



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 01:55 pm BST

PDB ID : 6P8Q  
Title : EGFR in complex with a dihydrodibenzodiazepinone allosteric inhibitor.  
Authors : Yun, C.H.; Heppner, D.E.; Eck, M.J.  
Deposited on : 2019-06-07  
Resolution : 1.90 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.

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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

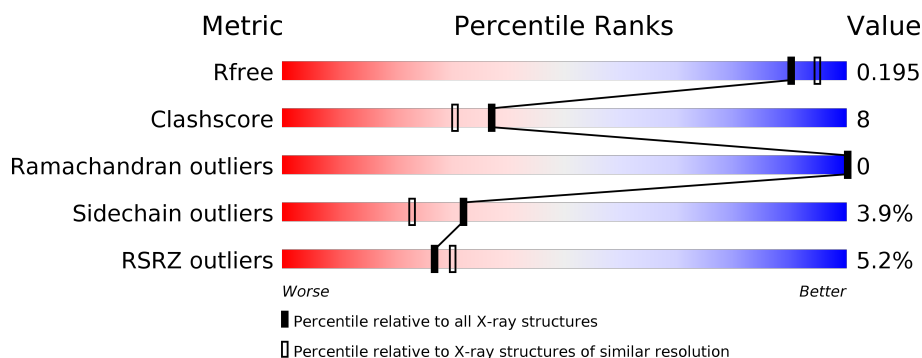
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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  $\geq 3$ , 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	327	<div> <div>3%</div> <div> <div></div> <div>82%</div> <div>12%</div> <div>6%</div> </div> </div>
1	B	327	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>14%</div> <div>8%</div> </div> </div>
1	C	327	<div> <div>8%</div> <div> <div></div> <div>80%</div> <div>15%</div> <div>• •</div> </div> </div>
1	D	327	<div> <div>6%</div> <div> <div></div> <div>74%</div> <div>15%</div> <div>• 9%</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
6	EDO	D	2004	-	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11202 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.

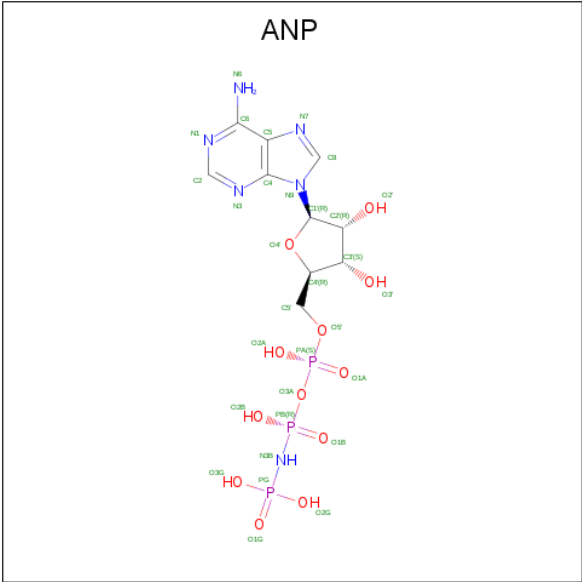
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	2	0
			2490	1603	416	452	19			
1	B	300	Total	C	N	O	S	0	9	0
			2452	1581	416	436	19			
1	C	316	Total	C	N	O	S	0	4	0
			2553	1638	434	461	20			
1	D	296	Total	C	N	O	S	0	5	0
			2418	1555	413	431	19			

There are 8 discrepancies between the modelled and reference sequences:

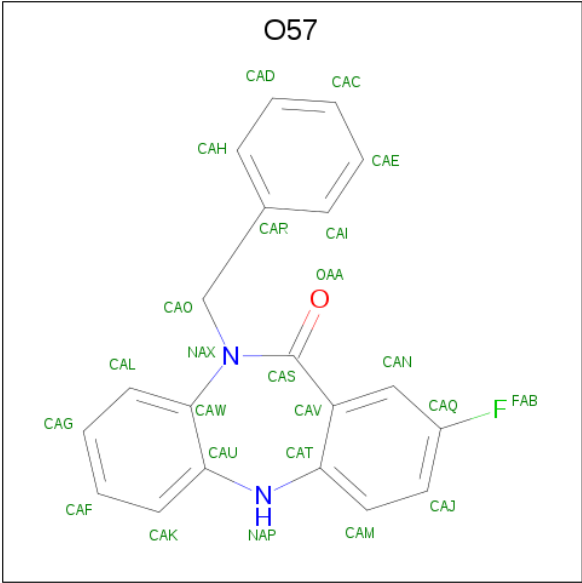
Chain	Residue	Modelled	Actual	Comment	Reference
A	790	MET	THR	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533
B	948	ARG	VAL	engineered mutation	UNP P00533
C	790	MET	THR	engineered mutation	UNP P00533
C	948	ARG	VAL	engineered mutation	UNP P00533
D	790	MET	THR	engineered mutation	UNP P00533
D	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 3 is 10-benzyl-2-fluoro-5,10-dihydro-11H-dibenzo[b,e][1,4]diazepin-11-one (three-letter code: O57) (formula: C<sub>20</sub>H<sub>15</sub>FN<sub>2</sub>O) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			24	20	1	2	1		
3	B	1	Total	C	F	N	O	0	0
			24	20	1	2	1		

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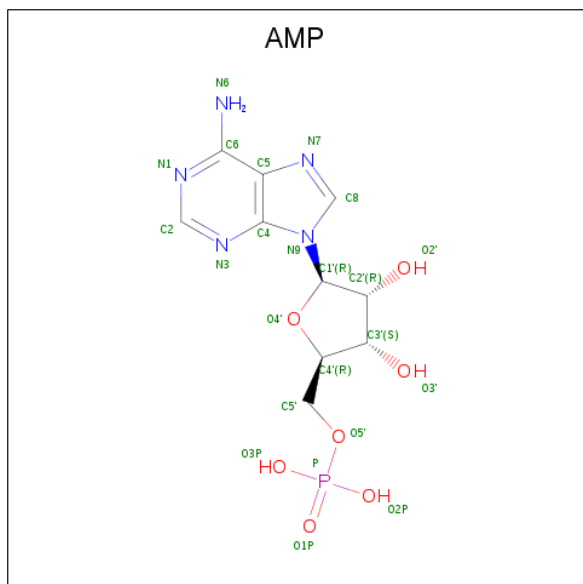
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	1	Total	C	F	N	O	0	0
			24	20	1	2	1		
3	D	1	Total	C	F	N	O	0	0
			24	20	1	2	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 5 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>7</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
5	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
5	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		
6	C	1	Total	C	O	0	0
			4	2	2		
6	C	1	Total	C	O	0	0
			4	2	2		
6	C	1	Total	C	O	0	0
			4	2	2		
6	C	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	301	Total	O	0	0
			301	301		
7	B	277	Total	O	0	0
			277	277		

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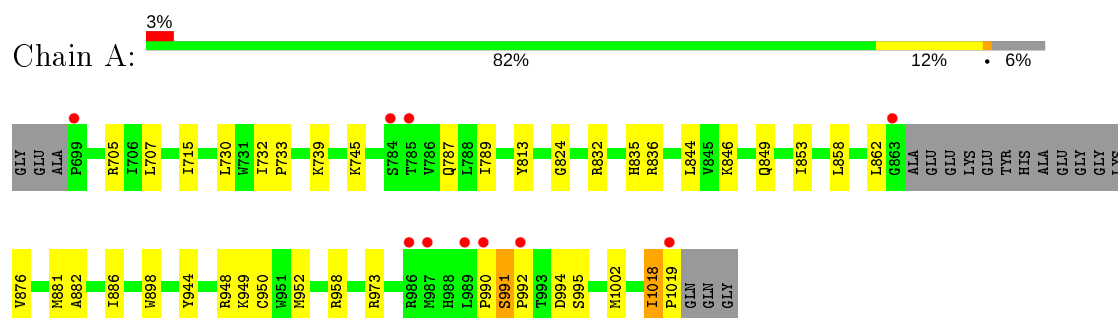
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	262	Total 262	O 262	0	0
7	D	212	Total 212	O 212	0	0



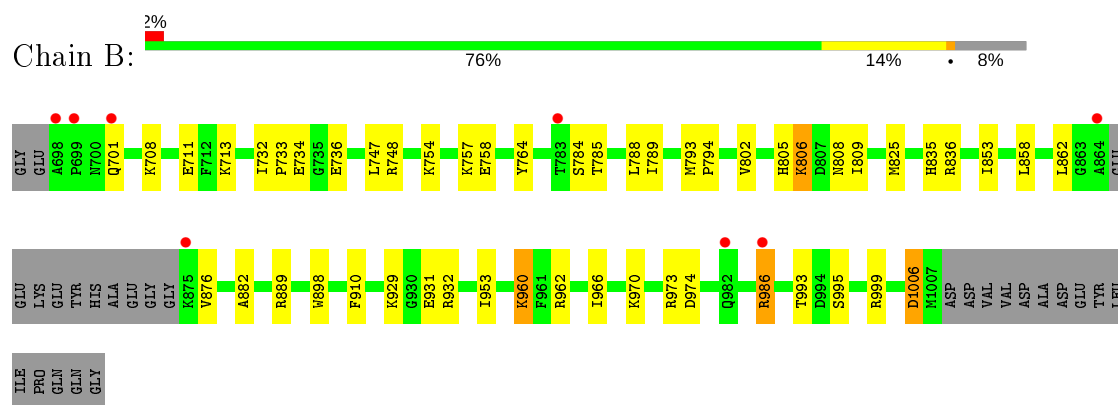
### 3 Residue-property plots [i](#)

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.

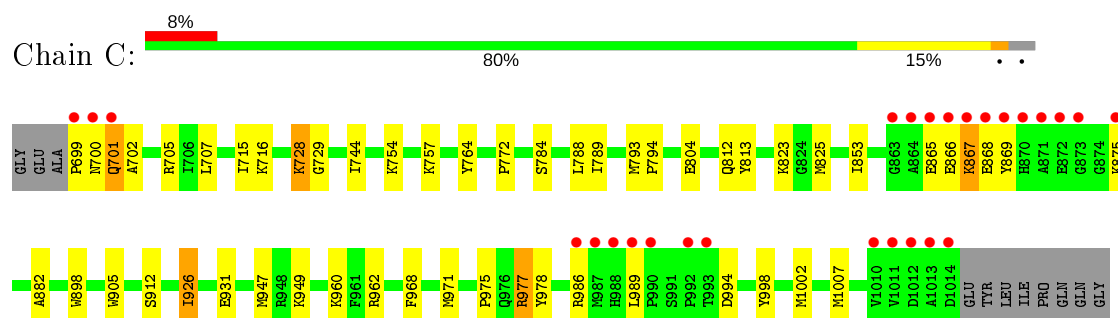
#### • Molecule 1: Epidermal growth factor receptor



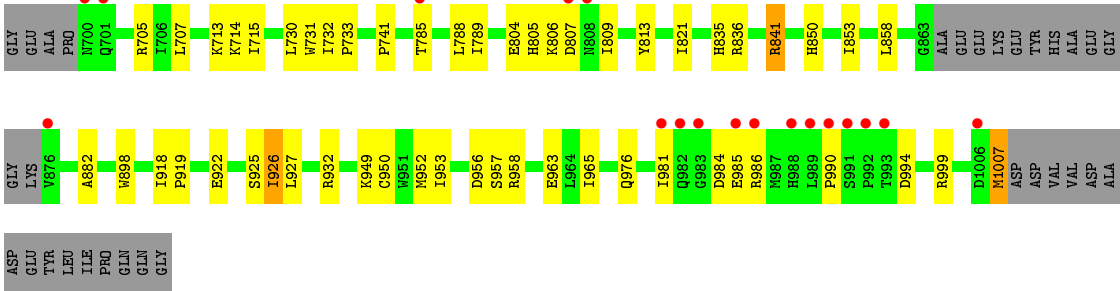
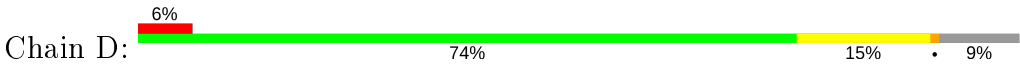
#### • Molecule 1: Epidermal growth factor receptor



#### • Molecule 1: Epidermal growth factor receptor



#### • Molecule 1: Epidermal growth factor receptor



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.15Å 72.87Å 79.93Å 100.16° 103.16° 95.61°	Depositor
Resolution (Å)	21.44 – 1.90 47.32 – 1.90	Depositor EDS
% Data completeness (in resolution range)	91.1 (21.44-1.90) 91.1 (47.32-1.90)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.27 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.15.2 _3472	Depositor
R, $R_{free}$	0.168 , 0.195 0.168 , 0.195	Depositor DCC
$R_{free}$ test set	4395 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.8	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 56.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11202	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.98% of the height of the origin peak. No significant pseudotranslation is detected.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AMP, MG, ANP, EDO, O57

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	0.94	0/2551	0.75	0/3454
1	B	0.95	1/2532 (0.0%)	0.79	2/3423 (0.1%)
1	C	0.93	0/2621	0.75	2/3543 (0.1%)
1	D	0.92	0/2485	0.74	0/3356
All	All	0.93	1/10189 (0.0%)	0.76	4/13776 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	974	ASP	C-N	7.43	1.48	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	995[A]	SER	CA-C-O	5.98	132.65	120.10
1	B	995[B]	SER	CA-C-O	5.98	132.65	120.10
1	C	926[A]	ILE	CA-C-O	5.50	131.65	120.10
1	C	926[B]	ILE	CA-C-O	5.50	131.65	120.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2490	0	2535	39	0
1	B	2452	0	2535	36	0
1	C	2553	0	2600	41	0
1	D	2418	0	2486	41	0
2	A	31	0	13	1	0
3	A	24	0	0	0	0
3	B	24	0	0	0	0
3	C	24	0	0	0	0
3	D	24	0	0	0	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	B	23	0	12	0	0
5	C	23	0	12	0	0
5	D	23	0	12	1	0
6	B	8	0	12	0	0
6	C	20	0	30	4	0
6	D	8	0	12	12	0
7	A	301	0	0	11	0
7	B	277	0	0	5	0
7	C	262	0	0	3	0
7	D	212	0	0	6	0
All	All	11202	0	10259	158	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (158) 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:A:813:TYR:CE1	1:A:990:PRO:HD3	2.03	0.94
1:C:868:GLU:HG2	1:C:869:TYR:N	1.90	0.85
1:C:865:GLU:O	1:C:866:GLU:CB	2.27	0.82
1:D:806:LYS:HD3	7:D:2117:HOH:O	1.79	0.82
1:C:812[A]:GLN:HG2	1:C:989:LEU:HG	1.62	0.81
1:A:949:LYS:HG2	1:A:952:MET:HE2	1.63	0.81
1:B:732:ILE:HD12	1:B:733:PRO:HD2	1.63	0.81
1:D:705:ARG:HH12	6:D:2004:EDO:H21	1.47	0.80
1:A:949:LYS:HA	1:A:952:MET:HE2	1.64	0.80
1:C:788:LEU:C	1:C:789:ILE:HD12	2.02	0.78
1:D:813:TYR:CE1	1:D:990:PRO:HD3	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:986:ARG:HH11	1:B:986:ARG:HG2	1.50	0.76
1:D:705:ARG:HH22	6:D:2004:EDO:H21	1.53	0.73
1:A:952:MET:HE1	7:A:2156:HOH:O	1.89	0.72
1:A:849:GLN:NE2	7:A:2102:HOH:O	2.22	0.71
1:D:731:TRP:HZ2	6:D:2004:EDO:H22	1.55	0.71
1:D:965:ILE:HD13	6:D:2005:EDO:H21	1.73	0.71
1:D:841[A]:ARG:NH1	5:D:2001:AMP:O3P	2.24	0.70
1:D:715:ILE:HD11	1:D:730:LEU:CD1	2.22	0.70
1:D:731:TRP:CZ2	6:D:2004:EDO:H22	2.27	0.69
1:A:732:ILE:CD1	1:A:739:LYS:HG2	2.24	0.68
1:C:868:GLU:CG	1:C:869:TYR:N	2.55	0.68
1:C:715:ILE:HG22	1:C:716:LYS:HG2	1.76	0.67
1:B:986:ARG:CG	1:B:986:ARG:HH11	2.07	0.67
1:D:705:ARG:NH1	6:D:2004:EDO:H21	2.11	0.66
1:A:832:ARG:NH1	7:A:2105:HOH:O	2.28	0.65
1:B:973[A]:ARG:HG2	1:B:973[A]:ARG:HH21	1.61	0.65
1:A:846:LYS:NZ	7:A:2106:HOH:O	2.30	0.65
1:A:949:LYS:HG2	1:A:952:MET:CE	2.26	0.65
1:B:960:LYS:HE3	7:B:2110:HOH:O	1.98	0.64
1:A:949:LYS:CA	1:A:952:MET:HE2	2.29	0.63
1:A:949:LYS:CG	1:A:952:MET:HE2	2.26	0.63
1:D:850:HIS:CE1	1:D:1007:MET:SD	2.92	0.63
1:A:949:LYS:CB	1:A:952:MET:HE2	2.29	0.62
1:C:754:LYS:HE2	7:C:2322:HOH:O	1.99	0.62
1:C:968:PHE:CD1	1:C:971:MET:HE3	2.35	0.61
1:D:952:MET:HE1	1:D:957:SER:O	2.01	0.60
1:D:999:ARG:HH11	1:D:999:ARG:HG2	1.66	0.60
1:B:825:MET:SD	1:B:853:ILE:HD13	2.41	0.59
1:C:823:LYS:HD3	6:C:2007:EDO:H21	1.84	0.59
1:B:788:LEU:C	1:B:789:ILE:HD12	2.22	0.59
1:A:707:LEU:HD13	1:A:789:ILE:HD13	1.83	0.59
1:B:836:ARG:NH2	7:B:2102:HOH:O	2.24	0.59
1:D:705:ARG:NH2	6:D:2004:EDO:H21	2.16	0.59
1:B:732:ILE:HD11	1:B:736:GLU:O	2.03	0.58
1:A:1018:ILE:HD13	1:D:741:PRO:HG3	1.86	0.58
1:C:905:TRP:HD1	1:C:947:MET:HE1	1.68	0.57
1:A:1019:PRO:HG2	7:A:2344:HOH:O	2.03	0.57
1:C:789:ILE:HD12	1:C:789:ILE:N	2.19	0.57
1:B:1006:ASP:OD1	1:B:1006:ASP:N	2.30	0.57
1:C:968:PHE:CD1	1:C:971:MET:CE	2.88	0.56
1:D:789:ILE:N	1:D:789:ILE:HD12	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:812[A]:GLN:HG2	1:C:989:LEU:CG	2.35	0.56
1:A:1018:ILE:HG22	1:A:1018:ILE:O	2.05	0.56
1:D:788:LEU:C	1:D:789:ILE:HD12	2.27	0.55
1:B:701:GLN:HG2	1:B:764:TYR:CE1	2.41	0.55
1:A:973:ARG:NH2	7:A:2103:HOH:O	2.26	0.55
1:A:835:HIS:O	1:A:836:ARG:HB2	2.07	0.54
1:A:844:LEU:HD21	7:A:2184:HOH:O	2.07	0.54
1:B:932:ARG:HH22	1:B:953:ILE:HD11	1.72	0.54
1:D:835:HIS:O	1:D:836:ARG:HB2	2.07	0.54
1:C:926[A]:ILE:HG23	1:C:931:GLU:HB3	1.88	0.54
1:C:728:LYS:HD2	1:C:729:GLY:N	2.23	0.54
1:B:825:MET:HG2	1:B:853:ILE:HD11	1.91	0.53
1:C:813:TYR:CE1	1:C:989:LEU:HD23	2.43	0.53
1:C:994:ASP:HB3	6:D:2004:EDO:O1	2.09	0.53
1:C:977:ARG:HG2	1:C:978:TYR:CE2	2.44	0.53
1:D:932:ARG:HH22	1:D:953:ILE:HD11	1.73	0.52
1:A:991:SER:OG	1:A:992:PRO:HD2	2.10	0.52
1:A:952:MET:CE	7:A:2156:HOH:O	2.52	0.52
1:B:732:ILE:HD12	1:B:733:PRO:CD	2.37	0.52
1:A:715:ILE:HD11	1:A:730:LEU:CD1	2.40	0.51
1:A:949:LYS:CB	1:A:952:MET:CE	2.88	0.51
1:D:813:TYR:CE1	1:D:990:PRO:CD	2.92	0.51
1:A:876:VAL:N	7:A:2109:HOH:O	2.42	0.51
1:D:821:ILE:HG23	1:D:853:ILE:HD11	1.92	0.51
1:B:747:LEU:O	1:B:785:THR:CG2	2.58	0.51
1:B:858:LEU:HD11	1:B:862:LEU:HD12	1.93	0.51
1:C:744:ILE:HG12	1:C:789:ILE:HG13	1.93	0.50
1:D:731:TRP:HZ2	6:D:2004:EDO:C2	2.23	0.50
2:A:2001:ANP:O2A	7:A:2101:HOH:O	2.20	0.50
1:D:950:CYS:O	1:D:958:ARG:HD3	2.12	0.50
1:D:785:THR:O	1:D:785:THR:HG23	2.12	0.49
1:B:835:HIS:O	1:B:836:ARG:HB2	2.12	0.49
1:C:825:MET:SD	1:C:853:ILE:HD13	2.52	0.49
1:D:922:GLU:HA	7:D:2102:HOH:O	2.13	0.49
1:D:963[A]:GLU:HG3	7:D:2270:HOH:O	2.11	0.49
1:B:805:HIS:O	1:B:809:ILE:HG13	2.12	0.49
1:C:772:PRO:HB3	1:C:1007:MET:HG3	1.94	0.49
1:D:882:ALA:HA	1:D:898:TRP:CD2	2.47	0.49
1:B:973[A]:ARG:HG2	1:B:973[A]:ARG:NH2	2.27	0.49
1:D:841[A]:ARG:CZ	7:D:2119:HOH:O	2.61	0.49
1:C:728:LYS:HD2	1:C:728:LYS:C	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:701:GLN:HG3	1:C:764:TYR:CE1	2.48	0.48
1:B:789:ILE:N	1:B:789:ILE:HD12	2.28	0.48
6:C:2007:EDO:H11	7:C:2151:HOH:O	2.14	0.48
1:C:804:GLU:OE2	6:C:2006:EDO:H22	2.14	0.47
1:C:794:PRO:HG2	1:C:1002:MET:CE	2.44	0.47
1:C:700:ASN:HD21	1:C:702:ALA:HB3	1.80	0.47
1:C:789:ILE:CD1	1:C:789:ILE:N	2.78	0.47
1:D:705:ARG:HH22	6:D:2004:EDO:C2	2.24	0.47
1:A:944:TYR:CZ	1:A:948:ARG:HD3	2.50	0.47
1:C:912:SER:CB	6:C:2005:EDO:H12	2.45	0.46
1:B:802[B]:VAL:CG1	1:B:910:PHE:HA	2.46	0.46
1:D:705:ARG:CZ	6:D:2004:EDO:H21	2.46	0.46
1:D:981:ILE:O	1:D:984:ASP:HB2	2.16	0.46
1:C:812[B]:GLN:HG2	1:C:975:PRO:HG3	1.97	0.45
1:D:985:GLU:H	1:D:985:GLU:CD	2.19	0.45
1:B:931:GLU:O	1:B:932:ARG:HD3	2.17	0.45
1:D:805:HIS:O	1:D:809:ILE:HG13	2.16	0.45
1:B:825:MET:HG2	1:B:853:ILE:CD1	2.46	0.45
1:C:867:LYS:HG3	1:C:868:GLU:H	1.82	0.45
1:A:858:LEU:HD11	1:A:862:LEU:CD1	2.47	0.44
1:D:999:ARG:HG2	1:D:999:ARG:NH1	2.31	0.44
1:C:949:LYS:HB3	1:C:949:LYS:HE2	1.63	0.44
1:B:966:ILE:O	1:B:970[A]:LYS:HG3	2.18	0.44
1:C:977:ARG:HG3	1:C:978:TYR:CD2	2.53	0.44
1:B:708:LYS:HB2	1:B:711:GLU:HG3	2.00	0.43
1:A:882:ALA:HA	1:A:898:TRP:CD2	2.53	0.43
1:B:882:ALA:HA	1:B:898:TRP:CD2	2.54	0.43
1:C:699:PRO:N	7:C:2114:HOH:O	2.51	0.43
1:A:715:ILE:CD1	1:A:730:LEU:HG	2.48	0.43
1:A:824:GLY:HA3	1:A:853:ILE:CD1	2.49	0.43
1:C:705:ARG:HD3	1:C:707:LEU:HD21	2.01	0.43
1:A:881:MET:HE2	1:A:886:ILE:HG12	1.99	0.43
1:C:882:ALA:HA	1:C:898:TRP:CD2	2.54	0.43
1:D:715:ILE:HD11	1:D:730:LEU:HD11	1.97	0.43
1:A:949:LYS:HB3	1:A:952:MET:CE	2.49	0.43
1:A:949:LYS:HA	1:A:952:MET:CE	2.43	0.42
1:D:918:ILE:HA	1:D:919:PRO:HD3	1.82	0.42
1:B:732:ILE:HA	1:B:733:PRO:HD3	1.76	0.42
1:A:858:LEU:HD11	1:A:862:LEU:HD12	2.00	0.42
1:B:793:MET:HA	1:B:794:PRO:HD2	1.79	0.42
1:A:705:ARG:HD3	1:B:993:THR:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:732:ILE:HD12	1:A:739:LYS:HG2	2.00	0.42
1:B:806:LYS:HE2	1:B:806:LYS:HB2	1.44	0.42
1:C:793:MET:HA	1:C:794:PRO:HD3	1.83	0.42
1:D:926:ILE:HG13	1:D:927:LEU:N	2.34	0.42
6:D:2004:EDO:H12	7:D:2109:HOH:O	2.19	0.42
1:C:705:ARG:HD3	1:C:707:LEU:CD2	2.49	0.42
1:C:989:LEU:HD23	1:C:989:LEU:HA	1.88	0.41
1:D:732:ILE:HA	1:D:733:PRO:HD3	1.79	0.41
1:B:734[A]:GLU:OE2	7:B:2101:HOH:O	2.22	0.41
1:D:715:ILE:HD11	1:D:730:LEU:HD12	1.99	0.41
1:B:794:PRO:HD2	7:B:2146:HOH:O	2.21	0.41
1:B:929:LYS:NZ	7:B:2113:HOH:O	2.53	0.41
1:D:976:GLN:HB2	7:D:2199:HOH:O	2.20	0.41
1:B:986:ARG:CG	1:B:986:ARG:NH1	2.73	0.41
1:A:876:VAL:N	7:A:2117:HOH:O	2.54	0.40
1:A:745:LYS:O	1:A:787:GLN:HA	2.22	0.40
1:A:950:CYS:O	1:A:958:ARG:HD3	2.21	0.40
1:B:748:ARG:HD3	1:B:748:ARG:HH11	1.75	0.40
1:C:977:ARG:CG	1:C:978:TYR:CE2	3.04	0.40
1:C:960:LYS:HD2	1:C:960:LYS:HA	1.97	0.40
1:C:812[A]:GLN:HG2	1:C:989:LEU:CD1	2.52	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	307/327 (94%)	303 (99%)	4 (1%)	0	100	100
1	B	305/327 (93%)	301 (99%)	4 (1%)	0	100	100
1	C	318/327 (97%)	315 (99%)	3 (1%)	0	100	100
1	D	297/327 (91%)	293 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1227/1308 (94%)	1212 (99%)	15 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	277/287 (96%)	272 (98%)	5 (2%)	59	55
1	B	274/287 (96%)	259 (94%)	15 (6%)	21	12
1	C	281/287 (98%)	271 (96%)	10 (4%)	35	26
1	D	269/287 (94%)	252 (94%)	17 (6%)	18	8
All	All	1101/1148 (96%)	1054 (96%)	47 (4%)	32	19

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	991	SER
1	A	994	ASP
1	A	995	SER
1	A	1002	MET
1	A	1018	ILE
1	B	713	LYS
1	B	754	LYS
1	B	757[A]	LYS
1	B	757[B]	LYS
1	B	758	GLU
1	B	784	SER
1	B	806	LYS
1	B	808[A]	ASN
1	B	808[B]	ASN
1	B	876	VAL
1	B	889	ARG
1	B	960	LYS

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Mol	Chain	Res	Type
1	B	962	ARG
1	B	986	ARG
1	B	1006	ASP
1	C	701	GLN
1	C	728	LYS
1	C	757	LYS
1	C	784	SER
1	C	867	LYS
1	C	875	LYS
1	C	962	ARG
1	C	977	ARG
1	C	986	ARG
1	C	998	TYR
1	D	707	LEU
1	D	713	LYS
1	D	714	LYS
1	D	804[A]	GLU
1	D	804[B]	GLU
1	D	807	ASP
1	D	841[A]	ARG
1	D	841[B]	ARG
1	D	858	LEU
1	D	925	SER
1	D	926	ILE
1	D	949[A]	LYS
1	D	949[B]	LYS
1	D	956	ASP
1	D	986	ARG
1	D	994	ASP
1	D	1007	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	982	GLN
1	C	870	HIS

### 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 ⓘ

Of 22 ligands modelled in this entry, 5 are monoatomic - leaving 17 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	O57	C	2002	-	22,27,27	1.21	1 (4%)	22,38,38	1.06	1 (4%)
6	EDO	D	2004	-	3,3,3	0.25	0	2,2,2	0.42	0
5	AMP	B	2001	4	22,25,25	1.89	5 (22%)	25,38,38	1.61	4 (16%)
6	EDO	C	2007	-	3,3,3	0.61	0	2,2,2	0.20	0
5	AMP	D	2001	-	22,25,25	1.89	5 (22%)	25,38,38	1.79	3 (12%)
5	AMP	C	2001	4	22,25,25	1.74	5 (22%)	25,38,38	1.43	4 (16%)
2	ANP	A	2001	4	29,33,33	2.34	10 (34%)	31,52,52	1.72	6 (19%)
6	EDO	C	2004	-	3,3,3	0.33	0	2,2,2	0.46	0
3	O57	D	2002	-	22,27,27	1.27	2 (9%)	22,38,38	1.00	1 (4%)
6	EDO	C	2005	-	3,3,3	0.41	0	2,2,2	0.50	0
6	EDO	B	2005	-	3,3,3	0.29	0	2,2,2	0.48	0
6	EDO	D	2005	-	3,3,3	0.35	0	2,2,2	0.34	0
6	EDO	B	2004	-	3,3,3	0.16	0	2,2,2	1.02	0
3	O57	B	2002	-	22,27,27	1.20	1 (4%)	22,38,38	1.00	1 (4%)
3	O57	A	2002	-	22,27,27	1.27	2 (9%)	22,38,38	1.03	2 (9%)
6	EDO	C	2006	-	3,3,3	0.42	0	2,2,2	0.39	0
6	EDO	C	2008	-	3,3,3	0.33	0	2,2,2	0.63	0

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	O57	C	2002	-	-	2/2/4/4	0/3/4/4
6	EDO	D	2004	-	-	1/1/1/1	-
5	AMP	B	2001	4	-	0/6/26/26	0/3/3/3
6	EDO	C	2007	-	-	1/1/1/1	-
5	AMP	D	2001	-	-	0/6/26/26	0/3/3/3
5	AMP	C	2001	4	-	0/6/26/26	0/3/3/3
2	ANP	A	2001	4	-	4/14/38/38	0/3/3/3
6	EDO	C	2004	-	-	1/1/1/1	-
3	O57	D	2002	-	-	2/2/4/4	0/3/4/4
6	EDO	C	2005	-	-	1/1/1/1	-
6	EDO	B	2005	-	-	0/1/1/1	-
6	EDO	D	2005	-	-	1/1/1/1	-
6	EDO	B	2004	-	-	1/1/1/1	-
3	O57	B	2002	-	-	2/2/4/4	0/3/4/4
3	O57	A	2002	-	-	2/2/4/4	0/3/4/4
6	EDO	C	2006	-	-	0/1/1/1	-
6	EDO	C	2008	-	-	1/1/1/1	-

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2001	ANP	PG-O1G	6.57	1.56	1.46
2	A	2001	ANP	C2'-C1'	-5.05	1.46	1.53
5	D	2001	AMP	C2'-C1'	-4.84	1.46	1.53
5	B	2001	AMP	C2'-C1'	-4.83	1.46	1.53
5	D	2001	AMP	C2'-C3'	-4.71	1.40	1.53
5	B	2001	AMP	C2'-C3'	-4.54	1.40	1.53
2	A	2001	ANP	C2'-C3'	-4.47	1.41	1.53
5	C	2001	AMP	C2'-C3'	-4.43	1.41	1.53
5	C	2001	AMP	C2'-C1'	-4.18	1.47	1.53
2	A	2001	ANP	PB-O1B	3.69	1.52	1.46
2	A	2001	ANP	PG-O3G	-3.08	1.48	1.56
5	B	2001	AMP	P-O5'	-2.76	1.51	1.60
5	B	2001	AMP	O4'-C4'	-2.75	1.38	1.45
5	D	2001	AMP	P-O5'	-2.67	1.51	1.60
2	A	2001	ANP	C6-N6	2.55	1.43	1.34
5	C	2001	AMP	P-O5'	-2.51	1.52	1.60
2	A	2001	ANP	O4'-C4'	-2.44	1.39	1.45
3	D	2002	O57	CAN-CAQ	2.41	1.40	1.36
5	B	2001	AMP	C6-N6	2.34	1.42	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	2001	AMP	C6-N6	2.30	1.42	1.34
5	C	2001	AMP	O4'-C4'	-2.28	1.39	1.45
5	D	2001	AMP	O4'-C4'	-2.27	1.39	1.45
2	A	2001	ANP	PA-O5'	-2.27	1.50	1.59
5	D	2001	AMP	C6-N6	2.27	1.42	1.34
3	A	2002	O57	CAN-CAQ	2.19	1.39	1.36
3	A	2002	O57	CAJ-CAQ	2.16	1.41	1.37
2	A	2001	ANP	PG-N3B	2.16	1.69	1.63
3	C	2002	O57	CAJ-CAQ	2.09	1.41	1.37
3	D	2002	O57	CAJ-CAQ	2.07	1.41	1.37
3	B	2002	O57	CAJ-CAQ	2.02	1.41	1.37
2	A	2001	ANP	PB-O2B	-2.02	1.51	1.56

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	2001	AMP	C1'-N9-C4	-5.76	116.52	126.64
5	D	2001	AMP	N3-C2-N1	-5.03	120.81	128.68
5	B	2001	AMP	C1'-N9-C4	-4.69	118.39	126.64
2	A	2001	ANP	N3-C2-N1	-4.65	121.41	128.68
5	B	2001	AMP	N3-C2-N1	-4.52	121.62	128.68
5	C	2001	AMP	N3-C2-N1	-4.36	121.86	128.68
2	A	2001	ANP	C1'-N9-C4	-3.61	120.29	126.64
2	A	2001	ANP	O5'-C5'-C4'	3.37	120.57	108.99
5	C	2001	AMP	C1'-N9-C4	-3.18	121.05	126.64
2	A	2001	ANP	O1G-PG-N3B	-3.15	107.12	111.77
3	D	2002	O57	CAK-CAU-CAW	2.60	122.38	118.83
5	C	2001	AMP	O5'-C5'-C4'	2.58	117.87	108.99
3	B	2002	O57	CAK-CAU-CAW	2.39	122.10	118.83
5	B	2001	AMP	O5'-C5'-C4'	2.35	117.09	108.99
2	A	2001	ANP	C4-C5-N7	-2.20	107.10	109.40
3	A	2002	O57	CAK-CAU-CAW	2.19	121.82	118.83
5	B	2001	AMP	C4-C5-N7	-2.13	107.18	109.40
3	A	2002	O57	CAJ-CAQ-CAN	-2.13	120.88	123.23
5	C	2001	AMP	O5'-P-O1P	2.11	112.39	106.47
2	A	2001	ANP	O2G-PG-O1G	-2.06	108.27	113.45
5	D	2001	AMP	O5'-C5'-C4'	2.04	116.00	108.99
3	C	2002	O57	CAQ-CAN-CAV	-2.01	118.00	119.43

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2001	ANP	PB-N3B-PG-O1G
2	A	2001	ANP	PG-N3B-PB-O1B
2	A	2001	ANP	PA-O3A-PB-O1B
2	A	2001	ANP	PA-O3A-PB-O2B
6	C	2005	EDO	O1-C1-C2-O2
6	C	2008	EDO	O1-C1-C2-O2
3	A	2002	O57	NAX-CAO-CAR-CAI
3	A	2002	O57	NAX-CAO-CAR-CAH
3	B	2002	O57	NAX-CAO-CAR-CAI
3	B	2002	O57	NAX-CAO-CAR-CAH
3	C	2002	O57	NAX-CAO-CAR-CAI
3	D	2002	O57	NAX-CAO-CAR-CAI
3	C	2002	O57	NAX-CAO-CAR-CAH
3	D	2002	O57	NAX-CAO-CAR-CAH
6	D	2004	EDO	O1-C1-C2-O2
6	C	2007	EDO	O1-C1-C2-O2
6	D	2005	EDO	O1-C1-C2-O2
6	C	2004	EDO	O1-C1-C2-O2
6	B	2004	EDO	O1-C1-C2-O2

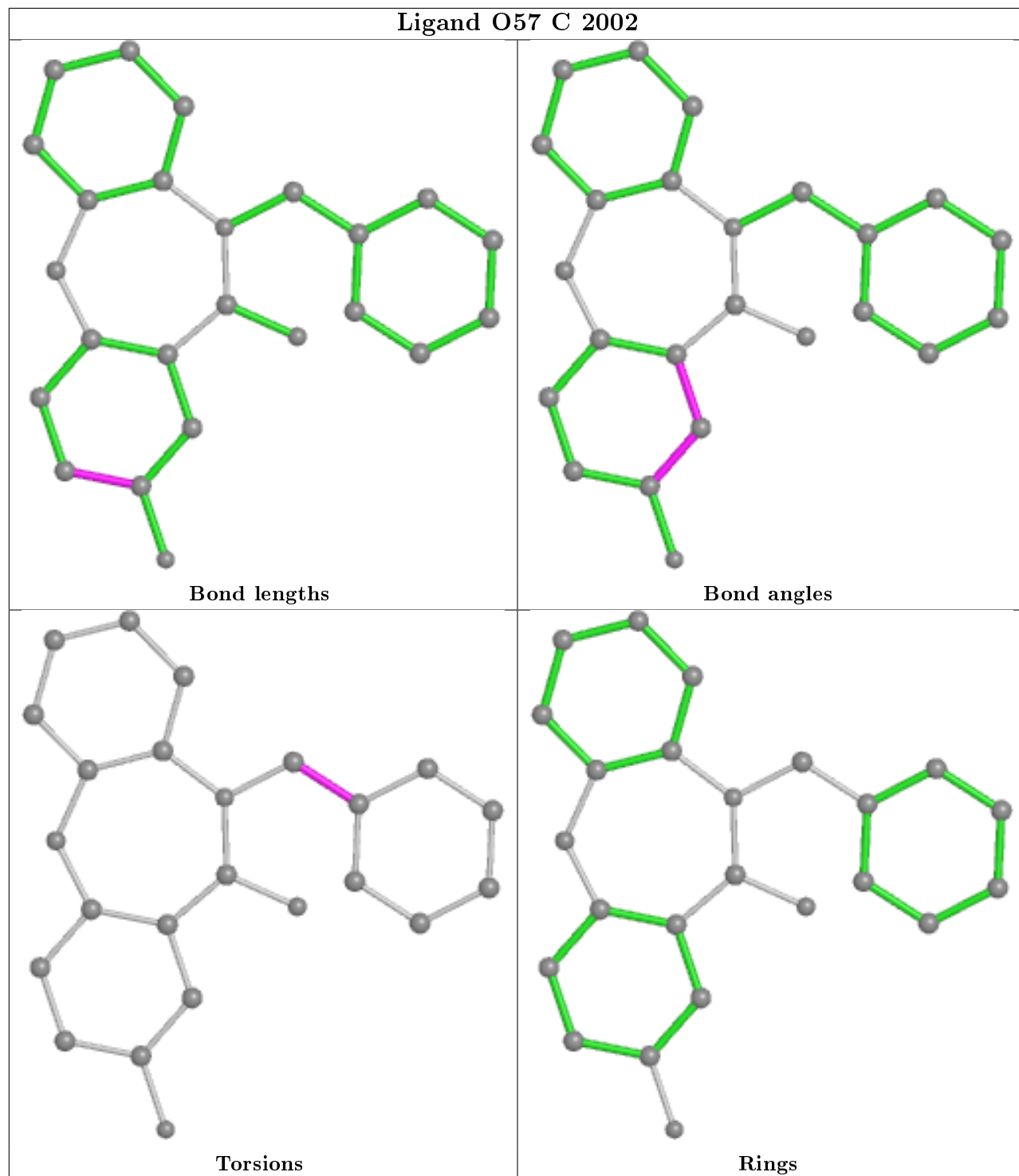
There are no ring outliers.

7 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	2004	EDO	11	0
6	C	2007	EDO	2	0
5	D	2001	AMP	1	0
2	A	2001	ANP	1	0
6	C	2005	EDO	1	0
6	D	2005	EDO	1	0
6	C	2006	EDO	1	0

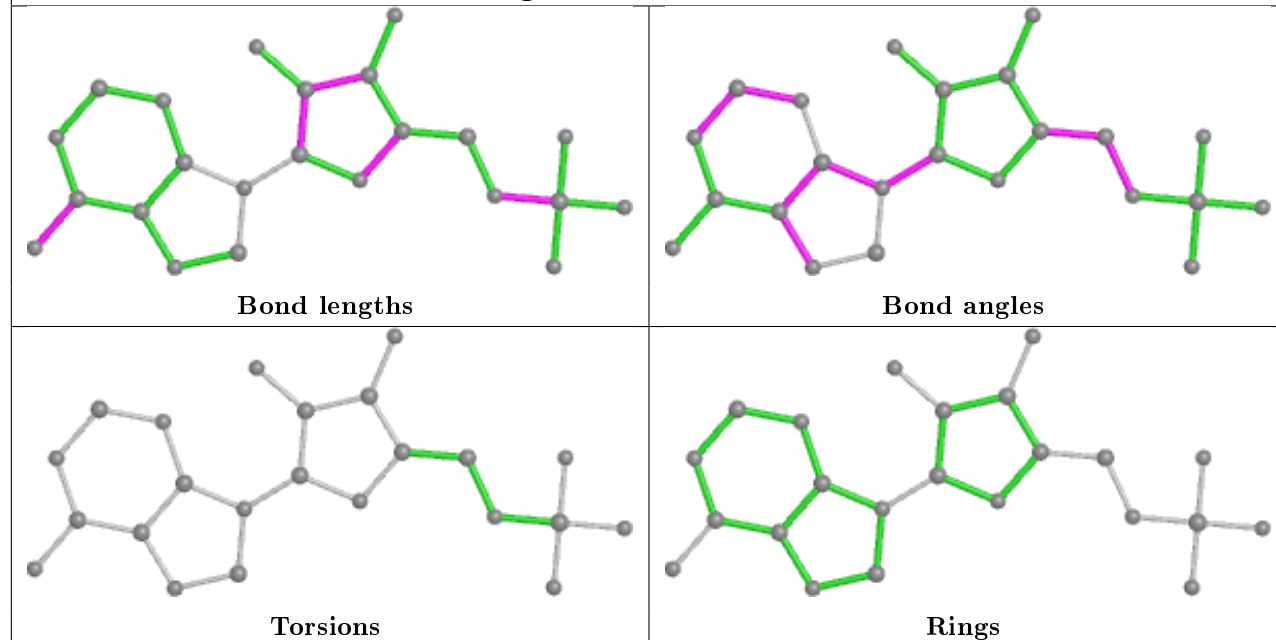
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

equivalents in the CSD to analyse the geometry.

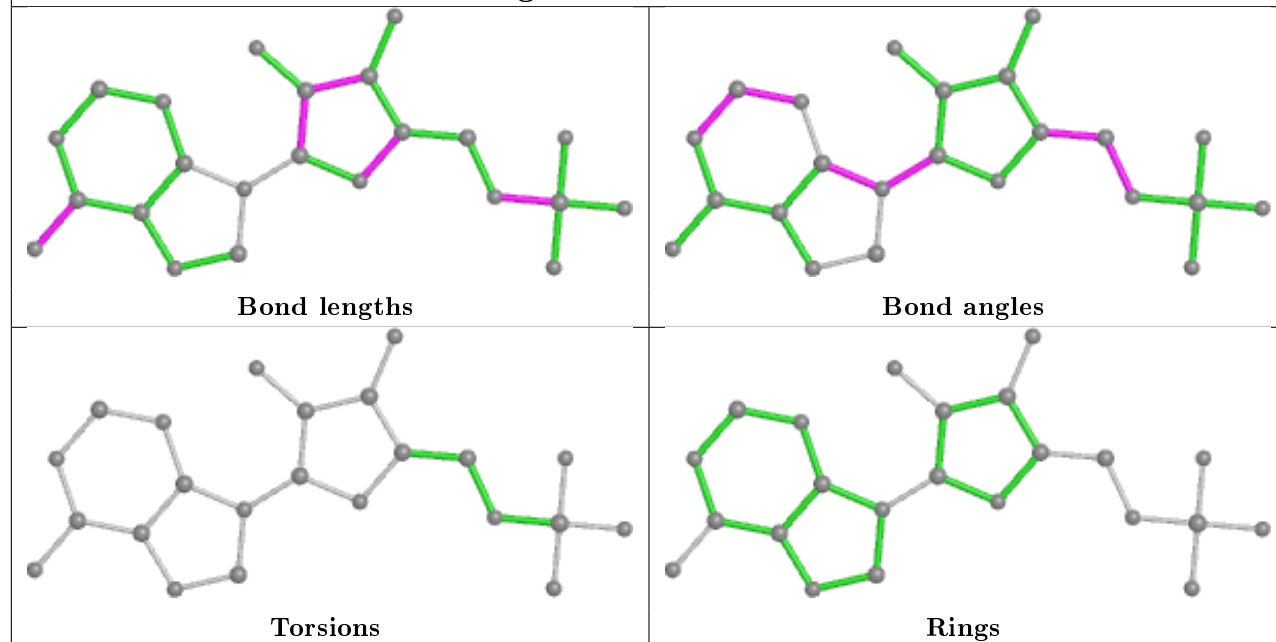




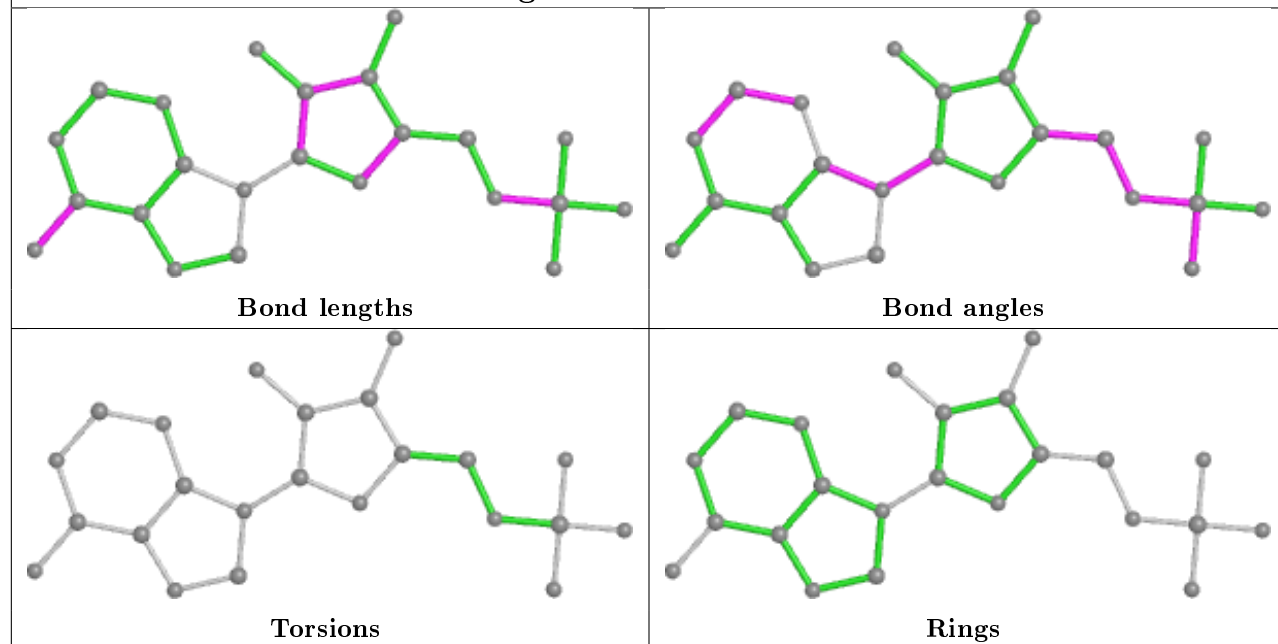
## Ligand AMP B 2001



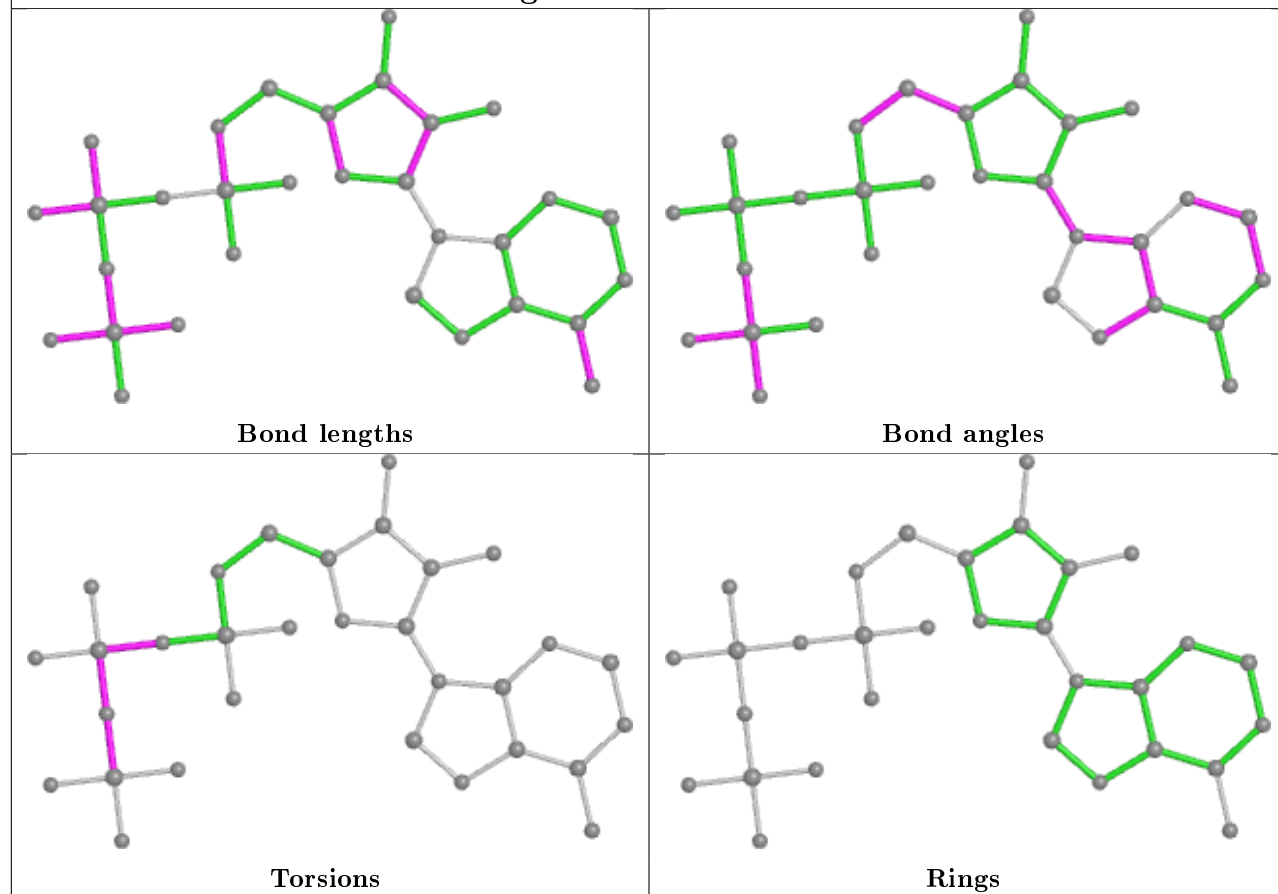
## Ligand AMP D 2001

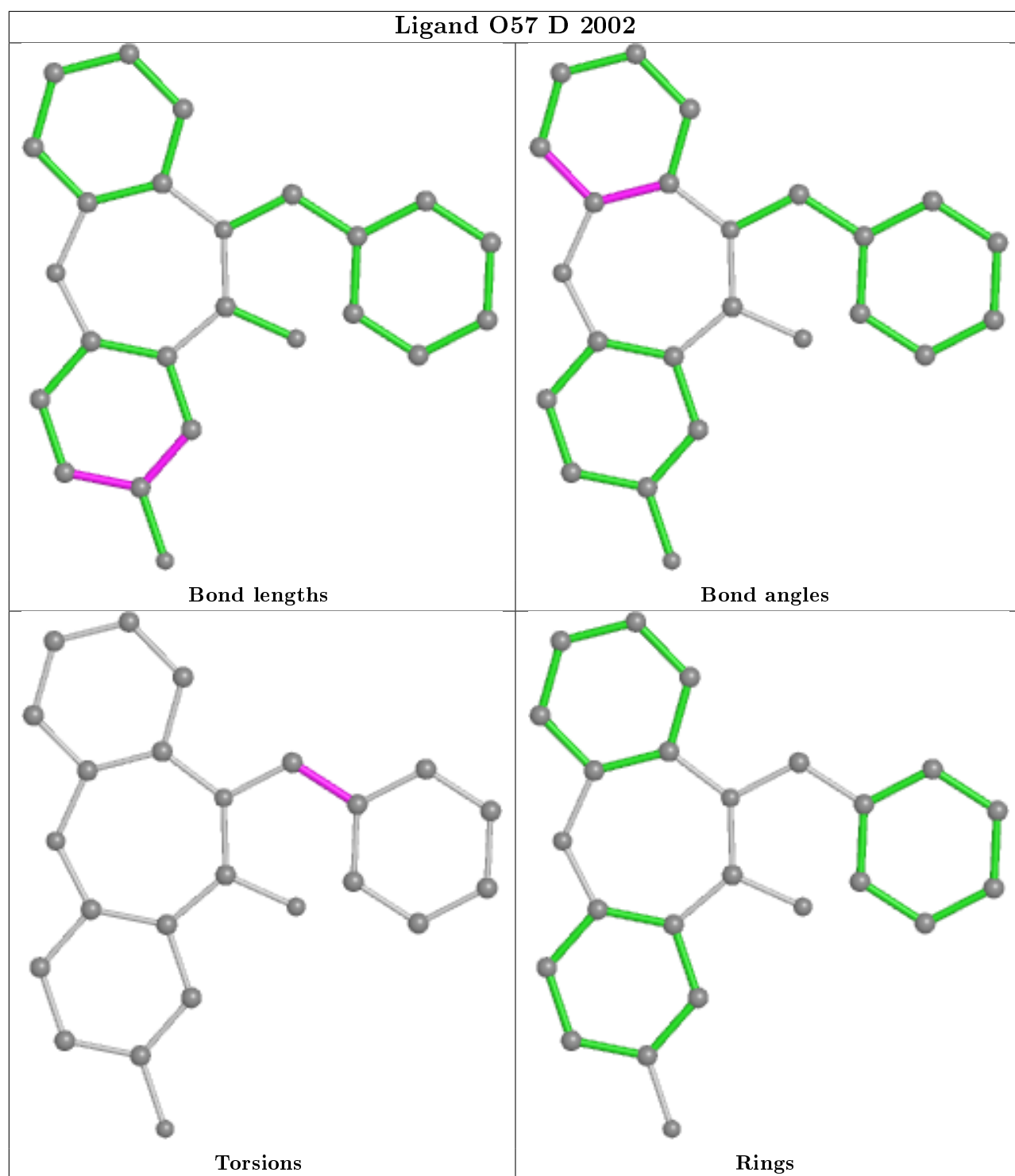


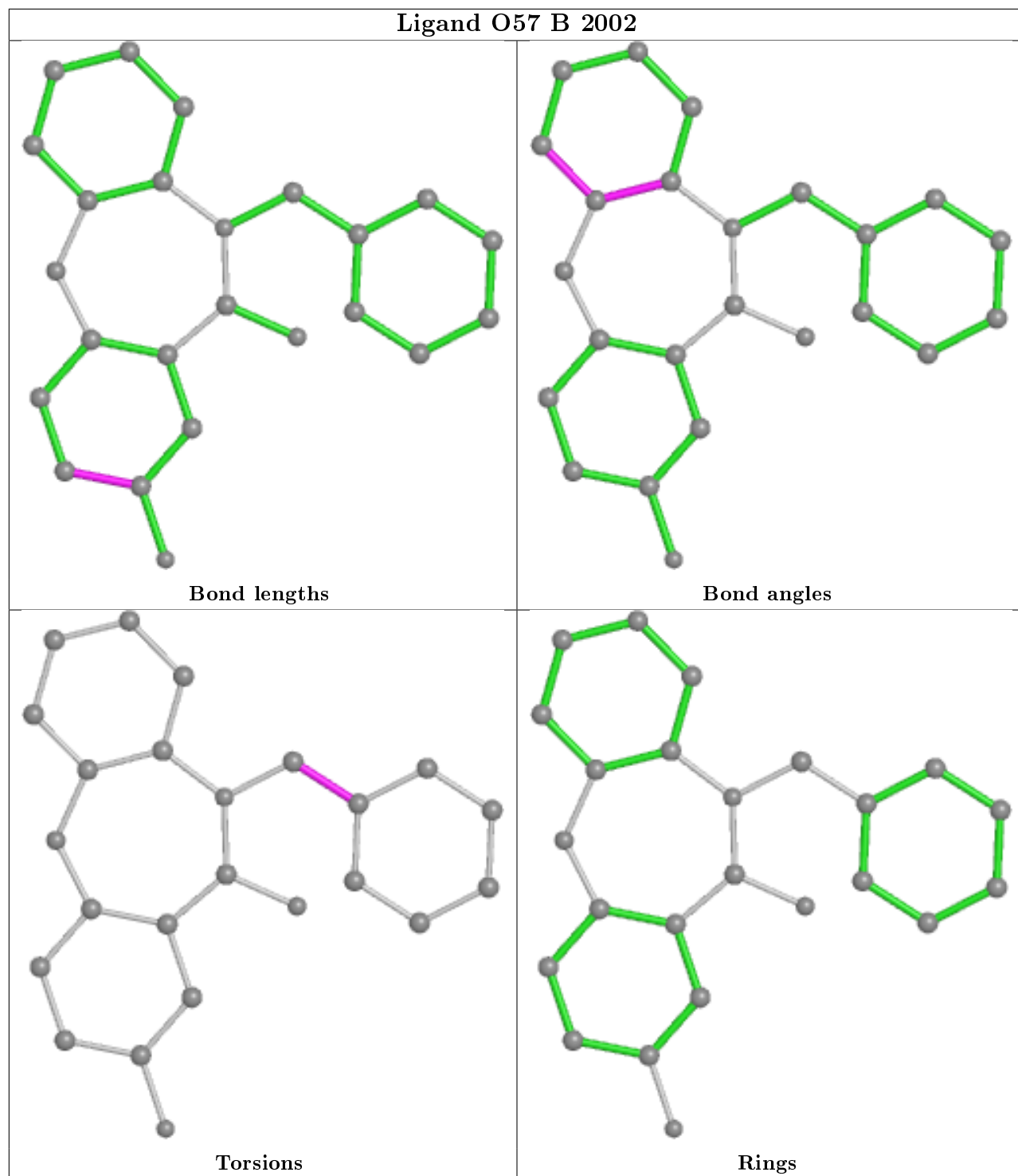
## Ligand AMP C 2001

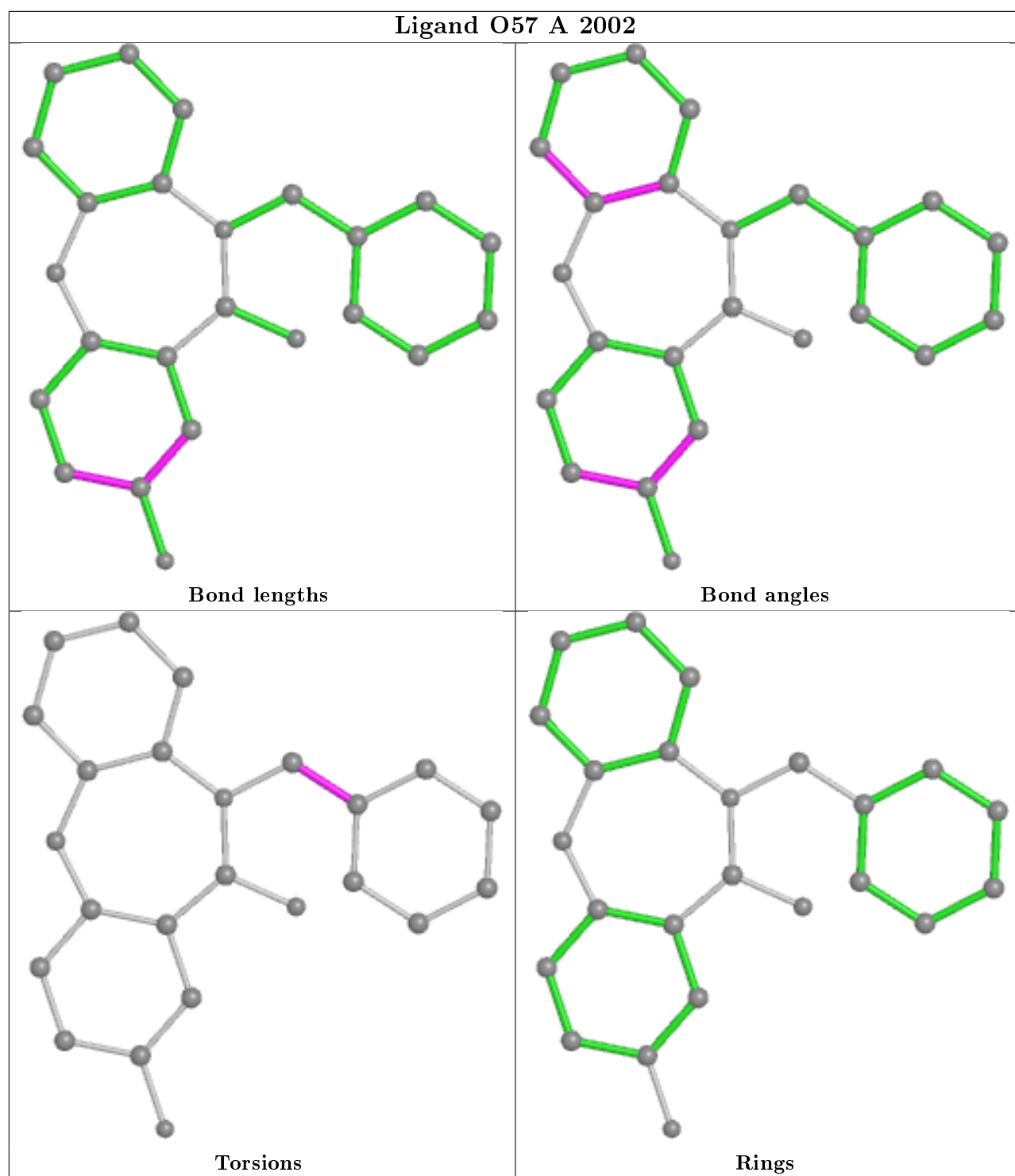


## Ligand ANP A 2001









## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	309/327 (94%)	-0.04	10 (3%) 47 50	11, 21, 40, 59	2 (0%)
1	B	300/327 (91%)	-0.07	8 (2%) 54 57	12, 22, 41, 60	2 (0%)
1	C	316/327 (96%)	0.16	27 (8%) 10 12	12, 23, 52, 83	7 (2%)
1	D	296/327 (90%)	0.04	18 (6%) 21 24	13, 24, 47, 59	1 (0%)
All	All	1221/1308 (93%)	0.02	63 (5%) 27 30	11, 23, 45, 83	12 (0%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	699	PRO	7.7
1	D	989	LEU	6.1
1	C	866	GLU	5.7
1	C	865	GLU	5.5
1	D	990	PRO	5.2
1	C	989	LEU	4.9
1	C	870	HIS	4.8
1	D	985	GLU	4.3
1	B	699	PRO	4.2
1	C	1010	VAL	4.2
1	C	699	PRO	4.1
1	C	864	ALA	4.0
1	C	988	HIS	3.9
1	C	869	TYR	3.8
1	C	1013	ALA	3.7
1	C	868	GLU	3.7
1	B	875	LYS	3.7
1	C	871	ALA	3.6
1	D	807	ASP	3.6
1	C	1012	ASP	3.6
1	A	992	PRO	3.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	C	873	GLY	3.4
1	A	989	LEU	3.4
1	C	867	LYS	3.2
1	D	701	GLN	3.1
1	C	1014	ASP	3.1
1	C	701	GLN	3.1
1	A	990	PRO	3.1
1	C	990	PRO	3.1
1	C	863	GLY	3.1
1	D	991	SER	3.0
1	D	988	HIS	3.0
1	C	1011	VAL	2.9
1	D	876	VAL	2.8
1	C	700	ASN	2.8
1	C	987	MET	2.8
1	C	993	THR	2.7
1	D	785	THR	2.7
1	C	872	GLU	2.7
1	B	986	ARG	2.6
1	D	982	GLN	2.6
1	C	875	LYS	2.6
1	C	992	PRO	2.6
1	C	986	ARG	2.5
1	A	785[A]	THR	2.5
1	A	986	ARG	2.5
1	D	986	ARG	2.5
1	D	808	ASN	2.4
1	A	784	SER	2.4
1	A	987	MET	2.4
1	B	701	GLN	2.4
1	B	864	ALA	2.3
1	A	863	GLY	2.3
1	D	992	PRO	2.3
1	B	982	GLN	2.2
1	B	698	ALA	2.1
1	D	981	ILE	2.1
1	D	700	ASN	2.1
1	B	783	THR	2.0
1	D	1006	ASP	2.0
1	A	1019	PRO	2.0
1	D	983	GLY	2.0
1	D	993	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](#)

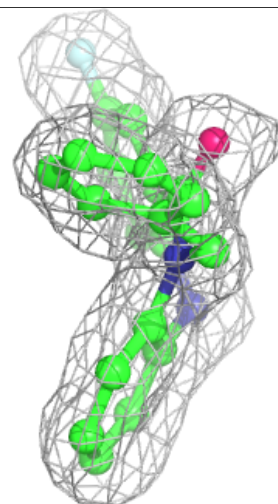
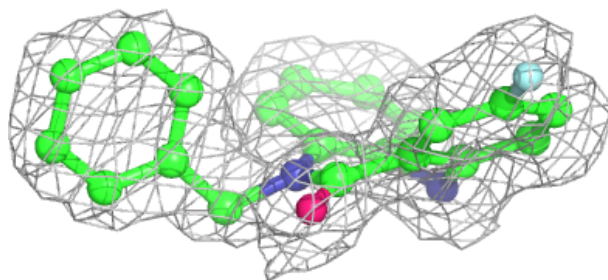
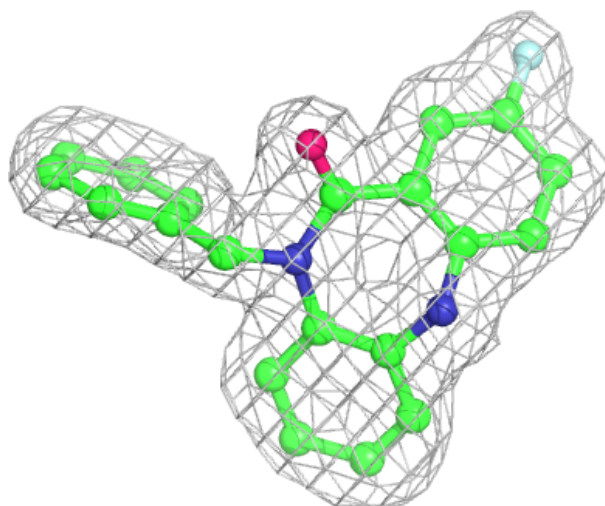
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	EDO	C	2005	4/4	0.70	0.22	29,37,42,45	0
6	EDO	C	2006	4/4	0.73	0.26	36,38,41,42	0
6	EDO	C	2008	4/4	0.77	0.16	35,37,45,49	0
6	EDO	C	2007	4/4	0.83	0.17	34,34,36,36	0
6	EDO	B	2005	4/4	0.88	0.12	42,49,52,68	0
6	EDO	B	2004	4/4	0.90	0.10	28,32,38,42	0
4	MG	A	2004	1/1	0.90	0.19	16,16,16,16	1
6	EDO	D	2004	4/4	0.92	0.26	37,38,43,51	0
6	EDO	C	2004	4/4	0.92	0.12	39,41,43,51	0
3	O57	D	2002	24/24	0.93	0.10	16,20,26,37	0
3	O57	C	2002	24/24	0.94	0.09	12,14,20,29	0
3	O57	A	2002	24/24	0.94	0.09	10,17,26,38	0
6	EDO	D	2005	4/4	0.94	0.18	35,38,40,46	0
5	AMP	D	2001	23/23	0.95	0.07	15,20,33,35	0
2	ANP	A	2001	31/31	0.96	0.09	11,20,28,33	6
3	O57	B	2002	24/24	0.96	0.09	13,18,20,32	0
5	AMP	B	2001	23/23	0.97	0.09	13,18,22,24	0
5	AMP	C	2001	23/23	0.97	0.11	10,15,18,19	0
4	MG	A	2003	1/1	0.98	0.12	28,28,28,28	0
4	MG	C	2003	1/1	0.99	0.20	10,10,10,10	0
4	MG	B	2003	1/1	0.99	0.19	18,18,18,18	0
4	MG	D	2003	1/1	1.00	0.10	22,22,22,22	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.

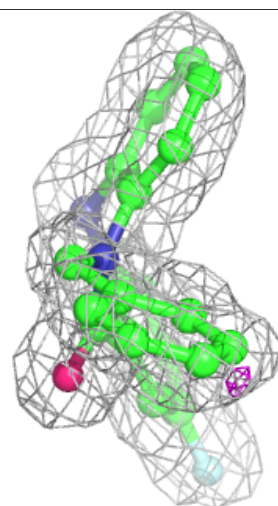
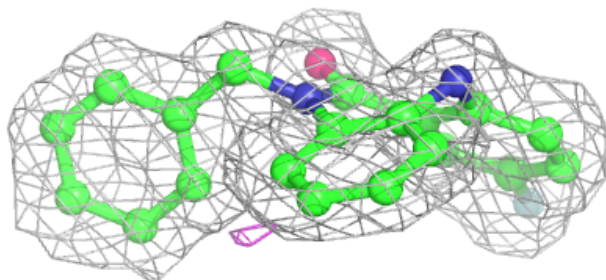
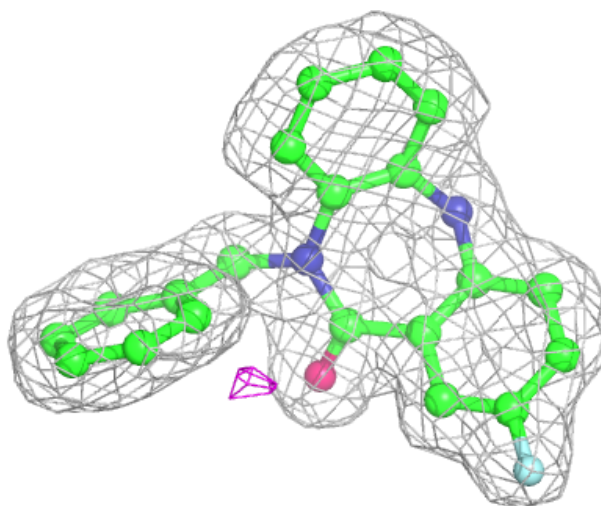
**Electron density around O57 D 2002:**

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



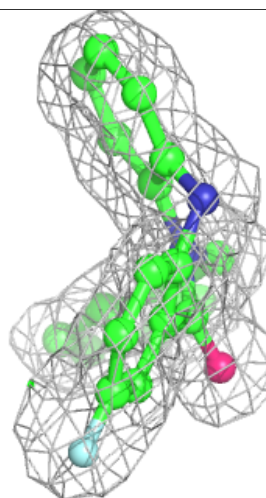
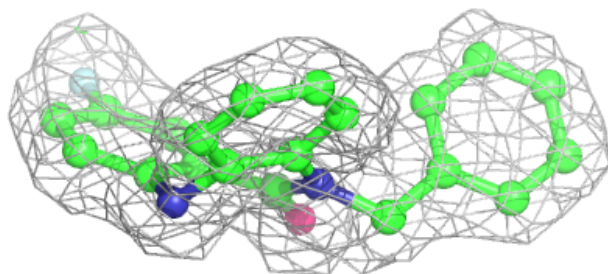
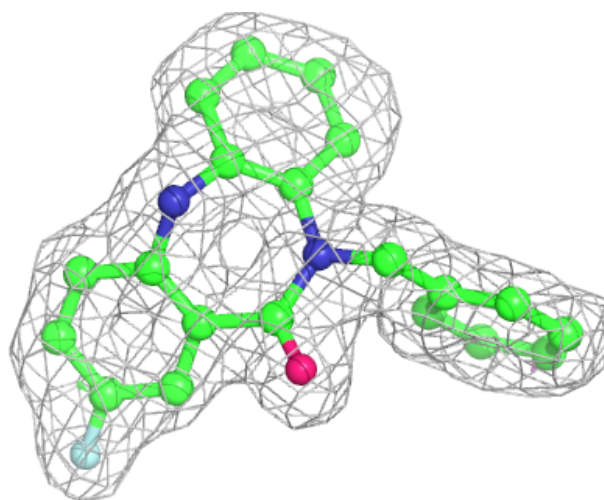
**Electron density around O57 C 2002:**

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



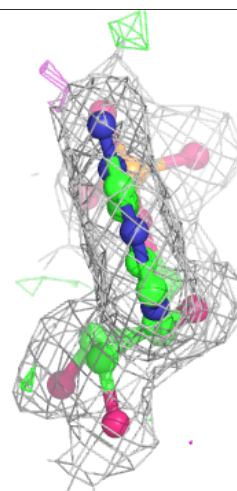
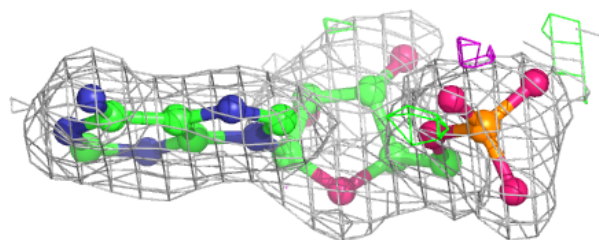
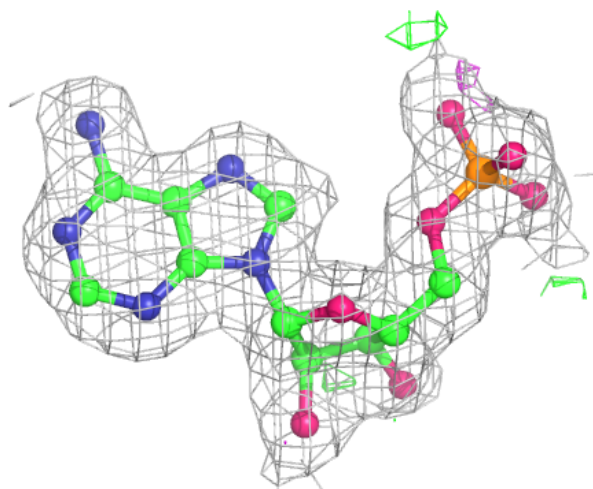
**Electron density around O57 A 2002:**

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



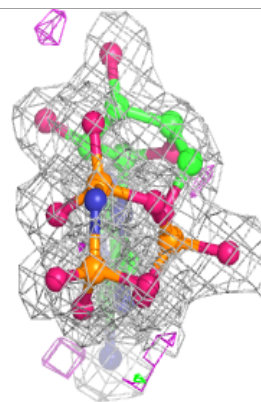
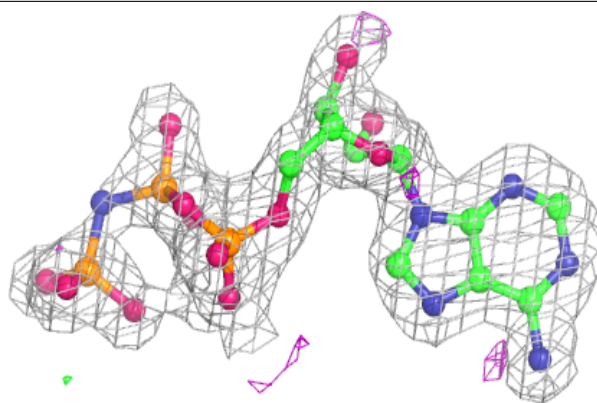
**Electron density around AMP D 2001:**

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



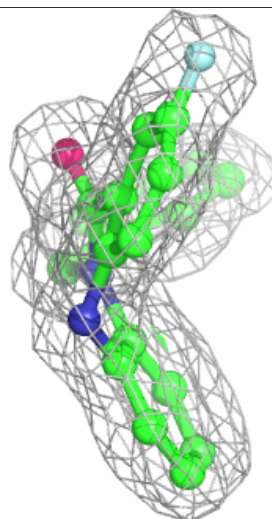
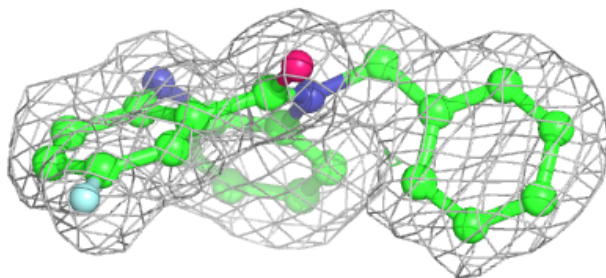
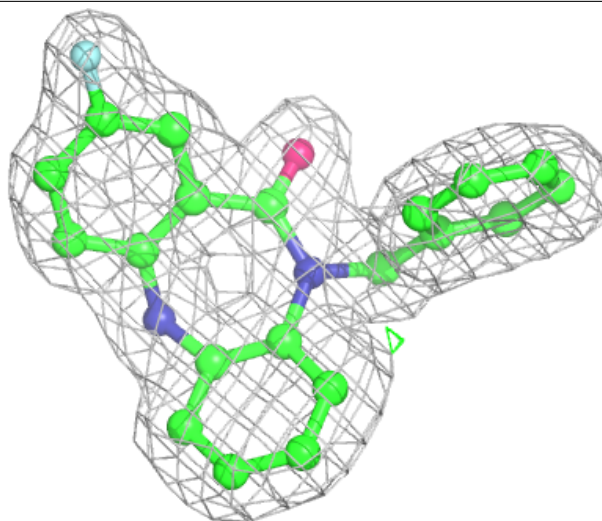
**Electron density around ANP A 2001:**

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and green (positive)



**Electron density around O57 B 2002:**

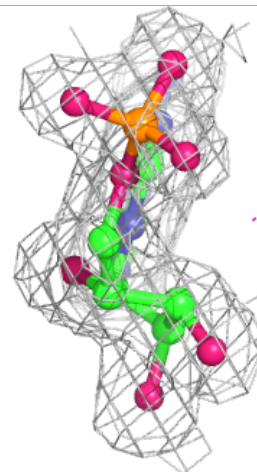
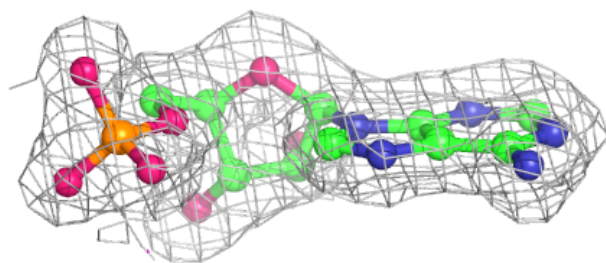
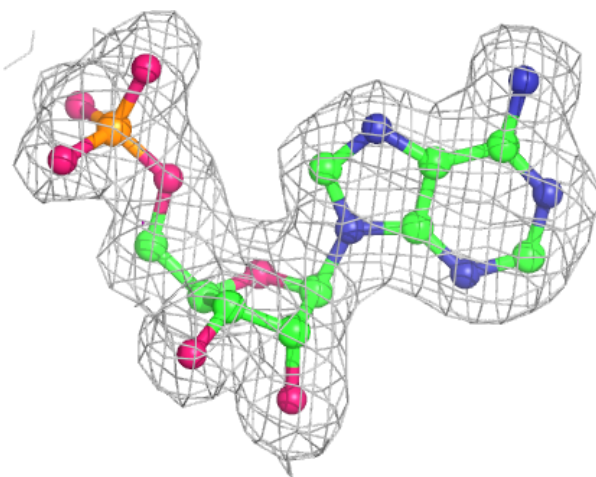
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around AMP B 2001:**

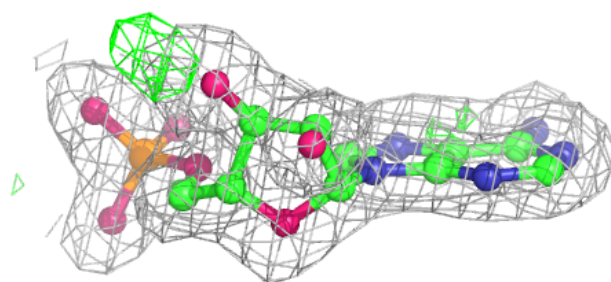
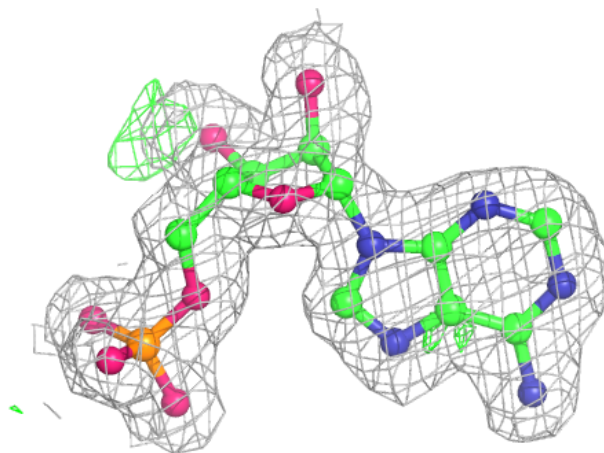
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around AMP C 2001:**

$2mF_o-DF_c$  (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.