



Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 05:41 AM BST

PDB ID : 2YQF
Title : Solution structure of the death domain of Ankyrin-1
Authors : Tanabe, W.; Suzuki, S.; Muto, Y.; Inoue, M.; Kigawa, T.; Terada, T.; Shirouzu, M.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2007-03-30

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
<http://wwpdb.org/validation/2016/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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

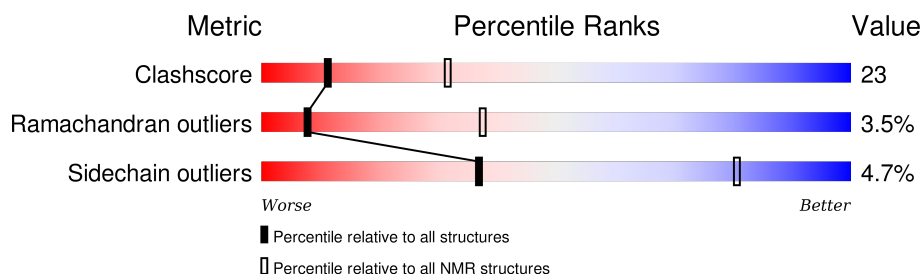
1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	111	

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 4 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:1405-A:1484 (80)	0.18	4

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 4 clusters and 7 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1694 atoms, of which 841 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ankyrin-1.

Mol	Chain	Residues	Atoms						Trace
1	A	111	Total	C	H	N	O	S	0
			1694	520	841	156	173	4	

There are 7 discrepancies between the modelled and reference sequences:

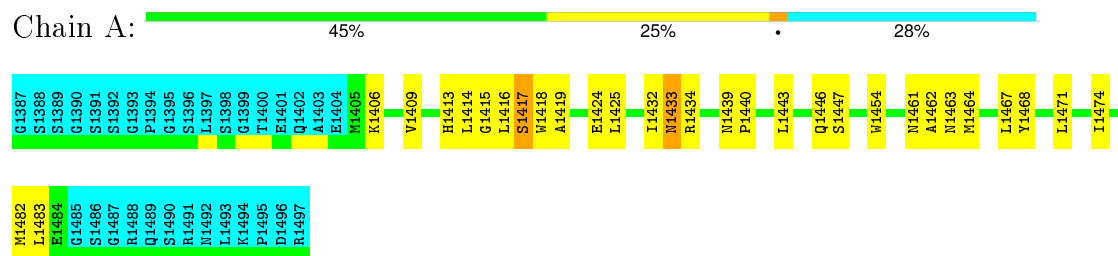
Chain	Residue	Modelled	Actual	Comment	Reference
A	1387	GLY	-	EXPRESSION TAG	UNP P16157
A	1388	SER	-	EXPRESSION TAG	UNP P16157
A	1389	SER	-	EXPRESSION TAG	UNP P16157
A	1390	GLY	-	EXPRESSION TAG	UNP P16157
A	1391	SER	-	EXPRESSION TAG	UNP P16157
A	1392	SER	-	EXPRESSION TAG	UNP P16157
A	1393	GLY	-	EXPRESSION TAG	UNP P16157

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: Ankyrin-1

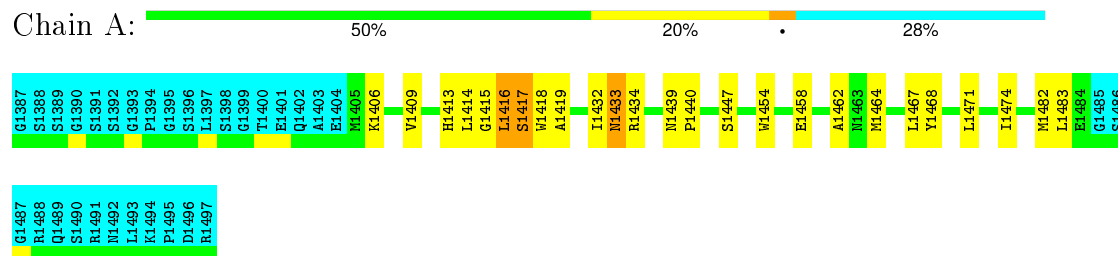


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

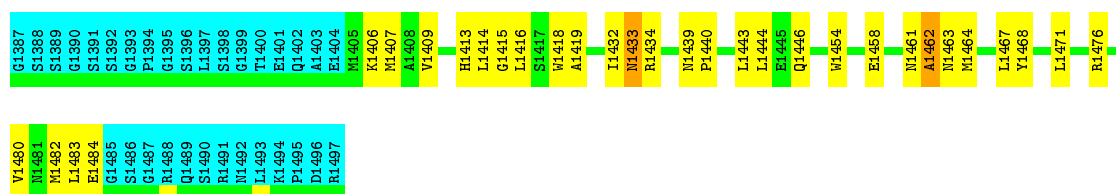
- Molecule 1: Ankyrin-1



4.2.2 Score per residue for model 2

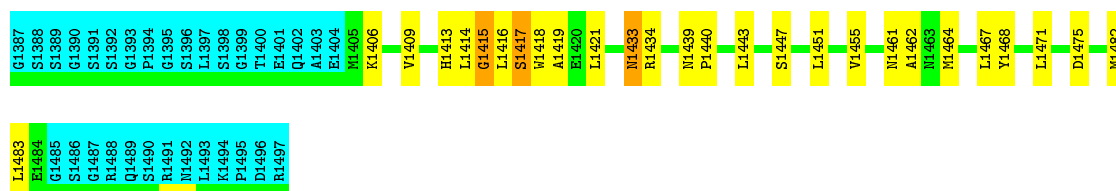
- Molecule 1: Ankyrin-1





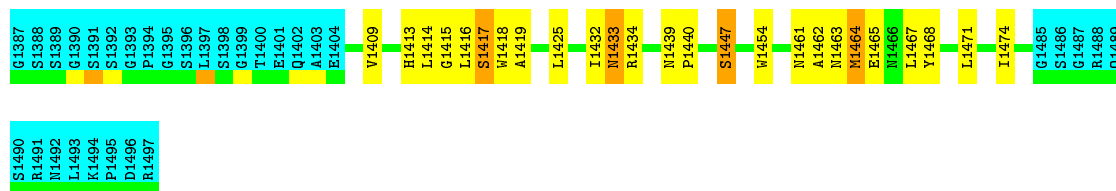
4.2.3 Score per residue for model 3

- Molecule 1: Ankyrin-1



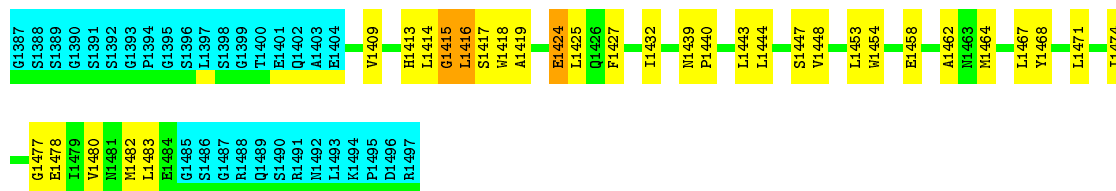
4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Ankyrin-1



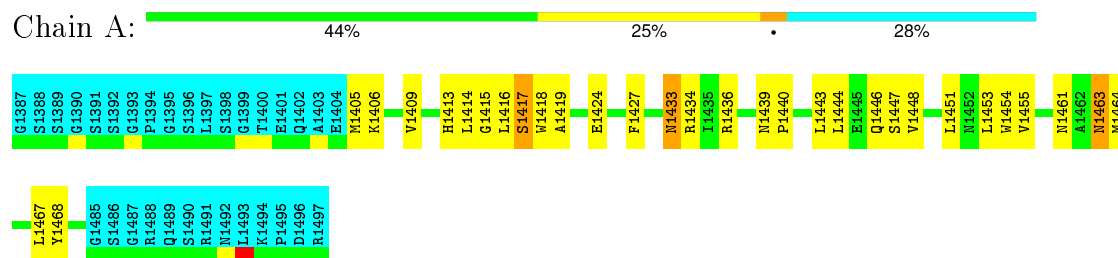
4.2.5 Score per residue for model 5

- Molecule 1: Ankyrin-1



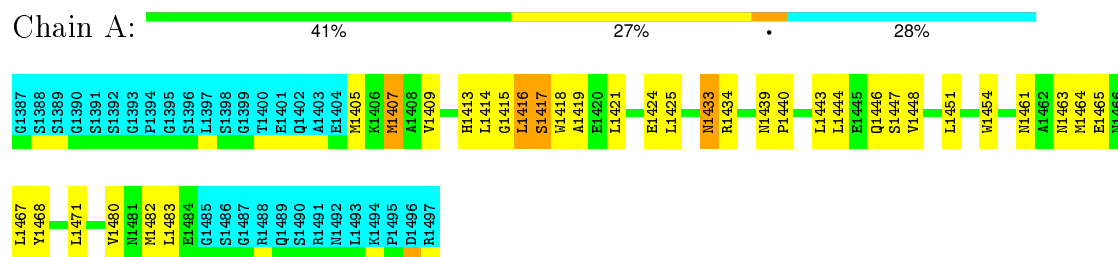
4.2.6 Score per residue for model 6

- Molecule 1: Ankyrin-1



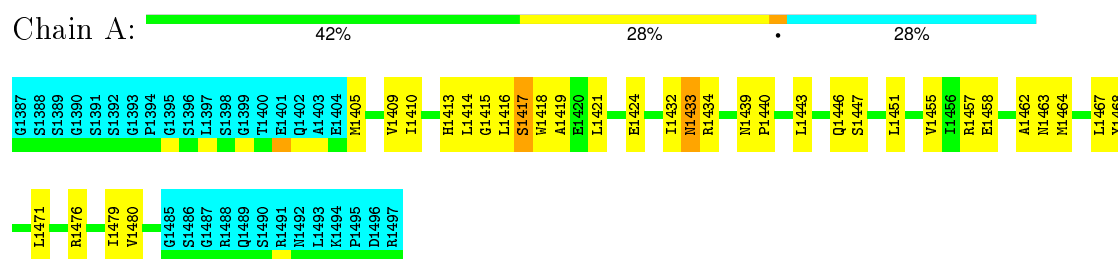
4.2.7 Score per residue for model 7

- Molecule 1: Ankyrin-1



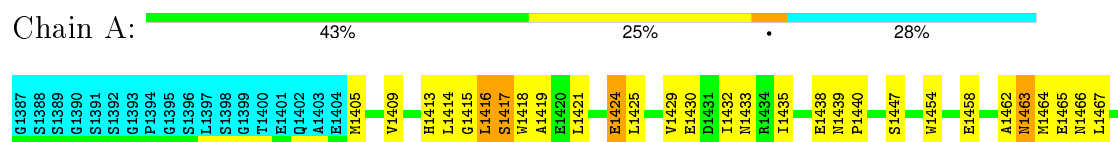
4.2.8 Score per residue for model 8

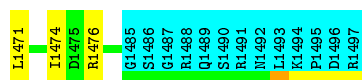
- Molecule 1: Ankyrin-1



4.2.9 Score per residue for model 9

- Molecule 1: Ankyrin-1

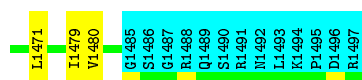
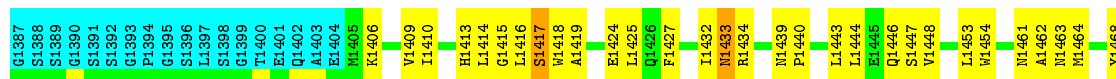




4.2.10 Score per residue for model 10

- Molecule 1: Ankyrin-1

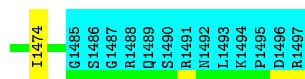
Chain A: 42% 28% 28%



4.2.11 Score per residue for model 11

- Molecule 1: Ankyrin-1

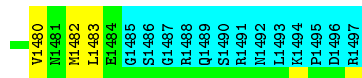
Chain A: 45% 25% 28%



4.2.12 Score per residue for model 12

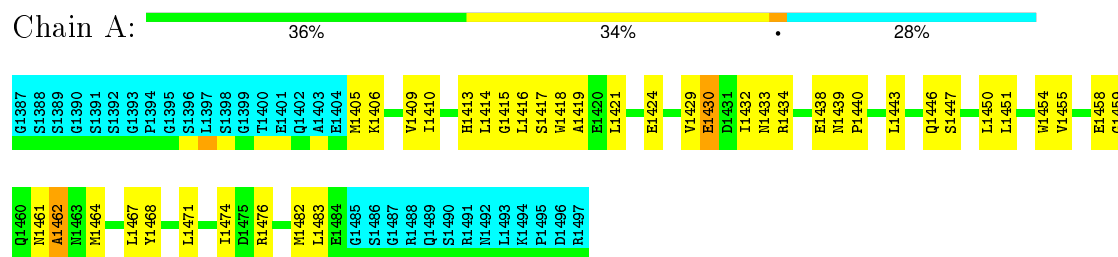
- Molecule 1: Ankyrin-1

Chain A: 43% 26% 28%



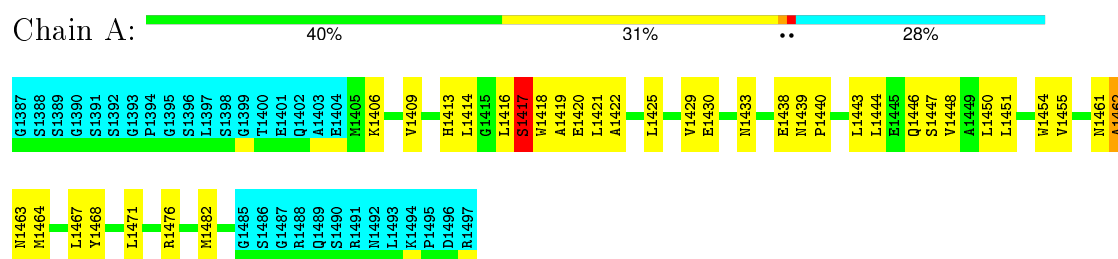
4.2.13 Score per residue for model 13

- Molecule 1: Ankyrin-1



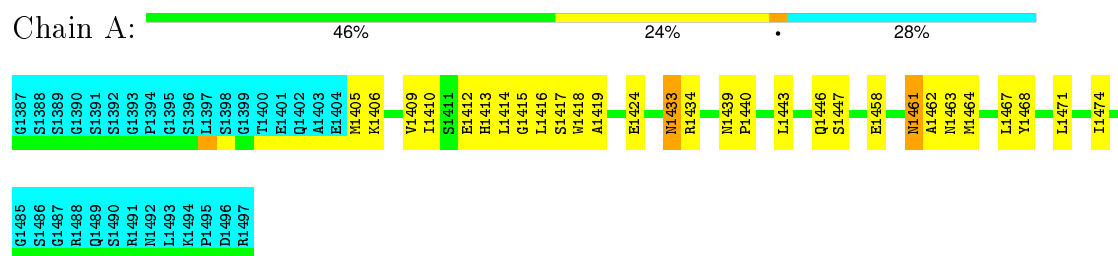
4.2.14 Score per residue for model 14

- Molecule 1: Ankyrin-1



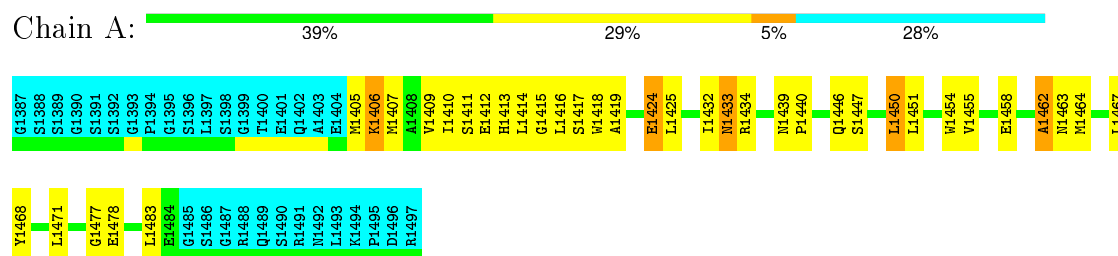
4.2.15 Score per residue for model 15

- Molecule 1: Ankyrin-1



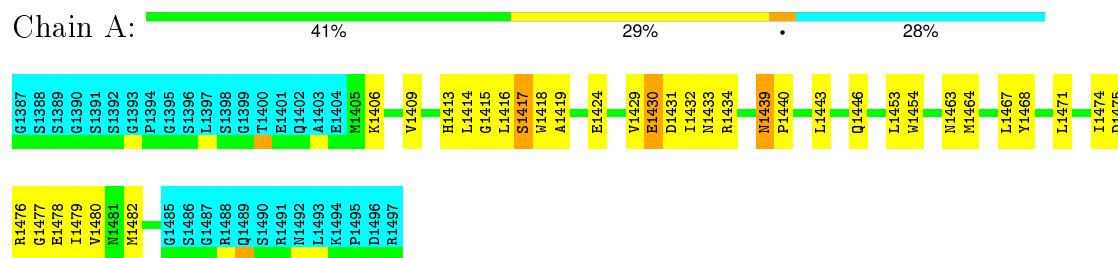
4.2.16 Score per residue for model 16

- Molecule 1: Ankyrin-1



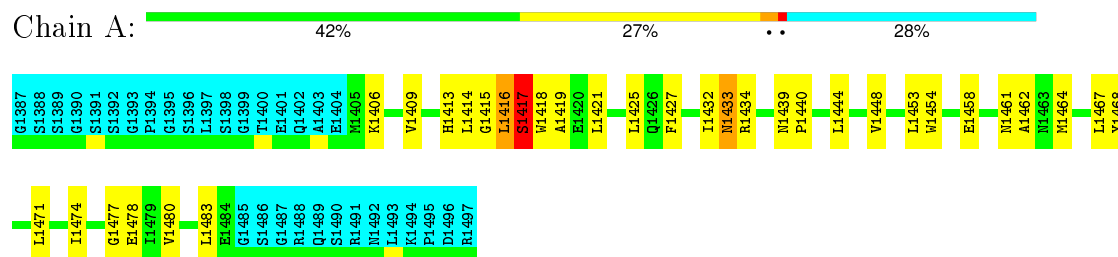
4.2.17 Score per residue for model 17

- Molecule 1: Ankyrin-1



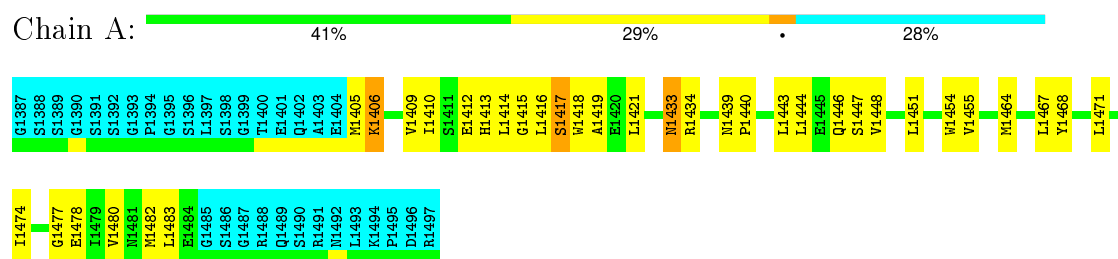
4.2.18 Score per residue for model 18

- Molecule 1: Ankyrin-1



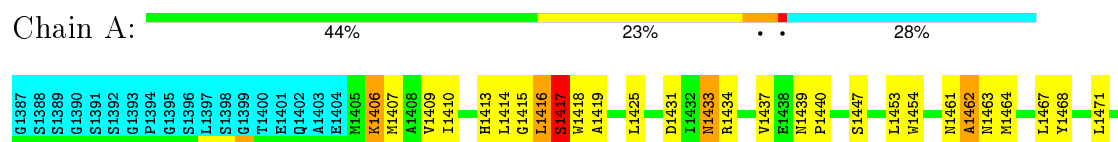
4.2.19 Score per residue for model 19

- Molecule 1: Ankyrin-1



4.2.20 Score per residue for model 20

- Molecule 1: Ankyrin-1



V1480
R1481
M1482
L1483
E1484
G1485
S1486
G1487
R1488
Q1489
S1490
R1491
N1492
L1493
R1494
P1495
D1496
R1497

5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *torsion angle dynamics, simulated annealing*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations, structures with the lowest energy, target function*.

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

Software name	Classification	Version
CYANA	structure solution	2.0.17
CYANA	refinement	2.0.17

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

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	641	642	642	30±5
All	All	12820	12840	12840	602

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 23.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1409:VAL:HG11	1:A:1483:LEU:HD21	0.81	1.51	13	11
1:A:1422:ALA:HB2	1:A:1450:LEU:HD11	0.75	1.59	14	1
1:A:1425:LEU:HD23	1:A:1454:TRP:CD1	0.73	2.18	18	2
1:A:1458:GLU:HB2	1:A:1462:ALA:HB2	0.71	1.62	13	7
1:A:1468:TYR:HA	1:A:1471:LEU:HD12	0.71	1.62	15	7
1:A:1425:LEU:CD2	1:A:1454:TRP:CD1	0.70	2.75	18	2
1:A:1414:LEU:HD23	1:A:1447:SER:CB	0.70	2.17	5	16
1:A:1414:LEU:HD23	1:A:1447:SER:OG	0.69	1.87	11	1
1:A:1409:VAL:CG1	1:A:1413:HIS:CE1	0.69	2.76	4	20
1:A:1467:LEU:CD2	1:A:1471:LEU:HD11	0.68	2.19	19	12
1:A:1421:LEU:HD23	1:A:1471:LEU:HD23	0.68	1.65	19	1
1:A:1458:GLU:CB	1:A:1462:ALA:HB2	0.67	2.20	18	7
1:A:1421:LEU:HD23	1:A:1421:LEU:O	0.65	1.91	3	2
1:A:1421:LEU:HD13	1:A:1471:LEU:HD23	0.65	1.66	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1422:ALA:HB2	1:A:1450:LEU:CD1	0.64	2.22	14	1
1:A:1444:LEU:O	1:A:1448:VAL:HG23	0.64	1.93	11	8
1:A:1414:LEU:HD23	1:A:1447:SER:HB3	0.64	1.68	8	7
1:A:1418:TRP:CG	1:A:1419:ALA:N	0.63	2.66	13	20
1:A:1421:LEU:CD2	1:A:1471:LEU:HD23	0.63	2.22	19	2
1:A:1416:LEU:O	1:A:1416:LEU:HD13	0.61	1.95	14	1
1:A:1451:LEU:O	1:A:1455:VAL:HG23	0.61	1.94	8	8
1:A:1409:VAL:CG1	1:A:1483:LEU:HD21	0.61	2.26	1	7
1:A:1429:VAL:CG1	1:A:1433:ASN:ND2	0.60	2.64	14	5
1:A:1416:LEU:HD13	1:A:1416:LEU:C	0.60	2.15	14	3
1:A:1413:HIS:CE1	1:A:1482:MET:SD	0.60	2.95	14	11
1:A:1464:MET:CG	1:A:1468:TYR:CE2	0.60	2.84	10	10
1:A:1409:VAL:HG13	1:A:1413:HIS:CE1	0.59	2.32	3	14
1:A:1439:ASN:N	1:A:1440:PRO:CD	0.59	2.65	13	20
1:A:1414:LEU:HD23	1:A:1447:SER:HB2	0.59	1.74	6	5
1:A:1425:LEU:HD13	1:A:1454:TRP:CD1	0.59	2.33	16	4
1:A:1429:VAL:HG13	1:A:1433:ASN:ND2	0.59	2.13	11	5
1:A:1421:LEU:HD13	1:A:1471:LEU:CD2	0.59	2.28	18	1
1:A:1421:LEU:O	1:A:1421:LEU:HD23	0.58	1.96	14	1
1:A:1405:MET:O	1:A:1409:VAL:HG23	0.58	1.97	8	7
1:A:1454:TRP:CZ3	1:A:1467:LEU:HD12	0.58	2.34	2	15
1:A:1413:HIS:CE1	1:A:1482:MET:CE	0.57	2.86	7	6
1:A:1476:ARG:HG3	1:A:1479:ILE:HD12	0.57	1.76	17	1
1:A:1409:VAL:HG11	1:A:1483:LEU:CD2	0.57	2.30	3	3
1:A:1468:TYR:CD1	1:A:1480:VAL:HG22	0.56	2.36	2	6
1:A:1414:LEU:HD21	1:A:1418:TRP:HA	0.55	1.79	8	10
1:A:1416:LEU:C	1:A:1416:LEU:CD2	0.54	2.76	7	2
1:A:1413:HIS:ND1	1:A:1479:ILE:HG23	0.53	2.18	10	2
1:A:1427:PHE:CE1	1:A:1453:LEU:CD2	0.53	2.91	10	3
1:A:1464:MET:HG3	1:A:1468:TYR:CE2	0.53	2.39	6	17
1:A:1416:LEU:CD2	1:A:1416:LEU:C	0.53	2.76	9	3
1:A:1422:ALA:CB	1:A:1450:LEU:HD11	0.53	2.33	14	1
1:A:1415:GLY:O	1:A:1443:LEU:HD22	0.52	2.03	5	2
1:A:1465:GLU:CD	1:A:1466:ASN:N	0.52	2.63	9	1
1:A:1432:ILE:HA	1:A:1435:ILE:HD12	0.52	1.82	9	1
1:A:1464:MET:HG2	1:A:1468:TYR:CE2	0.52	2.40	10	2
1:A:1409:VAL:HG12	1:A:1413:HIS:CE1	0.51	2.40	17	5
1:A:1416:LEU:O	1:A:1418:TRP:N	0.51	2.44	7	18
1:A:1416:LEU:CD1	1:A:1416:LEU:C	0.51	2.79	14	2
1:A:1433:ASN:OD1	1:A:1434:ARG:N	0.50	2.45	12	14
1:A:1427:PHE:CE1	1:A:1453:LEU:HD21	0.50	2.40	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1416:LEU:HD13	1:A:1416:LEU:O	0.50	2.06	15	2
1:A:1431:ASP:OD2	1:A:1453:LEU:HD21	0.50	2.07	20	1
1:A:1443:LEU:O	1:A:1446:GLN:N	0.49	2.45	2	11
1:A:1418:TRP:CE2	1:A:1446:GLN:OE1	0.49	2.65	10	1
1:A:1411:SER:OG	1:A:1451:LEU:HD11	0.49	2.07	16	1
1:A:1409:VAL:O	1:A:1412:GLU:N	0.49	2.45	15	3
1:A:1417:SER:O	1:A:1420:GLU:N	0.49	2.45	14	1
1:A:1418:TRP:NE1	1:A:1446:GLN:OE1	0.49	2.46	17	3
1:A:1468:TYR:CD1	1:A:1480:VAL:HG13	0.49	2.43	12	3
1:A:1464:MET:CG	1:A:1468:TYR:CZ	0.49	2.96	10	4
1:A:1450:LEU:O	1:A:1450:LEU:HD23	0.49	2.07	14	1
1:A:1474:ILE:HD11	1:A:1476:ARG:HG3	0.49	1.85	9	2
1:A:1463:ASN:ND2	1:A:1465:GLU:OE2	0.48	2.47	7	1
1:A:1421:LEU:HD13	1:A:1421:LEU:O	0.48	2.09	19	1
1:A:1405:MET:O	1:A:1409:VAL:CG2	0.48	2.61	8	1
1:A:1421:LEU:HD12	1:A:1471:LEU:CD2	0.48	2.39	7	1
1:A:1464:MET:HG3	1:A:1468:TYR:CZ	0.48	2.43	16	4
1:A:1439:ASN:N	1:A:1439:ASN:ND2	0.48	2.62	17	1
1:A:1418:TRP:CZ2	1:A:1446:GLN:OE1	0.48	2.67	10	1
1:A:1414:LEU:O	1:A:1416:LEU:N	0.47	2.46	7	8
1:A:1463:ASN:HD22	1:A:1464:MET:N	0.47	2.07	6	2
1:A:1431:ASP:OD1	1:A:1453:LEU:CD2	0.47	2.62	12	2
1:A:1424:GLU:OE2	1:A:1474:ILE:CG2	0.47	2.63	5	1
1:A:1463:ASN:OD1	1:A:1464:MET:N	0.47	2.48	7	1
1:A:1421:LEU:HD12	1:A:1471:LEU:HD23	0.46	1.87	7	1
1:A:1421:LEU:C	1:A:1421:LEU:CD2	0.46	2.84	14	1
1:A:1429:VAL:O	1:A:1430:GLU:C	0.46	2.54	9	5
1:A:1421:LEU:C	1:A:1421:LEU:HD23	0.46	2.30	14	1
1:A:1425:LEU:HD22	1:A:1454:TRP:CD1	0.45	2.46	7	2
1:A:1433:ASN:C	1:A:1433:ASN:OD1	0.45	2.55	16	8
1:A:1463:ASN:O	1:A:1465:GLU:N	0.45	2.49	4	1
1:A:1450:LEU:CD2	1:A:1450:LEU:O	0.45	2.65	16	1
1:A:1413:HIS:O	1:A:1414:LEU:C	0.45	2.55	10	16
1:A:1431:ASP:OD2	1:A:1453:LEU:CD2	0.45	2.64	17	1
1:A:1476:ARG:CG	1:A:1479:ILE:HD12	0.45	2.41	17	1
1:A:1421:LEU:HB2	1:A:1474:ILE:HD13	0.45	1.87	9	1
1:A:1417:SER:OG	1:A:1474:ILE:CD1	0.45	2.64	19	1
1:A:1410:ILE:HD11	1:A:1464:MET:CE	0.45	2.41	8	1
1:A:1463:ASN:O	1:A:1464:MET:C	0.45	2.55	8	11
1:A:1461:ASN:O	1:A:1462:ALA:C	0.45	2.55	13	9
1:A:1416:LEU:O	1:A:1416:LEU:CD2	0.45	2.64	5	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1434:ARG:NH1	1:A:1438:GLU:OE1	0.45	2.50	13	1
1:A:1450:LEU:C	1:A:1450:LEU:CD2	0.45	2.85	16	1
1:A:1416:LEU:C	1:A:1418:TRP:N	0.45	2.71	18	18
1:A:1439:ASN:N	1:A:1440:PRO:HD3	0.44	2.28	9	14
1:A:1407:MET:HE1	1:A:1467:LEU:HD11	0.44	1.87	7	1
1:A:1438:GLU:C	1:A:1440:PRO:CD	0.44	2.86	14	2
1:A:1425:LEU:CD1	1:A:1454:TRP:CD1	0.44	3.01	4	4
1:A:1433:ASN:OD1	1:A:1433:ASN:C	0.44	2.56	19	4
1:A:1417:SER:O	1:A:1418:TRP:C	0.44	2.56	14	13
1:A:1477:GLY:O	1:A:1480:VAL:N	0.44	2.50	5	2
1:A:1468:TYR:CE2	1:A:1484:GLU:OE2	0.44	2.71	2	1
1:A:1405:MET:O	1:A:1406:LYS:C	0.44	2.55	15	3
1:A:1421:LEU:O	1:A:1425:LEU:HD13	0.44	2.12	18	1
1:A:1407:MET:HE1	1:A:1451:LEU:HD22	0.43	1.88	7	1
1:A:1421:LEU:HD12	1:A:1450:LEU:HD21	0.43	1.90	13	1
1:A:1411:SER:OG	1:A:1451:LEU:CD1	0.43	2.66	16	1
1:A:1427:PHE:CE1	1:A:1453:LEU:HD23	0.43	2.48	10	2
1:A:1471:LEU:O	1:A:1474:ILE:CG1	0.43	2.66	4	2
1:A:1409:VAL:O	1:A:1410:ILE:C	0.43	2.56	19	4
1:A:1437:VAL:HG12	1:A:1437:VAL:O	0.43	2.13	20	1
1:A:1430:GLU:O	1:A:1434:ARG:CB	0.43	2.67	17	1
1:A:1416:LEU:O	1:A:1417:SER:C	0.43	2.57	19	8
1:A:1443:LEU:HD23	1:A:1446:GLN:OE1	0.43	2.13	2	1
1:A:1421:LEU:CD1	1:A:1471:LEU:CD2	0.43	2.96	7	1
1:A:1406:LYS:O	1:A:1410:ILE:HD12	0.43	2.14	13	1
1:A:1416:LEU:CD2	1:A:1416:LEU:O	0.43	2.67	18	3
1:A:1417:SER:OG	1:A:1474:ILE:HD11	0.43	2.14	19	1
1:A:1410:ILE:HD11	1:A:1464:MET:HE2	0.43	1.91	16	2
1:A:1450:LEU:HD23	1:A:1450:LEU:O	0.43	2.14	16	1
1:A:1410:ILE:HG23	1:A:1471:LEU:HD21	0.42	1.91	10	1
1:A:1433:ASN:CG	1:A:1434:ARG:N	0.42	2.72	12	9
1:A:1416:LEU:C	1:A:1416:LEU:HD22	0.42	2.34	7	2
1:A:1418:TRP:CH2	1:A:1432:ILE:HG23	0.42	2.48	17	1
1:A:1413:HIS:ND1	1:A:1482:MET:SD	0.42	2.92	12	1
1:A:1424:GLU:O	1:A:1424:GLU:CD	0.42	2.58	9	1
1:A:1477:GLY:O	1:A:1478:GLU:C	0.42	2.58	17	5
1:A:1482:MET:HG2	1:A:1483:LEU:N	0.42	2.30	12	1
1:A:1432:ILE:O	1:A:1435:ILE:N	0.42	2.52	9	1
1:A:1432:ILE:O	1:A:1433:ASN:C	0.42	2.58	9	2
1:A:1413:HIS:CD2	1:A:1413:HIS:N	0.41	2.87	20	2
1:A:1468:TYR:HD1	1:A:1480:VAL:HG22	0.41	1.75	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1429:VAL:HG13	1:A:1433:ASN:CG	0.41	2.35	9	1
1:A:1406:LYS:O	1:A:1407:MET:C	0.41	2.57	2	3
1:A:1424:GLU:CD	1:A:1424:GLU:O	0.41	2.59	16	2
1:A:1443:LEU:O	1:A:1444:LEU:C	0.41	2.58	14	2
1:A:1431:ASP:OD1	1:A:1431:ASP:N	0.41	2.52	11	1
1:A:1416:LEU:HD22	1:A:1416:LEU:C	0.41	2.35	9	1
1:A:1464:MET:HG2	1:A:1468:TYR:CZ	0.40	2.51	10	1
1:A:1407:MET:HE1	1:A:1467:LEU:CD1	0.40	2.47	7	1
1:A:1414:LEU:HG	1:A:1418:TRP:CA	0.40	2.47	9	1
1:A:1431:ASP:OD1	1:A:1453:LEU:HD21	0.40	2.16	17	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	80/111 (72%)	64±3 (80±3%)	13±3 (17±3%)	3±1 (4±1%)	8	37
All	All	1600/2220 (72%)	1277 (80%)	267 (17%)	56 (4%)	8	37

All 6 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	1415	GLY	19
1	A	1417	SER	17
1	A	1432	ILE	8
1	A	1462	ALA	6
1	A	1474	ILE	5
1	A	1464	MET	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	71/94 (76%)	68±1 (95±1%)	3±1 (5±1%)	37 80
All	All	1420/1880 (76%)	1353 (95%)	67 (5%)	37 80

All 17 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	1433	ASN	14
1	A	1424	GLU	11
1	A	1406	LYS	11
1	A	1416	LEU	6
1	A	1461	ASN	5
1	A	1417	SER	4
1	A	1476	ARG	3
1	A	1463	ASN	2
1	A	1430	GLU	2
1	A	1475	ASP	2
1	A	1439	ASN	1
1	A	1447	SER	1
1	A	1457	ARG	1
1	A	1407	MET	1
1	A	1436	ARG	1
1	A	1431	ASP	1
1	A	1450	LEU	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 ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided