



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:05 AM UTC

PDB ID : 4EXA / pdb_00004exa
Title : Crystal structure of the PA4992, the putative aldo-keto reductase from *Pseudomonas aeruginosa*
Authors : Sandalova, T.; Schnell, R.; Schneider, G.
Deposited on : 2012-04-30
Resolution : 2.80 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

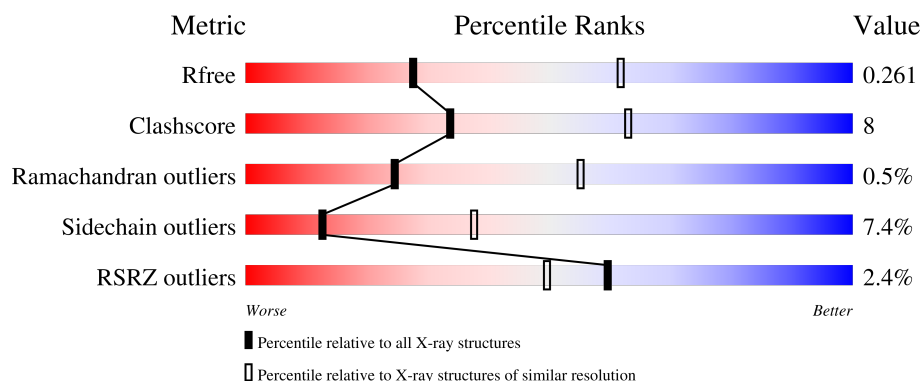
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	292	2% 72% 11% • 13%
1	B	292	2% 72% 11% • 14%
1	C	292	0% 71% 12% • 15%
1	D	292	2% 71% 12% • • 12%
1	E	292	2% 73% 11% • 12%

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Mol	Chain	Length	Quality of chain
1	F	292	3% 73% 12% • 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11958 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 Putative uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	0	0
			1935	1213	352	366	4			
1	B	252	Total	C	N	O	S	0	0	0
			1916	1200	350	362	4			
1	C	249	Total	C	N	O	S	0	0	0
			1891	1183	347	357	4			
1	D	256	Total	C	N	O	S	0	0	0
			1957	1227	355	371	4			
1	E	256	Total	C	N	O	S	0	0	0
			1956	1227	355	370	4			
1	F	259	Total	C	N	O	S	0	0	0
			1971	1235	360	372	4			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	expression tag	UNP Q9HUH3
A	-20	HIS	-	expression tag	UNP Q9HUH3
A	-19	HIS	-	expression tag	UNP Q9HUH3
A	-18	HIS	-	expression tag	UNP Q9HUH3
A	-17	HIS	-	expression tag	UNP Q9HUH3
A	-16	HIS	-	expression tag	UNP Q9HUH3
A	-15	HIS	-	expression tag	UNP Q9HUH3
A	-14	SER	-	expression tag	UNP Q9HUH3
A	-13	SER	-	expression tag	UNP Q9HUH3
A	-12	GLY	-	expression tag	UNP Q9HUH3
A	-11	VAL	-	expression tag	UNP Q9HUH3
A	-10	ASP	-	expression tag	UNP Q9HUH3
A	-9	LEU	-	expression tag	UNP Q9HUH3
A	-8	GLY	-	expression tag	UNP Q9HUH3
A	-7	THR	-	expression tag	UNP Q9HUH3
A	-6	GLU	-	expression tag	UNP Q9HUH3
A	-5	ASN	-	expression tag	UNP Q9HUH3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	LEU	-	expression tag	UNP Q9HUH3
A	-3	TYR	-	expression tag	UNP Q9HUH3
A	-2	PHE	-	expression tag	UNP Q9HUH3
A	-1	GLN	-	expression tag	UNP Q9HUH3
A	0	SER	-	expression tag	UNP Q9HUH3
B	-21	MET	-	expression tag	UNP Q9HUH3
B	-20	HIS	-	expression tag	UNP Q9HUH3
B	-19	HIS	-	expression tag	UNP Q9HUH3
B	-18	HIS	-	expression tag	UNP Q9HUH3
B	-17	HIS	-	expression tag	UNP Q9HUH3
B	-16	HIS	-	expression tag	UNP Q9HUH3
B	-15	HIS	-	expression tag	UNP Q9HUH3
B	-14	SER	-	expression tag	UNP Q9HUH3
B	-13	SER	-	expression tag	UNP Q9HUH3
B	-12	GLY	-	expression tag	UNP Q9HUH3
B	-11	VAL	-	expression tag	UNP Q9HUH3
B	-10	ASP	-	expression tag	UNP Q9HUH3
B	-9	LEU	-	expression tag	UNP Q9HUH3
B	-8	GLY	-	expression tag	UNP Q9HUH3
B	-7	THR	-	expression tag	UNP Q9HUH3
B	-6	GLU	-	expression tag	UNP Q9HUH3
B	-5	ASN	-	expression tag	UNP Q9HUH3
B	-4	LEU	-	expression tag	UNP Q9HUH3
B	-3	TYR	-	expression tag	UNP Q9HUH3
B	-2	PHE	-	expression tag	UNP Q9HUH3
B	-1	GLN	-	expression tag	UNP Q9HUH3
B	0	SER	-	expression tag	UNP Q9HUH3
C	-21	MET	-	expression tag	UNP Q9HUH3
C	-20	HIS	-	expression tag	UNP Q9HUH3
C	-19	HIS	-	expression tag	UNP Q9HUH3
C	-18	HIS	-	expression tag	UNP Q9HUH3
C	-17	HIS	-	expression tag	UNP Q9HUH3
C	-16	HIS	-	expression tag	UNP Q9HUH3
C	-15	HIS	-	expression tag	UNP Q9HUH3
C	-14	SER	-	expression tag	UNP Q9HUH3
C	-13	SER	-	expression tag	UNP Q9HUH3
C	-12	GLY	-	expression tag	UNP Q9HUH3
C	-11	VAL	-	expression tag	UNP Q9HUH3
C	-10	ASP	-	expression tag	UNP Q9HUH3
C	-9	LEU	-	expression tag	UNP Q9HUH3
C	-8	GLY	-	expression tag	UNP Q9HUH3
C	-7	THR	-	expression tag	UNP Q9HUH3

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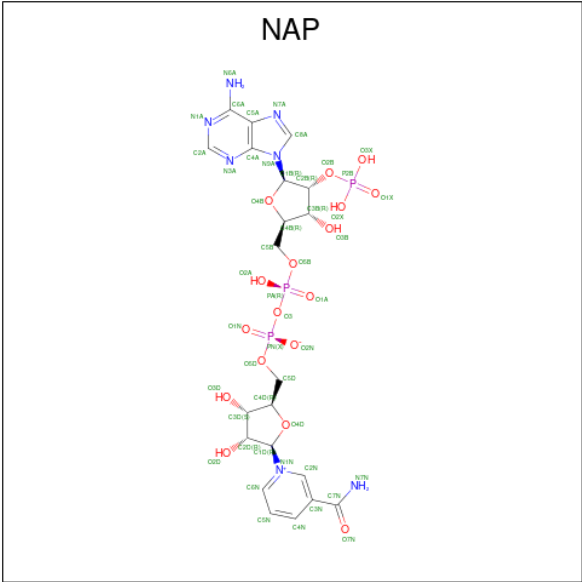
Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	GLU	-	expression tag	UNP Q9HUH3
C	-5	ASN	-	expression tag	UNP Q9HUH3
C	-4	LEU	-	expression tag	UNP Q9HUH3
C	-3	TYR	-	expression tag	UNP Q9HUH3
C	-2	PHE	-	expression tag	UNP Q9HUH3
C	-1	GLN	-	expression tag	UNP Q9HUH3
C	0	SER	-	expression tag	UNP Q9HUH3
D	-21	MET	-	expression tag	UNP Q9HUH3
D	-20	HIS	-	expression tag	UNP Q9HUH3
D	-19	HIS	-	expression tag	UNP Q9HUH3
D	-18	HIS	-	expression tag	UNP Q9HUH3
D	-17	HIS	-	expression tag	UNP Q9HUH3
D	-16	HIS	-	expression tag	UNP Q9HUH3
D	-15	HIS	-	expression tag	UNP Q9HUH3
D	-14	SER	-	expression tag	UNP Q9HUH3
D	-13	SER	-	expression tag	UNP Q9HUH3
D	-12	GLY	-	expression tag	UNP Q9HUH3
D	-11	VAL	-	expression tag	UNP Q9HUH3
D	-10	ASP	-	expression tag	UNP Q9HUH3
D	-9	LEU	-	expression tag	UNP Q9HUH3
D	-8	GLY	-	expression tag	UNP Q9HUH3
D	-7	THR	-	expression tag	UNP Q9HUH3
D	-6	GLU	-	expression tag	UNP Q9HUH3
D	-5	ASN	-	expression tag	UNP Q9HUH3
D	-4	LEU	-	expression tag	UNP Q9HUH3
D	-3	TYR	-	expression tag	UNP Q9HUH3
D	-2	PHE	-	expression tag	UNP Q9HUH3
D	-1	GLN	-	expression tag	UNP Q9HUH3
D	0	SER	-	expression tag	UNP Q9HUH3
E	-21	MET	-	expression tag	UNP Q9HUH3
E	-20	HIS	-	expression tag	UNP Q9HUH3
E	-19	HIS	-	expression tag	UNP Q9HUH3
E	-18	HIS	-	expression tag	UNP Q9HUH3
E	-17	HIS	-	expression tag	UNP Q9HUH3
E	-16	HIS	-	expression tag	UNP Q9HUH3
E	-15	HIS	-	expression tag	UNP Q9HUH3
E	-14	SER	-	expression tag	UNP Q9HUH3
E	-13	SER	-	expression tag	UNP Q9HUH3
E	-12	GLY	-	expression tag	UNP Q9HUH3
E	-11	VAL	-	expression tag	UNP Q9HUH3
E	-10	ASP	-	expression tag	UNP Q9HUH3
E	-9	LEU	-	expression tag	UNP Q9HUH3

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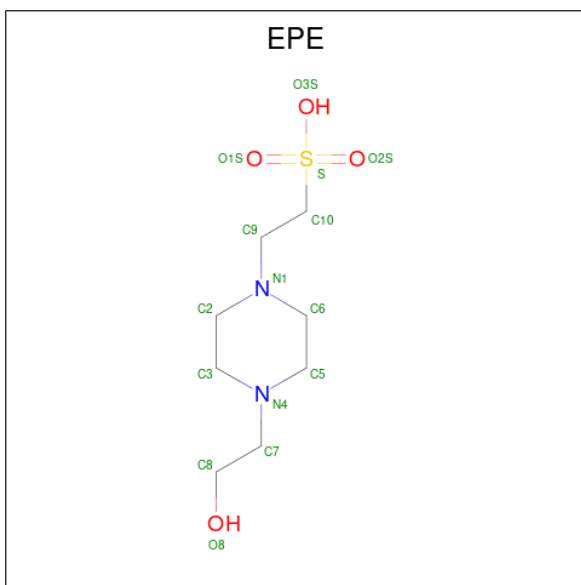
Chain	Residue	Modelled	Actual	Comment	Reference
E	-8	GLY	-	expression tag	UNP Q9HUH3
E	-7	THR	-	expression tag	UNP Q9HUH3
E	-6	GLU	-	expression tag	UNP Q9HUH3
E	-5	ASN	-	expression tag	UNP Q9HUH3
E	-4	LEU	-	expression tag	UNP Q9HUH3
E	-3	TYR	-	expression tag	UNP Q9HUH3
E	-2	PHE	-	expression tag	UNP Q9HUH3
E	-1	GLN	-	expression tag	UNP Q9HUH3
E	0	SER	-	expression tag	UNP Q9HUH3
F	-21	MET	-	expression tag	UNP Q9HUH3
F	-20	HIS	-	expression tag	UNP Q9HUH3
F	-19	HIS	-	expression tag	UNP Q9HUH3
F	-18	HIS	-	expression tag	UNP Q9HUH3
F	-17	HIS	-	expression tag	UNP Q9HUH3
F	-16	HIS	-	expression tag	UNP Q9HUH3
F	-15	HIS	-	expression tag	UNP Q9HUH3
F	-14	SER	-	expression tag	UNP Q9HUH3
F	-13	SER	-	expression tag	UNP Q9HUH3
F	-12	GLY	-	expression tag	UNP Q9HUH3
F	-11	VAL	-	expression tag	UNP Q9HUH3
F	-10	ASP	-	expression tag	UNP Q9HUH3
F	-9	LEU	-	expression tag	UNP Q9HUH3
F	-8	GLY	-	expression tag	UNP Q9HUH3
F	-7	THR	-	expression tag	UNP Q9HUH3
F	-6	GLU	-	expression tag	UNP Q9HUH3
F	-5	ASN	-	expression tag	UNP Q9HUH3
F	-4	LEU	-	expression tag	UNP Q9HUH3
F	-3	TYR	-	expression tag	UNP Q9HUH3
F	-2	PHE	-	expression tag	UNP Q9HUH3
F	-1	GLN	-	expression tag	UNP Q9HUH3
F	0	SER	-	expression tag	UNP Q9HUH3

- 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
			31	10	5	13	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	F	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
3	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

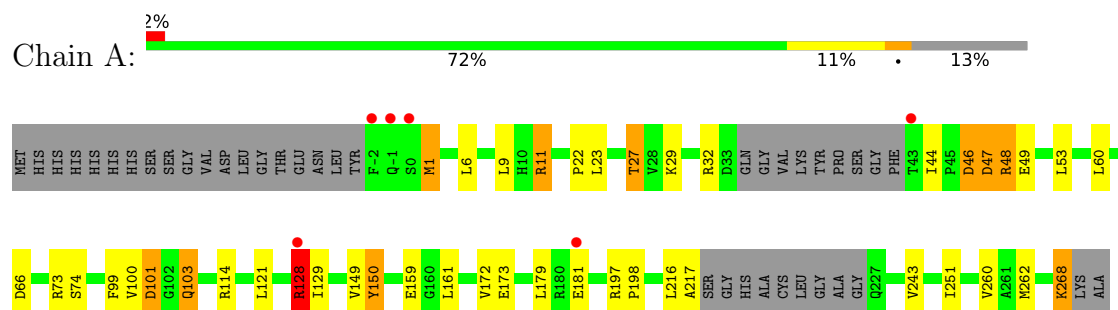
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	15	Total	O	0	0
			15	15		
4	B	18	Total	O	0	0
			18	18		
4	C	21	Total	O	0	0
			21	21		
4	D	25	Total	O	0	0
			25	25		
4	E	24	Total	O	0	0
			24	24		
4	F	13	Total	O	0	0
			13	13		

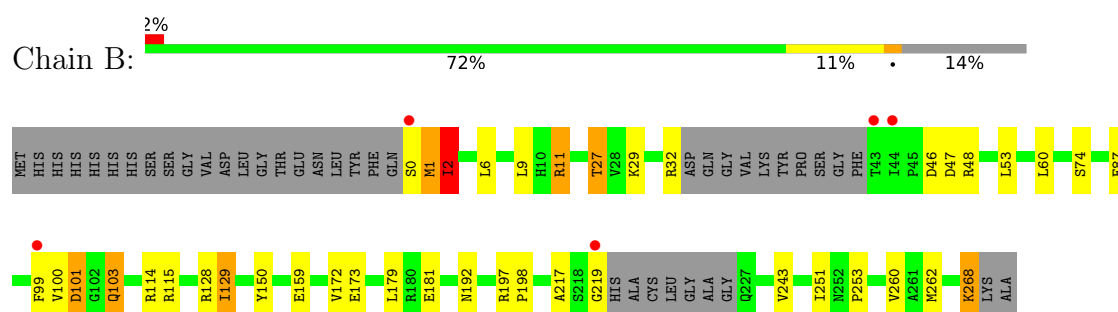
3 Residue-property plots [i](#)

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.

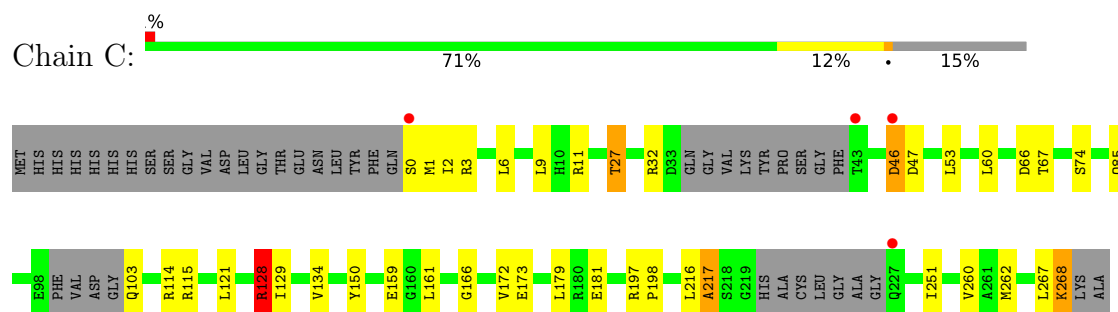
- Molecule 1: Putative uncharacterized protein



- Molecule 1: Putative uncharacterized protein

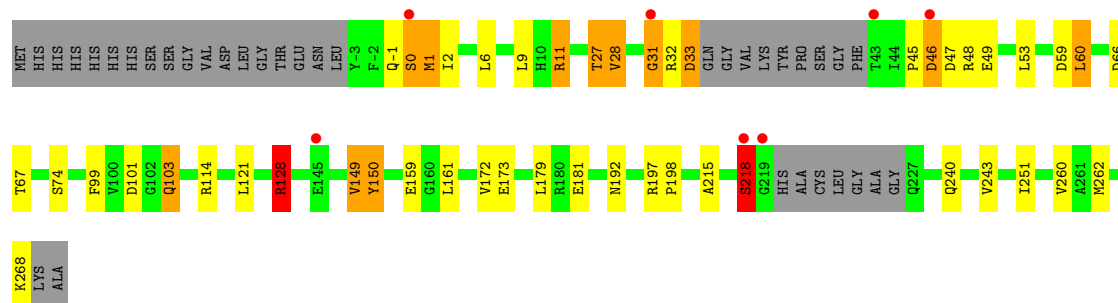


- Molecule 1: Putative uncharacterized protein

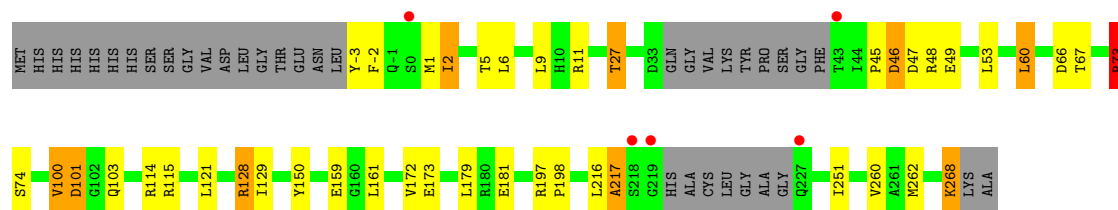
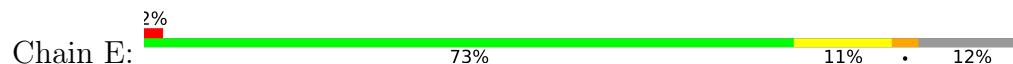


- Molecule 1: Putative uncharacterized protein

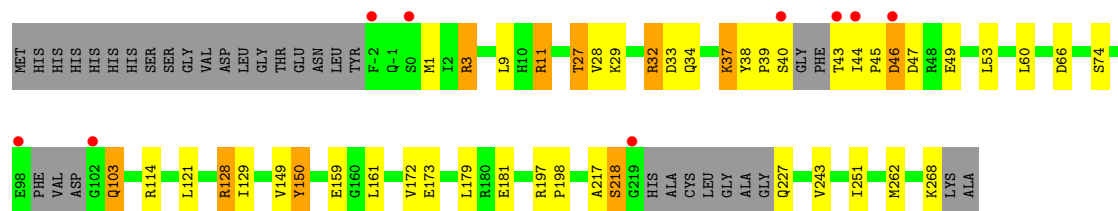




- Molecule 1: Putative uncharacterized protein



- Molecule 1: Putative uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	94.17Å 120.28Å 151.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	94.11 – 2.80 94.11 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.6 (94.11-2.80) 96.6 (94.11-2.80)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.227 , 0.272 0.224 , 0.261	Depositor DCC
R_{free} test set	2171 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 27.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	11958	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EPE, 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	0.79	1/1964 (0.1%)	0.93	7/2657 (0.3%)
1	B	0.86	1/1944 (0.1%)	0.92	3/2630 (0.1%)
1	C	0.84	0/1917	0.91	5/2592 (0.2%)
1	D	0.86	2/1987 (0.1%)	1.09	15/2688 (0.6%)
1	E	0.87	1/1986 (0.1%)	0.94	5/2687 (0.2%)
1	F	0.75	0/2000	0.88	4/2704 (0.1%)
All	All	0.83	5/11798 (0.0%)	0.95	39/15958 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	3
1	E	0	1
1	F	0	2
All	All	0	6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	129	ILE	C-O	-6.79	1.16	1.24
1	A	73	ARG	C-O	-5.69	1.16	1.24
1	E	73	ARG	C-O	-5.69	1.16	1.24
1	D	31	GLY	N-CA	5.65	1.49	1.44
1	D	215	ALA	CA-CB	-5.18	1.44	1.53

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	218	SER	O-C-N	-17.80	103.22	123.33
1	D	218	SER	CA-C-N	12.95	145.01	121.70
1	D	218	SER	C-N-CA	12.95	145.01	121.70
1	D	31	GLY	N-CA-C	-11.68	96.69	112.81
1	B	99	PHE	N-CA-C	10.58	123.29	110.91
1	D	46	ASP	CB-CA-C	-8.92	97.31	109.71
1	A	46	ASP	CB-CA-C	-8.67	97.66	109.71
1	D	99	PHE	N-CA-C	8.29	121.38	111.02
1	C	46	ASP	CB-CA-C	-8.04	98.53	109.71
1	A	46	ASP	N-CA-C	7.50	121.37	110.42
1	D	46	ASP	N-CA-C	7.49	121.36	110.42
1	E	46	ASP	CB-CA-C	-7.33	99.53	109.71
1	B	217	ALA	N-CA-C	6.94	117.75	108.38
1	C	217	ALA	N-CA-C	-6.84	96.23	110.80
1	E	46	ASP	N-CA-C	6.77	120.31	110.42
1	E	217	ALA	N-CA-C	-6.62	96.71	110.80
1	C	46	ASP	N-CA-C	6.51	119.92	110.42
1	B	103	GLN	N-CA-C	6.30	118.53	109.14
1	F	103	GLN	N-CA-C	6.09	117.83	109.18
1	D	103	GLN	N-CA-C	5.93	117.98	109.14
1	C	217	ALA	CB-CA-C	5.93	122.21	110.42
1	A	32	ARG	N-CA-C	5.79	118.54	108.76
1	E	217	ALA	CB-CA-C	5.74	121.84	110.42
1	A	99	PHE	N-CA-C	5.69	118.13	111.02
1	D	28	VAL	CB-CA-C	-5.68	104.60	112.04
1	D	218	SER	N-CA-C	5.63	117.83	108.99
1	F	46	ASP	CB-CA-C	-5.60	99.27	110.42
1	F	218	SER	N-CA-C	5.48	117.43	108.55
1	D	149	VAL	N-CA-C	5.43	116.16	110.62
1	D	1	MET	N-CA-C	-5.33	105.48	112.41
1	A	103	GLN	N-CA-C	5.30	117.04	109.14
1	E	73	ARG	N-CA-C	5.28	118.53	112.57
1	C	128	ARG	N-CA-C	5.23	115.44	108.38
1	A	44	ILE	CB-CA-C	-5.22	105.00	110.53
1	F	28	VAL	CB-CA-C	-5.18	105.26	112.04
1	A	128	ARG	N-CA-C	5.17	115.36	108.38
1	D	0	SER	CA-C-N	5.17	130.60	122.49
1	D	0	SER	C-N-CA	5.17	130.60	122.49
1	D	128	ARG	N-CA-C	5.13	115.31	108.38

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	218	SER	Peptide,Mainchain
1	D	45	PRO	Peptide
1	E	45	PRO	Peptide
1	F	217	ALA	Peptide
1	F	45	PRO	Peptide

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	1935	0	1951	26	0
1	B	1916	0	1935	26	0
1	C	1891	0	1911	25	0
1	D	1957	0	1968	33	0
1	E	1956	0	1968	39	0
1	F	1971	0	1987	38	0
2	A	31	0	11	1	0
2	B	31	0	11	1	0
2	C	31	0	11	2	0
2	D	31	0	11	0	0
2	E	31	0	11	0	0
2	F	31	0	11	0	0
3	B	15	0	17	0	0
3	C	15	0	17	0	0
4	A	15	0	0	0	0
4	B	18	0	0	2	0
4	C	21	0	0	1	0
4	D	25	0	0	1	0
4	E	24	0	0	1	0
4	F	13	0	0	1	0
All	All	11958	0	11820	182	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 8.

All (182) 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:F:32:ARG:C	1:F:44:ILE:HD11	1.78	1.08
1:F:32:ARG:C	1:F:44:ILE:CD1	2.35	1.00
1:E:27:THR:HG23	1:E:74:SER:OG	1.60	1.00
1:F:32:ARG:O	1:F:44:ILE:HD13	1.65	0.96
1:D:27:THR:HG23	1:D:74:SER:OG	1.67	0.92
1:B:27:THR:HG23	1:B:74:SER:OG	1.74	0.88
1:F:32:ARG:O	1:F:44:ILE:CD1	2.23	0.86
1:C:27:THR:HG23	1:C:74:SER:OG	1.74	0.86
1:E:100:VAL:HG12	1:E:100:VAL:O	1.78	0.84
1:B:197:ARG:HD3	4:B:413:HOH:O	1.79	0.82
1:A:27:THR:HG23	1:A:74:SER:OG	1.79	0.81
1:E:-3:TYR:HD1	1:E:-2:PHE:N	1.79	0.81
1:E:-3:TYR:HD1	1:E:-2:PHE:H	1.26	0.80
1:F:33:ASP:N	1:F:44:ILE:HD11	1.95	0.80
1:D:192:ASN:ND2	1:D:218:SER:HA	1.97	0.80
1:F:40:SER:C	1:F:43:THR:HA	2.09	0.77
1:F:39:PRO:O	1:F:40:SER:CB	2.32	0.76
1:E:-3:TYR:CD1	1:E:-2:PHE:N	2.54	0.74
1:E:27:THR:CG2	1:E:74:SER:OG	2.38	0.72
1:E:2:ILE:HD13	1:E:60:LEU:HD12	1.72	0.71
1:A:53:LEU:HD21	1:A:251:ILE:HA	1.73	0.70
1:E:2:ILE:CD1	1:E:5:THR:HG22	2.21	0.69
1:D:192:ASN:HD21	1:D:218:SER:HA	1.56	0.69
1:F:53:LEU:HD21	1:F:251:ILE:HA	1.75	0.68
1:E:2:ILE:HD13	1:E:60:LEU:CD1	2.25	0.67
1:D:27:THR:CG2	1:D:74:SER:OG	2.42	0.67
1:D:27:THR:HG23	1:D:74:SER:HG	1.57	0.67
1:D:53:LEU:HD21	1:D:251:ILE:HA	1.77	0.66
1:E:2:ILE:HD11	1:E:5:THR:CG2	2.26	0.66
1:F:32:ARG:C	1:F:44:ILE:HD13	2.15	0.65
1:F:27:THR:HG23	1:F:74:SER:OG	1.96	0.65
1:D:59:ASP:OD2	1:E:-2:PHE:CE1	2.50	0.65
1:E:53:LEU:HD21	1:E:251:ILE:HA	1.80	0.64
1:E:100:VAL:O	1:E:100:VAL:CG1	2.46	0.64
1:B:87:GLU:HB2	4:B:402:HOH:O	1.98	0.63
1:C:46:ASP:O	1:C:47:ASP:C	2.41	0.63
1:B:27:THR:CG2	1:B:74:SER:OG	2.46	0.61
2:C:301:NAP:PN	2:C:301:NAP:H51A	2.40	0.61
1:C:53:LEU:HD21	1:C:251:ILE:HA	1.82	0.61
1:C:2:ILE:HG23	1:F:1:MET:HE1	1.82	0.61
1:E:2:ILE:CD1	1:E:5:THR:CG2	2.79	0.60
1:D:59:ASP:OD2	1:E:-2:PHE:CZ	2.55	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:0:SER:OG	1:C:1:MET:N	2.34	0.59
1:D:121:LEU:HD21	1:D:128:ARG:HA	1.83	0.59
1:F:262:MET:HE2	1:F:262:MET:HA	1.84	0.59
1:B:192:ASN:HD21	1:B:219:GLY:H	1.49	0.58
1:F:121:LEU:HD21	1:F:128:ARG:HA	1.86	0.58
1:A:100:VAL:HG12	1:A:100:VAL:O	2.02	0.58
1:C:114:ARG:NH2	1:C:159:GLU:OE2	2.37	0.58
1:B:1:MET:O	1:B:2:ILE:HG23	2.03	0.58
1:C:27:THR:CG2	1:C:74:SER:OG	2.51	0.58
1:A:46:ASP:O	1:A:47:ASP:C	2.46	0.57
1:D:121:LEU:CD2	1:D:128:ARG:HA	2.34	0.57
1:F:121:LEU:CD2	1:F:128:ARG:HA	2.35	0.57
1:C:6:LEU:HG	1:C:260:VAL:HG13	1.87	0.57
1:A:121:LEU:HD21	1:A:128:ARG:HA	1.87	0.56
1:A:121:LEU:CD2	1:A:128:ARG:HA	2.35	0.56
1:B:27:THR:HG23	1:B:27:THR:O	2.06	0.56
2:C:301:NAP:H51A	2:C:301:NAP:O2N	2.06	0.56
1:C:121:LEU:HD21	1:C:128:ARG:HA	1.88	0.56
1:A:27:THR:CG2	1:A:74:SER:OG	2.51	0.56
1:E:6:LEU:HG	1:E:260:VAL:HG13	1.87	0.56
1:B:262:MET:HE2	1:B:262:MET:HA	1.88	0.55
1:D:1:MET:HE2	1:E:1:MET:HE2	1.88	0.55
1:A:29:LYS:NZ	2:A:301:NAP:O3B	2.39	0.55
1:F:40:SER:O	1:F:43:THR:HG23	2.06	0.55
1:B:100:VAL:O	1:B:101:ASP:HB2	2.06	0.55
1:B:1:MET:C	1:B:2:ILE:HG23	2.33	0.53
1:A:27:THR:HG23	1:A:27:THR:O	2.07	0.53
1:A:46:ASP:O	1:A:48:ARG:N	2.41	0.53
1:E:27:THR:HB	1:E:66:ASP:O	2.10	0.52
1:E:262:MET:HA	1:E:262:MET:HE2	1.90	0.52
1:E:46:ASP:O	1:E:47:ASP:C	2.53	0.52
1:F:32:ARG:HB2	1:F:44:ILE:HG12	1.91	0.52
1:A:46:ASP:O	1:A:49:GLU:N	2.42	0.52
1:C:121:LEU:CD2	1:C:128:ARG:HA	2.39	0.52
1:E:121:LEU:CD2	1:E:128:ARG:HA	2.39	0.52
1:E:216:LEU:O	1:E:217:ALA:HB2	2.09	0.52
1:F:27:THR:HG23	1:F:27:THR:O	2.10	0.52
1:D:27:THR:HG23	1:D:27:THR:O	2.09	0.51
1:F:38:TYR:HA	1:F:39:PRO:C	2.34	0.51
1:D:262:MET:HA	1:D:262:MET:HE2	1.93	0.51
1:B:6:LEU:HG	1:B:260:VAL:HG13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:40:SER:HA	1:F:43:THR:HA	1.93	0.51
1:D:28:VAL:O	1:D:31:GLY:O	2.29	0.51
1:D:46:ASP:O	1:D:47:ASP:C	2.54	0.51
1:F:114:ARG:NH2	1:F:159:GLU:OE2	2.44	0.51
1:A:216:LEU:O	1:A:217:ALA:HB2	2.11	0.50
1:C:262:MET:HA	1:C:262:MET:HE2	1.92	0.50
1:A:262:MET:HA	1:A:262:MET:HE2	1.93	0.50
1:F:40:SER:CA	1:F:43:THR:HA	2.41	0.50
1:C:3:ARG:NH2	4:C:413:HOH:O	2.44	0.50
1:A:11:ARG:NH1	1:A:243:VAL:O	2.45	0.49
1:B:114:ARG:NH2	1:B:159:GLU:OE2	2.45	0.49
1:C:128:ARG:HG2	1:C:129:ILE:N	2.24	0.49
1:F:46:ASP:O	1:F:47:ASP:C	2.56	0.48
1:D:27:THR:HG21	1:D:67:THR:HB	1.96	0.48
1:E:2:ILE:O	1:E:2:ILE:HG13	2.13	0.48
1:D:-1:GLN:C	1:D:1:MET:H	2.21	0.48
1:F:27:THR:HB	1:F:66:ASP:O	2.13	0.48
1:D:46:ASP:O	1:D:48:ARG:N	2.47	0.47
1:B:0:SER:O	1:B:0:SER:OG	2.29	0.47
1:D:6:LEU:HG	1:D:260:VAL:HG13	1.96	0.47
1:D:114:ARG:NH2	1:D:159:GLU:OE2	2.46	0.47
1:B:1:MET:O	1:B:2:ILE:CG2	2.62	0.47
1:C:27:THR:HG21	1:C:67:THR:HB	1.96	0.47
1:F:34:GLN:O	1:F:37:LYS:HB2	2.14	0.47
1:A:128:ARG:HG2	1:A:129:ILE:N	2.28	0.47
1:D:128:ARG:HB2	1:D:161:LEU:O	2.15	0.47
1:A:128:ARG:HB2	1:A:161:LEU:O	2.15	0.47
1:E:121:LEU:HD21	1:E:128:ARG:HA	1.96	0.47
1:F:128:ARG:HG2	1:F:129:ILE:N	2.26	0.47
1:F:3:ARG:HH11	1:F:3:ARG:CG	2.27	0.46
1:F:40:SER:HA	1:F:43:THR:CA	2.44	0.46
1:B:53:LEU:HD21	1:B:251:ILE:HA	1.98	0.46
1:B:197:ARG:N	1:B:198:PRO:CD	2.79	0.46
1:D:27:THR:HB	1:D:66:ASP:O	2.16	0.46
1:E:128:ARG:HG2	1:E:129:ILE:N	2.23	0.46
1:F:33:ASP:HA	1:F:44:ILE:CD1	2.46	0.46
1:A:27:THR:HB	1:A:66:ASP:O	2.16	0.45
1:E:27:THR:HG23	1:E:27:THR:O	2.16	0.45
1:E:197:ARG:HD3	4:E:424:HOH:O	2.15	0.45
1:D:59:ASP:OD2	1:E:-2:PHE:HE1	1.98	0.45
1:E:27:THR:HG22	1:E:67:THR:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:197:ARG:N	1:D:198:PRO:CD	2.79	0.45
1:D:46:ASP:O	1:D:49:GLU:N	2.50	0.45
1:C:128:ARG:HB2	1:C:161:LEU:O	2.17	0.45
1:A:1:MET:HB3	1:B:253:PRO:HB2	1.99	0.45
1:B:0:SER:C	1:B:2:ILE:N	2.75	0.45
1:A:6:LEU:HG	1:A:260:VAL:HG13	1.97	0.45
1:A:22:PRO:O	1:A:23:LEU:HD23	2.17	0.45
1:C:27:THR:HG22	1:C:67:THR:HA	1.99	0.45
1:F:149:VAL:HG13	1:F:150:TYR:N	2.31	0.45
1:D:149:VAL:HG13	1:D:150:TYR:N	2.32	0.44
1:E:100:VAL:O	1:E:101:ASP:HB2	2.17	0.44
1:A:149:VAL:HG13	1:A:150:TYR:N	2.32	0.44
1:D:33:ASP:OD2	1:D:33:ASP:C	2.60	0.44
1:D:2:ILE:HB	1:D:60:LEU:HD11	1.99	0.44
1:C:134:VAL:HG23	1:C:166:GLY:O	2.18	0.44
1:F:197:ARG:N	1:F:198:PRO:CD	2.81	0.44
1:E:27:THR:HG21	1:E:67:THR:HB	2.00	0.44
1:E:27:THR:HG23	1:E:74:SER:HG	1.77	0.43
1:E:114:ARG:NH2	1:E:159:GLU:OE2	2.51	0.43
1:E:268:LYS:HB3	1:E:268:LYS:HE3	1.86	0.43
1:A:197:ARG:N	1:A:198:PRO:CD	2.81	0.43
1:A:114:ARG:NH2	1:A:159:GLU:OE2	2.51	0.43
1:E:197:ARG:N	1:E:198:PRO:CD	2.80	0.43
1:F:27:THR:CG2	1:F:74:SER:OG	2.64	0.43
1:B:29:LYS:NZ	2:B:301:NAP:O3B	2.51	0.43
1:F:33:ASP:CA	1:F:44:ILE:HD11	2.49	0.43
1:A:268:LYS:HE3	1:A:268:LYS:HB3	1.86	0.42
1:B:0:SER:C	1:B:2:ILE:H	2.26	0.42
1:F:53:LEU:CD2	1:F:251:ILE:HA	2.47	0.42
1:B:48:ARG:HD2	1:B:48:ARG:HA	1.82	0.42
1:C:27:THR:HB	1:C:66:ASP:O	2.19	0.42
1:B:192:ASN:ND2	1:B:219:GLY:H	2.15	0.42
1:D:197:ARG:HE	1:D:240:GLN:HE22	1.68	0.42
1:C:1:MET:HE2	1:C:1:MET:HB2	1.64	0.42
1:C:197:ARG:N	1:C:198:PRO:CD	2.82	0.42
1:C:268:LYS:HE3	1:C:268:LYS:HB3	1.85	0.42
1:D:-1:GLN:C	1:D:1:MET:N	2.78	0.41
1:E:128:ARG:HB2	1:E:161:LEU:O	2.19	0.41
1:F:46:ASP:O	1:F:49:GLU:N	2.53	0.41
1:C:85:GLN:HB3	1:E:73:ARG:HH11	1.85	0.41
1:B:11:ARG:NH1	1:B:243:VAL:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:216:LEU:O	1:C:217:ALA:HB2	2.21	0.41
1:D:11:ARG:NH1	1:D:243:VAL:O	2.54	0.41
1:F:128:ARG:HB2	1:F:161:LEU:O	2.21	0.41
1:F:227:GLN:N	4:F:407:HOH:O	2.53	0.41
1:D:27:THR:HG22	1:D:67:THR:HA	2.02	0.41
1:C:267:LEU:O	1:C:268:LYS:C	2.63	0.41
1:E:46:ASP:O	1:E:48:ARG:N	2.54	0.41
1:F:11:ARG:NH1	1:F:243:VAL:O	2.53	0.41
1:F:29:LYS:HA	1:F:32:ARG:HD3	2.03	0.41
1:B:46:ASP:O	1:B:47:ASP:C	2.64	0.40
1:C:27:THR:HG23	1:C:27:THR:O	2.20	0.40
1:D:48:ARG:CZ	4:D:425:HOH:O	2.69	0.40
1:A:100:VAL:O	1:A:101:ASP:CB	2.70	0.40
1:B:128:ARG:HG2	1:B:129:ILE:N	2.27	0.40
1:B:268:LYS:HE3	1:B:268:LYS:HB3	1.88	0.40
1:E:46:ASP:O	1:E:49:GLU:N	2.54	0.40
1:A:46:ASP:C	1:A:48:ARG:N	2.78	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	247/292 (85%)	240 (97%)	5 (2%)	2 (1%)	16	44
1	B	246/292 (84%)	234 (95%)	10 (4%)	2 (1%)	16	44
1	C	241/292 (82%)	235 (98%)	6 (2%)	0	100	100
1	D	250/292 (86%)	241 (96%)	7 (3%)	2 (1%)	16	44
1	E	250/292 (86%)	242 (97%)	7 (3%)	1 (0%)	30	60
1	F	251/292 (86%)	241 (96%)	10 (4%)	0	100	100
All	All	1485/1752 (85%)	1433 (96%)	45 (3%)	7 (0%)	24	55

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	ASP
1	E	101	ASP
1	B	2	ILE
1	B	101	ASP
1	A	47	ASP
1	D	0	SER
1	D	101	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	201/230 (87%)	187 (93%)	14 (7%)	14	40
1	B	198/230 (86%)	183 (92%)	15 (8%)	12	36
1	C	195/230 (85%)	181 (93%)	14 (7%)	13	39
1	D	203/230 (88%)	189 (93%)	14 (7%)	14	41
1	E	203/230 (88%)	187 (92%)	16 (8%)	11	35
1	F	204/230 (89%)	188 (92%)	16 (8%)	11	35
All	All	1204/1380 (87%)	1115 (93%)	89 (7%)	13	37

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	9	LEU
1	A	11	ARG
1	A	27	THR
1	A	48	ARG
1	A	60	LEU
1	A	103	GLN
1	A	128	ARG
1	A	150	TYR
1	A	172	VAL

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Mol	Chain	Res	Type
1	A	173	GLU
1	A	179	LEU
1	A	181	GLU
1	A	268	LYS
1	B	1	MET
1	B	2	ILE
1	B	9	LEU
1	B	11	ARG
1	B	27	THR
1	B	32	ARG
1	B	60	LEU
1	B	103	GLN
1	B	115	ARG
1	B	150	TYR
1	B	172	VAL
1	B	173	GLU
1	B	179	LEU
1	B	181	GLU
1	B	268	LYS
1	C	9	LEU
1	C	11	ARG
1	C	27	THR
1	C	32	ARG
1	C	60	LEU
1	C	103	GLN
1	C	115	ARG
1	C	128	ARG
1	C	150	TYR
1	C	172	VAL
1	C	173	GLU
1	C	179	LEU
1	C	181	GLU
1	C	268	LYS
1	D	9	LEU
1	D	11	ARG
1	D	27	THR
1	D	32	ARG
1	D	33	ASP
1	D	60	LEU
1	D	103	GLN
1	D	128	ARG
1	D	150	TYR

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Mol	Chain	Res	Type
1	D	172	VAL
1	D	173	GLU
1	D	179	LEU
1	D	181	GLU
1	D	268	LYS
1	E	2	ILE
1	E	9	LEU
1	E	11	ARG
1	E	27	THR
1	E	60	LEU
1	E	73	ARG
1	E	100	VAL
1	E	103	GLN
1	E	115	ARG
1	E	128	ARG
1	E	150	TYR
1	E	172	VAL
1	E	173	GLU
1	E	179	LEU
1	E	181	GLU
1	E	268	LYS
1	F	3	ARG
1	F	9	LEU
1	F	11	ARG
1	F	27	THR
1	F	32	ARG
1	F	37	LYS
1	F	60	LEU
1	F	103	GLN
1	F	128	ARG
1	F	150	TYR
1	F	172	VAL
1	F	173	GLU
1	F	179	LEU
1	F	181	GLU
1	F	218	SER
1	F	268	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-1	GLN

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Mol	Chain	Res	Type
1	A	227	GLN
1	B	192	ASN
1	C	227	GLN
1	D	139	ASN
1	D	192	ASN
1	D	206	HIS
1	D	240	GLN
1	E	227	GLN
1	F	-1	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	EPE	C	302	-	15,15,15	0.48	0	19,20,20	1.89	4 (21%)
2	NAP	F	301	-	32,33,52	1.45	7 (21%)	50,52,80	1.77	8 (16%)
2	NAP	B	301	-	32,33,52	1.31	4 (12%)	50,52,80	1.92	11 (22%)
3	EPE	B	302	-	15,15,15	0.71	0	19,20,20	1.45	2 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAP	C	301	-	32,33,52	1.33	4 (12%)	50,52,80	1.72	9 (18%)
2	NAP	E	301	-	32,33,52	1.39	5 (15%)	50,52,80	2.06	12 (24%)
2	NAP	A	301	-	32,33,52	1.42	4 (12%)	50,52,80	1.85	9 (18%)
2	NAP	D	301	-	32,33,52	1.50	6 (18%)	50,52,80	1.98	10 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EPE	C	302	-	-	5/9/19/19	0/1/1/1
2	NAP	F	301	-	-	6/21/37/67	0/3/3/5
2	NAP	B	301	-	-	4/21/37/67	0/3/3/5
3	EPE	B	302	-	-	4/9/19/19	0/1/1/1
2	NAP	C	301	-	-	8/21/37/67	0/3/3/5
2	NAP	E	301	-	-	5/21/37/67	0/3/3/5
2	NAP	A	301	-	-	6/21/37/67	0/3/3/5
2	NAP	D	301	-	-	8/21/37/67	0/3/3/5

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	301	NAP	PN-O1N	4.10	1.63	1.50
2	E	301	NAP	PN-O1N	4.08	1.63	1.50
2	A	301	NAP	PN-O1N	4.03	1.63	1.50
2	F	301	NAP	PN-O1N	3.95	1.62	1.50
2	C	301	NAP	PN-O1N	3.92	1.62	1.50
2	B	301	NAP	PN-O1N	3.78	1.62	1.50
2	D	301	NAP	PA-O3	3.66	1.63	1.59
2	C	301	NAP	C2A-N1A	3.24	1.39	1.33
2	A	301	NAP	C2A-N1A	3.10	1.39	1.33
2	A	301	NAP	C2A-N3A	2.99	1.39	1.33
2	B	301	NAP	C2A-N3A	2.96	1.39	1.33
2	F	301	NAP	C2A-N1A	2.69	1.38	1.33
2	D	301	NAP	C2A-N1A	2.68	1.38	1.33
2	F	301	NAP	C2A-N3A	2.63	1.38	1.33
2	C	301	NAP	C2A-N3A	2.59	1.38	1.33
2	B	301	NAP	C2A-N1A	2.59	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	301	NAP	C2A-N3A	2.56	1.38	1.33
2	E	301	NAP	PA-O3	2.48	1.62	1.59
2	F	301	NAP	PA-O3	2.41	1.62	1.59
2	E	301	NAP	C2A-N1A	2.37	1.38	1.33
2	E	301	NAP	C2A-N3A	2.33	1.38	1.33
2	D	301	NAP	C5A-N7A	-2.33	1.34	1.39
2	F	301	NAP	C5A-N7A	-2.26	1.35	1.39
2	E	301	NAP	C5A-N7A	-2.24	1.35	1.39
2	A	301	NAP	C5A-N7A	-2.21	1.35	1.39
2	C	301	NAP	C8A-N7A	2.17	1.35	1.31
2	F	301	NAP	P2B-O2B	2.14	1.63	1.59
2	D	301	NAP	C8A-N7A	2.02	1.35	1.31
2	F	301	NAP	C8A-N7A	2.01	1.35	1.31
2	B	301	NAP	C8A-N7A	2.01	1.35	1.31

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	NAP	N3A-C2A-N1A	-6.67	118.48	128.58
2	D	301	NAP	N3A-C2A-N1A	-6.05	119.43	128.58
2	F	301	NAP	N3A-C2A-N1A	-5.55	120.18	128.58
2	D	301	NAP	C5A-C4A-N3A	-5.54	119.09	126.72
2	C	301	NAP	N3A-C2A-N1A	-5.31	120.54	128.58
2	B	301	NAP	N3A-C2A-N1A	-5.15	120.79	128.58
2	A	301	NAP	C5A-C4A-N3A	-5.09	119.70	126.72
2	A	301	NAP	N3A-C2A-N1A	-5.08	120.89	128.58
2	B	301	NAP	C5A-C4A-N3A	-5.00	119.83	126.72
3	C	302	EPE	O3S-S-C10	4.85	115.49	106.00
2	F	301	NAP	C5A-C4A-N3A	-4.70	120.25	126.72
2	E	301	NAP	C5A-C4A-N3A	-4.39	120.67	126.72
2	E	301	NAP	N9A-C8A-N7A	-4.23	107.94	113.94
3	C	302	EPE	C3-C2-N1	-4.17	102.24	110.65
2	A	301	NAP	N9A-C8A-N7A	-4.09	108.13	113.94
2	D	301	NAP	C2A-N3A-C4A	4.07	121.77	111.83
2	B	301	NAP	N9A-C8A-N7A	-4.06	108.17	113.94
2	A	301	NAP	C5A-N7A-C8A	4.05	109.81	103.45
2	F	301	NAP	N9A-C8A-N7A	-4.05	108.20	113.94
2	C	301	NAP	C5A-C4A-N3A	-4.03	121.16	126.72
2	E	301	NAP	O5D-PN-O2N	3.91	122.48	107.80
2	C	301	NAP	O5D-PN-O2N	3.90	122.41	107.80
2	B	301	NAP	C5A-N7A-C8A	3.83	109.47	103.45
2	D	301	NAP	C5A-N7A-C8A	3.81	109.44	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	NAP	C2A-N3A-C4A	3.81	121.13	111.83
2	D	301	NAP	N9A-C8A-N7A	-3.77	108.59	113.94
2	E	301	NAP	C5A-N7A-C8A	3.76	109.37	103.45
2	F	301	NAP	C5A-N7A-C8A	3.71	109.29	103.45
2	B	301	NAP	O5D-PN-O2N	3.68	121.62	107.80
2	E	301	NAP	C2B-C1B-N9A	-3.57	107.87	113.75
2	D	301	NAP	N3A-C4A-N9A	3.55	133.21	127.17
2	C	301	NAP	N9A-C8A-N7A	-3.55	108.90	113.94
2	B	301	NAP	N3A-C4A-N9A	3.53	133.18	127.17
2	A	301	NAP	N3A-C4A-N9A	3.42	132.99	127.17
2	B	301	NAP	C2A-N3A-C4A	3.38	120.09	111.83
2	F	301	NAP	C2A-N3A-C4A	3.35	120.02	111.83
2	E	301	NAP	O4B-C1B-N9A	3.34	114.51	108.09
2	C	301	NAP	C5A-N7A-C8A	3.31	108.65	103.45
3	C	302	EPE	C5-N4-C3	3.23	115.80	108.84
2	A	301	NAP	C2A-N3A-C4A	3.23	119.71	111.83
3	B	302	EPE	O2S-S-C10	3.19	111.54	106.73
2	E	301	NAP	N3A-C4A-N9A	3.18	132.57	127.17
2	D	301	NAP	O4B-C1B-N9A	3.09	114.03	108.09
2	A	301	NAP	C4A-C5A-N7A	-3.07	107.07	110.58
2	D	301	NAP	O5D-PN-O2N	3.07	119.33	107.80
2	F	301	NAP	N3A-C4A-N9A	3.04	132.34	127.17
2	E	301	NAP	C4A-C5A-N7A	-3.01	107.14	110.58
3	B	302	EPE	O3S-S-C10	2.96	111.79	106.00
2	E	301	NAP	C4A-N9A-C8A	2.92	108.80	105.74
2	C	301	NAP	C2A-N3A-C4A	2.92	118.96	111.83
2	B	301	NAP	C4A-C5A-N7A	-2.85	107.32	110.58
2	F	301	NAP	O5D-PN-O2N	2.76	118.16	107.80
2	D	301	NAP	C4A-C5A-N7A	-2.74	107.45	110.58
2	A	301	NAP	O5D-PN-O2N	2.72	118.01	107.80
2	A	301	NAP	C6A-C5A-C4A	2.70	120.86	117.18
2	F	301	NAP	C4A-C5A-N7A	-2.67	107.53	110.58
2	C	301	NAP	C4A-C5A-N7A	-2.64	107.57	110.58
3	C	302	EPE	C6-C5-N4	2.50	115.70	110.65
2	B	301	NAP	O2B-P2B-O1X	-2.45	100.60	109.33
2	C	301	NAP	N3A-C4A-N9A	2.43	131.29	127.17
2	D	301	NAP	O4B-C4B-C5B	2.36	116.89	109.33
2	B	301	NAP	C6A-C5A-C4A	2.26	120.26	117.18
2	C	301	NAP	C6A-C5A-C4A	2.23	120.23	117.18
2	B	301	NAP	C4A-N9A-C8A	2.18	108.03	105.74
2	E	301	NAP	O2X-P2B-O2B	2.17	114.29	105.85

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	NAP	C5B-O5B-PA-O1A
2	A	301	NAP	C5B-O5B-PA-O2A
2	A	301	NAP	PA-O3-PN-O5D
2	C	301	NAP	C5B-O5B-PA-O2A
2	C	301	NAP	C5B-O5B-PA-O3
2	C	301	NAP	O4B-C4B-C5B-O5B
2	C	301	NAP	PA-O3-PN-O2N
2	D	301	NAP	C5B-O5B-PA-O1A
2	D	301	NAP	C5B-O5B-PA-O2A
2	D	301	NAP	C5B-O5B-PA-O3
2	D	301	NAP	O4B-C4B-C5B-O5B
2	D	301	NAP	C3B-C4B-C5B-O5B
2	E	301	NAP	C5B-O5B-PA-O1A
2	E	301	NAP	C5B-O5B-PA-O3
2	E	301	NAP	PA-O3-PN-O5D
2	F	301	NAP	PA-O3-PN-O2N
3	B	302	EPE	C10-C9-N1-C2
3	B	302	EPE	S-C10-C9-N1
3	C	302	EPE	C9-C10-S-O2S
2	C	301	NAP	C3B-C4B-C5B-O5B
2	E	301	NAP	O4B-C4B-C5B-O5B
3	C	302	EPE	C9-C10-S-O3S
2	E	301	NAP	C3B-C4B-C5B-O5B
3	C	302	EPE	N4-C7-C8-O8
3	B	302	EPE	C8-C7-N4-C5
2	B	301	NAP	PN-O3-PA-O1A
2	F	301	NAP	PN-O3-PA-O5B
3	C	302	EPE	C9-C10-S-O1S
3	B	302	EPE	N4-C7-C8-O8
2	C	301	NAP	PA-O3-PN-O5D
2	F	301	NAP	O4B-C4B-C5B-O5B
2	A	301	NAP	C5B-O5B-PA-O3
3	C	302	EPE	C10-C9-N1-C6
2	F	301	NAP	C3B-C4B-C5B-O5B
2	D	301	NAP	C2B-O2B-P2B-O2X
2	B	301	NAP	C2B-O2B-P2B-O1X
2	C	301	NAP	C2B-O2B-P2B-O1X
2	A	301	NAP	PN-O3-PA-O1A
2	D	301	NAP	PA-O3-PN-O1N
2	A	301	NAP	PN-O3-PA-O2A
2	B	301	NAP	PN-O3-PA-O2A
2	B	301	NAP	C2B-O2B-P2B-O3X

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Mol	Chain	Res	Type	Atoms
2	C	301	NAP	PA-O3-PN-O1N
2	F	301	NAP	PA-O3-PN-O1N
2	D	301	NAP	C2B-O2B-P2B-O1X
2	F	301	NAP	PN-O3-PA-O2A

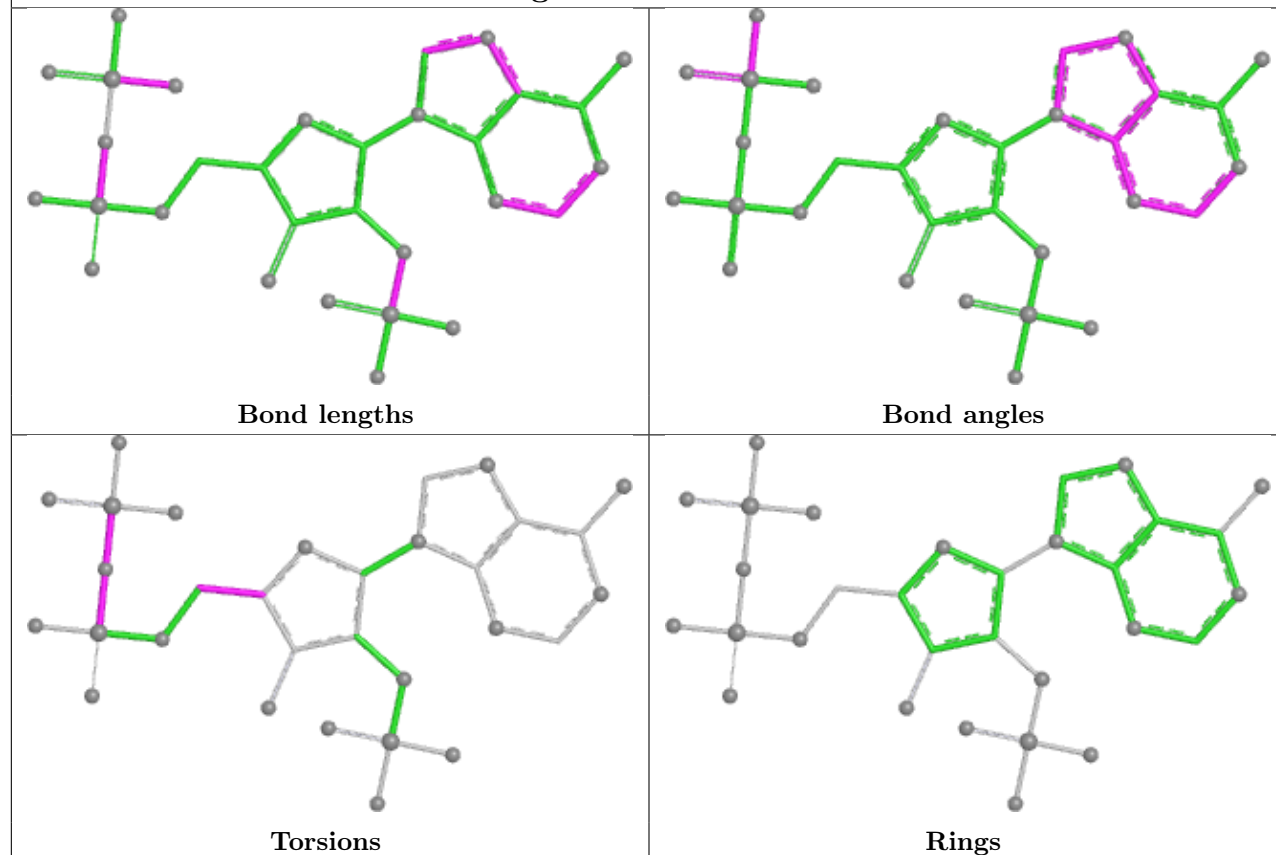
There are no ring outliers.

3 monomers are involved in 4 short contacts:

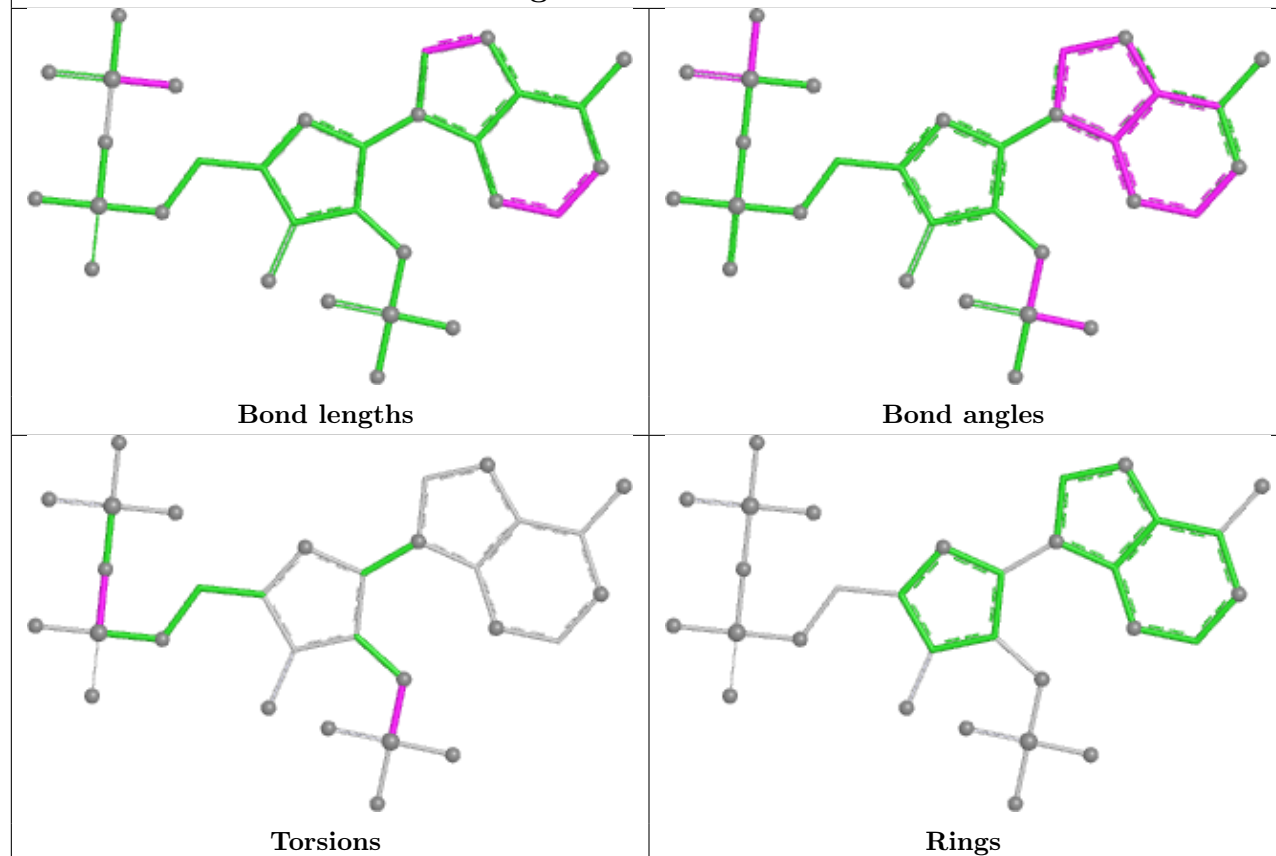
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	NAP	1	0
2	C	301	NAP	2	0
2	A	301	NAP	1	0

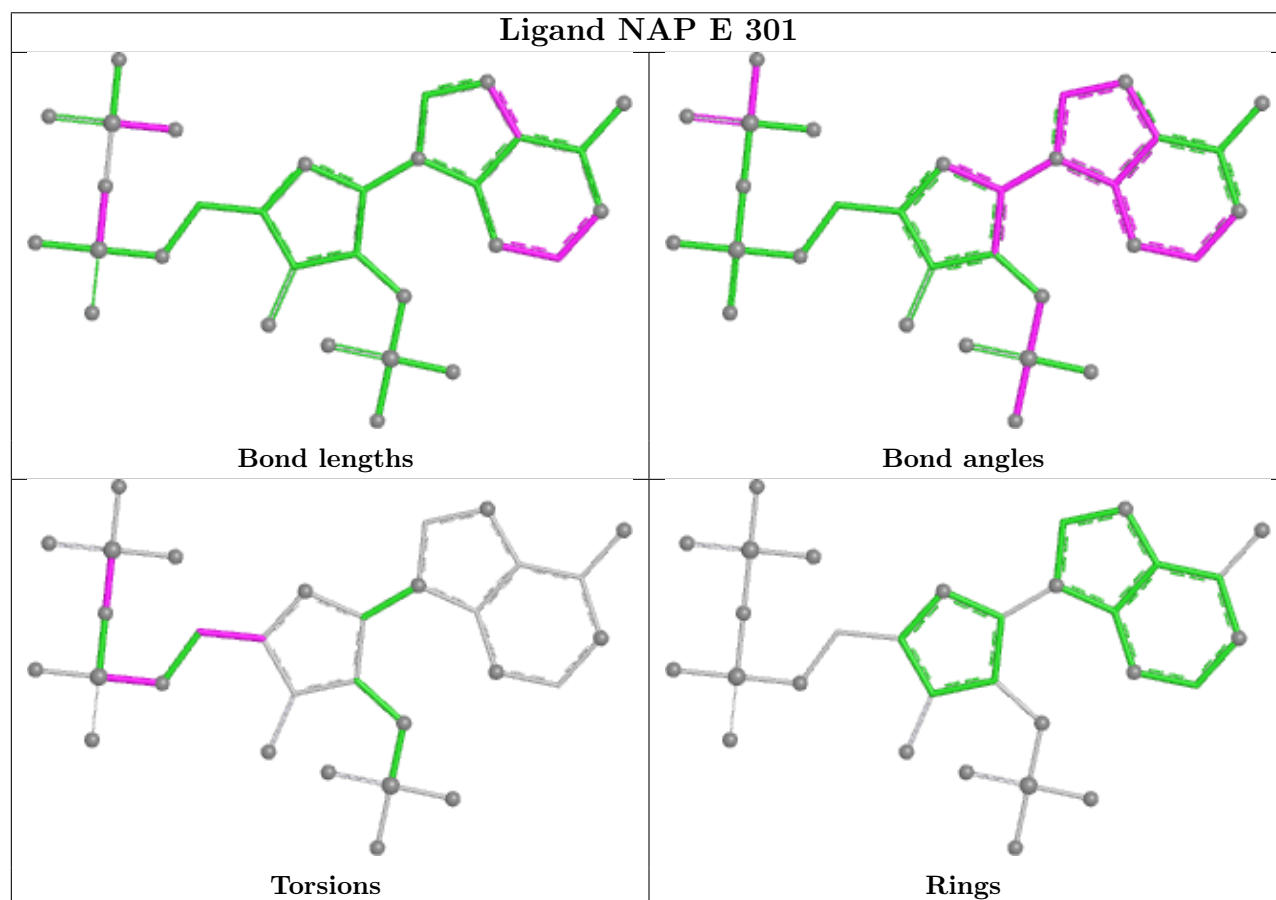
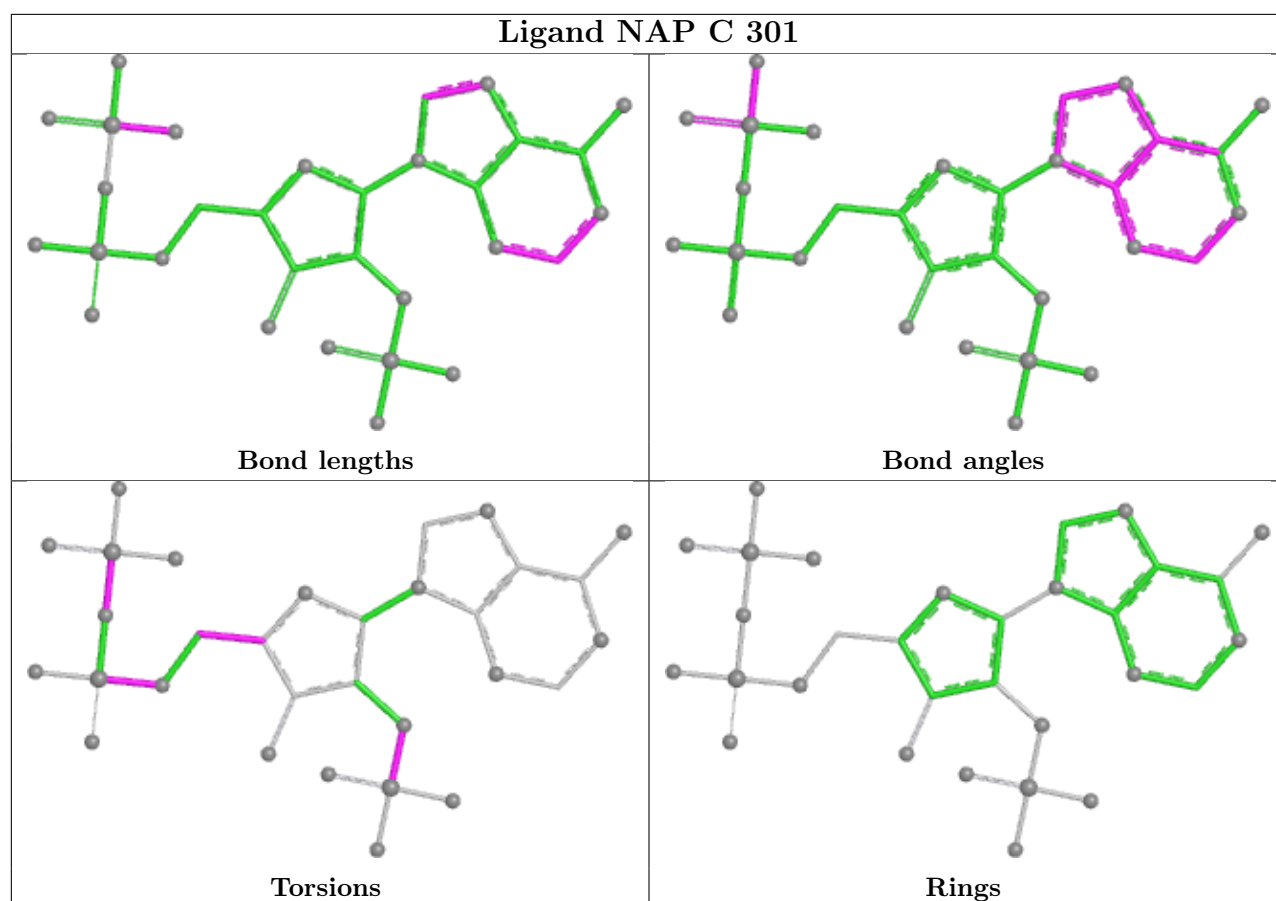
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

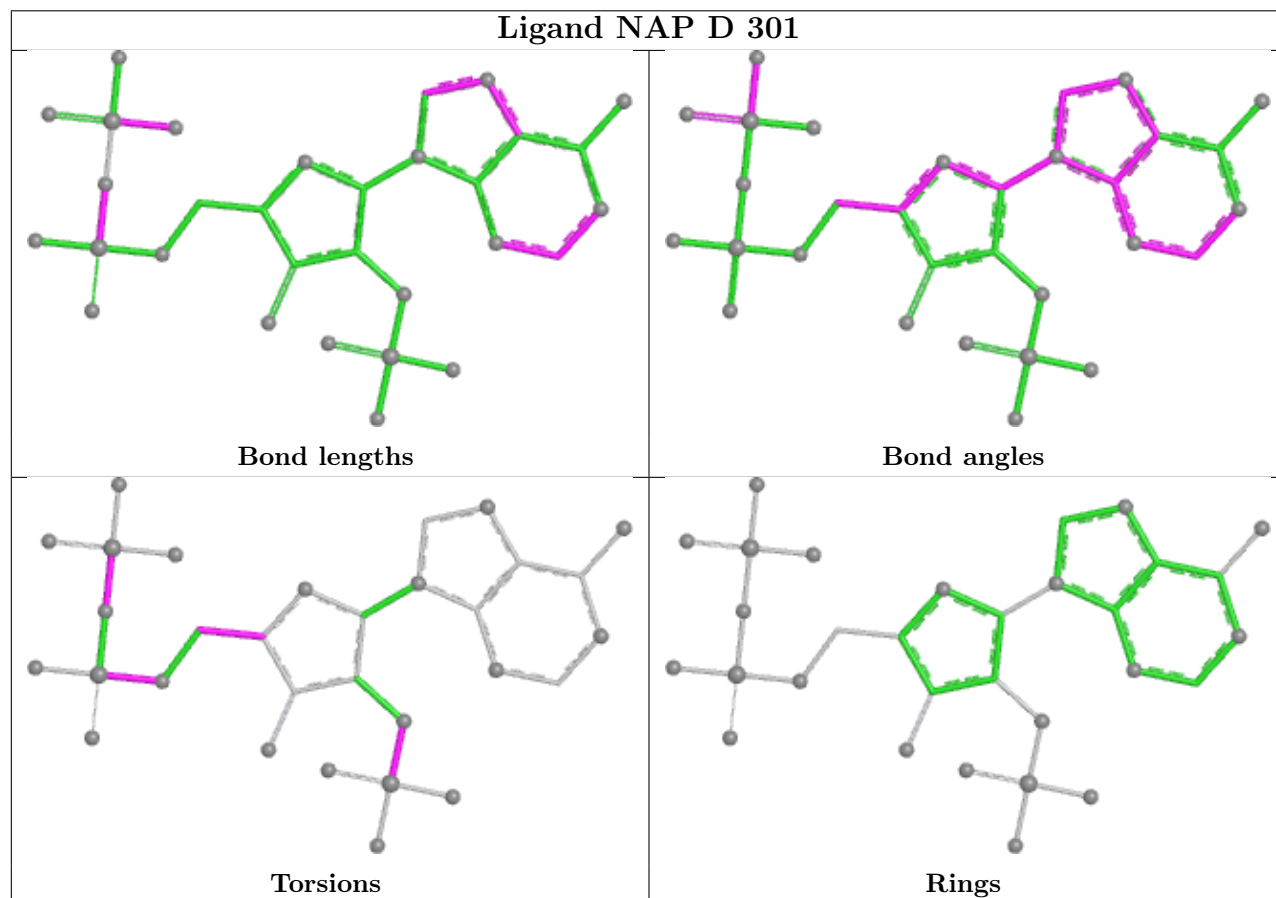
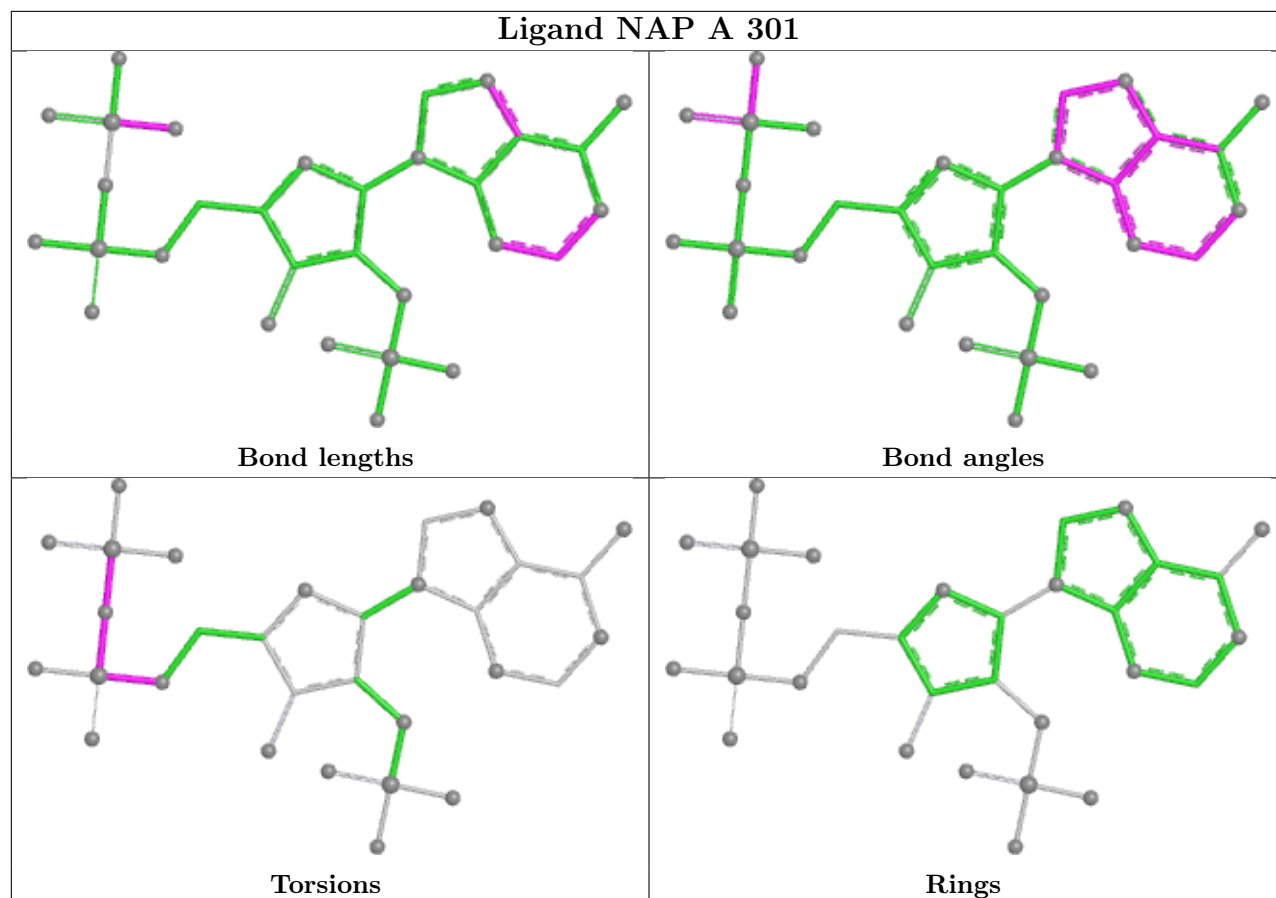
Ligand NAP F 301



Ligand NAP B 301







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	253/292 (86%)	-0.08	6 (2%) 59 49	14, 24, 44, 76	0
1	B	252/292 (86%)	-0.04	5 (1%) 65 56	14, 25, 44, 52	0
1	C	249/292 (85%)	0.00	4 (1%) 70 61	14, 24, 43, 56	0
1	D	256/292 (87%)	-0.03	7 (2%) 56 46	14, 25, 43, 50	0
1	E	256/292 (87%)	-0.03	5 (1%) 65 56	14, 25, 43, 49	0
1	F	259/292 (88%)	0.07	9 (3%) 47 38	14, 25, 44, 70	0
All	All	1525/1752 (87%)	-0.02	36 (2%) 59 49	14, 25, 44, 76	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	43	THR	5.5
1	F	43	THR	5.3
1	F	219	GLY	5.3
1	D	218	SER	4.5
1	E	219	GLY	4.2
1	F	-2	PHE	3.8
1	A	-2	PHE	3.7
1	C	0	SER	3.5
1	C	46	ASP	3.3
1	E	43	THR	3.2
1	A	43	THR	3.1
1	D	46	ASP	2.9
1	C	43	THR	2.9
1	A	-1	GLN	2.7
1	B	219	GLY	2.7
1	F	46	ASP	2.6
1	F	102	GLY	2.5
1	D	0	SER	2.5
1	B	0	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	43	THR	2.5
1	D	31	GLY	2.5
1	E	218	SER	2.5
1	A	181	GLU	2.4
1	F	0	SER	2.4
1	F	98	GLU	2.3
1	F	40	SER	2.3
1	A	0	SER	2.3
1	D	219	GLY	2.3
1	B	44	ILE	2.2
1	E	0	SER	2.2
1	A	128	ARG	2.2
1	D	145	GLU	2.1
1	B	99	PHE	2.0
1	F	44	ILE	2.0
1	C	227	GLN	2.0
1	E	227	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAP	B	301	31/48	0.88	0.10	38,46,59,61	0
2	NAP	F	301	31/48	0.88	0.10	38,46,77,79	0
2	NAP	A	301	31/48	0.89	0.12	32,45,67,67	0
2	NAP	D	301	31/48	0.91	0.10	32,40,58,59	0
2	NAP	C	301	31/48	0.91	0.10	27,36,54,54	0
3	EPE	C	302	15/15	0.92	0.14	33,49,57,57	0

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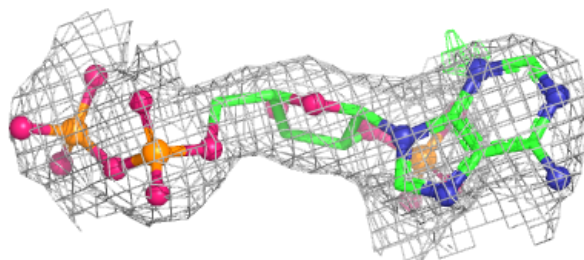
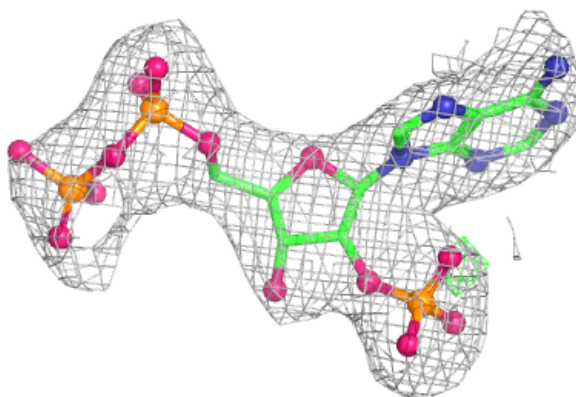
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAP	E	301	31/48	0.93	0.08	16,29,52,54	0
3	EPE	B	302	15/15	0.94	0.11	34,40,48,50	0

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.

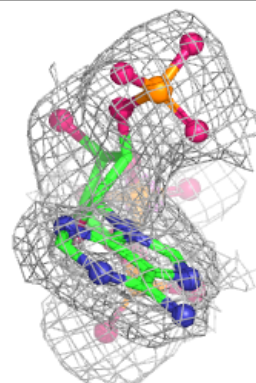
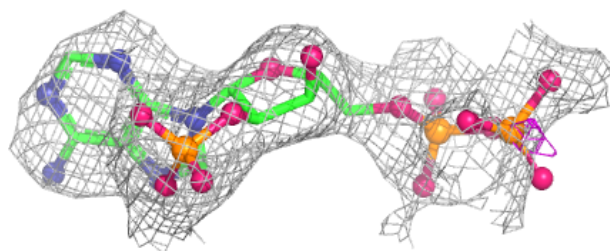
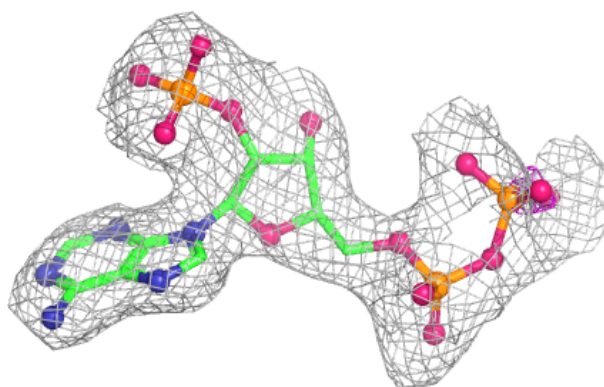
Electron density around NAP B 301:

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

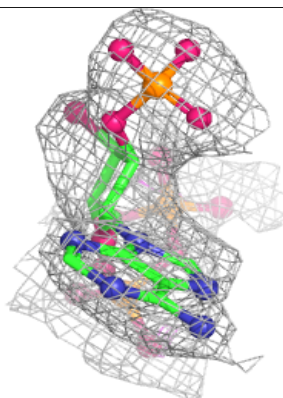
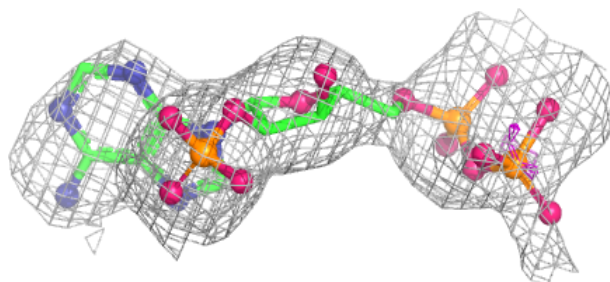
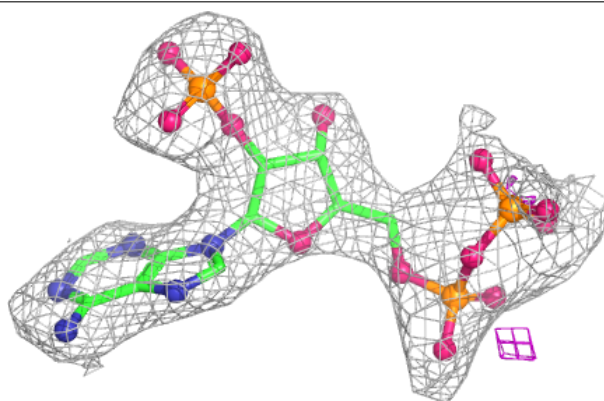


Electron density around NAP F 301:

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

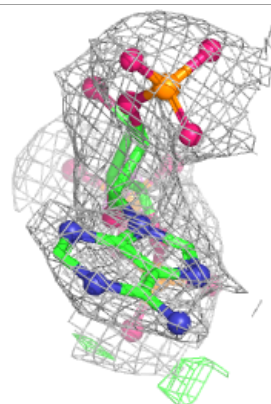
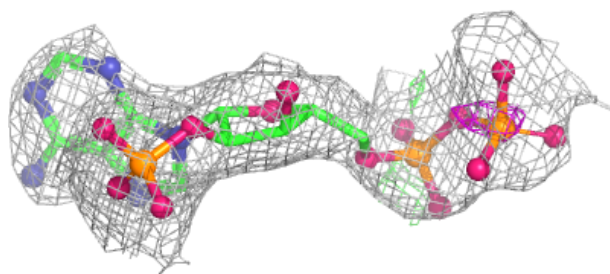
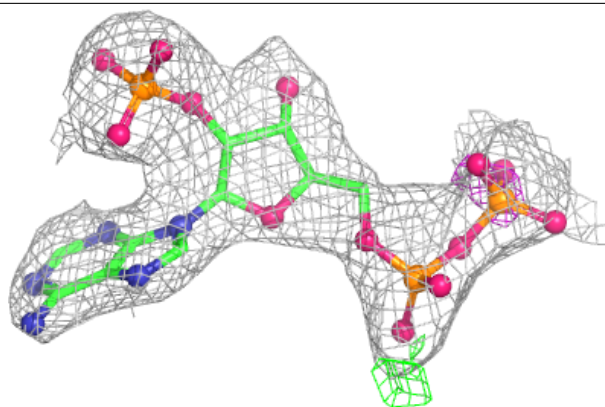
**Electron density around NAP A 301:**

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

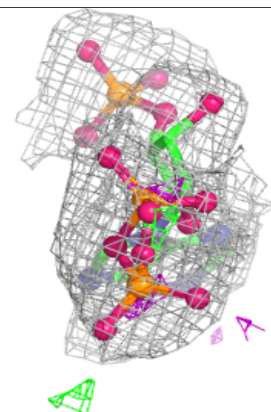
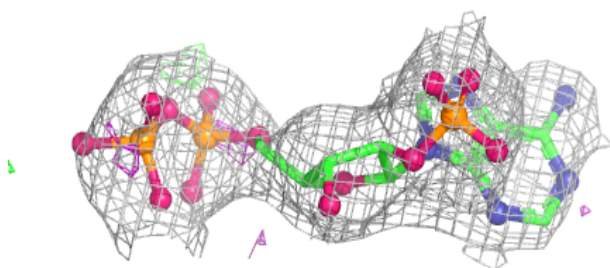
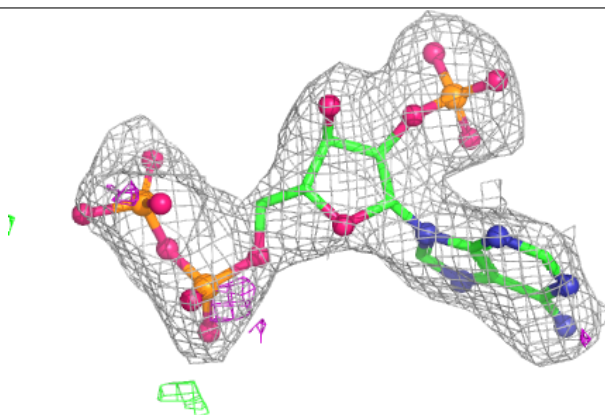


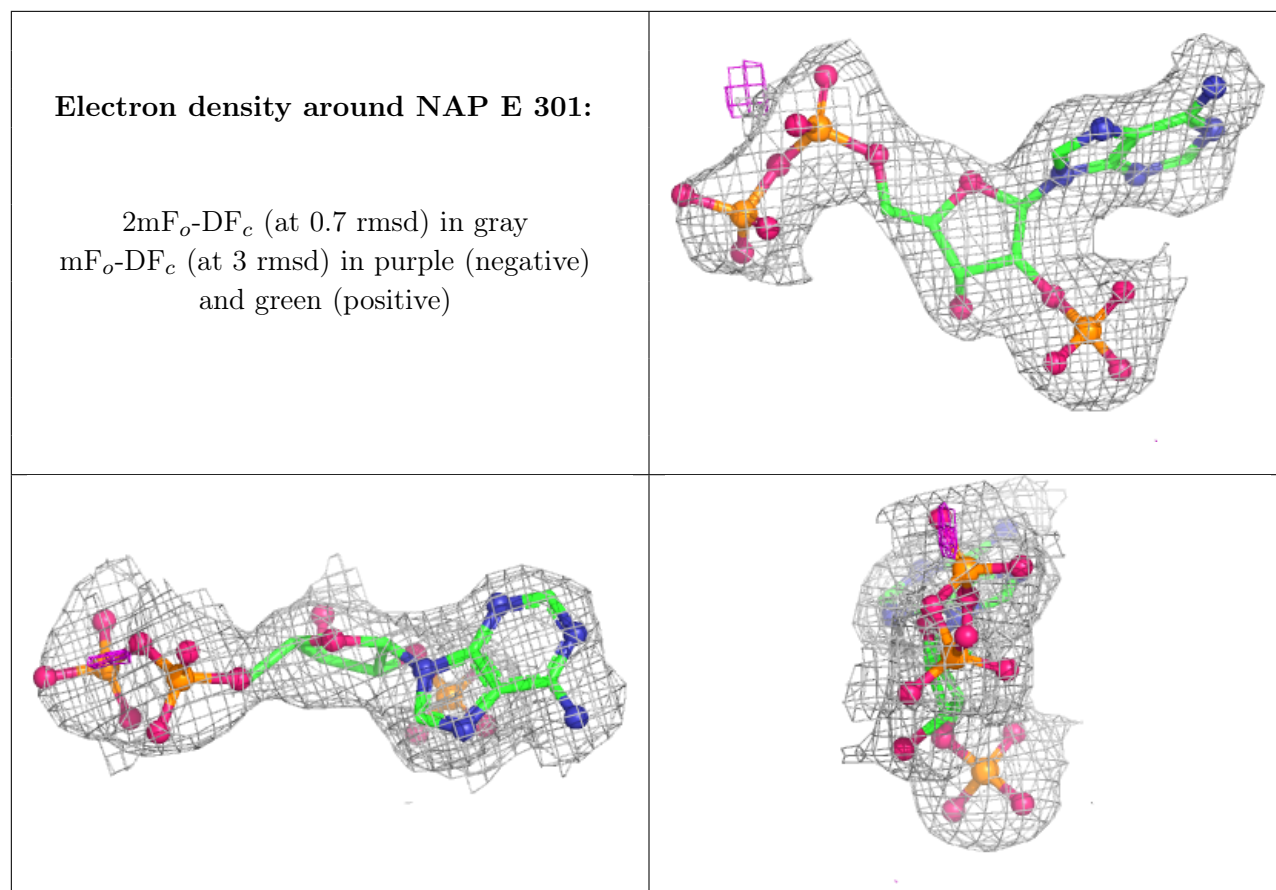
Electron density around NAP D 301:

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

**Electron density around NAP C 301:**

$2mF_o-DF_c$ (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.