Full wwPDB NMR Structure Validation Report (i)

Feb 17, 2022 – 08:34 AM EST

PDB ID	:	1NYG
Title	:	NMR STUDY OF THE SH3 DOMAIN FROM FYN PROTO-ONCOGENE TYROSINE KINASE, FAMILY OF 20 STRUCTURES
Authors	:	Morton, C.J.; Pugh, D.J.R.; Campbell, I.D.
Deposited on	:	1996-04-22

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 (i) symbol.

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

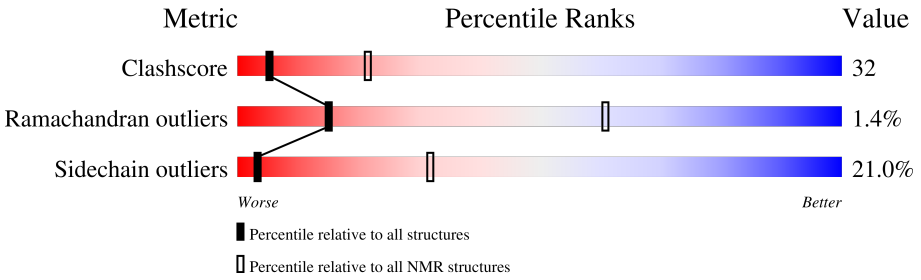
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

1 Overall quality at a glance (i)

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	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 <=5%

Mol	Chain	Length	Quality of chain
1	A	67	31% 46% • 7% 13%

2 Ensemble composition and analysis (i)

This entry contains 20 models. The atoms present in the NMR models are not consistent. Some calculations may have failed as a result. All residues are included in the validation scores. Model 8 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:86-A:114, A:118-A:141 (53)	0.27	8

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 in file

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 901 atoms, of which 432 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called FYN.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	58	901	301	432	73	95	0

4 Residue-property plots (i)

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: FYN

Chain A: 31% 46% • 7% 13%

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: FYN

Chain A: 36% 36% 7% 7% 13%

4.2.2 Score per residue for model 2

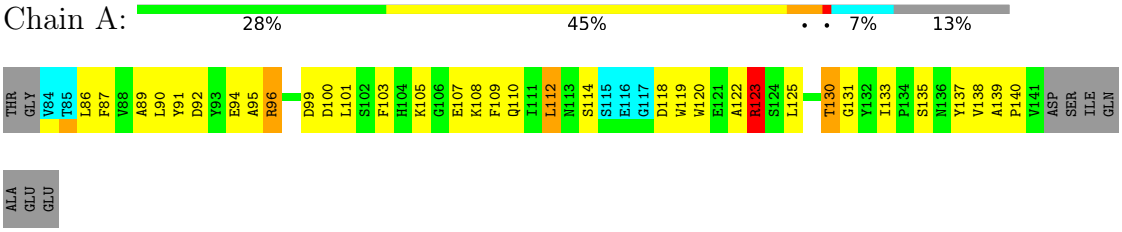
• Molecule 1: FYN

Chain A: 40% 31% 7% 7% 13%

4.2.3 Score per residue for model 3

- Molecule 1: FYN

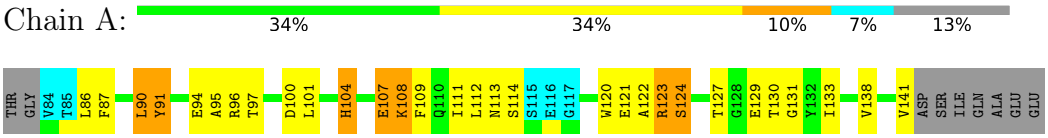
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: FYN

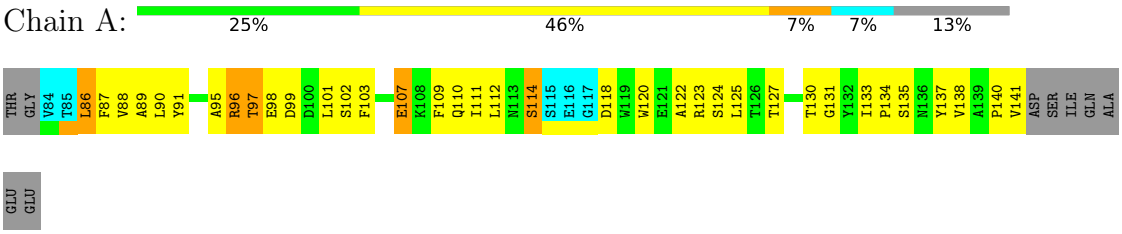
Chain A:



4.2.5 Score per residue for model 5

- Molecule 1: FYN

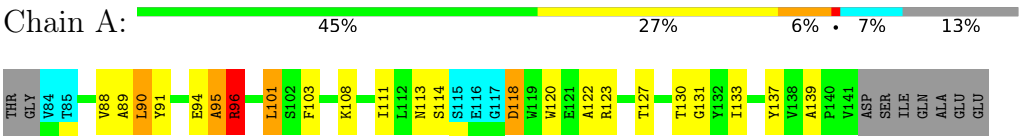
Chain A:



4.2.6 Score per residue for model 6

- Molecule 1: FYN

Chain A:



4.2.7 Score per residue for model 7

- Molecule 1: FYN

Chain A: 24% 48% 7% 7% 13%

THR GLY V84 T85 L86 F87 V88 A89 L90 Y91 D92 Y93 E94 A95 R96 T97 E98 D99 D100 L101 S102 F103 E107 K108 F109 Q110 I111 L112 N113 S114 S115 E116 G117 D118 W119 W120 E121 A122 R123 S124 L125 T126 T127 G131 Y132 I133 P134 S135 N136 Y137 V138 A139 P140 V141 ASP SER ILE GLN

ALA GLU GLU

4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: FYN

Chain A: 37% 37% • 7% 13%

THR GLY V84 T85 L86 F87 L90 R96 T97 E98 D99 D100 L101 S102 E107 K108 I111 L112 N113 S114 S115 E116 G117 D118 W119 W120 E121 A122 R123 S124 T127 G128 G131 Y132 I133 P134 S135 N136 Y137 V138 V141 ASP SER ILE GLN ALA GLU GLU

4.2.9 Score per residue for model 9

- Molecule 1: FYN

Chain A: 34% 36% 9% 7% 13%

THR GLY V84 T85 L86 F87 V88 A89 L90 Y91 D92 Y93 E94 A95 R96 D100 L101 S102 F103 H104 K105 K108 F109 Q110 I111 L112 N113 S114 S115 E116 G117 D118 W119 W120 E121 A122 R123 S124 L125 T126 T127 G131 Y132 I133 N136 V141 ASP SER ILE GLN ALA GLU GLU

4.2.10 Score per residue for model 10

- Molecule 1: FYN

Chain A: 37% 42% 7% 13%

THR GLY V84 T85 V88 A89 L90 Y91 D92 Y93 E94 A95 R96 L101 E107 K108 F109 Q110 I111 L112 N113 S114 S115 E116 G117 D118 W119 W120 E121 A122 R123 S124 T127 T130 G131 Y132 I133 P134 S135 N136 Y137 V138 V141 ASP SER ILE GLN ALA GLU GLU

4.2.11 Score per residue for model 11

- Molecule 1: FYN

Chain A: 30% 40% 7% • 7% 13%

THR GLY V84 T85 L86 F87 V88 A89 L90 Y91 D92 Y93 E94 A95 R96 D100 L101 S102 F103 H104 E107 K108 F109 Q110 I111 L112 N113 S114 S115 E116 G117 D118 W119 W120 E121 A122 R123 S124 T127 G131 Y132 I133 V138 V141 ASP SER ILE GLN ALA GLU GLU

4.2.12 Score per residue for model 12

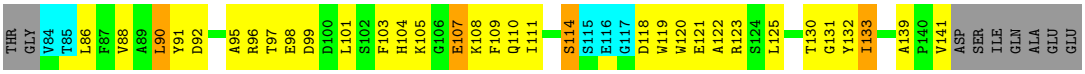
- Molecule 1: FYN

Chain A: 24% 45% 10% 7% 13%

4.2.13 Score per residue for model 13

- Molecule 1: FYN

Chain A: 30% 43% 6% 7% 13%



4.2.14 Score per residue for model 14

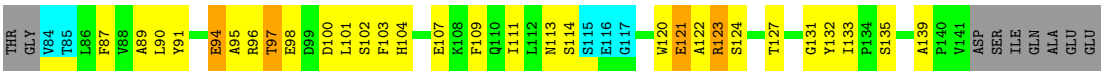
- Molecule 1: FYN

Chain A: 45% 28% 6% 7% 13%

4.2.15 Score per residue for model 15

- Molecule 1: FYN

Chain A: 34% 39% 6% 7% 13%



4.2.16 Score per residue for model 16

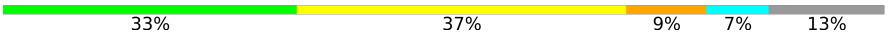
- Molecule 1: FYN

Chain A: 34% 33% 12% 7% 13%

4.2.17 Score per residue for model 17

- Molecule 1: FYN

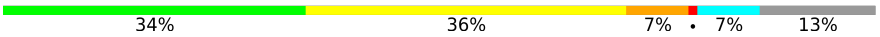
Chain A:



4.2.18 Score per residue for model 18

- Molecule 1: FYN

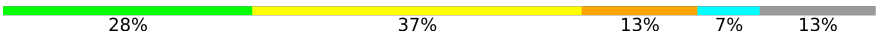
Chain A:



4.2.19 Score per residue for model 19

- Molecule 1: FYN

Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: FYN

Chain A:

5 Refinement protocol and experimental data overview (i)

Of the ? calculated structures, 20 were deposited, based on the following criterion: *?*.

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

Software name	Classification	Version
X-PLOR	refinement	3.1

No chemical shift data was provided.

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	1.9±0.2
All	All	0	39

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	123	ARG	Sidechain	20
1	A	96	ARG	Sidechain	19

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	437	403	403	27±6
All	All	8739	8060	8060	535

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 32.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:ILE:HD13	1:A:122:ALA:HB2	0.99	1.34	4	15
1:A:101:LEU:HD12	1:A:133:ILE:HG23	0.97	1.33	1	19
1:A:95:ALA:HB2	1:A:101:LEU:O	0.92	1.65	1	6
1:A:90:LEU:HD11	1:A:139:ALA:HB2	0.87	1.44	3	5
1:A:88:VAL:CG2	1:A:141:VAL:HG22	0.82	2.04	13	1
1:A:101:LEU:HD12	1:A:133:ILE:CG2	0.81	2.03	1	13
1:A:133:ILE:CD1	1:A:138:VAL:HG11	0.80	2.06	5	8
1:A:88:VAL:HG13	1:A:108:LYS:CD	0.79	2.08	17	1
1:A:101:LEU:CD1	1:A:133:ILE:HG23	0.79	2.07	5	16
1:A:133:ILE:HD12	1:A:138:VAL:HG11	0.78	1.53	5	4
1:A:101:LEU:HD11	1:A:131:GLY:C	0.75	2.01	10	18
1:A:101:LEU:HD11	1:A:131:GLY:CA	0.74	2.12	2	18
1:A:86:LEU:HD22	1:A:86:LEU:N	0.72	1.99	3	1
1:A:110:GLN:NE2	1:A:125:LEU:HD21	0.72	1.98	9	3
1:A:95:ALA:HB2	1:A:101:LEU:C	0.71	2.05	14	5
1:A:133:ILE:HD12	1:A:133:ILE:O	0.71	1.86	17	1
1:A:133:ILE:HD12	1:A:133:ILE:C	0.69	2.08	17	1
1:A:141:VAL:HG22	1:A:141:VAL:OXT	0.66	1.91	5	5
1:A:110:GLN:HG3	1:A:125:LEU:HD11	0.66	1.68	3	1
1:A:109:PHE:HB3	1:A:122:ALA:HB1	0.66	1.68	12	8
1:A:88:VAL:HG13	1:A:108:LYS:HD2	0.65	1.68	17	1
1:A:93:TYR:CE2	1:A:95:ALA:HB2	0.65	2.27	16	3
1:A:133:ILE:HD13	1:A:133:ILE:H	0.63	1.52	19	2
1:A:110:GLN:HG3	1:A:125:LEU:HD21	0.63	1.68	20	1
1:A:123:ARG:HG3	1:A:130:THR:HG23	0.62	1.71	3	1
1:A:133:ILE:HD12	1:A:138:VAL:CG1	0.61	2.24	5	2
1:A:101:LEU:HD21	1:A:131:GLY:N	0.61	2.10	16	6
1:A:133:ILE:HD13	1:A:138:VAL:HG11	0.61	1.72	4	2
1:A:90:LEU:HD21	1:A:139:ALA:HB3	0.61	1.73	13	1
1:A:86:LEU:O	1:A:141:VAL:HG12	0.60	1.97	1	2
1:A:95:ALA:HB1	1:A:100:ASP:OD1	0.59	1.98	14	1
1:A:123:ARG:CG	1:A:130:THR:HG23	0.58	2.28	18	1
1:A:90:LEU:O	1:A:91:TYR:CD1	0.58	2.57	12	15
1:A:101:LEU:HD11	1:A:131:GLY:N	0.58	2.14	1	4
1:A:111:ILE:CD1	1:A:122:ALA:HB2	0.58	2.27	9	9
1:A:114:SER:OG	1:A:120:TRP:CG	0.57	2.58	3	1
1:A:108:LYS:N	1:A:108:LYS:CD	0.57	2.67	18	5
1:A:90:LEU:HD21	1:A:139:ALA:CB	0.57	2.30	6	3
1:A:93:TYR:CD2	1:A:101:LEU:O	0.57	2.58	17	2
1:A:93:TYR:CE2	1:A:100:ASP:OD2	0.56	2.58	9	1
1:A:101:LEU:HD21	1:A:130:THR:C	0.56	2.21	20	2
1:A:86:LEU:CD2	1:A:125:LEU:HD11	0.56	2.30	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:100:ASP:OD1	1:A:119:TRP:CZ3	0.55	2.59	9	3
1:A:100:ASP:OD1	1:A:119:TRP:CE3	0.55	2.60	18	1
1:A:95:ALA:HB1	1:A:100:ASP:HB2	0.55	1.77	11	2
1:A:90:LEU:HB2	1:A:91:TYR:CE2	0.55	2.37	17	6
1:A:90:LEU:C	1:A:91:TYR:CG	0.55	2.81	17	8
1:A:114:SER:HB3	1:A:120:TRP:CD2	0.54	2.38	5	11
1:A:88:VAL:HG23	1:A:141:VAL:HG22	0.54	1.75	13	1
1:A:114:SER:CB	1:A:120:TRP:CD2	0.54	2.91	7	4
1:A:86:LEU:C	1:A:87:PHE:CD1	0.54	2.81	5	1
1:A:107:GLU:OE1	1:A:109:PHE:CZ	0.54	2.60	11	1
1:A:121:GLU:OE1	1:A:132:TYR:CD1	0.54	2.61	15	1
1:A:114:SER:HB2	1:A:120:TRP:CE2	0.54	2.38	6	10
1:A:90:LEU:O	1:A:91:TYR:CG	0.54	2.61	3	4
1:A:92:ASP:OD2	1:A:104:HIS:CD2	0.53	2.61	18	1
1:A:133:ILE:CD1	1:A:138:VAL:CG1	0.53	2.86	2	1
1:A:133:ILE:HD13	1:A:133:ILE:N	0.53	2.18	19	1
1:A:94:GLU:O	1:A:94:GLU:CG	0.53	2.56	4	3
1:A:90:LEU:C	1:A:91:TYR:CD1	0.53	2.82	12	3
1:A:86:LEU:N	1:A:86:LEU:CD2	0.53	2.71	3	1
1:A:114:SER:CB	1:A:120:TRP:CE2	0.53	2.92	1	4
1:A:121:GLU:N	1:A:121:GLU:OE1	0.53	2.42	1	1
1:A:110:GLN:HE21	1:A:125:LEU:HD21	0.52	1.64	7	1
1:A:95:ALA:CB	1:A:100:ASP:CB	0.52	2.87	16	1
1:A:87:PHE:CD2	1:A:139:ALA:C	0.52	2.83	1	2
1:A:97:THR:CG2	1:A:99:ASP:OD1	0.52	2.57	16	2
1:A:109:PHE:CD1	1:A:109:PHE:N	0.52	2.76	16	2
1:A:121:GLU:CG	1:A:121:GLU:O	0.52	2.58	4	1
1:A:134:PRO:HB2	1:A:137:TYR:CD1	0.52	2.40	7	2
1:A:94:GLU:O	1:A:96:ARG:N	0.52	2.43	3	4
1:A:100:ASP:OD2	1:A:119:TRP:CZ3	0.52	2.63	16	2
1:A:101:LEU:O	1:A:102:SER:CB	0.52	2.56	16	1
1:A:121:GLU:N	1:A:121:GLU:OE2	0.52	2.43	11	1
1:A:97:THR:CG2	1:A:100:ASP:OD2	0.52	2.57	15	2
1:A:108:LYS:C	1:A:109:PHE:CD1	0.51	2.83	16	2
1:A:87:PHE:N	1:A:87:PHE:CD1	0.51	2.78	2	4
1:A:120:TRP:CE2	1:A:135:SER:HB2	0.51	2.41	2	5
1:A:87:PHE:CD2	1:A:140:PRO:N	0.51	2.79	5	2
1:A:90:LEU:HD21	1:A:139:ALA:HB2	0.51	1.80	6	1
1:A:95:ALA:CB	1:A:100:ASP:HB2	0.51	2.35	16	1
1:A:100:ASP:OD2	1:A:119:TRP:CH2	0.51	2.63	11	1
1:A:88:VAL:HG13	1:A:108:LYS:HD3	0.51	1.78	17	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:118:ASP:OD2	1:A:136:ASN:ND2	0.51	2.44	8	1
1:A:94:GLU:N	1:A:94:GLU:OE2	0.51	2.43	11	1
1:A:86:LEU:O	1:A:141:VAL:CG1	0.51	2.59	1	1
1:A:101:LEU:HD21	1:A:131:GLY:HA3	0.51	1.82	12	5
1:A:109:PHE:CB	1:A:122:ALA:HB1	0.50	2.35	16	2
1:A:93:TYR:CZ	1:A:100:ASP:OD2	0.50	2.64	9	1
1:A:90:LEU:CB	1:A:91:TYR:CE2	0.50	2.95	17	2
1:A:103:PHE:CD2	1:A:109:PHE:CZ	0.50	2.99	15	9
1:A:90:LEU:HB2	1:A:91:TYR:CZ	0.50	2.42	12	2
1:A:108:LYS:HB3	1:A:125:LEU:HD12	0.50	1.83	19	2
1:A:133:ILE:C	1:A:133:ILE:CD1	0.50	2.80	17	1
1:A:105:LYS:O	1:A:105:LYS:CG	0.49	2.60	1	3
1:A:111:ILE:HD13	1:A:122:ALA:CB	0.49	2.35	9	1
1:A:141:VAL:OXT	1:A:141:VAL:CG2	0.49	2.60	5	3
1:A:132:TYR:CD1	1:A:132:TYR:N	0.49	2.80	12	5
1:A:100:ASP:CG	1:A:119:TRP:CZ3	0.49	2.86	18	2
1:A:141:VAL:OXT	1:A:141:VAL:HG13	0.49	2.08	20	1
1:A:92:ASP:OD1	1:A:93:TYR:N	0.49	2.46	7	3
1:A:97:THR:OG1	1:A:98:GLU:N	0.48	2.46	5	2
1:A:121:GLU:HG2	1:A:132:TYR:CE2	0.48	2.43	16	2
1:A:131:GLY:C	1:A:132:TYR:CD1	0.48	2.87	13	1
1:A:90:LEU:HD12	1:A:137:TYR:C	0.48	2.29	6	2
1:A:111:ILE:HG21	1:A:114:SER:OG	0.48	2.08	10	1
1:A:90:LEU:HB2	1:A:91:TYR:CE1	0.48	2.44	12	2
1:A:88:VAL:HG13	1:A:108:LYS:HE3	0.48	1.85	19	1
1:A:107:GLU:HB3	1:A:109:PHE:CE2	0.48	2.43	11	3
1:A:114:SER:HB3	1:A:120:TRP:CE2	0.47	2.44	10	2
1:A:108:LYS:N	1:A:108:LYS:HD2	0.47	2.24	8	1
1:A:120:TRP:CZ2	1:A:135:SER:HB2	0.47	2.44	18	1
1:A:89:ALA:CB	1:A:103:PHE:CE1	0.47	2.97	7	2
1:A:113:ASN:CB	1:A:121:GLU:CD	0.47	2.82	4	1
1:A:134:PRO:HG2	1:A:137:TYR:CG	0.47	2.44	5	2
1:A:91:TYR:HB2	1:A:137:TYR:CE2	0.47	2.44	3	1
1:A:113:ASN:CB	1:A:121:GLU:CG	0.47	2.93	7	1
1:A:121:GLU:HB3	1:A:132:TYR:CE1	0.47	2.43	11	2
1:A:111:ILE:CG2	1:A:114:SER:OG	0.47	2.62	10	1
1:A:86:LEU:HD21	1:A:125:LEU:HD11	0.47	1.87	12	2
1:A:121:GLU:O	1:A:121:GLU:HG3	0.47	2.10	4	1
1:A:101:LEU:CD1	1:A:133:ILE:CG2	0.47	2.88	5	3
1:A:120:TRP:CE2	1:A:135:SER:CB	0.47	2.97	18	2
1:A:87:PHE:CD1	1:A:87:PHE:N	0.46	2.82	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:90:LEU:HB2	1:A:91:TYR:CD1	0.46	2.45	13	1
1:A:104:HIS:CD2	1:A:104:HIS:N	0.46	2.82	4	1
1:A:123:ARG:CG	1:A:130:THR:OG1	0.46	2.63	18	1
1:A:136:ASN:OD1	1:A:137:TYR:CD1	0.46	2.69	20	1
1:A:114:SER:HB3	1:A:120:TRP:CG	0.46	2.45	5	2
1:A:92:ASP:OD1	1:A:103:PHE:O	0.46	2.33	3	2
1:A:86:LEU:O	1:A:141:VAL:HG23	0.46	2.11	4	1
1:A:112:LEU:N	1:A:112:LEU:HD23	0.46	2.25	16	2
1:A:101:LEU:CG	1:A:131:GLY:HA3	0.46	2.41	9	13
1:A:87:PHE:CE2	1:A:140:PRO:CD	0.46	2.99	3	1
1:A:93:TYR:CG	1:A:94:GLU:N	0.46	2.83	10	1
1:A:100:ASP:OD1	1:A:132:TYR:O	0.46	2.34	18	1
1:A:113:ASN:HB3	1:A:121:GLU:OE1	0.45	2.12	4	1
1:A:121:GLU:HB3	1:A:132:TYR:CD1	0.45	2.47	11	1
1:A:110:GLN:O	1:A:112:LEU:HD23	0.45	2.11	19	3
1:A:97:THR:HG23	1:A:100:ASP:OD2	0.45	2.11	2	1
1:A:87:PHE:CD2	1:A:111:ILE:CG1	0.45	3.00	8	1
1:A:97:THR:HG23	1:A:100:ASP:HB2	0.45	1.89	4	1
1:A:133:ILE:HD13	1:A:138:VAL:CG1	0.45	2.41	4	3
1:A:114:SER:OG	1:A:114:SER:O	0.45	2.33	14	1
1:A:114:SER:HA	1:A:120:TRP:CD1	0.45	2.47	16	2
1:A:95:ALA:N	1:A:102:SER:OG	0.45	2.49	11	1
1:A:93:TYR:CE1	1:A:134:PRO:HG3	0.44	2.47	16	1
1:A:124:SER:CB	1:A:127:THR:OG1	0.44	2.66	19	2
1:A:133:ILE:HG13	1:A:138:VAL:HG11	0.44	1.90	19	1
1:A:139:ALA:HB1	1:A:140:PRO:HD2	0.44	1.89	12	1
1:A:94:GLU:O	1:A:94:GLU:HG3	0.44	2.11	4	1
1:A:105:LYS:CG	1:A:105:LYS:O	0.44	2.64	14	1
1:A:111:ILE:C	1:A:112:LEU:HD23	0.44	2.32	4	1
1:A:113:ASN:CB	1:A:121:GLU:OE1	0.44	2.66	4	1
1:A:121:GLU:N	1:A:121:GLU:CD	0.44	2.71	15	2
1:A:103:PHE:HB3	1:A:107:GLU:OE1	0.44	2.13	1	1
1:A:101:LEU:CD1	1:A:131:GLY:C	0.44	2.84	7	4
1:A:132:TYR:N	1:A:132:TYR:CD1	0.44	2.85	10	2
1:A:101:LEU:CD2	1:A:131:GLY:HA3	0.44	2.43	12	1
1:A:94:GLU:O	1:A:95:ALA:C	0.44	2.56	1	7
1:A:97:THR:CG2	1:A:100:ASP:CG	0.44	2.86	8	1
1:A:124:SER:HB3	1:A:127:THR:OG1	0.43	2.13	4	2
1:A:123:ARG:HB2	1:A:130:THR:HG23	0.43	1.89	17	2
1:A:135:SER:O	1:A:138:VAL:CG2	0.43	2.66	10	1
1:A:93:TYR:CE2	1:A:101:LEU:O	0.43	2.71	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:110:GLN:O	1:A:112:LEU:CD2	0.43	2.66	17	1
1:A:97:THR:CG2	1:A:100:ASP:OD1	0.43	2.67	8	1
1:A:110:GLN:HB2	1:A:123:ARG:CG	0.43	2.43	14	1
1:A:113:ASN:HB3	1:A:121:GLU:OE2	0.43	2.13	8	1
1:A:87:PHE:CD1	1:A:140:PRO:HA	0.43	2.48	12	1
1:A:108:LYS:HD3	1:A:108:LYS:N	0.43	2.29	10	2
1:A:113:ASN:O	1:A:121:GLU:CD	0.43	2.57	8	1
1:A:97:THR:OG1	1:A:100:ASP:OD2	0.43	2.35	12	1
1:A:97:THR:HG1	1:A:100:ASP:CG	0.43	2.17	14	1
1:A:141:VAL:HG13	1:A:141:VAL:O	0.43	2.14	17	1
1:A:110:GLN:CG	1:A:125:LEU:HD21	0.43	2.43	20	1
1:A:114:SER:HB2	1:A:120:TRP:CD2	0.42	2.49	15	1
1:A:104:HIS:O	1:A:105:LYS:C	0.42	2.56	13	3
1:A:94:GLU:CD	1:A:94:GLU:N	0.42	2.72	16	1
1:A:127:THR:OG1	1:A:128:GLY:N	0.42	2.53	8	1
1:A:114:SER:OG	1:A:120:TRP:CE2	0.42	2.61	14	1
1:A:135:SER:HA	1:A:138:VAL:CG2	0.42	2.44	8	1
1:A:110:GLN:HB2	1:A:123:ARG:HG2	0.42	1.91	14	1
1:A:101:LEU:HD21	1:A:131:GLY:CA	0.42	2.44	17	1
1:A:133:ILE:HD11	1:A:138:VAL:HG11	0.42	1.90	2	1
1:A:113:ASN:HB2	1:A:121:GLU:HG3	0.42	1.92	7	1
1:A:103:PHE:CG	1:A:109:PHE:CZ	0.42	3.08	9	1
1:A:123:ARG:HG2	1:A:130:THR:CB	0.42	2.45	18	1
1:A:97:THR:HG23	1:A:99:ASP:OD1	0.42	2.15	16	1
1:A:103:PHE:CB	1:A:107:GLU:OE1	0.42	2.67	1	1
1:A:121:GLU:HG2	1:A:132:TYR:CE1	0.42	2.50	18	1
1:A:97:THR:OG1	1:A:100:ASP:CG	0.42	2.58	14	2
1:A:120:TRP:N	1:A:120:TRP:CD1	0.41	2.86	3	1
1:A:113:ASN:HB2	1:A:121:GLU:CD	0.41	2.35	4	1
1:A:140:PRO:O	1:A:141:VAL:C	0.41	2.57	7	1
1:A:89:ALA:O	1:A:105:LYS:HA	0.41	2.15	9	1
1:A:110:GLN:OE1	1:A:125:LEU:HD21	0.41	2.16	12	1
1:A:89:ALA:CB	1:A:103:PHE:CE2	0.41	3.03	6	3
1:A:120:TRP:O	1:A:132:TYR:HA	0.41	2.16	16	3
1:A:89:ALA:HB1	1:A:103:PHE:CE1	0.41	2.51	15	1
1:A:123:ARG:HG2	1:A:130:THR:HG23	0.41	1.93	18	1
1:A:89:ALA:HB1	1:A:103:PHE:HE2	0.41	1.76	19	1
1:A:90:LEU:C	1:A:91:TYR:CD2	0.41	2.94	3	1
1:A:87:PHE:CE1	1:A:140:PRO:HA	0.41	2.51	12	1
1:A:89:ALA:HA	1:A:137:TYR:O	0.40	2.16	5	1
1:A:110:GLN:CG	1:A:123:ARG:HB3	0.40	2.46	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:89:ALA:HB1	1:A:103:PHE:CE2	0.40	2.52	19	1
1:A:122:ALA:HB3	1:A:133:ILE:CD1	0.40	2.47	19	1
1:A:103:PHE:CD1	1:A:103:PHE:N	0.40	2.88	6	1
1:A:107:GLU:HB3	1:A:109:PHE:CE1	0.40	2.52	13	1
1:A:88:VAL:CG1	1:A:108:LYS:CD	0.40	2.92	17	1
1:A:123:ARG:HG2	1:A:130:THR:OG1	0.40	2.17	18	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	52/67 (78%)	48±2 (92±3%)	4±1 (7±3%)	1±1 (1±1%)	15	61
All	All	1040/1340 (78%)	955 (92%)	70 (7%)	15 (1%)	15	61

All 3 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	118	ASP	8
1	A	95	ALA	6
1	A	111	ILE	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	46/57 (81%)	36±2 (79±4%)	10±2 (21±4%)	3	32
All	All	920/1140 (81%)	727 (79%)	193 (21%)	3	32

All 32 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	107	GLU	13
1	A	118	ASP	11
1	A	127	THR	11
1	A	90	LEU	11
1	A	108	LYS	11
1	A	130	THR	11
1	A	88	VAL	10
1	A	114	SER	9
1	A	86	LEU	9
1	A	112	LEU	9
1	A	99	ASP	8
1	A	123	ARG	7
1	A	97	THR	7
1	A	124	SER	7
1	A	113	ASN	6
1	A	96	ARG	6
1	A	102	SER	6
1	A	98	GLU	5
1	A	105	LYS	4
1	A	91	TYR	4
1	A	104	HIS	4
1	A	121	GLU	4
1	A	136	ASN	3
1	A	94	GLU	3
1	A	92	ASP	2
1	A	137	TYR	2
1	A	129	GLU	2
1	A	101	LEU	2
1	A	110	GLN	2
1	A	133	ILE	2
1	A	100	ASP	1
1	A	138	VAL	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 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 (i)

No chemical shift data were provided