



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:49 PM UTC

PDB ID : 5XIQ / pdb_00005xiq
Title : Crystal Structure of Toxoplasma gondii Prolyl-tRNA Synthetase (TgPRS) in complex with Halofuginone
Authors : Jain, V.; Manickam, Y.; Sharma, A.
Deposited on : 2017-04-26
Resolution : 2.19 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

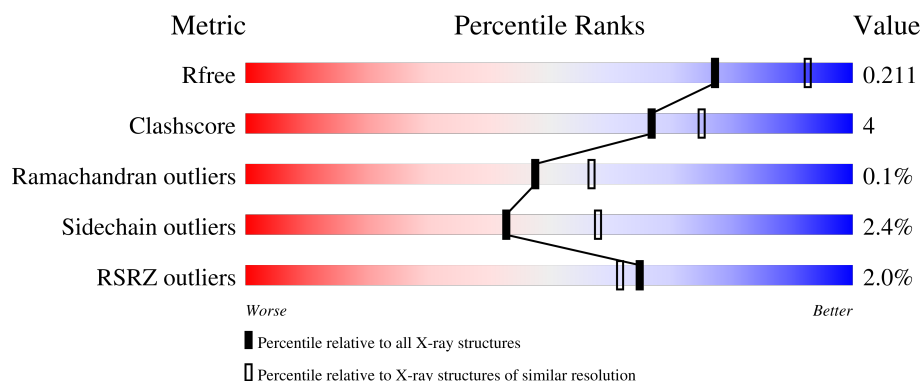
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	500	2% 86% 9% ..
1	B	500	% 83% 12% ..
1	C	500	2% 84% 11% ..
1	D	500	2% 85% 9% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16320 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.

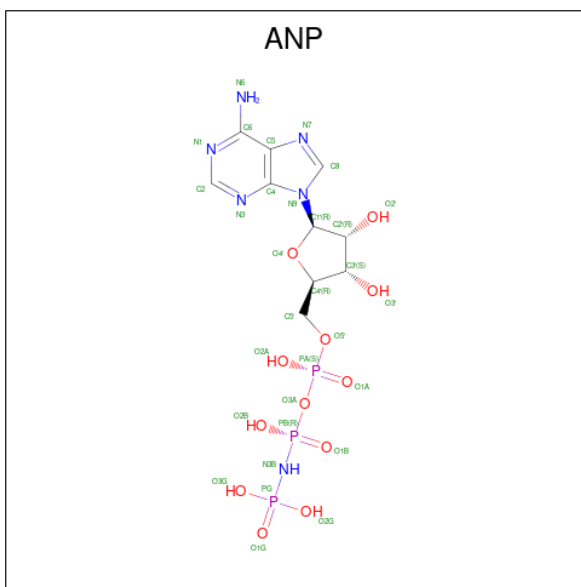
- Molecule 1 is a protein called Prolyl-tRNA synthetase (ProRS).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	478	Total	C	N	O	S	0	5	0
			3917	2521	671	703	22			
1	B	480	Total	C	N	O	S	0	1	0
			3905	2509	667	707	22			
1	C	481	Total	C	N	O	S	0	6	0
			3937	2533	681	701	22			
1	D	479	Total	C	N	O	S	0	6	0
			3941	2532	680	707	22			

There are 12 discrepancies between the modelled and reference sequences:

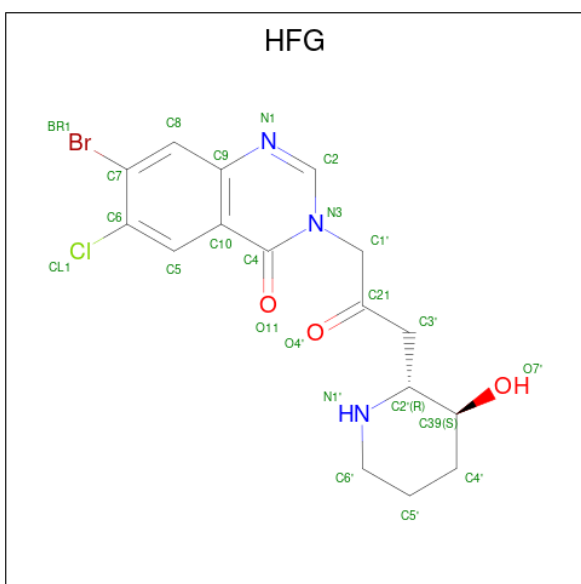
Chain	Residue	Modelled	Actual	Comment	Reference
A	331	GLY	-	expression tag	UNP S8G8I1
A	332	ALA	-	expression tag	UNP S8G8I1
A	333	MET	-	expression tag	UNP S8G8I1
B	331	GLY	-	expression tag	UNP S8G8I1
B	332	ALA	-	expression tag	UNP S8G8I1
B	333	MET	-	expression tag	UNP S8G8I1
C	331	GLY	-	expression tag	UNP S8G8I1
C	332	ALA	-	expression tag	UNP S8G8I1
C	333	MET	-	expression tag	UNP S8G8I1
D	331	GLY	-	expression tag	UNP S8G8I1
D	332	ALA	-	expression tag	UNP S8G8I1
D	333	MET	-	expression tag	UNP S8G8I1

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



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

- Molecule 3 is 7-bromo-6-chloro-3-{3-[(2R,3S)-3-hydroxypiperidin-2-yl]-2-oxopropyl}quinazolin-4(3H)-one (CCD ID: HFG) (formula: $C_{16}H_{17}BrClN_3O_3$).



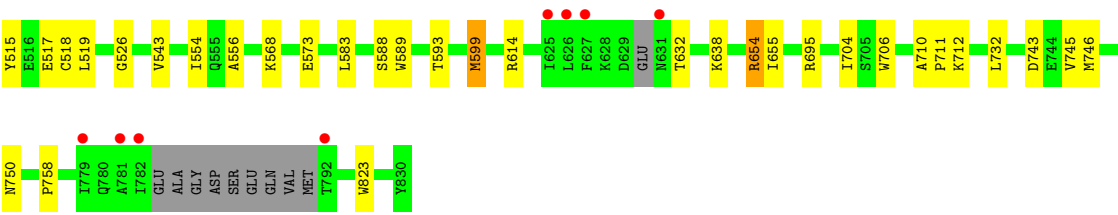
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	Br	C	Cl	N	O	0	0
			24	1	16	1	3	3		
3	B	1	Total	Br	C	Cl	N	O	0	0
			24	1	16	1	3	3		
3	C	1	Total	Br	C	Cl	N	O	0	0
			24	1	16	1	3	3		
3	D	1	Total	Br	C	Cl	N	O	0	0
			24	1	16	1	3	3		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

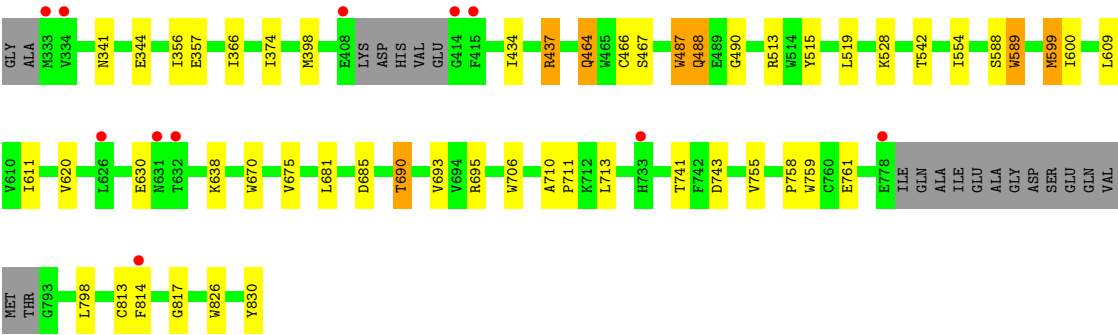
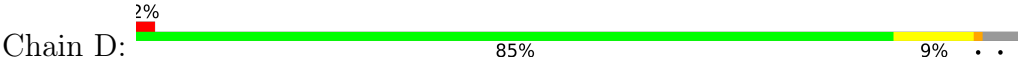
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mg	0	0
			2	2		
4	B	2	Total	Mg	0	0
			2	2		
4	C	2	Total	Mg	0	0
			2	2		
4	D	2	Total	Mg	0	0
			2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	130	Total	O	0	2
			132	132		
5	B	73	Total	O	0	0
			73	73		
5	C	109	Total	O	0	2
			111	111		
5	D	76	Total	O	0	0
			76	76		



● Molecule 1: Prolyl-tRNA synthetase (ProRS)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	76.85Å 90.90Å 92.87Å 89.86° 80.92° 75.82°	Depositor
Resolution (Å)	40.32 – 2.19 40.32 – 2.19	Depositor EDS
% Data completeness (in resolution range)	97.4 (40.32-2.19) 97.4 (40.32-2.19)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.165 , 0.207 0.173 , 0.211	Depositor DCC
R_{free} test set	6057 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	39.3	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	16320	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% 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: ANP, HFG, MG

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	1.24	4/4037 (0.1%)	1.17	10/5461 (0.2%)
1	B	1.13	3/4014 (0.1%)	1.14	15/5433 (0.3%)
1	C	1.18	7/4061 (0.2%)	1.12	8/5495 (0.1%)
1	D	1.14	2/4067 (0.0%)	1.11	6/5499 (0.1%)
All	All	1.17	16/16179 (0.1%)	1.14	39/21888 (0.2%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	608	GLY	C-O	-7.66	1.20	1.24
1	C	442	THR	N-CA	7.33	1.55	1.46
1	B	546	PHE	C-O	-7.13	1.16	1.23
1	A	547	ILE	CA-C	6.64	1.59	1.52
1	A	356	ILE	C-O	5.92	1.29	1.24
1	C	471	TRP	C-O	-5.77	1.16	1.23
1	D	467	SER	CA-C	-5.54	1.46	1.52
1	D	515	TYR	CA-C	5.51	1.59	1.52
1	A	381	PHE	N-CA	-5.50	1.40	1.46
1	C	526	GLY	C-O	-5.46	1.18	1.23
1	A	368	ARG	C-O	5.41	1.31	1.23
1	C	465	TRP	CA-CB	5.38	1.60	1.53
1	C	732	LEU	CA-C	5.25	1.59	1.52
1	C	436	ILE	C-O	5.24	1.30	1.24
1	C	508	LEU	C-O	5.24	1.30	1.24
1	B	400	VAL	N-CA	-5.01	1.40	1.46

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	368	ARG	CA-C-N	7.33	127.68	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	368	ARG	C-N-CA	7.33	127.68	119.32
1	A	507	ILE	N-CA-C	-7.21	103.44	110.72
1	C	440	SER	N-CA-C	7.18	122.14	112.88
1	D	437	ARG	N-CA-C	7.14	122.08	109.58
1	B	798	LEU	N-CA-C	-6.92	102.21	111.96
1	A	515	TYR	N-CA-C	6.88	118.57	111.14
1	B	745	VAL	N-CA-C	6.21	116.26	110.42
1	D	611	ILE	CB-CA-C	-5.76	104.42	110.53
1	A	428	SER	N-CA-C	5.76	116.92	109.72
1	B	416	SER	N-CA-C	5.66	122.32	109.81
1	B	800	ILE	CA-C-N	-5.66	114.14	119.85
1	B	800	ILE	C-N-CA	-5.66	114.14	119.85
1	D	690	THR	N-CA-C	5.58	117.10	109.18
1	B	438	PRO	CA-C-N	5.52	132.35	122.09
1	B	438	PRO	C-N-CA	5.52	132.35	122.09
1	A	745	VAL	N-CA-C	5.49	115.58	110.42
1	A	757	ALA	CA-C-N	-5.47	114.29	119.76
1	A	757	ALA	C-N-CA	-5.47	114.29	119.76
1	B	746	MET	CA-C-N	-5.47	113.26	119.28
1	B	746	MET	C-N-CA	-5.47	113.26	119.28
1	C	475[A]	GLN	CA-C-N	-5.35	115.06	120.31
1	C	475[A]	GLN	C-N-CA	-5.35	115.06	120.31
1	C	475[B]	GLN	CA-C-N	-5.35	115.06	120.31
1	C	475[B]	GLN	C-N-CA	-5.35	115.06	120.31
1	A	750	ASN	N-CA-C	-5.31	106.31	112.89
1	B	475	GLN	CA-C-N	-5.31	114.51	120.14
1	B	475	GLN	C-N-CA	-5.31	114.51	120.14
1	D	513	ARG	N-CA-C	5.30	117.14	111.36
1	A	688	LYS	N-CA-C	-5.28	101.11	109.76
1	D	817	GLY	N-CA-C	-5.25	107.65	113.79
1	A	592	THR	N-CA-C	5.25	116.64	109.18
1	C	745	VAL	N-CA-C	5.23	115.37	110.30
1	A	565	ASN	N-CA-C	5.17	116.99	111.36
1	B	809	GLU	N-CA-C	5.15	117.56	111.33
1	C	419	VAL	CB-CA-C	-5.07	104.56	111.15
1	C	695	ARG	CB-CA-C	-5.05	101.19	109.53
1	B	671	GLU	CB-CA-C	-5.05	103.18	110.96
1	D	798	LEU	N-CA-C	-5.03	104.86	111.96

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	3917	0	3872	28	0
1	B	3905	0	3838	33	0
1	C	3937	0	3895	30	0
1	D	3941	0	3890	33	0
2	A	31	0	13	0	0
2	B	31	0	13	0	0
2	C	31	0	13	1	0
2	D	31	0	13	0	0
3	A	24	0	17	2	0
3	B	24	0	17	1	0
3	C	24	0	17	2	0
3	D	24	0	17	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	132	0	0	2	0
5	B	73	0	0	0	0
5	C	111	0	0	3	0
5	D	76	0	0	0	0
All	All	16320	0	15615	117	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 (117) 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:398:MET:HE1	1:B:398:MET:HE1	1.17	1.14
1:C:398:MET:HE1	1:D:398:MET:CE	1.81	1.11
1:C:398:MET:CE	1:D:398:MET:HE1	1.87	1.04
1:C:398:MET:HE1	1:D:398:MET:HE1	1.07	1.03
1:A:685:ASP:O	1:A:688:LYS:O	1.93	0.86
1:A:519:LEU:HD22	1:A:599:MET:HE3	1.61	0.82
1:D:374:ILE:HD13	1:D:599:MET:HE1	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:807:MET:CE	1:B:820:ALA:HB3	2.17	0.75
1:D:437:ARG:NH2	1:D:466:CYS:HB2	2.02	0.74
1:B:543:VAL:HG23	1:B:556:ALA:HB3	1.70	0.73
1:D:398:MET:HA	1:D:437:ARG:HD3	1.72	0.72
1:A:519:LEU:HD22	1:A:599:MET:CE	2.24	0.66
2:C:1001:ANP:O2G	5:C:1101:HOH:O	2.13	0.66
1:A:398:MET:CE	1:B:398:MET:HE1	2.11	0.64
1:C:487:TRP:CH2	3:C:1002:HFG:H8	2.32	0.64
1:B:710:ALA:HB3	1:B:711:PRO:HD3	1.81	0.63
1:C:519:LEU:HD22	1:C:599:MET:HE3	1.81	0.63
1:A:437:ARG:O	1:A:437:ARG:HG2	2.01	0.61
1:D:519:LEU:HD22	1:D:599:MET:HE3	1.84	0.60
1:D:600:ILE:HG23	1:D:609:LEU:HD22	1.84	0.59
1:B:758:PRO:HB3	1:B:807:MET:HE1	1.86	0.58
1:B:626:LEU:HG	1:B:632:THR:HG22	1.86	0.58
1:C:543:VAL:HG23	1:C:556:ALA:HB3	1.86	0.57
1:A:398:MET:HE3	1:A:436:ILE:HG23	1.85	0.57
1:B:519:LEU:HD22	1:B:599:MET:HE3	1.88	0.56
1:C:710:ALA:HB3	1:C:711:PRO:HD3	1.89	0.55
1:D:758:PRO:HD2	1:D:814:PHE:HB3	1.88	0.55
1:A:688:LYS:O	1:A:690:THR:N	2.36	0.55
1:C:638:LYS:HE3	1:C:706:TRP:CZ3	2.42	0.54
1:D:528:LYS:HD3	1:D:542:THR:HG21	1.89	0.54
1:A:398:MET:CE	1:A:436:ILE:HG23	2.38	0.54
1:C:361:ILE:HD13	1:D:434:ILE:HD12	1.89	0.53
1:A:399:PHE:HB3	1:A:434[A]:ILE:HG21	1.92	0.52
1:B:807:MET:HE3	1:B:820:ALA:HB3	1.92	0.52
1:C:480:LEU:HD22	1:C:554:ILE:CD1	2.39	0.52
1:D:341:ASN:ND2	1:D:344:GLU:HG3	2.26	0.51
1:D:741:THR:OG1	1:D:743:ASP:OD1	2.28	0.51
1:A:399:PHE:HB3	1:A:434[A]:ILE:CG2	2.41	0.51
1:D:710:ALA:HB3	1:D:711:PRO:CD	2.42	0.50
1:B:374:ILE:HG21	1:B:599:MET:HE1	1.94	0.50
1:B:638:LYS:HE3	1:B:706:TRP:CE3	2.46	0.50
1:D:487:TRP:CH2	3:D:1002:HFG:H8	2.47	0.50
1:A:419:VAL:HG22	3:A:1002:HFG:BR1	2.67	0.50
1:D:670:TRP:CE3	1:D:675:VAL:HG21	2.46	0.49
1:C:455:HIS:ND1	5:C:1103:HOH:O	2.34	0.49
1:D:600:ILE:HG23	1:D:609:LEU:CD2	2.43	0.49
1:B:430:LEU:HD13	1:B:434:ILE:HG12	1.96	0.48
1:C:517:GLU:O	1:C:614[A]:ARG:HD2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:755:VAL:HG22	1:D:826:TRP:HB2	1.97	0.47
1:B:807:MET:HE1	1:B:820:ALA:HB3	1.96	0.47
1:C:519:LEU:HD22	1:C:599:MET:CE	2.44	0.47
1:C:514:TRP:O	1:C:518:CYS:HB2	2.15	0.47
1:D:437:ARG:HH21	1:D:466:CYS:HB2	1.79	0.47
1:B:399:PHE:HB3	1:B:434:ILE:CG2	2.45	0.47
1:D:490:GLY:O	1:D:588:SER:HA	2.14	0.46
1:A:487:TRP:CH2	3:A:1002:HFG:H8	2.50	0.46
1:B:645:MET:HE1	1:B:709:LEU:HB2	1.97	0.46
1:A:588:SER:C	1:A:589:TRP:CD1	2.94	0.46
1:C:361:ILE:CD1	1:D:434:ILE:HD12	2.46	0.46
1:C:758:PRO:HD3	1:C:823:TRP:CZ3	2.51	0.46
1:A:433:LYS:NZ	5:A:1108:HOH:O	2.49	0.46
1:A:437:ARG:HD3	5:A:1169:HOH:O	2.16	0.46
1:C:490:GLY:O	1:C:588:SER:HA	2.15	0.46
1:C:350:ILE:HD12	1:C:356:ILE:HG12	1.98	0.46
1:C:396:PHE:CE1	1:C:444:MET:HE3	2.50	0.46
1:C:486:LEU:HB2	1:C:593:THR:CG2	2.46	0.45
1:B:624:PRO:HB2	1:B:626:LEU:HD13	1.99	0.45
1:C:486:LEU:HB2	1:C:593:THR:HG23	1.98	0.45
1:D:638:LYS:HE2	1:D:706:TRP:CZ3	2.51	0.45
1:B:490:GLY:O	1:B:588:SER:HA	2.16	0.45
1:B:519:LEU:HD22	1:B:599:MET:CE	2.46	0.45
1:D:357:GLU:HB3	1:D:366:ILE:HB	1.99	0.45
1:A:660:ASN:ND2	1:B:456:ARG:CZ	2.80	0.45
1:A:774:GLN:OE1	1:A:792:THR:OG1	2.35	0.44
1:B:355:MET:HE3	1:B:609:LEU:CD1	2.47	0.44
1:B:612:PRO:HA	1:B:613:PRO:HD3	1.91	0.44
1:D:630:GLU:O	1:D:630:GLU:HG3	2.17	0.44
1:B:689:GLY:HA2	1:B:706:TRP:CH2	2.53	0.44
1:D:620:VAL:HG21	1:D:713:LEU:HD13	1.99	0.43
1:B:573:GLU:OE1	1:B:581:LYS:NZ	2.32	0.43
1:C:704:ILE:HD13	1:C:712:LYS:HG2	2.00	0.43
1:C:515:TYR:CZ	1:C:556:ALA:HB1	2.53	0.43
1:D:685:ASP:HB3	1:D:690:THR:O	2.18	0.43
1:C:441:GLU:OE2	3:C:1002:HFG:N1'	2.52	0.43
1:B:649:ALA:O	1:B:650:ASP:HB2	2.18	0.43
1:D:759:TRP:CE3	1:D:761:GLU:HA	2.54	0.43
1:B:487:TRP:CD1	1:B:487:TRP:C	2.95	0.43
1:C:746:MET:O	1:C:750:ASN:ND2	2.51	0.43
1:B:398:MET:CE	1:B:436:ILE:HG23	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:374:ILE:HG21	1:C:599:MET:HE1	2.01	0.42
1:D:710:ALA:HB3	1:D:711:PRO:HD3	2.00	0.42
1:B:350:ILE:HD12	1:B:356:ILE:HG12	2.00	0.42
1:C:402[A]:ARG:HD3	5:C:1204:HOH:O	2.19	0.42
1:A:490:GLY:O	1:A:588:SER:HA	2.19	0.42
1:B:333:MET:HG2	1:B:668:ASN:OD1	2.19	0.42
1:B:490:GLY:HA3	1:B:589:TRP:CZ3	2.55	0.42
1:B:643:LYS:O	1:B:647:GLU:HG2	2.20	0.42
1:A:570:PHE:O	1:A:571:GLU:HB2	2.20	0.42
1:C:477:THR:O	1:C:478:PRO:C	2.63	0.42
1:C:654[B]:ARG:HG2	1:C:655:ILE:N	2.35	0.42
1:A:515:TYR:CZ	1:A:556:ALA:HB1	2.55	0.41
1:D:695:ARG:HH11	1:D:695:ARG:HD2	1.72	0.41
1:A:685:ASP:HB3	1:A:690:THR:O	2.20	0.41
1:C:573:GLU:HG2	1:C:583:LEU:HD23	2.02	0.41
1:B:576:ASP:OD1	1:B:576:ASP:C	2.63	0.41
1:B:419:VAL:HG22	3:B:1002:HFG:BR1	2.75	0.41
1:A:612:PRO:HA	1:A:613:PRO:HD3	1.97	0.41
1:D:554:ILE:HG13	1:D:830:TYR:HB2	2.03	0.41
1:A:667:TYR:CD1	1:A:678:ARG:HD2	2.55	0.41
1:D:588:SER:C	1:D:589:TRP:CD1	2.98	0.41
1:B:486:LEU:HB2	1:B:593:THR:HG23	2.03	0.41
1:A:600:ILE:HG23	1:A:609:LEU:CD2	2.51	0.41
1:D:464:GLN:O	1:D:488:GLN:HA	2.21	0.40
1:A:449:ALA:O	1:A:453:ARG:NH1	2.54	0.40
1:A:374:ILE:HG21	1:A:599:MET:HE1	2.03	0.40
1:A:693:VAL:HG21	1:A:713:LEU:HD21	2.04	0.40
1:D:638:LYS:HE2	1:D:706:TRP:CH2	2.56	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	475/500 (95%)	464 (98%)	11 (2%)	0	100	100
1	B	475/500 (95%)	460 (97%)	14 (3%)	1 (0%)	43	51
1	C	479/500 (96%)	463 (97%)	16 (3%)	0	100	100
1	D	479/500 (96%)	468 (98%)	11 (2%)	0	100	100
All	All	1908/2000 (95%)	1855 (97%)	52 (3%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	438	PRO

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	416/436 (95%)	406 (98%)	10 (2%)	43	58
1	B	414/436 (95%)	403 (97%)	11 (3%)	39	53
1	C	417/436 (96%)	406 (97%)	11 (3%)	40	55
1	D	419/436 (96%)	410 (98%)	9 (2%)	47	63
All	All	1666/1744 (96%)	1625 (98%)	41 (2%)	43	56

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	356	ILE
1	A	407	LYS
1	A	437	ARG
1	A	487	TRP
1	A	488	GLN
1	A	589	TRP
1	A	593	THR
1	A	599	MET
1	A	686	LEU
1	A	775	LYS

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Mol	Chain	Res	Type
1	B	432	GLU
1	B	437	ARG
1	B	487	TRP
1	B	488	GLN
1	B	565	ASN
1	B	589	TRP
1	B	599	MET
1	B	626	LEU
1	B	718	GLU
1	B	772	GLU
1	B	813	CYS
1	C	356	ILE
1	C	361	ILE
1	C	487	TRP
1	C	488	GLN
1	C	568	LYS
1	C	589	TRP
1	C	599	MET
1	C	632	THR
1	C	654[A]	ARG
1	C	654[B]	ARG
1	C	743	ASP
1	D	356	ILE
1	D	464	GLN
1	D	487	TRP
1	D	488	GLN
1	D	589	TRP
1	D	599	MET
1	D	681	LEU
1	D	693	VAL
1	D	813	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	488	GLN
1	A	586	GLN
1	B	488	GLN
1	B	586	GLN
1	C	488	GLN
1	C	750	ASN
1	C	780	GLN

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Mol	Chain	Res	Type
1	D	379	GLN
1	D	488	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	HFG	D	1002	-	26,26,26	0.89	0	29,37,37	1.11	1 (3%)
2	ANP	D	1001	4	33,33,33	0.83	1 (3%)	45,52,52	0.89	3 (6%)
3	HFG	C	1002	-	26,26,26	0.69	0	29,37,37	0.82	0
3	HFG	A	1002	-	26,26,26	1.08	1 (3%)	29,37,37	0.95	1 (3%)
3	HFG	B	1002	-	26,26,26	1.01	0	29,37,37	0.93	1 (3%)
2	ANP	C	1001	4	33,33,33	0.72	0	45,52,52	0.90	4 (8%)
2	ANP	B	1001	4	33,33,33	1.44	3 (9%)	45,52,52	0.91	3 (6%)
2	ANP	A	1001	4	33,33,33	0.82	0	45,52,52	0.93	2 (4%)

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	HFG	D	1002	-	-	0/8/19/19	0/3/3/3
2	ANP	D	1001	4	-	6/18/38/38	0/3/3/3
3	HFG	C	1002	-	-	0/8/19/19	0/3/3/3
3	HFG	A	1002	-	-	0/8/19/19	0/3/3/3
3	HFG	B	1002	-	-	0/8/19/19	0/3/3/3
2	ANP	C	1001	4	-	5/18/38/38	0/3/3/3
2	ANP	B	1001	4	-	3/18/38/38	0/3/3/3
2	ANP	A	1001	4	-	4/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	ANP	PB-O1B	5.21	1.54	1.46
2	B	1001	ANP	PB-O2B	-4.86	1.43	1.56
3	A	1002	HFG	C1'-C21	2.51	1.54	1.51
2	B	1001	ANP	PB-O3A	2.09	1.61	1.59
2	D	1001	ANP	PB-O3A	2.02	1.61	1.59

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1002	HFG	C4'-C39-C2'	-3.29	108.74	110.89
2	A	1001	ANP	O1G-PG-N3B	-2.86	107.56	111.77
3	B	1002	HFG	C4'-C39-C2'	-2.68	109.14	110.89
2	C	1001	ANP	O1G-PG-N3B	-2.59	107.96	111.77
2	B	1001	ANP	O1G-PG-N3B	-2.58	107.97	111.77
2	D	1001	ANP	O1G-PG-N3B	-2.57	107.98	111.77
3	A	1002	HFG	C4'-C39-C2'	-2.36	109.34	110.89
2	A	1001	ANP	O1B-PB-N3B	2.29	115.14	111.77
2	D	1001	ANP	C5'-C4'-C3'	-2.28	107.00	115.21
2	B	1001	ANP	O1B-PB-N3B	2.25	115.09	111.77
2	C	1001	ANP	C5'-C4'-C3'	-2.22	107.23	115.21
2	C	1001	ANP	O1B-PB-N3B	2.11	114.88	111.77
2	D	1001	ANP	O1B-PB-N3B	2.10	114.86	111.77
2	B	1001	ANP	C5-C4-N3	-2.08	123.85	126.72
2	C	1001	ANP	C5-C4-N3	-2.03	123.92	126.72

There are no chirality outliers.

All (18) torsion outliers are listed below:

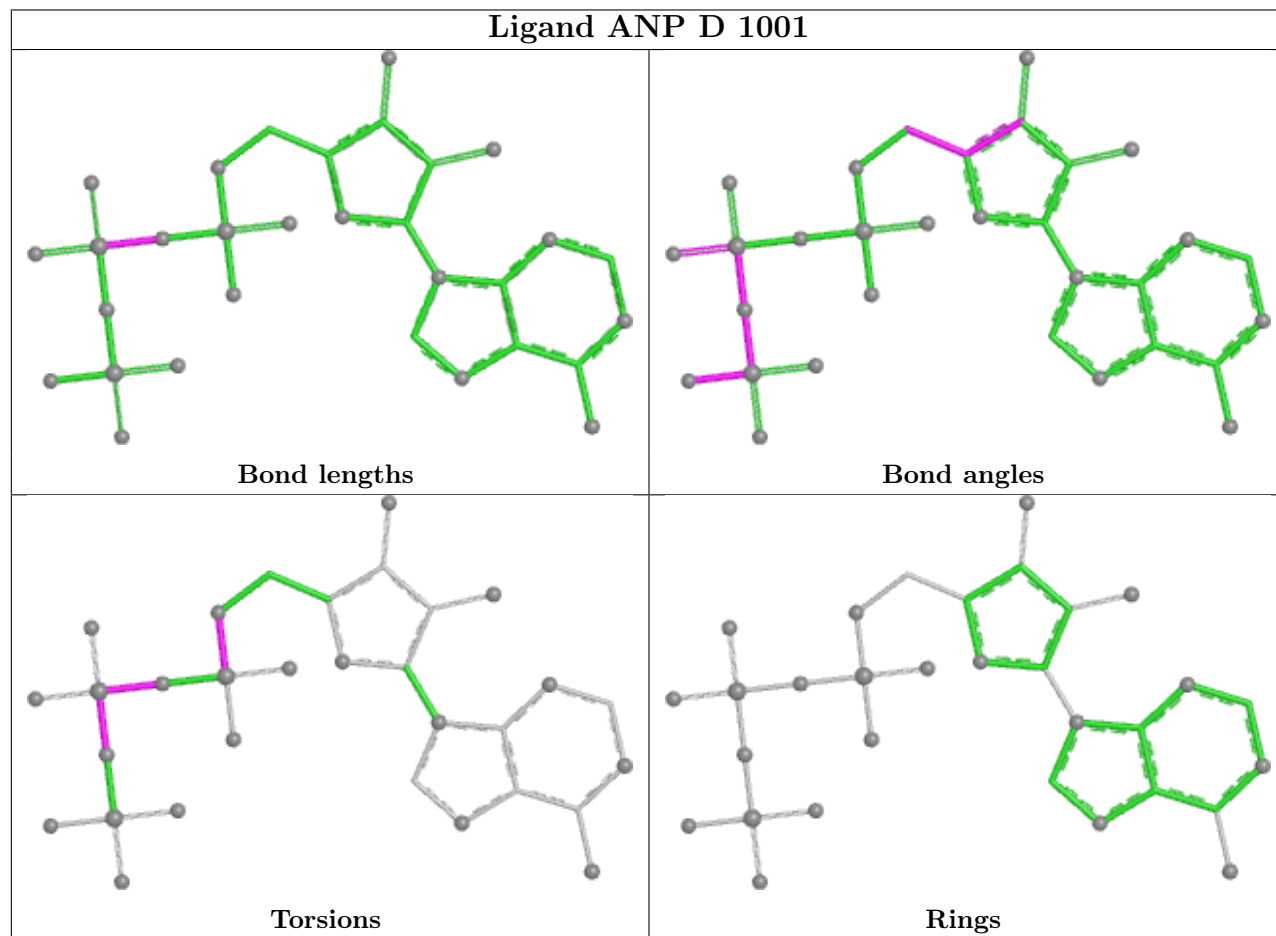
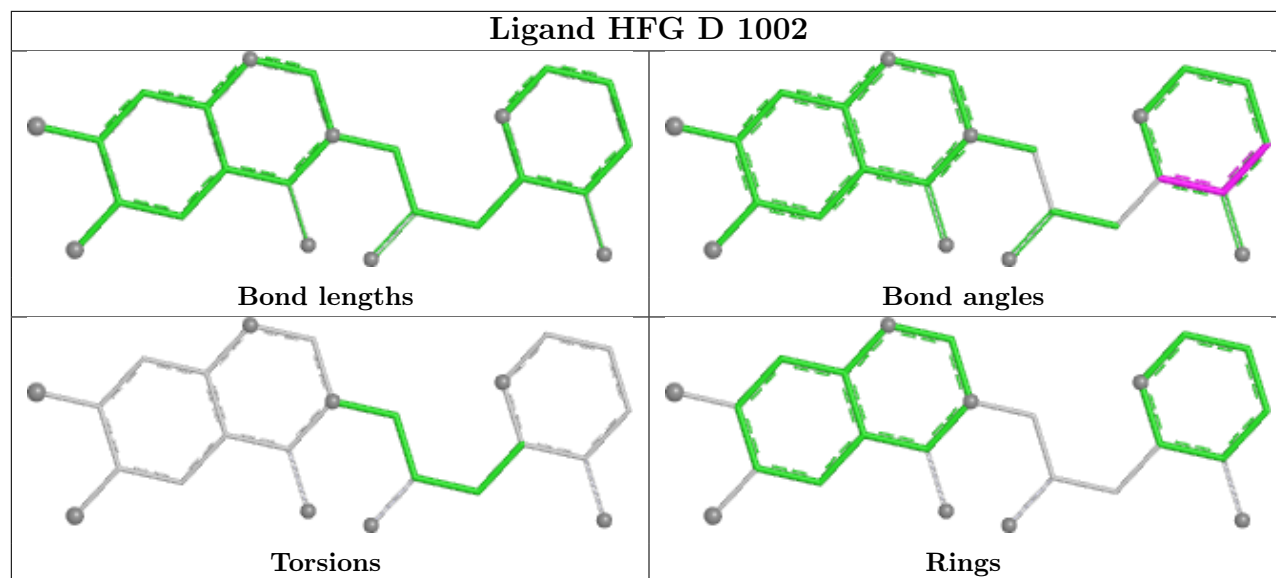
Mol	Chain	Res	Type	Atoms
2	A	1001	ANP	PG-N3B-PB-O1B
2	A	1001	ANP	C5'-O5'-PA-O1A
2	A	1001	ANP	C5'-O5'-PA-O3A
2	B	1001	ANP	C5'-O5'-PA-O1A
2	B	1001	ANP	C5'-O5'-PA-O3A
2	C	1001	ANP	PG-N3B-PB-O1B
2	C	1001	ANP	C5'-O5'-PA-O1A
2	D	1001	ANP	PG-N3B-PB-O1B
2	D	1001	ANP	PA-O3A-PB-O2B
2	D	1001	ANP	C5'-O5'-PA-O1A
2	D	1001	ANP	C5'-O5'-PA-O2A
2	D	1001	ANP	C5'-O5'-PA-O3A
2	A	1001	ANP	C5'-O5'-PA-O2A
2	B	1001	ANP	C5'-O5'-PA-O2A
2	C	1001	ANP	C5'-O5'-PA-O2A
2	C	1001	ANP	C5'-O5'-PA-O3A
2	D	1001	ANP	PA-O3A-PB-O1B
2	C	1001	ANP	O4'-C4'-C5'-O5'

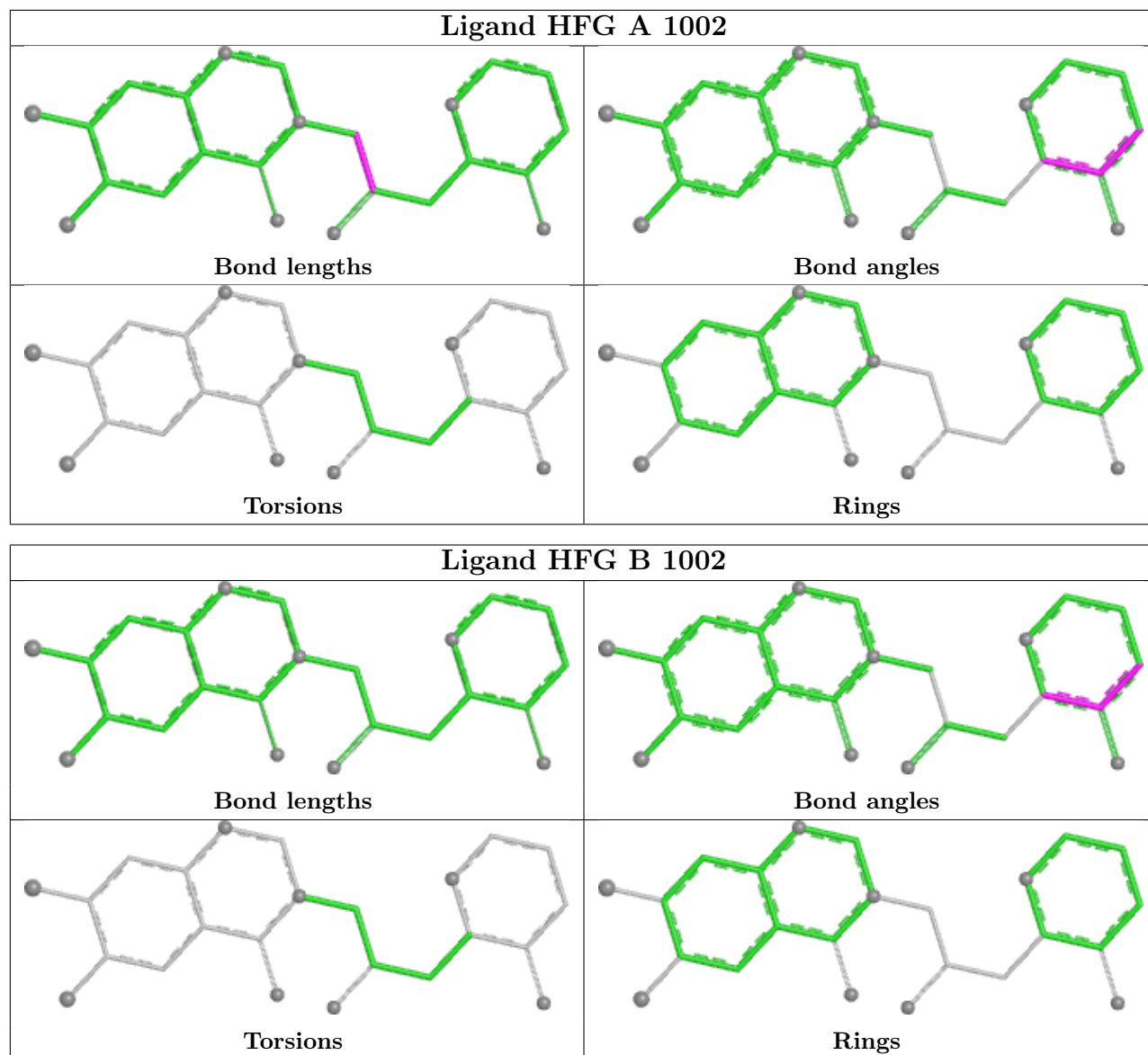
There are no ring outliers.

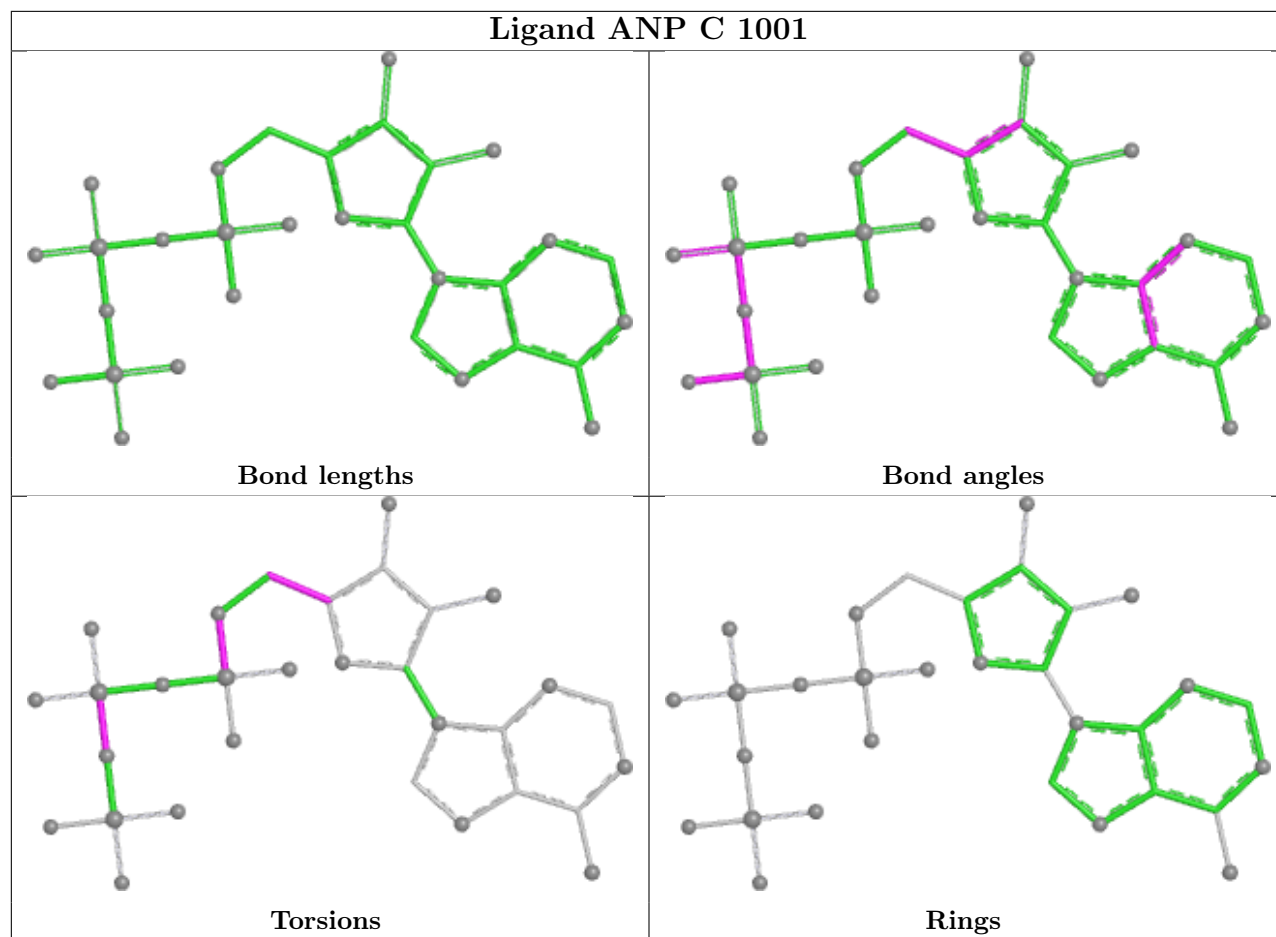
5 monomers are involved in 7 short contacts:

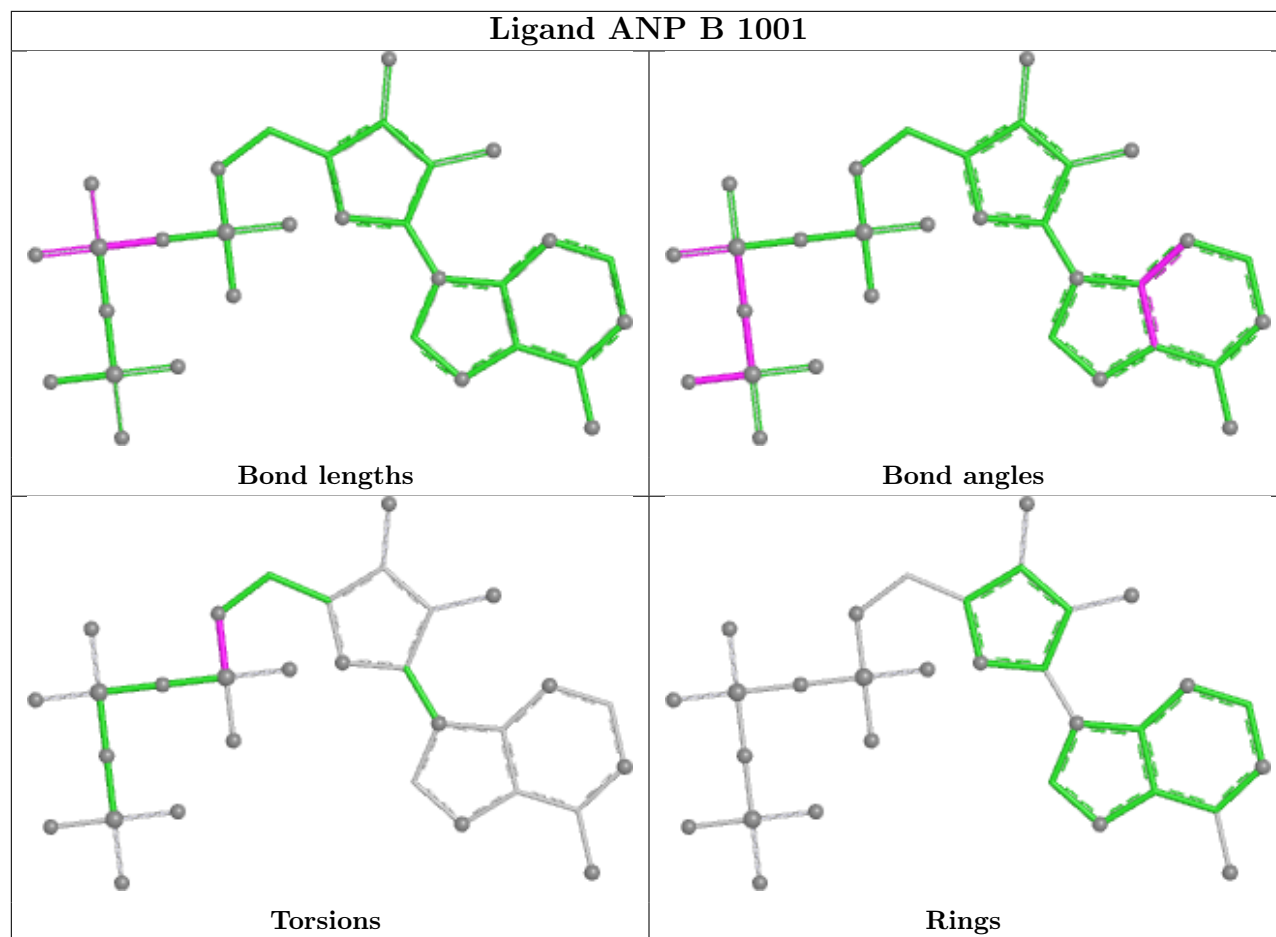
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1002	HFG	1	0
3	C	1002	HFG	2	0
3	A	1002	HFG	2	0
3	B	1002	HFG	1	0
2	C	1001	ANP	1	0

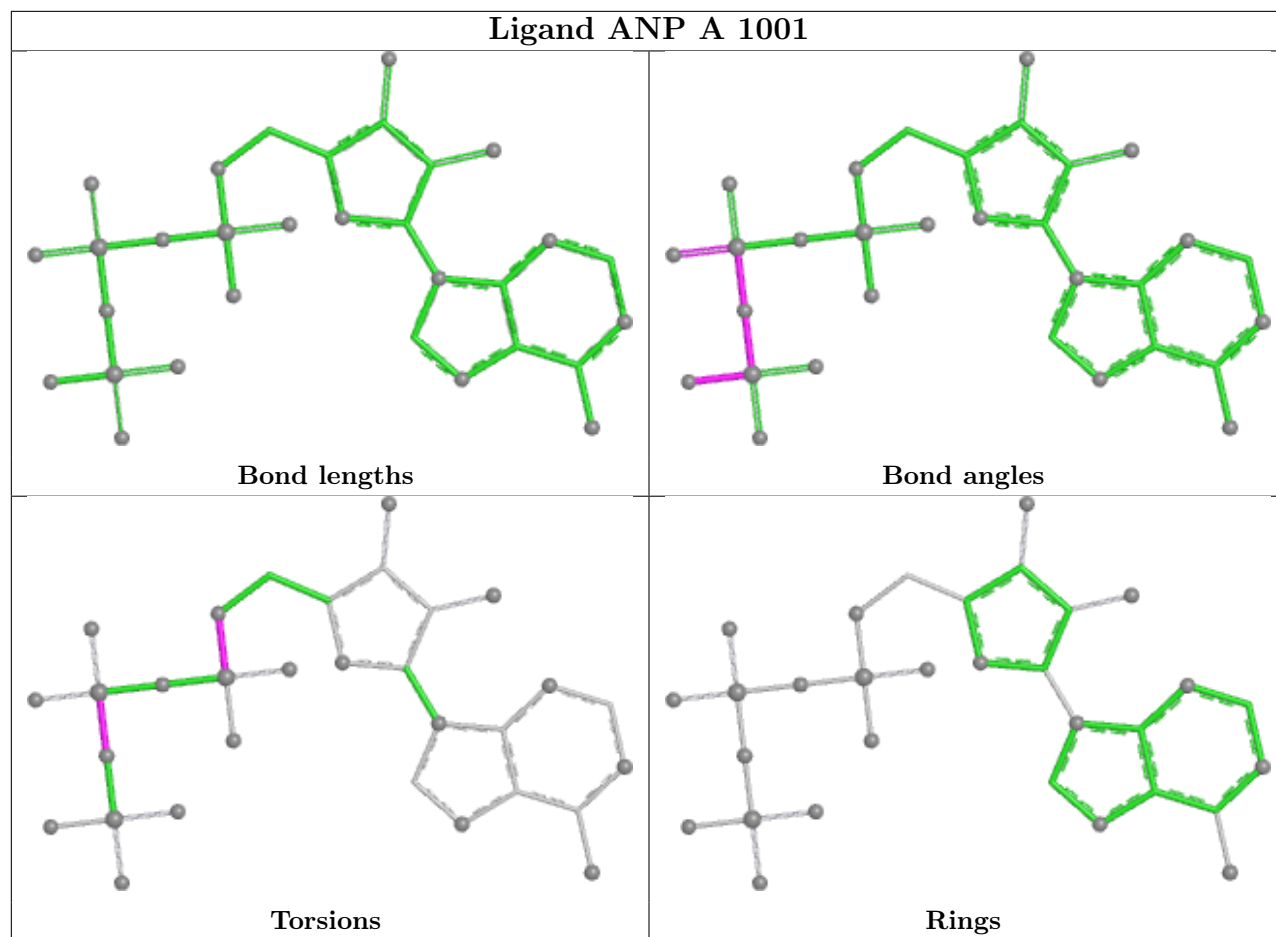
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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, 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	478/500 (95%)	-0.22	11 (2%) 61 58	20, 37, 62, 84	5 (1%)
1	B	480/500 (96%)	-0.08	6 (1%) 75 73	20, 43, 73, 94	2 (0%)
1	C	481/500 (96%)	-0.12	10 (2%) 63 60	22, 40, 73, 125	6 (1%)
1	D	479/500 (95%)	-0.02	11 (2%) 61 58	22, 44, 74, 111	6 (1%)
All	All	1918/2000 (95%)	-0.11	38 (1%) 65 62	20, 41, 72, 125	19 (0%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	415	PHE	10.1
1	C	782	ILE	6.1
1	C	627	PHE	5.4
1	B	792	THR	4.9
1	D	415	PHE	4.0
1	A	415	PHE	3.8
1	D	334	VAL	3.8
1	C	631	ASN	3.5
1	C	415	PHE	3.3
1	C	792	THR	3.2
1	D	414	GLY	3.2
1	D	631	ASN	3.1
1	B	781	ALA	3.1
1	A	659	SER	3.1
1	B	473	PHE	2.9
1	B	627	PHE	2.8
1	C	626	LEU	2.8
1	A	631	ASN	2.8
1	C	625	ILE	2.8
1	C	781	ALA	2.7
1	D	626	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	733[A]	HIS	2.7
1	C	407	LYS	2.7
1	A	779	ILE	2.6
1	A	333	MET	2.5
1	A	630	GLU	2.5
1	D	778	GLU	2.5
1	A	627	PHE	2.5
1	A	688	LYS	2.5
1	C	779	ILE	2.4
1	D	408	GLU	2.3
1	A	792	THR	2.3
1	A	626	LEU	2.3
1	D	333	MET	2.2
1	B	333	MET	2.2
1	D	632	THR	2.1
1	D	814	PHE	2.1
1	A	733	HIS	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	HFG	C	1002	24/24	0.92	0.10	26,31,43,64	0
3	HFG	B	1002	24/24	0.93	0.09	30,34,39,66	0
3	HFG	A	1002	24/24	0.93	0.09	27,32,42,59	0
3	HFG	D	1002	24/24	0.93	0.09	27,31,40,67	0
2	ANP	B	1001	31/31	0.96	0.07	30,35,41,42	0
2	ANP	D	1001	31/31	0.96	0.07	26,32,41,53	0

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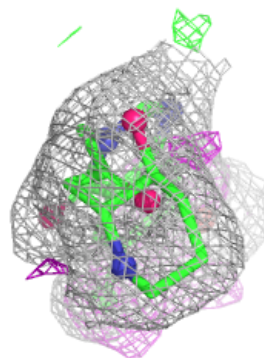
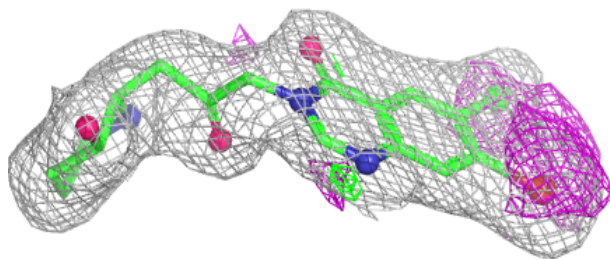
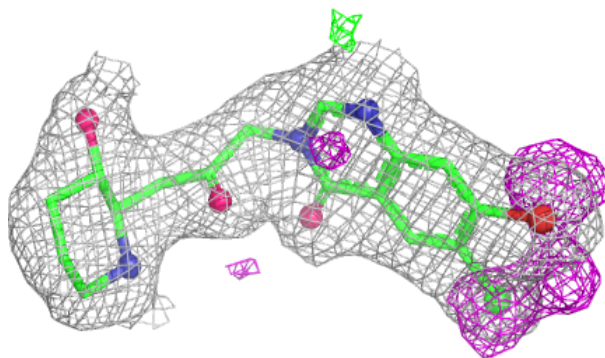
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MG	B	1004	1/1	0.96	0.05	56,56,56,56	0
4	MG	C	1004	1/1	0.96	0.04	44,44,44,44	0
2	ANP	C	1001	31/31	0.97	0.06	28,32,35,39	0
2	ANP	A	1001	31/31	0.97	0.06	27,30,35,36	0
4	MG	A	1003	1/1	0.98	0.03	32,32,32,32	0
4	MG	C	1003	1/1	0.98	0.03	37,37,37,37	0
4	MG	B	1003	1/1	0.98	0.04	36,36,36,36	0
4	MG	A	1004	1/1	0.99	0.03	51,51,51,51	0
4	MG	D	1003	1/1	0.99	0.02	29,29,29,29	0
4	MG	D	1004	1/1	0.99	0.05	50,50,50,50	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.

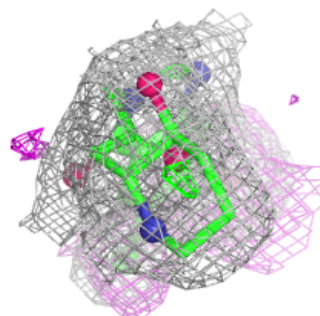
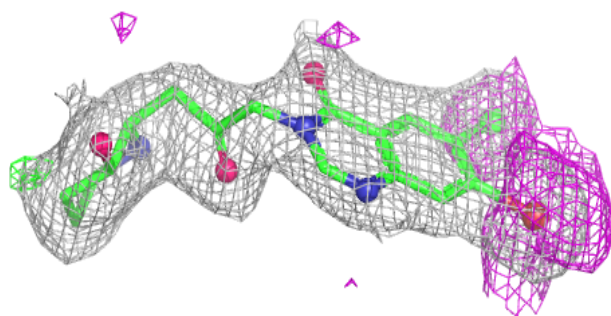
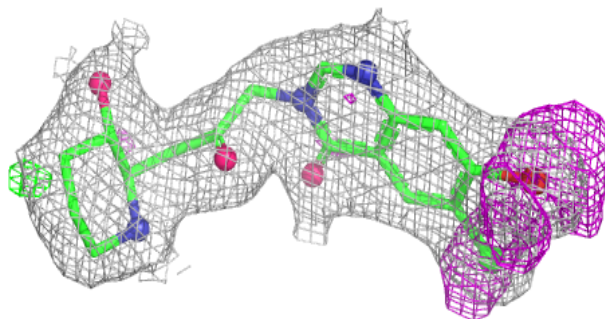
Electron density around HFG B 1002:

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

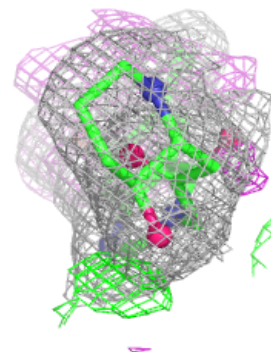
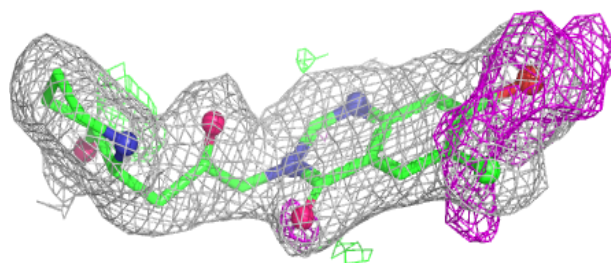
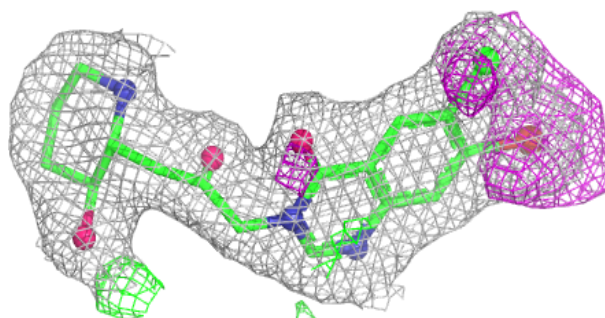


Electron density around HFG A 1002:

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

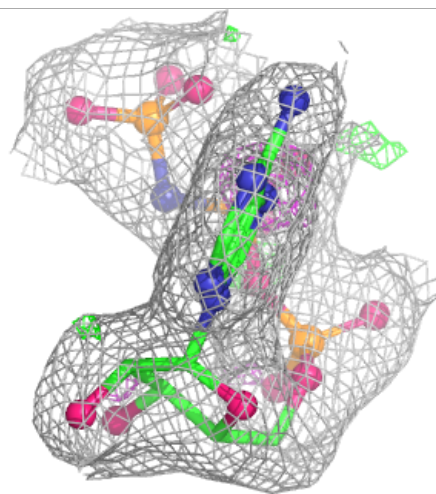
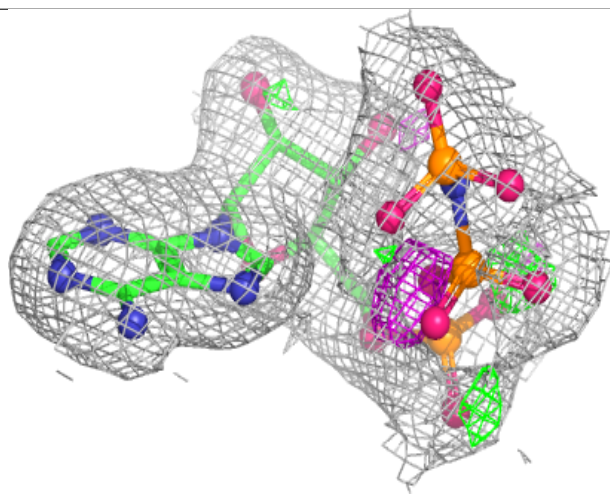
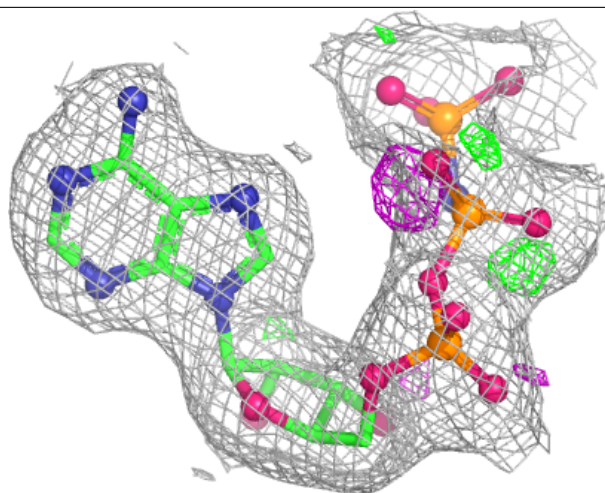
**Electron density around HFG D 1002:**

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



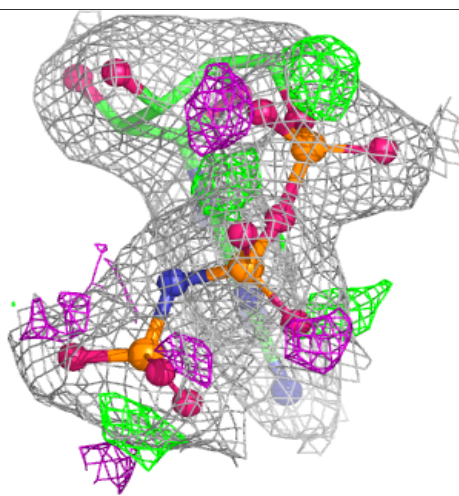
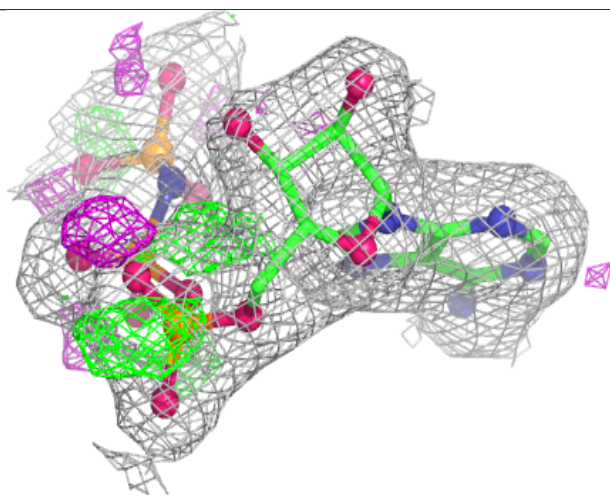
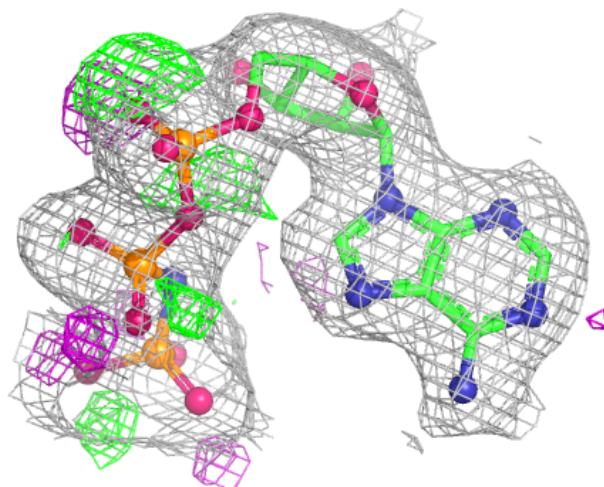
Electron density around ANP B 1001:

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



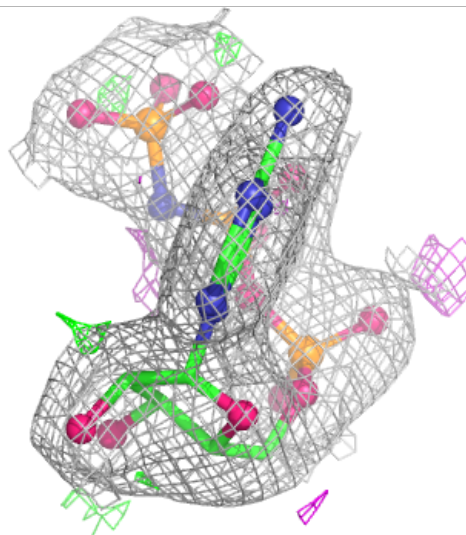
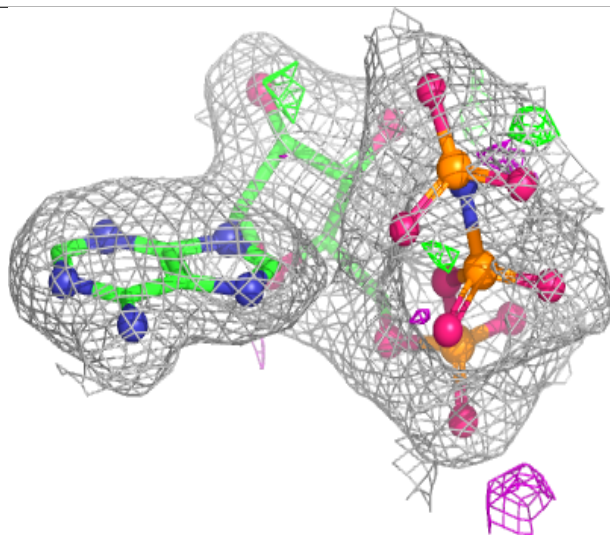
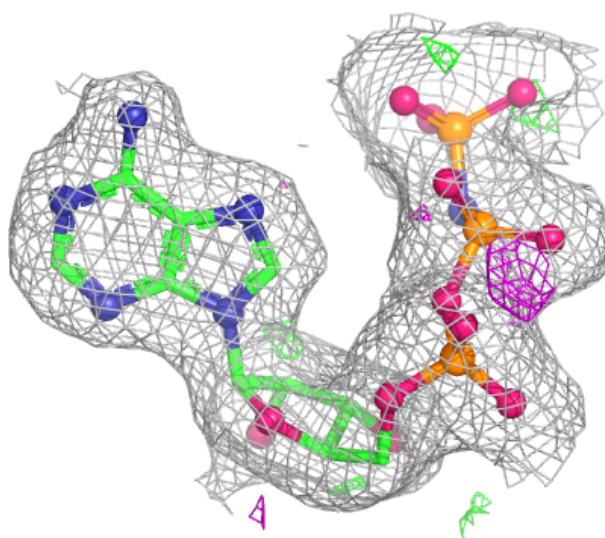
Electron density around ANP D 1001:

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



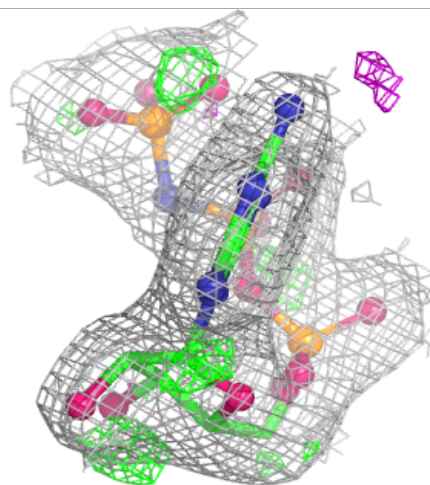
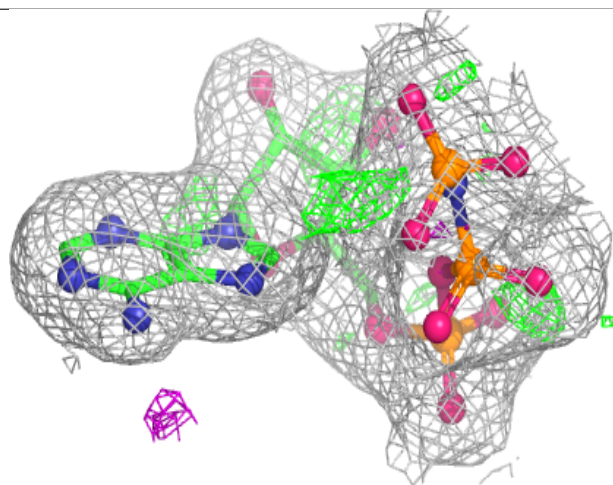
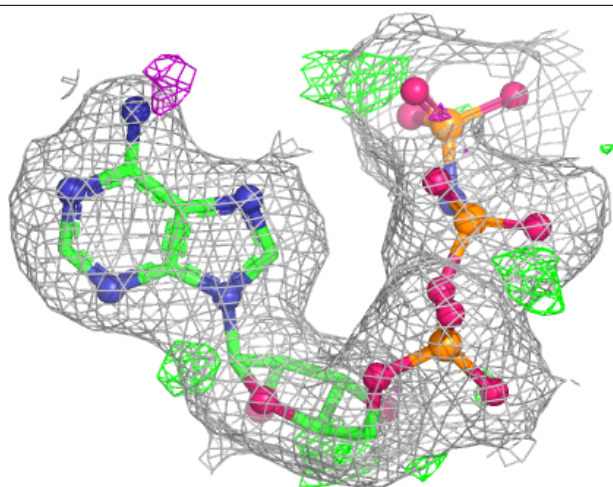
Electron density around ANP C 1001:

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



Electron density around ANP A 1001:

$2mF_o-DF_c$ (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.