



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 01:03 pm BST

PDB ID : 1XKQ  
Title : Crystal Structure of Short-Chain Dehydrogenase/Reductase of unknown Function from *Caenorhabditis Elegans* with Cofactor  
Authors : Schormann, N.; Zhou, J.; Karpova, E.; Zhang, Y.; Symersky, J.; Bunzel, B.; Huang, W.-Y.; Arabshahi, A.; Qiu, S.; Luan, C.-H.; Gray, R.; Carson, M.; Tsao, J.; Luo, M.; Johnson, D.; Lu, S.; Lin, G.; Luo, D.; Cao, Z.; Li, S.; McKinstry, A.; Shang, Q.; Chen, Y.-J.; Bray, T.; Nagy, L.; DeLucas, L.; Southeast Collaboratory for Structural Genomics (SECSG)  
Deposited on : 2004-09-29  
Resolution : 2.10 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

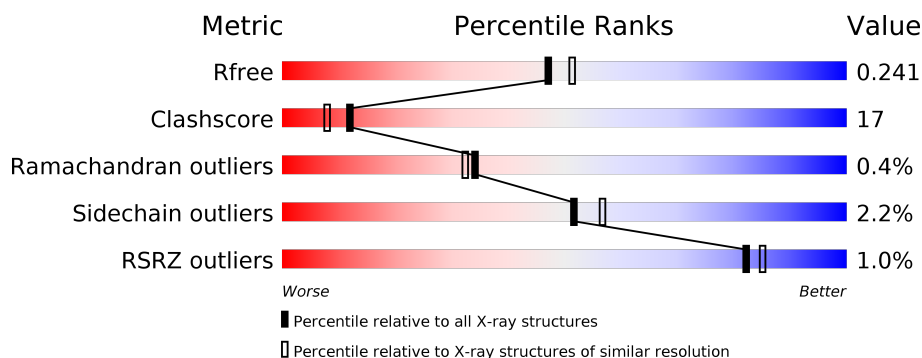
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	280	<div> <div>70%</div> <div>26%</div> <div>..</div> </div>
1	B	280	<div> <div>%</div> <div>71%</div> <div>24%</div> <div>..</div> </div>
1	C	280	<div> <div>2%</div> <div>68%</div> <div>28%</div> <div>..</div> </div>
1	D	280	<div> <div>%</div> <div>73%</div> <div>23%</div> <div>..</div> </div>

2 Entry composition ⓘ

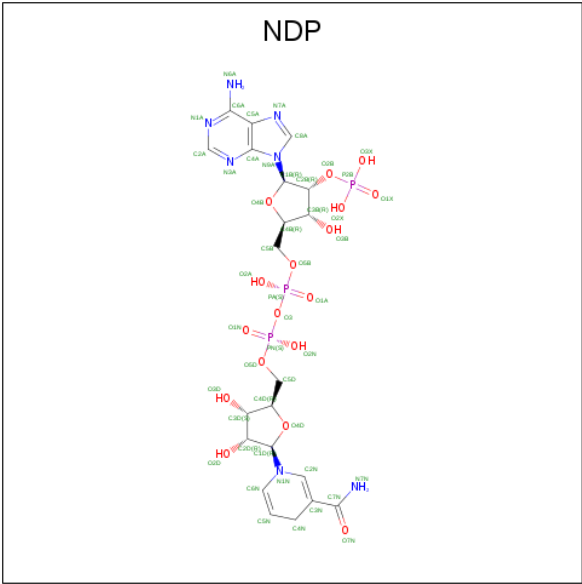
There are 3 unique types of molecules in this entry. The entry contains 8955 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 short-chain reductase family member (5D234).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	272	Total	C	N	O	S	0	0	0
			2039	1283	351	398	7			
1	B	271	Total	C	N	O	S	0	0	0
			2032	1278	350	397	7			
1	C	271	Total	C	N	O	S	0	0	0
			2032	1278	350	397	7			
1	D	271	Total	C	N	O	S	0	0	0
			2032	1278	350	397	7			

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C<sub>21</sub>H<sub>30</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



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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		

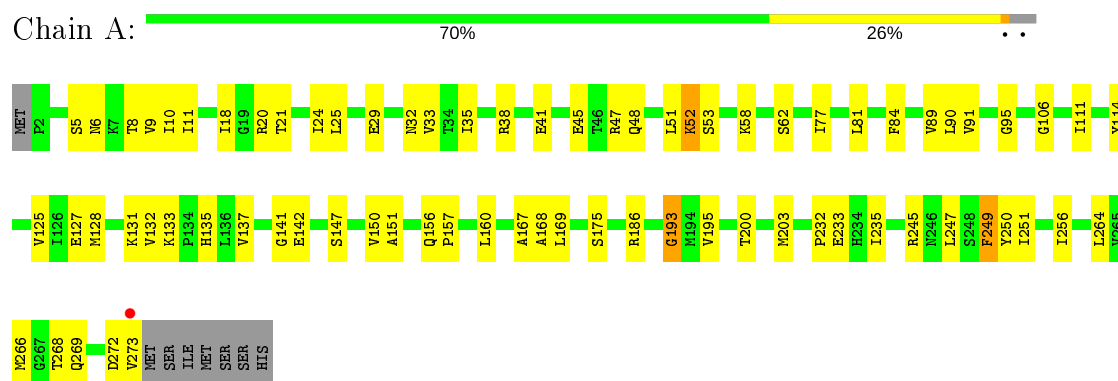
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	161	Total	O	0	0
			161	161		
3	B	167	Total	O	0	0
			167	167		
3	C	131	Total	O	0	0
			131	131		
3	D	169	Total	O	0	0
			169	169		

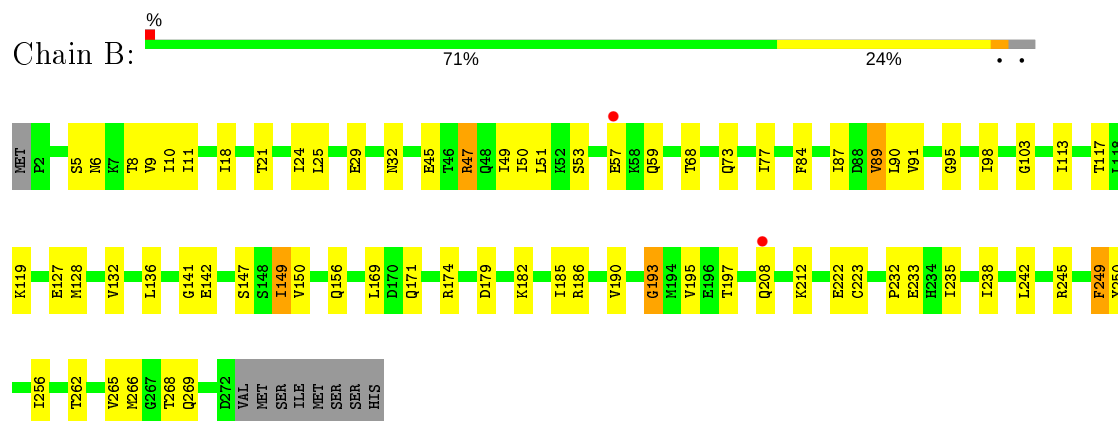
### 3 Residue-property plots [i](#)

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

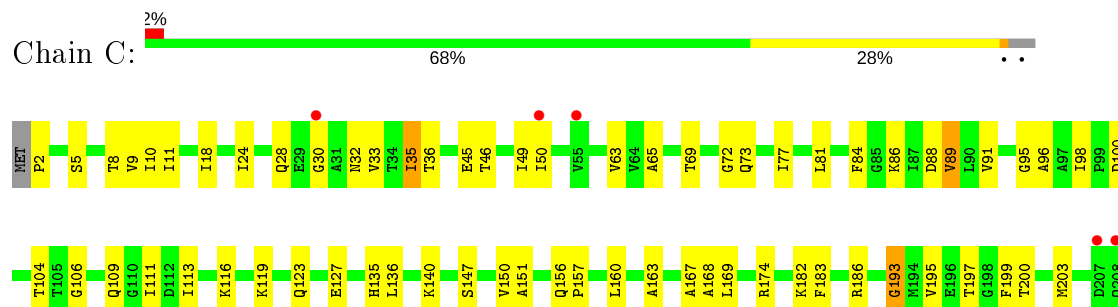
- Molecule 1: short-chain reductase family member (5D234)



- Molecule 1: short-chain reductase family member (5D234)

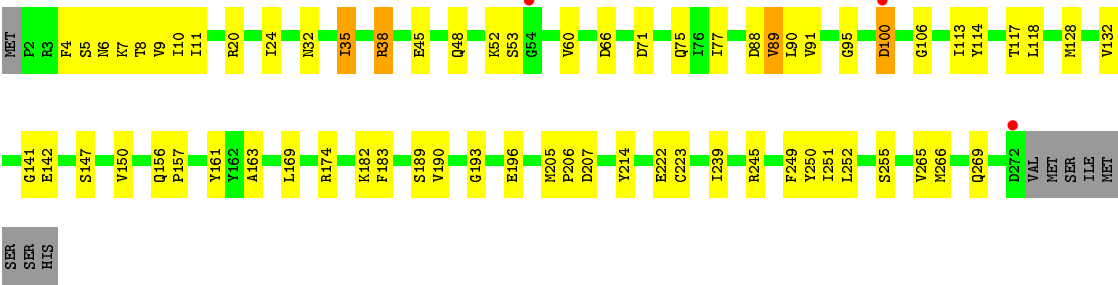


- Molecule 1: short-chain reductase family member (5D234)





- Molecule 1: short-chain reductase family member (5D234)



SER  
SER  
HIS

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	119.69Å 119.69Å 193.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.01 – 2.10 45.67 – 2.04	Depositor EDS
% Data completeness (in resolution range)	95.4 (34.01-2.10) 95.0 (45.67-2.04)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	9.42 (at 2.05Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.216 , 0.245 0.212 , 0.241	Depositor DCC
$R_{free}$ test set	4389 reflections (4.62%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.9	Xtriage
Anisotropy	0.378	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 43.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.076 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	8955	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.62% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.34	0/2069	0.61	1/2801 (0.0%)
1	B	0.33	0/2062	0.60	1/2791 (0.0%)
1	C	0.31	0/2062	0.57	1/2791 (0.0%)
1	D	0.34	0/2062	0.61	0/2791
All	All	0.33	0/8255	0.60	3/11174 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	193	GLY	N-CA-C	-5.70	98.86	113.10
1	B	193	GLY	N-CA-C	-5.58	99.14	113.10
1	A	193	GLY	N-CA-C	-5.47	99.43	113.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2039	0	2064	72	0
1	B	2032	0	2055	73	0
1	C	2032	0	2055	83	0
1	D	2032	0	2055	69	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	48	0	26	7	0
2	B	48	0	26	5	0
2	C	48	0	26	6	0
2	D	48	0	26	6	0
3	A	161	0	0	6	0
3	B	167	0	0	3	0
3	C	131	0	0	6	0
3	D	169	0	0	5	0
All	All	8955	0	8333	286	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 17.

All (286) 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:D:150:VAL:HG13	1:D:156:GLN:HG3	1.46	0.98
1:C:150:VAL:HG13	1:C:156:GLN:HG3	1.48	0.94
1:B:113:ILE:O	1:B:117:THR:HG23	1.68	0.90
1:C:35:ILE:HD13	1:C:35:ILE:H	1.33	0.90
1:B:235:ILE:O	1:B:238:ILE:HG22	1.70	0.90
1:A:11:ILE:HA	1:A:91:VAL:HG13	1.55	0.88
1:D:117:THR:HG21	1:D:161:TYR:HB3	1.56	0.87
1:A:150:VAL:HG13	1:A:156:GLN:HG3	1.58	0.86
1:D:35:ILE:HD13	1:D:35:ILE:H	1.43	0.84
1:B:136:LEU:O	1:B:185:ILE:HD11	1.79	0.83
1:C:69:THR:O	1:C:73:GLN:HG2	1.79	0.82
1:D:11:ILE:HA	1:D:91:VAL:CG1	2.11	0.80
1:B:11:ILE:HA	1:B:91:VAL:CG1	2.13	0.78
1:C:5:SER:HA	1:C:30:GLY:O	1.84	0.78
1:C:195:VAL:HG13	1:C:197:THR:HG23	1.66	0.76
1:A:21:THR:HG21	1:A:232:PRO:HB2	1.69	0.74
1:C:11:ILE:HA	1:C:91:VAL:HG13	1.68	0.74
1:A:11:ILE:HA	1:A:91:VAL:CG1	2.16	0.74
1:B:190:VAL:HG21	1:B:238:ILE:HG21	1.69	0.73
1:C:9:VAL:HG22	1:C:89:VAL:HG13	1.70	0.73
1:C:18:ILE:HD11	1:C:195:VAL:HG11	1.69	0.72
1:C:11:ILE:HA	1:C:91:VAL:CG1	2.20	0.72
1:D:117:THR:HG23	1:D:118:LEU:HD12	1.72	0.71
1:D:117:THR:HG21	1:D:161:TYR:CB	2.21	0.71
1:B:195:VAL:HG13	1:B:197:THR:HG23	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:GLY:HA2	1:A:157:PRO:O	1.90	0.70
1:C:9:VAL:HG22	1:C:89:VAL:CG1	2.22	0.69
1:B:9:VAL:HG22	1:B:89:VAL:CG1	2.23	0.68
1:C:224:ILE:HG22	1:C:226:ILE:HG22	1.73	0.68
1:B:266:MET:H	1:B:269:GLN:NE2	1.92	0.68
1:B:150:VAL:HG13	1:B:156:GLN:HG3	1.74	0.68
1:A:251:ILE:HD11	1:B:238:ILE:HD13	1.74	0.68
1:C:8:THR:HG21	1:C:84:PHE:HB3	1.76	0.67
1:D:35:ILE:HD13	1:D:35:ILE:N	2.11	0.66
1:B:11:ILE:HG23	1:B:91:VAL:HG11	1.77	0.66
1:B:45:GLU:O	1:B:49:ILE:HG12	1.95	0.66
1:D:38:ARG:HB2	1:D:38:ARG:HH11	1.61	0.65
1:A:235:ILE:N	1:A:235:ILE:HD12	2.12	0.65
1:A:41:GLU:HG2	3:A:1375:HOH:O	1.97	0.64
1:D:71:ASP:O	1:D:75:GLN:HG2	1.98	0.64
1:A:47:ARG:NH1	1:A:51:LEU:HD11	2.12	0.64
1:C:266:MET:HB3	1:C:269:GLN:HG3	1.78	0.64
1:A:200:THR:HA	1:A:203:MET:HE2	1.79	0.64
1:C:86:LYS:HE2	1:C:88:ASP:OD2	1.98	0.64
1:C:109:GLN:HB3	1:C:113:ILE:HD12	1.79	0.63
1:B:21:THR:HG21	1:B:232:PRO:HB2	1.78	0.63
1:A:235:ILE:H	1:A:235:ILE:HD12	1.62	0.63
1:D:150:VAL:HG13	1:D:156:GLN:CG	2.26	0.63
1:A:128:MET:O	1:A:132:VAL:HG13	2.00	0.61
1:D:266:MET:H	1:D:269:GLN:NE2	1.98	0.61
1:B:147:SER:O	2:B:2281:NDP:H6N	2.00	0.61
1:D:11:ILE:HG23	1:D:91:VAL:HG11	1.81	0.61
1:A:18:ILE:CD1	1:A:232:PRO:HA	2.30	0.61
1:B:91:VAL:O	1:B:91:VAL:HG13	2.01	0.61
1:D:9:VAL:HG13	1:D:89:VAL:HG22	1.80	0.61
1:C:182:LYS:HD2	1:C:183:PHE:CZ	2.36	0.61
1:D:38:ARG:HD2	1:D:66:ASP:HA	1.82	0.61
1:B:233:GLU:CD	1:B:233:GLU:H	2.03	0.61
1:A:233:GLU:H	1:A:233:GLU:CD	2.04	0.60
1:D:11:ILE:HA	1:D:91:VAL:HG13	1.82	0.60
1:A:18:ILE:HD13	1:A:232:PRO:HA	1.83	0.60
1:B:195:VAL:HG12	2:B:2281:NDP:C7N	2.32	0.60
1:D:265:VAL:HG13	3:D:4330:HOH:O	2.01	0.60
1:B:149:ILE:HD12	1:B:193:GLY:HA2	1.84	0.59
1:D:8:THR:HG22	1:D:32:ASN:HB2	1.83	0.59
1:A:11:ILE:HG13	1:A:91:VAL:HG11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:VAL:HG22	1:B:89:VAL:HG13	1.83	0.59
1:A:193:GLY:O	2:A:1281:NDP:H42N	2.02	0.59
1:A:266:MET:H	1:A:269:GLN:NE2	2.00	0.59
1:C:100:ASP:OD1	1:C:113:ILE:HD11	2.03	0.59
1:D:9:VAL:HG22	1:D:89:VAL:HG13	1.85	0.58
1:C:238:ILE:HD13	1:D:251:ILE:HD11	1.85	0.58
1:A:175:SER:HB3	1:C:160:LEU:HD22	1.86	0.58
1:C:8:THR:HG22	1:C:32:ASN:HB2	1.85	0.58
1:A:141:GLY:C	1:A:142:GLU:HG3	2.23	0.58
1:A:90:LEU:HD22	1:A:132:VAL:HG11	1.84	0.58
1:A:200:THR:HA	1:A:203:MET:CE	2.32	0.58
1:C:35:ILE:HD13	1:C:35:ILE:N	2.14	0.58
1:C:11:ILE:HD13	1:C:33:VAL:HG13	1.85	0.58
1:C:150:VAL:HG13	1:C:156:GLN:CG	2.30	0.57
1:C:106:GLY:HA2	1:C:157:PRO:O	2.05	0.57
1:D:128:MET:O	1:D:132:VAL:HG22	2.04	0.57
1:B:10:ILE:O	1:B:91:VAL:HG12	2.04	0.57
1:D:10:ILE:O	1:D:91:VAL:HG12	2.05	0.57
1:A:41:GLU:O	1:A:45:GLU:HG3	2.05	0.57
1:C:73:GLN:OE1	1:C:127:GLU:HB3	2.05	0.56
1:D:11:ILE:HD13	1:D:91:VAL:CG1	2.35	0.56
1:B:32:ASN:HD22	1:B:59:GLN:HG3	1.71	0.56
1:B:90:LEU:HD22	1:B:132:VAL:HG11	1.87	0.56
1:B:24:ILE:HD13	1:B:49:ILE:HG21	1.87	0.56
1:C:96:ALA:HA	1:C:199:PHE:CE1	2.41	0.56
1:C:156:GLN:O	1:C:160:LEU:HD23	2.05	0.56
1:A:10:ILE:O	1:A:91:VAL:HG12	2.06	0.55
1:B:11:ILE:HA	1:B:91:VAL:HG13	1.87	0.55
1:D:38:ARG:NH1	1:D:38:ARG:HB2	2.20	0.55
1:B:11:ILE:HA	1:B:91:VAL:HG12	1.87	0.55
1:A:11:ILE:CD1	1:A:33:VAL:HG13	2.37	0.54
1:C:169:LEU:HD23	1:C:169:LEU:O	2.08	0.54
1:D:91:VAL:O	1:D:91:VAL:HG13	2.06	0.54
1:B:222:GLU:O	1:B:265:VAL:HG11	2.07	0.54
1:A:8:THR:HG22	1:A:32:ASN:HB2	1.89	0.54
1:B:32:ASN:ND2	1:B:59:GLN:HG3	2.23	0.54
1:A:11:ILE:HD13	1:A:33:VAL:HG13	1.90	0.53
1:A:125:VAL:HG11	1:A:169:LEU:HD21	1.89	0.53
1:D:11:ILE:HA	1:D:91:VAL:HG12	1.88	0.53
1:C:200:THR:HA	1:C:203:MET:CE	2.39	0.53
1:C:195:VAL:HG13	1:C:197:THR:CG2	2.36	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:ILE:HD13	1:D:252:LEU:HD12	1.90	0.53
1:C:238:ILE:CD1	1:D:251:ILE:HD11	2.38	0.53
1:D:106:GLY:HA2	1:D:157:PRO:O	2.09	0.52
1:C:24:ILE:HA	1:C:50:ILE:CD1	2.39	0.52
1:C:35:ILE:H	1:C:35:ILE:CD1	2.13	0.52
1:C:81:LEU:HD12	3:C:3389:HOH:O	2.09	0.52
1:C:258:ALA:HB2	1:D:251:ILE:CD1	2.38	0.52
1:B:223:CYS:HA	1:C:268:THR:HG22	1.91	0.52
1:C:195:VAL:HG12	2:C:3281:NDP:C7N	2.39	0.52
1:D:193:GLY:O	2:D:4281:NDP:H42N	2.09	0.52
1:A:51:LEU:C	1:A:53:SER:H	2.13	0.52
1:A:150:VAL:HG13	1:A:156:GLN:CG	2.36	0.52
1:B:268:THR:HG23	3:C:3288:HOH:O	2.10	0.52
1:A:21:THR:HG23	3:A:1318:HOH:O	2.10	0.52
1:B:136:LEU:HB3	1:B:185:ILE:HD12	1.92	0.52
1:C:95:GLY:CA	2:C:3281:NDP:H3D	2.40	0.52
1:B:25:LEU:O	1:B:29:GLU:HG2	2.10	0.51
1:C:24:ILE:O	1:C:28:GLN:HG3	2.10	0.51
1:A:127:GLU:HG2	1:C:111:ILE:HD11	1.92	0.51
1:C:157:PRO:HA	1:C:160:LEU:HD21	1.92	0.51
1:D:48:GLN:O	1:D:52:LYS:HG3	2.10	0.51
2:D:4281:NDP:O1N	2:D:4281:NDP:H2N	2.11	0.51
1:B:150:VAL:HG13	1:B:156:GLN:CG	2.39	0.51
1:C:169:LEU:HD23	1:C:169:LEU:C	2.31	0.51
1:C:245:ARG:O	1:C:249:PHE:HB2	2.11	0.50
1:B:50:ILE:O	1:B:53:SER:HB3	2.09	0.50
1:D:174:ARG:NH2	3:D:4307:HOH:O	2.42	0.50
1:D:90:LEU:HD22	1:D:132:VAL:HG21	1.93	0.50
1:B:149:ILE:HD13	1:B:149:ILE:N	2.27	0.50
1:B:149:ILE:H	1:B:149:ILE:HD13	1.76	0.50
1:A:18:ILE:HD11	1:A:195:VAL:HG21	1.94	0.50
1:B:245:ARG:O	1:B:249:PHE:HB2	2.12	0.50
1:D:95:GLY:HA3	2:D:4281:NDP:H3D	1.93	0.50
1:A:256:ILE:HG12	1:B:256:ILE:HD12	1.93	0.50
1:C:151:ALA:HB1	1:C:167:ALA:HA	1.94	0.50
1:A:25:LEU:O	1:A:29:GLU:HG2	2.12	0.50
1:B:11:ILE:HD13	1:B:91:VAL:CG1	2.42	0.49
3:B:2330:HOH:O	1:C:268:THR:HG23	2.12	0.49
1:D:11:ILE:HD13	1:D:91:VAL:HG11	1.92	0.49
1:D:113:ILE:O	1:D:117:THR:HG22	2.12	0.49
1:A:133:LYS:O	1:A:137:VAL:HG23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LYS:HB2	1:A:52:LYS:NZ	2.27	0.49
1:B:9:VAL:HG13	1:B:89:VAL:HG13	1.92	0.49
1:D:222:GLU:O	1:D:265:VAL:HG11	2.12	0.49
1:A:268:THR:HG22	1:D:223:CYS:HA	1.94	0.49
1:B:179:ASP:O	1:B:182:LYS:HG2	2.13	0.49
1:B:186:ARG:NH2	1:B:242:LEU:O	2.45	0.49
1:D:114:TYR:O	1:D:117:THR:HG22	2.12	0.49
1:D:150:VAL:CG1	1:D:156:GLN:HG3	2.28	0.48
1:A:11:ILE:HG13	1:A:91:VAL:CG1	2.43	0.48
1:C:10:ILE:O	1:C:91:VAL:HG12	2.13	0.48
1:D:95:GLY:CA	2:D:4281:NDP:H3D	2.43	0.48
1:C:197:THR:HG22	1:C:232:PRO:HG3	1.96	0.48
1:B:8:THR:HG21	1:B:84:PHE:HB3	1.95	0.48
1:C:95:GLY:HA3	2:C:3281:NDP:H3D	1.96	0.48
2:A:1281:NDP:O1N	2:A:1281:NDP:H2N	2.14	0.48
1:B:136:LEU:C	1:B:185:ILE:HD11	2.33	0.48
1:C:77:ILE:HG22	3:C:3389:HOH:O	2.14	0.47
1:A:195:VAL:HG12	2:A:1281:NDP:C7N	2.44	0.47
1:B:103:GLY:HA2	3:B:2424:HOH:O	2.14	0.47
1:B:77:ILE:HD12	1:B:132:VAL:HG12	1.95	0.47
1:C:186:ARG:NH2	1:C:242:LEU:O	2.47	0.47
1:D:196:GLU:HG2	1:D:214:TYR:CE1	2.49	0.47
1:A:9:VAL:HG22	1:A:89:VAL:HB	1.96	0.47
1:D:77:ILE:HD12	1:D:132:VAL:HG12	1.95	0.47
1:B:179:ASP:O	1:B:182:LYS:HE2	2.14	0.47
1:C:224:ILE:CG2	1:C:226:ILE:HG22	2.43	0.47
1:C:147:SER:O	2:C:3281:NDP:H6N	2.15	0.47
1:A:111:ILE:O	1:A:114:TYR:HB3	2.14	0.47
1:B:262:THR:O	1:B:265:VAL:HG12	2.14	0.47
1:C:11:ILE:HD12	1:C:11:ILE:N	2.30	0.47
1:C:96:ALA:HA	1:C:199:PHE:HE1	1.79	0.47
1:B:11:ILE:CD1	1:B:91:VAL:HG11	2.45	0.47
1:C:150:VAL:HG12	1:C:163:ALA:HA	1.97	0.47
1:B:128:MET:O	1:B:132:VAL:HG13	2.14	0.47
1:D:265:VAL:CG1	3:D:4330:HOH:O	2.62	0.47
1:A:5:SER:O	1:A:6:ASN:HB2	2.15	0.46
1:C:150:VAL:HG12	1:C:150:VAL:O	2.15	0.46
1:D:150:VAL:HG12	1:D:163:ALA:HA	1.96	0.46
1:A:147:SER:O	2:A:1281:NDP:H6N	2.15	0.46
1:A:77:ILE:HG12	1:A:132:VAL:HG12	1.97	0.46
1:D:196:GLU:HG2	1:D:214:TYR:CD1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:258:ALA:CB	1:D:251:ILE:HD13	2.45	0.46
1:D:11:ILE:CD1	1:D:91:VAL:HG11	2.45	0.46
1:B:11:ILE:HD13	1:B:91:VAL:HG12	1.97	0.46
1:C:231:LYS:HE3	3:C:3379:HOH:O	2.15	0.46
1:D:77:ILE:HD12	1:D:132:VAL:CG1	2.46	0.45
1:D:60:VAL:HG23	1:D:60:VAL:O	2.17	0.45
1:A:95:GLY:CA	2:A:1281:NDP:H3D	2.47	0.45
1:A:8:THR:HG21	1:A:84:PHE:HB3	1.97	0.45
1:B:193:GLY:O	2:B:2281:NDP:H42N	2.17	0.45
1:D:147:SER:O	2:D:4281:NDP:H6N	2.17	0.45
1:C:200:THR:HA	1:C:203:MET:HE2	1.99	0.45
1:C:11:ILE:CD1	1:C:33:VAL:HG13	2.47	0.45
1:B:8:THR:HG22	1:B:32:ASN:HB2	1.98	0.45
1:C:111:ILE:HG12	3:C:3336:HOH:O	2.16	0.45
1:B:150:VAL:CG1	1:B:156:GLN:HG3	2.44	0.45
1:C:81:LEU:HD11	1:C:135:HIS:CE1	2.52	0.45
1:A:77:ILE:HD13	1:A:131:LYS:HB3	1.99	0.44
1:A:20:ARG:O	1:A:24:ILE:HG13	2.18	0.44
1:A:11:ILE:HD13	1:A:33:VAL:CG1	2.46	0.44
1:A:168:ALA:HB2	1:C:168:ALA:HB2	1.99	0.44
1:A:233:GLU:N	1:A:233:GLU:CD	2.68	0.44
1:D:20:ARG:O	1:D:24:ILE:HG13	2.17	0.44
1:D:88:ASP:O	1:D:141:GLY:HA3	2.17	0.44
1:A:142:GLU:OE2	1:A:245:ARG:HB2	2.18	0.44
1:B:149:ILE:CD1	1:B:149:ILE:H	2.30	0.44
1:B:10:ILE:HD11	1:B:87:ILE:HD12	2.00	0.44
1:C:233:GLU:CD	1:C:233:GLU:H	2.21	0.44
1:D:11:ILE:HD13	1:D:91:VAL:HG12	1.99	0.44
1:B:11:ILE:HG23	1:B:91:VAL:CG1	2.46	0.44
1:A:256:ILE:HG23	1:B:256:ILE:HD11	2.00	0.43
1:A:272:ASP:OD1	1:A:273:VAL:N	2.51	0.43
1:B:171:GLN:HA	1:B:171:GLN:OE1	2.18	0.43
2:B:2281:NDP:H2N	2:B:2281:NDP:O1N	2.19	0.43
1:D:8:THR:HG23	3:D:4301:HOH:O	2.18	0.43
1:C:193:GLY:O	2:C:3281:NDP:H42N	2.18	0.43
1:D:141:GLY:O	1:D:142:GLU:HG3	2.19	0.43
1:A:142:GLU:HG2	1:A:186:ARG:HB2	2.00	0.43
1:D:38:ARG:NH1	2:D:4281:NDP:O3X	2.52	0.43
1:B:73:GLN:NE2	1:B:127:GLU:OE1	2.42	0.43
1:B:18:ILE:HD11	1:B:195:VAL:HG11	2.01	0.43
1:B:68:THR:O	1:B:119:LYS:NZ	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:95:GLY:CA	2:B:2281:NDP:H3D	2.49	0.43
1:C:100:ASP:HB3	1:C:104:THR:H	1.84	0.43
2:C:3281:NDP:H2N	2:C:3281:NDP:O1N	2.19	0.43
1:B:117:THR:HG21	3:B:2306:HOH:O	2.18	0.43
1:B:150:VAL:O	1:B:156:GLN:HG3	2.19	0.43
1:C:36:THR:HA	1:C:63:VAL:O	2.19	0.43
1:D:60:VAL:HG23	3:D:4430:HOH:O	2.18	0.43
1:C:98:ILE:CD1	1:C:116:LYS:HB3	2.49	0.42
1:A:38:ARG:HD3	2:A:1281:NDP:O3X	2.19	0.42
1:A:81:LEU:HD11	1:A:135:HIS:CE1	2.54	0.42
1:A:264:LEU:HD22	1:B:174:ARG:HD2	2.01	0.42
1:A:52:LYS:HB2	1:A:52:LYS:HZ2	1.83	0.42
1:C:119:LYS:HA	1:C:123:GLN:HB3	2.01	0.42
1:C:200:THR:HA	1:C:203:MET:HE3	2.01	0.42
1:C:45:GLU:O	1:C:49:ILE:HG13	2.20	0.42
1:C:136:LEU:O	1:C:140:LYS:N	2.52	0.42
1:C:2:PRO:HB2	1:C:5:SER:HB3	2.01	0.42
1:B:51:LEU:HD21	1:B:57:GLU:OE1	2.20	0.42
1:B:5:SER:O	1:B:6:ASN:HB2	2.20	0.42
1:D:117:THR:HG23	1:D:118:LEU:N	2.34	0.42
1:C:157:PRO:HA	1:C:160:LEU:CD2	2.50	0.42
1:C:174:ARG:NH2	3:C:3321:HOH:O	2.43	0.42
1:C:212:LYS:O	1:C:212:LYS:HD3	2.18	0.42
1:A:35:ILE:HG13	1:A:62:SER:HA	2.02	0.42
1:C:258:ALA:HB2	1:D:251:ILE:HD13	2.01	0.42
1:D:100:ASP:OD1	1:D:113:ILE:HG13	2.20	0.42
1:D:117:THR:HG23	1:D:118:LEU:CD1	2.48	0.42
1:C:193:GLY:HA3	1:C:259:ASP:CB	2.50	0.41
1:A:186:ARG:NH2	1:A:245:ARG:HA	2.35	0.41
1:A:95:GLY:HA3	2:A:1281:NDP:H3D	2.02	0.41
1:C:65:ALA:HB1	1:C:72:GLY:HA2	2.02	0.41
1:D:245:ARG:O	1:D:249:PHE:HB2	2.20	0.41
1:D:4:PHE:O	1:D:7:LYS:HB2	2.20	0.41
1:A:18:ILE:CD1	1:A:235:ILE:HD13	2.50	0.41
1:A:8:THR:HG23	3:A:1311:HOH:O	2.20	0.41
1:C:98:ILE:HD12	1:C:116:LYS:HB3	2.02	0.41
1:D:189:SER:O	1:D:255:SER:HA	2.21	0.41
1:D:205:MET:HA	1:D:206:PRO:HD3	1.95	0.41
1:C:46:THR:O	1:C:50:ILE:HG12	2.20	0.41
1:A:151:ALA:HB1	1:A:167:ALA:HA	2.03	0.41
1:B:208:GLN:O	1:B:212:LYS:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:190:VAL:HG11	1:D:239:ILE:HD11	2.01	0.41
1:A:169:LEU:HD13	3:A:1288:HOH:O	2.21	0.41
1:A:245:ARG:O	1:A:249:PHE:HB2	2.20	0.41
1:B:150:VAL:HG12	1:B:150:VAL:O	2.21	0.41
1:A:48:GLN:HG3	3:A:1369:HOH:O	2.21	0.41
1:A:160:LEU:HB2	3:A:1435:HOH:O	2.21	0.40
1:B:141:GLY:C	1:B:142:GLU:HG3	2.41	0.40
1:B:98:ILE:HB	1:B:117:THR:HG22	2.02	0.40
1:D:5:SER:O	1:D:6:ASN:HB2	2.22	0.40
1:A:48:GLN:HB3	1:A:52:LYS:HE3	2.03	0.40
1:C:24:ILE:HA	1:C:50:ILE:HD11	2.03	0.40
1:A:18:ILE:HD12	1:A:235:ILE:HD13	2.04	0.40
1:B:47:ARG:HD2	1:B:57:GLU:OE1	2.22	0.40
1:B:8:THR:HA	1:B:32:ASN:HB2	2.02	0.40
1:D:182:LYS:HD2	1:D:183:PHE:CZ	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	270/280 (96%)	260 (96%)	8 (3%)	2 (1%)	22	18
1	B	269/280 (96%)	260 (97%)	8 (3%)	1 (0%)	34	32
1	C	269/280 (96%)	260 (97%)	9 (3%)	0	100	100
1	D	269/280 (96%)	259 (96%)	9 (3%)	1 (0%)	34	32
All	All	1077/1120 (96%)	1039 (96%)	34 (3%)	4 (0%)	34	32

All (4) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	52	LYS
1	A	249	PHE
1	B	249	PHE
1	D	53	SER

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	221/229 (96%)	218 (99%)	3 (1%)	67	73
1	B	220/229 (96%)	215 (98%)	5 (2%)	50	55
1	C	220/229 (96%)	217 (99%)	3 (1%)	67	73
1	D	220/229 (96%)	212 (96%)	8 (4%)	35	36
All	All	881/916 (96%)	862 (98%)	19 (2%)	52	57

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

Mol	Chain	Res	Type
1	A	58	LYS
1	A	247	LEU
1	A	250	TYR
1	B	47	ARG
1	B	89	VAL
1	B	149	ILE
1	B	169	LEU
1	B	250	TYR
1	C	35	ILE
1	C	89	VAL
1	C	250	TYR
1	D	35	ILE
1	D	38	ARG
1	D	45	GLU
1	D	89	VAL
1	D	100	ASP
1	D	169	LEU
1	D	207	ASP

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Mol	Chain	Res	Type
1	D	250	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	28	GLN
1	A	32	ASN
1	A	78	ASN
1	A	123	GLN
1	A	156	GLN
1	A	208	GLN
1	A	237	ASN
1	A	269	GLN
1	B	28	GLN
1	B	32	ASN
1	B	48	GLN
1	B	78	ASN
1	B	115	HIS
1	B	123	GLN
1	B	156	GLN
1	B	208	GLN
1	B	211	GLN
1	B	237	ASN
1	B	269	GLN
1	C	28	GLN
1	C	32	ASN
1	C	78	ASN
1	C	123	GLN
1	C	156	GLN
1	C	208	GLN
1	C	211	GLN
1	C	237	ASN
1	D	75	GLN
1	D	78	ASN
1	D	83	GLN
1	D	123	GLN
1	D	156	GLN
1	D	208	GLN
1	D	237	ASN
1	D	246	ASN
1	D	269	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

4 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	1281	-	45,52,52	1.96	15 (33%)	53,80,80	2.52	17 (32%)
2	NDP	C	3281	-	45,52,52	1.99	15 (33%)	53,80,80	2.48	16 (30%)
2	NDP	B	2281	-	45,52,52	1.94	16 (35%)	53,80,80	2.49	16 (30%)
2	NDP	D	4281	-	45,52,52	1.99	16 (35%)	53,80,80	2.50	16 (30%)

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	1281	-	-	8/30/77/77	0/5/5/5
2	NDP	C	3281	-	-	8/30/77/77	0/5/5/5
2	NDP	B	2281	-	-	9/30/77/77	0/5/5/5
2	NDP	D	4281	-	-	8/30/77/77	0/5/5/5

All (62) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	4281	NDP	C7N-C3N	6.08	1.61	1.48
2	A	1281	NDP	C7N-C3N	5.89	1.61	1.48
2	C	3281	NDP	C7N-C3N	5.87	1.61	1.48
2	B	2281	NDP	C7N-C3N	5.50	1.60	1.48
2	B	2281	NDP	O4B-C1B	-4.90	1.34	1.41
2	D	4281	NDP	O4B-C1B	-4.65	1.34	1.41
2	C	3281	NDP	O4B-C1B	-4.57	1.34	1.41
2	A	1281	NDP	O4B-C1B	-4.52	1.34	1.41
2	C	3281	NDP	P2B-O2B	4.05	1.67	1.59
2	D	4281	NDP	C6N-C5N	3.85	1.40	1.33
2	A	1281	NDP	C6N-C5N	3.75	1.40	1.33
2	C	3281	NDP	C6N-C5N	3.64	1.39	1.33
2	B	2281	NDP	C6N-C5N	3.55	1.39	1.33
2	D	4281	NDP	P2B-O2B	3.35	1.65	1.59
2	B	2281	NDP	P2B-O2B	3.35	1.65	1.59
2	A	1281	NDP	P2B-O2B	3.03	1.65	1.59
2	D	4281	NDP	C4N-C3N	-2.87	1.44	1.49
2	B	2281	NDP	C4N-C3N	-2.83	1.44	1.49
2	A	1281	NDP	C4N-C3N	-2.80	1.44	1.49
2	D	4281	NDP	PA-O2A	-2.76	1.42	1.55
2	C	3281	NDP	C4N-C3N	-2.72	1.44	1.49
2	A	1281	NDP	C1D-N1N	2.68	1.54	1.46
2	B	2281	NDP	C8A-N7A	-2.67	1.29	1.34
2	C	3281	NDP	C8A-N7A	-2.67	1.29	1.34
2	A	1281	NDP	PA-O2A	-2.64	1.42	1.55
2	A	1281	NDP	C2N-C3N	2.60	1.42	1.34
2	B	2281	NDP	PA-O2A	-2.59	1.43	1.55
2	D	4281	NDP	C8A-N7A	-2.55	1.30	1.34
2	A	1281	NDP	O4D-C4D	2.54	1.50	1.45
2	C	3281	NDP	C2A-N1A	2.52	1.38	1.33
2	C	3281	NDP	PA-O2A	-2.50	1.43	1.55
2	D	4281	NDP	PN-O2N	-2.50	1.43	1.55
2	B	2281	NDP	C2A-N1A	2.49	1.38	1.33
2	D	4281	NDP	C4A-N3A	2.49	1.39	1.35
2	B	2281	NDP	C4A-N3A	2.47	1.39	1.35
2	D	4281	NDP	C1D-N1N	2.45	1.53	1.46
2	B	2281	NDP	PN-O2N	-2.45	1.43	1.55
2	A	1281	NDP	C4A-N3A	2.44	1.39	1.35
2	B	2281	NDP	O4D-C4D	2.41	1.50	1.45
2	C	3281	NDP	C1D-N1N	2.39	1.53	1.46
2	A	1281	NDP	C2A-N1A	2.37	1.38	1.33
2	C	3281	NDP	C4A-N3A	2.37	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3281	NDP	C2N-C3N	2.35	1.41	1.34
2	C	3281	NDP	PN-O1N	-2.35	1.42	1.50
2	D	4281	NDP	C2A-N1A	2.34	1.38	1.33
2	D	4281	NDP	C2N-C3N	2.32	1.41	1.34
2	D	4281	NDP	P2B-O3X	-2.27	1.46	1.54
2	C	3281	NDP	O4D-C4D	2.25	1.50	1.45
2	C	3281	NDP	PN-O2N	-2.22	1.44	1.55
2	D	4281	NDP	O4D-C4D	2.21	1.49	1.45
2	B	2281	NDP	C1D-N1N	2.20	1.52	1.46
2	A	1281	NDP	P2B-O3X	-2.20	1.46	1.54
2	A	1281	NDP	PN-O2N	-2.20	1.45	1.55
2	C	3281	NDP	P2B-O3X	-2.20	1.46	1.54
2	A	1281	NDP	PN-O1N	-2.18	1.43	1.50
2	A	1281	NDP	C8A-N7A	-2.15	1.30	1.34
2	B	2281	NDP	C2N-C3N	2.15	1.40	1.34
2	D	4281	NDP	C4N-C5N	-2.13	1.43	1.48
2	B	2281	NDP	PN-O1N	-2.09	1.43	1.50
2	B	2281	NDP	C4N-C5N	-2.08	1.43	1.48
2	B	2281	NDP	P2B-O3X	-2.06	1.46	1.54
2	D	4281	NDP	PN-O1N	-2.05	1.43	1.50

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1281	NDP	O5D-PN-O1N	-6.99	81.75	109.07
2	D	4281	NDP	O5D-PN-O1N	-6.83	82.37	109.07
2	B	2281	NDP	O5D-PN-O1N	-6.80	82.51	109.07
2	C	3281	NDP	O5D-PN-O1N	-6.67	83.01	109.07
2	D	4281	NDP	O3X-P2B-O1X	-6.09	86.85	110.68
2	C	3281	NDP	O3X-P2B-O1X	-6.00	87.19	110.68
2	B	2281	NDP	O3X-P2B-O1X	-5.95	87.38	110.68
2	C	3281	NDP	O3X-P2B-O2X	-5.95	84.90	107.64
2	A	1281	NDP	O3X-P2B-O2X	-5.91	85.05	107.64
2	A	1281	NDP	O3X-P2B-O1X	-5.86	87.74	110.68
2	B	2281	NDP	O3X-P2B-O2X	-5.76	85.62	107.64
2	D	4281	NDP	O3X-P2B-O2X	-5.67	85.95	107.64
2	D	4281	NDP	O3X-P2B-O2B	-5.60	80.88	105.99
2	B	2281	NDP	O3X-P2B-O2B	-5.58	81.01	105.99
2	C	3281	NDP	O3X-P2B-O2B	-5.45	81.57	105.99
2	A	1281	NDP	O3X-P2B-O2B	-5.43	81.68	105.99
2	A	1281	NDP	O2X-P2B-O1X	4.90	129.86	110.68
2	C	3281	NDP	O2X-P2B-O1X	4.83	129.57	110.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2281	NDP	O2X-P2B-O1X	4.75	129.29	110.68
2	D	4281	NDP	O2X-P2B-O1X	4.74	129.24	110.68
2	D	4281	NDP	O2A-PA-O1A	4.46	134.29	112.24
2	A	1281	NDP	O2N-PN-O5D	-4.42	87.21	107.75
2	C	3281	NDP	O2A-PA-O1A	4.33	133.66	112.24
2	B	2281	NDP	O2A-PA-O1A	4.33	133.65	112.24
2	A	1281	NDP	O2A-PA-O1A	4.32	133.60	112.24
2	D	4281	NDP	O2N-PN-O5D	-4.30	87.76	107.75
2	C	3281	NDP	O2N-PN-O5D	-4.28	87.87	107.75
2	B	2281	NDP	O2N-PN-O5D	-4.27	87.90	107.75
2	A	1281	NDP	C5A-C6A-N6A	4.19	126.72	120.35
2	C	3281	NDP	C5A-C6A-N6A	3.93	126.32	120.35
2	D	4281	NDP	C5A-C6A-N6A	3.90	126.27	120.35
2	D	4281	NDP	C3N-C2N-N1N	-3.85	117.60	123.10
2	B	2281	NDP	C3N-C2N-N1N	-3.84	117.62	123.10
2	A	1281	NDP	C3N-C2N-N1N	-3.83	117.64	123.10
2	C	3281	NDP	C3N-C2N-N1N	-3.75	117.74	123.10
2	B	2281	NDP	C5A-C6A-N6A	3.72	126.01	120.35
2	A	1281	NDP	O3B-C3B-C2B	3.48	121.04	111.17
2	B	2281	NDP	O4D-C1D-N1N	3.46	114.82	108.06
2	D	4281	NDP	O4D-C1D-N1N	3.43	114.77	108.06
2	C	3281	NDP	O3B-C3B-C2B	3.43	120.90	111.17
2	C	3281	NDP	O4D-C1D-N1N	3.37	114.65	108.06
2	A	1281	NDP	O4D-C1D-N1N	3.30	114.50	108.06
2	B	2281	NDP	O3B-C3B-C2B	3.24	120.38	111.17
2	D	4281	NDP	O3B-C3B-C2B	3.22	120.31	111.17
2	D	4281	NDP	O7N-C7N-C3N	-2.40	116.38	120.90
2	B	2281	NDP	O7N-C7N-N7N	2.37	128.43	122.88
2	C	3281	NDP	O7N-C7N-N7N	2.34	128.35	122.88
2	D	4281	NDP	C1D-N1N-C2N	-2.32	117.25	121.11
2	A	1281	NDP	O7N-C7N-C3N	-2.31	116.54	120.90
2	B	2281	NDP	C1D-N1N-C2N	-2.28	117.32	121.11
2	D	4281	NDP	O2B-P2B-O1X	2.28	118.17	109.39
2	C	3281	NDP	C1D-N1N-C2N	-2.25	117.37	121.11
2	B	2281	NDP	O2B-P2B-O1X	2.24	118.03	109.39
2	B	2281	NDP	O7N-C7N-C3N	-2.22	116.71	120.90
2	A	1281	NDP	O7N-C7N-N7N	2.22	128.07	122.88
2	A	1281	NDP	C1D-N1N-C2N	-2.21	117.43	121.11
2	D	4281	NDP	O7N-C7N-N7N	2.21	128.05	122.88
2	C	3281	NDP	O7N-C7N-C3N	-2.18	116.79	120.90
2	D	4281	NDP	C1B-N9A-C4A	-2.15	122.87	126.64
2	A	1281	NDP	C1B-N9A-C4A	-2.12	122.91	126.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3281	NDP	O2B-P2B-O1X	2.11	117.55	109.39
2	B	2281	NDP	C1B-N9A-C4A	-2.11	122.94	126.64
2	A	1281	NDP	O2B-P2B-O1X	2.07	117.39	109.39
2	A	1281	NDP	C2B-C3B-C4B	-2.02	97.60	101.99
2	C	3281	NDP	O5B-C5B-C4B	-2.01	102.09	108.99

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1281	NDP	C5B-O5B-PA-O2A
2	A	1281	NDP	O4D-C1D-N1N-C6N
2	C	3281	NDP	C5B-O5B-PA-O2A
2	C	3281	NDP	O4D-C1D-N1N-C6N
2	B	2281	NDP	C5B-O5B-PA-O2A
2	B	2281	NDP	O4D-C1D-N1N-C6N
2	D	4281	NDP	C5B-O5B-PA-O2A
2	D	4281	NDP	O4D-C1D-N1N-C6N
2	A	1281	NDP	O4B-C4B-C5B-O5B
2	D	4281	NDP	O4B-C4B-C5B-O5B
2	C	3281	NDP	O4B-C4B-C5B-O5B
2	B	2281	NDP	O4B-C4B-C5B-O5B
2	C	3281	NDP	C2B-O2B-P2B-O2X
2	B	2281	NDP	C5B-O5B-PA-O3
2	D	4281	NDP	C5B-O5B-PA-O3
2	D	4281	NDP	C2B-O2B-P2B-O2X
2	C	3281	NDP	C4D-C5D-O5D-PN
2	A	1281	NDP	C4D-C5D-O5D-PN
2	B	2281	NDP	C4D-C5D-O5D-PN
2	D	4281	NDP	C4D-C5D-O5D-PN
2	A	1281	NDP	C3B-C4B-C5B-O5B
2	D	4281	NDP	C3B-C4B-C5B-O5B
2	A	1281	NDP	C5B-O5B-PA-O3
2	A	1281	NDP	C2B-O2B-P2B-O2X
2	C	3281	NDP	C5B-O5B-PA-O3
2	B	2281	NDP	C2B-O2B-P2B-O2X
2	C	3281	NDP	C3B-C4B-C5B-O5B
2	B	2281	NDP	C3B-C4B-C5B-O5B
2	A	1281	NDP	C2N-C3N-C7N-N7N
2	C	3281	NDP	C2N-C3N-C7N-N7N
2	B	2281	NDP	C2N-C3N-C7N-N7N
2	D	4281	NDP	C2N-C3N-C7N-N7N

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Mol	Chain	Res	Type	Atoms
2	B	2281	NDP	C3B-C2B-O2B-P2B

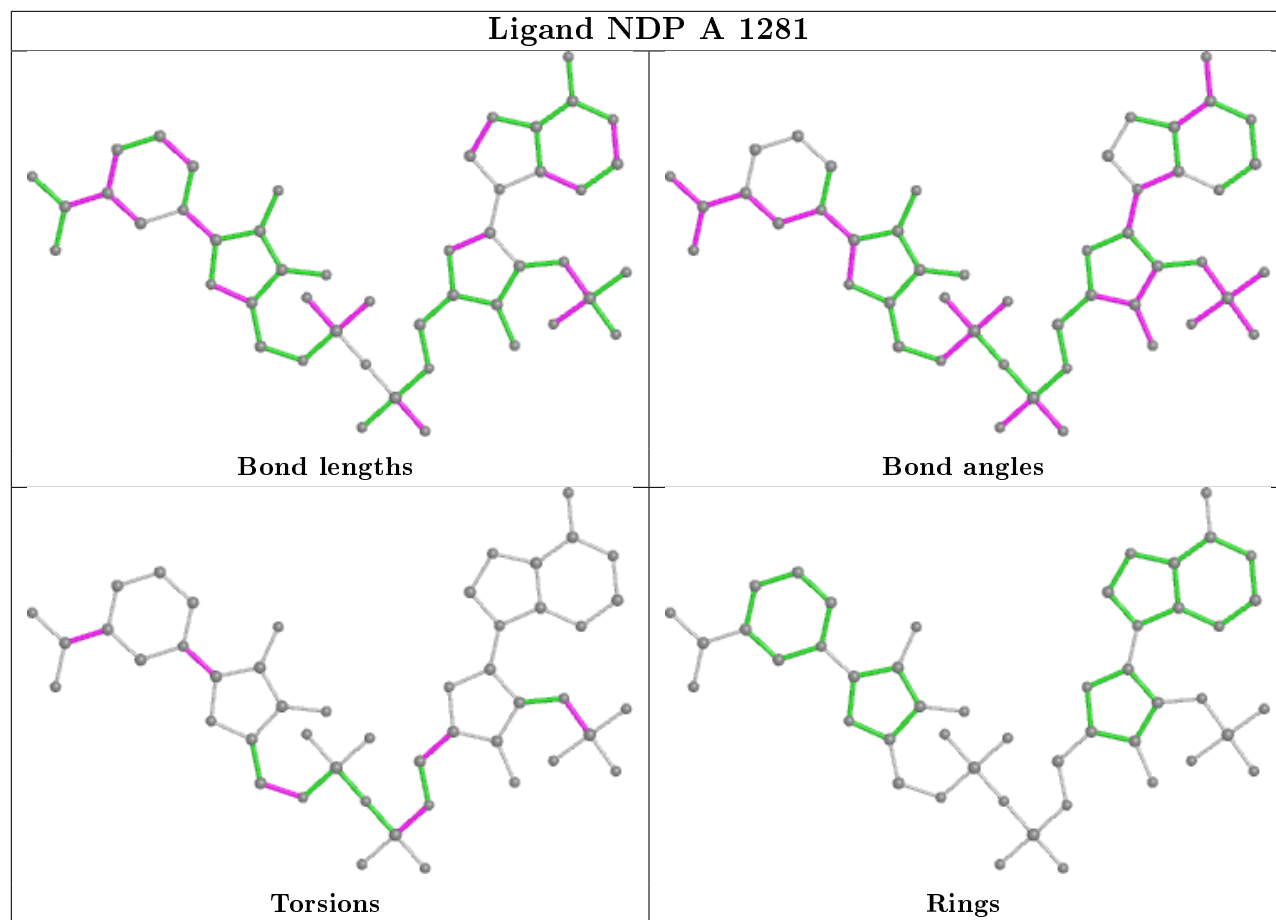
There are no ring outliers.

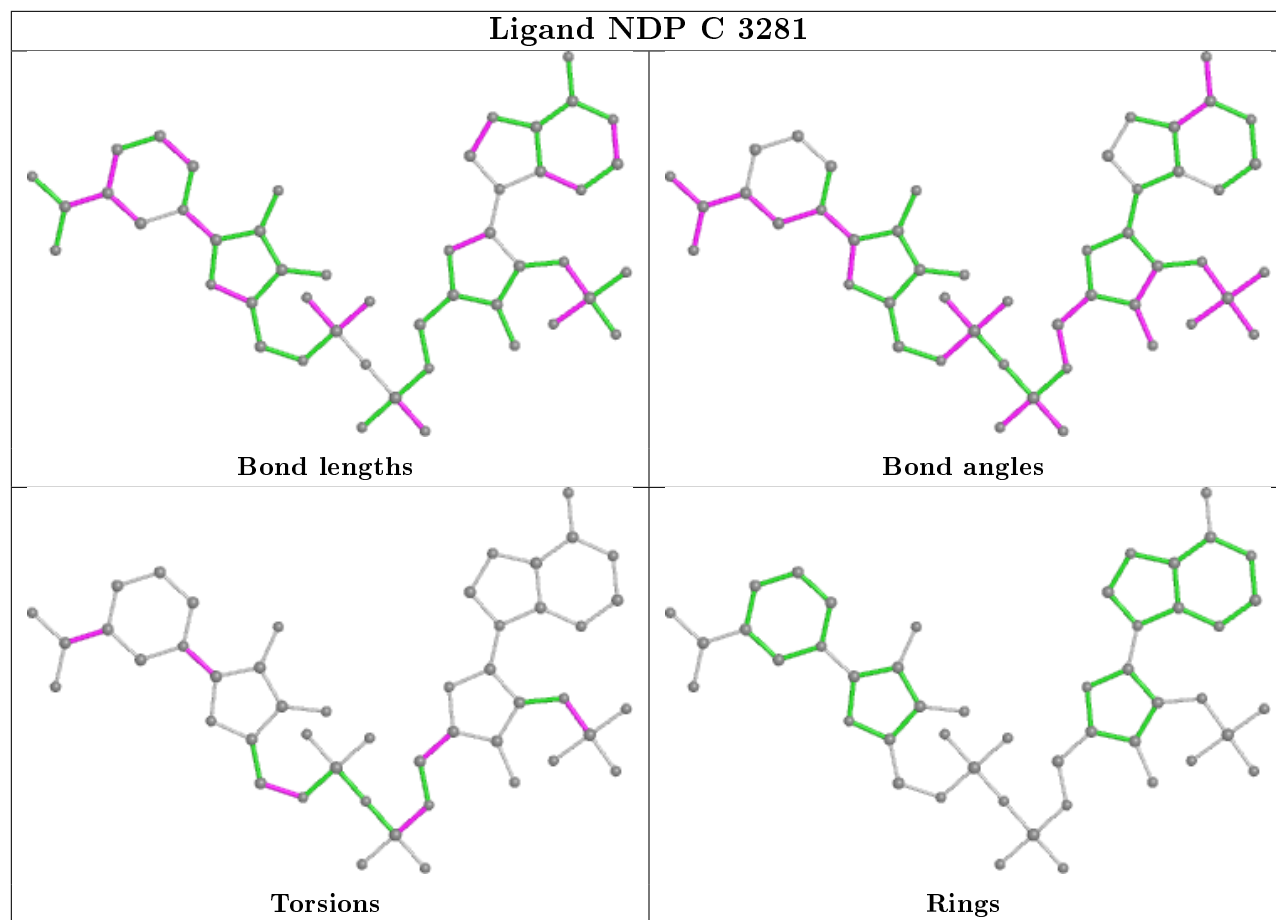
4 monomers are involved in 24 short contacts:

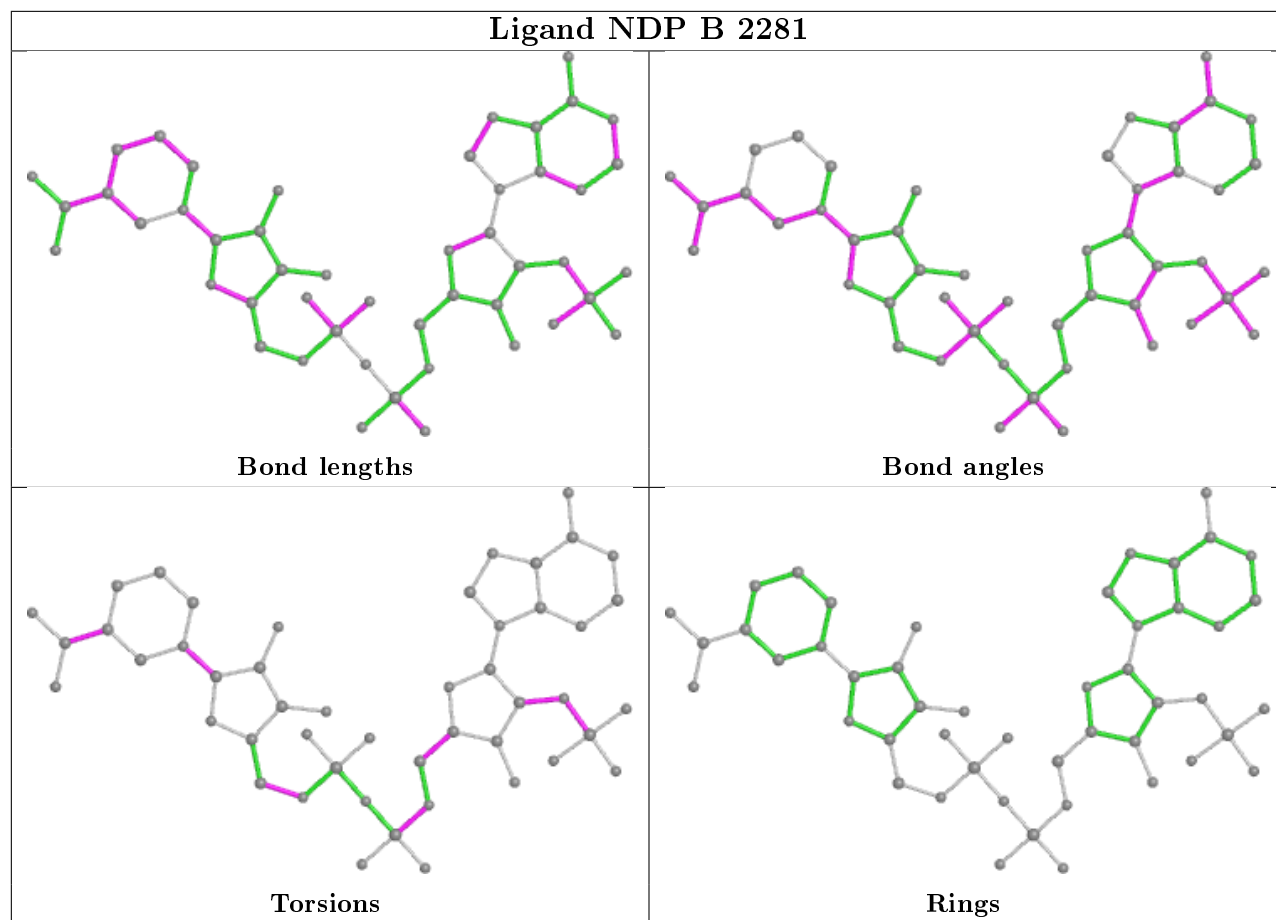
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1281	NDP	7	0
2	C	3281	NDP	6	0
2	B	2281	NDP	5	0
2	D	4281	NDP	6	0

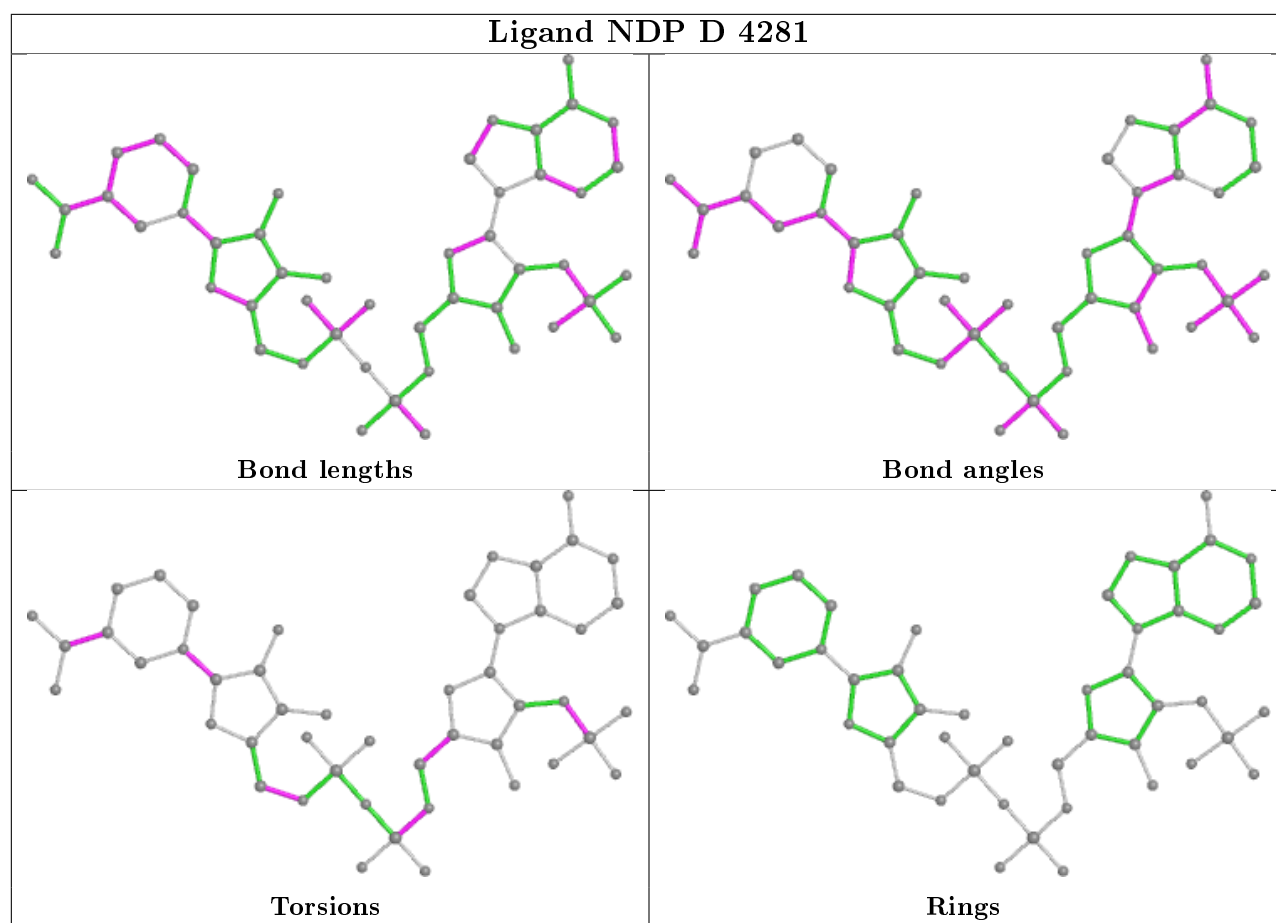
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	272/280 (97%)	-0.24	1 (0%) 92 93	13, 21, 37, 56	0
1	B	271/280 (96%)	-0.06	2 (0%) 87 89	13, 24, 44, 54	0
1	C	271/280 (96%)	-0.05	5 (1%) 68 72	13, 25, 48, 59	0
1	D	271/280 (96%)	-0.15	3 (1%) 80 84	13, 21, 39, 50	0
All	All	1085/1120 (96%)	-0.13	11 (1%) 82 85	13, 23, 43, 59	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	273	VAL	3.6
1	D	100	ASP	3.2
1	B	57	GLU	2.9
1	C	50	ILE	2.5
1	C	207	ASP	2.4
1	C	30	GLY	2.3
1	C	55	VAL	2.3
1	D	54	GLY	2.2
1	B	208	GLN	2.2
1	C	208	GLN	2.1
1	D	272	ASP	2.1

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

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

### 6.3 Carbohydrates [i](#)

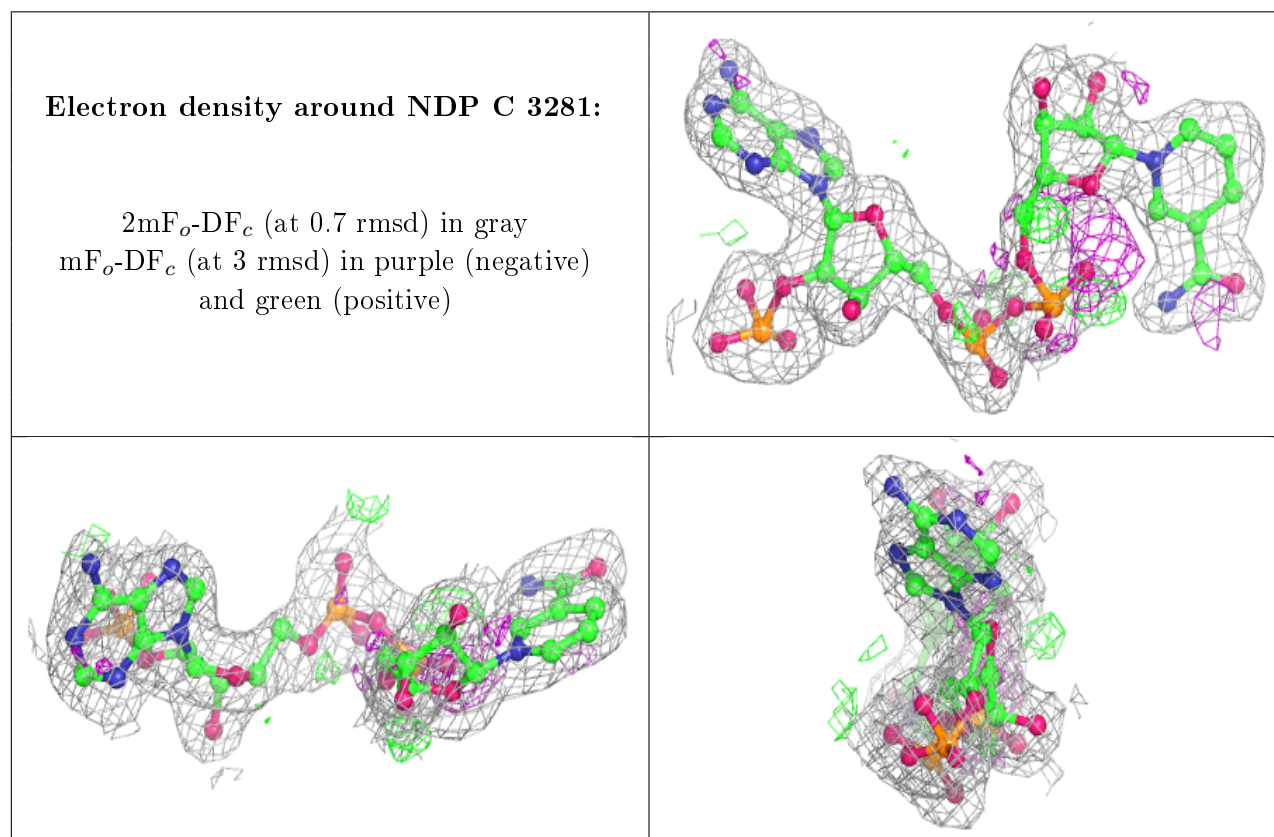
There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

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

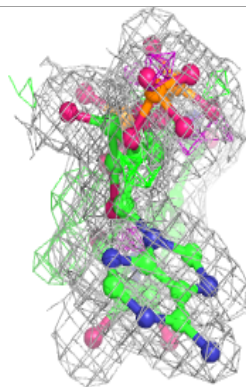
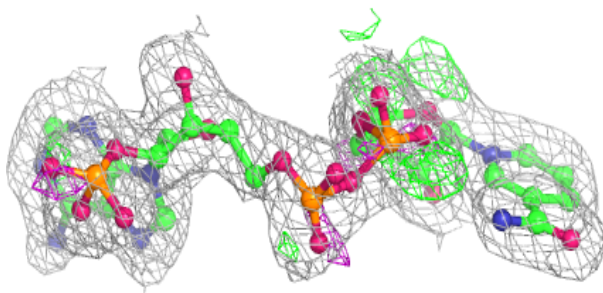
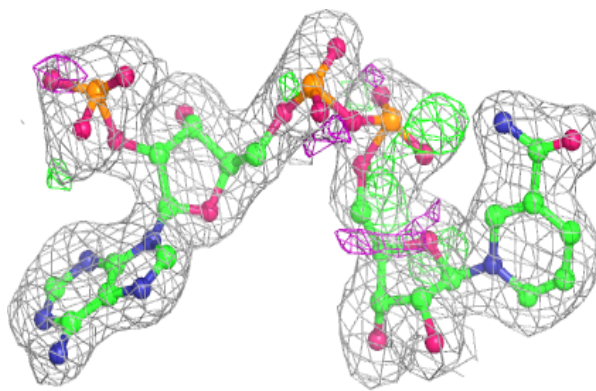
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NDP	C	3281	48/48	0.94	0.12	20,27,33,35	0
2	NDP	B	2281	48/48	0.94	0.12	18,22,31,35	0
2	NDP	A	1281	48/48	0.95	0.12	13,20,25,27	0
2	NDP	D	4281	48/48	0.95	0.13	14,20,26,32	0

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.

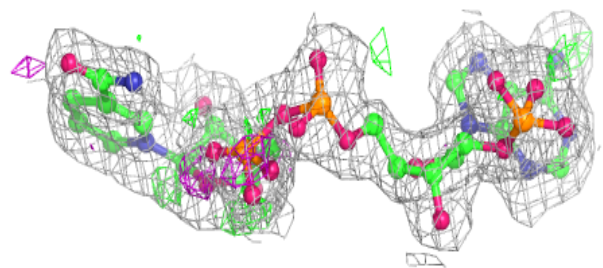
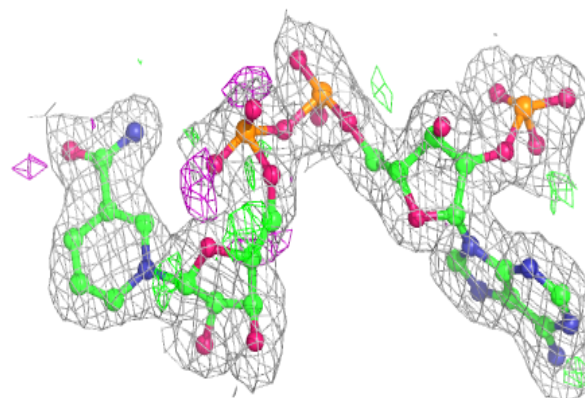


**Electron density around NDP B 2281:**

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

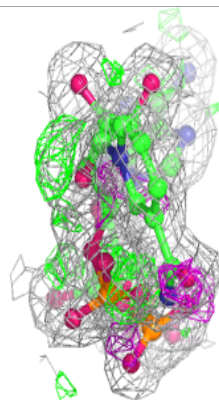
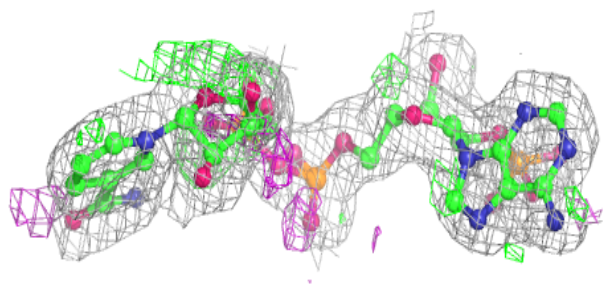
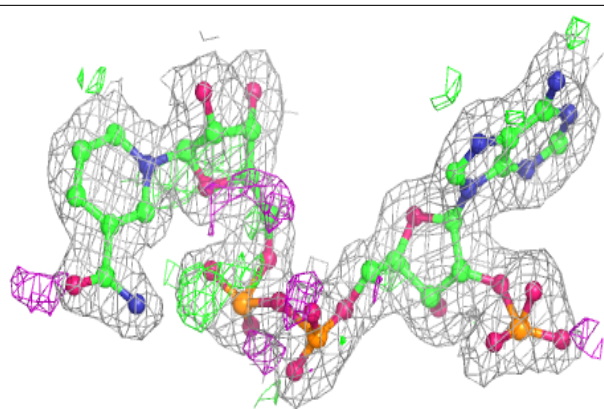
**Electron density around NDP A 1281:**

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



**Electron density around NDP D 4281:**

$2mF_o-DF_c$  (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.