



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 25, 2023 – 06:27 PM EDT

PDB ID : 3ANL
Title : Crystal structure of 1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR) complexed with pyridin-2-ylmethylphosphonic acid
Authors : Endo, K.; Kato, M.; Deng, L.; Song, Y.; Yajima, S.
Deposited on : 2010-09-03
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

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 : 1.8.5 (274361), 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

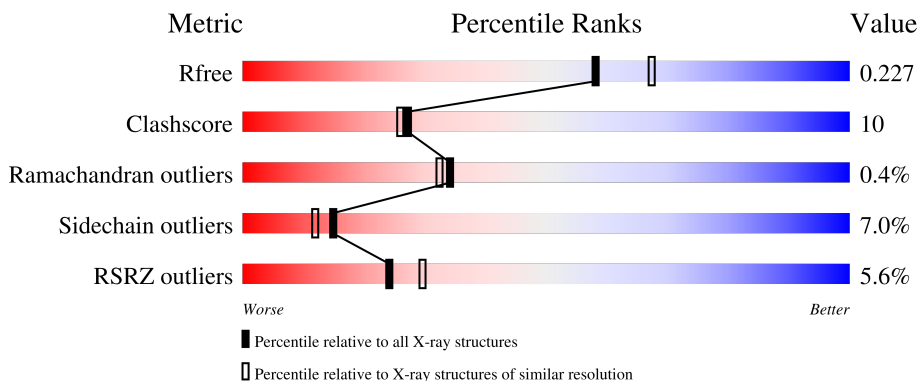
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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 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	420	 6% 75% 17% • 5%
1	B	420	 5% 73% 18% • 5%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6592 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 1-deoxy-D-xylulose 5-phosphate reductoisomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	400	3036	1895	536	579	26	0	0	0
1	B	398	3025	1889	534	576	26	0	0	0

There are 46 discrepancies between the modelled and reference sequences:

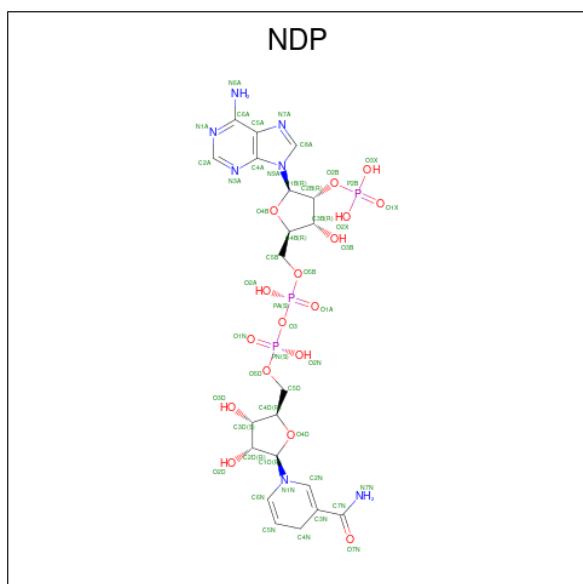
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	expression tag	UNP P45568
A	-9	ARG	-	expression tag	UNP P45568
A	-8	GLY	-	expression tag	UNP P45568
A	-7	SER	-	expression tag	UNP P45568
A	-6	HIS	-	expression tag	UNP P45568
A	-5	HIS	-	expression tag	UNP P45568
A	-4	HIS	-	expression tag	UNP P45568
A	-3	HIS	-	expression tag	UNP P45568
A	-2	HIS	-	expression tag	UNP P45568
A	-1	HIS	-	expression tag	UNP P45568
A	0	GLY	-	expression tag	UNP P45568
A	398	SER	-	expression tag	UNP P45568
A	399	ALA	-	expression tag	UNP P45568
A	400	CYS	-	expression tag	UNP P45568
A	401	ASP	-	expression tag	UNP P45568
A	402	LEU	-	expression tag	UNP P45568
A	403	GLY	-	expression tag	UNP P45568
A	404	THR	-	expression tag	UNP P45568
A	405	PRO	-	expression tag	UNP P45568
A	406	GLY	-	expression tag	UNP P45568
A	407	ARG	-	expression tag	UNP P45568
A	408	PRO	-	expression tag	UNP P45568
A	409	ALA	-	expression tag	UNP P45568
B	-10	MET	-	expression tag	UNP P45568
B	-9	ARG	-	expression tag	UNP P45568

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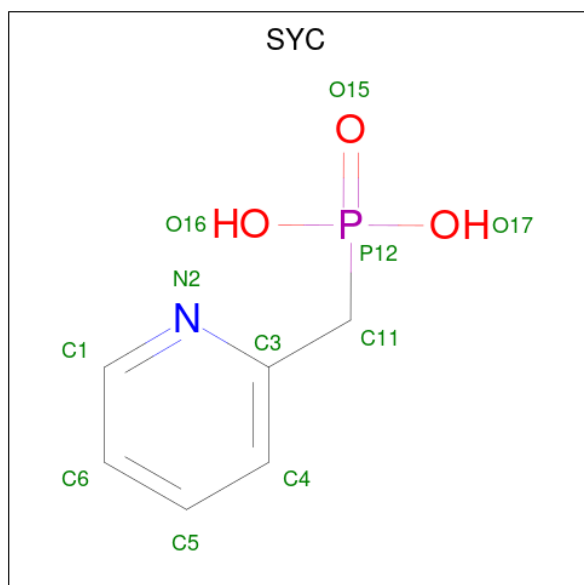
Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	GLY	-	expression tag	UNP P45568
B	-7	SER	-	expression tag	UNP P45568
B	-6	HIS	-	expression tag	UNP P45568
B	-5	HIS	-	expression tag	UNP P45568
B	-4	HIS	-	expression tag	UNP P45568
B	-3	HIS	-	expression tag	UNP P45568
B	-2	HIS	-	expression tag	UNP P45568
B	-1	HIS	-	expression tag	UNP P45568
B	0	GLY	-	expression tag	UNP P45568
B	398	SER	-	expression tag	UNP P45568
B	399	ALA	-	expression tag	UNP P45568
B	400	CYS	-	expression tag	UNP P45568
B	401	ASP	-	expression tag	UNP P45568
B	402	LEU	-	expression tag	UNP P45568
B	403	GLY	-	expression tag	UNP P45568
B	404	THR	-	expression tag	UNP P45568
B	405	PRO	-	expression tag	UNP P45568
B	406	GLY	-	expression tag	UNP P45568
B	407	ARG	-	expression tag	UNP P45568
B	408	PRO	-	expression tag	UNP P45568
B	409	ALA	-	expression tag	UNP P45568

- 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	48	21	7	17	3	0	0
2	B	1	48	21	7	17	3	0	0

- Molecule 3 is (pyridin-2-ylmethyl)phosphonic acid (three-letter code: SYC) (formula: $C_6H_8NO_3P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	11	6	1	3	1	0	0
3	B	1	11	6	1	3	1	0	0

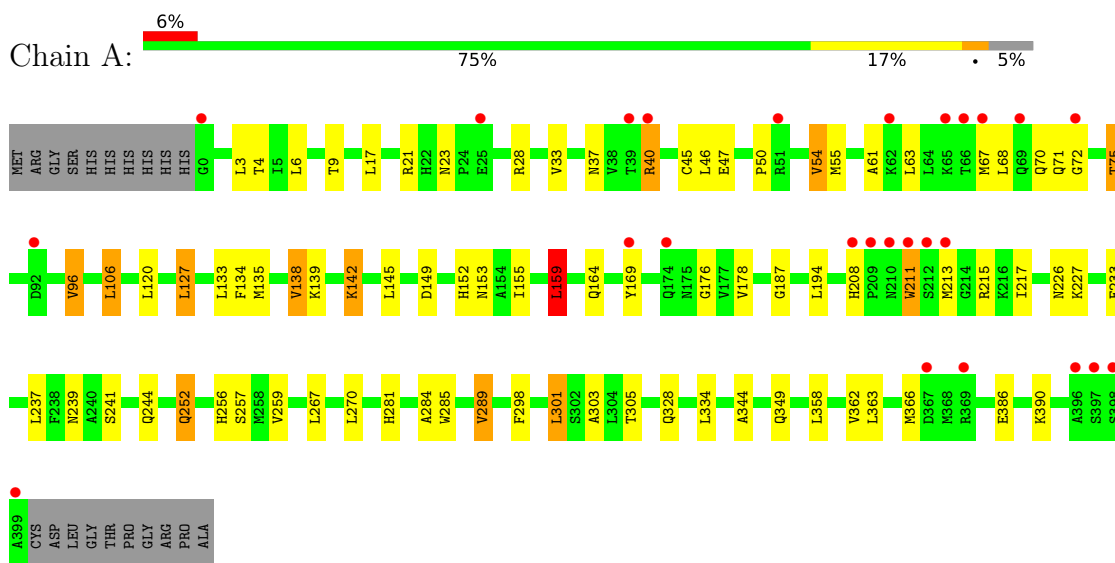
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	204	Total O 204 204	0	0
4	B	209	Total O 209 209	0	0

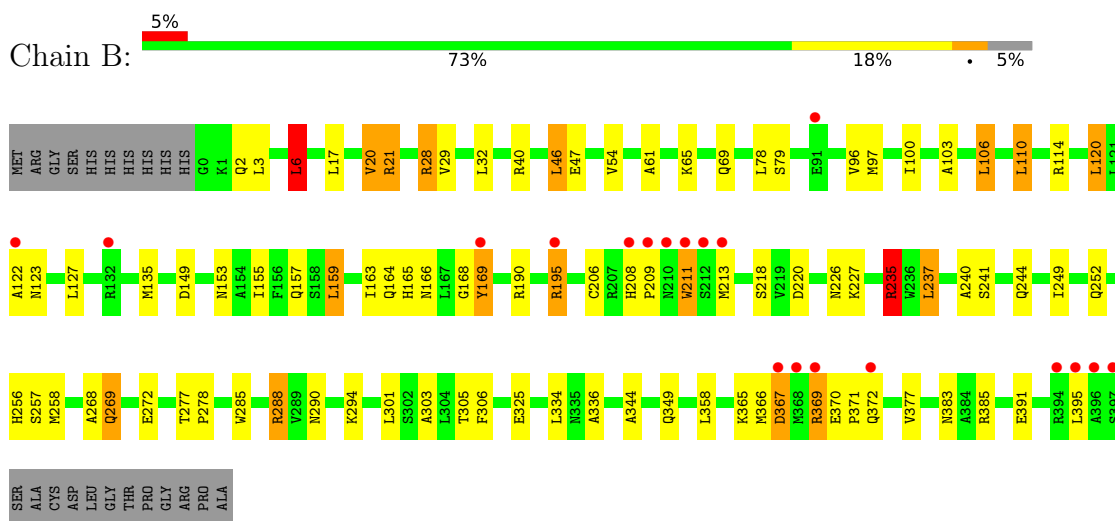
3 Residue-property plots [i](#)

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: 1-deoxy-D-xylulose 5-phosphate reductoisomerase



- Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	181.72Å 59.30Å 87.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.20 – 2.10 29.20 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.3 (29.20-2.10) 99.3 (29.20-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.29 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.184 , 0.225 0.186 , 0.227	Depositor DCC
R_{free} test set	2822 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	21.2	Xtrriage
Anisotropy	0.369	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 52.5	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	6592	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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: NDP, SYC

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	0.83	0/3084	0.84	3/4181 (0.1%)
1	B	0.82	0/3073	0.91	13/4166 (0.3%)
All	All	0.83	0/6157	0.87	16/8347 (0.2%)

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	235	ARG	NE-CZ-NH2	-11.24	114.68	120.30
1	B	21	ARG	NE-CZ-NH2	-9.12	115.74	120.30
1	B	21	ARG	NE-CZ-NH1	8.44	124.52	120.30
1	B	235	ARG	NE-CZ-NH1	8.26	124.43	120.30
1	B	237	LEU	CA-CB-CG	7.40	132.33	115.30
1	B	288	ARG	NE-CZ-NH2	-7.11	116.74	120.30
1	B	3	LEU	CA-CB-CG	6.56	130.38	115.30
1	B	46	LEU	CB-CG-CD1	5.85	120.94	111.00
1	A	106	LEU	CB-CG-CD1	5.69	120.67	111.00
1	A	215	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	B	6	LEU	CA-CB-CG	5.18	127.22	115.30
1	B	40	ARG	NE-CZ-NH2	5.16	122.88	120.30
1	B	6	LEU	CB-CG-CD1	5.14	119.74	111.00
1	A	159	LEU	CB-CG-CD1	5.04	119.56	111.00
1	B	28	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	B	288	ARG	CG-CD-NE	5.02	122.34	111.80

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	3036	0	3059	59	0
1	B	3025	0	3049	68	0
2	A	48	0	26	1	0
2	B	48	0	26	3	0
3	A	11	0	6	0	0
3	B	11	0	6	0	0
4	A	204	0	0	3	0
4	B	209	0	0	11	0
All	All	6592	0	6172	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 10.

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:B:122:ALA:C	4:B:410:HOH:O	1.91	1.06
1:B:256:HIS:CD2	1:B:269:GLN:HE22	1.81	0.96
1:B:256:HIS:HD2	1:B:269:GLN:HE22	0.99	0.95
1:A:6:LEU:CD2	1:A:96:VAL:HG23	2.03	0.88
1:B:123:ASN:N	4:B:410:HOH:O	2.04	0.85
1:B:241:SER:H	1:B:244:GLN:HE21	1.29	0.79
1:A:67:MET:O	1:A:71:GLN:HG2	1.84	0.77
1:B:21:ARG:HD3	1:B:47:GLU:OE2	1.87	0.75
1:A:6:LEU:HD23	1:A:96:VAL:HG23	1.70	0.72
1:B:122:ALA:O	2:B:702:NDP:O4D	2.08	0.71
1:B:272:GLU:OE1	4:B:465:HOH:O	2.10	0.70
1:A:6:LEU:HD21	1:A:96:VAL:HG23	1.74	0.69
1:A:21:ARG:HD3	1:A:47:GLU:OE2	1.94	0.68
1:A:241:SER:H	1:A:244:GLN:HE21	1.41	0.68
1:A:303:ALA:HB1	1:B:303:ALA:HB1	1.75	0.68
1:B:114:ARG:HH11	1:B:114:ARG:HG3	1.59	0.68
1:B:211:TRP:CE2	1:B:213:MET:HG3	2.30	0.66
1:B:256:HIS:CD2	1:B:269:GLN:NE2	2.61	0.65
1:A:6:LEU:HD21	1:A:96:VAL:CG2	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:MET:CE	1:A:145:LEU:HD11	2.28	0.64
1:B:164:GLN:NE2	1:B:285:TRP:HE1	1.96	0.64
1:A:153:ASN:HD21	1:A:281:HIS:CD2	2.18	0.61
1:A:211:TRP:CE2	1:A:213:MET:HG3	2.35	0.61
1:A:135:MET:HE3	1:A:145:LEU:HD11	1.82	0.61
1:A:252:GLN:HE22	1:A:305:THR:H	1.49	0.61
1:B:190:ARG:HD3	4:B:484:HOH:O	1.99	0.61
1:B:288:ARG:NE	4:B:412:HOH:O	1.99	0.61
1:A:40:ARG:NH2	4:A:414:HOH:O	2.34	0.60
1:B:241:SER:H	1:B:244:GLN:NE2	1.99	0.59
1:B:235:ARG:HD2	1:B:240:ALA:O	2.03	0.59
1:B:252:GLN:HE22	1:B:305:THR:H	1.49	0.59
1:B:153:ASN:ND2	1:B:157:GLN:HE21	2.00	0.59
1:B:294:LYS:HG2	4:B:557:HOH:O	2.02	0.58
1:B:383:ASN:HB2	4:B:494:HOH:O	2.03	0.58
1:B:288:ARG:NH2	4:B:412:HOH:O	2.30	0.58
1:A:159:LEU:HD13	1:A:259:VAL:HG21	1.84	0.57
1:B:17:LEU:HA	1:B:20:VAL:HG13	1.86	0.57
1:A:127:LEU:HD11	1:A:135:MET:CE	2.34	0.57
1:A:133:LEU:HG	1:A:328:GLN:HE22	1.68	0.57
1:A:127:LEU:HD11	1:A:135:MET:HE3	1.87	0.56
1:A:344:ALA:HA	1:A:349:GLN:HE21	1.70	0.56
1:B:135:MET:CE	1:B:168:GLY:HA3	2.35	0.56
1:A:6:LEU:CD2	1:A:96:VAL:CG2	2.81	0.56
1:B:252:GLN:NE2	1:B:305:THR:H	2.05	0.54
1:A:68:LEU:HD13	1:A:75:THR:HG23	1.88	0.54
1:A:45:CYS:HB3	1:A:75:THR:HG21	1.89	0.53
1:A:134:PHE:O	1:A:138:VAL:HG13	2.09	0.53
1:B:153:ASN:HD21	1:B:157:GLN:HE21	1.54	0.53
1:A:211:TRP:CZ2	1:A:213:MET:HG3	2.44	0.52
1:B:155:ILE:HG22	1:B:159:LEU:HD22	1.92	0.52
1:A:252:GLN:NE2	1:A:305:THR:H	2.07	0.52
1:B:195:ARG:HD3	1:B:195:ARG:H	1.75	0.52
1:A:164:GLN:NE2	1:A:285:TRP:HE1	2.08	0.52
1:A:362:VAL:O	1:A:366:MET:HG2	2.09	0.52
1:B:366:MET:O	1:B:367:ASP:C	2.48	0.52
1:B:235:ARG:NH2	1:B:325:GLU:OE2	2.43	0.52
1:A:50:PRO:O	1:A:75:THR:HB	2.10	0.51
1:B:2:GLN:NE2	4:B:605:HOH:O	2.43	0.51
1:B:235:ARG:CD	1:B:240:ALA:O	2.59	0.50
1:A:217:ILE:HD11	1:A:226:ASN:ND2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:VAL:HG22	1:A:54:VAL:HG13	1.93	0.49
1:A:187:GLY:HA2	1:A:208:HIS:CE1	2.48	0.49
1:A:55:MET:HB2	1:A:61:ALA:HB2	1.94	0.49
1:A:70:GLN:C	1:A:72:GLY:H	2.15	0.48
1:A:256:HIS:HE1	4:A:506:HOH:O	1.96	0.48
1:B:110:LEU:HD22	1:B:114:ARG:HG2	1.96	0.48
1:B:369:ARG:HD2	1:B:369:ARG:H	1.79	0.48
1:A:139:LYS:HE3	1:A:169:TYR:CE1	2.49	0.48
1:B:114:ARG:HG3	1:B:114:ARG:NH1	2.24	0.48
1:A:149:ASP:HA	2:A:701:NDP:H5N	1.96	0.47
1:B:135:MET:HE1	1:B:168:GLY:HA3	1.96	0.47
1:B:344:ALA:HA	1:B:349:GLN:HE21	1.79	0.47
1:B:54:VAL:HG22	1:B:78:LEU:HB2	1.96	0.47
1:B:166:ASN:HA	1:B:169:TYR:CZ	2.49	0.47
1:B:258:MET:HE2	1:B:268:ALA:HB2	1.96	0.47
1:B:258:MET:CE	1:B:268:ALA:HB2	2.45	0.47
1:B:29:VAL:HG11	1:B:32:LEU:HD21	1.97	0.47
1:B:100:ILE:HD12	2:B:702:NDP:N3A	2.30	0.46
1:A:152:HIS:HE1	1:A:233:GLU:OE2	1.99	0.46
1:B:21:ARG:CD	1:B:47:GLU:OE2	2.63	0.45
1:B:220:ASP:HB3	1:B:226:ASN:HB2	1.97	0.45
1:B:17:LEU:HA	1:B:17:LEU:HD23	1.87	0.45
1:B:211:TRP:CZ2	1:B:213:MET:HG3	2.51	0.45
1:A:142:LYS:HD2	1:A:142:LYS:N	2.31	0.45
1:A:155:ILE:HG22	1:A:159:LEU:HD22	1.98	0.45
1:A:135:MET:HE3	1:A:145:LEU:CD1	2.46	0.44
1:A:284:ALA:HB2	1:A:289:VAL:HB	1.99	0.44
1:B:103:ALA:O	1:B:106:LEU:HB2	2.17	0.44
1:A:386:GLU:O	1:A:390:LYS:HG3	2.17	0.44
1:A:270:LEU:HD12	1:A:270:LEU:N	2.33	0.44
1:B:127:LEU:HD11	1:B:237:LEU:HD13	2.00	0.43
1:A:6:LEU:N	1:A:6:LEU:HD22	2.33	0.43
1:B:65:LYS:O	1:B:69:GLN:HG3	2.18	0.43
1:A:4:THR:HG22	1:A:6:LEU:HD22	2.00	0.43
1:B:290:ASN:ND2	4:B:516:HOH:O	2.51	0.43
1:A:153:ASN:HD21	1:A:281:HIS:HD2	1.63	0.43
1:B:6:LEU:HD22	1:B:96:VAL:CG1	2.48	0.43
1:B:249:ILE:O	1:B:306:PHE:HA	2.18	0.43
1:A:71:GLN:HG2	1:A:71:GLN:H	1.68	0.43
1:A:21:ARG:NH2	4:A:463:HOH:O	2.46	0.42
1:B:149:ASP:HA	2:B:702:NDP:H5N	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:GLN:HE21	1:B:285:TRP:HE1	1.65	0.42
1:A:176:GLY:HA3	1:B:288:ARG:HB2	2.02	0.42
1:B:365:LYS:HE3	1:B:391:GLU:CD	2.39	0.42
1:A:139:LYS:HE3	1:A:169:TYR:HE1	1.84	0.42
1:B:97:MET:HA	1:B:120:LEU:HB2	2.01	0.42
1:A:67:MET:O	1:A:71:GLN:CG	2.64	0.42
1:A:70:GLN:C	1:A:72:GLY:N	2.74	0.42
1:A:46:LEU:HD23	1:A:46:LEU:HA	1.88	0.41
1:A:298:PHE:HA	1:A:301:LEU:HD22	2.02	0.41
1:B:6:LEU:HB2	1:B:97:MET:O	2.20	0.41
1:B:336:ALA:HB1	1:B:385:ARG:HG3	2.02	0.41
1:B:163:ILE:O	1:B:165:HIS:O	2.39	0.41
1:B:370:GLU:HA	1:B:371:PRO:HD3	1.98	0.41
1:A:37:ASN:OD1	1:A:40:ARG:HB2	2.21	0.41
1:B:208:HIS:HA	1:B:209:PRO:HD2	1.83	0.41
1:B:391:GLU:O	1:B:395:LEU:HD23	2.21	0.41
1:A:9:THR:HG22	1:A:40:ARG:HB3	2.02	0.41
1:B:61:ALA:CB	1:B:79:SER:HB3	2.50	0.41
1:B:206:CYS:HA	1:B:218:SER:HB3	2.02	0.41
1:A:252:GLN:NE2	1:A:252:GLN:H	2.19	0.41
1:B:226:ASN:ND2	4:B:576:HOH:O	2.54	0.41
1:A:23:ASN:ND2	1:A:289:VAL:HG22	2.36	0.40
1:A:127:LEU:HD21	1:A:237:LEU:HD13	2.02	0.40
1:B:277:THR:HB	1:B:278:PRO:CD	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	398/420 (95%)	390 (98%)	7 (2%)	1 (0%)	41 41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	396/420 (94%)	388 (98%)	6 (2%)	2 (0%)	29	26
All	All	794/840 (94%)	778 (98%)	13 (2%)	3 (0%)	34	32

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	367	ASP
1	A	257	SER
1	B	257	SER

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	328/344 (95%)	302 (92%)	26 (8%)	12	9
1	B	327/344 (95%)	307 (94%)	20 (6%)	18	16
All	All	655/688 (95%)	609 (93%)	46 (7%)	15	12

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	17	LEU
1	A	28	ARG
1	A	40	ARG
1	A	54	VAL
1	A	63	LEU
1	A	75	THR
1	A	96	VAL
1	A	106	LEU
1	A	120	LEU
1	A	127	LEU
1	A	138	VAL
1	A	142	LYS

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Mol	Chain	Res	Type
1	A	159	LEU
1	A	178	VAL
1	A	194	LEU
1	A	211	TRP
1	A	227	LYS
1	A	239	ASN
1	A	252	GLN
1	A	267	LEU
1	A	289	VAL
1	A	301	LEU
1	A	334	LEU
1	A	358	LEU
1	A	363	LEU
1	B	6	LEU
1	B	20	VAL
1	B	28	ARG
1	B	46	LEU
1	B	106	LEU
1	B	110	LEU
1	B	120	LEU
1	B	159	LEU
1	B	169	TYR
1	B	195	ARG
1	B	211	TRP
1	B	227	LYS
1	B	235	ARG
1	B	269	GLN
1	B	301	LEU
1	B	334	LEU
1	B	358	LEU
1	B	369	ARG
1	B	372	GLN
1	B	377	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	70	GLN
1	A	144	GLN
1	A	152	HIS
1	A	164	GLN

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Mol	Chain	Res	Type
1	A	175	ASN
1	A	208	HIS
1	A	226	ASN
1	A	239	ASN
1	A	244	GLN
1	A	252	GLN
1	A	256	HIS
1	A	281	HIS
1	A	328	GLN
1	A	349	GLN
1	B	82	GLN
1	B	123	ASN
1	B	144	GLN
1	B	153	ASN
1	B	164	GLN
1	B	175	ASN
1	B	210	ASN
1	B	244	GLN
1	B	252	GLN
1	B	256	HIS
1	B	269	GLN
1	B	281	HIS
1	B	290	ASN
1	B	349	GLN
1	B	383	ASN

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 monosaccharides 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	701	-	45,52,52	1.65	5 (11%)	53,80,80	1.33	5 (9%)
3	SYC	A	800	-	11,11,11	1.53	2 (18%)	13,15,15	1.95	5 (38%)
3	SYC	B	801	-	11,11,11	1.42	1 (9%)	13,15,15	1.81	4 (30%)
2	NDP	B	702	-	45,52,52	1.50	4 (8%)	53,80,80	1.39	4 (7%)

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	701	-	-	5/30/77/77	0/5/5/5
3	SYC	A	800	-	-	0/5/5/5	0/1/1/1
3	SYC	B	801	-	-	0/5/5/5	0/1/1/1
2	NDP	B	702	-	-	4/30/77/77	0/5/5/5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	NDP	O7N-C7N	6.60	1.40	1.24
2	B	702	NDP	O7N-C7N	6.02	1.38	1.24
2	A	701	NDP	C2A-N3A	4.62	1.39	1.32
2	B	702	NDP	C2A-N3A	3.91	1.38	1.32
2	B	702	NDP	C6N-C5N	3.62	1.39	1.33
3	B	801	SYC	P12-C11	3.50	1.85	1.79
2	A	701	NDP	C6N-C5N	3.42	1.39	1.33
2	A	701	NDP	C2A-N1A	3.38	1.40	1.33
3	A	800	SYC	P12-O16	3.05	1.61	1.54
3	A	800	SYC	P12-C11	2.84	1.84	1.79
2	B	702	NDP	C2A-N1A	2.12	1.37	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	NDP	P2B-O2B	2.05	1.63	1.59

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	NDP	N3A-C2A-N1A	-5.93	119.40	128.68
2	B	702	NDP	N3A-C2A-N1A	-5.58	119.95	128.68
2	B	702	NDP	C1B-N9A-C4A	-3.81	119.94	126.64
3	A	800	SYC	O17-P12-C11	3.76	115.69	106.92
3	B	801	SYC	C1-N2-C3	3.41	122.09	117.42
3	A	800	SYC	O17-P12-O16	-3.40	98.15	108.08
3	B	801	SYC	O17-P12-O16	-3.11	99.00	108.08
2	B	702	NDP	O7N-C7N-C3N	-2.97	115.30	120.90
2	B	702	NDP	C3N-C7N-N7N	2.97	122.94	117.67
3	A	800	SYC	C1-N2-C3	2.86	121.34	117.42
3	B	801	SYC	C6-C1-N2	-2.72	118.98	123.43
3	B	801	SYC	O17-P12-C11	2.70	113.22	106.92
2	A	701	NDP	C1B-N9A-C4A	-2.55	122.16	126.64
3	A	800	SYC	C6-C1-N2	-2.34	119.61	123.43
2	A	701	NDP	PN-O3-PA	-2.33	124.83	132.83
2	A	701	NDP	C5D-C4D-C3D	-2.19	106.99	115.18
3	A	800	SYC	C11-C3-C4	-2.05	119.94	121.42
2	A	701	NDP	O4D-C4D-C3D	2.00	109.08	105.11

There are no chirality outliers.

All (9) torsion outliers are listed below:

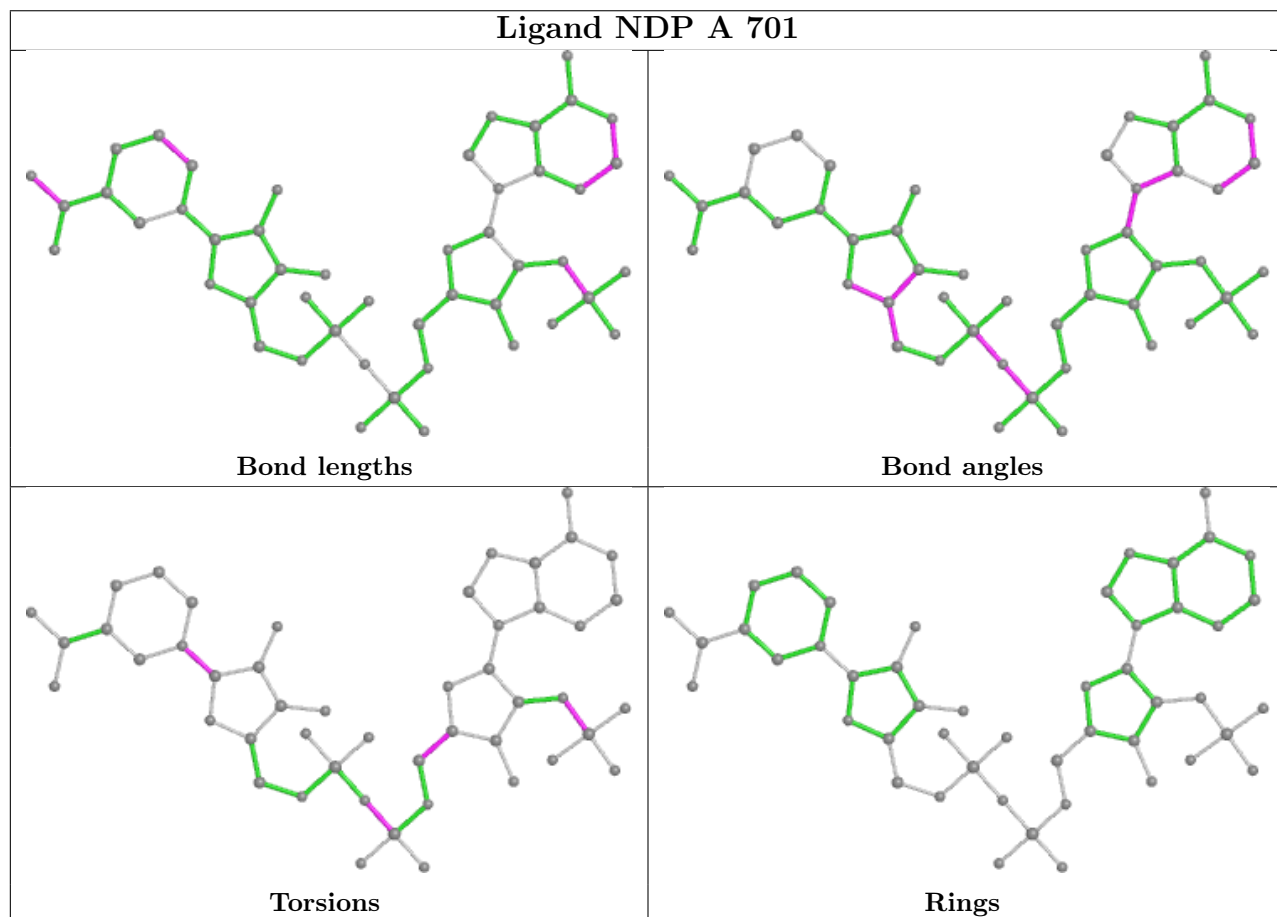
Mol	Chain	Res	Type	Atoms
2	A	701	NDP	C2B-O2B-P2B-O3X
2	A	701	NDP	O4D-C1D-N1N-C6N
2	B	702	NDP	O4D-C1D-N1N-C6N
2	A	701	NDP	C2D-C1D-N1N-C6N
2	B	702	NDP	C2D-C1D-N1N-C6N
2	B	702	NDP	O4B-C4B-C5B-O5B
2	A	701	NDP	PN-O3-PA-O1A
2	B	702	NDP	C2B-O2B-P2B-O2X
2	A	701	NDP	O4B-C4B-C5B-O5B

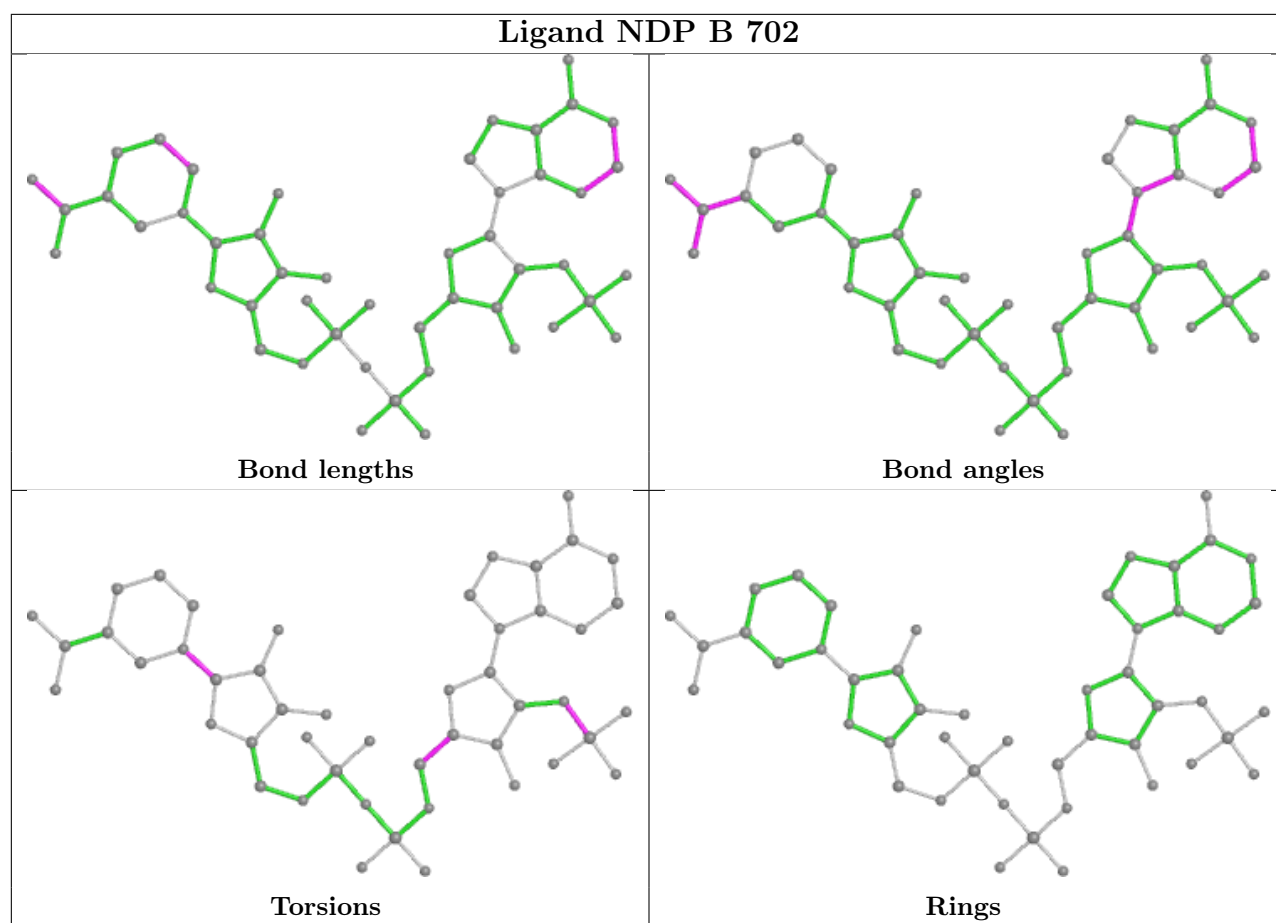
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	NDP	1	0
2	B	702	NDP	3	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	400/420 (95%)	0.22	26 (6%) 18 23	10, 19, 44, 64	0
1	B	398/420 (94%)	0.12	19 (4%) 30 36	10, 19, 36, 57	0
All	All	798/840 (95%)	0.17	45 (5%) 24 29	10, 19, 42, 64	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	209	PRO	10.1
1	B	209	PRO	7.9
1	A	399	ALA	7.4
1	A	210	ASN	6.7
1	A	211	TRP	6.3
1	A	169	TYR	6.2
1	B	211	TRP	6.2
1	B	210	ASN	5.9
1	B	212	SER	5.6
1	A	398	SER	5.1
1	B	367	ASP	4.0
1	B	397	SER	4.0
1	B	395	LEU	3.6
1	A	208	HIS	3.4
1	A	369	ARG	3.3
1	B	396	ALA	3.2
1	A	212	SER	3.2
1	A	397	SER	3.1
1	A	66	THR	3.1
1	A	25	GLU	3.1
1	A	367	ASP	3.1
1	B	213	MET	3.0
1	B	394	ARG	3.0
1	B	208	HIS	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	169	TYR	2.9
1	B	195	ARG	2.9
1	B	369	ARG	2.9
1	A	67	MET	2.9
1	A	174	GLN	2.6
1	B	368	MET	2.5
1	A	396	ALA	2.5
1	A	62	LYS	2.5
1	A	69	GLN	2.4
1	A	40	ARG	2.3
1	A	213	MET	2.3
1	A	92	ASP	2.2
1	A	39	THR	2.2
1	A	0	GLY	2.1
1	B	91	GLU	2.1
1	A	51	ARG	2.1
1	B	132	ARG	2.1
1	B	122	ALA	2.0
1	B	372	GLN	2.0
1	A	65	LYS	2.0
1	A	72	GLY	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.

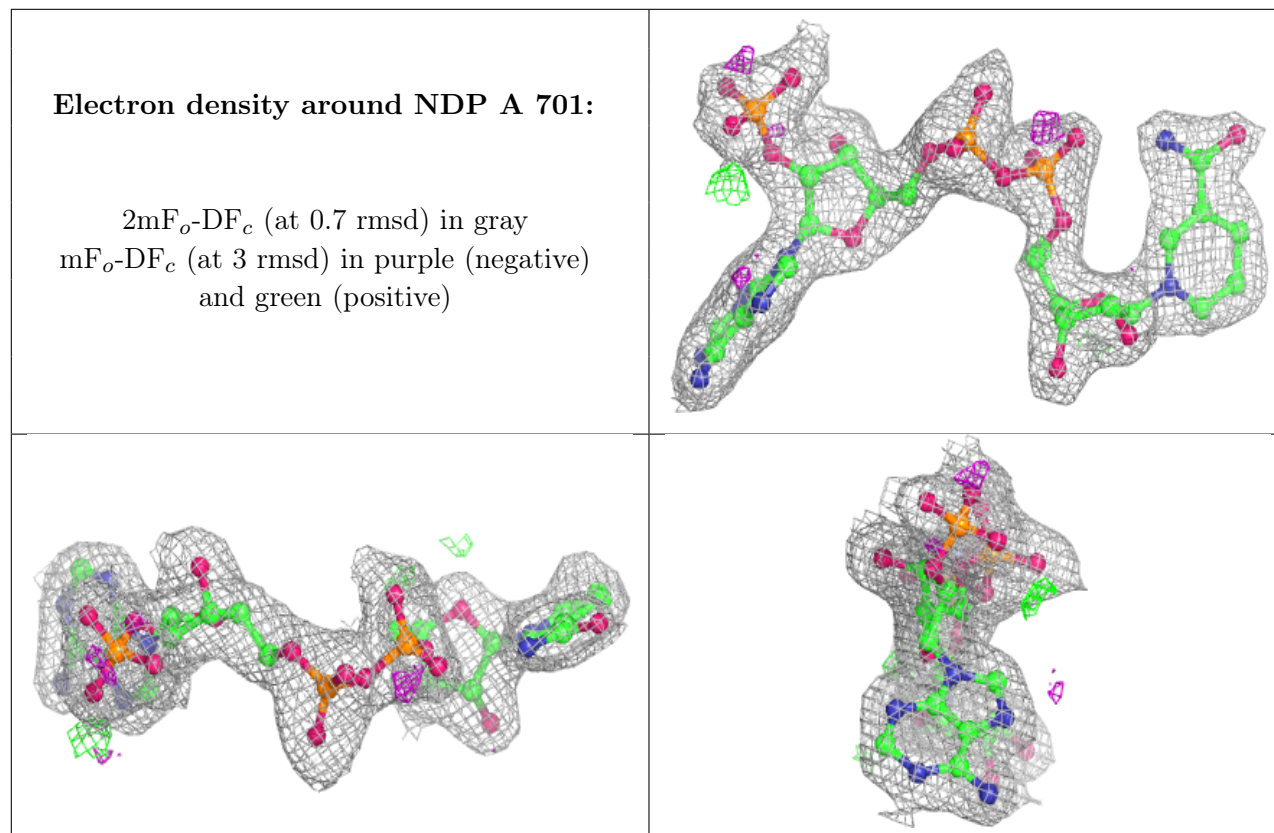
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NDP	A	701	48/48	0.95	0.11	19,26,35,38	0
2	NDP	B	702	48/48	0.97	0.10	16,21,27,29	0

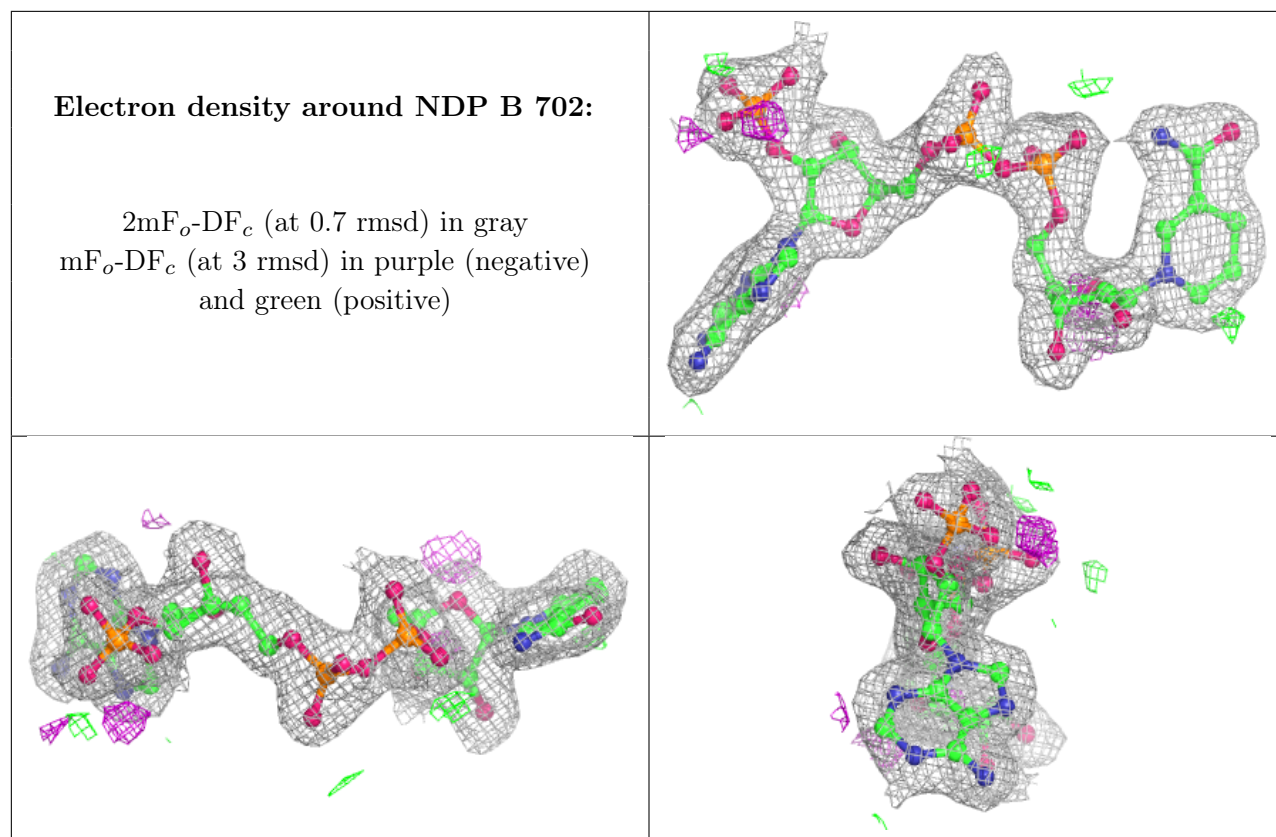
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SYC	A	800	11/11	0.97	0.11	12,18,22,23	0
3	SYC	B	801	11/11	0.97	0.11	12,15,17,18	0

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.





6.5 Other polymers [i](#)

There are no such residues in this entry.