-4.43	105.87	109.92
2	J	601	NAP	C4D-O4D-C1D	-4.37	105.92	109.92
2	B	601	NAP	C4B-O4B-C1B	-4.37	105.93	109.92
2	A	601	NAP	O7N-C7N-N7N	-4.28	116.43	122.62
2	I	601	NAP	C4D-O4D-C1D	-4.27	106.02	109.92
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	H	601	NAP	N6A-C6A-N1A	-4.08	109.62	118.33
2	G	601	NAP	O4B-C1B-C2B	-3.97	99.83	106.61
2	H	601	NAP	O2A-PA-O3	3.86	117.72	107.27
2	I	601	NAP	N6A-C6A-N1A	-3.84	110.14	118.33
2	E	601	NAP	N6A-C6A-N1A	-3.80	110.21	118.33
2	J	601	NAP	C4B-O4B-C1B	-3.78	106.46	109.92
2	B	601	NAP	N6A-C6A-N1A	-3.77	110.29	118.33
2	A	601	NAP	P2B-O2B-C2B	-3.69	113.58	123.43
2	E	601	NAP	C4D-O4D-C1D	-3.64	106.60	109.92
2	A	601	NAP	C6N-N1N-C2N	-3.61	118.81	121.88
2	F	601	NAP	C6N-N1N-C2N	-3.48	118.92	121.88
2	I	601	NAP	C1B-N9A-C4A	-3.46	120.56	126.64
2	A	601	NAP	N6A-C6A-N1A	-3.44	110.98	118.33
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	C	601	NAP	C1B-N9A-C4A	-3.31	120.83	126.64
2	C	601	NAP	C4B-O4B-C1B	-3.30	106.91	109.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
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	A	601	NAP	O4B-C1B-N9A	-3.23	104.46	108.75
2	E	601	NAP	C6N-N1N-C2N	-3.21	119.15	121.88
2	C	601	NAP	C5B-C4B-C3B	-3.17	103.80	115.21
2	G	601	NAP	N6A-C6A-N1A	-3.13	111.64	118.33
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	C	601	NAP	N6A-C6A-N1A	-3.03	111.86	118.33
2	H	601	NAP	O4B-C1B-N9A	3.03	112.76	108.75
2	A	601	NAP	C1B-N9A-C4A	-3.00	121.37	126.64
2	F	601	NAP	O3-PA-O1A	-2.84	102.17	110.70
2	G	601	NAP	C1B-N9A-C4A	-2.80	121.72	126.64
2	F	601	NAP	O2A-PA-O3	2.79	114.82	107.27
2	D	601	NAP	C6N-N1N-C2N	-2.74	119.54	121.88
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	I	601	NAP	O2N-PN-O3	2.61	114.32	107.27
2	J	601	NAP	C5B-C4B-C3B	-2.59	105.89	115.21
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	J	601	NAP	C4A-C5A-N7A	-2.52	106.67	109.34
2	I	601	NAP	C5D-C4D-C3D	-2.50	106.20	115.21
2	A	601	NAP	O2N-PN-O3	2.48	113.97	107.27
2	E	601	NAP	C4B-O4B-C1B	-2.47	107.66	109.92
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	J	601	NAP	P2B-O2B-C2B	-2.43	116.95	123.43
2	G	601	NAP	C4N-C3N-C7N	-2.38	114.59	121.06
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	C	601	NAP	O4B-C1B-C2B	-2.27	102.73	106.61
2	F	601	NAP	C5D-C4D-C3D	-2.25	107.11	115.21
2	H	601	NAP	O2B-C2B-C1B	-2.23	102.21	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	601	NAP	C5D-C4D-C3D	-2.22	107.21	115.21
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	C	601	NAP	C3N-C7N-N7N	2.08	120.31	117.74
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

There are no chirality outliers.

All (81) 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

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Mol	Chain	Res	Type	Atoms
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
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	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-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

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

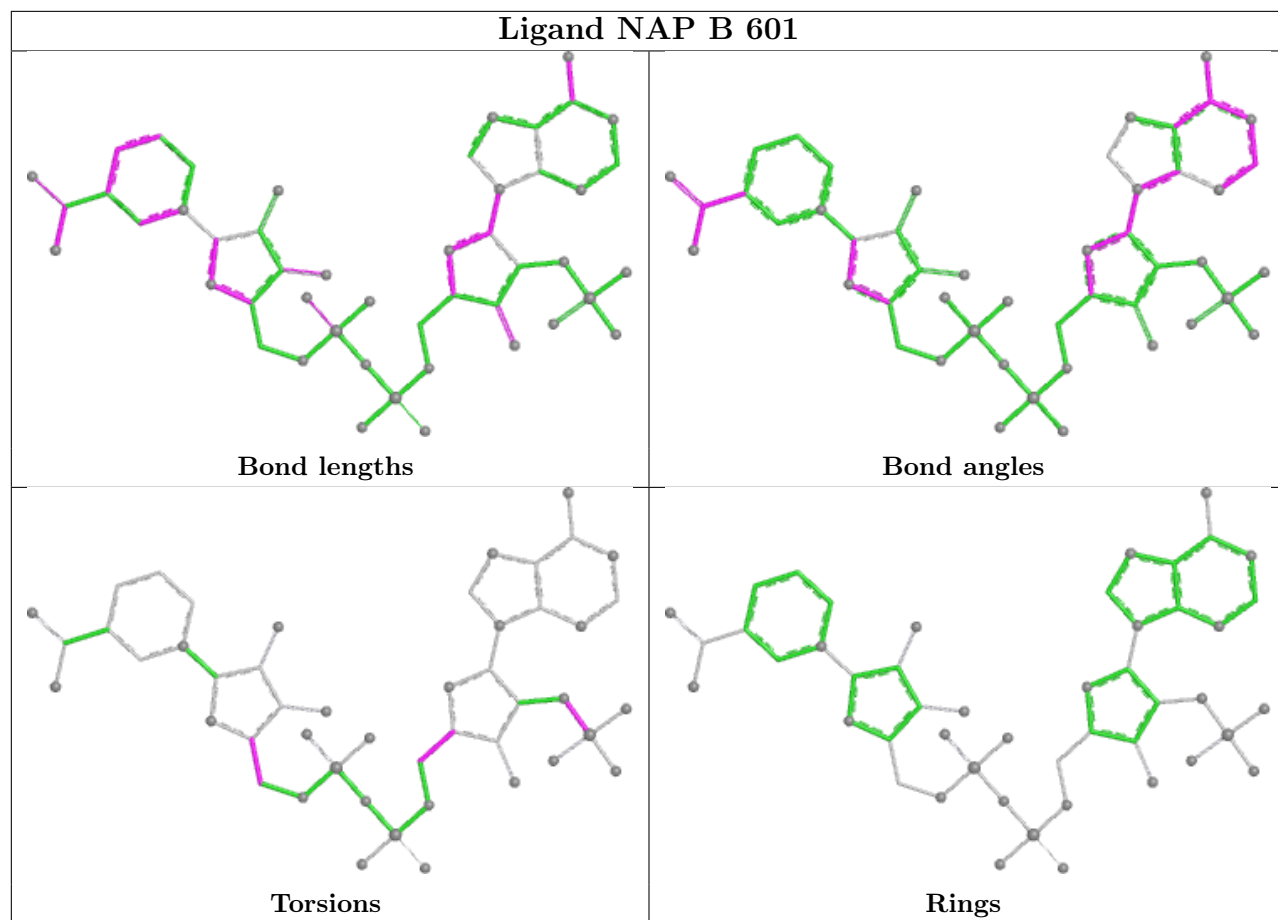
There are no ring outliers.

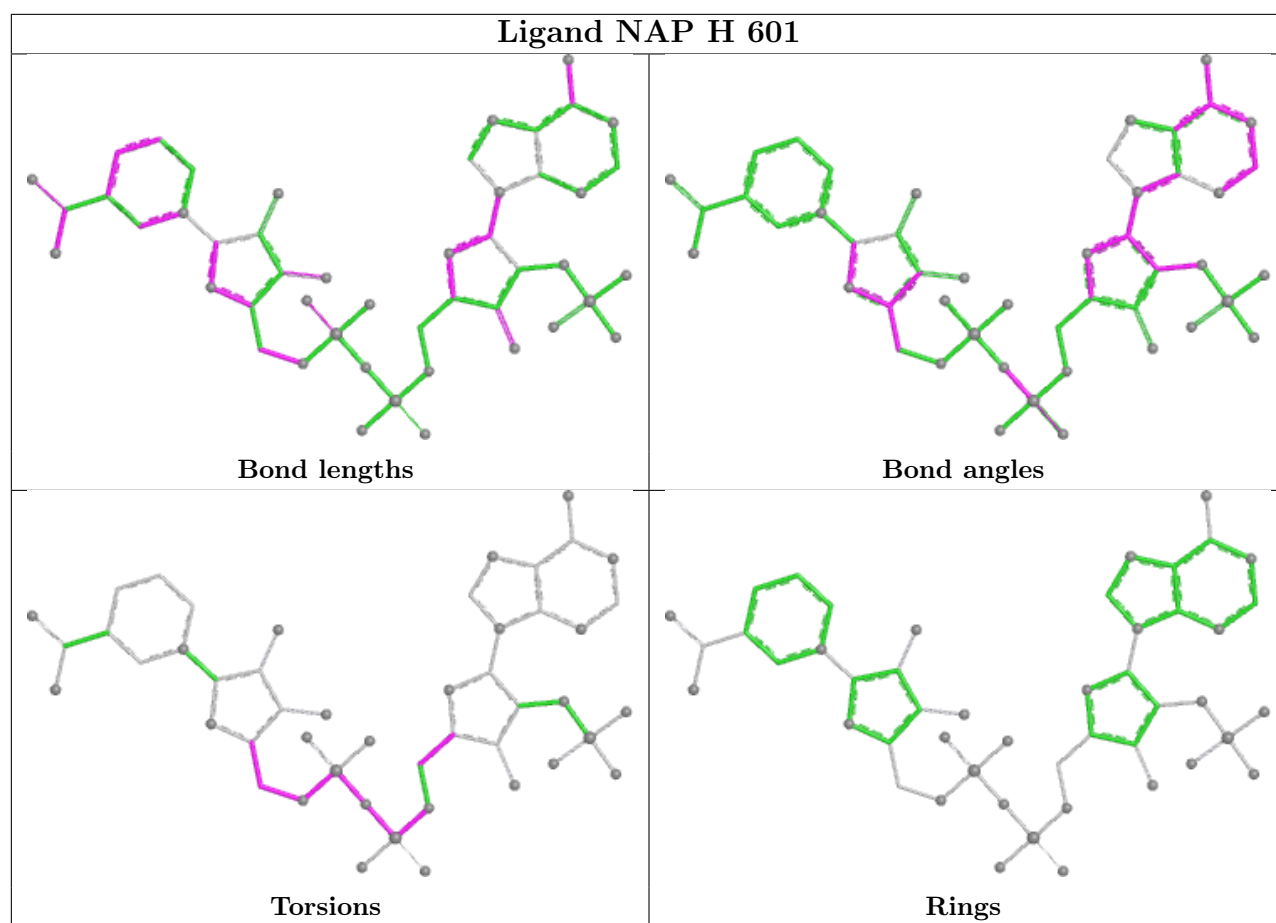
9 monomers are involved in 31 short contacts:

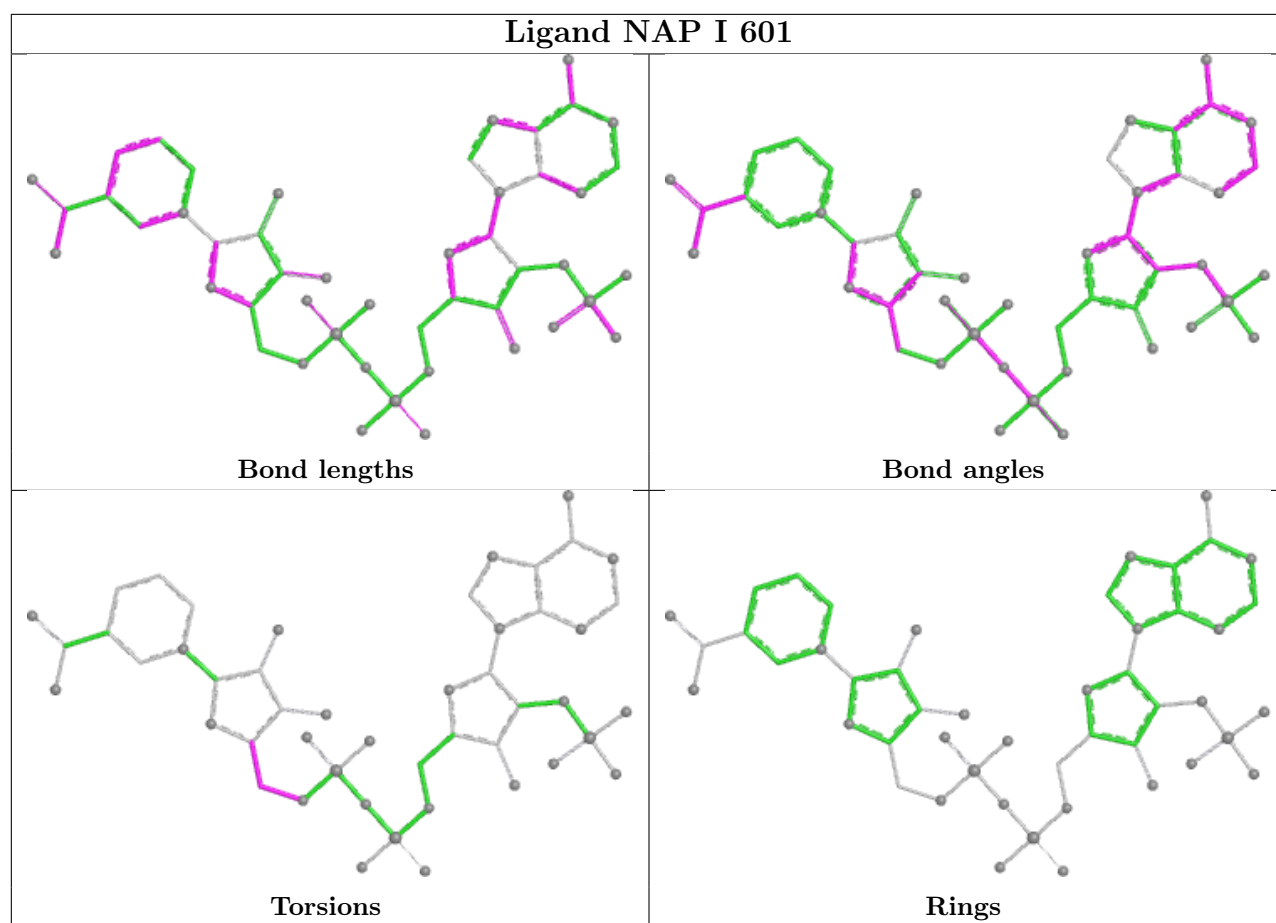
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	NAP	3	0
2	H	601	NAP	5	0
2	I	601	NAP	2	0
2	J	601	NAP	7	0
2	D	601	NAP	3	0
2	G	601	NAP	1	0
2	F	601	NAP	5	0
2	A	601	NAP	2	0
2	C	601	NAP	3	0

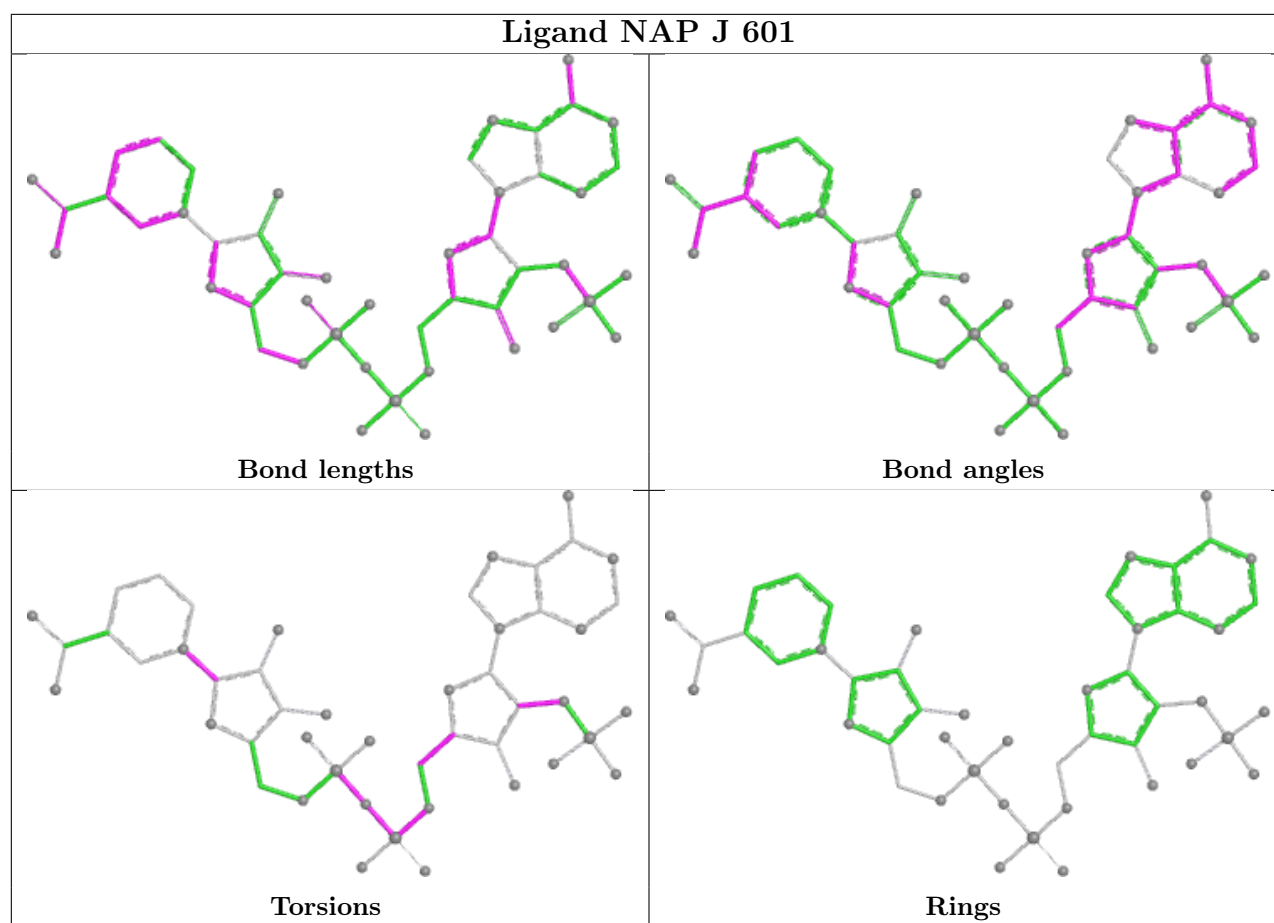
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

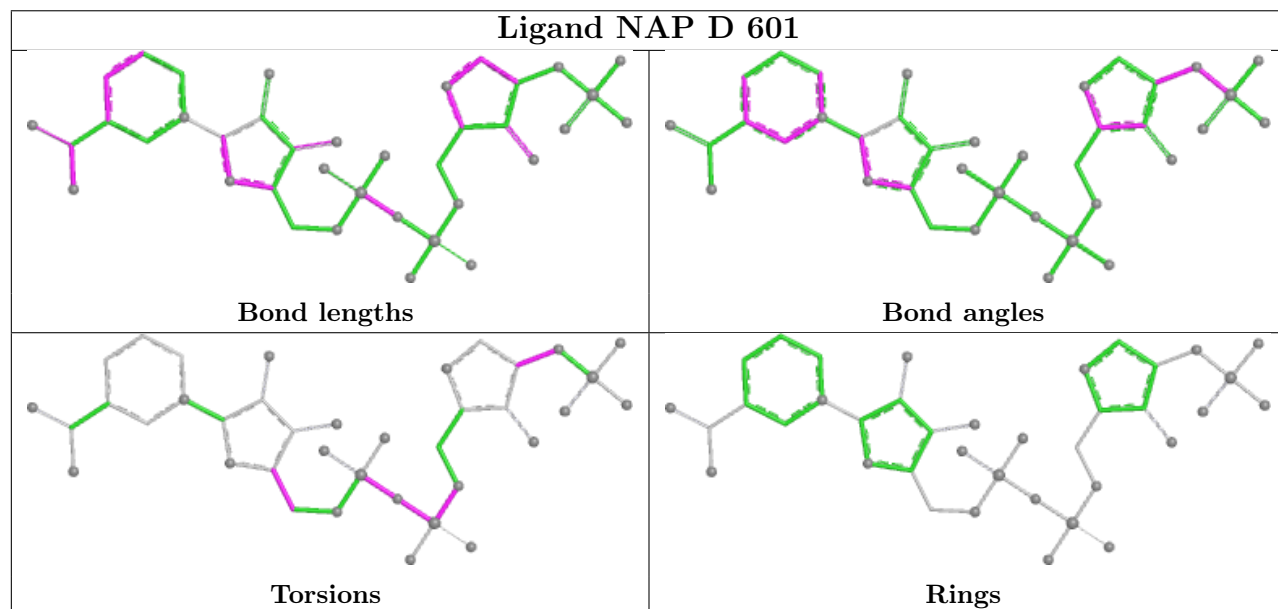
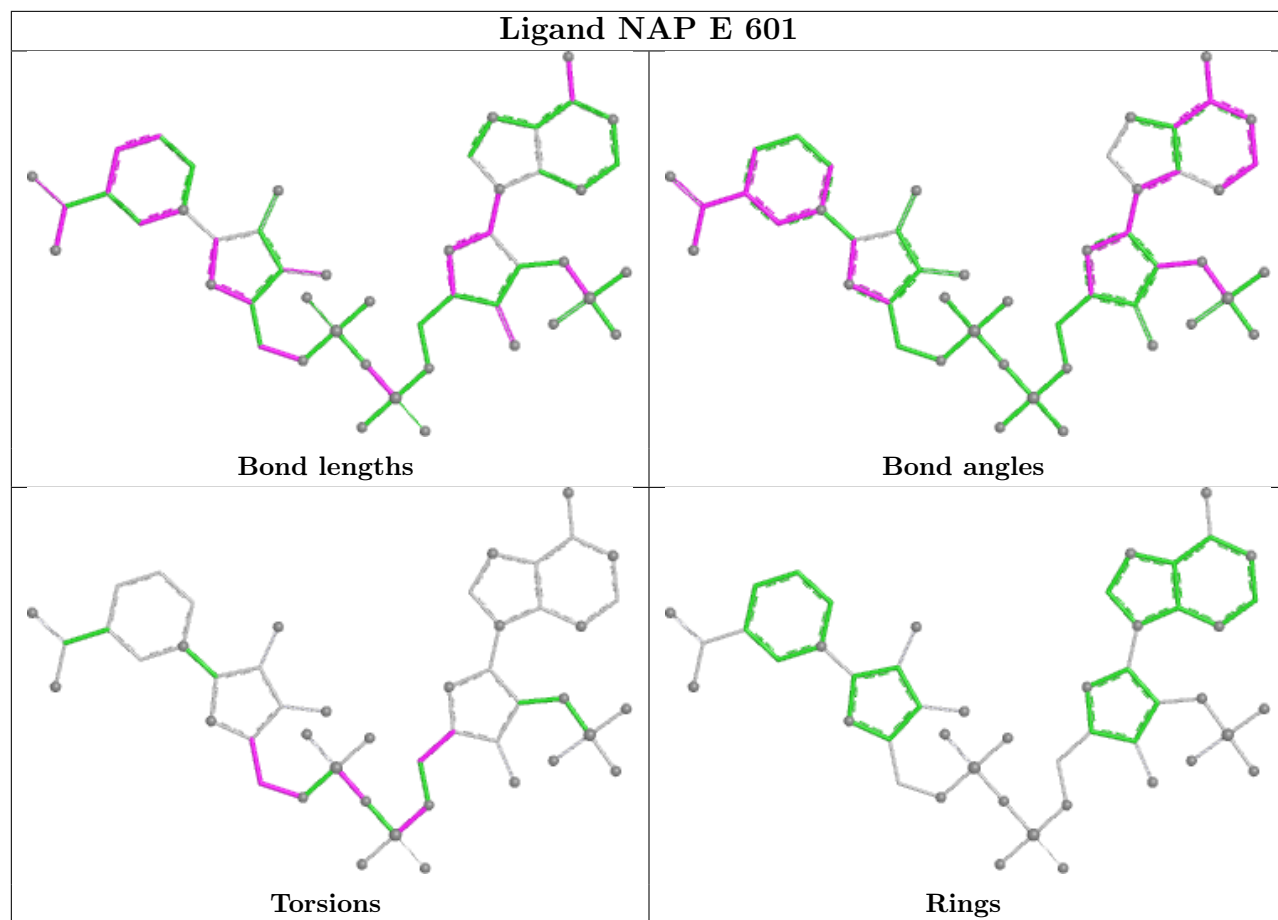


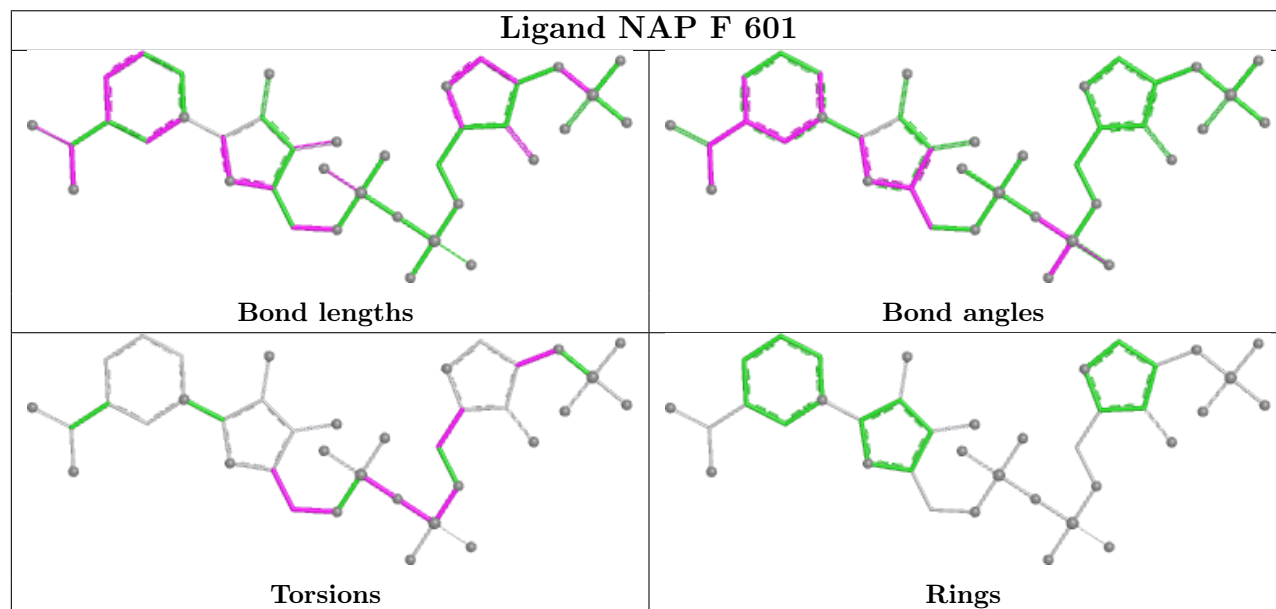
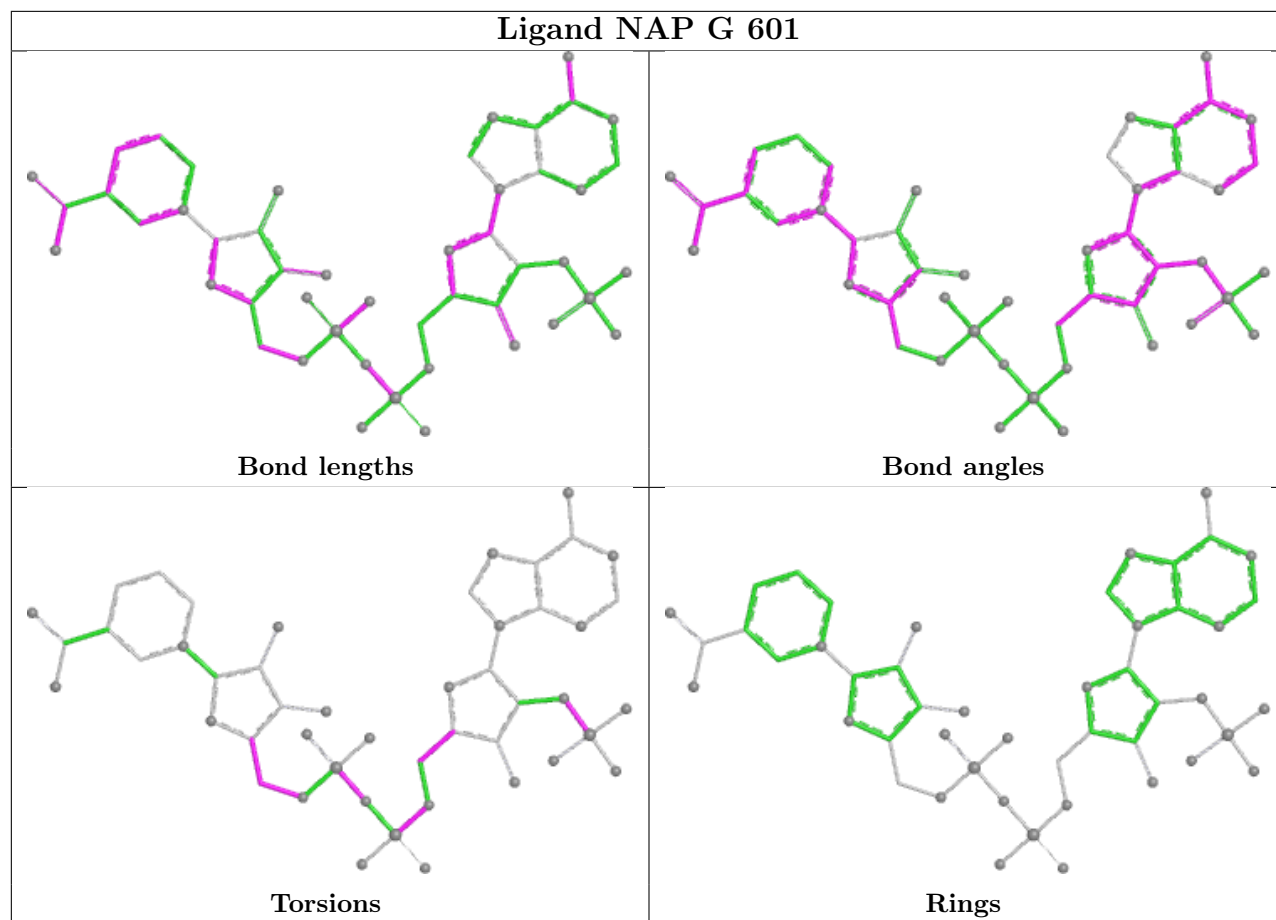


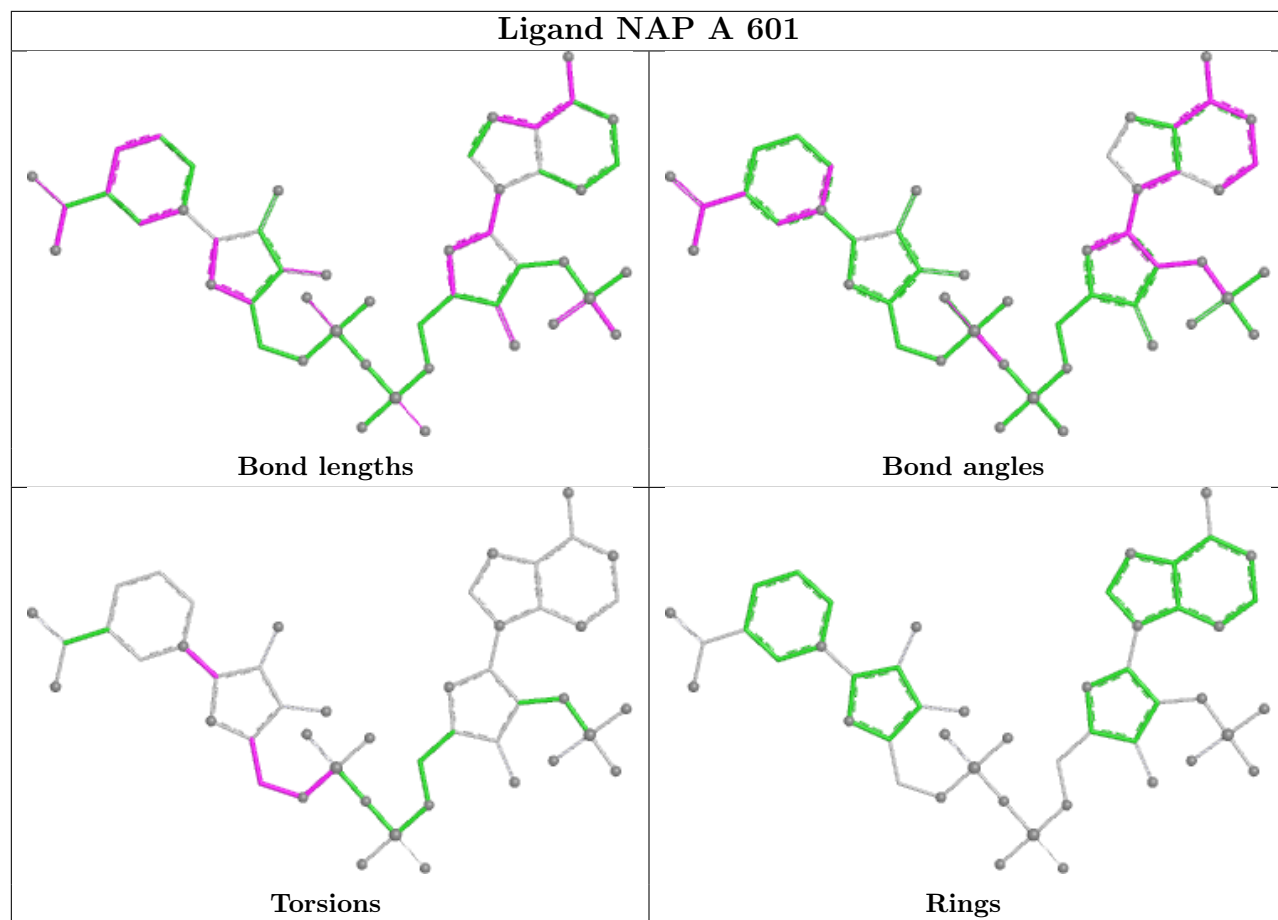


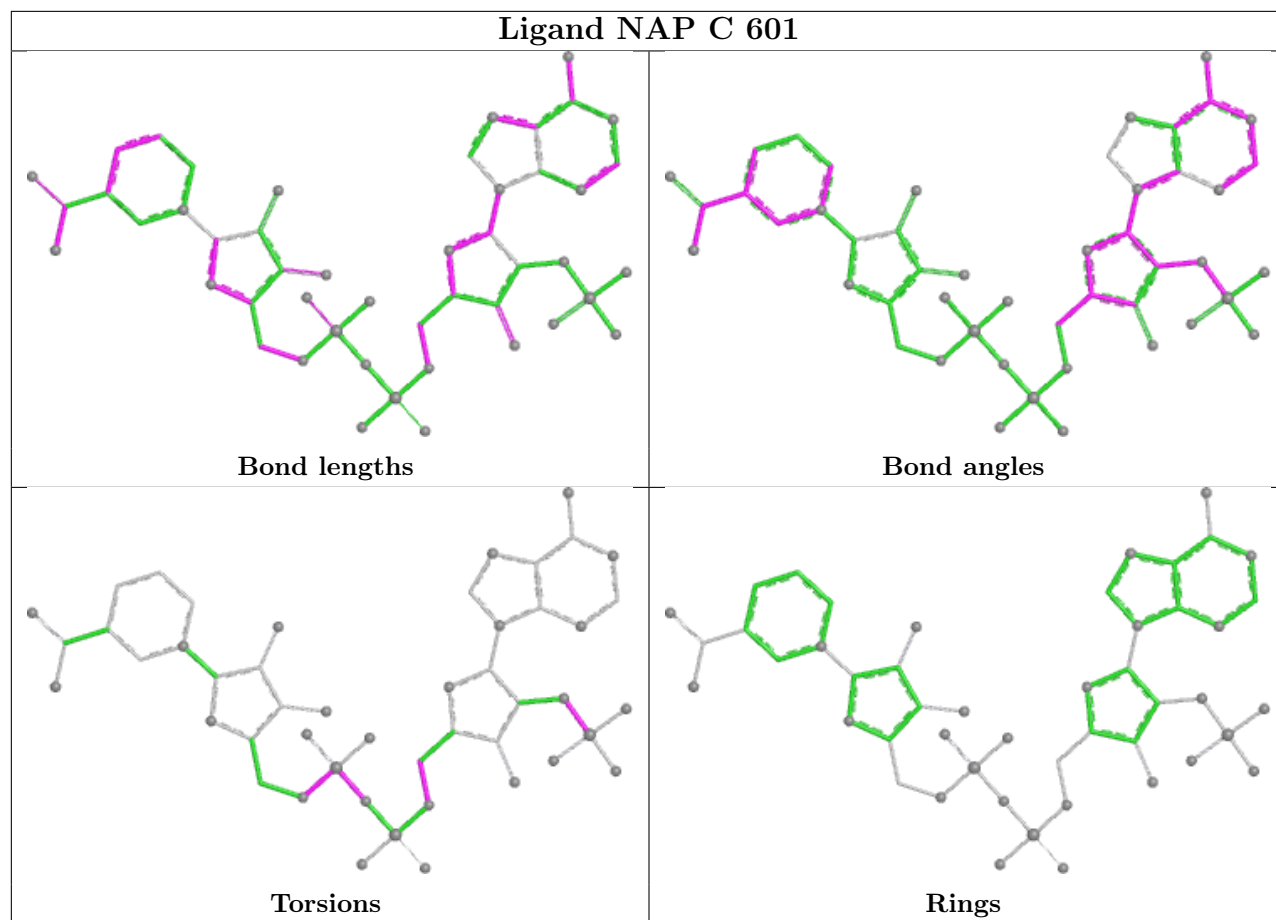












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	441/522 (84%)	-0.19	1 (0%) 95 95	38, 53, 75, 109	0
1	B	440/522 (84%)	-0.04	7 (1%) 72 69	40, 57, 82, 106	0
1	C	441/522 (84%)	-0.05	5 (1%) 80 79	40, 57, 79, 116	0
1	D	440/522 (84%)	0.02	9 (2%) 65 62	40, 63, 85, 116	0
1	E	441/522 (84%)	-0.20	4 (0%) 84 83	38, 54, 75, 117	0
1	F	441/522 (84%)	0.20	20 (4%) 33 29	37, 66, 91, 119	0
1	G	440/522 (84%)	-0.28	1 (0%) 95 95	34, 49, 67, 105	0
1	H	441/522 (84%)	-0.17	2 (0%) 91 90	36, 51, 72, 110	0
1	I	441/522 (84%)	-0.22	1 (0%) 95 95	36, 50, 69, 107	0
1	J	440/522 (84%)	-0.14	4 (0%) 84 83	37, 55, 77, 95	0
All	All	4406/5220 (84%)	-0.11	54 (1%) 79 77	34, 55, 80, 119	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	82	ALA	9.0
1	C	82	ALA	8.9
1	E	82	ALA	8.5
1	F	82	ALA	6.0
1	A	82	ALA	5.8
1	E	83	ALA	5.1
1	F	83	ALA	4.9
1	E	84	VAL	4.2
1	D	83	ALA	3.7
1	I	82	ALA	3.5
1	F	327	THR	3.2
1	F	204	CYS	3.2
1	H	83	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	83	ALA	3.1
1	F	373	LYS	3.1
1	B	398	ALA	3.0
1	D	392	ILE	2.9
1	F	328	CYS	2.9
1	D	91	THR	2.9
1	C	373	LYS	2.8
1	F	84	VAL	2.8
1	F	372	ALA	2.7
1	C	83	ALA	2.7
1	D	395	SER	2.7
1	C	84	VAL	2.6
1	F	365	LEU	2.6
1	F	197	ASN	2.5
1	D	373	LYS	2.4
1	F	89	PHE	2.4
1	J	83	ALA	2.4
1	D	262	ALA	2.4
1	D	492	THR	2.4
1	B	84	VAL	2.3
1	J	373	LYS	2.3
1	F	396	VAL	2.3
1	D	140	GLU	2.2
1	B	392	ILE	2.2
1	F	93	ASP	2.2
1	B	370	LEU	2.2
1	D	197	ASN	2.2
1	F	361	VAL	2.2
1	F	394	ILE	2.2
1	B	293	GLY	2.2
1	F	265	ALA	2.2
1	J	395	SER	2.2
1	F	326	ILE	2.1
1	E	258	GLU	2.1
1	F	369	VAL	2.1
1	J	84	VAL	2.1
1	G	83	ALA	2.1
1	F	367	ASP	2.1
1	B	328	CYS	2.1
1	F	354	TYR	2.1
1	C	261	LEU	2.1

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

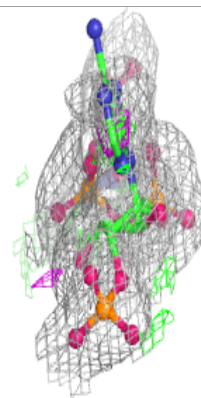
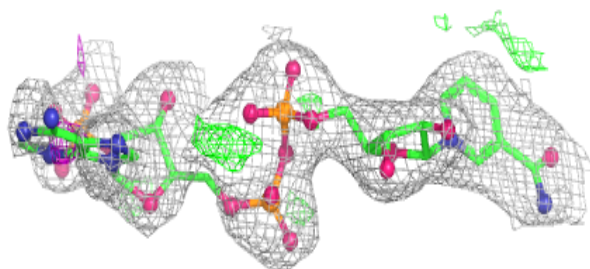
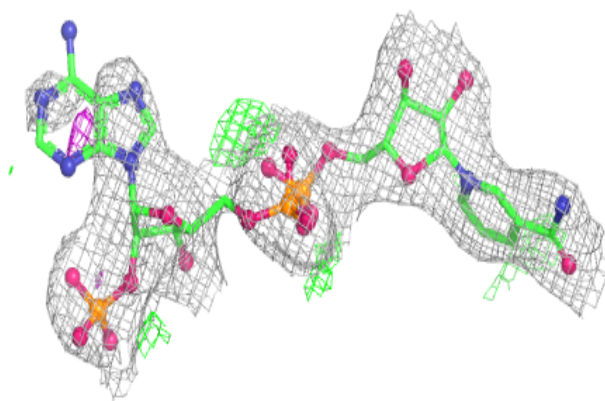
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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	B	601	48/48	0.85	0.23	35,99,134,138	0
2	NAP	J	601	48/48	0.85	0.24	46,91,111,117	48
2	NAP	H	601	48/48	0.86	0.21	50,87,108,112	48
2	NAP	C	601	48/48	0.86	0.20	52,95,122,124	48
2	NAP	E	601	48/48	0.87	0.20	35,106,156,159	0
2	NAP	F	601	38/48	0.87	0.19	64,93,140,142	0
2	NAP	D	601	38/48	0.89	0.20	46,88,121,122	0
2	NAP	G	601	48/48	0.89	0.21	35,84,131,132	0
3	K	D	602	1/1	0.89	0.07	76,76,76,76	0
3	K	J	602	1/1	0.89	0.09	64,64,64,64	0
3	K	E	602	1/1	0.90	0.07	60,60,60,60	0
3	K	B	602	1/1	0.90	0.09	64,64,64,64	0
2	NAP	I	601	48/48	0.91	0.18	39,65,84,88	0
2	NAP	A	601	48/48	0.91	0.17	48,72,96,101	0
3	K	C	602	1/1	0.92	0.11	67,67,67,67	0
3	K	I	602	1/1	0.94	0.07	58,58,58,58	0
3	K	F	602	1/1	0.96	0.12	70,70,70,70	0
3	K	G	602	1/1	0.96	0.09	51,51,51,51	0
3	K	A	602	1/1	0.98	0.09	63,63,63,63	0
3	K	H	602	1/1	0.98	0.11	58,58,58,58	0

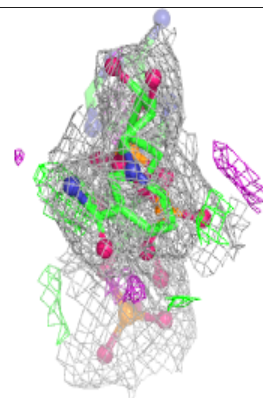
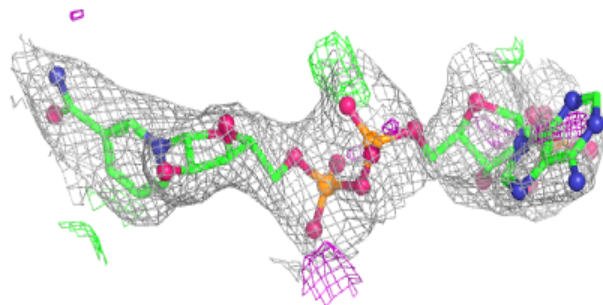
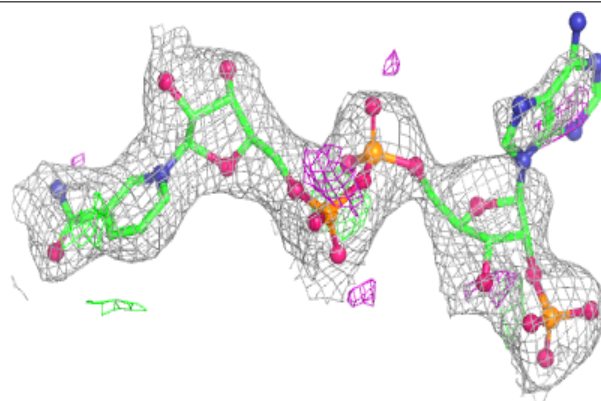
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around NAP 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)

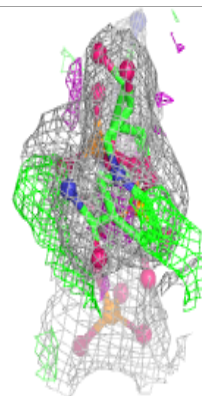
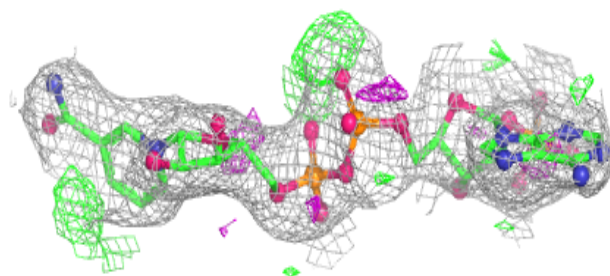
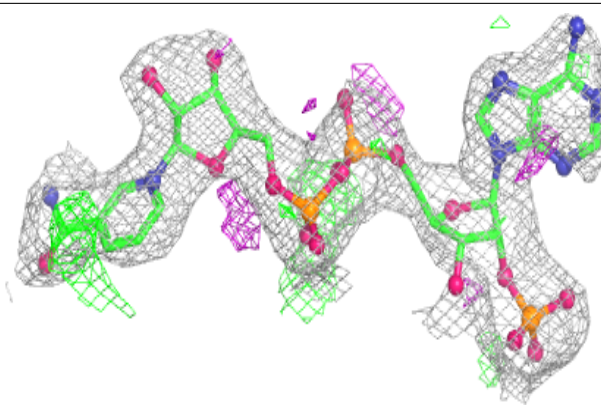
**Electron density around NAP J 601:**

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

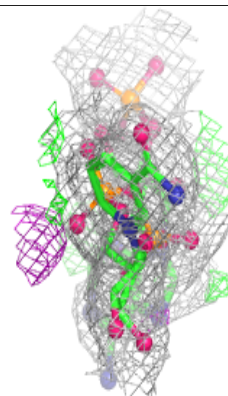
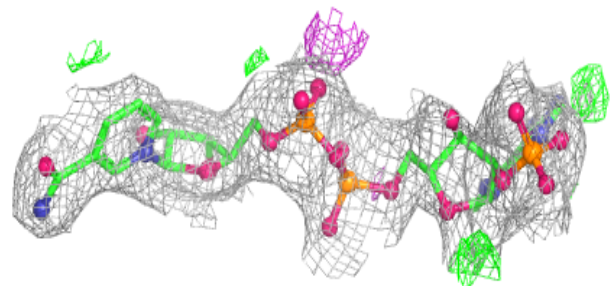
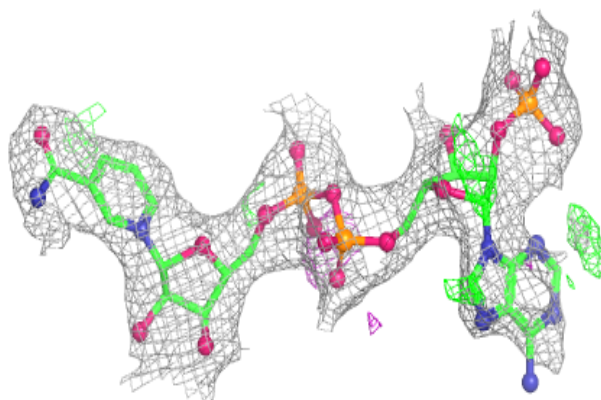


**Electron density around NAP H 601:**

$2mF_o-DF_c$  (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:**

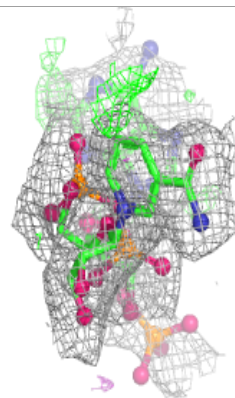
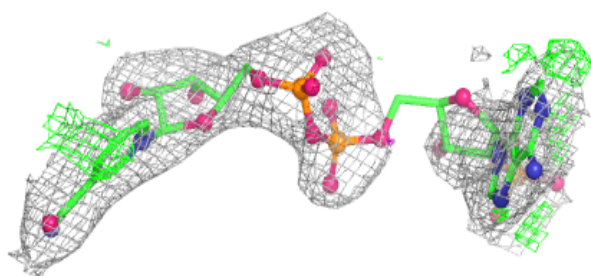
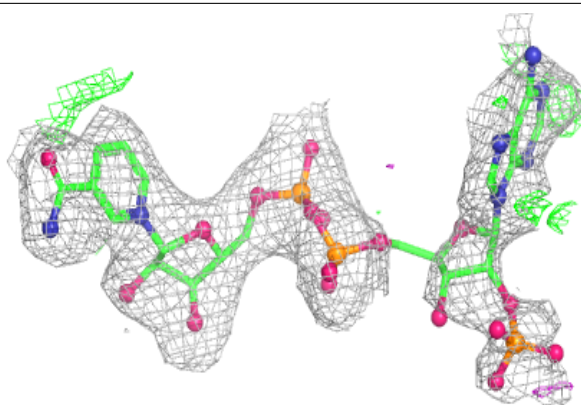
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



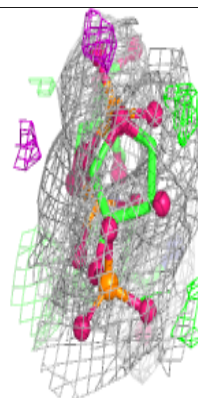
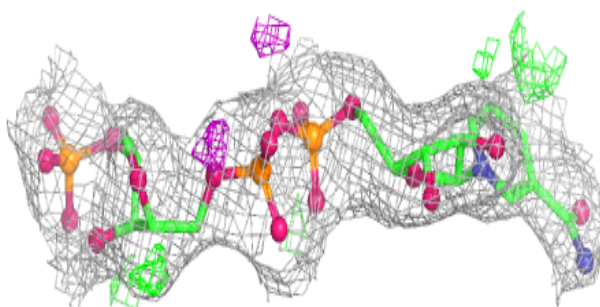
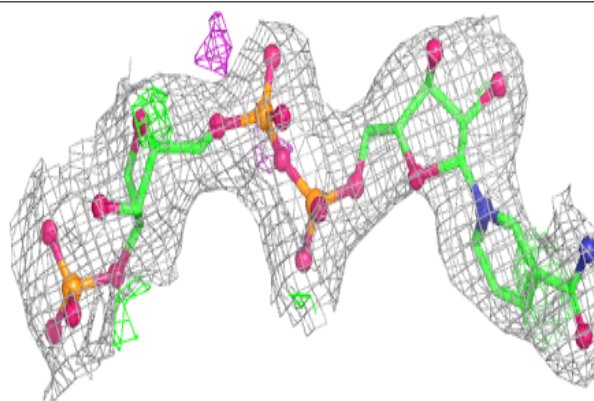


**Electron density around NAP E 601:**

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

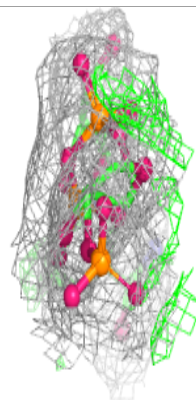
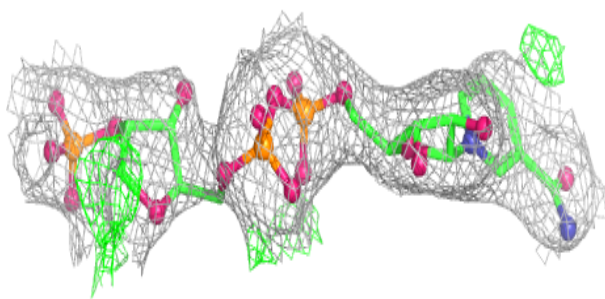
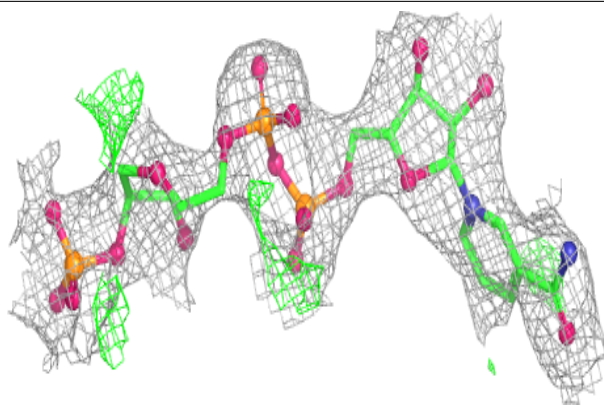
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

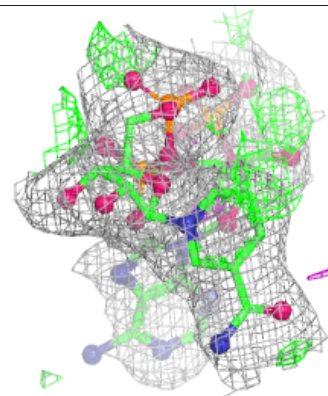
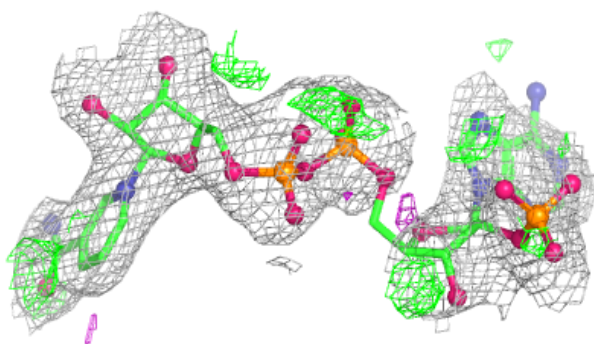
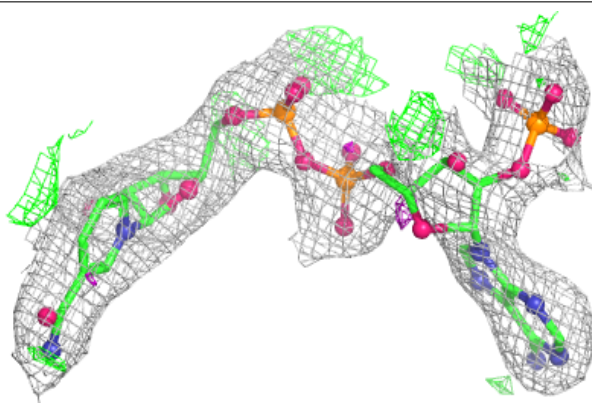


**Electron density around NAP D 601:**

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

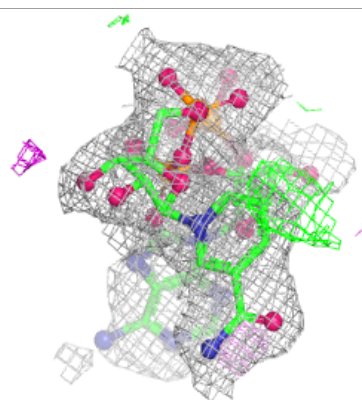
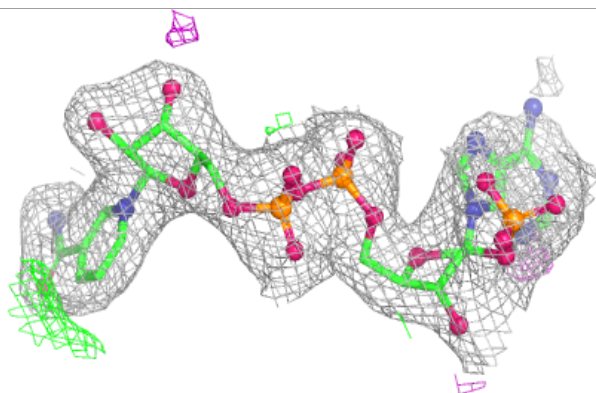
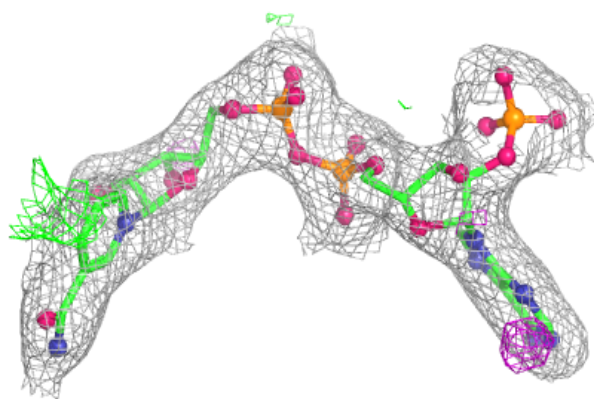
**Electron density around NAP G 601:**

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

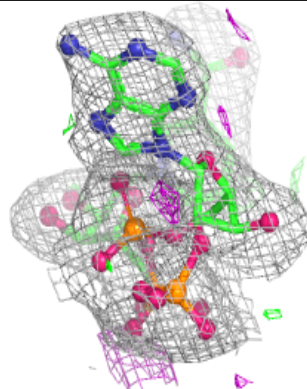
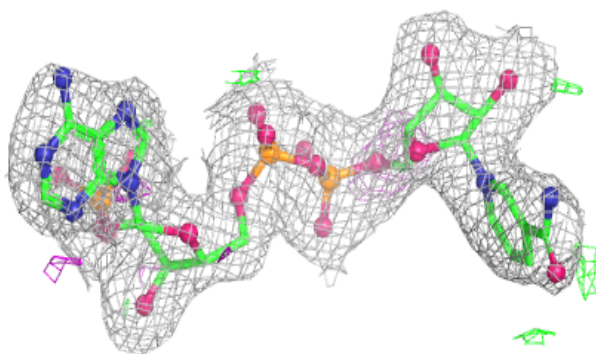
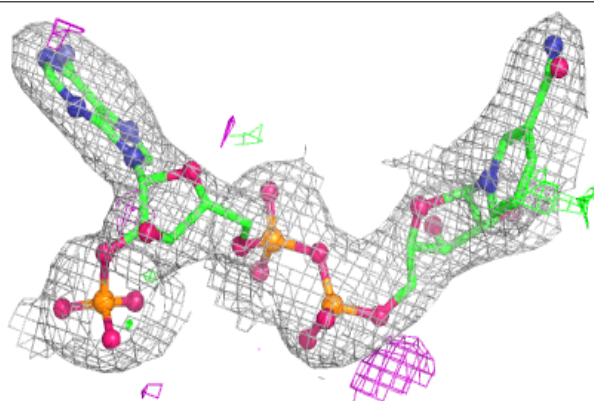


**Electron density around NAP I 601:**

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

**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)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.