



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:22 PM UTC

PDB ID : 2X99 / pdb_00002x99
Title : Thioredoxin glutathione reductase from Schistosoma mansoni in complex with NADPH
Authors : Angelucci, F.; Dimastrogiovanni, D.; Boumis, G.; Brunori, M.; Miele, A.E.; Saccoccia, F.; Bellelli, A.
Deposited on : 2010-03-15
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

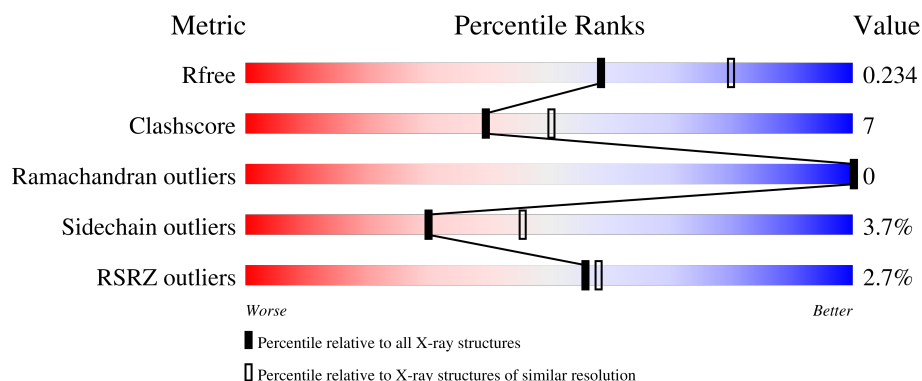
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	598	

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
4	GSH	A	604	X	-	-	-

2 Entry composition [i](#)

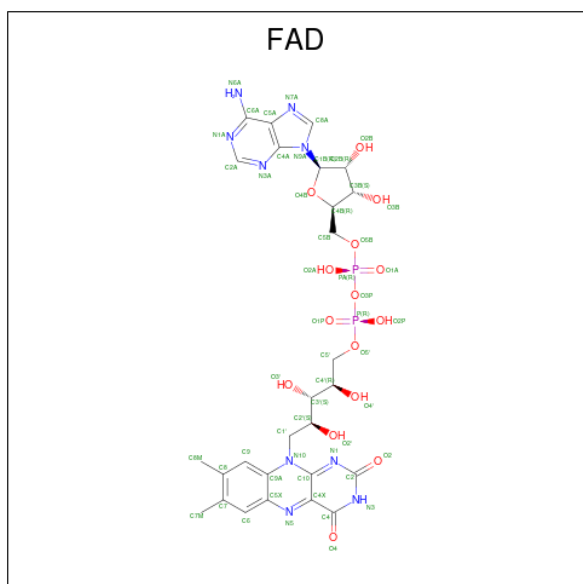
There are 8 unique types of molecules in this entry. The entry contains 4936 atoms, of which 0 are hydrogens and 0 are deuteriums.

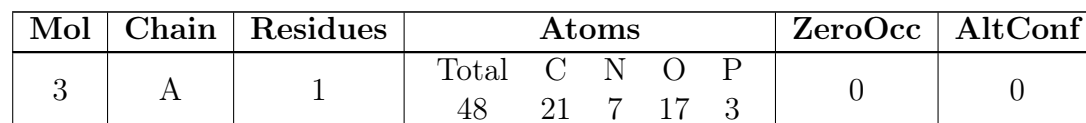
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called THIOREDOXIN GLUTATHIONE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	587	Total	C	N	O	S	0	2	0
			4502	2858	758	862	24			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).





- # GSH
-
- The diagram shows the chemical structure of reduced glutathione (GSH). The molecule consists of a glutamate (CA1(S)) and a cysteine (CA2(R)) residue linked by a peptide bond. The glutamate is further linked to a glycine (CA3) residue. The cysteine residue has a free thiol group (HS-) and is linked to a glycine (CA3) residue. The structure is labeled with atom names and numbers: N1, N2, N3, O1, O2, O31, O32, O11, O12, C1, C2, C3, CA1(S), CA2(R), CA3, CB1, CB2, CG1, CD1, SG2, and HS.
- NC(CCNC(=O)CCNC(=O)O)C(=O)O

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 20	C 10	N 3	O 6	S 1	0	0
4	A	1	Total 20	C 10	N 3	O 6	S 1	0	0

- 

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			13	8	5		
7	A	1	Total	C	O	0	0
			13	8	5		
7	A	1	Total	C	O	0	0
			13	8	5		
7	A	1	Total	C	O	0	0
			13	8	5		
7	A	1	Total	C	O	0	0
			13	8	5		

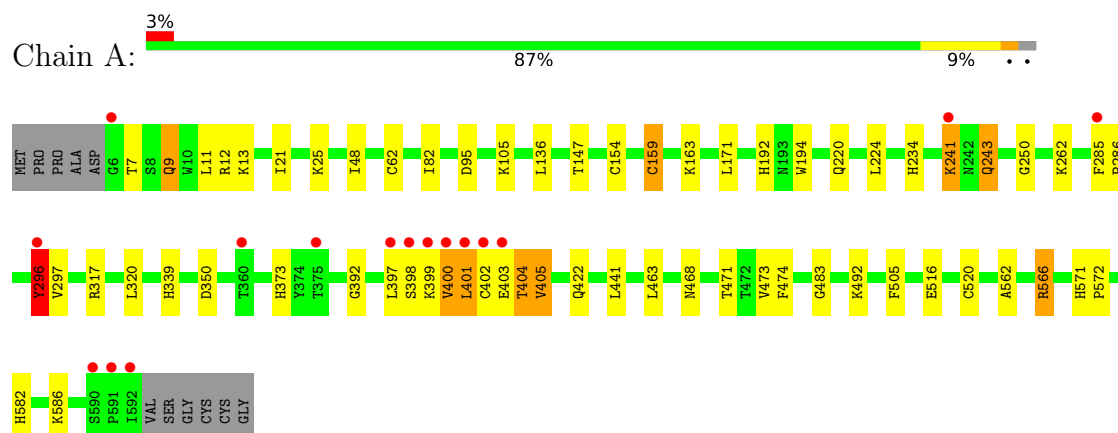
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	185	Total	O	0	0
			185	185		

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: THIOREDOXIN GLUTATHIONE REDUCTASE



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	141.50Å 102.61Å 59.94Å 90.00° 112.82° 90.00°	Depositor
Resolution (Å)	40.00 – 2.30 40.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (40.00-2.30) 99.8 (40.00-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.190 , 0.231 0.192 , 0.234	Depositor DCC
R_{free} test set	1743 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	35.0	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.022 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4936	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% 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, PG4, GSH, CA, PEG, FAD

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	0.68	1/4595 (0.0%)	0.86	6/6224 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	405	VAL	CA-CB	-5.39	1.48	1.54

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	397	LEU	CB-CA-C	-11.62	89.67	110.36
1	A	582	HIS	CB-CA-C	6.09	122.53	110.42
1	A	400	VAL	N-CA-C	5.80	116.85	111.45
1	A	296	TYR	N-CA-CB	5.67	119.06	110.28
1	A	296	TYR	CA-CB-CG	5.33	123.50	113.90

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	4502	0	4520	61	0
2	A	53	0	31	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	48	0	26	10	0
4	A	40	0	29	3	0
5	A	1	0	0	0	0
6	A	42	0	60	1	0
7	A	65	0	90	5	0
8	A	185	0	0	2	0
All	All	4936	0	4756	64	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 7.

The worst 5 of 64 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:441:LEU:HD11	1:A:471:THR:HG22	1.57	0.84
1:A:400:VAL:HG23	1:A:401:LEU:HD13	1.61	0.82
1:A:401:LEU:O	1:A:404:THR:HG23	1.77	0.82
1:A:296:TYR:CE1	3:A:602:NDP:H2D	2.15	0.81
1:A:399:LYS:O	1:A:403:GLU:HG2	1.81	0.80

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	587/598 (98%)	572 (97%)	15 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	490/496 (99%)	471 (96%)	19 (4%)	28	43

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	401	LEU
1	A	566	ARG
1	A	586	LYS
1	A	463	LEU
1	A	171	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	468	ASN
1	A	531	ASN
1	A	549	GLN
1	A	514	HIS
1	A	338	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 16 ligands modelled in this entry, 1 is monoatomic - leaving 15 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$
7	PG4	A	615	-	12,12,12	0.51	0	11,11,11	0.32	0
6	PEG	A	616	-	6,6,6	0.45	0	5,5,5	0.28	0
6	PEG	A	607	-	6,6,6	0.47	0	5,5,5	0.21	0
6	PEG	A	609	-	6,6,6	0.52	0	5,5,5	0.79	0
6	PEG	A	610	-	6,6,6	0.46	0	5,5,5	0.34	0
7	PG4	A	613	-	12,12,12	0.46	0	11,11,11	0.31	0
6	PEG	A	606	-	6,6,6	0.49	0	5,5,5	0.24	0
4	GSH	A	604	1	18,19,19	2.87	2 (11%)	21,24,24	0.94	2 (9%)
2	FAD	A	601	-	58,58,58	1.07	5 (8%)	85,89,89	1.69	16 (18%)
6	PEG	A	608	-	6,6,6	0.46	0	5,5,5	0.37	0
7	PG4	A	611	-	12,12,12	0.43	0	11,11,11	0.41	0
3	NDP	A	602	-	51,52,52	1.64	9 (17%)	71,80,80	1.61	9 (12%)
7	PG4	A	612	-	12,12,12	0.50	0	11,11,11	0.19	0
4	GSH	A	603	-	18,19,19	3.16	2 (11%)	21,24,24	1.10	1 (4%)
7	PG4	A	614	-	12,12,12	0.53	0	11,11,11	0.26	0

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
7	PG4	A	615	-	-	3/10/10/10	-
6	PEG	A	616	-	-	2/4/4/4	-
6	PEG	A	607	-	-	1/4/4/4	-
6	PEG	A	609	-	-	4/4/4/4	-
6	PEG	A	610	-	-	0/4/4/4	-
7	PG4	A	613	-	-	0/10/10/10	-
6	PEG	A	606	-	-	0/4/4/4	-
4	GSH	A	604	1	1/1/6/8	10/24/24/24	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	A	601	-	-	5/34/50/50	0/6/6/6
6	PEG	A	608	-	-	2/4/4/4	-
7	PG4	A	611	-	-	2/10/10/10	-
3	NDP	A	602	-	-	12/34/77/77	0/5/5/5
7	PG4	A	612	-	-	3/10/10/10	-
4	GSH	A	603	-	-	8/24/24/24	-
7	PG4	A	614	-	-	7/10/10/10	-

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	GSH	OE1-CD1	9.30	1.41	1.23
4	A	603	GSH	O2-C2	9.12	1.40	1.23
4	A	604	GSH	O2-C2	8.42	1.39	1.23
4	A	604	GSH	OE1-CD1	7.86	1.38	1.23
3	A	602	NDP	O7N-C7N	7.47	1.41	1.24

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	FAD	N3A-C2A-N1A	-6.05	119.42	128.58
3	A	602	NDP	N3A-C2A-N1A	-5.94	119.58	128.58
3	A	602	NDP	C5A-C4A-N3A	-5.16	119.62	126.72
2	A	601	FAD	C5A-C4A-N3A	-4.36	120.71	126.72
2	A	601	FAD	N9A-C8A-N7A	-4.32	107.80	113.94

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	604	GSH	CA1

5 of 59 torsion outliers are listed below:

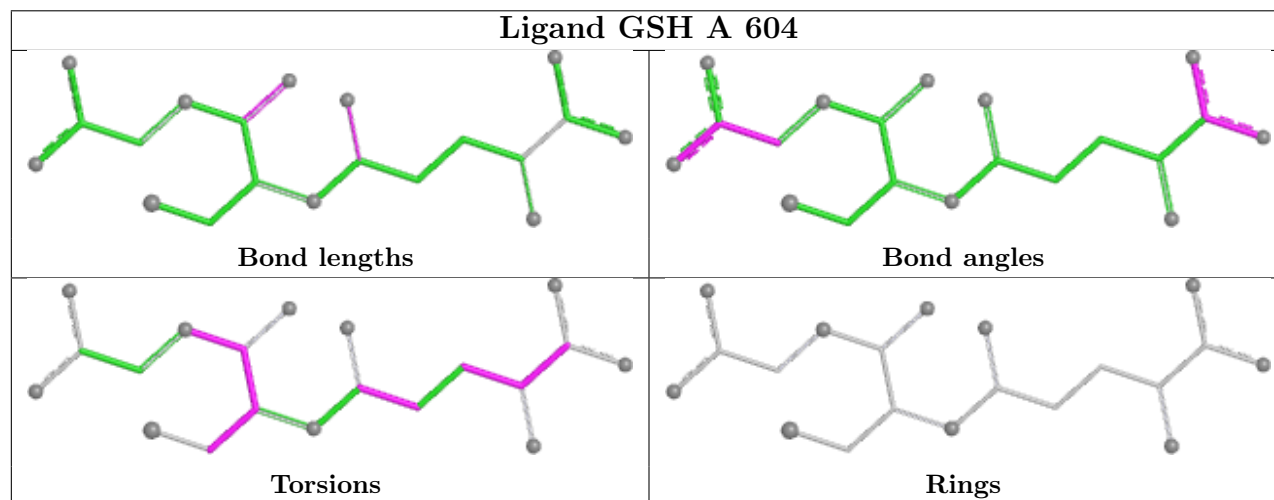
Mol	Chain	Res	Type	Atoms
3	A	602	NDP	C5B-O5B-PA-O1A
3	A	602	NDP	C5D-O5D-PN-O3
3	A	602	NDP	C5D-O5D-PN-O1N
3	A	602	NDP	C5D-O5D-PN-O2N
3	A	602	NDP	O4D-C4D-C5D-O5D

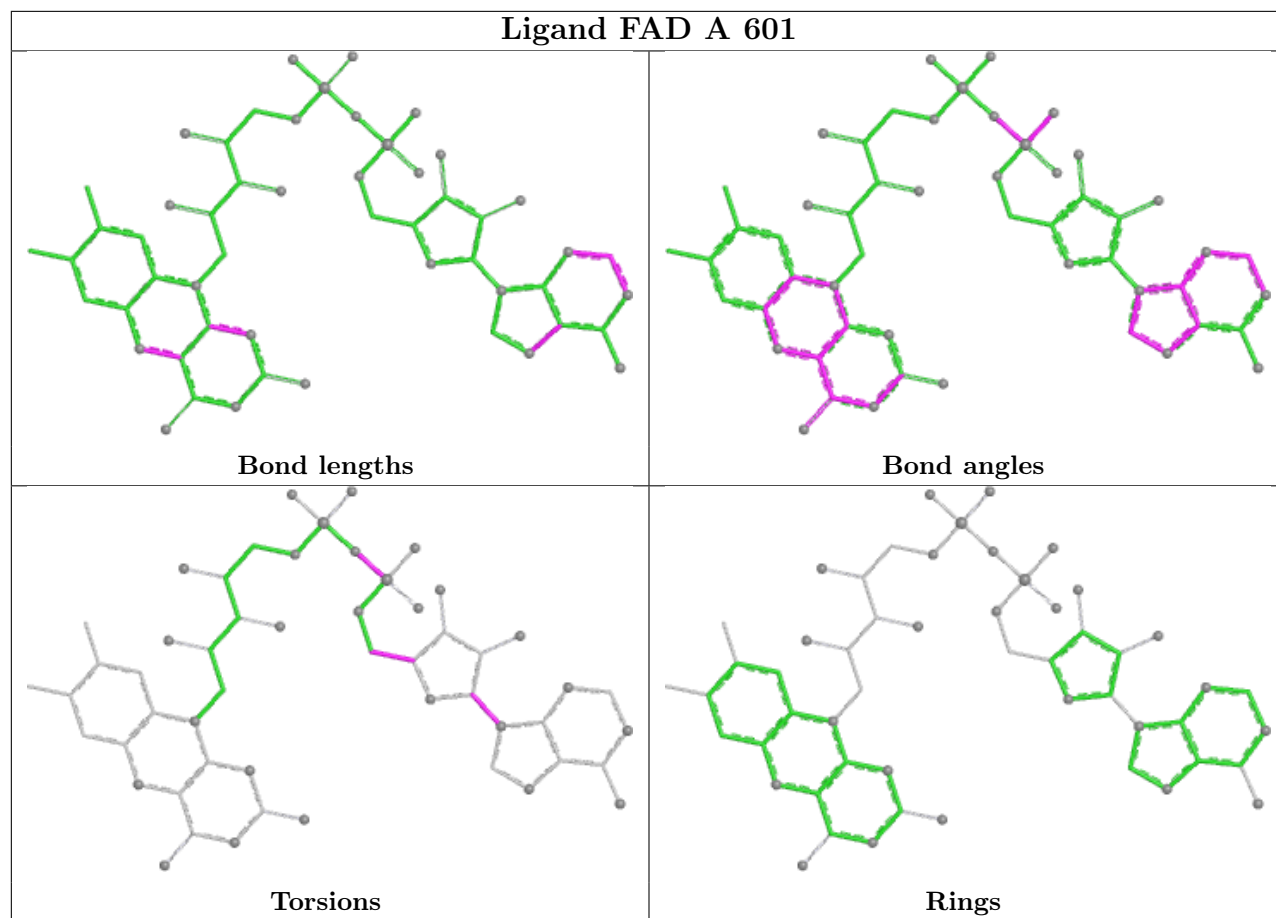
There are no ring outliers.

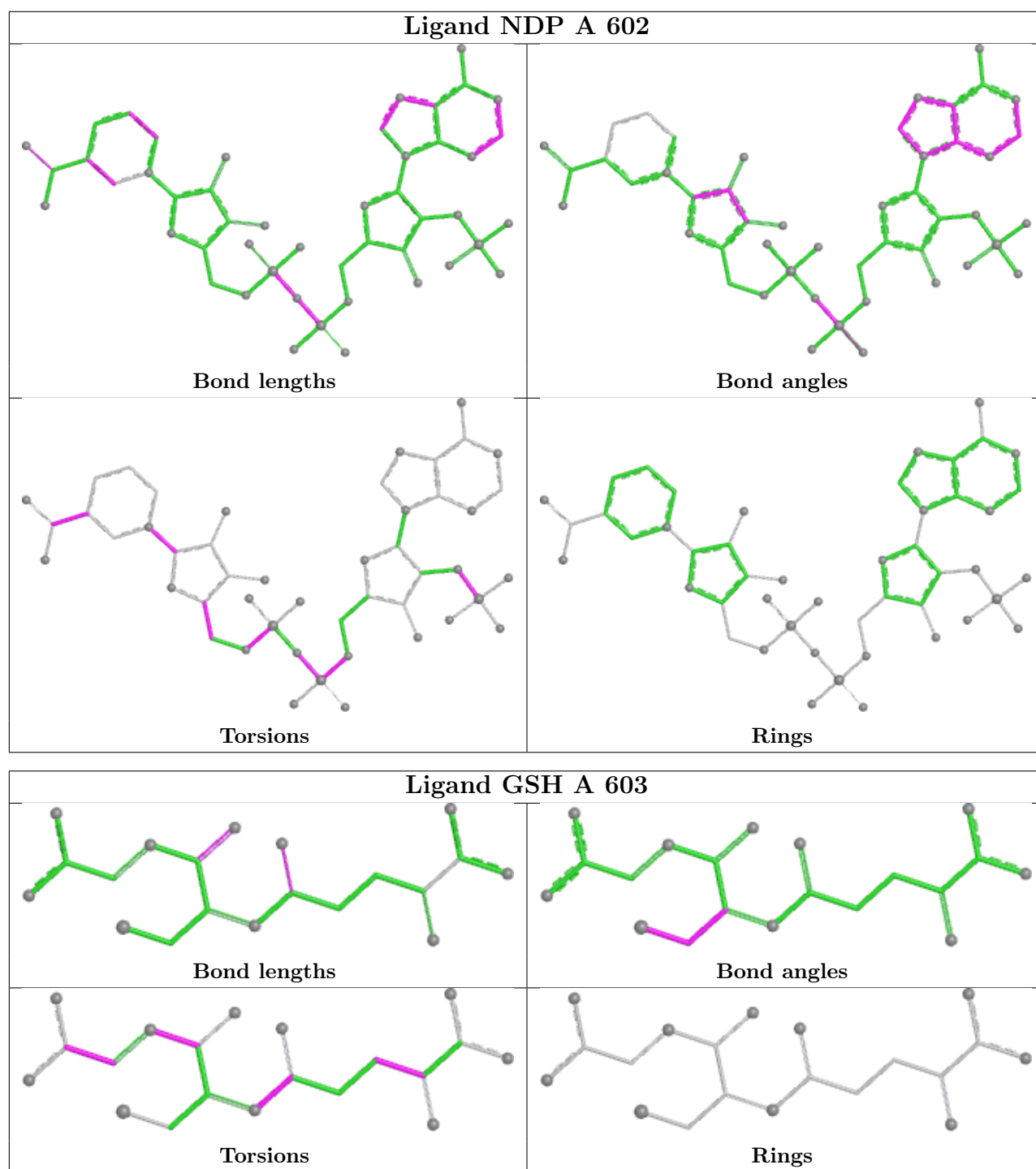
8 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	615	PG4	1	0
6	A	609	PEG	1	0
7	A	613	PG4	1	0
4	A	604	GSH	2	0
2	A	601	FAD	1	0
3	A	602	NDP	10	0
4	A	603	GSH	1	0
7	A	614	PG4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	587/598 (98%)	-0.05	16 (2%) 56 58	19, 30, 54, 64	3 (0%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	296	TYR	4.8
1	A	399	LYS	4.4
1	A	398	SER	4.4
1	A	592	ILE	4.0
1	A	397	LEU	3.9

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.

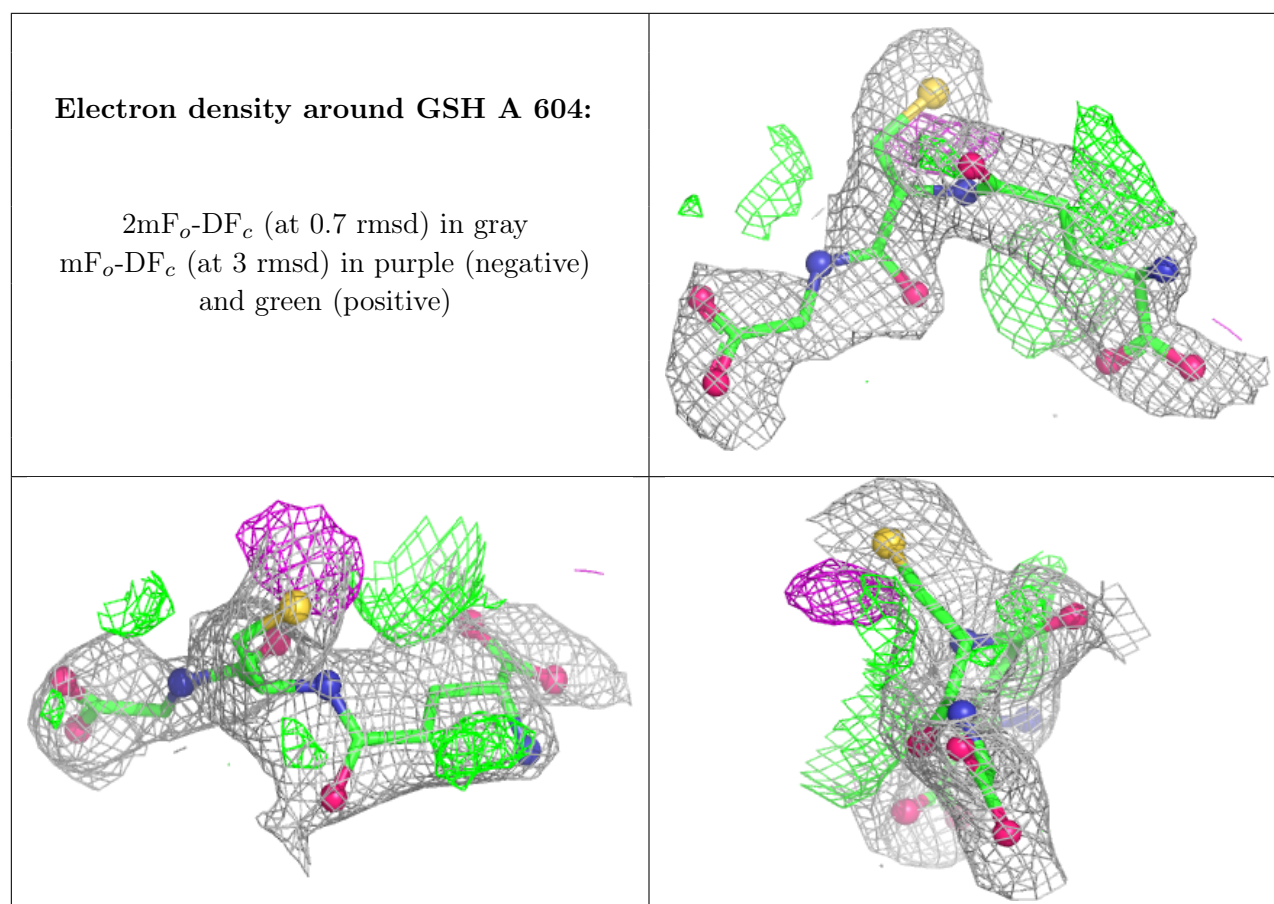
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GSH	A	604	20/20	0.73	0.19	64,68,72,72	0
4	GSH	A	603	20/20	0.84	0.14	56,58,62,62	0

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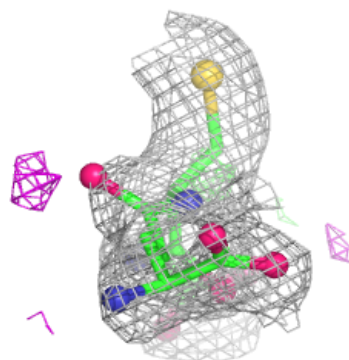
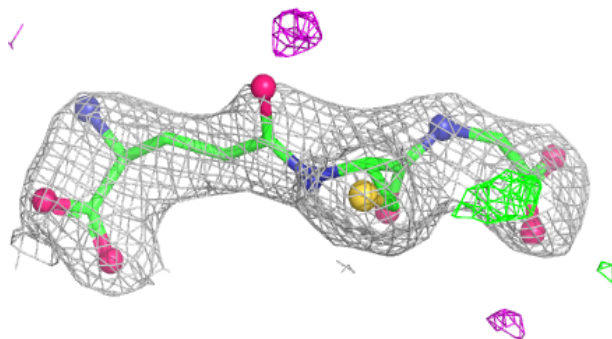
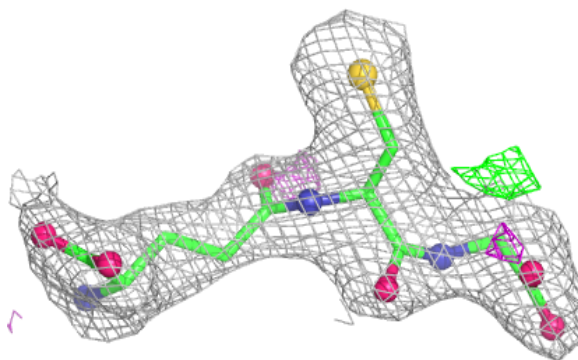
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	PEG	A	608	7/7	0.85	0.18	45,47,50,51	0
7	PG4	A	612	13/13	0.85	0.18	62,64,71,71	0
6	PEG	A	610	7/7	0.87	0.13	48,49,51,51	0
6	PEG	A	607	7/7	0.87	0.15	57,58,60,62	0
7	PG4	A	614	13/13	0.87	0.15	53,54,56,57	0
3	NDP	A	602	48/48	0.88	0.14	29,43,57,57	48
6	PEG	A	606	7/7	0.88	0.16	40,41,45,45	0
6	PEG	A	609	7/7	0.88	0.14	29,33,35,36	0
7	PG4	A	615	13/13	0.88	0.16	56,60,66,66	0
7	PG4	A	613	13/13	0.90	0.14	63,66,70,70	0
5	CA	A	605	1/1	0.91	0.16	71,71,71,71	0
6	PEG	A	616	7/7	0.92	0.13	56,59,61,62	0
7	PG4	A	611	13/13	0.93	0.10	37,39,42,43	0
2	FAD	A	601	53/53	0.95	0.08	24,28,38,40	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.

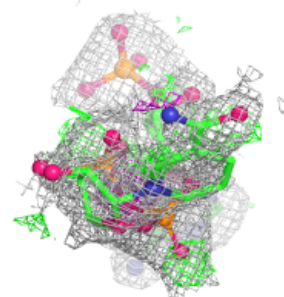
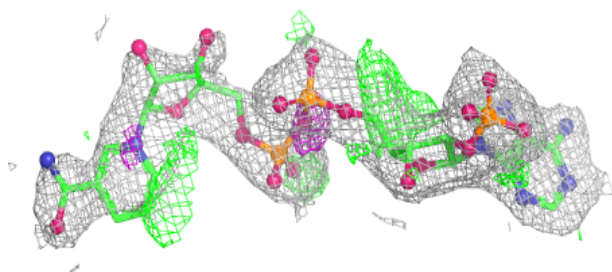
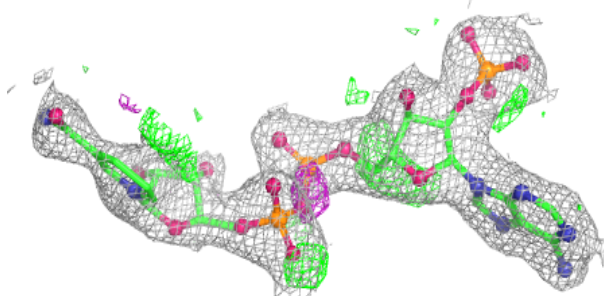


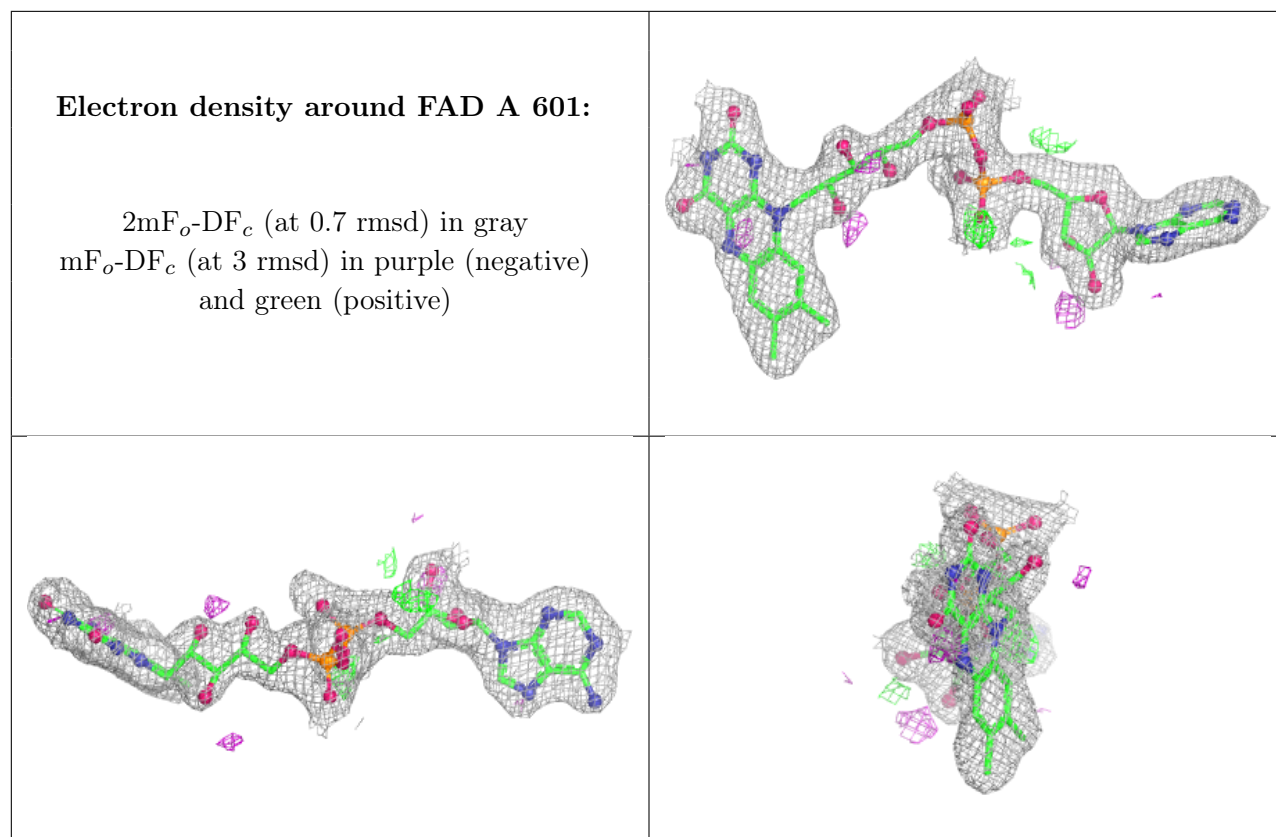
Electron density around GSH A 603:

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

**Electron density around NDP A 602:**

$2mF_o-DF_c$ (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.