



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:49 PM UTC

PDB ID : 8U2W / pdb_00008u2w
Title : Glucose-6-phosphate 1-dehydrogenase (G6PDH) from *Crithidia fasciculata* (NADP bound)
Authors : Seattle Structural Genomics Center for Infectious Disease; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2023-09-06
Resolution : 2.35 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

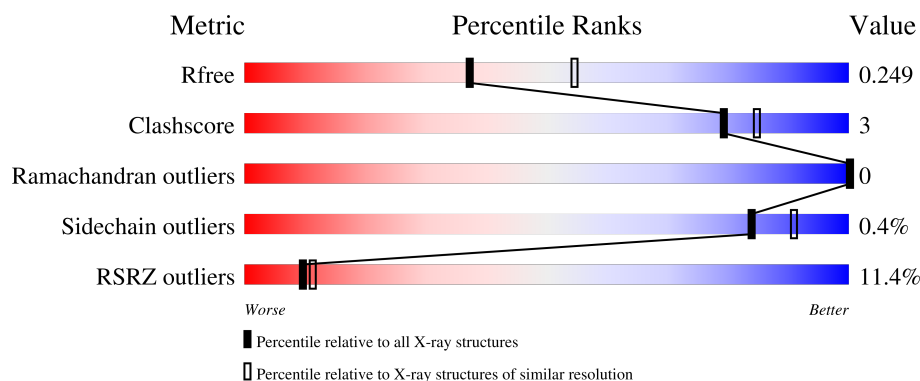
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	679	8% 66% 5% 29%
1	B	679	9% 66% 5% 29%

2 Entry composition [i](#)

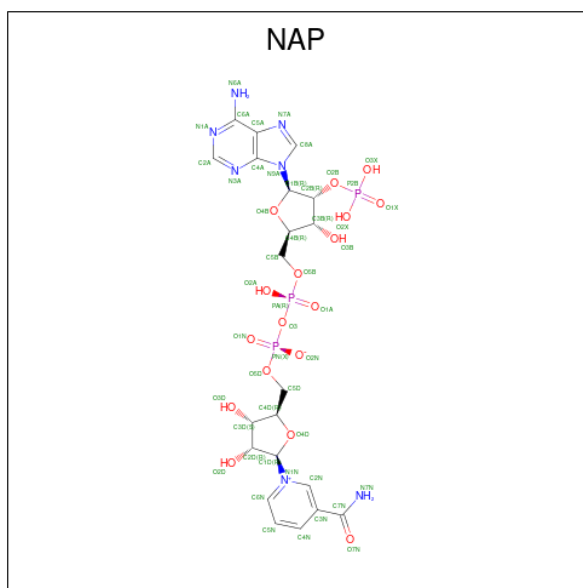
There are 3 unique types of molecules in this entry. The entry contains 7642 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Acetyl-coenzyme A synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	482	Total	C	N	O	S	0	0	0
			3778	2403	647	713	15			
1	B	481	Total	C	N	O	S	0	0	0
			3747	2388	642	702	15			

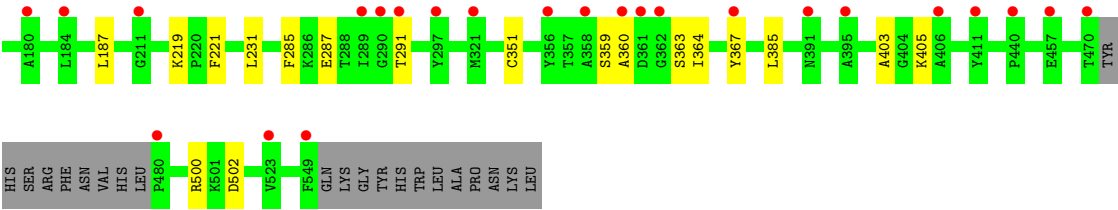
- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	26	Total 26	O 26	0	0
3	B	29	Total 29	O 29	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	121.33Å 123.26Å 162.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.87 – 2.35 33.87 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.9 (33.87-2.35) 99.9 (33.87-2.35)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 2.34Å)	Xtriage
Refinement program	PHENIX (1.21rc1_4933: ???)	Depositor
R, R_{free}	0.215 , 0.248 0.217 , 0.249	Depositor DCC
R_{free} test set	2529 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	55.7	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.020 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7642	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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: NAP

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	0.18	0/3858	0.40	0/5217
1	B	0.19	0/3828	0.40	0/5182
All	All	0.18	0/7686	0.40	0/10399

There are no bond length outliers.

There are no bond angle outliers.

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	3778	0	3706	20	0
1	B	3747	0	3670	21	0
2	A	31	0	11	0	0
2	B	31	0	11	0	0
3	A	26	0	0	0	0
3	B	29	0	0	0	0
All	All	7642	0	7398	41	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 3.

All (41) 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:221:PHE:HB2	1:A:504:LEU:HD21	1.79	0.63
1:B:148:THR:HG21	1:B:166:HIS:CE1	2.35	0.61
1:A:291:THR:HG21	1:A:367:TYR:HE1	1.69	0.58
1:B:56:CYS:SG	1:B:57:GLU:N	2.76	0.58
1:A:56:CYS:SG	1:A:57:GLU:N	2.77	0.57
1:B:500:ARG:HD2	1:B:502:ASP:OD1	2.05	0.56
1:A:444:MET:HE2	1:A:469:LEU:HD22	1.87	0.56
1:B:124:GLU:HG3	1:B:125:THR:HG23	1.87	0.56
1:B:351:CYS:HB2	1:B:385:LEU:HD23	1.89	0.54
1:B:121:TRP:CD1	1:B:125:THR:HG1	2.26	0.53
1:B:148:THR:HG21	1:B:166:HIS:NE2	2.24	0.52
1:B:148:THR:HG22	1:B:149:TYR:N	2.23	0.52
1:A:72:LEU:HD21	1:A:491:LEU:HD22	1.91	0.51
1:B:221:PHE:HB3	1:B:231:LEU:HD23	1.92	0.51
1:B:291:THR:HG21	1:B:367:TYR:CE1	2.47	0.50
1:B:287:GLU:OE1	1:B:405:LYS:NZ	2.44	0.50
1:B:291:THR:HG21	1:B:367:TYR:HE1	1.77	0.49
1:B:77:LEU:HD12	1:B:187:LEU:HD22	1.94	0.49
1:A:191:PRO:HG3	1:A:220:PRO:HD2	1.95	0.49
1:A:221:PHE:CB	1:A:504:LEU:HD21	2.43	0.49
1:B:359:SER:O	1:B:360:ALA:HB3	2.13	0.48
1:A:124:GLU:HG3	1:A:125:THR:HG23	1.96	0.48
1:B:351:CYS:HB2	1:B:385:LEU:CD2	2.44	0.47
1:A:291:THR:HG21	1:A:367:TYR:CE1	2.49	0.47
1:A:359:SER:O	1:A:360:ALA:HB3	2.15	0.46
1:A:149:TYR:HD1	1:A:150:PHE:N	2.14	0.46
1:A:174:PHE:O	1:A:179:LYS:NZ	2.49	0.46
1:A:63:VAL:CG1	1:A:67:GLN:HB2	2.47	0.45
1:A:361:ASP:OD1	1:A:363:SER:N	2.37	0.45
1:B:285:PHE:O	1:B:403:ALA:HA	2.17	0.45
1:B:363:SER:HB2	1:B:364:ILE:HD12	1.99	0.44
1:A:120:LYS:O	1:A:124:GLU:HG2	2.18	0.44
1:B:219:LYS:HG2	1:B:221:PHE:CE2	2.52	0.43
1:B:149:TYR:HD1	1:B:150:PHE:N	2.16	0.43
1:A:351:CYS:HB2	1:A:385:LEU:HD23	2.01	0.43
1:A:77:LEU:HD12	1:A:187:LEU:HD22	2.01	0.43
1:A:340:LEU:HB3	1:A:506:VAL:HG12	2.00	0.42
1:B:72:LEU:HD23	1:B:105:ILE:HD12	2.01	0.42
1:A:356:TYR:HA	1:A:528:TYR:O	2.19	0.42
1:A:356:TYR:HB3	1:A:528:TYR:CZ	2.56	0.41
1:B:73:THR:HA	1:B:106:ASN:O	2.21	0.41

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	474/679 (70%)	461 (97%)	13 (3%)	0	100	100
1	B	475/679 (70%)	462 (97%)	13 (3%)	0	100	100
All	All	949/1358 (70%)	923 (97%)	26 (3%)	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	400/591 (68%)	397 (99%)	3 (1%)	73	84
1	B	393/591 (66%)	393 (100%)	0	100	100
All	All	793/1182 (67%)	790 (100%)	3 (0%)	84	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	SER
1	A	138	CYS
1	A	148	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	GLN
1	A	223	HIS
1	A	249	HIS
1	B	94	GLN
1	B	223	HIS
1	B	249	HIS

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](#)

2 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	NAP	A	601	-	32,33,52	2.04	3 (9%)	50,52,80	0.92	2 (4%)
2	NAP	B	601	-	32,33,52	1.94	3 (9%)	50,52,80	1.12	5 (10%)

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	NAP	A	601	-	-	10/21/37/67	0/3/3/5
2	NAP	B	601	-	-	4/21/37/67	0/3/3/5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	NAP	P2B-O2B	8.70	1.74	1.59
2	B	601	NAP	P2B-O2B	8.15	1.73	1.59
2	A	601	NAP	PA-O3	5.84	1.65	1.59
2	B	601	NAP	PA-O3	5.37	1.65	1.59
2	A	601	NAP	PN-O5D	2.89	1.65	1.54
2	B	601	NAP	PN-O5D	2.84	1.65	1.54

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	NAP	O2N-PN-O1N	3.13	123.02	110.83
2	B	601	NAP	P2B-O2B-C2B	-3.06	115.27	123.43
2	A	601	NAP	O2N-PN-O1N	2.98	122.44	110.83
2	B	601	NAP	C2B-C3B-C4B	-2.47	96.68	101.99
2	B	601	NAP	O2B-P2B-O1X	-2.43	100.66	109.33
2	A	601	NAP	P2B-O2B-C2B	-2.26	117.39	123.43
2	B	601	NAP	O2A-PA-O1A	2.08	122.10	112.44

There are no chirality outliers.

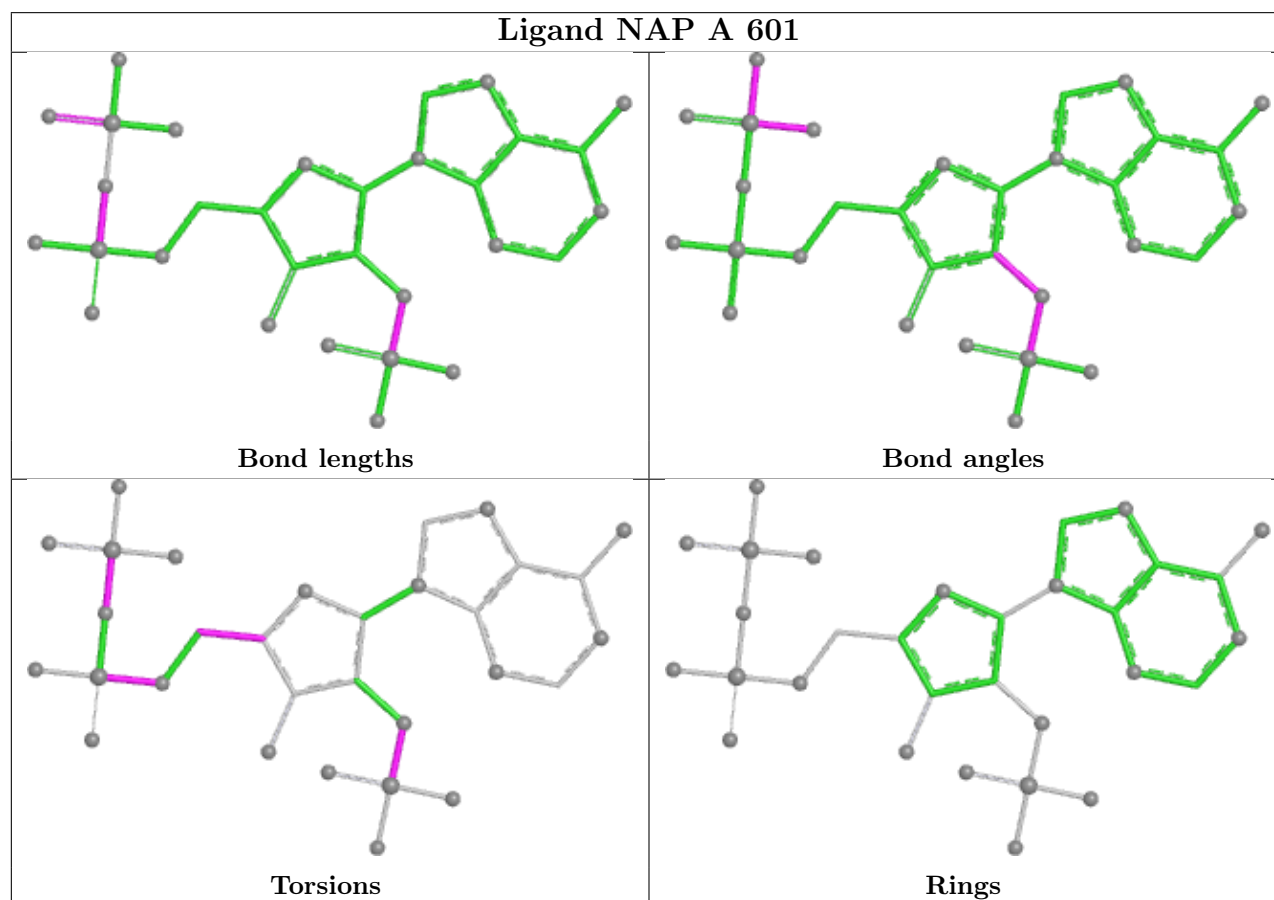
All (14) torsion outliers are listed below:

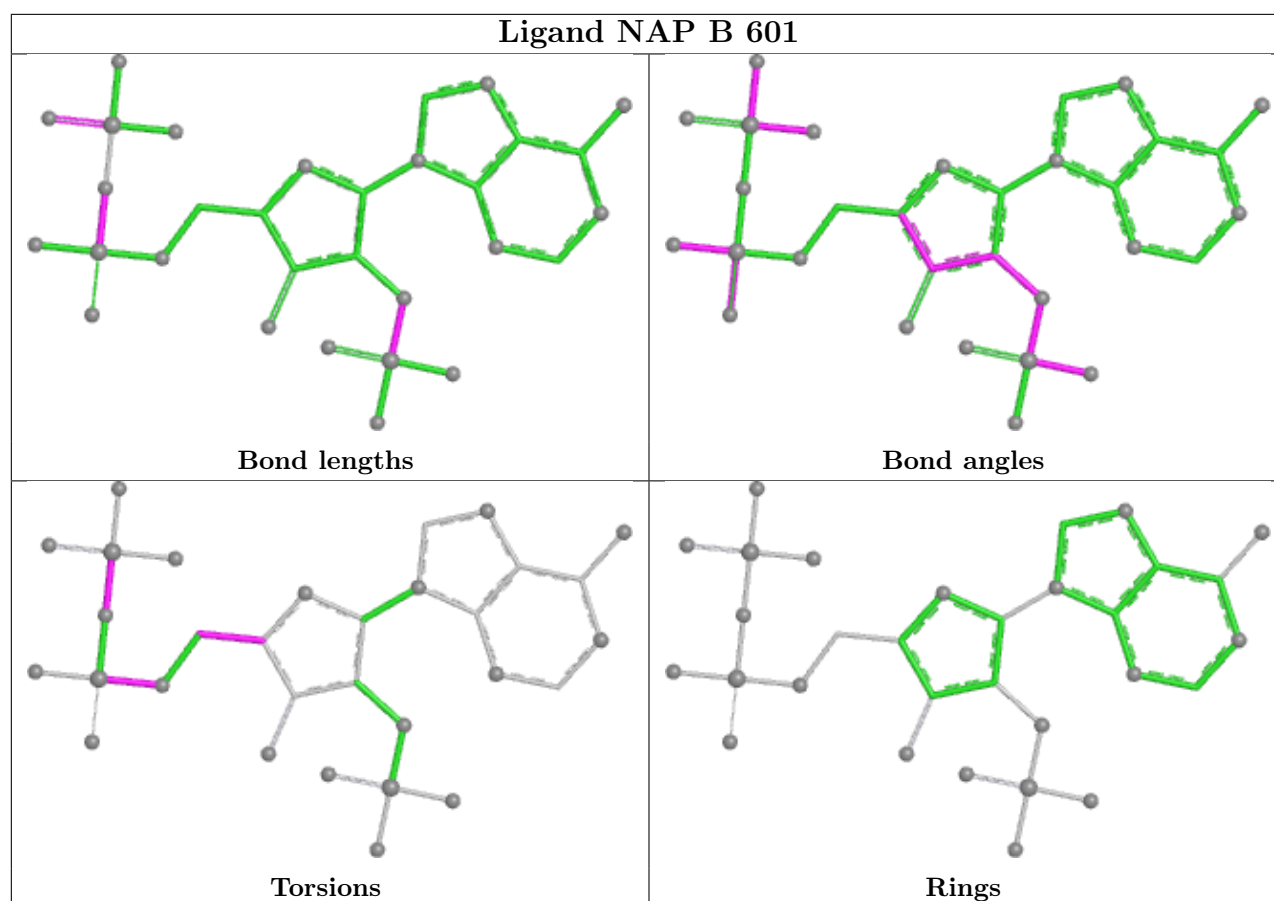
Mol	Chain	Res	Type	Atoms
2	A	601	NAP	C5B-O5B-PA-O1A
2	A	601	NAP	C5B-O5B-PA-O2A
2	A	601	NAP	C5B-O5B-PA-O3
2	B	601	NAP	PA-O3-PN-O5D
2	B	601	NAP	O4B-C4B-C5B-O5B
2	B	601	NAP	C3B-C4B-C5B-O5B
2	A	601	NAP	C3B-C4B-C5B-O5B
2	A	601	NAP	O4B-C4B-C5B-O5B
2	A	601	NAP	PA-O3-PN-O2N
2	B	601	NAP	C5B-O5B-PA-O1A
2	A	601	NAP	C2B-O2B-P2B-O2X
2	A	601	NAP	PA-O3-PN-O1N
2	A	601	NAP	C2B-O2B-P2B-O3X
2	A	601	NAP	C2B-O2B-P2B-O1X

There are no ring outliers.

No monomer is involved in short contacts.

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	482/679 (70%)	0.82	51 (10%) 11 13	41, 77, 137, 216	0
1	B	481/679 (70%)	0.82	59 (12%) 8 10	41, 75, 134, 172	0
All	All	963/1358 (70%)	0.82	110 (11%) 10 11	41, 76, 134, 216	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	126	LEU	7.4
1	A	121	TRP	5.0
1	B	118	VAL	5.0
1	A	459	LEU	4.9
1	A	125	THR	4.7
1	A	364	ILE	4.7
1	A	133	LEU	4.6
1	B	406	ALA	4.4
1	A	130	PHE	4.4
1	A	356	TYR	4.2
1	B	395	ALA	4.0
1	B	367	TYR	3.8
1	B	59	ILE	3.8
1	B	549	PHE	3.8
1	B	440	PRO	3.7
1	B	356	TYR	3.5
1	A	367	TYR	3.4
1	B	361	ASP	3.4
1	B	470	THR	3.3
1	A	525	PRO	3.2
1	A	210	GLY	3.2
1	A	360	ALA	3.1
1	A	526	ILE	3.1
1	A	523	VAL	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	113	THR	3.0
1	B	289	ILE	3.0
1	B	84	ALA	3.0
1	B	127	THR	3.0
1	B	67	GLN	3.0
1	A	122	LYS	3.0
1	B	65	GLU	3.0
1	A	550	GLN	3.0
1	B	133	LEU	2.9
1	A	355	GLN	2.9
1	B	126	LEU	2.9
1	B	60	VAL	2.9
1	B	321	MET	2.9
1	A	137	SER	2.8
1	B	176	GLY	2.8
1	B	83	LEU	2.8
1	B	124	GLU	2.8
1	A	231	LEU	2.8
1	B	149	TYR	2.8
1	B	170	LEU	2.8
1	A	362	GLY	2.7
1	B	71	PRO	2.7
1	A	132	ARG	2.7
1	B	174	PHE	2.7
1	B	360	ALA	2.7
1	B	391	ASN	2.7
1	A	235	ILE	2.7
1	B	56	CYS	2.7
1	B	411	TYR	2.6
1	A	131	SER	2.6
1	B	137	SER	2.6
1	B	457	GLU	2.6
1	A	118	VAL	2.6
1	B	112	ARG	2.6
1	B	123	HIS	2.6
1	A	111	ALA	2.5
1	A	321	MET	2.5
1	B	125	THR	2.5
1	A	363	SER	2.5
1	A	365	PRO	2.5
1	A	480	PRO	2.5
1	B	291	THR	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	58	ARG	2.4
1	A	549	PHE	2.4
1	A	69	ARG	2.4
1	A	124	GLU	2.4
1	B	100	LEU	2.4
1	B	107	ILE	2.4
1	B	108	VAL	2.4
1	B	175	ASP	2.4
1	B	180	ALA	2.4
1	B	358	ALA	2.4
1	B	57	GLU	2.4
1	A	297	TYR	2.3
1	B	290	GLY	2.3
1	B	130	PHE	2.3
1	A	209	GLU	2.3
1	B	297	TYR	2.3
1	B	211	GLY	2.3
1	A	455	LEU	2.3
1	B	111	ALA	2.3
1	A	176	GLY	2.2
1	A	547	PHE	2.2
1	B	523	VAL	2.2
1	B	480	PRO	2.2
1	A	129	TYR	2.2
1	A	353	LEU	2.2
1	A	358	ALA	2.2
1	B	362	GLY	2.2
1	A	460	ARG	2.1
1	B	121	TRP	2.1
1	B	167	VAL	2.1
1	A	370	ASP	2.1
1	A	123	HIS	2.1
1	A	379	CYS	2.1
1	B	68	LYS	2.1
1	A	110	TYR	2.1
1	A	75	VAL	2.1
1	B	140	VAL	2.1
1	A	83	LEU	2.1
1	B	184	LEU	2.1
1	A	150	PHE	2.1
1	A	285	PHE	2.1
1	B	142	PRO	2.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	373	VAL	2.0
1	B	64	SER	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 [i](#)

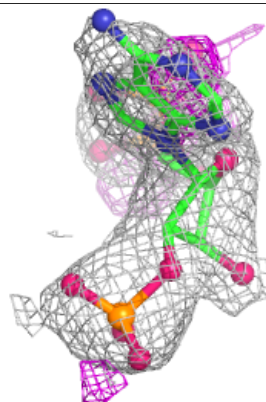
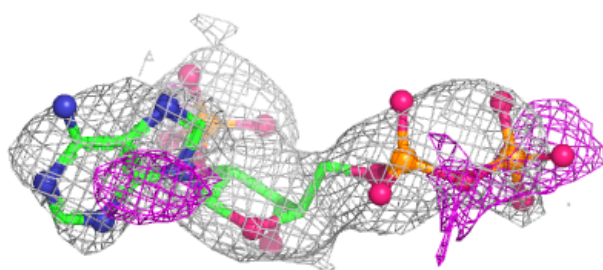
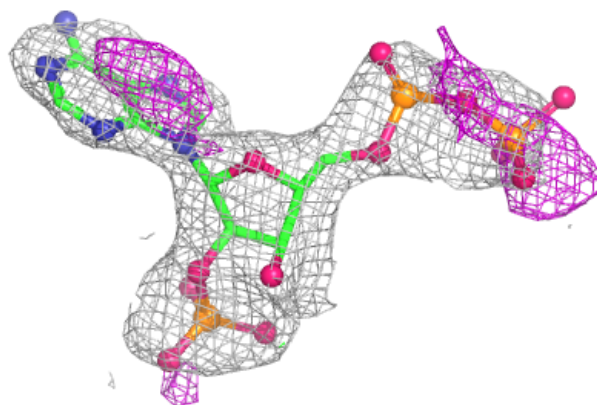
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAP	B	601	31/48	0.69	0.12	90,103,135,140	0
2	NAP	A	601	31/48	0.70	0.12	97,126,140,147	0

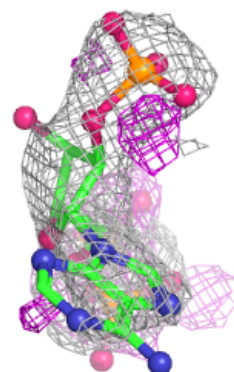
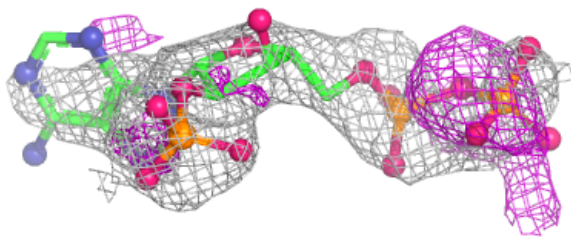
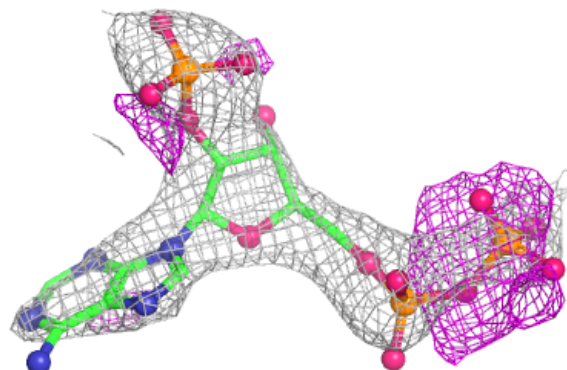
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NAP B 601:

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

**Electron density around NAP A 601:**

$2mF_o-DF_c$ (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.