



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 12:49 pm BST

PDB ID : 4YZ9
Title : Crystal Structure of human phosphorylated IRE1alpha in complex with a type III kinase inhibitor (GSK2850163A)
Authors : Concha, N.O.
Deposited on : 2015-03-24
Resolution : 2.46 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 : 2.11
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) : 2.11

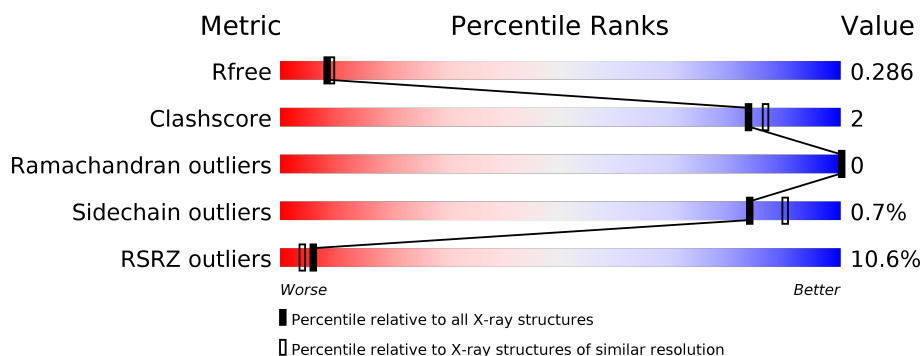
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.46 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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 on 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	405	<div> <div>6%</div> <div>87%</div> <div>7%</div> <div>6%</div> </div>
1	B	405	<div> <div>19%</div> <div>85%</div> <div>7%</div> <div>7%</div> </div>
1	C	405	<div> <div>5%</div> <div>88%</div> <div>5%</div> <div>7%</div> </div>

2 Entry composition [i](#)

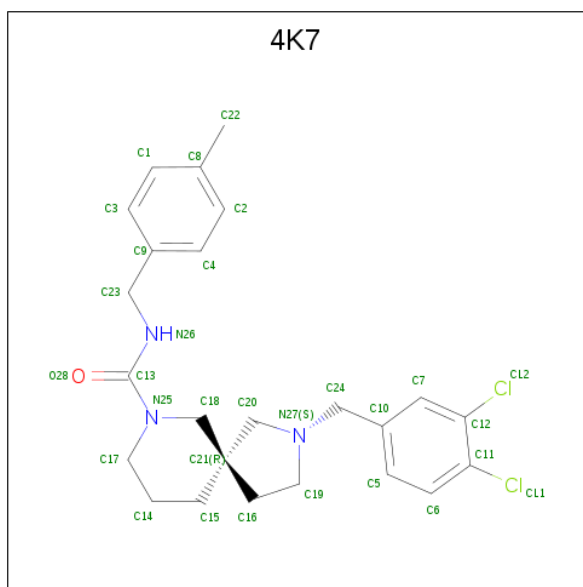
There are 3 unique types of molecules in this entry. The entry contains 17863 atoms, of which 8734 are hydrogens and 0 are deuteriums.

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 Serine/threonine-protein kinase/endoribonuclease IRE1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	381	Total	C	H	N	O	S	0	1	0
			5922	1926	2910	516	551	19			
1	B	375	Total	C	H	N	O	S	0	1	0
			5750	1880	2817	505	529	19			
1	C	378	Total	C	H	N	O	S	0	3	0
			5934	1926	2920	525	544	19			

- Molecule 2 is (5R)-2-(3,4-dichlorobenzyl)-N-(4-methylbenzyl)-2,7-diazaspiro[4.5]decane-7-carboxamide (three-letter code: 4K7) (formula: C₂₄H₂₉Cl₂N₃O).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	H	N	O	0	0
			59	24	2	29	3	1		
2	B	1	Total	C	Cl	H	N	O	0	0
			59	24	2	29	3	1		
2	C	1	Total	C	Cl	H	N	O	0	0
			59	24	2	29	3	1		


- Molecule 3 is water.

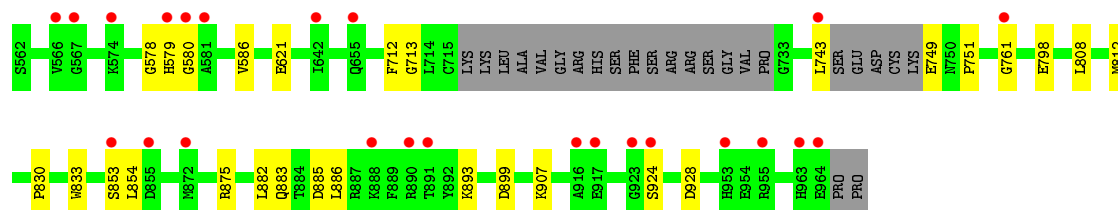
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	39	Total 39	O 39	0	0
3	B	9	Total 9	O 9	0	0
3	C	32	Total 32	O 32	0	0

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA 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.

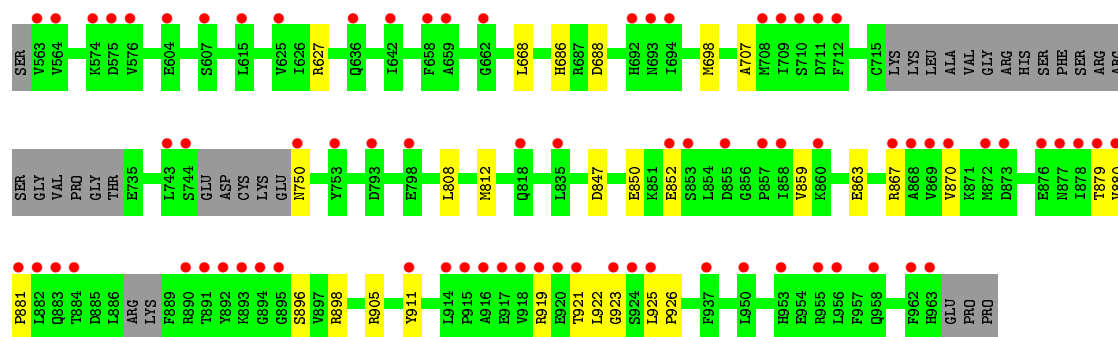
- Molecule 1: Serine/threonine-protein kinase/endoribonuclease IRE1

Chain A: 




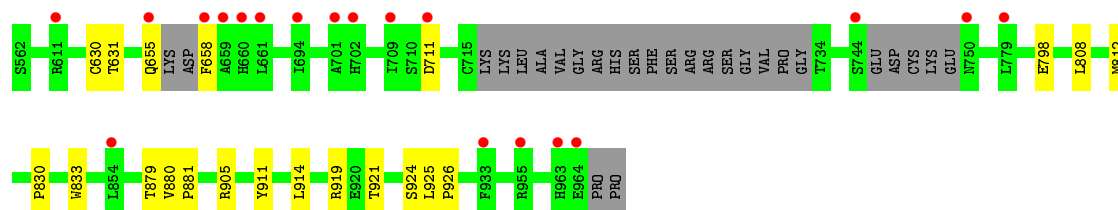
- Molecule 1: Serine/threonine-protein kinase/endoribonuclease IRE1

Chain B: 



- Molecule 1: Serine/threonine-protein kinase/endoribonuclease IRE1

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	244.00 Å 77.77 Å 88.31 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.18 – 2.46 30.18 – 2.46	Depositor EDS
% Data completeness (in resolution range)	96.7 (29.18-2.46) 96.7 (30.18-2.46)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 2.48 Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.235 , 0.283 0.240 , 0.286	Depositor DCC
R_{free} test set	3018 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	44.9	Xtriage
Anisotropy	0.688	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	17863	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4K7

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	0.27	0/3088	0.46	0/4186
1	B	0.26	0/3007	0.44	0/4078
1	C	0.28	0/3096	0.46	0/4191
All	All	0.27	0/9191	0.45	0/12455

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	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	580	GLY	Peptide
1	B	922	LEU	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	3012	2910	2899	14	0
1	B	2933	2817	2814	15	0
1	C	3014	2920	2922	15	0
2	A	30	29	29	0	0
2	B	30	29	29	0	0
2	C	30	29	29	0	0
3	A	39	0	0	2	0
3	B	9	0	0	0	0
3	C	32	0	0	1	0
All	All	9129	8734	8722	42	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 2.

All (42) 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:B:850:GLU:O	1:B:898:ARG:NH2	2.12	0.83
1:C:914:LEU:O	1:C:919:ARG:NH1	2.19	0.75
1:A:885:ASP:OD2	1:A:907:LYS:NZ	2.19	0.74
1:B:925:LEU:HD23	1:B:926:PRO:N	2.07	0.69
1:C:655:GLN:C	1:C:658:PHE:HA	2.15	0.67
1:B:847:ASP:OD1	1:B:905:ARG:NE	2.34	0.61
1:C:879:THR:HG21	1:C:921:THR:HB	1.82	0.60
1:A:875:ARG:O	1:A:883:GLN:NE2	2.34	0.59
1:A:621:GLU:OE2	3:A:1101:HOH:O	2.17	0.59
1:B:925:LEU:HD23	1:B:926:PRO:CA	2.37	0.55
1:A:798:GLU:HG3	1:C:798:GLU:HG3	1.90	0.53
1:C:630:CYS:SG	1:C:631:THR:N	2.84	0.51
1:C:881:PRO:HB2	1:C:921:THR:HG21	1.93	0.51
1:B:686:HIS:ND1	1:B:688:ASP:O	2.44	0.50
1:B:863:GLU:OE2	1:B:896:SER:OG	2.23	0.49
1:B:919:ARG:O	1:B:923:GLY:N	2.45	0.49
1:A:893:LYS:N	1:A:899:ASP:OD2	2.47	0.47
3:A:1101:HOH:O	1:B:627:ARG:NH1	2.47	0.46
1:C:711[B]:ASP:OD1	3:C:1101:HOH:O	2.21	0.46
1:B:911:TYR:OH	1:B:923:GLY:O	2.31	0.46
1:B:867:ARG:HA	1:B:870:VAL:HB	1.97	0.45
1:B:880:VAL:HB	1:B:881:PRO:HD3	1.98	0.45
1:B:852:GLU:HB2	1:B:859:VAL:CG2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:925:LEU:HD23	1:C:926:PRO:HA	1.98	0.45
1:B:879:THR:HG21	1:B:921:THR:HG21	1.98	0.45
1:C:808:LEU:HG	1:C:812:MET:HE2	1.99	0.44
1:A:808:LEU:HG	1:A:812:MET:HE2	1.99	0.44
1:A:749:GLU:HG2	1:A:751:PRO:HD3	1.98	0.44
1:A:578:GLY:HA3	1:A:713:GLY:O	2.17	0.44
1:C:911:TYR:CG	1:C:925:LEU:HD12	2.53	0.43
1:C:879:THR:HG21	1:C:921:THR:CB	2.48	0.43
1:B:808:LEU:HG	1:B:812:MET:HE2	2.00	0.43
1:A:853:SER:O	1:A:854:LEU:HB3	2.18	0.43
1:A:928:ASP:OD2	1:C:921:THR:HA	2.19	0.43
1:A:586:VAL:HG21	1:A:712:PHE:CG	2.54	0.42
1:A:882:LEU:O	1:A:886:LEU:HG	2.19	0.42
1:A:830:PRO:HA	1:A:833:TRP:CD2	2.55	0.42
1:B:668:LEU:HG	1:B:707:ALA:HB2	2.02	0.41
1:C:830:PRO:HA	1:C:833:TRP:CD2	2.56	0.41
1:C:880:VAL:HB	1:C:881:PRO:HD3	2.03	0.41
1:C:879:THR:HG23	1:C:881:PRO:HD2	2.03	0.40
1:A:761:GLY:HA2	1:A:812:MET:HE3	2.01	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	376/405 (93%)	366 (97%)	10 (3%)	0	100	100
1	B	368/405 (91%)	354 (96%)	14 (4%)	0	100	100
1	C	373/405 (92%)	359 (96%)	14 (4%)	0	100	100
All	All	1117/1215 (92%)	1079 (97%)	38 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	319/359 (89%)	316 (99%)	3 (1%)	78	86
1	B	307/359 (86%)	305 (99%)	2 (1%)	84	90
1	C	321/359 (89%)	319 (99%)	2 (1%)	86	91
All	All	947/1077 (88%)	940 (99%)	7 (1%)	84	90

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	579	HIS
1	A	743	LEU
1	A	924	SER
1	B	698	MET
1	B	750	ASN
1	C	905	ARG
1	C	924	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	825	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

There are no carbohydrates in this entry.

5.6 Ligand geometry

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	4K7	B	1001	-	33,33,33	0.74	0	43,47,47	2.19	7 (16%)
2	4K7	A	1001	-	33,33,33	0.73	0	43,47,47	1.86	6 (13%)
2	4K7	C	1001	-	33,33,33	0.72	0	43,47,47	1.55	5 (11%)

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	4K7	B	1001	-	-	0/13/36/36	0/4/4/4
2	4K7	A	1001	-	-	0/13/36/36	0/4/4/4
2	4K7	C	1001	-	-	0/13/36/36	0/4/4/4

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1001	4K7	N26-C13-N25	10.94	122.93	117.67
2	A	1001	4K7	N26-C13-N25	9.37	122.17	117.67
2	C	1001	4K7	N26-C13-N25	6.81	120.94	117.67
2	B	1001	4K7	C15-C21-C18	3.75	114.12	109.15
2	B	1001	4K7	C19-N27-C20	3.24	107.19	104.02
2	B	1001	4K7	O28-C13-N25	-3.05	117.50	121.78
2	C	1001	4K7	C19-N27-C20	3.04	106.99	104.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1001	4K7	C24-N27-C19	-2.93	108.92	113.18
2	A	1001	4K7	C24-N27-C19	-2.92	108.93	113.18
2	C	1001	4K7	C15-C21-C18	2.89	112.98	109.15
2	A	1001	4K7	C21-C18-N25	2.77	115.67	112.04
2	A	1001	4K7	C19-N27-C20	2.59	106.56	104.02
2	A	1001	4K7	O28-C13-N25	-2.52	118.24	121.78
2	B	1001	4K7	C21-C18-N25	2.50	115.31	112.04
2	A	1001	4K7	C15-C21-C18	2.45	112.41	109.15
2	C	1001	4K7	C24-N27-C19	-2.44	109.63	113.18
2	B	1001	4K7	C14-C17-N25	2.34	115.28	110.66
2	C	1001	4K7	C24-N27-C20	-2.14	110.20	112.93

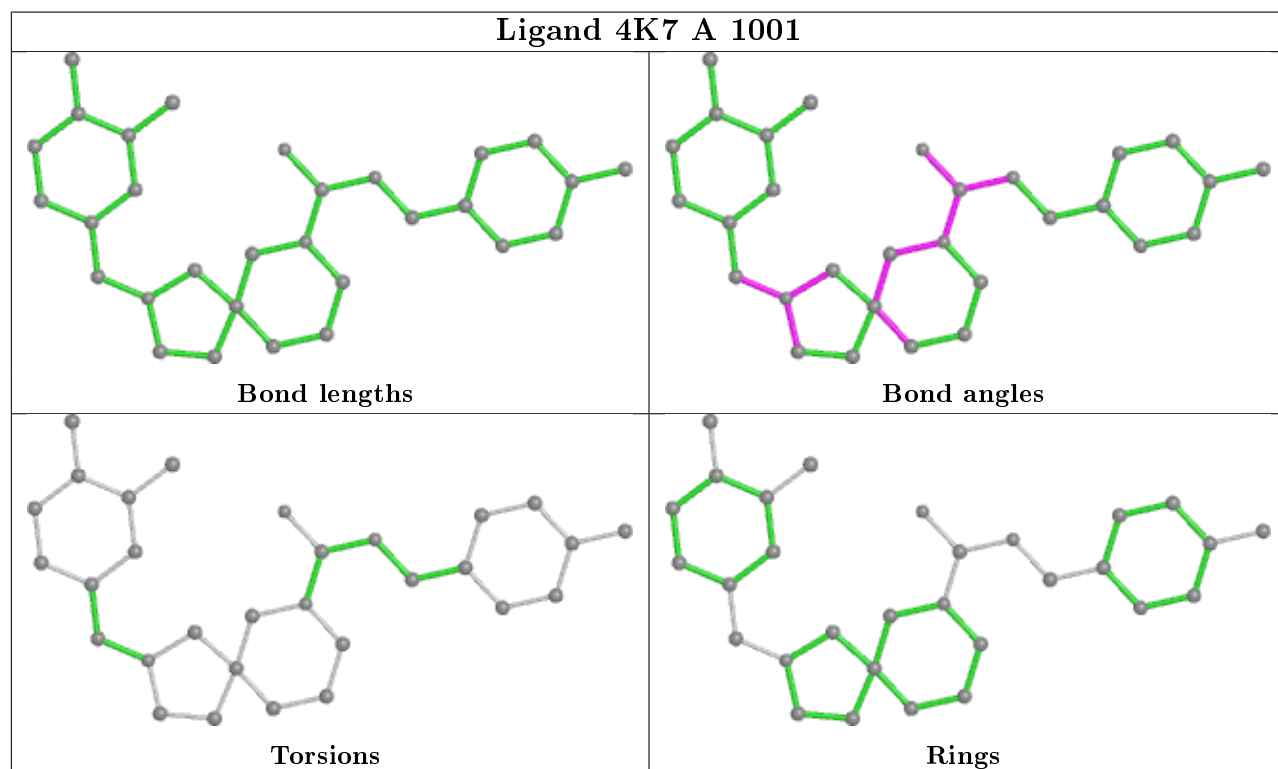
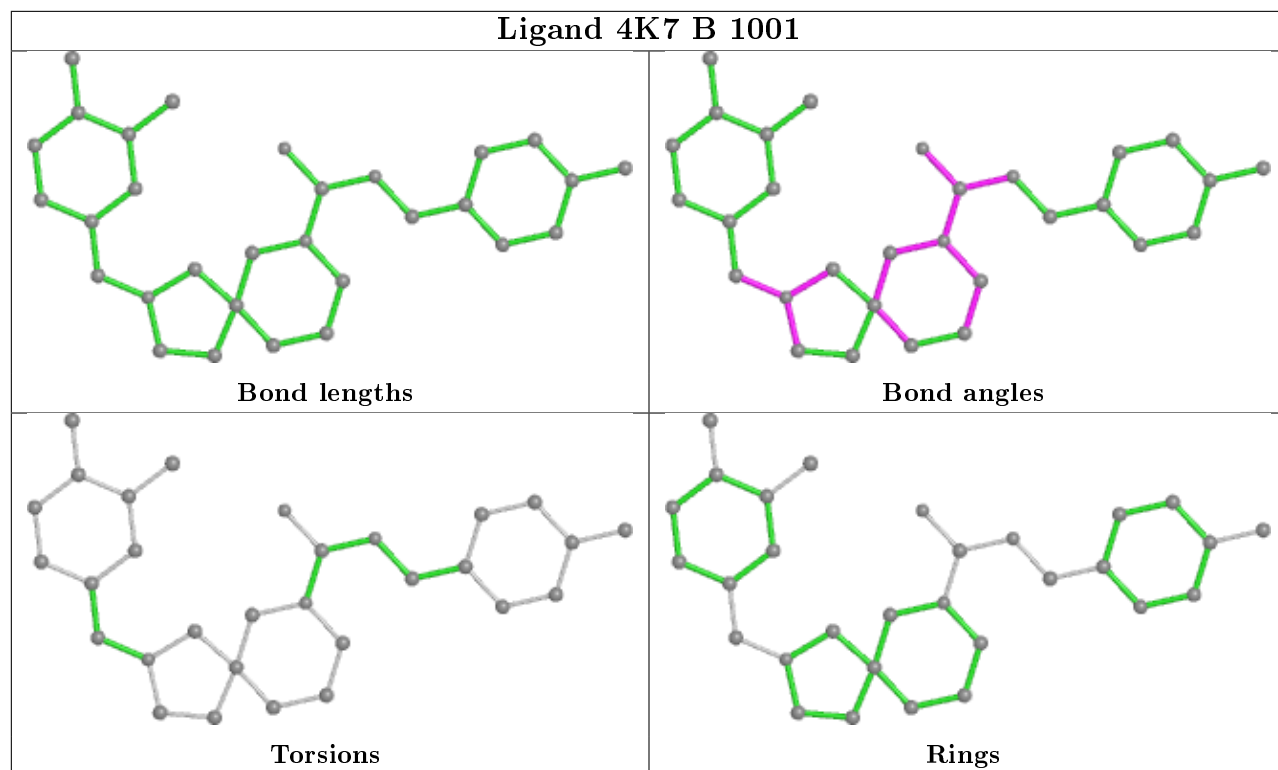
There are no chirality outliers.

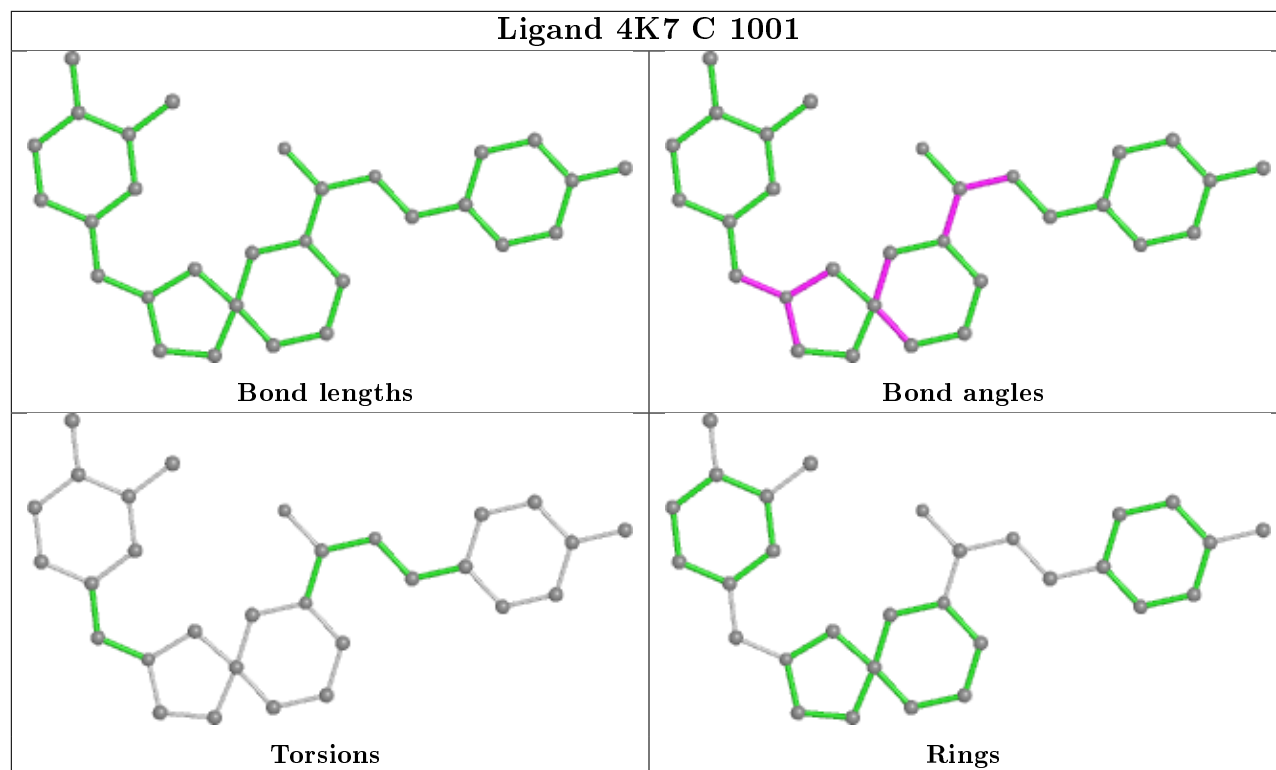
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	381/405 (94%)	0.36	24 (6%) 20 16	28, 49, 79, 111	0
1	B	375/405 (92%)	1.09	77 (20%) 1 0	38, 70, 105, 132	0
1	C	378/405 (93%)	0.30	19 (5%) 28 26	29, 53, 79, 113	0
All	All	1134/1215 (93%)	0.58	120 (10%) 6 4	28, 56, 95, 132	0

All (120) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	923	GLY	11.6
1	B	872	MET	8.0
1	C	964	GLU	7.1
1	B	891	THR	6.9
1	B	916	ALA	6.1
1	B	892	TYR	5.5
1	B	857	PRO	5.2
1	B	880	VAL	5.2
1	B	615	LEU	5.2
1	B	963	HIS	5.1
1	B	884	THR	5.0
1	A	963	HIS	5.0
1	C	963	HIS	5.0
1	B	955	ARG	4.8
1	C	702	HIS	4.8
1	B	962	PHE	4.8
1	B	917	GLU	4.7
1	B	853	SER	4.4
1	B	893	LYS	4.4
1	B	890	ARG	4.4
1	A	580	GLY	4.3
1	B	914	LEU	4.2
1	B	744	SER	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	662	GLY	4.1
1	C	659	ALA	4.1
1	B	882	LEU	4.0
1	B	878	ILE	4.0
1	A	955	ARG	4.0
1	C	750	ASN	3.9
1	B	574	LYS	3.8
1	A	872	MET	3.8
1	B	953	HIS	3.8
1	B	858	ILE	3.7
1	B	920	GLU	3.7
1	B	564	VAL	3.7
1	A	924	SER	3.6
1	B	818	GLN	3.6
1	B	876	GLU	3.6
1	B	604	GLU	3.6
1	B	750	ASN	3.6
1	B	709	ILE	3.5
1	B	883	GLN	3.5
1	B	869	VAL	3.5
1	C	655	GLN	3.5
1	B	879	THR	3.5
1	B	924	SER	3.4
1	A	743	LEU	3.4
1	B	855	ASP	3.3
1	B	870	VAL	3.3
1	A	923	GLY	3.3
1	A	574	LYS	3.2
1	A	890	ARG	3.1
1	B	958	GLN	3.1
1	C	955	ARG	3.1
1	B	743	LEU	3.1
1	C	933	PHE	3.0
1	C	779	LEU	3.0
1	B	915	PRO	3.0
1	B	576	VAL	3.0
1	A	566	VAL	3.0
1	B	867	ARG	2.9
1	B	919	ARG	2.9
1	A	964	GLU	2.9
1	B	956	LEU	2.9
1	A	888	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	744	SER	2.8
1	B	911	TYR	2.8
1	A	891	THR	2.7
1	B	950	LEU	2.7
1	B	877	ASN	2.7
1	B	694	ILE	2.7
1	B	852	GLU	2.7
1	B	693	ASN	2.7
1	A	916	ALA	2.7
1	A	642	ILE	2.7
1	B	658	PHE	2.7
1	B	710	SER	2.6
1	C	854	LEU	2.6
1	B	636	GLN	2.6
1	B	921	THR	2.6
1	B	642	ILE	2.6
1	A	579	HIS	2.5
1	A	853	SER	2.5
1	B	711	ASP	2.5
1	C	611	ARG	2.5
1	B	918	VAL	2.5
1	C	658	PHE	2.4
1	B	894	GLY	2.4
1	C	660	HIS	2.4
1	C	701	ALA	2.4
1	B	575	ASP	2.4
1	A	953	HIS	2.4
1	A	655	GLN	2.4
1	A	581	ALA	2.4
1	B	835	LEU	2.4
1	A	855	ASP	2.3
1	B	753	TYR	2.3
1	B	868	ALA	2.3
1	B	937	PHE	2.2
1	A	761	GLY	2.2
1	B	692	HIS	2.2
1	C	711[A]	ASP	2.2
1	B	659	ALA	2.2
1	B	881	PRO	2.2
1	B	895	GLY	2.1
1	B	708	MET	2.1
1	B	712	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	661	LEU	2.1
1	B	625	VAL	2.1
1	C	709	ILE	2.1
1	B	873	ASP	2.1
1	C	694	ILE	2.1
1	B	925	LEU	2.1
1	A	567	GLY	2.1
1	B	563	VAL	2.0
1	A	917	GLU	2.0
1	B	798	GLU	2.0
1	B	607	SER	2.0
1	B	793	ASP	2.0
1	B	860	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

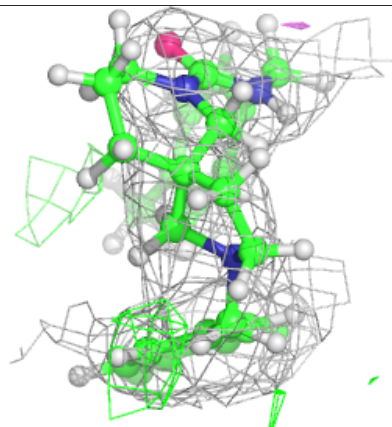
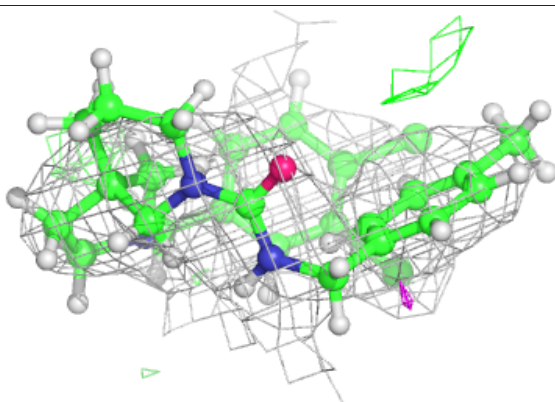
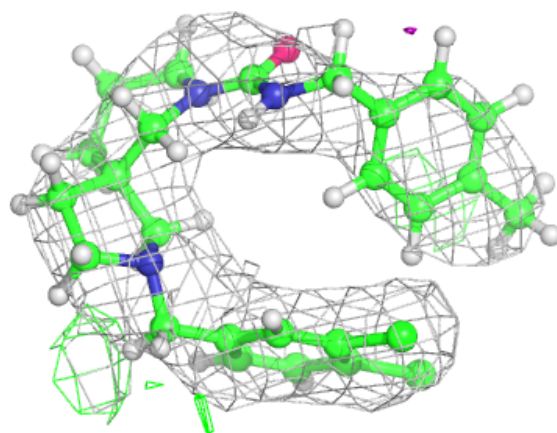
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	4K7	B	1001	30/30	0.87	0.24	57,80,106,117	0
2	4K7	C	1001	30/30	0.89	0.21	43,61,81,180	0
2	4K7	A	1001	30/30	0.96	0.18	32,48,70,89	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.

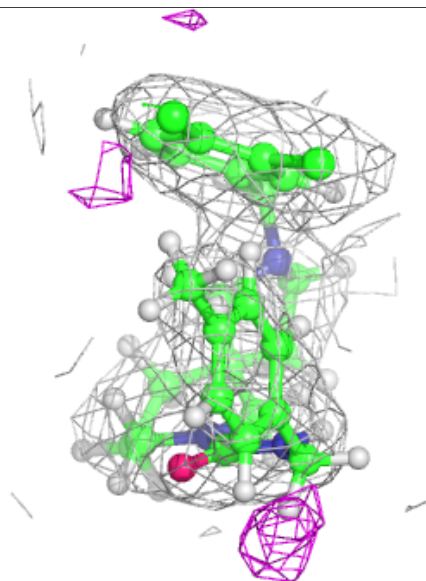
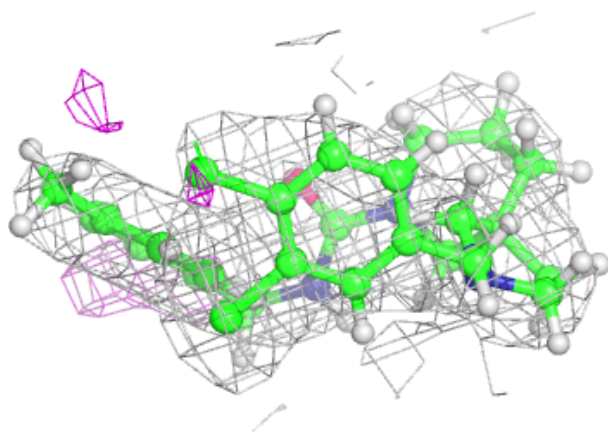
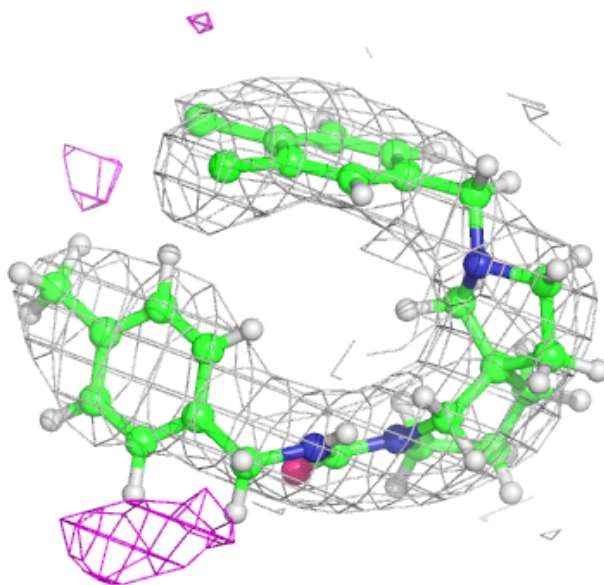
Electron density around 4K7 B 1001:

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



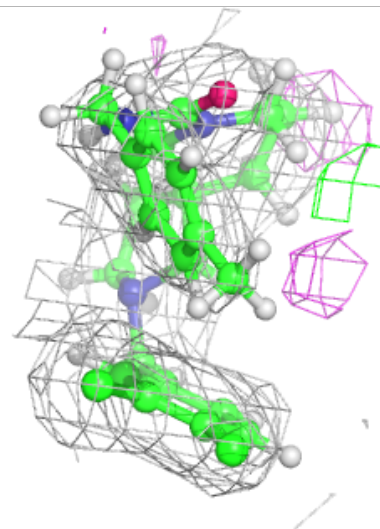
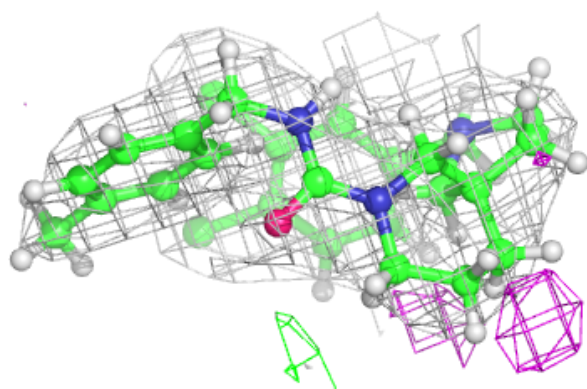
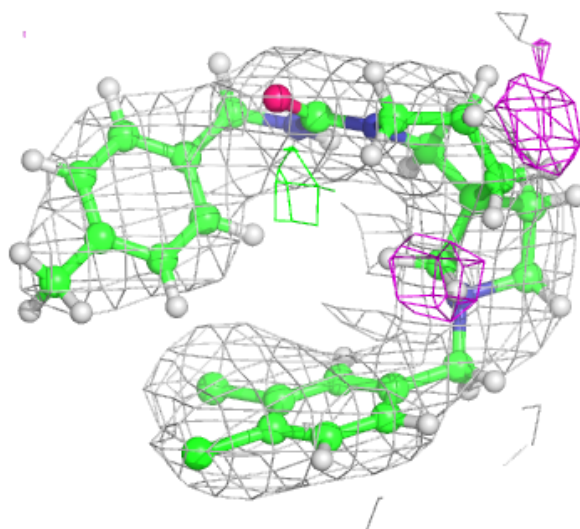
Electron density around 4K7 C 1001:

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



Electron density around 4K7 A 1001:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.