



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 12, 2022 – 01:03 PM EDT

PDB ID : 7M1Z
Title : Targeting Enterococcus faecalis HMG-CoA reductase with a novel non-statin inhibitor
Authors : Bose, S.; Steussy, C.N.; Stauffacher, C.V.
Deposited on : 2021-03-15
Resolution : 2.27 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
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)	:	2.29

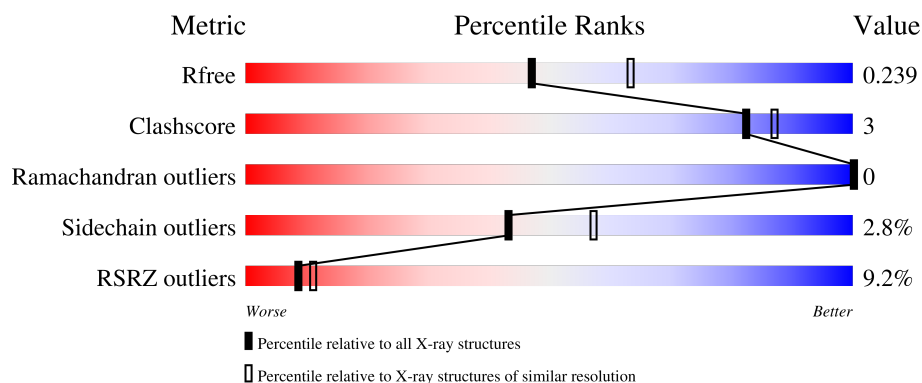
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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	430	<div> <div>2%</div> <div>78%</div> <div>5%</div> <div>17%</div> </div>
1	B	430	<div> <div>12%</div> <div>93%</div> <div>6%</div> <div>.</div> </div>
1	C	430	<div> <div>14%</div> <div>89%</div> <div>9%</div> <div>.</div> </div>
1	D	430	<div> <div>5%</div> <div>75%</div> <div>8%</div> <div>17%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	ACT	A	510	-	-	X	-
5	ACT	A	512	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 25332 atoms, of which 12529 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 Hydroxymethylglutaryl-CoA reductase, degradative.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	358	Total	C	H	N	O	S	2	28	0
			5714	1786	2876	483	553	16			
1	B	425	Total	C	H	N	O	S	10	4	0
			6582	2042	3322	574	629	15			
1	C	422	Total	C	H	N	O	S	2	4	0
			6554	2036	3307	569	627	15			
1	D	357	Total	C	H	N	O	S	3	13	0
			5562	1743	2791	472	541	15			

There are 28 discrepancies between the modelled and reference sequences:

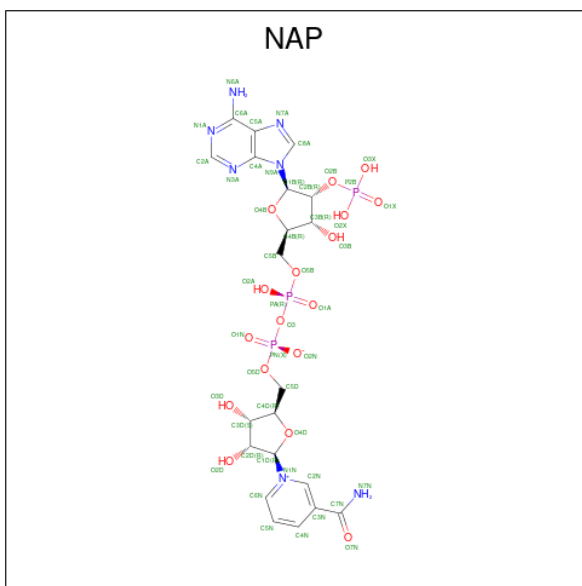
Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP A0A6M1FI83
A	-5	VAL	-	expression tag	UNP A0A6M1FI83
A	-4	PRO	-	expression tag	UNP A0A6M1FI83
A	-3	ARG	-	expression tag	UNP A0A6M1FI83
A	-2	GLY	-	expression tag	UNP A0A6M1FI83
A	-1	SER	-	expression tag	UNP A0A6M1FI83
A	0	HIS	-	expression tag	UNP A0A6M1FI83
B	-6	LEU	-	expression tag	UNP A0A6M1FI83
B	-5	VAL	-	expression tag	UNP A0A6M1FI83
B	-4	PRO	-	expression tag	UNP A0A6M1FI83
B	-3	ARG	-	expression tag	UNP A0A6M1FI83
B	-2	GLY	-	expression tag	UNP A0A6M1FI83
B	-1	SER	-	expression tag	UNP A0A6M1FI83
B	0	HIS	-	expression tag	UNP A0A6M1FI83
C	-6	LEU	-	expression tag	UNP A0A6M1FI83
C	-5	VAL	-	expression tag	UNP A0A6M1FI83
C	-4	PRO	-	expression tag	UNP A0A6M1FI83
C	-3	ARG	-	expression tag	UNP A0A6M1FI83
C	-2	GLY	-	expression tag	UNP A0A6M1FI83
C	-1	SER	-	expression tag	UNP A0A6M1FI83
C	0	HIS	-	expression tag	UNP A0A6M1FI83

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	LEU	-	expression tag	UNP A0A6M1FI83
D	-5	VAL	-	expression tag	UNP A0A6M1FI83
D	-4	PRO	-	expression tag	UNP A0A6M1FI83
D	-3	ARG	-	expression tag	UNP A0A6M1FI83
D	-2	GLY	-	expression tag	UNP A0A6M1FI83
D	-1	SER	-	expression tag	UNP A0A6M1FI83
D	0	HIS	-	expression tag	UNP A0A6M1FI83

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



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 73	C 21	H 25	N 7	O 17	P 3	0	0
2	B	1	Total 73	C 21	H 25	N 7	O 17	P 3	0	0
2	C	1	Total 73	C 21	H 25	N 7	O 17	P 3	0	0
2	D	1	Total 73	C 21	H 25	N 7	O 17	P 3	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	C	1	Total	C	H	O	0	0
			14	3	8	3		
3	C	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

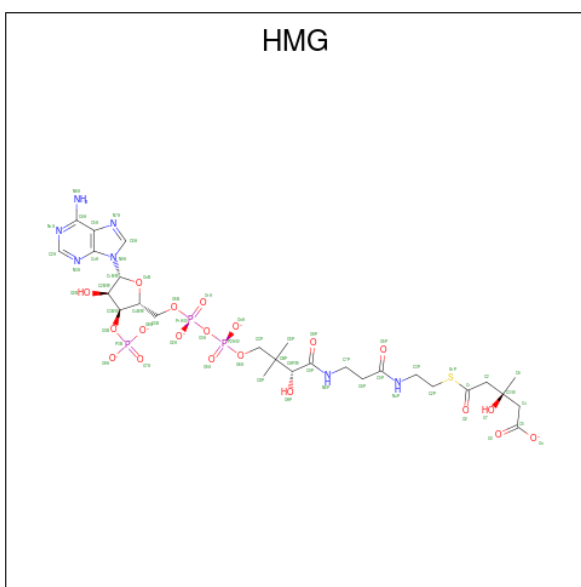
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Ca	0	0
			2	2		
4	B	1	Total	Ca	0	0
			1	1		
4	C	2	Total	Ca	0	0
			2	2		
4	D	2	Total	Ca	0	0
			2	2		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



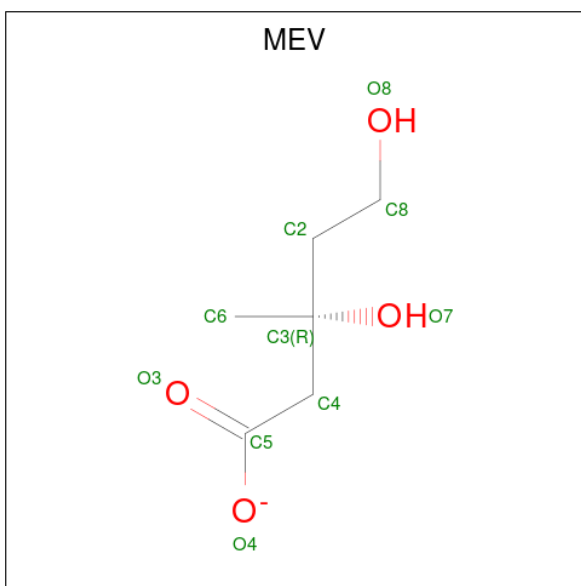
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			7	2	3	2		
5	A	1	Total	C	H	O	0	0
			7	2	3	2		
5	A	1	Total	C	H	O	0	0
			7	2	3	2		
5	A	1	Total	C	H	O	0	0
			7	2	3	2		
5	A	1	Total	C	H	O	0	0
			7	2	3	2		
5	B	1	Total	C	H	O	0	0
			7	2	3	2		
5	C	1	Total	C	H	O	0	0
			7	2	3	2		
5	C	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 6 is 3-HYDROXY-3-METHYLGLUTARYL-COENZYME A (three-letter code: HMG) (formula: $C_{27}H_{39}N_7O_{20}P_3S$).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	H	N	O	P	S		
6	B	1	97	27	39	7	20	3	1	0	0

- Molecule 7 is (R)-MEVALONATE (three-letter code: MEV) (formula: $C_6H_{11}O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
7	C	1	21	6	11	4	0	0

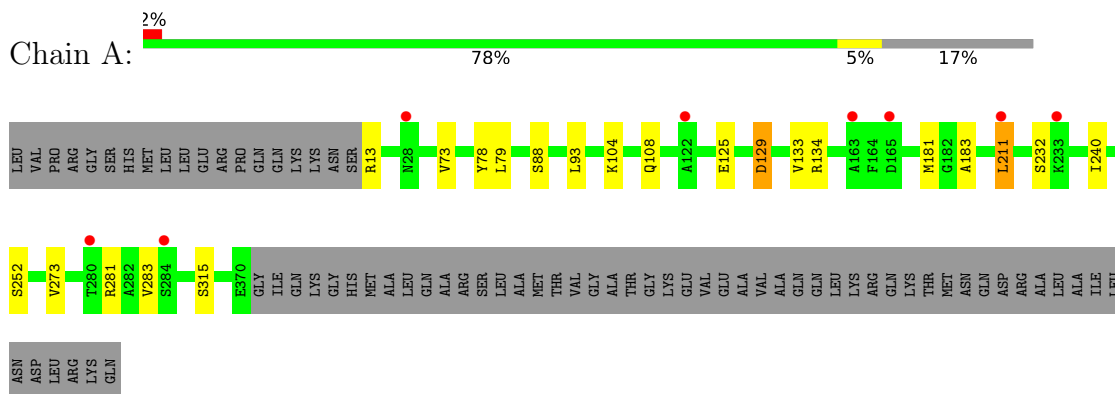
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	111	Total 112	O 112	0	1
8	B	103	Total 103	O 103	0	0
8	C	68	Total 68	O 68	0	0
8	D	58	Total 59	O 59	0	1

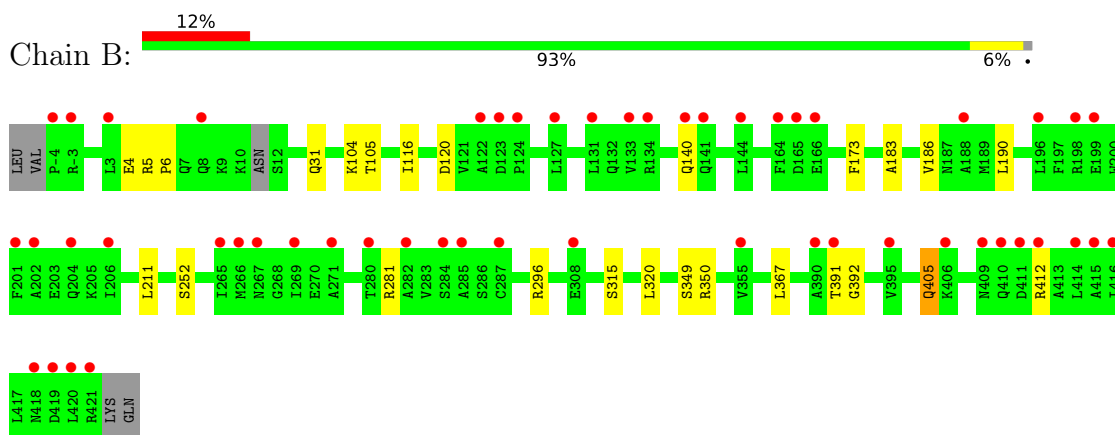
3 Residue-property plots [i](#)

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.

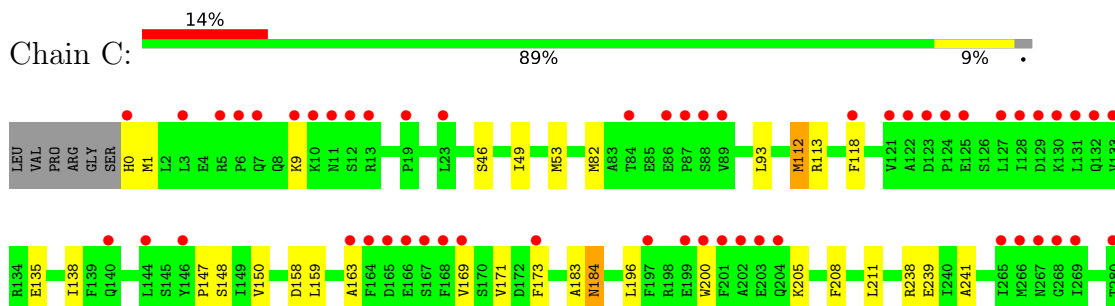
- Molecule 1: Hydroxymethylglutaryl-CoA reductase, degradative

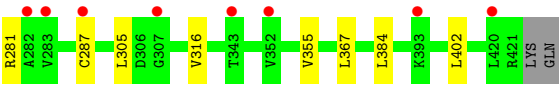


- Molecule 1: Hydroxymethylglutaryl-CoA reductase, degradative

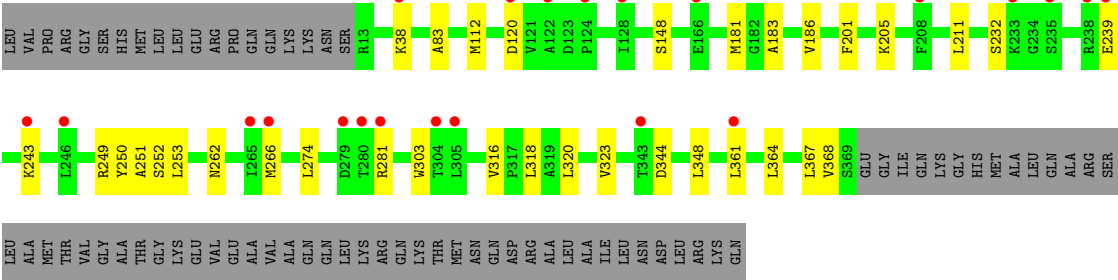
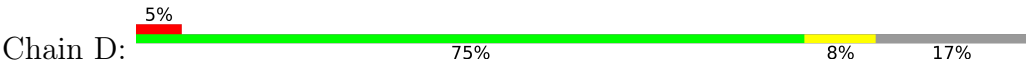


- Molecule 1: Hydroxymethylglutaryl-CoA reductase, degradative





● Molecule 1: Hydroxymethylglutaryl-CoA reductase, degradative



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	241.29Å 62.56Å 171.93Å 90.00° 133.49° 90.00°	Depositor
Resolution (Å)	39.54 – 2.27 39.53 – 2.27	Depositor EDS
% Data completeness (in resolution range)	88.1 (39.54-2.27) 88.1 (39.53-2.27)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 2.27Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.196 , 0.239 0.196 , 0.239	Depositor DCC
R_{free} test set	3840 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	38.1	Xtriage
Anisotropy	0.957	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for h+2*k,-h-l 0.007 for h,-k,-h-l 0.011 for -h-2*k,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	25332	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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: GOL, ACT, HMG, CA, MEV, 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	0.33	0/2993	0.52	0/4047
1	B	0.37	0/3318	0.55	0/4478
1	C	0.35	0/3296	0.54	0/4454
1	D	0.40	0/2848	0.54	0/3856
All	All	0.36	0/12455	0.54	0/16835

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	2838	2876	2745	13	0
1	B	3260	3322	3302	12	0
1	C	3247	3307	3302	20	0
1	D	2771	2791	2745	18	0
2	A	48	25	25	0	0
2	B	48	25	25	0	0
2	C	48	25	25	0	0
2	D	48	25	25	1	0
3	A	18	24	24	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	12	16	16	3	0
3	C	12	16	16	0	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	24	18	18	4	0
5	B	4	3	3	0	0
5	C	8	6	6	0	0
6	B	58	39	39	3	0
7	C	10	11	11	0	0
8	A	112	0	0	0	0
8	B	103	0	0	1	0
8	C	68	0	0	0	0
8	D	59	0	0	1	0
All	All	12803	12529	12327	63	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 3.

All (63) 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)
6:B:501:HMG:O4A	3:B:504:GOL:H11	1.70	0.92
6:B:501:HMG:O1A	3:B:504:GOL:H12	1.76	0.85
1:D:183:ALA:HA	1:D:211:LEU:HD13	1.69	0.73
1:B:116:ILE:HG13	1:B:190:LEU:HD12	1.74	0.68
1:C:241:ALA:HB1	1:C:305[B]:LEU:HD21	1.75	0.67
1:A:104:LYS:HE3	3:A:503:GOL:H31	1.75	0.66
1:C:384:LEU:HD23	1:C:402[B]:LEU:HD21	1.79	0.64
1:D:251:ALA:HB2	8:D:605:HOH:O	1.98	0.62
1:C:183:ALA:HA	1:C:211:LEU:HD13	1.82	0.61
1:D:249:ARG:O	1:D:253:LEU:HD12	2.02	0.59
1:C:208:PHE:HB2	1:D:367:LEU:HD11	1.85	0.58
1:A:183:ALA:HA	1:A:211:LEU:HD13	1.86	0.58
1:B:412:ARG:HD2	8:B:602:HOH:O	2.04	0.57
1:A:232:SER:HB2	1:A:240:ILE:HD12	1.88	0.56
1:C:163:ALA:HA	1:C:169:VAL:HG23	1.87	0.56
1:D:303:TRP:CH2	1:D:361:LEU:HD13	2.42	0.55
1:D:239:GLU:O	1:D:243:LYS:HG3	2.07	0.54
1:C:158:ASP:OD1	1:C:159:LEU:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:183:ALA:HA	1:B:211:LEU:HD22	1.91	0.53
1:C:171:VAL:HG12	1:C:173:PHE:CE1	2.44	0.53
1:D:83:ALA:HB3	1:D:274:LEU:HD12	1.89	0.53
5:A:509:ACT:H1	5:A:512:ACT:H1	1.91	0.52
1:D:83:ALA:CB	1:D:274:LEU:HD12	2.40	0.52
1:A:104:LYS:HG3	3:A:503:GOL:H31	1.93	0.51
1:C:196:LEU:HD11	1:C:200:TRP:HE1	1.75	0.51
1:D:320:LEU:HB3	1:D:348:LEU:HD23	1.93	0.51
1:D:250:TYR:HA	1:D:253:LEU:HD13	1.93	0.51
1:B:405:GLN:HE21	1:B:405:GLN:HA	1.77	0.50
1:C:93:LEU:HD13	1:C:355:VAL:HG13	1.92	0.50
1:C:135:GLU:HA	1:C:138:ILE:HD12	1.92	0.50
1:B:104:LYS:NZ	1:C:239:GLU:OE1	2.46	0.49
6:B:501:HMG:O4A	3:B:504:GOL:C1	2.53	0.49
1:C:82:MET:CE	1:C:93:LEU:HD22	2.42	0.49
1:C:287:CYS:SG	1:C:316:VAL:CG2	3.02	0.48
1:C:147:PRO:O	1:C:150:VAL:HG12	2.15	0.47
1:A:73:VAL:O	5:A:510:ACT:H1	2.16	0.46
1:A:93:LEU:C	1:A:93:LEU:HD13	2.35	0.46
1:B:391:THR:HG22	1:B:392:GLY:N	2.30	0.46
1:A:79:LEU:HD11	1:B:31:GLN:HG3	1.98	0.46
1:B:173:PHE:CD1	1:B:190:LEU:HD11	2.51	0.46
1:A:125:GLU:O	1:A:129:ASP:OD1	2.34	0.45
1:A:133:VAL:HG23	1:A:134:ARG:HG3	1.98	0.45
1:A:104:LYS:HE3	3:A:503:GOL:C3	2.43	0.44
1:C:208:PHE:CB	1:D:367:LEU:HD11	2.47	0.43
1:A:273:VAL:HG11	1:A:283:VAL:HG11	2.00	0.43
1:D:316:VAL:HG23	1:D:318:LEU:HD23	1.99	0.43
1:A:108:GLN:HB3	5:A:512:ACT:H2	2.01	0.43
1:A:78:TYR:OH	5:A:510:ACT:H2	2.19	0.42
1:C:112:MET:HE3	1:C:113:ARG:H	1.84	0.42
1:C:184:ASN:HD22	1:C:184:ASN:N	2.17	0.42
1:D:112[A]:MET:CE	1:D:181[A]:MET:O	2.67	0.42
1:B:186:VAL:O	1:B:190:LEU:HD23	2.20	0.42
1:D:323:VAL:HG11	2:D:501:NAP:C5A	2.50	0.42
1:D:120[B]:ASP:OD1	1:D:205:LYS:HE2	2.21	0.41
1:B:105:THR:OG1	1:B:350:ARG:HD2	2.20	0.41
1:C:118:PHE:HB2	1:C:169:VAL:HG12	2.02	0.41
1:C:49:ILE:O	1:C:53:MET:HG3	2.21	0.41
1:D:262:ASN:O	1:D:266:MET:HG2	2.21	0.41
1:D:364:LEU:O	1:D:368:VAL:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:LEU:HD12	1:B:349:SER:HA	2.03	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	382/430 (89%)	368 (96%)	14 (4%)	0	100	100
1	B	425/430 (99%)	411 (97%)	14 (3%)	0	100	100
1	C	424/430 (99%)	407 (96%)	17 (4%)	0	100	100
1	D	368/430 (86%)	354 (96%)	14 (4%)	0	100	100
All	All	1599/1720 (93%)	1540 (96%)	59 (4%)	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	317/350 (91%)	309 (98%)	8 (2%)	47	62
1	B	349/350 (100%)	339 (97%)	10 (3%)	42	56
1	C	347/350 (99%)	337 (97%)	10 (3%)	42	56
1	D	301/350 (86%)	294 (98%)	7 (2%)	50	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1314/1400 (94%)	1279 (97%)	35 (3%)	43 59

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	88	SER
1	A	129	ASP
1	A	181	MET
1	A	211	LEU
1	A	252	SER
1	A	281	ARG
1	A	315	SER
1	B	4	GLU
1	B	5	ARG
1	B	6	PRO
1	B	120	ASP
1	B	140	GLN
1	B	252	SER
1	B	281	ARG
1	B	296	ARG
1	B	315	SER
1	B	405	GLN
1	C	0	HIS
1	C	1	MET
1	C	9	LYS
1	C	46	SER
1	C	112	MET
1	C	148	SER
1	C	184	ASN
1	C	205	LYS
1	C	238	ARG
1	C	281	ARG
1	D	38	LYS
1	D	148	SER
1	D	201	PHE
1	D	232	SER
1	D	252	SER
1	D	281	ARG
1	D	344	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	204	GLN
1	B	405	GLN
1	C	184	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 29 ligands modelled in this entry, 7 are monoatomic - leaving 22 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	GOL	C	503	-	5,5,5	0.85	0	5,5,5	1.01	0
2	NAP	C	502	-	45,52,52	2.73	18 (40%)	56,80,80	2.00	12 (21%)
3	GOL	A	502	-	5,5,5	0.81	0	5,5,5	0.97	0
3	GOL	A	503	-	5,5,5	0.73	0	5,5,5	0.96	0
6	HMG	B	501	-	52,60,60	2.14	14 (26%)	62,90,90	1.34	8 (12%)
5	ACT	A	507	-	3,3,3	1.13	0	3,3,3	1.71	1 (33%)
3	GOL	B	504	-	5,5,5	0.35	0	5,5,5	0.50	0
2	NAP	D	501	-	45,52,52	2.56	17 (37%)	56,80,80	2.23	15 (26%)
2	NAP	A	501	-	45,52,52	2.89	20 (44%)	56,80,80	1.76	13 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ACT	C	507	-	3,3,3	1.08	0	3,3,3	1.56	1 (33%)
3	GOL	A	504	-	5,5,5	0.75	0	5,5,5	1.05	0
5	ACT	A	509	-	3,3,3	1.09	0	3,3,3	1.75	1 (33%)
7	MEV	C	501	-	8,9,9	1.08	0	6,12,12	1.18	0
5	ACT	A	512	-	3,3,3	1.08	0	3,3,3	1.69	1 (33%)
5	ACT	A	508	-	3,3,3	0.98	0	3,3,3	1.62	0
5	ACT	A	511	-	3,3,3	1.17	0	3,3,3	1.61	1 (33%)
5	ACT	A	510	-	3,3,3	1.08	0	3,3,3	1.47	1 (33%)
3	GOL	B	503	-	5,5,5	0.85	0	5,5,5	1.00	0
2	NAP	B	502	-	45,52,52	2.82	19 (42%)	56,80,80	1.89	15 (26%)
5	ACT	B	506	-	3,3,3	1.02	0	3,3,3	1.63	1 (33%)
3	GOL	C	504	-	5,5,5	0.73	0	5,5,5	0.93	0
5	ACT	C	508	-	3,3,3	0.93	0	3,3,3	1.65	1 (33%)

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	GOL	A	503	-	-	4/4/4/4	-
3	GOL	B	503	-	-	0/4/4/4	-
2	NAP	A	501	-	-	12/31/67/67	0/5/5/5
3	GOL	C	503	-	-	2/4/4/4	-
2	NAP	B	502	-	-	13/31/67/67	0/5/5/5
6	HMG	B	501	-	-	15/56/77/77	0/3/3/3
3	GOL	A	504	-	-	0/4/4/4	-
7	MEV	C	501	-	-	3/9/9/9	-
2	NAP	C	502	-	-	10/31/67/67	0/5/5/5
3	GOL	B	504	-	-	0/4/4/4	-
3	GOL	C	504	-	-	4/4/4/4	-
2	NAP	D	501	-	-	12/31/67/67	0/5/5/5
3	GOL	A	502	-	-	2/4/4/4	-

All (88) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NAP	O4D-C1D	9.05	1.53	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	502	NAP	O4D-C1D	8.35	1.52	1.41
2	B	502	NAP	O4D-C1D	8.34	1.52	1.41
6	B	501	HMG	O4B-C1B	7.88	1.52	1.41
2	D	501	NAP	O4D-C1D	7.60	1.51	1.41
2	A	501	NAP	C2N-N1N	7.42	1.44	1.35
2	B	502	NAP	C2N-N1N	7.11	1.43	1.35
2	A	501	NAP	C7N-N7N	6.76	1.45	1.33
2	B	502	NAP	C7N-N7N	6.72	1.45	1.33
2	C	502	NAP	C7N-N7N	6.61	1.45	1.33
2	C	502	NAP	C2N-N1N	6.57	1.43	1.35
2	A	501	NAP	O4B-C1B	6.32	1.49	1.41
2	B	502	NAP	O4B-C1B	6.13	1.49	1.41
2	D	501	NAP	O4B-C1B	6.09	1.49	1.41
2	C	502	NAP	O4B-C1B	5.94	1.49	1.41
2	D	501	NAP	C7N-N7N	5.88	1.44	1.33
6	B	501	HMG	C9P-N8P	5.22	1.45	1.33
6	B	501	HMG	C5P-N4P	5.06	1.44	1.33
2	D	501	NAP	O7N-C7N	-4.73	1.15	1.24
2	D	501	NAP	C2N-N1N	4.32	1.40	1.35
2	A	501	NAP	C6N-N1N	3.87	1.44	1.35
2	C	502	NAP	O7N-C7N	-3.82	1.16	1.24
2	B	502	NAP	C6N-N1N	3.62	1.44	1.35
2	A	501	NAP	O4D-C4D	3.61	1.53	1.45
2	B	502	NAP	O7N-C7N	-3.57	1.17	1.24
2	A	501	NAP	O7N-C7N	-3.53	1.17	1.24
2	B	502	NAP	O4D-C4D	3.52	1.52	1.45
2	C	502	NAP	C6N-N1N	3.52	1.44	1.35
2	D	501	NAP	C4A-N3A	-3.35	1.31	1.35
6	B	501	HMG	P3B-O3B	3.34	1.65	1.59
6	B	501	HMG	C4A-N3A	-3.28	1.31	1.35
6	B	501	HMG	O4B-C4B	3.26	1.52	1.45
6	B	501	HMG	C6A-N6A	3.23	1.45	1.34
2	C	502	NAP	O4D-C4D	3.21	1.52	1.45
2	B	502	NAP	C3N-C7N	3.17	1.55	1.50
2	D	501	NAP	C6N-N1N	3.12	1.43	1.35
2	D	501	NAP	O4D-C4D	3.10	1.51	1.45
2	D	501	NAP	P2B-O2X	-3.08	1.43	1.54
2	B	502	NAP	C4A-N3A	-3.07	1.31	1.35
2	B	502	NAP	C6A-N6A	3.06	1.45	1.34
2	C	502	NAP	C6A-N6A	3.04	1.45	1.34
2	A	501	NAP	C6A-N6A	3.00	1.45	1.34
2	D	501	NAP	C6A-N6A	2.99	1.44	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	NAP	P2B-O2B	2.97	1.64	1.59
2	A	501	NAP	C3N-C7N	2.90	1.54	1.50
2	A	501	NAP	C4A-N3A	-2.87	1.31	1.35
2	A	501	NAP	P2B-O2B	2.86	1.64	1.59
2	B	502	NAP	O3D-C3D	2.85	1.49	1.43
2	D	501	NAP	P2B-O3X	-2.83	1.43	1.54
6	B	501	HMG	O7-C3	-2.82	1.40	1.44
6	B	501	HMG	C2B-C1B	-2.80	1.49	1.53
6	B	501	HMG	C2B-C3B	-2.78	1.46	1.52
2	C	502	NAP	C3N-C7N	2.74	1.54	1.50
2	C	502	NAP	C4A-N3A	-2.72	1.31	1.35
2	C	502	NAP	P2B-O2B	2.67	1.64	1.59
6	B	501	HMG	C1-S1P	2.62	1.82	1.76
2	C	502	NAP	O3D-C3D	2.56	1.49	1.43
2	D	501	NAP	PN-O2N	-2.52	1.43	1.55
2	B	502	NAP	PN-O1N	-2.51	1.42	1.50
2	A	501	NAP	O4B-C4B	2.44	1.50	1.45
2	A	501	NAP	P2B-O2X	-2.39	1.45	1.54
2	A	501	NAP	O3D-C3D	2.35	1.48	1.43
2	B	502	NAP	O3B-C3B	2.35	1.48	1.43
6	B	501	HMG	C5A-N7A	2.34	1.48	1.39
2	D	501	NAP	P2B-O1X	-2.33	1.43	1.50
2	C	502	NAP	O3B-C3B	2.33	1.48	1.43
2	A	501	NAP	O2D-C2D	2.31	1.48	1.43
2	D	501	NAP	PA-O2A	-2.29	1.44	1.55
2	A	501	NAP	P2B-O3X	-2.29	1.46	1.54
2	A	501	NAP	O3B-C3B	2.28	1.48	1.43
2	B	502	NAP	P2B-O2X	-2.26	1.46	1.54
2	C	502	NAP	P2B-O3X	-2.25	1.46	1.54
2	C	502	NAP	P2B-O2X	-2.25	1.46	1.54
2	B	502	NAP	P2B-O3X	-2.23	1.46	1.54
2	D	501	NAP	O4B-C4B	2.21	1.49	1.45
2	C	502	NAP	O2D-C2D	2.21	1.48	1.43
2	C	502	NAP	C5N-C4N	2.20	1.43	1.38
2	A	501	NAP	PN-O1N	-2.17	1.43	1.50
6	B	501	HMG	O9P-C9P	-2.11	1.19	1.23
2	D	501	NAP	PN-O1N	-2.10	1.43	1.50
2	C	502	NAP	PA-O2A	-2.09	1.45	1.55
2	B	502	NAP	O4B-C4B	2.08	1.49	1.45
2	A	501	NAP	PN-O2N	-2.07	1.45	1.55
2	B	502	NAP	O2D-C2D	2.06	1.47	1.43
6	B	501	HMG	C2-C3	-2.06	1.52	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NAP	PA-O2A	-2.04	1.45	1.55
2	D	501	NAP	O2D-C2D	2.03	1.47	1.43
2	B	502	NAP	PA-O2A	-2.02	1.45	1.55

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	NAP	C6N-N1N-C2N	-7.34	115.28	121.97
2	C	502	NAP	C3N-C7N-N7N	6.87	126.00	117.75
2	D	501	NAP	C3N-C7N-N7N	6.78	125.89	117.75
2	B	502	NAP	C3N-C7N-N7N	6.44	125.48	117.75
2	C	502	NAP	C6N-N1N-C2N	-5.45	117.00	121.97
2	C	502	NAP	N3A-C2A-N1A	-5.00	120.86	128.68
2	D	501	NAP	O7N-C7N-C3N	-4.98	113.67	119.63
2	D	501	NAP	N3A-C2A-N1A	-4.95	120.93	128.68
2	A	501	NAP	N3A-C2A-N1A	-4.74	121.27	128.68
2	B	502	NAP	N3A-C2A-N1A	-4.68	121.36	128.68
2	A	501	NAP	C3N-C7N-N7N	4.68	123.36	117.75
2	B	502	NAP	O7N-C7N-N7N	-4.49	116.20	122.58
2	B	502	NAP	C6N-N1N-C2N	-4.34	118.01	121.97
6	B	501	HMG	C2-C1-S1P	4.23	118.86	113.63
2	A	501	NAP	C6N-N1N-C2N	-4.23	118.12	121.97
2	C	502	NAP	O7N-C7N-N7N	-4.18	116.64	122.58
2	D	501	NAP	C2N-C3N-C4N	3.93	122.72	118.26
6	B	501	HMG	N3A-C2A-N1A	-3.82	122.70	128.68
2	D	501	NAP	C1B-N9A-C4A	-3.62	120.28	126.64
2	D	501	NAP	C4A-C5A-N7A	-3.50	105.75	109.40
2	C	502	NAP	C1B-N9A-C4A	-3.40	120.67	126.64
2	A	501	NAP	PN-O3-PA	-3.39	121.19	132.83
2	A	501	NAP	C4A-C5A-N7A	-3.33	105.93	109.40
2	A	501	NAP	O7N-C7N-N7N	-3.30	117.88	122.58
2	C	502	NAP	O2A-PA-O1A	-3.28	96.01	112.24
2	B	502	NAP	C4A-C5A-N7A	-3.15	106.11	109.40
2	A	501	NAP	O4D-C1D-C2D	-3.09	102.41	106.93
2	B	502	NAP	PN-O3-PA	-3.05	122.38	132.83
2	B	502	NAP	C1B-N9A-C4A	-2.99	121.39	126.64
6	B	501	HMG	C4A-C5A-N7A	-2.96	106.31	109.40
2	D	501	NAP	C5N-C6N-N1N	2.90	124.57	120.40
2	C	502	NAP	C4A-C5A-N7A	-2.85	106.43	109.40
2	B	502	NAP	O4D-C1D-C2D	-2.78	102.87	106.93
2	C	502	NAP	C2A-N1A-C6A	2.77	123.49	118.75
6	B	501	HMG	P1A-O3A-P2A	-2.76	123.34	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	NAP	PN-O3-PA	-2.72	123.48	132.83
2	B	502	NAP	O2A-PA-O1A	-2.71	98.82	112.24
6	B	501	HMG	C1B-N9A-C4A	-2.70	121.90	126.64
2	D	501	NAP	O2A-PA-O1A	-2.69	98.93	112.24
6	B	501	HMG	C3B-C2B-C1B	2.68	105.83	99.89
2	A	501	NAP	C1B-N9A-C4A	-2.67	121.96	126.64
6	B	501	HMG	C6P-C7P-N8P	-2.65	106.56	111.90
2	D	501	NAP	C2A-N1A-C6A	2.44	122.94	118.75
2	C	502	NAP	O4B-C1B-C2B	-2.43	102.37	106.59
2	A	501	NAP	O2A-PA-O1A	-2.40	100.37	112.24
2	A	501	NAP	C2N-N1N-C1D	2.39	124.46	119.14
2	B	502	NAP	C2A-N1A-C6A	2.39	122.84	118.75
2	A	501	NAP	C2A-N1A-C6A	2.28	122.65	118.75
5	A	509	ACT	O-C-CH3	-2.28	113.47	122.33
6	B	501	HMG	C2P-C3P-N4P	-2.28	107.63	112.42
2	A	501	NAP	O5B-PA-O1A	2.27	117.92	109.07
2	B	502	NAP	O5B-PA-O1A	2.25	117.86	109.07
2	D	501	NAP	O3X-P2B-O2B	2.22	115.96	105.99
2	D	501	NAP	C5N-C4N-C3N	-2.22	117.72	120.34
2	D	501	NAP	O2N-PN-O1N	-2.22	101.28	112.24
2	C	502	NAP	PN-O3-PA	-2.21	125.23	132.83
5	A	507	ACT	O-C-CH3	-2.20	113.75	122.33
2	D	501	NAP	C3B-C2B-C1B	2.19	107.00	102.89
2	C	502	NAP	O5B-PA-O1A	2.16	117.51	109.07
5	A	512	ACT	O-C-CH3	-2.14	114.01	122.33
5	C	507	ACT	OXT-C-O	2.13	129.92	122.05
5	A	510	ACT	OXT-C-O	2.12	129.86	122.05
2	B	502	NAP	C2N-N1N-C1D	2.12	123.85	119.14
2	A	501	NAP	O2N-PN-O1N	-2.09	101.90	112.24
2	B	502	NAP	O2N-PN-O1N	-2.08	101.96	112.24
2	C	502	NAP	C3N-C2N-N1N	2.07	122.45	120.43
5	C	508	ACT	O-C-CH3	-2.06	114.31	122.33
2	B	502	NAP	O2X-P2B-O2B	2.04	115.15	105.99
2	B	502	NAP	O2X-P2B-O1X	-2.04	102.71	110.68
5	A	511	ACT	O-C-CH3	-2.02	114.46	122.33
5	B	506	ACT	OXT-C-O	2.02	129.48	122.05

There are no chirality outliers.

All (77) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	NAP	C5B-O5B-PA-O1A

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Mol	Chain	Res	Type	Atoms
2	A	501	NAP	PN-O3-PA-O5B
2	A	501	NAP	C4B-C5B-O5B-PA
2	A	501	NAP	O4D-C1D-N1N-C6N
2	A	501	NAP	C2D-C1D-N1N-C6N
2	B	502	NAP	C4B-C5B-O5B-PA
2	B	502	NAP	O4D-C1D-N1N-C6N
2	B	502	NAP	C2D-C1D-N1N-C6N
2	C	502	NAP	C4B-C5B-O5B-PA
2	C	502	NAP	C2D-C1D-N1N-C6N
2	D	501	NAP	C2B-O2B-P2B-O2X
2	D	501	NAP	O4D-C1D-N1N-C6N
2	D	501	NAP	C2D-C1D-N1N-C6N
3	A	503	GOL	O1-C1-C2-C3
3	A	503	GOL	C1-C2-C3-O3
3	A	503	GOL	O2-C2-C3-O3
3	C	504	GOL	O1-C1-C2-C3
6	B	501	HMG	C5B-O5B-P1A-O3A
6	B	501	HMG	O4B-C4B-C5B-O5B
6	B	501	HMG	C2-C1-S1P-C2P
7	C	501	MEV	C3-C2-C8-O8
6	B	501	HMG	C2B-C3B-O3B-P3B
6	B	501	HMG	C3B-C4B-C5B-O5B
2	B	502	NAP	C1B-C2B-O2B-P2B
2	B	502	NAP	C3B-C2B-O2B-P2B
2	D	501	NAP	C3B-C2B-O2B-P2B
3	A	502	GOL	O1-C1-C2-C3
3	C	504	GOL	C1-C2-C3-O3
6	B	501	HMG	C4B-C3B-O3B-P3B
3	A	503	GOL	O1-C1-C2-O2
3	C	504	GOL	O2-C2-C3-O3
2	D	501	NAP	C4B-C5B-O5B-PA
3	C	504	GOL	O1-C1-C2-O2
2	C	502	NAP	C3B-C2B-O2B-P2B
6	B	501	HMG	O2-C1-S1P-C2P
2	C	502	NAP	PN-O3-PA-O5B
2	D	501	NAP	PN-O3-PA-O5B
2	A	501	NAP	C4D-C5D-O5D-PN
2	B	502	NAP	C4D-C5D-O5D-PN
2	D	501	NAP	C4D-C5D-O5D-PN
2	A	501	NAP	C5B-O5B-PA-O3
2	A	501	NAP	C2B-O2B-P2B-O2X
2	B	502	NAP	C5B-O5B-PA-O3

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Mol	Chain	Res	Type	Atoms
2	B	502	NAP	C2B-O2B-P2B-O2X
3	A	502	GOL	O1-C1-C2-O2
3	C	503	GOL	O1-C1-C2-O2
6	B	501	HMG	C3B-O3B-P3B-O8A
2	C	502	NAP	C4D-C5D-O5D-PN
2	A	501	NAP	C5B-O5B-PA-O2A
2	B	502	NAP	C5B-O5B-PA-O2A
6	B	501	HMG	C5B-O5B-P1A-O1A
6	B	501	HMG	C5B-O5B-P1A-O2A
2	D	501	NAP	C1B-C2B-O2B-P2B
6	B	501	HMG	CEP-CBP-CCP-O6A
2	C	502	NAP	O4B-C4B-C5B-O5B
2	D	501	NAP	O4B-C4B-C5B-O5B
6	B	501	HMG	CDP-CBP-CCP-O6A
3	C	503	GOL	O1-C1-C2-C3
2	B	502	NAP	PN-O3-PA-O5B
2	C	502	NAP	C1B-C2B-O2B-P2B
6	B	501	HMG	C1-C2-C3-C4
2	B	502	NAP	O4B-C4B-C5B-O5B
2	A	501	NAP	C2D-C1D-N1N-C2N
2	B	502	NAP	C2B-O2B-P2B-O3X
2	B	502	NAP	C2D-C1D-N1N-C2N
2	C	502	NAP	C2D-C1D-N1N-C2N
2	D	501	NAP	C2D-C1D-N1N-C2N
2	A	501	NAP	O4B-C4B-C5B-O5B
2	A	501	NAP	PN-O3-PA-O1A
2	C	502	NAP	PA-O3-PN-O2N
2	D	501	NAP	PA-O3-PN-O2N
6	B	501	HMG	P2A-O3A-P1A-O2A
7	C	501	MEV	C3-C4-C5-O3
2	C	502	NAP	C5B-O5B-PA-O2A
2	D	501	NAP	C5D-O5D-PN-O1N
7	C	501	MEV	C3-C4-C5-O4
6	B	501	HMG	C1-C2-C3-O7

There are no ring outliers.

7 monomers are involved in 11 short contacts:

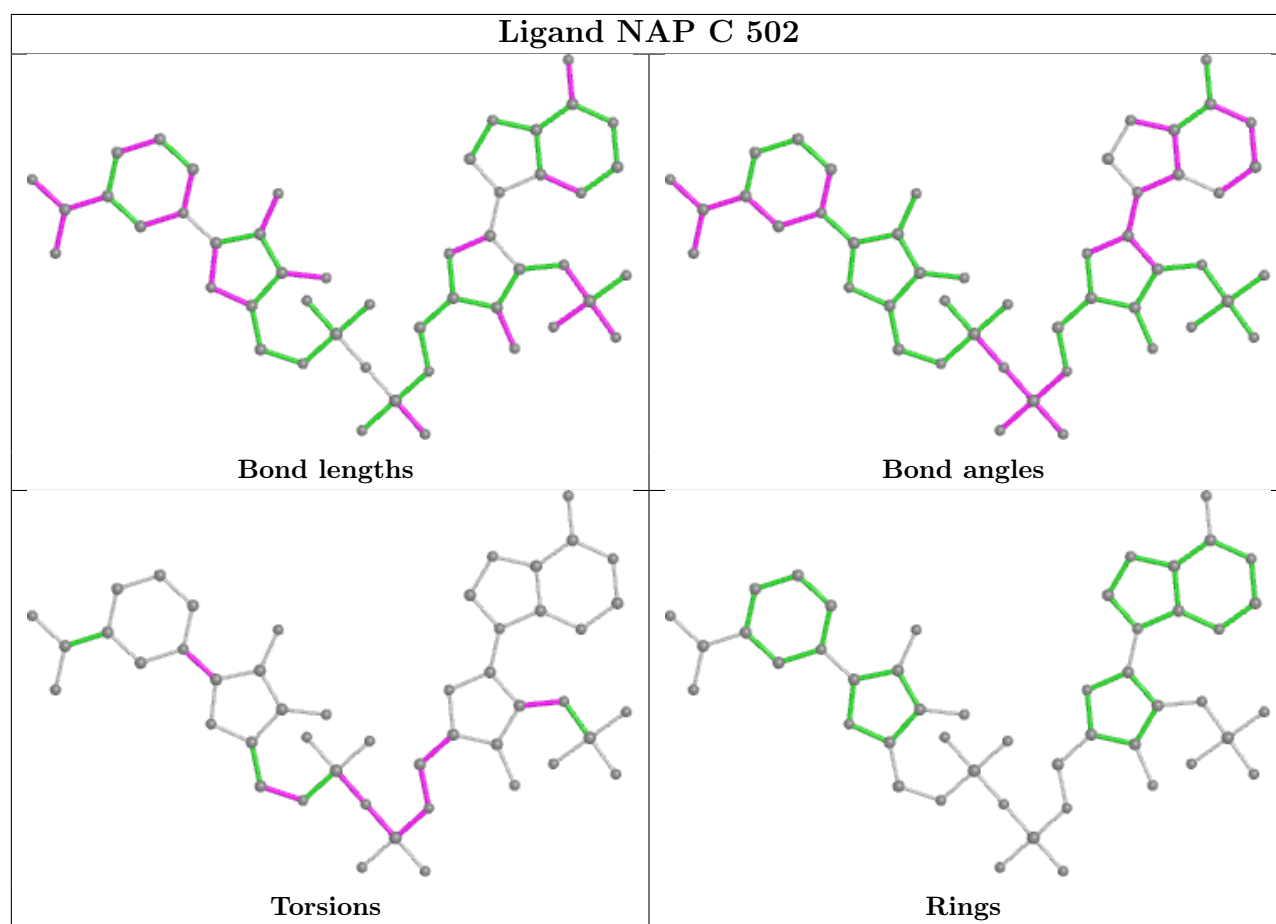
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	GOL	3	0
6	B	501	HMG	3	0
3	B	504	GOL	3	0

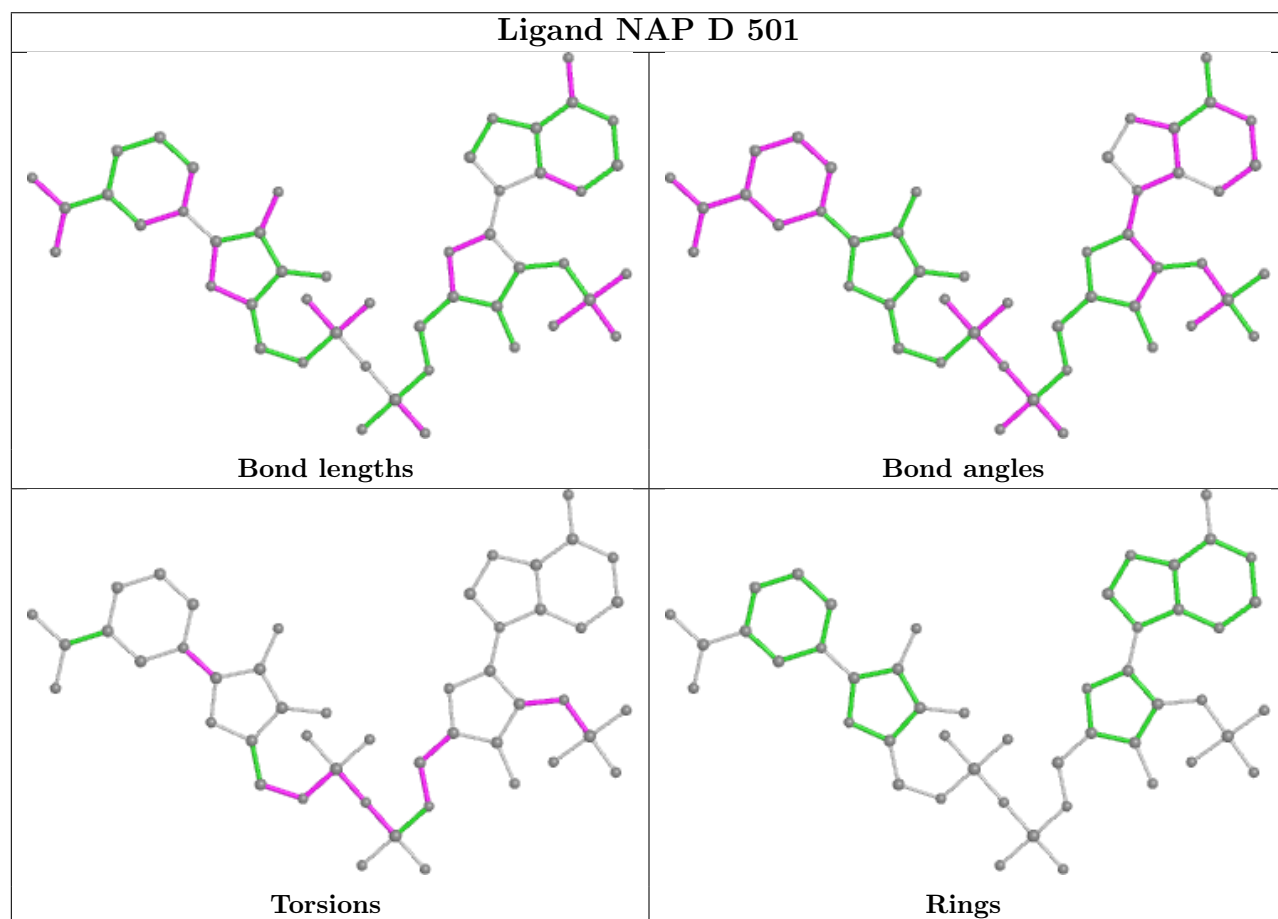
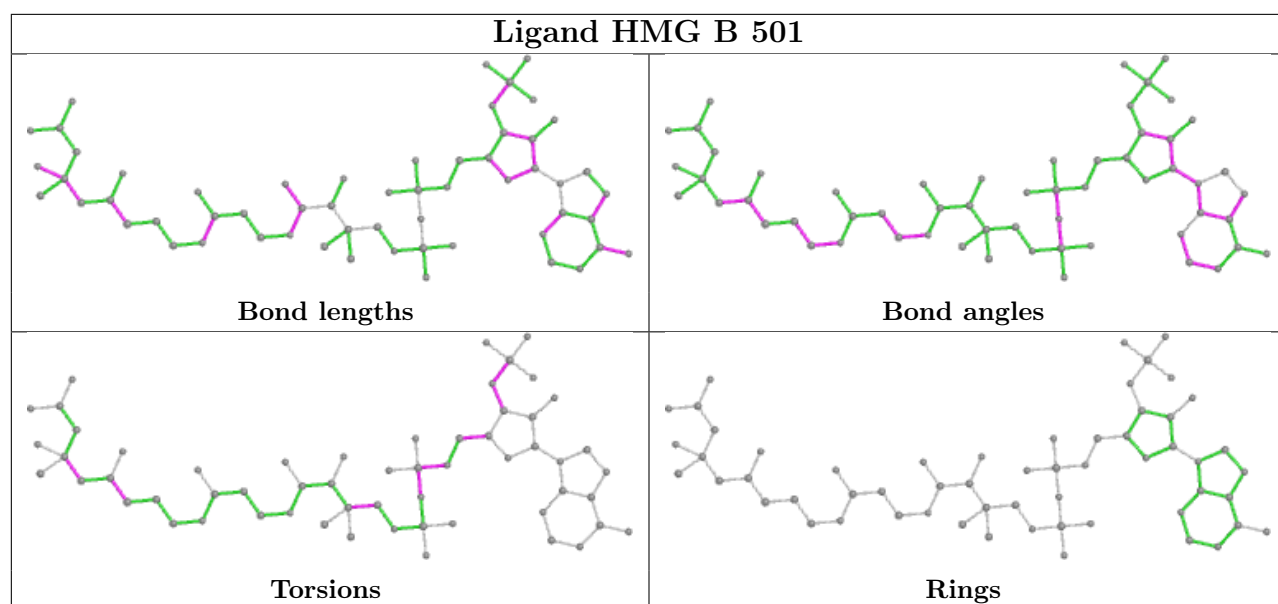
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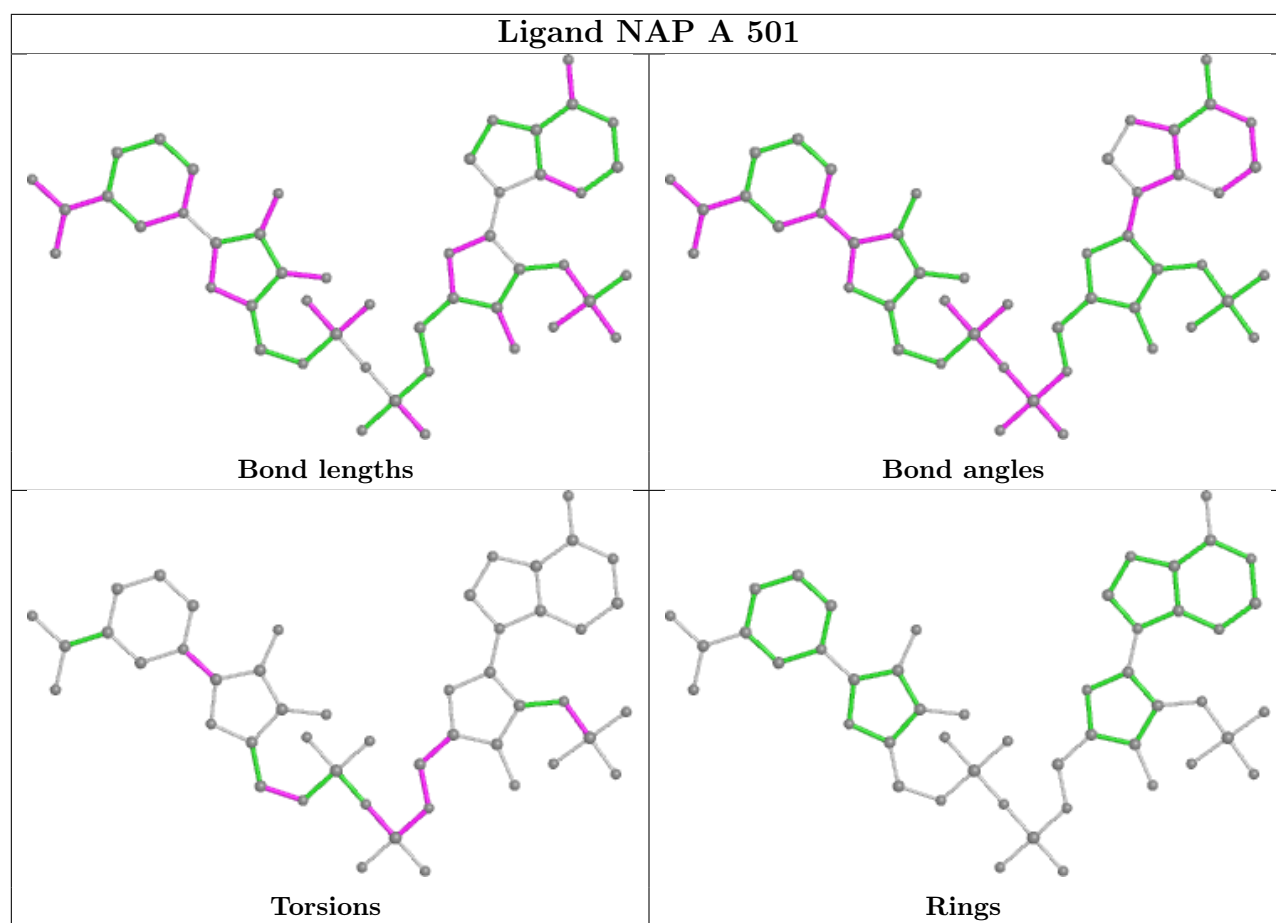
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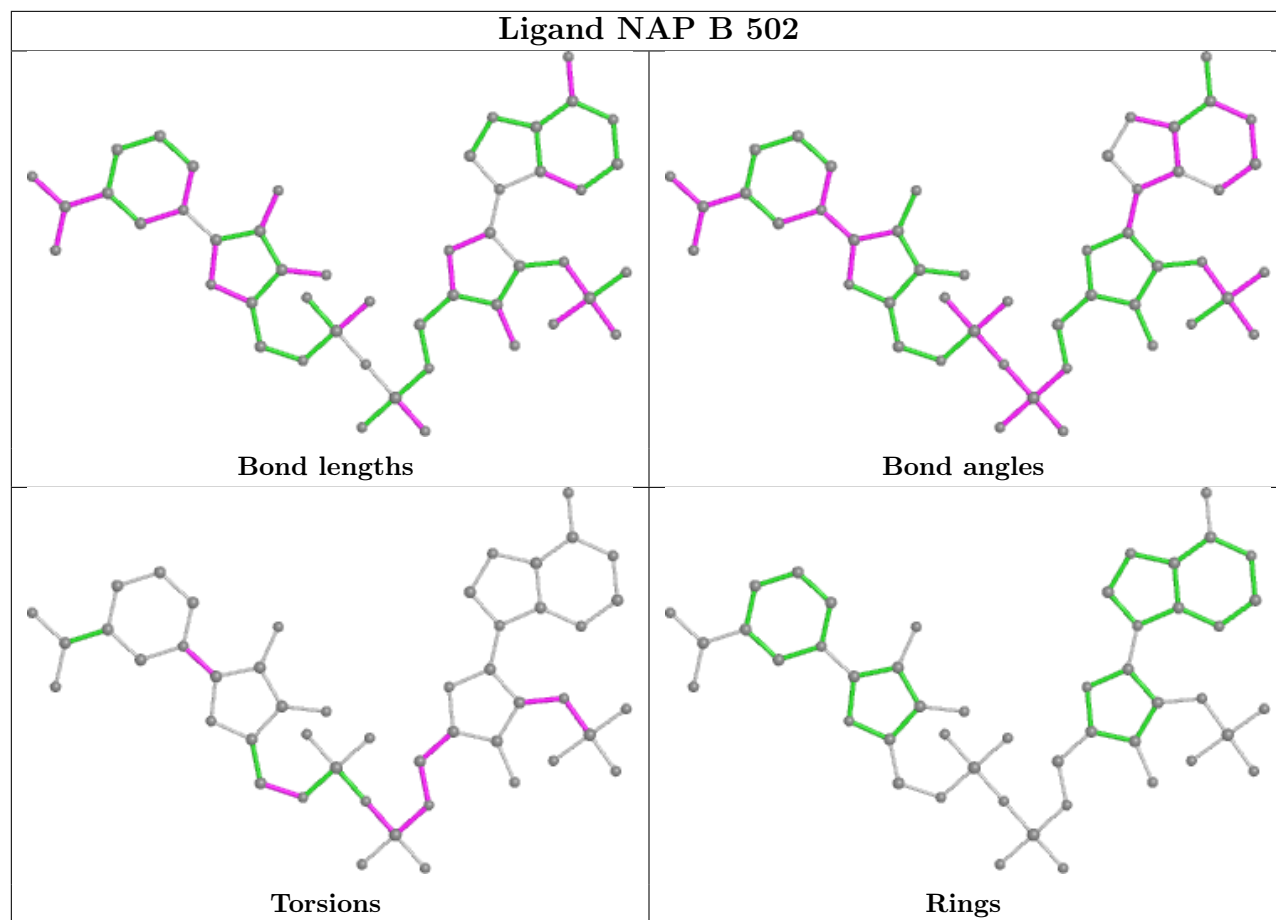
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	501	NAP	1	0
5	A	509	ACT	1	0
5	A	512	ACT	2	0
5	A	510	ACT	2	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	358/430 (83%)	0.21	8 (2%) 62 68	23, 40, 68, 89	12 (3%)
1	B	425/430 (98%)	0.62	52 (12%) 4 5	26, 45, 95, 122	16 (3%)
1	C	422/430 (98%)	0.84	62 (14%) 2 3	38, 59, 112, 135	12 (2%)
1	D	357/430 (83%)	0.50	22 (6%) 20 25	38, 66, 100, 122	7 (1%)
All	All	1562/1720 (90%)	0.56	144 (9%) 9 11	23, 54, 99, 135	47 (3%)

All (144) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	200	TRP	7.9
1	B	166	GLU	7.5
1	C	201	PHE	6.4
1	B	406	LYS	6.1
1	C	118	PHE	5.8
1	C	121	VAL	5.7
1	C	164	PHE	5.6
1	C	128	ILE	5.2
1	B	411	ASP	5.2
1	C	163	ALA	5.2
1	B	3	LEU	5.1
1	B	201	PHE	4.9
1	C	204	GLN	4.8
1	B	122	ALA	4.8
1	B	415	ALA	4.7
1	B	-3	ARG	4.7
1	D	305	LEU	4.7
1	C	131	LEU	4.7
1	C	129	ASP	4.7
1	C	122	ALA	4.7
1	C	168	PHE	4.6

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Mol	Chain	Res	Type	RSRZ
1	B	-4	PRO	4.2
1	B	133	VAL	4.2
1	C	166	GLU	4.2
1	C	169	VAL	4.1
1	C	203	GLU	4.0
1	B	418	ASN	4.0
1	D	243	LYS	3.9
1	C	124	PRO	3.9
1	C	13	ARG	3.8
1	B	414	LEU	3.7
1	C	133	VAL	3.7
1	B	144	LEU	3.6
1	B	199	GLU	3.6
1	C	199	GLU	3.6
1	C	123	ASP	3.5
1	B	416	ILE	3.5
1	C	280	THR	3.5
1	D	280	THR	3.4
1	C	125	GLU	3.4
1	C	6	PRO	3.4
1	D	266	MET	3.3
1	C	89	VAL	3.3
1	B	123	ASP	3.3
1	C	202	ALA	3.3
1	C	197	PHE	3.3
1	A	233	LYS	3.3
1	B	8	GLN	3.2
1	B	202	ALA	3.2
1	B	421	ARG	3.2
1	C	282	ALA	3.2
1	C	11	ASN	3.2
1	C	5	ARG	3.1
1	D	239	GLU	3.1
1	A	165	ASP	3.1
1	A	28[A]	ASN	3.1
1	D	343	THR	3.1
1	B	124	PRO	3.1
1	B	391	THR	3.0
1	C	267	ASN	3.0
1	A	284	SER	2.9
1	C	307	GLY	2.9
1	C	130	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	196	LEU	2.9
1	B	282	ALA	2.9
1	D	304	THR	2.9
1	B	395	VAL	2.9
1	C	3	LEU	2.9
1	B	410	GLN	2.8
1	C	9	LYS	2.8
1	C	127	LEU	2.8
1	C	420	LEU	2.8
1	D	124	PRO	2.8
1	B	164	PHE	2.8
1	C	173	PHE	2.8
1	A	122	ALA	2.8
1	C	10	LYS	2.8
1	B	269	ILE	2.8
1	C	268	GLY	2.7
1	B	419	ASP	2.7
1	D	128	ILE	2.7
1	D	122	ALA	2.7
1	B	127	LEU	2.7
1	C	0	HIS	2.7
1	C	165	ASP	2.7
1	C	266[A]	MET	2.6
1	C	23	LEU	2.6
1	B	204	GLN	2.6
1	C	84	THR	2.6
1	C	7	GLN	2.6
1	C	140	GLN	2.5
1	B	131	LEU	2.5
1	B	285	ALA	2.5
1	C	269	ILE	2.5
1	D	238	ARG	2.5
1	D	361	LEU	2.5
1	A	280	THR	2.5
1	C	144	LEU	2.5
1	D	235	SER	2.5
1	B	308	GLU	2.4
1	C	146	TYR	2.4
1	C	132	GLN	2.4
1	B	266	MET	2.4
1	D	120[A]	ASP	2.4
1	D	166	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	87	PRO	2.4
1	B	165	ASP	2.3
1	B	141	GLN	2.3
1	D	233	LYS	2.3
1	A	163	ALA	2.3
1	B	188	ALA	2.3
1	C	287	CYS	2.3
1	C	19	PRO	2.3
1	D	281	ARG	2.3
1	D	38	LYS	2.3
1	D	208	PHE	2.3
1	B	420	LEU	2.3
1	C	88	SER	2.3
1	B	284	SER	2.3
1	B	412	ARG	2.3
1	C	86	GLU	2.3
1	D	279	ASP	2.2
1	B	198	ARG	2.2
1	B	271	ALA	2.2
1	A	211	LEU	2.2
1	C	265	ILE	2.2
1	B	355	VAL	2.2
1	B	267	ASN	2.2
1	C	283	VAL	2.2
1	B	206	ILE	2.1
1	B	134	ARG	2.1
1	B	280	THR	2.1
1	B	140	GLN	2.1
1	C	352	VAL	2.1
1	B	409	ASN	2.1
1	B	287	CYS	2.1
1	B	390	ALA	2.1
1	B	265	ILE	2.0
1	D	246	LEU	2.0
1	D	265	ILE	2.0
1	C	343	THR	2.0
1	C	393	LYS	2.0
1	C	12	SER	2.0
1	C	167	SER	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 monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

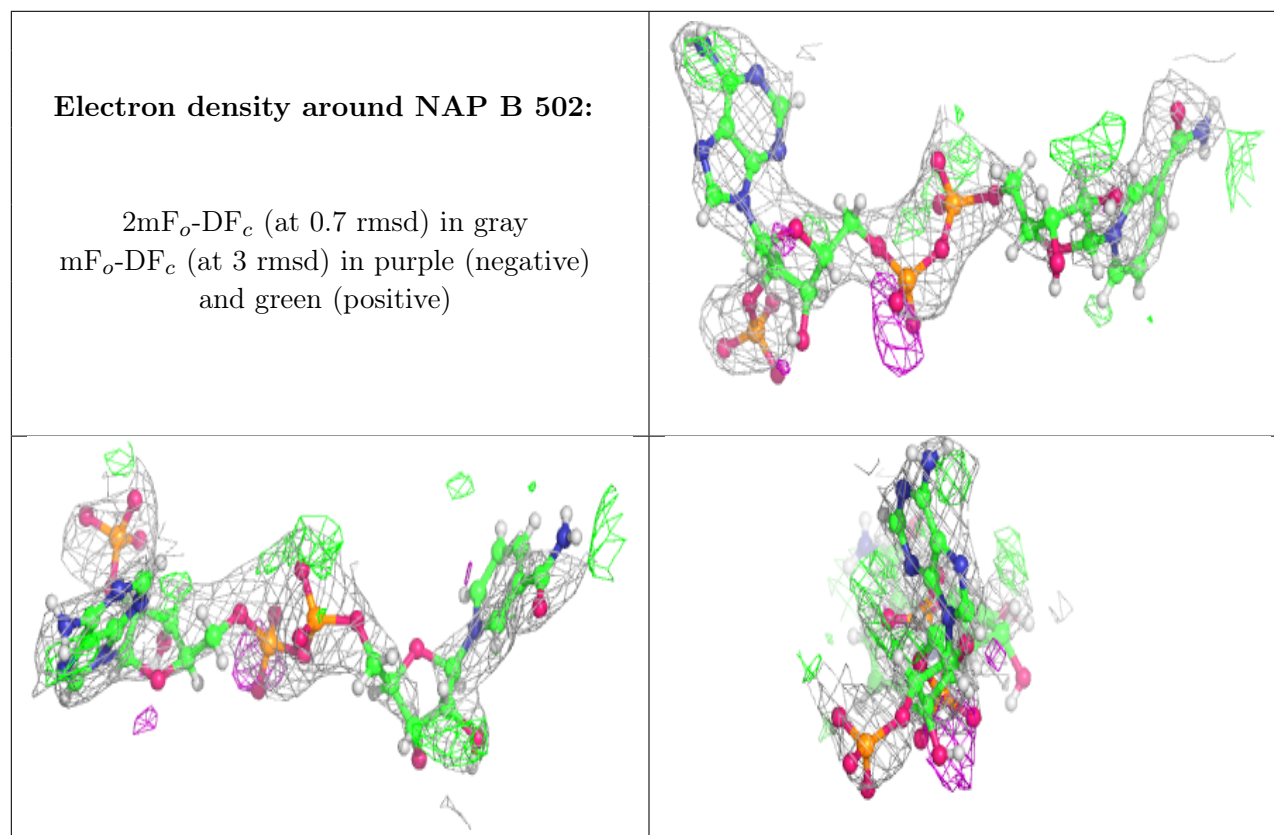
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	C	504	6/6	0.69	0.20	70,85,98,98	0
5	ACT	A	510	4/4	0.69	0.24	48,56,64,64	0
2	NAP	B	502	48/48	0.72	0.32	56,72,92,100	73
2	NAP	C	502	48/48	0.78	0.25	72,88,108,122	73
5	ACT	C	507	4/4	0.79	0.22	52,61,73,73	0
3	GOL	B	504	6/6	0.81	0.24	57,70,92,111	0
5	ACT	A	512	4/4	0.81	0.25	59,71,76,79	0
5	ACT	B	506	4/4	0.81	0.34	44,50,53,53	7
2	NAP	A	501	48/48	0.81	0.32	38,54,72,86	73
4	CA	D	503	1/1	0.82	0.07	89,89,89,89	0
5	ACT	A	507	4/4	0.84	0.24	55,64,86,86	0
5	ACT	A	511	4/4	0.88	0.22	60,67,72,72	0
3	GOL	B	503	6/6	0.88	0.20	71,89,101,107	0
5	ACT	C	508	4/4	0.88	0.64	56,68,81,81	0
3	GOL	A	504	6/6	0.89	0.21	76,91,98,101	0
3	GOL	A	502	6/6	0.90	0.16	60,72,85,85	0
3	GOL	A	503	6/6	0.90	0.30	62,75,87,91	0
5	ACT	A	509	4/4	0.91	0.13	51,57,63,63	0
4	CA	C	506	1/1	0.93	0.10	93,93,93,93	0
3	GOL	C	503	6/6	0.93	0.15	51,62,66,69	14
5	ACT	A	508	4/4	0.94	0.14	55,57,69,69	0
2	NAP	D	501	48/48	0.94	0.18	44,55,69,72	0
6	HMG	B	501	58/58	0.94	0.16	30,42,59,64	0
4	CA	A	505	1/1	0.95	0.12	58,58,58,58	0
4	CA	A	506	1/1	0.95	0.03	54,54,54,54	0
7	MEV	C	501	10/10	0.95	0.17	48,57,66,69	0
4	CA	C	505	1/1	0.97	0.43	103,103,103,103	0

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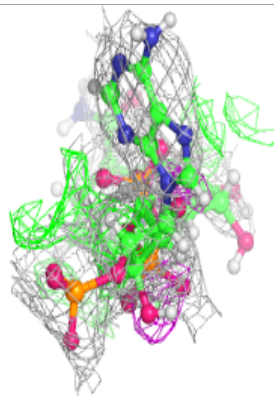
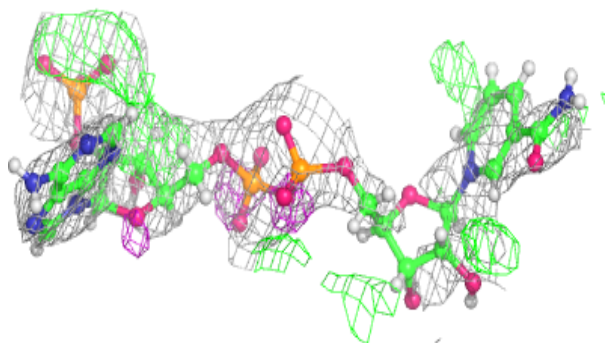
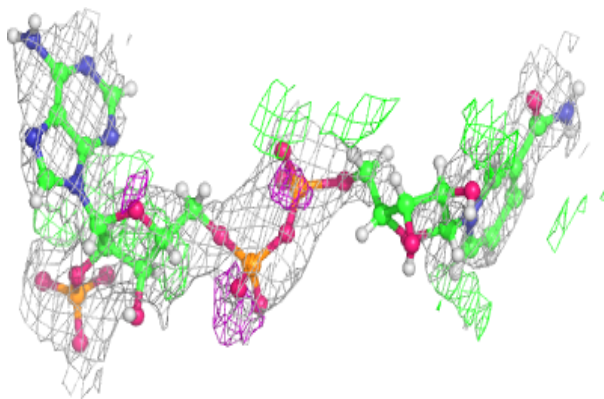
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CA	B	505	1/1	0.97	0.06	76,76,76,76	0
4	CA	D	502	1/1	0.97	0.10	77,77,77,77	0

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.

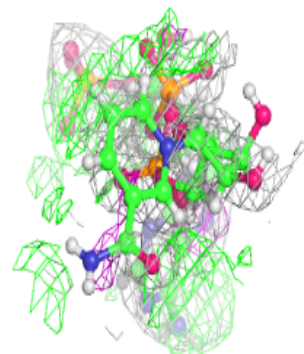
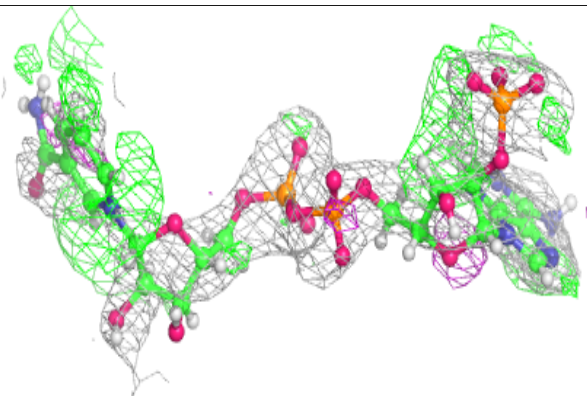
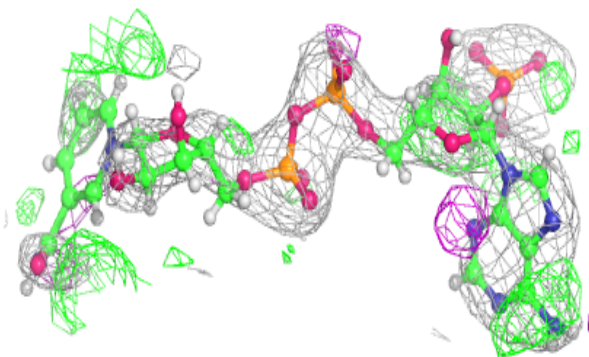


Electron density around NAP C 502:

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

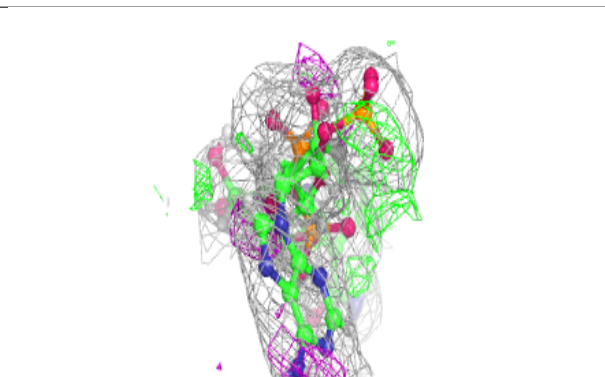
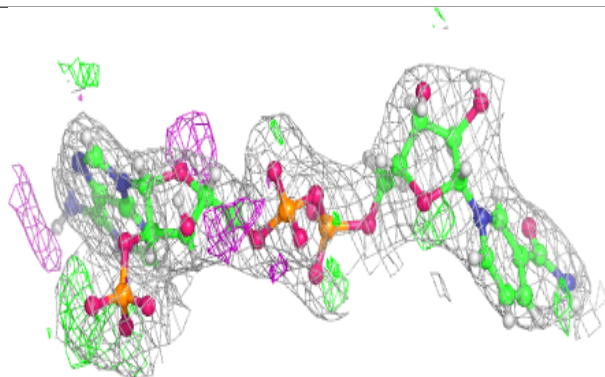
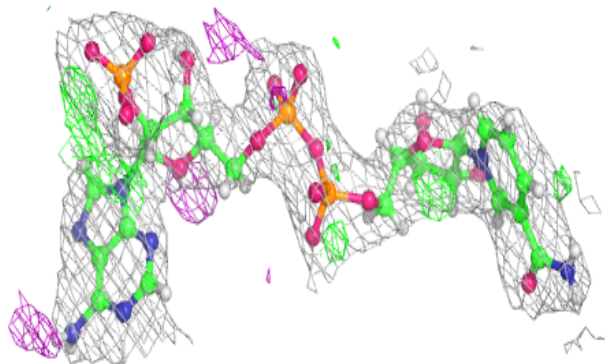
**Electron density around NAP A 501:**

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

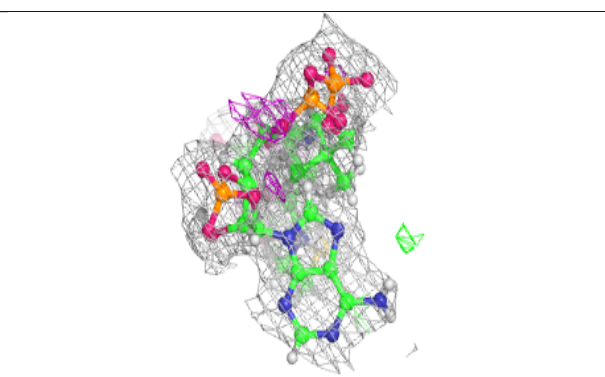
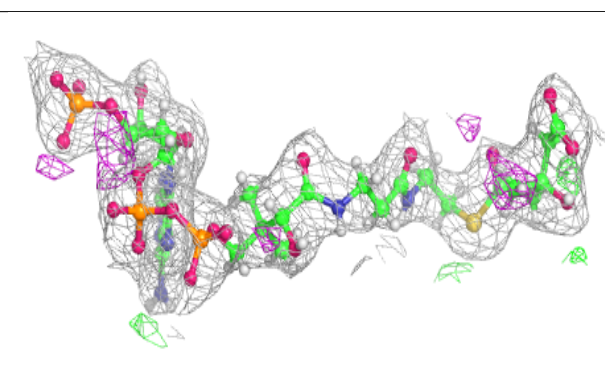
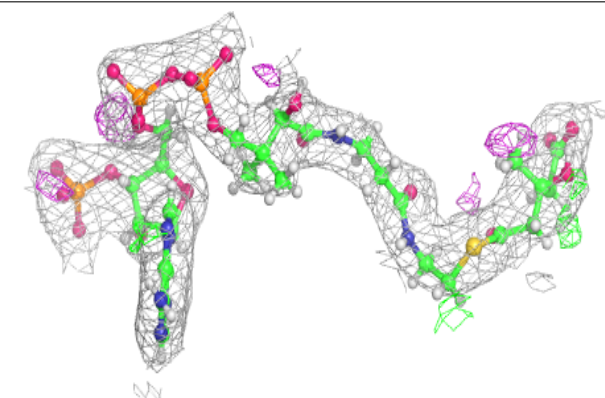


Electron density around NAP D 501:

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

**Electron density around HMG B 501:**

$2mF_o-DF_c$ (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.