



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 01:29 pm BST

PDB ID : 3VS3
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

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

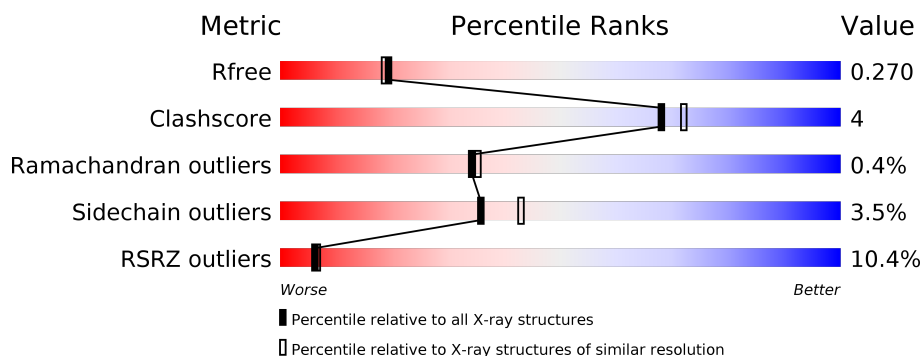
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.17 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}	130704	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (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 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	454	<div> <div>11%</div> <div>86%</div> <div>9%</div> <div>• •</div> </div>
1	B	454	<div> <div>9%</div> <div>82%</div> <div>12%</div> <div>• 5%</div> </div>

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.

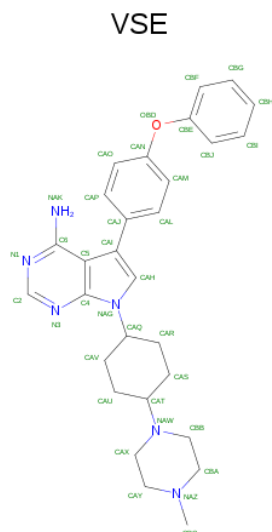
- Molecule 1 is a protein called Tyrosine-protein kinase HCK.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
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-pyrrolo[2,3-d]pyrimidin-4-amine (three-letter code: VSE) (formula: C₂₉H₃₄N₆O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 36	C 29	N 6	O 1	0	0
2	B	1	Total 36	C 29	N 6	O 1	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	164	Total O 164 164	0	0

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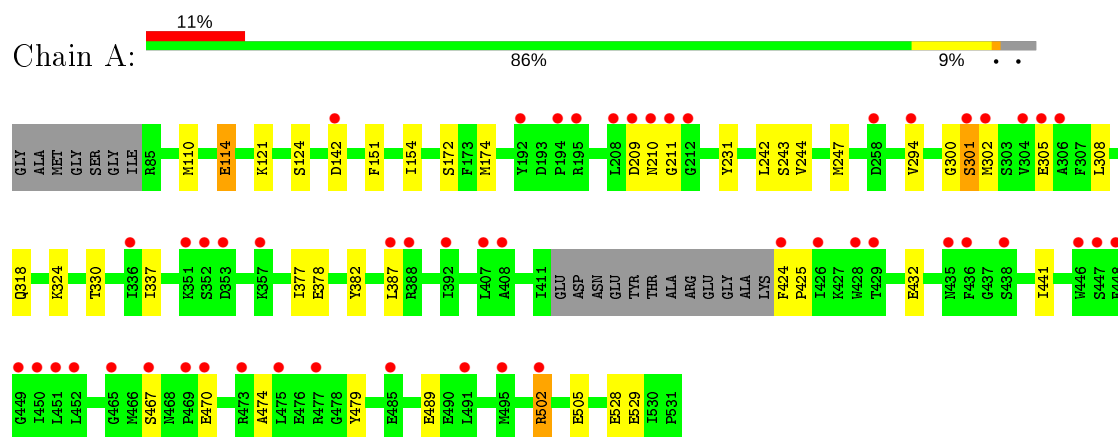
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	172	Total 172	O 172	0	0

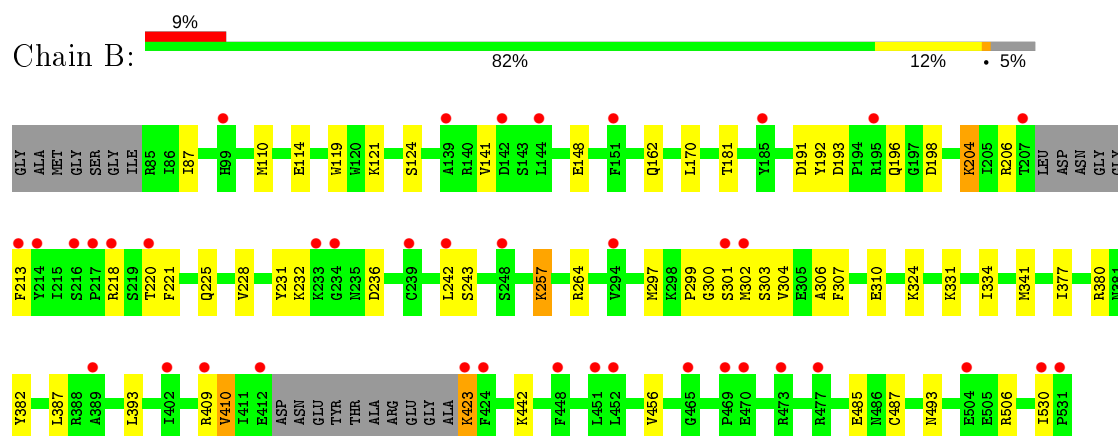
3 Residue-property plots [i](#)

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: 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, α , β , γ	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) 98.8 (31.46-2.17)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.18Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.226 , 0.279 0.220 , 0.270	Depositor DCC
R_{free} test set	3357 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7434	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage'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.*

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: CA, CL, VSE, PTR

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.24	0/3585	0.42	0/4839
1	B	0.25	0/3570	0.43	0/4816
All	All	0.24	0/7155	0.43	0/9655

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	3518	0	3490	24	0
1	B	3504	0	3481	28	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
5	A	164	0	0	1	0
5	B	172	0	0	2	0
All	All	7434	0	7039	53	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 (53) 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: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:257:LYS:NZ	5:B:852:HOH:O	2.34	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: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:B:423:LYS:HZ2	1:B:423:LYS:HB3	1.77	0.49
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: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:B:170:LEU:O	1:B:243:SER:OG	2.31	0.47
1:A:300:GLY:HA3	1:A:301:SER:CB	2.45	0.46
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:442:LYS:NZ	1:B:506:ARG:O	2.36	0.44
1:B:232:LYS:HA	1:B:242:LEU:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:601:VSE:H36	2:A:601:VSE:H17	1.64	0.43
1:B:218:ARG:NH1	1:B:236:ASP:OD2	2.52	0.43
1:A:502:ARG:HD2	1:A:502:ARG:H	1.84	0.43
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:B:341:MET:HG3	1:B:393:LEU:HD23	2.02	0.41
1:B:257:LYS:H	1:B:257:LYS:HD2	1.85	0.41
1:A:378:GLU:HG3	1:A:441:ILE:HG12	2.03	0.41
1:A:243:SER:OG	1:A:244:VAL:N	2.53	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
1:B:297:MET:HE3	1:B:297:MET:HB3	1.98	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	430/454 (95%)	415 (96%)	14 (3%)	1 (0%)	47	52
1	B	425/454 (94%)	409 (96%)	14 (3%)	2 (0%)	29	28
All	All	855/908 (94%)	824 (96%)	28 (3%)	3 (0%)	34	35

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	300	GLY
1	B	485	GLU

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Mol	Chain	Res	Type
1	A	425	PRO

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	381/393 (97%)	370 (97%)	11 (3%)	42	51
1	B	380/393 (97%)	364 (96%)	16 (4%)	30	35
All	All	761/786 (97%)	734 (96%)	27 (4%)	36	43

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	GLU
1	A	142	ASP
1	A	209	ASP
1	A	247	MET
1	A	301	SER
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
1	B	141	VAL
1	B	148	GLU
1	B	162	GLN
1	B	198	ASP
1	B	204	LYS
1	B	220	THR
1	B	257	LYS
1	B	302	MET
1	B	304	VAL
1	B	324	LYS

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Mol	Chain	Res	Type
1	B	387	LEU
1	B	410	VAL
1	B	423	LYS
1	B	493	ASN
1	B	530	ILE

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	B	527	1,3	15,16,17	1.21	1 (6%)	19,22,24	0.80	1 (5%)
1	PTR	A	527	1,3	15,16,17	1.32	1 (6%)	19,22,24	0.70	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	1,3	-	1/10/11/13	0/1/1/1
1	PTR	A	527	1,3	-	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	-4.39	1.30	1.40
1	B	527	PTR	OH-CZ	-4.33	1.30	1.40

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	527	PTR	CB-CA-C	2.46	116.08	111.47

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	527	PTR	C-CA-CB-CG
1	A	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 carbohydrates 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	-	39,41,41	0.80	1 (2%)	45,58,58	2.85	11 (24%)
2	VSE	A	601	-	39,41,41	0.75	1 (2%)	45,58,58	2.82	10 (22%)

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	-	-	4/12/36/36	0/6/6/6
2	VSE	A	601	-	-	3/12/36/36	0/6/6/6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	VSE	CAH-NAG	-3.33	1.33	1.38
2	A	601	VSE	CAH-NAG	-3.02	1.33	1.38

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	VSE	CBB-NAW-CAX	9.69	126.78	109.08
2	A	601	VSE	CBB-NAW-CAX	9.55	126.53	109.08
2	A	601	VSE	CBA-NAZ-CAY	8.56	121.50	109.52
2	B	601	VSE	CBA-NAZ-CAY	8.19	120.98	109.52
2	B	601	VSE	CBC-NAZ-CBA	6.69	120.67	110.66
2	A	601	VSE	CBC-NAZ-CBA	6.38	120.20	110.66
2	B	601	VSE	CAH-NAG-CAQ	-6.11	120.07	125.48
2	A	601	VSE	CAX-CAY-NAZ	-5.59	104.49	110.80
2	B	601	VSE	CAX-CAY-NAZ	-5.57	104.51	110.80
2	B	601	VSE	CBC-NAZ-CAY	5.13	118.34	110.66
2	A	601	VSE	CAH-NAG-CAQ	-5.11	120.95	125.48
2	A	601	VSE	CBC-NAZ-CAY	5.10	118.29	110.66
2	A	601	VSE	N3-C2-N1	-4.77	121.23	128.68
2	B	601	VSE	N3-C2-N1	-4.69	121.35	128.68
2	A	601	VSE	CAS-CAT-NAW	-3.13	104.39	112.52
2	B	601	VSE	CAH-CAI-CAJ	-2.87	119.92	125.37
2	A	601	VSE	CAY-CAX-NAW	-2.78	105.28	110.59
2	B	601	VSE	CAS-CAT-NAW	-2.60	105.76	112.52
2	A	601	VSE	CAH-CAI-CAJ	-2.42	120.78	125.37
2	B	601	VSE	CAY-CAX-NAW	-2.23	106.33	110.59
2	B	601	VSE	CBB-NAW-CAT	2.17	118.76	112.64

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	VSE	CAS-CAT-NAW-CAX

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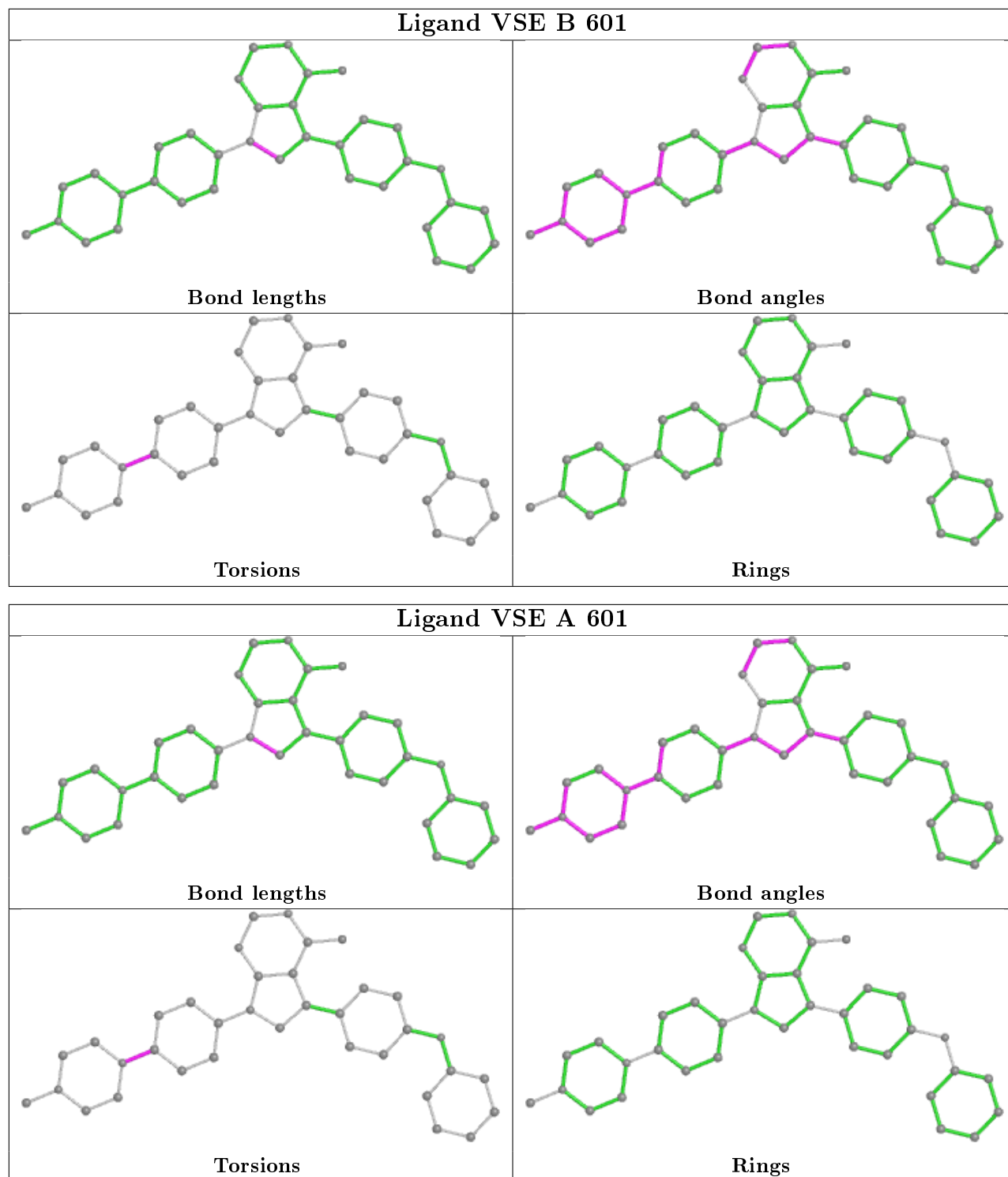
Mol	Chain	Res	Type	Atoms
2	B	601	VSE	CAU-CAT-NAW-CBB
2	A	601	VSE	CAU-CAT-NAW-CAX
2	B	601	VSE	CAU-CAT-NAW-CAX
2	B	601	VSE	CAS-CAT-NAW-CAX
2	A	601	VSE	CAU-CAT-NAW-CBB
2	B	601	VSE	CAS-CAT-NAW-CBB

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 ⓘ

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	434/454 (95%)	0.59	51 (11%) 4 4	28, 50, 85, 102	1 (0%)
1	B	431/454 (94%)	0.58	39 (9%) 9 9	25, 49, 88, 114	0
All	All	865/908 (95%)	0.59	90 (10%) 6 6	25, 50, 88, 114	1 (0%)

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	531	PRO	8.9
1	B	213	PHE	6.9
1	B	301	SER	6.4
1	A	209	ASP	6.2
1	A	301	SER	5.8
1	B	234	GLY	5.7
1	A	436	PHE	5.1
1	B	142	ASP	4.7
1	B	214	TYR	4.6
1	A	465	GLY	4.5
1	A	469	PRO	4.5
1	B	195	ARG	4.3
1	B	302	MET	4.2
1	A	305	GLU	4.2
1	A	473	ARG	4.0
1	B	530	ILE	3.9
1	A	477	ARG	3.8
1	A	353	ASP	3.7
1	A	208	LEU	3.6
1	A	448	PHE	3.5
1	A	435	ASN	3.4
1	A	424	PHE	3.4
1	A	387	LEU	3.4
1	A	302	MET	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	211	GLY	3.2
1	B	452	LEU	3.2
1	A	304	VAL	3.2
1	A	438	SER	3.2
1	A	452	LEU	3.1
1	B	233	LYS	3.1
1	B	424	PHE	3.0
1	A	192	TYR	3.0
1	B	465	GLY	3.0
1	B	139	ALA	2.9
1	B	207	THR	2.9
1	A	451	LEU	2.8
1	B	412	GLU	2.7
1	A	449	GLY	2.7
1	A	426	ILE	2.7
1	A	194	PRO	2.7
1	A	142	ASP	2.7
1	A	195	ARG	2.6
1	A	470	GLU	2.6
1	A	502	ARG	2.6
1	A	408	ALA	2.6
1	B	99	HIS	2.6
1	B	451	LEU	2.6
1	A	495	MET	2.5
1	B	469	PRO	2.5
1	A	212	GLY	2.5
1	A	352	SER	2.5
1	B	218	ARG	2.5
1	B	216	SER	2.4
1	A	258	ASP	2.4
1	B	448	PHE	2.4
1	A	450	ILE	2.3
1	A	467	SER	2.3
1	A	407	LEU	2.3
1	B	185	TYR	2.3
1	A	306	ALA	2.3
1	B	239	CYS	2.3
1	B	294	VAL	2.2
1	A	351	LYS	2.2
1	A	294	VAL	2.2
1	A	357	LYS	2.2
1	B	409	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	423	LYS	2.2
1	B	389	ALA	2.2
1	A	491	LEU	2.1
1	B	151	PHE	2.1
1	B	477	ARG	2.1
1	A	210	ASN	2.1
1	A	428	TRP	2.1
1	B	248	SER	2.1
1	A	336	ILE	2.1
1	B	402	ILE	2.1
1	B	470	GLU	2.1
1	A	475	LEU	2.1
1	B	144	LEU	2.1
1	A	388	ARG	2.1
1	A	446	TRP	2.1
1	B	217	PRO	2.0
1	A	485	GLU	2.0
1	B	242	LEU	2.0
1	A	429	THR	2.0
1	B	220	THR	2.0
1	B	504	GLU	2.0
1	A	447	SER	2.0
1	A	392	ILE	2.0
1	B	473	ARG	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, 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
1	PTR	B	527	16/17	0.96	0.14	45,58,64,67	0
1	PTR	A	527	16/17	0.97	0.12	24,36,44,46	0

6.3 Carbohydrates [i](#)

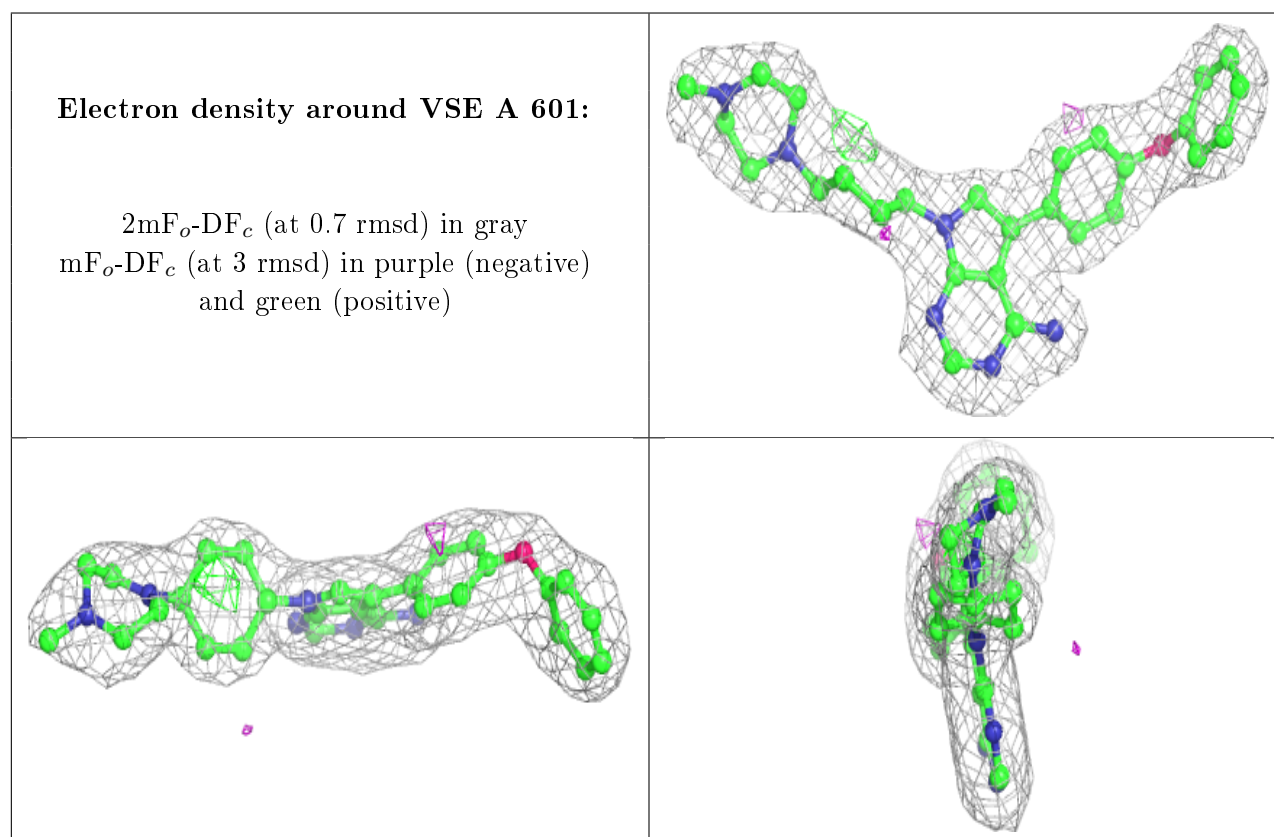
There are no carbohydrates in this entry.

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.

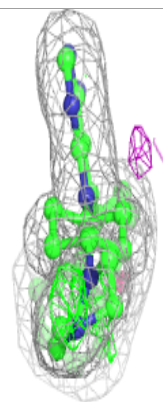
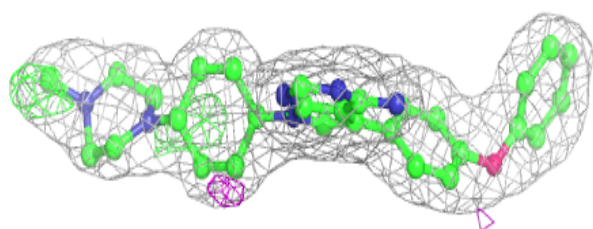
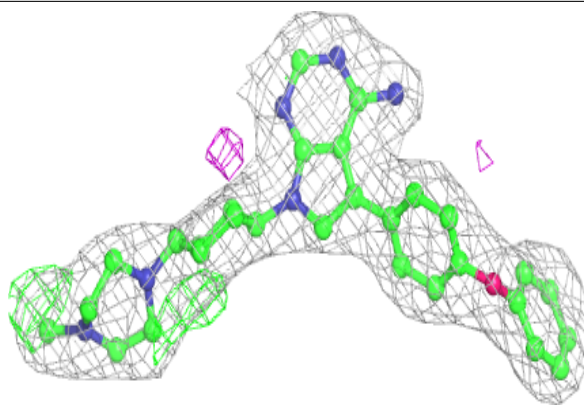
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	CA	B	602	1/1	0.15	0.37	74,74,74,74	0
3	CA	A	602	1/1	0.76	0.30	52,52,52,52	0
2	VSE	A	601	36/36	0.91	0.16	26,37,56,63	0
2	VSE	B	601	36/36	0.94	0.17	23,30,55,60	0
4	CL	A	603	1/1	0.95	0.07	53,53,53,53	0
4	CL	B	603	1/1	0.98	0.08	60,60,60,60	0

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.



Electron density around VSE 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.