



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 08:37 PM UTC

PDB ID : 2BFA / pdb_00002bfa
Title : Leishmania major pteridine reductase 1 in complex with NADP and CB3717
Authors : Schuettelkopf, A.W.; Hunter, W.N.
Deposited on : 2004-12-06
Resolution : 2.70 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

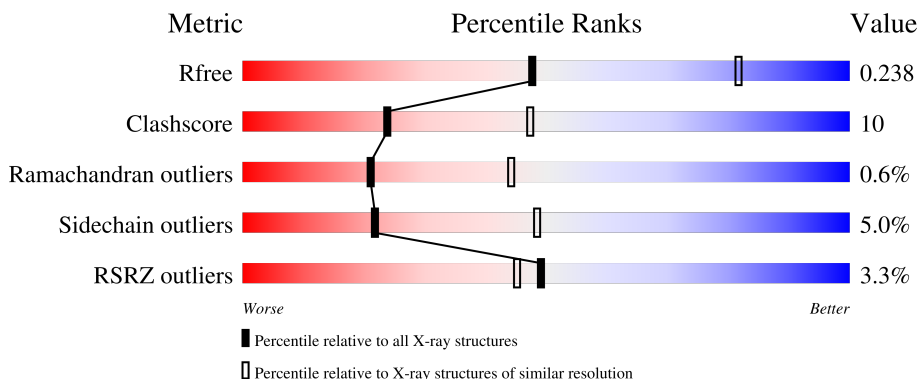
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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% 73% 18% • 8%
1	B	288	 3% 72% 18% • 8%
1	C	288	 2% 72% 14% • 12%
1	D	288	 3% 73% 15% • 11%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CB3	C	1290	-	-	-	X
4	EDO	A	1291	-	-	X	-
4	EDO	A	1293	-	-	X	-
4	EDO	B	1291	-	-	X	-
4	EDO	D	1291	-	-	X	-
4	EDO	D	1292	-	-	X	-

2 Entry composition [i](#)

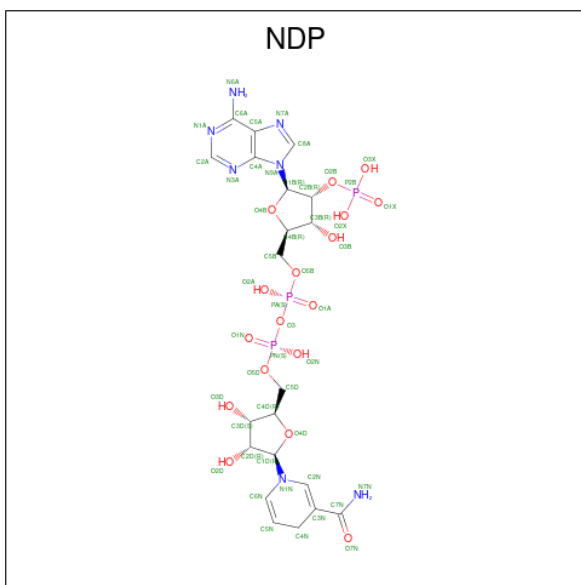
There are 5 unique types of molecules in this entry. The entry contains 8319 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			Total	C	N	O	S			
1	A	265	Total 1980	C 1248	N 352	O 369	S 11	0	0	0
1	B	266	Total 1984	C 1250	N 353	O 370	S 11	0	0	0
1	C	253	Total 1885	C 1189	N 337	O 349	S 10	0	0	0
1	D	255	Total 1903	C 1199	N 341	O 353	S 10	0	0	0

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



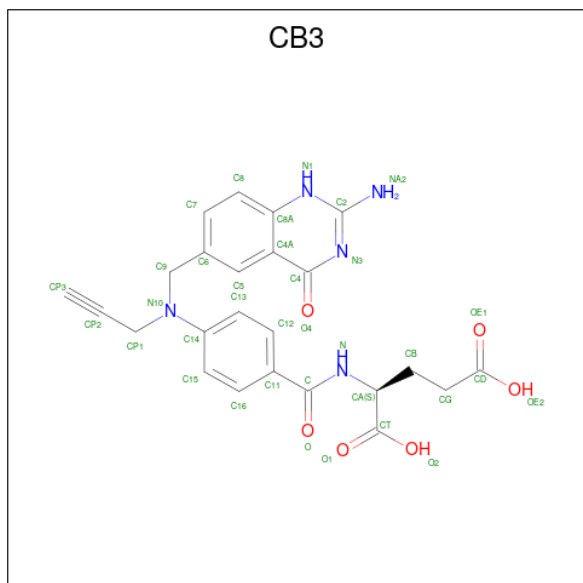
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0

Continued on next page...

Continued from previous page...

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

- Molecule 3 is 10-PROPARGYL-5,8-DIDEAZAFOLIC ACID (CCD ID: CB3) (formula: $C_{24}H_{23}N_5O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			35	24	5	6		
3	B	1	Total	C	N	O	0	0
			35	24	5	6		
3	C	1	Total	C	N	O	0	0
			35	24	5	6		
3	D	1	Total	C	N	O	0	0
			35	24	5	6		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

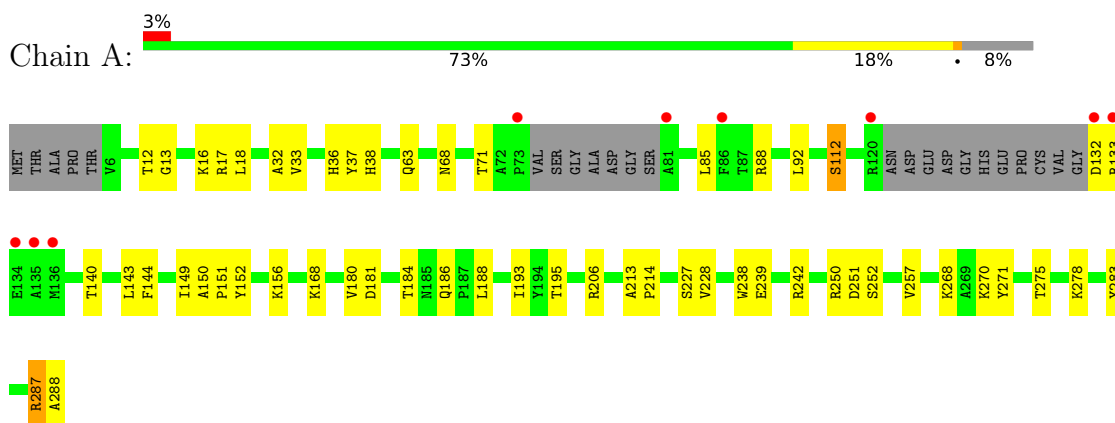
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	59	Total O 59 59	0	0
5	B	42	Total O 42 42	0	0
5	C	63	Total O 63 63	0	0
5	D	47	Total O 47 47	0	0

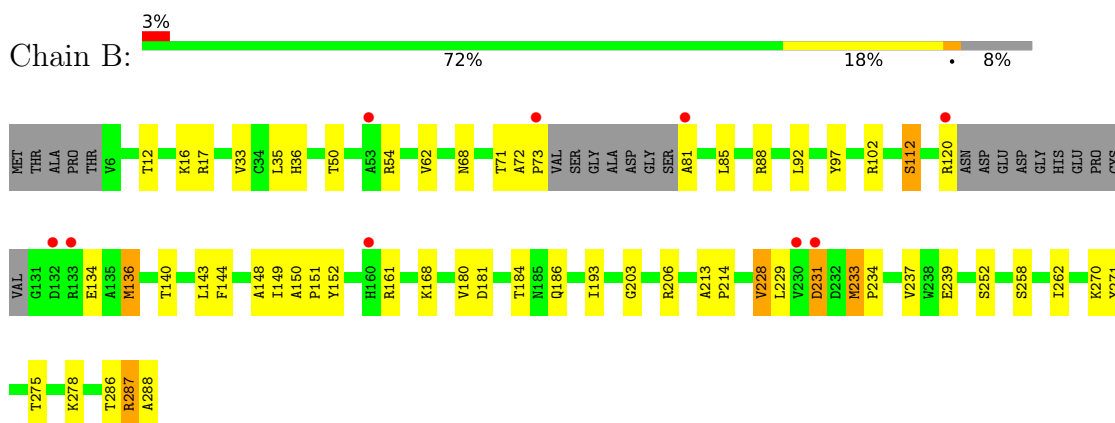
3 Residue-property plots [i](#)

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.

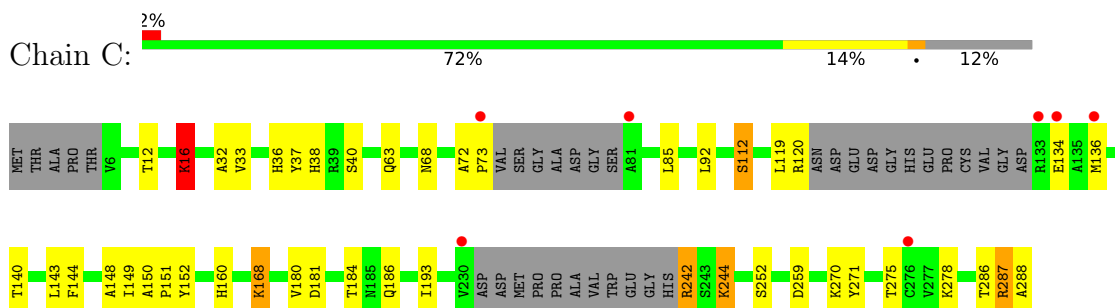
• Molecule 1: PTERIDINE REDUCTASE 1




• Molecule 1: PTERIDINE REDUCTASE 1

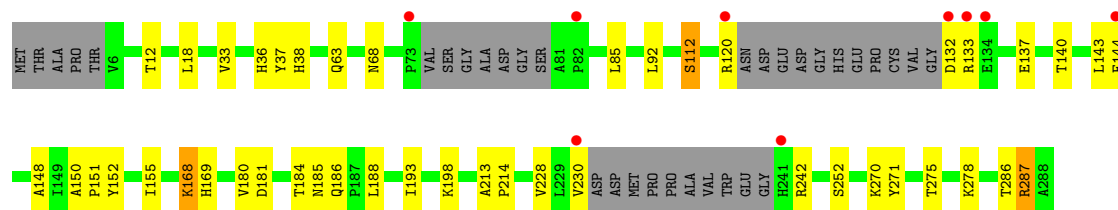


• Molecule 1: PTERIDINE REDUCTASE 1



● Molecule 1: PTERIDINE REDUCTASE 1

Chain D:  3% 73% 15% 11%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	94.54Å 103.83Å 137.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.50 – 2.70 24.50 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (24.50-2.70) 93.2 (24.50-2.70)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.68Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.203 , 0.236 0.203 , 0.238	Depositor DCC
R_{free} test set	1775 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	21.3	Xtrriage
Anisotropy	0.191	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8319	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.00 % 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 1.6721e-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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, EDO, CB3

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	0.48	0/2019	0.82	2/2750 (0.1%)
1	B	0.49	0/2023	0.82	0/2755
1	C	0.46	0/1918	0.82	3/2608 (0.1%)
1	D	0.48	0/1937	0.82	1/2634 (0.0%)
All	All	0.48	0/7897	0.82	6/10747 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	16	LYS	N-CA-C	5.58	115.64	108.34
1	C	33	VAL	N-CA-C	5.50	115.81	108.11
1	A	33	VAL	N-CA-C	5.39	115.65	108.11
1	D	33	VAL	N-CA-C	5.33	115.58	108.11
1	A	32	ALA	N-CA-C	-5.30	101.82	110.20
1	C	32	ALA	N-CA-C	-5.09	102.16	110.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1980	0	1987	45	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1984	0	1990	57	0
1	C	1885	0	1911	39	0
1	D	1903	0	1922	37	0
2	A	48	0	26	1	0
2	B	48	0	26	2	0
2	C	48	0	26	1	0
2	D	48	0	26	2	0
3	A	35	0	21	7	0
3	B	35	0	21	6	0
3	C	35	0	21	4	0
3	D	35	0	21	7	0
4	A	12	0	18	17	0
4	B	4	0	6	7	0
4	D	8	0	12	12	0
5	A	59	0	0	1	0
5	B	42	0	0	1	0
5	C	63	0	0	1	0
5	D	47	0	0	1	0
All	All	8319	0	8034	162	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 10.

All (162) 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:B:68:ASN:HD22	4:B:1291:EDO:H21	1.17	1.07
1:B:275:THR:HG21	1:D:278:LYS:HB2	1.43	0.99
1:A:278:LYS:HB2	1:C:275:THR:HG21	1.46	0.98
3:A:1290:CB3:H12	1:D:287:ARG:HH21	1.27	0.97
1:C:149:ILE:CD1	4:D:1292:EDO:H21	1.95	0.96
1:D:188:LEU:HD22	4:D:1291:EDO:H21	1.46	0.96
1:B:278:LYS:HB2	1:D:275:THR:HG21	1.49	0.93
1:A:156:LYS:HE3	1:B:136:MET:HE3	1.49	0.93
1:A:188:LEU:HD22	4:A:1291:EDO:H21	1.53	0.90
1:A:275:THR:HG21	1:C:278:LYS:HB2	1.51	0.89
1:B:68:ASN:ND2	4:B:1291:EDO:H21	1.89	0.86
1:B:12:THR:HA	1:B:36:HIS:HB3	1.56	0.85
3:A:1290:CB3:H12	1:D:287:ARG:NH2	1.93	0.84
1:D:68:ASN:HD22	4:D:1292:EDO:H12	1.42	0.84
1:A:287:ARG:HH21	3:D:1290:CB3:H12	1.43	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1290:CB3:H13	4:A:1291:EDO:O2	1.77	0.83
1:A:181:ASP:OD2	4:A:1291:EDO:H12	1.79	0.82
1:C:149:ILE:HD11	4:D:1292:EDO:H21	1.65	0.79
1:A:287:ARG:NH2	3:D:1290:CB3:H12	1.97	0.78
1:B:68:ASN:HD22	4:B:1291:EDO:C2	1.96	0.77
4:A:1293:EDO:H21	1:B:203:GLY:CA	2.14	0.77
1:B:287:ARG:HH21	3:C:1290:CB3:H12	1.50	0.76
1:A:186:GLN:O	1:D:287:ARG:NH1	2.21	0.73
1:A:195:THR:CG2	4:A:1293:EDO:H12	2.17	0.73
1:A:242:ARG:NH1	1:A:251:ASP:OD1	2.23	0.72
1:B:17:ARG:NH1	1:B:228:VAL:HG23	2.05	0.72
1:C:168:LYS:HD3	1:C:168:LYS:H	1.53	0.71
1:B:97:TYR:CE1	1:B:102:ARG:HA	2.26	0.71
1:C:12:THR:HA	1:C:36:HIS:HB3	1.74	0.69
1:C:181:ASP:HB3	1:C:184:THR:HG23	1.73	0.69
1:A:287:ARG:NH1	1:D:186:GLN:O	2.26	0.68
4:A:1293:EDO:H21	1:B:203:GLY:HA3	1.74	0.67
1:D:12:THR:HA	1:D:36:HIS:HB3	1.77	0.67
1:C:112:SER:HB2	1:C:143:LEU:HD23	1.77	0.67
1:A:112:SER:HB2	1:A:143:LEU:HD23	1.74	0.67
1:D:181:ASP:HB3	1:D:184:THR:HG23	1.75	0.66
1:B:112:SER:HB2	1:B:143:LEU:HD23	1.77	0.66
1:A:12:THR:HA	1:A:36:HIS:HB3	1.77	0.66
1:B:228:VAL:HG23	1:B:228:VAL:O	1.94	0.66
3:B:1290:CB3:H13	5:C:2057:HOH:O	1.94	0.66
3:B:1290:CB3:H12	1:C:287:ARG:NH2	2.10	0.66
1:D:112:SER:HB2	1:D:143:LEU:HD23	1.79	0.65
1:D:133:ARG:O	1:D:137:GLU:HG2	1.97	0.65
1:A:252:SER:HB3	1:C:271:TYR:CE2	2.32	0.65
3:B:1290:CB3:H12	1:C:287:ARG:HH21	1.63	0.64
1:D:68:ASN:ND2	4:D:1292:EDO:H12	2.12	0.64
1:A:242:ARG:HB3	1:A:250:ARG:HA	1.81	0.63
3:A:1290:CB3:H7	4:A:1291:EDO:H22	1.79	0.63
1:A:288:ALA:HB2	1:D:286:THR:HB	1.82	0.62
1:B:229:LEU:HD11	3:B:1290:CB3:H15	1.81	0.62
1:C:150:ALA:HB3	1:C:151:PRO:HD3	1.82	0.62
1:A:181:ASP:HB3	1:A:184:THR:HG23	1.81	0.61
1:B:97:TYR:CE2	1:B:161:ARG:HB3	2.35	0.61
1:B:287:ARG:NH2	3:C:1290:CB3:H12	2.15	0.61
3:D:1290:CB3:H7	4:D:1291:EDO:H22	1.82	0.61
1:D:132:ASP:OD1	1:D:132:ASP:C	2.43	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:ARG:NH1	1:C:186:GLN:O	2.31	0.60
1:D:150:ALA:HB3	1:D:151:PRO:HD3	1.83	0.60
3:A:1290:CB3:C7	4:A:1291:EDO:H22	2.31	0.60
1:A:150:ALA:HB3	1:A:151:PRO:HD3	1.84	0.60
1:B:288:ALA:HB2	1:C:286:THR:HB	1.83	0.59
1:B:186:GLN:O	1:C:287:ARG:NH1	2.33	0.59
1:A:149:ILE:HD11	4:B:1291:EDO:H12	1.85	0.59
1:A:271:TYR:CE2	1:C:252:SER:HB3	2.38	0.58
4:A:1293:EDO:H21	1:B:203:GLY:HA2	1.85	0.58
1:A:278:LYS:HB2	1:C:275:THR:CG2	2.29	0.58
1:B:271:TYR:CE2	1:D:252:SER:HB3	2.38	0.58
1:A:195:THR:HG22	4:A:1293:EDO:H12	1.85	0.57
1:B:150:ALA:HB3	1:B:151:PRO:HD3	1.84	0.57
1:C:193:ILE:HD11	1:D:152:TYR:CE2	2.40	0.57
1:A:206:ARG:HH22	4:A:1292:EDO:H11	1.69	0.56
1:B:149:ILE:HD11	4:B:1291:EDO:H11	1.86	0.56
1:B:181:ASP:HB3	1:B:184:THR:HG23	1.87	0.56
1:A:268:LYS:HG2	1:C:259:ASP:OD2	2.06	0.56
1:B:17:ARG:HH12	1:B:228:VAL:HG23	1.71	0.55
1:B:50:THR:HG21	1:B:54:ARG:HH21	1.73	0.54
1:B:252:SER:HB3	1:D:271:TYR:CE2	2.43	0.54
1:A:149:ILE:CD1	4:B:1291:EDO:H12	2.39	0.53
1:A:278:LYS:CB	1:C:275:THR:HG21	2.30	0.53
1:C:152:TYR:CE2	1:D:193:ILE:HD11	2.44	0.53
1:B:50:THR:CG2	1:B:54:ARG:HH21	2.22	0.52
1:C:149:ILE:HD11	4:D:1292:EDO:C2	2.38	0.52
1:A:13:GLY:HA2	5:A:2058:HOH:O	2.09	0.52
1:A:193:ILE:HD11	1:B:152:TYR:CE2	2.46	0.51
1:B:286:THR:HB	1:C:288:ALA:HB2	1.91	0.50
1:C:140:THR:O	1:C:144:PHE:HB2	2.10	0.50
1:C:68:ASN:HA	1:C:85:LEU:HD22	1.94	0.50
1:B:97:TYR:CE2	1:B:161:ARG:CB	2.94	0.49
2:B:1289:NDP:H41N	3:B:1290:CB3:C7	2.41	0.49
1:A:287:ARG:NH2	4:D:1291:EDO:O2	2.39	0.49
1:C:119:LEU:O	1:C:120:ARG:C	2.55	0.49
1:A:283:TYR:OH	3:A:1290:CB3:O	2.28	0.48
1:A:71:THR:HG23	1:A:88:ARG:NH1	2.28	0.48
1:B:231:ASP:HA	1:B:233:MET:HE2	1.95	0.48
1:A:140:THR:O	1:A:144:PHE:HB2	2.14	0.48
1:B:233:MET:HB2	1:B:234:PRO:HD2	1.96	0.48
1:B:140:THR:O	1:B:144:PHE:HB2	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:68:ASN:HA	1:B:85:LEU:HD22	1.96	0.47
1:D:148:ALA:C	1:D:151:PRO:HD2	2.40	0.47
2:D:1289:NDP:H41N	3:D:1290:CB3:C7	2.44	0.47
1:B:73:PRO:HG3	1:B:81:ALA:O	2.14	0.46
1:A:206:ARG:HH22	4:A:1292:EDO:C1	2.27	0.46
1:D:68:ASN:HD22	4:D:1292:EDO:C1	2.21	0.46
2:D:1289:NDP:H2D	3:D:1290:CB3:C2	2.45	0.46
1:A:275:THR:CG2	1:C:278:LYS:HB2	2.34	0.46
2:A:1289:NDP:H41N	3:A:1290:CB3:C7	2.46	0.45
1:D:140:THR:O	1:D:144:PHE:HB2	2.16	0.45
4:A:1293:EDO:O1	1:B:206:ARG:NE	2.39	0.45
1:C:72:ALA:O	1:C:73:PRO:C	2.58	0.45
1:A:227:SER:O	1:A:228:VAL:C	2.59	0.45
1:D:151:PRO:O	1:D:155:ILE:HG13	2.17	0.45
1:D:168:LYS:HE2	1:D:169:HIS:CE1	2.52	0.45
1:C:193:ILE:HD11	1:D:152:TYR:CD2	2.51	0.45
1:A:17:ARG:NH1	1:A:228:VAL:HG23	2.32	0.44
1:B:258:SER:O	1:B:262:ILE:HD13	2.18	0.44
1:C:242:ARG:C	1:C:244:LYS:H	2.25	0.44
1:D:185:ASN:HB2	5:D:2017:HOH:O	2.18	0.44
4:A:1293:EDO:O1	1:B:203:GLY:HA2	2.18	0.44
1:C:16:LYS:HE3	1:C:40:SER:OG	2.18	0.44
1:C:181:ASP:HB3	1:C:184:THR:CG2	2.46	0.44
1:B:278:LYS:CB	1:D:275:THR:HG21	2.35	0.43
1:D:181:ASP:HB3	1:D:184:THR:CG2	2.46	0.43
1:B:71:THR:HG23	1:B:88:ARG:NH1	2.33	0.43
1:A:18:LEU:HD13	1:A:257:VAL:HG11	2.00	0.43
1:B:33:VAL:HG12	1:B:35:LEU:HD23	1.99	0.43
1:B:148:ALA:C	1:B:151:PRO:HD2	2.43	0.43
2:B:1289:NDP:H2D	3:B:1290:CB3:C2	2.48	0.43
4:A:1293:EDO:HO1	1:B:206:ARG:HE	1.65	0.43
1:C:149:ILE:CD1	4:D:1292:EDO:C2	2.84	0.43
1:A:193:ILE:HD11	1:B:152:TYR:CD2	2.54	0.43
1:D:68:ASN:HA	1:D:85:LEU:HD22	2.01	0.43
4:A:1293:EDO:H22	1:B:206:ARG:HH21	1.83	0.43
3:D:1290:CB3:C7	4:D:1291:EDO:H22	2.48	0.43
1:B:288:ALA:O	1:C:244:LYS:HD2	2.19	0.42
1:C:148:ALA:C	1:C:151:PRO:HD2	2.44	0.42
1:D:37:TYR:CE1	1:D:63:GLN:HG2	2.54	0.42
5:B:2039:HOH:O	3:C:1290:CB3:H13	2.19	0.42
1:A:152:TYR:CE2	1:B:193:ILE:HD11	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:233:MET:HG3	1:B:237:VAL:HB	2.01	0.42
1:A:68:ASN:HA	1:A:85:LEU:HD22	2.01	0.42
1:B:213:ALA:N	1:B:214:PRO:CD	2.82	0.42
1:D:36:HIS:CG	1:D:37:TYR:N	2.88	0.42
1:D:198:LYS:HD2	1:D:198:LYS:HA	1.90	0.42
1:A:37:TYR:O	1:A:63:GLN:HA	2.20	0.41
1:A:213:ALA:N	1:A:214:PRO:CD	2.82	0.41
3:D:1290:CB3:H13	4:D:1291:EDO:C2	2.51	0.41
1:D:38:HIS:HD2	1:D:63:GLN:NE2	2.18	0.41
1:C:38:HIS:HD2	1:C:63:GLN:NE2	2.19	0.41
1:A:38:HIS:HD2	1:A:63:GLN:NE2	2.19	0.41
1:C:160:HIS:HB2	1:D:120:ARG:NH1	2.36	0.41
1:D:37:TYR:CD1	1:D:37:TYR:C	2.99	0.41
1:D:213:ALA:N	1:D:214:PRO:CD	2.84	0.41
4:A:1293:EDO:C2	1:B:203:GLY:HA2	2.51	0.41
2:C:1289:NDP:H41N	3:C:1290:CB3:C7	2.51	0.41
1:B:228:VAL:O	1:B:228:VAL:CG2	2.65	0.41
1:B:149:ILE:CD1	4:B:1291:EDO:C2	3.00	0.40
1:C:37:TYR:O	1:C:63:GLN:HA	2.21	0.40
1:C:37:TYR:CD1	1:C:37:TYR:C	2.98	0.40
1:A:152:TYR:CD2	1:B:193:ILE:HD11	2.57	0.40
1:A:238:TRP:CZ2	1:A:242:ARG:HD2	2.57	0.40
1:B:72:ALA:HA	1:B:73:PRO:HD3	1.80	0.40
1:B:213:ALA:HB3	1:B:214:PRO:HD3	2.04	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	259/288 (90%)	241 (93%)	17 (7%)	1 (0%)	30 54

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	260/288 (90%)	244 (94%)	14 (5%)	2 (1%)	16	37
1	C	245/288 (85%)	229 (94%)	15 (6%)	1 (0%)	30	54
1	D	247/288 (86%)	233 (94%)	12 (5%)	2 (1%)	16	37
All	All	1011/1152 (88%)	947 (94%)	58 (6%)	6 (1%)	21	44

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	180	VAL
1	B	180	VAL
1	C	180	VAL
1	D	180	VAL
1	B	228	VAL
1	D	228	VAL

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	206/223 (92%)	197 (96%)	9 (4%)	25	53
1	B	206/223 (92%)	193 (94%)	13 (6%)	16	39
1	C	196/223 (88%)	186 (95%)	10 (5%)	21	48
1	D	198/223 (89%)	190 (96%)	8 (4%)	28	56
All	All	806/892 (90%)	766 (95%)	40 (5%)	22	48

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
1	A	92	LEU
1	A	112	SER
1	A	132	ASP
1	A	133	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	168	LYS
1	A	239	GLU
1	A	270	LYS
1	A	287	ARG
1	B	16	LYS
1	B	62	VAL
1	B	92	LEU
1	B	112	SER
1	B	120	ARG
1	B	134	GLU
1	B	136	MET
1	B	168	LYS
1	B	231	ASP
1	B	233	MET
1	B	239	GLU
1	B	270	LYS
1	B	287	ARG
1	C	16	LYS
1	C	92	LEU
1	C	112	SER
1	C	134	GLU
1	C	136	MET
1	C	168	LYS
1	C	242	ARG
1	C	244	LYS
1	C	270	LYS
1	C	287	ARG
1	D	18	LEU
1	D	92	LEU
1	D	112	SER
1	D	168	LYS
1	D	230	VAL
1	D	242	ARG
1	D	270	LYS
1	D	287	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	HIS
1	A	63	GLN
1	A	108	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	185	ASN
1	B	38	HIS
1	B	63	GLN
1	B	68	ASN
1	B	185	ASN
1	C	38	HIS
1	C	63	GLN
1	C	185	ASN
1	D	38	HIS
1	D	63	GLN
1	D	68	ASN
1	D	169	HIS

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](#)

14 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	NDP	A	1289	-	51,52,52	1.74	9 (17%)	71,80,80	1.46	11 (15%)
4	EDO	D	1291	-	3,3,3	0.29	0	2,2,2	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NDP	B	1289	-	51,52,52	1.73	9 (17%)	71,80,80	1.47	8 (11%)
3	CB3	A	1290	-	37,37,37	2.84	15 (40%)	50,51,51	1.47	8 (16%)
2	NDP	C	1289	-	51,52,52	1.75	8 (15%)	71,80,80	1.55	11 (15%)
2	NDP	D	1289	-	51,52,52	1.70	8 (15%)	71,80,80	1.51	10 (14%)
4	EDO	A	1292	-	3,3,3	0.27	0	2,2,2	0.39	0
4	EDO	B	1291	-	3,3,3	0.33	0	2,2,2	0.15	0
4	EDO	A	1293	-	3,3,3	0.27	0	2,2,2	0.41	0
3	CB3	D	1290	-	37,37,37	2.87	15 (40%)	50,51,51	1.51	6 (12%)
4	EDO	D	1292	-	3,3,3	0.28	0	2,2,2	0.28	0
3	CB3	B	1290	-	37,37,37	2.84	15 (40%)	50,51,51	1.52	7 (14%)
3	CB3	C	1290	-	37,37,37	2.86	15 (40%)	50,51,51	1.45	6 (12%)
4	EDO	A	1291	-	3,3,3	0.31	0	2,2,2	0.16	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	NDP	A	1289	-	-	1/34/77/77	0/5/5/5
4	EDO	D	1291	-	-	1/1/1/1	-
2	NDP	B	1289	-	-	2/34/77/77	0/5/5/5
3	CB3	A	1290	-	-	16/27/28/28	0/3/3/3
2	NDP	C	1289	-	-	2/34/77/77	0/5/5/5
2	NDP	D	1289	-	-	2/34/77/77	0/5/5/5
4	EDO	A	1292	-	-	0/1/1/1	-
4	EDO	B	1291	-	-	0/1/1/1	-
4	EDO	A	1293	-	-	0/1/1/1	-
3	CB3	D	1290	-	-	20/27/28/28	0/3/3/3
4	EDO	D	1292	-	-	0/1/1/1	-
3	CB3	B	1290	-	-	17/27/28/28	0/3/3/3
3	CB3	C	1290	-	-	8/27/28/28	0/3/3/3
4	EDO	A	1291	-	-	1/1/1/1	-

All (94) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1290	CB3	O4-C4	9.68	1.39	1.23
3	D	1290	CB3	O4-C4	9.28	1.39	1.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1290	CB3	O4-C4	9.20	1.39	1.23
3	B	1290	CB3	O4-C4	9.08	1.38	1.23
2	D	1289	NDP	O7N-C7N	7.32	1.41	1.24
2	C	1289	NDP	O7N-C7N	7.24	1.41	1.24
3	C	1290	CB3	CP1-N10	7.23	1.53	1.46
2	B	1289	NDP	O7N-C7N	7.16	1.41	1.24
3	D	1290	CB3	CP1-N10	6.99	1.52	1.46
3	B	1290	CB3	CP1-N10	6.86	1.52	1.46
2	A	1289	NDP	O7N-C7N	6.76	1.40	1.24
3	A	1290	CB3	CP1-N10	6.70	1.52	1.46
3	A	1290	CB3	C9-N10	6.42	1.55	1.46
3	B	1290	CB3	C9-N10	6.29	1.55	1.46
3	C	1290	CB3	C9-N10	6.22	1.55	1.46
3	D	1290	CB3	C9-N10	6.19	1.55	1.46
2	A	1289	NDP	C4N-C3N	-5.62	1.39	1.50
2	C	1289	NDP	C4N-C3N	-5.47	1.39	1.50
2	D	1289	NDP	C4N-C3N	-5.34	1.39	1.50
2	B	1289	NDP	C4N-C3N	-5.32	1.39	1.50
3	A	1290	CB3	C15-C14	4.38	1.47	1.39
3	C	1290	CB3	C15-C14	4.33	1.47	1.39
3	D	1290	CB3	C15-C14	4.31	1.47	1.39
3	B	1290	CB3	C15-C14	4.25	1.47	1.39
2	C	1289	NDP	C4N-C5N	-3.84	1.39	1.49
2	B	1289	NDP	C4N-C5N	-3.73	1.39	1.49
2	A	1289	NDP	C4N-C5N	-3.70	1.39	1.49
2	D	1289	NDP	C4N-C5N	-3.66	1.39	1.49
3	B	1290	CB3	C5-C6	3.50	1.45	1.39
3	D	1290	CB3	C5-C6	3.49	1.45	1.39
3	D	1290	CB3	C8-C7	3.35	1.44	1.38
3	D	1290	CB3	C16-C11	3.33	1.44	1.39
3	C	1290	CB3	C8-C7	3.32	1.44	1.38
3	C	1290	CB3	C5-C6	3.31	1.44	1.39
3	A	1290	CB3	C5-C6	3.31	1.44	1.39
3	C	1290	CB3	C4A-C4	-3.27	1.42	1.48
2	C	1289	NDP	PN-O3	3.27	1.63	1.59
3	C	1290	CB3	C16-C11	3.26	1.44	1.39
3	B	1290	CB3	C8-C7	3.18	1.43	1.38
3	D	1290	CB3	C4A-C8A	3.17	1.46	1.41
3	A	1290	CB3	C8-C7	3.12	1.43	1.38
3	A	1290	CB3	C4A-C8A	3.08	1.45	1.41
3	B	1290	CB3	C16-C11	3.06	1.44	1.39
2	B	1289	NDP	PN-O3	2.98	1.62	1.59

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1290	CB3	C16-C11	2.97	1.43	1.39
3	B	1290	CB3	CA-N	2.95	1.52	1.45
3	C	1290	CB3	C4A-C8A	2.95	1.45	1.41
3	D	1290	CB3	C4A-C4	-2.93	1.43	1.48
3	B	1290	CB3	C4A-C8A	2.92	1.45	1.41
2	A	1289	NDP	C2A-N1A	2.84	1.39	1.33
3	B	1290	CB3	C4A-C4	-2.84	1.43	1.48
3	C	1290	CB3	C16-C15	2.83	1.43	1.38
3	D	1290	CB3	C5-C4A	2.81	1.44	1.39
3	D	1290	CB3	C16-C15	2.73	1.43	1.38
3	B	1290	CB3	C5-C4A	2.71	1.44	1.39
3	A	1290	CB3	C5-C4A	2.70	1.44	1.39
3	B	1290	CB3	C13-C14	2.69	1.44	1.39
2	C	1289	NDP	C2A-N1A	2.69	1.38	1.33
2	A	1289	NDP	PA-O3	2.67	1.62	1.59
3	C	1290	CB3	C13-C14	2.66	1.44	1.39
3	B	1290	CB3	C16-C15	2.63	1.43	1.38
3	A	1290	CB3	C13-C14	2.62	1.44	1.39
2	A	1289	NDP	PN-O3	2.61	1.62	1.59
2	B	1289	NDP	C2A-N1A	2.60	1.38	1.33
3	D	1290	CB3	C13-C14	2.58	1.44	1.39
3	A	1290	CB3	C16-C15	2.56	1.43	1.38
2	C	1289	NDP	C2A-N3A	2.52	1.38	1.33
2	D	1289	NDP	C2A-N3A	2.52	1.38	1.33
2	D	1289	NDP	C2A-N1A	2.51	1.38	1.33
3	A	1290	CB3	C4A-C4	-2.41	1.44	1.48
2	C	1289	NDP	PA-O3	2.38	1.62	1.59
2	B	1289	NDP	PA-O3	2.37	1.62	1.59
2	A	1289	NDP	C5A-N7A	-2.37	1.34	1.39
3	C	1290	CB3	C7-C6	2.36	1.43	1.38
3	D	1290	CB3	C12-C11	2.34	1.43	1.39
3	D	1290	CB3	C7-C6	2.33	1.43	1.38
3	C	1290	CB3	C5-C4A	2.30	1.43	1.39
2	A	1289	NDP	C2A-N3A	2.29	1.38	1.33
2	D	1289	NDP	C8A-N7A	2.28	1.36	1.31
2	C	1289	NDP	C8A-N7A	2.27	1.36	1.31
2	B	1289	NDP	C2A-N3A	2.25	1.37	1.33
3	A	1290	CB3	C12-C11	2.13	1.42	1.39
2	D	1289	NDP	C6N-C5N	2.10	1.39	1.33
2	A	1289	NDP	C6N-C5N	2.10	1.39	1.33
3	C	1290	CB3	C12-C11	2.09	1.42	1.39
2	D	1289	NDP	PN-O3	2.09	1.61	1.59

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1289	NDP	C6N-C5N	2.07	1.39	1.33
3	A	1290	CB3	C7-C6	2.05	1.43	1.38
3	B	1290	CB3	C11-C	-2.05	1.45	1.50
3	A	1290	CB3	C11-C	-2.04	1.45	1.50
3	C	1290	CB3	C8-C8A	2.04	1.43	1.39
2	B	1289	NDP	C5A-N7A	-2.02	1.35	1.39
3	D	1290	CB3	C8-C8A	2.01	1.43	1.39
3	B	1290	CB3	C12-C11	2.01	1.42	1.39

All (67) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1289	NDP	N3A-C2A-N1A	-5.63	120.06	128.58
2	A	1289	NDP	N3A-C2A-N1A	-5.63	120.06	128.58
2	D	1289	NDP	N3A-C2A-N1A	-5.50	120.26	128.58
2	C	1289	NDP	N3A-C2A-N1A	-5.38	120.43	128.58
3	D	1290	CB3	C6-C9-N10	4.74	121.81	114.13
3	B	1290	CB3	C6-C9-N10	4.70	121.74	114.13
3	C	1290	CB3	C6-C9-N10	4.63	121.63	114.13
2	D	1289	NDP	N9A-C8A-N7A	-4.47	107.60	113.94
2	C	1289	NDP	C5A-C4A-N3A	-4.46	120.58	126.72
3	A	1290	CB3	C6-C9-N10	4.35	121.18	114.13
2	C	1289	NDP	N9A-C8A-N7A	-4.28	107.86	113.94
2	D	1289	NDP	C5A-C4A-N3A	-4.20	120.94	126.72
2	B	1289	NDP	C5A-C4A-N3A	-4.04	121.15	126.72
2	B	1289	NDP	N9A-C8A-N7A	-3.99	108.28	113.94
2	A	1289	NDP	C5A-C4A-N3A	-3.89	121.36	126.72
2	A	1289	NDP	N9A-C8A-N7A	-3.88	108.43	113.94
3	A	1290	CB3	C8A-C4A-C4	-3.80	116.01	120.11
3	B	1290	CB3	C8A-C4A-C4	-3.70	116.12	120.11
2	D	1289	NDP	C5A-N7A-C8A	3.65	109.19	103.45
3	D	1290	CB3	C8A-C4A-C4	-3.62	116.20	120.11
2	C	1289	NDP	C2A-N3A-C4A	3.49	120.36	111.83
3	D	1290	CB3	CP2-CP1-N10	3.49	116.67	113.45
2	C	1289	NDP	C5A-N7A-C8A	3.47	108.90	103.45
2	D	1289	NDP	C2A-N3A-C4A	3.40	120.12	111.83
2	B	1289	NDP	C5A-N7A-C8A	3.29	108.62	103.45
2	A	1289	NDP	C5A-N7A-C8A	3.25	108.56	103.45
2	B	1289	NDP	C2A-N3A-C4A	3.23	119.73	111.83
3	B	1290	CB3	NA2-C2-N1	3.18	123.47	116.77
2	A	1289	NDP	C2A-N3A-C4A	3.07	119.34	111.83
3	C	1290	CB3	C8A-C4A-C4	-3.06	116.80	120.11

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1290	CB3	CP2-CP1-N10	3.05	116.26	113.45
3	A	1290	CB3	NA2-C2-N1	3.01	123.11	116.77
3	B	1290	CB3	CP2-CP1-N10	3.00	116.22	113.45
3	D	1290	CB3	NA2-C2-N1	2.88	122.84	116.77
3	C	1290	CB3	NA2-C2-N1	2.83	122.73	116.77
2	C	1289	NDP	N3A-C4A-N9A	2.79	131.91	127.17
2	D	1289	NDP	C4A-C5A-N7A	-2.78	107.40	110.58
2	C	1289	NDP	C4A-C5A-N7A	-2.70	107.49	110.58
2	C	1289	NDP	O4B-C1B-N9A	2.67	113.22	108.09
2	B	1289	NDP	N3A-C4A-N9A	2.65	131.67	127.17
3	D	1290	CB3	CP1-CP2-CP3	-2.59	173.43	177.63
3	A	1290	CB3	CP2-CP1-N10	2.59	115.84	113.45
2	A	1289	NDP	N3A-C4A-N9A	2.56	131.52	127.17
2	D	1289	NDP	N3A-C4A-N9A	2.54	131.49	127.17
2	B	1289	NDP	C3N-C2N-N1N	-2.52	119.50	123.20
2	C	1289	NDP	C3N-C2N-N1N	-2.49	119.55	123.20
2	D	1289	NDP	C4A-N9A-C8A	2.38	108.24	105.74
2	C	1289	NDP	C4A-N9A-C8A	2.36	108.22	105.74
2	D	1289	NDP	C3N-C2N-N1N	-2.34	119.77	123.20
2	A	1289	NDP	C4A-C5A-N7A	-2.30	107.95	110.58
2	B	1289	NDP	C4A-C5A-N7A	-2.18	108.09	110.58
2	C	1289	NDP	C2B-C1B-N9A	-2.17	110.18	113.75
2	D	1289	NDP	O4B-C1B-N9A	2.16	112.24	108.09
3	B	1290	CB3	N1-C2-N3	-2.14	119.40	123.32
3	A	1290	CB3	N1-C2-N3	-2.13	119.42	123.32
2	A	1289	NDP	O2A-PA-O3	2.12	113.01	107.27
3	C	1290	CB3	CP1-CP2-CP3	-2.10	174.22	177.63
3	B	1290	CB3	CT-CA-N	2.10	115.44	110.57
2	A	1289	NDP	C4A-N9A-C8A	2.10	107.94	105.74
3	A	1290	CB3	C5-C4A-C4	2.09	124.23	119.51
2	A	1289	NDP	O4B-C1B-N9A	2.09	112.10	108.09
3	B	1290	CB3	CP1-CP2-CP3	-2.08	174.26	177.63
3	A	1290	CB3	CP1-CP2-CP3	-2.07	174.28	177.63
3	D	1290	CB3	N1-C2-N3	-2.04	119.59	123.32
3	C	1290	CB3	N1-C2-N3	-2.03	119.60	123.32
3	A	1290	CB3	C9-N10-C14	2.02	124.23	120.72
2	A	1289	NDP	C3N-C2N-N1N	-2.02	120.24	123.20

There are no chirality outliers.

All (70) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1290	CB3	CP2-CP1-N10-C9
3	A	1290	CB3	CP2-CP1-N10-C14
3	A	1290	CB3	N-CA-CB-CG
3	B	1290	CB3	CP2-CP1-N10-C9
3	B	1290	CB3	CP2-CP1-N10-C14
3	C	1290	CB3	CP2-CP1-N10-C14
3	D	1290	CB3	CP2-CP1-N10-C14
3	B	1290	CB3	CT-CA-N-C
3	D	1290	CB3	CT-CA-N-C
3	B	1290	CB3	C15-C14-N10-C9
3	B	1290	CB3	C13-C14-N10-CP1
3	B	1290	CB3	C13-C14-N10-C9
3	B	1290	CB3	C15-C14-N10-CP1
3	A	1290	CB3	N-C-C11-C12
3	B	1290	CB3	N-CA-CB-CG
3	D	1290	CB3	N-CA-CB-CG
3	A	1290	CB3	O-C-C11-C12
3	A	1290	CB3	C15-C14-N10-C9
3	A	1290	CB3	C13-C14-N10-CP1
3	C	1290	CB3	C15-C14-N10-C9
3	C	1290	CB3	C13-C14-N10-CP1
3	D	1290	CB3	C15-C14-N10-C9
3	A	1290	CB3	C13-C14-N10-C9
3	D	1290	CB3	C13-C14-N10-CP1
3	C	1290	CB3	C13-C14-N10-C9
3	C	1290	CB3	C15-C14-N10-CP1
3	A	1290	CB3	N-C-C11-C16
3	A	1290	CB3	C15-C14-N10-CP1
3	D	1290	CB3	C13-C14-N10-C9
3	A	1290	CB3	O-C-C11-C16
3	D	1290	CB3	C15-C14-N10-CP1
2	B	1289	NDP	O4D-C1D-N1N-C6N
3	D	1290	CB3	CT-CA-CB-CG
3	C	1290	CB3	CB-CA-N-C
3	D	1290	CB3	N-CA-CT-O1
3	A	1290	CB3	CT-CA-CB-CG
3	C	1290	CB3	CP2-CP1-N10-C9
3	D	1290	CB3	CP2-CP1-N10-C9
2	C	1289	NDP	O4D-C1D-N1N-C6N
3	D	1290	CB3	N-CA-CT-O2
2	A	1289	NDP	O4D-C1D-N1N-C6N
2	D	1289	NDP	O4D-C1D-N1N-C6N
3	B	1290	CB3	N-CA-CT-O1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	B	1290	CB3	N-CA-CT-O2
3	D	1290	CB3	CB-CA-CT-O2
3	B	1290	CB3	CT-CA-CB-CG
3	D	1290	CB3	C6-C9-N10-C14
3	D	1290	CB3	N-C-C11-C12
3	D	1290	CB3	CB-CA-CT-O1
3	A	1290	CB3	C6-C9-N10-CP1
3	B	1290	CB3	C6-C9-N10-CP1
3	D	1290	CB3	O-C-C11-C12
2	B	1289	NDP	O4D-C4D-C5D-O5D
2	D	1289	NDP	C2N-C3N-C7N-N7N
3	C	1290	CB3	C6-C9-N10-C14
3	B	1290	CB3	C6-C9-N10-C14
3	D	1290	CB3	OE2-CD-CG-CB
3	A	1290	CB3	OE2-CD-CG-CB
3	D	1290	CB3	N-C-C11-C16
2	C	1289	NDP	O4D-C4D-C5D-O5D
3	D	1290	CB3	OE1-CD-CG-CB
3	A	1290	CB3	C6-C9-N10-C14
3	A	1290	CB3	OE1-CD-CG-CB
4	A	1291	EDO	O1-C1-C2-O2
3	B	1290	CB3	C11-C-N-CA
4	D	1291	EDO	O1-C1-C2-O2
3	B	1290	CB3	O-C-N-CA
3	B	1290	CB3	O-C-C11-C12
3	B	1290	CB3	N-C-C11-C12
3	D	1290	CB3	O-C-C11-C16

There are no ring outliers.

14 monomers are involved in 54 short contacts:

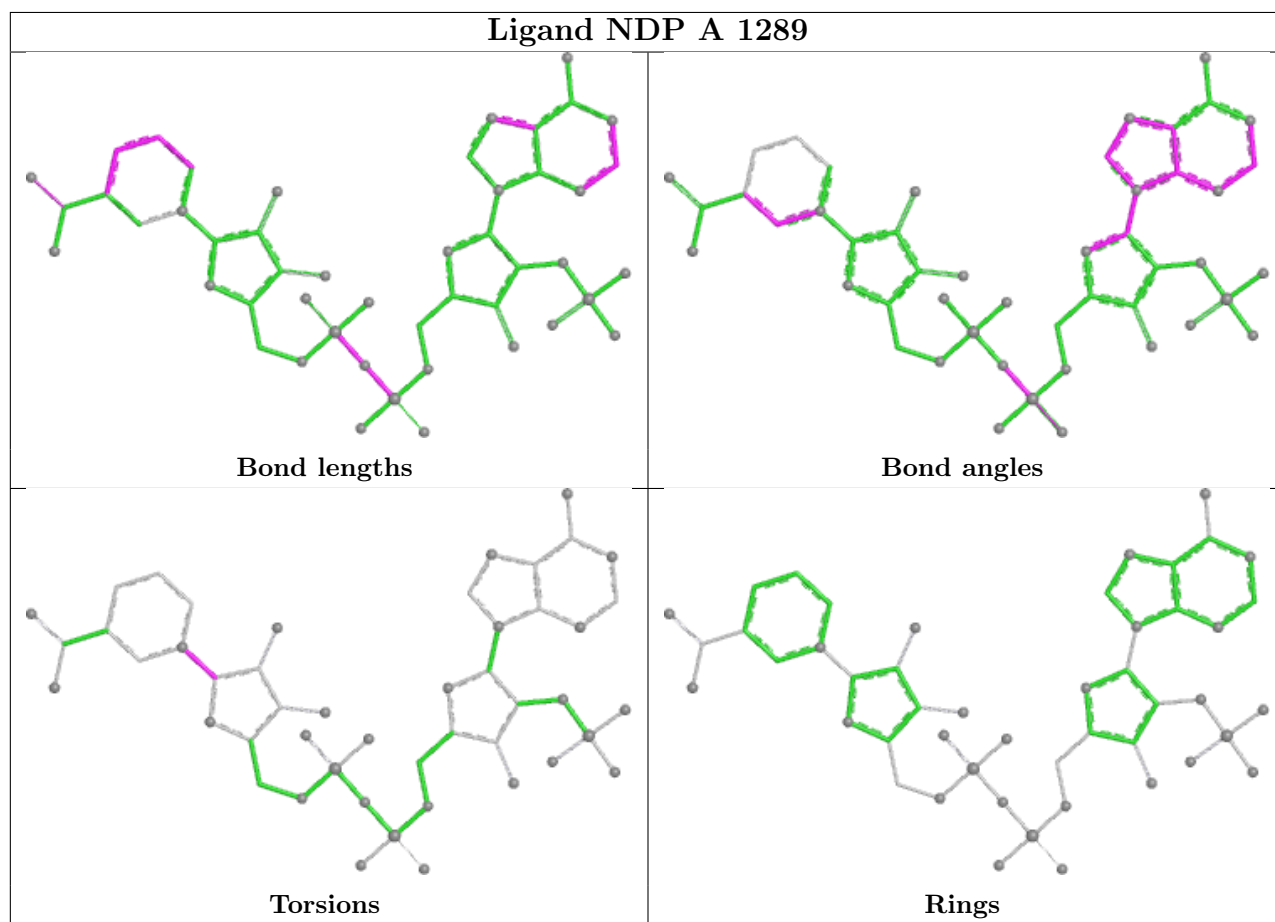
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1289	NDP	1	0
4	D	1291	EDO	5	0
2	B	1289	NDP	2	0
3	A	1290	CB3	7	0
2	C	1289	NDP	1	0
2	D	1289	NDP	2	0
4	A	1292	EDO	2	0
4	B	1291	EDO	7	0
4	A	1293	EDO	10	0
3	D	1290	CB3	7	0

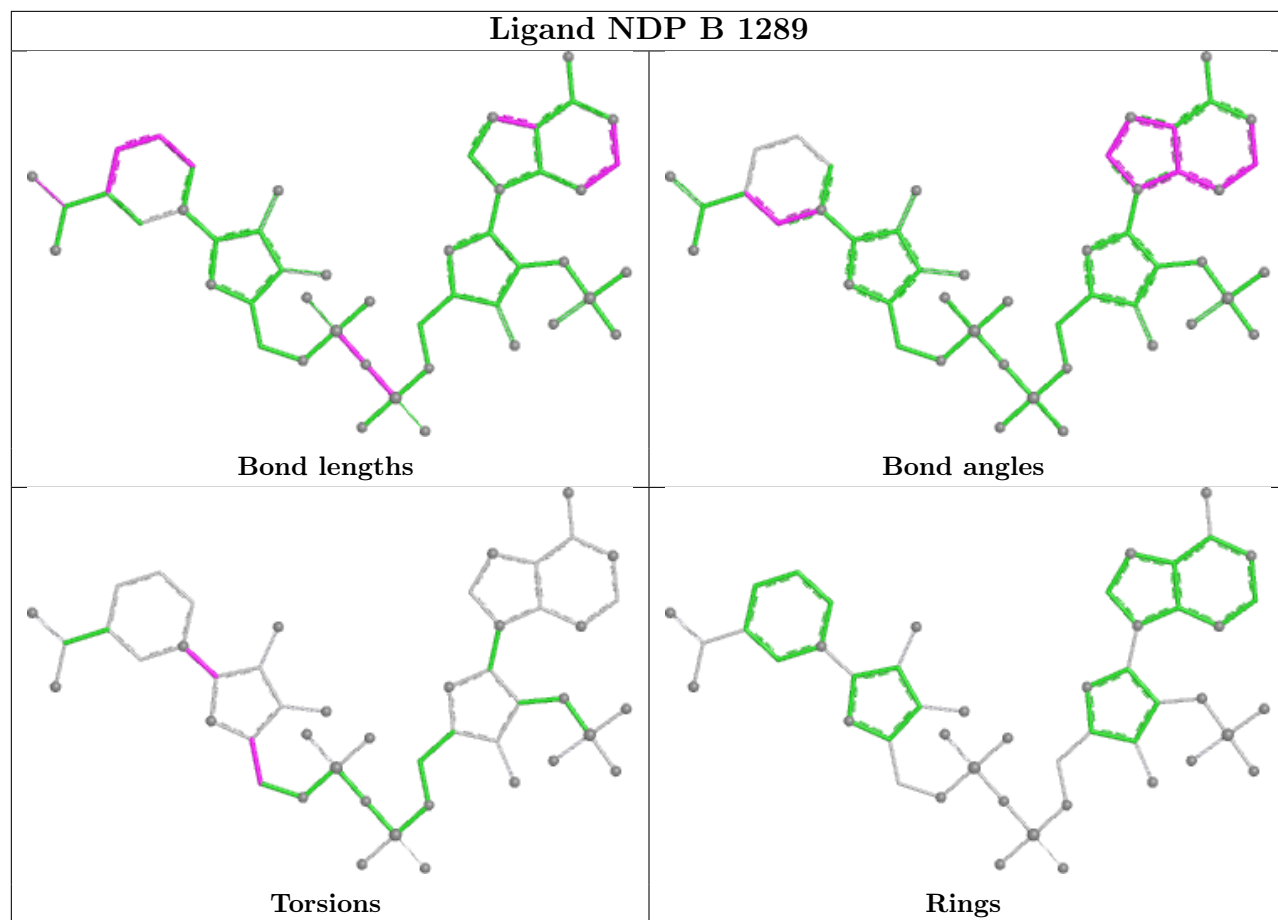
Continued on next page...

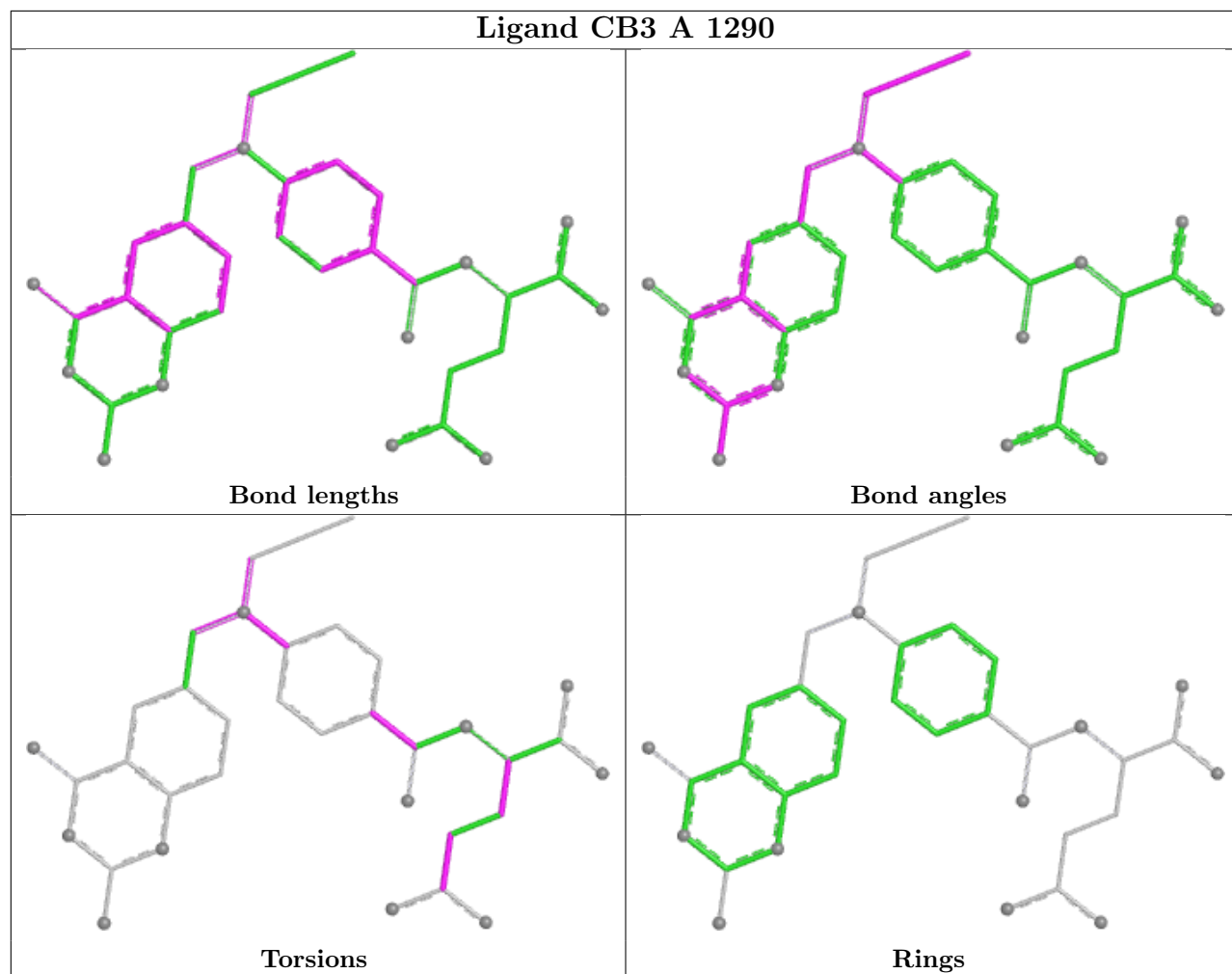
Continued from previous page...

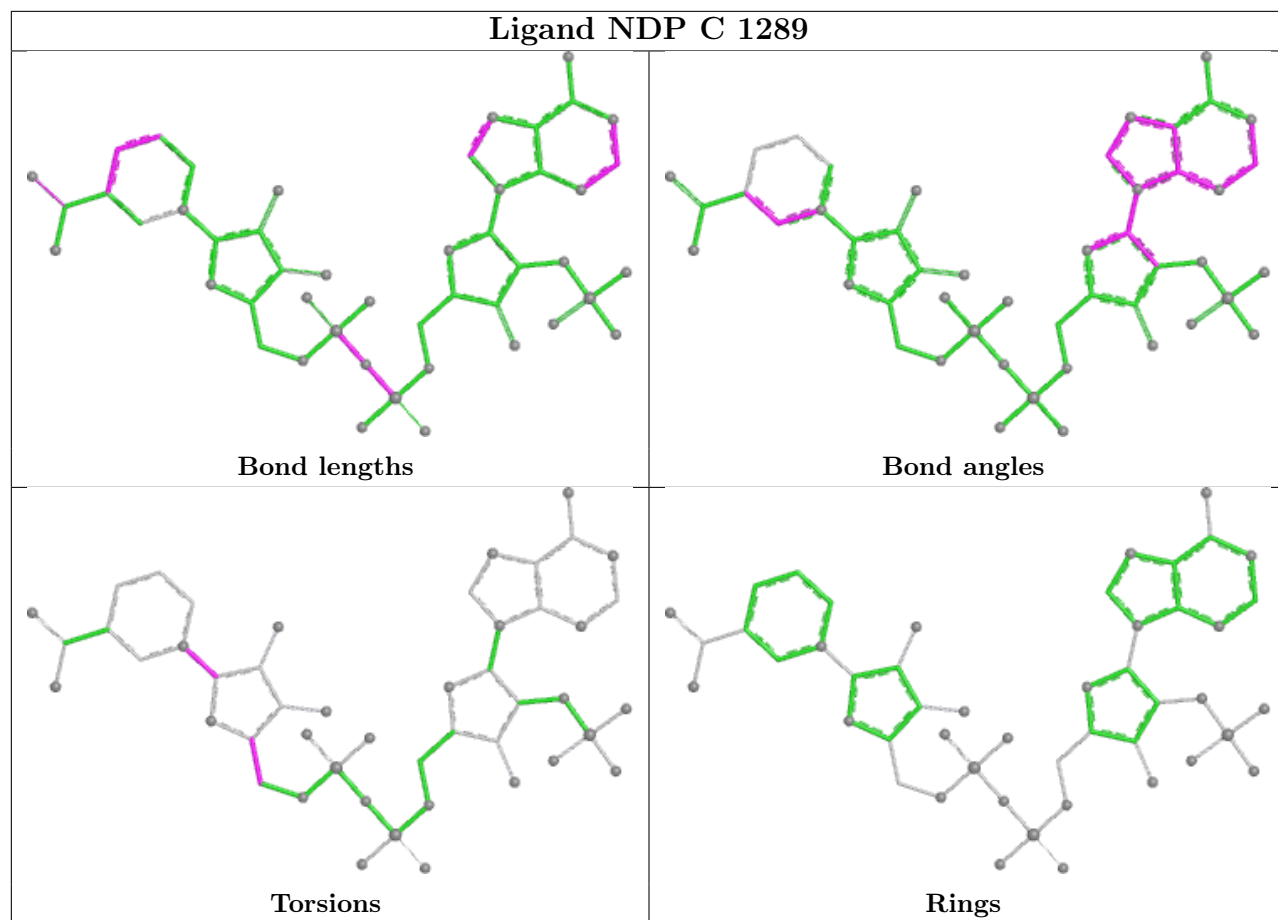
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1292	EDO	7	0
3	B	1290	CB3	6	0
3	C	1290	CB3	4	0
4	A	1291	EDO	5	0

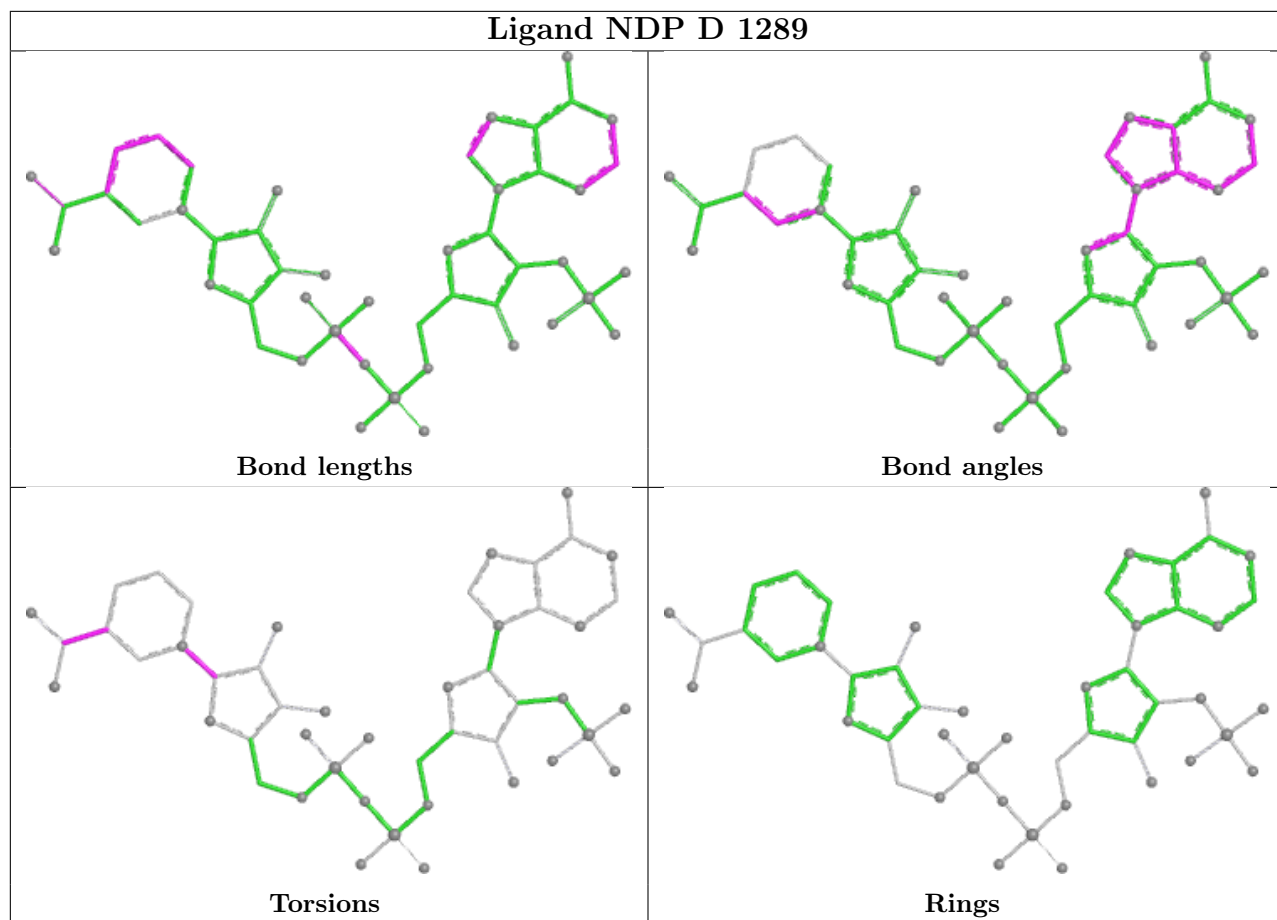
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

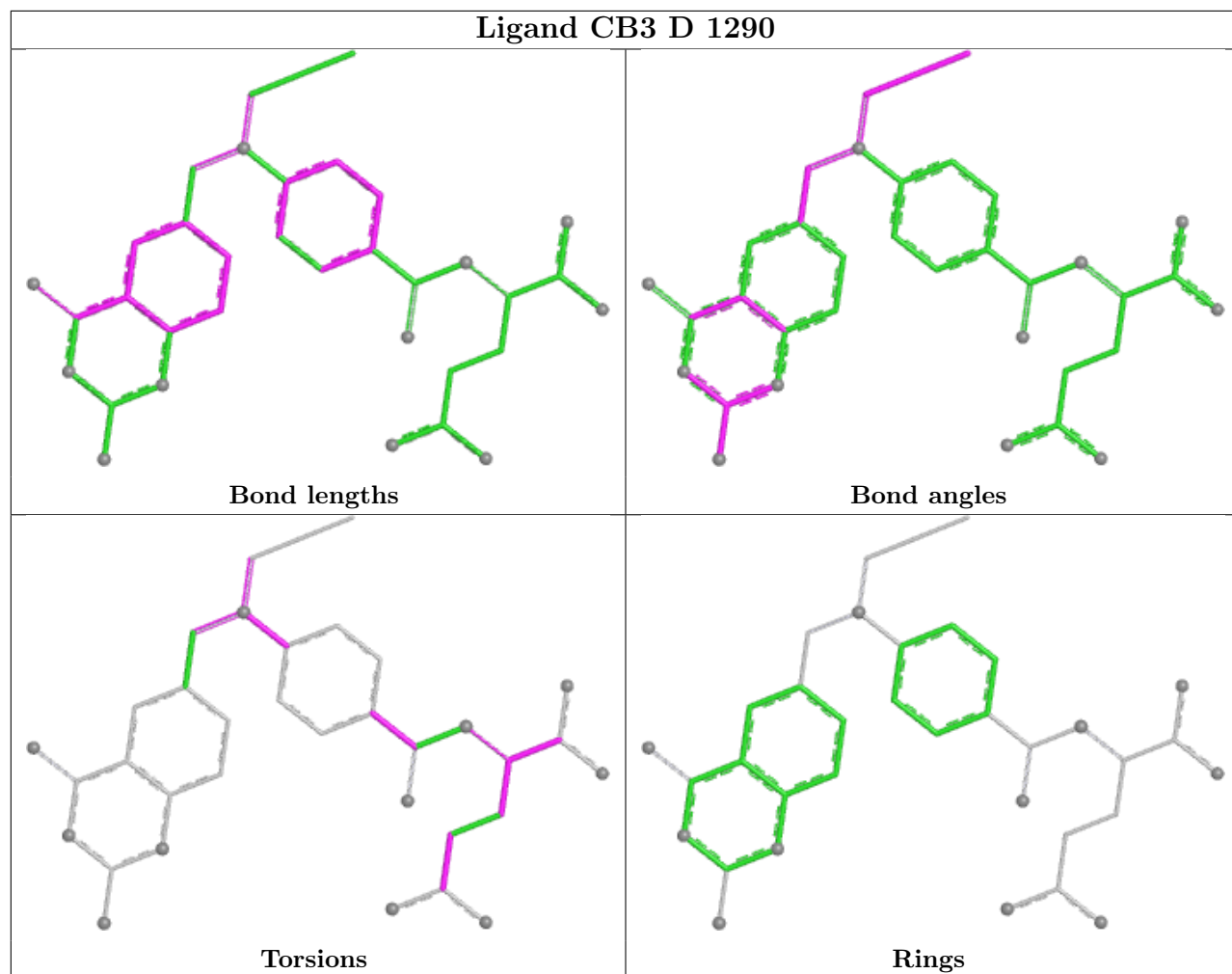


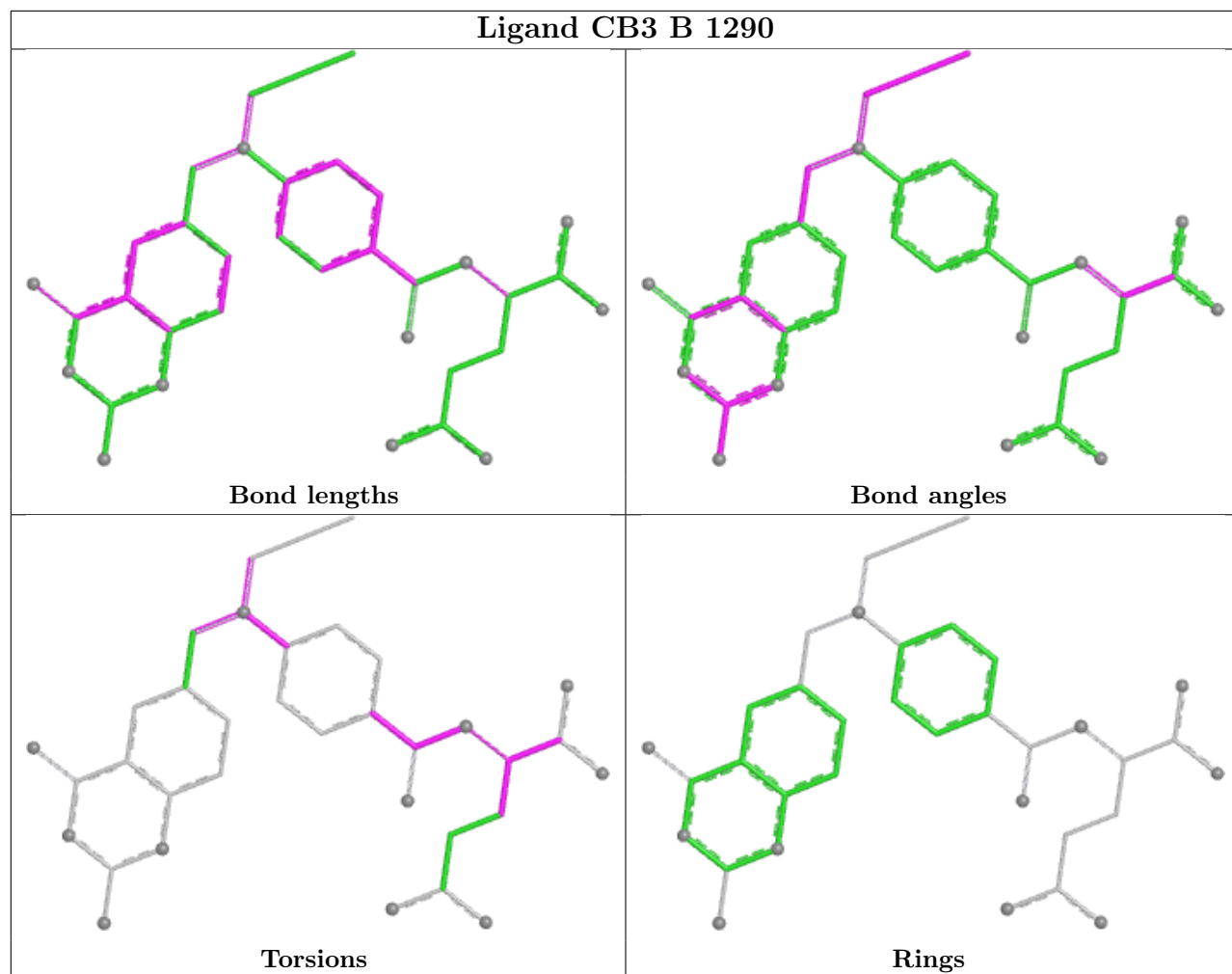


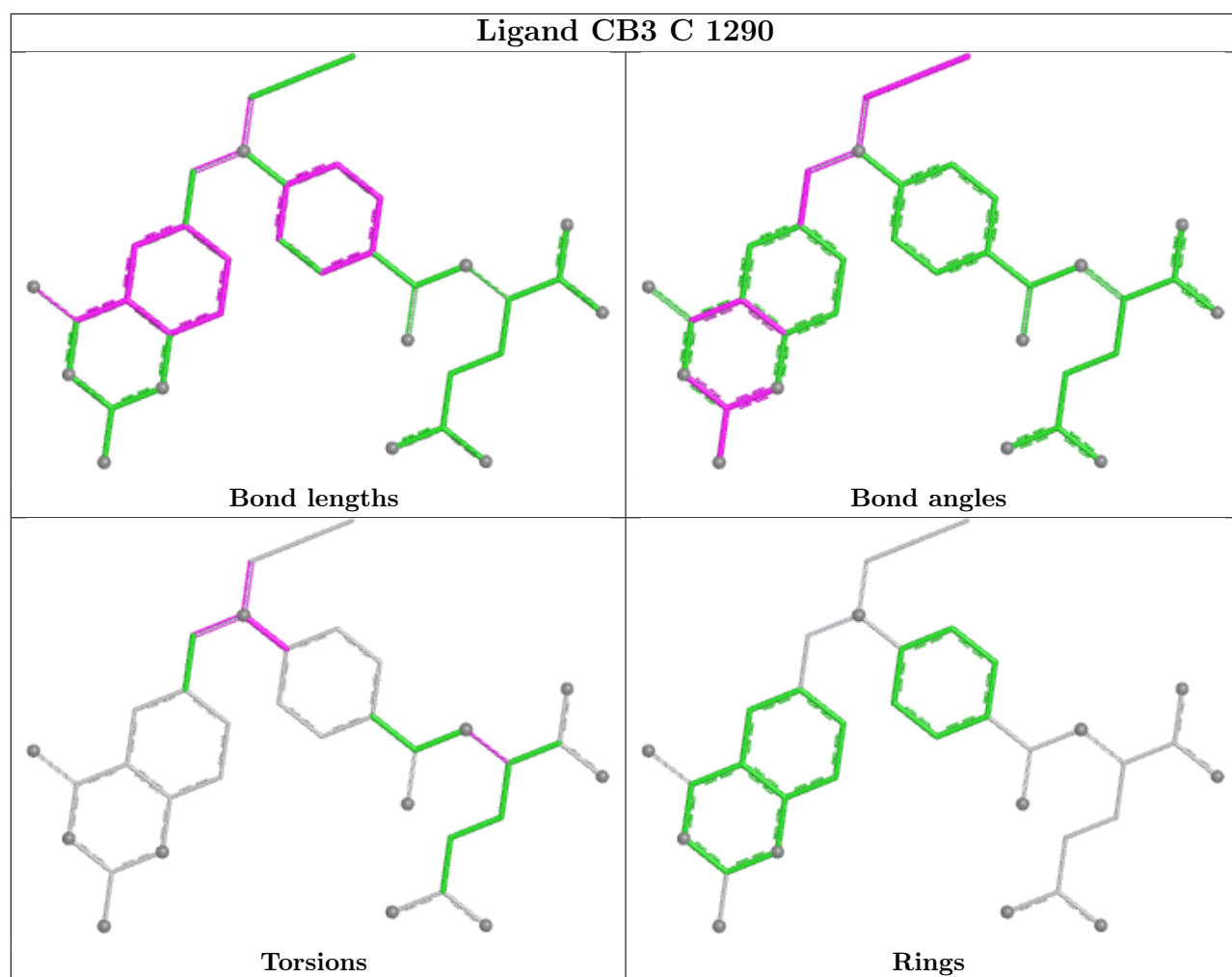












5.7 Other polymers [i](#)

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	265/288 (92%)	-0.00	9 (3%) 48 44	17, 25, 41, 93	1 (0%)
1	B	266/288 (92%)	0.07	9 (3%) 48 44	17, 26, 46, 67	2 (0%)
1	C	253/288 (87%)	-0.10	7 (2%) 55 51	17, 25, 46, 92	0
1	D	255/288 (88%)	0.07	9 (3%) 47 43	17, 25, 46, 75	3 (1%)
All	All	1039/1152 (90%)	0.01	34 (3%) 49 45	17, 25, 46, 93	6 (0%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	133	ARG	10.9
1	A	120	ARG	9.8
1	D	241	HIS	8.6
1	B	133	ARG	7.1
1	B	132	ASP	6.3
1	D	134	GLU	6.2
1	C	230	VAL	5.4
1	C	133	ARG	4.7
1	D	132	ASP	3.9
1	C	81	ALA	3.8
1	A	81	ALA	3.6
1	A	133	ARG	3.1
1	A	136	MET	3.0
1	A	132	ASP	3.0
1	A	135	ALA	2.6
1	D	120	ARG	2.5
1	B	230	VAL	2.5
1	A	86	PHE	2.4
1	B	81	ALA	2.4
1	D	73	PRO	2.4
1	A	73	PRO	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	160	HIS	2.3
1	B	120	ARG	2.3
1	D	230	VAL	2.3
1	A	134	GLU	2.3
1	C	276	CYS	2.2
1	B	231	ASP	2.2
1	D	144	PHE	2.2
1	C	73	PRO	2.2
1	B	53	ALA	2.1
1	C	134	GLU	2.1
1	D	82	PRO	2.1
1	B	73	PRO	2.1
1	C	136	MET	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.

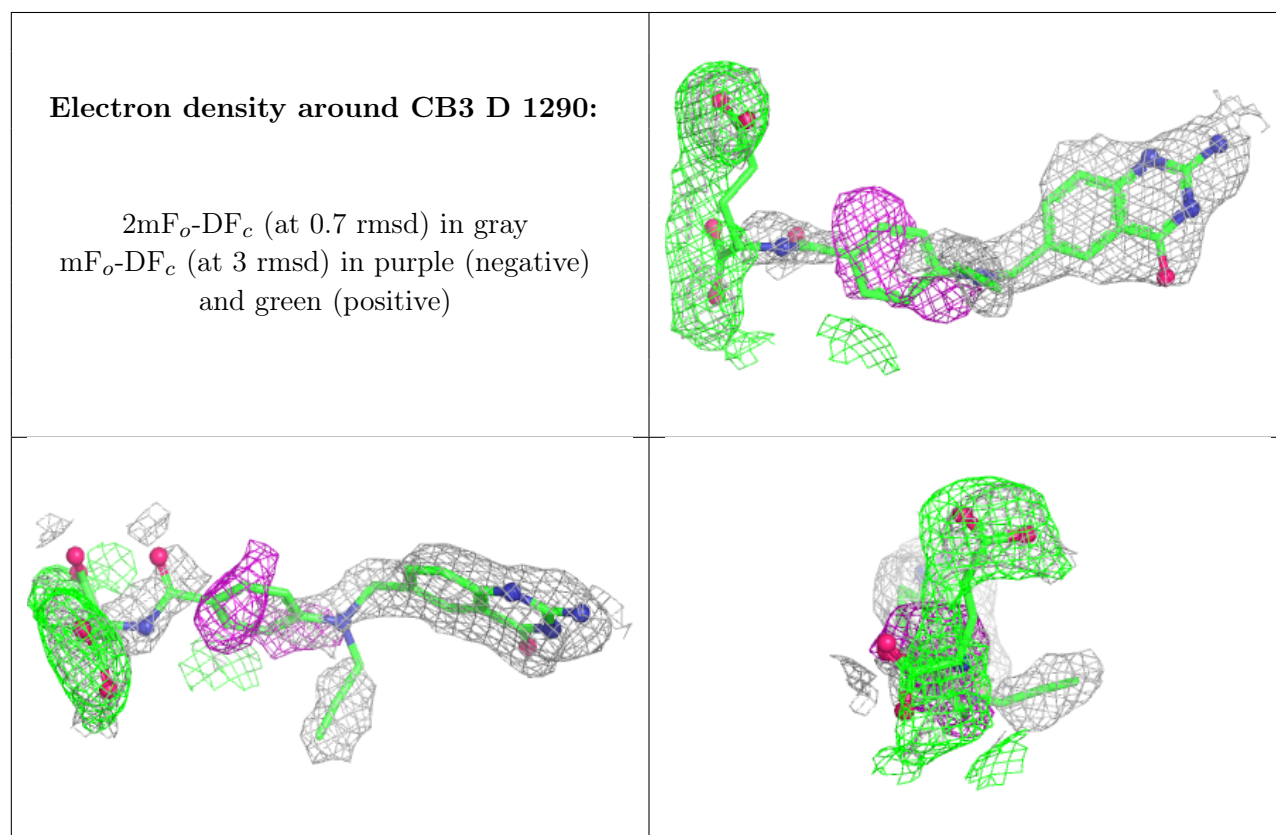
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CB3	D	1290	35/35	0.64	0.38	48,64,69,70	9
3	CB3	C	1290	35/35	0.68	0.41	50,81,93,93	9
3	CB3	A	1290	35/35	0.75	0.33	39,66,82,83	9
3	CB3	B	1290	35/35	0.80	0.32	41,73,89,89	9
4	EDO	D	1291	4/4	0.91	0.23	48,49,49,50	0
4	EDO	D	1292	4/4	0.91	0.12	34,36,37,39	0
4	EDO	B	1291	4/4	0.92	0.09	24,25,26,27	0
4	EDO	A	1291	4/4	0.94	0.13	46,47,47,48	0
2	NDP	C	1289	48/48	0.96	0.09	26,29,32,33	0
4	EDO	A	1292	4/4	0.96	0.11	37,39,40,41	0

Continued on next page...

Continued from previous page...

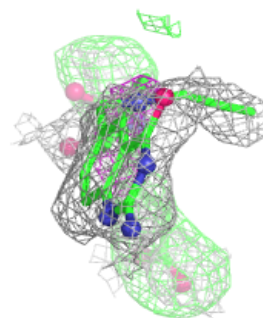
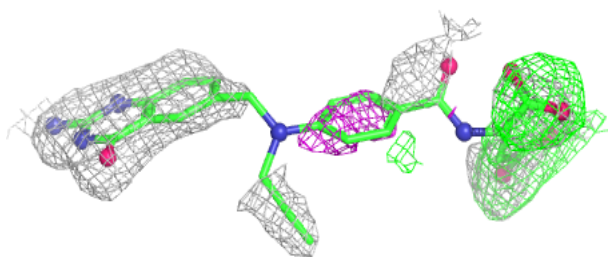
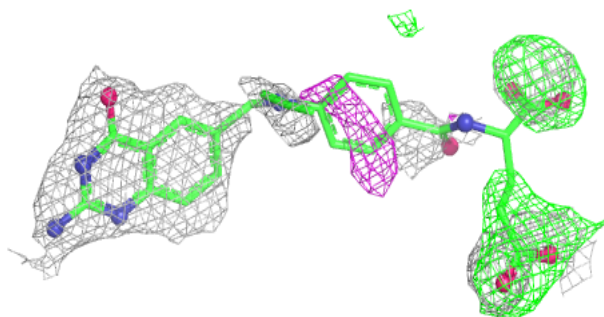
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	A	1293	4/4	0.96	0.11	50,51,51,51	0
2	NDP	A	1289	48/48	0.97	0.08	26,29,31,33	0
2	NDP	D	1289	48/48	0.97	0.07	26,29,32,33	0
2	NDP	B	1289	48/48	0.97	0.07	26,29,31,33	0

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.

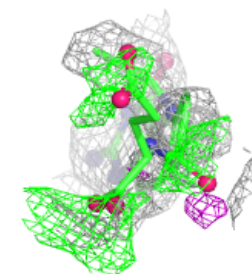
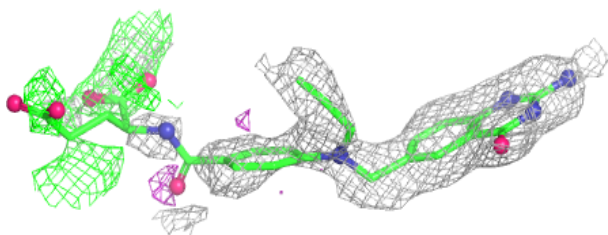
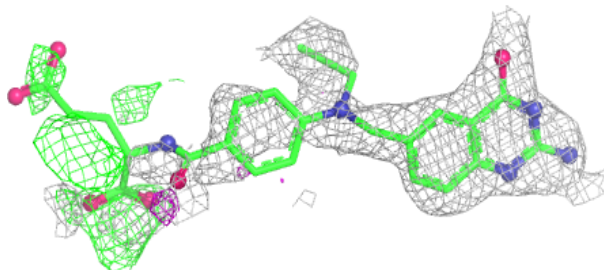


Electron density around CB3 C 1290:

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

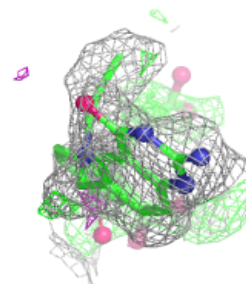
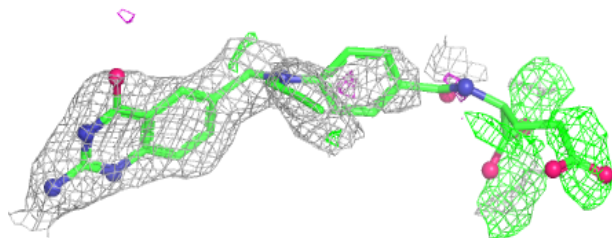
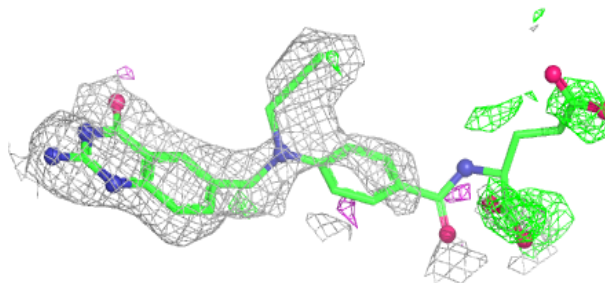
**Electron density around CB3 A 1290:**

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

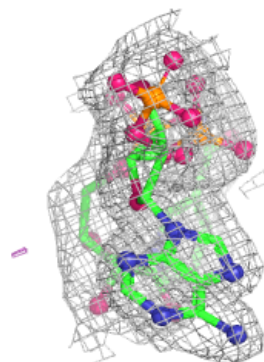
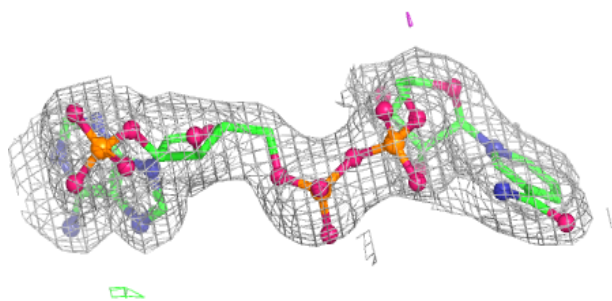
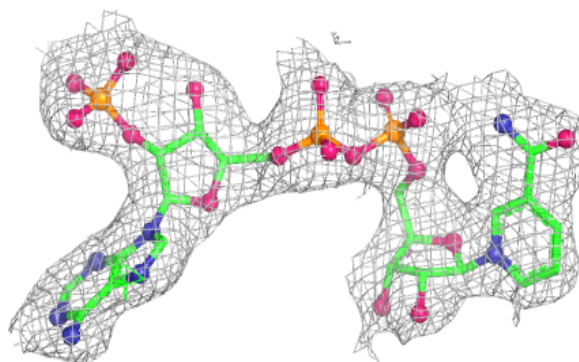


Electron density around CB3 B 1290:

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

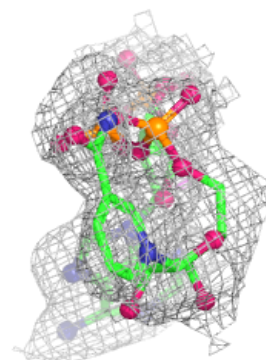
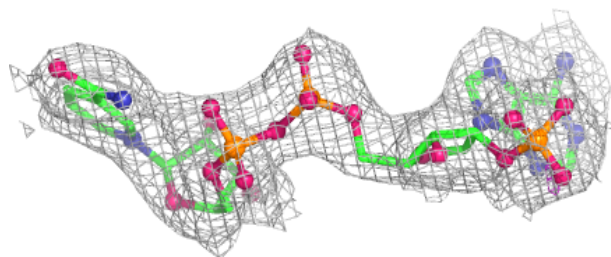
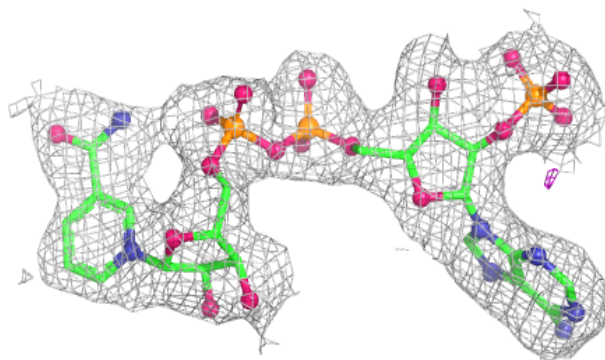
**Electron density around NDP C 1289:**

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

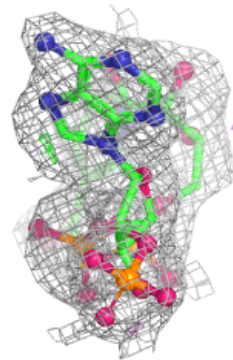
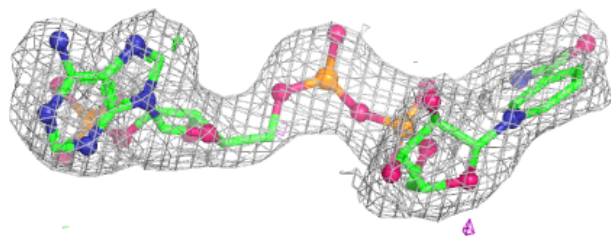


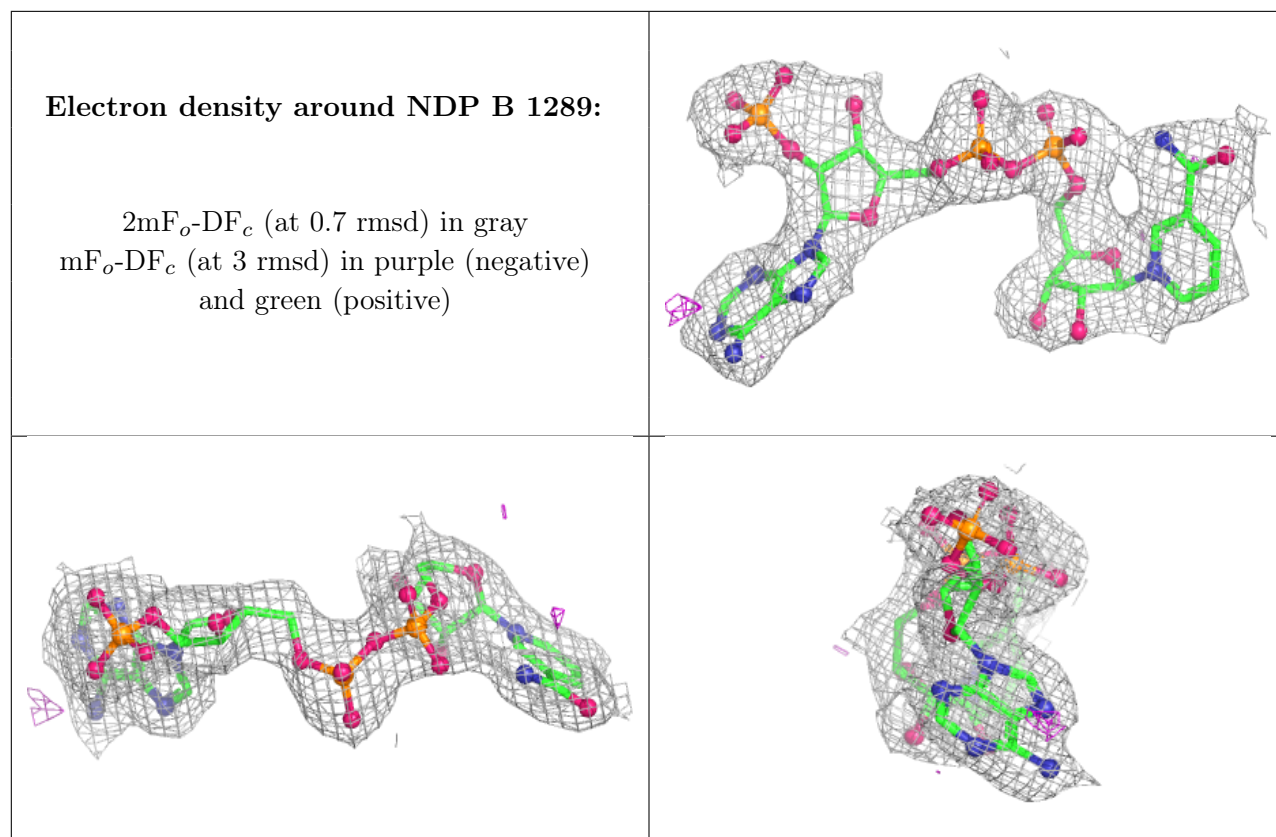
Electron density around NDP A 1289:

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

**Electron density around NDP D 1289:**

$2mF_o-DF_c$ (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.