



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 12:15 PM UTC

PDB ID : 3VS3 / pdb\_00003vs3  
Title : Crystal structure of HCK complexed with a pyrrolo-pyrimidine inhibitor 7-[trans-4-(4-methylpiperazin-1-yl)cyclohexyl]-5-(4-phenoxyphenyl)-7H-pyrrolo[2,3-d]pyrimidin-4-amine  
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Deposited on : 2012-04-21  
Resolution : 2.17 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

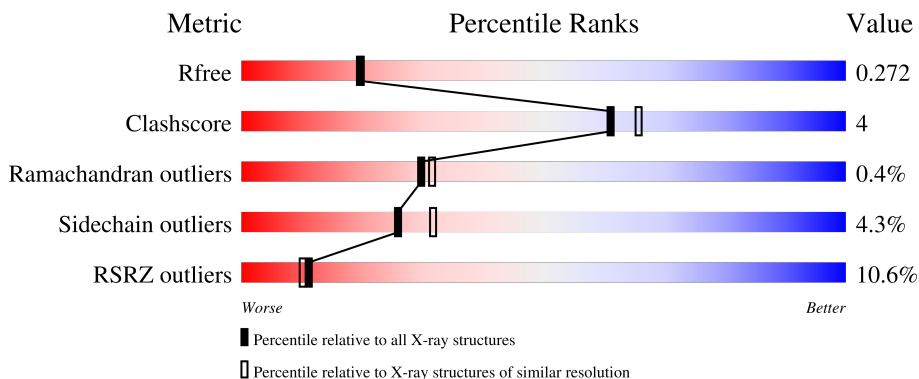
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.17 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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  $\geq 3$ , 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	454	
1	B	454	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7434 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
			Total	C	N	O	P	S			
1	A	435	Total	C	N	O	P	S	0	0	0
			3518	2250	592	655	1	20			
1	B	432	Total	C	N	O	P	S	0	0	0
			3504	2243	589	651	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 7-[trans-4-(4-methylpiperazin-1-yl)cyclohexyl]-5-(4-phenoxyphenyl)-7H-pyrrol o[2,3-d]pyrimidin-4-amine (CCD ID: VSE) (formula: C<sub>29</sub>H<sub>34</sub>N<sub>6</sub>O).



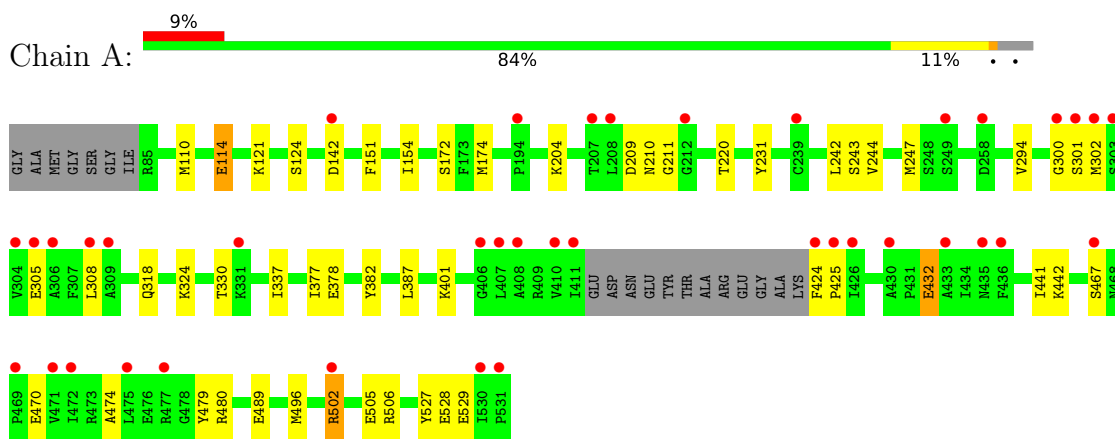
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	B	172	Total 172	O 172	0	0

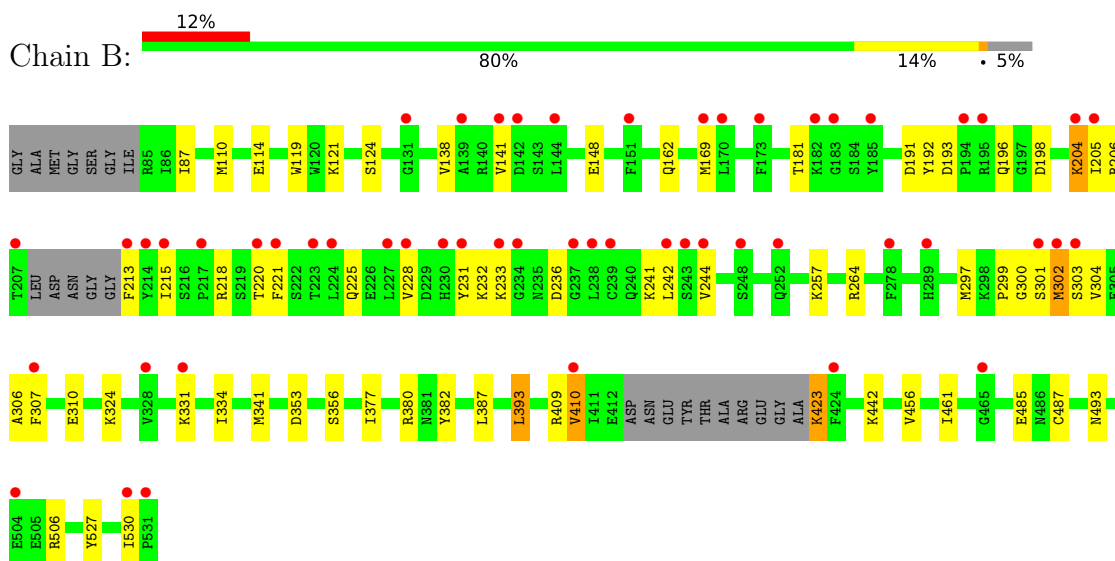
### 3 Residue-property plots

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



- Molecule 1: Tyrosine-protein kinase HCK



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.45Å 73.59Å 180.71Å 90.00° 96.30° 90.00°	Depositor
Resolution (Å)	31.46 – 2.17 31.46 – 2.17	Depositor EDS
% Data completeness (in resolution range)	98.8 (31.46-2.17) 98.7 (31.46-2.17)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.38 (at 2.18Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.226 , 0.279 0.221 , 0.272	Depositor DCC
$R_{free}$ test set	3357 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.8	Xtrriage
Anisotropy	0.272	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 52.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7434	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.75% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PTR, CL, CA, VSE

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	0.29	0/3585	0.71	0/4839
1	B	0.30	0/3570	0.70	1/4816 (0.0%)
All	All	0.30	0/7155	0.71	1/9655 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	215	ILE	N-CA-C	-5.71	106.90	111.81

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	3518	0	3490	28	0
1	B	3504	0	3481	30	0
2	A	36	0	34	2	0
2	B	36	0	34	0	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	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	164	0	0	2	0
5	B	172	0	0	2	0
All	All	7434	0	7039	59	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 (59) 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:210:ASN:H	1:A:211:GLY:HA3	1.38	0.86
1:A:110:MET:HG2	1:A:124:SER:HA	1.76	0.68
1:B:191:ASP:OD1	1:B:192:TYR:N	2.30	0.65
1:B:193:ASP:HB3	1:B:196:GLN:HB2	1.78	0.65
1:B:257:LYS:NZ	5:B:852:HOH:O	2.34	0.60
1:A:301:SER:N	1:A:302:MET:HA	2.16	0.60
1:A:300:GLY:HA3	1:A:301:SER:HB3	1.84	0.59
1:A:377:ILE:HG23	1:A:382:TYR:HB3	1.83	0.59
1:B:181:THR:OG1	1:B:204:LYS:NZ	2.35	0.59
1:B:114:GLU:HG2	1:B:121:LYS:HB3	1.85	0.58
1:B:456:VAL:HG11	1:B:487:CYS:HB2	1.87	0.56
1:A:301:SER:O	1:A:301:SER:OG	2.20	0.55
1:A:528:GLU:OE2	5:A:832:HOH:O	2.18	0.55
1:A:210:ASN:N	1:A:211:GLY:HA3	2.16	0.53
1:B:423:LYS:HZ3	1:B:423:LYS:HB3	1.74	0.53
1:B:310:GLU:OE2	1:B:409:ARG:NH2	2.41	0.53
1:B:213:PHE:N	1:B:221:PHE:O	2.42	0.53
1:B:110:MET:HB3	1:B:124:SER:HA	1.90	0.52
1:A:318:GLN:OE1	1:A:324:LYS:NZ	2.37	0.51
1:B:307:PHE:CE2	1:B:334:ILE:HG21	2.46	0.51
1:B:307:PHE:HA	1:B:410:VAL:HG21	1.93	0.50
1:A:474:ALA:HB1	1:A:479:TYR:HB3	1.94	0.49
1:A:151:PHE:HB3	1:A:154:ILE:HG13	1.94	0.49
1:A:489:GLU:OE2	1:B:206:ARG:NH2	2.45	0.49
1:B:299:PRO:O	1:B:301:SER:N	2.47	0.48
1:A:480:ARG:HG3	1:A:496:MET:HE1	1.94	0.48
1:A:231:TYR:HB2	1:A:242:LEU:HD22	1.96	0.48
1:A:308:LEU:HD21	1:A:330:THR:HG22	1.95	0.48
1:A:467:SER:H	1:A:470:GLU:HB3	1.79	0.47
1:B:377:ILE:HG23	1:B:382:TYR:HB3	1.97	0.47
1:A:300:GLY:HA3	1:A:301:SER:CB	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:PHE:CD1	1:A:174:MET:HB2	2.51	0.46
1:A:294:VAL:HG22	1:A:337:ILE:HG13	1.98	0.45
1:B:380:ARG:NH1	5:B:717:HOH:O	2.29	0.45
1:B:303:SER:HB2	1:B:306:ALA:HB3	1.99	0.45
1:B:353:ASP:O	1:B:356:SER:OG	2.34	0.45
1:B:110:MET:HE3	1:B:138:VAL:HG11	1.98	0.44
1:B:442:LYS:NZ	1:B:506:ARG:O	2.36	0.44
1:A:401:LYS:NZ	5:A:704:HOH:O	2.50	0.44
1:B:232:LYS:HA	1:B:242:LEU:HB2	1.98	0.44
2:A:601:VSE:H17	2:A:601:VSE:H36	1.64	0.43
1:B:218:ARG:NH1	1:B:236:ASP:OD2	2.52	0.43
1:A:502:ARG:H	1:A:502:ARG:HD2	1.84	0.43
1:B:297:MET:HE2	1:B:302:MET:HE3	2.02	0.42
1:A:114:GLU:HB2	1:A:121:LYS:HB3	2.02	0.42
1:B:119:TRP:CD1	1:B:257:LYS:HG3	2.54	0.42
1:A:172:SER:HA	1:A:244:VAL:O	2.20	0.42
1:B:264:ARG:NH2	1:B:331:LYS:O	2.48	0.42
1:B:231:TYR:CE1	1:B:236:ASP:HB3	2.55	0.42
1:A:442:LYS:NZ	1:A:506:ARG:O	2.38	0.41
1:B:169:MET:HE3	1:B:169:MET:HB2	1.95	0.41
1:B:341:MET:HG3	1:B:393:LEU:HD23	2.02	0.41
1:B:257:LYS:HD2	1:B:257:LYS:H	1.85	0.41
1:A:243:SER:OG	1:A:244:VAL:N	2.53	0.41
1:A:378:GLU:HG3	1:A:441:ILE:HG12	2.03	0.41
1:A:432:GLU:CD	1:A:432:GLU:H	2.28	0.41
1:B:225:GLN:HA	1:B:228:VAL:HG22	2.03	0.41
2:A:601:VSE:H1	2:A:601:VSE:CAP	2.34	0.40
1:A:502:ARG:HD3	1:A:505:GLU:HB2	2.04	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	430/454 (95%)	415 (96%)	14 (3%)	1 (0%)	43	49
1	B	425/454 (94%)	409 (96%)	14 (3%)	2 (0%)	24	25
All	All	855/908 (94%)	824 (96%)	28 (3%)	3 (0%)	30	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	300	GLY
1	B	485	GLU
1	A	425	PRO

### 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	381/393 (97%)	369 (97%)	12 (3%)	35	45
1	B	380/393 (97%)	359 (94%)	21 (6%)	19	22
All	All	761/786 (97%)	728 (96%)	33 (4%)	26	32

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	GLU
1	A	142	ASP
1	A	204	LYS
1	A	209	ASP
1	A	220	THR
1	A	247	MET
1	A	305	GLU
1	A	387	LEU
1	A	424	PHE
1	A	432	GLU
1	A	502	ARG
1	A	529	GLU
1	B	87	ILE

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Mol	Chain	Res	Type
1	B	141	VAL
1	B	148	GLU
1	B	162	GLN
1	B	198	ASP
1	B	204	LYS
1	B	205	ILE
1	B	220	THR
1	B	233	LYS
1	B	241	LYS
1	B	244	VAL
1	B	302	MET
1	B	304	VAL
1	B	324	LYS
1	B	387	LEU
1	B	393	LEU
1	B	410	VAL
1	B	423	LYS
1	B	461	ILE
1	B	493	ASN
1	B	530	ILE

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	230	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](#)

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	B	527	3,1	15,16,17	1.21	1 (6%)	17,22,24	0.50	0
1	PTR	A	527	3,1	15,16,17	1.32	1 (6%)	17,22,24	0.53	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	B	527	3,1	-	1/10/11/13	0/1/1/1
1	PTR	A	527	3,1	-	1/10/11/13	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	-4.44	1.30	1.40
1	B	527	PTR	OH-CZ	-4.38	1.30	1.40

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	527	PTR	C-CA-CB-CG
1	B	527	PTR	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	VSE	B	601	-	41,41,41	0.92	3 (7%)	55,58,58	2.63	16 (29%)
2	VSE	A	601	-	41,41,41	0.90	3 (7%)	55,58,58	2.62	14 (25%)

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	VSE	B	601	-	-	6/16/36/36	0/6/6/6
2	VSE	A	601	-	-	6/16/36/36	0/6/6/6

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	VSE	CAH-NAG	-2.89	1.33	1.38
2	B	601	VSE	C5-CAI	-2.77	1.39	1.46
2	A	601	VSE	C5-CAI	-2.71	1.39	1.46
2	A	601	VSE	CAH-NAG	-2.62	1.33	1.38
2	B	601	VSE	C5-C6	-2.29	1.39	1.42
2	A	601	VSE	C5-C6	-2.27	1.39	1.42

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	VSE	CBB-NAW-CAX	9.26	126.78	109.13
2	A	601	VSE	CBB-NAW-CAX	9.13	126.53	109.13
2	A	601	VSE	CBA-NAZ-CAY	7.51	121.50	109.54
2	A	601	VSE	C5-C4-N3	-7.45	119.07	126.97
2	B	601	VSE	C5-C4-N3	-7.41	119.11	126.97
2	B	601	VSE	CBA-NAZ-CAY	7.19	120.98	109.54
2	B	601	VSE	CBC-NAZ-CBA	5.27	120.67	110.63
2	A	601	VSE	CBC-NAZ-CBA	5.02	120.20	110.63
2	A	601	VSE	N1-C2-N3	-4.86	121.23	128.58
2	B	601	VSE	N1-C2-N3	-4.78	121.35	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	VSE	CBC-NAZ-CAY	4.04	118.34	110.63
2	A	601	VSE	CBC-NAZ-CAY	4.02	118.29	110.63
2	A	601	VSE	CAX-CAY-NAZ	-3.96	104.49	110.86
2	B	601	VSE	CAX-CAY-NAZ	-3.95	104.51	110.86
2	B	601	VSE	C6-C5-C4	3.85	118.63	115.74
2	A	601	VSE	C2-N3-C4	3.75	120.99	111.83
2	B	601	VSE	C2-N3-C4	3.63	120.70	111.83
2	A	601	VSE	C6-C5-C4	3.61	118.45	115.74
2	A	601	VSE	CAS-CAT-NAW	-3.23	104.39	112.66
2	B	601	VSE	N3-C4-NAG	3.09	132.42	127.17
2	A	601	VSE	N3-C4-NAG	3.04	132.34	127.17
2	A	601	VSE	CAY-CAX-NAW	-3.02	105.28	110.61
2	B	601	VSE	CAS-CAT-NAW	-2.69	105.76	112.66
2	B	601	VSE	CAY-CAX-NAW	-2.43	106.33	110.61
2	B	601	VSE	CBB-NAW-CAT	2.35	118.76	112.79
2	B	601	VSE	CAV-CAQ-NAG	2.35	114.00	111.40
2	B	601	VSE	C4-NAG-CAQ	2.33	131.10	125.82
2	B	601	VSE	CAJ-CAI-CAH	-2.29	119.92	124.37
2	A	601	VSE	CAV-CAQ-NAG	2.26	113.90	111.40
2	A	601	VSE	CBB-NAW-CAT	2.01	117.91	112.79

There are no chirality outliers.

All (12) torsion outliers are listed below:

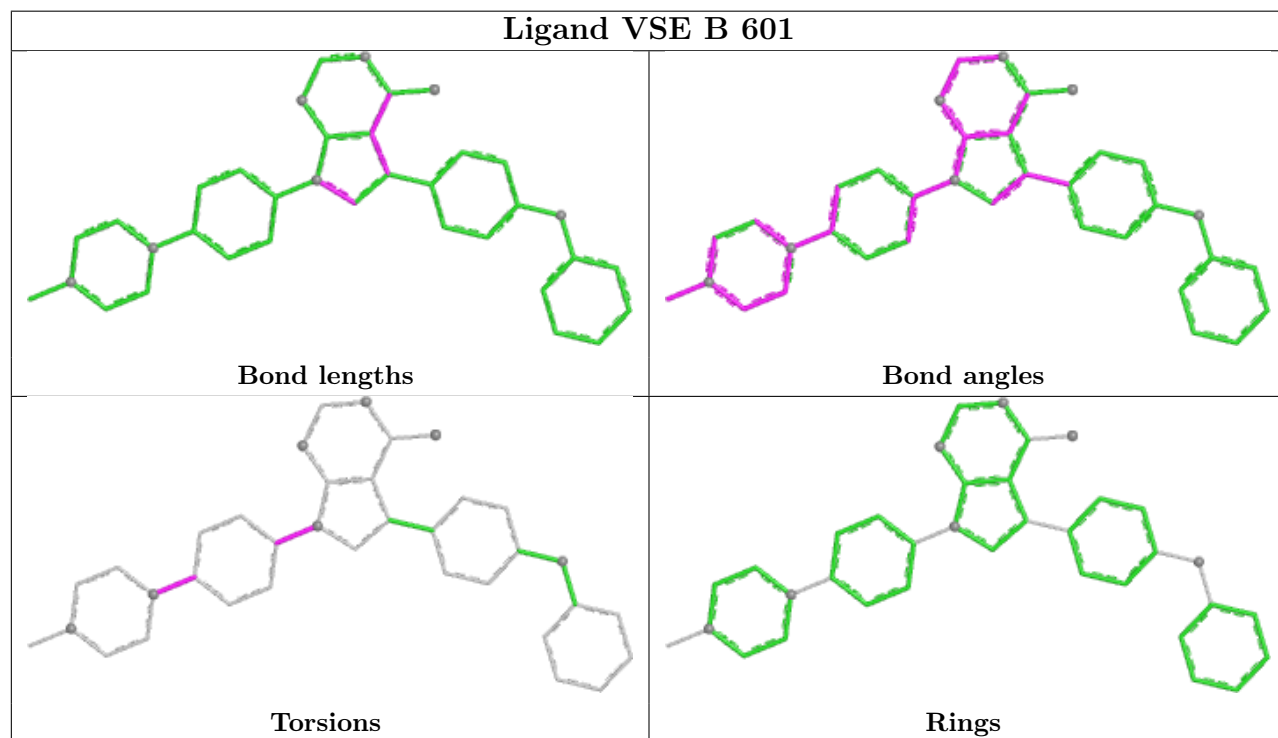
Mol	Chain	Res	Type	Atoms
2	A	601	VSE	CAV-CAQ-NAG-CAH
2	A	601	VSE	CAV-CAQ-NAG-C4
2	A	601	VSE	CAS-CAT-NAW-CAX
2	B	601	VSE	CAV-CAQ-NAG-CAH
2	B	601	VSE	CAV-CAQ-NAG-C4
2	B	601	VSE	CAU-CAT-NAW-CBB
2	A	601	VSE	CAU-CAT-NAW-CAX
2	B	601	VSE	CAU-CAT-NAW-CAX
2	B	601	VSE	CAS-CAT-NAW-CAX
2	A	601	VSE	CAU-CAT-NAW-CBB
2	B	601	VSE	CAS-CAT-NAW-CBB
2	A	601	VSE	CAR-CAQ-NAG-CAH

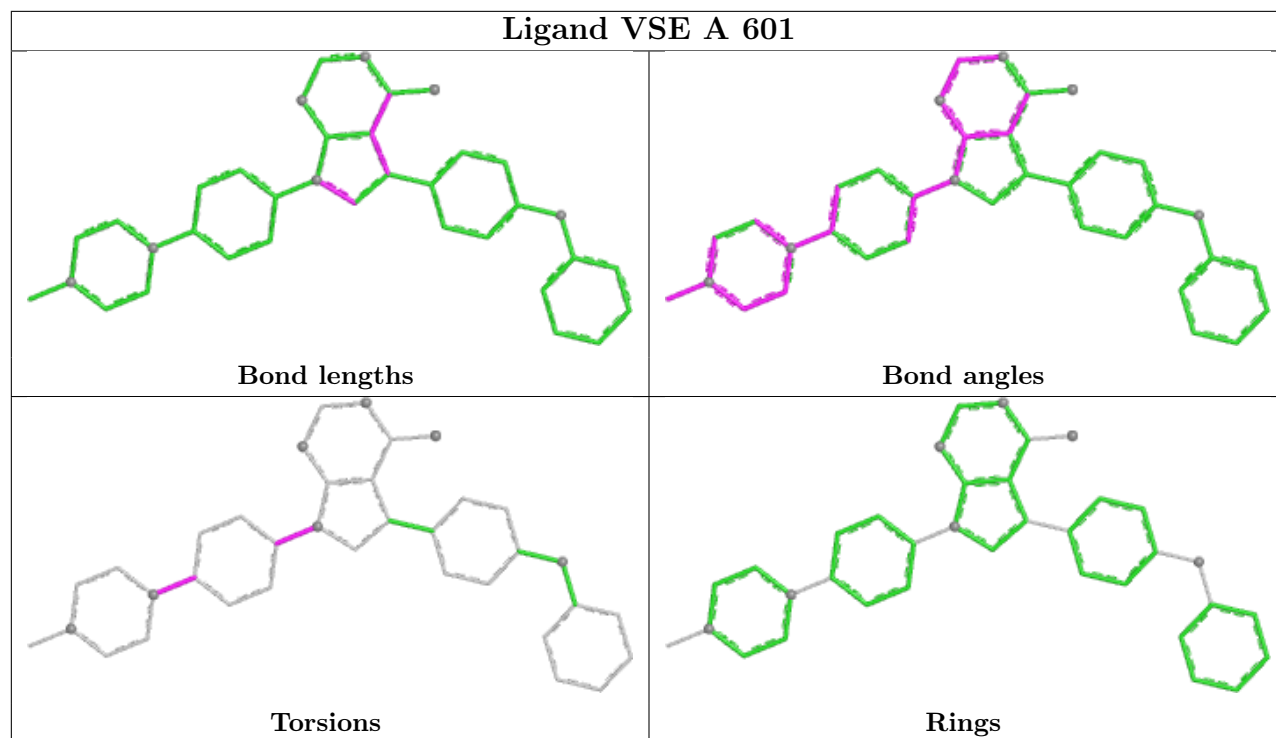
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	VSE	2	0

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





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	434/454 (95%)	0.66	39 (8%) 15 14	28, 50, 85, 102	1 (0%)
1	B	431/454 (94%)	0.78	53 (12%) 8 7	25, 49, 88, 114	0
All	All	865/908 (95%)	0.72	92 (10%) 11 10	25, 50, 88, 114	1 (0%)

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	213	PHE	6.7
1	B	207	THR	5.4
1	B	530	ILE	5.4
1	B	234	GLY	5.0
1	A	424	PHE	5.0
1	B	531	PRO	4.6
1	B	214	TYR	4.4
1	B	231	TYR	4.4
1	B	302	MET	4.1
1	B	194	PRO	4.0
1	A	467	SER	4.0
1	A	302	MET	3.9
1	B	215	ILE	3.7
1	B	303	SER	3.6
1	A	406	GLY	3.6
1	B	301	SER	3.5
1	B	228	VAL	3.5
1	B	151	PHE	3.4
1	A	426	ILE	3.3
1	A	309	ALA	3.2
1	A	207	THR	3.2
1	A	304	VAL	3.2
1	B	239	CYS	3.2
1	B	139	ALA	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	238	LEU	3.1
1	A	408	ALA	3.1
1	B	244	VAL	3.1
1	B	223	THR	3.0
1	A	258	ASP	3.0
1	B	221	PHE	3.0
1	A	477	ARG	3.0
1	B	242	LEU	3.0
1	A	411	ILE	2.9
1	A	410	VAL	2.9
1	B	169	MET	2.9
1	A	471	VAL	2.8
1	A	436	PHE	2.8
1	B	331	LYS	2.8
1	B	195	ARG	2.8
1	B	183	GLY	2.8
1	A	331	LYS	2.8
1	A	425	PRO	2.8
1	B	410	VAL	2.7
1	B	144	LEU	2.7
1	A	306	ALA	2.7
1	B	217	PRO	2.6
1	A	208	LEU	2.6
1	A	407	LEU	2.6
1	B	233	LYS	2.6
1	A	475	LEU	2.6
1	B	141	VAL	2.5
1	B	248	SER	2.5
1	B	224	LEU	2.5
1	A	300	GLY	2.5
1	A	305	GLU	2.4
1	A	301	SER	2.4
1	A	212	GLY	2.4
1	A	239	CYS	2.4
1	B	220	THR	2.4
1	A	469	PRO	2.4
1	B	182	LYS	2.4
1	B	142	ASP	2.4
1	A	303	SER	2.4
1	B	504	GLU	2.3
1	A	502	ARG	2.3
1	B	205	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	194	PRO	2.3
1	B	252	GLN	2.3
1	B	185	TYR	2.3
1	B	465	GLY	2.3
1	B	230	HIS	2.3
1	B	289	HIS	2.3
1	A	530	ILE	2.2
1	A	433	ALA	2.2
1	B	243	SER	2.2
1	B	424	PHE	2.2
1	A	430	ALA	2.2
1	A	308	LEU	2.1
1	A	249	SER	2.1
1	A	531	PRO	2.1
1	B	173	PHE	2.1
1	B	307	PHE	2.1
1	B	328	VAL	2.1
1	B	278	PHE	2.1
1	B	204	LYS	2.1
1	B	131	GLY	2.1
1	A	435	ASN	2.0
1	A	142	ASP	2.0
1	B	237	GLY	2.0
1	A	472	ILE	2.0
1	B	170	LEU	2.0
1	B	227	LEU	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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	PTR	B	527	16/17	0.95	0.10	45,58,64,67	0
1	PTR	A	527	16/17	0.96	0.09	24,36,44,46	0

## 6.3 Carbohydrates [i](#)

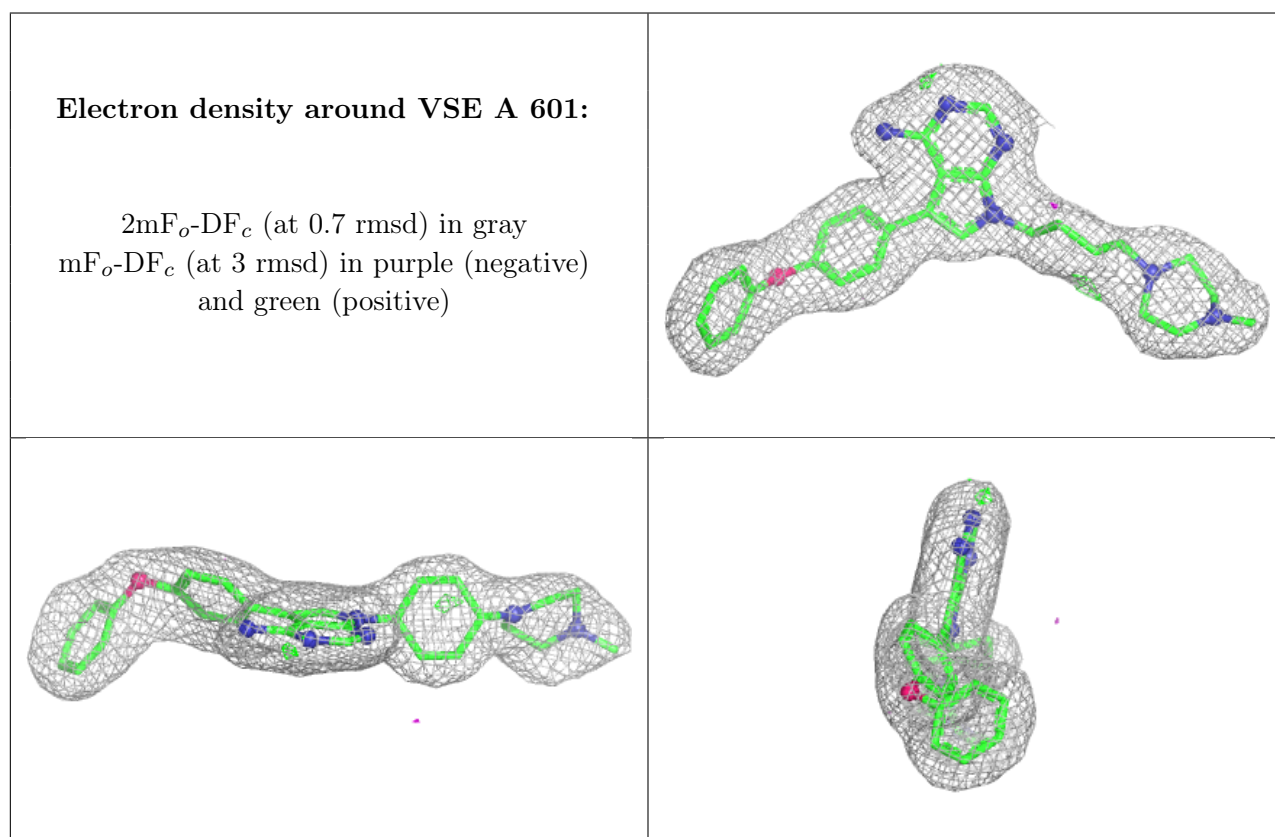
There are no oligosaccharides in this entry.

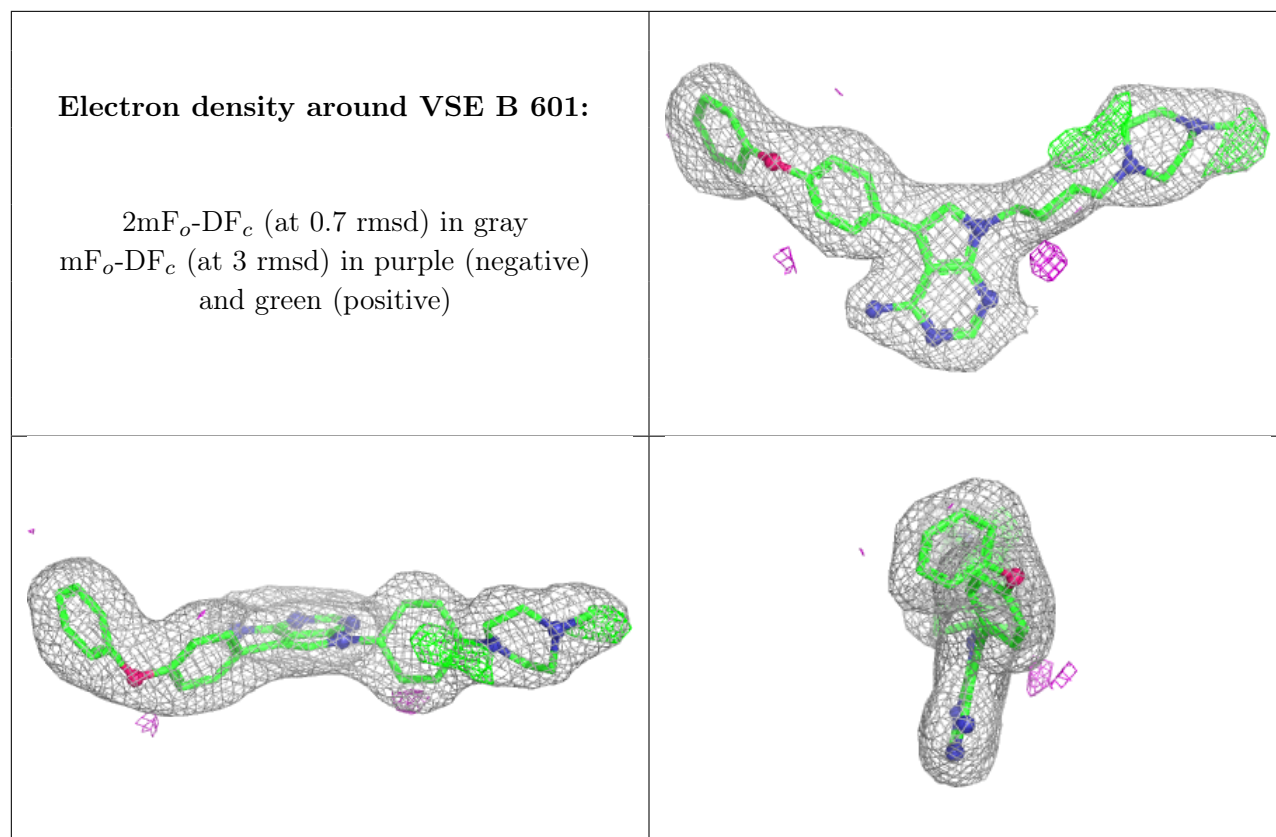
## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	CA	B	602	1/1	0.68	0.24	74,74,74,74	0
3	CA	A	602	1/1	0.85	0.19	52,52,52,52	0
2	VSE	A	601	36/36	0.94	0.09	26,37,56,63	0
2	VSE	B	601	36/36	0.94	0.09	23,30,55,60	0
4	CL	A	603	1/1	0.96	0.08	53,53,53,53	0
4	CL	B	603	1/1	0.96	0.08	60,60,60,60	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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.