



Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 08:13 pm BST

PDB ID : 1XHL
Title : Crystal Structure of putative Tropinone Reductase-II from *Caenorhabditis El-*
egans with Cofactor and Substrate
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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 : 2004-09-20
Resolution : 2.40 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 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

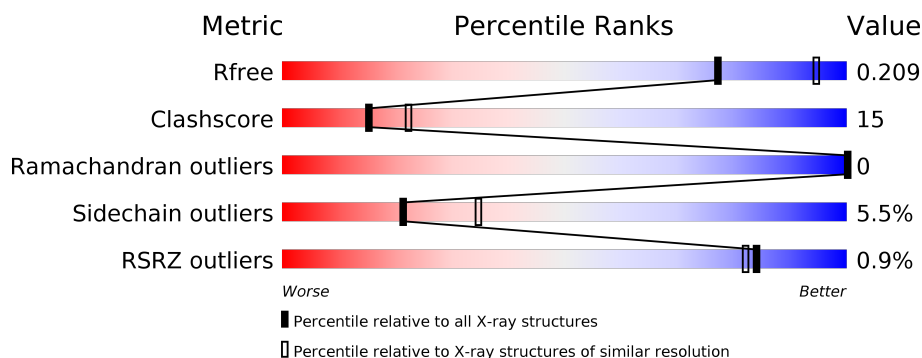
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 ≥ 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	297	<div> <div>%</div> <div> <div></div> <div>65%</div> <div>23%</div> <div>•</div> <div>8%</div> </div> </div>
1	B	297	<div> <div>%</div> <div> <div></div> <div>70%</div> <div>20%</div> <div>•</div> <div>8%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4418 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 dehydrogenase/reductase family member (5L265), putative Tropinone Reductase-II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	0
			2034	1273	351	400	10			
1	B	274	Total	C	N	O	S	0	0	0
			2034	1273	351	400	10			

There are 40 discrepancies between the modelled and reference sequences:

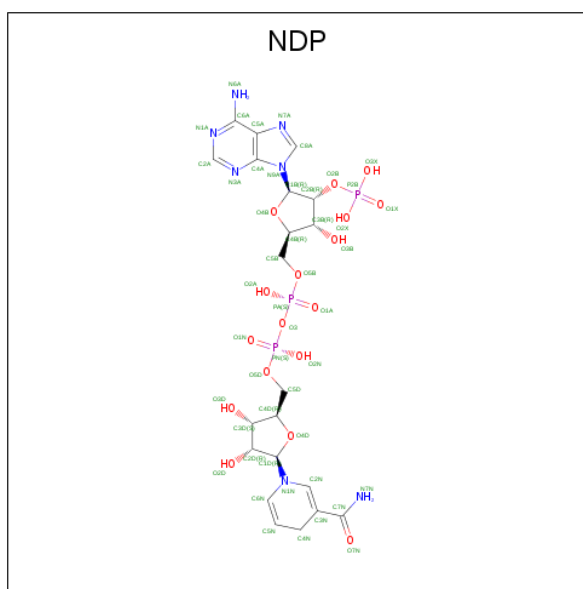
Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q19774
A	-18	GLY	-	EXPRESSION TAG	UNP Q19774
A	-17	SER	-	EXPRESSION TAG	UNP Q19774
A	-16	SER	-	EXPRESSION TAG	UNP Q19774
A	-15	HIS	-	EXPRESSION TAG	UNP Q19774
A	-14	HIS	-	EXPRESSION TAG	UNP Q19774
A	-13	HIS	-	EXPRESSION TAG	UNP Q19774
A	-12	HIS	-	EXPRESSION TAG	UNP Q19774
A	-11	HIS	-	EXPRESSION TAG	UNP Q19774
A	-10	HIS	-	EXPRESSION TAG	UNP Q19774
A	-9	SER	-	EXPRESSION TAG	UNP Q19774
A	-8	SER	-	EXPRESSION TAG	UNP Q19774
A	-7	GLY	-	EXPRESSION TAG	UNP Q19774
A	-6	LEU	-	EXPRESSION TAG	UNP Q19774
A	-5	VAL	-	EXPRESSION TAG	UNP Q19774
A	-4	PRO	-	EXPRESSION TAG	UNP Q19774
A	-3	ARG	-	EXPRESSION TAG	UNP Q19774
A	-2	GLY	-	EXPRESSION TAG	UNP Q19774
A	-1	SER	-	EXPRESSION TAG	UNP Q19774
A	0	HIS	-	EXPRESSION TAG	UNP Q19774
B	-19	MET	-	EXPRESSION TAG	UNP Q19774
B	-18	GLY	-	EXPRESSION TAG	UNP Q19774
B	-17	SER	-	EXPRESSION TAG	UNP Q19774
B	-16	SER	-	EXPRESSION TAG	UNP Q19774

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	HIS	-	EXPRESSION TAG	UNP Q19774
B	-14	HIS	-	EXPRESSION TAG	UNP Q19774
B	-13	HIS	-	EXPRESSION TAG	UNP Q19774
B	-12	HIS	-	EXPRESSION TAG	UNP Q19774
B	-11	HIS	-	EXPRESSION TAG	UNP Q19774
B	-10	HIS	-	EXPRESSION TAG	UNP Q19774
B	-9	SER	-	EXPRESSION TAG	UNP Q19774
B	-8	SER	-	EXPRESSION TAG	UNP Q19774
B	-7	GLY	-	EXPRESSION TAG	UNP Q19774
B	-6	LEU	-	EXPRESSION TAG	UNP Q19774
B	-5	VAL	-	EXPRESSION TAG	UNP Q19774
B	-4	PRO	-	EXPRESSION TAG	UNP Q19774
B	-3	ARG	-	EXPRESSION TAG	UNP Q19774
B	-2	GLY	-	EXPRESSION TAG	UNP Q19774
B	-1	SER	-	EXPRESSION TAG	UNP Q19774
B	0	HIS	-	EXPRESSION TAG	UNP Q19774

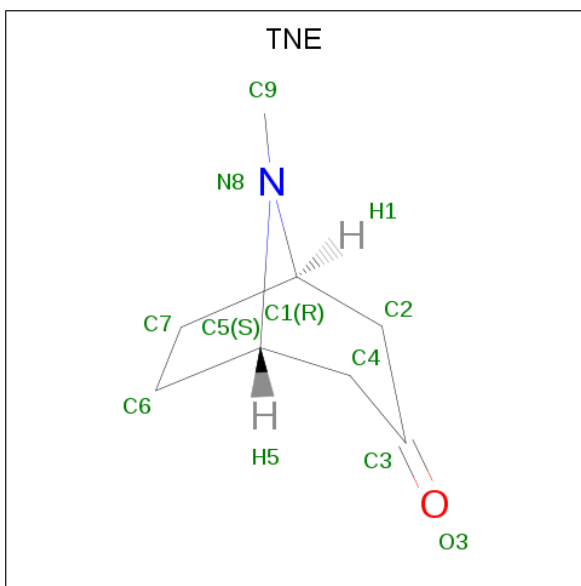
- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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

- Molecule 3 is 8-METHYL-8-AZABICYCLO[3,2,1]OCTAN-3-ONE (three-letter code: TNE)

(formula: C₈H₁₃NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	8	1	1		
3	B	1	Total	C	N	O	0	0
			10	8	1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	112	Total	O	0	0
			112	112		
4	B	122	Total	O	0	0
			122	122		

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.

- Chain A:
-
- 65% 23% 8%
- MET GLY SER SER HIS HIS HIS HIS HIS SER SER SER VAL PRO ARG GLY HIS MET MET ALA R3 F4 K7 I10 I11 G17 R20 V24 I25 K28 E29 G30 A31 Q32 V33 T34 I35 I39 E40 D41 Q48 K52 P56 A57 E58 K59 I60 K61 I76 T80 V91 G95 N104 T105 P108 E110 I124 T127 T130 K131 L134 I135 K136 V142 S145 I146 I147 V148 S155 G156 Y157 A161 K164 L167 D168 Q169 T174 D177 L178 I179 Q180 V183 R184 S187 K188 I192 V193 A194 T195 G196 F197 M198 L203 L204 Y212 T222 P223 V224 I233 I236 I237 L240 R243 M244 L245 S246 S247 S253 I254 V255 M264 Q267 M272 S276 GLN

- Chain B:
-
- | Category | Value (%) |
|----------|-----------|
| Q234 | 10 |
| N235 | 10 |
| I236 | 10 |
| L240 | 10 |
| A241 | 10 |
| D242 | 10 |
| R243 | 10 |
| N244 | 10 |
| L245 | 10 |
| S246 | 10 |
| S247 | 10 |
| S253 | 10 |
| I254 | 10 |
| M264 | 10 |
| Q267 | 10 |
| M272 | 10 |
| S276 | 10 |
| GLN | 10 |
| TU05 | 10 |
| D106 | 10 |
| Q107 | 10 |
| P108 | 10 |
| V109 | 10 |
| E110 | 10 |
| T127 | 10 |
| T130 | 10 |
| K131 | 10 |
| E132 | 10 |
| H133 | 10 |
| L134 | 10 |
| I135 | 10 |
| E140 | 10 |
| V144 | 10 |
| S145 | 10 |
| S146 | 10 |
| I147 | 10 |
| V148 | 10 |
| P151 | 10 |
| Q152 | 10 |
| S155 | 10 |
| G156 | 10 |
| Y157 | 10 |
| P158 | 10 |
| Y159 | 10 |
| Y160 | 10 |
| A161 | 10 |
| L167 | 10 |
| D168 | 10 |
| Q169 | 10 |
| D177 | 10 |
| L178 | 10 |
| Y183 | 10 |
| R184 | 10 |
| S187 | 10 |
| G191 | 10 |
| T195 | 10 |
| L211 | 10 |
| T222 | 10 |
| F223 | 10 |
| V224 | 10 |
| P230 | 10 |
| T232 | 10 |
| MET | 10 |
| GLY | 10 |
| SER | 10 |
| SER | 10 |
| HIS | 10 |
| HIS | 10 |
| HIS | 10 |
| HIS | 10 |
| HIS | 10 |
| HIS | 10 |
| HIS | 10 |
| SER | 10 |
| SER | 10 |
| GLY | 10 |
| LEU | 10 |
| VAL | 10 |
| PRO | 10 |
| ARG | 10 |
| GLY | 10 |
| HIS | 10 |
| HIS | 10 |
| MET | 10 |
| ALA | 10 |
| R3 | 10 |
| I10 | 10 |
| I11 | 10 |
| S15 | 10 |
| S21 | 10 |
| V24 | 10 |
| I25 | 10 |
| T34 | 10 |
| R42 | 10 |
| P56 | 10 |
| A57 | 10 |
| E58 | 10 |
| K59 | 10 |
| I76 | 10 |
| I77 | 10 |
| T80 | 10 |
| L81 | 10 |
| A82 | 10 |
| K83 | 10 |
| F84 | 10 |
| G85 | 10 |
| I89 | 10 |
| L90 | 10 |
| V91 | 10 |
| G95 | 10 |
| V104 | 10 |

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	109.59Å 109.59Å 162.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.17 – 2.40 27.17 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.1 (27.17-2.40) 95.1 (27.17-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.66 (at 2.39Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.191 , 0.215 0.185 , 0.209	Depositor DCC
R_{free} test set	1957 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4418	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% 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: TNE, 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	0.35	0/2061	0.61	0/2788
1	B	0.33	0/2061	0.61	1/2788 (0.0%)
All	All	0.34	0/4122	0.61	1/5576 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	191	GLY	N-CA-C	-5.03	100.52	113.10

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	2034	0	2058	74	0
1	B	2034	0	2058	56	0
2	A	48	0	26	7	0
2	B	48	0	26	5	0
3	A	10	0	13	1	0
3	B	10	0	13	1	0
4	A	112	0	0	1	0
4	B	122	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4418	0	4194	125	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 15.

All (125) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:THR:HG23	1:A:197:PHE:H	1.28	0.96
1:A:105:THR:HG22	1:B:177:ASP:OD2	1.75	0.86
1:A:148:VAL:HG13	1:A:161:ALA:HA	1.57	0.84
1:B:56:PRO:HG2	1:B:59:LYS:HG3	1.59	0.82
1:B:76:ILE:O	1:B:80:THR:HG22	1.79	0.81
1:A:76:ILE:O	1:A:80:THR:HG23	1.81	0.80
1:B:10:ILE:HD11	1:B:80:THR:HG21	1.63	0.79
1:B:130:THR:HG22	1:B:134:LEU:HG	1.64	0.78
1:B:178:LEU:HB3	1:B:183:VAL:HG22	1.66	0.78
1:A:11:ILE:HA	1:A:91:VAL:HG13	1.66	0.77
1:A:148:VAL:CG1	1:A:161:ALA:HA	2.18	0.73
1:B:140:GLU:OE2	1:B:243:ARG:HG2	1.90	0.71
1:A:178:LEU:HB3	1:A:183:VAL:HG13	1.71	0.71
1:A:177:ASP:O	1:A:180:GLN:HG2	1.92	0.69
1:B:195:THR:HG22	1:B:230:PRO:HG3	1.74	0.69
1:A:34:THR:OG1	1:A:80:THR:HG22	1.92	0.69
1:B:264:MET:H	1:B:267:GLN:NE2	1.93	0.67
1:A:105:THR:HG21	1:B:178:LEU:HD21	1.77	0.66
1:A:155:SER:HB2	1:B:177:ASP:HB2	1.78	0.66
1:A:35:ILE:HG12	1:A:60:ILE:HD11	1.77	0.66
1:A:130:THR:HG22	1:A:134:LEU:HG	1.77	0.65
1:A:108:PRO:HB2	1:A:110:GLU:HG2	1.78	0.65
1:A:39:ASN:HD22	1:A:39:ASN:C	2.00	0.64
1:B:178:LEU:HB3	1:B:183:VAL:CG2	2.27	0.64
1:A:145:SER:O	2:A:1278:NDP:H6N	1.98	0.64
1:A:104:ASN:HA	1:A:155:SER:O	1.99	0.63
1:B:222:ILE:HG22	1:B:224:VAL:HG12	1.80	0.62
1:B:264:MET:H	1:B:267:GLN:HE21	1.46	0.62
1:A:191:GLY:O	2:A:1278:NDP:H42N	2.01	0.61
1:A:195:THR:HG21	2:A:1278:NDP:PN	2.42	0.60
1:A:177:ASP:OD2	1:B:105:THR:HG23	2.01	0.60
1:A:187:SER:O	1:A:253:SER:HA	2.01	0.60
1:B:145:SER:O	2:B:2278:NDP:H6N	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:ASN:HD21	1:A:41:ASP:HB2	1.67	0.59
1:A:146:SER:HB3	1:A:164:LYS:HG2	1.85	0.59
1:A:264:MET:H	1:A:267:GLN:NE2	2.01	0.58
1:B:108:PRO:HB2	1:B:110:GLU:HG2	1.85	0.58
1:A:177:ASP:HB2	1:B:155:SER:HB2	1.86	0.58
2:B:2278:NDP:O1N	2:B:2278:NDP:H2N	2.04	0.58
1:B:131:LYS:O	1:B:135:ILE:HG23	2.04	0.58
1:B:191:GLY:O	2:B:2278:NDP:H42N	2.04	0.57
1:A:56:PRO:HG2	1:A:59:LYS:HG2	1.88	0.56
1:B:254:ILE:HD13	1:B:254:ILE:O	2.06	0.55
1:A:222:ILE:HG22	1:A:224:VAL:HG12	1.89	0.55
1:B:151:PRO:HG2	1:B:152:GLN:NE2	2.22	0.54
1:B:77:ILE:O	1:B:80:THR:HG23	2.08	0.53
1:A:195:THR:HG23	1:A:197:PHE:N	2.10	0.53
1:B:130:THR:HG22	1:B:134:LEU:CG	2.37	0.53
1:B:187:SER:O	1:B:253:SER:HA	2.09	0.53
1:A:264:MET:H	1:A:267:GLN:HE21	1.54	0.53
1:B:233:ILE:O	1:B:236:ILE:HG23	2.09	0.52
1:B:21:SER:O	1:B:24:VAL:HG22	2.10	0.52
3:A:1279:TNE:H62	4:A:1368:HOH:O	2.10	0.52
1:B:58:GLU:H	1:B:58:GLU:CD	2.13	0.52
1:B:104:ASN:HA	1:B:155:SER:O	2.10	0.51
1:A:243:ARG:O	1:A:247:SER:HB3	2.10	0.51
1:A:48:GLN:HG3	1:A:52:LYS:HE3	1.91	0.51
1:A:142:VAL:HG11	1:A:237:ILE:HG23	1.92	0.51
1:A:178:LEU:HB3	1:A:183:VAL:CG1	2.40	0.50
1:A:195:THR:HG23	1:A:196:GLY:N	2.26	0.50
1:B:21:SER:O	1:B:25:ILE:HG12	2.12	0.50
1:A:131:LYS:O	1:A:135:ILE:HG23	2.12	0.50
1:A:58:GLU:CD	1:A:58:GLU:H	2.14	0.50
1:A:131:LYS:NZ	1:B:106:ASP:OD2	2.45	0.49
2:A:1278:NDP:O1N	2:A:1278:NDP:H2N	2.12	0.49
1:A:95:GLY:CA	2:A:1278:NDP:H3D	2.43	0.49
1:B:243:ARG:O	1:B:247:SER:HB3	2.13	0.48
1:B:140:GLU:OE2	1:B:243:ARG:NH1	2.41	0.48
1:B:127:THR:O	1:B:131:LYS:HG3	2.13	0.48
1:A:127:THR:O	1:A:131:LYS:HG3	2.13	0.48
1:A:4:PHE:CB	1:A:31:ALA:HB2	2.44	0.48
1:B:169:GLN:OE1	1:B:169:GLN:HA	2.13	0.47
1:B:34:THR:OG1	1:B:80:THR:HB	2.14	0.47
1:A:56:PRO:HG2	1:A:59:LYS:CG	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:SER:HB3	1:B:148:VAL:HG12	1.96	0.47
1:A:35:ILE:CD1	1:A:60:ILE:HD11	2.45	0.47
1:A:184:ARG:NH2	1:A:240:LEU:O	2.48	0.46
1:A:60:ILE:HD12	1:A:61:ASN:N	2.30	0.46
1:A:11:ILE:CD1	1:A:33:VAL:HG23	2.46	0.46
1:A:4:PHE:HB3	1:A:31:ALA:HB2	1.97	0.46
1:B:58:GLU:O	1:B:83:LYS:HE2	2.16	0.46
1:A:135:ILE:HD12	1:A:135:ILE:O	2.16	0.45
1:A:95:GLY:HA3	2:A:1278:NDP:H3D	1.98	0.45
1:B:135:ILE:O	1:B:135:ILE:HD12	2.17	0.45
1:A:3:ARG:HD2	1:A:3:ARG:HA	1.74	0.45
1:A:35:ILE:CG1	1:A:60:ILE:HD11	2.44	0.45
1:A:11:ILE:HD12	1:A:11:ILE:N	2.32	0.44
1:A:193:VAL:HG13	2:A:1278:NDP:C7N	2.47	0.44
1:A:110:GLU:H	1:A:110:GLU:CD	2.20	0.44
1:A:25:ILE:O	1:A:29:GLU:HG2	2.18	0.44
1:A:169:GLN:HA	1:A:169:GLN:OE1	2.17	0.44
1:A:174:THR:HG22	1:B:105:THR:CG2	2.47	0.44
1:B:89:ILE:HD13	1:B:241:ALA:HB1	1.99	0.44
1:A:11:ILE:HG13	1:A:91:VAL:CG1	2.48	0.44
1:A:146:SER:OG	1:A:148:VAL:HB	2.18	0.44
1:A:20:ARG:O	1:A:24:VAL:HG13	2.18	0.44
1:A:17:GLY:HA3	1:A:195:THR:OG1	2.18	0.43
1:B:110:GLU:H	1:B:110:GLU:CD	2.22	0.43
1:B:236:ILE:CD1	1:B:254:ILE:HD12	2.48	0.43
1:A:24:VAL:O	1:A:28:LYS:HG3	2.18	0.43
1:A:4:PHE:O	1:A:7:LYS:HB2	2.19	0.43
1:B:15:SER:O	1:B:42:ARG:HB3	2.18	0.42
1:B:11:ILE:N	1:B:11:ILE:HD12	2.33	0.42
1:B:146:SER:CB	1:B:148:VAL:HG12	2.48	0.42
1:A:254:ILE:HD12	1:A:255:VAL:N	2.35	0.42
1:B:148:VAL:HG22	1:B:161:ALA:CB	2.49	0.42
1:A:124:ILE:HD13	1:B:159:TYR:CE1	2.55	0.42
1:A:233:ILE:HD13	1:A:233:ILE:N	2.34	0.42
1:A:174:THR:HG22	1:B:105:THR:HG22	2.02	0.42
1:B:184:ARG:HA	4:B:2302:HOH:O	2.19	0.41
1:A:11:ILE:HG13	1:A:91:VAL:HG11	2.02	0.41
1:B:148:VAL:CG2	1:B:157:TYR:HE2	2.33	0.41
1:A:10:ILE:HG12	1:A:80:THR:HG21	2.00	0.41
1:B:81:LEU:O	1:B:85:GLY:HA2	2.20	0.41
1:A:203:LEU:HA	1:A:204:PRO:HD3	1.95	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:VAL:HG22	1:A:157:TYR:HE1	1.86	0.41
1:B:184:ARG:NH2	1:B:240:LEU:O	2.53	0.41
1:B:95:GLY:CA	2:B:2278:NDP:H3D	2.51	0.41
1:A:131:LYS:HB2	1:A:131:LYS:HE3	1.95	0.41
1:A:35:ILE:HG12	1:A:60:ILE:CD1	2.47	0.41
1:B:235:ASN:HD22	1:B:235:ASN:HA	1.70	0.41
1:B:133:HIS:HD2	4:B:2356:HOH:O	2.02	0.41
1:A:198:MET:HG2	1:A:212:TYR:OH	2.21	0.40
1:A:188:VAL:HG21	1:A:236:ILE:HG12	2.02	0.40
2:B:2278:NDP:H41N	3:B:2279:TNE:C7	2.52	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	272/297 (92%)	261 (96%)	11 (4%)	0	100	100
1	B	272/297 (92%)	263 (97%)	9 (3%)	0	100	100
All	All	544/594 (92%)	524 (96%)	20 (4%)	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	219/238 (92%)	204 (93%)	15 (7%)	16	25
1	B	219/238 (92%)	210 (96%)	9 (4%)	30	48
All	All	438/476 (92%)	414 (94%)	24 (6%)	21	35

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	60	ILE
1	A	91	VAL
1	A	110	GLU
1	A	135	ILE
1	A	136	LYS
1	A	148	VAL
1	A	164	LYS
1	A	167	LEU
1	A	183	VAL
1	A	193	VAL
1	A	233	ILE
1	A	236	ILE
1	A	245	LEU
1	A	254	ILE
1	B	80	THR
1	B	110	GLU
1	B	135	ILE
1	B	167	LEU
1	B	211	LEU
1	B	236	ILE
1	B	243	ARG
1	B	245	LEU
1	B	254	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	49	GLN
1	A	73	GLN
1	A	78	ASN
1	A	121	GLN
1	A	180	GLN

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Mol	Chain	Res	Type
1	A	235	ASN
1	A	244	ASN
1	A	267	GLN
1	B	48	GLN
1	B	49	GLN
1	B	73	GLN
1	B	78	ASN
1	B	121	GLN
1	B	235	ASN
1	B	244	ASN
1	B	267	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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
3	TNE	B	2279	-	11,11,11	3.12	4 (36%)	16,16,16	1.48	2 (12%)
2	NDP	A	1278	-	45,52,52	1.95	14 (31%)	53,80,80	2.47	16 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	TNE	A	1279	-	11,11,11	3.20	5 (45%)	16,16,16	1.36	2 (12%)
2	NDP	B	2278	-	45,52,52	1.99	13 (28%)	53,80,80	2.48	15 (28%)

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	TNE	B	2279	-	-	-	0/3/2/2
2	NDP	A	1278	-	-	7/30/77/77	0/5/5/5
3	TNE	A	1279	-	-	-	0/3/2/2
2	NDP	B	2278	-	-	8/30/77/77	0/5/5/5

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1279	TNE	C2-C3	6.69	1.61	1.50
3	B	2279	TNE	C4-C3	6.64	1.61	1.50
3	A	1279	TNE	C4-C3	6.61	1.61	1.50
3	B	2279	TNE	C2-C3	6.54	1.61	1.50
2	B	2278	NDP	C7N-C3N	5.82	1.61	1.48
2	A	1278	NDP	C7N-C3N	5.54	1.60	1.48
2	B	2278	NDP	O4B-C1B	-4.92	1.34	1.41
2	A	1278	NDP	O4B-C1B	-4.75	1.34	1.41
2	B	2278	NDP	C6N-C5N	3.82	1.40	1.33
2	A	1278	NDP	P2B-O2B	3.62	1.66	1.59
2	B	2278	NDP	P2B-O2B	3.54	1.66	1.59
2	A	1278	NDP	C6N-C5N	3.49	1.39	1.33
2	A	1278	NDP	C4N-C3N	-3.41	1.43	1.49
2	B	2278	NDP	C4N-C3N	-2.95	1.44	1.49
2	A	1278	NDP	C8A-N7A	-2.92	1.29	1.34
2	B	2278	NDP	C4A-N3A	2.90	1.39	1.35
3	A	1279	TNE	C2-C1	2.75	1.59	1.53
2	B	2278	NDP	C8A-N7A	-2.71	1.29	1.34
2	A	1278	NDP	C2A-N1A	2.68	1.38	1.33
2	B	2278	NDP	C2A-N1A	2.63	1.38	1.33
3	A	1279	TNE	C9-N8	2.61	1.51	1.47
2	A	1278	NDP	PA-O2A	-2.52	1.43	1.55
2	B	2278	NDP	PA-O2A	-2.49	1.43	1.55
2	A	1278	NDP	C4A-N3A	2.48	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2279	TNE	C2-C1	2.47	1.58	1.53
2	B	2278	NDP	PN-O1N	-2.27	1.42	1.50
3	B	2279	TNE	C9-N8	2.26	1.50	1.47
2	B	2278	NDP	C2N-C3N	2.16	1.41	1.34
2	A	1278	NDP	C2N-C3N	2.14	1.40	1.34
2	B	2278	NDP	PN-O2N	-2.13	1.45	1.55
2	A	1278	NDP	C4N-C5N	-2.11	1.43	1.48
2	A	1278	NDP	PN-O2N	-2.10	1.45	1.55
2	A	1278	NDP	C1D-N1N	2.08	1.52	1.46
2	A	1278	NDP	PN-O1N	-2.07	1.43	1.50
2	B	2278	NDP	C4N-C5N	-2.07	1.43	1.48
3	A	1279	TNE	C4-C5	2.00	1.57	1.53

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1278	NDP	O5D-PN-O1N	-7.18	80.99	109.07
2	B	2278	NDP	O5D-PN-O1N	-7.18	81.02	109.07
2	B	2278	NDP	O3X-P2B-O1X	-6.08	86.89	110.68
2	A	1278	NDP	O3X-P2B-O1X	-6.05	87.01	110.68
2	A	1278	NDP	O3X-P2B-O2X	-5.81	85.44	107.64
2	B	2278	NDP	O3X-P2B-O2X	-5.75	85.65	107.64
2	A	1278	NDP	O3X-P2B-O2B	-5.65	80.69	105.99
2	B	2278	NDP	O3X-P2B-O2B	-5.61	80.87	105.99
2	A	1278	NDP	O2X-P2B-O1X	4.76	129.30	110.68
2	B	2278	NDP	O2X-P2B-O1X	4.73	129.19	110.68
2	B	2278	NDP	O2A-PA-O1A	4.32	133.58	112.24
2	A	1278	NDP	O2A-PA-O1A	4.30	133.48	112.24
2	A	1278	NDP	O2N-PN-O5D	-3.94	89.44	107.75
2	B	2278	NDP	O2N-PN-O5D	-3.91	89.59	107.75
2	A	1278	NDP	C5A-C6A-N6A	3.78	126.09	120.35
2	A	1278	NDP	C3N-C2N-N1N	-3.70	117.82	123.10
2	B	2278	NDP	C3N-C2N-N1N	-3.65	117.89	123.10
2	B	2278	NDP	C5A-C6A-N6A	3.63	125.87	120.35
3	B	2279	TNE	C6-C5-C4	-3.53	108.26	111.63
2	B	2278	NDP	O3B-C3B-C2B	3.35	120.69	111.17
2	A	1278	NDP	O3B-C3B-C2B	3.17	120.16	111.17
3	A	1279	TNE	C6-C5-C4	-3.07	108.69	111.63
2	A	1278	NDP	O4D-C1D-N1N	2.89	113.70	108.06
2	B	2278	NDP	O4D-C1D-N1N	2.71	113.35	108.06
2	B	2278	NDP	O7N-C7N-N7N	2.55	128.83	122.88
2	A	1278	NDP	O7N-C7N-N7N	2.51	128.74	122.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2278	NDP	C1D-N1N-C2N	-2.49	116.97	121.11
2	A	1278	NDP	C1D-N1N-C2N	-2.37	117.17	121.11
2	A	1278	NDP	O7N-C7N-C3N	-2.30	116.56	120.90
2	B	2278	NDP	O7N-C7N-C3N	-2.25	116.65	120.90
2	B	2278	NDP	O2B-P2B-O1X	2.23	118.01	109.39
3	B	2279	TNE	C4-C3-C2	2.21	119.26	115.99
3	A	1279	TNE	C4-C3-C2	2.12	119.12	115.99
2	A	1278	NDP	O2B-P2B-O1X	2.11	117.53	109.39
2	A	1278	NDP	O5B-C5B-C4B	-2.09	101.81	108.99

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1278	NDP	C5B-O5B-PA-O2A
2	A	1278	NDP	O4D-C1D-N1N-C6N
2	B	2278	NDP	C5B-O5B-PA-O2A
2	B	2278	NDP	O4D-C1D-N1N-C6N
2	A	1278	NDP	C5B-O5B-PA-O3
2	B	2278	NDP	O4B-C4B-C5B-O5B
2	A	1278	NDP	C4D-C5D-O5D-PN
2	B	2278	NDP	C4D-C5D-O5D-PN
2	A	1278	NDP	C2B-O2B-P2B-O2X
2	B	2278	NDP	C5B-O5B-PA-O3
2	B	2278	NDP	C2B-O2B-P2B-O2X
2	A	1278	NDP	O4B-C4B-C5B-O5B
2	A	1278	NDP	C2N-C3N-C7N-N7N
2	B	2278	NDP	C2N-C3N-C7N-N7N
2	B	2278	NDP	C3B-C4B-C5B-O5B

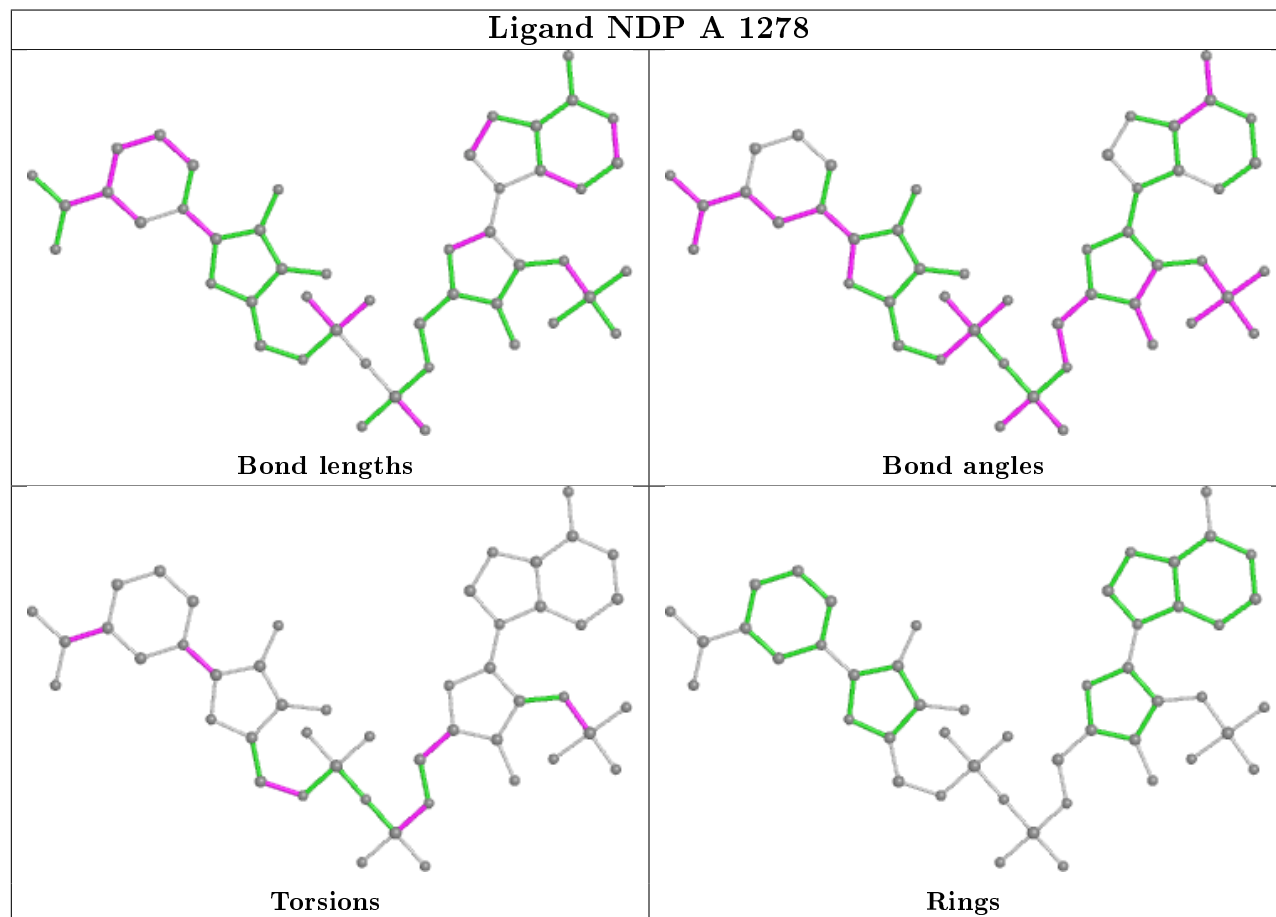
There are no ring outliers.

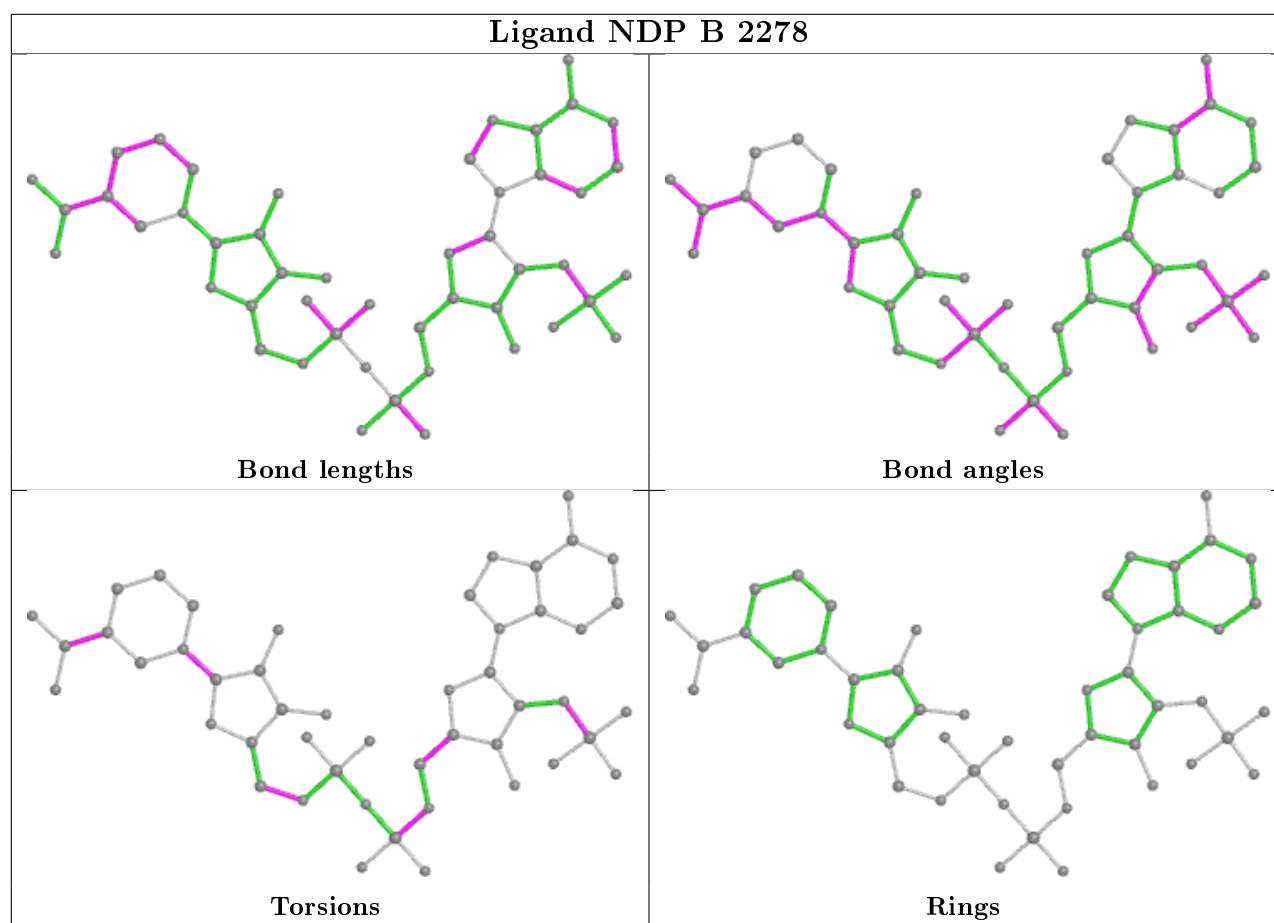
4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2279	TNE	1	0
2	A	1278	NDP	7	0
3	A	1279	TNE	1	0
2	B	2278	NDP	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 [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, 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	274/297 (92%)	-0.36	2 (0%) 87 86	30, 39, 58, 71	0
1	B	274/297 (92%)	-0.44	3 (1%) 80 79	29, 38, 53, 76	0
All	All	548/594 (92%)	-0.40	5 (0%) 84 82	29, 38, 56, 76	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	91	VAL	2.7
1	B	91	VAL	2.6
1	A	272	MET	2.2
1	B	272	MET	2.2
1	B	144	VAL	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 carbohydrates in this entry.

6.4 Ligands [i](#)

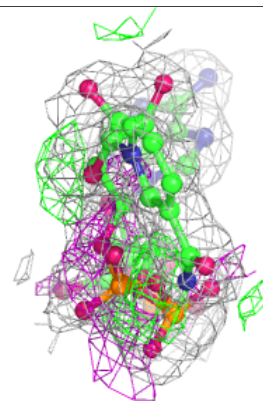
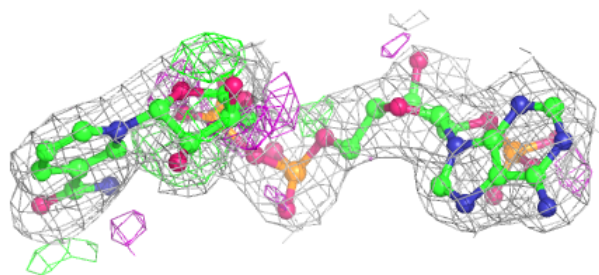
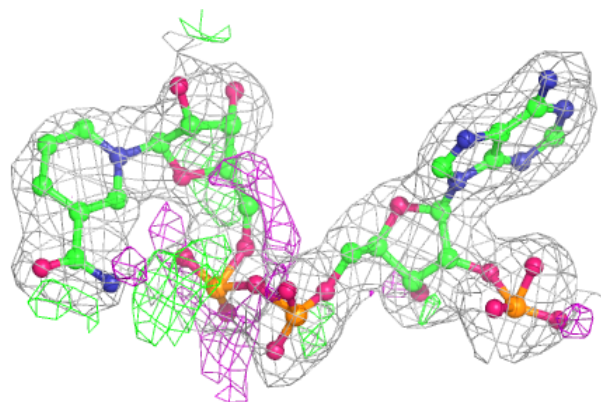
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

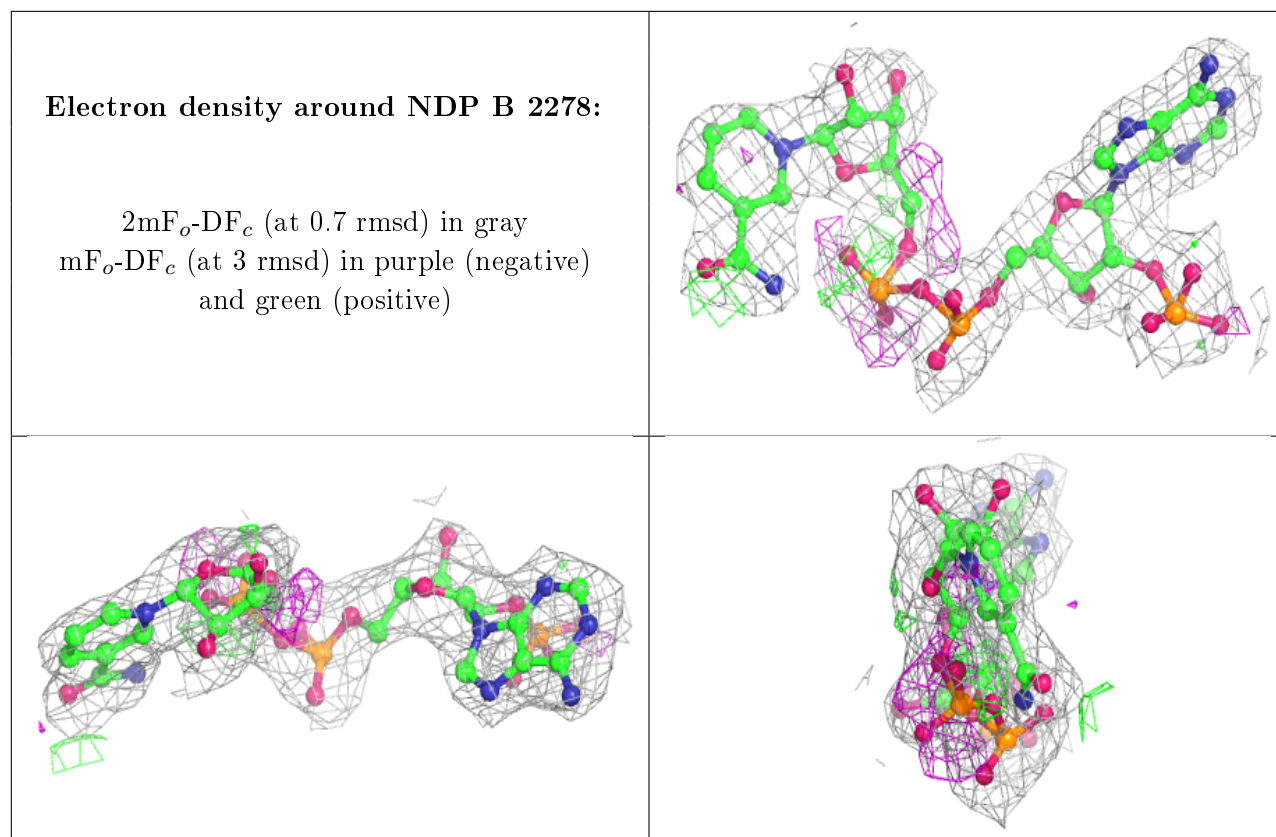
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	TNE	A	1279	10/10	0.90	0.22	65,67,67,68	0
2	NDP	A	1278	48/48	0.93	0.16	42,46,51,55	0
3	TNE	B	2279	10/10	0.93	0.24	65,65,66,68	0
2	NDP	B	2278	48/48	0.95	0.14	39,42,46,49	0

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 A 1278:

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.