



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 9, 2023 – 10:01 am GMT

PDB ID : 1H6C
Title : Oxidized Precursor Form of Glucose-Fructose Oxidoreductase from *Zy-*
momonas mobilis complexed with succinate
Authors : Nurizzo, D.; Baker, E.N.
Deposited on : 2001-06-11
Resolution : 2.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

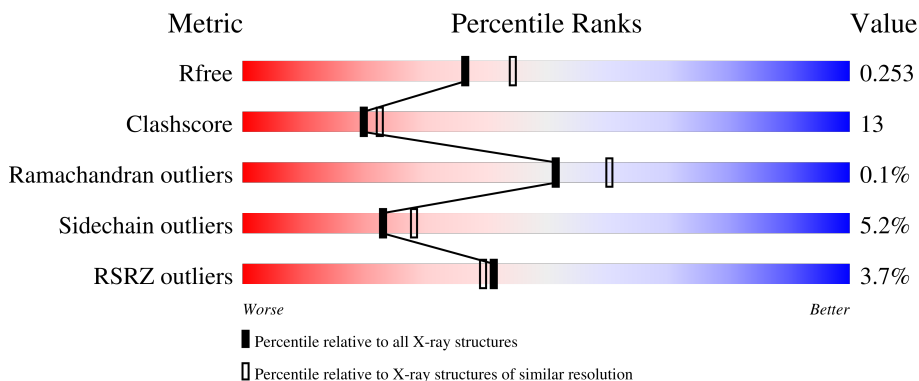
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	433	 6% 73% 12% • 12%
1	B	433	 6% 57% 29% • 12%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SIN	B	600	-	X	-	-

2 Entry composition i

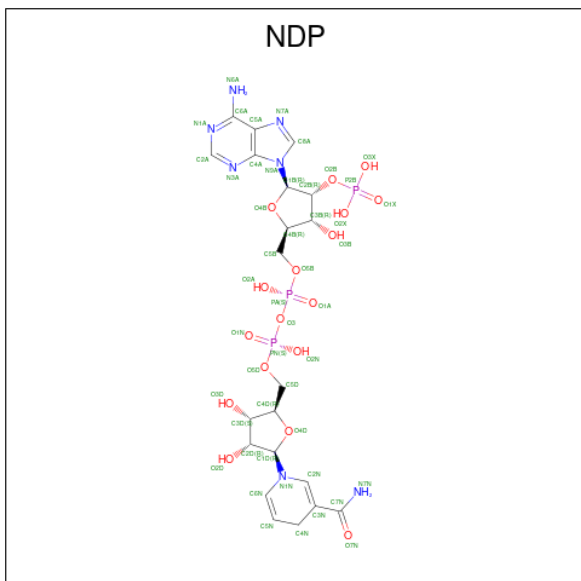
There are 5 unique types of molecules in this entry. The entry contains 6506 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE.

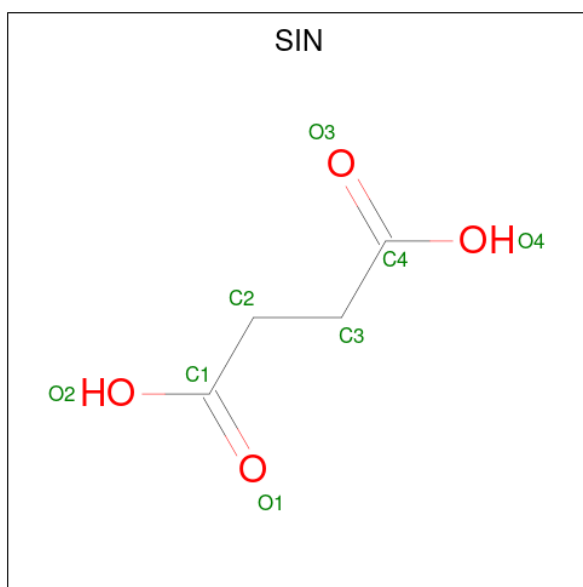
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	381	Total 2960	C 1856	N 530	O 554	S 20	0	0	0
1	B	381	Total 2960	C 1856	N 530	O 554	S 20	0	0	0

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



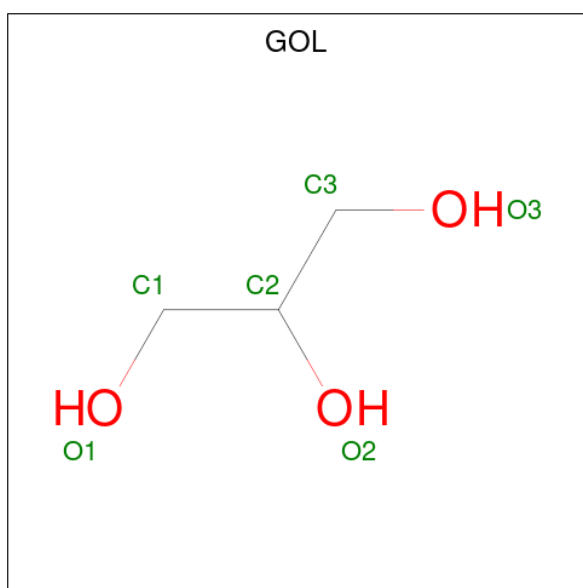
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 3 is SUCCINIC ACID (three-letter code: SIN) (formula: C₄H₆O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	4	4		
3	B	1	Total	C	O	0	0
			8	4	4		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

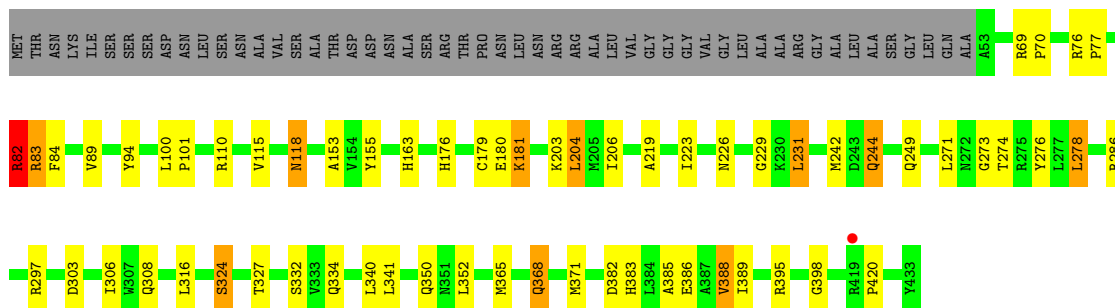
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	326	Total 326	O 326	0	0
5	B	136	Total 136	O 136	0	0

3 Residue-property plots

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.

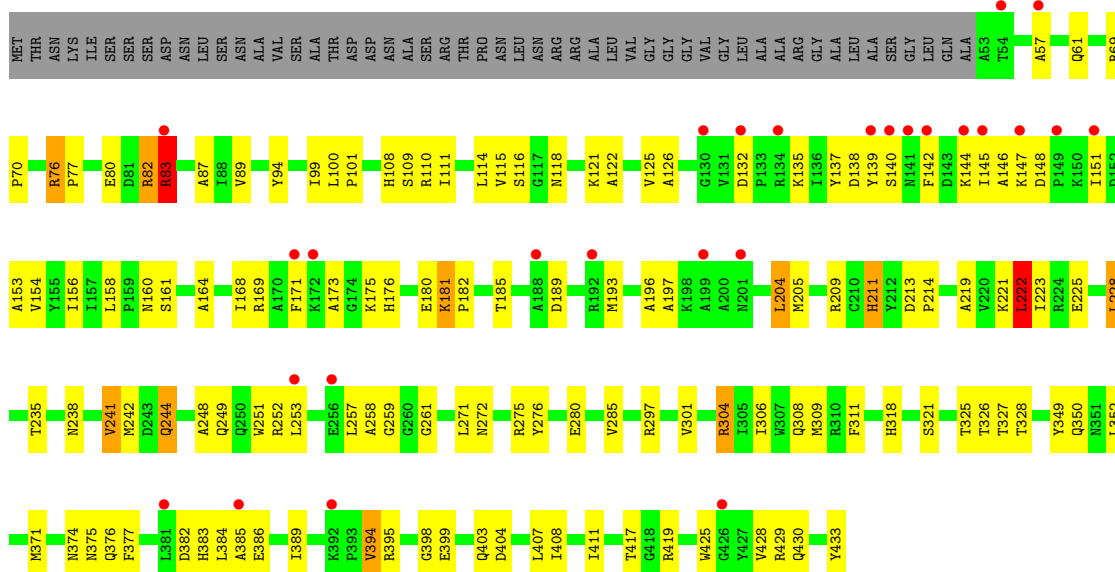
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain A: 



• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	84.10Å 93.30Å 115.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.20 15.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (15.00-2.20) 99.6 (15.00-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.06 (at 2.20Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.215 , 0.267 0.204 , 0.253	Depositor DCC
R_{free} test set	1382 reflections (2.98%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtrriage
Anisotropy	0.584	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6506	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.56% 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, SIN, GOL

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	0.38	0/3024	0.68	2/4093 (0.0%)
1	B	0.33	0/3024	0.61	3/4093 (0.1%)
All	All	0.36	0/6048	0.64	5/8186 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	ARG	NE-CZ-NH2	7.41	124.01	120.30
1	B	82	ARG	NE-CZ-NH2	6.64	123.62	120.30
1	A	83	ARG	NE-CZ-NH2	6.47	123.54	120.30
1	B	83	ARG	NE-CZ-NH2	6.32	123.46	120.30
1	B	222	LEU	CA-CB-CG	6.18	129.51	115.30

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	2960	0	2920	49	0
1	B	2960	0	2920	107	0
2	A	48	0	26	3	0
2	B	48	0	26	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	8	0	4	1	0
3	B	8	0	4	0	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
5	A	326	0	0	2	0
5	B	136	0	0	1	0
All	All	6506	0	5916	151	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 13.

All (151) 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:244:GLN:H	1:A:244:GLN:NE2	1.64	0.96
1:B:211:HIS:HE1	1:B:272:ASN:HD21	1.13	0.95
1:A:368:GLN:HE21	1:A:368:GLN:H	1.14	0.92
1:A:244:GLN:HE21	1:A:244:GLN:N	1.66	0.92
1:B:82:ARG:HG3	1:B:110:ARG:HB3	1.52	0.91
1:A:176:HIS:HD2	1:A:203:LYS:H	1.19	0.86
1:B:211:HIS:CE1	1:B:272:ASN:HD21	1.97	0.83
1:B:153:ALA:HB2	1:B:176:HIS:HB2	1.61	0.82
1:B:382:ASP:O	1:B:386:GLU:HG2	1.80	0.81
1:B:132:ASP:HB3	1:B:135:LYS:HD2	1.67	0.76
1:A:286:ARG:NH1	1:A:420:PRO:HB3	2.00	0.75
1:B:89:VAL:HG13	1:B:156:ILE:HA	1.69	0.74
1:A:368:GLN:H	1:A:368:GLN:NE2	1.85	0.74
1:B:82:ARG:CG	1:B:110:ARG:HB3	2.18	0.73
1:B:181:LYS:HD2	1:B:181:LYS:C	2.09	0.73
1:A:383:HIS:HE1	1:A:395:ARG:H	1.37	0.72
1:A:77:PRO:HD2	1:A:371:MET:HE2	1.72	0.70
1:A:176:HIS:CD2	1:A:203:LYS:H	2.08	0.68
1:A:118:ASN:C	1:A:118:ASN:HD22	1.97	0.67
1:A:244:GLN:H	1:A:244:GLN:HE21	0.81	0.67
1:A:385:ALA:O	1:A:389:ILE:HG12	1.95	0.66
1:B:185:THR:O	1:B:185:THR:HG22	1.96	0.65
1:B:209:ARG:HH11	1:B:376:GLN:HE22	1.44	0.65
1:B:403:GLN:HA	1:B:403:GLN:HE21	1.62	0.65
1:B:242:MET:SD	1:B:249:GLN:HB3	2.38	0.63
1:A:181:LYS:O	1:A:181:LYS:HD3	1.97	0.63
1:B:222:LEU:HD23	1:B:223:ILE:N	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:PRO:HD2	1:A:371:MET:CE	2.29	0.62
1:B:223:ILE:HG12	1:B:228:LEU:HD22	1.79	0.62
1:A:383:HIS:CE1	1:A:395:ARG:H	2.16	0.62
1:B:57:ALA:O	1:B:61:GLN:HG3	2.00	0.61
1:A:82:ARG:HB3	1:A:110:ARG:HB3	1.82	0.60
1:A:350:GLN:HB3	5:A:2243:HOH:O	2.01	0.60
1:B:82:ARG:HD2	1:B:109:SER:O	2.01	0.60
1:B:383:HIS:HE1	1:B:395:ARG:H	1.50	0.60
1:B:209:ARG:HH11	1:B:376:GLN:NE2	2.00	0.60
1:B:204:LEU:HD13	1:B:398:GLY:HA3	1.83	0.59
1:B:168:ILE:HG23	1:B:196:ALA:HB2	1.85	0.59
1:B:403:GLN:HE22	1:B:425:TRP:HE1	1.51	0.59
1:A:84:PHE:HE1	1:A:388:VAL:HG21	1.67	0.58
1:B:417:THR:HB	1:B:419:ARG:HD3	1.85	0.58
1:B:189:ASP:O	1:B:193:MET:HG3	2.04	0.58
1:B:285:VAL:HG22	1:B:309:MET:HG2	1.86	0.57
1:A:100:LEU:HB2	1:A:101:PRO:HD3	1.87	0.57
1:A:231:LEU:HD23	1:A:278:LEU:HD12	1.87	0.56
1:A:180:GLU:OE1	2:A:500:NDP:H2N	2.06	0.56
1:A:94:TYR:CD1	2:A:500:NDP:H41N	2.41	0.55
1:B:404:ASP:O	1:B:408:ILE:HG13	2.07	0.55
1:B:326:THR:HG22	1:B:327:THR:N	2.22	0.55
1:A:273:GLY:HA2	1:A:276:TYR:CE2	2.42	0.55
1:A:244:GLN:HE22	1:A:297:ARG:HD3	1.71	0.54
1:A:242:MET:SD	1:A:249:GLN:HB3	2.48	0.54
1:A:303:ASP:OD2	1:A:324:SER:HB2	2.07	0.54
1:B:238:ASN:HA	1:B:328:THR:O	2.07	0.54
1:B:100:LEU:HB2	1:B:101:PRO:HD3	1.89	0.54
1:B:161:SER:OG	1:B:257:LEU:HD12	2.08	0.54
1:B:69:ARG:HB3	1:B:70:PRO:HD2	1.91	0.53
1:B:205:MET:SD	1:B:394:VAL:HG21	2.49	0.53
1:B:301:VAL:HG22	5:B:2081:HOH:O	2.08	0.53
1:A:153:ALA:HB2	1:A:176:HIS:HB2	1.91	0.53
1:B:116:SER:HB3	1:B:122:ALA:HB2	1.91	0.52
1:B:89:VAL:CG1	1:B:156:ILE:HA	2.39	0.52
1:B:222:LEU:HD23	1:B:222:LEU:C	2.30	0.51
1:B:211:HIS:HE1	1:B:272:ASN:ND2	1.96	0.51
1:B:114:LEU:HD12	1:B:114:LEU:O	2.10	0.51
1:A:226:ASN:HD21	1:A:229:GLY:HA2	1.76	0.51
1:A:306:ILE:HD13	1:B:318:HIS:HB3	1.93	0.50
1:B:385:ALA:O	1:B:389:ILE:HG13	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:PRO:CD	1:A:371:MET:HE2	2.41	0.50
1:B:94:TYR:CE2	1:B:99:ILE:HD11	2.46	0.50
1:B:407:LEU:O	1:B:411:ILE:HG13	2.11	0.50
1:B:138:ASP:OD1	1:B:138:ASP:C	2.50	0.50
1:A:204:LEU:HD13	1:A:398:GLY:HA3	1.94	0.49
1:B:151:ILE:O	1:B:175:LYS:HD2	2.12	0.49
1:A:352:LEU:HD23	1:A:365:MET:HB3	1.95	0.48
1:B:125:VAL:HG23	1:B:126:ALA:N	2.29	0.48
1:B:89:VAL:HG22	1:B:158:LEU:HD21	1.95	0.48
1:B:251:TRP:HB2	1:B:257:LEU:HD23	1.95	0.48
1:B:115:VAL:HG22	1:B:137:TYR:HB2	1.95	0.48
1:B:76:ARG:HH11	1:B:76:ARG:HG2	1.79	0.48
1:B:76:ARG:HG2	1:B:77:PRO:N	2.27	0.47
1:B:100:LEU:HD22	1:B:111:ILE:HD13	1.95	0.47
1:A:286:ARG:NH1	1:A:420:PRO:CB	2.76	0.47
1:B:138:ASP:OD1	1:B:140:SER:N	2.48	0.47
1:B:87:ALA:O	1:B:154:VAL:HG23	2.15	0.47
1:B:153:ALA:CB	1:B:176:HIS:HB2	2.38	0.47
1:B:209:ARG:NH1	1:B:376:GLN:HE22	2.10	0.47
1:B:94:TYR:CD1	2:B:500:NDP:H41N	2.50	0.47
1:B:244:GLN:HE21	1:B:244:GLN:H	1.61	0.47
1:B:180:GLU:OE1	2:B:500:NDP:H2N	2.14	0.46
1:B:160:ASN:ND2	1:B:182:PRO:HD2	2.30	0.46
1:B:164:ALA:HB2	1:B:189:ASP:HB3	1.98	0.46
1:B:146:ALA:HA	1:B:175:LYS:HE2	1.97	0.46
1:A:308:GLN:HE22	1:B:306:ILE:HB	1.80	0.46
1:B:352:LEU:C	1:B:352:LEU:HD13	2.36	0.45
1:B:403:GLN:HA	1:B:403:GLN:NE2	2.31	0.45
1:A:83:ARG:NH2	1:A:389:ILE:HD12	2.31	0.45
1:B:221:LYS:HE2	1:B:225:GLU:OE2	2.17	0.45
1:B:139:TYR:O	1:B:169:ARG:NH2	2.50	0.45
1:B:326:THR:HG22	1:B:327:THR:H	1.82	0.45
1:A:316:LEU:HD12	1:B:304:ARG:HG3	1.98	0.45
1:A:274:THR:O	1:A:278:LEU:HB2	2.17	0.45
1:A:69:ARG:HB3	1:A:70:PRO:CD	2.47	0.44
1:B:244:GLN:H	1:B:244:GLN:NE2	2.14	0.44
1:A:382:ASP:O	1:A:386:GLU:HG3	2.17	0.44
1:B:280:GLU:HG3	1:B:311:PHE:CD2	2.52	0.44
1:B:252:ARG:HA	1:B:258:ALA:HB2	1.98	0.44
1:A:308:GLN:NE2	1:B:306:ILE:HB	2.32	0.44
1:B:185:THR:HG23	1:B:259:GLY:HA3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:ALA:HA	2:B:500:NDP:O1A	2.17	0.44
1:A:316:LEU:HG	1:B:304:ARG:NH1	2.33	0.44
1:B:144:LYS:HD2	1:B:147:LYS:HE3	1.99	0.44
1:B:429:ARG:NH1	1:B:433:TYR:HA	2.33	0.44
1:A:332:SER:HA	1:A:340:LEU:O	2.17	0.44
1:B:253:LEU:HD22	1:B:297:ARG:O	2.18	0.44
1:B:76:ARG:HH11	1:B:76:ARG:CG	2.30	0.43
1:B:77:PRO:HD3	1:B:371:MET:O	2.18	0.43
1:B:428:VAL:HG13	1:B:428:VAL:O	2.17	0.43
2:A:500:NDP:H42N	3:A:600:SIN:C1	2.48	0.43
1:A:89:VAL:HA	1:A:115:VAL:HB	2.00	0.43
1:B:185:THR:O	1:B:185:THR:CG2	2.65	0.43
1:B:238:ASN:O	1:B:321:SER:HA	2.19	0.43
1:B:135:LYS:NZ	1:B:148:ASP:OD2	2.51	0.43
1:B:142:PHE:O	1:B:145:ILE:HG23	2.19	0.42
1:B:83:ARG:HD3	1:B:389:ILE:CD1	2.49	0.42
1:B:271:LEU:O	1:B:275:ARG:HG3	2.18	0.42
1:A:226:ASN:ND2	1:A:229:GLY:HA2	2.34	0.42
1:B:257:LEU:HD12	1:B:257:LEU:HA	1.86	0.42
1:B:118:ASN:HB3	1:B:121:LYS:HE2	2.01	0.42
1:B:219:ALA:O	1:B:222:LEU:HD22	2.20	0.42
1:B:276:TYR:CB	1:B:433:TYR:HB3	2.49	0.42
1:B:375:ASN:ND2	1:B:377:PHE:HB2	2.35	0.42
1:B:213:ASP:HA	1:B:214:PRO:HD3	1.93	0.42
1:B:146:ALA:HB2	1:B:173:ALA:HA	2.02	0.42
1:B:276:TYR:HB2	1:B:433:TYR:HB3	2.01	0.41
1:B:383:HIS:CE1	1:B:394:VAL:HG22	2.55	0.41
1:A:219:ALA:O	1:A:223:ILE:HG13	2.21	0.41
1:A:383:HIS:HD2	5:A:2130:HOH:O	2.02	0.41
1:B:132:ASP:CB	1:B:135:LYS:HD2	2.42	0.41
1:B:261:GLY:HA2	1:B:301:VAL:HB	2.03	0.41
1:A:334:GLN:NE2	1:B:325:THR:OG1	2.54	0.41
1:B:80:GLU:OE1	1:B:108:HIS:HE1	2.03	0.41
1:B:235:THR:HA	1:B:318:HIS:O	2.20	0.41
1:B:241:VAL:O	1:B:241:VAL:HG22	2.19	0.41
1:B:383:HIS:CE1	1:B:395:ARG:H	2.32	0.41
1:B:261:GLY:CA	1:B:301:VAL:HB	2.50	0.41
1:B:222:LEU:CD2	1:B:223:ILE:HG13	2.50	0.41
1:A:163:HIS:HB3	1:A:179:CYS:SG	2.61	0.40
1:B:171:PHE:CZ	1:B:197:ALA:HB2	2.56	0.40
1:A:179:CYS:O	1:A:206:ILE:HA	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:ARG:CG	1:B:76:ARG:NH1	2.84	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	379/433 (88%)	367 (97%)	11 (3%)	1 (0%)	41	46
1	B	379/433 (88%)	366 (97%)	13 (3%)	0	100	100
All	All	758/866 (88%)	733 (97%)	24 (3%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	327	THR

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	308/345 (89%)	294 (96%)	14 (4%)	27	34
1	B	308/345 (89%)	290 (94%)	18 (6%)	20	23
All	All	616/690 (89%)	584 (95%)	32 (5%)	23	28

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	ARG
1	A	82	ARG
1	A	118	ASN
1	A	155	TYR
1	A	181	LYS
1	A	204	LEU
1	A	231	LEU
1	A	244	GLN
1	A	271	LEU
1	A	278	LEU
1	A	324	SER
1	A	341	LEU
1	A	368	GLN
1	A	388	VAL
1	B	76	ARG
1	B	83	ARG
1	B	181	LYS
1	B	204	LEU
1	B	211	HIS
1	B	222	LEU
1	B	228	LEU
1	B	241	VAL
1	B	244	GLN
1	B	304	ARG
1	B	308	GLN
1	B	349	TYR
1	B	350	GLN
1	B	374	ASN
1	B	384	LEU
1	B	394	VAL
1	B	399	GLU
1	B	430	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	A	118	ASN
1	A	176	HIS
1	A	191	GLN
1	A	226	ASN

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Mol	Chain	Res	Type
1	A	227	GLN
1	A	244	GLN
1	A	250	GLN
1	A	308	GLN
1	A	334	GLN
1	A	368	GLN
1	A	383	HIS
1	A	390	ASN
1	A	409	GLN
1	B	98	GLN
1	B	160	ASN
1	B	211	HIS
1	B	226	ASN
1	B	227	GLN
1	B	244	GLN
1	B	250	GLN
1	B	272	ASN
1	B	308	GLN
1	B	363	GLN
1	B	374	ASN
1	B	375	ASN
1	B	376	GLN
1	B	380	GLN
1	B	383	HIS
1	B	403	GLN
1	B	422	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

6 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	SIN	B	600	-	7,7,7	1.87	3 (42%)	8,8,8	1.84	3 (37%)
3	SIN	A	600	-	7,7,7	1.65	2 (28%)	8,8,8	1.69	2 (25%)
2	NDP	A	500	-	45,52,52	1.70	12 (26%)	53,80,80	1.31	5 (9%)
4	GOL	B	700	-	5,5,5	1.01	0	5,5,5	0.36	0
4	GOL	A	700	-	5,5,5	0.94	0	5,5,5	0.50	0
2	NDP	B	500	-	45,52,52	1.78	13 (28%)	53,80,80	1.25	5 (9%)

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	SIN	B	600	-	-	3/5/5/5	-
3	SIN	A	600	-	-	3/5/5/5	-
2	NDP	A	500	-	-	6/30/77/77	0/5/5/5
4	GOL	B	700	-	-	0/4/4/4	-
4	GOL	A	700	-	-	0/4/4/4	-
2	NDP	B	500	-	-	8/30/77/77	0/5/5/5

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	NDP	C6N-C5N	4.62	1.41	1.33
2	B	500	NDP	P2B-O2X	-4.51	1.37	1.54
2	A	500	NDP	C6N-C5N	4.44	1.41	1.33
2	A	500	NDP	P2B-O2X	-4.38	1.38	1.54
2	B	500	NDP	P2B-O2B	3.93	1.66	1.59
2	B	500	NDP	C7N-C3N	3.28	1.55	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	NDP	P2B-O2B	3.03	1.65	1.59
2	A	500	NDP	C6N-N1N	2.98	1.44	1.37
2	A	500	NDP	C7N-C3N	2.95	1.55	1.48
2	B	500	NDP	C4N-C3N	-2.94	1.44	1.49
3	B	600	SIN	O4-C4	-2.94	1.20	1.30
2	B	500	NDP	C6N-N1N	2.87	1.44	1.37
3	A	600	SIN	O4-C4	-2.87	1.21	1.30
2	A	500	NDP	C4N-C3N	-2.83	1.44	1.49
3	B	600	SIN	O2-C1	-2.81	1.21	1.30
2	A	500	NDP	O4B-C1B	2.73	1.44	1.41
2	B	500	NDP	C2N-C3N	2.59	1.42	1.34
2	B	500	NDP	O4B-C1B	2.55	1.44	1.41
3	A	600	SIN	O2-C1	-2.48	1.22	1.30
2	A	500	NDP	P2B-O1X	2.30	1.58	1.50
2	B	500	NDP	P2B-O1X	2.29	1.57	1.50
3	B	600	SIN	C3-C4	2.23	1.55	1.50
2	A	500	NDP	C2N-C3N	2.22	1.41	1.34
2	B	500	NDP	C4A-N3A	2.20	1.38	1.35
2	A	500	NDP	O4D-C1D	2.11	1.47	1.42
2	A	500	NDP	C5A-N7A	-2.11	1.32	1.39
2	B	500	NDP	O4D-C1D	2.10	1.47	1.42
2	A	500	NDP	C2A-N3A	2.09	1.35	1.32
2	B	500	NDP	C2A-N3A	2.04	1.35	1.32
2	B	500	NDP	C5A-N7A	-2.04	1.32	1.39

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	NDP	N3A-C2A-N1A	-5.02	120.83	128.68
2	B	500	NDP	N3A-C2A-N1A	-4.94	120.96	128.68
2	A	500	NDP	C3N-C2N-N1N	-3.40	118.24	123.10
2	B	500	NDP	C3N-C2N-N1N	-3.32	118.36	123.10
3	B	600	SIN	C3-C2-C1	2.97	119.98	113.60
2	A	500	NDP	C4A-C5A-N7A	2.77	112.28	109.40
3	B	600	SIN	C2-C3-C4	2.56	119.11	113.60
3	A	600	SIN	C3-C2-C1	2.51	119.00	113.60
2	A	500	NDP	C1D-N1N-C2N	-2.46	117.02	121.11
2	B	500	NDP	C1D-N1N-C2N	-2.41	117.09	121.11
2	B	500	NDP	C4A-C5A-N7A	2.29	111.78	109.40
3	A	600	SIN	O2-C1-C2	2.15	120.95	114.03
2	B	500	NDP	O2X-P2B-O2B	2.06	115.24	105.99
2	A	500	NDP	O2X-P2B-O2B	2.04	115.15	105.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	600	SIN	O2-C1-C2	2.02	120.51	114.03

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	500	NDP	C5D-O5D-PN-O2N
3	B	600	SIN	C1-C2-C3-C4
3	A	600	SIN	C1-C2-C3-C4
2	B	500	NDP	C5D-O5D-PN-O3
2	A	500	NDP	PA-O3-PN-O2N
2	B	500	NDP	PA-O3-PN-O2N
2	B	500	NDP	C5D-O5D-PN-O1N
2	B	500	NDP	O4D-C1D-N1N-C2N
2	A	500	NDP	O4D-C1D-N1N-C2N
3	B	600	SIN	O1-C1-C2-C3
3	B	600	SIN	O2-C1-C2-C3
2	B	500	NDP	O4B-C4B-C5B-O5B
3	A	600	SIN	O2-C1-C2-C3
2	A	500	NDP	O4B-C4B-C5B-O5B
3	A	600	SIN	C2-C3-C4-O3
2	A	500	NDP	C5D-O5D-PN-O3
2	B	500	NDP	C2B-O2B-P2B-O2X
2	A	500	NDP	C2N-C3N-C7N-N7N
2	B	500	NDP	C2N-C3N-C7N-N7N
2	A	500	NDP	C2D-C1D-N1N-C2N

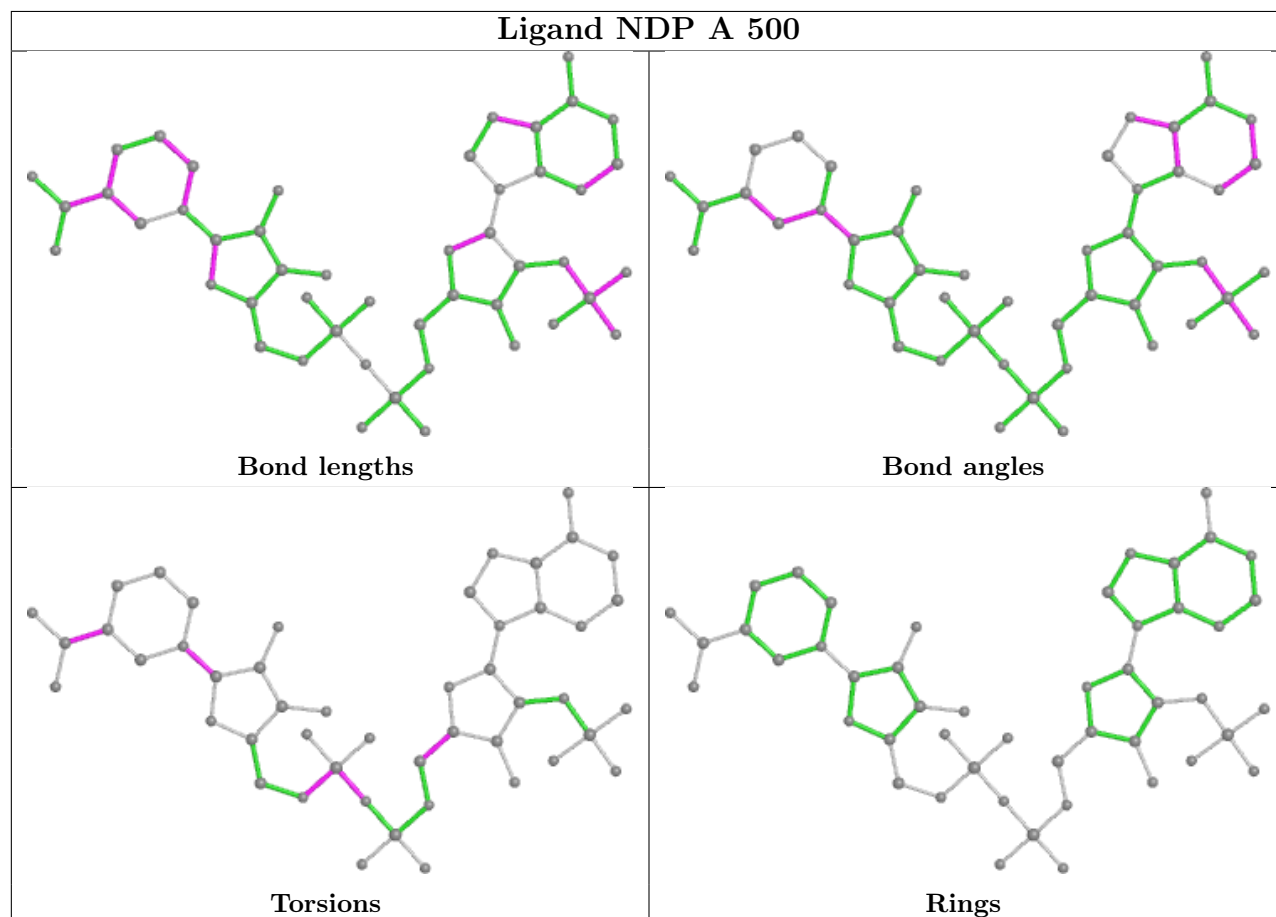
There are no ring outliers.

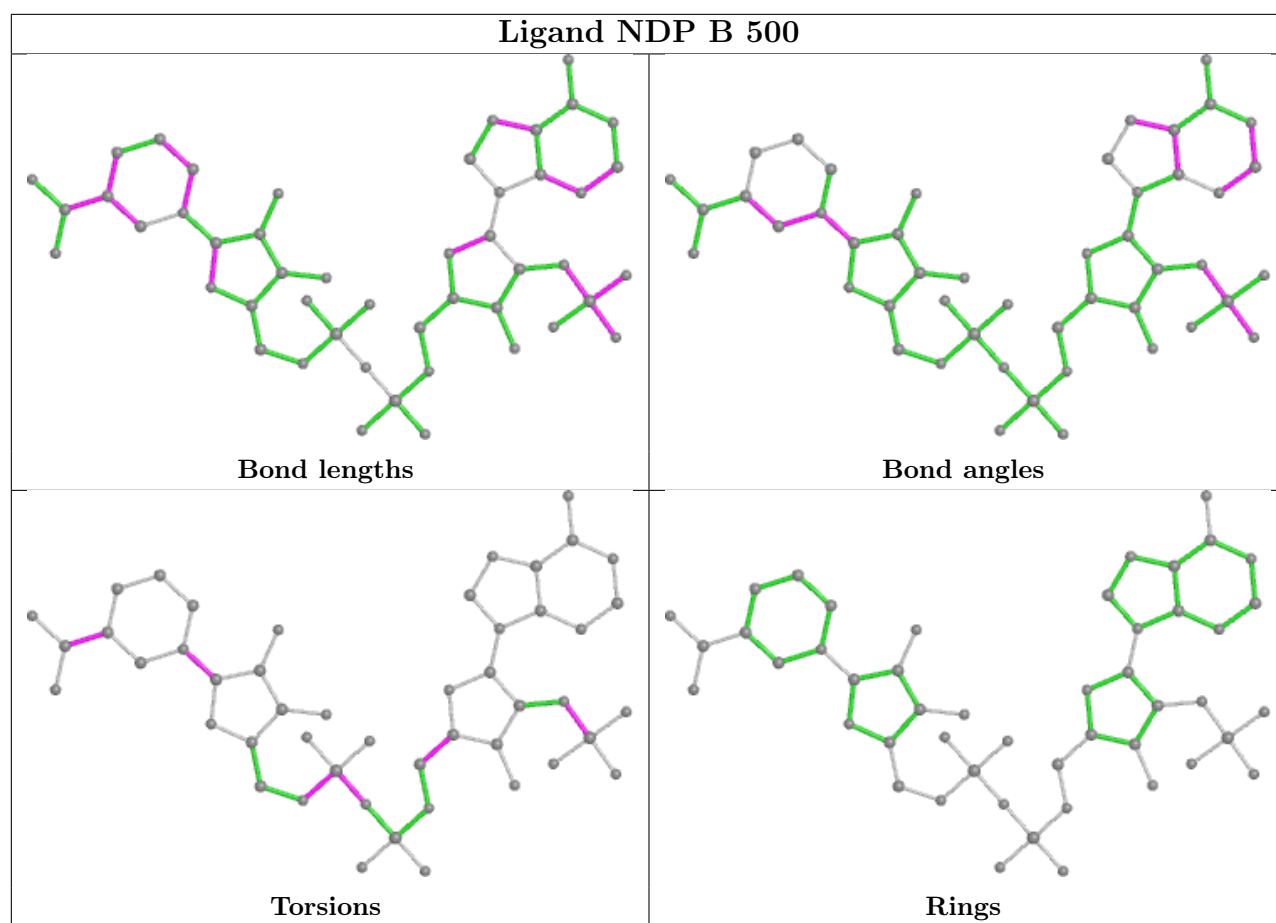
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	600	SIN	1	0
2	A	500	NDP	3	0
2	B	500	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	381/433 (87%)	-0.54	1 (0%) 94 93	18, 28, 41, 54	0
1	B	381/433 (87%)	0.33	27 (7%) 16 14	23, 49, 73, 82	0
All	All	762/866 (87%)	-0.11	28 (3%) 41 39	18, 35, 70, 82	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	147	LYS	4.2
1	B	134	ARG	3.8
1	B	145	ILE	3.2
1	B	132	ASP	3.2
1	B	140	SER	3.1
1	B	151	ILE	3.1
1	B	144	LYS	3.1
1	B	253	LEU	3.1
1	B	392	LYS	2.9
1	B	256	GLU	2.9
1	B	201	ASN	2.9
1	A	419	ARG	2.7
1	B	83	ARG	2.7
1	B	139	TYR	2.7
1	B	54	THR	2.6
1	B	130	GLY	2.6
1	B	426	GLY	2.6
1	B	381	LEU	2.5
1	B	385	ALA	2.5
1	B	171	PHE	2.5
1	B	142	PHE	2.4
1	B	172	LYS	2.4
1	B	192	ARG	2.4
1	B	141	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	57	ALA	2.1
1	B	199	ALA	2.1
1	B	188	ALA	2.1
1	B	149	PRO	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](#)

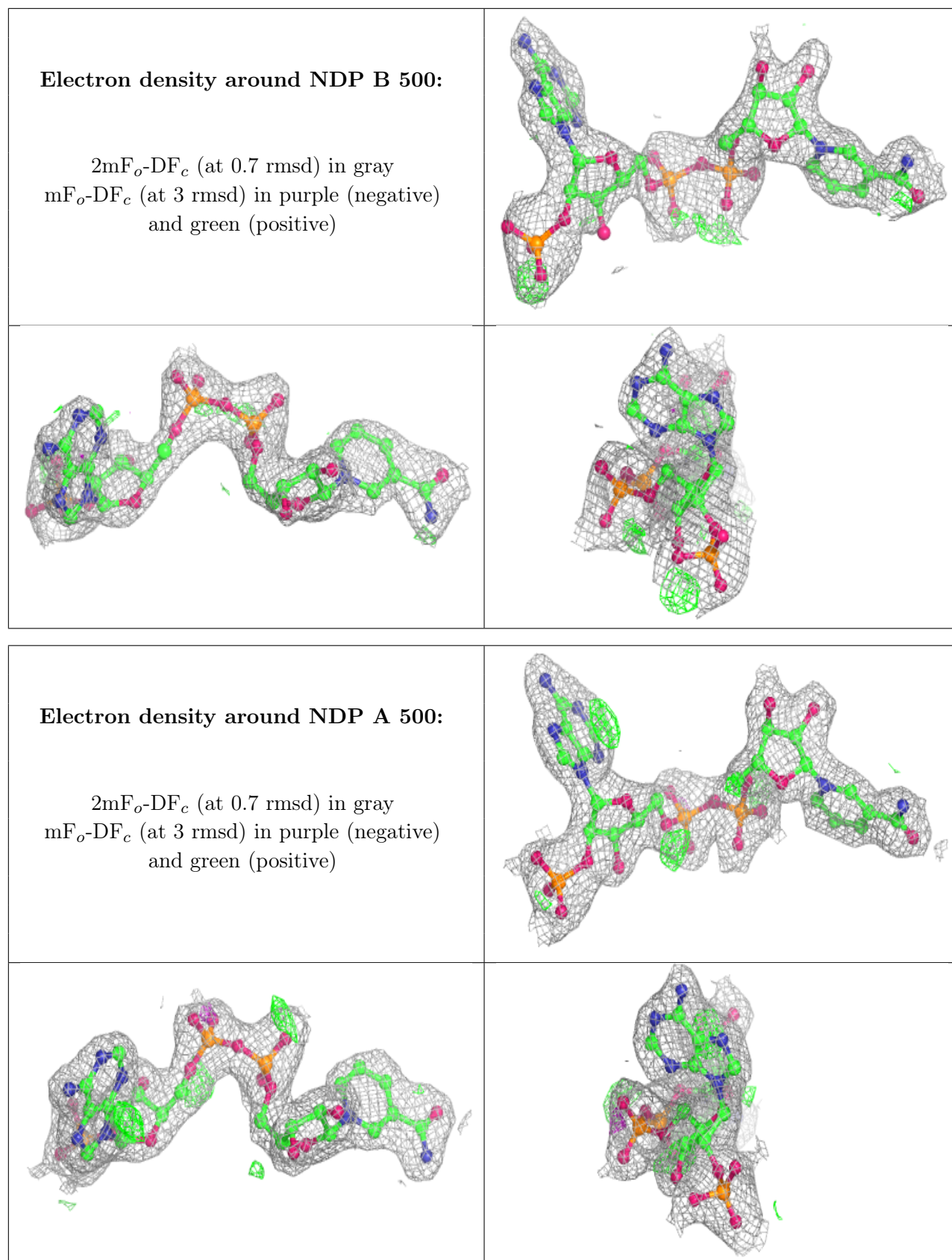
There are no monosaccharides in this entry.

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
4	GOL	B	700	6/6	0.79	0.20	63,64,64,64	0
3	SIN	B	600	8/8	0.82	0.18	62,67,68,68	0
4	GOL	A	700	6/6	0.85	0.26	57,58,60,61	0
3	SIN	A	600	8/8	0.86	0.16	34,36,37,38	0
2	NDP	B	500	48/48	0.92	0.14	47,54,62,63	0
2	NDP	A	500	48/48	0.97	0.10	16,25,28,29	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.