



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:00 PM GMT

PDB ID : 3VS5
Title : Crystal structure of HCK complexed with a pyrrolo-pyrimidine inhibitor 7-(1-methylpiperidin-4-yl)-5-(4-phenoxyphenyl)-7H-pyrrolo[2,3-d]pyrimidin-4-amine
Authors : Kuratani, M.; Tomabechi, Y.; Handa, N.; Yokoyama, S.
Deposited on : 2012-04-21
Resolution : 2.85 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

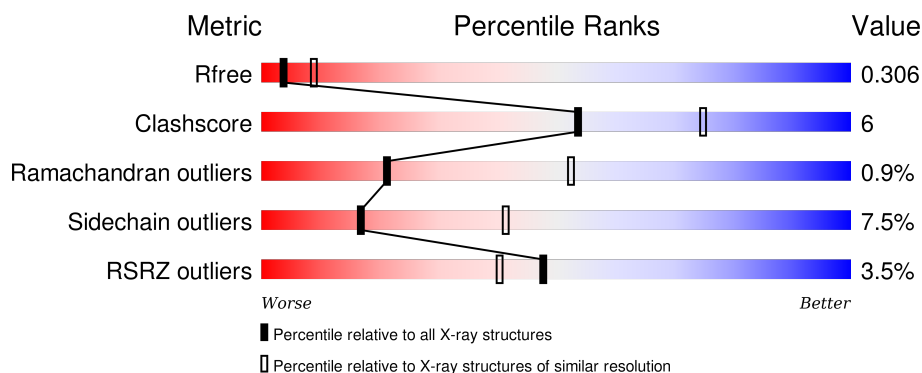
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

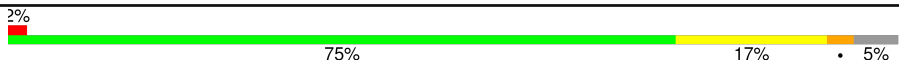
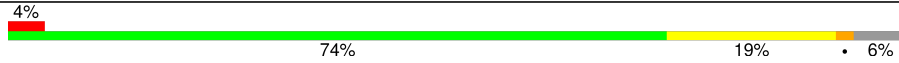
The reported resolution of this entry is 2.85 Å.

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}	91344	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

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. 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	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CA	B	602	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7027 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.

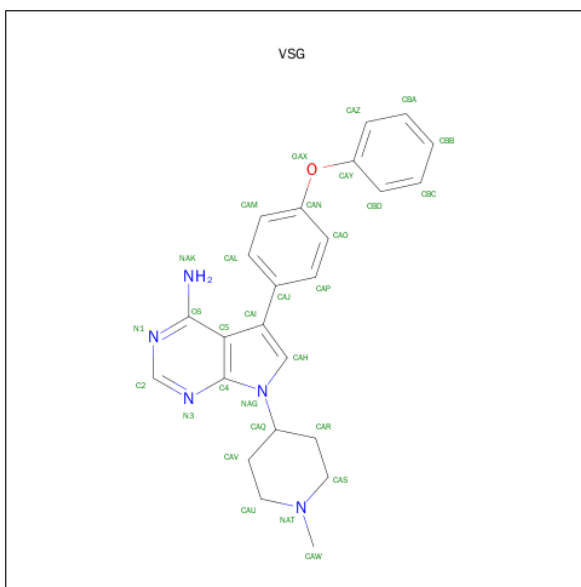
- Molecule 1 is a protein called Tyrosine-protein kinase HCK.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	P	S	0	0	0
			3468	2217	583	647	1	20			
1	B	428	Total	C	N	O	P	S	0	0	0
			3459	2213	581	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 7-(1-METHYLPYPERIDIN-4-YL)-5-(4-PHENOXYPHENYL)-7H-PYRROLO [2,3-D]PYRIMIDIN-4-AMINE (three-letter code: VSG) (formula: C₂₄H₂₅N₅O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			30	24	5	1		
2	B	1	Total	C	N	O	0	0
			30	24	5	1		

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

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

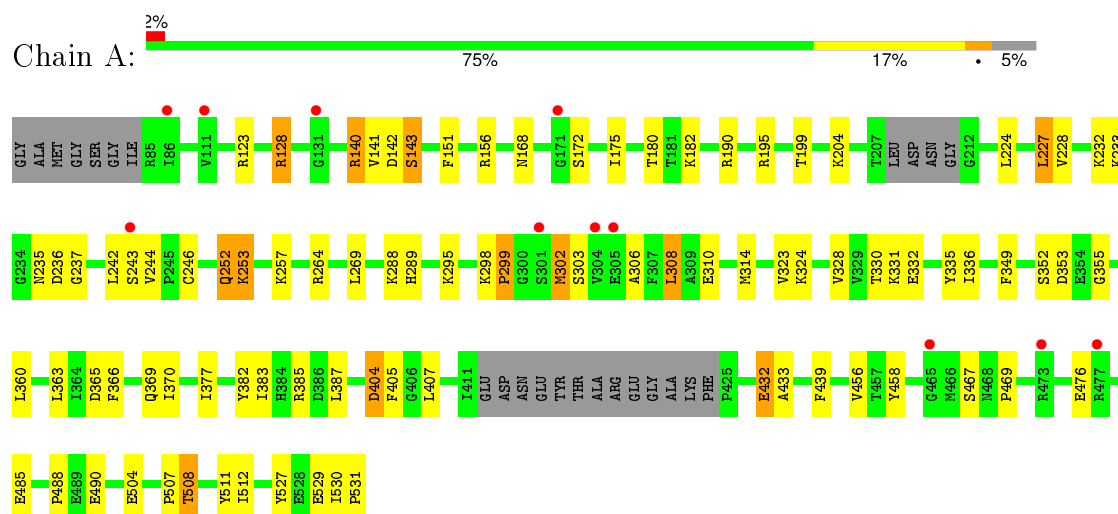
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	18	Total	O	0	0
			18	18		
4	B	20	Total	O	0	0
			20	20		

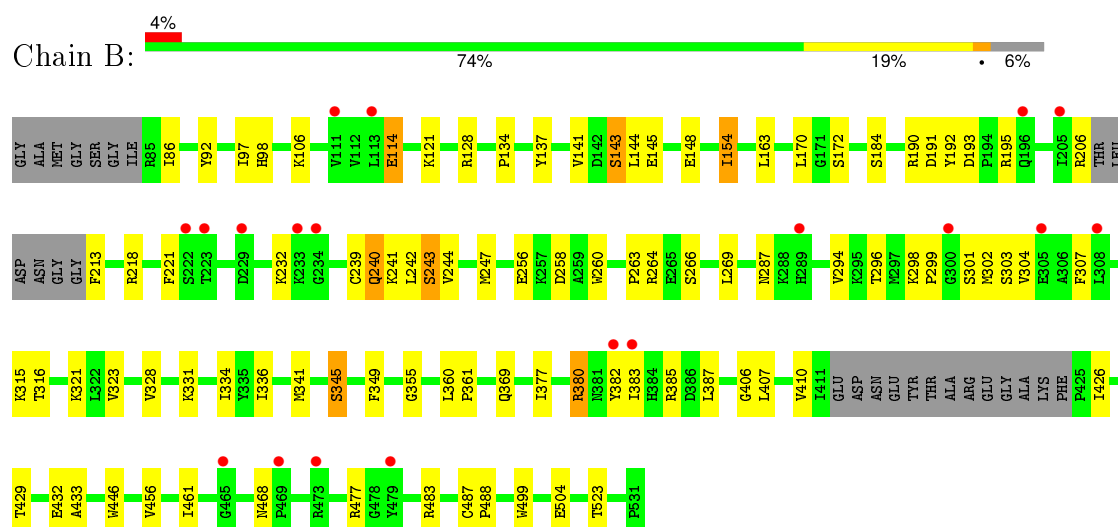
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.49 Å 94.83 Å 179.98 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.80 – 2.85 48.80 – 2.85	Depositor EDS
% Data completeness (in resolution range)	88.9 (48.80-2.85) 89.0 (48.80-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.86 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.255 , 0.309 0.250 , 0.306	Depositor DCC
R_{free} test set	2000 reflections (8.06%)	DCC
Wilson B-factor (Å ²)	48.6	Xtriage
Anisotropy	0.796	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 28.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	4 of 26805 reflections (0.015%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7027	wwPDB-VP
Average B, all atoms (Å ²)	53.0	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 40.36 % 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 2.7682e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: CA, PTR, VSG

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	0.37	0/3533	0.53	1/4767 (0.0%)
1	B	0.36	0/3524	0.54	0/4755
All	All	0.36	0/7057	0.54	1/9522 (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	A	227	LEU	CA-CB-CG	5.69	128.38	115.30

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	3468	0	3430	43	0
1	B	3459	0	3427	44	0
2	A	30	0	25	6	0
2	B	30	0	25	6	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	18	0	0	1	0
4	B	20	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7027	0	6907	90	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 6.

All (90) 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:298:LYS:HD3	1:B:299:PRO:HD2	1.70	0.73
1:A:123:ARG:HH21	1:A:128:ARG:HH22	1.42	0.68
1:B:213:PHE:N	1:B:221:PHE:O	2.29	0.66
1:B:483:ARG:NH1	1:B:487:CYS:O	2.31	0.64
1:A:360:LEU:HD21	1:A:488:PRO:HD3	1.79	0.63
1:B:191:ASP:OD1	1:B:192:TYR:N	2.32	0.63
2:A:601:VSG:H17	2:A:601:VSG:H18	1.64	0.63
1:B:239:CYS:O	1:B:240:GLN:NE2	2.31	0.63
1:A:252:GLN:NE2	4:A:712:HOH:O	2.31	0.62
1:A:308:LEU:HD11	1:A:330:THR:HG22	1.82	0.62
1:B:264:ARG:NH2	1:B:331:LYS:O	2.28	0.61
2:A:601:VSG:CAP	2:A:601:VSG:H17	2.15	0.60
1:A:404:ASP:OD1	2:A:601:VSG:H21	2.01	0.60
1:A:508:THR:HG23	1:A:511:TYR:H	1.68	0.59
1:A:235:ASN:O	1:A:237:GLY:N	2.33	0.58
1:B:287:ASN:OD1	4:B:704:HOH:O	2.17	0.58
1:B:307:PHE:CZ	1:B:336:ILE:HD11	2.39	0.58
1:B:163:LEU:O	1:B:190:ARG:NH1	2.36	0.57
1:B:321:LYS:HD2	1:B:369:GLN:HB3	1.85	0.57
1:A:377:ILE:HG23	1:A:382:TYR:HB3	1.87	0.55
1:A:383:ILE:HG22	1:A:385:ARG:HG3	1.89	0.54
1:A:323:VAL:HG11	2:A:601:VSG:H26	1.89	0.53
1:B:377:ILE:HG23	1:B:382:TYR:HB3	1.89	0.53
2:B:601:VSG:CAP	2:B:601:VSG:H17	2.23	0.52
1:A:467:SER:OG	1:A:469:PRO:HD2	2.10	0.51
1:A:180:THR:OG1	1:A:204:LYS:NZ	2.39	0.51
1:B:296:THR:O	1:B:296:THR:OG1	2.29	0.51
2:A:601:VSG:NAK	2:A:601:VSG:H18	2.27	0.50
1:B:341:MET:O	2:B:601:VSG:H15	2.12	0.50
1:B:461:ILE:HD12	1:B:461:ILE:H	1.77	0.49
1:B:260:TRP:CZ3	1:B:315:LYS:HD3	2.47	0.49
1:A:123:ARG:HH21	1:A:128:ARG:NH2	2.10	0.49
1:B:97:ILE:HG13	1:B:98:HIS:ND1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:232:LYS:HG2	1:B:242:LEU:HB2	1.93	0.49
1:A:175:ILE:HD13	1:A:224:LEU:HD22	1.94	0.49
1:B:114:GLU:HB2	1:B:121:LYS:HB3	1.95	0.49
1:A:168:ASN:HB2	1:A:190:ARG:HH11	1.78	0.48
1:A:349:PHE:O	1:A:355:GLY:HA3	2.14	0.48
1:A:507:PRO:HG2	1:A:512:ILE:HD11	1.95	0.47
1:B:106:LYS:NZ	1:B:148:GLU:OE2	2.33	0.47
1:A:404:ASP:N	1:A:404:ASP:OD1	2.46	0.47
1:B:323:VAL:HG11	2:B:601:VSG:H26	1.95	0.47
1:A:232:LYS:HA	1:A:242:LEU:HB2	1.97	0.47
1:B:154:ILE:HD12	1:B:154:ILE:HA	1.70	0.47
1:A:156:ARG:HD3	1:A:527:PTR:CE2	2.45	0.47
1:B:407:LEU:HD13	2:B:601:VSG:H23	1.95	0.47
1:A:407:LEU:HD13	2:A:601:VSG:H23	1.97	0.46
1:A:530:ILE:HA	1:A:531:PRO:HD3	1.64	0.46
1:B:349:PHE:O	1:B:355:GLY:HA3	2.16	0.46
1:A:140:ARG:O	1:A:143:SER:HB3	2.15	0.46
1:A:303:SER:HB3	1:A:306:ALA:HB3	1.98	0.46
1:A:172:SER:HA	1:A:244:VAL:O	2.16	0.46
1:B:360:LEU:HD21	1:B:488:PRO:HD3	1.98	0.45
1:B:345:SER:HB2	2:B:601:VSG:CAU	2.47	0.45
1:A:310:GLU:O	1:A:314:MET:HG3	2.17	0.45
1:A:168:ASN:HB2	1:A:190:ARG:NH1	2.32	0.44
1:B:301:SER:O	1:B:303:SER:N	2.50	0.44
1:B:446:TRP:CE3	1:B:499:TRP:HA	2.53	0.44
1:B:263:PRO:O	1:B:266:SER:OG	2.34	0.44
1:B:134:PRO:HB2	1:B:137:TYR:CD1	2.53	0.44
1:B:191:ASP:OD2	1:B:239:CYS:HB2	2.18	0.43
1:B:172:SER:HA	1:B:244:VAL:O	2.18	0.43
1:A:141:VAL:C	1:A:143:SER:H	2.20	0.43
1:A:243:SER:OG	1:A:244:VAL:N	2.50	0.43
1:A:299:PRO:HB3	1:A:332:GLU:HG2	2.00	0.43
1:A:264:ARG:HD3	1:A:335:TYR:CE2	2.54	0.43
1:A:365:ASP:O	1:A:369:GLN:HG3	2.18	0.43
1:B:141:VAL:C	1:B:143:SER:H	2.21	0.43
1:A:295:LYS:HB3	1:A:336:ILE:HB	2.01	0.43
1:A:253:LYS:H	1:A:253:LYS:HG3	1.54	0.43
1:B:382:TYR:OH	1:B:406:GLY:HA3	2.19	0.43
1:B:345:SER:HB2	2:B:601:VSG:H10	2.01	0.43
1:A:151:PHE:CZ	1:A:246:CYS:HB3	2.54	0.43
1:B:304:VAL:HG13	1:B:334:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:383:ILE:HG22	1:B:385:ARG:HG3	2.00	0.42
1:B:426:ILE:HD11	1:B:468:ASN:HB3	2.01	0.42
1:B:316:THR:O	1:B:380:ARG:NH2	2.53	0.42
1:B:134:PRO:HB2	1:B:137:TYR:HD1	1.84	0.42
1:B:170:LEU:O	1:B:243:SER:OG	2.32	0.42
1:A:433:ALA:HB1	1:A:439:PHE:CE2	2.54	0.41
1:B:429:THR:HG22	1:B:433:ALA:HB3	2.02	0.41
1:A:432:GLU:CD	1:A:432:GLU:H	2.23	0.41
1:A:228:VAL:O	1:A:232:LYS:HB2	2.20	0.41
1:B:269:LEU:HD22	1:B:294:VAL:HG21	2.02	0.41
1:A:504:GLU:CD	1:A:504:GLU:H	2.24	0.41
1:A:180:THR:HG1	1:A:204:LYS:HZ1	1.61	0.41
1:A:490:GLU:HG2	1:B:523:THR:O	2.19	0.41
1:B:360:LEU:HB3	1:B:361:PRO:HD3	2.03	0.41
1:A:363:LEU:HD11	1:A:458:TYR:CZ	2.56	0.40
1:A:366:PHE:O	1:A:370:ILE:HG13	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	423/454 (93%)	400 (95%)	19 (4%)	4 (1%)	21	52
1	B	421/454 (93%)	400 (95%)	17 (4%)	4 (1%)	19	49
All	All	844/908 (93%)	800 (95%)	36 (4%)	8 (1%)	21	52

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	195	ARG
1	B	302	MET

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Mol	Chain	Res	Type
1	A	236	ASP
1	A	302	MET
1	B	243	SER
1	A	142	ASP
1	B	256	GLU
1	A	299	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	374/393 (95%)	343 (92%)	31 (8%)	14	36
1	B	374/393 (95%)	349 (93%)	25 (7%)	20	47
All	All	748/786 (95%)	692 (92%)	56 (8%)	17	41

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	128	ARG
1	A	140	ARG
1	A	143	SER
1	A	182	LYS
1	A	195	ARG
1	A	199	THR
1	A	227	LEU
1	A	233	LYS
1	A	252	GLN
1	A	253	LYS
1	A	257	LYS
1	A	269	LEU
1	A	288	LYS
1	A	289	HIS
1	A	298	LYS
1	A	302	MET
1	A	308	LEU

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Mol	Chain	Res	Type
1	A	324	LYS
1	A	328	VAL
1	A	331	LYS
1	A	352	SER
1	A	353	ASP
1	A	387	LEU
1	A	404	ASP
1	A	405	PHE
1	A	432	GLU
1	A	456	VAL
1	A	476	GLU
1	A	485	GLU
1	A	508	THR
1	A	529	GLU
1	B	86	ILE
1	B	92	TYR
1	B	114	GLU
1	B	128	ARG
1	B	143	SER
1	B	144	LEU
1	B	145	GLU
1	B	154	ILE
1	B	184	SER
1	B	193	ASP
1	B	206	ARG
1	B	218	ARG
1	B	240	GLN
1	B	241	LYS
1	B	247	MET
1	B	258	ASP
1	B	328	VAL
1	B	345	SER
1	B	380	ARG
1	B	387	LEU
1	B	410	VAL
1	B	432	GLU
1	B	456	VAL
1	B	477	ARG
1	B	504	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	14,16,17	1.20	1 (7%)	18,22,24	0.68	1 (5%)
1	PTR	B	527	1,3	14,16,17	1.13	1 (7%)	18,22,24	0.76	1 (5%)

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	-	0/9/11/13	0/1/1/1
1	PTR	B	527	1,3	-	0/9/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	527	PTR	OH-CZ	-4.04	1.30	1.40
1	A	527	PTR	OH-CZ	-3.95	1.31	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	527	PTR	O-C-CA	-2.16	119.86	125.49
1	A	527	PTR	O-C-CA	-2.06	120.12	125.49

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	A	527	PTR	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 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	VSG	A	601	-	32,34,34	0.69	1 (3%)	37,48,48	3.01	9 (24%)
2	VSG	B	601	-	32,34,34	0.71	1 (3%)	37,48,48	2.94	9 (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	VSG	A	601	-	-	0/8/22/22	0/5/5/5
2	VSG	B	601	-	-	0/8/22/22	0/5/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	VSG	CAH-NAG	-2.36	1.34	1.38
2	A	601	VSG	CAH-NAG	-2.14	1.35	1.38

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	VSG	N3-C2-N1	-9.95	121.27	128.89
2	B	601	VSG	N3-C2-N1	-9.39	121.71	128.89
2	B	601	VSG	CAR-CAS-NAT	-4.98	104.38	111.32
2	A	601	VSG	CAR-CAS-NAT	-3.99	105.77	111.32
2	B	601	VSG	CAV-CAU-NAT	-2.27	108.16	111.32
2	A	601	VSG	CAV-CAU-NAT	-2.16	108.31	111.32
2	B	601	VSG	CAU-CAV-CAQ	2.45	112.34	110.41
2	B	601	VSG	CAY-OAX-CAN	3.60	127.77	118.81
2	A	601	VSG	CAY-OAX-CAN	3.66	127.93	118.81
2	A	601	VSG	CAU-CAV-CAQ	4.82	114.22	110.41
2	A	601	VSG	CAS-CAR-CAQ	4.84	114.23	110.41
2	B	601	VSG	CAS-CAR-CAQ	5.38	114.66	110.41
2	A	601	VSG	CAW-NAT-CAS	5.86	119.77	110.63
2	B	601	VSG	CAW-NAT-CAU	5.87	119.79	110.63
2	A	601	VSG	CAW-NAT-CAU	6.05	120.05	110.63
2	B	601	VSG	CAW-NAT-CAS	6.24	120.36	110.63
2	B	601	VSG	CAU-NAT-CAS	7.87	119.85	109.53
2	A	601	VSG	CAU-NAT-CAS	8.10	120.16	109.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	VSG	6	0
2	B	601	VSG	6	0

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, 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	429/454 (94%)	0.38	11 (2%) 59 54	28, 49, 72, 89	1 (0%)
1	B	427/454 (94%)	0.48	19 (4%) 38 31	29, 52, 86, 102	1 (0%)
All	All	856/908 (94%)	0.43	30 (3%) 48 40	28, 51, 80, 102	2 (0%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	301	SER	4.1
1	B	300	GLY	3.6
1	B	223	THR	3.2
1	B	111	VAL	3.0
1	B	465	GLY	2.8
1	B	382	TYR	2.7
1	A	473	ARG	2.7
1	B	473	ARG	2.7
1	A	304	VAL	2.7
1	B	222	SER	2.7
1	B	479	TYR	2.6
1	A	305	GLU	2.6
1	B	205	ILE	2.6
1	B	233	LYS	2.6
1	B	469	PRO	2.5
1	A	465	GLY	2.5
1	B	234	GLY	2.5
1	B	308	LEU	2.4
1	B	113	LEU	2.3
1	B	305	GLU	2.3
1	A	86	ILE	2.2
1	A	131	GLY	2.2
1	B	229	ASP	2.2
1	B	289	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	111	VAL	2.1
1	A	171	GLY	2.1
1	B	196	GLN	2.1
1	B	383	ILE	2.1
1	A	243	SER	2.0
1	A	477	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
1	PTR	B	527	16/17	0.95	0.18	-	36,53,59,60	0
1	PTR	A	527	16/17	0.96	0.19	-	34,42,49,65	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	CA	B	602	1/1	0.65	0.28	2.65	71,71,71,71	0
2	VSG	A	601	30/30	0.95	0.25	0.99	45,59,65,71	0
2	VSG	B	601	30/30	0.93	0.24	0.48	50,60,66,69	0
3	CA	A	602	1/1	0.64	0.30	-	66,66,66,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.