



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:05 PM UTC

PDB ID : 1UXT / pdb_00001uxt
Title : Structural basis for allosteric regulation and substrate specificity of the non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase (GAPN) from *Thermoproteus tenax*
Authors : Lorentzen, E.; Hensel, R.; Pohl, E.
Deposited on : 2004-03-01
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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

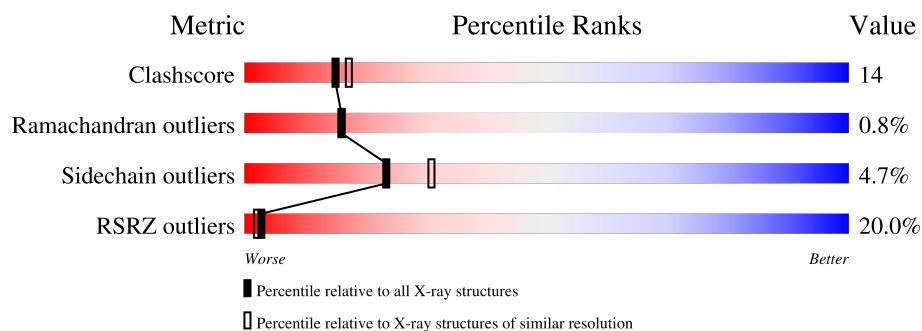
1 Overall quality at a glance

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))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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	501	20% 70% 25% .

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4106 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.

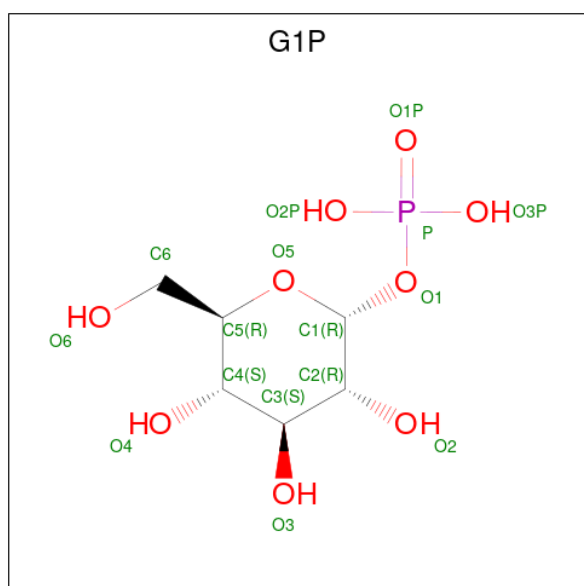
- Molecule 1 is a protein called GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total	C	N	O	S	0	0	0
			3777	2416	649	703	9			

There are 2 discrepancies between the modelled and reference sequences:

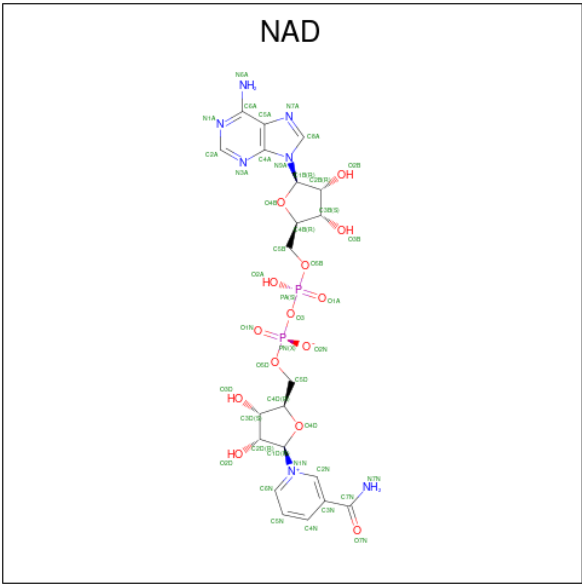
Chain	Residue	Modelled	Actual	Comment	Reference
A	378	PHE	LEU	engineered mutation	UNP O57693
A	402	LEU	SER	conflict	UNP O57693

- Molecule 2 is 1-O-phosphono-alpha-D-glucopyranose (CCD ID: G1P) (formula: $C_6H_{13}O_9P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			16	6	9	1		

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		

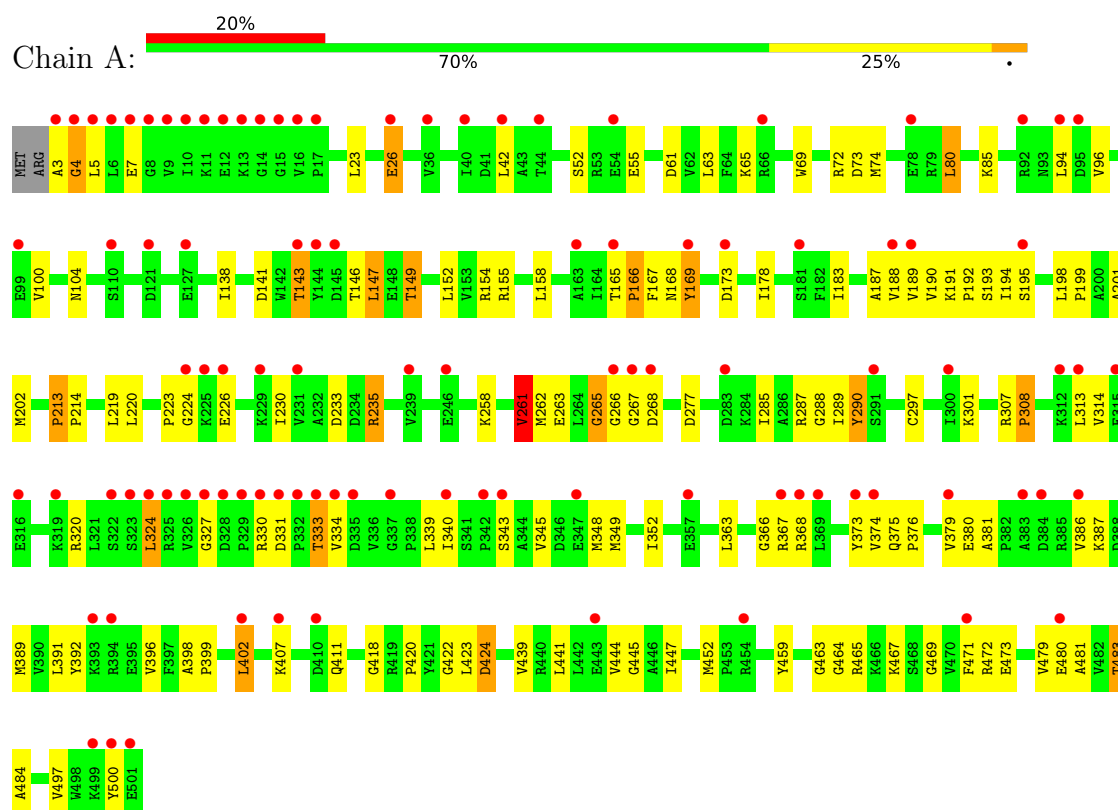
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	268	Total	O	0	0
			268	268		

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: GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NADP+)



4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α , β , γ	185.35Å 185.35Å 134.70Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.20 30.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.0 (30.00-2.20) 95.7 (30.00-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.32 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.224 , 0.242 0.238 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	49.3	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4106	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: G1P, NAD, NA

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	0.64	2/3847 (0.1%)	1.09	25/5219 (0.5%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	74	MET	SD-CE	5.98	1.94	1.79
1	A	262	MET	SD-CE	-5.23	1.66	1.79

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	266	GLY	CA-C-N	-9.43	112.94	122.27
1	A	266	GLY	C-N-CA	-9.43	112.94	122.27
1	A	266	GLY	N-CA-C	-8.18	101.23	111.70
1	A	187	ALA	N-CA-C	-7.90	98.82	110.52
1	A	168	ASN	N-CA-C	7.90	122.48	113.01
1	A	497	VAL	N-CA-C	-7.80	103.64	110.74
1	A	261	VAL	N-CA-C	-7.36	96.87	107.77
1	A	308	PRO	N-CA-C	6.47	122.25	113.84
1	A	265	GLY	N-CA-C	6.29	122.62	111.73
1	A	340	ILE	N-CA-C	6.02	118.58	111.05
1	A	138	ILE	N-CA-C	6.02	113.51	107.55
1	A	169	TYR	N-CA-C	-5.85	100.59	109.30
1	A	290	TYR	N-CA-C	5.82	120.66	113.50
1	A	465	ARG	N-CA-C	-5.64	100.78	109.52
1	A	441	LEU	N-CA-C	5.58	120.15	113.23
1	A	339	LEU	N-CA-C	-5.58	102.27	110.52
1	A	213	PRO	CA-C-N	5.46	125.80	119.47
1	A	213	PRO	C-N-CA	5.46	125.80	119.47
1	A	23	LEU	N-CA-C	5.21	118.69	111.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	277	ASP	N-CA-C	-5.18	100.64	108.67
1	A	464	GLY	N-CA-C	5.17	121.51	112.10
1	A	188	VAL	N-CA-C	5.16	116.09	108.45
1	A	459	TYR	N-CA-C	-5.10	105.85	111.71
1	A	473	GLU	N-CA-C	-5.01	101.93	109.85
1	A	469	GLY	N-CA-C	5.01	119.39	112.52

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	3777	0	3857	106	0
2	A	16	0	11	1	0
3	A	44	0	26	4	0
4	A	1	0	0	0	0
5	A	268	0	0	7	0
All	All	4106	0	3894	106	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 14.

All (106) 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:100:VAL:HG11	1:A:202:MET:HE1	1.36	1.07
1:A:267:GLY:HA3	1:A:301:LYS:HG3	1.37	1.01
1:A:223:PRO:HG2	1:A:226:GLU:HG3	1.51	0.92
1:A:265:GLY:H	3:A:1503:NAD:H71N	1.25	0.82
1:A:386:VAL:HG23	1:A:389:MET:HE2	1.63	0.80
1:A:165:THR:CG2	1:A:192:PRO:HA	2.13	0.79
1:A:233:ASP:OD1	1:A:235:ARG:HD3	1.87	0.74
1:A:330:ARG:HB2	5:A:2177:HOH:O	1.88	0.73
1:A:100:VAL:CG1	1:A:202:MET:HE1	2.17	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:THR:HG23	1:A:192:PRO:HA	1.72	0.72
1:A:154:ARG:NH1	5:A:2098:HOH:O	2.22	0.72
1:A:100:VAL:HG11	1:A:202:MET:CE	2.17	0.72
1:A:391:LEU:HD13	1:A:402:LEU:HD11	1.77	0.66
1:A:363:LEU:HD11	1:A:380:GLU:HB2	1.78	0.65
1:A:480:GLU:HG2	5:A:2102:HOH:O	1.96	0.65
1:A:261:VAL:HG22	1:A:481:ALA:HB1	1.79	0.65
1:A:158:LEU:HD21	1:A:484:ALA:HB2	1.79	0.65
1:A:63:LEU:HD13	1:A:189:VAL:HG22	1.77	0.64
1:A:386:VAL:HG23	1:A:389:MET:CE	2.28	0.64
1:A:331:ASP:HB2	1:A:334:VAL:HG23	1.79	0.62
1:A:143:THR:HG22	1:A:146:THR:H	1.64	0.62
1:A:345:VAL:HG13	1:A:374:VAL:HG11	1.81	0.62
1:A:285:ILE:O	1:A:289:ILE:HG13	2.01	0.60
1:A:96:VAL:HG23	5:A:2061:HOH:O	2.01	0.60
1:A:386:VAL:HA	1:A:389:MET:HE2	1.84	0.59
1:A:479:VAL:O	1:A:483:THR:HB	2.01	0.59
1:A:201:ALA:HA	1:A:219:LEU:CD2	2.33	0.58
1:A:165:THR:OG1	1:A:166:PRO:HD2	2.04	0.58
1:A:345:VAL:HG13	1:A:374:VAL:CG1	2.34	0.58
1:A:420:PRO:O	1:A:467:LYS:HB2	2.04	0.57
1:A:287:ARG:HG3	1:A:287:ARG:HH11	1.70	0.57
1:A:439:VAL:HA	1:A:447:ILE:HD13	1.86	0.57
1:A:391:LEU:HB3	1:A:402:LEU:HD11	1.85	0.57
1:A:265:GLY:N	3:A:1503:NAD:H71N	2.00	0.57
1:A:391:LEU:CD1	1:A:402:LEU:HD11	2.34	0.56
1:A:381:ALA:CB	1:A:389:MET:HE1	2.36	0.56
1:A:261:VAL:CG2	1:A:481:ALA:HB1	2.36	0.56
1:A:261:VAL:HG22	1:A:481:ALA:CB	2.35	0.56
1:A:63:LEU:CD1	1:A:189:VAL:HG22	2.35	0.56
1:A:407:LYS:HG3	1:A:411:GLN:OE1	2.07	0.55
1:A:307:ARG:HB2	1:A:308:PRO:CD	2.37	0.55
1:A:391:LEU:HD13	1:A:402:LEU:CD1	2.37	0.55
1:A:307:ARG:HB2	1:A:308:PRO:HD3	1.89	0.55
1:A:391:LEU:CB	1:A:402:LEU:HD11	2.36	0.55
1:A:169:TYR:HB2	1:A:173:ASP:OD2	2.07	0.54
1:A:146:THR:O	1:A:149:THR:HB	2.08	0.54
1:A:80:LEU:HD13	1:A:183:ILE:HD11	1.90	0.54
1:A:290:TYR:CD2	1:A:324:LEU:HD21	2.44	0.53
1:A:265:GLY:HA2	1:A:423:LEU:HD22	1.91	0.53
1:A:268:ASP:OD2	1:A:424:ASP:HB2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:ALA:O	1:A:5:LEU:N	2.43	0.52
1:A:155:ARG:NH2	5:A:2102:HOH:O	2.42	0.52
1:A:26:GLU:HG3	5:A:2011:HOH:O	2.09	0.51
1:A:263:GLU:HB3	3:A:1503:NAD:C7N	2.40	0.51
1:A:381:ALA:HB2	1:A:389:MET:HE1	1.92	0.51
1:A:158:LEU:CD2	1:A:484:ALA:HB2	2.41	0.50
1:A:141:ASP:HA	1:A:147:LEU:HD12	1.94	0.50
1:A:331:ASP:C	1:A:333:THR:H	2.19	0.50
1:A:61:ASP:OD1	1:A:65:LYS:HE3	2.14	0.48
1:A:52:SER:OG	1:A:55:GLU:HG3	2.14	0.48
1:A:314:VAL:CG1	1:A:363:LEU:HD13	2.44	0.48
1:A:327:GLY:O	1:A:373:TYR:HE2	1.97	0.48
1:A:348:MET:O	1:A:352:ILE:HG13	2.14	0.48
1:A:288:GLY:HA2	1:A:452:MET:HE3	1.96	0.47
1:A:483:THR:HG22	5:A:2101:HOH:O	2.13	0.47
1:A:165:THR:HG22	1:A:192:PRO:HA	1.93	0.47
1:A:324:LEU:HD23	1:A:376:PRO:HG3	1.96	0.47
1:A:100:VAL:HG21	1:A:202:MET:HE1	1.95	0.47
1:A:3:ALA:O	1:A:4:GLY:C	2.58	0.47
1:A:261:VAL:HG13	1:A:471:PHE:HB3	1.97	0.47
1:A:301:LYS:NZ	1:A:396:VAL:O	2.48	0.46
1:A:94:LEU:O	1:A:94:LEU:HD12	2.14	0.46
1:A:297:CYS:SG	3:A:1503:NAD:C4N	3.03	0.46
1:A:220:LEU:HD12	1:A:230:ILE:HD11	1.98	0.46
1:A:313:LEU:HD13	1:A:313:LEU:C	2.41	0.46
1:A:167:PHE:C	1:A:167:PHE:CD1	2.94	0.45
1:A:367:ARG:HB2	1:A:375:GLN:OE1	2.17	0.45
1:A:201:ALA:HA	1:A:219:LEU:HD21	1.96	0.45
1:A:193:SER:OG	1:A:195:SER:HB3	2.17	0.45
1:A:368:ARG:HA	1:A:374:VAL:HG12	1.99	0.45
1:A:198:LEU:HB2	1:A:199:PRO:HD3	1.98	0.44
1:A:445:GLY:HA3	1:A:463:GLY:O	2.17	0.44
1:A:85:LYS:HA	1:A:85:LYS:HD2	1.74	0.44
1:A:331:ASP:C	1:A:333:THR:N	2.75	0.44
1:A:349:MET:HE1	1:A:366:GLY:O	2.19	0.43
1:A:178:ILE:HD11	1:A:190:VAL:HG21	2.00	0.43
1:A:233:ASP:OD1	1:A:235:ARG:CD	2.61	0.43
1:A:94:LEU:HD12	1:A:94:LEU:C	2.44	0.42
1:A:194:ILE:HD12	1:A:194:ILE:HA	1.86	0.42
1:A:104:ASN:O	1:A:104:ASN:ND2	2.52	0.42
1:A:287:ARG:HG3	1:A:287:ARG:NH1	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:VAL:O	1:A:402:LEU:HA	2.20	0.42
1:A:42:LEU:HD12	1:A:42:LEU:N	2.35	0.42
1:A:72:ARG:NH2	2:A:1502:G1P:O2P	2.43	0.42
1:A:392:TYR:OH	1:A:418:GLY:HA3	2.19	0.42
1:A:422:GLY:HA2	1:A:444:VAL:HG12	2.01	0.42
1:A:320:ARG:O	1:A:324:LEU:HD13	2.20	0.41
1:A:386:VAL:HG13	1:A:387:LYS:N	2.34	0.41
1:A:290:TYR:CD1	1:A:290:TYR:C	2.98	0.41
1:A:100:VAL:CB	1:A:202:MET:HE1	2.50	0.41
1:A:96:VAL:O	1:A:100:VAL:HG23	2.21	0.41
1:A:69:TRP:O	1:A:73:ASP:HB2	2.20	0.41
1:A:213:PRO:HA	1:A:214:PRO:HD2	1.78	0.41
1:A:307:ARG:NH2	1:A:407:LYS:HG2	2.36	0.40
1:A:398:ALA:HB1	1:A:399:PRO:HD2	2.02	0.40
1:A:402:LEU:CD1	1:A:402:LEU:N	2.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	497/501 (99%)	474 (95%)	19 (4%)	4 (1%)	16 16

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	GLY
1	A	224	GLY
1	A	500	TYR
1	A	7	GLU

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	386/393 (98%)	368 (95%)	18 (5%)	23	31

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	GLU
1	A	80	LEU
1	A	143	THR
1	A	147	LEU
1	A	149	THR
1	A	152	LEU
1	A	166	PRO
1	A	191	LYS
1	A	235	ARG
1	A	258	LYS
1	A	261	VAL
1	A	324	LEU
1	A	333	THR
1	A	343	SER
1	A	402	LEU
1	A	424	ASP
1	A	472	ARG
1	A	483	THR

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

Mol	Chain	Res	Type
1	A	221	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	NAD	A	1503	-	46,48,48	2.23	12 (26%)	64,73,73	1.77	8 (12%)
2	G1P	A	1502	-	15,16,16	1.63	3 (20%)	24,24,24	2.39	8 (33%)

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	NAD	A	1503	-	-	8/30/62/62	0/5/5/5
2	G1P	A	1502	-	-	2/7/27/27	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1503	NAD	C2N-N1N	7.32	1.43	1.35
3	A	1503	NAD	PN-O3	-4.56	1.54	1.59
3	A	1503	NAD	C5N-C4N	4.55	1.46	1.38
3	A	1503	NAD	C6N-N1N	4.28	1.45	1.35
2	A	1502	G1P	P-O2P	4.07	1.69	1.54
3	A	1503	NAD	C3N-C7N	3.97	1.56	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1503	NAD	C4N-C3N	3.93	1.45	1.39
3	A	1503	NAD	O4D-C1D	3.70	1.45	1.40
3	A	1503	NAD	PA-O3	-3.42	1.55	1.59
3	A	1503	NAD	C5A-N7A	-2.63	1.34	1.39
3	A	1503	NAD	C4A-N3A	2.59	1.39	1.34
2	A	1502	G1P	P-O3P	2.58	1.64	1.54
3	A	1503	NAD	O5B-C5B	-2.50	1.35	1.44
3	A	1503	NAD	C8A-N7A	2.28	1.36	1.31
2	A	1502	G1P	P-O1	2.05	1.63	1.59

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1503	NAD	C5A-C4A-N3A	-5.88	118.62	126.72
3	A	1503	NAD	O4B-C4B-C5B	-5.46	91.86	109.33
3	A	1503	NAD	N3A-C2A-N1A	-5.10	120.86	128.58
3	A	1503	NAD	N3A-C4A-N9A	4.69	135.14	127.17
2	A	1502	G1P	P-O1-C1	4.59	135.85	123.54
2	A	1502	G1P	O1-C1-C2	-4.58	99.99	108.38
2	A	1502	G1P	O5-C1-C2	4.29	119.18	110.37
2	A	1502	G1P	C4-C3-C2	-3.99	103.83	110.83
2	A	1502	G1P	O5-C5-C4	3.86	116.65	109.70
3	A	1503	NAD	C2A-N3A-C4A	3.84	121.22	111.83
2	A	1502	G1P	C1-O5-C5	3.75	121.03	113.72
2	A	1502	G1P	O4-C4-C3	-3.34	102.50	110.38
3	A	1503	NAD	O3-PN-O1N	-2.54	103.05	110.70
3	A	1503	NAD	N9A-C8A-N7A	-2.53	110.34	113.94
2	A	1502	G1P	O1-P-O1P	2.47	118.12	109.33
3	A	1503	NAD	C6A-C5A-C4A	2.17	120.14	117.18

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1502	G1P	O5-C1-O1-P
3	A	1503	NAD	PN-O3-PA-O5B
3	A	1503	NAD	C2B-C1B-N9A-C8A
3	A	1503	NAD	C4D-C5D-O5D-PN
3	A	1503	NAD	PA-O3-PN-O2N
2	A	1502	G1P	C2-C1-O1-P
3	A	1503	NAD	C2B-C1B-N9A-C4A
3	A	1503	NAD	O4B-C1B-N9A-C8A

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Mol	Chain	Res	Type	Atoms
3	A	1503	NAD	PA-O3-PN-O1N
3	A	1503	NAD	O4B-C4B-C5B-O5B

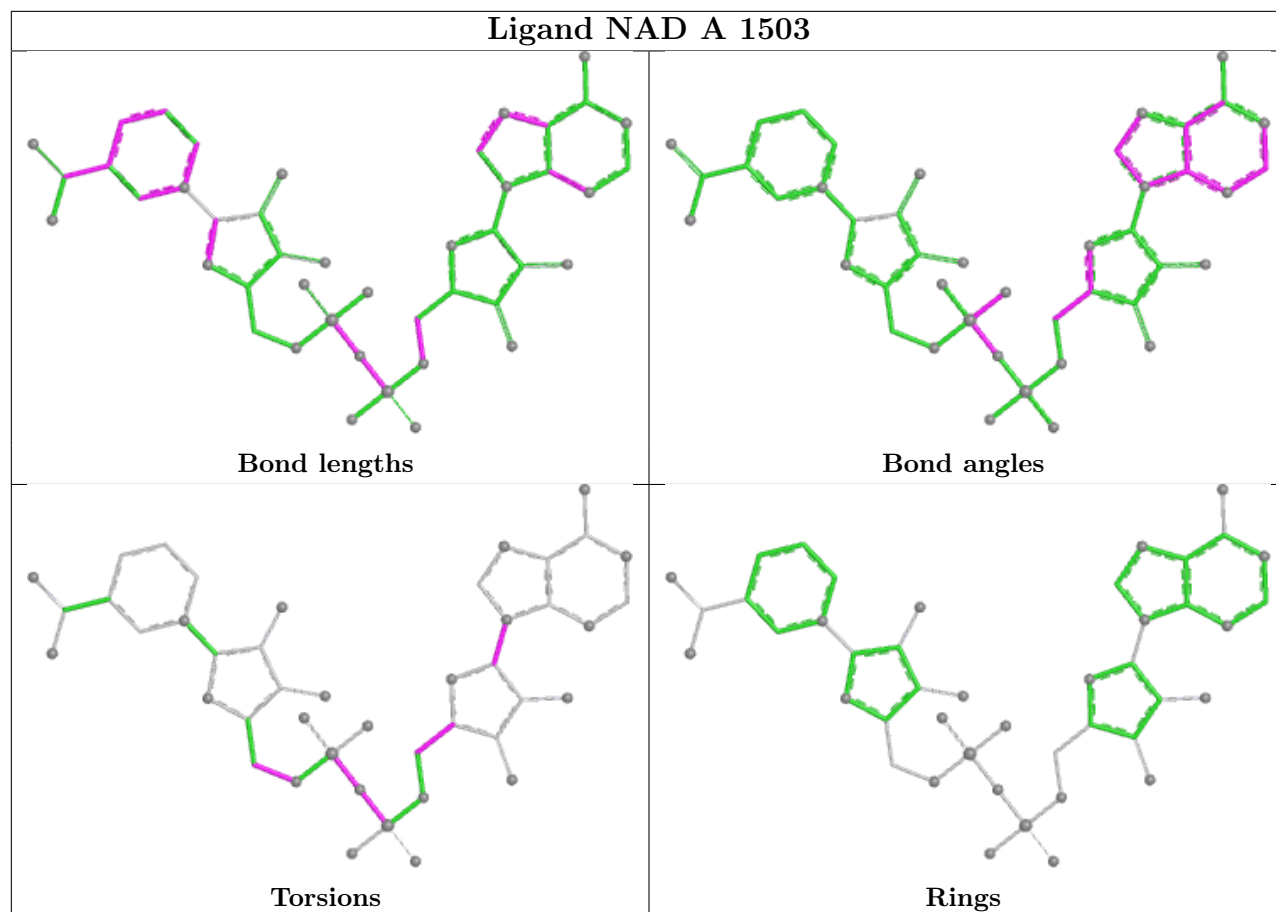
There are no ring outliers.

2 monomers are involved in 5 short contacts:

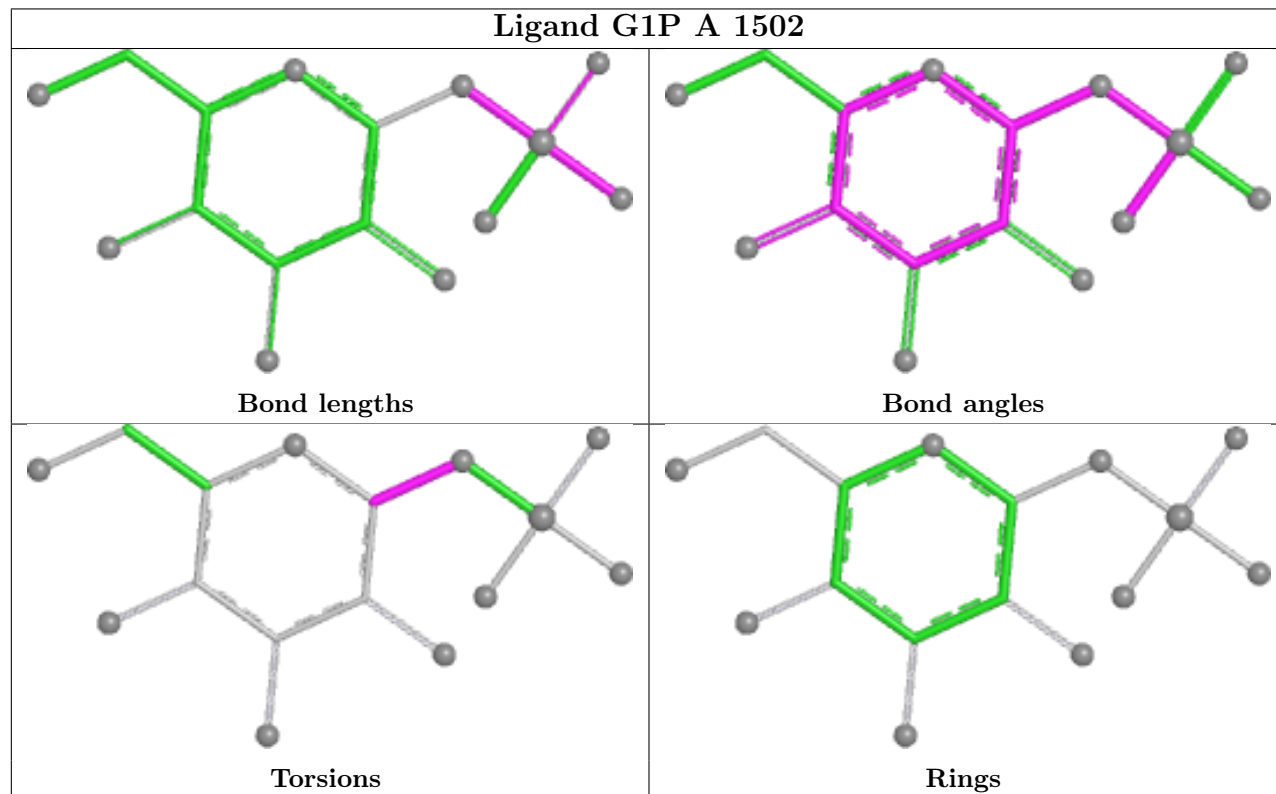
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1503	NAD	4	0
2	A	1502	G1P	1	0

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.

Ligand NAD A 1503



Ligand G1P A 1502



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	499/501 (99%)	1.36	100 (20%) 3 2	40, 55, 81, 105	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	ALA	16.3
1	A	500	TYR	9.3
1	A	4	GLY	7.9
1	A	327	GLY	5.6
1	A	13	LYS	5.0
1	A	331	ASP	4.9
1	A	333	THR	4.7
1	A	267	GLY	4.7
1	A	325	ARG	4.6
1	A	326	VAL	4.4
1	A	347	GLU	4.4
1	A	169	TYR	4.4
1	A	334	VAL	4.2
1	A	330	ARG	3.8
1	A	328	ASP	3.7
1	A	332	PRO	3.7
1	A	407	LYS	3.6
1	A	246	GLU	3.6
1	A	189	VAL	3.5
1	A	322	SER	3.5
1	A	54	GLU	3.5
1	A	127	GLU	3.4
1	A	5	LEU	3.4
1	A	480	GLU	3.3
1	A	501	GLU	3.3
1	A	95	ASP	3.3
1	A	229	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	324	LEU	3.3
1	A	373	TYR	3.2
1	A	11	LYS	3.1
1	A	329	PRO	3.1
1	A	335	ASP	3.0
1	A	42	LEU	3.0
1	A	14	GLY	3.0
1	A	471	PHE	3.0
1	A	9	VAL	3.0
1	A	291	SER	3.0
1	A	226	GLU	3.0
1	A	383	ALA	2.9
1	A	402	LEU	2.9
1	A	145	ASP	2.9
1	A	195	SER	2.9
1	A	369	LEU	2.8
1	A	92	ARG	2.8
1	A	454	ARG	2.8
1	A	268	ASP	2.8
1	A	7	GLU	2.7
1	A	239	VAL	2.7
1	A	337	GLY	2.7
1	A	410	ASP	2.6
1	A	6	LEU	2.5
1	A	15	GLY	2.5
1	A	181	SER	2.5
1	A	319	LYS	2.5
1	A	300	ILE	2.5
1	A	144	TYR	2.5
1	A	394	ARG	2.5
1	A	384	ASP	2.5
1	A	26	GLU	2.4
1	A	78	GLU	2.4
1	A	121	ASP	2.4
1	A	283	ASP	2.4
1	A	357	GLU	2.4
1	A	143	THR	2.4
1	A	165	THR	2.4
1	A	66	ARG	2.4
1	A	17	PRO	2.3
1	A	312	LYS	2.3
1	A	188	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	386	VAL	2.3
1	A	443	GLU	2.3
1	A	266	GLY	2.3
1	A	110	SER	2.3
1	A	12	GLU	2.3
1	A	316	GLU	2.3
1	A	173	ASP	2.3
1	A	163	ALA	2.3
1	A	99	GLU	2.3
1	A	225	LYS	2.3
1	A	16	VAL	2.2
1	A	368	ARG	2.2
1	A	315	GLU	2.2
1	A	40	ILE	2.2
1	A	36	VAL	2.2
1	A	374	VAL	2.2
1	A	342	PRO	2.2
1	A	224	GLY	2.2
1	A	94	LEU	2.1
1	A	340	ILE	2.1
1	A	323	SER	2.1
1	A	393	LYS	2.1
1	A	379	VAL	2.1
1	A	44	THR	2.1
1	A	367	ARG	2.1
1	A	499	LYS	2.1
1	A	231	VAL	2.1
1	A	8	GLY	2.1
1	A	343	SER	2.1
1	A	313	LEU	2.0
1	A	10	ILE	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 oligosaccharides in this entry.

6.4 Ligands

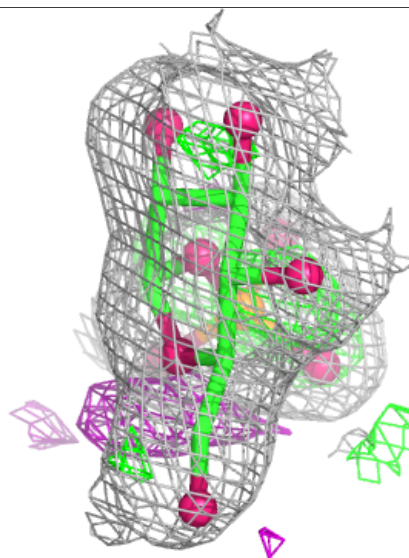
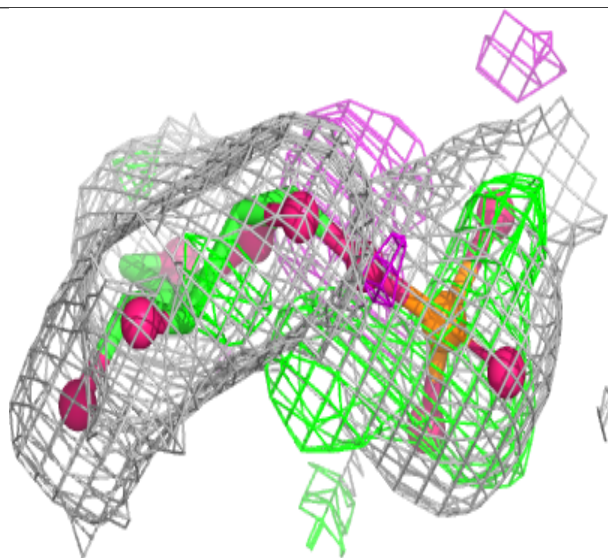
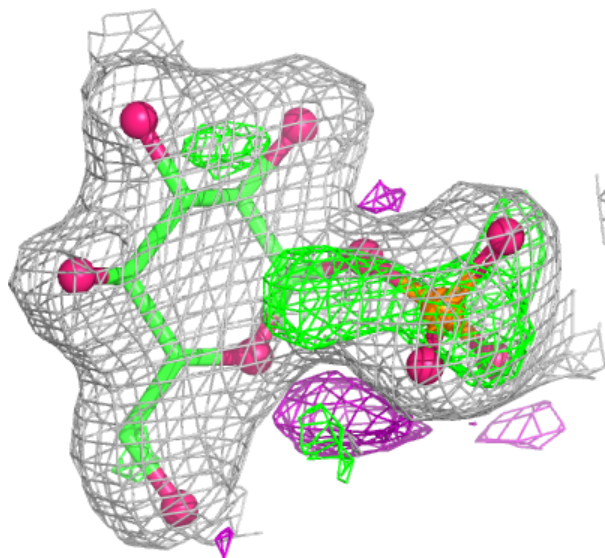
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	G1P	A	1502	16/16	0.93	0.14	43,48,53,54	0
3	NAD	A	1503	44/44	0.94	0.13	49,53,59,59	0
4	NA	A	1504	1/1	0.97	0.06	55,55,55,55	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.

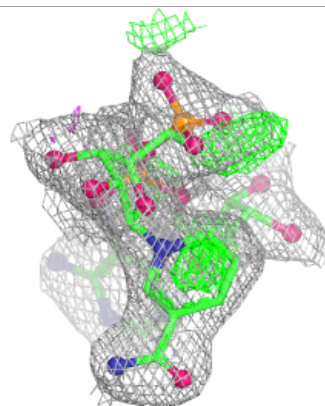
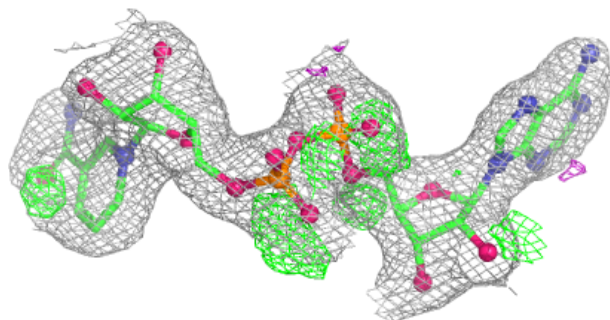
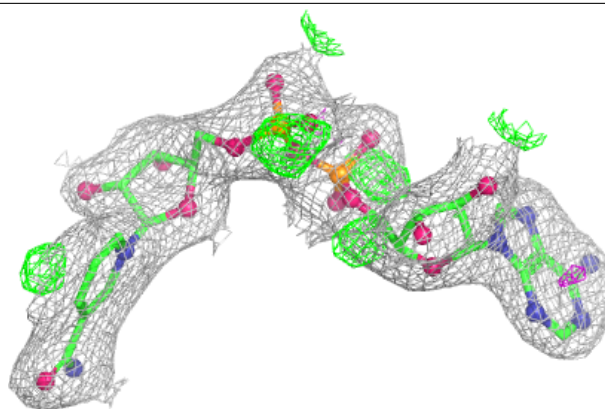
Electron density around G1P A 1502:

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



Electron density around NAD A 1503:

$2mF_o-DF_c$ (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.