Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 11:31 AM BST

PDB ID	:	3VS7
Title	:	Crystal structure of HCK complexed with a pyrazolo-pyrimidine inhibitor 1-cyclopentyl-3-(1H-pyrrolo[2,3-b]pyridin-5-yl)-1H-pyrazolo[3,4-d]pyrimidin-4-amine
Authors	:	Kuratani, M.; Honda, K.; Niwa, H.; Toyama, M.; Handa, N.; Yokoyama, S.
Deposited on	:	2012-04-21
Resolution	:	3.00 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:

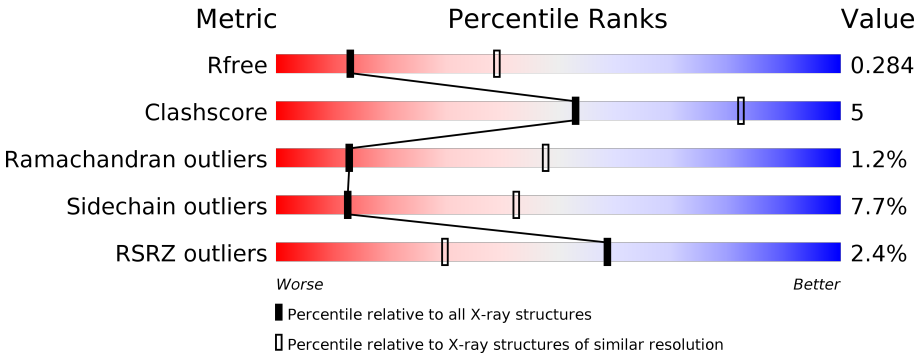
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 <=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	454	2% 75% 18% • 5%
1	B	454	2% 75% 17% • 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7020 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.

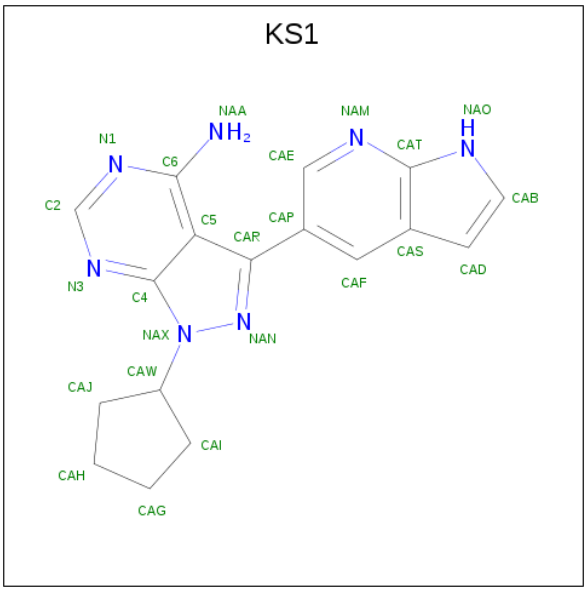
- Molecule 1 is a protein called Tyrosine-protein kinase HCK.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	433	Total	C	N	O	P	S	0	0	0
			3493	2232	587	653	1	20			
1	B	427	Total	C	N	O	P	S	0	0	0
			3454	2209	580	644	1	20			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	78	GLY	-	EXPRESSION TAG	UNP P08631
A	79	ALA	-	EXPRESSION TAG	UNP P08631
A	80	MET	-	EXPRESSION TAG	UNP P08631
A	81	GLY	-	EXPRESSION TAG	UNP P08631
A	82	SER	-	EXPRESSION TAG	UNP P08631
A	83	GLY	-	EXPRESSION TAG	UNP P08631
A	84	ILE	-	EXPRESSION TAG	UNP P08631
A	85	ARG	-	EXPRESSION TAG	UNP P08631
A	528	GLU	GLN	ENGINEERED MUTATION	UNP P08631
A	529	GLU	GLN	ENGINEERED MUTATION	UNP P08631
A	530	ILE	GLN	ENGINEERED MUTATION	UNP P08631
B	78	GLY	-	EXPRESSION TAG	UNP P08631
B	79	ALA	-	EXPRESSION TAG	UNP P08631
B	80	MET	-	EXPRESSION TAG	UNP P08631
B	81	GLY	-	EXPRESSION TAG	UNP P08631
B	82	SER	-	EXPRESSION TAG	UNP P08631
B	83	GLY	-	EXPRESSION TAG	UNP P08631
B	84	ILE	-	EXPRESSION TAG	UNP P08631
B	85	ARG	-	EXPRESSION TAG	UNP P08631
B	528	GLU	GLN	ENGINEERED MUTATION	UNP P08631
B	529	GLU	GLN	ENGINEERED MUTATION	UNP P08631
B	530	ILE	GLN	ENGINEERED MUTATION	UNP P08631

- Molecule 2 is 1-cyclopentyl-3-(1H-pyrrolo[2,3-b]pyridin-5-yl)-1H-pyrazolo[3,4-d]pyrimidin-4-amine (three-letter code: KS1) (formula: $C_{17}H_{17}N_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N 24 17 7	0	0
2	B	1	Total C N 24 17 7	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Ca 1 1	0	0
3	A	1	Total Ca 1 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Cl 1 1	0	0
4	A	1	Total Cl 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	12	Total O 12 12	0	0

Continued on next page...

Continued from previous page...

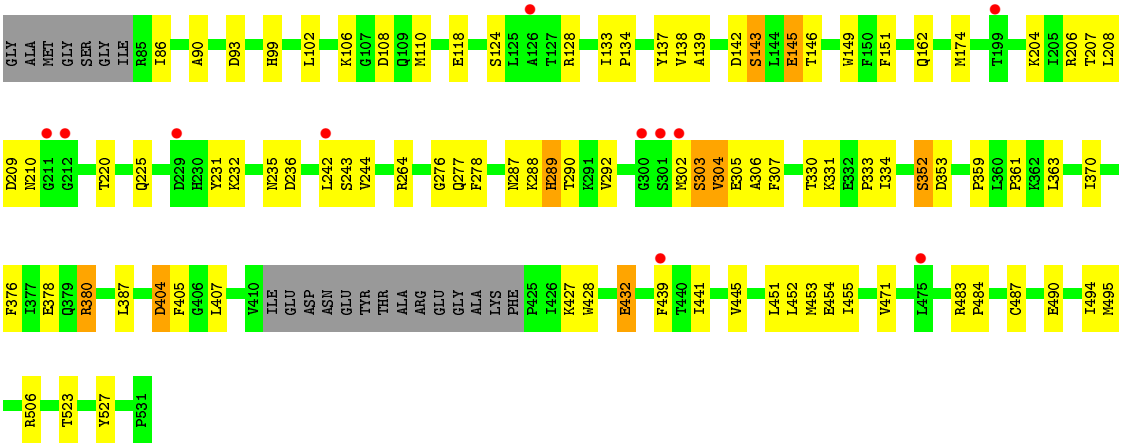
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	9	Total O 9 9	0	0

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.

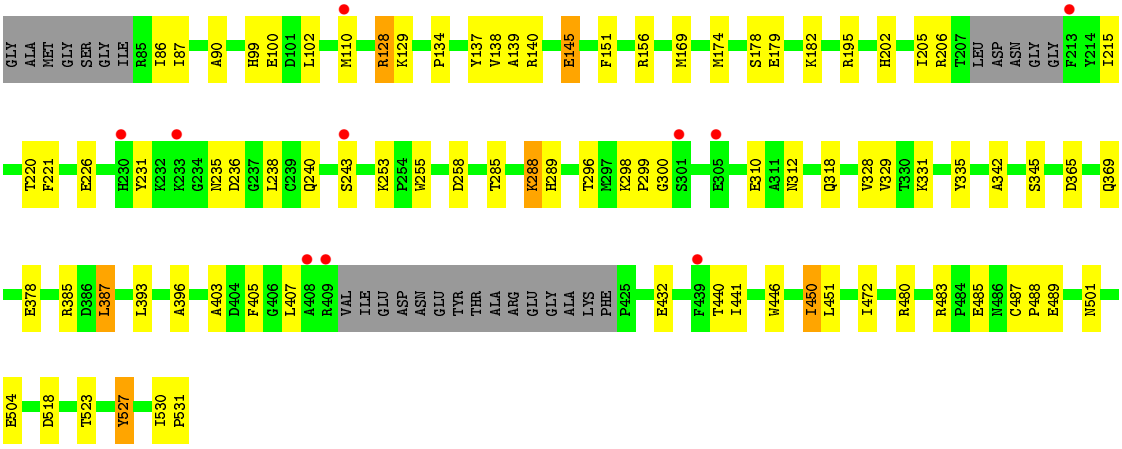
- Molecule 1: Tyrosine-protein kinase HCK

Chain A:



- Molecule 1: Tyrosine-protein kinase HCK

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	72.80Å 96.02Å 182.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.51 – 3.00 42.51 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.0 (42.51-3.00) 99.3 (42.51-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.29 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.233 , 0.290 0.227 , 0.284	Depositor DCC
R_{free} test set	1309 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	79.3	Xtriage
Anisotropy	0.785	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 69.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7020	wwPDB-VP
Average B, all atoms (Å^2)	108.0	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 34.41 % 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 6.8559e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: CA, KS1, PTR, CL

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	0.22	0/3559	0.40	0/4804
1	B	0.22	0/3519	0.40	0/4748
All	All	0.22	0/7078	0.40	0/9552

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

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	3493	0	3460	40	0
1	B	3454	0	3423	35	0
2	A	24	0	17	1	0
2	B	24	0	17	3	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	1	0
5	A	12	0	0	0	0
5	B	9	0	0	0	0
All	All	7020	0	6917	75	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 5.

All (75) 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:204:LYS:HE3	1:B:489:GLU:HG2	1.75	0.66
1:B:345:SER:HB2	2:B:601:KS1:HAHA	1.80	0.64
1:B:483:ARG:NH1	1:B:487:CYS:O	2.33	0.62
1:B:215:ILE:HG22	1:B:530:ILE:HG21	1.81	0.62
1:A:110:MET:HG2	1:A:124:SER:HA	1.84	0.59
1:A:143:SER:O	1:A:143:SER:OG	2.17	0.58
1:B:378:GLU:HG3	1:B:441:ILE:HG12	1.88	0.56
1:A:232:LYS:HA	1:A:242:LEU:HB2	1.90	0.54
1:B:288:LYS:O	1:B:289:HIS:ND1	2.41	0.53
1:A:276:GLY:O	1:A:278:PHE:N	2.42	0.52
1:A:303:SER:OG	1:A:304:VAL:N	2.42	0.52
1:A:432:GLU:OE2	1:A:506:ARG:NH1	2.29	0.52
1:A:142:ASP:H	1:A:146:THR:HG21	1.74	0.51
1:A:428:TRP:NE1	1:A:454:GLU:OE1	2.38	0.51
1:B:178:SER:OG	1:B:527:PTR:O3P	2.25	0.51
1:B:90:ALA:HA	1:B:138:VAL:HG12	1.93	0.51
1:B:480:ARG:NH2	1:B:501:ASN:OD1	2.41	0.51
1:B:156:ARG:NH1	1:B:518:ASP:OD1	2.36	0.51
1:A:452:LEU:HD23	1:A:495:MET:HG2	1.93	0.51
1:A:427:LYS:HE2	1:A:471:VAL:HG21	1.92	0.50
1:A:139:ALA:HB1	1:A:145:GLU:HG3	1.93	0.49
1:A:287:ASN:O	1:A:289:HIS:N	2.44	0.48
1:A:378:GLU:HG3	1:A:441:ILE:HG12	1.96	0.48
1:A:404:ASP:HB2	1:A:407:LEU:HD22	1.94	0.48
1:A:432:GLU:HG3	1:A:432:GLU:H	1.44	0.48
1:B:342:ALA:HB3	1:B:396:ALA:HB2	1.95	0.47
1:B:99:HIS:CD2	1:B:100:GLU:HG3	2.51	0.46
1:A:231:TYR:CE1	1:A:236:ASP:HB3	2.51	0.46
1:A:363:LEU:HB3	1:A:455:ILE:HG22	1.98	0.46
1:B:365:ASP:O	1:B:369:GLN:HG3	2.15	0.46
1:A:303:SER:HB3	1:A:306:ALA:HB3	1.97	0.45
1:A:352:SER:OG	1:A:353:ASP:N	2.49	0.45
1:B:151:PHE:CD1	1:B:174:MET:HB2	2.51	0.45
1:B:128:ARG:NH2	4:B:603:CL:CL	2.86	0.45
1:A:359:PRO:HB2	1:A:361:PRO:HD2	1.97	0.45
1:B:235:ASN:HB2	1:B:238:LEU:HB2	1.98	0.45
1:B:231:TYR:CE1	1:B:236:ASP:HB3	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:LEU:C	1:A:210:ASN:HA	2.38	0.45
1:B:329:VAL:HB	1:B:335:TYR:HB2	1.99	0.45
1:A:376:PHE:O	1:A:380:ARG:HG2	2.18	0.44
1:B:221:PHE:HD2	1:B:226:GLU:HG2	1.81	0.44
1:A:149:TRP:HZ2	1:A:225:GLN:HG2	1.83	0.44
1:B:530:ILE:HD12	1:B:531:PRO:HD2	2.00	0.44
1:A:143:SER:O	1:A:145:GLU:HG2	2.17	0.44
1:B:139:ALA:HB1	1:B:145:GLU:HG3	2.00	0.44
1:B:298:LYS:O	1:B:300:GLY:N	2.51	0.43
1:A:243:SER:OG	1:A:244:VAL:N	2.51	0.43
1:B:487:CYS:HA	1:B:488:PRO:HD3	1.91	0.43
1:A:110:MET:HE1	1:A:133:ILE:HG21	2.01	0.43
1:A:483:ARG:NH1	1:A:487:CYS:O	2.50	0.43
1:B:403:ALA:HB1	2:B:601:KS1:NAM	2.33	0.43
1:A:304:VAL:HG23	1:A:305:GLU:H	1.83	0.43
2:A:601:KS1:HNAB	2:A:601:KS1:CAF	2.32	0.43
1:B:134:PRO:HG2	1:B:137:TYR:HB2	2.01	0.43
1:A:93:ASP:OD1	1:A:106:LYS:N	2.44	0.42
1:B:102:LEU:HD21	1:B:129:LYS:HB2	2.00	0.42
1:B:253:LYS:H	1:B:253:LYS:HG3	1.55	0.42
1:A:231:TYR:HE1	1:A:236:ASP:HB3	1.84	0.42
1:B:102:LEU:HD11	1:B:129:LYS:O	2.19	0.42
2:B:601:KS1:HNAB	2:B:601:KS1:CAF	2.32	0.42
1:B:446:TRP:HE1	1:B:450:ILE:HD11	1.85	0.42
1:B:179:GLU:HA	1:B:182:LYS:HE2	2.02	0.42
1:A:134:PRO:HG2	1:A:137:TYR:HB2	2.02	0.42
1:B:156:ARG:HG2	1:B:202:HIS:CE1	2.54	0.42
1:A:151:PHE:CD1	1:A:174:MET:HB2	2.55	0.41
1:A:264:ARG:NH1	1:A:333:PRO:O	2.50	0.41
1:A:370:ILE:HD13	1:A:451:LEU:HD21	2.02	0.41
1:B:387:LEU:HD22	1:B:451:LEU:HD22	2.02	0.41
1:A:490:GLU:O	1:A:494:ILE:HG13	2.20	0.41
1:A:90:ALA:HA	1:A:138:VAL:HG12	2.02	0.41
1:A:490:GLU:HG2	1:B:523:THR:O	2.21	0.40
1:B:504:GLU:N	1:B:504:GLU:OE2	2.55	0.40
1:A:483:ARG:HA	1:A:484:PRO:HD3	1.91	0.40
1:B:393:LEU:HG	1:B:403:ALA:HB2	2.03	0.40
1:A:441:ILE:O	1:A:445:VAL:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	428/454 (94%)	386 (90%)	37 (9%)	5 (1%)	13	48
1	B	420/454 (92%)	391 (93%)	24 (6%)	5 (1%)	13	48
All	All	848/908 (93%)	777 (92%)	61 (7%)	10 (1%)	13	48

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	209	ASP
1	A	277	GLN
1	B	255	TRP
1	A	290	THR
1	A	404	ASP
1	A	303	SER
1	B	299	PRO
1	B	385	ARG
1	B	288	LYS
1	B	243	SER

5.3.2 Protein sidechains

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	378/393 (96%)	348 (92%)	30 (8%)	12	41
1	B	374/393 (95%)	346 (92%)	28 (8%)	13	43
All	All	752/786 (96%)	694 (92%)	58 (8%)	13	42

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	ILE
1	A	99	HIS
1	A	102	LEU
1	A	108	ASP
1	A	118	GLU
1	A	128	ARG
1	A	143	SER
1	A	145	GLU
1	A	162	GLN
1	A	206	ARG
1	A	207	THR
1	A	220	THR
1	A	235	ASN
1	A	288	LYS
1	A	289	HIS
1	A	292	VAL
1	A	302	MET
1	A	304	VAL
1	A	307	PHE
1	A	330	THR
1	A	331	LYS
1	A	334	ILE
1	A	352	SER
1	A	380	ARG
1	A	387	LEU
1	A	405	PHE
1	A	432	GLU
1	A	439	PHE
1	A	453	MET
1	A	523	THR
1	B	86	ILE
1	B	87	ILE
1	B	110	MET
1	B	128	ARG
1	B	140	ARG
1	B	145	GLU
1	B	169	MET
1	B	195	ARG
1	B	205	ILE
1	B	206	ARG
1	B	220	THR
1	B	240	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	258	ASP
1	B	285	THR
1	B	296	THR
1	B	310	GLU
1	B	312	ASN
1	B	318	GLN
1	B	328	VAL
1	B	331	LYS
1	B	387	LEU
1	B	405	PHE
1	B	407	LEU
1	B	432	GLU
1	B	440	THR
1	B	450	ILE
1	B	472	ILE
1	B	485	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	PTR	A	527	1,3	15,16,17	1.26	1 (6%)	19,22,24	0.62	0
1	PTR	B	527	1,3	15,16,17	1.22	1 (6%)	19,22,24	0.61	0

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
1	PTR	A	527	1,3	-	0/10/11/13	0/1/1/1
1	PTR	B	527	1,3	-	0/10/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	PTR	OH-CZ	-4.54	1.30	1.40
1	B	527	PTR	OH-CZ	-4.26	1.31	1.40

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	527	PTR	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 4 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	$\#\|Z\| > 2$
2	KS1	A	601	-	25,28,28	0.87	1 (4%)	25,41,41	1.92	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	KS1	B	601	-	25,28,28	0.88	1 (4%)	25,41,41	1.94	6 (24%)

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	KS1	A	601	-	-	2/4/15/15	0/5/5/5
2	KS1	B	601	-	-	2/4/15/15	0/5/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	KS1	CAS-CAT	-2.26	1.37	1.43
2	B	601	KS1	CAS-CAT	-2.24	1.37	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	601	KS1	CAP-CAE-NAM	-4.91	121.00	125.55
2	B	601	KS1	CAP-CAE-NAM	-4.80	121.11	125.55
2	B	601	KS1	N3-C2-N1	-4.19	122.14	128.68
2	A	601	KS1	N3-C2-N1	-4.10	122.27	128.68
2	B	601	KS1	CAF-CAP-CAE	3.02	120.46	116.24
2	A	601	KS1	CAF-CAP-CAE	2.89	120.28	116.24
2	B	601	KS1	CAP-CAF-CAS	-2.36	117.45	121.53
2	B	601	KS1	CAI-CAW-NAX	-2.34	110.37	113.35
2	A	601	KS1	CAP-CAF-CAS	-2.23	117.67	121.53
2	A	601	KS1	CAR-NAN-NAX	2.13	106.88	105.17
2	B	601	KS1	CAR-NAN-NAX	2.01	106.78	105.17

There are no chirality outliers.

All (4) torsion outliers are listed below:

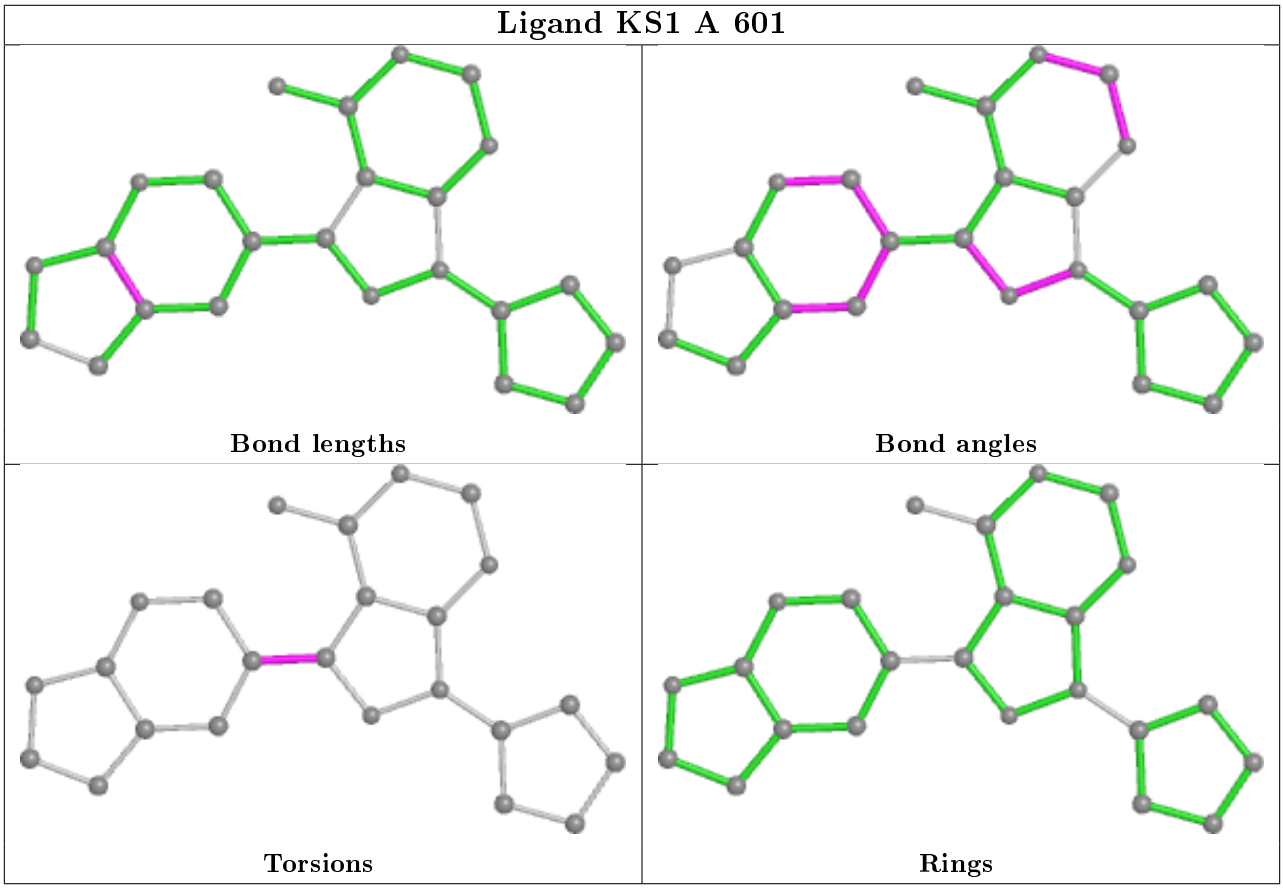
Mol	Chain	Res	Type	Atoms
2	A	601	KS1	CAF-CAP-CAR-NAN
2	A	601	KS1	CAE-CAP-CAR-NAN
2	B	601	KS1	CAF-CAP-CAR-NAN
2	B	601	KS1	CAE-CAP-CAR-NAN

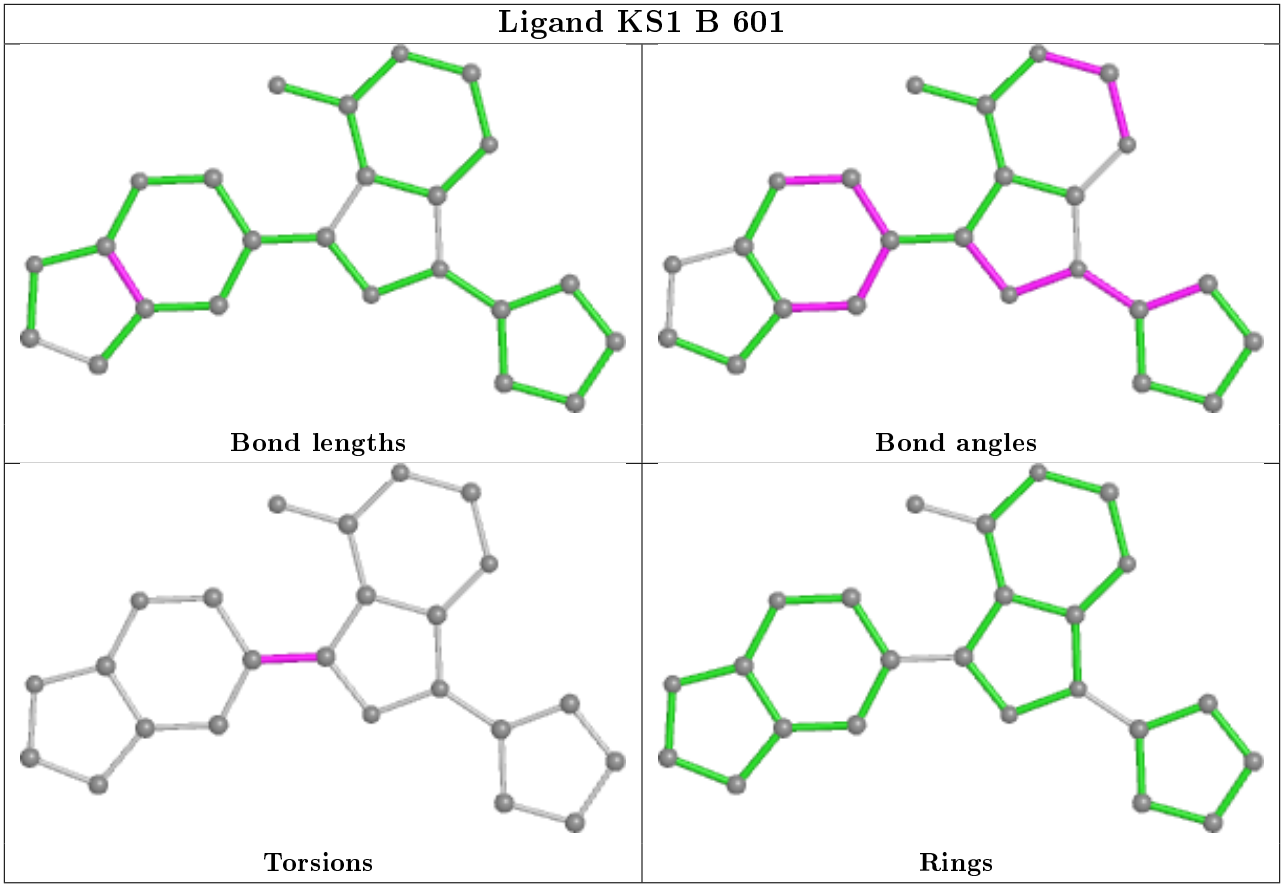
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	KS1	1	0
2	B	601	KS1	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.





5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	432/454 (95%)	0.18	11 (2%)	57	29	67, 104, 144, 177	1 (0%)
1	B	426/454 (93%)	0.34	10 (2%)	60	31	63, 109, 154, 187	1 (0%)
All	All	858/908 (94%)	0.26	21 (2%)	59	30	63, 106, 151, 187	2 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	301	SER	3.1
1	A	301	SER	2.9
1	B	213	PHE	2.8
1	B	408	ALA	2.6
1	A	212	GLY	2.6
1	B	439	PHE	2.5
1	A	300	GLY	2.5
1	A	242	LEU	2.4
1	A	211	GLY	2.3
1	B	305	GLU	2.3
1	A	475	LEU	2.2
1	B	110	MET	2.2
1	B	409	ARG	2.2
1	A	199	THR	2.2
1	B	243	SER	2.2
1	A	302	MET	2.1
1	A	229	ASP	2.1
1	B	233	LYS	2.1
1	A	126	ALA	2.1
1	A	439	PHE	2.0
1	B	230	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	PTR	A	527	16/17	0.96	0.20	67,88,105,109	0
1	PTR	B	527	16/17	0.96	0.19	67,90,104,105	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

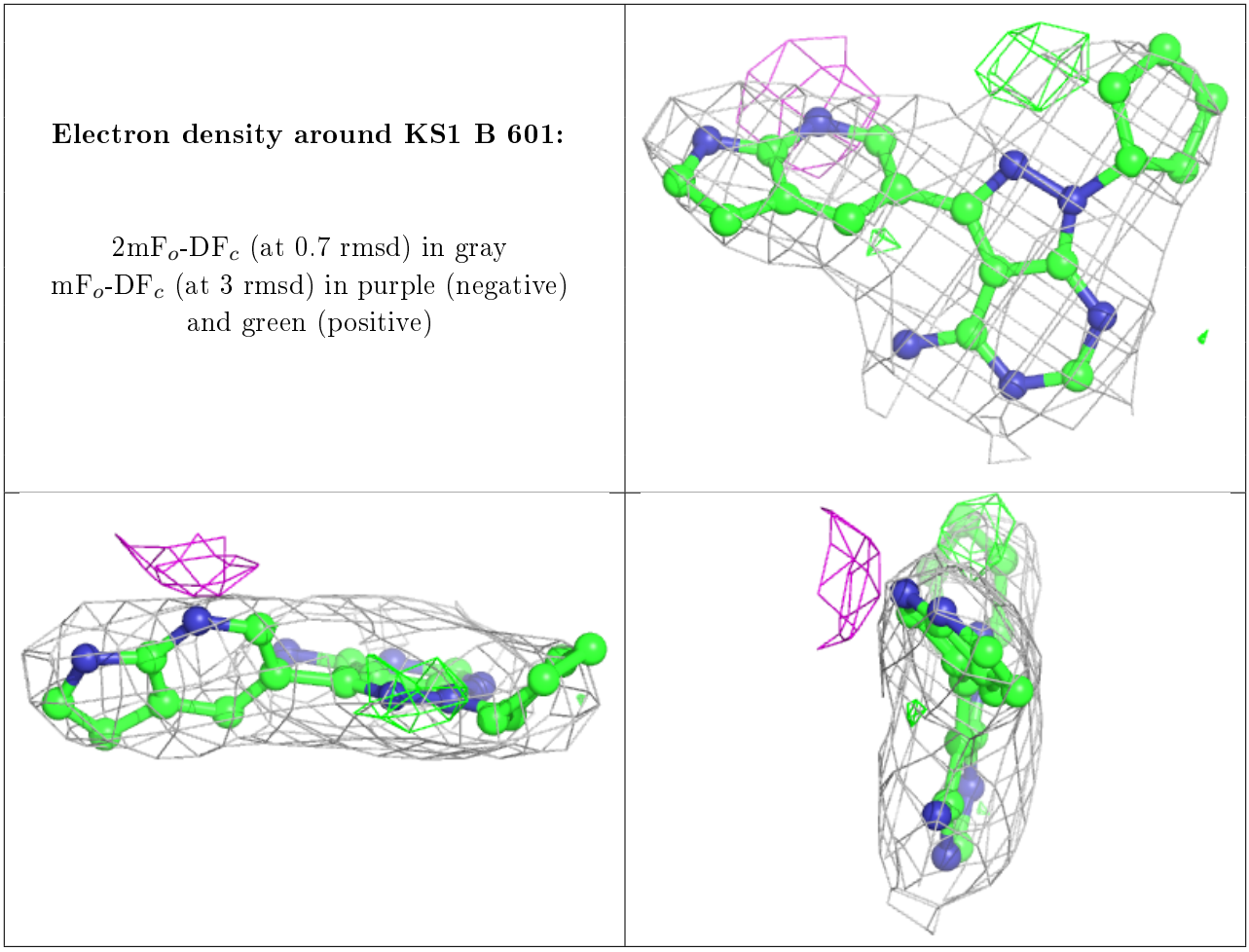
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	CA	A	602	1/1	0.60	0.32	99,99,99,99	0
3	CA	B	602	1/1	0.66	0.34	90,90,90,90	0
4	CL	B	603	1/1	0.84	0.88	119,119,119,119	0
4	CL	A	603	1/1	0.85	0.68	122,122,122,122	0
2	KS1	B	601	24/24	0.94	0.25	61,88,109,113	0
2	KS1	A	601	24/24	0.96	0.27	62,82,104,111	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.

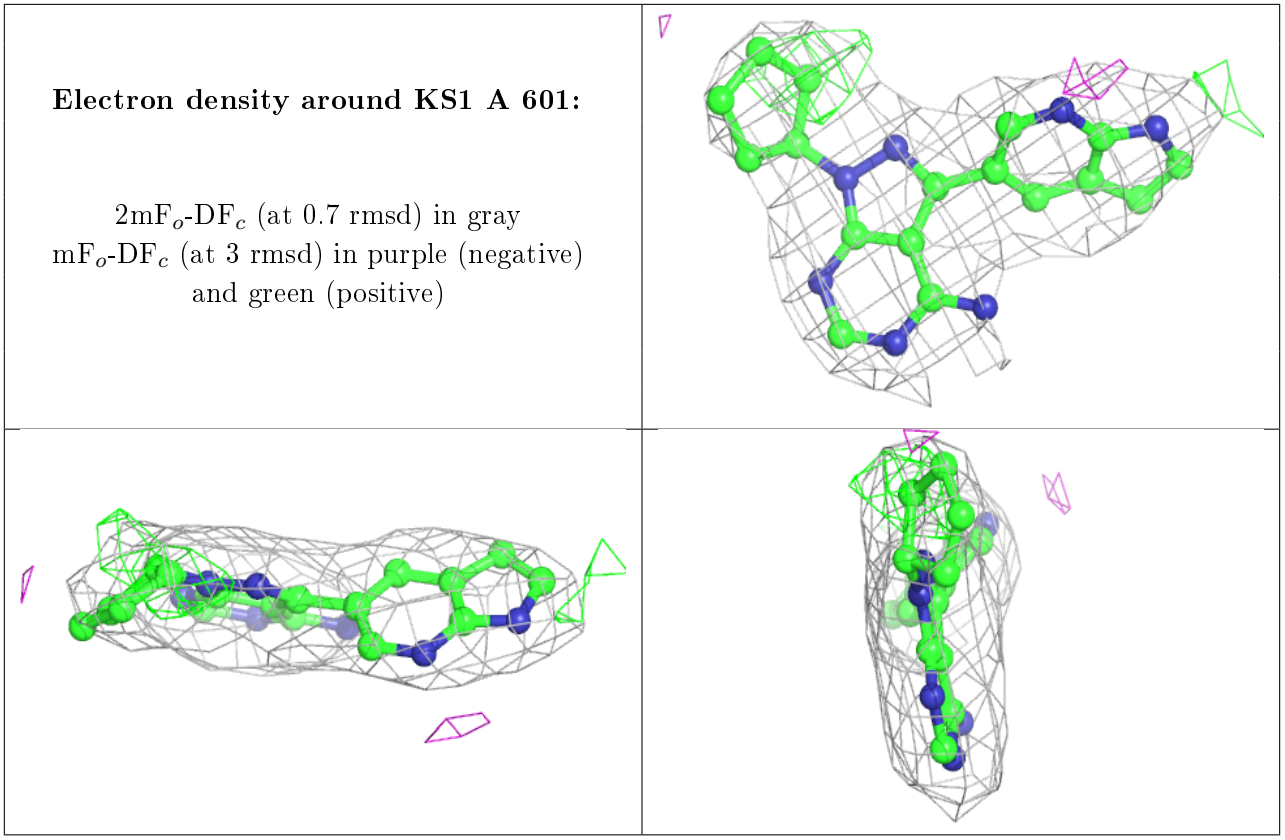
Electron density around KS1 B 601:

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



Electron density around KS1 A 601:

$2mF_o$-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.