



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:49 PM UTC

PDB ID : 6GEX / pdb\_00006gex  
Title : Trypanosoma brucei PTR1 in complex with inhibitor 2h (F246)  
Authors : Pozzi, C.; Landi, G.; Mangani, S.  
Deposited on : 2018-04-27  
Resolution : 1.78 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 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

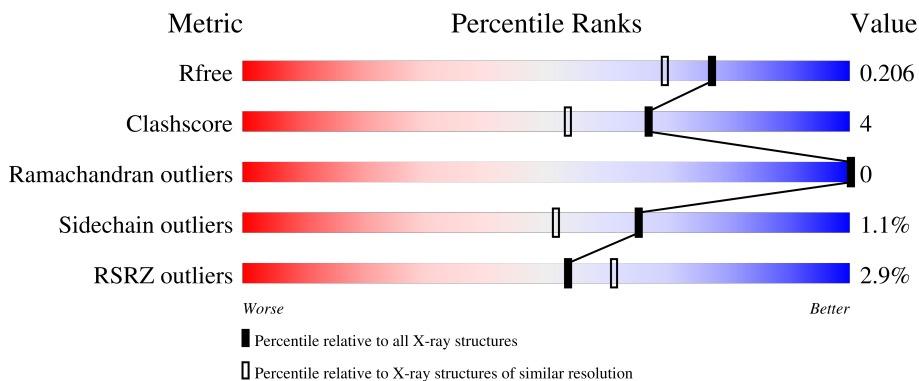
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.78 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	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	288	 0% 75% 11% 14%
1	B	288	 2% 77% 9% 14%
1	C	288	 6% 74% 11% 14%
1	D	288	 0% 74% 12% 14%

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	GOL	B	303[A]	-	X	-	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8383 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 Pteridine reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	248	1864	1178	327	348	11	0	9	0
1	B	248	1878	1189	326	351	12	0	9	0
1	C	248	1842	1159	324	348	11	0	6	0
1	D	247	1850	1171	321	346	12	0	6	0

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP O76290
A	-18	GLY	-	expression tag	UNP O76290
A	-17	SER	-	expression tag	UNP O76290
A	-16	SER	-	expression tag	UNP O76290
A	-15	HIS	-	expression tag	UNP O76290
A	-14	HIS	-	expression tag	UNP O76290
A	-13	HIS	-	expression tag	UNP O76290
A	-12	HIS	-	expression tag	UNP O76290
A	-11	HIS	-	expression tag	UNP O76290
A	-10	HIS	-	expression tag	UNP O76290
A	-9	SER	-	expression tag	UNP O76290
A	-8	SER	-	expression tag	UNP O76290
A	-7	GLY	-	expression tag	UNP O76290
A	-6	LEU	-	expression tag	UNP O76290
A	-5	VAL	-	expression tag	UNP O76290
A	-4	PRO	-	expression tag	UNP O76290
A	-3	ARG	-	expression tag	UNP O76290
A	-2	GLY	-	expression tag	UNP O76290
A	-1	SER	-	expression tag	UNP O76290
A	0	HIS	-	expression tag	UNP O76290
B	-19	MET	-	initiating methionine	UNP O76290

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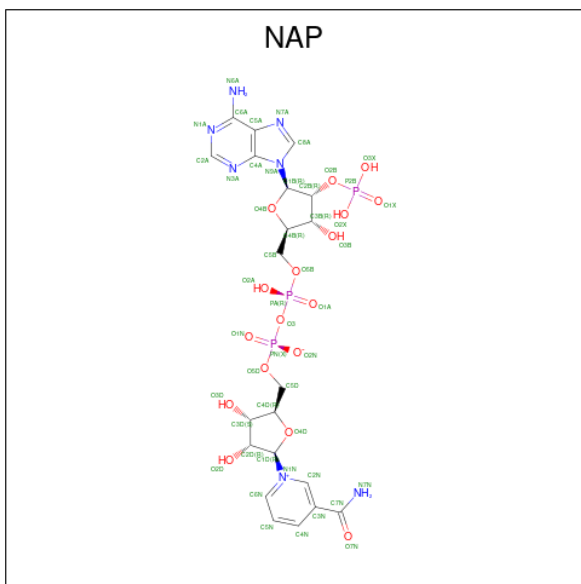
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP O76290
B	-17	SER	-	expression tag	UNP O76290
B	-16	SER	-	expression tag	UNP O76290
B	-15	HIS	-	expression tag	UNP O76290
B	-14	HIS	-	expression tag	UNP O76290
B	-13	HIS	-	expression tag	UNP O76290
B	-12	HIS	-	expression tag	UNP O76290
B	-11	HIS	-	expression tag	UNP O76290
B	-10	HIS	-	expression tag	UNP O76290
B	-9	SER	-	expression tag	UNP O76290
B	-8	SER	-	expression tag	UNP O76290
B	-7	GLY	-	expression tag	UNP O76290
B	-6	LEU	-	expression tag	UNP O76290
B	-5	VAL	-	expression tag	UNP O76290
B	-4	PRO	-	expression tag	UNP O76290
B	-3	ARG	-	expression tag	UNP O76290
B	-2	GLY	-	expression tag	UNP O76290
B	-1	SER	-	expression tag	UNP O76290
B	0	HIS	-	expression tag	UNP O76290
C	-19	MET	-	initiating methionine	UNP O76290
C	-18	GLY	-	expression tag	UNP O76290
C	-17	SER	-	expression tag	UNP O76290
C	-16	SER	-	expression tag	UNP O76290
C	-15	HIS	-	expression tag	UNP O76290
C	-14	HIS	-	expression tag	UNP O76290
C	-13	HIS	-	expression tag	UNP O76290
C	-12	HIS	-	expression tag	UNP O76290
C	-11	HIS	-	expression tag	UNP O76290
C	-10	HIS	-	expression tag	UNP O76290
C	-9	SER	-	expression tag	UNP O76290
C	-8	SER	-	expression tag	UNP O76290
C	-7	GLY	-	expression tag	UNP O76290
C	-6	LEU	-	expression tag	UNP O76290
C	-5	VAL	-	expression tag	UNP O76290
C	-4	PRO	-	expression tag	UNP O76290
C	-3	ARG	-	expression tag	UNP O76290
C	-2	GLY	-	expression tag	UNP O76290
C	-1	SER	-	expression tag	UNP O76290
C	0	HIS	-	expression tag	UNP O76290
D	-19	MET	-	initiating methionine	UNP O76290
D	-18	GLY	-	expression tag	UNP O76290
D	-17	SER	-	expression tag	UNP O76290

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP O76290
D	-15	HIS	-	expression tag	UNP O76290
D	-14	HIS	-	expression tag	UNP O76290
D	-13	HIS	-	expression tag	UNP O76290
D	-12	HIS	-	expression tag	UNP O76290
D	-11	HIS	-	expression tag	UNP O76290
D	-10	HIS	-	expression tag	UNP O76290
D	-9	SER	-	expression tag	UNP O76290
D	-8	SER	-	expression tag	UNP O76290
D	-7	GLY	-	expression tag	UNP O76290
D	-6	LEU	-	expression tag	UNP O76290
D	-5	VAL	-	expression tag	UNP O76290
D	-4	PRO	-	expression tag	UNP O76290
D	-3	ARG	-	expression tag	UNP O76290
D	-2	GLY	-	expression tag	UNP O76290
D	-1	SER	-	expression tag	UNP O76290
D	0	HIS	-	expression tag	UNP O76290

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



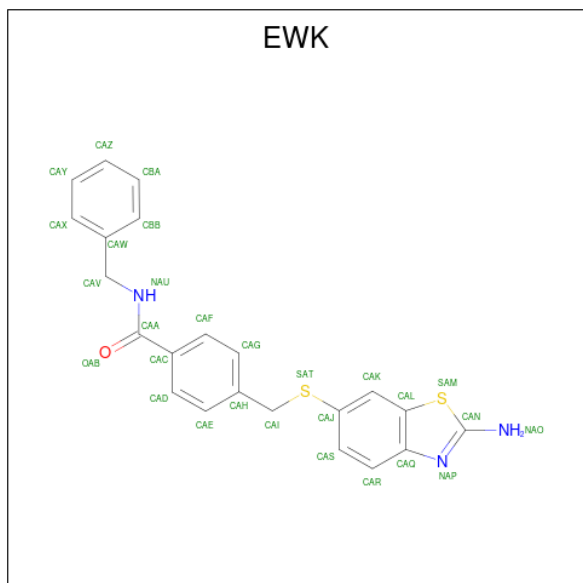
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	A	1	48	21	7	17	3	0	0
2	B	1	48	21	7	17	3	0	0

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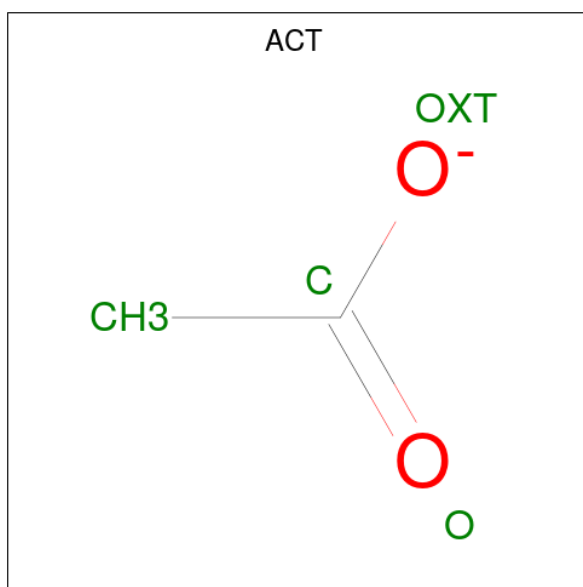
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is 4-[(2-azanyl-1,3-benzothiazol-6-yl)sulfanylmethyl]- {N}-(phenylmethyl)benzamide (CCD ID: EWK) (formula: C<sub>22</sub>H<sub>19</sub>N<sub>3</sub>OS<sub>2</sub>).



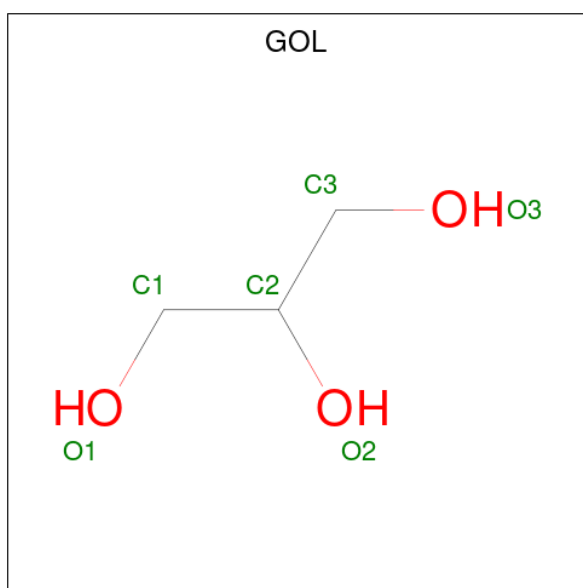
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total	C	N	O	S	0	0
			21	15	3	1	2		
3	B	1	Total	C	N	O	S	0	0
			21	15	3	1	2		
3	D	1	Total	C	N	O	S	0	0
			28	22	3	1	2		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	1
			12	6	6		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	167	Total 170	O 170	0	6
6	B	180	Total 181	O 181	0	3
6	C	149	Total 150	O 150	0	2
6	D	165	Total 166	O 166	0	4





## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.88Å 90.21Å 83.15Å 90.00° 115.76° 90.00°	Depositor
Resolution (Å)	74.89 – 1.78 74.89 – 1.78	Depositor EDS
% Data completeness (in resolution range)	99.1 (74.89-1.78) 99.1 (74.89-1.78)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 1.78Å)	Xtrriage
Refinement program	REFMAC 5.8.0222	Depositor
R, $R_{free}$	0.166 , 0.207 0.167 , 0.206	Depositor DCC
$R_{free}$ test set	4859 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.5	Xtrriage
Anisotropy	0.182	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 46.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.008 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8383	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.12 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.4186e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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

## 5 Model quality i

### 5.1 Standard geometry i

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

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	1.28	10/1915 (0.5%)	1.18	1/2602 (0.0%)
1	B	1.33	5/1932 (0.3%)	1.21	2/2623 (0.1%)
1	C	1.29	9/1881 (0.5%)	1.19	5/2560 (0.2%)
1	D	1.28	7/1895 (0.4%)	1.20	4/2575 (0.2%)
All	All	1.30	31/7623 (0.4%)	1.20	12/10360 (0.1%)

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	155	SER	C-O	7.03	1.32	1.23
1	C	69	LEU	N-CA	6.60	1.53	1.46
1	D	69	LEU	N-CA	6.52	1.53	1.46
1	C	64	THR	N-CA	6.48	1.54	1.46
1	B	25	GLN	N-CA	6.37	1.54	1.46
1	A	20	ALA	N-CA	6.26	1.53	1.46
1	D	24	HIS	N-CA	6.22	1.53	1.46
1	C	239	ASP	N-CA	6.03	1.53	1.46
1	A	133	LEU	N-CA	6.02	1.53	1.46
1	C	78	ASN	N-CA	5.99	1.53	1.46
1	D	125	GLY	N-CA	5.96	1.53	1.45
1	C	180	ALA	N-CA	5.81	1.53	1.46
1	C	208	LEU	N-CA	5.80	1.53	1.46
1	D	263	LEU	N-CA	5.78	1.53	1.46
1	B	125	GLY	N-CA	5.74	1.52	1.45
1	B	189	ALA	N-CA	5.73	1.53	1.46
1	A	204	PRO	C-O	5.72	1.30	1.23
1	A	136	MET	N-CA	5.67	1.53	1.46
1	A	267	HIS	N-CA	5.56	1.53	1.45
1	D	222	ARG	C-O	5.41	1.30	1.24
1	D	130	ALA	C-O	5.31	1.30	1.24
1	D	186	GLN	C-O	5.25	1.30	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	188	ALA	N-CA	5.23	1.53	1.46
1	C	267	HIS	CE1-NE2	5.19	1.37	1.32
1	C	261	GLY	N-CA	5.19	1.52	1.45
1	A	94	ALA	N-CA	5.18	1.52	1.46
1	B	69	LEU	N-CA	5.08	1.51	1.46
1	A	180	ALA	N-CA	5.08	1.52	1.46
1	A	187	SER	C-O	5.07	1.29	1.24
1	A	177	GLY	N-CA	5.02	1.52	1.45
1	B	85	GLY	N-CA	5.02	1.52	1.45

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	117	GLU	CB-CG-CD	5.74	122.36	112.60
1	D	235	GLU	CB-CG-CD	5.72	122.33	112.60
1	B	216	GLU	CB-CG-CD	5.69	122.27	112.60
1	D	204	PRO	CB-CA-C	-5.51	103.73	110.95
1	C	75	GLU	CB-CG-CD	5.46	121.89	112.60
1	B	29	ARG	CD-NE-CZ	-5.44	116.79	124.40
1	C	64	THR	CA-CB-OG1	-5.38	101.54	109.60
1	C	250	GLN	CB-CG-CD	5.23	121.49	112.60
1	C	101	PRO	N-CA-CB	5.21	107.95	103.31
1	C	141	ARG	CB-CG-CD	5.21	123.27	111.30
1	D	196	GLY	CA-C-N	-5.07	116.55	122.93
1	D	196	GLY	C-N-CA	-5.07	116.55	122.93

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	1864	0	1884	11	0
1	B	1878	0	1917	18	0
1	C	1842	0	1827	15	0
1	D	1850	0	1875	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	48	0	25	0	0
2	B	48	0	25	1	0
2	C	48	0	25	1	0
2	D	48	0	25	1	0
3	A	21	0	0	0	0
3	B	21	0	0	0	0
3	D	28	0	0	2	0
4	A	4	0	3	0	0
4	C	4	0	3	0	0
5	B	12	0	16	3	0
6	A	170	0	0	0	0
6	B	181	0	0	1	0
6	C	150	0	0	4	0
6	D	166	0	0	5	0
All	All	8383	0	7625	57	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (57) 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:208:LEU:HD21	6:C:511:HOH:O	1.73	0.89
1:B:42:VAL:HG13	5:B:303[A]:GOL:H11	1.67	0.77
1:D:164:VAL:HG22	1:D:179:HIS:CD2	2.32	0.64
1:B:103:VAL:HG22	6:D:403:HOH:O	1.99	0.62
1:A:22:LYS:HG2	1:A:242:ILE:HG13	1.82	0.60
1:B:161:ASP:O	1:B:164:VAL:HG22	2.02	0.59
1:D:250[B]:GLN:HG2	6:D:423:HOH:O	2.03	0.57
1:A:65:ASN:HA	1:A:69:LEU:HD22	1.86	0.57
1:C:138:PHE:O	1:C:142:GLN:HG2	2.05	0.56
1:C:164:VAL:HG22	1:C:179:HIS:CD2	2.39	0.56
1:B:163:MET:HE1	6:B:491:HOH:O	2.06	0.55
1:D:9:THR:HA	1:D:33:HIS:HB3	1.89	0.55
1:C:78:ASN:OD1	1:C:141:ARG:NH1	2.33	0.55
1:B:15:ILE:HB	2:B:301:NAP:H51N	1.90	0.54
1:A:265:LEU:HB2	1:B:190[B]:LEU:HD21	1.91	0.53
1:C:2:GLU:N	6:C:408:HOH:O	2.42	0.52
1:D:114:LYS:HD2	6:D:447:HOH:O	2.10	0.51
1:B:70:PRO:HG2	1:D:117[A]:GLU:HG2	1.93	0.50
1:D:65:ASN:HA	1:D:69:LEU:HD22	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:138:PHE:O	1:B:142:GLN:HG2	2.12	0.49
1:B:115:THR:OG1	1:B:117[B]:GLU:HG2	2.13	0.49
1:C:123:LEU:O	1:C:127[B]:ASN:HB2	2.13	0.49
1:B:190[B]:LEU:HD12	1:D:167:PRO:HG2	1.95	0.49
1:B:125:GLY:HA2	1:B:129[B]:ILE:HB	1.94	0.49
1:A:251:TYR:CE2	1:B:232:ALA:HB2	2.49	0.48
1:C:228:GLY:O	1:C:229:ARG:C	2.56	0.47
1:D:138:PHE:O	1:D:142:GLN:HG2	2.14	0.47
1:D:205:GLY:O	2:D:301:NAP:H4N	2.15	0.47
1:C:205:GLY:O	2:C:301:NAP:H4N	2.15	0.47
1:B:9:THR:HA	1:B:33:HIS:HB3	1.97	0.47
1:D:219:ASP:HB3	1:D:223:ARG:NH1	2.30	0.47
1:A:130:ALA:HB3	1:A:131:PRO:HD3	1.97	0.46
1:B:117[A]:GLU:HG3	1:D:67:ASN:HA	1.98	0.46
1:D:115:THR:OG1	1:D:117[B]:GLU:HG2	2.16	0.46
1:A:9:THR:HA	1:A:33:HIS:HB3	1.98	0.45
1:C:230:ARG:HD2	6:C:407:HOH:O	2.16	0.45
1:D:213:MET:CE	3:D:302:EWK:CAD	2.95	0.45
1:B:78:ASN:OD1	1:B:141:ARG:NH2	2.42	0.44
1:D:133:LEU:HA	1:D:136[B]:MET:HE3	1.98	0.44
1:C:9:THR:HA	1:C:33:HIS:HB3	2.00	0.43
1:C:232:ALA:HB2	1:D:251:TYR:CE2	2.53	0.43
1:C:236:GLN:HE21	1:D:250[B]:GLN:CD	2.26	0.43
1:A:26:THR:HG22	1:A:26:THR:O	2.19	0.42
1:A:179:HIS:ND1	6:C:403:HOH:O	2.37	0.42
1:B:46:ASP:OD1	5:B:303[A]:GOL:H12	2.20	0.42
1:D:230:ARG:NE	6:D:415:HOH:O	2.52	0.42
1:C:218:LYS:O	1:C:222:ARG:HG3	2.20	0.42
1:D:133:LEU:HD23	1:D:136[B]:MET:HE1	2.02	0.42
1:A:193:ALA:HB3	1:A:194:PRO:HD3	2.01	0.41
1:D:213:MET:HE1	3:D:302:EWK:CAD	2.51	0.41
1:C:169:MET:O	1:C:170:ALA:HB3	2.21	0.41
1:A:225:VAL:O	1:A:229:ARG:HD3	2.20	0.41
1:C:65:ASN:HA	1:C:69:LEU:HD22	2.02	0.41
1:A:266:VAL:HB	1:D:268:ALA:HB2	2.02	0.41
1:B:45:ALA:CB	5:B:303[A]:GOL:H32	2.50	0.41
1:B:103:VAL:HG21	1:D:195:TYR:CZ	2.56	0.41
1:D:140:GLN:NE2	6:D:402:HOH:O	2.27	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	250/288 (87%)	241 (96%)	9 (4%)	0	100	100
1	B	251/288 (87%)	245 (98%)	6 (2%)	0	100	100
1	C	248/288 (86%)	237 (96%)	11 (4%)	0	100	100
1	D	247/288 (86%)	241 (98%)	6 (2%)	0	100	100
All	All	996/1152 (86%)	964 (97%)	32 (3%)	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	196/231 (85%)	193 (98%)	3 (2%)	57	41
1	B	200/231 (87%)	199 (100%)	1 (0%)	81	73
1	C	190/231 (82%)	187 (98%)	3 (2%)	55	38
1	D	195/231 (84%)	194 (100%)	1 (0%)	81	73
All	All	781/924 (84%)	773 (99%)	8 (1%)	65	55

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

Mol	Chain	Res	Type
1	A	141	ARG
1	A	164	VAL

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Mol	Chain	Res	Type
1	A	209	LEU
1	B	164	VAL
1	C	22	LYS
1	C	74	GLU
1	C	141	ARG
1	D	215	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	92	ASN
1	A	127	ASN
1	A	140[A]	GLN
1	A	179	HIS
1	B	92	ASN
1	B	236	GLN
1	C	36	ASN
1	C	92	ASN
1	C	236	GLN
1	C	250	GLN
1	D	92	ASN
1	D	119	GLN
1	D	127	ASN

### 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

11 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	EWK	A	302	-	23,23,31	2.29	7 (30%)	32,32,42	4.21	8 (25%)
5	GOL	B	303[B]	-	5,5,5	0.56	0	5,5,5	1.16	0
4	ACT	A	303	-	3,3,3	0.94	0	3,3,3	0.95	0
2	NAP	C	301	-	50,52,52	1.63	8 (16%)	71,80,80	1.80	16 (22%)
2	NAP	A	301	-	50,52,52	1.85	11 (22%)	71,80,80	1.87	19 (26%)
3	EWK	D	302	-	31,31,31	2.49	9 (29%)	42,42,42	3.73	12 (28%)
4	ACT	C	302	-	3,3,3	0.86	0	3,3,3	1.05	0
2	NAP	B	301	-	50,52,52	1.81	11 (22%)	71,80,80	2.02	19 (26%)
5	GOL	B	303[A]	-	5,5,5	0.49	0	5,5,5	1.98	2 (40%)
2	NAP	D	301	-	50,52,52	1.75	14 (28%)	71,80,80	1.95	20 (28%)
3	EWK	B	302	-	23,23,31	3.33	8 (34%)	32,32,42	3.41	7 (21%)

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	EWK	A	302	-	-	4/9/9/14	0/3/3/4
5	GOL	B	303[B]	-	-	3/4/4/4	-
2	NAP	C	301	-	-	1/35/67/67	0/5/5/5
2	NAP	A	301	-	-	0/35/67/67	0/5/5/5
3	EWK	D	302	-	-	4/14/14/14	0/4/4/4
2	NAP	B	301	-	-	0/35/67/67	0/5/5/5
5	GOL	B	303[A]	-	-	4/4/4/4	-
2	NAP	D	301	-	-	0/35/67/67	0/5/5/5
3	EWK	B	302	-	-	4/9/9/14	0/3/3/4

All (68) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	302	EWK	CAJ-SAT	9.06	1.95	1.76
3	B	302	EWK	CAN-SAM	-7.18	1.68	1.76
3	D	302	EWK	CAN-SAM	-7.15	1.68	1.76
3	A	302	EWK	CAC-CAA	-6.32	1.41	1.50
2	C	301	NAP	C5A-C4A	6.22	1.50	1.39
3	B	302	EWK	CAC-CAA	-5.86	1.41	1.50
2	B	301	NAP	PA-O3	5.54	1.65	1.59
2	A	301	NAP	PA-O3	5.39	1.65	1.59
2	D	301	NAP	C5A-C4A	5.09	1.48	1.39
3	A	302	EWK	CAI-CAH	-4.90	1.40	1.51
3	D	302	EWK	CAI-CAH	-4.78	1.40	1.51
2	A	301	NAP	C5A-C4A	4.68	1.47	1.39
3	B	302	EWK	CAI-CAH	-4.66	1.40	1.51
2	B	301	NAP	O4D-C1D	4.54	1.46	1.40
3	B	302	EWK	CAL-SAM	-4.41	1.65	1.74
3	D	302	EWK	CAC-CAA	-4.24	1.40	1.50
2	B	301	NAP	C5A-C4A	4.02	1.46	1.39
2	A	301	NAP	O4D-C1D	3.98	1.46	1.40
2	C	301	NAP	C8A-N7A	3.89	1.39	1.31
3	D	302	EWK	CAJ-SAT	3.87	1.84	1.76
2	A	301	NAP	PN-O3	3.85	1.63	1.59
3	D	302	EWK	CAN-NAP	3.83	1.35	1.31
3	D	302	EWK	CAV-CAW	-3.78	1.43	1.51
2	D	301	NAP	PA-O3	3.77	1.63	1.59
2	D	301	NAP	P2B-O2B	3.75	1.66	1.59
2	D	301	NAP	O4D-C1D	3.70	1.45	1.40
2	B	301	NAP	C5A-C6A	3.60	1.51	1.41
3	D	302	EWK	CAK-CAL	-3.55	1.33	1.39
2	B	301	NAP	PN-O3	3.49	1.63	1.59
2	C	301	NAP	O4D-C1D	3.40	1.45	1.40
2	A	301	NAP	P2B-O2B	3.38	1.65	1.59
2	A	301	NAP	C5A-C6A	3.30	1.50	1.41
3	A	302	EWK	CAJ-SAT	3.25	1.83	1.76
3	B	302	EWK	CAK-CAL	-3.17	1.34	1.39
3	B	302	EWK	CAN-NAP	3.12	1.35	1.31
2	B	301	NAP	P2B-O2B	3.07	1.64	1.59
2	C	301	NAP	C5A-C6A	3.04	1.49	1.41
3	A	302	EWK	CAK-CAL	-3.01	1.34	1.39
2	D	301	NAP	C2A-N3A	3.01	1.39	1.33
3	A	302	EWK	CAN-NAP	2.98	1.34	1.31
2	D	301	NAP	C8A-N7A	2.98	1.37	1.31
2	A	301	NAP	C8A-N7A	2.95	1.37	1.31
2	D	301	NAP	C5A-C6A	2.77	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	301	NAP	PN-O3	2.67	1.62	1.59
2	B	301	NAP	C8A-N7A	2.66	1.36	1.31
2	C	301	NAP	PA-O3	2.61	1.62	1.59
2	C	301	NAP	O2D-C2D	2.54	1.49	1.43
3	D	302	EWK	CAL-SAM	-2.53	1.69	1.74
2	D	301	NAP	C4N-C3N	2.46	1.43	1.39
2	A	301	NAP	C2N-N1N	2.44	1.37	1.35
2	B	301	NAP	C4A-N3A	2.44	1.39	1.34
2	C	301	NAP	PN-O3	2.39	1.62	1.59
2	A	301	NAP	C2A-N3A	2.39	1.38	1.33
3	A	302	EWK	CAS-CAR	2.34	1.42	1.38
2	D	301	NAP	C7N-N7N	2.34	1.37	1.33
2	B	301	NAP	C2A-N1A	2.32	1.38	1.33
2	A	301	NAP	C2N-C3N	2.26	1.42	1.39
3	D	302	EWK	CAR-CAQ	-2.24	1.36	1.40
2	D	301	NAP	O2D-C2D	2.22	1.48	1.43
2	D	301	NAP	C2A-N1A	2.20	1.37	1.33
3	B	302	EWK	CAQ-NAP	-2.19	1.35	1.39
2	D	301	NAP	C4A-N9A	-2.19	1.33	1.37
2	A	301	NAP	C4A-N3A	2.15	1.38	1.34
2	D	301	NAP	PN-O5D	2.11	1.67	1.59
3	A	302	EWK	CAR-CAQ	-2.10	1.36	1.40
2	B	301	NAP	C2A-N3A	2.09	1.37	1.33
2	C	301	NAP	C4A-N9A	-2.02	1.33	1.37
2	B	301	NAP	C2B-C1B	2.00	1.58	1.53

All (103) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	EWK	SAM-CAN-NAP	-15.04	106.39	115.72
3	D	302	EWK	CAL-SAM-CAN	14.13	95.57	88.89
3	D	302	EWK	SAM-CAN-NAP	-13.46	107.37	115.72
3	A	302	EWK	CAL-SAM-CAN	11.76	94.45	88.89
3	B	302	EWK	CAL-SAM-CAN	11.50	94.32	88.89
3	B	302	EWK	SAM-CAN-NAP	-11.19	108.78	115.72
3	A	302	EWK	CAQ-NAP-CAN	10.34	116.70	110.57
3	D	302	EWK	CAQ-NAP-CAN	9.59	116.26	110.57
3	B	302	EWK	CAQ-NAP-CAN	7.08	114.77	110.57
3	A	302	EWK	SAM-CAN-NAO	6.74	127.46	120.13
2	B	301	NAP	C4A-N9A-C8A	5.96	112.00	105.74
2	D	301	NAP	C4A-N9A-C8A	5.84	111.87	105.74
2	A	301	NAP	C4A-N9A-C8A	5.64	111.66	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	NAP	C2B-C1B-N9A	-5.60	104.53	113.75
2	C	301	NAP	O2B-P2B-O1X	-5.14	91.02	109.33
3	D	302	EWK	SAM-CAN-NAO	5.13	125.71	120.13
2	B	301	NAP	O7N-C7N-C3N	-5.10	113.37	119.60
2	D	301	NAP	O4B-C1B-N9A	4.70	117.12	108.09
2	C	301	NAP	C2B-C1B-N9A	-4.66	106.08	113.75
2	D	301	NAP	C2B-C1B-N9A	-4.64	106.12	113.75
3	B	302	EWK	NAO-CAN-NAP	4.62	127.77	124.13
2	B	301	NAP	O4B-C1B-N9A	4.33	116.41	108.09
2	D	301	NAP	N9A-C8A-N7A	-4.20	107.98	113.94
2	C	301	NAP	C4A-N9A-C1B	-4.10	117.04	126.63
2	D	301	NAP	N3A-C4A-N9A	4.04	134.04	127.17
2	A	301	NAP	C4A-N9A-C1B	-4.01	117.26	126.63
2	A	301	NAP	C2B-C1B-N9A	-3.98	107.21	113.75
2	A	301	NAP	N9A-C8A-N7A	-3.89	108.42	113.94
2	B	301	NAP	C4A-N9A-C1B	-3.88	117.57	126.63
2	D	301	NAP	C5A-C4A-N3A	-3.87	121.39	126.72
3	D	302	EWK	CAR-CAS-CAJ	-3.86	116.04	120.48
2	A	301	NAP	C5N-C4N-C3N	-3.83	116.60	120.36
2	A	301	NAP	N3A-C4A-N9A	3.77	133.58	127.17
2	C	301	NAP	O4B-C1B-N9A	3.66	115.12	108.09
2	A	301	NAP	C2N-C3N-C4N	3.57	122.41	118.26
2	C	301	NAP	C4A-N9A-C8A	3.55	109.47	105.74
2	A	301	NAP	C5A-C4A-N3A	-3.55	121.82	126.72
2	B	301	NAP	N3A-C2A-N1A	-3.54	123.23	128.58
3	D	302	EWK	NAO-CAN-NAP	3.53	126.91	124.13
2	D	301	NAP	C4A-N9A-C1B	-3.50	118.45	126.63
5	B	303[A]	GOL	O2-C2-C1	-3.47	94.82	109.18
2	B	301	NAP	N9A-C8A-N7A	-3.35	109.18	113.94
2	C	301	NAP	C3N-C7N-N7N	3.35	121.86	117.74
3	A	302	EWK	CAR-CAS-CAJ	-3.34	116.63	120.48
2	B	301	NAP	C3N-C7N-N7N	3.29	121.79	117.74
2	A	301	NAP	O4B-C1B-N9A	3.28	114.39	108.09
2	B	301	NAP	N3A-C4A-N9A	3.25	132.69	127.17
2	C	301	NAP	C2A-N1A-C6A	3.20	123.99	118.73
2	C	301	NAP	C5A-C4A-N3A	-3.17	122.35	126.72
2	B	301	NAP	C2A-N1A-C6A	3.13	123.88	118.73
2	B	301	NAP	O2A-PA-O1A	3.12	126.97	112.44
2	D	301	NAP	N3A-C2A-N1A	-3.11	123.87	128.58
3	A	302	EWK	CAI-SAT-CAJ	3.10	109.24	103.08
3	B	302	EWK	CAR-CAS-CAJ	-3.08	116.93	120.48
3	B	302	EWK	SAM-CAN-NAO	3.06	123.45	120.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	NAP	C5A-C6A-N6A	-3.03	115.78	123.29
3	D	302	EWK	CAV-NAU-CAA	2.97	128.86	121.89
2	C	301	NAP	N3A-C2A-N1A	-2.91	124.18	128.58
2	D	301	NAP	O7N-C7N-C3N	-2.81	116.16	119.60
2	D	301	NAP	O2N-PN-O1N	2.77	125.33	112.44
2	C	301	NAP	C4A-C5A-N7A	-2.75	107.43	110.58
2	A	301	NAP	O2X-P2B-O1X	2.75	121.54	110.83
2	D	301	NAP	C5A-N7A-C8A	2.74	107.75	103.45
2	B	301	NAP	N6A-C6A-N1A	2.73	124.46	118.38
2	C	301	NAP	C1B-N9A-C8A	2.66	133.00	127.09
2	C	301	NAP	N3A-C4A-N9A	2.65	131.67	127.17
2	D	301	NAP	C2A-N3A-C4A	2.62	118.22	111.83
2	A	301	NAP	C6A-C5A-N7A	2.60	137.10	132.09
2	D	301	NAP	N6A-C6A-N1A	2.58	124.13	118.38
2	C	301	NAP	C6A-C5A-N7A	2.58	137.07	132.09
2	B	301	NAP	O2N-PN-O3	2.58	114.24	107.27
3	A	302	EWK	NAO-CAN-NAP	2.58	126.16	124.13
3	B	302	EWK	CAI-SAT-CAJ	2.57	108.18	103.08
2	A	301	NAP	O4B-C4B-C3B	-2.56	100.07	105.15
2	A	301	NAP	C5A-N7A-C8A	2.55	107.46	103.45
2	A	301	NAP	C4A-C5A-N7A	-2.53	107.69	110.58
2	A	301	NAP	N3A-C2A-N1A	-2.47	124.84	128.58
2	A	301	NAP	C4D-O4D-C1D	2.47	112.18	109.92
2	B	301	NAP	C5A-C4A-N9A	-2.46	103.12	105.81
2	D	301	NAP	C4A-C5A-N7A	-2.45	107.79	110.58
2	D	301	NAP	C4D-O4D-C1D	2.44	112.16	109.92
2	A	301	NAP	C2A-N3A-C4A	2.43	117.76	111.83
5	B	303[A]	GOL	O1-C1-C2	-2.36	99.73	110.38
2	B	301	NAP	C5A-C6A-N6A	-2.36	117.43	123.29
3	D	302	EWK	CAW-CAV-NAU	-2.35	108.13	113.07
2	C	301	NAP	O7N-C7N-N7N	-2.34	119.23	122.62
3	D	302	EWK	CAI-SAT-CAJ	2.34	107.72	103.08
2	B	301	NAP	O2B-P2B-O1X	-2.31	101.11	109.33
2	D	301	NAP	O2X-P2B-O1X	2.30	119.81	110.83
2	D	301	NAP	C2N-C3N-C4N	2.27	120.89	118.26
2	D	301	NAP	C6A-C5A-N7A	2.25	136.43	132.09
2	C	301	NAP	C2A-N3A-C4A	2.22	117.26	111.83
3	D	302	EWK	CAC-CAA-NAU	-2.19	112.58	117.12
2	D	301	NAP	O2B-P2B-O1X	-2.16	101.62	109.33
2	B	301	NAP	O3X-P2B-O2X	2.14	115.83	107.80
2	A	301	NAP	O2N-PN-O1N	2.12	122.32	112.44
2	B	301	NAP	O3D-C3D-C2D	-2.12	105.02	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	NAP	O3-PN-O1N	-2.09	104.41	110.70
3	A	302	EWK	CAS-CAR-CAQ	2.09	123.44	119.97
2	A	301	NAP	O2B-P2B-O1X	-2.08	101.93	109.33
2	C	301	NAP	O2N-PN-O1N	2.07	122.07	112.44
3	D	302	EWK	CAD-CAE-CAH	-2.07	118.28	121.00
3	D	302	EWK	CAE-CAD-CAC	2.05	122.99	120.80

There are no chirality outliers.

All (20) torsion outliers are listed below:

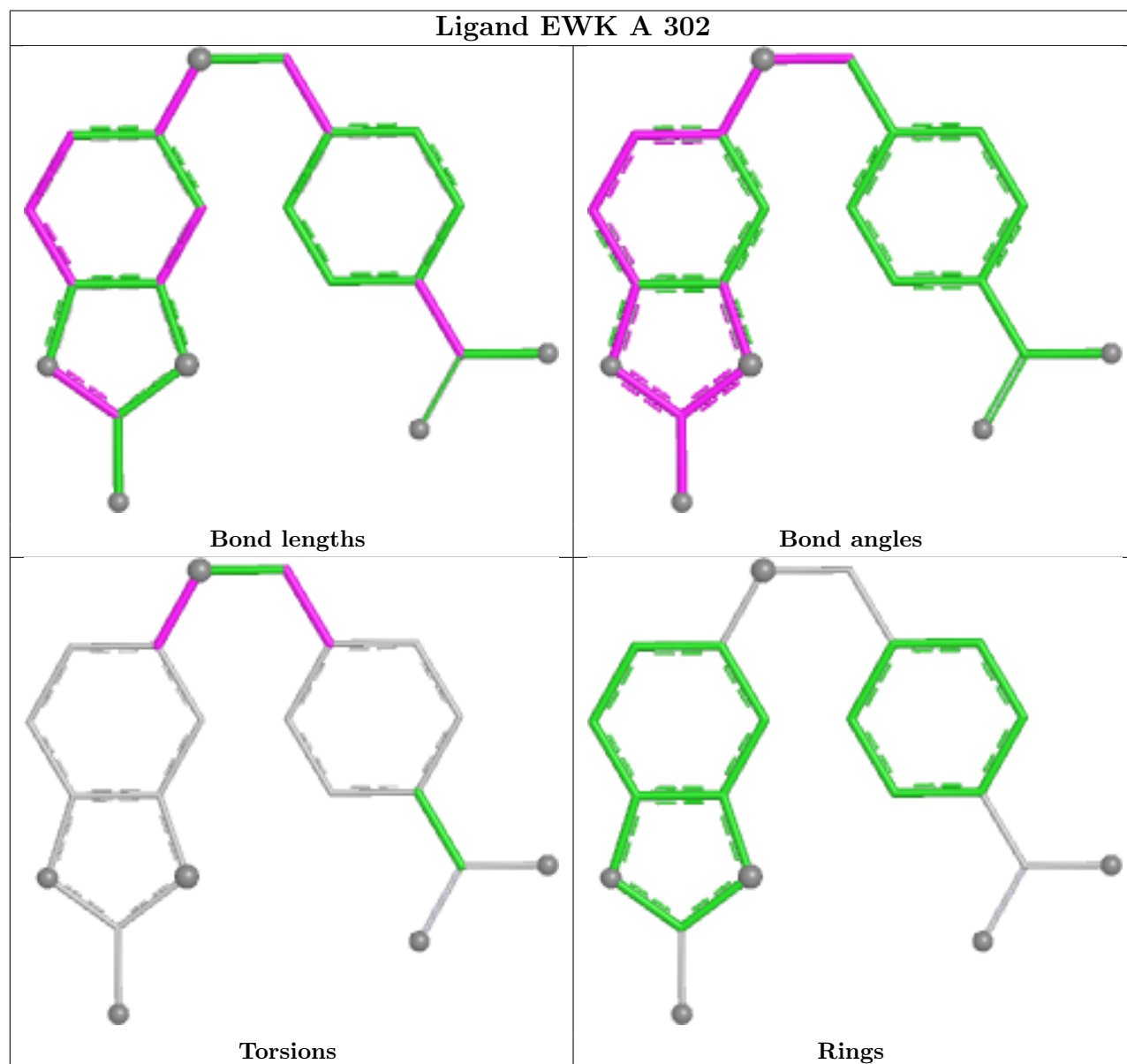
Mol	Chain	Res	Type	Atoms
5	B	303[A]	GOL	O1-C1-C2-C3
5	B	303[A]	GOL	C1-C2-C3-O3
5	B	303[B]	GOL	O1-C1-C2-C3
5	B	303[A]	GOL	O1-C1-C2-O2
5	B	303[A]	GOL	O2-C2-C3-O3
5	B	303[B]	GOL	O1-C1-C2-O2
3	A	302	EWK	CAE-CAH-CAI-SAT
5	B	303[B]	GOL	C1-C2-C3-O3
3	A	302	EWK	CAG-CAH-CAI-SAT
3	D	302	EWK	CAE-CAH-CAI-SAT
2	C	301	NAP	C5B-O5B-PA-O1A
3	B	302	EWK	CAE-CAH-CAI-SAT
3	D	302	EWK	CAG-CAH-CAI-SAT
3	B	302	EWK	CAG-CAH-CAI-SAT
3	A	302	EWK	CAK-CAJ-SAT-CAI
3	A	302	EWK	CAS-CAJ-SAT-CAI
3	B	302	EWK	CAS-CAJ-SAT-CAI
3	B	302	EWK	CAK-CAJ-SAT-CAI
3	D	302	EWK	CAK-CAJ-SAT-CAI
3	D	302	EWK	CAS-CAJ-SAT-CAI

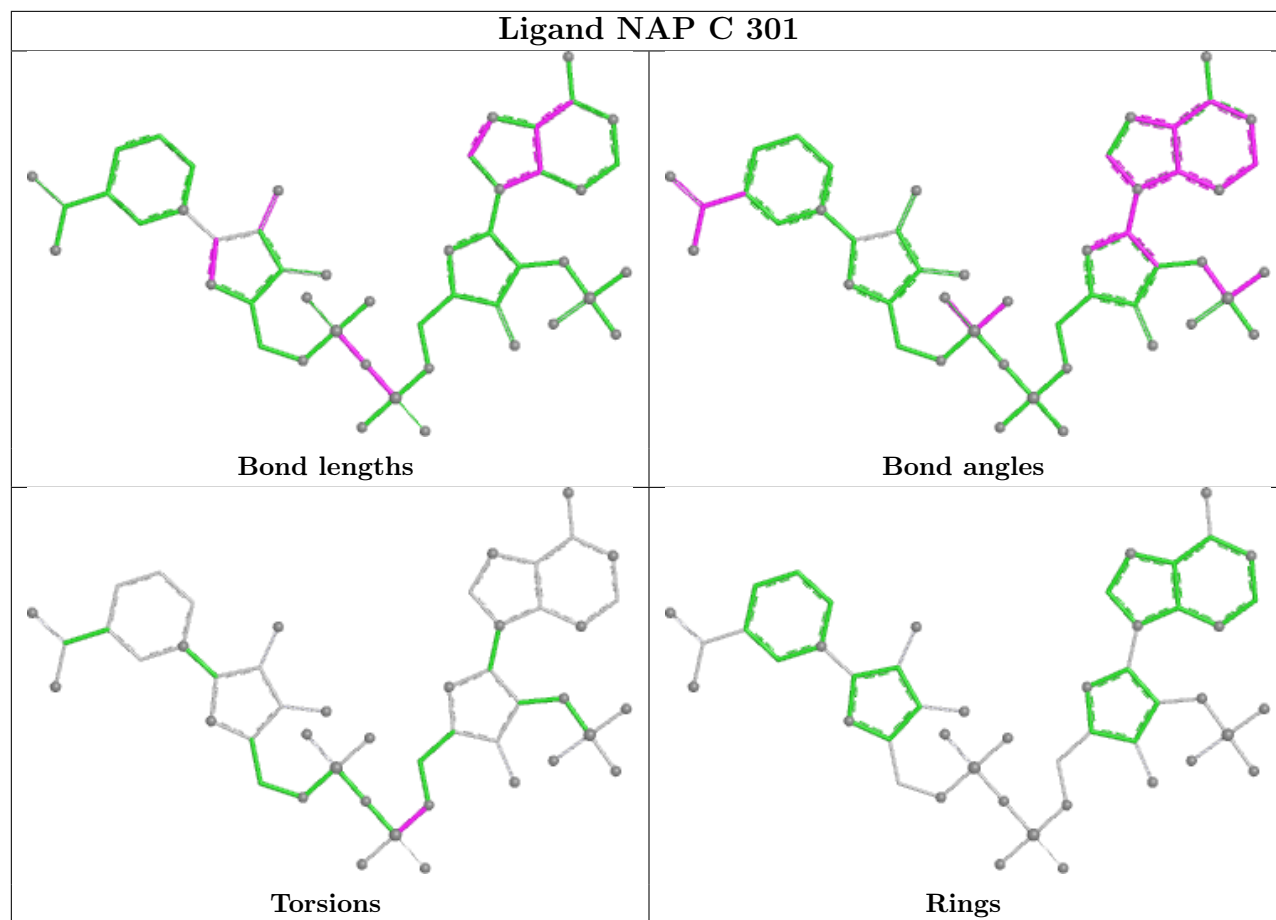
There are no ring outliers.

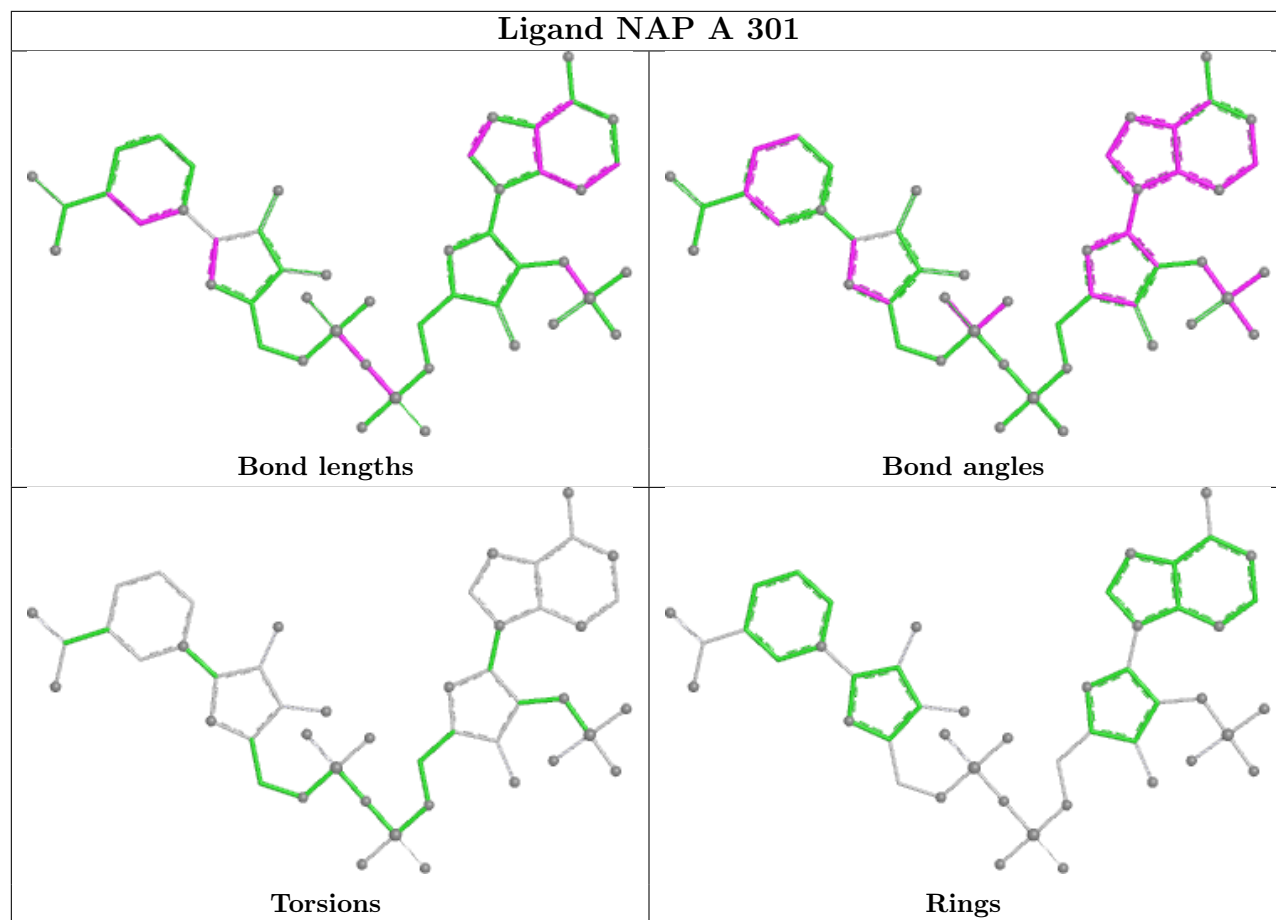
5 monomers are involved in 8 short contacts:

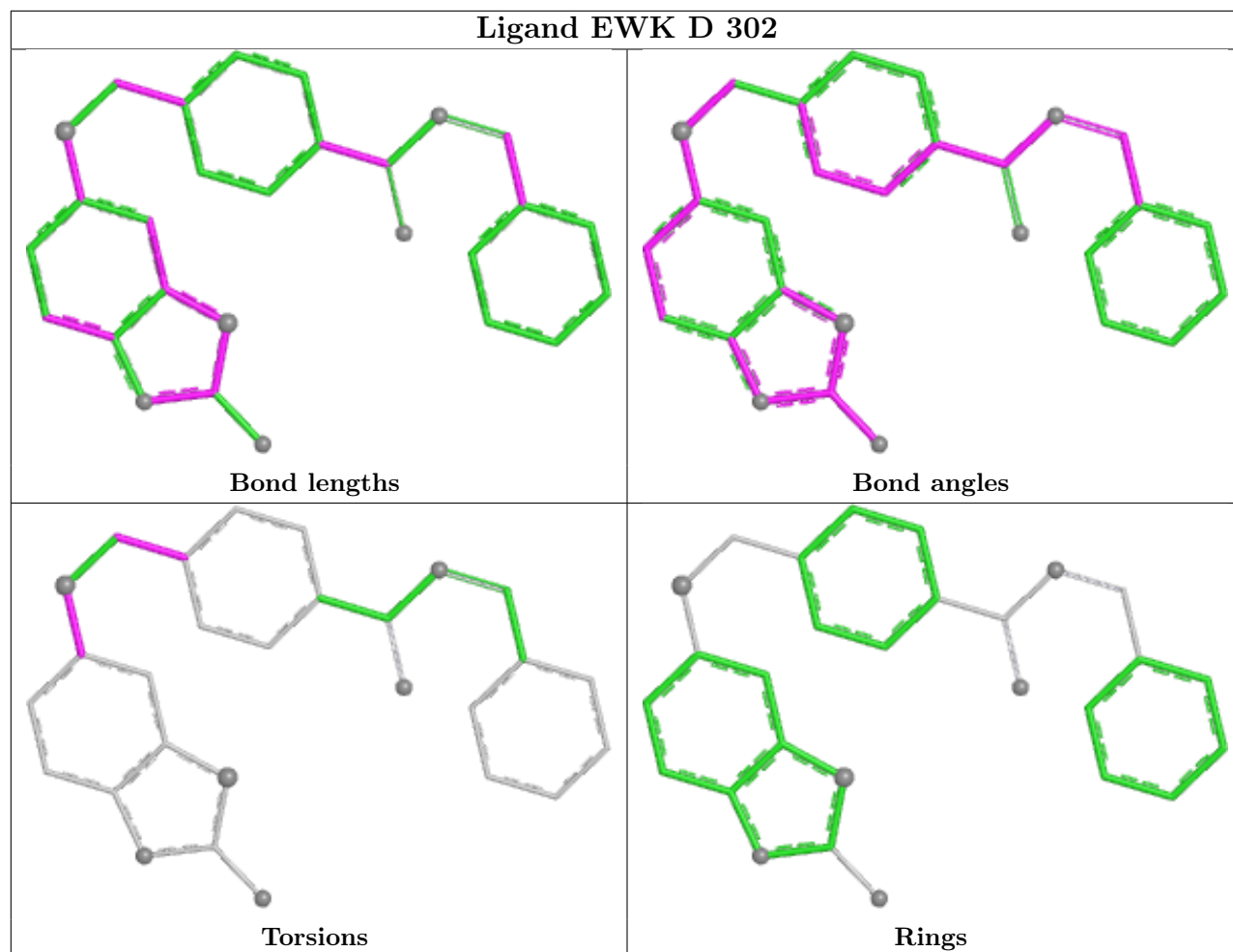
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	NAP	1	0
3	D	302	EWK	2	0
2	B	301	NAP	1	0
5	B	303[A]	GOL	3	0
2	D	301	NAP	1	0

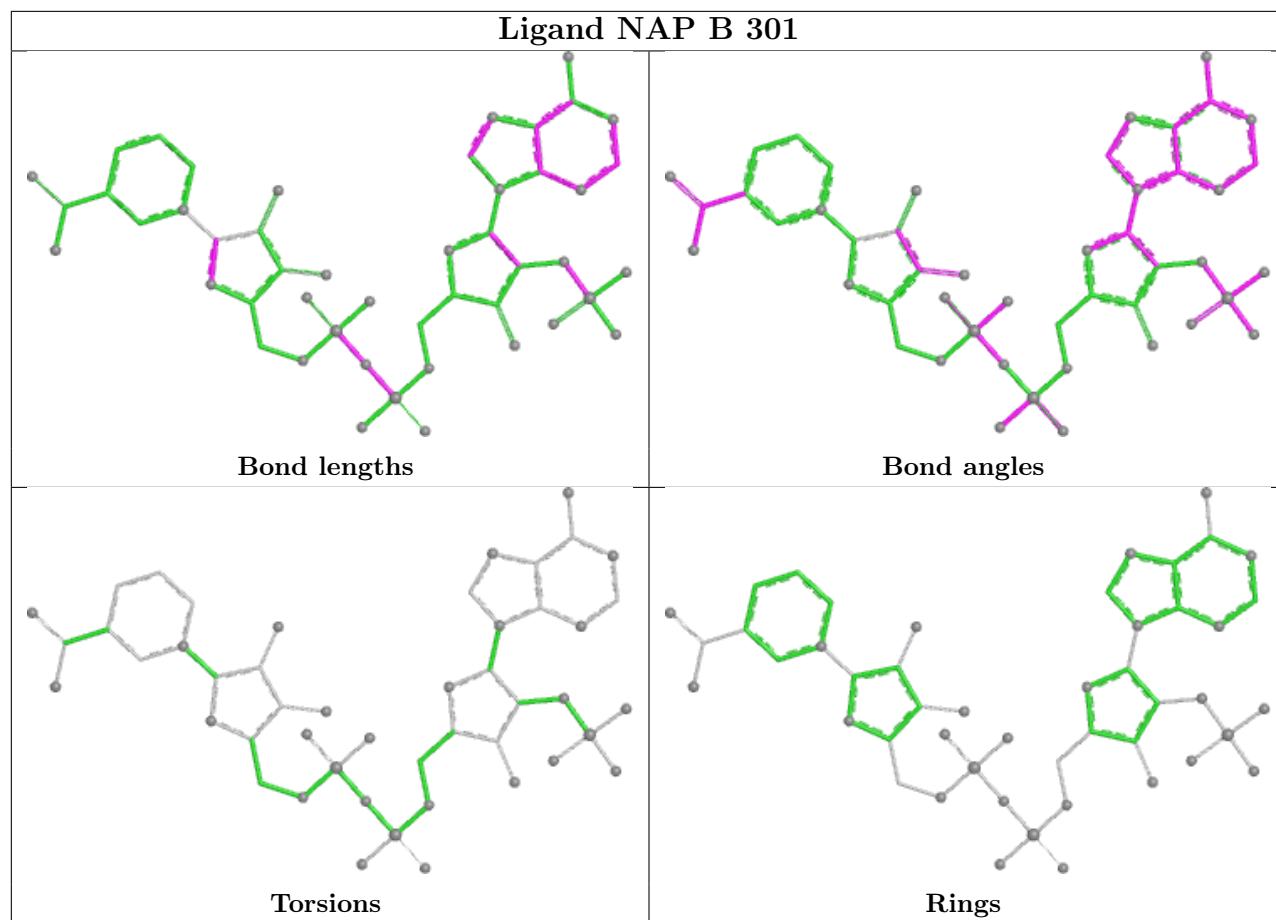
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

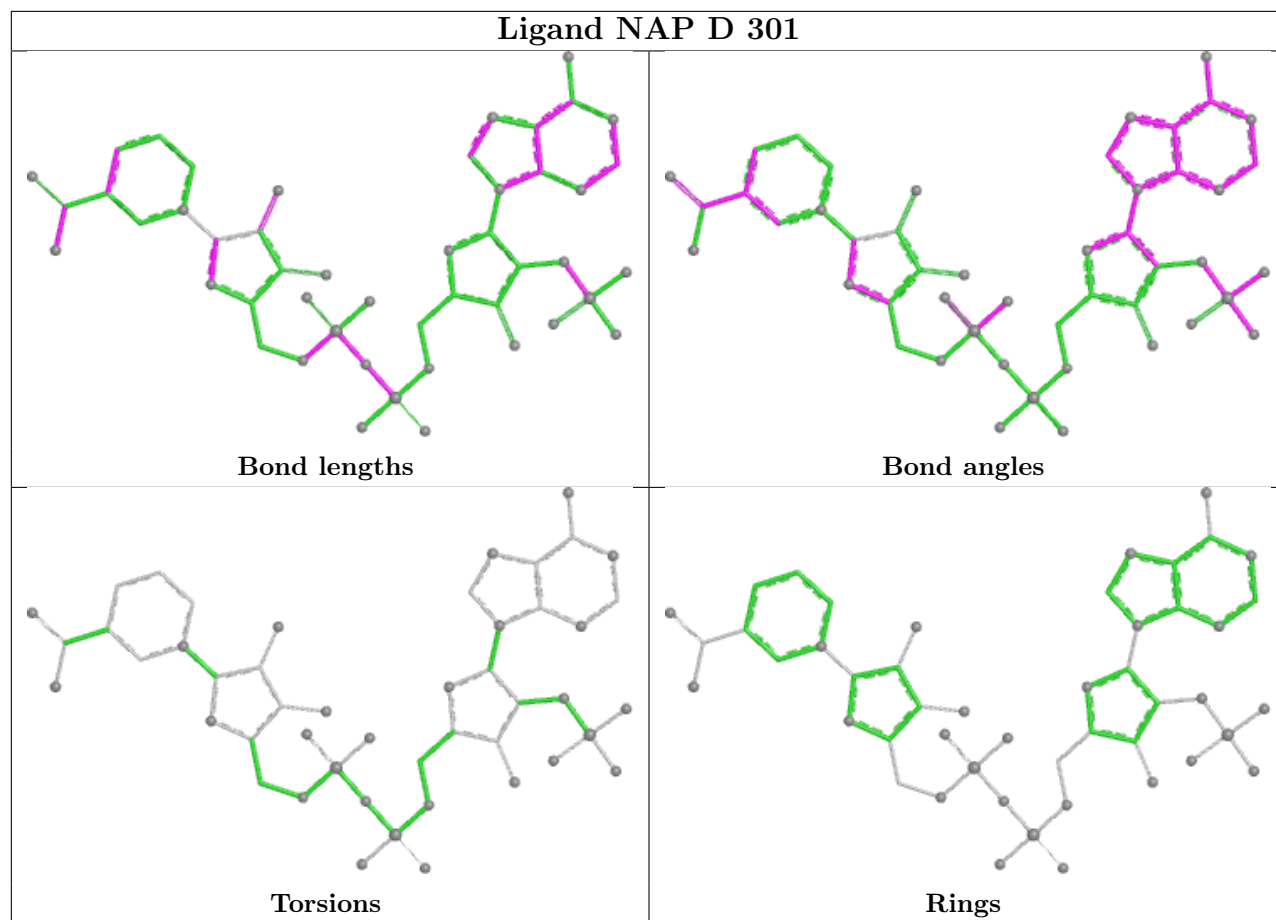


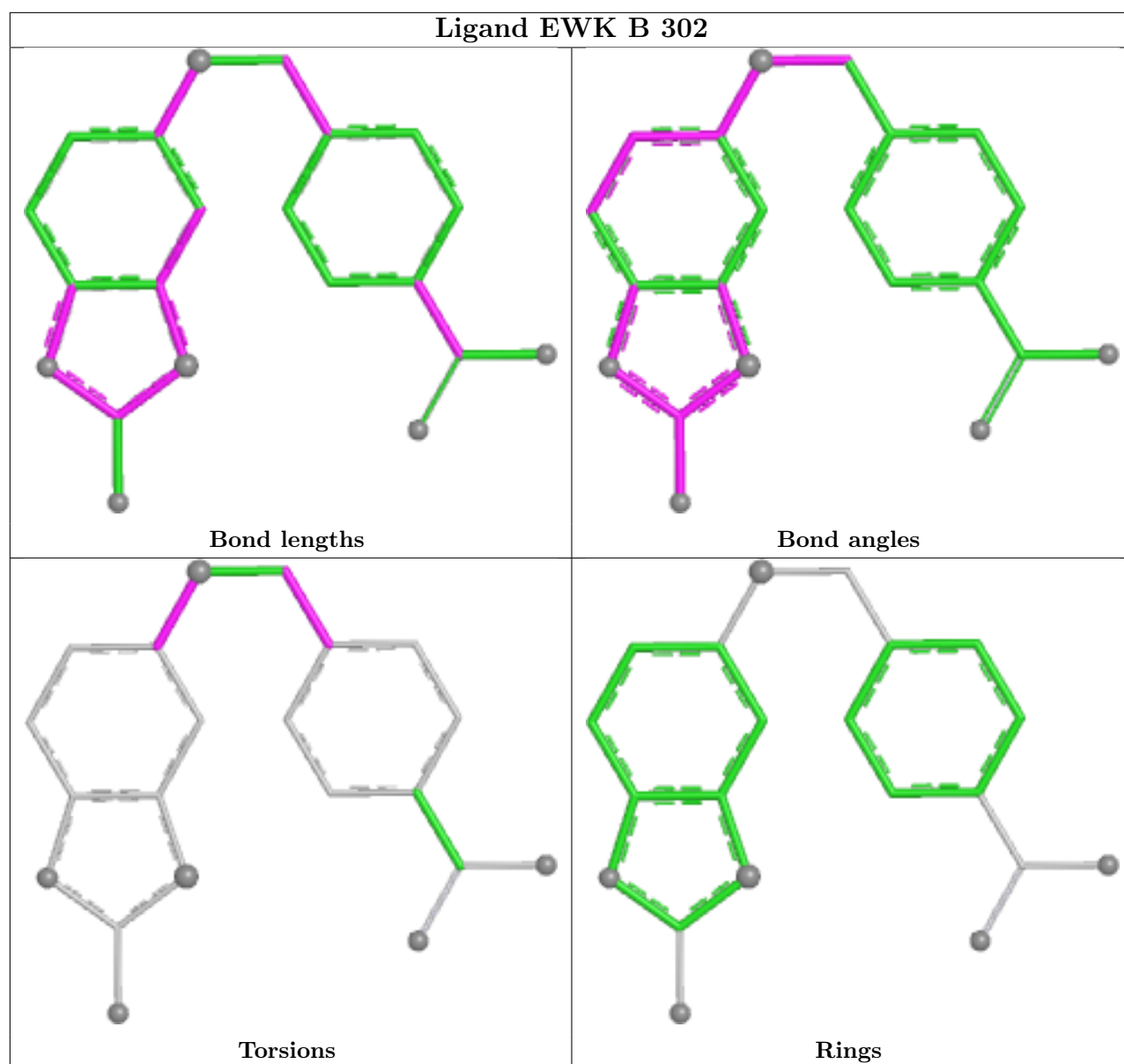












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	248/288 (86%)	-0.21	4 (1%) 70 77	5, 15, 30, 40	12 (4%)
1	B	248/288 (86%)	-0.28	5 (2%) 65 73	5, 12, 27, 53	18 (7%)
1	C	248/288 (86%)	0.05	17 (6%) 23 27	7, 16, 40, 75	17 (6%)
1	D	247/288 (85%)	-0.13	3 (1%) 76 82	4, 15, 33, 48	12 (4%)
All	All	991/1152 (86%)	-0.14	29 (2%) 53 61	4, 14, 32, 75	59 (5%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	212	ALA	6.9
1	B	211	VAL	4.9
1	C	208	LEU	4.8
1	B	210	PRO	4.0
1	C	221	TRP	3.7
1	C	217	GLU	3.6
1	C	211	VAL	3.4
1	C	212	ALA	3.3
1	C	195	TYR	3.1
1	C	152	SER	2.9
1	D	211	VAL	2.9
1	B	1	MET	2.9
1	C	214	GLY	2.8
1	A	103	VAL	2.7
1	A	212	ALA	2.7
1	D	215	GLU	2.6
1	C	209	LEU	2.6
1	B	164	VAL	2.6
1	C	215	GLU	2.4
1	A	195	TYR	2.3
1	C	213	MET	2.2

*Continued on next page...*

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Mol	Chain	Res	Type	RSRZ
1	C	207	SER	2.2
1	C	103	VAL	2.1
1	C	232	ALA	2.1
1	C	229	ARG	2.1
1	D	212	ALA	2.1
1	C	216	GLU	2.1
1	C	230	ARG	2.0
1	A	211	VAL	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

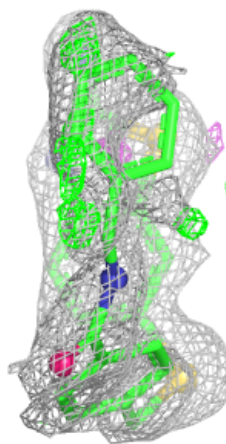
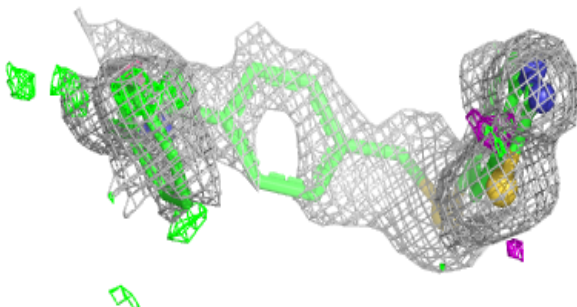
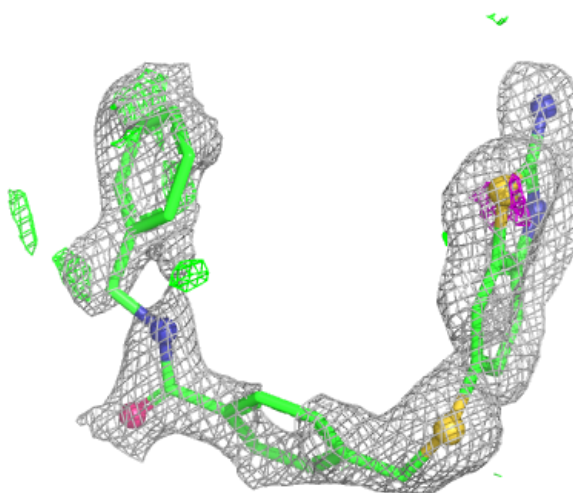
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	EWK	D	302	28/28	0.85	0.19	24,38,57,61	28
5	GOL	B	303[A]	6/6	0.86	0.15	15,23,25,26	6
5	GOL	B	303[B]	6/6	0.86	0.15	10,14,15,16	6
3	EWK	B	302	21/28	0.87	0.16	23,36,54,55	21
3	EWK	A	302	21/28	0.88	0.14	23,34,44,47	21
2	NAP	C	301	48/48	0.90	0.11	13,19,26,28	48
4	ACT	C	302	4/4	0.91	0.10	22,24,26,27	0
4	ACT	A	303	4/4	0.93	0.20	26,26,26,29	0
2	NAP	A	301	48/48	0.97	0.06	13,16,18,22	0
2	NAP	D	301	48/48	0.97	0.06	12,17,21,27	0
2	NAP	B	301	48/48	0.97	0.05	11,16,18,22	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.

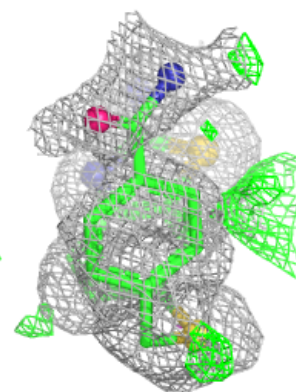
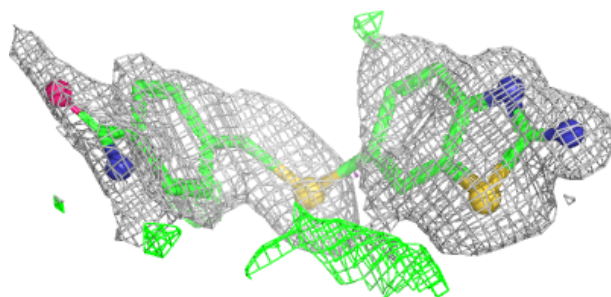
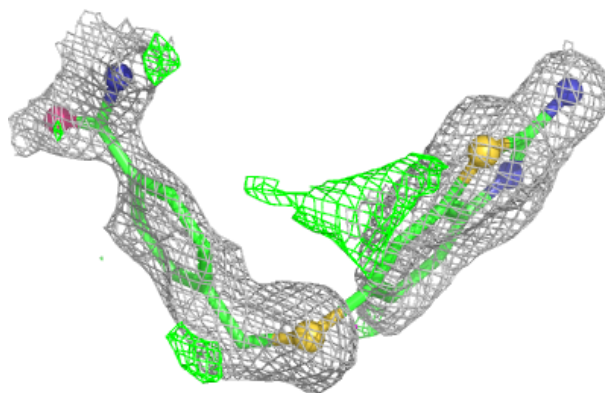
**Electron density around EWK D 302:**

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

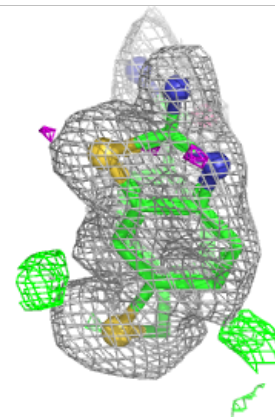
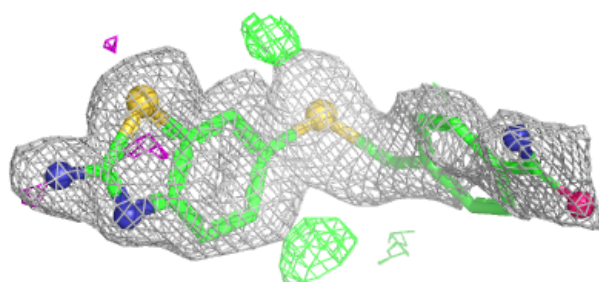
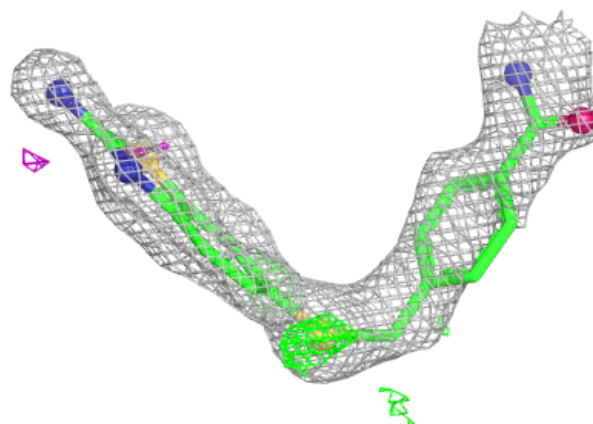


**Electron density around EWK B 302:**

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

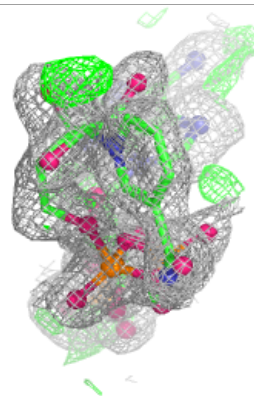
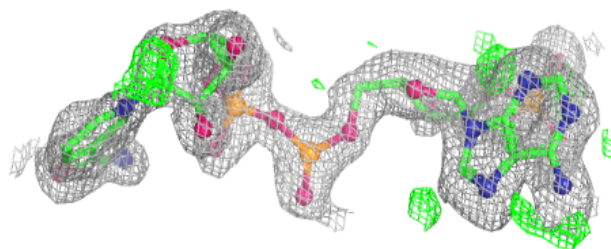
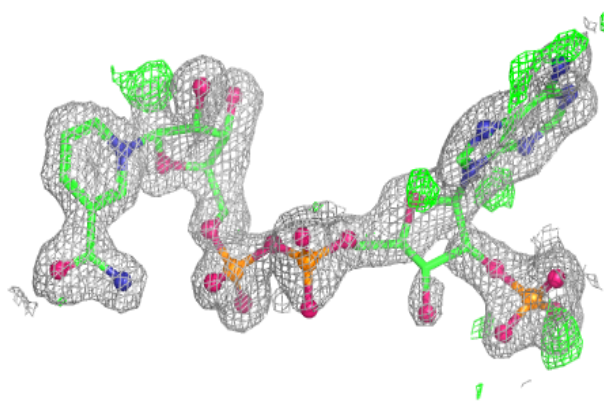
**Electron density around EWK A 302:**

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

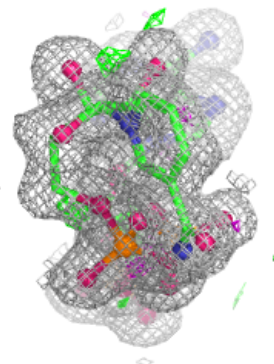
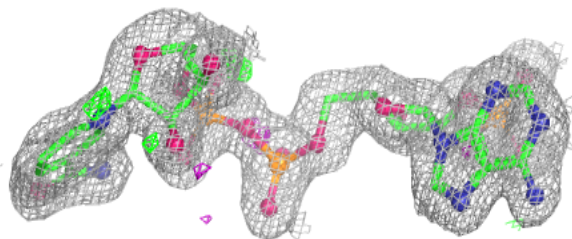
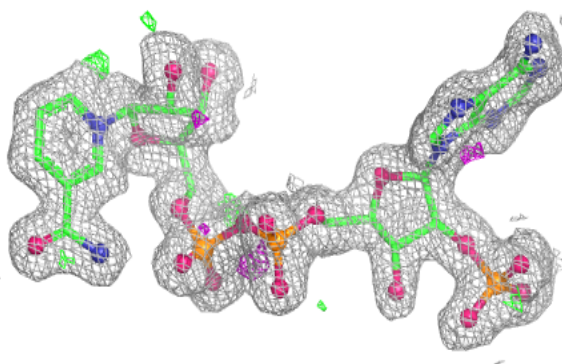


**Electron density around NAP C 301:**

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

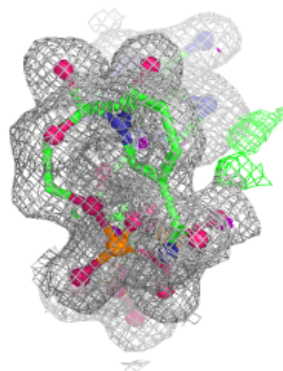
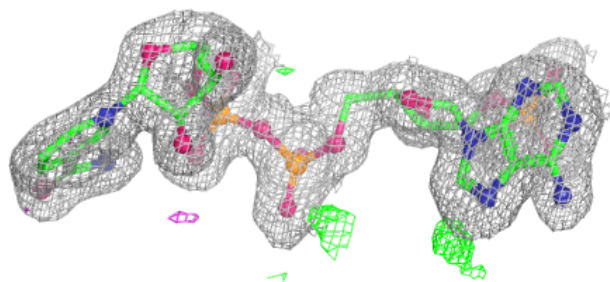
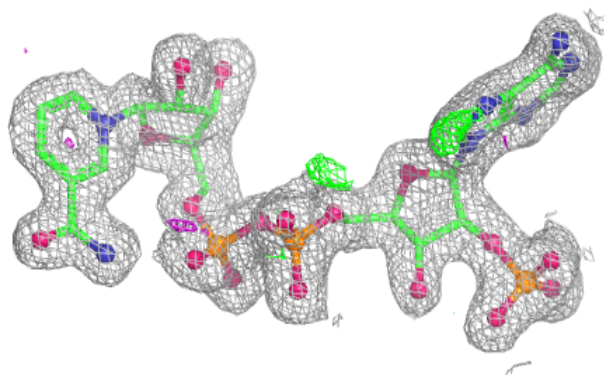
**Electron density around NAP A 301:**

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

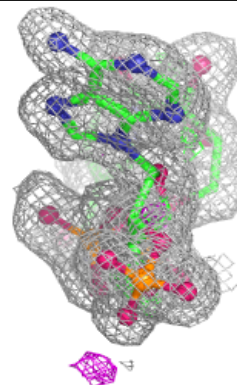
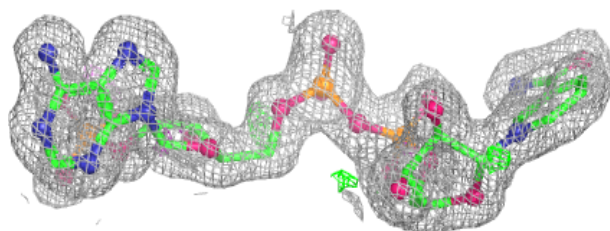
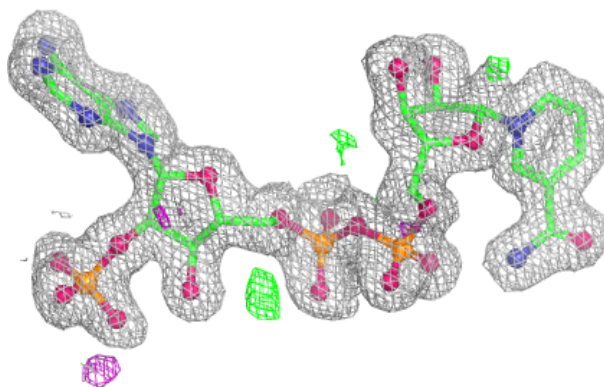


**Electron density around NAP D 301:**

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

**Electron density around NAP B 301:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.