



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:37 AM UTC

PDB ID : 4IDP / pdb_00004idp
Title : human atlastin-1 1-446, N440T, GppNHp
Authors : Byrnes, L.J.; Singh, A.; Szeto, K.; Benveniste, N.M.; O'Donnell, J.P.; Zipfel, W.R.;
Sondermann, H.
Deposited on : 2012-12-12
Resolution : 2.59 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

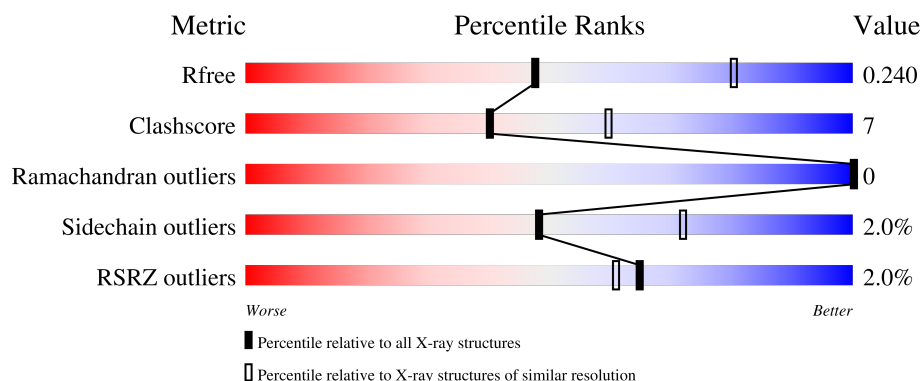
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

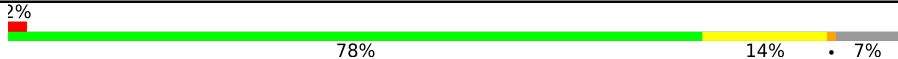
The reported resolution of this entry is 2.59 Å.

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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	447	
1	B	447	
1	C	447	
1	D	447	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14015 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 Atlastin-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	Se	0	4	0
			3376	2159	565	639	4	9			
1	B	416	Total	C	N	O	S	Se	0	4	0
			3378	2160	569	636	4	9			
1	C	416	Total	C	N	O	S	Se	0	0	0
			3351	2143	562	633	4	9			
1	D	417	Total	C	N	O	S	Se	0	3	0
			3375	2158	566	638	4	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q8WXF7
A	440	THR	ASN	engineered mutation	UNP Q8WXF7
B	0	SER	-	expression tag	UNP Q8WXF7
B	440	THR	ASN	engineered mutation	UNP Q8WXF7
C	0	SER	-	expression tag	UNP Q8WXF7
C	440	THR	ASN	engineered mutation	UNP Q8WXF7
D	0	SER	-	expression tag	UNP Q8WXF7
D	440	THR	ASN	engineered mutation	UNP Q8WXF7

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
2	B	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
2	C	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
2	D	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	110	Total	O	0	0
			110	110		

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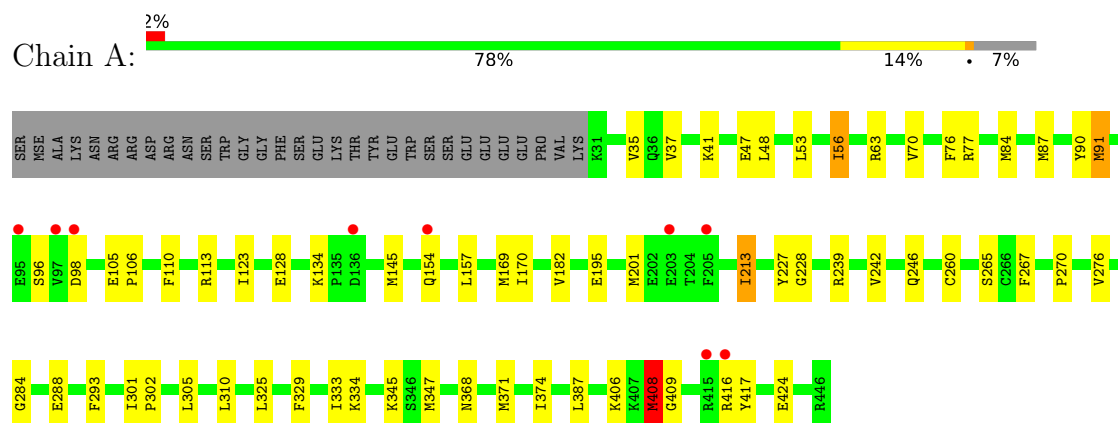
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	99	Total	O	0	0
			99	99		
4	C	99	Total	O	0	0
			99	99		
4	D	95	Total	O	0	0
			95	95		

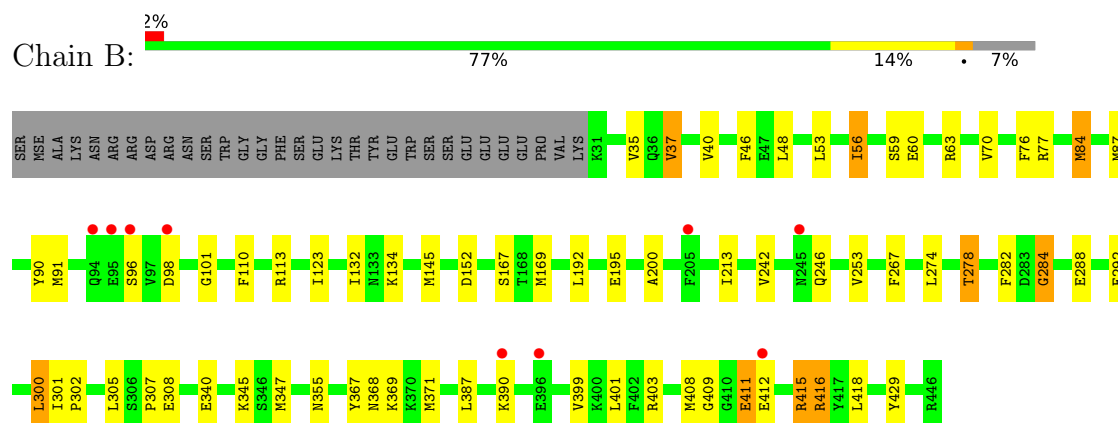
3 Residue-property plots [i](#)

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.

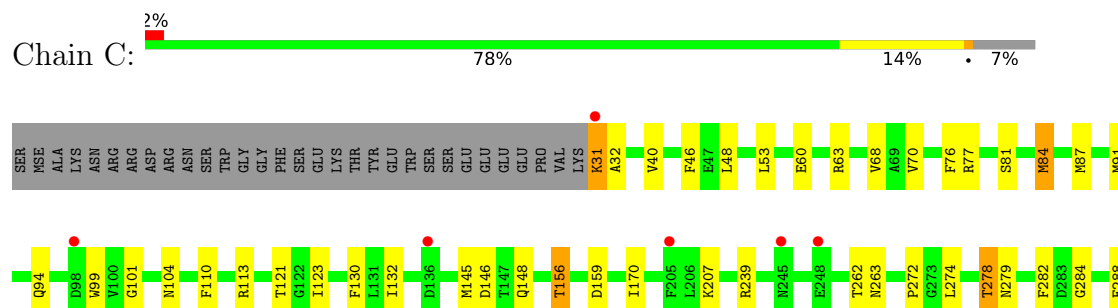
• Molecule 1: Atlastin-1



• Molecule 1: Atlastin-1

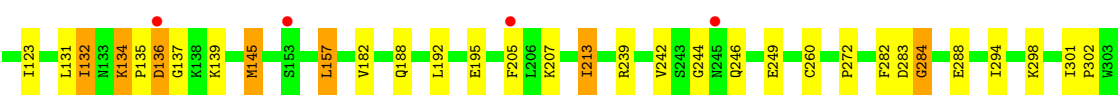
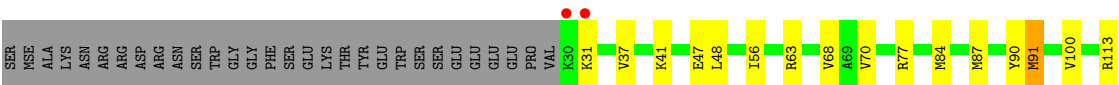
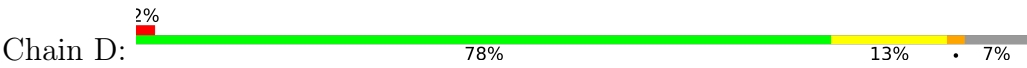


• Molecule 1: Atlastin-1





● Molecule 1: Atlantin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	131.95Å 268.12Å 62.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.68 – 2.59 49.68 – 2.59	Depositor EDS
% Data completeness (in resolution range)	80.3 (49.68-2.59) 80.7 (49.68-2.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.58Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.201 , 0.236 0.205 , 0.240	Depositor DCC
R_{free} test set	2000 reflections (3.53%)	wwPDB-VP
Wilson B-factor (Å ²)	27.5	Xtriage
Anisotropy	0.611	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.56$, $\langle L^2 \rangle = 0.41$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14015	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 65.46 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.0629e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GNP, MG

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	0.84	2/3450 (0.1%)	1.10	7/4637 (0.2%)
1	B	0.80	1/3452 (0.0%)	1.07	7/4638 (0.2%)
1	C	0.80	1/3413 (0.0%)	1.10	10/4587 (0.2%)
1	D	0.81	1/3446 (0.0%)	1.08	17/4631 (0.4%)
All	All	0.81	5/13761 (0.0%)	1.09	41/18493 (0.2%)

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

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	301	ILE	CA-CB	6.82	1.58	1.54
1	A	91	MSE	SE-CE	-5.43	1.79	1.95
1	A	368	ASN	CA-C	5.38	1.59	1.52
1	B	368	ASN	CA-C	5.24	1.59	1.52
1	D	91	MSE	SE-CE	-5.09	1.80	1.95

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	99	TRP	N-CA-C	-8.97	103.44	114.75
1	B	415	ARG	N-CA-C	8.94	120.64	111.07
1	B	101	GLY	N-CA-C	8.52	120.73	112.04
1	C	31	LYS	CG-CD-CE	-7.71	93.57	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	284	GLY	N-CA-C	7.17	126.11	115.64
1	D	132	ILE	CG1-CB-CG2	-7.05	89.56	110.70
1	B	284	GLY	N-CA-C	6.88	125.69	115.64
1	B	288	GLU	CA-CB-CG	-6.58	100.93	114.10
1	D	56	ILE	N-CA-C	6.49	117.12	110.82
1	D	134	LYS	CA-C-N	6.48	126.17	119.82
1	D	134	LYS	C-N-CA	6.48	126.17	119.82
1	A	56	ILE	N-CA-C	6.42	117.05	110.82
1	D	207	LYS	CA-C-N	6.32	126.06	119.05
1	D	207	LYS	C-N-CA	6.32	126.06	119.05
1	C	408	MSE	CA-CB-CG	6.16	126.42	114.10
1	D	284	GLY	N-CA-C	6.16	124.63	115.64
1	D	135	PRO	N-CA-C	-5.94	106.32	113.98
1	C	101	GLY	N-CA-C	5.90	118.06	112.04
1	B	300	LEU	N-CA-C	5.77	117.24	111.07
1	D	283	ASP	N-CA-C	-5.75	104.83	112.94
1	C	207	LYS	CA-C-N	5.63	125.48	119.28
1	C	207	LYS	C-N-CA	5.63	125.48	119.28
1	D	370	LYS	CA-CB-CG	-5.34	103.42	114.10
1	A	288	GLU	CA-CB-CG	-5.34	103.42	114.10
1	B	411	GLU	N-CA-C	5.31	117.07	111.28
1	C	288	GLU	CA-CB-CG	-5.28	103.55	114.10
1	C	279	ASN	CA-C-N	5.25	124.86	119.56
1	C	279	ASN	C-N-CA	5.25	124.86	119.56
1	A	374	ILE	N-CA-C	-5.24	107.66	111.90
1	D	188	GLN	N-CA-C	5.21	116.96	111.28
1	D	137	GLY	N-CA-C	-5.20	108.44	115.21
1	D	244	GLY	N-CA-C	5.18	118.51	112.50
1	D	288	GLU	CA-CB-CG	-5.18	103.75	114.10
1	A	408	MSE	N-CA-C	-5.15	103.24	110.50
1	B	56	ILE	N-CA-C	5.11	115.78	110.82
1	D	145	MSE	CA-CB-CG	5.09	124.29	114.10
1	A	154	GLN	CA-CB-CG	-5.09	103.92	114.10
1	D	260	CYS	N-CA-C	5.05	118.59	112.23
1	C	300	LEU	N-CA-C	5.05	116.47	111.07
1	D	157	LEU	CB-CG-CD2	-5.02	95.63	110.70
1	A	260	CYS	N-CA-C	5.02	117.86	111.69

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	408	MSE	Peptide

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	3376	0	3356	48	0
1	B	3378	0	3367	51	0
1	C	3351	0	3328	49	0
1	D	3375	0	3352	48	0
2	A	32	0	13	1	0
2	B	32	0	13	0	0
2	C	32	0	13	2	0
2	D	32	0	13	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	110	0	0	4	0
4	B	99	0	0	2	0
4	C	99	0	0	3	0
4	D	95	0	0	3	0
All	All	14015	0	13455	179	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.

All (179) 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:C:91:MSE:HE1	1:C:305:LEU:HD13	1.39	1.00
1:D:41:LYS:NZ	1:D:47:GLU:OE1	1.99	0.95
1:B:152:ASP:OD2	4:B:606:HOH:O	1.92	0.88
1:A:96:SER:OG	1:A:98:ASP:OD1	1.98	0.81
1:C:87:MSE:HE3	1:C:305:LEU:HD11	1.66	0.76
1:B:123:ILE:HG21	1:B:145:MSE:HE3	1.68	0.76
1:A:41:LYS:NZ	1:A:47:GLU:OE1	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:TYR:CD2	1:A:91:MSE:HE2	2.22	0.75
1:D:249:GLU:OE2	4:D:673:HOH:O	2.06	0.73
1:A:406:LYS:HZ1	1:B:340[A]:GLU:CD	1.97	0.72
1:C:156:THR:HG22	1:C:159:ASP:H	1.55	0.71
1:A:276:VAL:O	4:A:608:HOH:O	2.09	0.70
1:B:87:MSE:HE3	1:B:305:LEU:HD11	1.72	0.70
1:D:87:MSE:HE3	1:D:305:LEU:HD11	1.73	0.69
1:B:145:MSE:HE1	1:B:167:SER:HA	1.76	0.68
1:D:131:LEU:HB3	1:D:139:LYS:HE3	1.76	0.68
1:A:91:MSE:HE3	1:A:305:LEU:HD13	1.76	0.67
1:A:77:ARG:NH2	1:A:113:ARG:O	2.28	0.67
1:C:347:MSE:CE	1:D:157:LEU:HD21	2.26	0.66
1:C:340:GLU:OE1	1:C:340:GLU:N	2.27	0.66
1:A:87:MSE:HE3	1:A:305:LEU:HD11	1.78	0.65
1:B:429:TYR:HE2	1:D:415:ARG:HH12	1.44	0.65
1:A:90:TYR:HD2	1:A:91:MSE:HE2	1.59	0.65
1:C:274:LEU:O	1:C:278:THR:HB	1.96	0.65
1:C:347:MSE:HE3	1:D:345:LYS:O	1.96	0.65
1:B:90:TYR:CD2	1:B:91:MSE:HE3	2.32	0.64
1:A:408:MSE:HE3	1:B:195:GLU:HG3	1.80	0.64
1:A:70:VAL:HG11	1:A:87:MSE:HE1	1.80	0.63
1:D:365:ASP:OD1	1:D:369:LYS:HE2	1.99	0.62
1:C:48:LEU:HD11	1:C:53:LEU:HD22	1.80	0.62
1:D:90:TYR:CD2	1:D:91:MSE:HE2	2.35	0.62
1:A:371:MSE:HE1	1:A:387:LEU:HD11	1.82	0.61
1:C:345:LYS:HE3	4:C:660:HOH:O	2.00	0.61
1:B:355:ASN:HD22	1:B:408:MSE:H	1.48	0.61
1:C:347:MSE:CE	1:D:192:LEU:HD22	2.30	0.61
1:C:416:ARG:NE	4:C:630:HOH:O	2.34	0.60
1:A:424:GLU:OE2	4:A:638:HOH:O	2.17	0.59
1:D:77:ARG:NH2	1:D:113:ARG:O	2.34	0.59
1:A:91:MSE:CE	1:A:305:LEU:HB3	2.31	0.59
1:A:91:MSE:HE3	1:A:305:LEU:HB3	1.85	0.59
1:C:123:ILE:HD13	1:C:145:MSE:HE2	1.83	0.59
1:B:274:LEU:O	1:B:278:THR:HB	2.03	0.59
1:B:416[A]:ARG:HH12	1:D:426:ASP:HB3	1.68	0.58
1:A:128:GLU:OE1	4:A:662:HOH:O	2.17	0.58
1:A:123:ILE:HG21	1:A:145:MSE:HE2	1.86	0.58
1:B:411:GLU:O	1:B:415:ARG:HG3	2.04	0.57
1:D:424:GLU:OE2	4:D:667:HOH:O	2.17	0.57
1:D:91:MSE:HE3	1:D:305:LEU:HB3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:347:MSE:HE1	1:D:157:LEU:HD21	1.86	0.57
1:D:371:MSE:HE1	1:D:387:LEU:HD11	1.87	0.57
1:B:76:PHE:CD2	1:B:77:ARG:HG2	2.41	0.56
1:B:345:LYS:HE3	4:B:623:HOH:O	2.04	0.56
1:D:294:ILE:HG22	1:D:298:LYS:HD2	1.88	0.56
1:A:409:GLY:HA2	1:B:195:GLU:OE2	2.06	0.55
1:B:96:SER:OG	1:B:98:ASP:OD1	2.24	0.55
1:D:419:GLN:HG3	4:D:669:HOH:O	2.05	0.55
1:A:182:VAL:O	1:A:239:ARG:NH1	2.40	0.55
1:B:123:ILE:HD13	1:B:145:MSE:CE	2.37	0.54
1:A:35:VAL:HG21	1:A:56:ILE:HD11	1.89	0.54
1:A:301:ILE:HB	1:A:302:PRO:HD3	1.90	0.54
1:B:77:ARG:NH2	1:B:113:ARG:O	2.40	0.54
1:B:123:ILE:HG21	1:B:145:MSE:CE	2.38	0.54
1:C:31:LYS:HG2	1:C:32:ALA:O	2.08	0.54
1:B:90:TYR:HD2	1:B:91:MSE:HE3	1.72	0.53
1:B:355:ASN:ND2	1:B:408:MSE:H	2.06	0.53
1:A:227:TYR:CZ	1:A:270:PRO:HB3	2.44	0.53
1:C:48:LEU:HB2	1:C:333:ILE:HD13	1.90	0.53
1:D:301:ILE:HB	1:D:302:PRO:HD3	1.91	0.52
1:D:90:TYR:HD2	1:D:91:MSE:HE2	1.74	0.52
1:A:87:MSE:CE	1:A:305:LEU:HD11	2.39	0.52
1:C:411:GLU:O	1:C:415:ARG:HG3	2.09	0.52
1:A:48:LEU:HB2	1:A:333:ILE:HD13	1.92	0.51
1:D:182:VAL:O	1:D:239:ARG:NH1	2.44	0.51
1:C:40:VAL:HG22	1:C:46:PHE:CD1	2.46	0.51
1:C:123:ILE:HG21	1:C:145:MSE:HE3	1.93	0.51
1:A:48:LEU:HD11	1:A:53:LEU:HD22	1.92	0.51
1:C:347:MSE:HE1	1:D:192:LEU:HD22	1.93	0.50
1:C:76:PHE:CD2	1:C:77:ARG:HG2	2.47	0.50
1:D:48:LEU:HB2	1:D:333:ILE:HD13	1.93	0.50
1:B:40:VAL:HG22	1:B:46:PHE:CD1	2.47	0.50
1:D:70:VAL:HG11	1:D:87:MSE:HE1	1.93	0.50
1:D:100:VAL:HG11	1:D:298:LYS:CG	2.41	0.50
1:A:90:TYR:HD2	1:A:91:MSE:CE	2.25	0.49
1:A:91:MSE:HE3	1:A:305:LEU:CD1	2.41	0.49
1:D:68:VAL:HG21	1:D:310:LEU:HB3	1.94	0.49
1:D:91:MSE:CE	1:D:305:LEU:HB3	2.42	0.49
1:D:63:ARG:HD3	1:D:323[A]:ARG:NH2	2.28	0.48
1:C:170:ILE:HG23	1:C:325:LEU:HD11	1.95	0.48
1:A:242:VAL:HA	1:A:246:GLN:OE1	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:TYR:CD2	1:A:91:MSE:CE	2.95	0.48
1:C:123:ILE:HD13	1:C:145:MSE:CE	2.43	0.48
1:B:35:VAL:HG21	1:B:56:ILE:HD11	1.95	0.48
1:D:90:TYR:HD2	1:D:91:MSE:CE	2.27	0.48
1:C:70:VAL:HG11	1:C:87:MSE:HE1	1.96	0.48
1:B:60:GLU:HA	1:B:63:ARG:HH21	1.79	0.48
1:D:134:LYS:C	1:D:136:ASP:H	2.22	0.48
1:C:94:GLN:O	4:C:607:HOH:O	2.19	0.47
1:C:409:GLY:HA2	1:D:195:GLU:OE2	2.12	0.47
1:B:416[A]:ARG:H	1:B:416[A]:ARG:HG2	1.45	0.47
1:C:68:VAL:HG21	1:C:310:LEU:HB3	1.97	0.47
1:B:371:MSE:HE1	1:B:387:LEU:HD11	1.97	0.47
1:D:90:TYR:CD2	1:D:91:MSE:CE	2.98	0.46
1:C:91:MSE:HE2	1:C:91:MSE:HB2	1.64	0.46
1:A:228:GLY:HA2	1:A:267:PHE:CZ	2.51	0.46
1:B:91:MSE:HA	1:B:91:MSE:HE2	1.97	0.46
1:D:134:LYS:C	1:D:136:ASP:N	2.71	0.46
1:D:323[B]:ARG:HG3	1:D:324:GLY:N	2.30	0.46
1:D:242:VAL:HA	1:D:246:GLN:OE1	2.16	0.46
1:D:390:LYS:HA	1:D:390:LYS:HD2	1.77	0.46
1:B:59:SER:O	1:B:63:ARG:HB3	2.15	0.46
1:B:48:LEU:HD11	1:B:53:LEU:HD22	1.97	0.46
1:C:81:SER:OG	1:C:146:ASP:OD2	2.34	0.46
1:B:301:ILE:HB	1:B:302:PRO:HD3	1.97	0.45
1:B:84:MSE:HE2	1:B:84:MSE:HB2	1.71	0.45
1:B:282:PHE:CZ	1:B:284:GLY:HA2	2.52	0.45
1:C:40:VAL:HG22	1:C:46:PHE:HD1	1.82	0.45
1:C:84:MSE:HE2	1:C:84:MSE:HB2	1.82	0.45
1:C:429:TYR:CZ	1:C:433:ILE:HD11	2.52	0.45
1:B:267:PHE:CG	1:B:300:LEU:HD13	2.52	0.45
1:D:282:PHE:CZ	1:D:284:GLY:HA2	2.52	0.45
1:B:134:LYS:HE2	1:B:307:PRO:O	2.16	0.45
1:A:345:LYS:HE3	4:A:622:HOH:O	2.17	0.44
1:C:371:MSE:HE1	1:C:387:LEU:HD11	1.99	0.44
1:B:70:VAL:HG11	1:B:87:MSE:HE1	1.99	0.44
1:B:412:GLU:HG2	1:D:388:GLN:OE1	2.17	0.44
1:C:91:MSE:HG2	1:C:130:PHE:CD2	2.52	0.44
1:A:76:PHE:CD2	1:A:77:ARG:HG2	2.53	0.44
1:B:60:GLU:CA	1:B:63:ARG:HH21	2.31	0.44
1:C:262:THR:HG22	1:C:263:ASN:OD1	2.17	0.44
1:C:282:PHE:CZ	1:C:284:GLY:HA2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:84:MSE:HG2	1:B:110:PHE:CE2	2.53	0.43
1:A:77:ARG:NH1	2:A:501:GNP:HNB3	2.16	0.43
1:A:84:MSE:HE3	1:A:110:PHE:CE2	2.53	0.43
1:D:123:ILE:HG21	1:D:145:MSE:HE3	1.99	0.43
1:C:301:ILE:HB	1:C:302:PRO:HD3	2.01	0.43
1:B:40:VAL:HG22	1:B:46:PHE:HD1	1.82	0.43
1:C:390:LYS:HD3	1:C:390:LYS:HA	1.66	0.43
1:C:399:VAL:HG13	1:C:418:LEU:HD11	2.00	0.43
1:C:113:ARG:O	2:C:501:GNP:H5'1	2.19	0.43
1:A:134:LYS:HE2	1:A:310:LEU:O	2.18	0.42
1:A:91:MSE:HE3	1:A:305:LEU:CB	2.48	0.42
1:C:401:LEU:HD12	1:C:401:LEU:HA	1.86	0.42
1:C:411:GLU:HA	1:C:414:SER:HB2	2.00	0.42
1:C:84:MSE:HG2	1:C:110:PHE:CD2	2.54	0.42
1:B:399:VAL:HG13	1:B:418:LEU:HD11	2.01	0.42
1:C:60:GLU:CA	1:C:63:ARG:HH21	2.32	0.42
1:C:347:MSE:HE3	1:D:157:LEU:HD21	1.99	0.42
1:A:347:MSE:SE	1:B:192:LEU:HD22	2.70	0.42
1:D:91:MSE:HE3	1:D:305:LEU:CB	2.49	0.42
1:C:272:PRO:HG3	2:C:501:GNP:C6	2.50	0.42
1:D:272:PRO:HG3	2:D:501:GNP:C6	2.49	0.42
1:C:379:LYS:HA	1:C:379:LYS:HD3	1.89	0.42
1:D:123:ILE:HD13	1:D:145:MSE:HE2	2.01	0.42
1:A:213:ILE:HD13	1:A:265:SER:OG	2.20	0.41
1:A:195:GLU:OE2	1:B:409:GLY:HA2	2.20	0.41
1:D:70:VAL:CG1	1:D:87:MSE:HE1	2.50	0.41
1:A:170:ILE:HG23	1:A:325:LEU:HD11	2.02	0.41
1:D:41:LYS:NZ	1:D:47:GLU:CD	2.76	0.41
1:A:70:VAL:CG1	1:A:87:MSE:HE1	2.47	0.41
1:A:157:LEU:HD21	1:B:347:MSE:SE	2.71	0.41
1:B:242:VAL:HA	1:B:246:GLN:OE1	2.21	0.41
1:C:84:MSE:HG2	1:C:110:PHE:CE2	2.56	0.41
1:A:270:PRO:HG2	1:A:293:PHE:HA	2.03	0.41
1:B:169:MSE:HE1	1:B:200:ALA:HB3	2.03	0.41
1:C:347:MSE:HB3	1:C:347:MSE:HE2	1.91	0.41
1:A:416:ARG:NE	1:A:417:TYR:CE2	2.88	0.40
1:B:367:TYR:CZ	1:B:371:MSE:HG3	2.56	0.40
1:A:169:MSE:HE3	1:A:201:MSE:HG3	2.04	0.40
1:B:37:VAL:O	1:B:48:LEU:HD12	2.21	0.40
1:C:121:THR:HA	1:C:148:GLN:HB2	2.02	0.40
1:B:401:LEU:HA	1:B:401:LEU:HD12	1.83	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:84:MSE:HE2	1:D:84:MSE:HB2	1.81	0.40
1:D:205:PHE:HD1	1:D:205:PHE:HA	1.73	0.40
1:A:91:MSE:HE1	1:A:305:LEU:HB3	2.00	0.40
1:A:105[A]:GLU:HA	1:A:106:PRO:HD3	1.95	0.40
1:B:90:TYR:CE2	1:B:91:MSE:HE3	2.57	0.40
1:A:195:GLU:HG2	1:B:408:MSE:HG3	2.03	0.40
1:B:390:LYS:HD3	1:B:390:LYS:HA	1.84	0.40
1:D:213:ILE:HD12	1:D:304:LEU:CD2	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	418/447 (94%)	411 (98%)	7 (2%)	0	100	100
1	B	418/447 (94%)	412 (99%)	6 (1%)	0	100	100
1	C	414/447 (93%)	407 (98%)	7 (2%)	0	100	100
1	D	418/447 (94%)	412 (99%)	6 (1%)	0	100	100
All	All	1668/1788 (93%)	1642 (98%)	26 (2%)	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	371/385 (96%)	365 (98%)	6 (2%)	55	77
1	B	371/385 (96%)	358 (96%)	13 (4%)	32	57
1	C	367/385 (95%)	360 (98%)	7 (2%)	50	73
1	D	370/385 (96%)	364 (98%)	6 (2%)	55	77
All	All	1479/1540 (96%)	1447 (98%)	32 (2%)	48	70

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

Mol	Chain	Res	Type
1	A	37	VAL
1	A	63	ARG
1	A	213	ILE
1	A	329	PHE
1	A	334	LYS
1	A	408	MSE
1	B	37	VAL
1	B	84	MSE
1	B	132	ILE
1	B	213	ILE
1	B	253	VAL
1	B	278	THR
1	B	292	GLU
1	B	308	GLU
1	B	369	LYS
1	B	403[A]	ARG
1	B	403[B]	ARG
1	B	416[A]	ARG
1	B	416[B]	ARG
1	C	84	MSE
1	C	104	ASN
1	C	132	ILE
1	C	156	THR
1	C	239	ARG
1	C	278	THR
1	C	414	SER
1	D	31	LYS
1	D	37	VAL
1	D	132	ILE
1	D	136	ASP
1	D	213	ILE
1	D	329	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	GLN
1	A	183	GLN
1	A	251	GLN
1	A	318	ASN
1	A	393	GLN
1	B	93	ASN
1	B	174	GLN
1	B	183	GLN
1	B	318	ASN
1	B	355	ASN
1	B	393	GLN
1	C	133	ASN
1	C	431	GLN
1	C	443	HIS
1	D	174	GLN
1	D	393	GLN
1	D	435	HIS
1	D	443	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](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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
2	GNP	D	501	3	34,34,34	1.50	6 (17%)	47,54,54	1.45	7 (14%)
2	GNP	A	501	3	34,34,34	1.54	5 (14%)	47,54,54	1.01	2 (4%)
2	GNP	C	501	3	34,34,34	1.45	6 (17%)	47,54,54	1.13	4 (8%)
2	GNP	B	501	3	34,34,34	1.55	6 (17%)	47,54,54	1.07	4 (8%)

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	GNP	D	501	3	-	3/18/38/38	0/3/3/3
2	GNP	A	501	3	-	3/18/38/38	0/3/3/3
2	GNP	C	501	3	-	2/18/38/38	0/3/3/3
2	GNP	B	501	3	-	2/18/38/38	0/3/3/3

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	GNP	PG-O1G	5.08	1.53	1.46
2	A	501	GNP	PG-O1G	4.37	1.52	1.46
2	D	501	GNP	PA-O3A	-4.20	1.55	1.59
2	B	501	GNP	PA-O3A	-3.80	1.55	1.59
2	A	501	GNP	PA-O3A	-3.67	1.55	1.59
2	A	501	GNP	PB-O3A	-3.66	1.54	1.59
2	C	501	GNP	PB-O3A	-3.63	1.54	1.59
2	C	501	GNP	PG-O1G	3.53	1.51	1.46
2	B	501	GNP	PB-O3A	-3.49	1.54	1.59
2	D	501	GNP	PB-O3A	-3.29	1.55	1.59
2	A	501	GNP	PB-O2B	-3.24	1.48	1.56
2	D	501	GNP	PG-O1G	3.24	1.51	1.46
2	D	501	GNP	PB-O2B	-3.20	1.48	1.56
2	C	501	GNP	PA-O3A	-3.12	1.56	1.59
2	A	501	GNP	PG-O2G	-3.06	1.48	1.56
2	C	501	GNP	PB-O2B	-3.04	1.48	1.56
2	B	501	GNP	PB-O2B	-2.93	1.49	1.56
2	D	501	GNP	PG-O2G	-2.60	1.49	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	GNP	PG-O2G	-2.47	1.50	1.56
2	C	501	GNP	PG-O2G	-2.24	1.50	1.56
2	C	501	GNP	PG-O3G	-2.14	1.51	1.56
2	B	501	GNP	PB-O1B	2.05	1.49	1.46
2	D	501	GNP	PB-N3B	-2.01	1.58	1.63

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	GNP	O1G-PG-N3B	-5.21	104.11	111.77
2	A	501	GNP	O1G-PG-N3B	-3.96	105.94	111.77
2	B	501	GNP	O3G-PG-O1G	-3.71	104.14	113.45
2	D	501	GNP	O4'-C1'-N9	-3.54	100.35	108.36
2	C	501	GNP	O3G-PG-O1G	-3.43	104.85	113.45
2	D	501	GNP	O2G-PG-O3G	3.24	116.29	107.59
2	D	501	GNP	O4'-C1'-C2'	-3.04	100.11	106.62
2	B	501	GNP	O2G-PG-O3G	2.91	115.42	107.59
2	C	501	GNP	O2G-PG-O3G	2.88	115.33	107.59
2	D	501	GNP	O2B-PB-O1B	2.66	115.58	109.87
2	C	501	GNP	O4'-C1'-C2'	-2.65	100.94	106.62
2	C	501	GNP	O4'-C1'-N9	-2.65	102.35	108.36
2	B	501	GNP	O1G-PG-N3B	-2.15	108.60	111.77
2	D	501	GNP	O2B-PB-O3A	2.11	111.67	104.64
2	A	501	GNP	O4'-C1'-C2'	-2.10	102.13	106.62
2	B	501	GNP	O2A-PA-O3A	2.07	112.86	107.27
2	D	501	GNP	O3G-PG-O1G	-2.05	108.30	113.45

There are no chirality outliers.

All (10) torsion outliers are listed below:

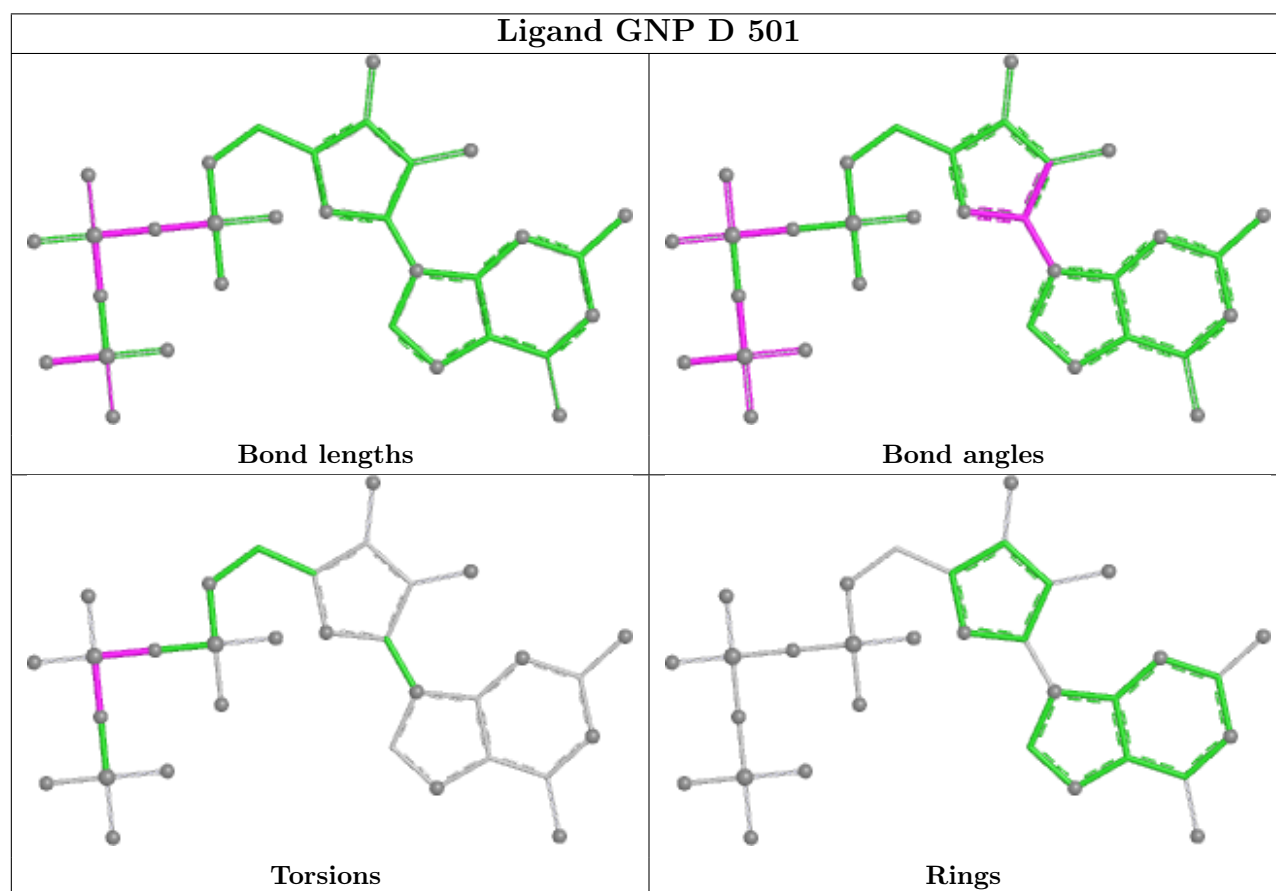
Mol	Chain	Res	Type	Atoms
2	A	501	GNP	PG-N3B-PB-O1B
2	A	501	GNP	PA-O3A-PB-O2B
2	B	501	GNP	PG-N3B-PB-O1B
2	C	501	GNP	PG-N3B-PB-O1B
2	D	501	GNP	PG-N3B-PB-O1B
2	D	501	GNP	PA-O3A-PB-O2B
2	A	501	GNP	PA-O3A-PB-O1B
2	B	501	GNP	PA-O3A-PB-O1B
2	C	501	GNP	PA-O3A-PB-O1B
2	D	501	GNP	PA-O3A-PB-O1B

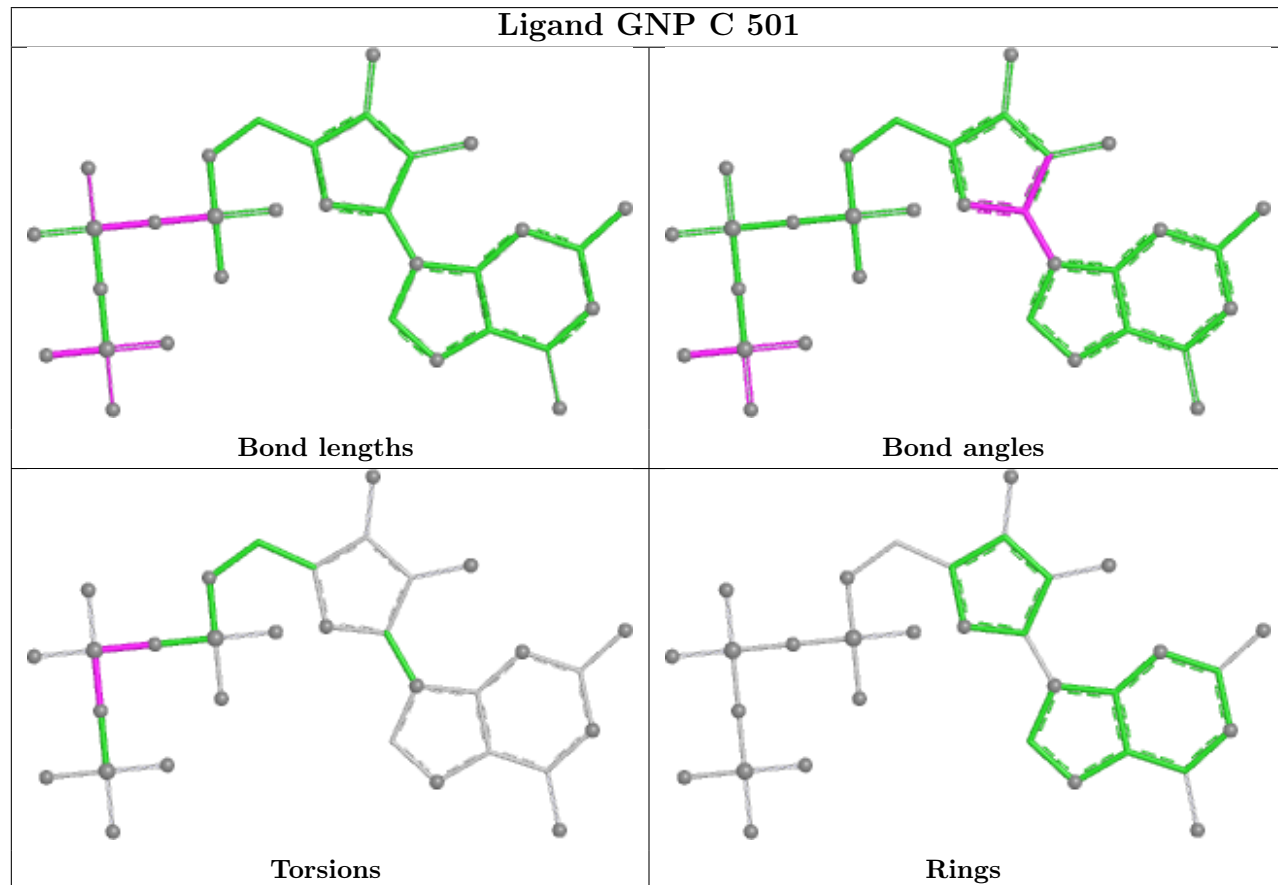
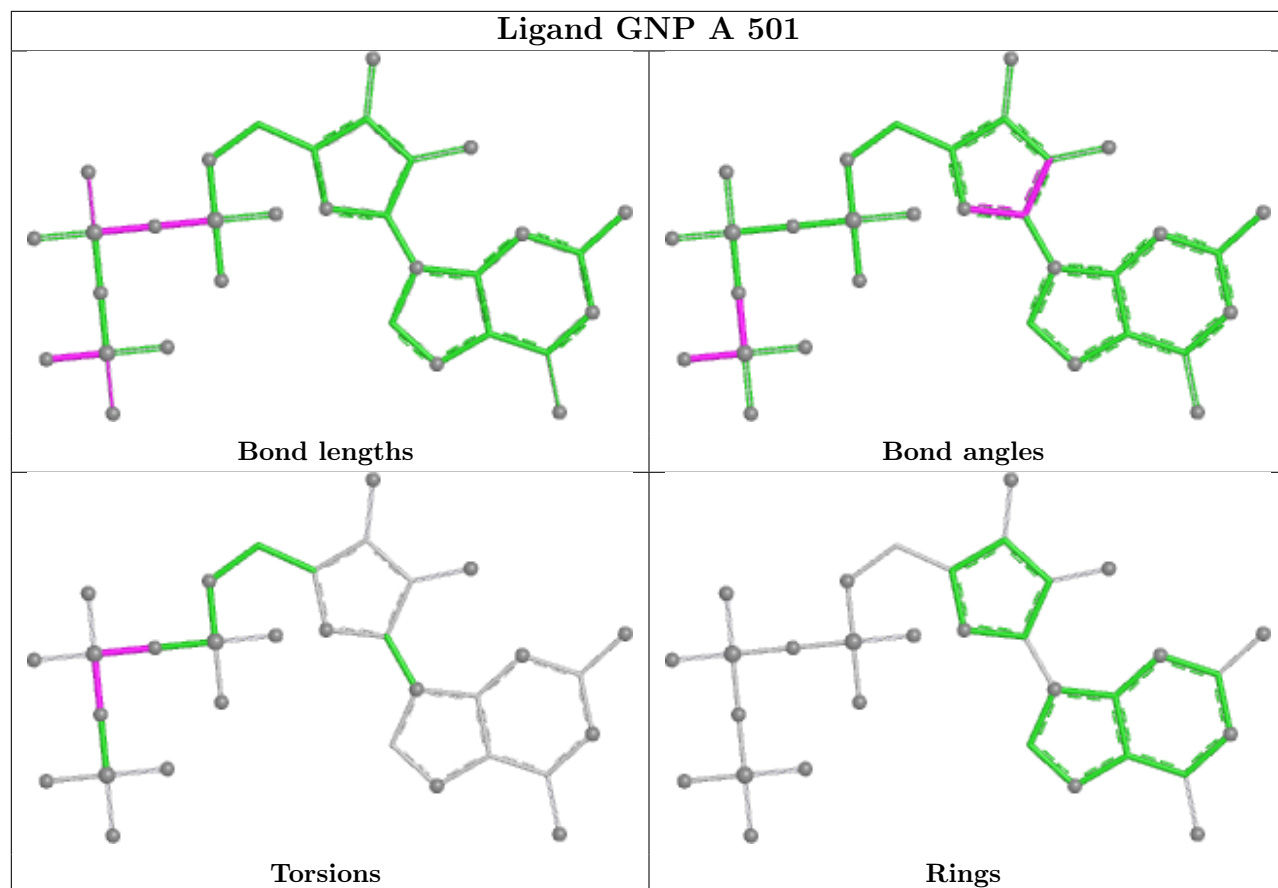
There are no ring outliers.

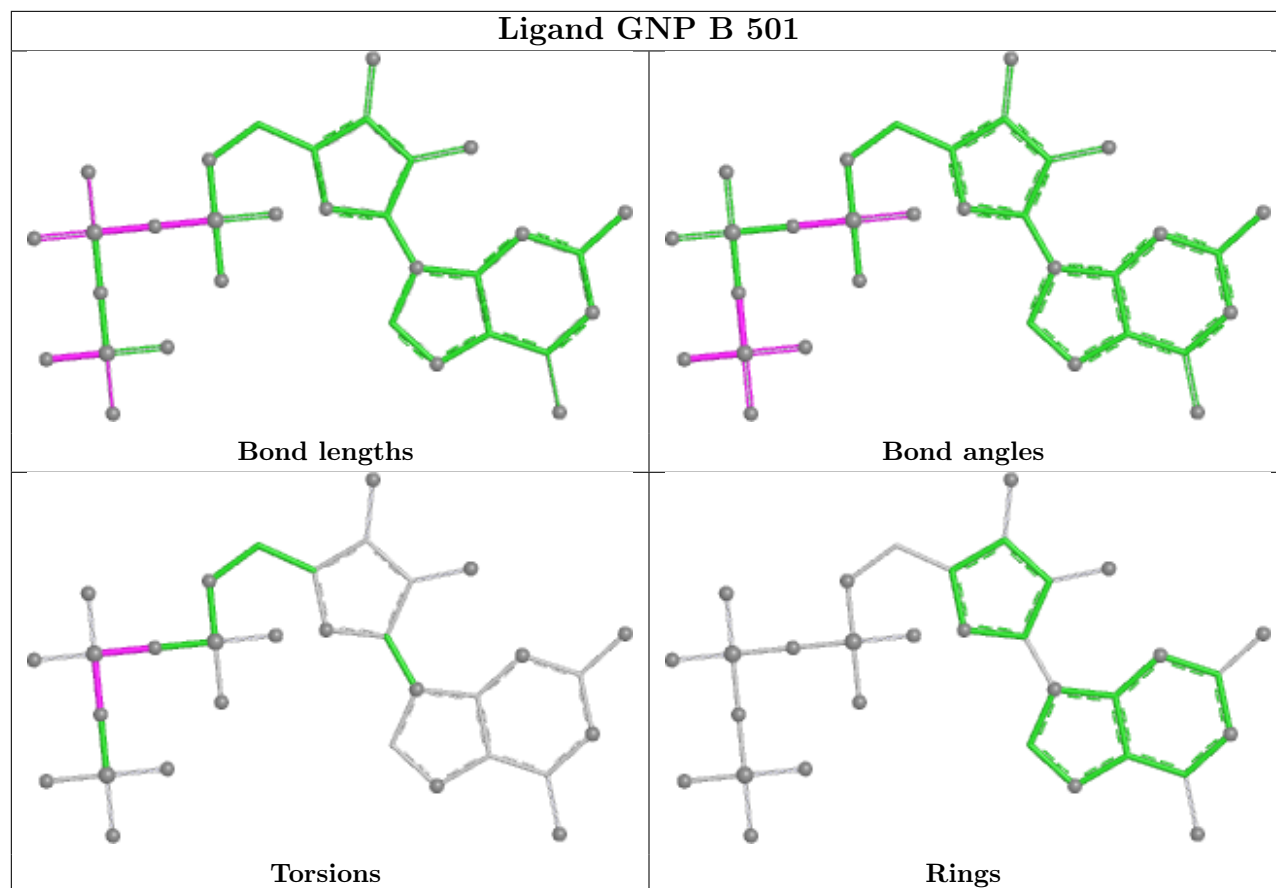
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	501	GNP	1	0
2	A	501	GNP	1	0
2	C	501	GNP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	407/447 (91%)	-0.11	9 (2%) 62 58	11, 24, 54, 95	4 (0%)
1	B	407/447 (91%)	-0.10	9 (2%) 62 58	11, 24, 54, 92	4 (0%)
1	C	407/447 (91%)	-0.16	8 (1%) 65 61	10, 25, 51, 90	0
1	D	408/447 (91%)	-0.22	7 (1%) 69 65	11, 24, 50, 85	3 (0%)
All	All	1629/1788 (91%)	-0.15	33 (2%) 65 61	10, 24, 53, 95	11 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	415	ARG	4.1
1	D	205	PHE	3.8
1	D	415	ARG	3.6
1	D	30	LYS	3.4
1	C	416	ARG	3.3
1	A	97	VAL	3.2
1	A	416	ARG	3.1
1	B	390	LYS	2.9
1	C	136	ASP	2.9
1	A	205	PHE	2.9
1	A	154	GLN	2.8
1	C	205	PHE	2.8
1	B	96	SER	2.8
1	C	245	ASN	2.7
1	B	98	ASP	2.7
1	A	98	ASP	2.6
1	A	136	ASP	2.6
1	D	31	LYS	2.5
1	C	98	ASP	2.5
1	D	136	ASP	2.4
1	A	95	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	31	LYS	2.3
1	B	95	GLU	2.3
1	B	205	PHE	2.2
1	D	245	ASN	2.2
1	B	94	GLN	2.2
1	B	396	GLU	2.2
1	A	203	GLU	2.2
1	C	248	GLU	2.2
1	B	245[A]	ASN	2.1
1	C	340	GLU	2.1
1	B	412	GLU	2.1
1	D	153	SER	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no 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.

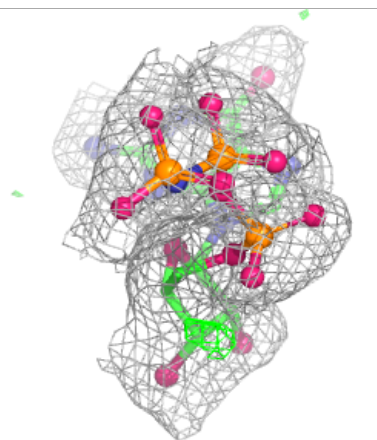
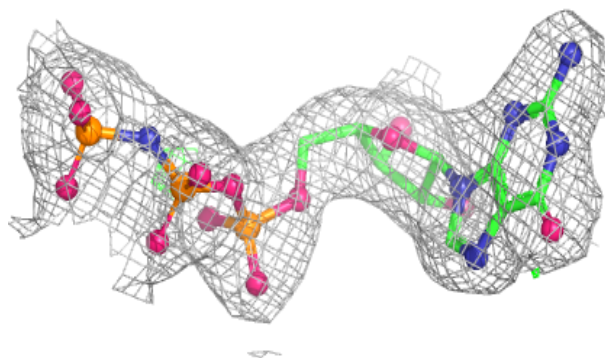
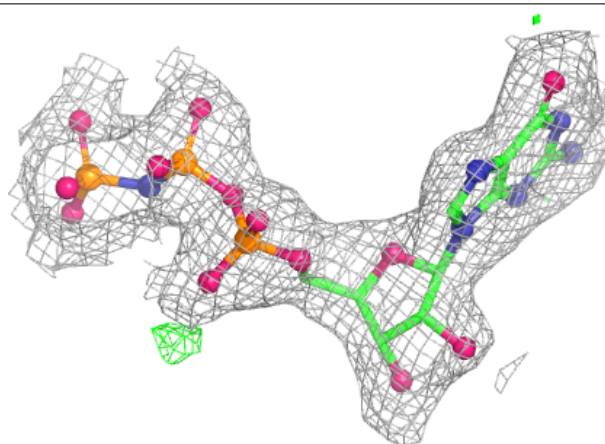
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	B	502	1/1	0.95	0.12	44,44,44,44	0
3	MG	C	502	1/1	0.97	0.11	35,35,35,35	0
2	GNP	A	501	32/32	0.98	0.05	8,17,22,23	0
2	GNP	D	501	32/32	0.99	0.04	8,18,23,24	0
3	MG	A	502	1/1	0.99	0.06	35,35,35,35	0
2	GNP	B	501	32/32	0.99	0.04	7,15,20,22	0
2	GNP	C	501	32/32	0.99	0.04	6,18,21,22	0
3	MG	D	502	1/1	0.99	0.05	31,31,31,31	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.

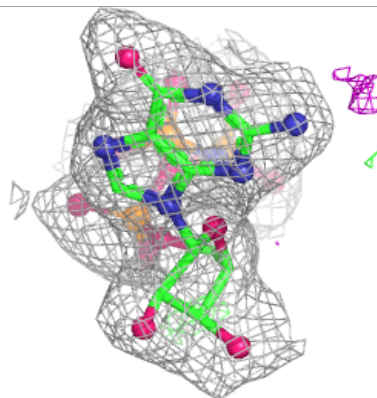
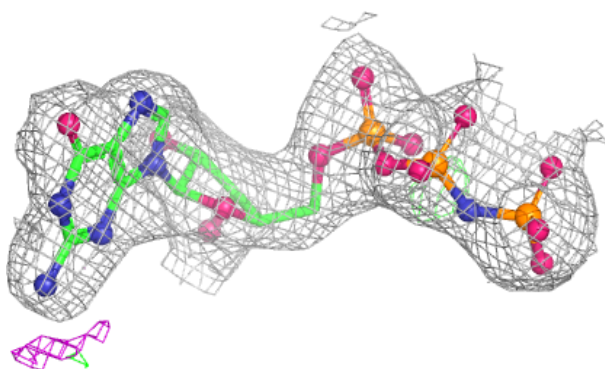
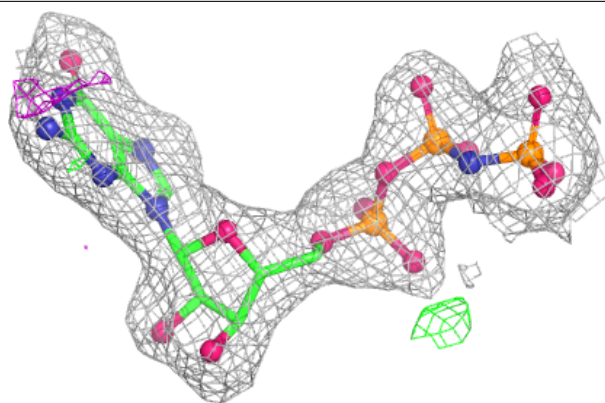
Electron density around GNP A 501:

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

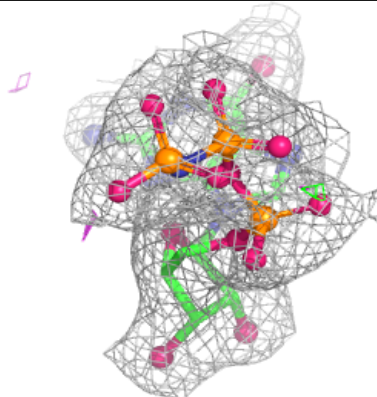
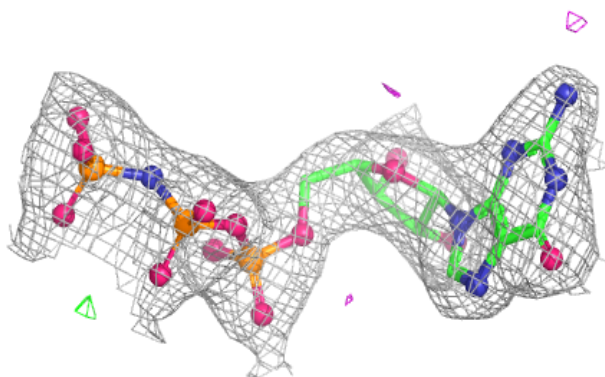
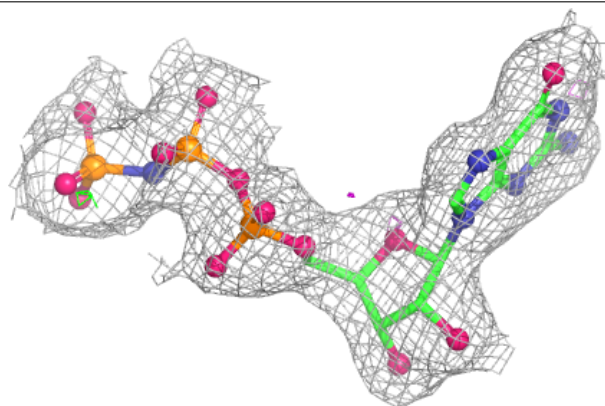


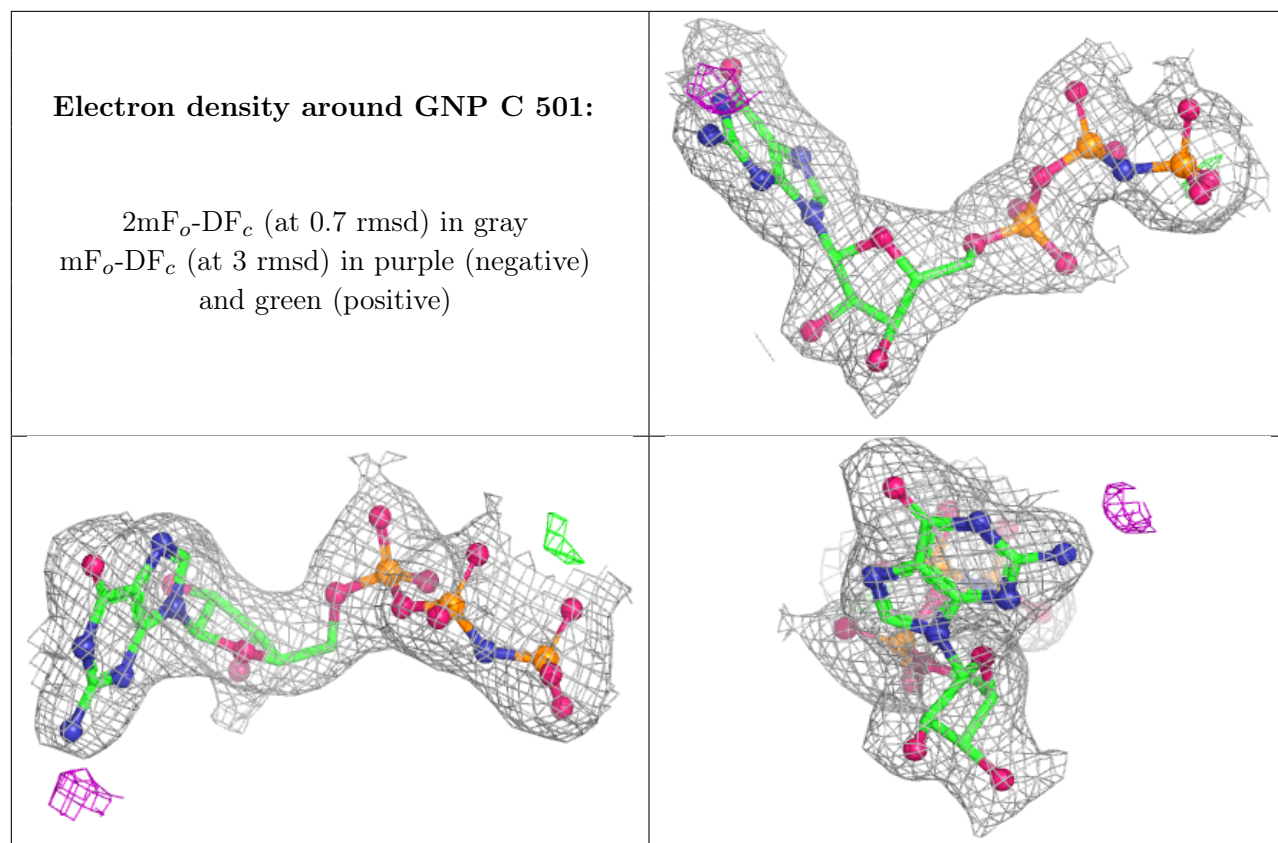
Electron density around GNP D 501:

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

**Electron density around GNP B 501:**

$2mF_o-DF_c$ (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.