



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 09:37 AM UTC

PDB ID : 1Q7B / pdb_00001q7b
Title : The structure of betaketoacyl-[ACP] reductase from E. coli in complex with NADP+
Authors : Price, A.C.; Zhang, Y.-M.; Rock, C.O.; White, S.M.
Deposited on : 2003-08-17
Resolution : 2.05 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

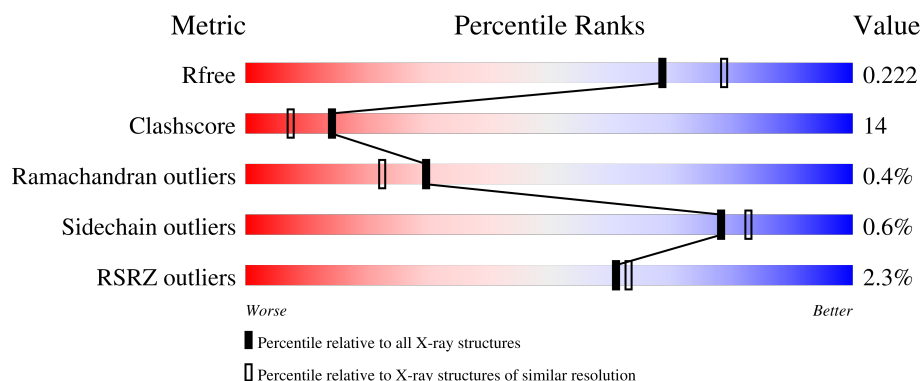
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	244	0% 82% 16% .
1	B	244	3% 76% 21% ..
1	C	244	2% 78% 20% .
1	D	244	2% 78% 19% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7809 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 3-oxoacyl-[acyl-carrier protein] reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	14	0	0
			1780	1103	322	345	10			
1	B	241	Total	C	N	O	S	39	0	0
			1767	1094	320	343	10			
1	C	243	Total	C	N	O	S	7	0	0
			1780	1103	322	345	10			
1	D	243	Total	C	N	O	S	18	0	0
			1780	1103	322	345	10			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Ca	0	0
			3	3		
2	B	3	Total	Ca	0	0
			3	3		
2	C	1	Total	Ca	0	0
			1	1		
2	D	1	Total	Ca	0	0
			1	1		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
3	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
3	C	1	Total 48	C 21	N 7	O 17	P 3	0	0
3	D	1	Total 48	C 21	N 7	O 17	P 3	0	0

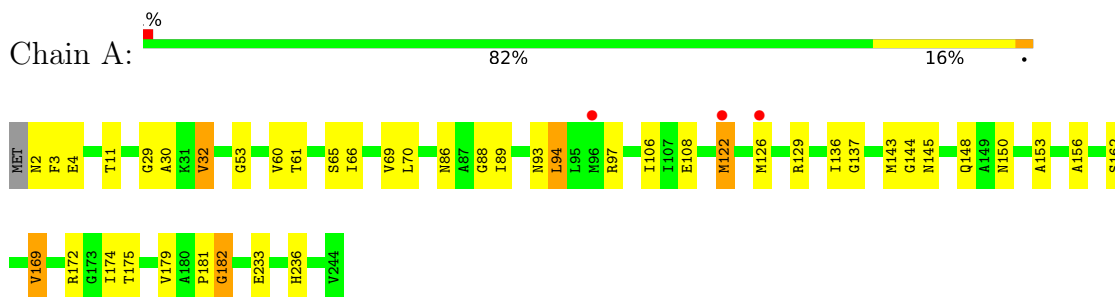
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	135	Total O 135 135	0	0
4	B	118	Total O 118 118	0	0
4	C	134	Total O 134 134	0	0
4	D	115	Total O 115 115	0	0

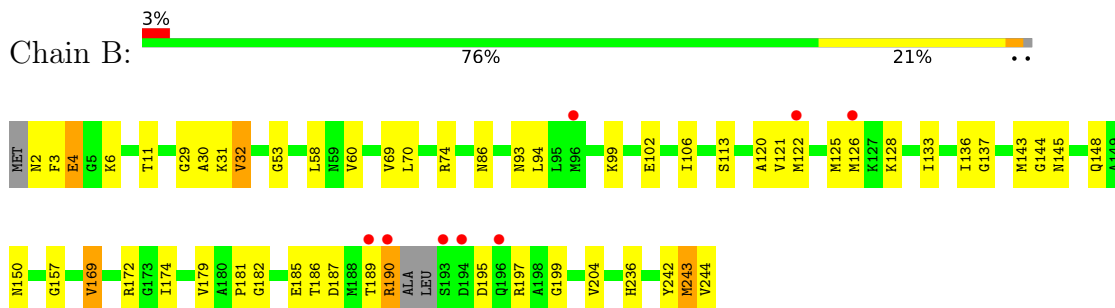
3 Residue-property plots [i](#)

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.

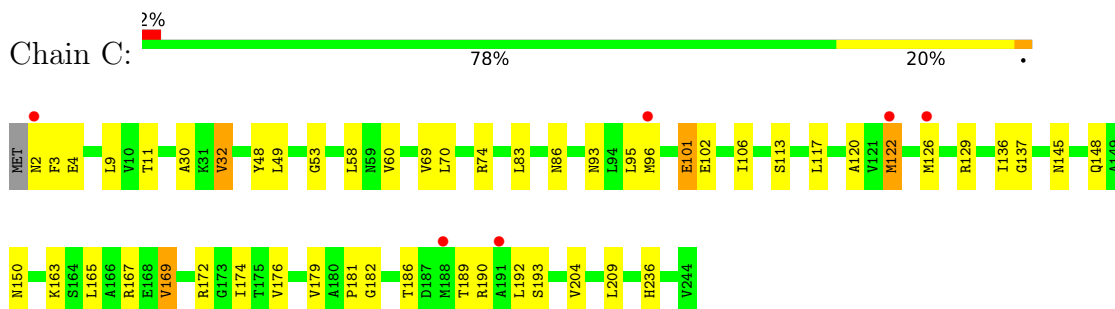
- Molecule 1: 3-oxoacyl-[acyl-carrier protein] reductase



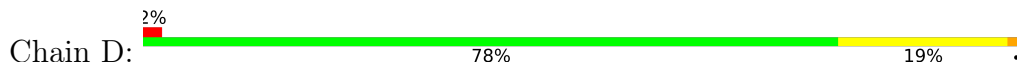
- Molecule 1: 3-oxoacyl-[acyl-carrier protein] reductase

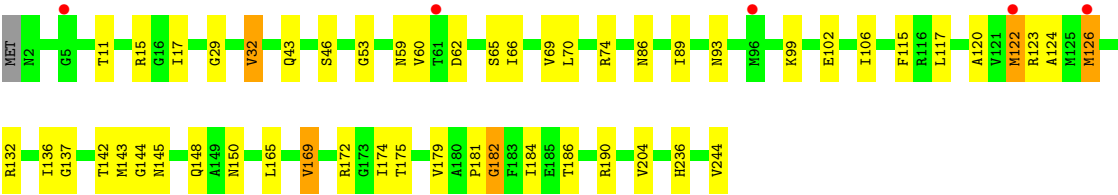


- Molecule 1: 3-oxoacyl-[acyl-carrier protein] reductase



- Molecule 1: 3-oxoacyl-[acyl-carrier protein] reductase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	72.75Å 76.18Å 99.73Å 90.00° 109.47° 90.00°	Depositor
Resolution (Å)	20.00 – 2.05 20.00 – 2.06	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.05) 95.1 (20.00-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.06Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.200 , 0.221 0.203 , 0.222	Depositor DCC
R_{free} test set	3083 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	31.7	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.021 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7809	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.97% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.40	0/1796	0.90	5/2418 (0.2%)
1	B	0.44	1/1782 (0.1%)	0.92	9/2397 (0.4%)
1	C	0.41	0/1796	0.88	5/2418 (0.2%)
1	D	0.48	2/1796 (0.1%)	0.87	5/2418 (0.2%)
All	All	0.44	3/7170 (0.0%)	0.89	24/9651 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	122	MET	SD-CE	-10.65	1.52	1.79
1	D	126	MET	SD-CE	-5.54	1.65	1.79
1	B	243	MET	SD-CE	-5.31	1.66	1.79

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	195	ASP	N-CA-C	-8.90	101.75	114.12
1	C	182	GLY	N-CA-C	-7.82	101.65	112.13
1	C	204	VAL	N-CA-C	7.66	115.80	107.60
1	A	32	VAL	N-CA-C	7.62	118.84	108.17
1	D	182	GLY	N-CA-C	-7.57	101.99	112.13
1	A	182	GLY	N-CA-C	-7.32	102.32	112.13
1	B	182	GLY	N-CA-C	-7.31	102.34	112.13
1	D	204	VAL	N-CA-C	7.00	115.09	107.60
1	C	32	VAL	N-CA-C	6.90	118.54	108.53
1	B	204	VAL	N-CA-C	6.76	114.84	107.60
1	B	32	VAL	N-CA-C	6.48	117.92	108.53
1	D	32	VAL	N-CA-C	6.32	117.70	108.53
1	A	169	VAL	N-CA-C	6.10	118.76	112.90
1	B	31	LYS	N-CA-C	-6.07	99.32	108.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	169	VAL	N-CA-C	5.67	118.34	112.90
1	B	169	VAL	N-CA-C	5.61	118.54	113.10
1	C	122	MET	N-CA-C	5.60	117.06	111.07
1	B	199	GLY	N-CA-C	-5.52	105.97	113.37
1	D	29	GLY	N-CA-C	5.47	122.03	114.92
1	D	169	VAL	N-CA-C	5.43	118.37	113.10
1	B	94	LEU	N-CA-C	-5.25	103.10	110.50
1	A	94	LEU	N-CA-C	-5.24	103.11	110.50
1	A	122	MET	N-CA-C	5.05	116.47	110.97
1	B	29	GLY	N-CA-C	5.01	121.44	114.92

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	1780	0	1813	39	0
1	B	1767	0	1796	55	0
1	C	1780	0	1813	66	0
1	D	1780	0	1813	66	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	48	0	25	6	0
3	B	48	0	25	3	0
3	C	48	0	25	3	0
3	D	48	0	25	5	0
4	A	135	0	0	13	0
4	B	118	0	0	13	0
4	C	134	0	0	10	0
4	D	115	0	0	20	0
All	All	7809	0	7335	206	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 14.

All (206) 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:B:122:MET:HE3	1:B:125:MET:HE3	1.38	1.05
1:C:83:LEU:HA	4:C:3205:HOH:O	1.56	1.03
1:B:187:ASP:HA	1:B:190:ARG:HE	1.23	1.00
1:D:43:GLN:HA	4:D:4237:HOH:O	1.60	0.98
1:A:156:ALA:HB3	4:B:2178:HOH:O	1.61	0.98
1:C:9:LEU:HB3	4:C:3205:HOH:O	1.63	0.97
1:A:233:GLU:HA	4:A:1146:HOH:O	1.64	0.95
1:B:187:ASP:CA	1:B:190:ARG:HE	1.80	0.95
1:C:95:LEU:HB3	1:D:122:MET:HE1	1.49	0.94
1:C:129:ARG:HH12	1:C:172:ARG:HH11	1.17	0.93
1:D:244:VAL:HG21	4:D:4231:HOH:O	1.67	0.92
1:A:145:ASN:HD22	1:A:148:GLN:HE21	1.14	0.91
1:C:95:LEU:HD23	1:D:122:MET:CE	2.02	0.89
1:C:49:LEU:HD23	4:C:3203:HOH:O	1.72	0.88
1:C:145:ASN:HD22	1:C:148:GLN:HE21	1.15	0.87
1:D:145:ASN:HD22	1:D:148:GLN:HE21	1.18	0.87
1:B:122:MET:CE	1:B:125:MET:HE3	2.07	0.84
1:B:242:TYR:HA	4:D:4228:HOH:O	1.80	0.82
1:A:175:THR:HG22	4:A:1156:HOH:O	1.77	0.82
1:D:126:MET:SD	1:D:174:ILE:HD12	2.19	0.81
1:D:145:ASN:HD22	1:D:148:GLN:NE2	1.78	0.81
1:C:145:ASN:HD22	1:C:148:GLN:NE2	1.79	0.81
1:D:126:MET:CE	1:D:172:ARG:HG3	2.13	0.79
1:D:126:MET:HE1	1:D:172:ARG:HG3	1.65	0.78
1:C:126:MET:HE1	1:C:172:ARG:HG3	1.67	0.77
1:C:126:MET:CE	1:C:172:ARG:HG3	2.15	0.76
1:C:129:ARG:HH12	1:C:172:ARG:NH1	1.83	0.75
1:C:129:ARG:NH1	1:C:172:ARG:HH11	1.83	0.75
1:B:187:ASP:HA	1:B:190:ARG:NE	2.02	0.75
1:B:121:VAL:HG23	1:B:125:MET:HE2	1.69	0.75
1:C:95:LEU:HD23	1:D:122:MET:HE1	1.67	0.75
1:D:66:ILE:HD11	4:D:4227:HOH:O	1.86	0.74
1:C:49:LEU:HA	4:C:3203:HOH:O	1.88	0.73
1:A:145:ASN:HD22	1:A:148:GLN:NE2	1.88	0.72
1:B:187:ASP:N	1:B:190:ARG:HE	1.88	0.71
1:B:186:THR:O	1:B:190:ARG:HG3	1.90	0.71
1:B:70:LEU:CD1	1:B:120:ALA:HB1	2.21	0.71
1:B:243:MET:HE2	1:C:167:ARG:NE	2.05	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:MET:HE1	1:B:133:ILE:HD11	1.73	0.70
1:C:96:MET:HE2	1:D:123:ARG:HG3	1.73	0.70
1:C:48:TYR:HD1	4:C:3203:HOH:O	1.73	0.69
1:C:193:SER:N	4:C:3206:HOH:O	2.25	0.69
1:A:162:SER:HB3	4:A:1154:HOH:O	1.93	0.69
1:B:157:GLY:HA2	4:B:2178:HOH:O	1.92	0.69
3:A:1901:NAP:H3D	4:A:1133:HOH:O	1.93	0.68
1:B:99:LYS:HB2	1:B:102:GLU:HG3	1.76	0.68
1:A:153:ALA:HA	4:B:2178:HOH:O	1.95	0.67
1:D:122:MET:HE2	1:D:165:LEU:HD11	1.77	0.67
1:B:122:MET:SD	1:B:169:VAL:HG11	2.36	0.66
1:C:95:LEU:CB	1:D:122:MET:HE1	2.24	0.66
1:C:96:MET:SD	1:D:123:ARG:HG2	2.36	0.65
1:B:244:VAL:HG13	4:B:2176:HOH:O	1.96	0.65
1:C:106:ILE:HG13	1:C:150:ASN:ND2	2.10	0.65
1:C:101:GLU:HG2	1:C:102:GLU:N	2.10	0.65
3:C:3901:NAP:H52A	4:C:3113:HOH:O	1.97	0.64
1:B:70:LEU:HD11	1:B:120:ALA:HB1	1.80	0.63
3:D:4901:NAP:H52A	4:D:4113:HOH:O	1.98	0.62
1:A:143:MET:HE2	4:A:2082:HOH:O	1.99	0.62
1:D:137:GLY:O	3:D:4901:NAP:H6N	2.00	0.61
1:D:106:ILE:HG13	1:D:150:ASN:ND2	2.16	0.61
1:C:96:MET:CE	1:D:123:ARG:HG3	2.30	0.61
1:B:106:ILE:HG13	1:B:150:ASN:ND2	2.14	0.61
1:C:86:ASN:HD22	1:C:136:ILE:HG13	1.68	0.59
1:C:96:MET:SD	1:D:123:ARG:CG	2.91	0.58
1:D:142:THR:HG21	4:D:4231:HOH:O	2.03	0.58
1:D:86:ASN:HD22	1:D:136:ILE:HG13	1.68	0.58
1:A:86:ASN:HD22	1:A:136:ILE:HG13	1.68	0.58
1:C:95:LEU:CD2	1:D:122:MET:HE1	2.34	0.58
1:B:189:THR:O	1:B:197:ARG:NH1	2.37	0.58
1:D:126:MET:HE3	1:D:172:ARG:HG3	1.86	0.57
1:D:46:SER:HB2	4:D:4237:HOH:O	2.05	0.56
1:B:187:ASP:N	1:B:190:ARG:NE	2.53	0.56
1:D:99:LYS:HB2	1:D:102:GLU:HG3	1.87	0.56
1:B:243:MET:HE2	1:C:167:ARG:HE	1.69	0.55
1:C:3:PHE:HB3	1:C:30:ALA:HB2	1.87	0.55
1:B:236:HIS:HD2	4:B:2021:HOH:O	1.89	0.55
1:B:145:ASN:HD22	1:B:148:GLN:HE21	1.53	0.55
1:D:65:SER:O	1:D:69:VAL:HG23	2.07	0.55
1:A:60:VAL:HG22	3:A:1901:NAP:N1A	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:ILE:HG13	1:A:106:ILE:HD13	1.89	0.55
1:B:86:ASN:HD22	1:B:136:ILE:HG13	1.70	0.55
1:C:95:LEU:HD23	1:D:122:MET:HE3	1.85	0.54
1:D:184:ILE:HD11	4:D:4236:HOH:O	2.07	0.54
1:B:2:ASN:OD1	1:B:4:GLU:HB2	2.07	0.54
1:A:129:ARG:HG2	4:A:1143:HOH:O	2.07	0.54
1:B:243:MET:HE2	1:C:167:ARG:CZ	2.38	0.53
1:C:70:LEU:O	1:C:74:ARG:HG3	2.09	0.53
1:C:186:THR:O	1:C:190:ARG:HG3	2.08	0.53
1:D:17:ILE:HD12	4:D:4234:HOH:O	2.09	0.53
1:D:184:ILE:CD1	4:D:4236:HOH:O	2.57	0.52
1:C:70:LEU:CD1	1:C:120:ALA:HB1	2.40	0.52
1:A:137:GLY:O	3:A:1901:NAP:H6N	2.10	0.52
1:B:243:MET:HE3	1:C:163:LYS:HB3	1.91	0.52
1:D:182:GLY:N	4:D:4236:HOH:O	2.38	0.52
1:B:58:LEU:HB2	1:B:69:VAL:HG21	1.92	0.51
1:D:17:ILE:CD1	4:D:4234:HOH:O	2.59	0.51
1:D:70:LEU:HB3	1:D:74:ARG:NH1	2.26	0.51
1:A:129:ARG:CD	1:A:172:ARG:HH21	2.24	0.51
1:B:70:LEU:O	1:B:74:ARG:HG3	2.11	0.51
1:C:2:ASN:OD1	1:C:4:GLU:HB2	2.11	0.51
1:D:60:VAL:C	4:D:4227:HOH:O	2.53	0.51
4:B:3051:HOH:O	1:C:236:HIS:HE1	1.93	0.50
1:C:122:MET:CE	1:C:174:ILE:HD13	2.41	0.50
1:B:244:VAL:HG22	4:B:2176:HOH:O	2.11	0.50
1:B:243:MET:CE	1:C:163:LYS:HB3	2.41	0.50
1:A:122:MET:CE	1:A:174:ILE:HD13	2.42	0.49
1:B:143:MET:HG3	1:B:144:GLY:O	2.13	0.49
1:C:95:LEU:HD11	1:D:115:PHE:CD1	2.48	0.49
1:C:137:GLY:O	3:C:3901:NAP:H6N	2.12	0.49
1:A:122:MET:SD	1:A:169:VAL:HG11	2.53	0.49
1:B:128:LYS:NZ	4:B:2172:HOH:O	2.45	0.49
1:B:190:ARG:NH1	4:B:2170:HOH:O	2.45	0.49
1:B:243:MET:CE	1:C:167:ARG:NE	2.75	0.49
1:D:70:LEU:HB3	1:D:74:ARG:HH12	1.77	0.49
1:D:11:THR:HG21	1:D:117:LEU:CD1	2.43	0.49
1:B:186:THR:O	1:B:187:ASP:C	2.56	0.48
1:A:162:SER:CB	4:A:1154:HOH:O	2.58	0.48
1:A:236:HIS:HE1	4:D:1051:HOH:O	1.96	0.48
3:D:4901:NAP:H3D	4:D:4113:HOH:O	2.11	0.48
1:C:122:MET:HE1	1:C:174:ILE:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:137:GLY:O	3:B:2901:NAP:H6N	2.13	0.48
1:A:106:ILE:HG13	1:A:150:ASN:ND2	2.29	0.48
1:D:46:SER:CB	4:D:4237:HOH:O	2.62	0.48
1:D:86:ASN:ND2	3:D:4901:NAP:H4D	2.29	0.48
1:D:236:HIS:CE1	4:D:4231:HOH:O	2.67	0.48
1:D:236:HIS:HD2	4:D:4021:HOH:O	1.96	0.48
1:A:122:MET:HE1	1:A:174:ILE:HD13	1.96	0.48
1:C:95:LEU:HD11	1:D:115:PHE:HD1	1.78	0.48
1:C:2:ASN:OD1	1:C:4:GLU:CB	2.63	0.47
1:C:86:ASN:ND2	3:C:3901:NAP:H4D	2.29	0.47
1:C:236:HIS:HD2	4:C:3021:HOH:O	1.96	0.47
1:C:58:LEU:HB2	1:C:69:VAL:HG21	1.95	0.47
1:A:94:LEU:HD12	1:A:97:ARG:NH2	2.30	0.47
1:A:3:PHE:HB2	1:A:30:ALA:HB2	1.96	0.47
1:A:129:ARG:NE	1:A:172:ARG:HH21	2.13	0.46
1:B:187:ASP:H	1:B:190:ARG:HH21	1.62	0.46
1:C:96:MET:HE1	1:D:123:ARG:HA	1.95	0.46
1:A:86:ASN:ND2	3:A:1901:NAP:H4D	2.31	0.46
1:A:236:HIS:HD2	4:A:1021:HOH:O	1.97	0.46
1:D:70:LEU:O	1:D:74:ARG:HG3	2.16	0.46
1:A:88:GLY:N	4:A:1133:HOH:O	2.48	0.46
1:C:11:THR:O	1:C:86:ASN:HB3	2.15	0.46
1:C:95:LEU:CG	1:D:122:MET:HE1	2.46	0.46
1:B:11:THR:O	1:B:86:ASN:HB3	2.15	0.46
1:C:189:THR:HA	1:C:192:LEU:HG	1.96	0.45
1:C:96:MET:HE1	1:D:123:ARG:N	2.32	0.45
1:B:122:MET:HE3	1:B:125:MET:CE	2.27	0.45
1:B:86:ASN:ND2	3:B:2901:NAP:H4D	2.31	0.45
1:D:11:THR:O	1:D:86:ASN:HB3	2.15	0.45
1:C:172:ARG:HG2	4:C:3049:HOH:O	2.15	0.45
1:B:145:ASN:HD22	1:B:148:GLN:NE2	2.14	0.45
1:B:185:GLU:CG	4:B:2170:HOH:O	2.65	0.45
1:A:11:THR:O	1:A:86:ASN:HB3	2.16	0.44
1:B:243:MET:CE	1:C:167:ARG:HE	2.30	0.44
1:A:175:THR:CG2	4:A:1156:HOH:O	2.50	0.44
1:C:60:VAL:HB	1:C:113:SER:HB2	1.99	0.44
1:B:6:LYS:HE3	4:B:2172:HOH:O	2.18	0.44
1:B:122:MET:CE	1:B:174:ILE:HD13	2.48	0.44
1:B:60:VAL:HG22	3:B:2901:NAP:N1A	2.32	0.43
1:C:11:THR:HG21	1:C:117:LEU:HD13	2.00	0.43
1:B:122:MET:HE1	1:B:174:ILE:HD13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ASN:HA	4:A:1130:HOH:O	2.18	0.43
1:C:96:MET:SD	1:D:123:ARG:HG3	2.58	0.43
1:B:60:VAL:HB	1:B:113:SER:HB2	2.01	0.43
3:A:1901:NAP:H52A	4:A:1133:HOH:O	2.18	0.43
1:D:126:MET:SD	1:D:174:ILE:CD1	2.99	0.43
1:C:122:MET:SD	1:C:169:VAL:HG11	2.59	0.43
1:B:3:PHE:HB2	1:B:30:ALA:HB2	2.00	0.43
1:A:179:VAL:O	1:A:181:PRO:HD3	2.19	0.43
4:A:4051:HOH:O	1:D:236:HIS:HE1	2.01	0.43
1:A:4:GLU:HA	1:A:29:GLY:O	2.18	0.42
1:A:66:ILE:O	1:A:70:LEU:HD23	2.19	0.42
1:C:32:VAL:O	1:C:53:GLY:HA3	2.19	0.42
1:D:143:MET:HG3	1:D:144:GLY:O	2.19	0.42
1:A:32:VAL:O	1:A:53:GLY:HA3	2.19	0.42
1:C:179:VAL:O	1:C:181:PRO:HD3	2.19	0.42
1:D:60:VAL:HG22	3:D:4901:NAP:N1A	2.34	0.42
1:D:186:THR:O	1:D:190:ARG:HG3	2.19	0.42
1:A:3:PHE:CB	1:A:30:ALA:HB2	2.49	0.42
1:B:32:VAL:O	1:B:53:GLY:HA3	2.20	0.42
1:A:143:MET:HG3	1:A:144:GLY:O	2.19	0.42
1:D:132:ARG:HD3	1:D:175:THR:OG1	2.20	0.41
1:B:179:VAL:O	1:B:181:PRO:HD3	2.20	0.41
1:C:96:MET:CE	1:D:123:ARG:CG	2.97	0.41
1:A:126:MET:HE1	1:A:172:ARG:HG3	2.02	0.41
1:C:96:MET:CE	1:D:123:ARG:N	2.83	0.41
1:C:165:LEU:HG	1:C:176:VAL:HG21	2.03	0.41
1:D:172:ARG:NH1	4:D:4230:HOH:O	2.36	0.41
1:B:126:MET:SD	1:B:174:ILE:HD12	2.61	0.41
1:A:182:GLY:O	3:A:1901:NAP:H4N	2.21	0.41
1:D:70:LEU:CD1	1:D:120:ALA:HB1	2.50	0.41
1:D:165:LEU:O	1:D:169:VAL:HG22	2.19	0.41
1:D:32:VAL:O	1:D:53:GLY:HA3	2.20	0.41
1:B:172:ARG:HG2	4:B:2049:HOH:O	2.20	0.41
1:A:65:SER:O	1:A:69:VAL:HG23	2.20	0.41
1:D:89:ILE:HG13	1:D:106:ILE:HD13	2.01	0.41
1:D:145:ASN:ND2	1:D:148:GLN:HE21	2.01	0.41
1:B:185:GLU:HG3	4:B:2170:HOH:O	2.21	0.41
1:D:59:ASN:HD22	1:D:62:ASP:HB2	1.86	0.41
1:D:179:VAL:O	1:D:181:PRO:HD3	2.20	0.41
1:C:145:ASN:ND2	1:C:148:GLN:HE21	1.97	0.40
1:D:124:ALA:HB3	4:D:4003:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3:PHE:CB	1:C:30:ALA:HB2	2.49	0.40
1:D:15:ARG:HH11	1:D:15:ARG:HG2	1.86	0.40
1:A:61:THR:HG22	1:A:108:GLU:HG2	2.03	0.40
1:C:193:SER:HB3	4:C:3206:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	241/244 (99%)	231 (96%)	9 (4%)	1 (0%)	30	22
1	B	237/244 (97%)	230 (97%)	6 (2%)	1 (0%)	30	22
1	C	241/244 (99%)	235 (98%)	5 (2%)	1 (0%)	30	22
1	D	241/244 (99%)	234 (97%)	6 (2%)	1 (0%)	30	22
All	All	960/976 (98%)	930 (97%)	26 (3%)	4 (0%)	30	22

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	93	ASN
1	A	93	ASN
1	B	93	ASN
1	C	93	ASN

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	179/180 (99%)	179 (100%)	0	100	100
1	B	178/180 (99%)	176 (99%)	2 (1%)	65	68
1	C	179/180 (99%)	177 (99%)	2 (1%)	65	68
1	D	179/180 (99%)	179 (100%)	0	100	100
All	All	715/720 (99%)	711 (99%)	4 (1%)	78	83

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	4	GLU
1	B	190	ARG
1	C	101	GLU
1	C	209	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	ASN
1	A	85	ASN
1	A	86	ASN
1	A	148	GLN
1	A	236	HIS
1	B	85	ASN
1	B	86	ASN
1	B	104	ASN
1	B	148	GLN
1	B	236	HIS
1	C	85	ASN
1	C	86	ASN
1	C	148	GLN
1	C	236	HIS
1	D	59	ASN
1	D	85	ASN
1	D	86	ASN
1	D	148	GLN
1	D	236	HIS

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](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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$
3	NAP	B	2901	-	50,52,52	2.10	11 (22%)	71,80,80	1.43	12 (16%)
3	NAP	A	1901	-	50,52,52	2.07	12 (24%)	71,80,80	1.43	12 (16%)
3	NAP	C	3901	-	50,52,52	2.04	10 (20%)	71,80,80	1.45	12 (16%)
3	NAP	D	4901	-	50,52,52	2.08	12 (24%)	71,80,80	1.43	12 (16%)

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	NAP	B	2901	-	-	7/35/67/67	0/5/5/5
3	NAP	A	1901	-	-	7/35/67/67	0/5/5/5
3	NAP	C	3901	-	-	8/35/67/67	0/5/5/5
3	NAP	D	4901	-	-	8/35/67/67	0/5/5/5

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	4901	NAP	C2N-N1N	8.33	1.44	1.35
3	B	2901	NAP	C2N-N1N	8.20	1.44	1.35
3	A	1901	NAP	C2N-N1N	8.01	1.43	1.35
3	C	3901	NAP	C2N-N1N	7.87	1.43	1.35
3	B	2901	NAP	C4N-C3N	5.12	1.47	1.39
3	A	1901	NAP	C4N-C3N	5.05	1.47	1.39
3	C	3901	NAP	C4N-C3N	4.92	1.46	1.39
3	D	4901	NAP	C4N-C3N	4.86	1.46	1.39
3	C	3901	NAP	O4D-C1D	4.65	1.47	1.40
3	A	1901	NAP	O4D-C1D	4.62	1.47	1.40
3	B	2901	NAP	O4D-C1D	4.60	1.46	1.40
3	D	4901	NAP	O4D-C1D	4.44	1.46	1.40
3	C	3901	NAP	C2A-N1A	4.03	1.41	1.33
3	B	2901	NAP	C2A-N1A	4.01	1.41	1.33
3	A	1901	NAP	C2A-N1A	3.80	1.40	1.33
3	D	4901	NAP	C2A-N1A	3.73	1.40	1.33
3	B	2901	NAP	C6N-N1N	3.26	1.42	1.35
3	A	1901	NAP	C6N-N1N	3.24	1.42	1.35
3	C	3901	NAP	C6N-N1N	3.15	1.42	1.35
3	A	1901	NAP	C2A-N3A	3.12	1.39	1.33
3	D	4901	NAP	C6N-N1N	3.05	1.42	1.35
3	B	2901	NAP	C2A-N3A	3.03	1.39	1.33
3	B	2901	NAP	P2B-O2B	2.93	1.64	1.59
3	C	3901	NAP	C2A-N3A	2.93	1.39	1.33
3	D	4901	NAP	C2A-N3A	2.91	1.39	1.33
3	A	1901	NAP	P2B-O2B	2.90	1.64	1.59
3	C	3901	NAP	P2B-O2B	2.84	1.64	1.59
3	D	4901	NAP	P2B-O2B	2.73	1.64	1.59
3	C	3901	NAP	PA-O1A	-2.72	1.41	1.50
3	D	4901	NAP	PA-O1A	-2.69	1.41	1.50
3	A	1901	NAP	PA-O1A	-2.66	1.41	1.50
3	C	3901	NAP	O4B-C4B	2.62	1.50	1.45
3	B	2901	NAP	PA-O1A	-2.57	1.41	1.50
3	A	1901	NAP	C4A-N3A	2.55	1.39	1.34
3	D	4901	NAP	O4B-C4B	2.55	1.50	1.45
3	B	2901	NAP	O4B-C4B	2.54	1.50	1.45
3	A	1901	NAP	O4B-C4B	2.47	1.50	1.45
3	D	4901	NAP	C4A-N3A	2.44	1.39	1.34
3	C	3901	NAP	C4A-N3A	2.37	1.38	1.34
3	B	2901	NAP	C4A-N3A	2.35	1.38	1.34
3	D	4901	NAP	C3N-C7N	2.25	1.53	1.50
3	B	2901	NAP	C5N-C4N	2.07	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	4901	NAP	C5N-C4N	2.07	1.42	1.38
3	A	1901	NAP	C5N-C4N	2.05	1.42	1.38
3	A	1901	NAP	C3N-C7N	2.00	1.53	1.50

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	4901	NAP	C6N-N1N-C1D	-4.06	111.76	119.73
3	C	3901	NAP	C6N-N1N-C1D	-4.02	111.84	119.73
3	A	1901	NAP	C6N-N1N-C1D	-3.95	111.97	119.73
3	B	2901	NAP	C6N-N1N-C1D	-3.90	112.07	119.73
3	A	1901	NAP	N3A-C2A-N1A	-3.63	123.09	128.58
3	B	2901	NAP	N3A-C2A-N1A	-3.63	123.09	128.58
3	C	3901	NAP	N3A-C2A-N1A	-3.59	123.15	128.58
3	D	4901	NAP	N3A-C2A-N1A	-3.58	123.16	128.58
3	C	3901	NAP	C3N-C7N-N7N	3.07	121.53	117.74
3	D	4901	NAP	C3N-C7N-N7N	3.02	121.46	117.74
3	C	3901	NAP	O7N-C7N-C3N	-3.01	115.92	119.60
3	A	1901	NAP	C3N-C7N-N7N	2.96	121.38	117.74
3	D	4901	NAP	O2A-PA-O1A	2.93	126.08	112.44
3	B	2901	NAP	C3N-C7N-N7N	2.91	121.32	117.74
3	C	3901	NAP	O2A-PA-O1A	2.90	125.96	112.44
3	A	1901	NAP	O2A-PA-O1A	2.89	125.89	112.44
3	B	2901	NAP	O2A-PA-O1A	2.88	125.85	112.44
3	C	3901	NAP	C2N-C3N-C4N	2.76	121.47	118.26
3	D	4901	NAP	C2N-N1N-C1D	2.71	125.11	119.13
3	B	2901	NAP	O7N-C7N-C3N	-2.69	116.31	119.60
3	A	1901	NAP	O7N-C7N-C3N	-2.68	116.32	119.60
3	B	2901	NAP	O4B-C1B-N9A	2.64	113.17	108.09
3	C	3901	NAP	C2N-N1N-C1D	2.64	124.95	119.13
3	A	1901	NAP	C2N-N1N-C1D	2.63	124.95	119.13
3	B	2901	NAP	C2N-C3N-C4N	2.63	121.32	118.26
3	B	2901	NAP	C2N-N1N-C1D	2.63	124.94	119.13
3	C	3901	NAP	O4B-C1B-N9A	2.62	113.13	108.09
3	A	1901	NAP	O4B-C1B-N9A	2.60	113.09	108.09
3	D	4901	NAP	O4B-C1B-N9A	2.59	113.06	108.09
3	B	2901	NAP	O5B-C5B-C4B	-2.59	100.18	108.99
3	A	1901	NAP	C2N-C3N-C4N	2.57	121.25	118.26
3	C	3901	NAP	O5B-C5B-C4B	-2.52	100.40	108.99
3	A	1901	NAP	O5B-C5B-C4B	-2.51	100.44	108.99
3	D	4901	NAP	O5B-C5B-C4B	-2.51	100.45	108.99
3	D	4901	NAP	O7N-C7N-C3N	-2.50	116.54	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	4901	NAP	C2N-C3N-C4N	2.41	121.06	118.26
3	C	3901	NAP	C2B-C1B-N9A	-2.36	109.87	113.75
3	B	2901	NAP	C2B-C1B-N9A	-2.33	109.92	113.75
3	C	3901	NAP	O3X-P2B-O2X	2.30	116.43	107.80
3	A	1901	NAP	C2B-C1B-N9A	-2.28	109.99	113.75
3	A	1901	NAP	O3X-P2B-O2X	2.28	116.36	107.80
3	B	2901	NAP	O3X-P2B-O2X	2.27	116.33	107.80
3	D	4901	NAP	C2B-C1B-N9A	-2.26	110.04	113.75
3	D	4901	NAP	O3X-P2B-O2X	2.24	116.21	107.80
3	C	3901	NAP	C1B-N9A-C8A	2.17	131.92	127.09
3	D	4901	NAP	C1B-N9A-C8A	2.17	131.92	127.09
3	B	2901	NAP	C1B-N9A-C8A	2.16	131.90	127.09
3	A	1901	NAP	C1B-N9A-C8A	2.15	131.88	127.09

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1901	NAP	C5B-O5B-PA-O1A
3	B	2901	NAP	C5B-O5B-PA-O1A
3	C	3901	NAP	C5B-O5B-PA-O1A
3	D	4901	NAP	C5B-O5B-PA-O1A
3	A	1901	NAP	C3B-C2B-O2B-P2B
3	B	2901	NAP	C3B-C2B-O2B-P2B
3	C	3901	NAP	C3B-C2B-O2B-P2B
3	D	4901	NAP	C3B-C2B-O2B-P2B
3	C	3901	NAP	C3D-C4D-C5D-O5D
3	D	4901	NAP	C3D-C4D-C5D-O5D
3	A	1901	NAP	C1B-C2B-O2B-P2B
3	B	2901	NAP	C1B-C2B-O2B-P2B
3	C	3901	NAP	C1B-C2B-O2B-P2B
3	D	4901	NAP	C1B-C2B-O2B-P2B
3	A	1901	NAP	O4D-C4D-C5D-O5D
3	B	2901	NAP	C3D-C4D-C5D-O5D
3	C	3901	NAP	O4D-C4D-C5D-O5D
3	D	4901	NAP	O4D-C4D-C5D-O5D
3	A	1901	NAP	C3D-C4D-C5D-O5D
3	B	2901	NAP	O4D-C4D-C5D-O5D
3	A	1901	NAP	C5B-O5B-PA-O3
3	B	2901	NAP	C5B-O5B-PA-O3
3	C	3901	NAP	C5B-O5B-PA-O3
3	D	4901	NAP	C5B-O5B-PA-O3

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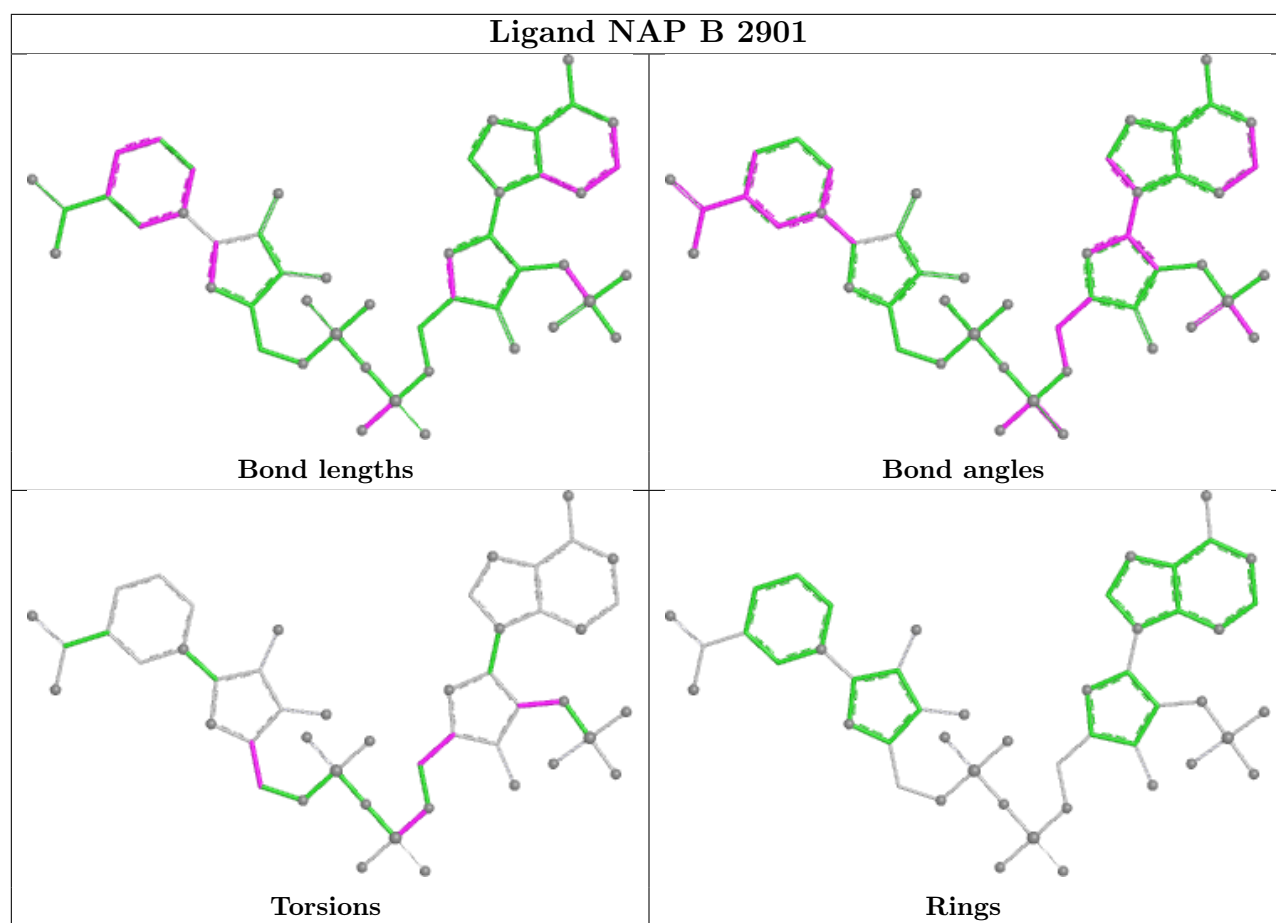
Mol	Chain	Res	Type	Atoms
3	D	4901	NAP	O4D-C1D-N1N-C6N
3	A	1901	NAP	O4B-C4B-C5B-O5B
3	B	2901	NAP	O4B-C4B-C5B-O5B
3	C	3901	NAP	O4B-C4B-C5B-O5B
3	D	4901	NAP	O4B-C4B-C5B-O5B
3	C	3901	NAP	PN-O3-PA-O1A

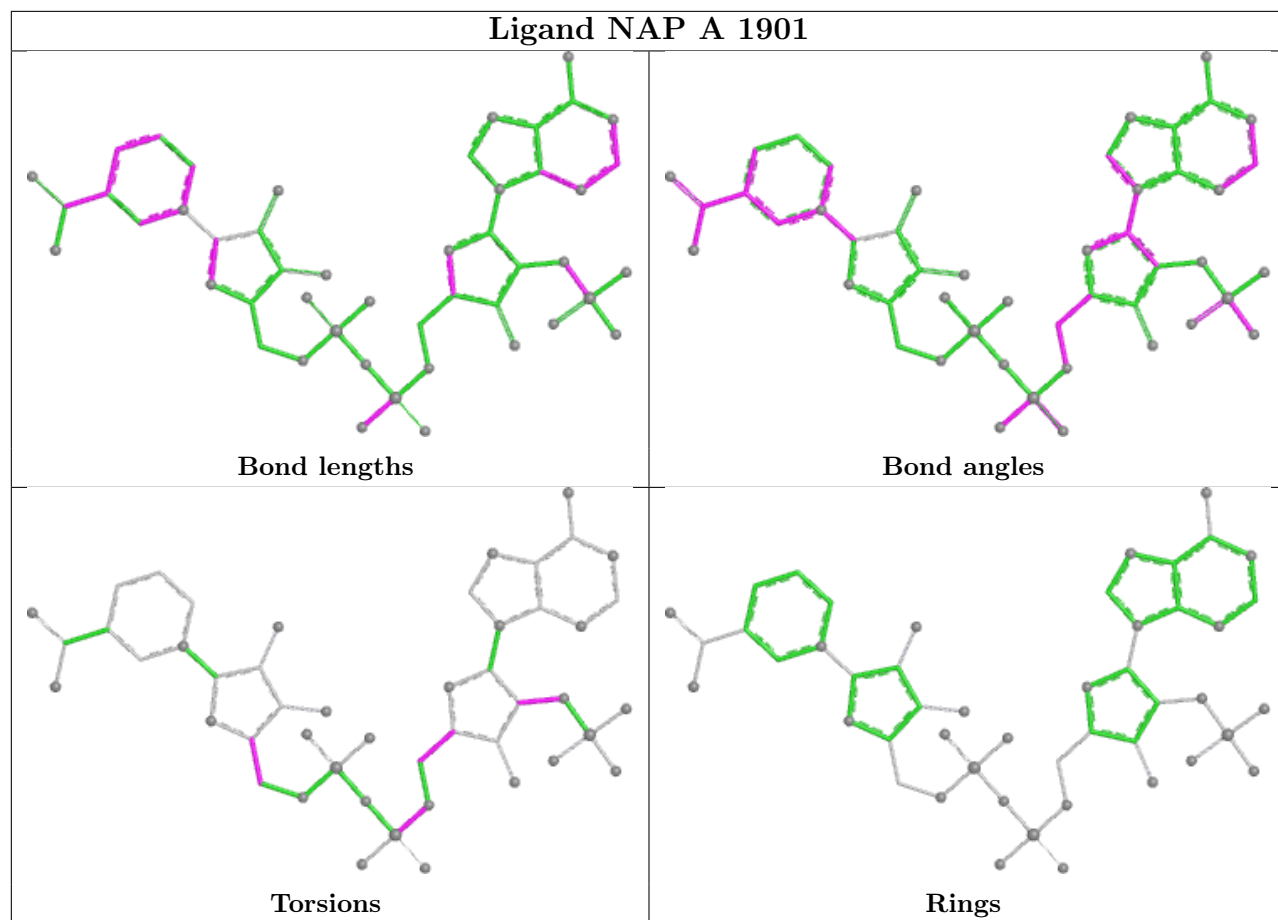
There are no ring outliers.

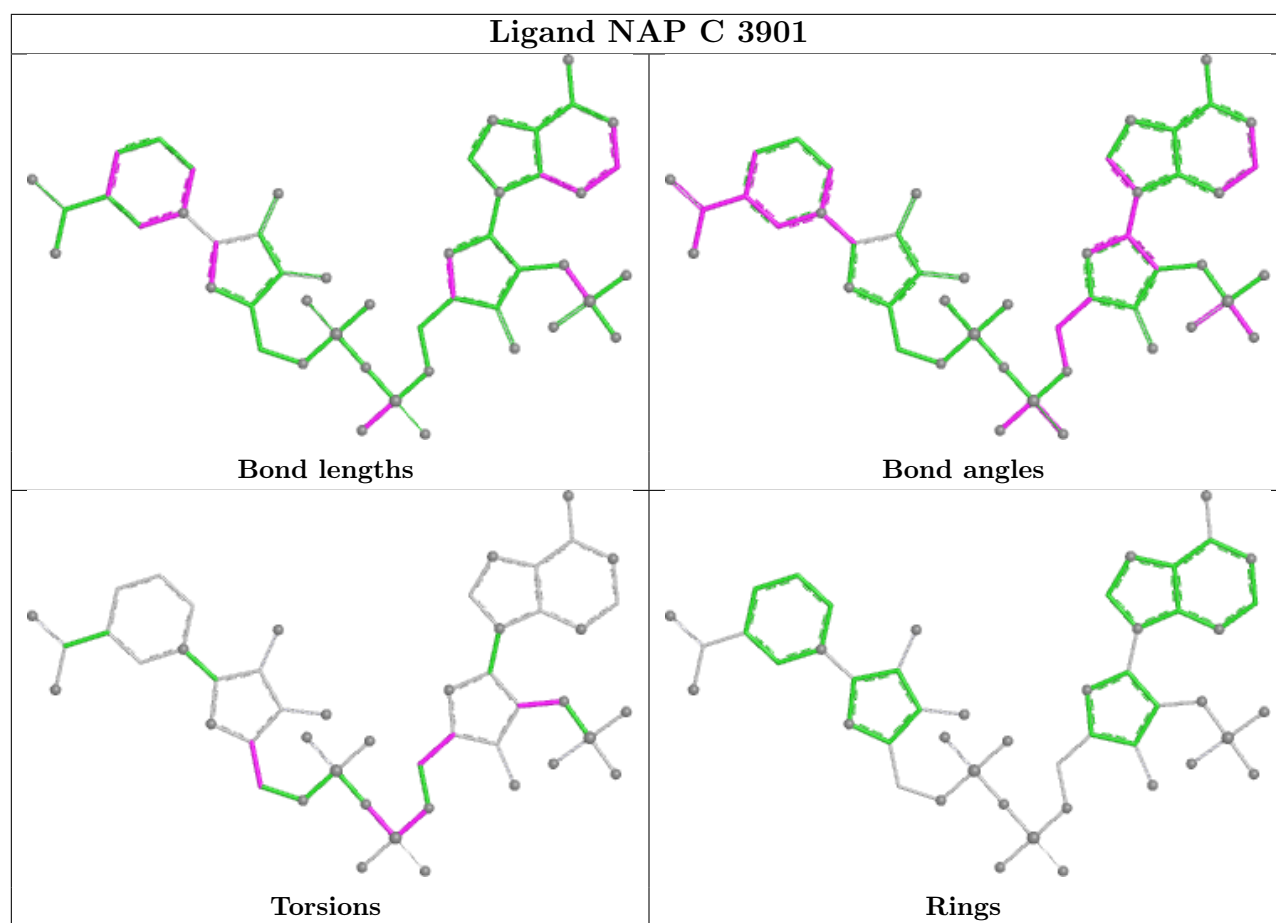
4 monomers are involved in 17 short contacts:

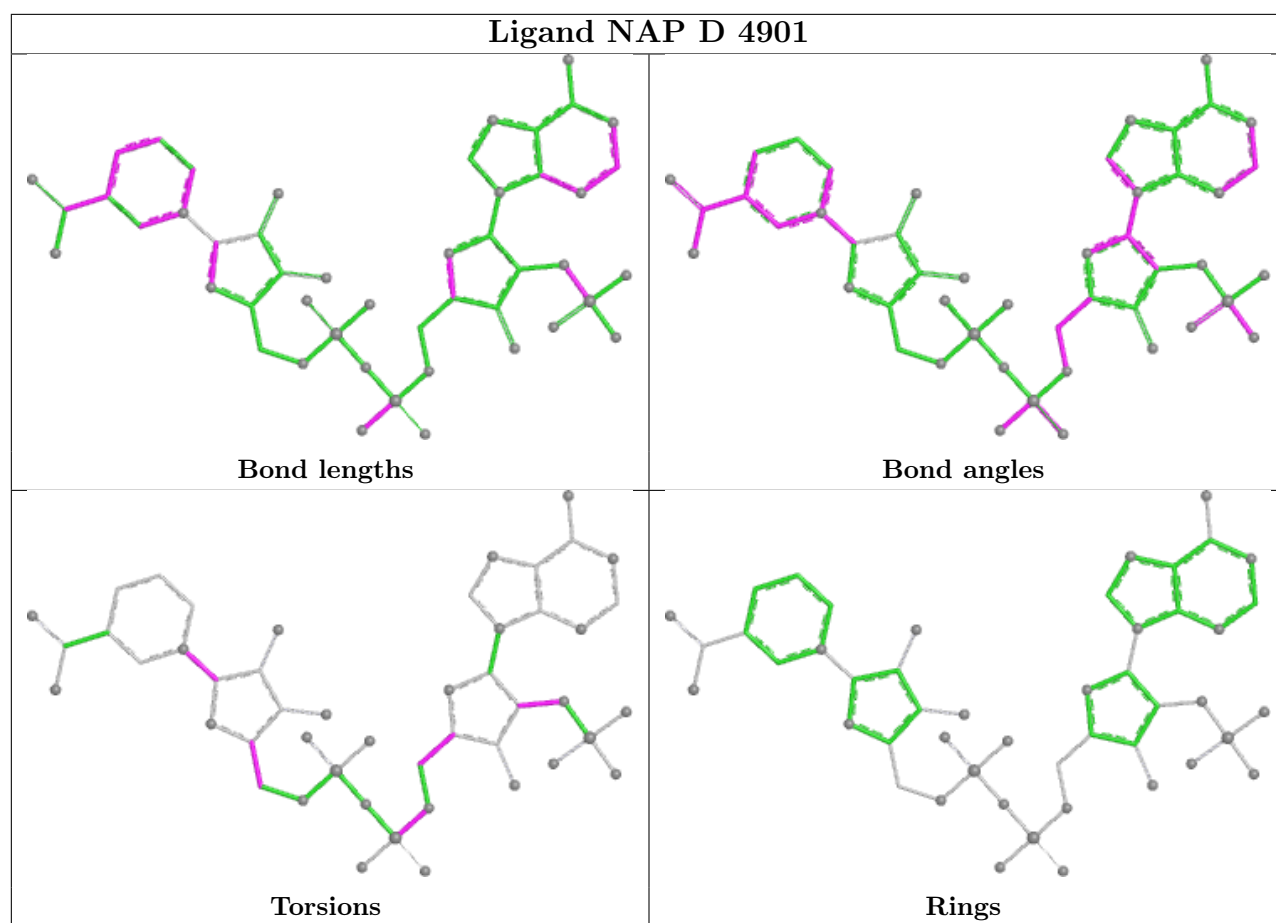
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2901	NAP	3	0
3	A	1901	NAP	6	0
3	C	3901	NAP	3	0
3	D	4901	NAP	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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, 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	243/244 (99%)	-0.09	3 (1%) 76 78	17, 30, 45, 54	8 (3%)
1	B	241/244 (98%)	-0.02	8 (3%) 49 49	16, 29, 45, 81	13 (5%)
1	C	243/244 (99%)	-0.08	6 (2%) 58 60	16, 28, 43, 53	6 (2%)
1	D	243/244 (99%)	0.03	5 (2%) 63 65	18, 31, 48, 55	7 (2%)
All	All	970/976 (99%)	-0.04	22 (2%) 61 63	16, 29, 46, 81	34 (3%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	126	MET	8.0
1	B	96	MET	7.2
1	B	126	MET	7.0
1	A	126	MET	7.0
1	B	122	MET	6.6
1	C	122	MET	6.3
1	C	126	MET	6.2
1	D	122	MET	5.1
1	A	122	MET	5.0
1	B	193	SER	5.0
1	A	96	MET	4.8
1	C	96	MET	4.4
1	C	188	MET	4.3
1	D	96	MET	4.0
1	C	2	ASN	3.2
1	D	61	THR	2.7
1	B	189	THR	2.7
1	C	191	ALA	2.5
1	D	5	GLY	2.5
1	B	194	ASP	2.4
1	B	196	GLN	2.1
1	B	190	ARG	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

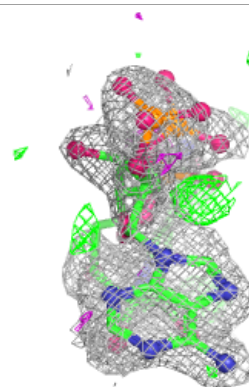
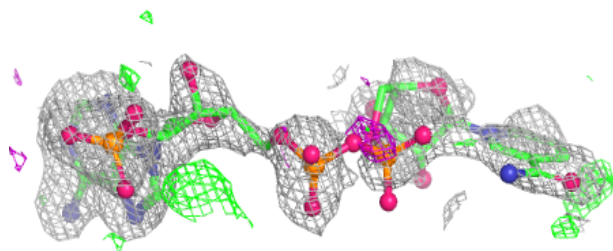
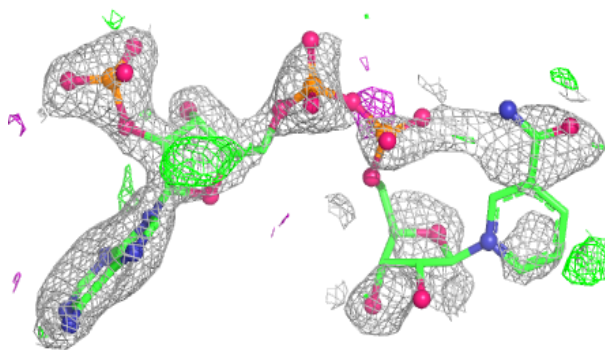
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	NAP	D	4901	48/48	0.80	0.16	32,41,47,48	48
3	NAP	A	1901	48/48	0.86	0.16	31,38,45,46	48
2	CA	A	9006	1/1	0.87	0.08	56,56,56,56	0
3	NAP	B	2901	48/48	0.88	0.12	32,40,45,47	26
3	NAP	C	3901	48/48	0.89	0.13	31,39,45,45	26
2	CA	C	9004	1/1	0.90	0.07	53,53,53,53	0
2	CA	B	9008	1/1	0.91	0.07	60,60,60,60	0
2	CA	A	9007	1/1	0.95	0.05	50,50,50,50	0
2	CA	B	9003	1/1	0.96	0.05	42,42,42,42	0
2	CA	A	9002	1/1	0.99	0.02	24,24,24,24	0
2	CA	D	9005	1/1	0.99	0.03	55,55,55,55	0
2	CA	B	9001	1/1	0.99	0.03	24,24,24,24	0

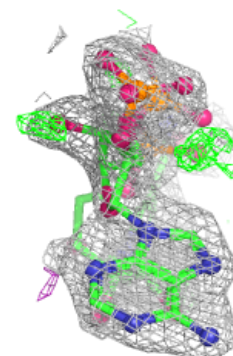
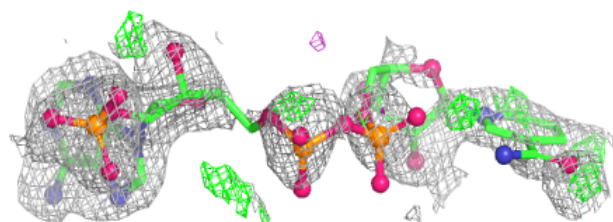
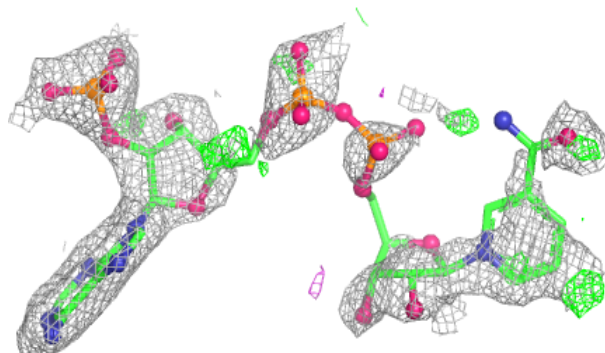
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAP D 4901:

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

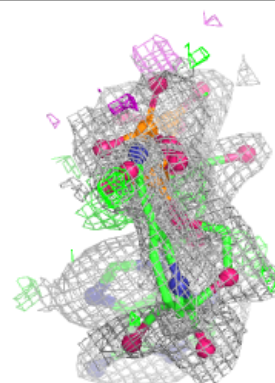
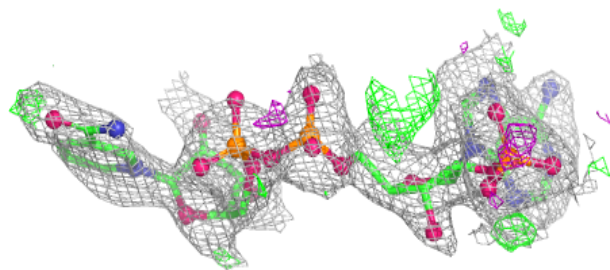
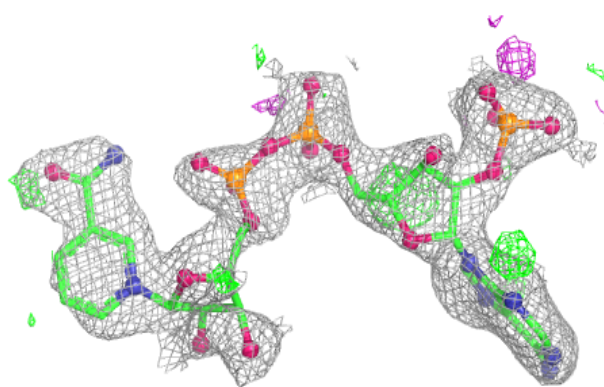
**Electron density around NAP A 1901:**

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

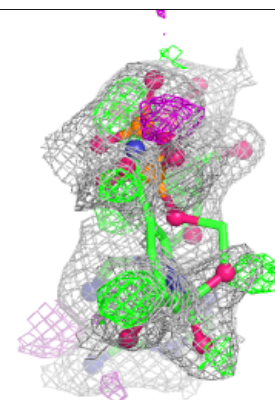
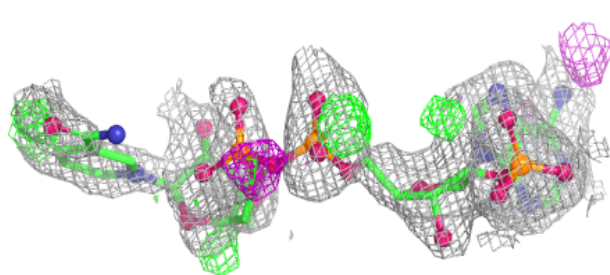
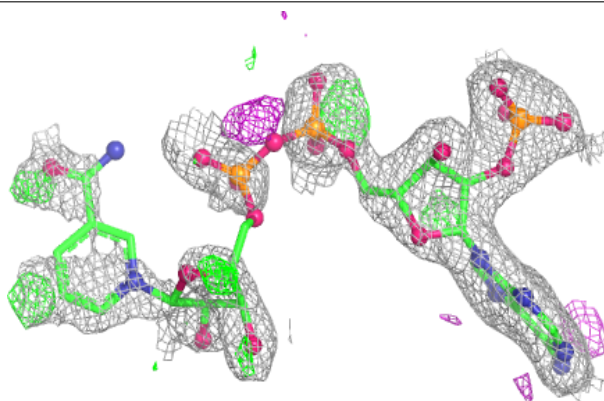


Electron density around NAP B 2901:

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

**Electron density around NAP C 3901:**

$2mF_o-DF_c$ (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.