



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2022 – 03:16 PM EDT

PDB ID : 7SIZ
Title : C-type inactivation in a voltage gated K⁺ channel
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Deposited on : 2021-10-15
Resolution : 3.10 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.28.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.28.1

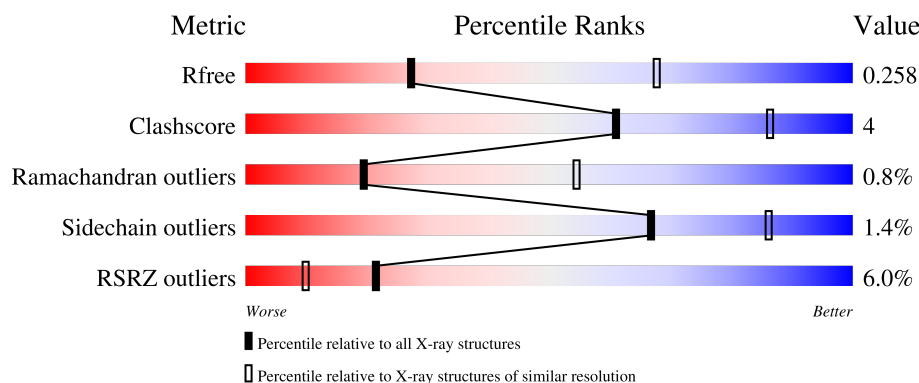
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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	333	
1	C	333	
2	B	514	
2	D	514	

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	K	B	502	-	-	-	X
4	K	D	503	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10688 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 Voltage-gated potassium channel subunit beta-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	0	0
			2552	1624	442	470	16			
1	C	326	Total	C	N	O	S	0	0	0
			2556	1627	443	470	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	35	MET	-	initiating methionine	UNP P62483
C	35	MET	-	initiating methionine	UNP P62483

- Molecule 2 is a protein called Voltage gated potassium channel Kv1.2-Kv2.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	334	Total	C	N	O	S	0	0	0
			2731	1805	440	473	13			
2	D	333	Total	C	N	O	S	0	0	0
			2703	1790	434	466	13			

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
3	C	1	Total 48	C 21	N 7	O 17	P 3	0	0

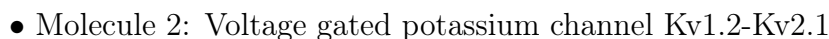
- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

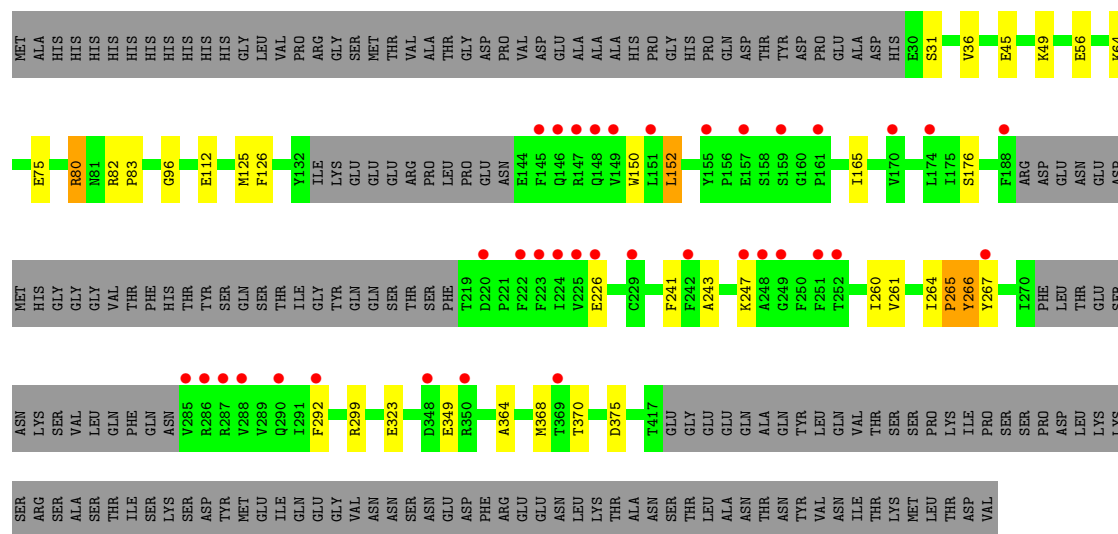
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	6	Total K 6 6	0	0
4	D	6	Total K 6 6	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	7	Total O 7 7	0	0
5	C	24	Total O 24 24	0	0
5	D	7	Total O 7 7	0	0

- Molecule 1: Voltage-gated potassium channel subunit beta-2





4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	130.73Å 130.73Å 278.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.75 – 3.10 47.75 – 2.95	Depositor EDS
% Data completeness (in resolution range)	89.9 (47.75-3.10) 88.2 (47.75-2.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.77 (at 2.96Å)	Xtriage
Refinement program	PHENIX 1.14_3260, PHENIX 1.14_3260	Depositor
R, R_{free}	0.236 , 0.265 0.227 , 0.258	Depositor DCC
R_{free} test set	2650 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	78.6	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 71.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10688	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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, K

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	0.24	0/2604	0.40	0/3520
1	C	0.24	0/2608	0.39	0/3524
2	B	0.25	0/2801	0.38	0/3793
2	D	0.25	0/2772	0.38	0/3755
All	All	0.24	0/10785	0.39	0/14592

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	2552	0	2571	23	0
1	C	2556	0	2582	15	0
2	B	2731	0	2750	36	0
2	D	2703	0	2716	18	0
3	A	48	0	25	9	0
3	C	48	0	25	3	0
4	B	6	0	0	0	0
4	D	6	0	0	0	0
5	A	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	24	0	0	0	0
5	D	7	0	0	1	0
All	All	10688	0	10669	95	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 4.

All (95) 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:244:SER:OG	3:A:401:NAP:O2N	1.93	0.86
2:B:296:ARG:HG2	2:B:299:ARG:HE	1.46	0.79
1:A:118:LYS:HG2	1:A:156:PHE:HB2	1.67	0.76
1:A:329:GLN:O	1:A:333:ASN:ND2	2.21	0.73
2:B:176:SER:OG	2:B:299:ARG:NH1	2.21	0.72
1:C:118:LYS:HG3	1:C:156:PHE:HB2	1.73	0.70
1:C:254:LYS:NZ	3:C:1001:NAP:O1X	2.25	0.68
2:B:241:PHE:O	2:B:247:LYS:NZ	2.28	0.67
2:B:351:ASP:OD1	2:B:351:ASP:N	2.29	0.65
2:D:226:GLU:HG3	2:D:266:TYR:HE1	1.61	0.65
1:A:85:ASP:OD1	1:A:118:LYS:NZ	2.30	0.65
2:D:152:LEU:HD23	2:D:165:ILE:HG13	1.80	0.63
1:A:244:SER:HA	3:A:401:NAP:O2N	1.99	0.63
2:D:261:VAL:HA	2:D:264:ILE:HG12	1.80	0.63
2:D:241:PHE:O	2:D:247:LYS:NZ	2.32	0.62
1:A:333:ASN:HD21	3:A:401:NAP:H61A	1.49	0.59
2:D:36:VAL:HG22	2:D:45:GLU:HG2	1.83	0.59
2:B:255:MET:HE1	2:B:305:ARG:HA	1.84	0.59
2:D:80:ARG:NH1	2:D:112:GLU:OE2	2.36	0.58
2:B:153:PHE:O	2:B:240:ARG:NE	2.36	0.58
1:C:52:LEU:HD13	1:C:322:LEU:HD11	1.86	0.58
2:D:265:PRO:O	2:D:267:TYR:N	2.38	0.57
2:B:236:GLU:OE2	2:B:240:ARG:NH1	2.38	0.56
1:C:85:ASP:OD1	1:C:118:LYS:NZ	2.37	0.56
2:D:150:TRP:HB2	2:D:243:ALA:HB1	1.88	0.56
2:B:29:HIS:O	2:B:29:HIS:ND1	2.38	0.56
2:B:153:PHE:HE1	2:B:165:ILE:HG21	1.70	0.55
2:D:323:GLU:OE1	2:D:323:GLU:N	2.37	0.54
1:A:236:ILE:HG13	1:A:238:VAL:HG23	1.88	0.54
1:A:97:VAL:O	1:A:101:ASN:ND2	2.40	0.54
2:D:31:SER:HA	2:D:49:LYS:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:217:TYR:HB2	1:C:225:VAL:HG21	1.90	0.54
2:B:156:PRO:HB2	2:B:163:ARG:HD2	1.91	0.53
2:B:349:GLU:HB3	2:B:352:SER:HB2	1.91	0.53
1:C:56:THR:HB	1:C:60:PHE:HB2	1.92	0.52
2:B:260:ILE:O	2:B:264:ILE:HG13	2.10	0.52
1:A:216:GLU:HB2	1:A:243:TRP:CH2	2.46	0.51
3:C:1001:NAP:H8A	3:C:1001:NAP:H52A	1.92	0.51
1:A:293:GLN:HE21	1:A:297:GLU:HG3	1.75	0.51
2:D:265:PRO:HB3	2:D:292:PHE:HB3	1.93	0.51
2:B:180:PHE:HE1	2:B:293:ARG:HE	1.58	0.51
2:B:105:PRO:HG2	2:B:108:ILE:HD12	1.93	0.50
2:B:312:ILE:HD13	2:B:413:TYR:HA	1.94	0.50
1:C:310:TRP:O	1:C:313:ARG:NH1	2.38	0.49
2:B:260:ILE:O	2:B:263:ILE:HG12	2.12	0.49
2:B:264:ILE:HG22	2:B:292:PHE:HE2	1.78	0.49
1:C:325:SER:OG	3:C:1001:NAP:O3X	2.25	0.49
1:A:244:SER:CA	3:A:401:NAP:O2N	2.60	0.49
1:A:340:LEU:HD12	1:A:343:LEU:HD12	1.95	0.48
1:C:225:VAL:HA	1:C:229:LEU:HD12	1.96	0.47
2:B:226:GLU:OE1	2:B:296:ARG:NH2	2.46	0.47
2:B:340:SER:HA	2:B:357:ILE:HD12	1.96	0.47
3:A:401:NAP:H6N	3:A:401:NAP:H3D	1.97	0.46
1:A:287:ALA:HA	1:A:290:LYS:HE2	1.98	0.46
2:B:98:LEU:HD21	2:B:113:ILE:HD13	1.98	0.45
3:A:401:NAP:H6N	3:A:401:NAP:C3D	2.47	0.45
1:A:75:LEU:HD23	1:A:331:MET:HG3	1.98	0.45
1:A:244:SER:CB	3:A:401:NAP:O2N	2.65	0.45
2:B:183:GLU:OE2	2:B:296:ARG:NH2	2.43	0.45
2:B:172:VAL:HG11	2:B:232:TRP:CD1	2.52	0.44
1:C:216:GLU:HB2	1:C:243:TRP:CZ2	2.53	0.44
2:B:51:LEU:HD13	2:B:59:LEU:HB3	2.00	0.44
1:A:333:ASN:ND2	3:A:401:NAP:H61A	2.15	0.44
2:D:260:ILE:O	2:D:264:ILE:HG23	2.18	0.44
1:C:216:GLU:HB2	1:C:243:TRP:CH2	2.53	0.43
2:D:75:GLU:OE2	5:D:601:HOH:O	2.21	0.43
2:B:346:GLU:OE2	2:B:380:THR:N	2.38	0.43
2:B:242:PHE:HA	2:B:247:LYS:HZ1	1.83	0.43
2:D:176:SER:HB2	2:D:299:ARG:HH11	1.84	0.43
2:B:150:TRP:HB2	2:B:243:ALA:HB1	1.99	0.43
1:A:191:SER:OG	1:A:194:GLU:HG3	2.19	0.43
1:A:298:ARG:NH2	1:A:350:GLU:OE2	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:400:LEU:HB2	2:B:401:PRO:HD3	2.01	0.42
2:D:82:ARG:HB2	2:D:83:PRO:HD3	2.02	0.42
1:C:87:ALA:HB2	1:C:118:LYS:HE2	2.00	0.42
2:B:255:MET:HE1	2:B:305:ARG:CA	2.49	0.42
2:D:364:ALA:O	2:D:368:MET:HB2	2.19	0.42
2:B:256:ASN:OD1	2:B:305:ARG:NH2	2.39	0.42
2:B:113:ILE:HG23	2:B:118:LEU:HD12	2.02	0.42
1:A:167:GLU:HA	1:A:201:VAL:HG11	2.01	0.41
2:B:255:MET:HE2	2:B:255:MET:HB3	1.75	0.41
1:C:202:ALA:HA	1:C:207:LEU:HB2	2.03	0.41
1:C:212:CYS:SG	1:C:213:GLU:N	2.94	0.41
2:B:396:LEU:O	2:B:400:LEU:HG	2.21	0.41
1:A:212:CYS:SG	1:A:213:GLU:N	2.93	0.41
1:A:338:GLN:O	1:A:341:PRO:HD2	2.21	0.41
2:B:83:PRO:HB2	2:B:104:VAL:HG22	2.02	0.41
2:D:56:GLU:O	2:D:64:LYS:NZ	2.51	0.41
1:A:264:ARG:NH2	3:A:401:NAP:O3B	2.54	0.41
2:B:299:ARG:H	2:B:299:ARG:HG2	1.24	0.41
1:A:120:PHE:HE1	1:A:161:ASP:HB2	1.86	0.41
2:B:290:GLN:O	2:B:294:ILE:HG12	2.21	0.41
2:D:375:ASP:N	2:D:375:ASP:OD1	2.51	0.41
1:C:57:TRP:CD2	1:C:58:VAL:HG23	2.57	0.40
2:B:163:ARG:HD2	2:B:163:ARG:HA	1.93	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	324/333 (97%)	313 (97%)	9 (3%)	2 (1%)	25 59
1	C	324/333 (97%)	313 (97%)	9 (3%)	2 (1%)	25 59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	326/514 (63%)	311 (95%)	13 (4%)	2 (1%)	25	59
2	D	325/514 (63%)	300 (92%)	21 (6%)	4 (1%)	13	44
All	All	1299/1694 (77%)	1237 (95%)	52 (4%)	10 (1%)	19	54

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	266	TYR
1	A	62	GLY
2	D	265	PRO
2	B	154	GLU
2	B	245	PRO
1	A	120	PHE
1	C	120	PHE
2	D	370	THR
2	D	96	GLY
1	C	62	GLY

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	272/280 (97%)	270 (99%)	2 (1%)	84	93
1	C	273/280 (98%)	273 (100%)	0	100	100
2	B	299/459 (65%)	290 (97%)	9 (3%)	41	71
2	D	293/459 (64%)	288 (98%)	5 (2%)	60	83
All	All	1137/1478 (77%)	1121 (99%)	16 (1%)	67	86

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	268	LYS
1	A	331	MET

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Mol	Chain	Res	Type
2	B	224	ILE
2	B	227	THR
2	B	230	ILE
2	B	236	GLU
2	B	289	VAL
2	B	296	ARG
2	B	297	ILE
2	B	299	ARG
2	B	351	ASP
2	D	80	ARG
2	D	125	MET
2	D	126	PHE
2	D	152	LEU
2	D	349	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	218	HIS
1	A	293	GLN
1	C	221	GLN
1	C	333	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 12 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAP	C	1001	-	45,52,52	1.34	6 (13%)	56,80,80	1.27	5 (8%)
3	NAP	A	401	-	45,52,52	1.26	5 (11%)	56,80,80	1.19	5 (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
3	NAP	C	1001	-	-	3/31/67/67	0/5/5/5
3	NAP	A	401	-	-	6/31/67/67	0/5/5/5

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	NAP	C2D-C1D	-2.97	1.49	1.53
3	C	1001	NAP	C2D-C1D	-2.73	1.49	1.53
3	C	1001	NAP	C2N-N1N	-2.52	1.31	1.35
3	A	401	NAP	C2N-N1N	-2.25	1.32	1.35
3	C	1001	NAP	O4B-C4B	-2.17	1.40	1.45
3	A	401	NAP	P2B-O2X	-2.15	1.46	1.54
3	C	1001	NAP	C3N-C7N	-2.10	1.47	1.50
3	A	401	NAP	P2B-O3X	-2.06	1.46	1.54
3	C	1001	NAP	O7N-C7N	-2.04	1.20	1.24
3	A	401	NAP	O7N-C7N	-2.02	1.20	1.24
3	C	1001	NAP	C4N-C3N	-2.01	1.35	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1001	NAP	PN-O3-PA	-3.74	119.99	132.83
3	A	401	NAP	N3A-C2A-N1A	-3.35	123.45	128.68
3	A	401	NAP	PN-O3-PA	-3.33	121.41	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1001	NAP	N3A-C2A-N1A	-3.26	123.58	128.68
3	C	1001	NAP	C4A-C5A-N7A	-2.65	106.64	109.40
3	A	401	NAP	C4A-C5A-N7A	-2.62	106.67	109.40
3	A	401	NAP	C3D-C2D-C1D	2.58	104.86	100.98
3	C	1001	NAP	C3D-C2D-C1D	2.58	104.86	100.98
3	A	401	NAP	C5N-C4N-C3N	-2.29	117.64	120.34
3	C	1001	NAP	C5N-C4N-C3N	-2.05	117.91	120.34

There are no chirality outliers.

All (9) torsion outliers are listed below:

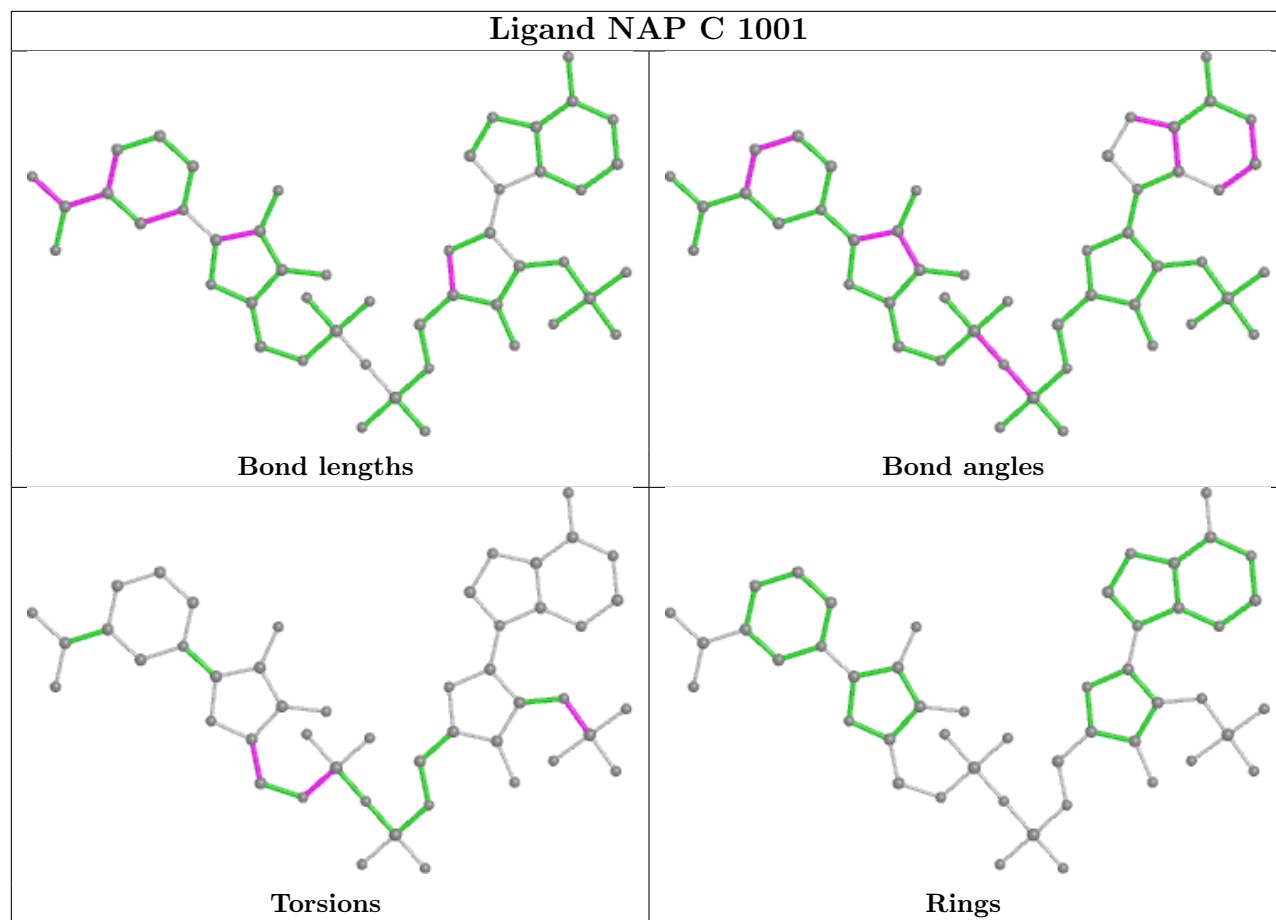
Mol	Chain	Res	Type	Atoms
3	A	401	NAP	C5B-O5B-PA-O1A
3	A	401	NAP	C5B-O5B-PA-O3
3	A	401	NAP	O4D-C1D-N1N-C6N
3	A	401	NAP	O4D-C4D-C5D-O5D
3	A	401	NAP	C3D-C4D-C5D-O5D
3	C	1001	NAP	C2B-O2B-P2B-O1X
3	A	401	NAP	C2B-O2B-P2B-O1X
3	C	1001	NAP	C5D-O5D-PN-O1N
3	C	1001	NAP	O4D-C4D-C5D-O5D

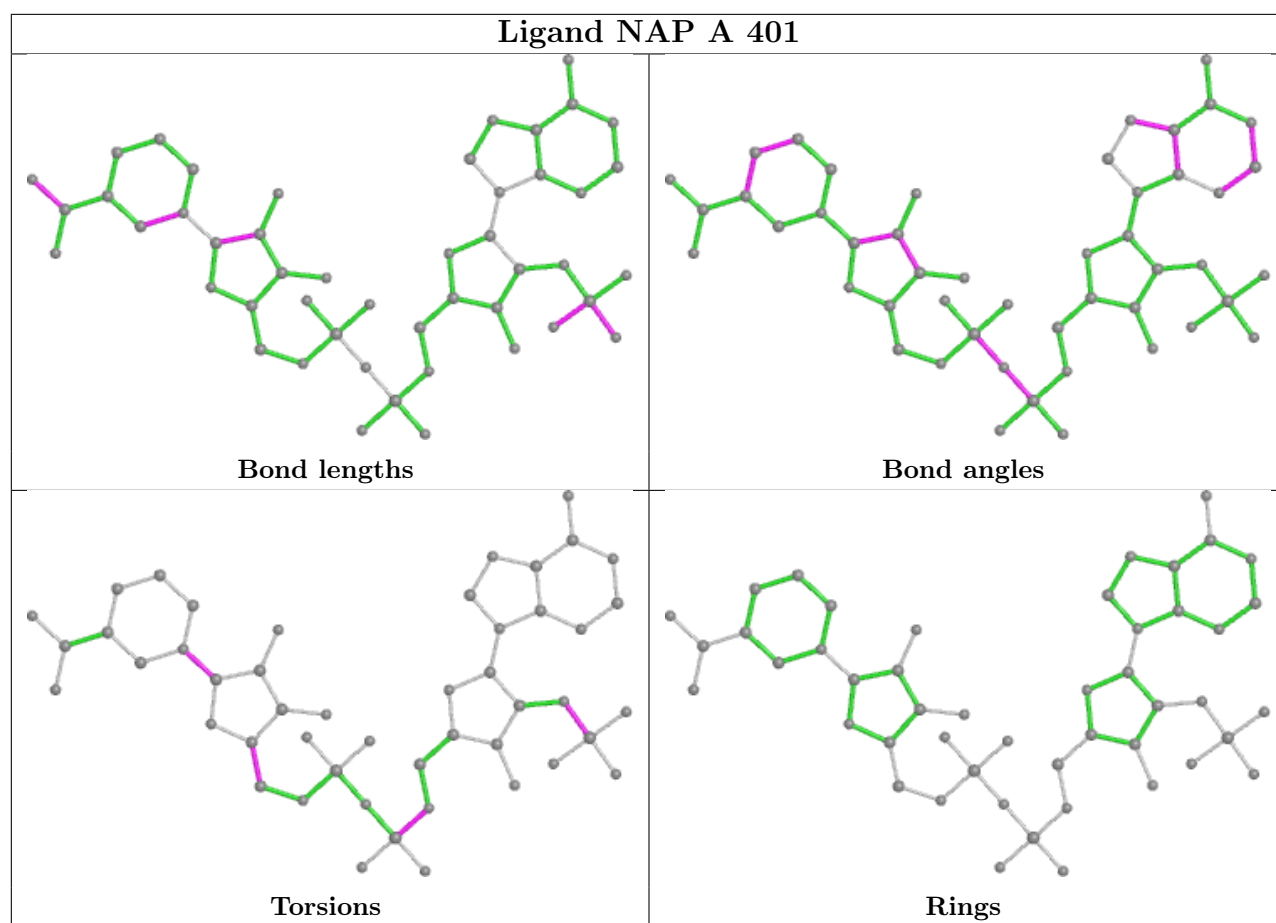
There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1001	NAP	3	0
3	A	401	NAP	9	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	326/333 (97%)	0.01	7 (2%) 63 43	48, 74, 120, 162	0
1	C	326/333 (97%)	-0.05	3 (0%) 84 69	47, 70, 110, 160	0
2	B	334/514 (64%)	0.33	33 (9%) 7 2	56, 116, 182, 232	0
2	D	333/514 (64%)	0.41	36 (10%) 5 2	54, 133, 199, 236	0
All	All	1319/1694 (77%)	0.18	79 (5%) 21 10	47, 89, 181, 236	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	285	VAL	7.4
1	A	361	SER	7.0
1	C	361	SER	6.7
2	D	222	PHE	4.9
2	D	287	ARG	4.8
2	D	188	PHE	4.7
2	B	248	ALA	4.6
2	D	251	PHE	4.5
2	B	188	PHE	4.4
1	A	360	TYR	4.2
2	B	242	PHE	4.2
2	D	350	ARG	4.1
2	B	145	PHE	3.8
2	B	31	SER	3.8
2	B	159	SER	3.8
2	B	288	VAL	3.8
2	D	286	ARG	3.7
2	D	248	ALA	3.7
2	B	249	GLY	3.6
2	B	269	THR	3.6
2	D	174	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
2	D	145	PHE	3.5
2	D	226	GLU	3.4
2	D	242	PHE	3.3
2	D	224	ILE	3.3
2	D	149	VAL	3.3
2	B	251	PHE	3.3
2	B	292	PHE	3.3
2	D	249	GLY	3.3
2	D	369	THR	3.2
2	B	265	PRO	3.2
2	D	288	VAL	3.2
2	D	159	SER	3.1
2	B	240	ARG	3.1
2	D	348	ASP	3.0
2	D	146	GLN	3.0
2	B	163	ARG	3.0
2	D	220	ASP	2.9
2	D	252	THR	2.8
2	B	164	ILE	2.8
2	B	222	PHE	2.8
2	D	225	VAL	2.7
1	A	359	PRO	2.7
2	D	290	GLN	2.7
2	B	187	ILE	2.6
1	A	262	TYR	2.6
1	A	223	GLU	2.5
2	B	32	SER	2.5
1	C	359	PRO	2.5
2	B	158	SER	2.5
2	D	292	PHE	2.5
2	D	157	GLU	2.5
2	D	147	ARG	2.4
2	D	161	PRO	2.4
2	D	223	PHE	2.4
1	A	358	LYS	2.3
2	B	270	ILE	2.3
2	B	267	TYR	2.3
2	B	286	ARG	2.3
2	B	287	ARG	2.3
2	D	229	CYS	2.3
2	B	291	ILE	2.3
1	A	285	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
2	D	247	LYS	2.3
2	D	155	TYR	2.3
2	D	170	VAL	2.2
2	B	166	ALA	2.2
2	D	151	LEU	2.2
2	B	246	SER	2.2
2	B	250	PHE	2.2
2	B	238	LEU	2.2
2	B	124	GLU	2.2
1	C	360	TYR	2.2
2	B	160	GLY	2.2
2	B	167	ILE	2.1
2	D	267	TYR	2.1
2	D	148	GLN	2.1
2	B	233	PHE	2.1
2	B	128	GLU	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 monosaccharides 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(\AA^2)	Q<0.9
4	K	D	502	1/1	0.39	0.15	90,90,90,90	1
4	K	B	504	1/1	0.51	0.34	83,83,83,83	1
4	K	D	504	1/1	0.58	0.09	191,191,191,191	1
4	K	B	502	1/1	0.62	0.77	173,173,173,173	1
4	K	D	503	1/1	0.66	0.81	193,193,193,193	1
4	K	B	505	1/1	0.79	0.26	71,71,71,71	1
4	K	D	501	1/1	0.89	0.04	132,132,132,132	1

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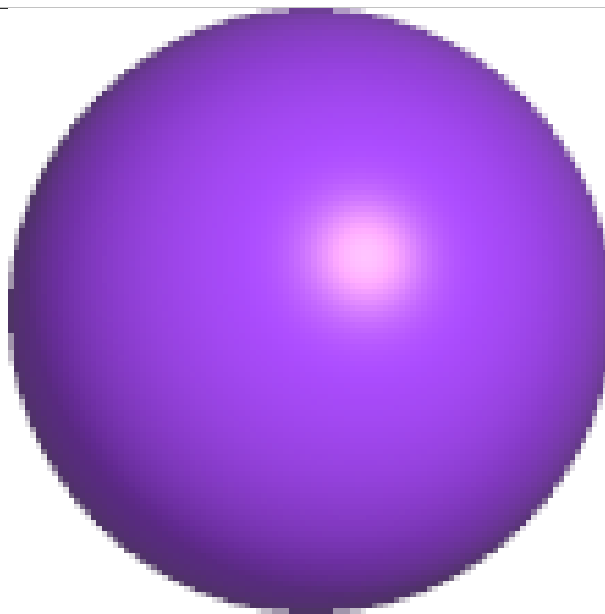
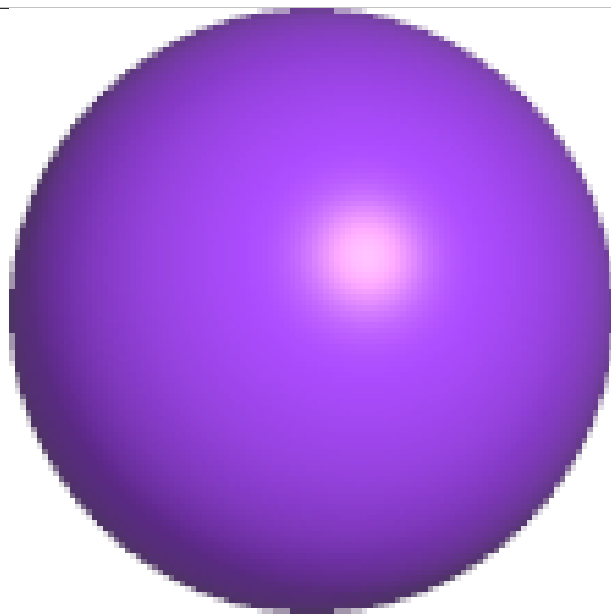
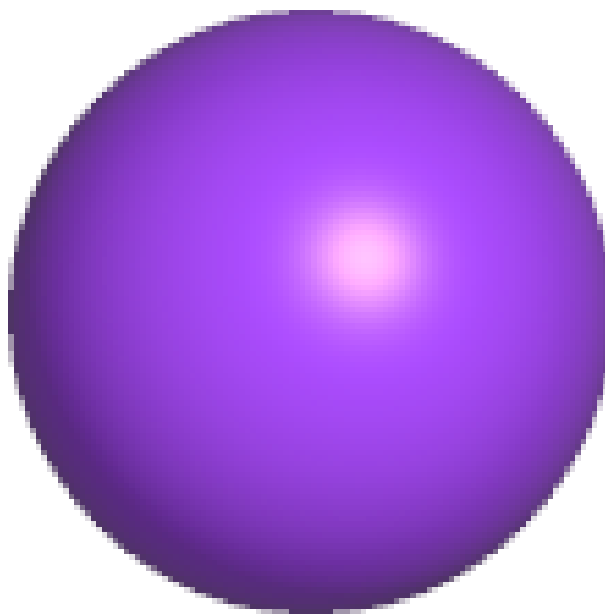
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	K	D	505	1/1	0.93	0.76	168,168,168,168	1
4	K	D	506	1/1	0.93	0.56	145,145,145,145	1
4	K	B	503	1/1	0.94	0.25	79,79,79,79	1
3	NAP	A	401	48/48	0.95	0.20	81,85,92,95	0
4	K	B	501	1/1	0.95	0.54	122,122,122,122	1
4	K	B	506	1/1	0.95	0.18	87,87,87,87	1
3	NAP	C	1001	48/48	0.97	0.17	68,81,90,92	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.

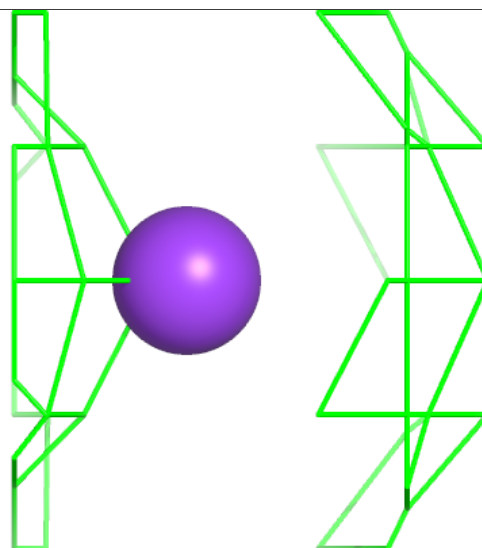
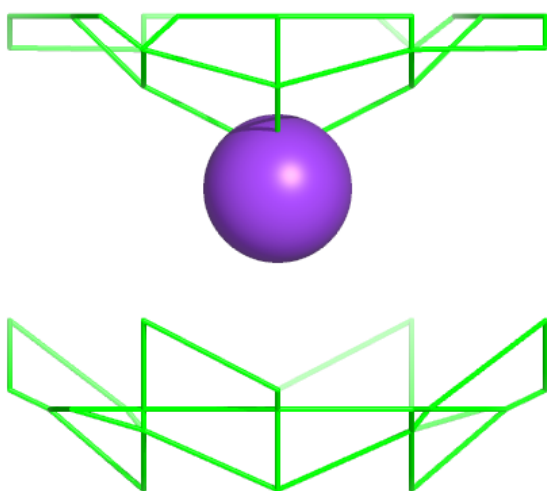
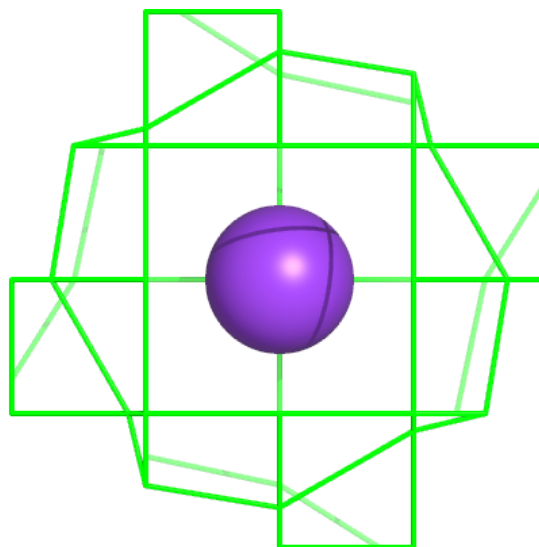
Electron density around K D 502:

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



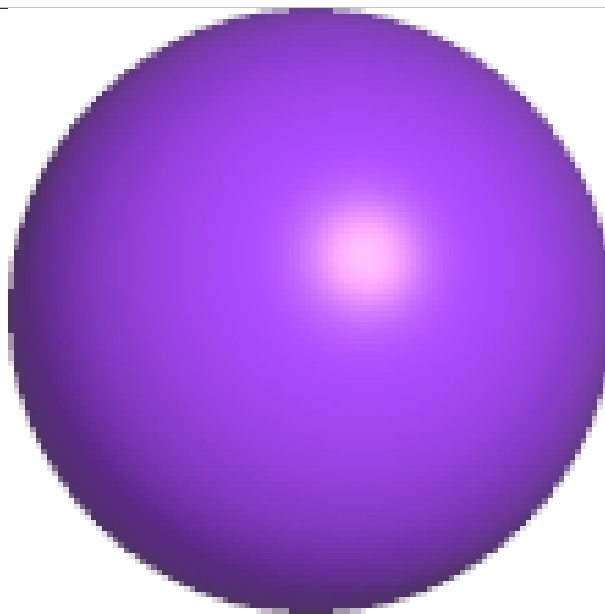
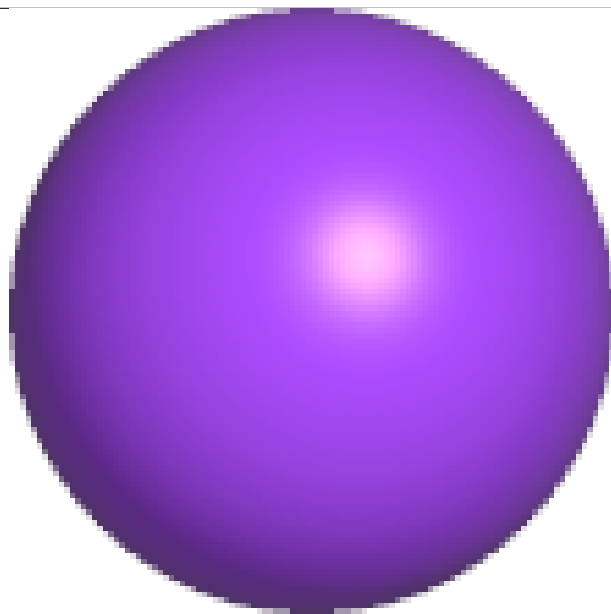
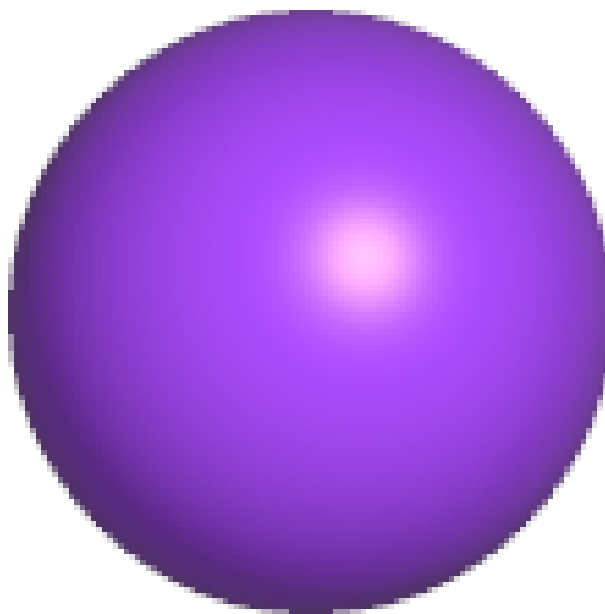
Electron density around K B 504:

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



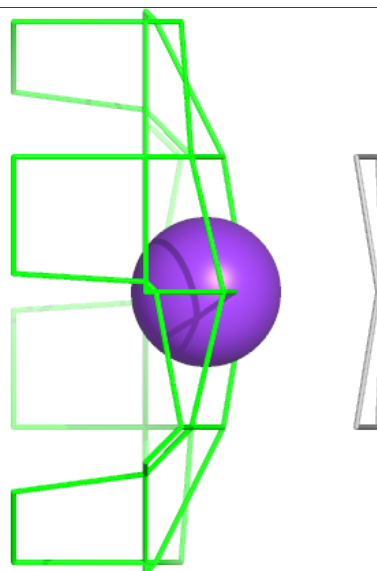
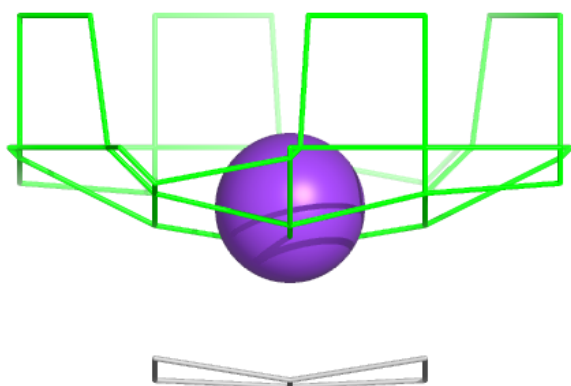
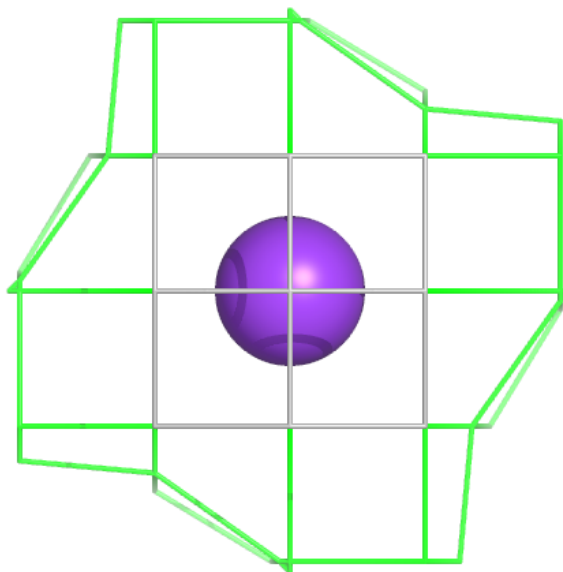
Electron density around K D 504:

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



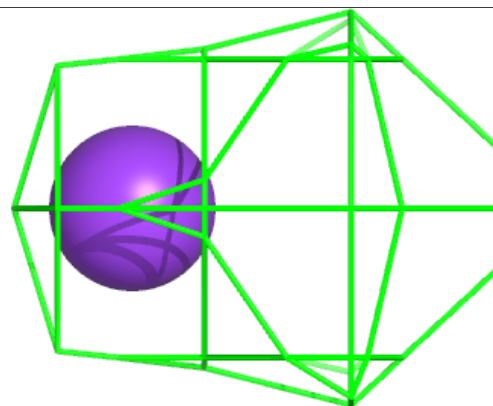
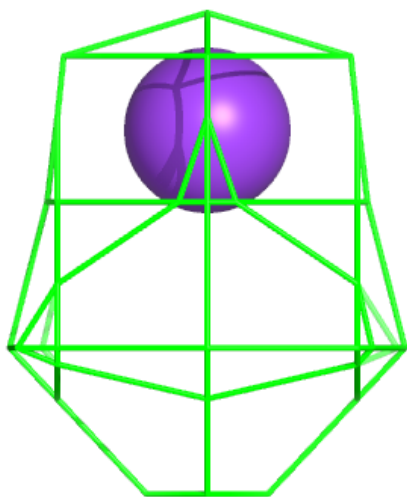
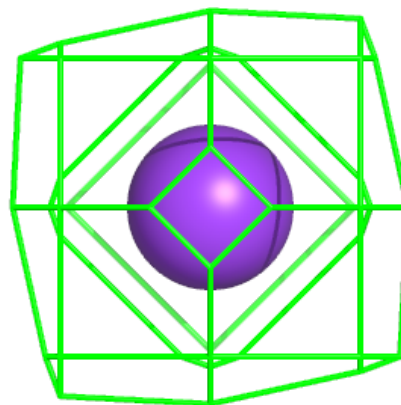
Electron density around K B 502:

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



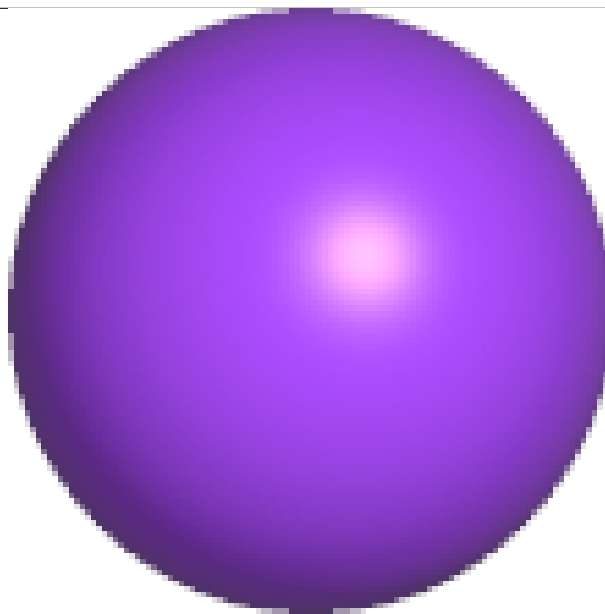
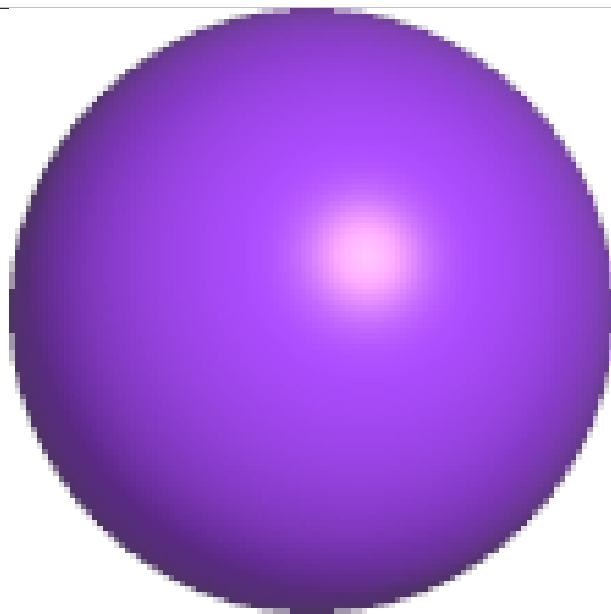
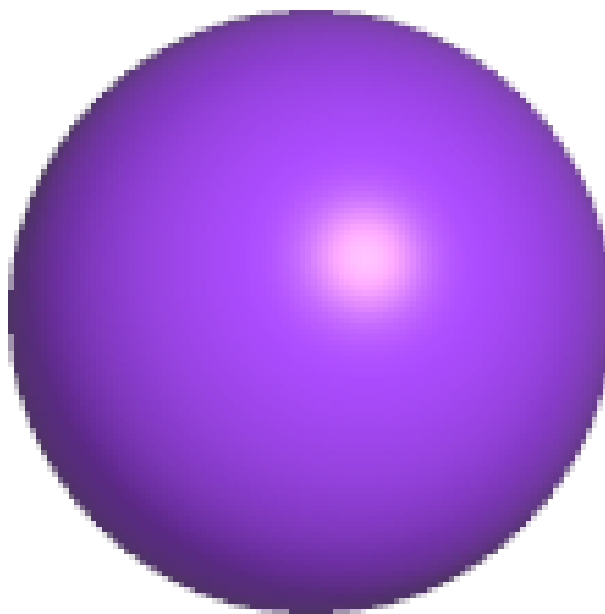
Electron density around K D 503:

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and green (positive)



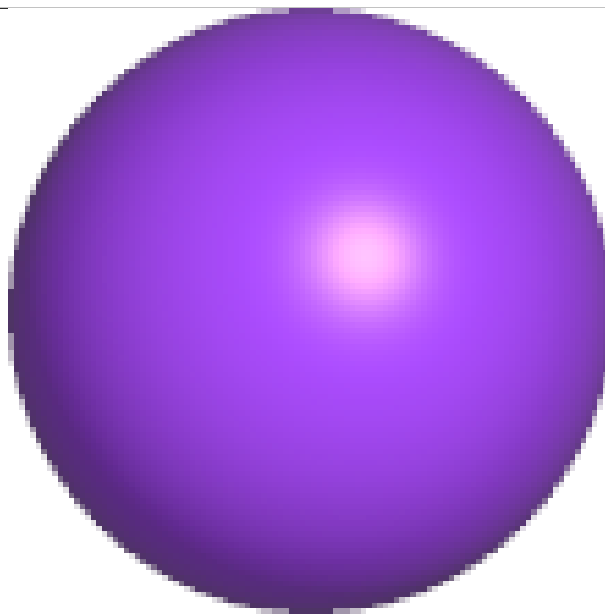
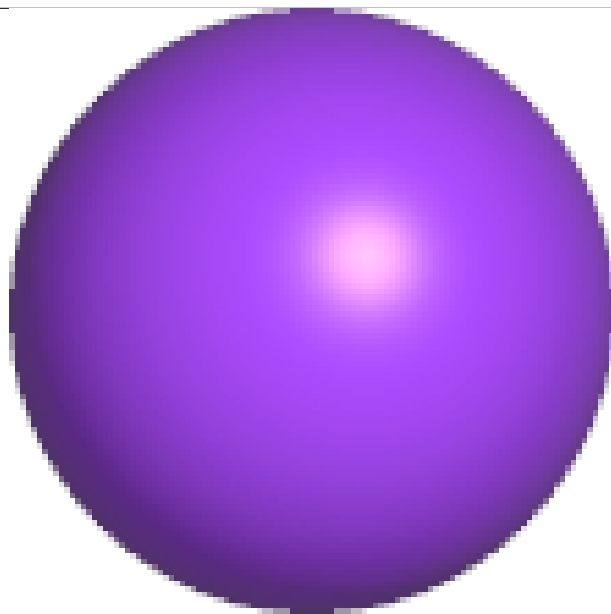
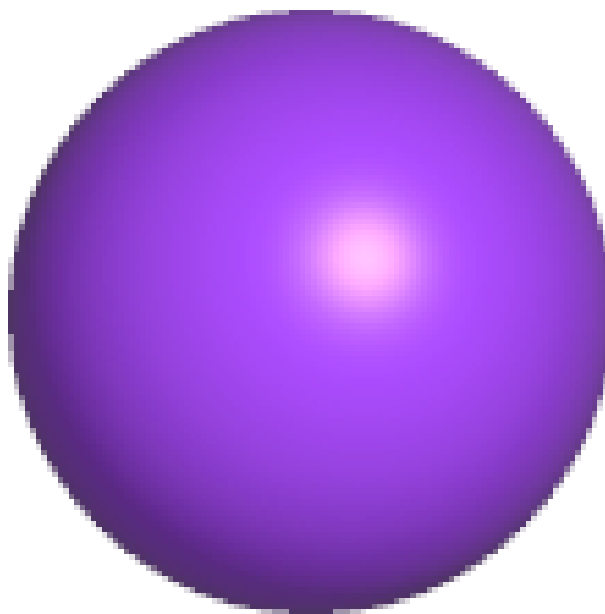
Electron density around K B 505:

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



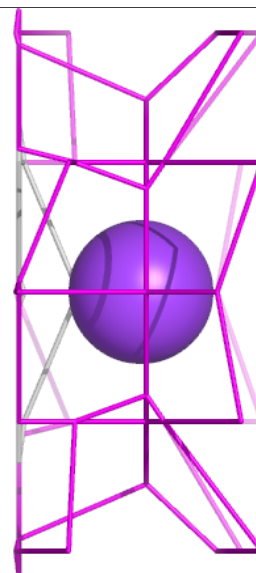
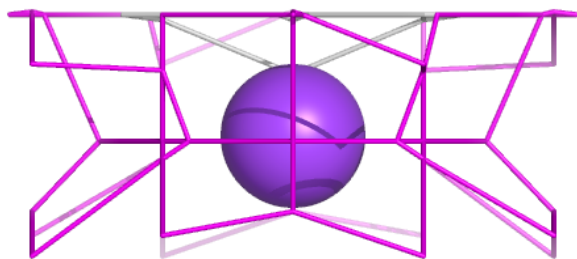
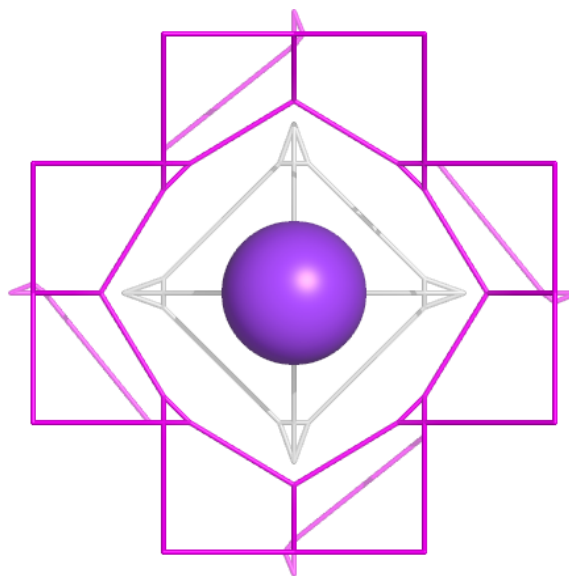
Electron density around K D 501:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



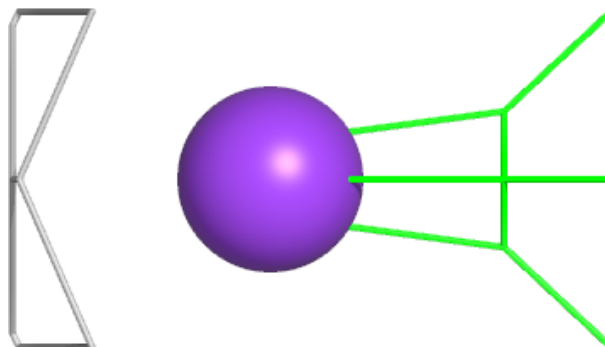
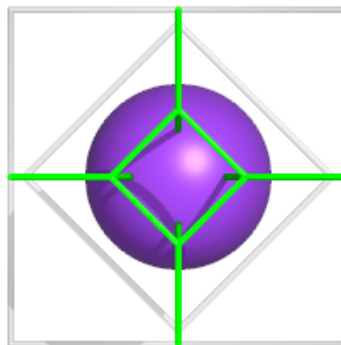
Electron density around K D 505:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



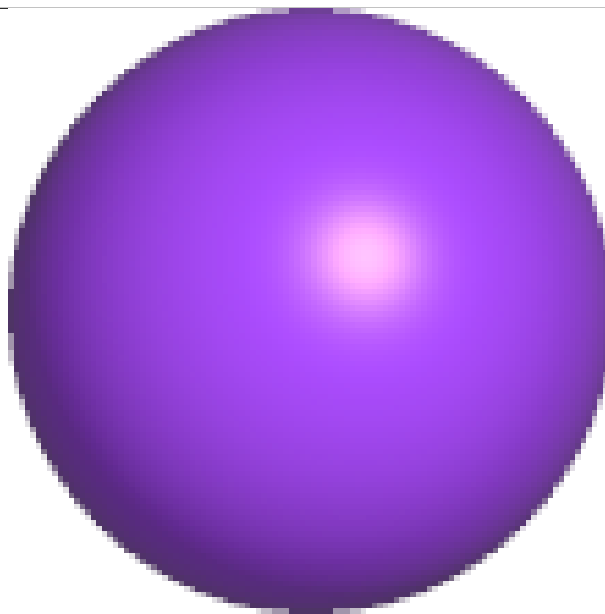
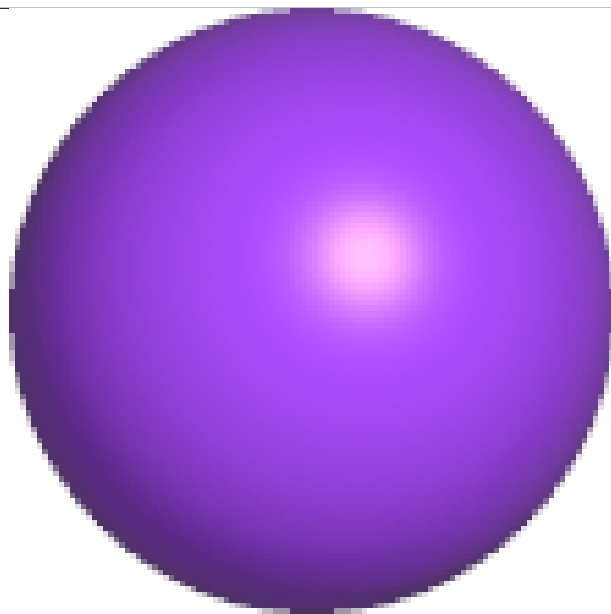
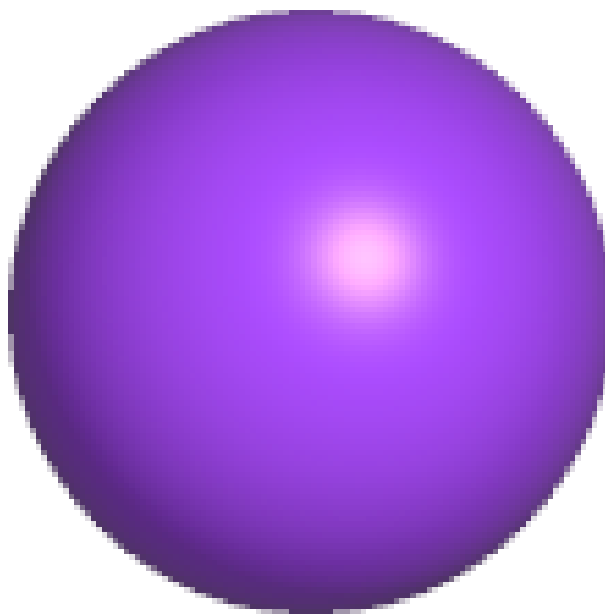
Electron density around K D 506:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



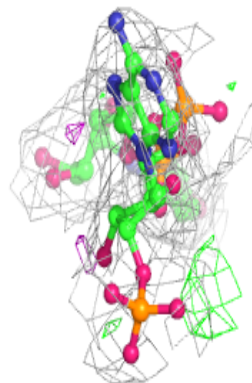
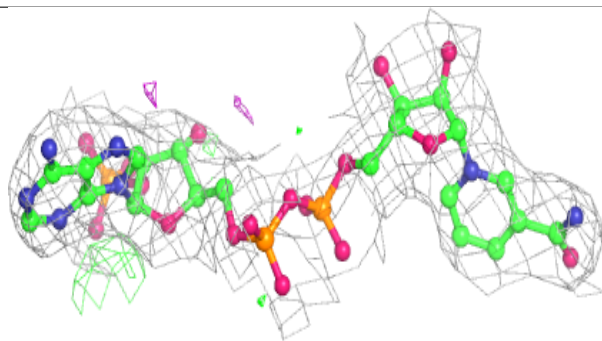
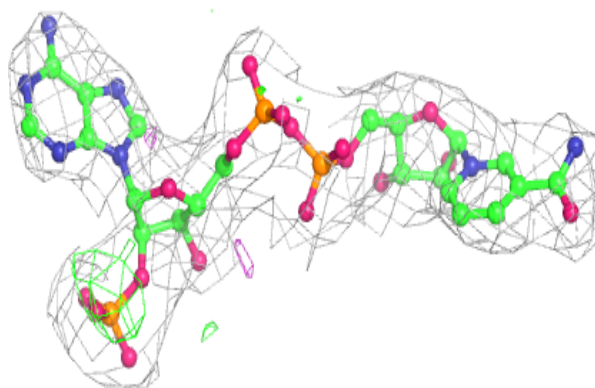
Electron density around K B 503:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



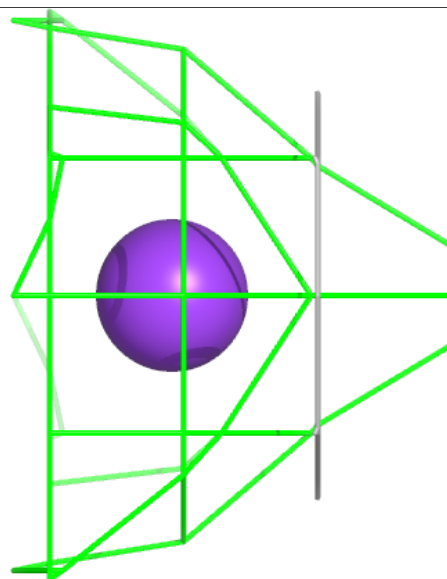
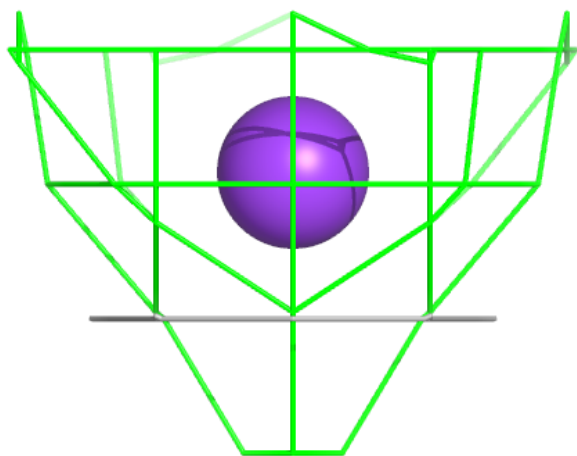
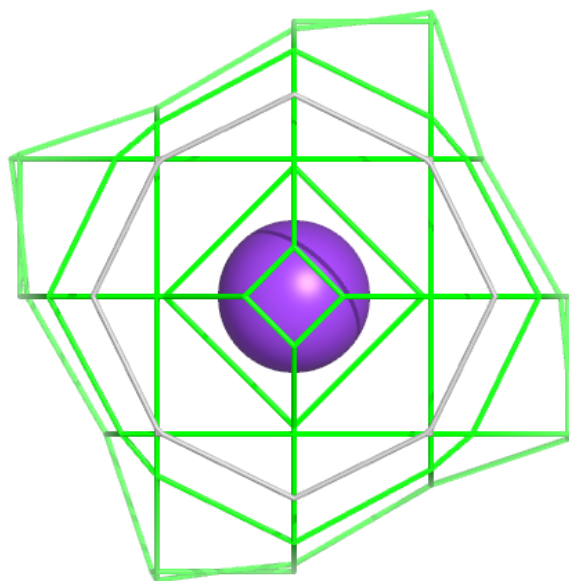
Electron density around NAP A 401:

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and green (positive)



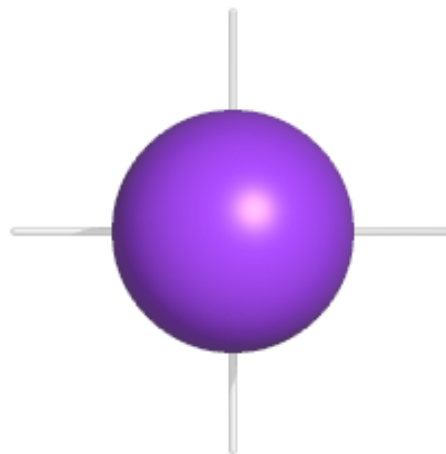
Electron density around K B 501:

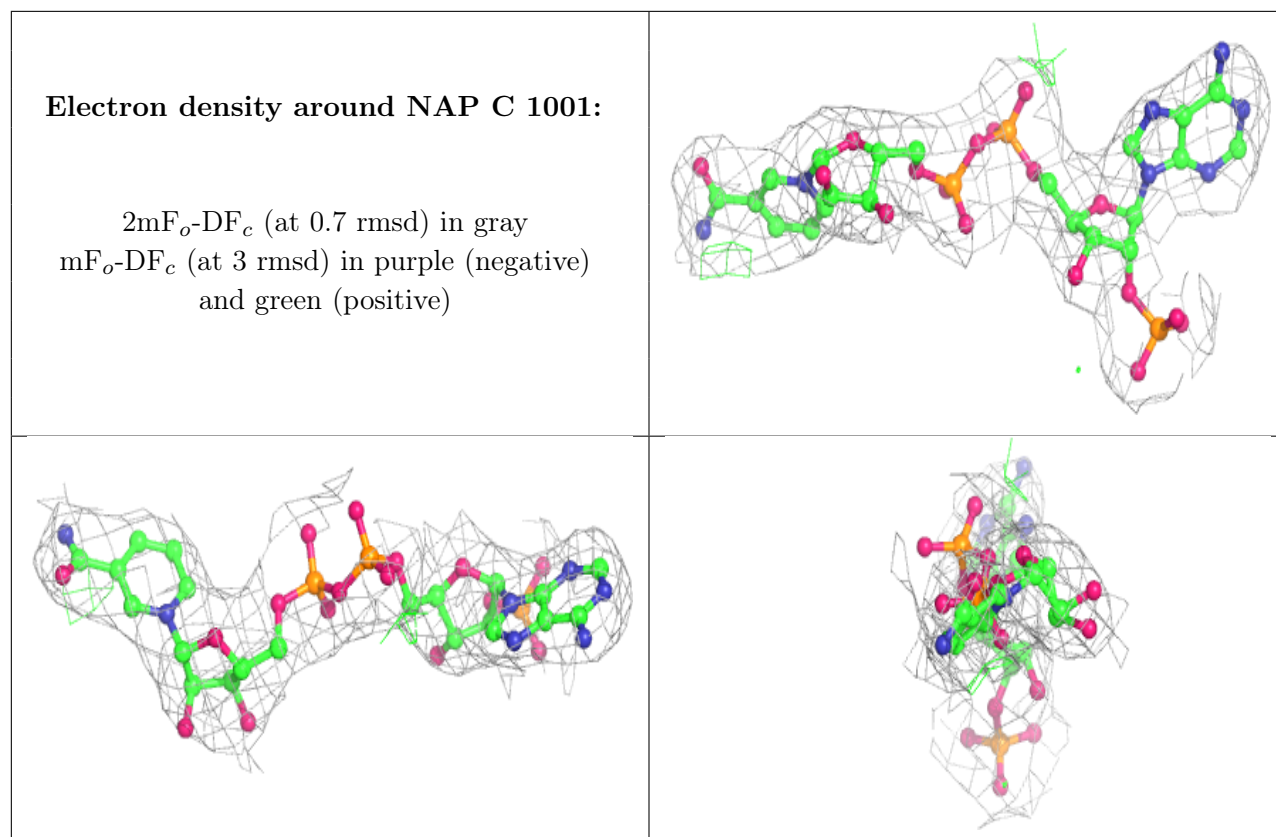
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and green (positive)



Electron density around K B 506:

$2mF_o-DF_c$ (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.