Full wwPDB X-ray Structure Validation Report (i)

Sep 23, 2023 – 06:16 PM EDT

PDB ID	:	5T3N
Title	:	Sp-2Cl-cAMPS bound to PKAR CBD2
Authors	:	Littler, D.R.; Gilson, P.
Deposited on	:	2016-08-26
Resolution	:	2.40 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

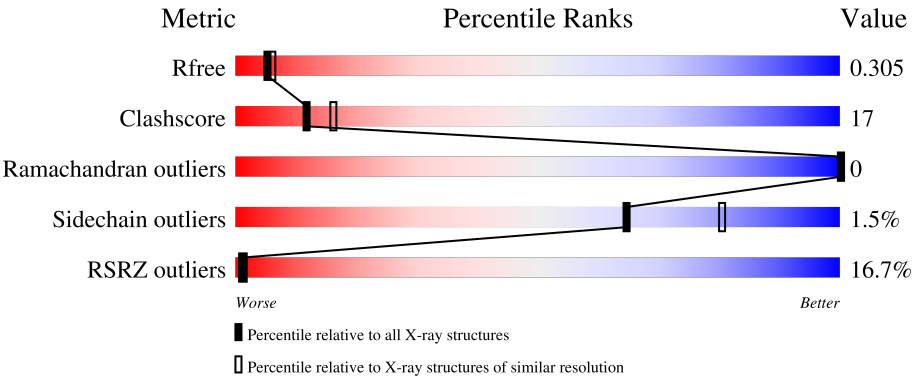
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	161	7% 73% 22% 5%
1	B	161	24% 58% 29% . 9%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2453 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 cAMP-dependent protein kinase regulatory subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	0	0	0
			1228	781	210	231	6			
1	B	146	Total	C	N	O	S	0	0	0
			1164	739	198	221	6			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	281	MET	-	initiating methionine	UNP Q7KQK0
A	282	ALA	-	expression tag	UNP Q7KQK0
A	283	HIS	-	expression tag	UNP Q7KQK0
A	284	HIS	-	expression tag	UNP Q7KQK0
A	285	HIS	-	expression tag	UNP Q7KQK0
A	286	HIS	-	expression tag	UNP Q7KQK0
A	287	HIS	-	expression tag	UNP Q7KQK0
A	288	HIS	-	expression tag	UNP Q7KQK0
A	289	GLU	-	expression tag	UNP Q7KQK0
A	290	VAL	-	expression tag	UNP Q7KQK0
A	291	LEU	-	expression tag	UNP Q7KQK0
A	292	PHE	-	expression tag	UNP Q7KQK0
A	293	GLN	-	expression tag	UNP Q7KQK0
A	294	GLY	-	expression tag	UNP Q7KQK0
A	295	PRO	-	expression tag	UNP Q7KQK0
A	296	GLY	-	expression tag	UNP Q7KQK0
B	281	MET	-	initiating methionine	UNP Q7KQK0
B	282	ALA	-	expression tag	UNP Q7KQK0
B	283	HIS	-	expression tag	UNP Q7KQK0
B	284	HIS	-	expression tag	UNP Q7KQK0
B	285	HIS	-	expression tag	UNP Q7KQK0
B	286	HIS	-	expression tag	UNP Q7KQK0
B	287	HIS	-	expression tag	UNP Q7KQK0
B	288	HIS	-	expression tag	UNP Q7KQK0
B	289	GLU	-	expression tag	UNP Q7KQK0

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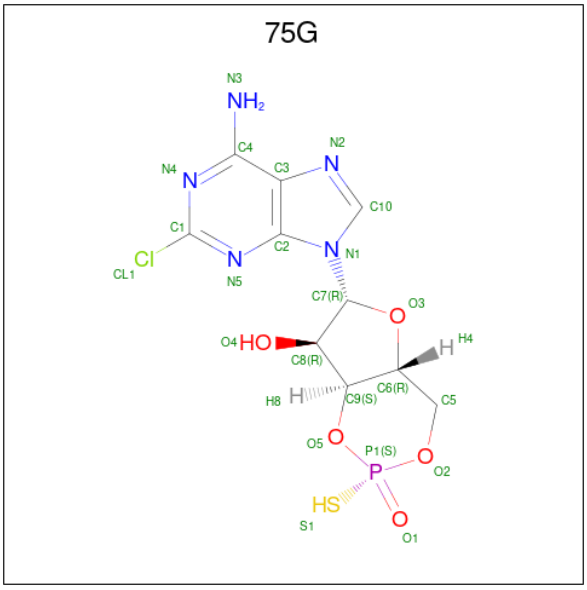
Chain	Residue	Modelled	Actual	Comment	Reference
B	290	VAL	-	expression tag	UNP Q7KQK0
B	291	LEU	-	expression tag	UNP Q7KQK0
B	292	PHE	-	expression tag	UNP Q7KQK0
B	293	GLN	-	expression tag	UNP Q7KQK0
B	294	GLY	-	expression tag	UNP Q7KQK0
B	295	PRO	-	expression tag	UNP Q7KQK0
B	296	GLY	-	expression tag	UNP Q7KQK0

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total I 2 2	0	0
2	B	3	Total I 3 3	0	0

- Molecule 3 is (2S,4aR,6R,7R,7aS)-6-(6-amino-2-chloro-9H-purin-9-yl)-7-hydroxy-2-sulfanyltetrahydro-2H,4H-2lambda 5 -furo[3,2-d][1,3,2]dioxaphosphinin-2-one (three-letter code: 75G) (formula: $C_{10}H_{11}ClN_5O_5PS$).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	P	S	0	0
			23	10	1	5	5	1	1		
3	B	1	Total	C	Cl	N	O	P	S	0	0
			23	10	1	5	5	1	1		

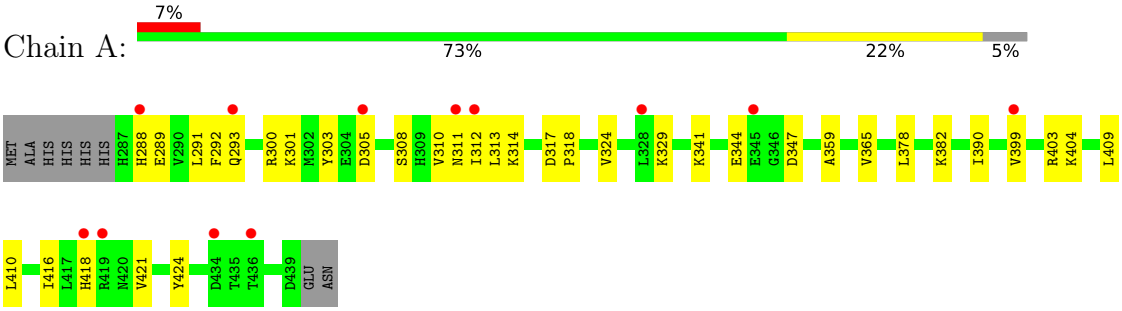
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	7	Total O 7 7	0	0
4	B	3	Total O 3 3	0	0

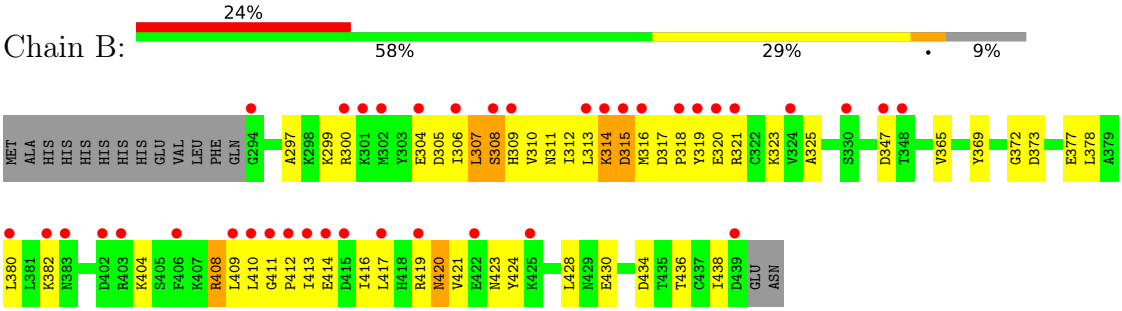
3 Residue-property plots (i)

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

• Molecule 1: cAMP-dependent protein kinase regulatory subunit



• Molecule 1: cAMP-dependent protein kinase regulatory subunit



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	64.19Å 64.19Å 195.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.42 – 2.40 33.42 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.8 (33.42-2.40) 99.7 (33.42-2.40)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.19 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.251 , 0.307 0.252 , 0.305	Depositor DCC
R_{free} test set	863 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å^2)	47.8	Xtriage
Anisotropy	0.943	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 55.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	2453	wwPDB-VP
Average B, all atoms (Å^2)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.24% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 75G, IOD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.68	0/1248	0.99	1/1675 (0.1%)
1	B	0.60	1/1181 (0.1%)	0.99	4/1584 (0.3%)
All	All	0.64	1/2429 (0.0%)	0.99	5/3259 (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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	318	PRO	N-CD	5.57	1.55	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	310	VAL	N-CA-C	-6.09	94.55	111.00
1	B	307	LEU	CB-CA-C	-5.53	99.69	110.20
1	B	419	ARG	C-N-CA	-5.24	108.59	121.70
1	B	317	ASP	C-N-CD	5.14	139.19	128.40
1	B	308	SER	O-C-N	5.10	130.87	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	420	ASN	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1228	0	1246	25	0
1	B	1164	0	1189	61	5
2	A	2	0	0	0	0
2	B	3	0	0	1	0
3	A	23	0	0	0	0
3	B	23	0	0	3	0
4	A	7	0	0	0	0
4	B	3	0	0	0	0
All	All	2453	0	2435	85	5

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 17.

All (85) 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:307:LEU:HD21	1:B:313:LEU:CD2	1.96	0.95
1:B:411:GLY:HA2	1:B:414:GLU:HG3	1.47	0.94
1:B:316:MET:SD	1:B:412:PRO:HB2	2.09	0.92
1:B:307:LEU:HD21	1:B:313:LEU:HD23	1.52	0.90
1:A:311:ASN:HA	1:A:314:LYS:HE3	1.55	0.88
1:B:411:GLY:HA2	1:B:414:GLU:CG	2.12	0.80
1:B:310:VAL:HG22	1:B:372:GLY:HA2	1.63	0.79
1:B:411:GLY:CA	1:B:414:GLU:HG3	2.17	0.74
1:A:312:ILE:HG23	1:A:313:LEU:HD12	1.70	0.74
1:B:299:LYS:HE2	1:B:325:ALA:O	1.92	0.68
1:B:312:ILE:HG13	1:B:312:ILE:O	1.94	0.68
1:A:378:LEU:HD11	1:A:382:LYS:HE3	1.76	0.67
1:A:289:GLU:O	1:A:293:GLN:HG3	1.95	0.66
1:B:307:LEU:CD2	1:B:313:LEU:HD23	2.23	0.66
1:B:320:GLU:OE1	1:B:323:LYS:HD3	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:307:LEU:HD11	1:B:313:LEU:CD2	2.28	0.64
1:B:304:GLU:O	1:B:307:LEU:HB3	2.00	0.62
1:B:316:MET:HE3	1:B:412:PRO:CB	2.29	0.62
1:B:312:ILE:HD11	1:B:417:LEU:HD23	1.83	0.60
1:B:307:LEU:O	1:B:307:LEU:HD23	2.01	0.60
1:B:307:LEU:C	1:B:309:HIS:H	2.05	0.59
1:B:310:VAL:HG12	1:B:312:ILE:HG22	1.84	0.59
1:B:411:GLY:HA2	1:B:414:GLU:CD	2.23	0.59
1:B:307:LEU:HD21	1:B:313:LEU:CB	2.32	0.59
1:A:305:ASP:O	1:A:308:SER:OG	2.14	0.58
1:A:312:ILE:HD11	1:A:416:ILE:CG2	2.34	0.57
1:B:316:MET:HE3	1:B:412:PRO:HB3	1.87	0.56
1:A:317:ASP:HB2	1:A:318:PRO:CD	2.35	0.56
1:A:418:HIS:O	1:A:421:VAL:HB	2.06	0.56
1:B:316:MET:CE	1:B:412:PRO:CB	2.85	0.54
1:A:341:LYS:HE2	1:A:344:GLU:OE2	2.10	0.52
1:A:347:ASP:OD1	1:A:403:ARG:NH1	2.43	0.52
1:B:315:ASP:OD2	1:B:315:ASP:N	2.35	0.52
1:A:421:VAL:HA	1:A:424:TYR:CD2	2.45	0.51
1:B:410:LEU:HD22	1:B:413:ILE:HD11	1.93	0.51
1:A:312:ILE:HD11	1:A:416:ILE:HG22	1.93	0.51
1:B:316:MET:SD	1:B:412:PRO:CB	2.92	0.50
1:B:378:LEU:HB3	3:B:504:75G:S1	2.51	0.50
1:B:307:LEU:O	1:B:310:VAL:N	2.29	0.49
1:B:310:VAL:HG13	1:B:372:GLY:O	2.13	0.49
1:A:288:HIS:ND1	1:A:288:HIS:N	2.60	0.48
1:B:307:LEU:HD11	1:B:313:LEU:HD23	1.94	0.48
1:A:359:ALA:HB2	1:A:390:ILE:HG12	1.96	0.48
1:B:305:ASP:O	1:B:306:ILE:C	2.52	0.48
1:B:316:MET:CE	1:B:412:PRO:HG2	2.44	0.48
1:B:305:ASP:O	1:B:308:SER:N	2.45	0.47
1:B:316:MET:HE1	1:B:412:PRO:HG2	1.96	0.47
1:B:307:LEU:HD21	1:B:313:LEU:HD22	1.91	0.47
1:B:382:LYS:HE3	1:B:438:ILE:O	2.15	0.46
1:A:291:LEU:O	1:A:300:ARG:HD2	2.14	0.46
1:B:307:LEU:HD23	1:B:307:LEU:C	2.36	0.46
1:B:307:LEU:C	1:B:309:HIS:N	2.67	0.46
1:A:365:VAL:HG21	1:B:365:VAL:HG21	1.98	0.46
1:B:311:ASN:O	1:B:314:LYS:HB2	2.15	0.46
1:B:424:TYR:O	1:B:428:LEU:HG	2.15	0.46
1:B:404:LYS:HA	1:B:404:LYS:HD3	1.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:ASN:O	1:A:314:LYS:HG2	2.16	0.45
1:A:312:ILE:HD11	1:A:416:ILE:HG21	1.98	0.45
1:B:369:TYR:HD1	1:B:373:ASP:HB3	1.81	0.45
1:B:312:ILE:CD1	1:B:417:LEU:HD23	2.46	0.45
1:A:329:LYS:O	1:A:399:VAL:HA	2.17	0.44
1:B:299:LYS:O	1:B:300:ARG:C	2.53	0.44
1:B:434:ASP:OD1	1:B:436:THR:HG23	2.17	0.44
1:A:303:TYR:HD1	1:A:303:TYR:HA	1.68	0.44
1:B:421:VAL:O	1:B:424:TYR:HB2	2.18	0.44
1:B:304:GLU:CD	1:B:321:ARG:HH11	2.21	0.43
1:B:305:ASP:OD2	1:B:305:ASP:C	2.55	0.43
1:A:317:ASP:CB	1:A:318:PRO:CD	2.96	0.43
1:B:377:GLU:OE1	3:B:504:75G:O4	2.37	0.43
1:B:430:GLU:HG3	2:B:501:IOD:I	2.89	0.43
1:B:420:ASN:HD21	1:B:423:ASN:ND2	2.16	0.42
1:A:292:PHE:HB3	1:A:301:LYS:HE3	2.00	0.42
1:B:320:GLU:OE1	1:B:323:LYS:CD	2.65	0.42
1:B:408:ARG:H	1:B:408:ARG:HG2	1.20	0.42
1:B:310:VAL:HG22	1:B:372:GLY:CA	2.44	0.42
1:A:410:LEU:HD23	1:A:410:LEU:HA	1.88	0.41
1:B:297:ALA:O	1:B:300:ARG:HB2	2.21	0.41
1:B:409:LEU:HD23	1:B:409:LEU:HA	1.71	0.41
1:B:420:ASN:OD1	1:B:423:ASN:N	2.48	0.41
1:A:324:VAL:HA	1:A:409:LEU:HD13	2.02	0.41
1:B:320:GLU:O	1:B:323:LYS:HB2	2.20	0.41
1:B:369:TYR:OH	3:B:504:75G:C10	2.69	0.41
1:B:413:ILE:HA	1:B:416:ILE:HD12	2.03	0.41
1:A:312:ILE:CG2	1:A:313:LEU:HD12	2.44	0.40
1:B:347:ASP:HA	1:B:380:LEU:HD21	2.04	0.40

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:319:TYR:CD1	1:B:319:TYR:CD1[8_885]	0.44	1.76
1:B:319:TYR:CE1	1:B:319:TYR:CE1[8_885]	1.26	0.94
1:B:319:TYR:CD1	1:B:319:TYR:CE1[8_885]	1.55	0.65
1:B:319:TYR:CG	1:B:319:TYR:CD1[8_885]	1.56	0.64
1:B:319:TYR:CB	1:B:319:TYR:CB[8_885]	2.09	0.11

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	151/161 (94%)	147 (97%)	4 (3%)	0	100	100
1	B	144/161 (89%)	136 (94%)	8 (6%)	0	100	100
All	All	295/322 (92%)	283 (96%)	12 (4%)	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	135/142 (95%)	134 (99%)	1 (1%)	84	92
1	B	128/142 (90%)	125 (98%)	3 (2%)	50	70
All	All	263/284 (93%)	259 (98%)	4 (2%)	65	80

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	404	LYS
1	B	314	LYS
1	B	315	ASP
1	B	408	ARG

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

Mol	Chain	Res	Type
1	B	423	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 7 ligands modelled in this entry, 5 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	75G	B	504	-	19,26,26	4.48	11 (57%)	26,41,41	3.41	10 (38%)
3	75G	A	503	-	19,26,26	4.77	11 (57%)	26,41,41	3.61	13 (50%)

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	75G	B	504	-	-	0/0/31/31	0/4/4/4
3	75G	A	503	-	-	0/0/31/31	0/4/4/4

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	504	75G	O3-C7	12.53	1.58	1.41
3	A	503	75G	O3-C7	11.83	1.57	1.41
3	A	503	75G	O2-C5	10.20	1.60	1.46
3	A	503	75G	C1-N5	9.61	1.37	1.30
3	B	504	75G	O2-C5	8.55	1.58	1.46
3	B	504	75G	C1-N5	8.42	1.37	1.30
3	A	503	75G	C8-C7	-4.44	1.47	1.53
3	A	503	75G	C5-C6	-3.86	1.45	1.51
3	A	503	75G	O5-C9	-3.72	1.38	1.44
3	B	504	75G	O5-C9	-3.63	1.38	1.44
3	B	504	75G	C5-C6	-3.38	1.46	1.51
3	B	504	75G	C8-C7	-3.28	1.48	1.53
3	A	503	75G	C1-N4	3.27	1.38	1.32
3	B	504	75G	O3-C6	3.14	1.52	1.45
3	A	503	75G	O3-C6	2.88	1.51	1.45
3	A	503	75G	C8-C9	-2.76	1.46	1.52
3	A	503	75G	C9-C6	-2.72	1.45	1.52
3	B	504	75G	C4-N3	2.71	1.43	1.34
3	B	504	75G	C9-C6	-2.59	1.45	1.52
3	B	504	75G	C1-N4	2.48	1.36	1.32
3	B	504	75G	C8-C9	-2.40	1.47	1.52
3	A	503	75G	C4-N3	2.37	1.42	1.34

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	503	75G	C1-N5-C2	9.13	121.32	114.09
3	A	503	75G	N5-C1-N4	-8.93	121.62	130.62
3	B	504	75G	N5-C1-N4	-7.93	122.63	130.62
3	B	504	75G	C1-N5-C2	7.70	120.18	114.09
3	B	504	75G	C3-C4-N4	-7.64	116.00	121.01
3	A	503	75G	C3-C4-N4	-6.27	116.89	121.01
3	A	503	75G	P1-O2-C5	-5.83	105.63	118.64
3	B	504	75G	CL1-C1-N5	5.44	120.34	115.70
3	B	504	75G	O5-P1-O2	4.95	111.35	104.14
3	A	503	75G	CL1-C1-N5	4.62	119.64	115.70
3	A	503	75G	C2-C3-N2	-4.49	104.72	109.40
3	A	503	75G	O5-P1-O2	4.24	110.32	104.14
3	B	504	75G	C2-C3-N2	-3.83	105.41	109.40
3	B	504	75G	C1-N4-C4	3.29	120.71	116.64
3	B	504	75G	C9-C8-C7	3.22	107.02	99.89
3	A	503	75G	C1-N4-C4	2.83	120.15	116.64
3	A	503	75G	P1-O5-C9	-2.55	107.81	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	504	75G	O5-C9-C6	2.50	112.60	110.71
3	A	503	75G	CL1-C1-N4	2.50	118.72	115.15
3	A	503	75G	C9-C8-C7	2.37	105.14	99.89
3	A	503	75G	O5-C9-C8	-2.17	113.48	115.61
3	A	503	75G	N3-C4-N4	2.06	122.67	117.07
3	B	504	75G	P1-O2-C5	-2.02	114.13	118.64

There are no chirality outliers.

There are no torsion outliers.

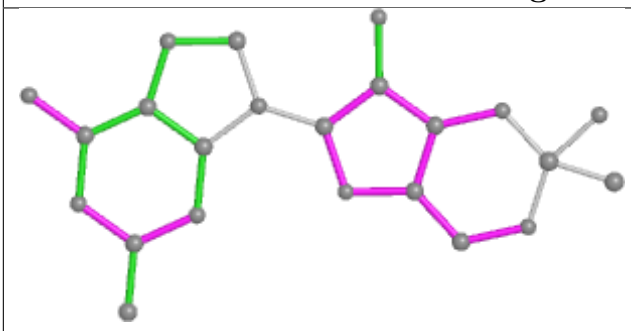
There are no ring outliers.

1 monomer is involved in 3 short contacts:

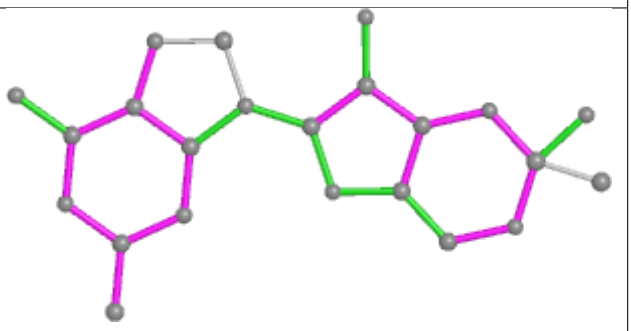
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	504	75G	3	0

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

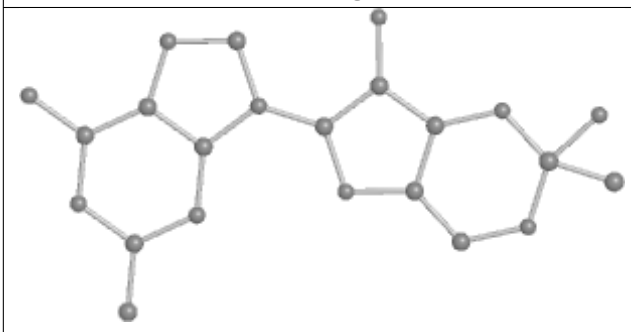
Ligand 75G B 504



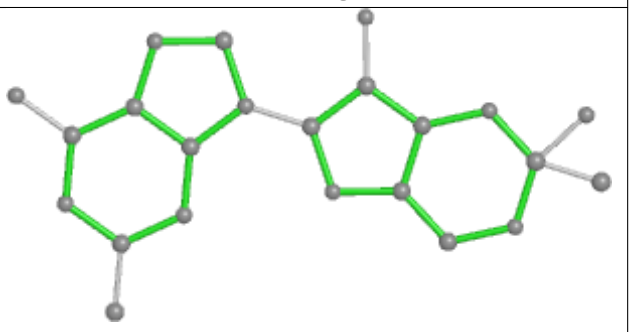
Bond lengths



Bond angles

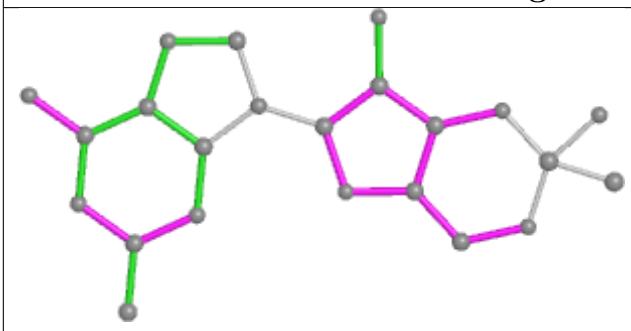


Torsions

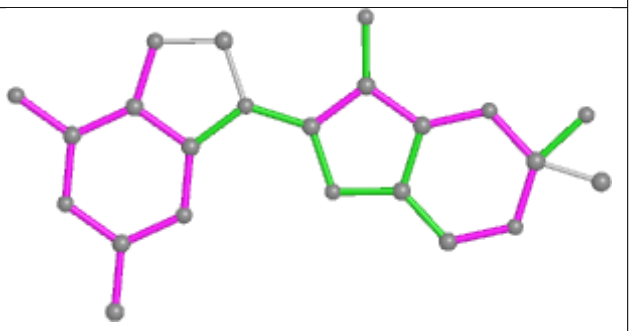


Rings

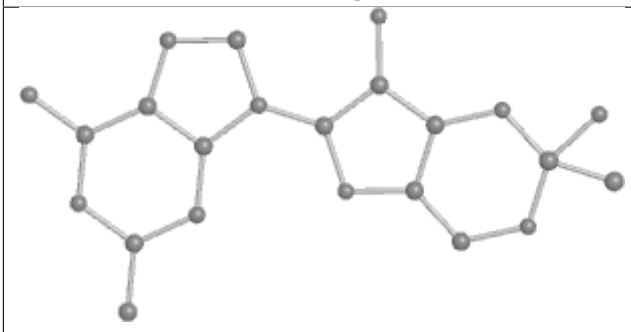
Ligand 75G A 503



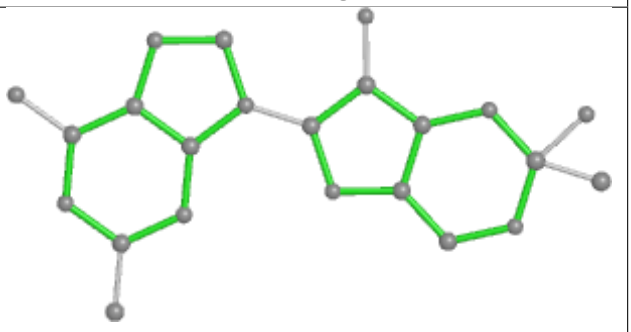
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	153/161 (95%)	0.52	12 (7%)	13	11	43, 69, 113, 144	0
1	B	146/161 (90%)	1.58	38 (26%)	0	0	46, 98, 201, 378	0
All	All	299/322 (92%)	1.04	50 (16%)	1	1	43, 80, 179, 378	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	319	TYR	18.6
1	B	415	ASP	8.6
1	B	410	LEU	7.5
1	B	411	GLY	6.7
1	B	409	LEU	6.7
1	B	306	ILE	5.9
1	B	304	GLU	5.4
1	B	413	ILE	5.0
1	B	419	ARG	5.0
1	B	406	PHE	5.0
1	B	315	ASP	4.9
1	B	316	MET	4.8
1	A	419	ARG	4.8
1	B	417	LEU	4.8
1	B	324	VAL	4.6
1	B	414	GLU	4.5
1	B	320	GLU	4.1
1	A	436	THR	3.7
1	B	412	PRO	3.6
1	B	347	ASP	3.6
1	B	302	MET	3.4
1	B	309	HIS	3.4
1	B	380	LEU	3.3
1	B	402	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	422	GLU	3.1
1	A	288	HIS	3.1
1	B	403	ARG	3.0
1	A	311	ASN	3.0
1	A	345	GLU	2.9
1	A	434	ASP	2.9
1	A	418	HIS	2.9
1	A	293	GLN	2.8
1	B	348	THR	2.8
1	B	314	LYS	2.8
1	B	439	ASP	2.7
1	B	313	LEU	2.7
1	B	301	LYS	2.7
1	A	312	ILE	2.4
1	B	321	ARG	2.4
1	B	425	LYS	2.4
1	B	318	PRO	2.4
1	B	330	SER	2.3
1	B	294	GLY	2.2
1	B	308	SER	2.2
1	A	305	ASP	2.1
1	A	399	VAL	2.1
1	B	383	ASN	2.1
1	B	382	LYS	2.1
1	B	300	ARG	2.1
1	A	328	LEU	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)

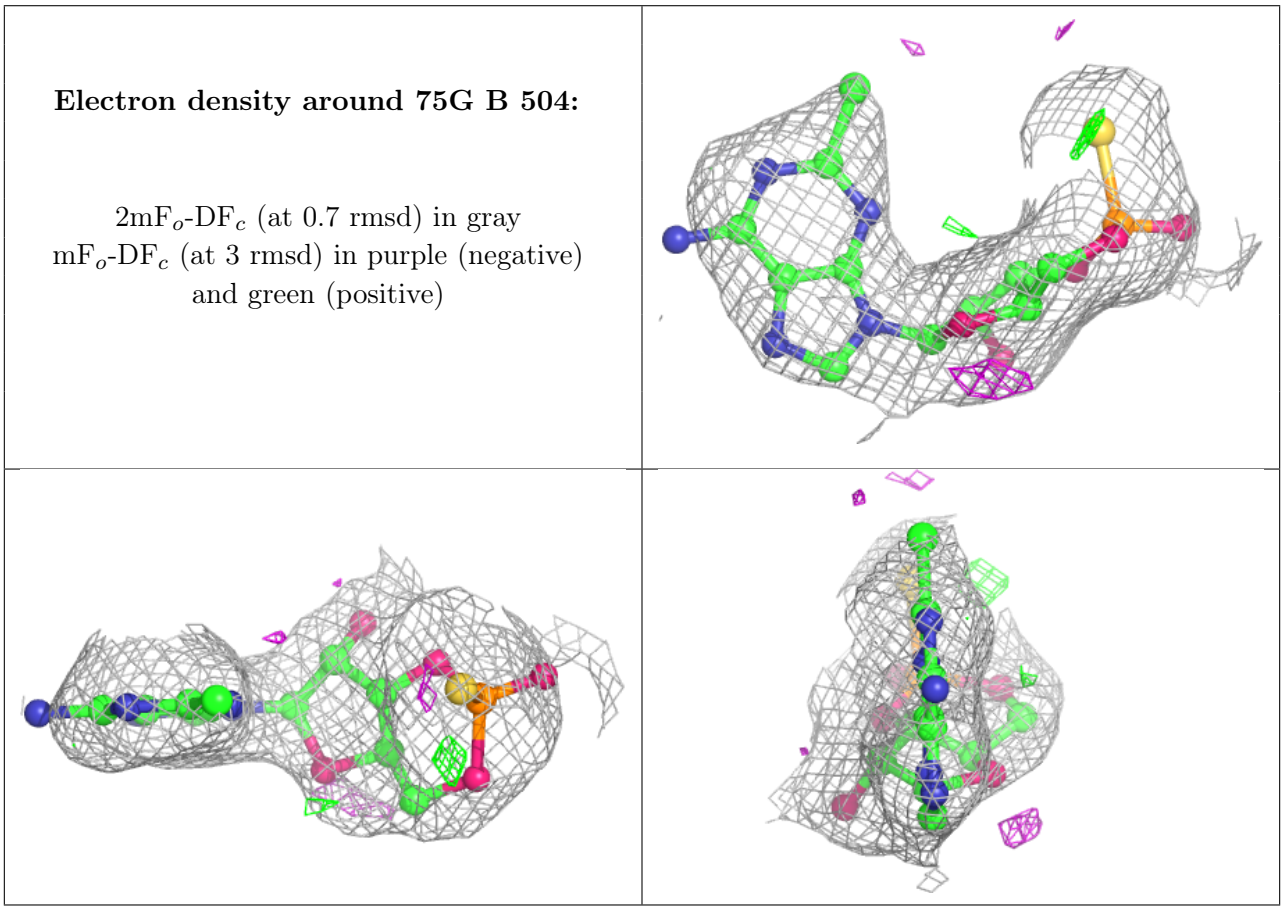
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	IOD	A	502	1/1	0.80	0.15	201,201,201,201	0
2	IOD	B	502	1/1	0.80	0.19	207,207,207,207	0
3	75G	B	504	23/23	0.91	0.17	70,79,90,129	0
2	IOD	B	503	1/1	0.92	0.10	85,85,85,85	0
3	75G	A	503	23/23	0.97	0.14	39,49,59,108	0
2	IOD	B	501	1/1	0.97	0.03	93,93,93,93	0
2	IOD	A	501	1/1	0.99	0.18	67,67,67,67	1

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.

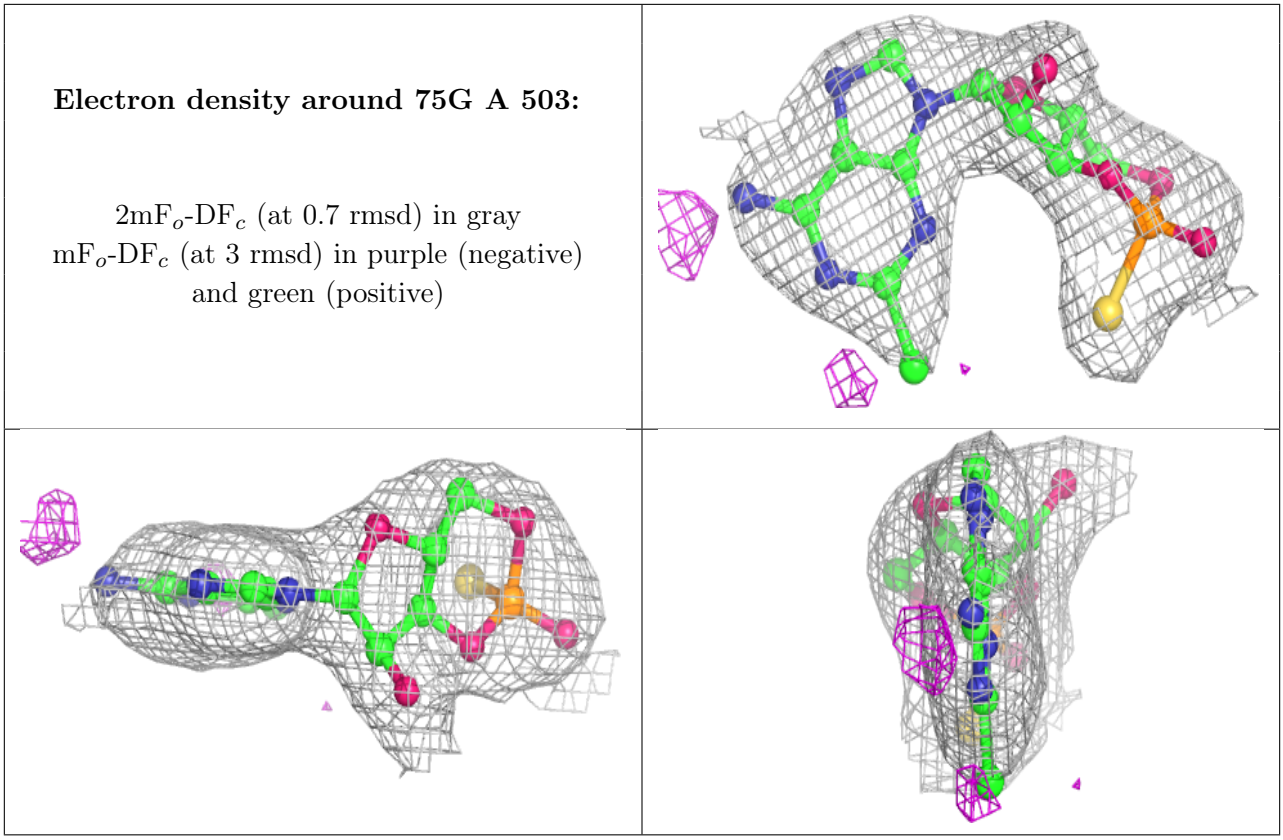
Electron density around 75G B 504:

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



Electron density around 75G A 503:

$2mF_o$-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.