



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:40 PM GMT

PDB ID : 3RNY
Title : Crystal structure of human RSK1 C-terminal kinase domain
Authors : Li, D.; Fu, T.-M.; Nan, J.; Su, X.-D.
Deposited on : 2011-04-24
Resolution : 2.70 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

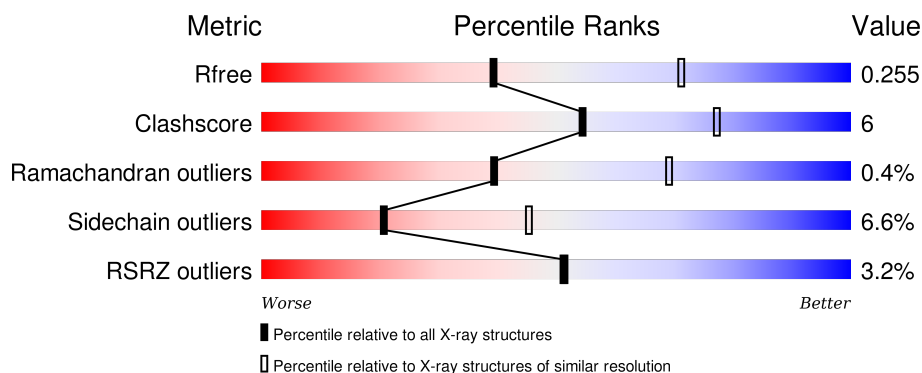
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	346	 2% 63% 12% • 24%
1	B	346	 3% 68% 10% • 22%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4068 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 Ribosomal protein S6 kinase alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	1	0
			1985	1264	330	380	11			
1	B	271	Total	C	N	O	S	0	0	0
			2038	1296	347	384	11			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	390	MET	-	EXPRESSION TAG	UNP Q15418
A	391	GLY	-	EXPRESSION TAG	UNP Q15418
A	392	SER	-	EXPRESSION TAG	UNP Q15418
A	393	SER	-	EXPRESSION TAG	UNP Q15418
A	394	HIS	-	EXPRESSION TAG	UNP Q15418
A	395	HIS	-	EXPRESSION TAG	UNP Q15418
A	396	HIS	-	EXPRESSION TAG	UNP Q15418
A	397	HIS	-	EXPRESSION TAG	UNP Q15418
A	398	HIS	-	EXPRESSION TAG	UNP Q15418
A	399	HIS	-	EXPRESSION TAG	UNP Q15418
A	400	SER	-	EXPRESSION TAG	UNP Q15418
A	401	SER	-	EXPRESSION TAG	UNP Q15418
A	402	GLY	-	EXPRESSION TAG	UNP Q15418
A	403	LEU	-	EXPRESSION TAG	UNP Q15418
A	404	VAL	-	EXPRESSION TAG	UNP Q15418
A	405	PRO	-	EXPRESSION TAG	UNP Q15418
A	406	ARG	-	EXPRESSION TAG	UNP Q15418
A	407	GLY	-	EXPRESSION TAG	UNP Q15418
A	408	SER	-	EXPRESSION TAG	UNP Q15418
A	409	HIS	-	EXPRESSION TAG	UNP Q15418
A	410	MET	-	INITIATING METHIONINE	UNP Q15418
B	390	MET	-	EXPRESSION TAG	UNP Q15418
B	391	GLY	-	EXPRESSION TAG	UNP Q15418
B	392	SER	-	EXPRESSION TAG	UNP Q15418
B	393	SER	-	EXPRESSION TAG	UNP Q15418

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Chain	Residue	Modelled	Actual	Comment	Reference
B	394	HIS	-	EXPRESSION TAG	UNP Q15418
B	395	HIS	-	EXPRESSION TAG	UNP Q15418
B	396	HIS	-	EXPRESSION TAG	UNP Q15418
B	397	HIS	-	EXPRESSION TAG	UNP Q15418
B	398	HIS	-	EXPRESSION TAG	UNP Q15418
B	399	HIS	-	EXPRESSION TAG	UNP Q15418
B	400	SER	-	EXPRESSION TAG	UNP Q15418
B	401	SER	-	EXPRESSION TAG	UNP Q15418
B	402	GLY	-	EXPRESSION TAG	UNP Q15418
B	403	LEU	-	EXPRESSION TAG	UNP Q15418
B	404	VAL	-	EXPRESSION TAG	UNP Q15418
B	405	PRO	-	EXPRESSION TAG	UNP Q15418
B	406	ARG	-	EXPRESSION TAG	UNP Q15418
B	407	GLY	-	EXPRESSION TAG	UNP Q15418
B	408	SER	-	EXPRESSION TAG	UNP Q15418
B	409	HIS	-	EXPRESSION TAG	UNP Q15418
B	410	MET	-	INITIATING METHIONINE	UNP Q15418

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Na 1 1	0	0
2	A	1	Total Na 1 1	0	0

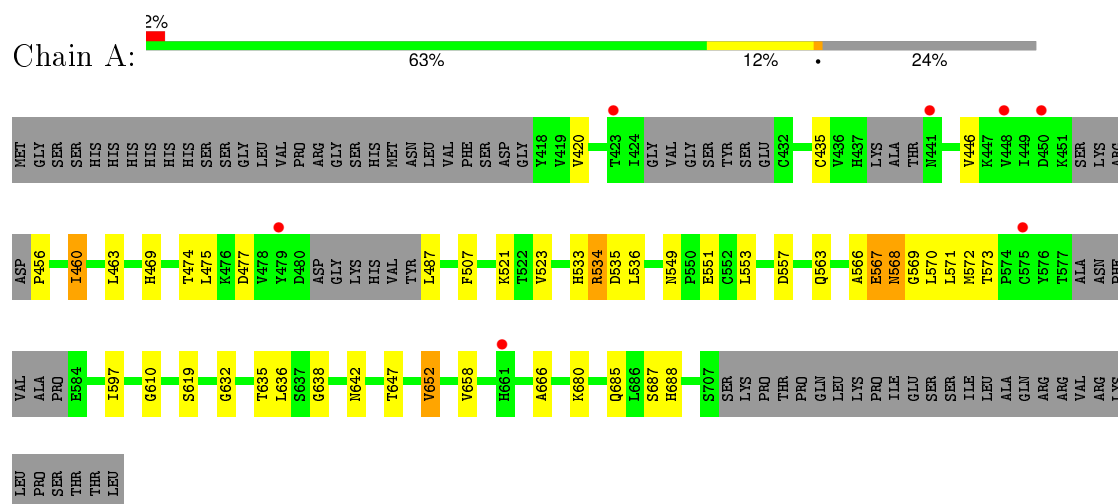
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	22	Total O 22 22	0	0
3	B	21	Total O 21 21	0	0

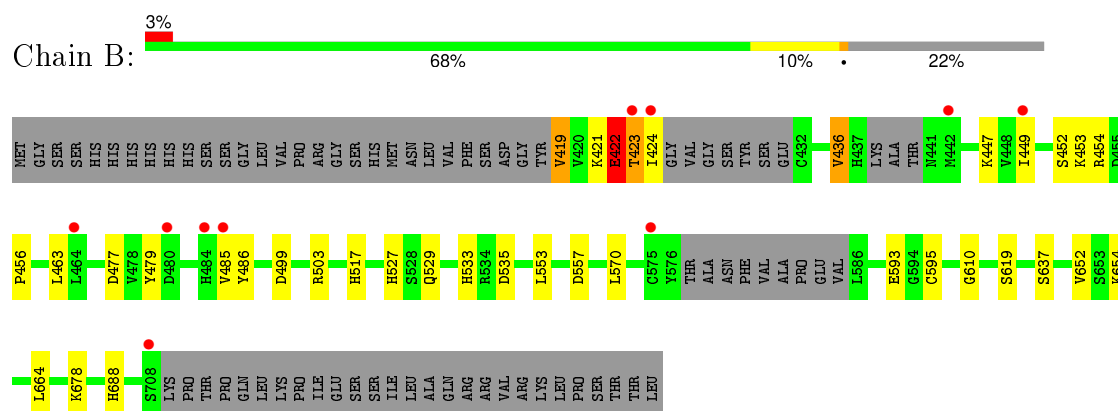
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Ribosomal protein S6 kinase alpha-1



- Molecule 1: Ribosomal protein S6 kinase alpha-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	39.86 Å 143.47 Å 59.92 Å 90.00° 95.77° 90.00°	Depositor
Resolution (Å)	11.98 – 2.70 11.96 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (11.98-2.70) 98.2 (11.96-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 2.70 Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.188 , 0.238 0.205 , 0.255	Depositor DCC
R_{free} test set	920 reflections (5.16%)	DCC
Wilson B-factor (Å ²)	38.2	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 50.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 17838 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4068	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NA

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	0.53	0/2024	0.71	0/2749
1	B	0.52	0/2076	0.73	0/2820
All	All	0.52	0/4100	0.72	0/5569

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	1985	0	1868	33	0
1	B	2038	0	1939	19	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	22	0	0	0	0
3	B	21	0	0	1	0
All	All	4068	0	3807	50	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 (50) 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:632:GLY:HA3	1:A:658:VAL:HG12	1.47	0.94
1:A:568:ASN:N	1:A:569:GLY:HA2	1.83	0.94
1:A:568:ASN:ND2	1:A:570:LEU:CD2	2.44	0.81
1:B:421:LYS:O	1:B:422:GLU:HB2	1.80	0.81
1:A:568:ASN:ND2	1:A:570:LEU:HD22	1.98	0.79
1:B:447:LYS:HE2	1:B:449:ILE:HD11	1.67	0.74
1:A:566:ALA:O	1:A:567:GLU:CB	2.37	0.72
1:B:452:SER:O	1:B:453:LYS:CB	2.37	0.71
1:A:534:ARG:HH11	1:A:534:ARG:HB2	1.55	0.70
1:A:568:ASN:N	1:A:568:ASN:OD1	2.30	0.65
1:A:563[B]:GLN:HG2	1:A:571:LEU:HD22	1.78	0.64
1:B:447:LYS:HE2	1:B:449:ILE:CD1	2.29	0.62
1:A:570:LEU:H	1:A:570:LEU:HD23	1.63	0.62
1:B:499:ASP:O	1:B:503:ARG:HD2	2.00	0.62
1:A:568:ASN:N	1:A:569:GLY:CA	2.61	0.61
1:A:469:HIS:HA	1:B:570:LEU:HD11	1.81	0.61
1:B:527:HIS:CE1	1:B:593:GLU:HB2	2.42	0.55
1:A:573:THR:HG23	1:B:529:GLN:HE22	1.72	0.55
1:A:568:ASN:HD22	1:A:570:LEU:HD22	1.72	0.54
1:A:636:LEU:HD21	1:A:652:VAL:HG21	1.89	0.54
1:B:419:VAL:HG13	1:B:436:VAL:HG13	1.91	0.52
1:B:535:ASP:OD1	3:B:28:HOH:O	2.19	0.52
1:A:632:GLY:CA	1:A:658:VAL:HG12	2.33	0.51
1:B:423:THR:HG23	1:B:424:ILE:H	1.76	0.51
1:B:610:GLY:HA3	1:B:688:HIS:HA	1.92	0.51
1:A:610:GLY:HA3	1:A:688:HIS:HA	1.93	0.50
1:A:534:ARG:NH1	1:A:534:ARG:HB2	2.25	0.50
1:A:568:ASN:H	1:A:569:GLY:HA2	1.73	0.49
1:A:638:GLY:H	1:A:642:ASN:ND2	2.12	0.47
1:A:638:GLY:H	1:A:642:ASN:HD21	1.62	0.47
1:A:456:PRO:O	1:A:460:ILE:HG13	2.14	0.47
1:B:447:LYS:CE	1:B:449:ILE:HD11	2.41	0.47
1:A:475:LEU:HD11	1:A:487:LEU:HB2	1.96	0.47
1:A:632:GLY:HA3	1:A:658:VAL:CG1	2.33	0.46
1:A:570:LEU:HD23	1:A:570:LEU:N	2.30	0.46
1:B:456:PRO:HG3	1:B:485:VAL:HG11	1.96	0.46
1:A:507:PHE:H	1:A:685:GLN:HE22	1.62	0.46
1:B:517:HIS:ND1	1:B:678:LYS:NZ	2.65	0.44
1:A:435:CYS:SG	1:A:446:VAL:HG23	2.60	0.42
1:A:533:HIS:CE1	1:A:557:ASP:O	2.72	0.42
1:A:597:ILE:HD11	1:A:666:ALA:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:566:ALA:HB2	1:A:572:MET:SD	2.60	0.42
1:B:479:TYR:HB2	1:B:486:TYR:HB2	2.02	0.42
1:A:549:ASN:HB3	1:A:551:GLU:OE1	2.20	0.41
1:B:654:LYS:HB3	1:B:664:LEU:HG	2.02	0.41
1:B:533:HIS:NE2	1:B:557:ASP:O	2.52	0.41
1:A:533:HIS:HD2	1:A:535:ASP:H	1.68	0.41
1:B:423:THR:HG23	1:B:424:ILE:N	2.37	0.40
1:A:533:HIS:CG	1:A:536:LEU:HD13	2.56	0.40
1:A:523:VAL:HG21	1:A:536:LEU:HD21	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	253/346 (73%)	243 (96%)	9 (4%)	1 (0%)	39	69
1	B	263/346 (76%)	254 (97%)	8 (3%)	1 (0%)	39	69
All	All	516/692 (75%)	497 (96%)	17 (3%)	2 (0%)	39	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	422	GLU
1	A	567	GLU

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	203/305 (67%)	188 (93%)	15 (7%)	17	39
1	B	208/305 (68%)	196 (94%)	12 (6%)	25	52
All	All	411/610 (67%)	384 (93%)	27 (7%)	21	45

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

Mol	Chain	Res	Type
1	A	420	VAL
1	A	460	ILE
1	A	463	LEU
1	A	474	THR
1	A	477	ASP
1	A	521	LYS
1	A	534	ARG
1	A	553	LEU
1	A	568	ASN
1	A	619	SER
1	A	635	THR
1	A	647	THR
1	A	652	VAL
1	A	680	LYS
1	A	687	SER
1	B	419	VAL
1	B	422	GLU
1	B	423	THR
1	B	436	VAL
1	B	454	ARG
1	B	463	LEU
1	B	477	ASP
1	B	553	LEU
1	B	595	CYS
1	B	619	SER
1	B	637	SER
1	B	652	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	533	HIS

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Mol	Chain	Res	Type
1	A	642	ASN
1	A	685	GLN
1	B	529	GLN
1	B	563	GLN
1	B	616	ASN
1	B	689	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	264/346 (76%)	-0.37	7 (2%) 58 58	21, 42, 80, 111	0
1	B	271/346 (78%)	-0.29	10 (3%) 45 45	18, 42, 84, 108	0
All	All	535/692 (77%)	-0.33	17 (3%) 51 51	18, 42, 83, 111	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	449	ILE	6.4
1	A	450	ASP	5.3
1	B	480	ASP	4.1
1	A	448	VAL	3.5
1	A	423	THR	2.9
1	B	442	MET	2.8
1	B	464	LEU	2.6
1	B	575	CYS	2.5
1	A	479	TYR	2.3
1	B	708	SER	2.1
1	A	441	ASN	2.1
1	A	661	HIS	2.1
1	B	423	THR	2.1
1	A	575	CYS	2.1
1	B	485	VAL	2.0
1	B	424	ILE	2.0
1	B	484	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

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(\AA^2)	Q<0.9
2	NA	B	1	1/1	0.90	0.13	-0.52	52,52,52,52	0
2	NA	A	1	1/1	0.92	0.12	-2.17	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.