



Full wwPDB NMR Structure Validation Report ⓘ

Sep 28, 2020 – 11:45 AM EDT

PDB ID : 6XR7
Title : Abl isoform 1b inactive1 state
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Deposited on : 2020-07-11

This is a Full wwPDB NMR 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/NMRValidationReportHelp>

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:

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.14.6
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

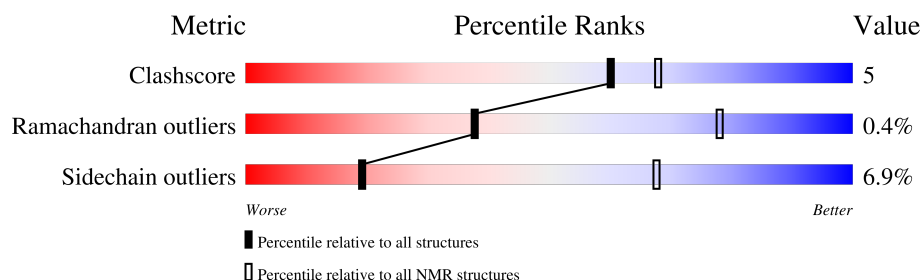
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 8%.

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)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	287	

2 Ensemble composition and analysis

This entry contains 20 models. Model 15 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:252-A:268, A:274-A:292, A:298-A:404, A:421-A:519 (242)	0.63	15

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 3 single-model clusters were found.

Cluster number	Models
1	1, 2, 5, 9, 10, 12, 14, 15, 17, 20
2	4, 6, 7, 16, 19
3	3, 18
Single-model clusters	8; 11; 13

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 4616 atoms, of which 2286 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Tyrosine-protein kinase ABL1.

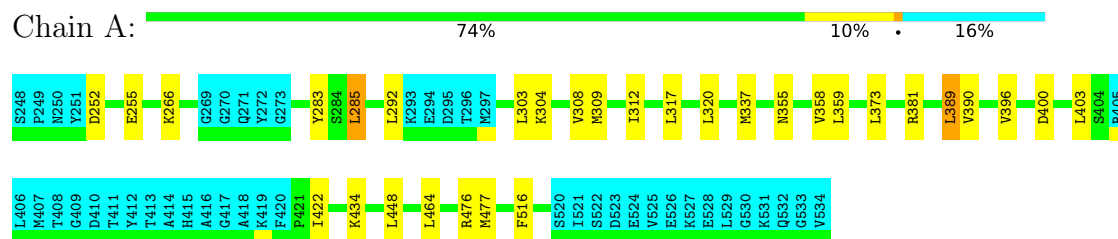
Mol	Chain	Residues	Atoms						Trace
1	A	287	Total	C	H	N	O	S	0
			4616	1495	2286	379	439	17	

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Tyrosine-protein kinase ABL1

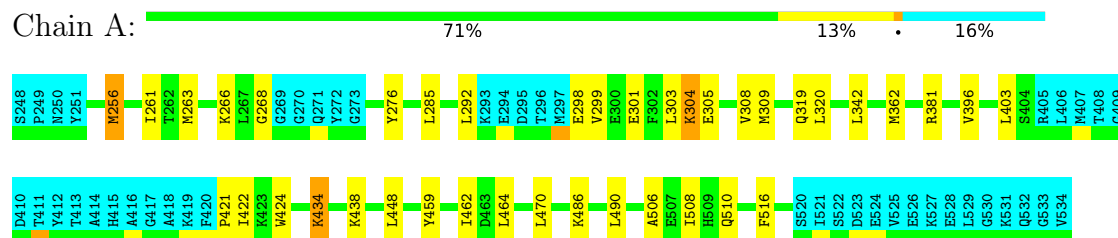


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

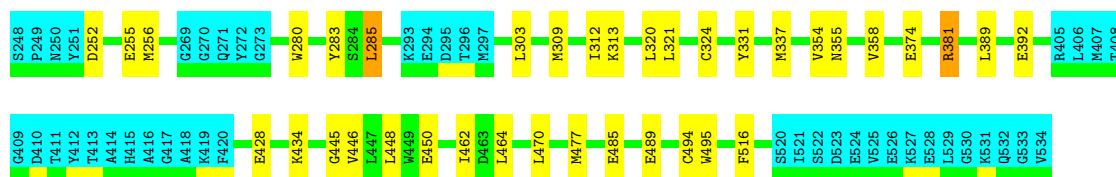
- Molecule 1: Tyrosine-protein kinase ABL1



4.2.2 Score per residue for model 2

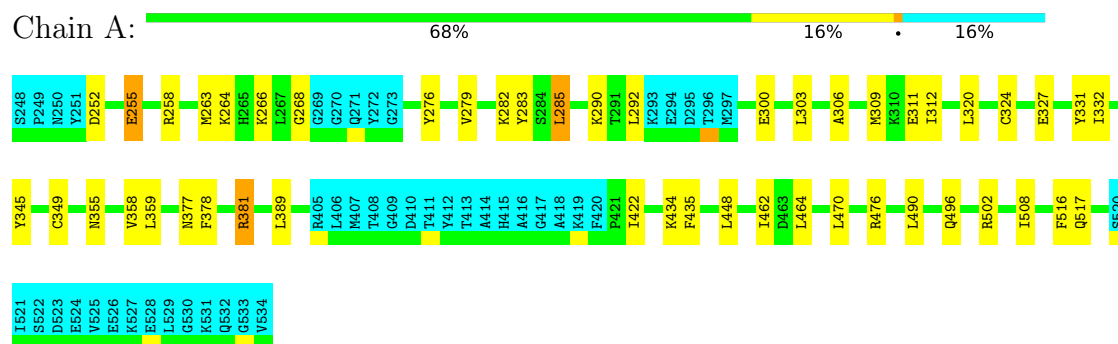
- Molecule 1: Tyrosine-protein kinase ABL1





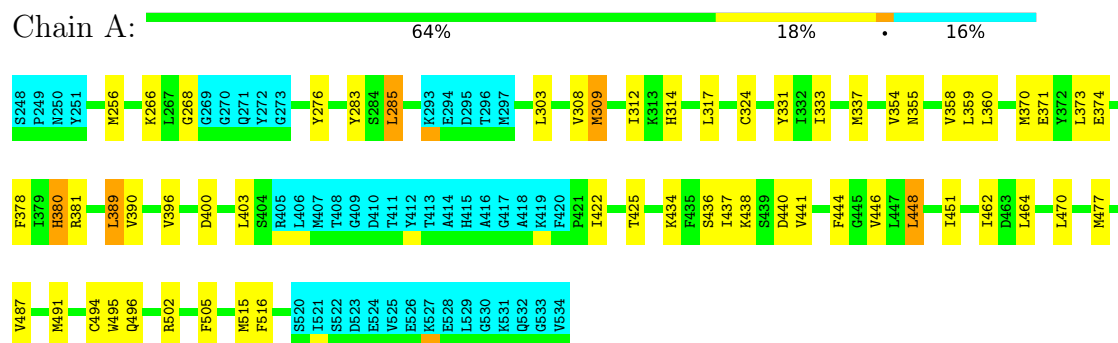
4.2.3 Score per residue for model 3

- Molecule 1: Tyrosine-protein kinase ABL1



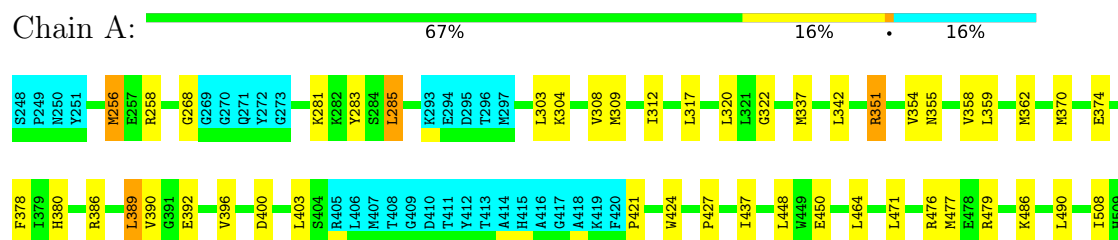
4.2.4 Score per residue for model 4

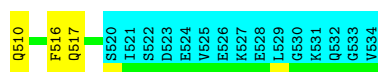
- Molecule 1: Tyrosine-protein kinase ABL1



4.2.5 Score per residue for model 5

- Molecule 1: Tyrosine-protein kinase ABL1

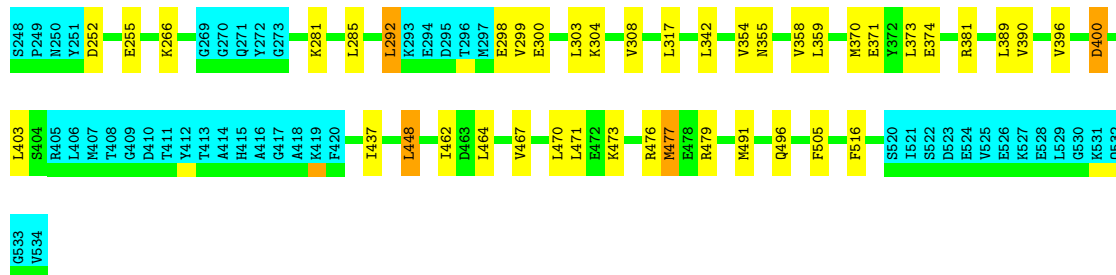




4.2.6 Score per residue for model 6

- Molecule 1: Tyrosine-protein kinase ABL1

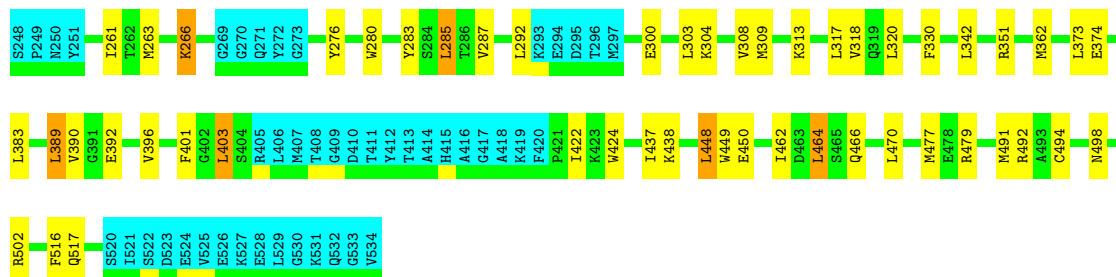
Chain A: 69% 14% 16%



4.2.7 Score per residue for model 7

- Molecule 1: Tyrosine-protein kinase ABL1

Chain A: 67% 16% 16%



4.2.8 Score per residue for model 8

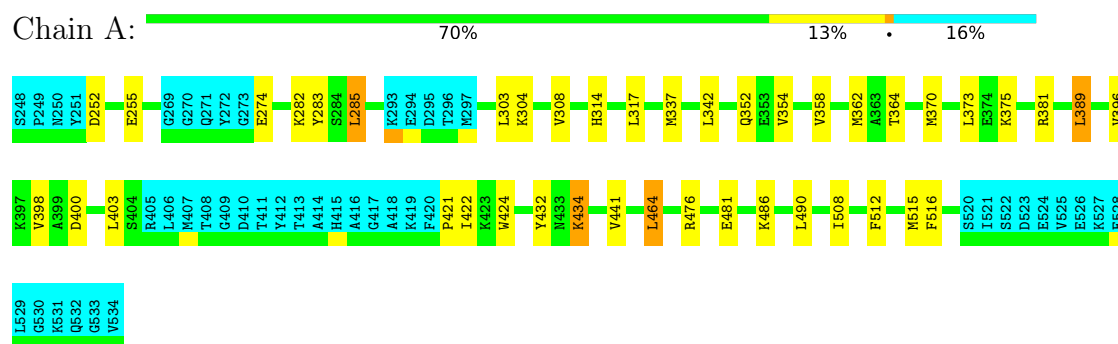
- Molecule 1: Tyrosine-protein kinase ABL1

Chain A: 67% 16% 16%



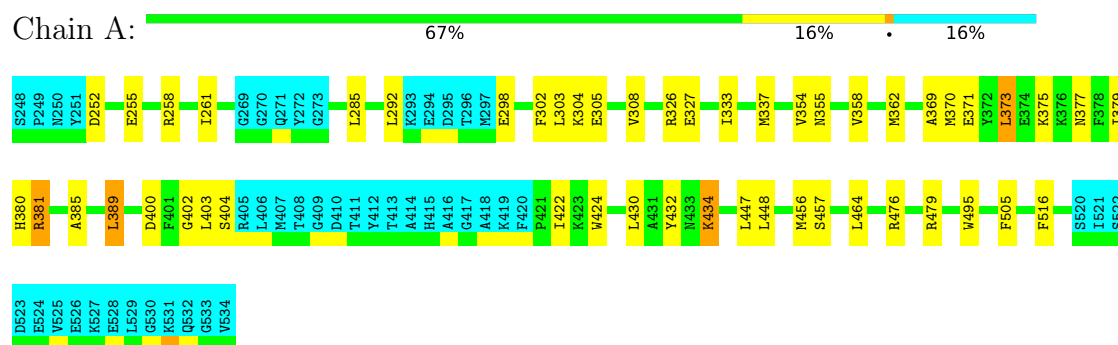
4.2.9 Score per residue for model 9

- Molecule 1: Tyrosine-protein kinase ABL1



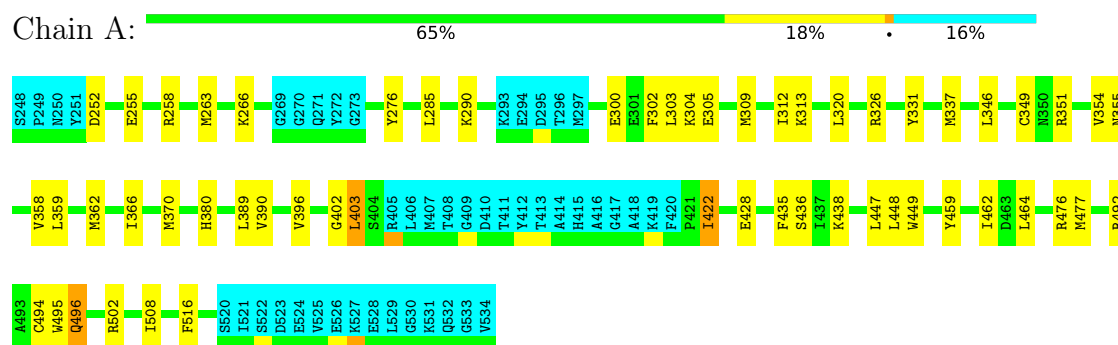
4.2.10 Score per residue for model 10

- Molecule 1: Tyrosine-protein kinase ABL1



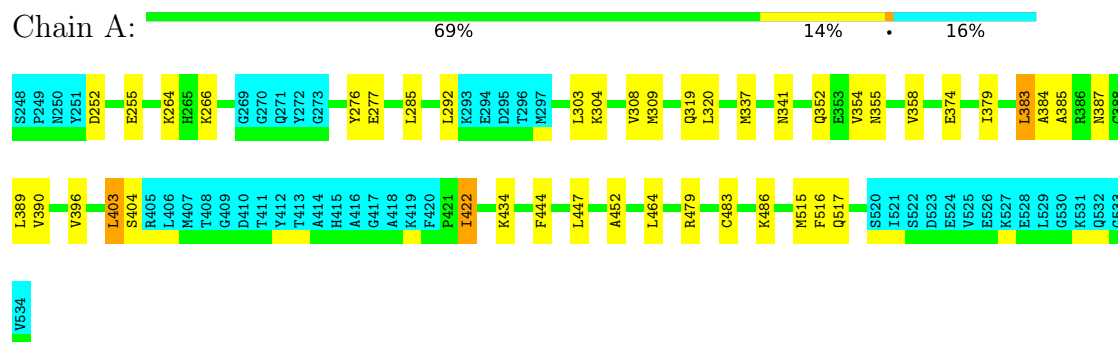
4.2.11 Score per residue for model 11

- Molecule 1: Tyrosine-protein kinase ABL1



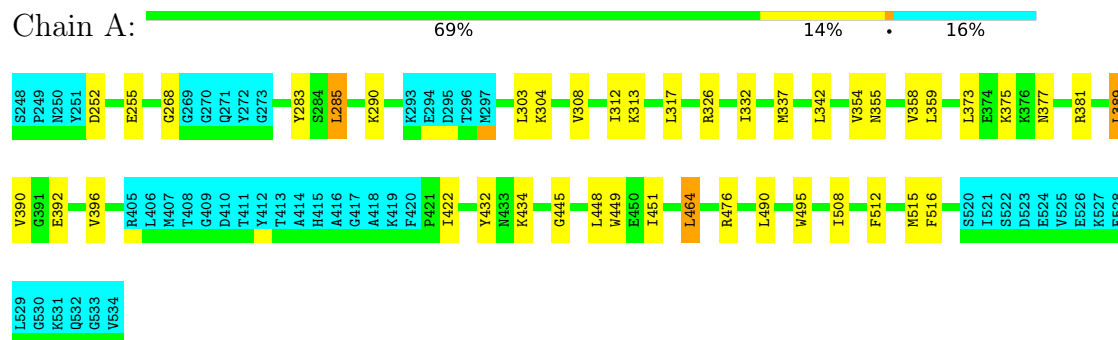
4.2.12 Score per residue for model 12

- Molecule 1: Tyrosine-protein kinase ABL1



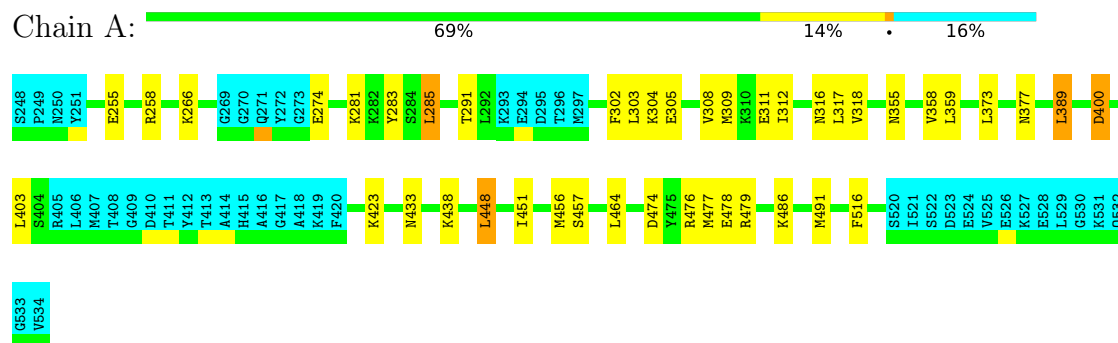
4.2.13 Score per residue for model 13

- Molecule 1: Tyrosine-protein kinase ABL1



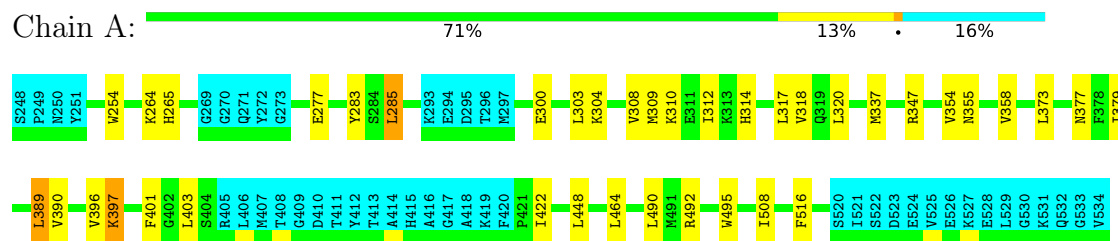
4.2.14 Score per residue for model 14

- Molecule 1: Tyrosine-protein kinase ABL1



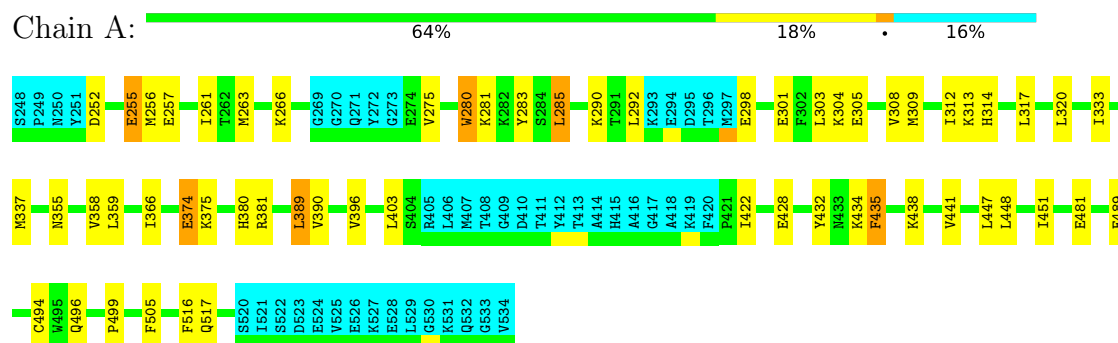
4.2.15 Score per residue for model 15 (medoid)

- Molecule 1: Tyrosine-protein kinase ABL1



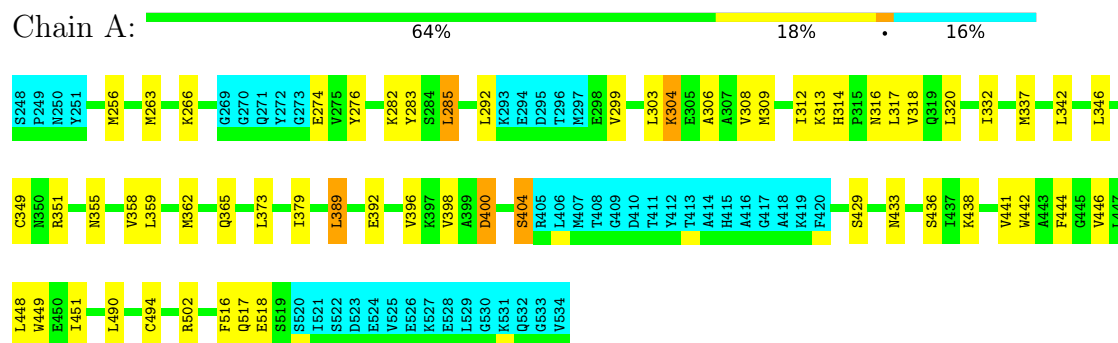
4.2.16 Score per residue for model 16

- Molecule 1: Tyrosine-protein kinase ABL1



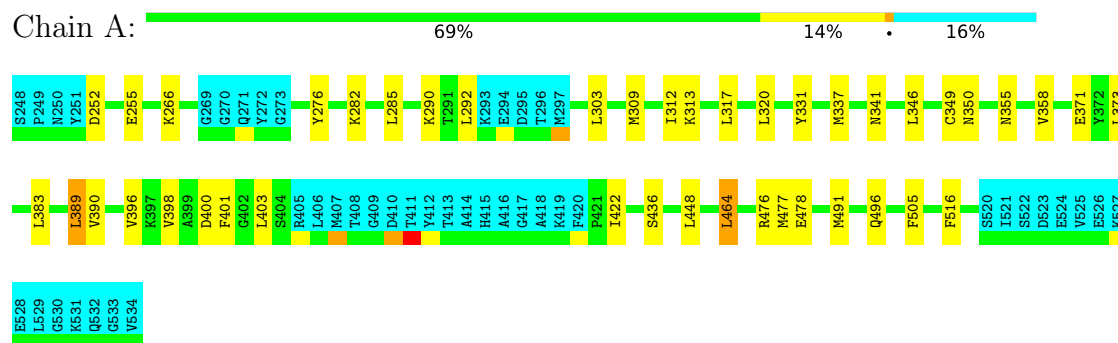
4.2.17 Score per residue for model 17

- Molecule 1: Tyrosine-protein kinase ABL1



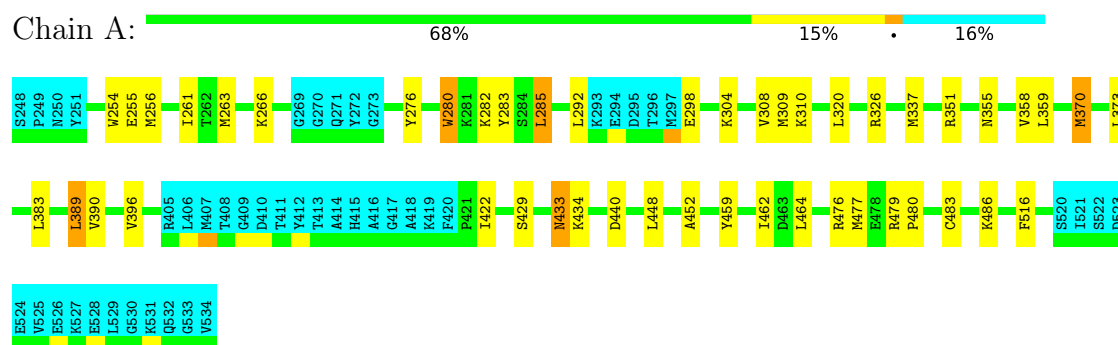
4.2.18 Score per residue for model 18

- Molecule 1: Tyrosine-protein kinase ABL1



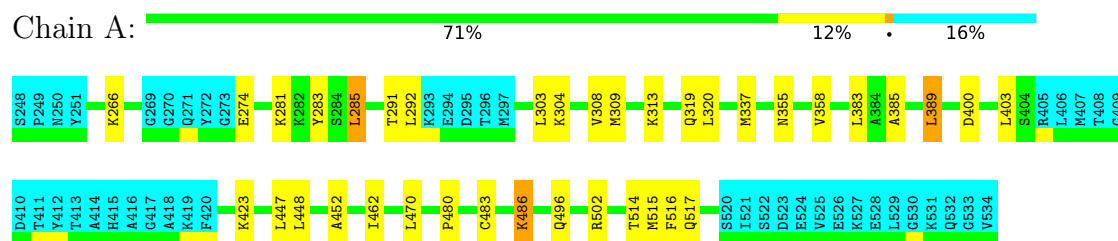
4.2.19 Score per residue for model 19

- Molecule 1: Tyrosine-protein kinase ABL1



4.2.20 Score per residue for model 20

- Molecule 1: Tyrosine-protein kinase ABL1



5 Refinement protocol and experimental data overview

The models were refined using the following method: *molecular dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CNS	refinement	
CYANA	structure calculation	
TALOS	geometry optimization	
PSVS	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	544
Number of shifts mapped to atoms	544
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	8%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

There are no covalent bond-length or bond-angle outliers.

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	1.0±0.0
All	All	0	20

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	516	PHE	Peptide	20

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1989	1962	1957	18±4
All	All	39780	39240	39140	367

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:452:ALA:HB1	1:A:483:CYS:SG	0.73	2.24	19	3
1:A:317:LEU:HD11	1:A:373:LEU:HD11	0.69	1.64	8	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:309:MET:SD	1:A:320:LEU:HD13	0.69	2.28	11	4
1:A:337:MET:HG2	1:A:389:LEU:HB3	0.66	1.67	12	3
1:A:370:MET:SD	1:A:380:HIS:NE2	0.64	2.70	11	2
1:A:462:ILE:HD13	1:A:470:LEU:HD21	0.63	1.68	1	5
1:A:337:MET:HG3	1:A:389:LEU:HD13	0.63	1.70	10	2
1:A:436:SER:HB2	1:A:438:LYS:HG2	0.61	1.72	11	3
1:A:309:MET:HB3	1:A:320:LEU:HB2	0.60	1.72	15	9
1:A:422:ILE:HD13	1:A:464:LEU:HD11	0.60	1.72	10	5
1:A:422:ILE:HD12	1:A:464:LEU:HD11	0.60	1.72	12	2
1:A:252:ASP:HB3	1:A:255:GLU:HB2	0.59	1.74	10	10
1:A:432:TYR:HB2	1:A:434:LYS:HD2	0.59	1.74	10	1
1:A:374:GLU:HG2	1:A:437:ILE:HD11	0.58	1.75	7	4
1:A:264:LYS:HB2	1:A:277:GLU:HG3	0.57	1.75	15	2
1:A:480:PRO:HG2	1:A:483:CYS:SG	0.57	2.39	20	1
1:A:400:ASP:HA	1:A:403:LEU:HD12	0.57	1.76	18	3
1:A:274:GLU:HB3	1:A:291:THR:HB	0.56	1.77	20	1
1:A:342:LEU:HD11	1:A:362:MET:SD	0.56	2.40	5	6
1:A:309:MET:HA	1:A:312:ILE:HG22	0.56	1.77	14	6
1:A:480:PRO:HB2	1:A:483:CYS:SG	0.56	2.41	19	1
1:A:337:MET:HG2	1:A:389:LEU:HB2	0.56	1.78	5	8
1:A:308:VAL:HG22	1:A:404:SER:HB2	0.56	1.77	17	1
1:A:441:VAL:HG11	1:A:502:ARG:HD3	0.56	1.78	17	1
1:A:342:LEU:HD22	1:A:396:VAL:HG11	0.55	1.76	9	7
1:A:371:GLU:HA	1:A:505:PHE:HB2	0.55	1.76	6	4
1:A:422:ILE:HG12	1:A:464:LEU:HD11	0.54	1.79	9	3
1:A:318:VAL:HA	1:A:397:LYS:HE3	0.54	1.79	15	1
1:A:283:TYR:HB2	1:A:285:LEU:HD12	0.54	1.78	16	12
1:A:386:ARG:HH22	1:A:421:PRO:HG3	0.54	1.63	5	1
1:A:448:LEU:HB3	1:A:491:MET:SD	0.54	2.43	4	2
1:A:479:ARG:HD2	1:A:479:ARG:H	0.54	1.63	5	1
1:A:444:PHE:HB2	1:A:494:CYS:SG	0.54	2.42	17	1
1:A:432:TYR:HB2	1:A:434:LYS:HG2	0.53	1.80	8	4
1:A:346:LEU:HA	1:A:349:CYS:SG	0.53	2.43	18	3
1:A:422:ILE:HG13	1:A:464:LEU:HD21	0.53	1.80	18	1
1:A:438:LYS:HA	1:A:502:ARG:NH1	0.53	2.18	7	1
1:A:266:LYS:HA	1:A:276:TYR:HA	0.53	1.80	1	9
1:A:360:LEU:HD21	1:A:515:MET:SD	0.53	2.44	4	1
1:A:312:ILE:HD12	1:A:317:LEU:HD13	0.53	1.81	17	5
1:A:448:LEU:HB3	1:A:491:MET:HE2	0.53	1.79	18	1
1:A:459:TYR:HB3	1:A:462:ILE:HD11	0.53	1.81	8	4
1:A:380:HIS:HA	1:A:403:LEU:HG	0.52	1.81	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:490:LEU:HD21	1:A:508:ILE:HG23	0.51	1.82	13	7
1:A:318:VAL:HG22	1:A:389:LEU:HD11	0.51	1.81	14	2
1:A:364:THR:HG22	1:A:512:PHE:HB3	0.51	1.83	9	1
1:A:304:LYS:O	1:A:308:VAL:HG23	0.51	2.06	5	14
1:A:354:VAL:HA	1:A:358:VAL:HG11	0.50	1.82	2	10
1:A:283:TYR:HB3	1:A:285:LEU:HD12	0.50	1.82	5	1
1:A:494:CYS:SG	1:A:508:ILE:HD11	0.50	2.46	11	1
1:A:487:VAL:HG22	1:A:515:MET:SD	0.50	2.47	4	1
1:A:317:LEU:HD11	1:A:373:LEU:HD13	0.50	1.82	6	1
1:A:309:MET:HB2	1:A:320:LEU:HD12	0.50	1.84	19	1
1:A:355:ASN:O	1:A:358:VAL:HG12	0.50	2.07	20	17
1:A:326:ARG:HG3	1:A:327:GLU:HG3	0.50	1.84	10	1
1:A:308:VAL:HG11	1:A:403:LEU:HB3	0.49	1.82	16	3
1:A:441:VAL:HG13	1:A:508:ILE:HD11	0.49	1.83	9	1
1:A:261:ILE:HD11	1:A:287:VAL:HG21	0.49	1.85	7	1
1:A:264:LYS:HD2	1:A:279:VAL:HG23	0.48	1.85	3	1
1:A:486:LYS:HG3	1:A:515:MET:SD	0.48	2.49	12	1
1:A:256:MET:HE1	1:A:261:ILE:HD11	0.48	1.84	1	1
1:A:274:GLU:HB2	1:A:291:THR:HB	0.48	1.85	14	1
1:A:384:ALA:HB3	1:A:387:ASN:HD22	0.48	1.69	12	1
1:A:308:VAL:HG21	1:A:403:LEU:HB3	0.47	1.86	7	1
1:A:496:GLN:HB3	1:A:502:ARG:HD2	0.47	1.87	3	1
1:A:252:ASP:HB2	1:A:255:GLU:HB2	0.47	1.85	16	1
1:A:370:MET:SD	1:A:383:LEU:HD22	0.47	2.49	19	1
1:A:390:VAL:HG22	1:A:396:VAL:HG22	0.47	1.85	7	11
1:A:462:ILE:HD12	1:A:470:LEU:HD21	0.47	1.86	2	2
1:A:355:ASN:O	1:A:359:LEU:HG	0.47	2.10	11	9
1:A:512:PHE:HA	1:A:515:MET:HE2	0.47	1.86	13	1
1:A:498:ASN:HB2	1:A:501:ASP:HB3	0.47	1.86	8	1
1:A:380:HIS:O	1:A:381:ARG:HD3	0.47	2.09	10	1
1:A:385:ALA:N	1:A:447:LEU:HD13	0.47	2.24	20	3
1:A:309:MET:HG3	1:A:400:ASP:HB2	0.46	1.87	20	1
1:A:374:GLU:HB3	1:A:505:PHE:HB3	0.46	1.85	16	1
1:A:309:MET:HB3	1:A:320:LEU:HD22	0.46	1.88	3	1
1:A:444:PHE:HD2	1:A:494:CYS:SG	0.46	2.33	4	1
1:A:304:LYS:HE3	1:A:304:LYS:HA	0.46	1.88	1	1
1:A:427:PRO:HB3	1:A:471:LEU:HB3	0.46	1.88	5	1
1:A:369:ALA:O	1:A:373:LEU:HD22	0.46	2.11	10	1
1:A:441:VAL:O	1:A:494:CYS:SG	0.46	2.73	16	1
1:A:486:LYS:HB2	1:A:515:MET:SD	0.46	2.51	20	1
1:A:438:LYS:HA	1:A:502:ARG:HH12	0.46	1.71	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:445:GLY:HA2	1:A:494:CYS:SG	0.45	2.50	2	1
1:A:258:ARG:HH22	1:A:327:GLU:HG3	0.45	1.72	3	1
1:A:306:ALA:HB2	1:A:332:ILE:HD11	0.45	1.89	3	1
1:A:290:LYS:O	1:A:331:TYR:HA	0.45	2.11	3	3
1:A:514:THR:O	1:A:517:GLN:HG2	0.45	2.10	20	1
1:A:312:ILE:HD12	1:A:317:LEU:HG	0.45	1.88	5	1
1:A:261:ILE:HB	1:A:280:TRP:HD1	0.45	1.70	16	3
1:A:456:MET:SD	1:A:457:SER:N	0.45	2.89	10	2
1:A:256:MET:SD	1:A:322:GLY:HA3	0.45	2.52	5	1
1:A:300:GLU:O	1:A:304:LYS:HG2	0.45	2.12	7	4
1:A:379:ILE:HB	1:A:404:SER:HB2	0.45	1.88	10	1
1:A:441:VAL:HG21	1:A:502:ARG:HH11	0.45	1.72	4	1
1:A:421:PRO:HG2	1:A:424:TRP:HB2	0.44	1.89	5	1
1:A:302:PHE:O	1:A:305:GLU:HG2	0.44	2.11	10	3
1:A:421:PRO:HB2	1:A:424:TRP:CE3	0.44	2.48	1	1
1:A:466:GLN:HG3	1:A:470:LEU:HD23	0.44	1.88	7	1
1:A:370:MET:SD	1:A:398:VAL:HG21	0.44	2.52	9	1
1:A:292:LEU:HD21	1:A:299:VAL:HG22	0.44	1.88	6	2
1:A:290:LYS:HB2	1:A:332:ILE:HB	0.44	1.89	13	1
1:A:362:MET:HB2	1:A:396:VAL:HG21	0.44	1.90	5	1
1:A:438:LYS:HD3	1:A:499:PRO:HB3	0.44	1.88	16	1
1:A:309:MET:HA	1:A:312:ILE:HG12	0.44	1.88	17	1
1:A:292:LEU:HD21	1:A:299:VAL:HA	0.44	1.90	1	1
1:A:256:MET:HE3	1:A:333:ILE:HG13	0.44	1.90	16	2
1:A:358:VAL:O	1:A:362:MET:HG3	0.44	2.13	8	2
1:A:309:MET:SD	1:A:400:ASP:HB3	0.43	2.53	17	1
1:A:506:ALA:O	1:A:510:GLN:HG2	0.43	2.13	1	1
1:A:496:GLN:HG2	1:A:502:ARG:HB3	0.43	1.90	11	1
1:A:383:LEU:HD12	1:A:444:PHE:HA	0.43	1.88	12	1
1:A:362:MET:HB3	1:A:396:VAL:HG21	0.43	1.90	11	1
1:A:316:ASN:ND2	1:A:365:GLN:HB3	0.43	2.28	17	1
1:A:446:VAL:HG22	1:A:495:TRP:HE1	0.43	1.74	2	2
1:A:422:ILE:HG23	1:A:464:LEU:HD21	0.43	1.89	3	1
1:A:403:LEU:HD23	1:A:404:SER:H	0.43	1.73	12	1
1:A:400:ASP:HB3	1:A:403:LEU:HG	0.43	1.90	14	1
1:A:258:ARG:NH2	1:A:324:CYS:SG	0.43	2.91	3	1
1:A:496:GLN:HG3	1:A:502:ARG:HB3	0.43	1.90	20	1
1:A:421:PRO:HB2	1:A:424:TRP:HB2	0.43	1.91	9	1
1:A:306:ALA:HB2	1:A:332:ILE:HD12	0.43	1.91	17	1
1:A:318:VAL:CG2	1:A:389:LEU:HD11	0.42	2.44	7	2
1:A:261:ILE:HD12	1:A:333:ILE:HD13	0.42	1.91	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:254:TRP:HE1	1:A:310:LYS:HG3	0.42	1.73	15	1
1:A:429:SER:O	1:A:433:ASN:HA	0.42	2.14	17	2
1:A:324:CYS:HB3	1:A:331:TYR:HB2	0.42	1.90	4	3
1:A:305:GLU:HB3	1:A:401:PHE:HD2	0.42	1.74	8	1
1:A:359:LEU:HB3	1:A:451:ILE:HG22	0.42	1.91	17	2
1:A:254:TRP:HE1	1:A:310:LYS:HA	0.42	1.75	19	1
1:A:448:LEU:HD13	1:A:491:MET:HB3	0.42	1.92	7	1
1:A:359:LEU:HD13	1:A:451:ILE:O	0.42	2.15	14	4
1:A:381:ARG:HB2	1:A:435:PHE:HB3	0.42	1.91	3	1
1:A:448:LEU:HB3	1:A:491:MET:HG3	0.42	1.91	6	1
1:A:477:MET:N	1:A:477:MET:SD	0.42	2.93	6	1
1:A:292:LEU:HD22	1:A:330:PHE:CD2	0.42	2.50	7	1
1:A:380:HIS:ND1	1:A:381:ARG:N	0.42	2.68	16	1
1:A:304:LYS:HE2	1:A:304:LYS:HA	0.42	1.92	6	1
1:A:493:ALA:HA	1:A:496:GLN:HG2	0.42	1.91	8	1
1:A:445:GLY:HA3	1:A:495:TRP:CH2	0.42	2.50	13	1
1:A:467:VAL:O	1:A:471:LEU:HG	0.42	2.15	6	1
1:A:366:ILE:HD13	1:A:447:LEU:HD21	0.42	1.92	11	2
1:A:317:LEU:HD23	1:A:398:VAL:HB	0.41	1.91	17	1
1:A:301:GLU:O	1:A:305:GLU:HG3	0.41	2.15	16	2
1:A:459:TYR:CE1	1:A:477:MET:SD	0.41	3.14	8	1
1:A:282:LYS:HE2	1:A:282:LYS:HA	0.41	1.91	18	1
1:A:366:ILE:HG21	1:A:447:LEU:HD21	0.41	1.93	8	1
1:A:491:MET:HA	1:A:494:CYS:SG	0.41	2.56	7	1
1:A:428:GLU:HB2	1:A:434:LYS:HE3	0.41	1.92	2	1
1:A:442:TRP:O	1:A:446:VAL:HG23	0.41	2.16	17	1
1:A:337:MET:HG2	1:A:389:LEU:HD13	0.41	1.91	4	1
1:A:275:VAL:HG22	1:A:290:LYS:HG2	0.41	1.91	8	2
1:A:265:HIS:O	1:A:277:GLU:HG2	0.41	2.16	15	1
1:A:351:ARG:H	1:A:351:ARG:NE	0.41	2.14	5	1
1:A:256:MET:SD	1:A:280:TRP:NE1	0.40	2.94	2	1
1:A:345:TYR:O	1:A:349:CYS:SG	0.40	2.79	3	1
1:A:389:LEU:HD23	1:A:389:LEU:N	0.40	2.32	16	1
1:A:309:MET:SD	1:A:400:ASP:HB2	0.40	2.56	4	1
1:A:380:HIS:HA	1:A:403:LEU:HD23	0.40	1.93	5	1
1:A:486:LYS:HB3	1:A:515:MET:SD	0.40	2.56	9	1
1:A:422:ILE:HG13	1:A:430:LEU:HD21	0.40	1.92	10	1
1:A:317:LEU:HA	1:A:398:VAL:O	0.40	2.16	18	1
1:A:300:GLU:O	1:A:304:LYS:HB2	0.40	2.17	15	1

6.3 Torsion angles [i](#)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	242/287 (84%)	229±2 (95±1%)	12±2 (5±1%)	1±1 (0±0%)	38	78
All	All	4840/5740 (84%)	4588 (95%)	232 (5%)	20 (0%)	38	78

All 7 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	268	GLY	5
1	A	401	PHE	4
1	A	403	LEU	3
1	A	400	ASP	3
1	A	402	GLY	2
1	A	298	GLU	2
1	A	404	SER	1

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	216/251 (86%)	201±4 (93±2%)	15±4 (7±2%)	19	68
All	All	4320/5020 (86%)	4020 (93%)	300 (7%)	19	68

All 76 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	285	LEU	20
1	A	303	LEU	19
1	A	448	LEU	17

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Mol	Chain	Res	Type	Models (Total)
1	A	389	LEU	15
1	A	476	ARG	11
1	A	464	LEU	10
1	A	477	MET	9
1	A	313	LYS	8
1	A	263	MET	7
1	A	381	ARG	7
1	A	292	LEU	7
1	A	266	LYS	6
1	A	377	ASN	6
1	A	479	ARG	6
1	A	392	GLU	5
1	A	496	GLN	5
1	A	370	MET	5
1	A	351	ARG	5
1	A	434	LYS	5
1	A	314	HIS	5
1	A	281	LYS	5
1	A	486	LYS	5
1	A	495	TRP	4
1	A	258	ARG	4
1	A	449	TRP	4
1	A	282	LYS	4
1	A	256	MET	4
1	A	255	GLU	4
1	A	403	LEU	4
1	A	375	LYS	4
1	A	422	ILE	4
1	A	383	LEU	4
1	A	374	GLU	3
1	A	326	ARG	3
1	A	373	LEU	3
1	A	492	ARG	3
1	A	450	GLU	3
1	A	319	GLN	3
1	A	478	GLU	2
1	A	489	GLU	2
1	A	321	LEU	2
1	A	428	GLU	2
1	A	298	GLU	2
1	A	400	ASP	2
1	A	341	ASN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	311	GLU	2
1	A	481	GLU	2
1	A	440	ASP	2
1	A	280	TRP	2
1	A	438	LYS	2
1	A	304	LYS	2
1	A	423	LYS	2
1	A	433	ASN	2
1	A	424	TRP	2
1	A	274	GLU	1
1	A	474	ASP	1
1	A	498	ASN	1
1	A	425	THR	1
1	A	300	GLU	1
1	A	435	PHE	1
1	A	473	LYS	1
1	A	397	LYS	1
1	A	276	TYR	1
1	A	347	ARG	1
1	A	518	GLU	1
1	A	257	GLU	1
1	A	490	LEU	1
1	A	517	GLN	1
1	A	316	ASN	1
1	A	485	GLU	1
1	A	350	ASN	1
1	A	352	GLN	1
1	A	380	HIS	1
1	A	510	GLN	1
1	A	379	ILE	1
1	A	309	MET	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 8% for the well-defined parts and 7% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: 07102020_inactive1_BMRB.cs.str

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	544
Number of shifts mapped to atoms	544
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 8%, i.e. 241 atoms were assigned a chemical shift out of a possible 3099. 0 out of 42 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/1188 (0%)	0/473 (0%)	0/484 (0%)	0/231 (0%)
Sidechain	217/1593 (14%)	107/937 (11%)	110/593 (19%)	0/63 (0%)
Aromatic	24/318 (8%)	12/164 (7%)	12/137 (9%)	0/17 (0%)
Overall	241/3099 (8%)	119/1574 (8%)	122/1214 (10%)	0/311 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 7%, i.e. 266 atoms were assigned a chemical shift out of a possible 3610. 0 out of 46 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/1411 (0%)	0/562 (0%)	0/574 (0%)	0/275 (0%)
Sidechain	242/1840 (13%)	119/1082 (11%)	123/685 (18%)	0/73 (0%)
Aromatic	24/359 (7%)	12/185 (6%)	12/155 (8%)	0/19 (0%)
Overall	266/3610 (7%)	131/1829 (7%)	135/1414 (10%)	0/367 (0%)

7.1.4 Statistically unusual chemical shifts [i](#)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	453	THR	HG21	-0.20	2.29 – -0.01	-5.8
1	A	453	THR	HG22	-0.20	2.29 – -0.01	-5.8
1	A	453	THR	HG23	-0.20	2.29 – -0.01	-5.8

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

