



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:28 AM UTC

PDB ID : 5L4N / pdb_00005l4n
Title : Leishmania major Pteridine reductase 1 (PTR1) in complex with compound 1
Authors : Dello Iacono, L.; Di Pisa, F.; Pozzi, C.; Landi, G.; Mangani, S.
Deposited on : 2016-05-26
Resolution : 2.35 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

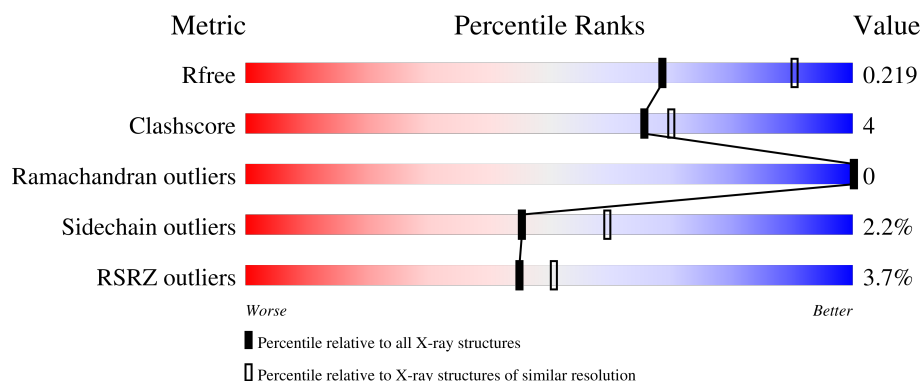
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	288	3% 81% 7% 12%
1	B	288	3% 79% 8% 12%
1	C	288	4% 76% 16% 8%
1	D	288	3% 84% 7% 8%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 8568 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.

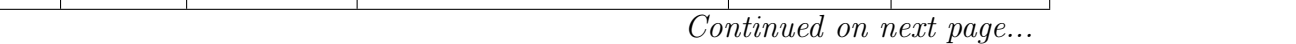
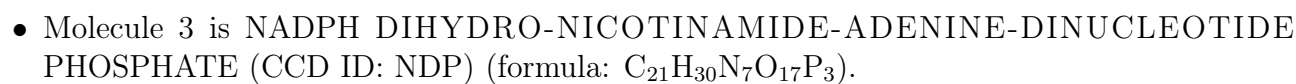
- Molecule 1 is a protein called Pteridine reductase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	7	0
			1887	1201	327	350	9			
1	B	254	Total	C	N	O	S	0	8	0
			1893	1202	332	350	9			
1	C	265	Total	C	N	O	S	0	8	0
			1983	1259	349	365	10			
1	D	264	Total	C	N	O	S	0	10	0
			1976	1253	346	366	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	162	VAL	PHE	variant	UNP Q01782
B	162	VAL	PHE	variant	UNP Q01782
C	162	VAL	PHE	variant	UNP Q01782
D	162	VAL	PHE	variant	UNP Q01782

- Molecule 2 is (2 {R})-2-(3-hydroxyphenyl)-6-oxidanyl-2,3-dihydrochromen-4-one (CCD ID: 6QT) (formula: C₁₅H₁₂O₄).



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

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

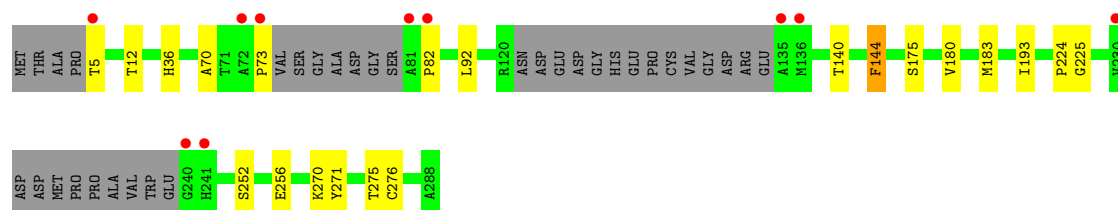
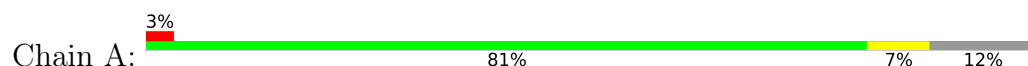
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	122	Total 122	O 122	0	0
9	B	155	Total 155	O 155	0	0
9	C	120	Total 120	O 120	0	0
9	D	166	Total 166	O 166	0	0

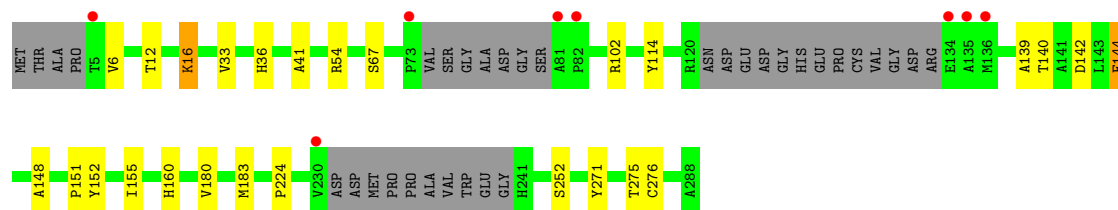
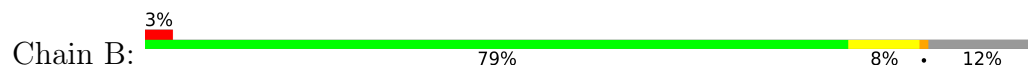
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

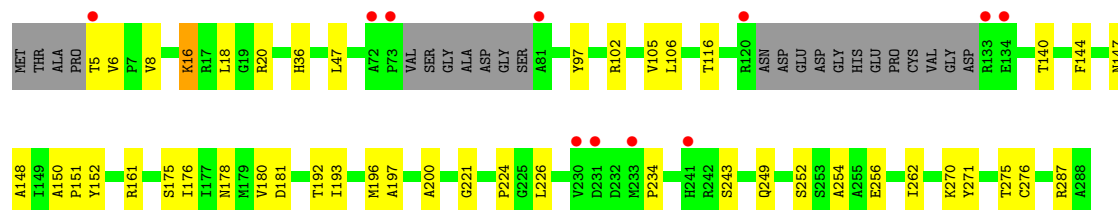
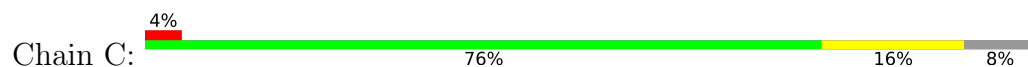
• Molecule 1: Pteridine reductase 1



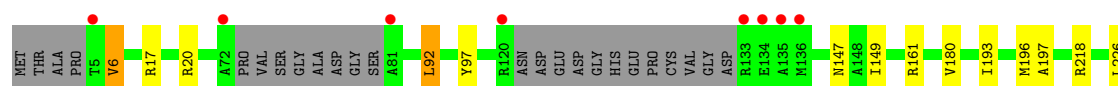
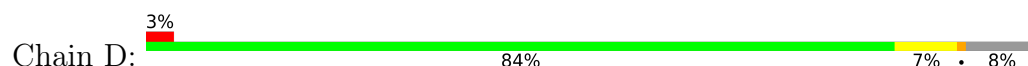
• Molecule 1: Pteridine reductase 1

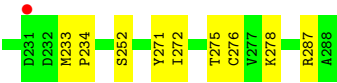


• Molecule 1: Pteridine reductase 1



• Molecule 1: Pteridine reductase 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	94.70Å 104.25Å 137.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	82.97 – 2.35 82.97 – 2.35	Depositor EDS
% Data completeness (in resolution range)	94.6 (82.97-2.35) 94.6 (82.97-2.35)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.163 , 0.218 0.166 , 0.219	Depositor DCC
R_{free} test set	2714 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8568	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.68 % 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 4.4448e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6QT, ACT, NDP, GOL, CSX, PEG, PGE, EDO

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	1.10	1/1934 (0.1%)	1.11	1/2635 (0.0%)
1	B	1.10	1/1944 (0.1%)	1.06	0/2646
1	C	1.12	1/2028 (0.0%)	1.12	4/2767 (0.1%)
1	D	1.14	1/2027 (0.0%)	1.10	1/2765 (0.0%)
All	All	1.11	4/7933 (0.1%)	1.10	6/10813 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	225	GLY	N-CA	7.24	1.50	1.45
1	C	234	PRO	CA-C	6.79	1.55	1.51
1	B	41	ALA	N-CA	5.63	1.53	1.46
1	D	234	PRO	CA-C	5.25	1.57	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	144	PHE	N-CA-C	6.00	117.90	111.36
1	D	149	ILE	N-CA-C	5.82	116.00	110.42
1	C	6	VAL	CA-C-N	-5.14	114.94	120.03
1	C	6	VAL	C-N-CA	-5.14	114.94	120.03
1	C	181	ASP	N-CA-CB	-5.11	102.23	110.81
1	C	16	LYS	N-CA-C	5.03	115.96	108.86

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	1887	0	1908	14	0
1	B	1893	0	1899	16	0
1	C	1983	0	1991	24	0
1	D	1976	0	1975	18	0
2	A	19	0	0	0	0
2	B	19	0	0	0	0
3	A	48	0	26	0	0
3	B	48	0	26	0	0
3	C	48	0	26	0	0
3	D	48	0	26	1	0
4	A	6	0	8	0	0
5	B	4	0	3	0	0
6	C	7	0	10	0	0
7	D	7	0	9	0	0
8	D	12	0	18	3	0
9	A	122	0	0	3	0
9	B	155	0	0	1	0
9	C	120	0	0	1	0
9	D	166	0	0	0	0
All	All	8568	0	7925	60	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 (60) 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:175:SER:HB2	9:A:759:HOH:O	1.63	0.97
1:D:20:ARG:HH22	8:D:305:EDO:H21	1.46	0.79
1:C:116:THR:HG21	1:C:193[B]:ILE:HD12	1.66	0.77
1:D:17:ARG:HG2	1:D:17:ARG:HH11	1.57	0.70
9:B:793:HOH:O	1:D:278:LYS:HD2	1.89	0.70
1:B:12:THR:HA	1:B:36:HIS:HB3	1.74	0.69
1:D:17:ARG:HG2	1:D:17:ARG:NH1	2.13	0.64
1:A:12:THR:HA	1:A:36:HIS:HB3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:20:ARG:NH2	8:D:305:EDO:H21	2.15	0.61
1:A:5:THR:HB	9:A:753:HOH:O	2.04	0.58
1:A:144:PHE:CE1	1:B:144:PHE:HE2	2.21	0.58
1:D:17:ARG:HD3	3:D:301:NDP:O2A	2.06	0.56
1:A:180:VAL:O	1:A:224:PRO:HD2	2.06	0.55
1:A:270[B]:LYS:HE3	1:C:256:GLU:OE2	2.08	0.54
1:A:70:ALA:HB1	1:A:82:PRO:HB2	1.90	0.53
1:C:18:LEU:HD22	1:C:254:ALA:HA	1.90	0.53
1:D:6:VAL:HG11	8:D:304:EDO:H21	1.90	0.53
1:C:192:THR:O	1:C:196:MET:HG3	2.10	0.52
1:A:183:MET:HB3	1:D:287:ARG:NH2	2.25	0.51
1:C:20:ARG:HG3	1:C:47:LEU:HD22	1.92	0.50
1:B:151:PRO:O	1:B:155:ILE:HG13	2.11	0.49
1:A:193:ILE:HD11	1:B:152:TYR:CE2	2.47	0.49
1:A:256:GLU:OE2	1:C:270:LYS:HE3	2.13	0.48
1:C:140:THR:O	1:C:144:PHE:HB2	2.14	0.48
1:D:147:ASN:HB2	1:D:197:ALA:HB1	1.96	0.48
1:D:180:VAL:HG21	1:D:276[B]:CSX:HG	1.78	0.48
1:B:140:THR:O	1:B:144:PHE:HB2	2.13	0.47
1:B:252:SER:HB3	1:D:271:TYR:CE2	2.50	0.47
1:A:140:THR:O	1:A:144:PHE:HB2	2.16	0.46
1:A:73:PRO:HD3	1:A:82:PRO:HA	1.98	0.46
1:B:271:TYR:CE2	1:D:252:SER:HB3	2.51	0.46
1:C:8:VAL:HG23	1:C:102:ARG:HG3	1.98	0.45
1:C:152:TYR:CE2	1:D:193:ILE:HD11	2.52	0.45
1:D:92:LEU:HD12	1:D:92:LEU:HA	1.69	0.44
1:C:147:ASN:HB2	1:C:197:ALA:HB1	1.99	0.44
1:B:6:VAL:O	1:B:102:ARG:HD3	2.17	0.44
1:C:97:TYR:CZ	1:C:161:ARG:HB3	2.54	0.43
1:D:161:ARG:HD2	1:D:161:ARG:HA	1.70	0.43
1:A:252:SER:HB3	1:C:271:TYR:CE2	2.54	0.43
1:C:105:VAL:HA	1:C:175:SER:O	2.19	0.43
1:C:180:VAL:O	1:C:224:PRO:HD2	2.19	0.43
1:C:97:TYR:CE1	1:C:161:ARG:HG3	2.54	0.43
1:C:200:ALA:HB1	1:D:196:MET:HB3	2.00	0.42
1:D:218:ARG:HD2	1:D:272:ILE:O	2.20	0.42
1:D:97:TYR:CZ	1:D:161:ARG:HB3	2.55	0.42
1:C:106:LEU:HB3	1:C:176:ILE:HG12	2.01	0.42
1:B:180:VAL:O	1:B:224:PRO:HD2	2.19	0.42
1:C:5:THR:HA	9:C:489:HOH:O	2.19	0.42
1:B:67[A]:SER:OG	1:B:142:ASP:HA	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:150:ALA:HB3	1:C:151:PRO:HD3	2.03	0.41
9:A:796:HOH:O	1:B:160[B]:HIS:HE1	2.02	0.41
1:B:183:MET:HB3	1:C:287:ARG:NH2	2.35	0.41
1:A:271:TYR:CE2	1:C:252:SER:HB3	2.56	0.41
1:C:178:ASN:O	1:C:221:GLY:HA2	2.21	0.41
1:C:243:SER:HA	1:C:249:GLN:HB3	2.01	0.41
1:B:114:TYR:OH	1:B:139:ALA:HA	2.21	0.41
1:B:180:VAL:HG21	1:B:276:CSX:HG	1.84	0.41
1:B:16[B]:LYS:HB2	1:B:16[B]:LYS:HE2	1.84	0.40
1:B:148:ALA:C	1:B:151:PRO:HD2	2.47	0.40
1:C:148:ALA:C	1:C:151:PRO:HD2	2.47	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	252/288 (88%)	240 (95%)	12 (5%)	0	100	100
1	B	253/288 (88%)	243 (96%)	10 (4%)	0	100	100
1	C	265/288 (92%)	250 (94%)	15 (6%)	0	100	100
1	D	266/288 (92%)	252 (95%)	14 (5%)	0	100	100
All	All	1036/1152 (90%)	985 (95%)	51 (5%)	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	194/222 (87%)	192 (99%)	2 (1%)	68	81
1	B	193/222 (87%)	186 (96%)	7 (4%)	31	41
1	C	202/222 (91%)	197 (98%)	5 (2%)	42	55
1	D	202/222 (91%)	197 (98%)	5 (2%)	42	55
All	All	791/888 (89%)	772 (98%)	19 (2%)	45	57

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	LEU
1	A	275	THR
1	B	16[A]	LYS
1	B	16[B]	LYS
1	B	33[A]	VAL
1	B	33[B]	VAL
1	B	54	ARG
1	B	144	PHE
1	B	275	THR
1	C	16	LYS
1	C	36	HIS
1	C	226	LEU
1	C	262	ILE
1	C	275	THR
1	D	6	VAL
1	D	92	LEU
1	D	226	LEU
1	D	233	MET
1	D	275	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	ASN
1	A	147	ASN
1	A	185	ASN
1	B	38	HIS
1	B	169	HIS
1	B	249	GLN

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Mol	Chain	Res	Type
1	C	108	ASN
1	D	249	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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
1	CSX	C	276[B]	1	3,6,7	0.52	0	1,6,8	2.83	1 (100%)
1	CSX	A	276	1	3,6,7	0.92	0	1,6,8	3.26	1 (100%)
1	CSX	D	276[B]	-	3,6,7	0.43	0	1,6,8	0.12	0
1	CSX	C	276[A]	1	3,6,7	0.89	0	1,6,8	3.53	1 (100%)
1	CSX	D	276[A]	-	3,6,7	0.64	0	1,6,8	0.66	0
1	CSX	B	276	1	3,6,7	1.17	0	1,6,8	0.60	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
1	CSX	C	276[B]	1	-	0/2/5/7	-
1	CSX	A	276	1	-	0/2/5/7	-
1	CSX	D	276[B]	-	-	0/2/5/7	-
1	CSX	C	276[A]	1	-	2/2/5/7	-
1	CSX	D	276[A]	-	-	2/2/5/7	-
1	CSX	B	276	1	-	0/2/5/7	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	276[A]	CSX	CA-CB-SG	-3.53	104.87	113.17
1	A	276	CSX	CA-CB-SG	-3.26	105.50	113.17
1	C	276[B]	CSX	CA-CB-SG	-2.83	106.53	113.17

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	276[A]	CSX	N-CA-CB-SG
1	C	276[A]	CSX	C-CA-CB-SG
1	D	276[A]	CSX	N-CA-CB-SG
1	D	276[A]	CSX	C-CA-CB-SG

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	276[B]	CSX	1	0
1	B	276	CSX	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

13 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
2	6QT	A	601	-	21,21,21	1.98	4 (19%)	30,30,30	1.40	5 (16%)
3	NDP	A	602	-	51,52,52	1.53	8 (15%)	71,80,80	1.91	19 (26%)
4	GOL	A	603	-	5,5,5	0.80	0	5,5,5	0.93	0
7	PGE	D	302	-	6,6,9	0.69	0	5,5,8	0.35	0
8	EDO	D	305	-	3,3,3	0.50	0	2,2,2	0.63	0
8	EDO	D	304	-	3,3,3	0.75	0	2,2,2	0.07	0
2	6QT	B	601	-	21,21,21	2.35	3 (14%)	30,30,30	2.15	9 (30%)
3	NDP	D	301	-	51,52,52	1.39	8 (15%)	71,80,80	2.03	18 (25%)
8	EDO	D	303	-	3,3,3	0.53	0	2,2,2	0.93	0
3	NDP	C	301	-	51,52,52	1.44	8 (15%)	71,80,80	1.67	17 (23%)
3	NDP	B	602	-	51,52,52	1.48	7 (13%)	71,80,80	1.93	18 (25%)
6	PEG	C	302	-	6,6,6	0.67	0	5,5,5	0.70	0
5	ACT	B	603	-	3,3,3	0.86	0	3,3,3	1.16	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
2	6QT	A	601	-	-	0/4/16/16	0/3/3/3
3	NDP	A	602	-	-	2/34/77/77	0/5/5/5
4	GOL	A	603	-	-	0/4/4/4	-
7	PGE	D	302	-	-	4/4/4/7	-
8	EDO	D	305	-	-	0/1/1/1	-
8	EDO	D	304	-	-	1/1/1/1	-
2	6QT	B	601	-	-	0/4/16/16	0/3/3/3
3	NDP	D	301	-	-	2/34/77/77	0/5/5/5
8	EDO	D	303	-	-	1/1/1/1	-
3	NDP	C	301	-	-	1/34/77/77	0/5/5/5
3	NDP	B	602	-	-	3/34/77/77	0/5/5/5
6	PEG	C	302	-	-	3/4/4/4	-

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	6QT	CAM-CAJ	-7.57	1.38	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	6QT	CAM-CAJ	-5.40	1.42	1.51
3	C	301	NDP	C5A-C4A	5.15	1.48	1.39
3	A	602	NDP	PA-O3	5.05	1.65	1.59
2	B	601	6QT	CAE-CAH	-4.73	1.42	1.48
3	A	602	NDP	C5A-C4A	4.66	1.47	1.39
3	B	602	NDP	C5A-C4A	4.50	1.47	1.39
3	D	301	NDP	PA-O3	4.49	1.64	1.59
3	B	602	NDP	PN-O3	4.15	1.64	1.59
3	B	602	NDP	PA-O3	4.15	1.64	1.59
2	A	601	6QT	CAI-CAH	-4.13	1.42	1.50
2	B	601	6QT	CAI-CAH	-3.83	1.43	1.50
3	B	602	NDP	C5A-C6A	3.73	1.51	1.41
3	A	602	NDP	PN-O3	3.59	1.63	1.59
3	D	301	NDP	C5A-C4A	3.43	1.45	1.39
3	C	301	NDP	PA-O3	3.30	1.63	1.59
3	D	301	NDP	C8A-N7A	3.26	1.37	1.31
3	C	301	NDP	C8A-N7A	3.12	1.37	1.31
3	A	602	NDP	C5A-N7A	-2.86	1.33	1.39
3	A	602	NDP	C8A-N7A	2.85	1.37	1.31
2	A	601	6QT	CAE-CAH	-2.75	1.44	1.48
3	C	301	NDP	C5A-C6A	2.74	1.48	1.41
3	D	301	NDP	C5A-N7A	-2.70	1.34	1.39
3	A	602	NDP	C5A-C6A	2.65	1.48	1.41
3	A	602	NDP	P2B-O2B	2.43	1.63	1.59
3	B	602	NDP	C8A-N7A	2.40	1.36	1.31
3	C	301	NDP	C2N-C3N	2.35	1.41	1.35
3	B	602	NDP	C7N-C3N	2.31	1.53	1.48
3	D	301	NDP	C8A-N9A	-2.28	1.33	1.37
2	A	601	6QT	CAD-CAC	2.27	1.42	1.39
3	C	301	NDP	C6N-C5N	2.26	1.40	1.33
3	C	301	NDP	C4A-N3A	2.23	1.38	1.34
3	B	602	NDP	C6N-C5N	2.23	1.39	1.33
3	D	301	NDP	C5A-C6A	2.18	1.47	1.41
3	A	602	NDP	C6N-C5N	2.15	1.39	1.33
3	D	301	NDP	C2A-N1A	2.13	1.37	1.33
3	C	301	NDP	PN-O3	2.07	1.61	1.59
3	D	301	NDP	P2B-O2B	2.00	1.63	1.59

All (86) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	6QT	CAF-CAE-CAH	-5.92	116.61	119.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	NDP	C5A-C4A-N3A	-5.81	118.72	126.72
3	D	301	NDP	C5A-C4A-N3A	-5.68	118.90	126.72
3	A	602	NDP	C5A-C4A-N3A	-5.35	119.35	126.72
3	B	602	NDP	C4A-C5A-N7A	-5.32	104.49	110.58
3	A	602	NDP	C4A-C5A-N7A	-5.09	104.76	110.58
3	C	301	NDP	C4A-N9A-C8A	4.67	110.64	105.74
3	D	301	NDP	C4A-C5A-N7A	-4.51	105.43	110.58
3	D	301	NDP	N9A-C8A-N7A	-4.42	107.66	113.94
3	A	602	NDP	C5A-N7A-C8A	4.42	110.40	103.45
3	D	301	NDP	N3A-C4A-N9A	4.37	134.59	127.17
3	D	301	NDP	C4A-N9A-C8A	4.35	110.30	105.74
3	B	602	NDP	C5A-N7A-C8A	4.26	110.14	103.45
3	D	301	NDP	C5A-N7A-C8A	4.23	110.09	103.45
2	B	601	6QT	CAI-CAH-CAE	4.22	123.25	116.63
3	B	602	NDP	N3A-C4A-N9A	4.19	134.29	127.17
3	A	602	NDP	N9A-C8A-N7A	-4.00	108.26	113.94
3	C	301	NDP	N3A-C4A-N9A	3.93	133.86	127.17
3	A	602	NDP	N3A-C4A-N9A	3.86	133.73	127.17
3	B	602	NDP	C4A-N9A-C8A	3.83	109.76	105.74
3	B	602	NDP	O4B-C1B-N9A	3.80	115.40	108.09
3	C	301	NDP	C5A-C4A-N3A	-3.80	121.49	126.72
3	B	602	NDP	C2A-N3A-C4A	3.79	121.10	111.83
3	B	602	NDP	N9A-C8A-N7A	-3.75	108.61	113.94
3	A	602	NDP	C4A-N9A-C8A	3.72	109.65	105.74
3	C	301	NDP	N3A-C2A-N1A	-3.67	123.03	128.58
3	D	301	NDP	N3A-C2A-N1A	-3.53	123.24	128.58
3	D	301	NDP	C2A-N3A-C4A	3.45	120.25	111.83
3	D	301	NDP	O4B-C1B-N9A	3.40	114.61	108.09
3	D	301	NDP	O7N-C7N-C3N	-3.35	114.59	120.90
3	D	301	NDP	C2B-C1B-N9A	-3.33	108.27	113.75
2	A	601	6QT	OAG-CAF-CAE	-3.31	118.32	122.16
3	A	602	NDP	C2A-N3A-C4A	3.25	119.76	111.83
3	A	602	NDP	O4B-C1B-N9A	3.25	114.33	108.09
3	C	301	NDP	N9A-C8A-N7A	-3.16	109.45	113.94
2	B	601	6QT	CAO-CAN-CAM	3.10	122.76	120.09
2	B	601	6QT	OAG-CAJ-CAM	3.10	113.23	107.47
3	B	602	NDP	C6A-C5A-N7A	3.08	138.03	132.09
3	B	602	NDP	O2A-PA-O3	3.06	115.53	107.27
3	A	602	NDP	N3A-C2A-N1A	-3.04	123.98	128.58
3	C	301	NDP	C2A-N1A-C6A	3.02	123.68	118.73
3	D	301	NDP	C1D-N1N-C6N	-2.99	114.45	120.77
3	A	602	NDP	C2B-C1B-N9A	-2.99	108.84	113.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	6QT	OAG-CAF-CAE	-2.93	118.75	122.16
3	A	602	NDP	C6N-N1N-C2N	2.93	122.45	119.32
3	B	602	NDP	O4D-C1D-N1N	2.91	113.64	108.08
3	C	301	NDP	C2A-N3A-C4A	2.88	118.86	111.83
3	D	301	NDP	C3N-C7N-N7N	2.86	122.74	117.67
3	C	301	NDP	C4A-N9A-C1B	-2.82	120.03	126.63
3	A	602	NDP	C6A-C5A-N7A	2.82	137.52	132.09
3	C	301	NDP	O2B-P2B-O1X	-2.82	99.30	109.33
3	D	301	NDP	C6N-N1N-C2N	2.81	122.33	119.32
2	B	601	6QT	CAD-CAE-CAH	2.79	124.18	119.51
3	D	301	NDP	O3X-P2B-O1X	2.66	121.21	110.83
3	B	602	NDP	N3A-C2A-N1A	-2.63	124.60	128.58
3	D	301	NDP	O2A-PA-O3	2.61	114.33	107.27
2	A	601	6QT	CAI-CAH-CAE	2.60	120.71	116.63
3	B	602	NDP	C6N-N1N-C2N	2.59	122.09	119.32
3	C	301	NDP	C5A-N7A-C8A	2.51	107.40	103.45
3	A	602	NDP	C1D-N1N-C6N	-2.42	115.67	120.77
3	A	602	NDP	C3N-C2N-N1N	-2.40	119.67	123.20
3	A	602	NDP	O7N-C7N-C3N	-2.39	116.39	120.90
3	A	602	NDP	C3N-C7N-N7N	2.36	121.86	117.67
3	B	602	NDP	C1D-N1N-C6N	-2.36	115.78	120.77
3	C	301	NDP	C4A-C5A-N7A	-2.35	107.89	110.58
3	D	301	NDP	C4B-O4B-C1B	-2.32	104.34	109.47
2	A	601	6QT	CAD-CAE-CAH	2.28	123.32	119.51
3	C	301	NDP	O4B-C1B-N9A	2.27	112.45	108.09
2	B	601	6QT	OAS-CAH-CAE	-2.26	119.18	121.71
3	C	301	NDP	C1D-N1N-C6N	-2.26	116.00	120.77
3	D	301	NDP	O4B-C4B-C5B	2.25	116.55	109.33
3	C	301	NDP	C2B-C1B-N9A	-2.23	110.09	113.75
3	B	602	NDP	C4D-O4D-C1D	2.21	114.35	109.47
3	B	602	NDP	C2B-C1B-N9A	-2.20	110.13	113.75
2	A	601	6QT	CAO-CAN-CAM	2.17	121.96	120.09
2	B	601	6QT	OAS-CAH-CAI	-2.15	117.30	120.81
3	C	301	NDP	O4D-C1D-N1N	2.13	112.14	108.08
2	B	601	6QT	CAA-CAB-CAC	2.13	122.13	119.88
3	C	301	NDP	C6A-C5A-N7A	2.12	136.17	132.09
3	A	602	NDP	O2B-P2B-O1X	-2.09	101.87	109.33
2	A	601	6QT	OAS-CAH-CAI	-2.08	117.41	120.81
3	A	602	NDP	O3X-P2B-O2X	2.06	115.53	107.80
3	A	602	NDP	C2A-N1A-C6A	2.04	122.08	118.73
3	C	301	NDP	O3X-P2B-O2X	2.04	115.44	107.80
3	B	602	NDP	C3N-C7N-N7N	2.02	121.25	117.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	NDP	O3X-P2B-O2X	2.00	115.31	107.80

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	NDP	O4D-C1D-N1N-C6N
3	B	602	NDP	O4D-C1D-N1N-C6N
3	C	301	NDP	O4D-C1D-N1N-C6N
7	D	302	PGE	O1-C1-C2-O2
7	D	302	PGE	O2-C3-C4-O3
3	D	301	NDP	O4D-C1D-N1N-C6N
6	C	302	PEG	O1-C1-C2-O2
8	D	304	EDO	O1-C1-C2-O2
7	D	302	PGE	C4-C3-O2-C2
6	C	302	PEG	C4-C3-O2-C2
8	D	303	EDO	O1-C1-C2-O2
6	C	302	PEG	C1-C2-O2-C3
3	A	602	NDP	C2N-C3N-C7N-N7N
3	B	602	NDP	C2N-C3N-C7N-N7N
3	D	301	NDP	PN-O3-PA-O1A
3	B	602	NDP	O4D-C4D-C5D-O5D
7	D	302	PGE	C1-C2-O2-C3

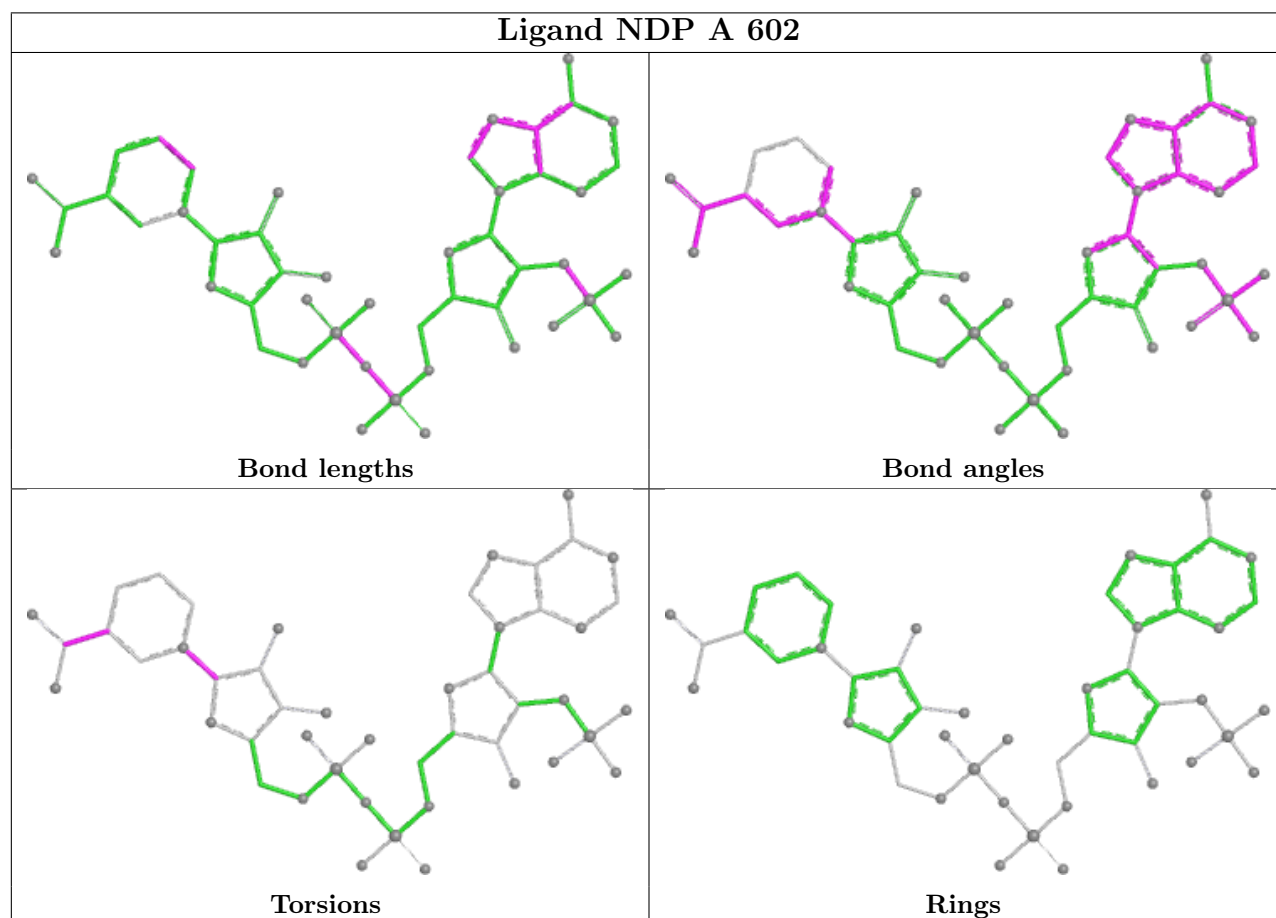
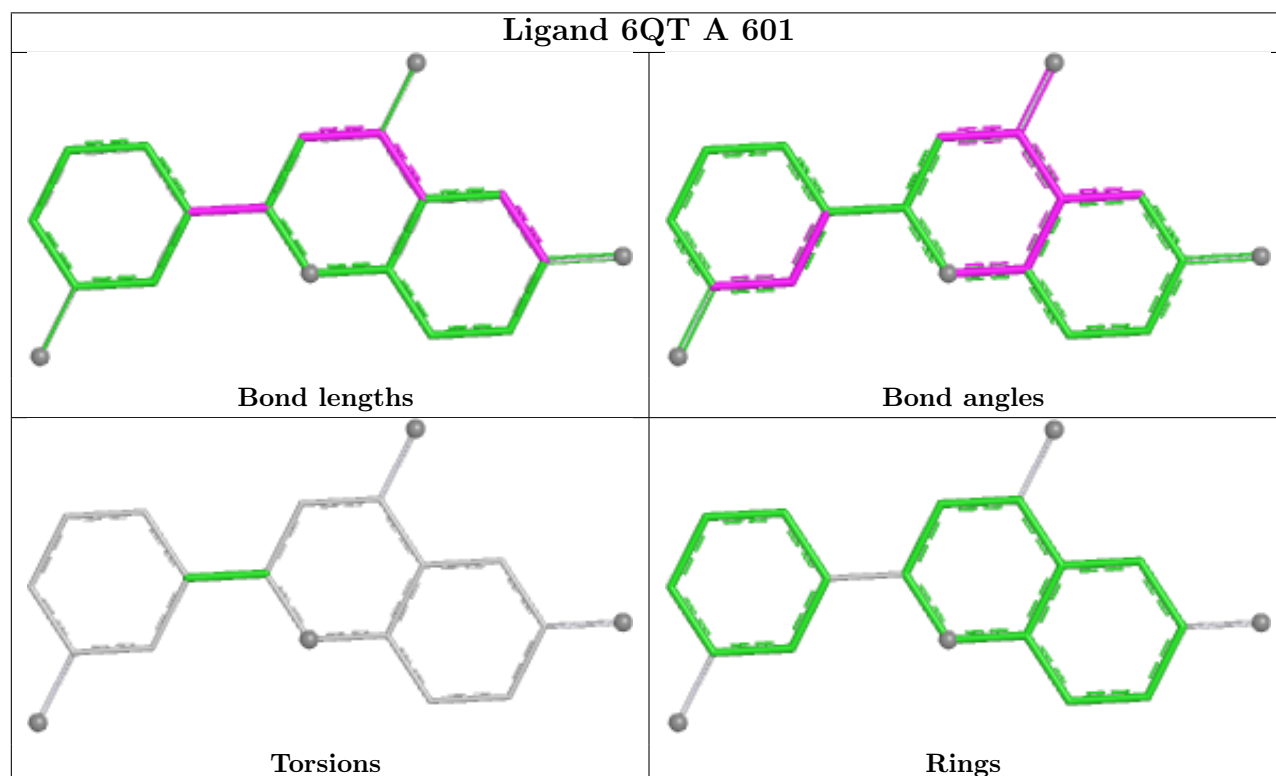
There are no ring outliers.

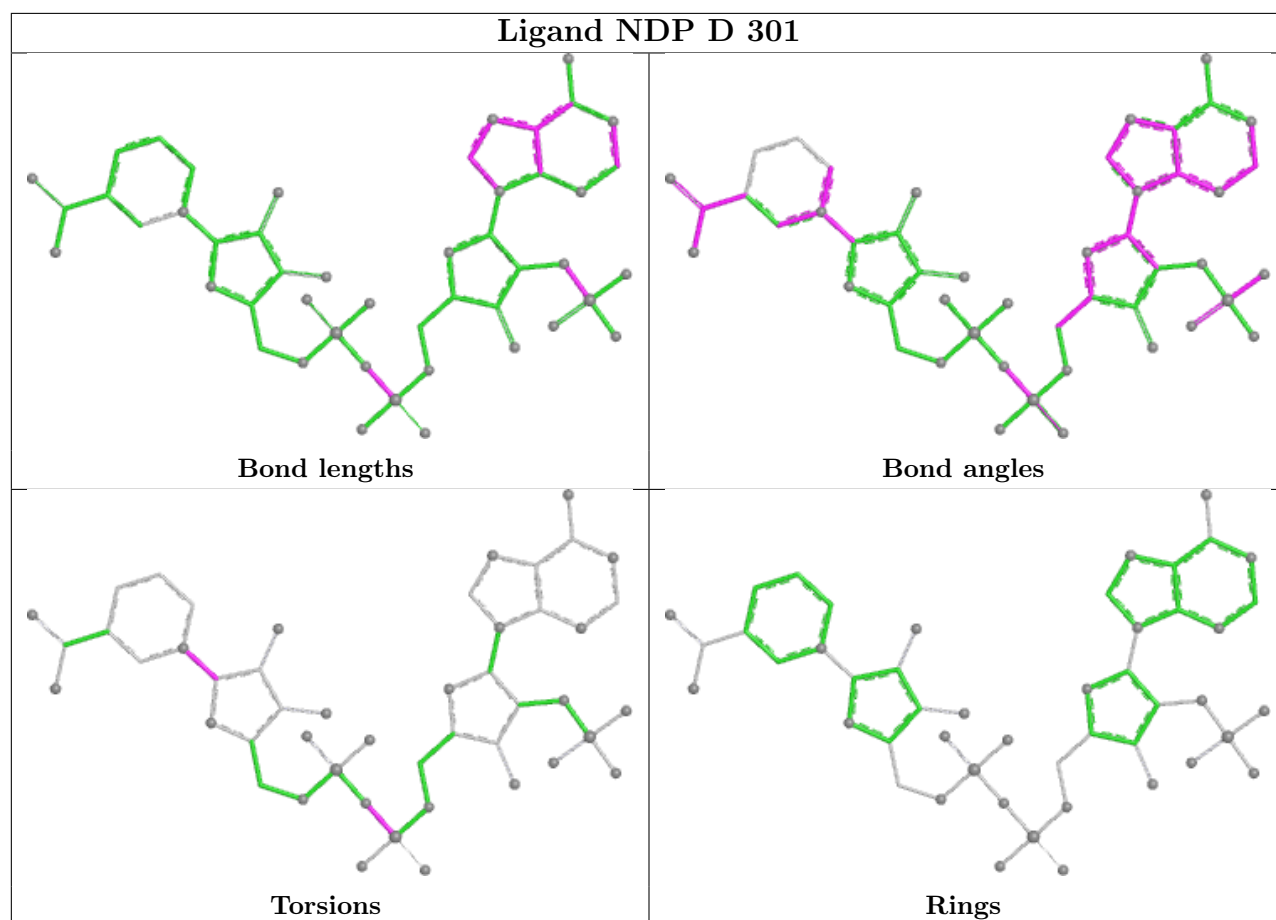
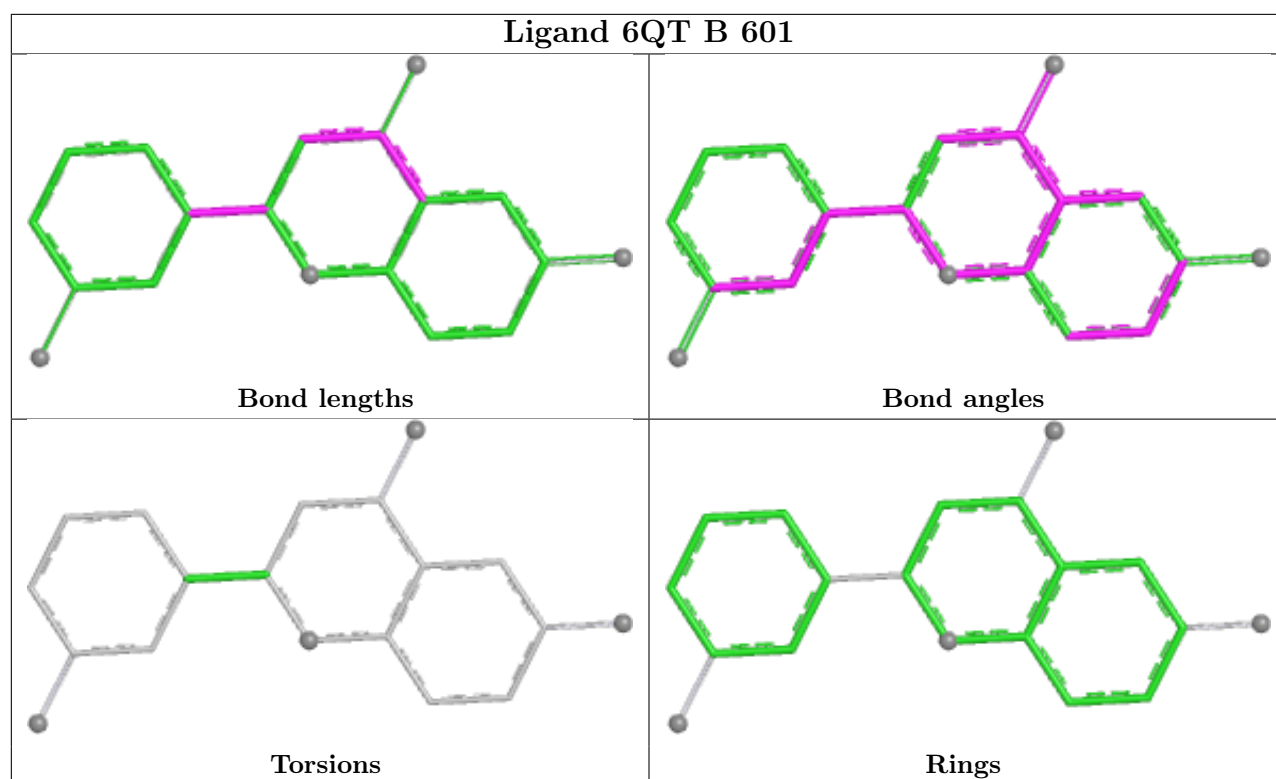
3 monomers are involved in 4 short contacts:

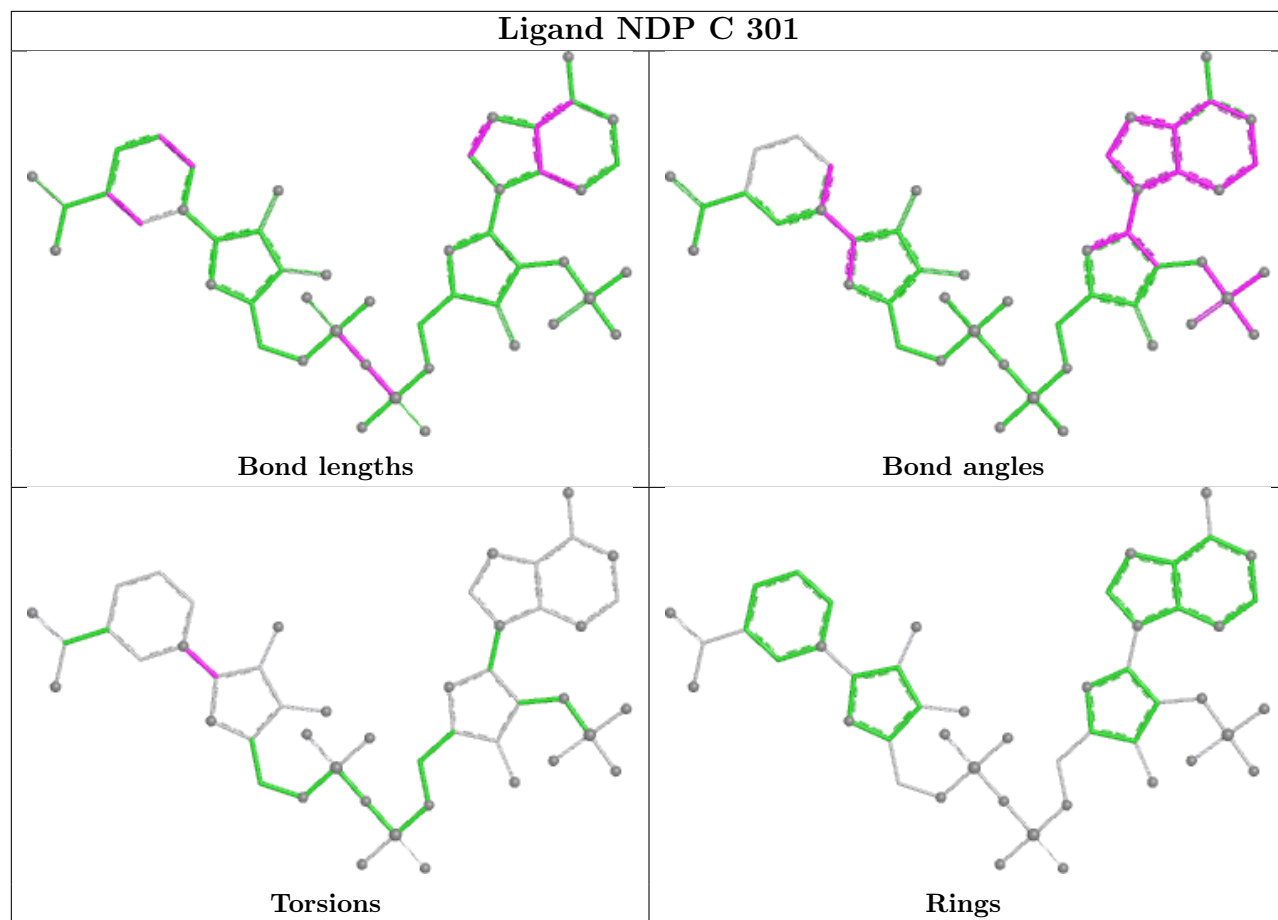
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	D	305	EDO	2	0
8	D	304	EDO	1	0
3	D	301	NDP	1	0

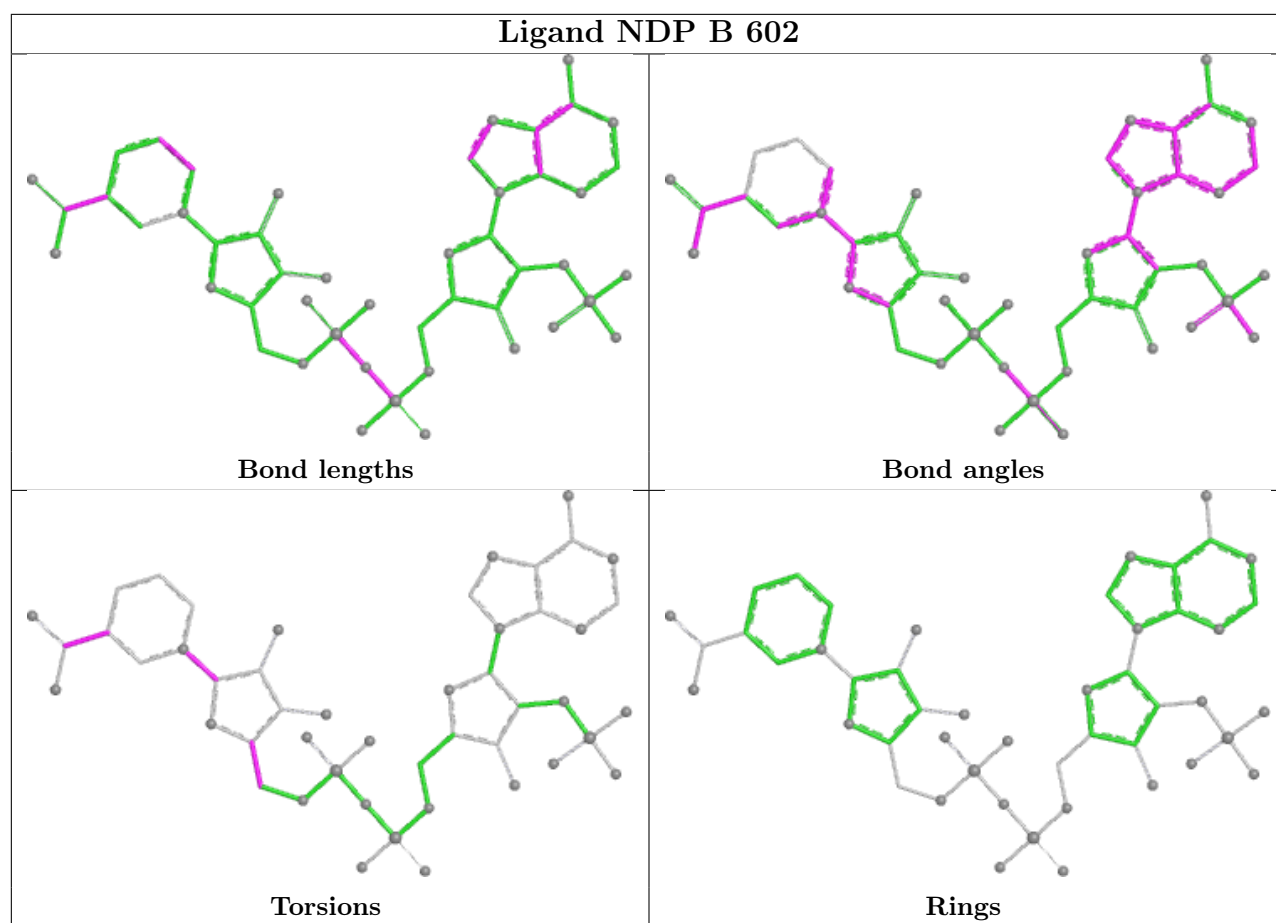
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	253/288 (87%)	-0.41	10 (3%)	42 48	11, 22, 51, 98	10 (3%)
1	B	253/288 (87%)	-0.48	8 (3%)	50 57	11, 19, 47, 89	10 (3%)
1	C	264/288 (91%)	-0.31	11 (4%)	40 46	9, 23, 48, 77	8 (3%)
1	D	263/288 (91%)	-0.55	9 (3%)	48 55	8, 17, 37, 77	9 (3%)
All	All	1033/1152 (89%)	-0.44	38 (3%)	45 51	8, 20, 50, 98	37 (3%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	231	ASP	5.7
1	B	134	GLU	5.1
1	A	73	PRO	4.9
1	A	230	VAL	4.6
1	B	135	ALA	4.6
1	C	133	ARG	4.6
1	C	230	VAL	4.1
1	B	136	MET	4.1
1	C	73	PRO	3.9
1	C	5	THR	3.7
1	D	72	ALA	3.6
1	D	133	ARG	3.6
1	B	81	ALA	3.5
1	D	231	ASP	3.4
1	D	120	ARG	3.3
1	A	72	ALA	3.2
1	B	5	THR	3.2
1	A	136	MET	3.1
1	D	134	GLU	3.0
1	D	5	THR	3.0
1	A	240	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	81	ALA	2.9
1	B	73	PRO	2.8
1	A	81	ALA	2.8
1	D	135	ALA	2.8
1	A	82	PRO	2.7
1	A	5	THR	2.6
1	D	81	ALA	2.5
1	C	120	ARG	2.5
1	C	72	ALA	2.5
1	B	230	VAL	2.4
1	C	233	MET	2.4
1	D	136	MET	2.2
1	B	82	PRO	2.1
1	C	134	GLU	2.1
1	A	135	ALA	2.1
1	C	241	HIS	2.0
1	A	241	HIS	2.0

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

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(Å ²)	Q<0.9
1	CSX	C	276[A]	7/8	0.95	0.08	23,24,29,32	7
1	CSX	C	276[B]	7/8	0.95	0.08	23,24,29,30	7
1	CSX	A	276	7/8	0.96	0.06	23,27,53,59	0
1	CSX	D	276[A]	7/8	0.97	0.07	22,23,28,29	4
1	CSX	D	276[B]	7/8	0.97	0.07	22,23,26,28	4
1	CSX	B	276	7/8	0.98	0.05	21,24,46,49	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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,

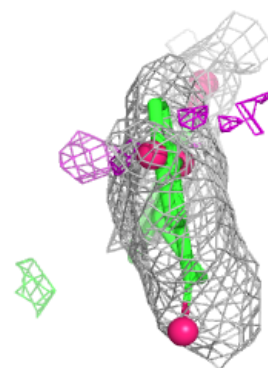
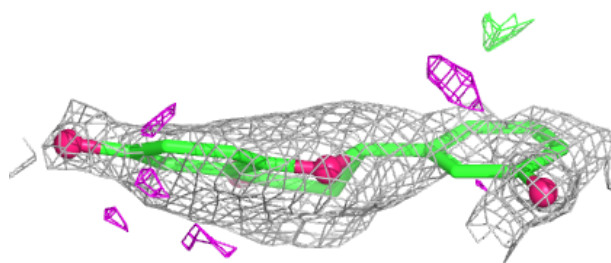
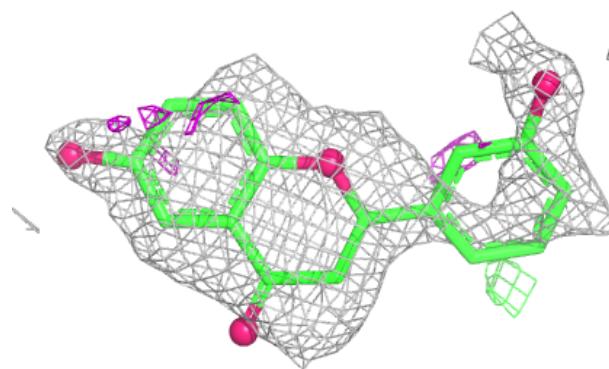
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	EDO	D	303	4/4	0.59	0.23	37,38,38,42	0
7	PGE	D	302	7/10	0.78	0.23	48,53,55,58	0
5	ACT	B	603	4/4	0.83	0.16	54,55,58,59	0
2	6QT	B	601	19/19	0.86	0.20	54,72,86,89	0
6	PEG	C	302	7/7	0.88	0.16	48,52,58,60	0
2	6QT	A	601	19/19	0.89	0.19	51,76,91,92	0
8	EDO	D	305	4/4	0.89	0.11	36,38,41,42	0
4	GOL	A	603	6/6	0.90	0.13	47,55,56,57	0
8	EDO	D	304	4/4	0.93	0.12	45,46,49,51	0
3	NDP	D	301	48/48	0.98	0.05	15,20,22,24	0
3	NDP	A	602	48/48	0.98	0.05	26,29,34,38	0
3	NDP	B	602	48/48	0.98	0.05	26,31,37,37	0
3	NDP	C	301	48/48	0.98	0.05	18,25,28,30	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.

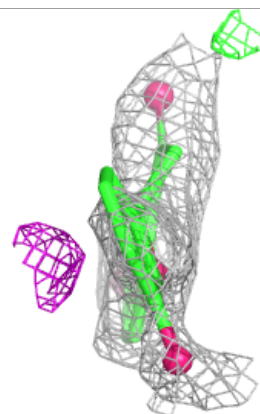
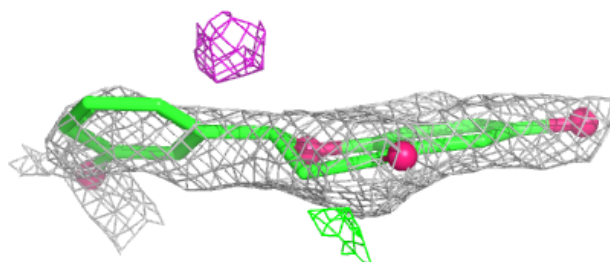
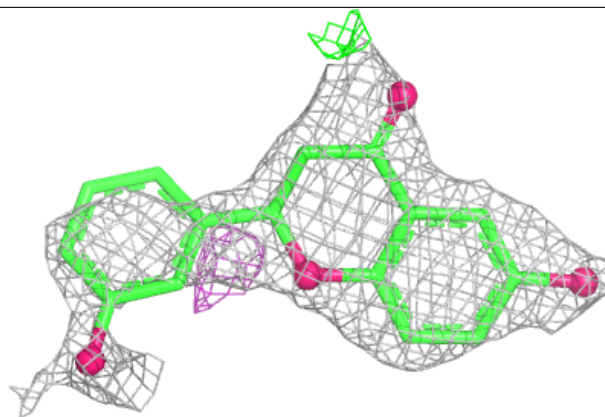
Electron density around 6QT B 601:

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

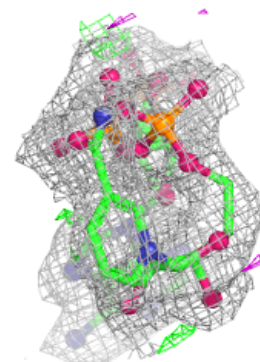
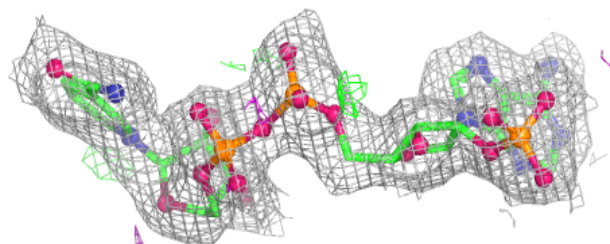
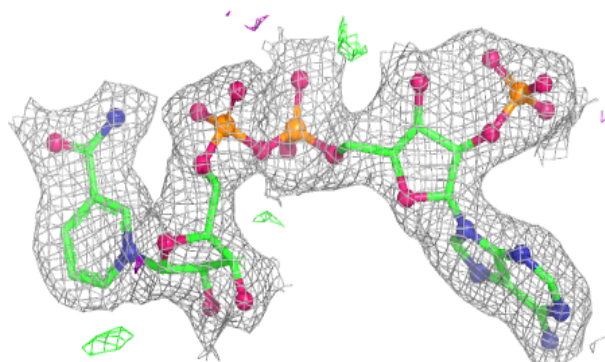


Electron density around 6QT A 601:

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

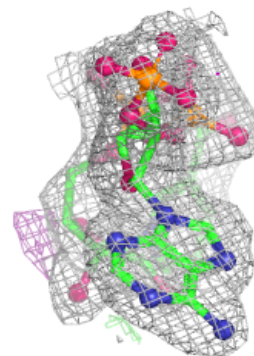
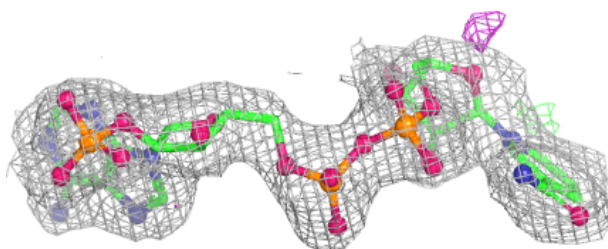
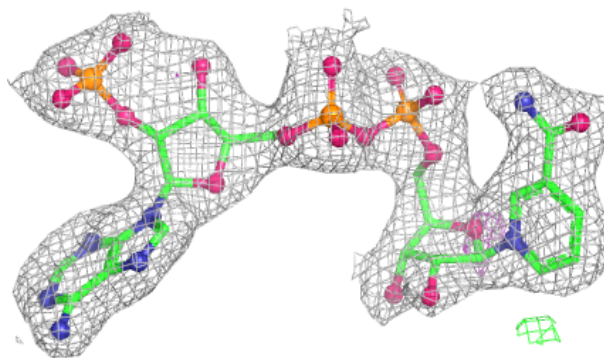
**Electron density around NDP D 301:**

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

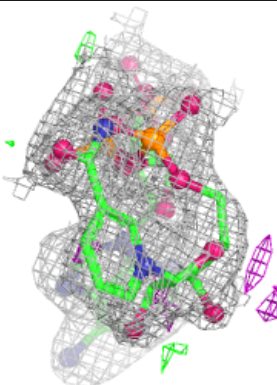
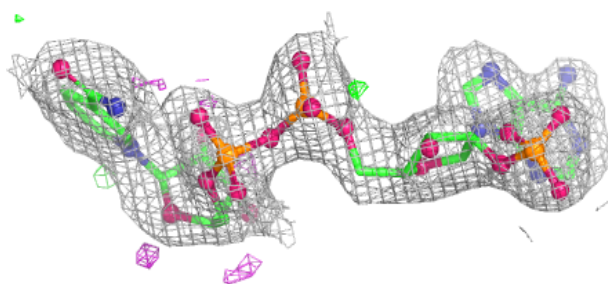
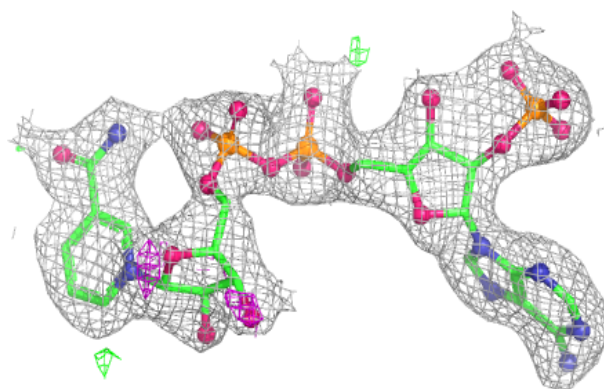


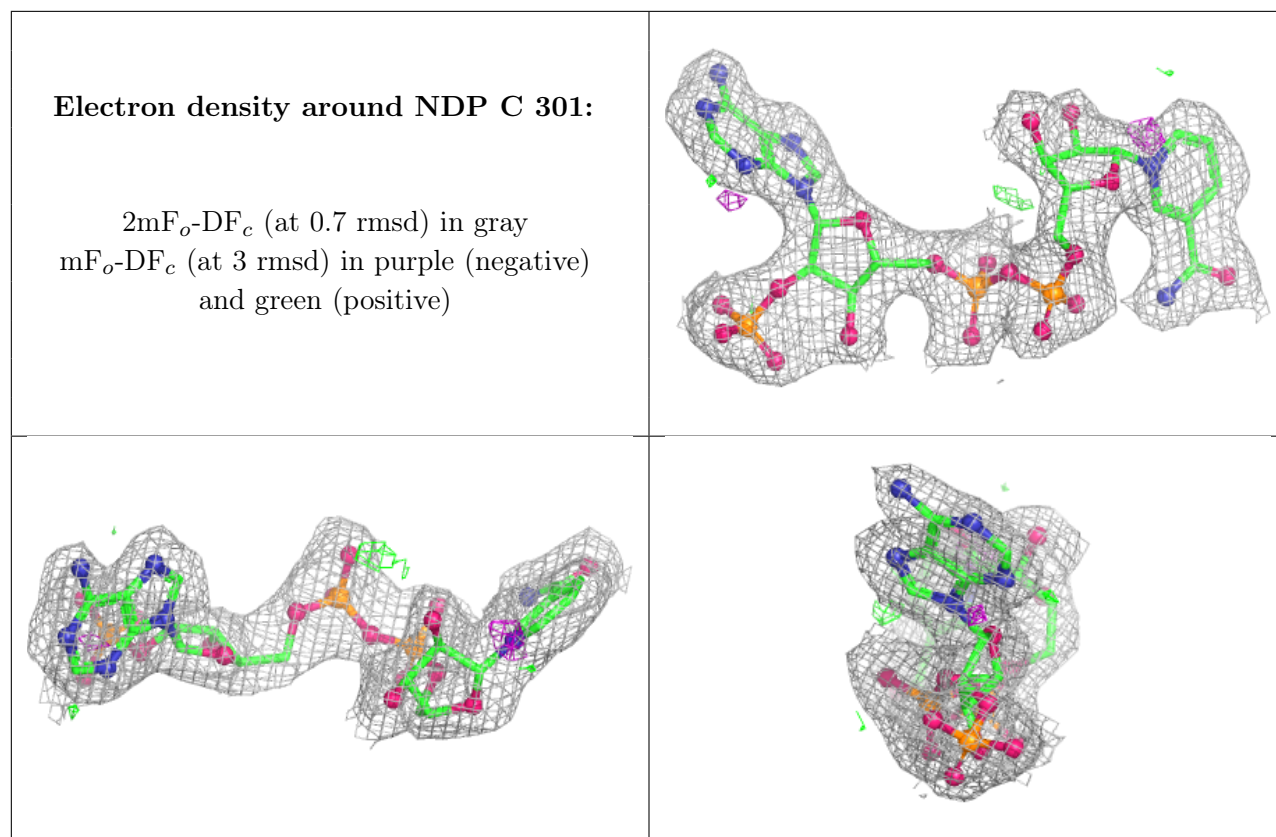
Electron density around NDP A 602:

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

**Electron density around NDP B 602:**

$2mF_o-DF_c$ (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.