



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 11:48 AM UTC

PDB ID : 1K3J / pdb_00001k3j
Title : Refined NMR Structure of the FHA1 Domain of Yeast Rad53
Authors : Yuan, C.; Yongkiettrakul, S.; Byeon, I.-J.L.; Zhou, S.; Tsai, M.-D.
Deposited on : 2001-10-03

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 types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

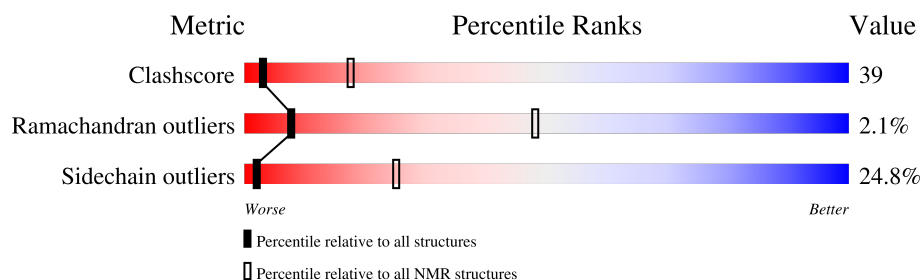
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	151	25% 42% 7% 26%

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 12 is the overall representative, medoid model (most similar to other models).

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:16-A:24 (9)	0.19	15
2	A:31-A:51, A:63-A:77, A:81-A:93, A:99-A:151 (102)	0.27	12

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

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

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2424 atoms, of which 1224 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein Kinase SPK1.

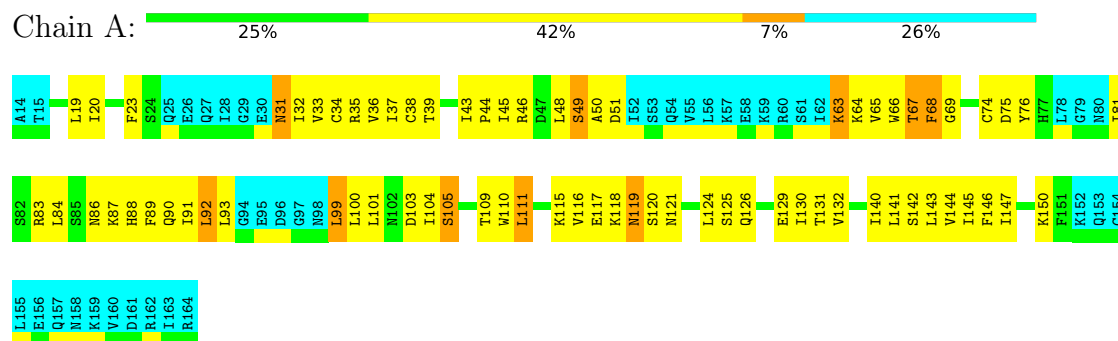
Mol	Chain	Residues	Atoms						Trace
1	A	151	Total	C	H	N	O	S	0
			2424	751	1224	215	230	4	

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: Protein Kinase SPK1

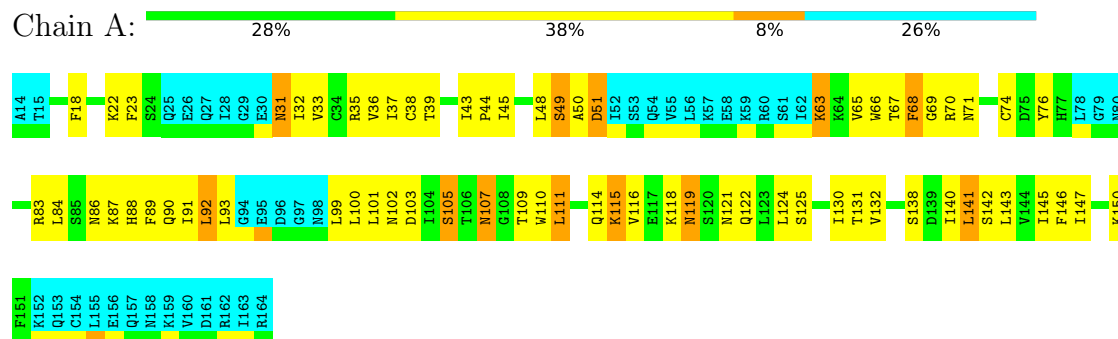


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

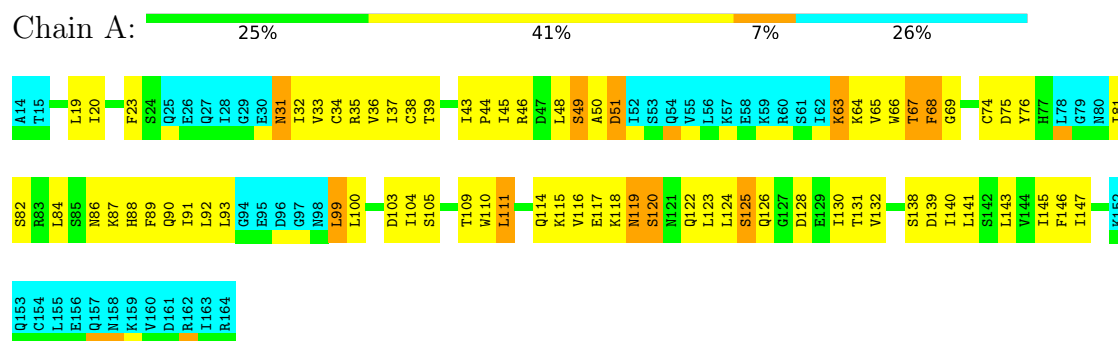
4.2.1 Score per residue for model 1

- Molecule 1: Protein Kinase SPK1



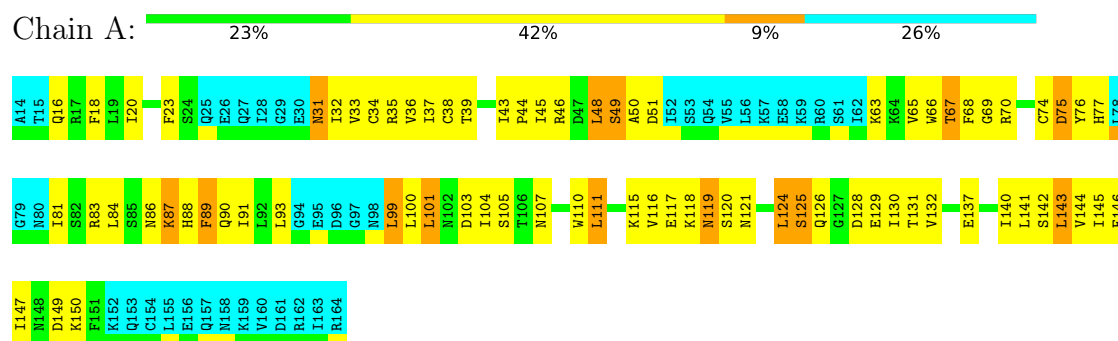
4.2.2 Score per residue for model 2

- Molecule 1: Protein Kinase SPK1



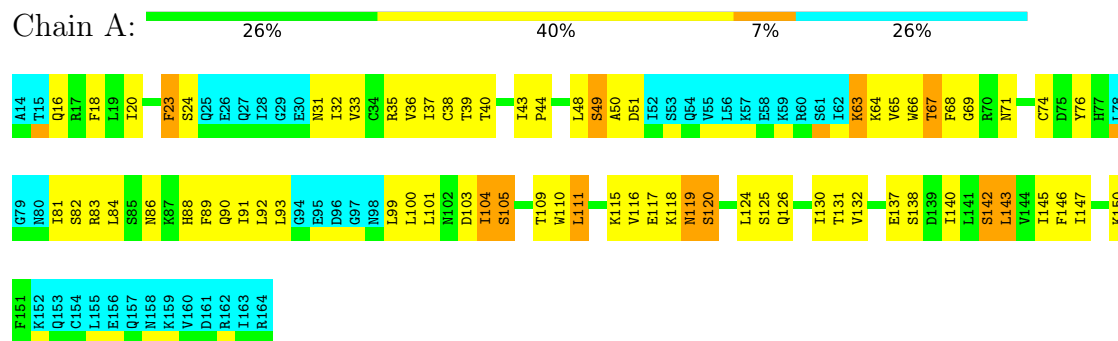
4.2.3 Score per residue for model 3

- Molecule 1: Protein Kinase SPK1



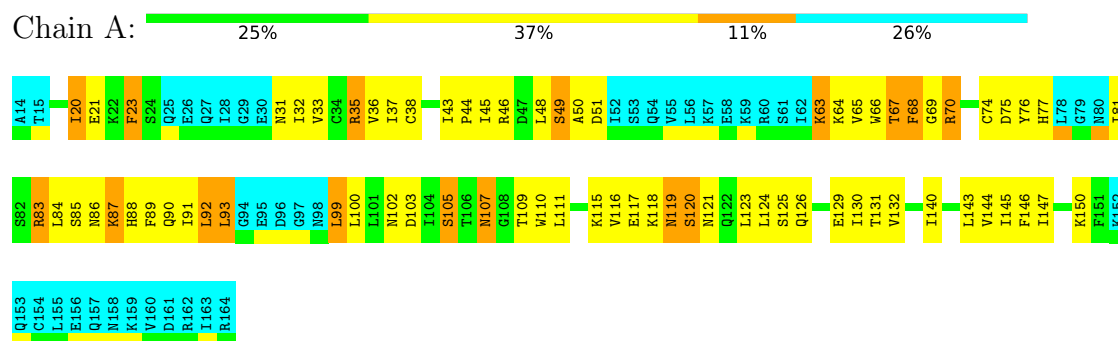
4.2.4 Score per residue for model 4

- Molecule 1: Protein Kinase SPK1



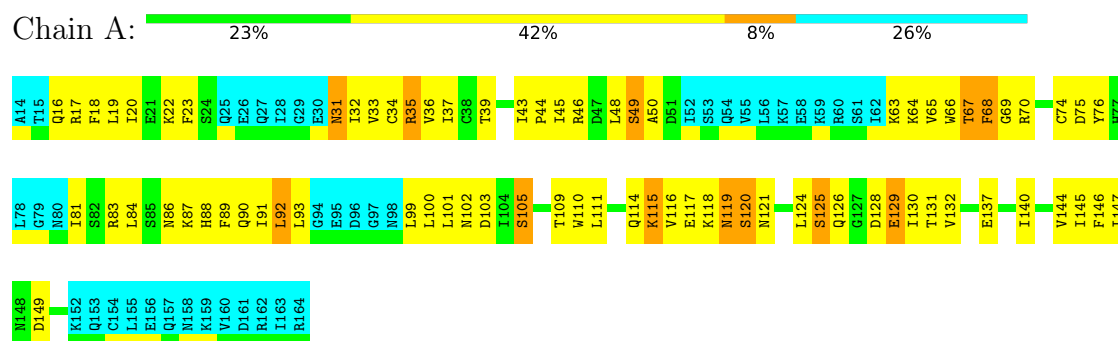
4.2.5 Score per residue for model 5

- Molecule 1: Protein Kinase SPK1



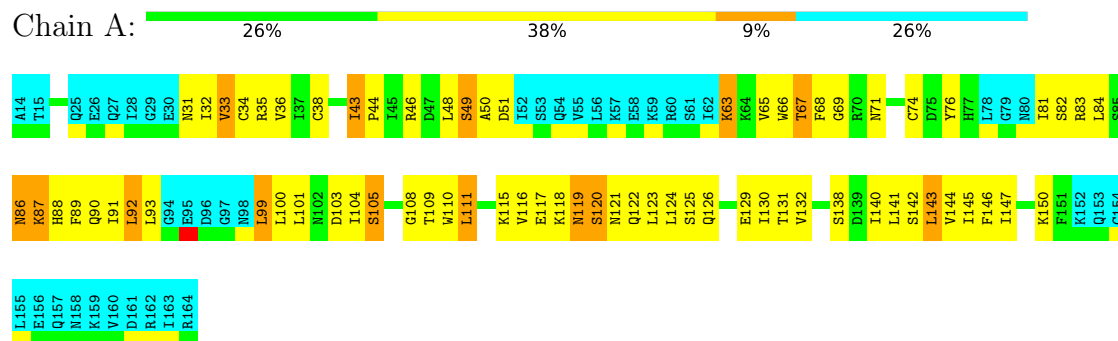
4.2.6 Score per residue for model 6

- Molecule 1: Protein Kinase SPK1



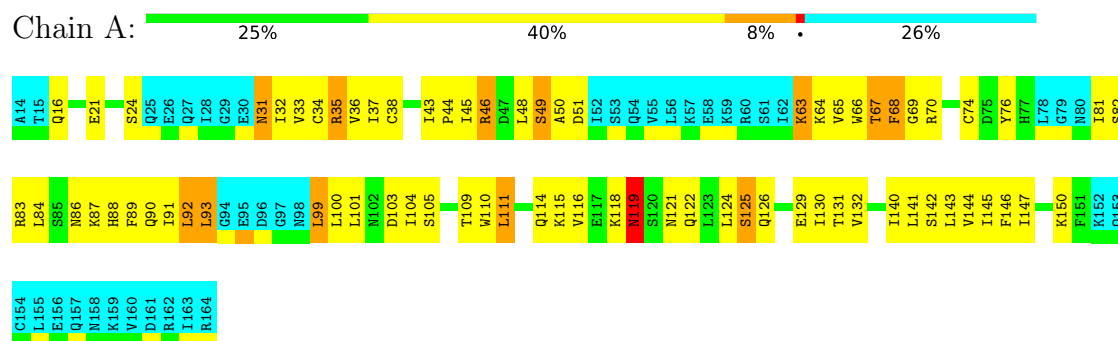
4.2.7 Score per residue for model 7

- Molecule 1: Protein Kinase SPK1



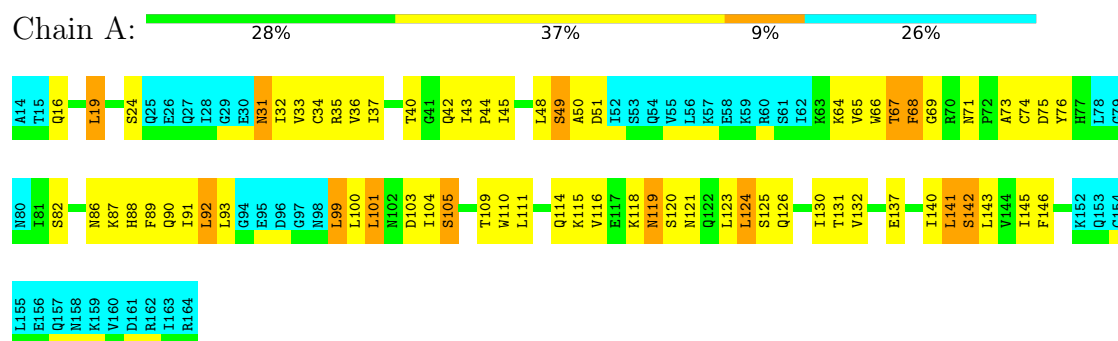
4.2.8 Score per residue for model 8

- Molecule 1: Protein Kinase SPK1



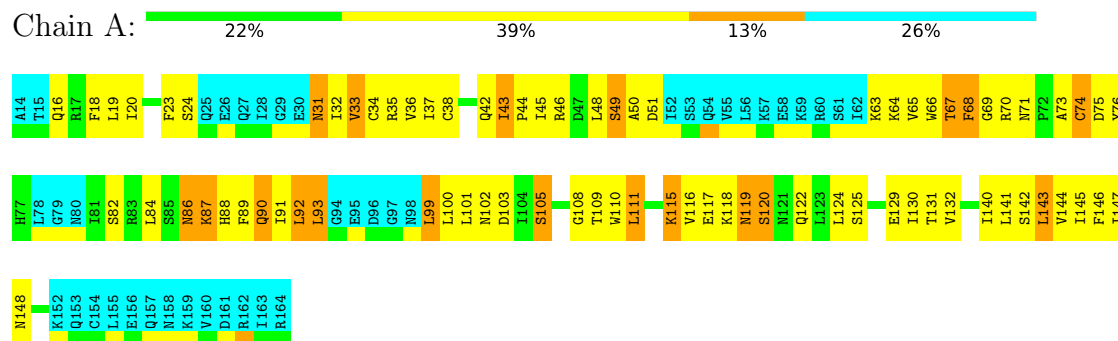
4.2.9 Score per residue for model 9

- Molecule 1: Protein Kinase SPK1



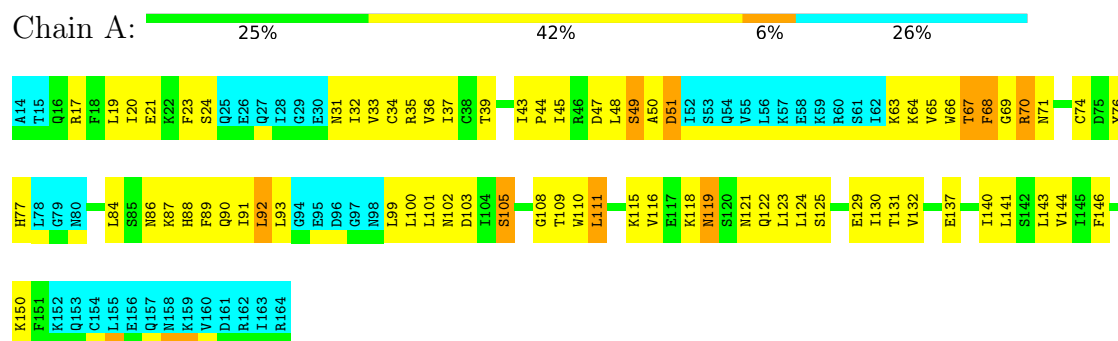
4.2.10 Score per residue for model 10

- Molecule 1: Protein Kinase SPK1



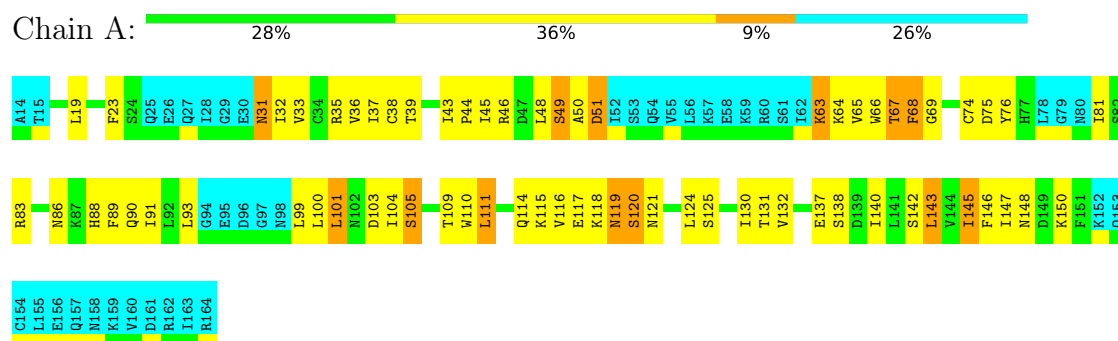
4.2.11 Score per residue for model 11

- Molecule 1: Protein Kinase SPK1



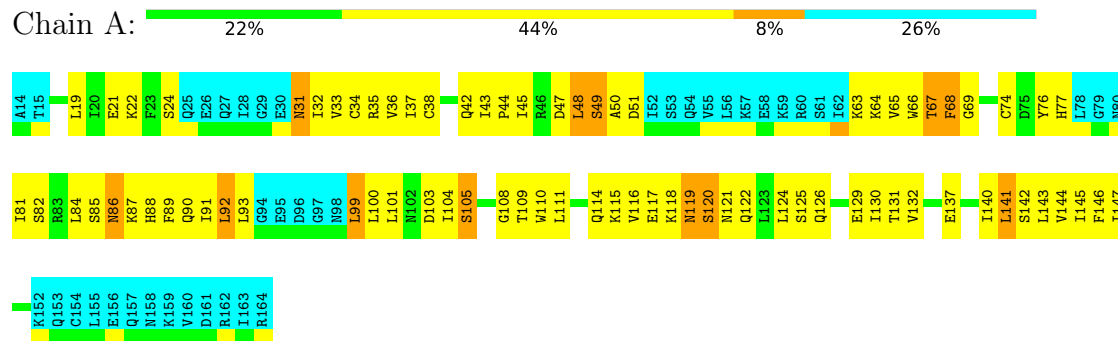
4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: Protein Kinase SPK1



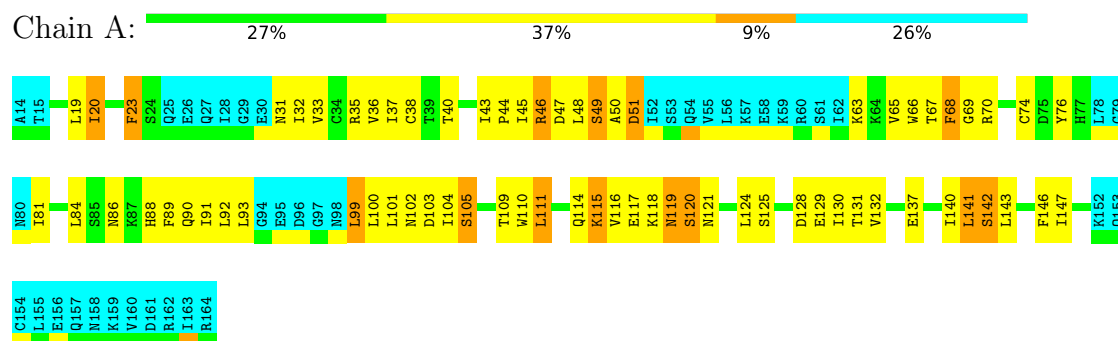
4.2.13 Score per residue for model 13

- Molecule 1: Protein Kinase SPK1



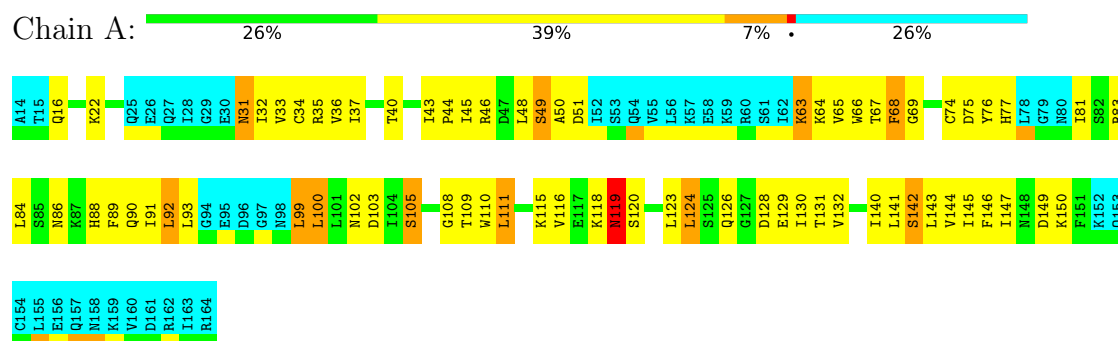
4.2.14 Score per residue for model 14

- Molecule 1: Protein Kinase SPK1



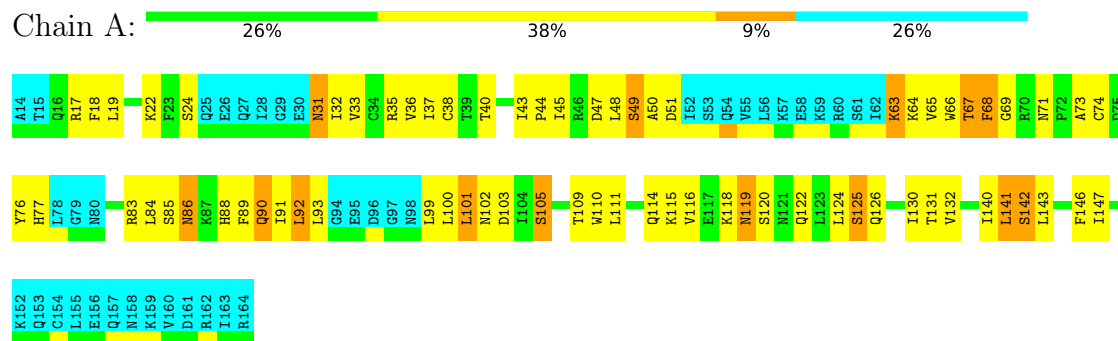
4.2.15 Score per residue for model 15

- Molecule 1: Protein Kinase SPK1



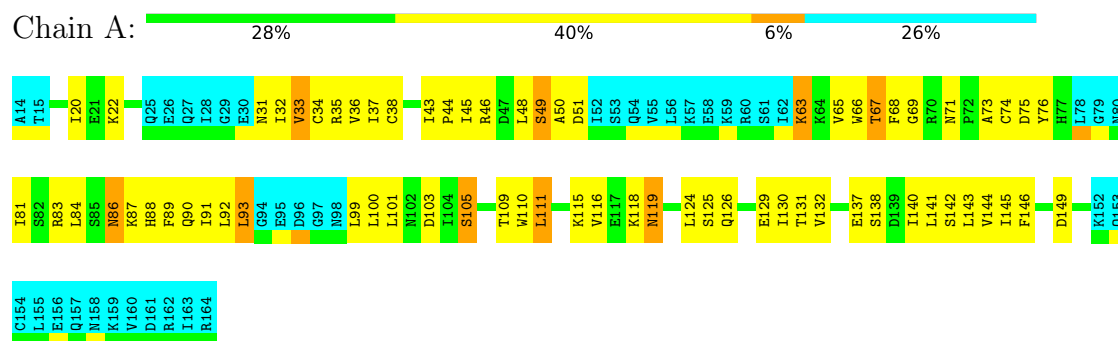
4.2.16 Score per residue for model 16

- Molecule 1: Protein Kinase SPK1



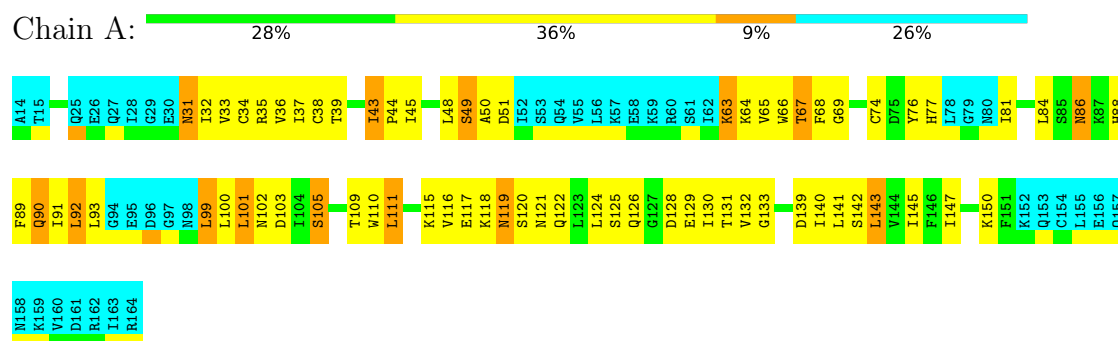
4.2.17 Score per residue for model 17

- Molecule 1: Protein Kinase SPK1



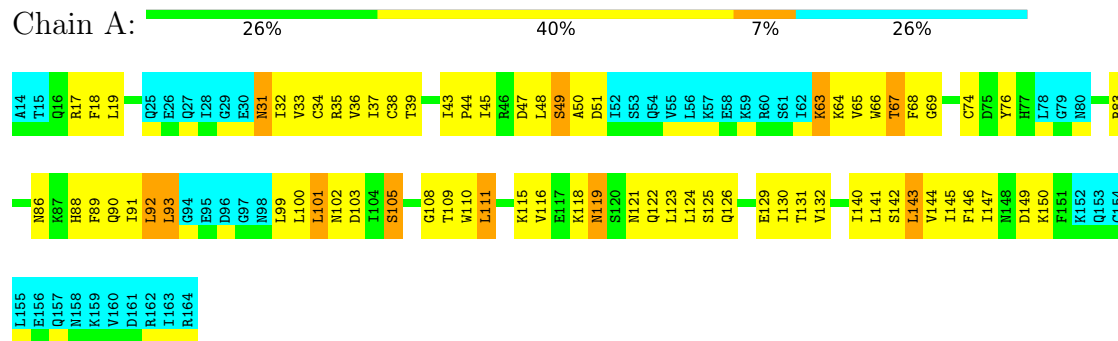
4.2.18 Score per residue for model 18

- Molecule 1: Protein Kinase SPK1



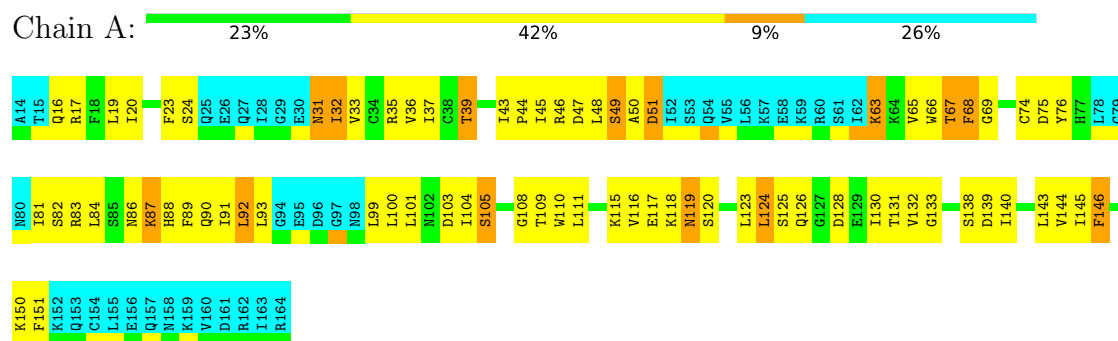
4.2.19 Score per residue for model 19

- Molecule 1: Protein Kinase SPK1



4.2.20 Score per residue for model 20

• Molecule 1: Protein Kinase SPK1



5 Refinement protocol and experimental data overview

The models were refined using the following method: *The structures are based on a total of 2377 restraints. Among them, 2107 are NOE-derived distance constraints, 192 TALOS-derived dihedral angle restraints, and 78 restraints from hydrogen bonds..*

Of the 50 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations, structures with the lowest energy.*

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

Software name	Classification	Version
CNS	structure solution	1.0
CNS	refinement	1.0

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 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 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	884	903	901	69±5
All	All	17680	18060	18020	1379

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 39.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:130:ILE:HD11	1:A:145:ILE:HD11	1.00	1.29	15	9
1:A:101:LEU:HD21	1:A:124:LEU:HD13	0.96	1.36	10	2
1:A:81:ILE:HD13	1:A:84:LEU:HD12	0.94	1.38	3	5
1:A:33:VAL:HG23	1:A:49:SER:HA	0.88	1.46	19	16
1:A:124:LEU:HD11	1:A:145:ILE:HG21	0.87	1.47	1	8
1:A:129:GLU:CG	1:A:144:VAL:HG22	0.82	2.04	6	10
1:A:101:LEU:HD11	1:A:130:ILE:HD11	0.82	1.46	12	4
1:A:67:THR:HG23	1:A:90:GLN:HG3	0.81	1.50	16	15
1:A:67:THR:HG23	1:A:90:GLN:CG	0.81	2.05	18	5
1:A:68:PHE:CE1	1:A:91:ILE:HD12	0.80	2.12	18	3
1:A:111:LEU:HD12	1:A:116:VAL:HG11	0.78	1.55	14	3
1:A:100:LEU:HD13	1:A:122:GLN:O	0.78	1.78	7	5
1:A:33:VAL:HG12	1:A:99:LEU:HD11	0.77	1.56	14	5
1:A:103:ASP:OD2	1:A:116:VAL:HG23	0.77	1.79	3	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:110:TRP:CE2	1:A:115:LYS:HB2	0.76	2.15	17	20
1:A:68:PHE:CZ	1:A:91:ILE:HD12	0.76	2.14	1	9
1:A:92:LEU:HD13	1:A:100:LEU:HD12	0.75	1.57	15	1
1:A:130:ILE:CD1	1:A:145:ILE:HD11	0.75	2.11	15	4
1:A:48:LEU:HD22	1:A:66:TRP:CD1	0.74	2.17	7	4
1:A:35:ARG:NE	1:A:45:ILE:HG21	0.74	1.97	8	1
1:A:33:VAL:CG1	1:A:93:LEU:HD13	0.73	2.11	9	4
1:A:100:LEU:HD22	1:A:121:ASN:HB3	0.72	1.60	11	5
1:A:48:LEU:HD23	1:A:66:TRP:CD2	0.72	2.19	5	8
1:A:33:VAL:HG23	1:A:49:SER:CA	0.72	2.13	5	15
1:A:36:VAL:HG21	1:A:68:PHE:CZ	0.71	2.21	17	4
1:A:37:ILE:HG23	1:A:45:ILE:HG12	0.70	1.62	17	17
1:A:36:VAL:HG13	1:A:48:LEU:HD11	0.70	1.62	3	3
1:A:129:GLU:HG3	1:A:144:VAL:HG22	0.70	1.63	3	4
1:A:100:LEU:HD23	1:A:122:GLN:O	0.69	1.86	8	5
1:A:33:VAL:HG11	1:A:93:LEU:HD22	0.69	1.63	14	12
1:A:40:THR:HG21	1:A:142:SER:OG	0.69	1.87	14	5
1:A:33:VAL:CG1	1:A:93:LEU:HD22	0.69	2.18	4	12
1:A:69:GLY:HA3	1:A:86:ASN:O	0.68	1.88	13	20
1:A:129:GLU:HG2	1:A:144:VAL:HG22	0.68	1.65	6	7
1:A:37:ILE:HD12	1:A:146:PHE:CD1	0.68	2.23	4	3
1:A:92:LEU:HD21	1:A:121:ASN:OD1	0.67	1.90	8	2
1:A:33:VAL:HG22	1:A:93:LEU:HD13	0.67	1.65	7	2
1:A:101:LEU:HD11	1:A:130:ILE:CD1	0.67	2.18	8	3
1:A:71:ASN:OD1	1:A:73:ALA:HB3	0.67	1.89	10	4
1:A:123:LEU:HD23	1:A:124:LEU:O	0.66	1.91	2	1
1:A:81:ILE:HD13	1:A:84:LEU:CD1	0.66	2.17	3	3
1:A:84:LEU:HD21	1:A:132:VAL:CG2	0.66	2.21	18	2
1:A:34:CYS:SG	1:A:48:LEU:HD12	0.66	2.31	7	6
1:A:103:ASP:CG	1:A:118:LYS:HA	0.65	2.16	5	20
1:A:141:LEU:HD23	1:A:142:SER:N	0.65	2.06	10	7
1:A:92:LEU:HD11	1:A:121:ASN:OD1	0.65	1.90	8	2
1:A:39:THR:HG21	1:A:129:GLU:OE2	0.65	1.91	19	1
1:A:81:ILE:HD12	1:A:84:LEU:CD1	0.65	2.21	7	4
1:A:124:LEU:HD21	1:A:147:ILE:HG12	0.64	1.69	6	8
1:A:33:VAL:HG12	1:A:99:LEU:HD21	0.64	1.67	18	4
1:A:92:LEU:HD11	1:A:102:ASN:HB2	0.64	1.68	15	3
1:A:34:CYS:SG	1:A:99:LEU:HD22	0.64	2.33	2	1
1:A:33:VAL:CG2	1:A:50:ALA:HB3	0.63	2.24	10	4
1:A:147:ILE:HD12	1:A:147:ILE:N	0.63	2.08	5	2
1:A:81:ILE:HB	1:A:84:LEU:HD13	0.63	1.69	20	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:LEU:HD12	1:A:116:VAL:CG1	0.63	2.24	14	3
1:A:36:VAL:HG11	1:A:68:PHE:CE2	0.63	2.29	5	5
1:A:43:ILE:HG23	1:A:44:PRO:HD2	0.62	1.70	14	4
1:A:70:ARG:NH2	1:A:84:LEU:HD22	0.62	2.08	11	2
1:A:111:LEU:CD1	1:A:116:VAL:HG11	0.62	2.24	14	3
1:A:40:THR:HG23	1:A:142:SER:HB2	0.62	1.72	16	2
1:A:99:LEU:HB2	1:A:124:LEU:HD21	0.62	1.71	15	1
1:A:131:THR:HG22	1:A:140:ILE:CG2	0.62	2.24	16	19
1:A:99:LEU:O	1:A:100:LEU:HD22	0.62	1.93	10	5
1:A:99:LEU:O	1:A:100:LEU:HD12	0.62	1.95	9	9
1:A:93:LEU:HD12	1:A:99:LEU:HG	0.62	1.70	10	1
1:A:65:VAL:HG23	1:A:91:ILE:C	0.61	2.21	5	1
1:A:65:VAL:HG13	1:A:91:ILE:C	0.61	2.21	6	18
1:A:36:VAL:HG21	1:A:68:PHE:CE2	0.60	2.30	19	13
1:A:101:LEU:HD23	1:A:130:ILE:HD11	0.60	1.74	14	2
1:A:99:LEU:HB2	1:A:124:LEU:HD22	0.60	1.72	6	1
1:A:100:LEU:HD13	1:A:122:GLN:C	0.59	2.22	7	5
1:A:33:VAL:HG21	1:A:50:ALA:HB3	0.59	1.73	10	2
1:A:67:THR:HG23	1:A:90:GLN:CD	0.59	2.22	4	2
1:A:141:LEU:HD22	1:A:143:LEU:CD2	0.59	2.28	9	3
1:A:141:LEU:HD22	1:A:143:LEU:HD13	0.59	1.73	14	1
1:A:38:CYS:HA	1:A:143:LEU:HD13	0.59	1.73	16	12
1:A:142:SER:C	1:A:143:LEU:HD22	0.59	2.22	13	11
1:A:36:VAL:HG23	1:A:48:LEU:HD11	0.58	1.75	9	3
1:A:124:LEU:HD11	1:A:145:ILE:CG2	0.58	2.24	1	3
1:A:43:ILE:HG21	1:A:76:TYR:CE2	0.58	2.34	2	2
1:A:93:LEU:C	1:A:93:LEU:HD13	0.58	2.24	13	3
1:A:42:GLN:CD	1:A:141:LEU:HD11	0.58	2.23	13	1
1:A:65:VAL:HG13	1:A:91:ILE:O	0.58	1.99	3	19
1:A:36:VAL:HG21	1:A:68:PHE:HE2	0.58	1.58	11	9
1:A:68:PHE:CD2	1:A:76:TYR:CG	0.57	2.92	18	11
1:A:39:THR:HG23	1:A:144:VAL:HG21	0.57	1.76	20	1
1:A:93:LEU:HD12	1:A:99:LEU:CD1	0.57	2.28	17	1
1:A:124:LEU:CD2	1:A:147:ILE:HD11	0.57	2.30	4	1
1:A:124:LEU:HD21	1:A:147:ILE:HG13	0.57	1.75	13	2
1:A:32:ILE:HA	1:A:49:SER:HB3	0.57	1.76	3	20
1:A:33:VAL:HG13	1:A:93:LEU:HD13	0.57	1.77	10	1
1:A:84:LEU:HD12	1:A:84:LEU:N	0.57	2.15	20	4
1:A:38:CYS:HA	1:A:143:LEU:HD23	0.57	1.75	5	2
1:A:100:LEU:HD23	1:A:122:GLN:C	0.57	2.24	11	5
1:A:68:PHE:CD1	1:A:76:TYR:HB2	0.57	2.34	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:33:VAL:CG1	1:A:99:LEU:HD21	0.57	2.30	15	2
1:A:81:ILE:HD11	1:A:141:LEU:HD12	0.56	1.77	7	1
1:A:37:ILE:HG23	1:A:45:ILE:CG1	0.56	2.30	8	6
1:A:33:VAL:HG21	1:A:93:LEU:HD22	0.56	1.77	10	2
1:A:37:ILE:HG23	1:A:45:ILE:HD11	0.56	1.76	11	1
1:A:33:VAL:HG23	1:A:50:ALA:N	0.56	2.13	3	2
1:A:65:VAL:HG23	1:A:91:ILE:O	0.56	2.00	5	1
1:A:101:LEU:HD11	1:A:124:LEU:HA	0.56	1.77	13	1
1:A:68:PHE:CE2	1:A:76:TYR:CG	0.56	2.94	17	5
1:A:99:LEU:C	1:A:100:LEU:HD22	0.56	2.25	10	5
1:A:129:GLU:CD	1:A:144:VAL:HG22	0.56	2.26	11	7
1:A:20:ILE:HG23	1:A:23:PHE:CE2	0.56	2.36	11	1
1:A:111:LEU:HD13	1:A:128:ASP:OD2	0.56	2.01	15	2
1:A:92:LEU:HD23	1:A:92:LEU:N	0.55	2.16	5	2
1:A:32:ILE:HG22	1:A:32:ILE:O	0.55	2.00	20	1
1:A:65:VAL:HG22	1:A:92:LEU:CB	0.55	2.30	4	5
1:A:101:LEU:HD12	1:A:101:LEU:N	0.55	2.16	14	1
1:A:88:HIS:CE1	1:A:105:SER:OG	0.55	2.60	8	3
1:A:68:PHE:CG	1:A:89:PHE:CE2	0.54	2.95	5	17
1:A:40:THR:HG21	1:A:142:SER:CB	0.54	2.31	14	1
1:A:81:ILE:HD12	1:A:84:LEU:HD11	0.54	1.78	7	2
1:A:65:VAL:HG12	1:A:90:GLN:HG2	0.54	1.79	6	13
1:A:37:ILE:HD12	1:A:146:PHE:CE1	0.54	2.37	4	1
1:A:23:PHE:CD1	1:A:24:SER:N	0.54	2.75	11	1
1:A:91:ILE:HD11	1:A:145:ILE:HD11	0.53	1.79	3	1
1:A:130:ILE:HD11	1:A:145:ILE:CD1	0.53	2.25	9	2
1:A:124:LEU:CD1	1:A:145:ILE:HG21	0.53	2.28	1	2
1:A:36:VAL:CG2	1:A:48:LEU:HD11	0.53	2.34	9	3
1:A:68:PHE:CD2	1:A:89:PHE:CE2	0.53	2.96	17	9
1:A:88:HIS:CD2	1:A:105:SER:OG	0.53	2.62	5	17
1:A:88:HIS:CD2	1:A:105:SER:HB2	0.53	2.38	3	3
1:A:68:PHE:CD2	1:A:76:TYR:CB	0.53	2.91	1	12
1:A:48:LEU:HD21	1:A:68:PHE:HZ	0.53	1.63	6	7
1:A:34:CYS:SG	1:A:48:LEU:HD22	0.53	2.44	15	2
1:A:101:LEU:HD21	1:A:145:ILE:HD12	0.53	1.80	6	1
1:A:93:LEU:HD23	1:A:99:LEU:HG	0.53	1.80	13	2
1:A:48:LEU:HD23	1:A:66:TRP:CG	0.52	2.38	2	5
1:A:126:GLN:HA	1:A:147:ILE:HD13	0.52	1.81	7	5
1:A:87:LYS:CB	1:A:104:ILE:HD12	0.52	2.35	2	3
1:A:81:ILE:CD1	1:A:84:LEU:HD12	0.52	2.26	3	1
1:A:68:PHE:N	1:A:68:PHE:CD1	0.52	2.77	8	14

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:VAL:HG22	1:A:90:GLN:HG2	0.52	1.81	5	1
1:A:33:VAL:HG12	1:A:34:CYS:N	0.52	2.19	7	1
1:A:68:PHE:CD2	1:A:76:TYR:CD2	0.52	2.98	17	2
1:A:123:LEU:HD13	1:A:124:LEU:O	0.52	2.05	15	1
1:A:129:GLU:OE2	1:A:144:VAL:HG22	0.52	2.05	19	1
1:A:43:ILE:CG2	1:A:44:PRO:HD2	0.52	2.35	16	20
1:A:33:VAL:HG21	1:A:50:ALA:CB	0.52	2.35	10	3
1:A:125:SER:O	1:A:147:ILE:HD11	0.51	2.05	3	4
1:A:43:ILE:CD1	1:A:143:LEU:HD21	0.51	2.35	7	1
1:A:42:GLN:HB2	1:A:43:ILE:HD12	0.51	1.82	9	1
1:A:67:THR:HG22	1:A:87:LYS:HB3	0.51	1.81	13	3
1:A:111:LEU:HD23	1:A:128:ASP:OD2	0.51	2.05	18	1
1:A:84:LEU:HD21	1:A:132:VAL:HG21	0.51	1.80	18	2
1:A:101:LEU:CD1	1:A:130:ILE:HD11	0.51	2.27	12	2
1:A:92:LEU:HD21	1:A:102:ASN:HB2	0.51	1.83	1	2
1:A:92:LEU:HD11	1:A:100:LEU:HD13	0.51	1.81	18	1
1:A:87:LYS:HB2	1:A:104:ILE:HD12	0.51	1.83	9	6
1:A:101:LEU:HD11	1:A:124:LEU:HD13	0.51	1.82	14	1
1:A:84:LEU:HD21	1:A:132:VAL:HG23	0.51	1.81	16	5
1:A:33:VAL:CG2	1:A:93:LEU:HD13	0.51	2.35	17	2
1:A:91:ILE:HG12	1:A:101:LEU:HD12	0.51	1.82	18	2
1:A:33:VAL:CG2	1:A:50:ALA:N	0.50	2.74	4	17
1:A:124:LEU:HD21	1:A:147:ILE:HD11	0.50	1.84	4	1
1:A:66:TRP:O	1:A:90:GLN:HA	0.50	2.06	7	14
1:A:131:THR:CG2	1:A:140:ILE:CG2	0.50	2.90	16	20
1:A:40:THR:CG2	1:A:142:SER:CB	0.50	2.89	4	5
1:A:88:HIS:CE1	1:A:105:SER:HB3	0.50	2.41	4	17
1:A:43:ILE:HD12	1:A:141:LEU:HD11	0.50	1.84	14	1
1:A:66:TRP:HB3	1:A:68:PHE:CE1	0.50	2.41	3	1
1:A:85:SER:O	1:A:86:ASN:C	0.50	2.55	5	2
1:A:33:VAL:HG22	1:A:93:LEU:CD1	0.50	2.35	17	2
1:A:93:LEU:HD12	1:A:99:LEU:HD11	0.50	1.83	17	1
1:A:99:LEU:HD23	1:A:124:LEU:HD22	0.50	1.82	16	1
1:A:124:LEU:HD22	1:A:147:ILE:HG12	0.50	1.84	15	1
1:A:43:ILE:CD1	1:A:141:LEU:HD21	0.49	2.37	1	1
1:A:67:THR:O	1:A:75:ASP:N	0.49	2.45	2	8
1:A:103:ASP:O	1:A:119:ASN:N	0.49	2.42	2	19
1:A:99:LEU:HB3	1:A:124:LEU:HD13	0.49	1.85	4	1
1:A:141:LEU:C	1:A:141:LEU:HD23	0.49	2.32	2	3
1:A:33:VAL:HG23	1:A:49:SER:C	0.49	2.32	5	15
1:A:100:LEU:HD23	1:A:121:ASN:HB3	0.49	1.84	3	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:88:HIS:CD2	1:A:132:VAL:CG1	0.49	2.96	9	20
1:A:39:THR:CG2	1:A:144:VAL:HG21	0.49	2.37	20	1
1:A:66:TRP:O	1:A:90:GLN:CG	0.49	2.60	3	8
1:A:88:HIS:CE1	1:A:132:VAL:HB	0.49	2.43	2	11
1:A:92:LEU:O	1:A:99:LEU:HD23	0.49	2.06	8	1
1:A:48:LEU:HD23	1:A:66:TRP:CE3	0.49	2.42	14	8
1:A:33:VAL:HG11	1:A:66:TRP:CH2	0.49	2.43	7	2
1:A:92:LEU:HD13	1:A:100:LEU:CD1	0.49	2.36	15	1
1:A:39:THR:HG23	1:A:144:VAL:CG2	0.48	2.38	20	1
1:A:124:LEU:HD21	1:A:147:ILE:CG1	0.48	2.39	5	4
1:A:40:THR:CG2	1:A:142:SER:HB2	0.48	2.38	9	5
1:A:68:PHE:HZ	1:A:91:ILE:HD12	0.48	1.68	2	1
1:A:48:LEU:HD11	1:A:68:PHE:HZ	0.48	1.67	7	1
1:A:93:LEU:HD13	1:A:99:LEU:CD2	0.48	2.38	12	3
1:A:43:ILE:HG22	1:A:44:PRO:HD2	0.48	1.84	2	1
1:A:36:VAL:HG11	1:A:68:PHE:HE2	0.48	1.69	16	2
1:A:101:LEU:HD21	1:A:124:LEU:CD1	0.48	2.25	10	1
1:A:33:VAL:HG11	1:A:93:LEU:HD13	0.48	1.83	9	1
1:A:43:ILE:CG2	1:A:76:TYR:CZ	0.48	2.96	6	6
1:A:141:LEU:HD22	1:A:143:LEU:CD1	0.48	2.39	14	1
1:A:92:LEU:HD12	1:A:100:LEU:HB3	0.48	1.85	6	1
1:A:123:LEU:HD13	1:A:124:LEU:N	0.48	2.24	19	2
1:A:35:ARG:NH1	1:A:45:ILE:HG21	0.47	2.24	6	1
1:A:20:ILE:O	1:A:23:PHE:HB2	0.47	2.09	4	8
1:A:68:PHE:CD2	1:A:76:TYR:HB2	0.47	2.44	2	6
1:A:48:LEU:HB3	1:A:66:TRP:CE2	0.47	2.44	20	11
1:A:100:LEU:HD12	1:A:121:ASN:HB3	0.47	1.85	7	1
1:A:42:GLN:OE1	1:A:141:LEU:HD11	0.47	2.09	13	1
1:A:81:ILE:N	1:A:81:ILE:HD12	0.47	2.24	15	1
1:A:68:PHE:CD2	1:A:89:PHE:CZ	0.47	3.02	19	2
1:A:99:LEU:HD13	1:A:124:LEU:CD2	0.47	2.39	7	1
1:A:88:HIS:CD2	1:A:132:VAL:HG11	0.47	2.44	4	11
1:A:35:ARG:HE	1:A:45:ILE:HG21	0.47	1.68	8	1
1:A:111:LEU:HD23	1:A:128:ASP:OD1	0.47	2.09	14	1
1:A:49:SER:O	1:A:66:TRP:HZ2	0.47	1.92	17	9
1:A:142:SER:O	1:A:143:LEU:HD22	0.47	2.09	13	6
1:A:88:HIS:CG	1:A:105:SER:HB2	0.47	2.44	2	2
1:A:48:LEU:HG	1:A:66:TRP:CD1	0.47	2.45	17	8
1:A:68:PHE:CE2	1:A:76:TYR:CD2	0.47	3.03	4	2
1:A:111:LEU:C	1:A:111:LEU:HD12	0.47	2.35	11	10
1:A:141:LEU:HD22	1:A:143:LEU:HD21	0.47	1.85	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:83:ARG:O	1:A:107:ASN:ND2	0.47	2.48	5	2
1:A:100:LEU:C	1:A:101:LEU:HD12	0.47	2.34	14	1
1:A:49:SER:O	1:A:64:LYS:CE	0.47	2.64	5	11
1:A:101:LEU:HD12	1:A:124:LEU:CD1	0.46	2.40	3	1
1:A:101:LEU:HD11	1:A:145:ILE:HD12	0.46	1.86	9	1
1:A:33:VAL:HG13	1:A:93:LEU:HD22	0.46	1.86	5	2
1:A:93:LEU:CD1	1:A:99:LEU:HD11	0.46	2.40	17	1
1:A:124:LEU:CD1	1:A:124:LEU:C	0.46	2.89	20	2
1:A:99:LEU:CD1	1:A:147:ILE:HG23	0.46	2.40	18	1
1:A:31:ASN:O	1:A:49:SER:HB3	0.46	2.11	10	1
1:A:43:ILE:CD1	1:A:141:LEU:HD11	0.46	2.40	14	1
1:A:68:PHE:CG	1:A:76:TYR:HB3	0.46	2.46	4	2
1:A:93:LEU:HD13	1:A:99:LEU:CD1	0.46	2.40	12	2
1:A:70:ARG:NH1	1:A:85:SER:O	0.46	2.49	5	1
1:A:68:PHE:O	1:A:88:HIS:N	0.46	2.49	2	9
1:A:68:PHE:CE1	1:A:91:ILE:CD1	0.46	2.99	17	2
1:A:65:VAL:CG1	1:A:91:ILE:O	0.46	2.63	3	12
1:A:105:SER:HB2	1:A:108:GLY:H	0.46	1.71	10	7
1:A:33:VAL:CG1	1:A:99:LEU:HD11	0.45	2.41	12	1
1:A:100:LEU:HD23	1:A:100:LEU:N	0.45	2.26	15	1
1:A:109:THR:HG22	1:A:130:ILE:CG2	0.45	2.41	8	19
1:A:92:LEU:HD21	1:A:121:ASN:HD22	0.45	1.72	9	2
1:A:129:GLU:HG3	1:A:144:VAL:HG13	0.45	1.88	13	1
1:A:88:HIS:O	1:A:105:SER:N	0.45	2.49	2	16
1:A:110:TRP:NE1	1:A:115:LYS:HB2	0.45	2.26	4	14
1:A:70:ARG:CZ	1:A:84:LEU:HB2	0.45	2.41	11	2
1:A:84:LEU:CD2	1:A:88:HIS:CE1	0.45	3.00	17	2
1:A:89:PHE:CD1	1:A:89:PHE:N	0.45	2.85	3	1
1:A:124:LEU:HG	1:A:125:SER:N	0.45	2.26	8	2
1:A:84:LEU:N	1:A:84:LEU:CD1	0.45	2.80	20	2
1:A:99:LEU:HB3	1:A:124:LEU:HD23	0.45	1.88	20	1
1:A:48:LEU:CD2	1:A:66:TRP:CG	0.44	3.00	2	6
1:A:109:THR:CG2	1:A:130:ILE:CG2	0.44	2.95	20	7
1:A:67:THR:CG2	1:A:90:GLN:HG3	0.44	2.37	7	1
1:A:19:LEU:O	1:A:19:LEU:HD13	0.44	2.12	9	1
1:A:43:ILE:HD12	1:A:143:LEU:HD21	0.44	1.89	20	1
1:A:92:LEU:HD11	1:A:100:LEU:CD2	0.44	2.42	9	1
1:A:20:ILE:O	1:A:23:PHE:CD2	0.44	2.70	11	1
1:A:38:CYS:SG	1:A:43:ILE:HB	0.44	2.53	14	1
1:A:88:HIS:NE2	1:A:132:VAL:HB	0.44	2.28	6	5
1:A:33:VAL:CG2	1:A:93:LEU:HD22	0.44	2.43	10	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:43:ILE:HG21	1:A:76:TYR:CZ	0.44	2.48	20	5
1:A:65:VAL:HG21	1:A:92:LEU:HD23	0.43	1.91	6	1
1:A:101:LEU:HG	1:A:124:LEU:HD11	0.43	1.90	9	1
1:A:74:CYS:HG	1:A:87:LYS:HA	0.43	1.72	10	1
1:A:81:ILE:CD1	1:A:141:LEU:HD12	0.43	2.43	7	1
1:A:48:LEU:HD21	1:A:68:PHE:CZ	0.43	2.49	14	3
1:A:90:GLN:CG	1:A:104:ILE:HD13	0.43	2.43	4	1
1:A:68:PHE:CZ	1:A:91:ILE:CD1	0.43	3.01	7	2
1:A:99:LEU:CB	1:A:124:LEU:HD13	0.43	2.43	4	1
1:A:68:PHE:CD1	1:A:76:TYR:CB	0.43	3.01	3	1
1:A:132:VAL:HG22	1:A:141:LEU:O	0.43	2.13	3	1
1:A:101:LEU:N	1:A:101:LEU:CD1	0.43	2.81	14	1
1:A:88:HIS:CD2	1:A:105:SER:HG	0.43	2.31	5	1
1:A:123:LEU:C	1:A:123:LEU:HD13	0.43	2.39	5	3
1:A:45:ILE:HG22	1:A:46:ARG:N	0.43	2.28	14	1
1:A:88:HIS:NE2	1:A:132:VAL:CG1	0.43	2.82	3	4
1:A:117:GLU:O	1:A:120:SER:HB2	0.43	2.14	7	10
1:A:70:ARG:CZ	1:A:84:LEU:CB	0.43	2.96	5	1
1:A:70:ARG:NH2	1:A:84:LEU:CD2	0.43	2.82	5	1
1:A:49:SER:O	1:A:64:LYS:HE2	0.43	2.14	6	3
1:A:66:TRP:N	1:A:91:ILE:O	0.43	2.49	12	3
1:A:118:LYS:HG2	1:A:119:ASN:N	0.42	2.29	12	2
1:A:66:TRP:O	1:A:90:GLN:HG2	0.42	2.13	7	4
1:A:92:LEU:CD2	1:A:102:ASN:HB2	0.42	2.43	5	1
1:A:81:ILE:HD12	1:A:84:LEU:HD12	0.42	1.90	7	1
1:A:68:PHE:CG	1:A:76:TYR:CB	0.42	3.03	17	1
1:A:118:LYS:O	1:A:119:ASN:C	0.42	2.62	19	5
1:A:89:PHE:HA	1:A:104:ILE:HG12	0.42	1.91	7	1
1:A:90:GLN:O	1:A:102:ASN:N	0.42	2.48	15	8
1:A:64:LYS:O	1:A:66:TRP:CZ3	0.42	2.73	5	1
1:A:66:TRP:CD1	1:A:75:ASP:OD2	0.42	2.72	15	1
1:A:20:ILE:HG23	1:A:23:PHE:HE2	0.42	1.71	11	1
1:A:23:PHE:CD1	1:A:23:PHE:C	0.42	2.98	11	1
1:A:65:VAL:HA	1:A:91:ILE:O	0.42	2.15	6	4
1:A:33:VAL:CG1	1:A:34:CYS:N	0.41	2.83	7	1
1:A:92:LEU:HD21	1:A:100:LEU:HB3	0.41	1.90	14	1
1:A:93:LEU:HD13	1:A:99:LEU:HG	0.41	1.90	3	1
1:A:36:VAL:HG23	1:A:48:LEU:HD13	0.41	1.91	1	1
1:A:103:ASP:HB3	1:A:109:THR:HB	0.41	1.90	1	4
1:A:130:ILE:N	1:A:143:LEU:O	0.41	2.52	9	4
1:A:35:ARG:CD	1:A:45:ILE:CG2	0.41	2.98	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:107:ASN:OD1	1:A:107:ASN:N	0.41	2.54	1	1
1:A:33:VAL:HG11	1:A:93:LEU:HG	0.41	1.93	18	1
1:A:42:GLN:CB	1:A:141:LEU:HD11	0.41	2.45	10	1
1:A:118:LYS:O	1:A:120:SER:N	0.41	2.54	10	1
1:A:84:LEU:CD2	1:A:132:VAL:HG21	0.41	2.45	11	1
1:A:129:GLU:CG	1:A:143:LEU:O	0.41	2.69	14	1
1:A:110:TRP:O	1:A:130:ILE:HG23	0.41	2.15	3	1
1:A:50:ALA:HB3	1:A:93:LEU:CD2	0.41	2.45	6	1
1:A:92:LEU:HD21	1:A:121:ASN:ND2	0.41	2.31	9	1
1:A:101:LEU:HD11	1:A:145:ILE:CD1	0.41	2.46	9	1
1:A:63:LYS:N	1:A:63:LYS:CD	0.41	2.84	7	1
1:A:40:THR:HG21	1:A:142:SER:H	0.41	1.76	4	1
1:A:92:LEU:HD13	1:A:121:ASN:HD22	0.41	1.76	6	1
1:A:65:VAL:HG22	1:A:92:LEU:HB3	0.41	1.92	8	1
1:A:124:LEU:CD2	1:A:147:ILE:CD1	0.41	2.99	4	1
1:A:88:HIS:CG	1:A:105:SER:HB3	0.41	2.51	10	2
1:A:68:PHE:CD2	1:A:76:TYR:CD1	0.41	3.09	19	1
1:A:50:ALA:CB	1:A:93:LEU:HD23	0.40	2.46	12	2
1:A:111:LEU:HD12	1:A:111:LEU:C	0.40	2.41	8	1
1:A:84:LEU:HD22	1:A:88:HIS:CE1	0.40	2.51	13	1
1:A:49:SER:O	1:A:66:TRP:CZ2	0.40	2.74	17	1
1:A:66:TRP:O	1:A:91:ILE:N	0.40	2.51	6	2
1:A:23:PHE:CG	1:A:24:SER:N	0.40	2.89	11	1
1:A:130:ILE:HG13	1:A:145:ILE:HD11	0.40	1.92	12	1
1:A:101:LEU:CD2	1:A:145:ILE:CD1	0.40	2.99	19	1
1:A:33:VAL:CG2	1:A:50:ALA:CB	0.40	2.99	17	1
1:A:133:GLY:O	1:A:139:ASP:O	0.40	2.40	18	2
1:A:70:ARG:N	1:A:86:ASN:O	0.40	2.55	3	1
1:A:46:ARG:HB2	1:A:76:TYR:CE2	0.40	2.51	8	1
1:A:129:GLU:HA	1:A:143:LEU:O	0.40	2.17	15	1
1:A:103:ASP:N	1:A:103:ASP:OD1	0.40	2.54	3	1

6.3 Torsion angles ⓘ

6.3.1 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 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	111/151 (74%)	100±1 (90±1%)	8±1 (8±1%)	2±0 (2±0%)	8	48
All	All	2220/3020 (74%)	2003 (90%)	170 (8%)	47 (2%)	8	48

All 5 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	31	ASN	20
1	A	119	ASN	20
1	A	128	ASP	3
1	A	104	ILE	3
1	A	86	ASN	1

6.3.2 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 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	102/137 (74%)	77±2 (75±2%)	25±2 (25±2%)	2	25
All	All	2040/2740 (74%)	1534 (75%)	506 (25%)	2	25

All 65 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	35	ARG	20
1	A	49	SER	20
1	A	67	THR	20
1	A	74	CYS	20
1	A	111	LEU	20
1	A	125	SER	18
1	A	105	SER	17
1	A	146	PHE	17
1	A	63	LYS	15
1	A	92	LEU	15
1	A	68	PHE	14
1	A	120	SER	14
1	A	31	ASN	13

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Mol	Chain	Res	Type	Models (Total)
1	A	150	LYS	12
1	A	46	ARG	12
1	A	83	ARG	12
1	A	101	LEU	11
1	A	19	LEU	11
1	A	99	LEU	11
1	A	126	GLN	10
1	A	39	THR	9
1	A	87	LYS	9
1	A	114	GLN	9
1	A	137	GLU	9
1	A	82	SER	8
1	A	16	GLN	8
1	A	70	ARG	7
1	A	138	SER	7
1	A	141	LEU	7
1	A	143	LEU	7
1	A	24	SER	7
1	A	18	PHE	6
1	A	22	LYS	6
1	A	51	ASP	6
1	A	77	HIS	6
1	A	47	ASP	6
1	A	23	PHE	5
1	A	124	LEU	5
1	A	149	ASP	5
1	A	142	SER	5
1	A	93	LEU	5
1	A	86	ASN	5
1	A	71	ASN	4
1	A	115	LYS	4
1	A	21	GLU	4
1	A	34	CYS	4
1	A	17	ARG	4
1	A	107	ASN	3
1	A	145	ILE	3
1	A	20	ILE	3
1	A	33	VAL	3
1	A	43	ILE	3
1	A	90	GLN	3
1	A	48	LEU	2
1	A	75	ASP	2

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Mol	Chain	Res	Type	Models (Total)
1	A	129	GLU	2
1	A	123	LEU	2
1	A	119	ASN	2
1	A	148	ASN	2
1	A	117	GLU	2
1	A	139	ASP	1
1	A	89	PHE	1
1	A	100	LEU	1
1	A	85	SER	1
1	A	32	ILE	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides 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

No chemical shift data were provided