



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 4, 2024 – 10:13 pm GMT

PDB ID : 5A03
Title : Crystal structure of aldose-aldose oxidoreductase from *Caulobacter crescentus* complexed with xylose
Authors : Taberman, H.; Rouvinen, J.; Parkkinen, T.
Deposited on : 2015-04-17
Resolution : 1.85 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

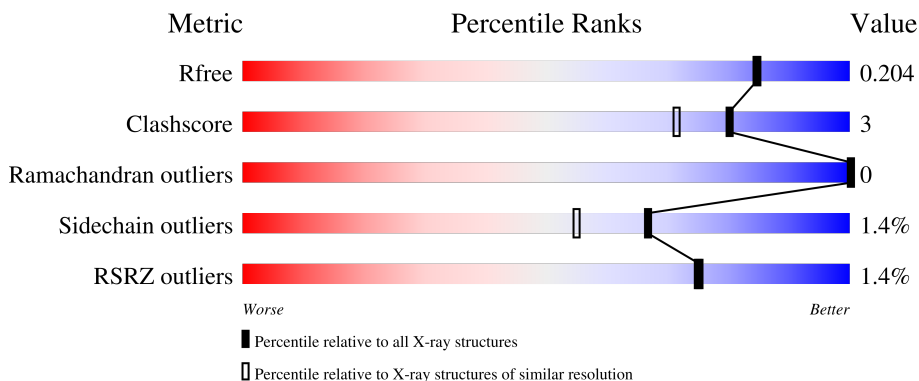
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



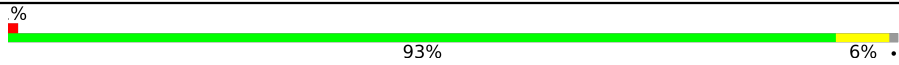
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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	339	93% 6% .
1	B	339	90% 8% ..
1	C	339	93% 6% .
1	D	339	93% 6% .
1	E	339	94% ..

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Mol	Chain	Length	Quality of chain
1	F	339	 <p>A horizontal bar chart representing the quality of the chain. The bar is primarily green, indicating a high quality score of 93%. A small yellow segment at the end indicates a lower quality score of 6%. The bar is labeled with a '%' symbol at the start and '93%' and '6%' at the corresponding positions along the bar.</p>

2 Entry composition [i](#)

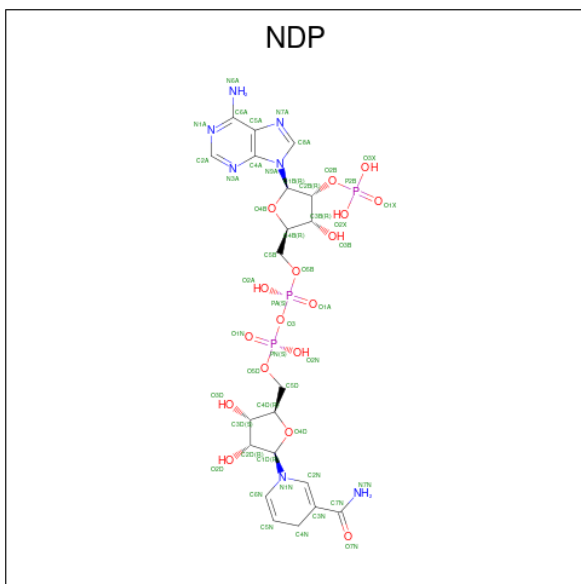
There are 7 unique types of molecules in this entry. The entry contains 17880 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ALDOSE-ALDOSE OXIDOREDUCTASE.

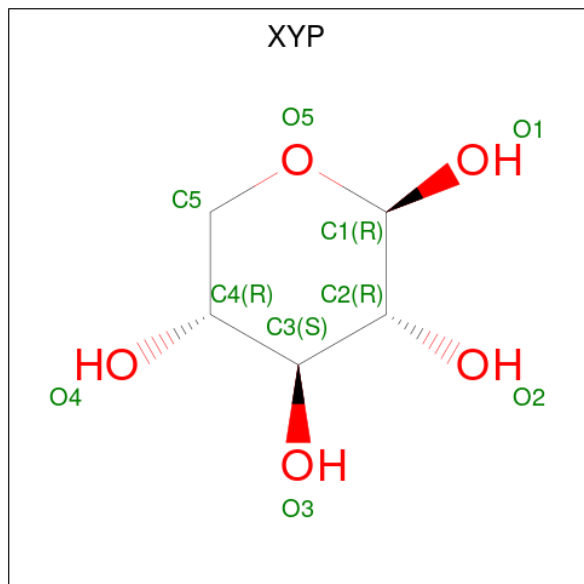
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	335	Total 2593	C 1626	N 471	O 482	S 14	0	0	0
1	B	335	Total 2593	C 1626	N 471	O 482	S 14	0	0	0
1	C	336	Total 2597	C 1628	N 472	O 483	S 14	0	0	0
1	D	335	Total 2593	C 1626	N 471	O 482	S 14	0	0	0
1	E	335	Total 2593	C 1626	N 471	O 482	S 14	0	0	0
1	F	335	Total 2604	C 1632	N 475	O 483	S 14	0	1	0

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: 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
2	C	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	D	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	E	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	F	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 3 is beta-D-xylopyranose (three-letter code: XYP) (formula: C₅H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	Total 10	C 5	O 5	0	0
3	A	1	Total 10	C 5	O 5	0	0
3	A	1	Total 10	C 5	O 5	0	0
3	A	1	Total 10	C 5	O 5	0	0
3	B	1	Total 10	C 5	O 5	0	0
3	C	1	Total 10	C 5	O 5	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 10 5 5	0	0
3	D	1	Total C O 10 5 5	0	0
3	D	1	Total C O 10 5 5	0	0
3	E	1	Total C O 10 5 5	0	0
3	E	1	Total C O 10 5 5	0	0
3	E	1	Total C O 10 5 5	0	0
3	F	1	Total C O 10 5 5	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



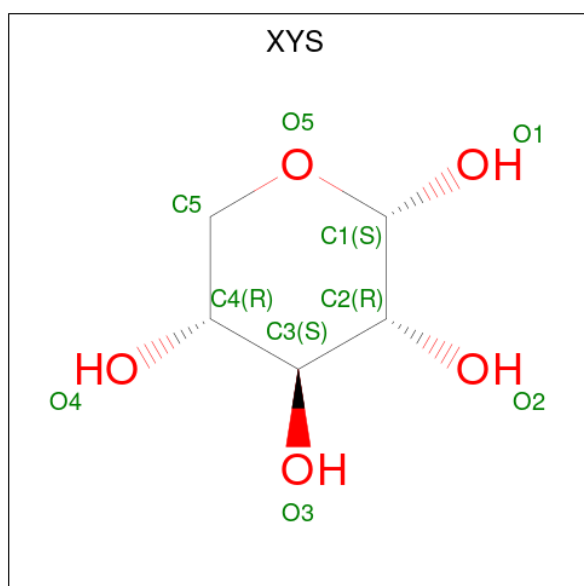
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	D	1	Total O S 5 4 1	0	0

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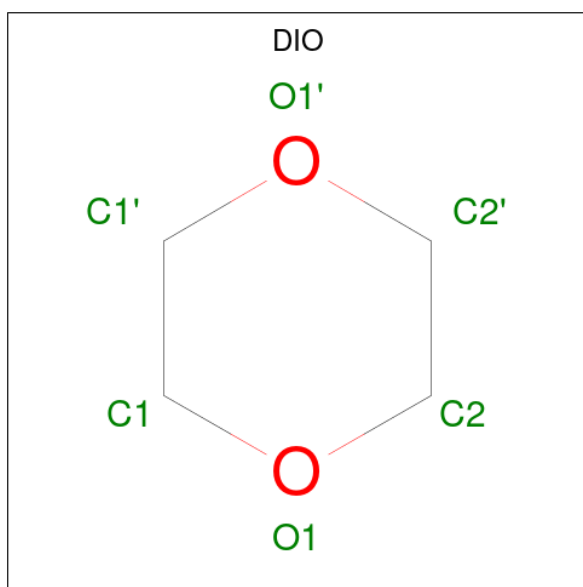
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	1	Total O S 5 4 1	0	0
4	E	1	Total O S 5 4 1	0	0
4	E	1	Total O S 5 4 1	0	0
4	E	1	Total O S 5 4 1	0	0
4	F	1	Total O S 5 4 1	0	0

- Molecule 5 is alpha-D-xylopyranose (three-letter code: XY5) (formula: C₅H₁₀O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C O 10 5 5	0	0
5	E	1	Total C O 10 5 5	0	0

- Molecule 6 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: C₄H₈O₂).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	374	Total O 374 374	0	0
7	B	286	Total O 286 286	0	0
7	C	303	Total O 303 303	0	0
7	D	285	Total O 285 285	0	0
7	E	275	Total O 275 275	0	0
7	F	289	Total O 289 289	0	0

3 Residue-property plots [i](#)

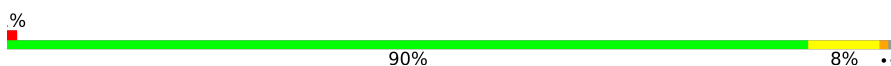
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

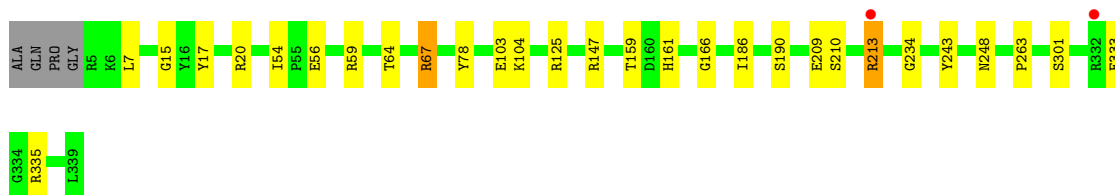
- Molecule 1: ALDOSE-ALDOSE OXIDOREDUCTASE

Chain A: 

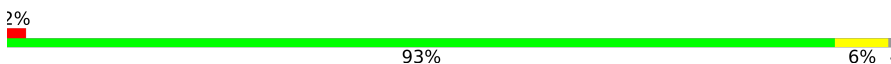


- Molecule 1: ALDOSE-ALDOSE OXIDOREDUCTASE

Chain B: 

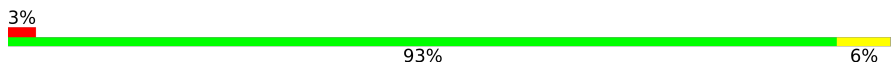


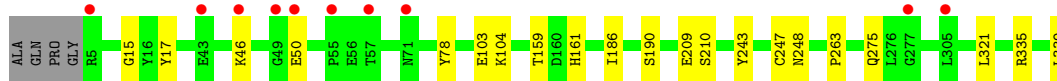
- Molecule 1: ALDOSE-ALDOSE OXIDOREDUCTASE

Chain C: 



- Molecule 1: ALDOSE-ALDOSE OXIDOREDUCTASE

Chain D: 

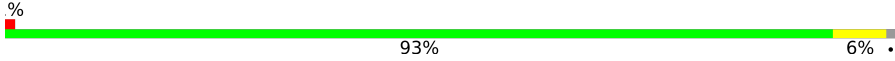


- Molecule 1: ALDOSE-ALDOSE OXIDOREDUCTASE

Chain E: 



● Molecule 1: ALDOSE-ALDOSE OXIDOREDUCTASE

Chain F:  %



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	101.06Å 153.48Å 107.33Å 90.00° 109.42° 90.00°	Depositor
Resolution (Å)	49.99 – 1.85 49.99 – 1.85	Depositor EDS
% Data completeness (in resolution range)	97.4 (49.99-1.85) 97.5 (49.99-1.85)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 1.84Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.167 , 0.195 0.178 , 0.204	Depositor DCC
R_{free} test set	12814 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.4	Xtrriage
Anisotropy	0.366	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17880	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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: XYS, DIO, XYP, NDP, SO4

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	0.39	0/2648	0.53	0/3586
1	B	0.35	0/2648	0.52	0/3586
1	C	0.35	0/2652	0.51	0/3591
1	D	0.35	0/2648	0.51	0/3586
1	E	0.37	0/2648	0.52	0/3586
1	F	0.38	0/2659	0.52	0/3600
All	All	0.36	0/15903	0.52	0/21535

There are no bond length outliers.

There are no bond angle outliers.

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	2593	0	2580	15	0
1	B	2593	0	2580	22	0
1	C	2597	0	2583	15	0
1	D	2593	0	2580	12	0
1	E	2593	0	2580	9	0
1	F	2604	0	2592	12	0
2	A	48	0	26	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	48	0	26	4	0
2	C	48	0	26	4	0
2	D	48	0	26	4	0
2	E	48	0	26	6	0
2	F	48	0	26	4	0
3	A	40	0	0	2	0
3	B	10	0	0	1	0
3	C	20	0	0	0	0
3	D	20	0	0	1	0
3	E	30	0	0	2	0
3	F	10	0	0	1	0
4	A	10	0	0	0	0
4	C	5	0	0	0	0
4	D	10	0	0	0	0
4	E	15	0	0	0	0
4	F	5	0	0	0	0
5	B	10	0	10	0	0
5	E	10	0	10	0	0
6	D	12	0	16	1	0
7	A	374	0	0	4	2
7	B	286	0	0	4	0
7	C	303	0	0	5	0
7	D	285	0	0	0	0
7	E	275	0	0	0	0
7	F	289	0	0	3	2
All	All	17880	0	15687	85	2

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 3.

All (85) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:TYR:CD1	2:C:1340:NDP:H41N	2.24	0.72
1:A:17:TYR:CD1	2:A:1340:NDP:H41N	2.25	0.72
1:A:147:ARG:NH2	7:A:2187:HOH:O	2.23	0.71
1:C:175:ARG:NH2	7:C:2191:HOH:O	2.24	0.70
1:E:17:TYR:CD1	2:E:1340:NDP:H41N	2.29	0.68
1:B:147:ARG:NH2	7:B:2149:HOH:O	2.27	0.67
1:D:17:TYR:CD1	2:D:1340:NDP:H41N	2.30	0.67
1:F:17:TYR:CD1	2:F:1340:NDP:H41N	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2184:HOH:O	1:B:20:ARG:NH2	2.29	0.65
3:A:1343:XYP:O2	7:A:2010:HOH:O	2.15	0.64
1:C:147:ARG:NH2	7:C:2150:HOH:O	2.32	0.63
1:C:5:ARG:NH2	7:C:2002:HOH:O	2.33	0.61
1:C:335:ARG:NH2	7:C:2293:HOH:O	2.32	0.61
1:B:67:ARG:NH1	7:B:2069:HOH:O	2.05	0.61
1:F:15:GLY:HA3	2:F:1340:NDP:O5B	2.00	0.60
1:D:15:GLY:HA3	2:D:1340:NDP:O5B	2.02	0.59
1:A:15:GLY:HA3	2:A:1340:NDP:O5B	2.04	0.58
1:C:14:LEU:HD22	1:C:39:SER:HB2	1.87	0.55
1:A:161:HIS:HB3	1:A:186:ILE:HG13	1.89	0.55
1:B:333:GLU:OE1	1:B:335:ARG:NE	2.37	0.54
1:E:161:HIS:HB3	1:E:186:ILE:HG13	1.88	0.54
1:B:17:TYR:CD1	2:B:1340:NDP:H41N	2.43	0.54
1:E:15:GLY:HA3	2:E:1340:NDP:O5B	2.07	0.53
1:B:213:ARG:HD3	7:B:2204:HOH:O	2.09	0.53
1:A:335:ARG:HA	1:E:335:ARG:HA	1.90	0.53
1:F:161:HIS:HB3	1:F:186:ILE:HG13	1.91	0.53
1:F:147[A]:ARG:NH2	7:F:2148:HOH:O	2.38	0.52
1:F:103:GLU:OE1	2:F:1340:NDP:H2N	2.10	0.51
1:F:147[B]:ARG:HG3	7:F:2151:HOH:O	2.10	0.51
1:B:54:ILE:O	1:B:59:ARG:NH1	2.34	0.51
2:B:1340:NDP:H42N	3:B:1341:XYP:C1	2.42	0.50
1:D:103:GLU:OE1	2:D:1340:NDP:H2N	2.11	0.50
1:B:234:GLY:HA3	6:D:1343:DIO:H2'1	1.94	0.50
1:B:161:HIS:HB3	1:B:186:ILE:HG13	1.93	0.49
1:A:144:LYS:HG3	7:A:2183:HOH:O	2.12	0.49
2:E:1340:NDP:H42N	3:E:1342:XYP:C1	2.43	0.49
1:B:15:GLY:HA3	2:B:1340:NDP:O5B	2.13	0.48
2:D:1340:NDP:H42N	3:D:1341:XYP:C1	2.43	0.48
1:B:335:ARG:HA	1:D:335:ARG:HA	1.94	0.48
1:E:213:ARG:HE	3:E:1343:XYP:C5	2.26	0.47
1:A:141:GLU:CD	1:B:20:ARG:HH22	2.17	0.47
2:F:1340:NDP:H42N	3:F:1341:XYP:C1	2.44	0.47
1:A:141:GLU:OE1	1:B:20:ARG:NH2	2.43	0.47
1:C:335:ARG:HA	1:F:335:ARG:HA	1.97	0.47
1:F:248:ASN:O	1:F:263:PRO:HA	2.14	0.47
1:B:103:GLU:OE1	2:B:1340:NDP:H2N	2.15	0.46
1:E:209:GLU:HG2	1:E:210:SER:N	2.29	0.46
1:C:161:HIS:HB3	1:C:186:ILE:HG13	1.98	0.46
1:C:103:GLU:OE1	2:C:1340:NDP:H2N	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:GLU:OE1	2:A:1340:NDP:H2N	2.16	0.46
1:A:248:ASN:O	1:A:263:PRO:HA	2.15	0.46
1:C:169:LYS:HA	1:C:169:LYS:HD3	1.76	0.46
1:D:248:ASN:O	1:D:263:PRO:HA	2.15	0.46
1:B:209:GLU:HG2	1:B:210:SER:N	2.31	0.46
1:D:209:GLU:HG2	1:D:210:SER:N	2.31	0.45
1:F:284:GLU:OE1	7:F:2250:HOH:O	2.21	0.45
1:C:15:GLY:HA3	2:C:1340:NDP:O5B	2.16	0.45
1:B:159:THR:HG23	1:B:190:SER:HB3	1.99	0.45
1:E:103:GLU:OE1	2:E:1340:NDP:H2N	2.17	0.45
1:A:44:LYS:HZ1	3:A:1343:XYP:C1	2.30	0.44
1:C:17:TYR:CE1	2:C:1340:NDP:H41N	2.53	0.44
1:C:248:ASN:O	1:C:263:PRO:HA	2.17	0.44
1:E:248:ASN:O	1:E:263:PRO:HA	2.18	0.43
2:E:1340:NDP:O5D	2:E:1340:NDP:H6N	2.18	0.43
1:B:248:ASN:O	1:B:263:PRO:HA	2.18	0.43
1:A:39:SER:O	1:A:61:SER:HA	2.19	0.43
1:C:247:CYS:HB3	7:C:2232:HOH:O	2.19	0.43
1:D:159:THR:HG23	1:D:190:SER:HB3	2.01	0.42
1:B:56:GLU:HA	1:B:59:ARG:HD3	2.01	0.42
1:D:46:LYS:NZ	1:D:50:GLU:OE2	2.47	0.42
1:A:17:TYR:CE1	2:A:1340:NDP:H41N	2.55	0.42
1:F:108:ASN:HA	1:F:184:MET:HE1	2.02	0.42
7:B:2226:HOH:O	1:D:247:CYS:HB3	2.19	0.41
1:C:167:ASP:HA	1:C:168:PRO:HD2	1.98	0.41
1:D:321:LEU:HD13	1:D:321:LEU:HA	1.92	0.41
2:E:1340:NDP:N3A	2:E:1340:NDP:H3B	2.36	0.41
1:A:224:ILE:HD11	1:E:155:ARG:HB3	2.02	0.41
1:B:7:LEU:HD12	1:B:301:SER:HA	2.02	0.41
1:D:161:HIS:HB3	1:D:186:ILE:HG13	2.03	0.41
1:A:276:LEU:O	1:B:166:GLY:HA3	2.21	0.41
1:F:7:LEU:HD12	1:F:301:SER:HA	2.04	0.40
1:B:64:THR:O	1:B:67:ARG:HD3	2.20	0.40
1:D:339:LEU:HD23	1:D:339:LEU:HA	1.89	0.40
1:B:125:ARG:HD3	1:B:125:ARG:HA	1.91	0.40
1:F:83:ASN:OD1	1:F:105:PRO:HD2	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2138:HOH:O	7:F:2289:HOH:O[2_656]	2.12	0.08
7:A:2220:HOH:O	7:F:2016:HOH:O[2_656]	2.18	0.02

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	333/339 (98%)	324 (97%)	9 (3%)	0	100	100
1	B	333/339 (98%)	325 (98%)	8 (2%)	0	100	100
1	C	334/339 (98%)	326 (98%)	8 (2%)	0	100	100
1	D	333/339 (98%)	326 (98%)	7 (2%)	0	100	100
1	E	333/339 (98%)	327 (98%)	6 (2%)	0	100	100
1	F	334/339 (98%)	325 (97%)	9 (3%)	0	100	100
All	All	2000/2034 (98%)	1953 (98%)	47 (2%)	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	270/272 (99%)	267 (99%)	3 (1%)	73	64
1	B	270/272 (99%)	265 (98%)	5 (2%)	57	42
1	C	270/272 (99%)	266 (98%)	4 (2%)	65	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	270/272 (99%)	266 (98%)	4 (2%)	65	52
1	E	270/272 (99%)	267 (99%)	3 (1%)	73	64
1	F	271/272 (100%)	268 (99%)	3 (1%)	73	64
All	All	1621/1632 (99%)	1599 (99%)	22 (1%)	67	55

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	TYR
1	A	104	LYS
1	A	243	TYR
1	B	67	ARG
1	B	78	TYR
1	B	104	LYS
1	B	213	ARG
1	B	243	TYR
1	C	5	ARG
1	C	78	TYR
1	C	104	LYS
1	C	243	TYR
1	D	78	TYR
1	D	104	LYS
1	D	243	TYR
1	D	275	GLN
1	E	78	TYR
1	E	104	LYS
1	E	243	TYR
1	F	78	TYR
1	F	104	LYS
1	F	243	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	GLN

5.3.3 RNA

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

32 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	XYP	E	1342	-	10,10,10	0.66	0	14,14,14	1.00	1 (7%)
4	SO4	E	1346	-	4,4,4	0.14	0	6,6,6	0.17	0
4	SO4	C	1343	-	4,4,4	0.14	0	6,6,6	0.09	0
3	XYP	C	1341	-	10,10,10	0.61	0	14,14,14	1.42	1 (7%)
3	XYP	D	1342	-	10,10,10	0.65	0	14,14,14	1.12	1 (7%)
2	NDP	B	1340	-	45,52,52	2.14	7 (15%)	53,80,80	1.44	7 (13%)
3	XYP	A	1341	-	10,10,10	0.50	0	14,14,14	1.15	1 (7%)
4	SO4	D	1345	-	4,4,4	0.11	0	6,6,6	0.14	0
6	DIO	D	1343	-	6,6,6	0.46	0	6,6,6	0.84	0
5	XYS	B	1342	-	10,10,10	1.68	1 (10%)	14,14,14	1.01	1 (7%)
4	SO4	F	1342	-	4,4,4	0.21	0	6,6,6	0.17	0
6	DIO	D	1344	-	6,6,6	0.46	0	6,6,6	0.59	0
2	NDP	E	1340	-	45,52,52	2.05	5 (11%)	53,80,80	1.46	9 (16%)
4	SO4	E	1347	-	4,4,4	0.12	0	6,6,6	0.09	0
4	SO4	A	1345	-	4,4,4	0.19	0	6,6,6	0.11	0
3	XYP	E	1341	-	10,10,10	0.92	0	14,14,14	1.21	1 (7%)
2	NDP	A	1340	-	45,52,52	1.71	6 (13%)	53,80,80	1.41	7 (13%)
3	XYP	A	1343	-	10,10,10	0.74	0	14,14,14	0.97	1 (7%)
3	XYP	F	1341	-	10,10,10	0.67	0	14,14,14	1.24	1 (7%)
4	SO4	D	1346	-	4,4,4	0.16	0	6,6,6	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	XYS	E	1344	-	10,10,10	1.39	1 (10%)	14,14,14	1.57	3 (21%)
3	XYP	A	1342	-	10,10,10	0.66	0	14,14,14	0.78	0
3	XYP	C	1342	-	10,10,10	0.68	0	14,14,14	0.89	1 (7%)
3	XYP	B	1341	-	10,10,10	0.66	0	14,14,14	1.32	1 (7%)
3	XYP	D	1341	-	10,10,10	0.70	0	14,14,14	1.12	1 (7%)
4	SO4	A	1346	-	4,4,4	0.16	0	6,6,6	0.13	0
4	SO4	E	1345	-	4,4,4	0.16	0	6,6,6	0.09	0
3	XYP	E	1343	-	10,10,10	0.88	0	14,14,14	1.79	2 (14%)
2	NDP	D	1340	-	45,52,52	2.11	7 (15%)	53,80,80	1.45	6 (11%)
3	XYP	A	1344	-	10,10,10	0.71	0	14,14,14	0.76	0
2	NDP	C	1340	-	45,52,52	2.07	6 (13%)	53,80,80	1.42	7 (13%)
2	NDP	F	1340	-	45,52,52	2.04	7 (15%)	53,80,80	1.49	7 (13%)

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	XYP	E	1342	-	-	-	0/1/1/1
3	XYP	C	1341	-	-	-	0/1/1/1
3	XYP	D	1342	-	-	-	0/1/1/1
2	NDP	B	1340	-	-	4/30/77/77	0/5/5/5
3	XYP	A	1341	-	-	-	0/1/1/1
6	DIO	D	1343	-	-	-	0/1/1/1
5	XYS	B	1342	-	-	-	0/1/1/1
6	DIO	D	1344	-	-	-	0/1/1/1
2	NDP	E	1340	-	-	4/30/77/77	0/5/5/5
3	XYP	E	1341	-	-	-	0/1/1/1
2	NDP	A	1340	-	-	3/30/77/77	0/5/5/5
3	XYP	A	1343	-	-	-	0/1/1/1
3	XYP	F	1341	-	-	-	0/1/1/1
5	XYS	E	1344	-	-	-	0/1/1/1
3	XYP	A	1342	-	-	-	0/1/1/1
3	XYP	C	1342	-	-	-	0/1/1/1
3	XYP	B	1341	-	-	-	0/1/1/1
3	XYP	D	1341	-	-	-	0/1/1/1
3	XYP	E	1343	-	-	-	0/1/1/1
2	NDP	D	1340	-	-	4/30/77/77	0/5/5/5
3	XYP	A	1344	-	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NDP	C	1340	-	-	4/30/77/77	0/5/5/5
2	NDP	F	1340	-	-	4/30/77/77	0/5/5/5

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1340	NDP	P2B-O2B	11.20	1.80	1.59
2	C	1340	NDP	P2B-O2B	10.66	1.79	1.59
2	D	1340	NDP	P2B-O2B	10.62	1.79	1.59
2	E	1340	NDP	P2B-O2B	10.41	1.79	1.59
2	F	1340	NDP	P2B-O2B	9.72	1.77	1.59
2	A	1340	NDP	P2B-O2B	7.70	1.73	1.59
5	B	1342	XYS	O5-C1	-4.94	1.36	1.43
2	F	1340	NDP	PN-O5D	4.87	1.79	1.59
2	D	1340	NDP	PN-O5D	4.72	1.78	1.59
2	C	1340	NDP	PN-O5D	4.34	1.76	1.59
2	B	1340	NDP	PN-O5D	4.30	1.76	1.59
2	A	1340	NDP	PN-O5D	4.28	1.76	1.59
2	E	1340	NDP	PN-O5D	4.28	1.76	1.59
5	E	1344	XYS	O5-C1	-4.11	1.37	1.43
2	F	1340	NDP	O2B-C2B	-3.91	1.29	1.44
2	A	1340	NDP	O2B-C2B	-3.52	1.31	1.44
2	E	1340	NDP	O2B-C2B	-3.46	1.31	1.44
2	C	1340	NDP	O2B-C2B	-3.35	1.31	1.44
2	D	1340	NDP	O2B-C2B	-3.34	1.31	1.44
2	B	1340	NDP	O2B-C2B	-3.14	1.32	1.44
2	B	1340	NDP	C2A-N1A	2.65	1.38	1.33
2	B	1340	NDP	C7N-N7N	2.53	1.40	1.33
2	F	1340	NDP	O4B-C1B	2.51	1.44	1.41
2	E	1340	NDP	O4B-C1B	2.49	1.44	1.41
2	D	1340	NDP	C2A-N1A	2.47	1.38	1.33
2	C	1340	NDP	C7N-N7N	2.42	1.39	1.33
2	A	1340	NDP	C2A-N1A	2.41	1.38	1.33
2	D	1340	NDP	C7N-N7N	2.35	1.39	1.33
2	A	1340	NDP	C4A-N3A	2.30	1.38	1.35
2	F	1340	NDP	C2A-N1A	2.30	1.38	1.33
2	F	1340	NDP	C7N-N7N	2.27	1.39	1.33
2	D	1340	NDP	C3D-C4D	2.25	1.58	1.53
2	F	1340	NDP	C3D-C4D	2.22	1.58	1.53
2	D	1340	NDP	C4A-N3A	2.16	1.38	1.35
2	B	1340	NDP	C6N-N1N	2.07	1.42	1.37
2	C	1340	NDP	O4B-C1B	2.04	1.43	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1340	NDP	C7N-N7N	2.03	1.38	1.33
2	C	1340	NDP	C2A-N1A	2.03	1.37	1.33
2	E	1340	NDP	C2A-N1A	2.03	1.37	1.33
2	B	1340	NDP	C4A-N3A	2.00	1.38	1.35

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1340	NDP	PN-O3-PA	-5.73	113.15	132.83
3	E	1343	XYP	C5-O5-C1	-5.60	103.29	112.71
2	D	1340	NDP	PN-O3-PA	-5.49	113.98	132.83
2	E	1340	NDP	PN-O3-PA	-5.24	114.85	132.83
2	B	1340	NDP	PN-O3-PA	-5.13	115.22	132.83
2	C	1340	NDP	PN-O3-PA	-5.06	115.46	132.83
2	A	1340	NDP	PN-O3-PA	-4.80	116.37	132.83
3	C	1341	XYP	C4-C3-C2	-4.18	103.66	110.89
3	E	1341	XYP	C5-O5-C1	-3.78	106.35	112.71
3	B	1341	XYP	C5-O5-C1	-3.64	106.58	112.71
3	A	1341	XYP	C5-O5-C1	-3.52	106.79	112.71
3	F	1341	XYP	C5-O5-C1	-3.31	107.15	112.71
5	E	1344	XYS	C5-O5-C1	3.23	118.14	112.71
3	D	1341	XYP	C5-O5-C1	-3.08	107.53	112.71
5	E	1344	XYS	O5-C1-C2	3.03	113.93	109.43
5	E	1344	XYS	O5-C5-C4	2.98	115.37	110.77
5	B	1342	XYS	C5-O5-C1	2.85	117.50	112.71
3	E	1342	XYP	C5-O5-C1	-2.67	108.22	112.71
2	E	1340	NDP	O3X-P2B-O2X	2.66	117.82	107.64
2	D	1340	NDP	O3X-P2B-O2X	2.63	117.70	107.64
2	F	1340	NDP	O3X-P2B-O2X	2.61	117.60	107.64
3	D	1342	XYP	C4-C3-C2	-2.60	106.39	110.89
2	B	1340	NDP	O3X-P2B-O2X	2.60	117.56	107.64
2	A	1340	NDP	O3X-P2B-O2X	2.57	117.45	107.64
3	A	1343	XYP	C5-O5-C1	-2.55	108.42	112.71
2	C	1340	NDP	O3X-P2B-O2X	2.50	117.20	107.64
2	D	1340	NDP	O2B-P2B-O1X	-2.50	99.74	109.39
2	D	1340	NDP	PA-O5B-C5B	-2.49	107.06	121.68
2	B	1340	NDP	PA-O5B-C5B	-2.48	107.14	121.68
2	E	1340	NDP	O2B-P2B-O1X	-2.44	99.97	109.39
2	A	1340	NDP	C3N-C2N-N1N	-2.44	119.62	123.10
2	E	1340	NDP	PA-O5B-C5B	-2.43	107.42	121.68
2	B	1340	NDP	O2B-P2B-O1X	-2.37	100.24	109.39
2	F	1340	NDP	PA-O5B-C5B	-2.36	107.82	121.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1340	NDP	PA-O5B-C5B	-2.34	107.96	121.68
2	F	1340	NDP	C2A-N1A-C6A	-2.29	114.84	118.75
2	C	1340	NDP	C5B-C4B-C3B	-2.25	106.75	115.18
2	B	1340	NDP	C2A-N1A-C6A	-2.25	114.91	118.75
2	D	1340	NDP	C3N-C2N-N1N	-2.21	119.95	123.10
2	A	1340	NDP	O2N-PN-O1N	2.20	123.10	112.24
2	C	1340	NDP	O2B-P2B-O1X	-2.20	100.92	109.39
2	A	1340	NDP	PA-O5B-C5B	-2.18	108.87	121.68
2	A	1340	NDP	O2B-P2B-O1X	-2.18	100.96	109.39
2	E	1340	NDP	O7N-C7N-N7N	-2.18	117.77	122.88
2	F	1340	NDP	O2B-P2B-O1X	-2.16	101.06	109.39
2	F	1340	NDP	C5B-C4B-C3B	-2.15	107.13	115.18
3	C	1342	XYP	C5-O5-C1	-2.15	109.10	112.71
3	E	1343	XYP	C5-C4-C3	2.14	112.30	109.67
2	B	1340	NDP	O7N-C7N-N7N	-2.14	117.87	122.88
2	B	1340	NDP	O2N-PN-O1N	2.12	122.73	112.24
2	D	1340	NDP	C2A-N1A-C6A	-2.11	115.15	118.75
2	E	1340	NDP	C5B-C4B-C3B	-2.09	107.34	115.18
2	E	1340	NDP	C2A-N1A-C6A	-2.09	115.17	118.75
2	E	1340	NDP	O5D-PN-O1N	-2.09	100.91	109.07
2	A	1340	NDP	C2A-N1A-C6A	-2.06	115.23	118.75
2	E	1340	NDP	O2N-PN-O1N	2.06	122.43	112.24
2	C	1340	NDP	O2N-PN-O5D	-2.05	98.22	107.75
2	C	1340	NDP	C2A-N1A-C6A	-2.02	115.30	118.75
2	F	1340	NDP	C3N-C2N-N1N	-2.01	120.23	123.10

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1340	NDP	O4B-C4B-C5B-O5B
2	E	1340	NDP	O4B-C4B-C5B-O5B
2	B	1340	NDP	O4B-C4B-C5B-O5B
2	C	1340	NDP	O4B-C4B-C5B-O5B
2	F	1340	NDP	O4B-C4B-C5B-O5B
2	D	1340	NDP	C3B-C4B-C5B-O5B
2	E	1340	NDP	C3B-C4B-C5B-O5B
2	C	1340	NDP	C3B-C4B-C5B-O5B
2	B	1340	NDP	C3B-C4B-C5B-O5B
2	F	1340	NDP	C3B-C4B-C5B-O5B
2	C	1340	NDP	O4D-C1D-N1N-C2N
2	F	1340	NDP	C2D-C1D-N1N-C2N

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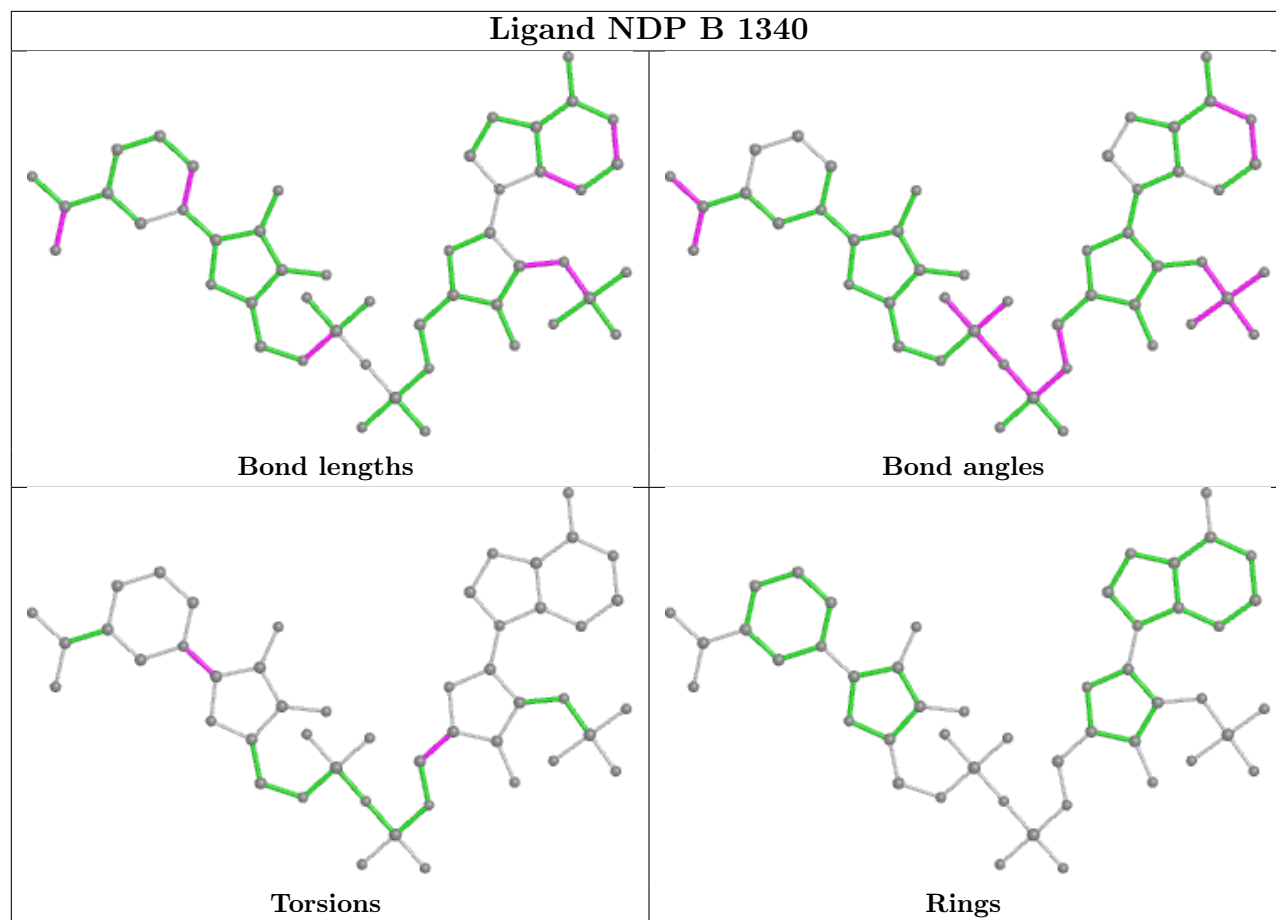
Mol	Chain	Res	Type	Atoms
2	A	1340	NDP	O4D-C1D-N1N-C2N
2	D	1340	NDP	O4D-C1D-N1N-C2N
2	E	1340	NDP	O4D-C1D-N1N-C2N
2	F	1340	NDP	O4D-C1D-N1N-C2N
2	A	1340	NDP	C2D-C1D-N1N-C2N
2	D	1340	NDP	C2D-C1D-N1N-C2N
2	E	1340	NDP	C2D-C1D-N1N-C2N
2	B	1340	NDP	O4D-C1D-N1N-C2N
2	B	1340	NDP	C2D-C1D-N1N-C2N
2	C	1340	NDP	C2D-C1D-N1N-C2N
2	A	1340	NDP	O4B-C4B-C5B-O5B

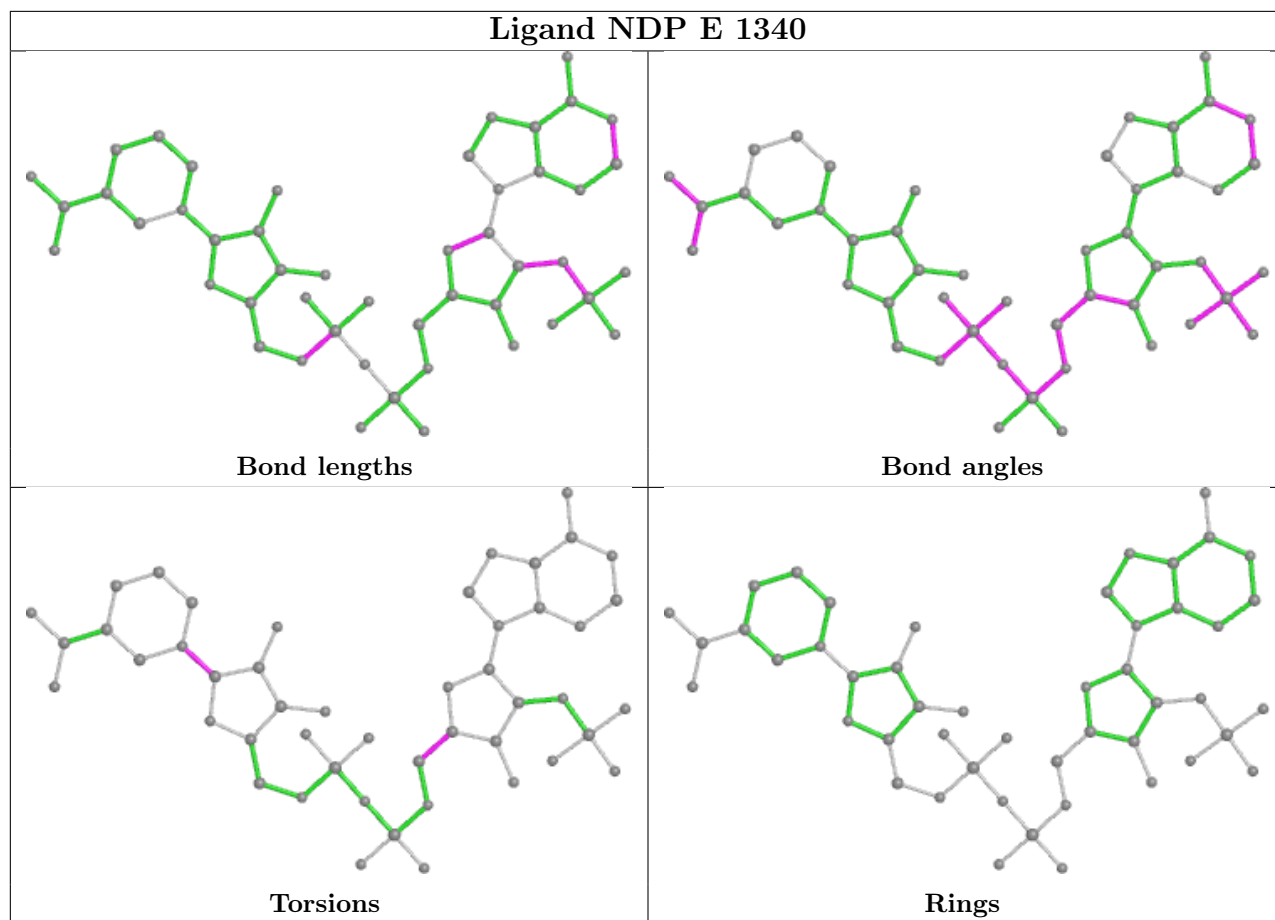
There are no ring outliers.

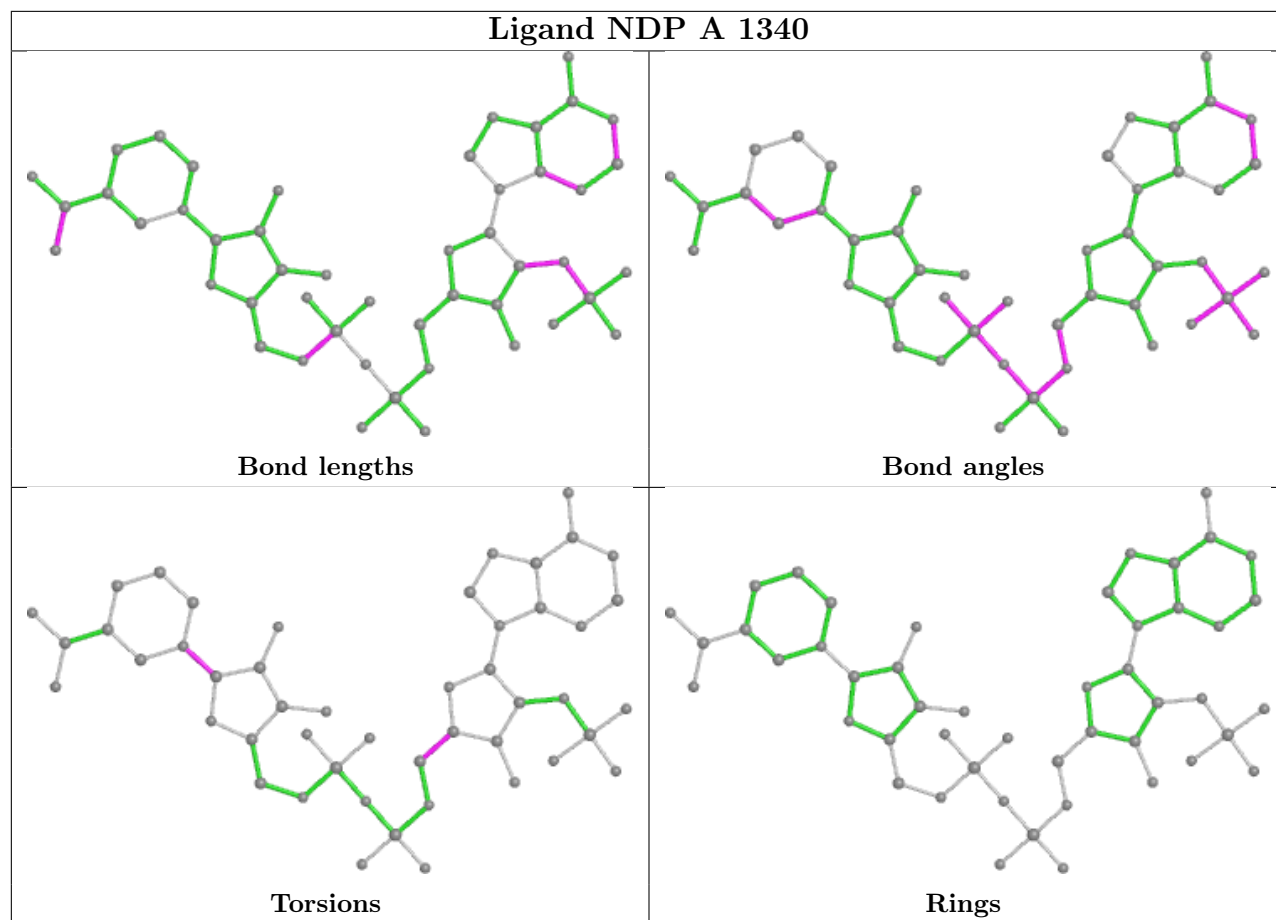
13 monomers are involved in 30 short contacts:

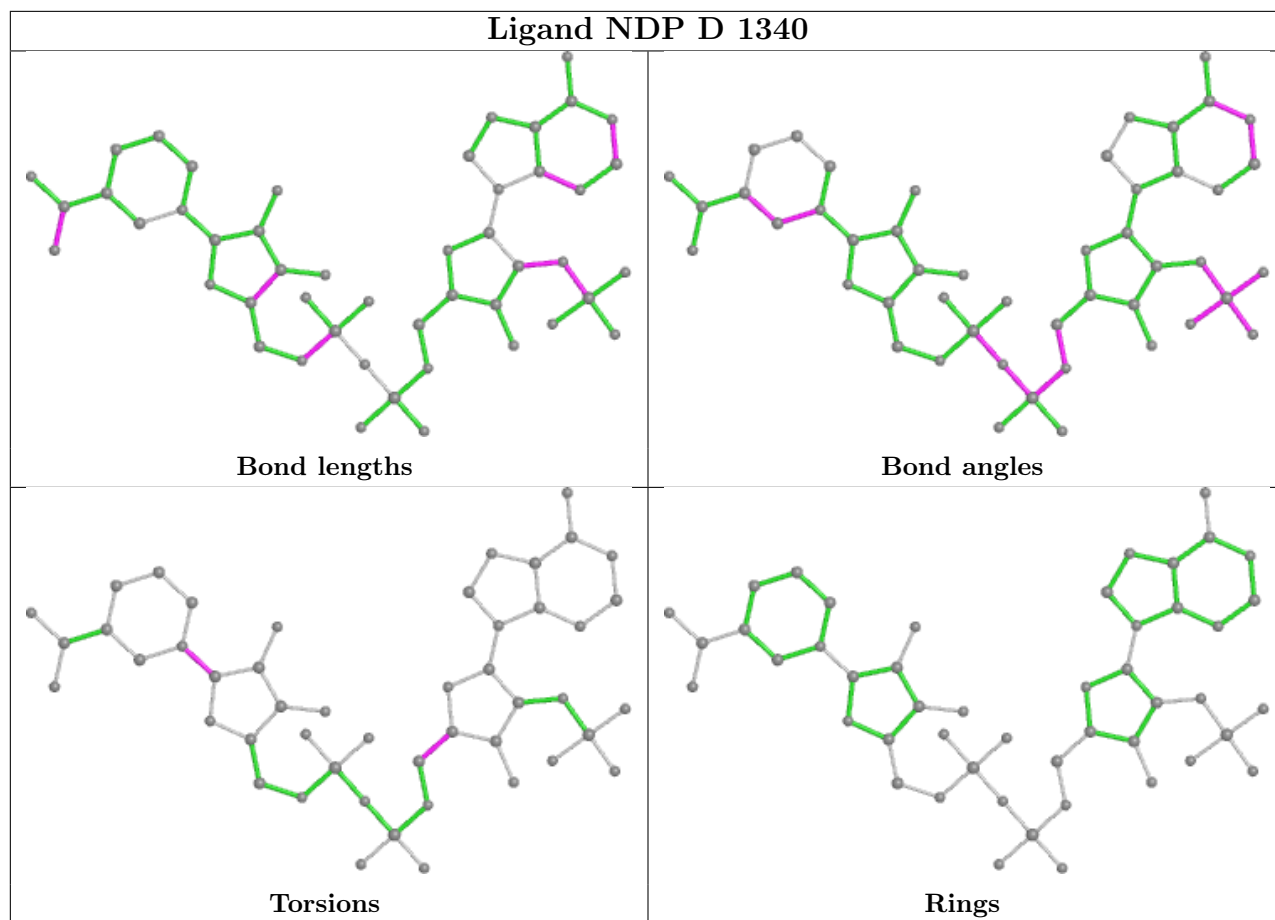
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	1342	XYP	1	0
2	B	1340	NDP	4	0
6	D	1343	DIO	1	0
2	E	1340	NDP	6	0
2	A	1340	NDP	4	0
3	A	1343	XYP	2	0
3	F	1341	XYP	1	0
3	B	1341	XYP	1	0
3	D	1341	XYP	1	0
3	E	1343	XYP	1	0
2	D	1340	NDP	4	0
2	C	1340	NDP	4	0
2	F	1340	NDP	4	0

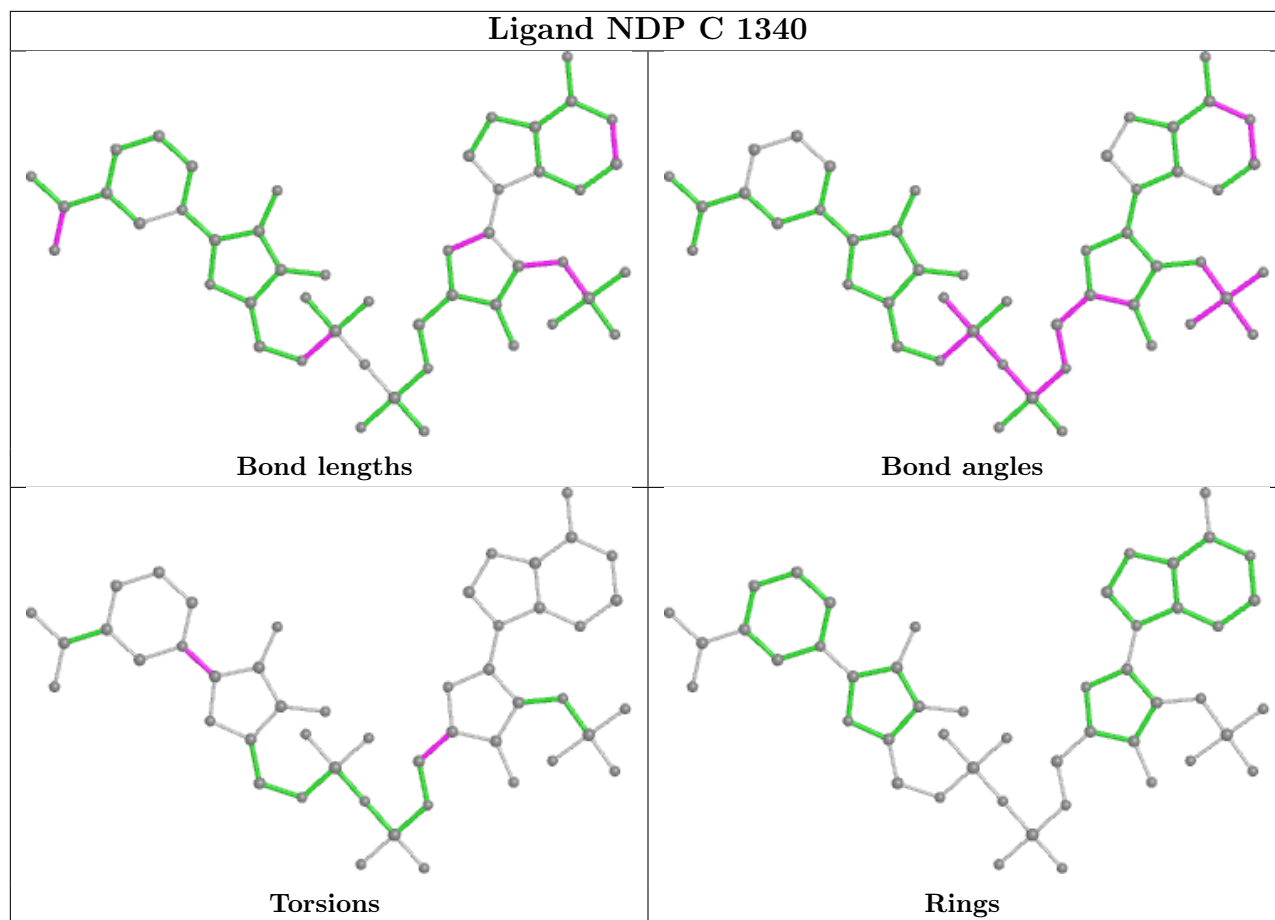
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

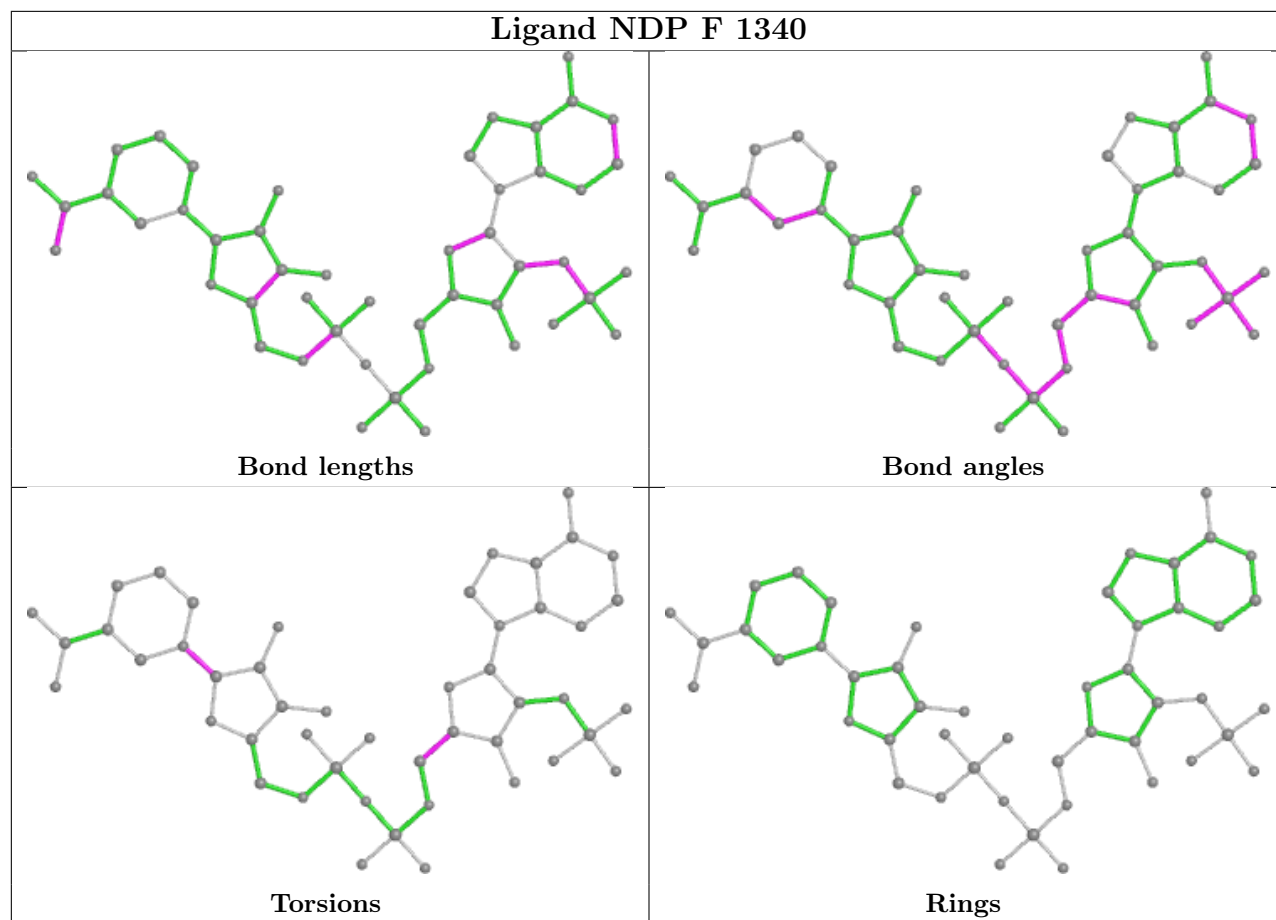












5.7 Other polymers [i](#)

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	335/339 (98%)	-0.34	2 (0%) 89 89	14, 19, 30, 50	0
1	B	335/339 (98%)	-0.16	2 (0%) 89 89	15, 23, 36, 53	0
1	C	336/339 (99%)	-0.16	6 (1%) 68 67	14, 22, 36, 53	0
1	D	335/339 (98%)	-0.17	10 (2%) 50 47	15, 22, 37, 52	0
1	E	335/339 (98%)	-0.06	5 (1%) 73 73	14, 21, 33, 46	0
1	F	335/339 (98%)	-0.14	3 (0%) 84 84	13, 20, 35, 52	0
All	All	2011/2034 (98%)	-0.17	28 (1%) 75 75	13, 21, 35, 53	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	5	ARG	5.1
1	C	4	GLY	5.1
1	A	5	ARG	4.5
1	D	5	ARG	4.2
1	D	43	GLU	3.5
1	D	50	GLU	3.5
1	D	277	GLY	3.1
1	D	49	GLY	2.9
1	F	56	GLU	2.9
1	E	57	THR	2.7
1	A	307	GLY	2.7
1	C	5	ARG	2.7
1	E	46	LYS	2.6
1	B	332	ARG	2.6
1	D	55	PRO	2.4
1	E	5	ARG	2.3
1	C	47	THR	2.3
1	D	57	THR	2.3
1	E	50	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	214	SER	2.2
1	F	308	ARG	2.2
1	C	72	PRO	2.1
1	C	335	ARG	2.1
1	E	277	GLY	2.1
1	D	46	LYS	2.1
1	D	305	LEU	2.1
1	D	71	ASN	2.1
1	B	213	ARG	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 monosaccharides 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	XYP	A	1343	10/10	0.71	0.32	37,43,48,51	0
3	XYP	E	1343	10/10	0.78	0.20	28,39,42,46	0
3	XYP	A	1344	10/10	0.79	0.19	29,36,42,43	0
4	SO4	E	1346	5/5	0.82	0.18	39,40,56,63	0
4	SO4	F	1342	5/5	0.82	0.22	45,48,54,62	0
3	XYP	C	1341	10/10	0.83	0.28	30,39,45,52	0
6	DIO	D	1343	6/6	0.83	0.27	36,38,42,44	0
3	XYP	D	1342	10/10	0.85	0.25	36,41,47,49	0
5	XYS	E	1344	10/10	0.86	0.10	21,29,34,34	0
3	XYP	F	1341	10/10	0.86	0.13	24,28,32,40	0
3	XYP	B	1341	10/10	0.88	0.11	29,33,36,38	0
3	XYP	E	1341	10/10	0.88	0.23	37,43,50,51	0
4	SO4	E	1347	5/5	0.89	0.34	56,57,69,71	0
3	XYP	D	1341	10/10	0.90	0.12	23,25,30,30	0

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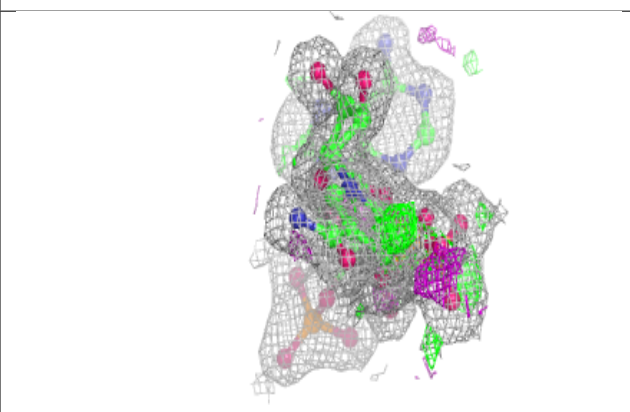
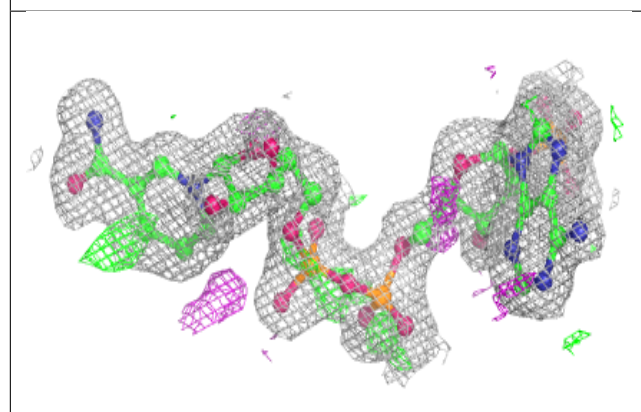
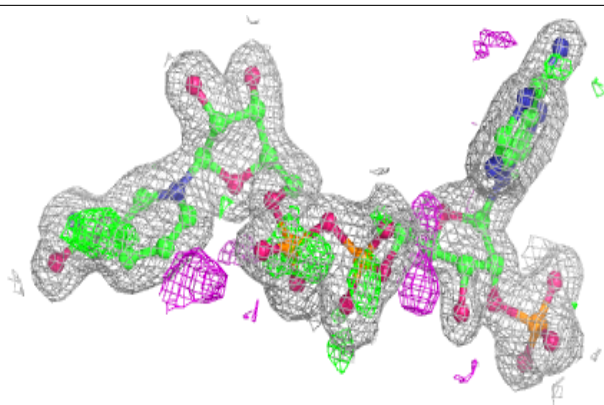
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	DIO	D	1344	6/6	0.91	0.25	48,50,54,60	0
3	XYP	A	1342	10/10	0.93	0.10	22,25,32,34	0
3	XYP	A	1341	10/10	0.93	0.10	20,22,29,30	0
4	SO4	D	1346	5/5	0.93	0.21	50,61,64,69	0
3	XYP	C	1342	10/10	0.94	0.08	22,25,30,33	0
2	NDP	E	1340	48/48	0.94	0.11	18,24,29,33	0
3	XYP	E	1342	10/10	0.94	0.09	19,23,29,30	0
5	XYS	B	1342	10/10	0.95	0.06	27,30,32,34	0
2	NDP	B	1340	48/48	0.96	0.09	19,23,27,28	0
2	NDP	C	1340	48/48	0.96	0.10	18,24,26,27	0
2	NDP	D	1340	48/48	0.96	0.09	20,26,30,33	0
4	SO4	A	1345	5/5	0.96	0.15	25,33,42,46	0
2	NDP	A	1340	48/48	0.96	0.10	16,20,24,26	0
2	NDP	F	1340	48/48	0.96	0.09	19,24,27,29	0
4	SO4	A	1346	5/5	0.97	0.20	37,42,49,50	0
4	SO4	D	1345	5/5	0.97	0.06	33,39,45,45	0
4	SO4	E	1345	5/5	0.98	0.08	31,35,40,43	0
4	SO4	C	1343	5/5	0.98	0.18	32,41,42,43	0

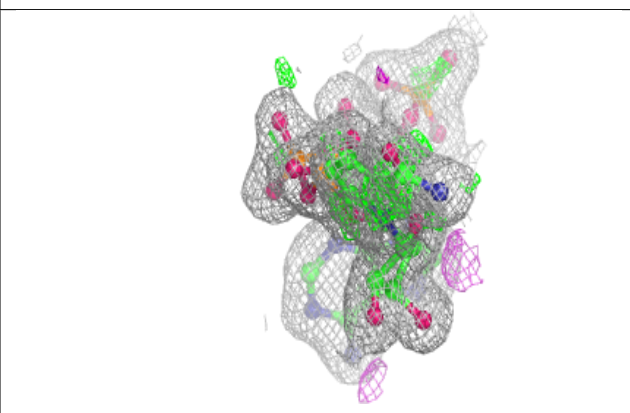
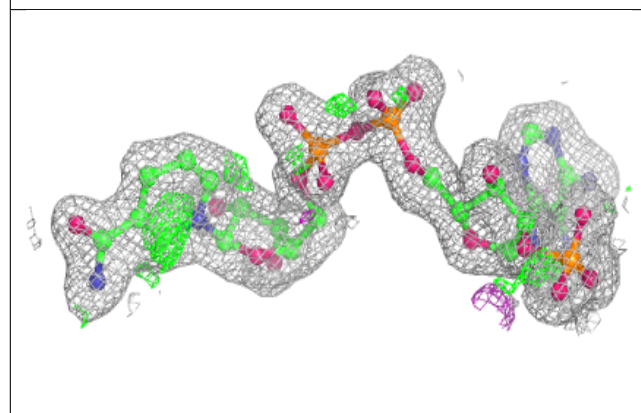
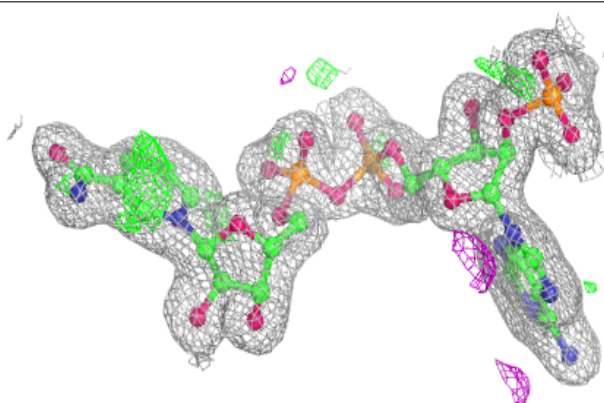
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NDP E 1340:

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

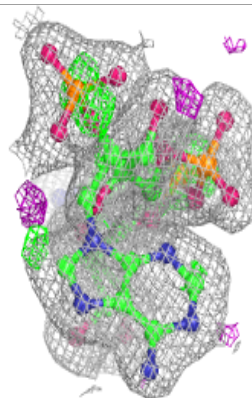
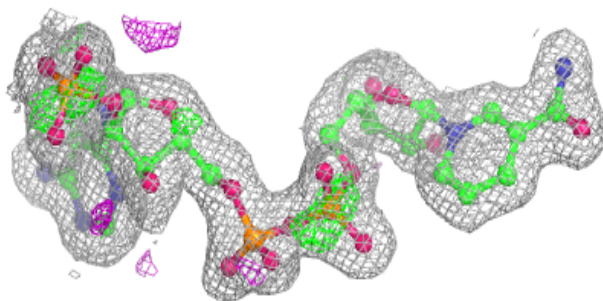
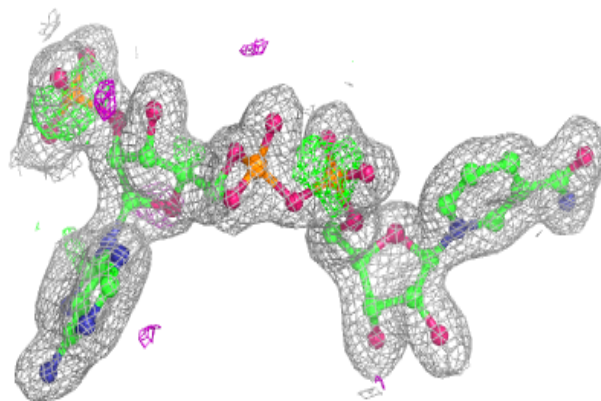
**Electron density around NDP B 1340:**

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

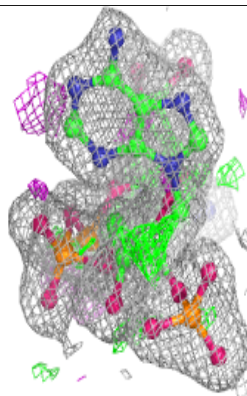
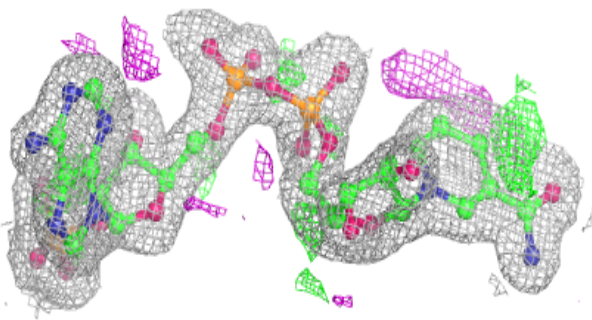
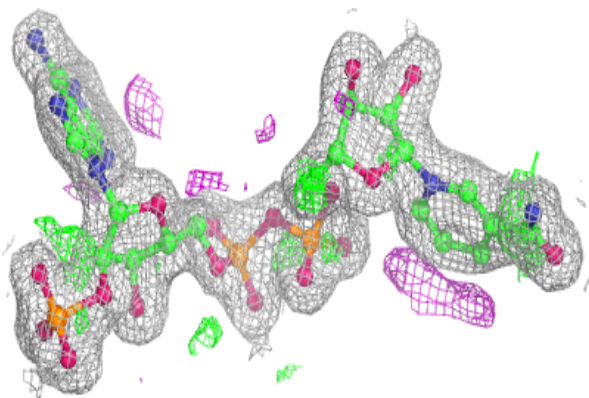


Electron density around NDP C 1340:

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

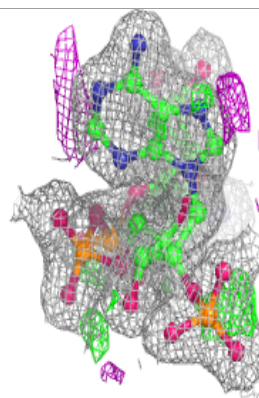
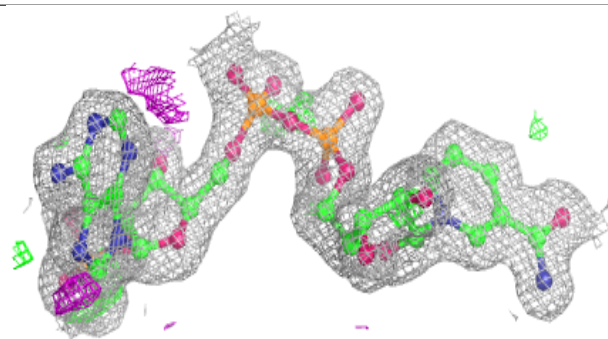
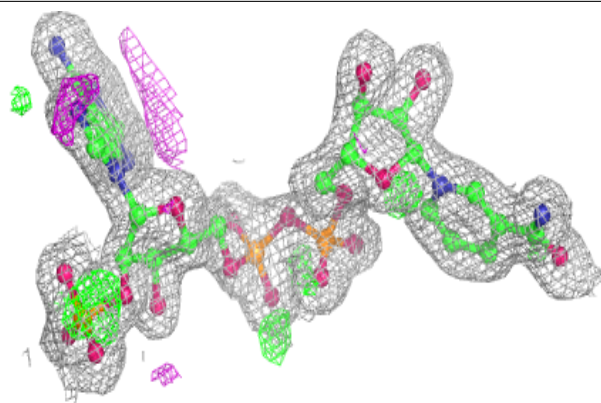
**Electron density around NDP D 1340:**

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

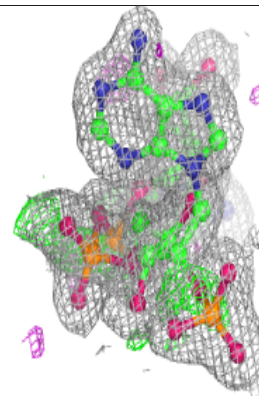
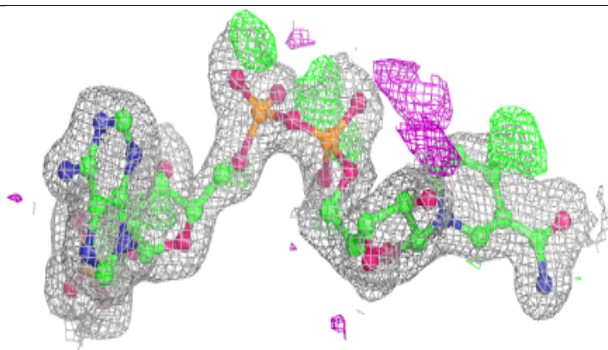
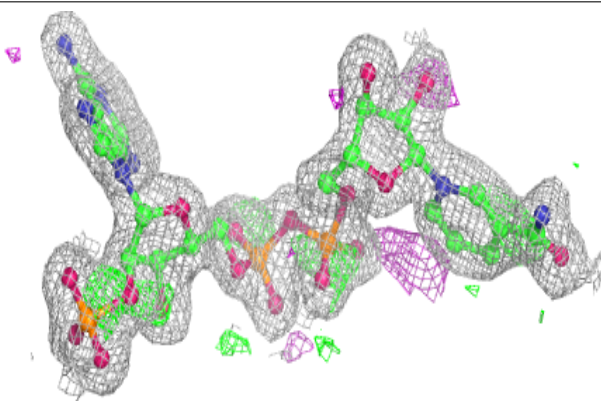


Electron density around NDP A 1340:

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

**Electron density around NDP F 1340:**

$2mF_o-DF_c$ (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.