wwPDB X-ray Structure Validation Summary Report (i)

Aug 4, 2026 – 03:47 AM EDT

PDB ID	:	2NYA / pdb_00002nya
Title	:	Crystal structure of the periplasmic nitrate reductase (NAP) from Escherichia coli
Authors	:	Jepson, B.J.N.; Richardson, D.J.; Hemmings, A.M.
Deposited on	:	2006-11-20
Resolution	:	2.50 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 (i) 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 (i)) were used in the production of this report:

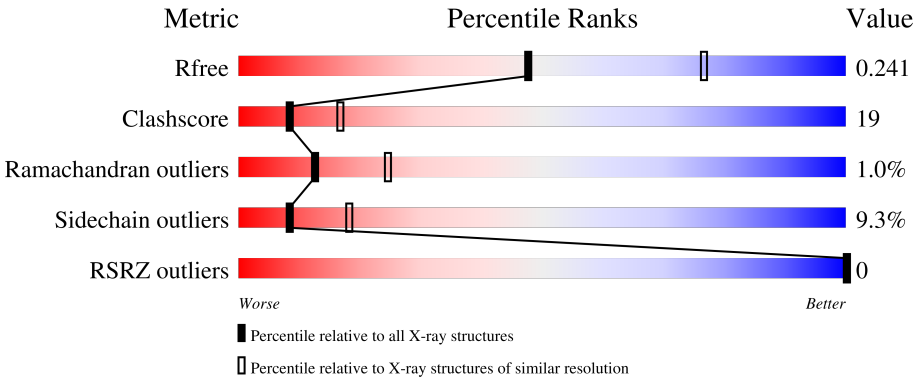
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 <=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	792	66% 28% 6%
1	F	792	63% 31% 6%

2 Entry composition (i)

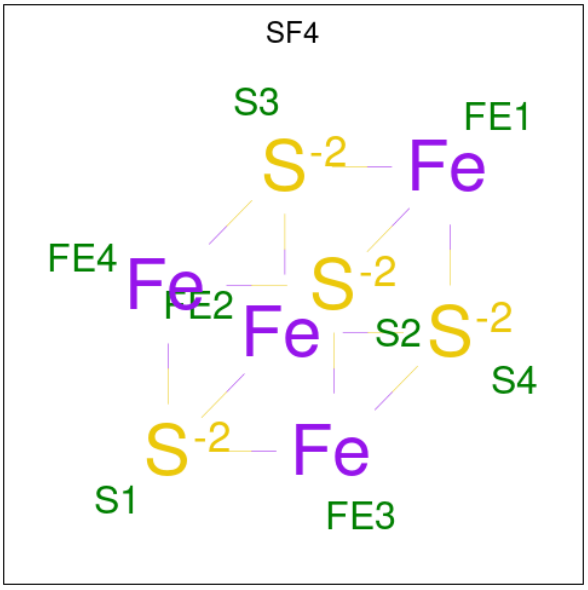
There are 5 unique types of molecules in this entry. The entry contains 13733 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Periplasmic nitrate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	791	Total	C	N	O	S	0	0	0
			6301	4012	1100	1157	32			
1	F	791	Total	C	N	O	S	0	0	0
			6301	4012	1100	1157	32			

- Molecule 2 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).

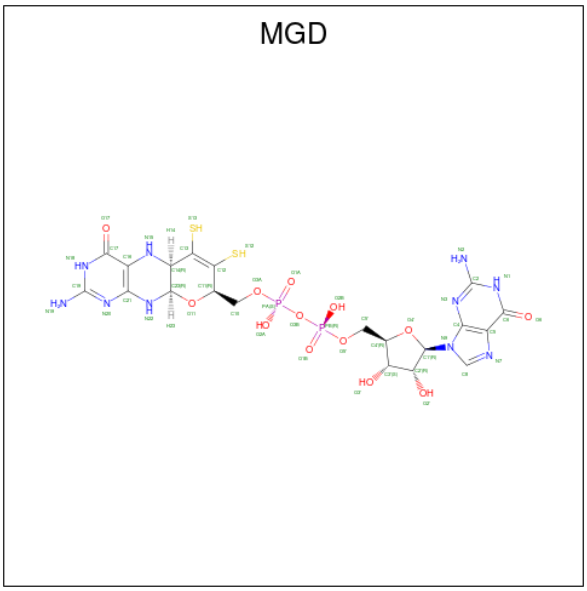


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	Fe	S		0	0
			8	4	4			
2	F	1	Total	Fe	S		0	0
			8	4	4			

- Molecule 3 is MOLYBDENUM(VI) ION (CCD ID: 6MO) (formula: Mo).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mo 1 1	0	0
3	F	1	Total Mo 1 1	0	0

- Molecule 4 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA -1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (CCD ID: MGD) (formula: $C_{20}H_{26}N_{10}O_{13}P_2S_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O P S 47 20 10 13 2 2	0	0
4	A	1	Total C N O P S 47 20 10 13 2 2	0	0
4	F	1	Total C N O P S 47 20 10 13 2 2	0	0
4	F	1	Total C N O P S 47 20 10 13 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	489	Total O 489 489	0	0
5	F	436	Total O 436 436	0	0

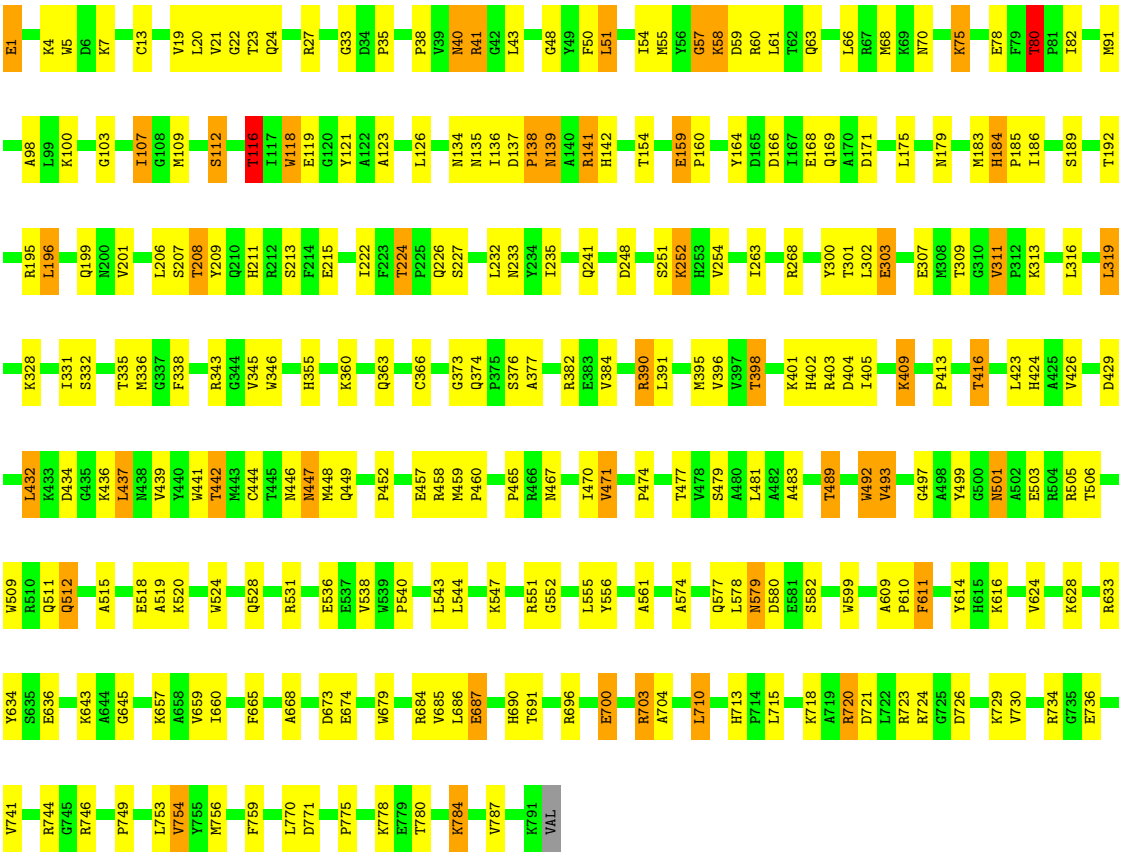
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Periplasmic nitrate reductase

Chain A:

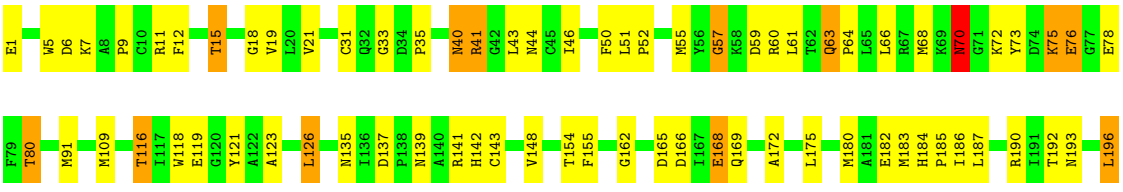


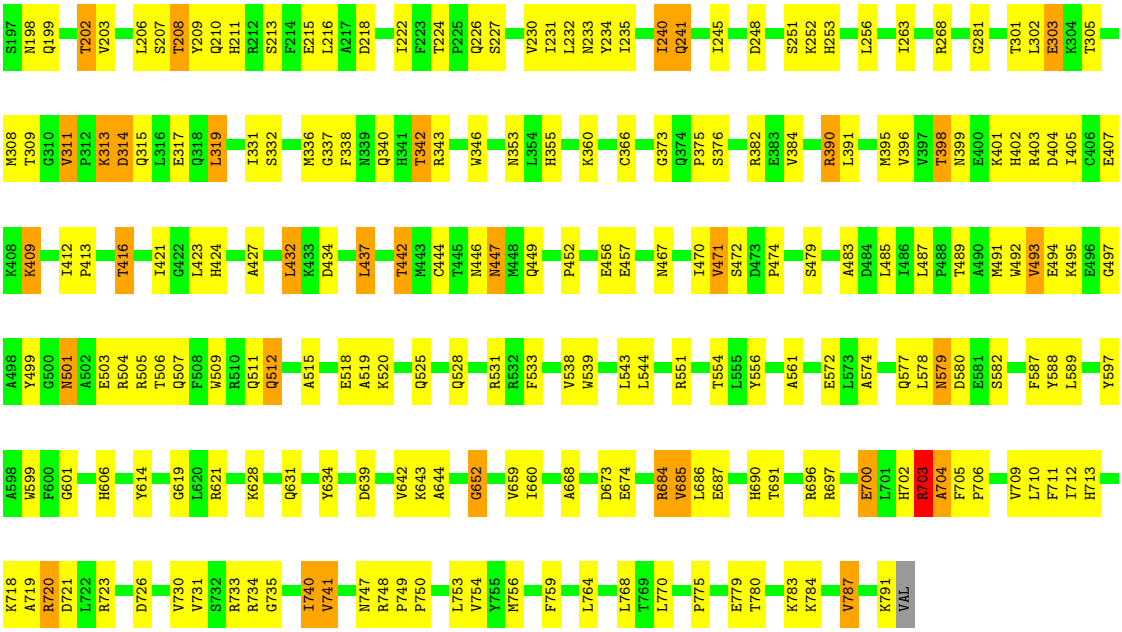


• Molecule 1: Periplasmic nitrate reductase

Chain F:






S197 N198 Q199 T202 V203 L206 S207 T208 Y209 Q210 H211 R212 S213 F214 E215 L216 A217 D218 I222 F223 T224 P225 Q226 S227 V230 I231 L232 N233 Y234 I235 I240 Q241 I245 D248 S251 K252 H253 L256 I263 R268 G281 T301 L302 E303 K304 T305
M308 T309 G310 V311 P312 K313 D314 Q315 L316 E317 Q318 L319 I331 S332 M336 G337 F338 N339 Q340 H341 T342 R343 W346 N353 L354 H355 K360 C366 G373 Q374 P375 S376 R382 E383 V384 R390 L391 M395 V396 V397 T398 N399 E400 K401 H402 R403 D404 I405 C406 E407
K408 K409 I412 P413 T416 I421 G422 L423 H424 A427 L432 K433 D434 L437 T442 M443 C444 T445 N446 N447 M448 Q449 P452 E456 E457 N467 I470 V471 S472 D473 P474 S479 A483 D484 L485 I486 L487 P488 T489 A490 M491 W492 V493 E494 K495 E496 G497
A498 Y499 G500 N501 A502 E503 R504 R505 T506 Q507 F508 W509 R510 Q511 Q512 A515 E518 A519 K520 Q525 Q528 R531 R532 F533 V538 W539 L543 L544 R551 T554 L555 Y556 A561 E572 L573 A574 Q577 L578 N579 D580 E581 S582 F587 Y588 L589 Y597
A598 W599 F600 G601 H606 Y614 G619 L620 R621 K628 Q631 Y634 D639 V642 K643 A644 G652 V659 I660 A668 D673 E674 R684 V685 L686 E687 H690 T691 R696 R697 E700 L701 H702 R703 A704 F705 P706 V709 L710 F711 I712 H713
K718 A719 R720 D721 L722 R723 D726 V730 V731 S732 R733 R734 G735 I740 V741 N747 R748 P749 P750 L753 V754 Y755 M756 F759 L764 L768 T769 L770 P775 E779 T780 K783 K784 V787 K791 VAL

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	69.45Å 94.60Å 131.21Å 90.00° 96.34° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50 50.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.1 (50.00-2.50) 97.1 (50.00-2.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	2.50 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.181 , 0.243 0.181 , 0.241	Depositor DCC
R_{free} test set	2860 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å^2)	27.6	Xtriage
Anisotropy	0.729	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 43.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	13733	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.11% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: 6MO, MGD, SF4

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	0.88	2/6470 (0.0%)	1.07	13/8770 (0.1%)
1	F	0.83	0/6470	1.03	9/8770 (0.1%)
All	All	0.86	2/12940 (0.0%)	1.05	22/17540 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	F	0	2
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	224	THR	CA-CB	5.12	1.63	1.53
1	A	80	THR	CA-CB	5.05	1.62	1.54

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	57	GLY	O-C-N	-7.37	113.12	122.70
1	F	263	ILE	N-CA-C	7.33	118.44	111.91
1	A	103	GLY	CA-C-N	7.23	127.85	119.47
1	A	103	GLY	C-N-CA	7.23	127.85	119.47
1	F	126	LEU	N-CA-C	-6.48	104.13	111.07

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	138	PRO	Peptide
1	F	313	LYS	Peptide
1	F	57	GLY	Peptide

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	6301	0	6155	227	0
1	F	6301	0	6155	258	0
2	A	8	0	0	0	0
2	F	8	0	0	0	0
3	A	1	0	0	0	0
3	F	1	0	0	0	0
4	A	94	0	44	14	0
4	F	94	0	44	17	0
5	A	489	0	0	15	0
5	F	436	0	0	29	1
All	All	13733	0	12398	481	1

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 19.

The worst 5 of 481 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:F:783:LYS:HG3	5:F:7033:HOH:O	1.43	1.18
1:F:109:MET:CE	1:F:123:ALA:HB1	1.95	0.96
1:F:684:ARG:NH2	4:F:6001:MGD:H15	1.63	0.95
1:F:193:ASN:HB3	5:F:7024:HOH:O	1.68	0.93
1:F:668:ALA:HA	5:F:7032:HOH:O	1.67	0.93

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:7379:HOH:O	5:F:7409:HOH:O[2_655]	1.98	0.22

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	789/792 (100%)	736 (93%)	47 (6%)	6 (1%)	16 31
1	F	789/792 (100%)	725 (92%)	55 (7%)	9 (1%)	11 22
All	All	1578/1584 (100%)	1461 (93%)	102 (6%)	15 (1%)	12 24

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	139	ASN
1	F	70	ASN
1	F	215	GLU
1	F	314	ASP
1	F	241	GLN

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	661/663 (100%)	595 (90%)	66 (10%)	7 15
1	F	661/663 (100%)	604 (91%)	57 (9%)	10 21
All	All	1322/1326 (100%)	1199 (91%)	123 (9%)	8 18

5 of 123 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	700	GLU
1	F	518	GLU
1	F	51	LEU
1	F	512	GLN
1	F	700	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	135	ASN
1	F	606	HIS
1	F	233	ASN
1	F	604	HIS
1	F	501	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 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	$\#\|Z\|>2$
4	MGD	F	7001	3	47,52,52	1.47	7 (14%)	58,81,81	2.22	16 (27%)
4	MGD	F	6001	3	47,52,52	1.45	8 (17%)	58,81,81	2.26	21 (36%)
2	SF4	F	5001	1	0,12,12	-	-	-		
4	MGD	A	3001	3	47,52,52	1.33	4 (8%)	58,81,81	2.16	18 (31%)
2	SF4	A	2001	1	0,12,12	-	-	-		
4	MGD	A	4001	3	47,52,52	1.46	7 (14%)	58,81,81	1.97	13 (22%)

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
4	MGD	F	7001	3	-	6/22/66/66	0/6/6/6
4	MGD	F	6001	3	-	4/22/66/66	0/6/6/6
2	SF4	F	5001	1	-	-	0/6/5/5
4	MGD	A	3001	3	-	6/22/66/66	0/6/6/6
2	SF4	A	2001	1	-	-	0/6/5/5
4	MGD	A	4001	3	-	7/22/66/66	0/6/6/6

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	4001	MGD	C16-C21	5.58	1.48	1.38
4	F	7001	MGD	C16-C21	5.58	1.48	1.38
4	F	6001	MGD	C16-C21	5.01	1.47	1.38
4	A	3001	MGD	C16-C21	4.72	1.46	1.38
4	A	4001	MGD	C17-N18	-3.40	1.32	1.38

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	F	7001	MGD	C23-C14-N15	7.73	115.46	107.87
4	A	4001	MGD	C5-C4-N3	-5.92	118.97	128.39
4	F	7001	MGD	C5-C4-N3	-5.68	119.35	128.39
4	F	7001	MGD	C2-N3-C4	5.59	121.93	112.30
4	A	3001	MGD	C19-N20-C21	5.42	122.92	113.36

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	3001	MGD	PA-O3B-PB-O5'
4	A	3001	MGD	C5'-O5'-PB-O2B
4	A	3001	MGD	C5'-O5'-PB-O3B
4	A	4001	MGD	C5'-O5'-PB-O1B
4	A	4001	MGD	C5'-O5'-PB-O2B

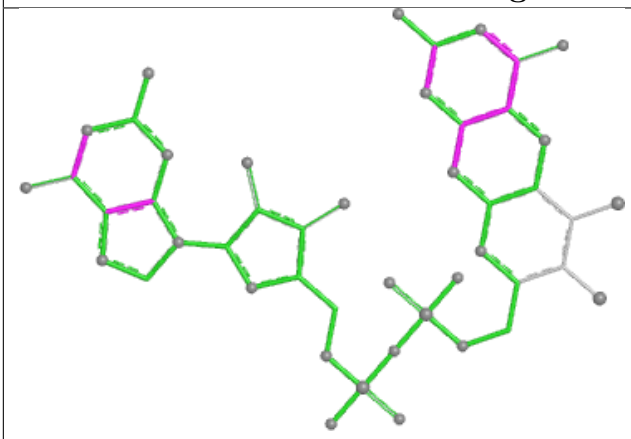
There are no ring outliers.

4 monomers are involved in 31 short contacts:

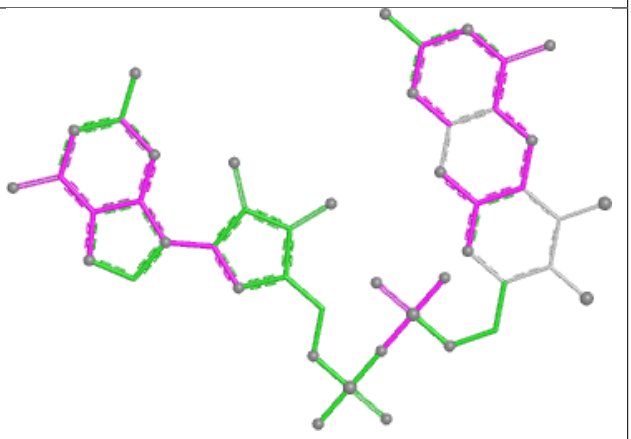
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	7001	MGD	8	0
4	F	6001	MGD	9	0
4	A	3001	MGD	7	0
4	A	4001	MGD	7	0

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 then 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.

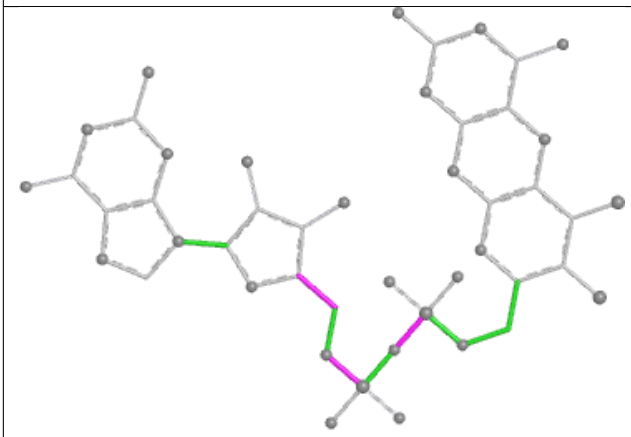
Ligand MGD F 7001



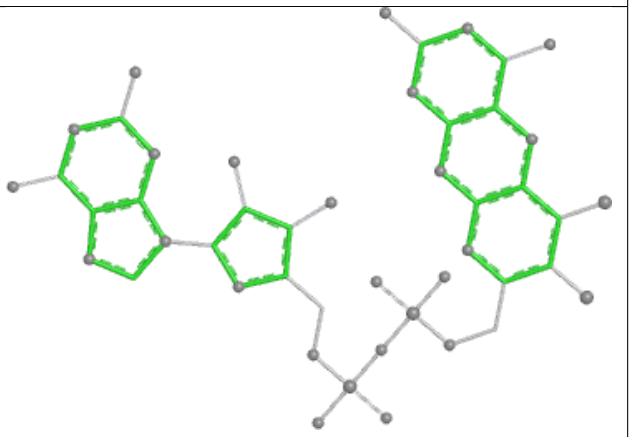
Bond lengths



Bond angles

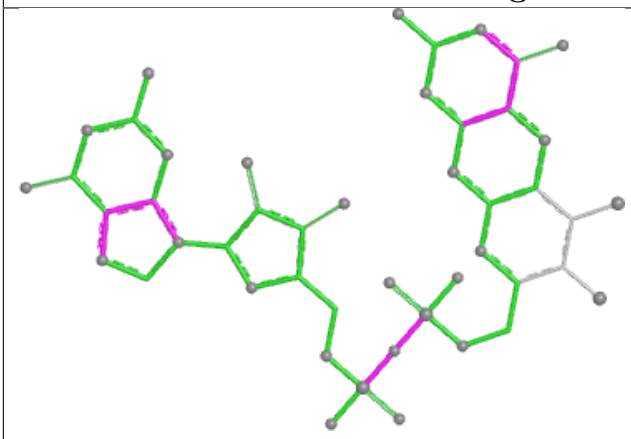


Torsions

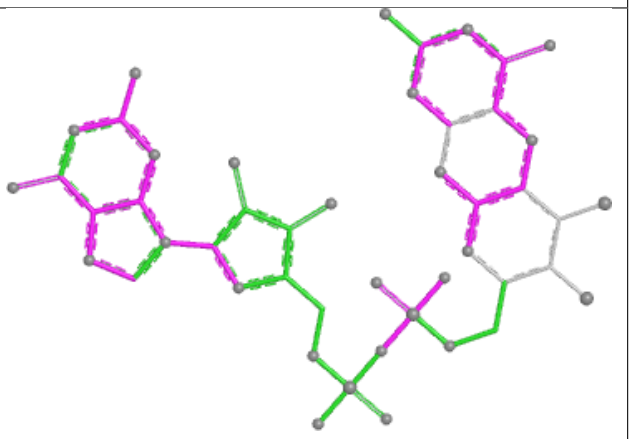


Rings

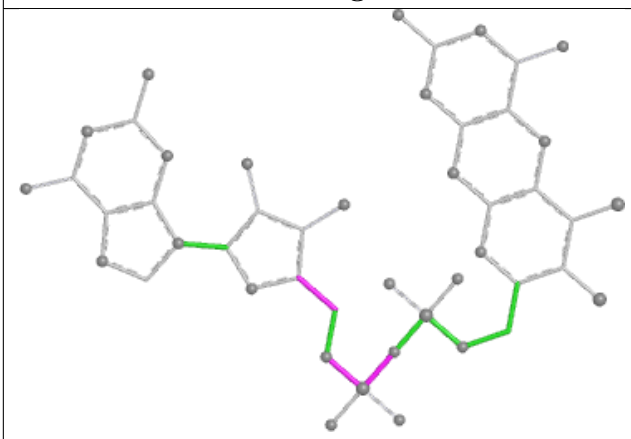
Ligand MGD F 6001



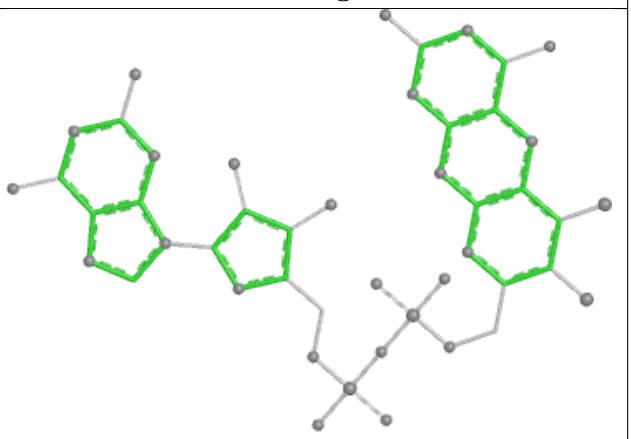
Bond lengths



Bond angles

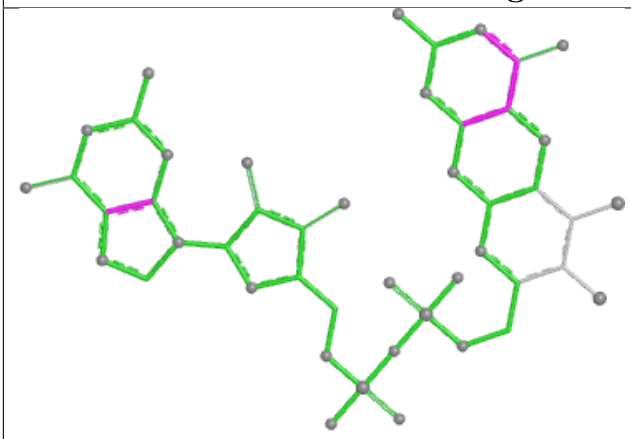


Torsions

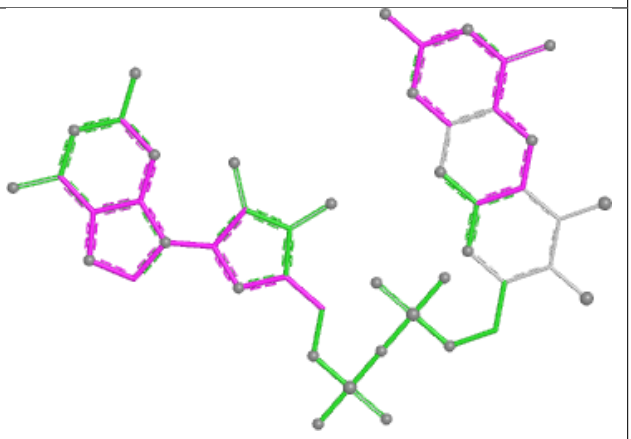


Rings

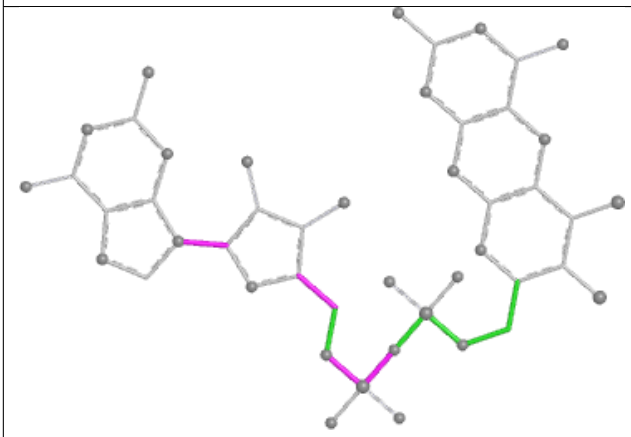
Ligand MGD A 3001



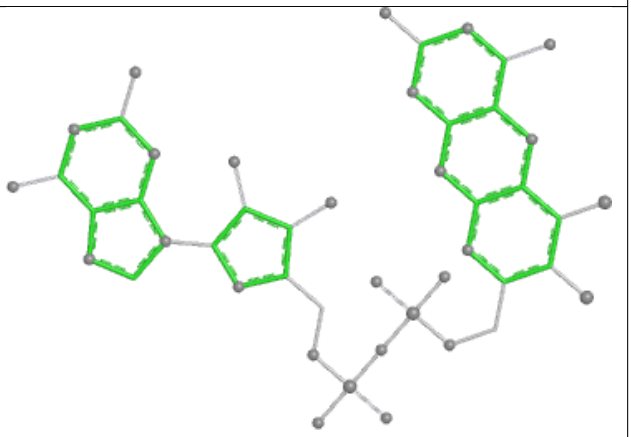
Bond lengths



Bond angles

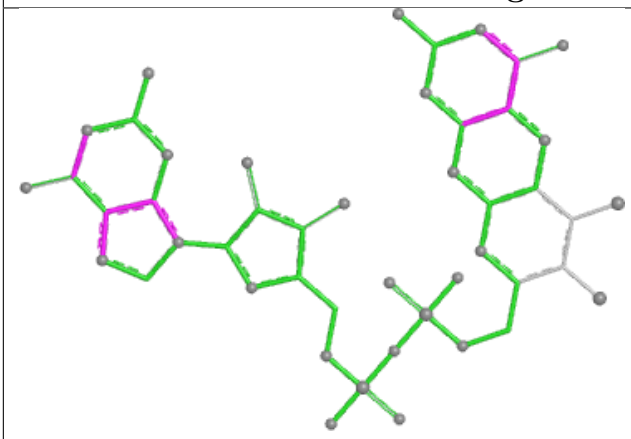


Torsions

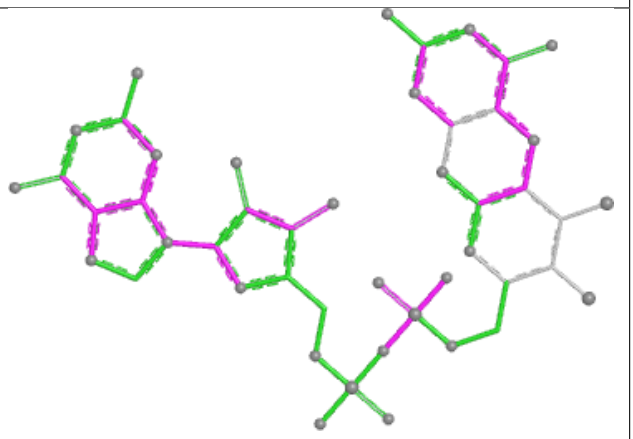


Rings

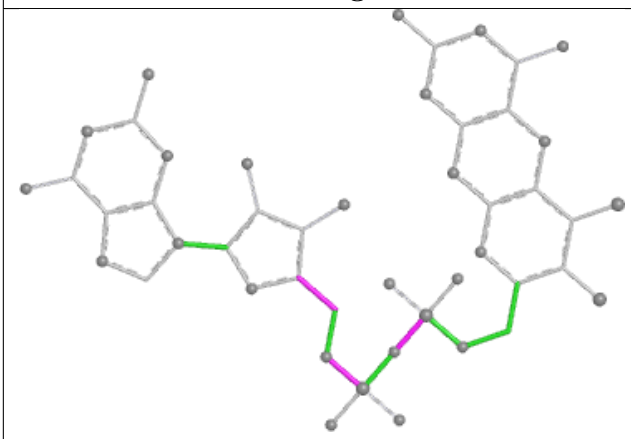
Ligand MGD A 4001



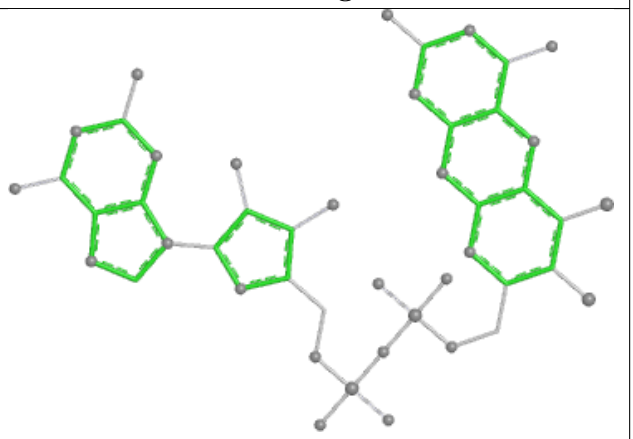
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} 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	791/792 (99%)	-0.47	0	100	100	13, 24, 37, 46	0
1	F	791/792 (99%)	-0.30	0	100	100	17, 30, 45, 55	0
All	All	1582/1584 (99%)	-0.38	0	100	100	13, 27, 42, 55	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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, 95^{th} 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	MGD	F	7001	47/47	0.97	0.06	18,22,27,31	0
4	MGD	A	3001	47/47	0.98	0.05	11,16,17,20	0
4	MGD	A	4001	47/47	0.98	0.06	13,21,26,30	0
4	MGD	F	6001	47/47	0.98	0.05	15,19,21,22	0
2	SF4	F	5001	8/8	0.98	0.03	25,26,29,30	0
2	SF4	A	2001	8/8	0.99	0.03	24,26,28,28	0
3	6MO	A	2002	1/1	0.99	0.03	20,20,20,20	0

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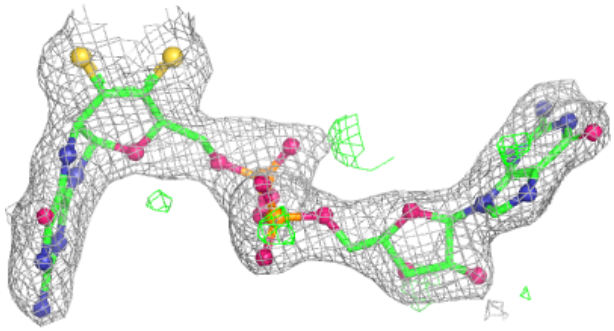
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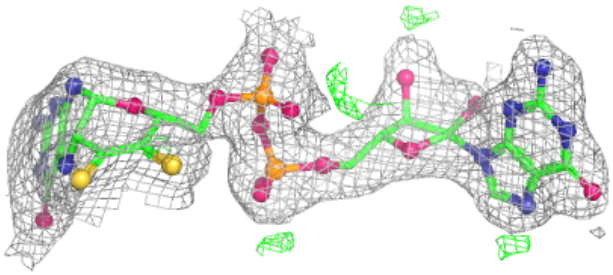
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	6MO	F	5002	1/1	1.00	0.02	24,24,24,24	0

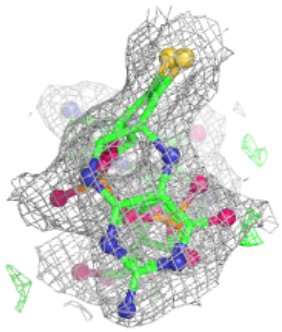
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around MGD F 7001:

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

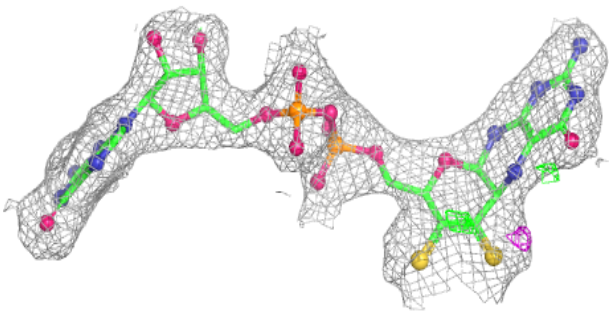


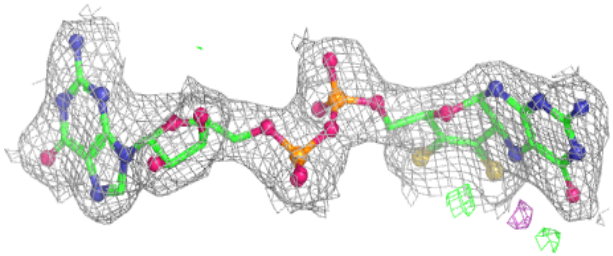


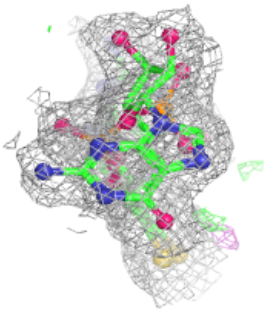


Electron density around MGD A 3001:

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



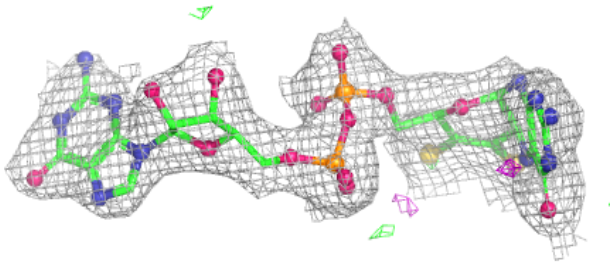


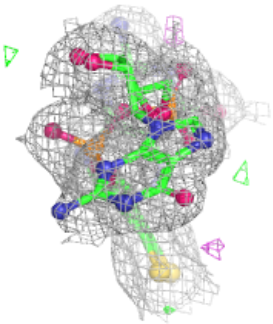


Electron density around MGD A 4001:

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

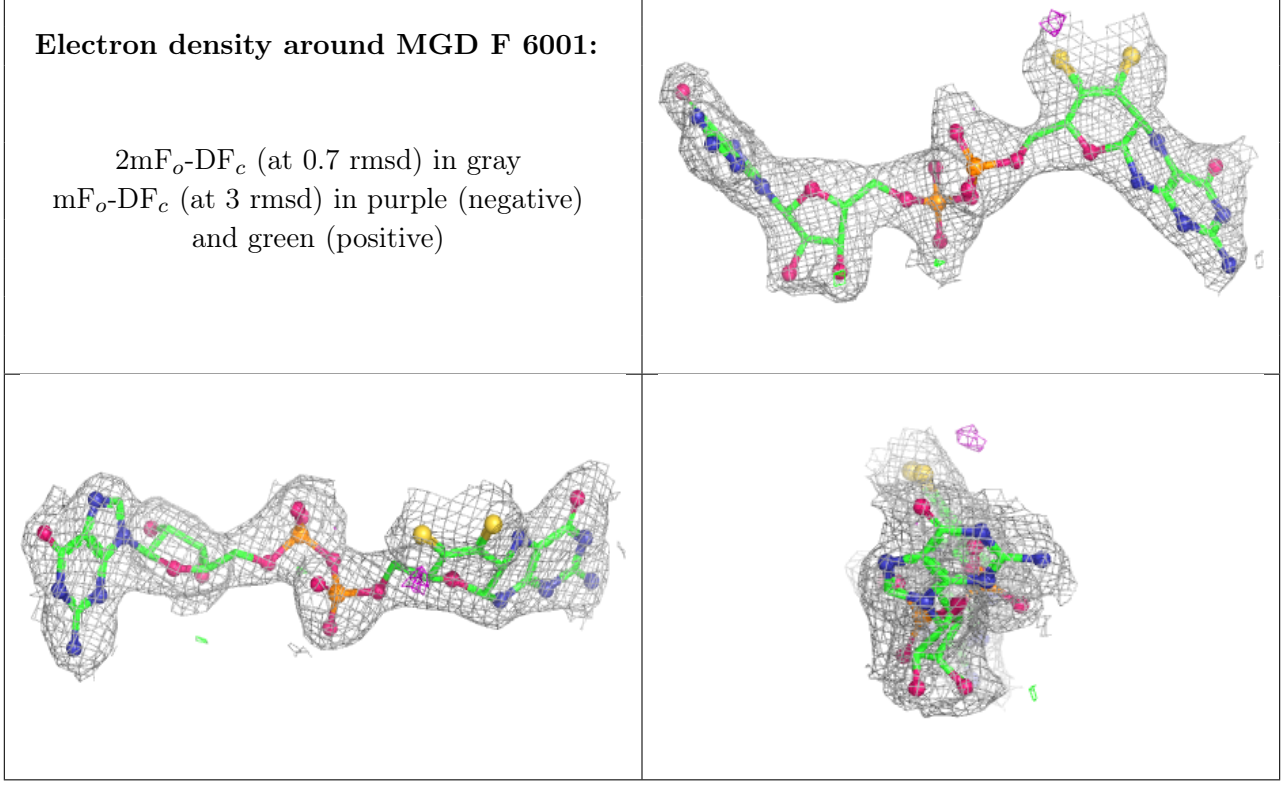






Electron density around MGD F 6001:

$2mF_o$-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.