



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 08:15 am BST

PDB ID : 6EOW
Title : Structure of Raspberry Ketone Synthase with Hydroxybenzalacetone
Authors : Tosi, T.; Moore, S.J.; Freemont, P.S.
Deposited on : 2017-10-10
Resolution : 1.80 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

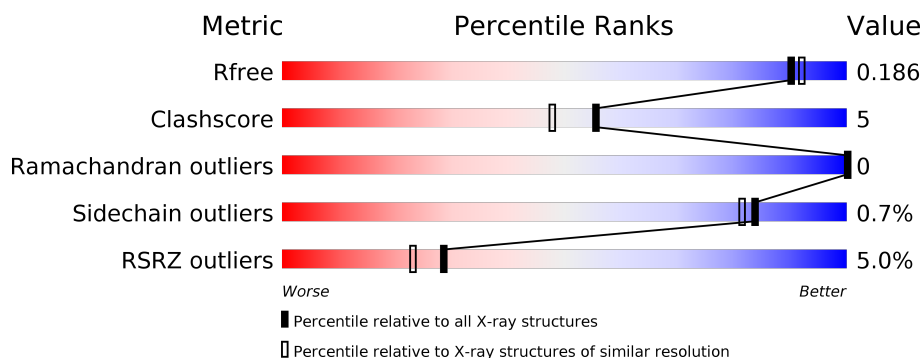
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 on 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	368	<div> <div>5%</div> <div> <div></div> <div>83%</div> <div>9%</div> <div>7%</div> </div> </div>
1	B	368	<div> <div>5%</div> <div> <div></div> <div>83%</div> <div>6%</div> <div>10%</div> </div> </div>
1	C	368	<div> <div>5%</div> <div> <div></div> <div>80%</div> <div>8%</div> <div>11%</div> </div> </div>
1	D	368	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>8%</div> <div>10%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BKZ	B	401	-	X	X	-
3	BKZ	C	401	-	-	X	-
3	BKZ	D	401	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11256 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 Ketone/zingerone synthase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	79	5	0
			2685	1732	439	495	19			
1	B	331	Total	C	N	O	S	94	2	0
			2587	1671	420	480	16			
1	C	327	Total	C	N	O	S	97	3	0
			2572	1665	417	474	16			
1	D	330	Total	C	N	O	S	90	2	0
			2579	1664	419	479	17			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP G1FCG0
A	-18	GLY	-	expression tag	UNP G1FCG0
A	-17	SER	-	expression tag	UNP G1FCG0
A	-16	SER	-	expression tag	UNP G1FCG0
A	-15	HIS	-	expression tag	UNP G1FCG0
A	-14	HIS	-	expression tag	UNP G1FCG0
A	-13	HIS	-	expression tag	UNP G1FCG0
A	-12	HIS	-	expression tag	UNP G1FCG0
A	-11	HIS	-	expression tag	UNP G1FCG0
A	-10	HIS	-	expression tag	UNP G1FCG0
A	-9	SER	-	expression tag	UNP G1FCG0
A	-8	SER	-	expression tag	UNP G1FCG0
A	-7	GLY	-	expression tag	UNP G1FCG0
A	-6	LEU	-	expression tag	UNP G1FCG0
A	-5	VAL	-	expression tag	UNP G1FCG0
A	-4	PRO	-	expression tag	UNP G1FCG0
A	-3	ARG	-	expression tag	UNP G1FCG0
A	-2	GLY	-	expression tag	UNP G1FCG0
A	-1	SER	-	expression tag	UNP G1FCG0
A	0	HIS	-	expression tag	UNP G1FCG0
B	-19	MET	-	initiating methionine	UNP G1FCG0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP G1FCG0
B	-17	SER	-	expression tag	UNP G1FCG0
B	-16	SER	-	expression tag	UNP G1FCG0
B	-15	HIS	-	expression tag	UNP G1FCG0
B	-14	HIS	-	expression tag	UNP G1FCG0
B	-13	HIS	-	expression tag	UNP G1FCG0
B	-12	HIS	-	expression tag	UNP G1FCG0
B	-11	HIS	-	expression tag	UNP G1FCG0
B	-10	HIS	-	expression tag	UNP G1FCG0
B	-9	SER	-	expression tag	UNP G1FCG0
B	-8	SER	-	expression tag	UNP G1FCG0
B	-7	GLY	-	expression tag	UNP G1FCG0
B	-6	LEU	-	expression tag	UNP G1FCG0
B	-5	VAL	-	expression tag	UNP G1FCG0
B	-4	PRO	-	expression tag	UNP G1FCG0
B	-3	ARG	-	expression tag	UNP G1FCG0
B	-2	GLY	-	expression tag	UNP G1FCG0
B	-1	SER	-	expression tag	UNP G1FCG0
B	0	HIS	-	expression tag	UNP G1FCG0
C	-19	MET	-	initiating methionine	UNP G1FCG0
C	-18	GLY	-	expression tag	UNP G1FCG0
C	-17	SER	-	expression tag	UNP G1FCG0
C	-16	SER	-	expression tag	UNP G1FCG0
C	-15	HIS	-	expression tag	UNP G1FCG0
C	-14	HIS	-	expression tag	UNP G1FCG0
C	-13	HIS	-	expression tag	UNP G1FCG0
C	-12	HIS	-	expression tag	UNP G1FCG0
C	-11	HIS	-	expression tag	UNP G1FCG0
C	-10	HIS	-	expression tag	UNP G1FCG0
C	-9	SER	-	expression tag	UNP G1FCG0
C	-8	SER	-	expression tag	UNP G1FCG0
C	-7	GLY	-	expression tag	UNP G1FCG0
C	-6	LEU	-	expression tag	UNP G1FCG0
C	-5	VAL	-	expression tag	UNP G1FCG0
C	-4	PRO	-	expression tag	UNP G1FCG0
C	-3	ARG	-	expression tag	UNP G1FCG0
C	-2	GLY	-	expression tag	UNP G1FCG0
C	-1	SER	-	expression tag	UNP G1FCG0
C	0	HIS	-	expression tag	UNP G1FCG0
D	-19	MET	-	initiating methionine	UNP G1FCG0
D	-18	GLY	-	expression tag	UNP G1FCG0
D	-17	SER	-	expression tag	UNP G1FCG0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP G1FCG0
D	-15	HIS	-	expression tag	UNP G1FCG0
D	-14	HIS	-	expression tag	UNP G1FCG0
D	-13	HIS	-	expression tag	UNP G1FCG0
D	-12	HIS	-	expression tag	UNP G1FCG0
D	-11	HIS	-	expression tag	UNP G1FCG0
D	-10	HIS	-	expression tag	UNP G1FCG0
D	-9	SER	-	expression tag	UNP G1FCG0
D	-8	SER	-	expression tag	UNP G1FCG0
D	-7	GLY	-	expression tag	UNP G1FCG0
D	-6	LEU	-	expression tag	UNP G1FCG0
D	-5	VAL	-	expression tag	UNP G1FCG0
D	-4	PRO	-	expression tag	UNP G1FCG0
D	-3	ARG	-	expression tag	UNP G1FCG0
D	-2	GLY	-	expression tag	UNP G1FCG0
D	-1	SER	-	expression tag	UNP G1FCG0
D	0	HIS	-	expression tag	UNP G1FCG0

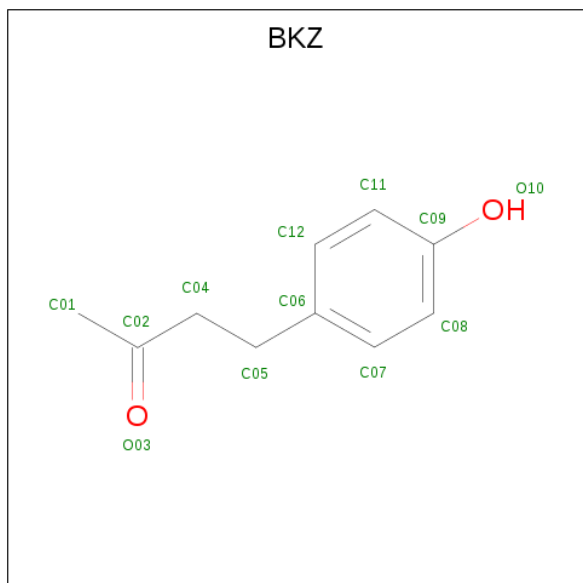
- [illegible]

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

- Molecule 3 is 4-(4-hydroxyphenyl)butan-2-one (three-letter code: BKZ) (formula: $C_{10}H_{12}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			12	10	2		
3	C	1	Total	C	O	0	0
			12	10	2		
3	D	1	Total	C	O	0	0
			12	10	2		

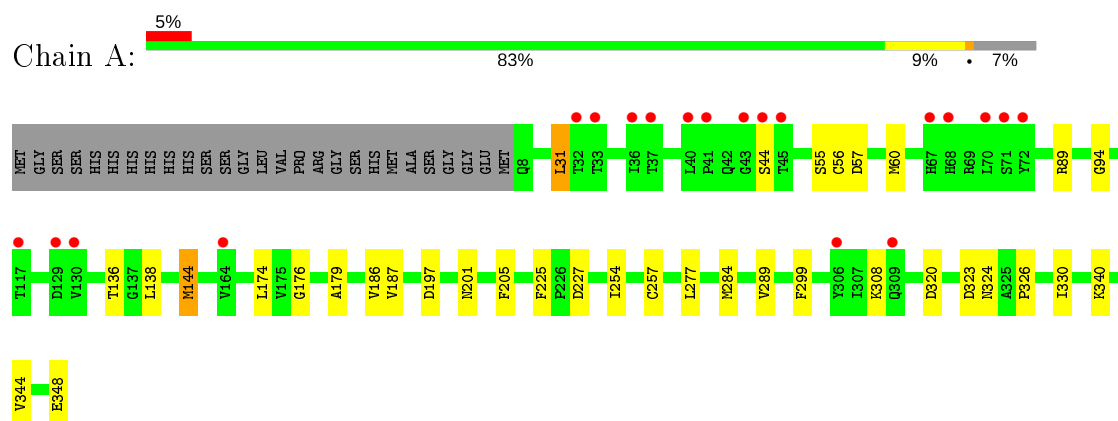
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	183	Total	O	0	0
			183	183		
4	B	151	Total	O	0	0
			151	151		
4	C	139	Total	O	0	0
			139	139		
4	D	132	Total	O	0	0
			132	132		

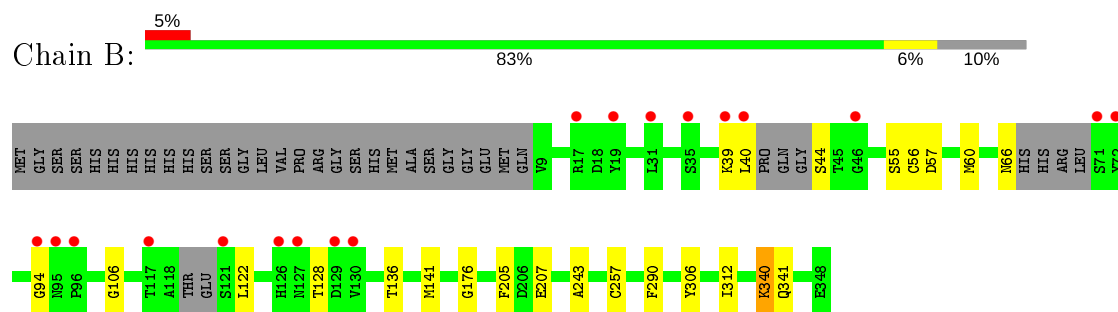
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

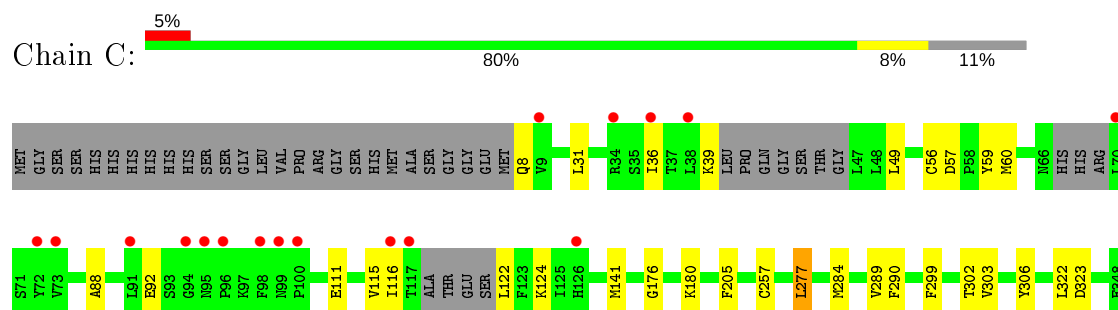
- Molecule 1: Ketone/zingerone synthase 1



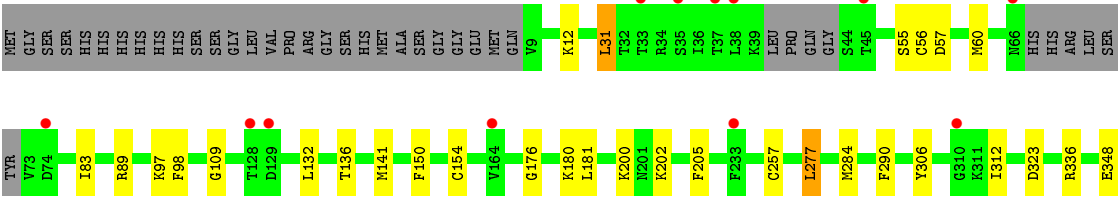
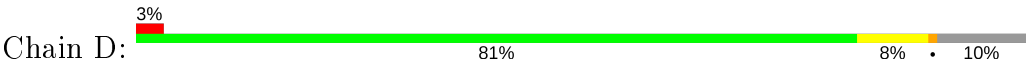
- Molecule 1: Ketone/zingerone synthase 1



- Molecule 1: Ketone/zingerone synthase 1



- Molecule 1: Ketone/zingerone synthase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.04Å 81.73Å 93.05Å 77.68° 85.13° 72.70°	Depositor
Resolution (Å)	29.11 – 1.80 29.11 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.4 (29.11-1.80) 97.4 (29.11-1.80)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.07 (at 1.80Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.162 , 0.187 0.161 , 0.186	Depositor DCC
R_{free} test set	6025 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtriage
Anisotropy	0.325	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 56.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11256	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.84% 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: NAP, BKZ

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	0.53	0/2761	0.65	2/3731 (0.1%)
1	B	0.53	0/2648	0.66	1/3576 (0.0%)
1	C	0.49	0/2636	0.61	1/3560 (0.0%)
1	D	0.45	0/2640	0.60	2/3566 (0.1%)
All	All	0.50	0/10685	0.63	6/14433 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	340	LYS	CD-CE-NZ	-7.01	95.59	111.70
1	D	277	LEU	CB-CG-CD1	-6.57	99.83	111.00
1	A	31	LEU	CA-CB-CG	-6.00	101.51	115.30
1	D	31	LEU	CB-CG-CD2	-5.81	101.12	111.00
1	C	277	LEU	CB-CG-CD1	-5.53	101.60	111.00
1	A	227	ASP	CB-CG-OD1	5.41	123.17	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2685	0	2692	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2587	0	2591	20	0
1	C	2572	0	2583	23	0
1	D	2579	0	2584	19	0
2	A	48	0	25	2	0
2	B	48	0	25	5	0
2	C	48	0	25	6	0
2	D	48	0	25	4	0
3	B	12	0	0	9	0
3	C	12	0	0	11	0
3	D	12	0	0	7	0
4	A	183	0	0	0	0
4	B	151	0	0	2	0
4	C	139	0	0	2	0
4	D	132	0	0	0	0
All	All	11256	0	10550	103	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 5.

All (103) 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:C:290:PHE:CZ	3:C:401:BKZ:O03	2.17	0.96
1:C:277:LEU:HD11	1:C:284:MET:HE2	1.55	0.86
1:C:290:PHE:HZ	3:C:401:BKZ:O03	1.56	0.85
3:C:401:BKZ:C08	2:C:402:NAP:O2D	2.25	0.84
3:B:401:BKZ:C05	2:B:402:NAP:C4N	2.56	0.83
1:B:141:MET:SD	3:B:401:BKZ:C01	2.69	0.80
1:C:141:MET:HG3	3:C:401:BKZ:C01	2.12	0.78
1:A:254:ILE:HD12	1:A:284[B]:MET:HE2	1.66	0.78
3:C:401:BKZ:C05	2:C:402:NAP:C4N	2.63	0.77
3:D:401:BKZ:C05	2:D:402:NAP:C4N	2.64	0.75
1:A:197:ASP:OD1	1:A:201:ASN:ND2	2.18	0.74
1:D:277:LEU:HD11	1:D:284:MET:CE	2.20	0.71
1:B:340:LYS:HD2	1:B:341:GLN:N	2.06	0.70
1:C:141:MET:CG	3:C:401:BKZ:C01	2.69	0.70
1:C:141:MET:SD	3:C:401:BKZ:C01	2.80	0.70
1:A:277:LEU:HD21	1:A:284[B]:MET:HE3	1.75	0.68
1:B:290:PHE:CZ	3:B:401:BKZ:O03	2.47	0.67
1:A:144:MET:CE	1:A:299:PHE:CD2	2.78	0.67
1:A:89:ARG:NH1	1:A:348:GLU:OE1	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:401:BKZ:O10	4:C:501:HOH:O	2.14	0.65
3:D:401:BKZ:C08	2:D:402:NAP:O2D	2.45	0.65
1:A:144:MET:HE1	1:A:299:PHE:CB	2.27	0.64
1:A:254:ILE:HB	1:A:284[B]:MET:HG3	1.78	0.64
3:B:401:BKZ:C08	2:B:402:NAP:O2D	2.46	0.63
1:A:277:LEU:HD21	1:A:284[B]:MET:CE	2.29	0.62
1:B:141:MET:CG	3:B:401:BKZ:C01	2.79	0.61
1:B:141:MET:HG3	3:B:401:BKZ:C01	2.30	0.60
1:A:138:LEU:HD12	1:A:174:LEU:HD11	1.81	0.60
1:A:289:VAL:H	2:A:401:NAP:H72N	1.50	0.60
1:D:56:CYS:HA	1:D:60[A]:MET:HE1	1.83	0.60
1:C:289:VAL:H	2:C:402:NAP:H72N	1.51	0.59
1:B:340:LYS:C	1:B:340:LYS:HD2	2.23	0.58
1:D:141:MET:HG3	3:D:401:BKZ:C01	2.32	0.58
1:A:144:MET:HE1	1:A:299:PHE:HB3	1.86	0.58
1:A:144:MET:CE	1:A:299:PHE:CG	2.88	0.57
1:C:299:PHE:CE1	1:C:303[B]:VAL:HG21	2.40	0.56
1:B:44:SER:O	1:B:94:GLY:HA3	2.05	0.56
1:A:31:LEU:HD22	1:A:323:ASP:HA	1.87	0.56
1:B:56:CYS:HA	1:B:60[A]:MET:HE3	1.88	0.55
1:A:326:PRO:O	1:A:330:ILE:HG12	2.06	0.54
1:A:144:MET:HE1	1:A:299:PHE:CD2	2.42	0.54
1:B:39:LYS:O	1:B:40:LEU:HG	2.08	0.54
1:D:306:TYR:HB3	1:D:312:ILE:HG12	1.89	0.54
1:D:89:ARG:NH1	1:D:348:GLU:OE1	2.40	0.54
1:A:56:CYS:HA	1:A:60[B]:MET:HE1	1.90	0.54
1:D:290:PHE:CZ	3:D:401:BKZ:O03	2.60	0.53
1:B:306:TYR:HB3	1:B:312:ILE:HG12	1.89	0.53
1:A:320:ASP:O	1:A:324:ASN:ND2	2.34	0.53
1:B:57:ASP:H	1:B:60[A]:MET:HE3	1.74	0.53
1:C:56:CYS:HA	1:C:60[B]:MET:HE1	1.91	0.53
1:A:144:MET:HE1	1:A:299:PHE:CG	2.44	0.53
1:B:257:CYS:O	2:B:402:NAP:H2N	2.10	0.52
1:D:257:CYS:O	2:D:402:NAP:H2N	2.09	0.51
1:B:57:ASP:H	1:B:60[A]:MET:CE	2.24	0.51
1:A:144:MET:CE	1:A:144:MET:HA	2.41	0.51
1:D:290:PHE:HZ	3:D:401:BKZ:O03	1.94	0.51
3:C:401:BKZ:C06	2:C:402:NAP:C3N	2.89	0.50
1:A:257:CYS:O	2:A:401:NAP:H2N	2.12	0.48
1:B:243:ALA:N	4:B:501:HOH:O	2.47	0.48
1:D:141:MET:CG	3:D:401:BKZ:C01	2.92	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:GLY:HA3	1:A:205:PHE:CZ	2.49	0.48
1:D:176:GLY:HA3	1:D:205:PHE:CZ	2.49	0.48
1:D:97:LYS:HE3	1:D:98:PHE:CE2	2.49	0.47
1:A:144:MET:HE3	1:A:299:PHE:CD2	2.49	0.47
1:A:57:ASP:H	1:A:60[B]:MET:CE	2.28	0.47
1:C:277:LEU:HD11	1:C:284:MET:CE	2.36	0.47
1:C:59:TYR:HB3	3:C:401:BKZ:C07	2.45	0.46
1:B:207:GLU:OE1	4:B:502:HOH:O	2.20	0.45
1:D:55:SER:HB2	1:D:136:THR:HB	1.99	0.45
1:C:115:VAL:C	1:C:116:ILE:HD12	2.37	0.45
1:B:176:GLY:HA3	1:B:205:PHE:CZ	2.52	0.45
1:C:57:ASP:H	1:C:60[B]:MET:CE	2.30	0.44
1:C:180:LYS:HA	1:C:180:LYS:HD2	1.85	0.44
1:C:8:GLN:HA	1:C:36:ILE:O	2.18	0.44
1:B:290:PHE:CE2	3:B:401:BKZ:O03	2.70	0.44
1:A:136:THR:O	1:A:340:LYS:HE2	2.18	0.44
1:A:55:SER:HB2	1:A:136:THR:HB	2.00	0.44
3:B:401:BKZ:C06	2:B:402:NAP:C3N	2.96	0.44
1:D:31:LEU:HD21	1:D:323:ASP:HA	1.99	0.44
1:C:302:THR:O	1:C:306:TYR:HD2	2.01	0.43
1:C:176:GLY:HA3	1:C:205:PHE:CZ	2.52	0.43
1:D:57:ASP:H	1:D:60[A]:MET:CE	2.31	0.43
3:B:401:BKZ:C05	2:B:402:NAP:C3N	2.96	0.43
1:C:257:CYS:O	2:C:402:NAP:H2N	2.18	0.43
1:C:49:LEU:HB3	1:C:88:ALA:HB1	2.01	0.43
1:D:180:LYS:HA	1:D:180:LYS:HD2	1.78	0.43
1:C:31:LEU:HD21	1:C:323:ASP:HA	2.00	0.43
1:A:179:ALA:HB3	1:A:186:VAL:HG21	2.02	0.42
1:D:132:LEU:HD23	1:D:132:LEU:HA	1.91	0.42
1:D:181:LEU:HD11	1:D:312:ILE:HD11	2.01	0.42
1:C:111:GLU:HA	1:C:322:LEU:HD21	2.02	0.42
1:B:106:GLY:HA3	1:B:122:LEU:HD23	2.01	0.42
1:D:150:PHE:O	1:D:154:CYS:HB2	2.19	0.42
1:A:187:VAL:HB	1:A:225:PHE:CZ	2.55	0.41
1:C:39:LYS:HA	1:C:92:GLU:OE1	2.20	0.41
3:C:401:BKZ:C07	2:C:402:NAP:C2N	2.98	0.41
1:D:83:ILE:HD13	1:D:109:GLY:HA2	2.03	0.41
1:A:320:ASP:HA	1:A:344:VAL:CG1	2.51	0.40
1:C:122:LEU:N	4:C:509:HOH:O	2.54	0.40
1:B:55:SER:HB2	1:B:136:THR:HB	2.02	0.40
1:A:44:SER:O	1:A:94:GLY:HA3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:401:BKZ:C06	2:D:402:NAP:C3N	2.99	0.40
1:B:128:THR:O	1:B:128:THR:HG22	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	344/368 (94%)	340 (99%)	4 (1%)	0	100	100
1	B	325/368 (88%)	320 (98%)	5 (2%)	0	100	100
1	C	322/368 (88%)	318 (99%)	4 (1%)	0	100	100
1	D	326/368 (89%)	322 (99%)	4 (1%)	0	100	100
All	All	1317/1472 (90%)	1300 (99%)	17 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	291/307 (95%)	289 (99%)	2 (1%)	84	81
1	B	279/307 (91%)	278 (100%)	1 (0%)	91	89
1	C	278/307 (91%)	277 (100%)	1 (0%)	91	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	278/307 (91%)	274 (99%)	4 (1%)	67	59
All	All	1126/1228 (92%)	1118 (99%)	8 (1%)	84	81

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	MET
1	A	308	LYS
1	B	66	ASN
1	C	124	LYS
1	D	12	LYS
1	D	200	LYS
1	D	202	LYS
1	D	336	ARG

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

7 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	BKZ	D	401	-	12,12,12	2.21	4 (33%)	14,15,15	2.17	6 (42%)
2	NAP	D	402	-	45,52,52	1.84	14 (31%)	56,80,80	1.25	7 (12%)
2	NAP	B	402	-	45,52,52	2.12	15 (33%)	56,80,80	1.17	5 (8%)
3	BKZ	C	401	-	12,12,12	2.34	5 (41%)	14,15,15	1.72	5 (35%)
2	NAP	C	402	-	45,52,52	2.01	12 (26%)	56,80,80	1.13	3 (5%)
2	NAP	A	401	-	45,52,52	1.92	12 (26%)	56,80,80	1.04	2 (3%)
3	BKZ	B	401	-	12,12,12	2.14	5 (41%)	14,15,15	2.89	7 (50%)

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	BKZ	D	401	-	-	2/5/5/5	0/1/1/1
2	NAP	D	402	-	-	9/31/67/67	0/5/5/5
2	NAP	B	402	-	-	5/31/67/67	0/5/5/5
3	BKZ	C	401	-	-	2/5/5/5	0/1/1/1
2	NAP	C	402	-	-	5/31/67/67	0/5/5/5
2	NAP	A	401	-	-	5/31/67/67	0/5/5/5
3	BKZ	B	401	-	-	2/5/5/5	0/1/1/1

All (67) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	402	NAP	C2N-N1N	-5.06	1.28	1.35
2	B	402	NAP	P2B-O3X	-4.70	1.36	1.54
2	C	402	NAP	P2B-O3X	-4.42	1.37	1.54
3	D	401	BKZ	C08-C07	-4.39	1.30	1.38
3	C	401	BKZ	C08-C07	-4.36	1.30	1.38
2	B	402	NAP	O7N-C7N	-4.32	1.15	1.24
2	B	402	NAP	C2N-N1N	-4.21	1.29	1.35
3	D	401	BKZ	C05-C04	-4.14	1.32	1.52
2	B	402	NAP	P2B-O2X	-4.06	1.39	1.54
2	A	401	NAP	PA-O2A	-4.05	1.36	1.55
3	C	401	BKZ	C05-C04	-3.91	1.33	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	402	NAP	PN-O1N	-3.86	1.37	1.50
3	B	401	BKZ	C05-C04	-3.86	1.33	1.52
2	A	401	NAP	PN-O1N	-3.83	1.37	1.50
2	D	402	NAP	P2B-O3X	-3.74	1.40	1.54
2	C	402	NAP	P2B-O2X	-3.72	1.40	1.54
3	B	401	BKZ	C11-C09	-3.71	1.31	1.38
2	B	402	NAP	PA-O2A	-3.67	1.38	1.55
2	A	401	NAP	PA-O1A	-3.60	1.38	1.50
2	C	402	NAP	PN-O1N	-3.58	1.38	1.50
2	A	401	NAP	P2B-O3X	-3.51	1.41	1.54
3	C	401	BKZ	C12-C11	-3.49	1.32	1.38
2	D	402	NAP	PN-O2N	-3.49	1.38	1.55
2	C	402	NAP	C4A-N3A	-3.43	1.30	1.35
2	A	401	NAP	C2N-N1N	-3.40	1.30	1.35
2	D	402	NAP	PA-O2A	-3.40	1.39	1.55
2	D	402	NAP	P2B-O2X	-3.36	1.41	1.54
2	C	402	NAP	PN-O2N	-3.31	1.39	1.55
3	D	401	BKZ	C11-C09	-3.30	1.32	1.38
2	A	401	NAP	P2B-O1X	-3.25	1.40	1.50
2	C	402	NAP	PA-O2A	-3.21	1.40	1.55
3	B	401	BKZ	C12-C11	-3.19	1.33	1.38
2	C	402	NAP	PA-O1A	-3.15	1.39	1.50
2	A	401	NAP	PN-O2N	-3.15	1.40	1.55
2	A	401	NAP	C4A-N3A	-3.12	1.31	1.35
2	D	402	NAP	PA-O1A	-3.10	1.39	1.50
2	A	401	NAP	P2B-O2X	-3.06	1.43	1.54
2	B	402	NAP	C5A-N7A	-3.05	1.28	1.39
2	D	402	NAP	C4A-N3A	-3.00	1.31	1.35
3	C	401	BKZ	C11-C09	-2.98	1.33	1.38
2	B	402	NAP	PN-O2N	-2.90	1.41	1.55
2	C	402	NAP	C5A-N7A	-2.81	1.29	1.39
2	D	402	NAP	PN-O1N	-2.80	1.41	1.50
2	B	402	NAP	P2B-O1X	-2.75	1.41	1.50
2	A	401	NAP	C5A-N7A	-2.70	1.29	1.39
2	D	402	NAP	O7N-C7N	-2.69	1.19	1.24
2	D	402	NAP	P2B-O1X	-2.67	1.41	1.50
3	C	401	BKZ	C12-C06	-2.64	1.33	1.38
2	D	402	NAP	O4D-C4D	-2.62	1.39	1.45
2	A	401	NAP	O4B-C4B	-2.60	1.39	1.45
3	B	401	BKZ	C08-C07	-2.60	1.34	1.38
3	B	401	BKZ	C12-C06	-2.58	1.33	1.38
2	B	402	NAP	C4A-N3A	-2.57	1.32	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	402	NAP	C5A-N7A	-2.53	1.30	1.39
2	B	402	NAP	O4D-C4D	-2.48	1.39	1.45
2	B	402	NAP	PA-O1A	-2.47	1.42	1.50
2	D	402	NAP	C2N-N1N	-2.46	1.32	1.35
2	B	402	NAP	O4B-C4B	-2.42	1.39	1.45
3	D	401	BKZ	C12-C11	-2.41	1.34	1.38
2	D	402	NAP	O2D-C2D	-2.32	1.37	1.43
2	B	402	NAP	C2A-N1A	-2.30	1.29	1.33
2	D	402	NAP	O4B-C4B	-2.19	1.40	1.45
2	B	402	NAP	C6N-N1N	-2.17	1.30	1.35
2	C	402	NAP	O4B-C4B	-2.16	1.40	1.45
2	A	401	NAP	O4D-C4D	-2.12	1.40	1.45
2	C	402	NAP	O4D-C4D	-2.09	1.40	1.45
2	C	402	NAP	O7N-C7N	-2.05	1.20	1.24

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	BKZ	C08-C07-C06	-6.54	112.03	121.03
3	B	401	BKZ	C07-C08-C09	4.46	124.77	119.88
3	B	401	BKZ	C12-C11-C09	-4.23	115.24	119.88
3	D	401	BKZ	C08-C07-C06	-3.89	115.67	121.03
2	D	402	NAP	C4A-C5A-N7A	-3.81	105.43	109.40
3	D	401	BKZ	C12-C11-C09	-3.80	115.70	119.88
2	C	402	NAP	C4A-C5A-N7A	-3.46	105.80	109.40
3	B	401	BKZ	C05-C06-C12	-3.41	112.60	121.23
3	D	401	BKZ	C12-C06-C07	3.38	123.47	118.17
2	A	401	NAP	C4A-C5A-N7A	-3.22	106.04	109.40
3	C	401	BKZ	C12-C06-C07	3.15	123.12	118.17
3	B	401	BKZ	C12-C06-C07	3.11	123.06	118.17
2	B	402	NAP	C2A-N1A-C6A	3.05	123.96	118.75
2	B	402	NAP	N3A-C2A-N1A	-3.01	123.97	128.68
2	D	402	NAP	O3X-P2B-O2X	2.85	118.52	107.64
3	D	401	BKZ	C05-C06-C12	-2.81	114.13	121.23
2	D	402	NAP	N3A-C2A-N1A	-2.59	124.63	128.68
2	D	402	NAP	O4D-C1D-C2D	-2.59	103.15	106.93
3	C	401	BKZ	C11-C09-C08	2.56	124.08	119.77
3	C	401	BKZ	C12-C11-C09	-2.53	117.10	119.88
2	D	402	NAP	O4B-C4B-C3B	-2.42	100.33	105.11
2	C	402	NAP	N6A-C6A-N1A	2.41	123.57	118.57
2	B	402	NAP	C4A-C5A-N7A	-2.39	106.91	109.40
2	C	402	NAP	N3A-C2A-N1A	-2.38	124.96	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	402	NAP	N6A-C6A-N1A	2.34	123.43	118.57
3	C	401	BKZ	O10-C09-C11	-2.34	113.36	120.02
3	B	401	BKZ	C11-C12-C06	2.33	124.23	121.03
2	A	401	NAP	C3N-C2N-N1N	2.23	122.61	120.43
3	D	401	BKZ	O10-C09-C11	-2.22	113.69	120.02
2	D	402	NAP	PN-O3-PA	-2.18	125.35	132.83
3	C	401	BKZ	C08-C07-C06	-2.16	118.06	121.03
2	B	402	NAP	O4D-C1D-C2D	-2.11	103.84	106.93
2	D	402	NAP	O4B-C1B-C2B	-2.08	102.98	106.59
3	D	401	BKZ	C11-C09-C08	2.06	123.24	119.77
3	B	401	BKZ	O10-C09-C11	-2.01	114.30	120.02

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	401	BKZ	C01-C02-C04-C05
3	D	401	BKZ	O03-C02-C04-C05
2	D	402	NAP	O4D-C1D-N1N-C6N
2	B	402	NAP	O4D-C1D-N1N-C6N
3	C	401	BKZ	O03-C02-C04-C05
2	C	402	NAP	O4D-C1D-N1N-C2N
2	C	402	NAP	O4D-C1D-N1N-C6N
2	A	401	NAP	O4D-C1D-N1N-C2N
2	A	401	NAP	O4D-C1D-N1N-C6N
3	B	401	BKZ	C01-C02-C04-C05
3	B	401	BKZ	O03-C02-C04-C05
3	C	401	BKZ	C01-C02-C04-C05
2	A	401	NAP	C4B-C5B-O5B-PA
2	D	402	NAP	C4B-C5B-O5B-PA
2	B	402	NAP	C4B-C5B-O5B-PA
2	D	402	NAP	C3B-C4B-C5B-O5B
2	C	402	NAP	C4B-C5B-O5B-PA
2	B	402	NAP	O4B-C4B-C5B-O5B
2	A	401	NAP	O4B-C4B-C5B-O5B
2	D	402	NAP	O4B-C4B-C5B-O5B
2	C	402	NAP	O4B-C4B-C5B-O5B
2	D	402	NAP	PA-O3-PN-O2N
2	A	401	NAP	C3B-C4B-C5B-O5B
2	D	402	NAP	C2B-O2B-P2B-O1X
2	D	402	NAP	C2B-O2B-P2B-O2X
2	D	402	NAP	C2B-O2B-P2B-O3X

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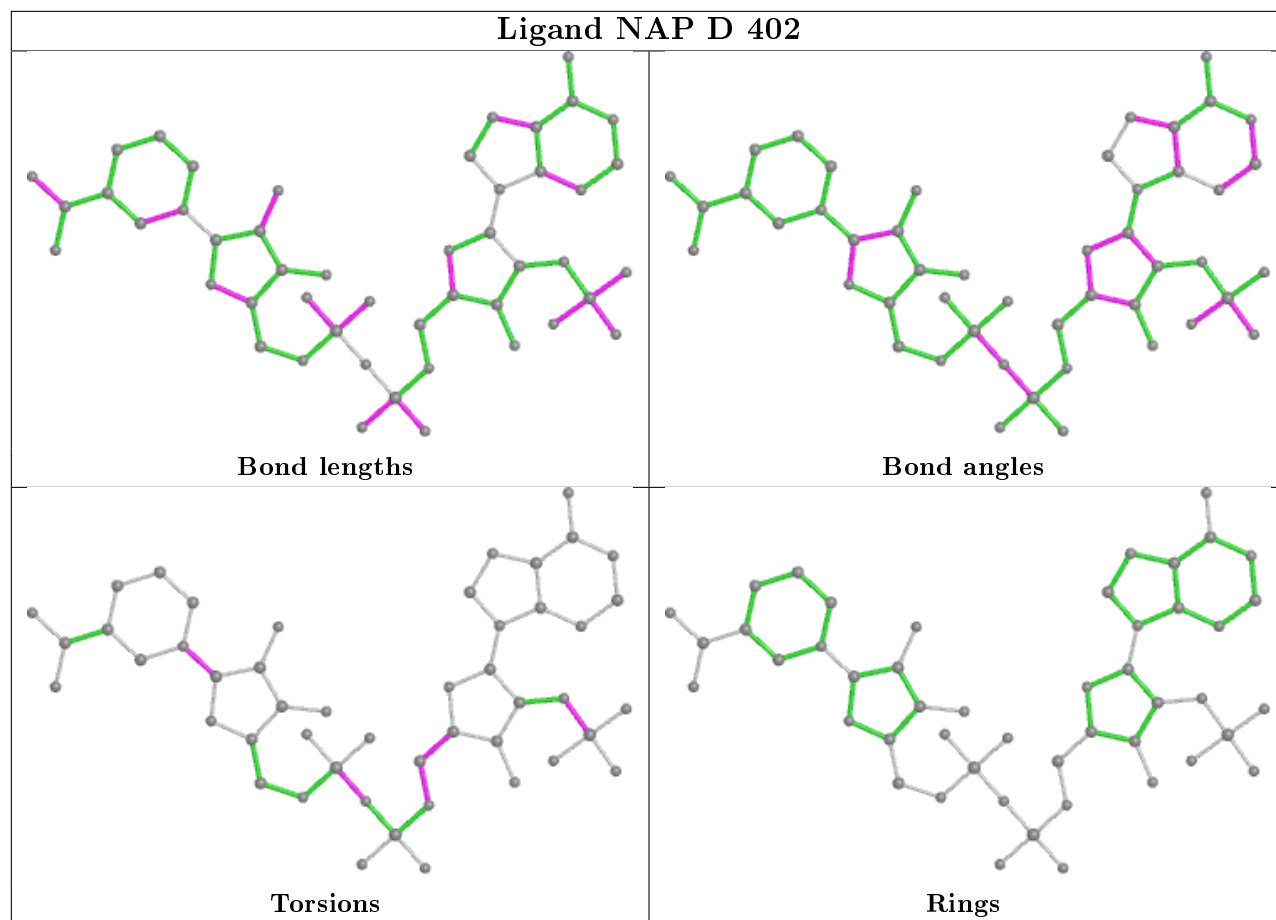
Mol	Chain	Res	Type	Atoms
2	B	402	NAP	C2B-O2B-P2B-O3X
2	C	402	NAP	C2D-C1D-N1N-C2N
2	B	402	NAP	C3B-C4B-C5B-O5B
2	D	402	NAP	PA-O3-PN-O1N

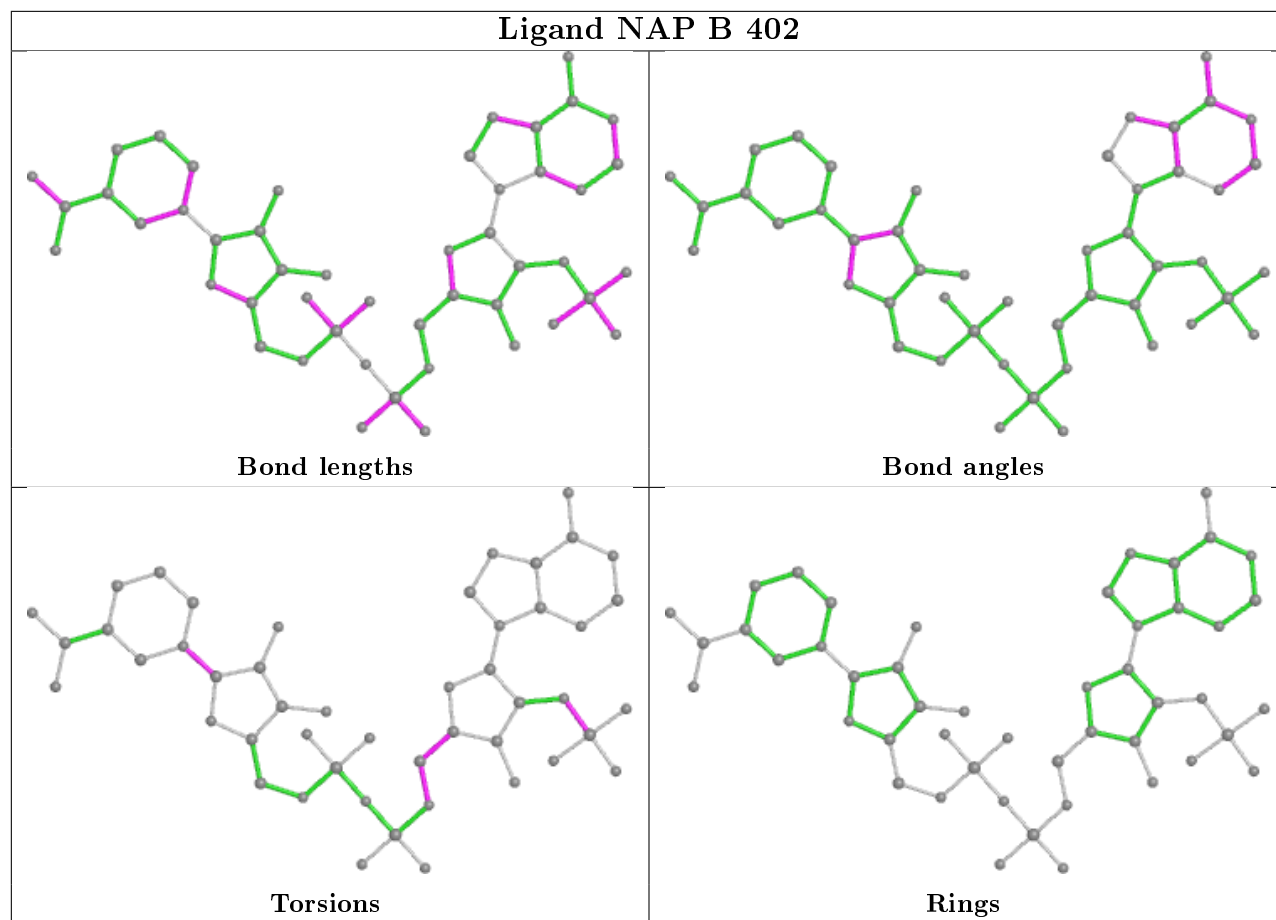
There are no ring outliers.

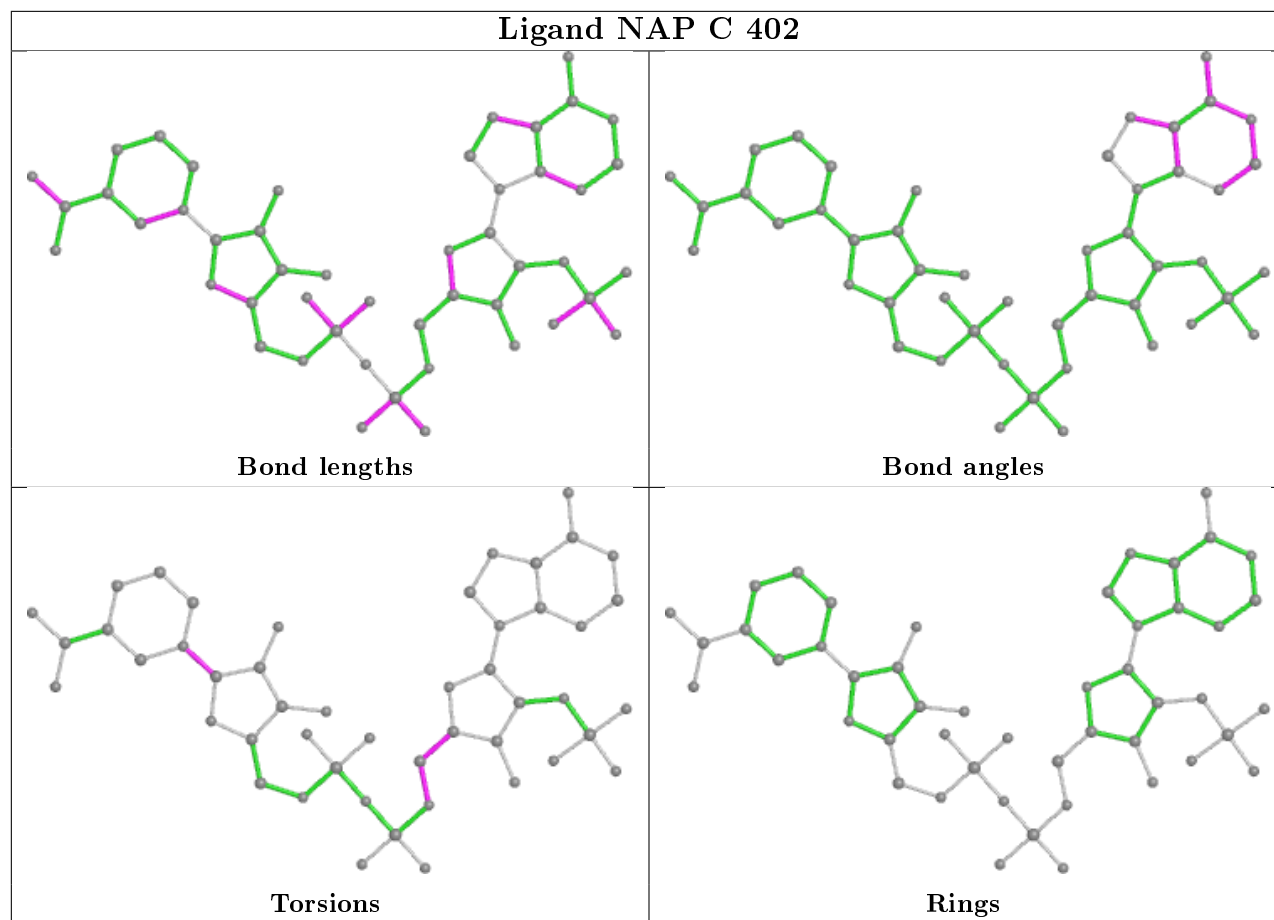
7 monomers are involved in 33 short contacts:

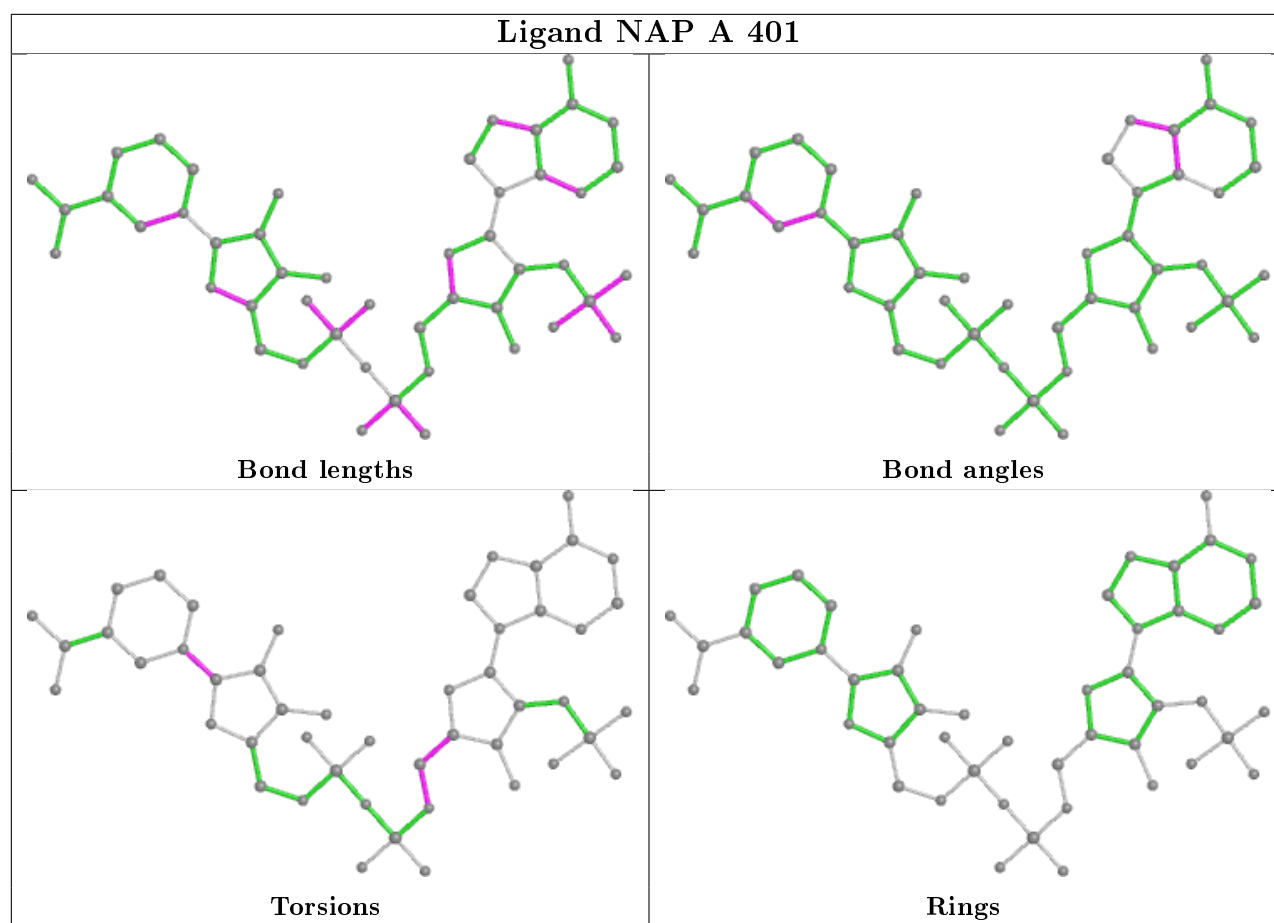
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	401	BKZ	7	0
2	D	402	NAP	4	0
2	B	402	NAP	5	0
3	C	401	BKZ	11	0
2	C	402	NAP	6	0
2	A	401	NAP	2	0
3	B	401	BKZ	9	0

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	341/368 (92%)	0.01	20 (5%)	22 17	14, 29, 55, 64	20 (5%)
1	B	331/368 (89%)	0.01	18 (5%)	25 20	14, 29, 61, 73	25 (7%)
1	C	327/368 (88%)	-0.05	17 (5%)	27 22	17, 31, 62, 82	26 (7%)
1	D	330/368 (89%)	-0.02	12 (3%)	42 37	17, 33, 54, 68	26 (7%)
All	All	1329/1472 (90%)	-0.01	67 (5%)	28 23	14, 31, 58, 82	97 (7%)

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	96	PRO	5.7
1	D	37	THR	5.0
1	B	71	SER	4.7
1	A	72	TYR	4.4
1	D	38	LEU	4.1
1	B	72	TYR	3.9
1	A	70	LEU	3.8
1	B	35	SER	3.7
1	A	41	PRO	3.4
1	D	35	SER	3.3
1	C	98	PHE	3.3
1	A	306	TYR	3.2
1	A	43	GLY	3.1
1	B	126	HIS	3.1
1	C	9	VAL	3.1
1	C	73	VAL	3.1
1	C	117	THR	2.9
1	C	116	ILE	2.9
1	D	66	ASN	2.9
1	D	45	THR	2.8
1	B	94	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	94	GLY	2.8
1	A	129	ASP	2.8
1	A	45	THR	2.8
1	A	33	THR	2.8
1	C	70	LEU	2.6
1	A	36	ILE	2.6
1	D	33	THR	2.6
1	B	127	ASN	2.6
1	A	40	LEU	2.5
1	A	44	SER	2.5
1	A	309	GLN	2.5
1	D	164	VAL	2.5
1	C	100	PRO	2.5
1	C	72	TYR	2.5
1	B	19	TYR	2.5
1	B	121	SER	2.4
1	C	91	LEU	2.4
1	A	71	SER	2.4
1	B	46	GLY	2.4
1	B	17	ARG	2.3
1	C	95	ASN	2.3
1	B	129	ASP	2.3
1	B	95	ASN	2.3
1	B	130	VAL	2.3
1	B	96	PRO	2.3
1	C	126	HIS	2.3
1	A	130	VAL	2.3
1	A	32	THR	2.3
1	D	74	ASP	2.3
1	A	68	HIS	2.2
1	D	129	ASP	2.2
1	C	36	ILE	2.2
1	A	67	HIS	2.1
1	B	31	LEU	2.1
1	B	40	LEU	2.1
1	B	39	LYS	2.1
1	D	233	PHE	2.1
1	A	164	VAL	2.1
1	C	99	ASN	2.1
1	D	128	THR	2.0
1	C	34	ARG	2.0
1	C	38	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	117	THR	2.0
1	D	310	GLY	2.0
1	A	37	THR	2.0
1	B	117	THR	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 carbohydrates in this entry.

6.4 Ligands [i](#)

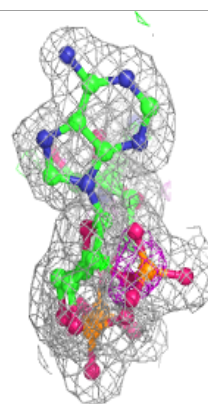
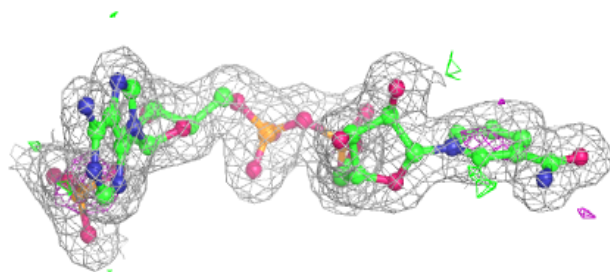
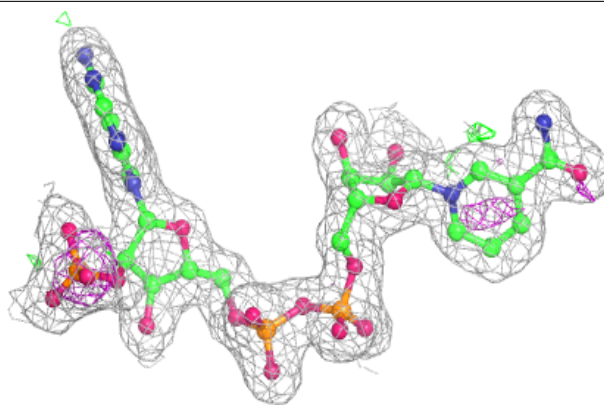
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	BKZ	D	401	12/12	0.85	0.20	37,48,67,67	0
3	BKZ	C	401	12/12	0.86	0.23	39,45,58,61	0
3	BKZ	B	401	12/12	0.91	0.19	23,43,59,60	0
2	NAP	D	402	48/48	0.96	0.10	19,22,25,28	0
2	NAP	C	402	48/48	0.98	0.11	19,22,25,27	0
2	NAP	A	401	48/48	0.98	0.10	17,21,24,27	0
2	NAP	B	402	48/48	0.98	0.11	16,20,23,25	0

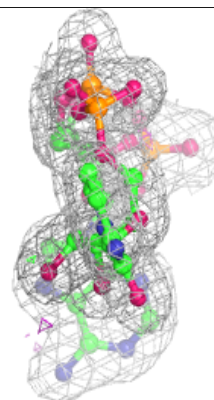
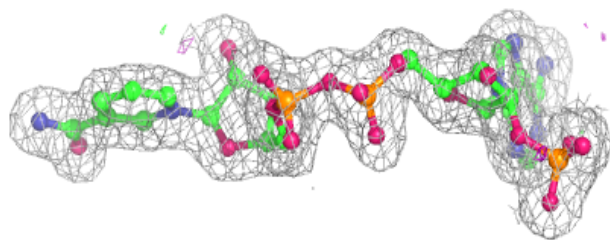
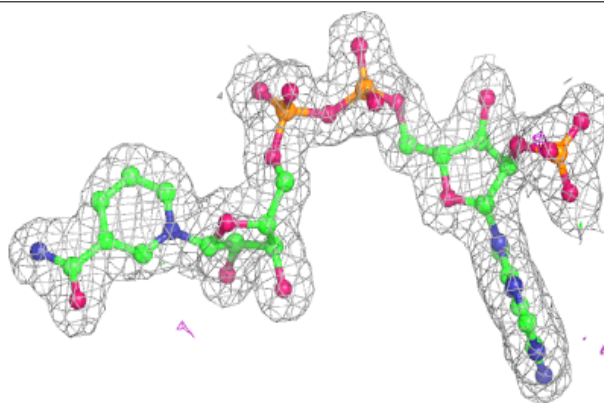
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAP D 402:

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

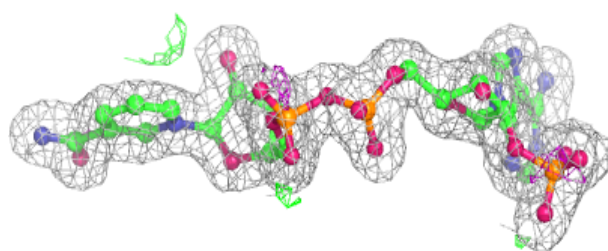
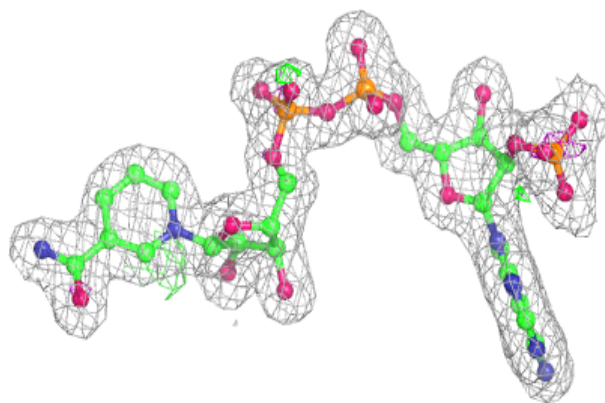
**Electron density around NAP C 402:**

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

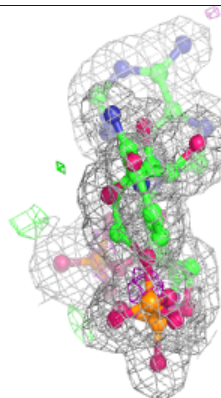
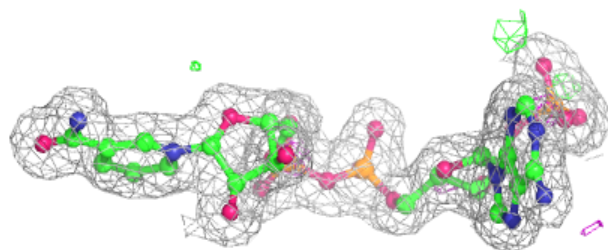
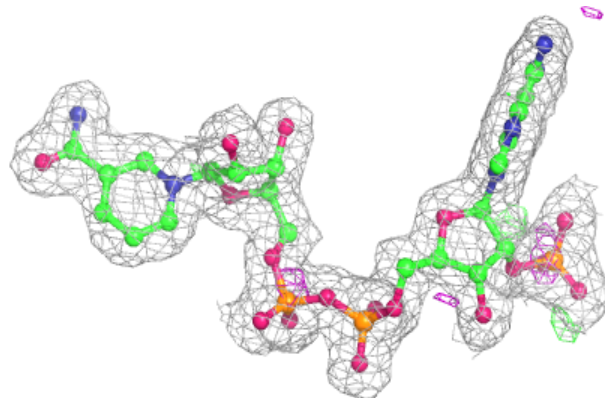


Electron density around NAP A 401:

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

**Electron density around NAP B 402:**

$2mF_o-DF_c$ (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.