



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 07:26 AM UTC

PDB ID : 2Z5V / pdb_00002z5v
Title : Solution structure of the TIR domain of human MyD88
Authors : Ohnishi, H.; Tochio, H.; Hiroaki, H.; Kondo, N.; Kato, Z.; Shirakawa, M.
Deposited on : 2007-07-19

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

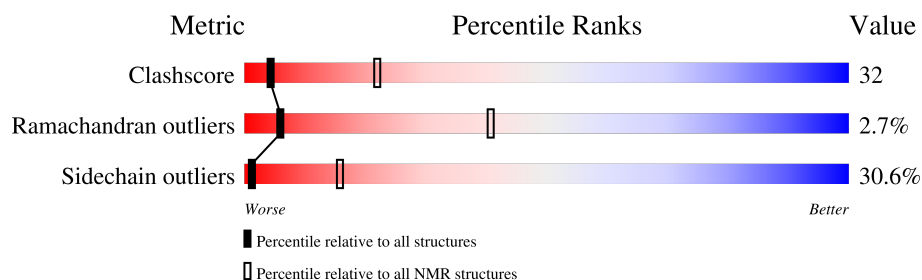
1 Overall quality at a glance

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	149	35% 42% 7% 11% 5%

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:10-A:37, A:42-A:47, A:57-A:147 (125)	0.54	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 5 clusters. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2336 atoms, of which 1177 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Myeloid differentiation primary response protein MyD88.

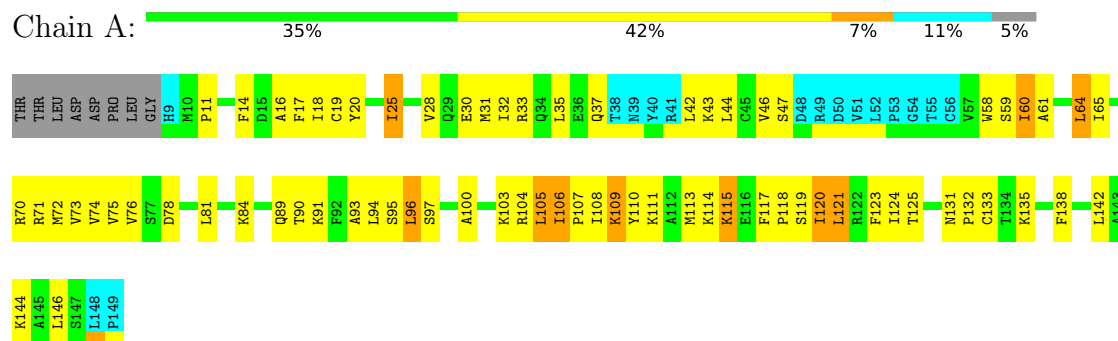
Mol	Chain	Residues	Atoms						Trace
1	A	141	Total	C	H	N	O	S	0
			2336	745	1177	198	204	12	

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: Myeloid differentiation primary response protein MyD88

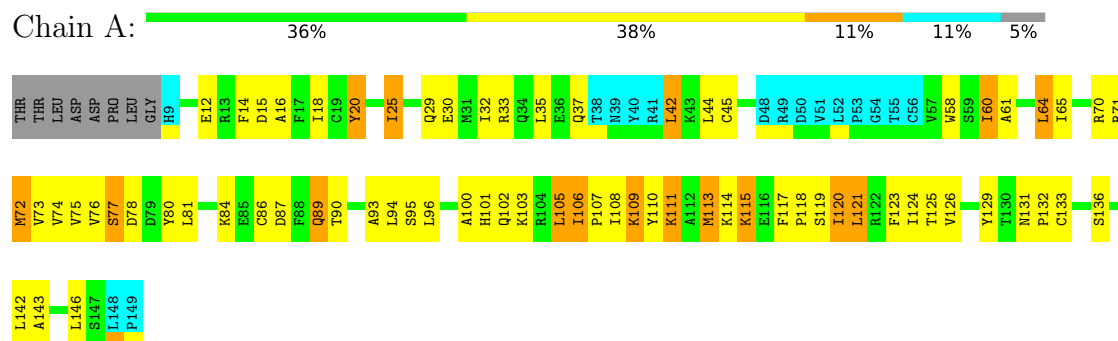


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

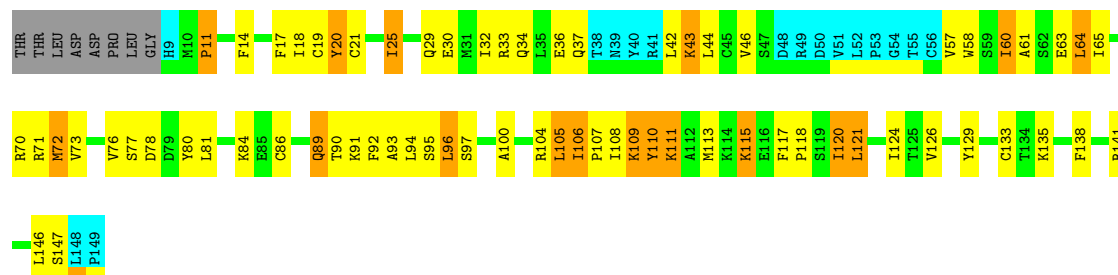
- Molecule 1: Myeloid differentiation primary response protein MyD88



4.2.2 Score per residue for model 2

- Molecule 1: Myeloid differentiation primary response protein MyD88

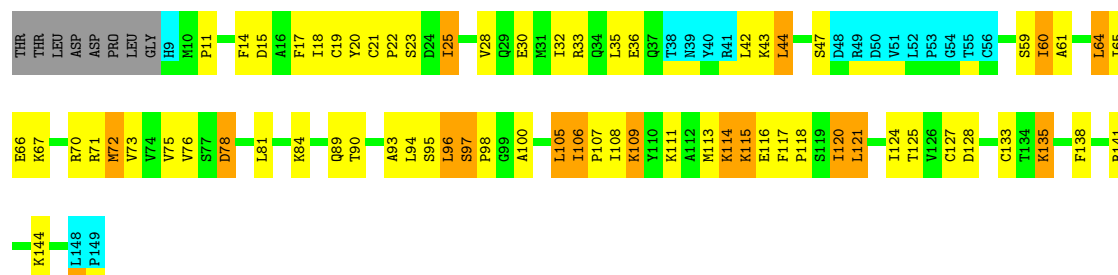
Chain A:  37% 36% 11% 11% 5%



4.2.3 Score per residue for model 3

- Molecule 1: Myeloid differentiation primary response protein MyD88

Chain A:  38% 36% 11% 11% 5%



4.2.4 Score per residue for model 4

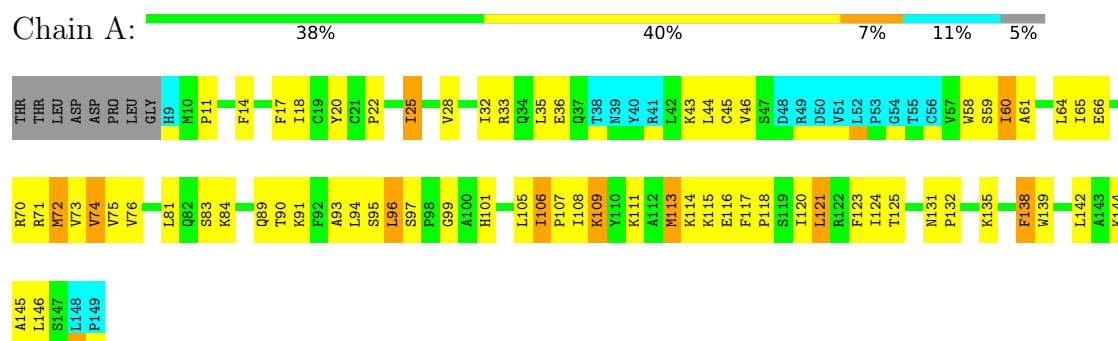
- Molecule 1: Myeloid differentiation primary response protein MyD88

Chain A:  36% 35% 13% 11% 5%



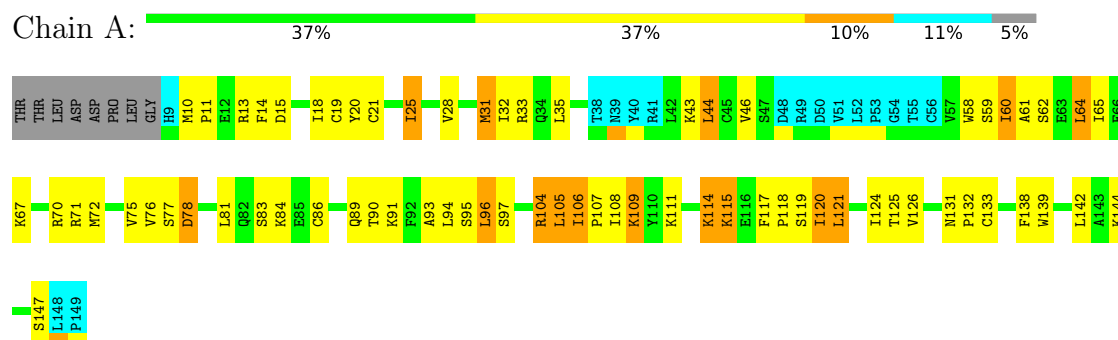
4.2.5 Score per residue for model 5

- Molecule 1: Myeloid differentiation primary response protein MyD88



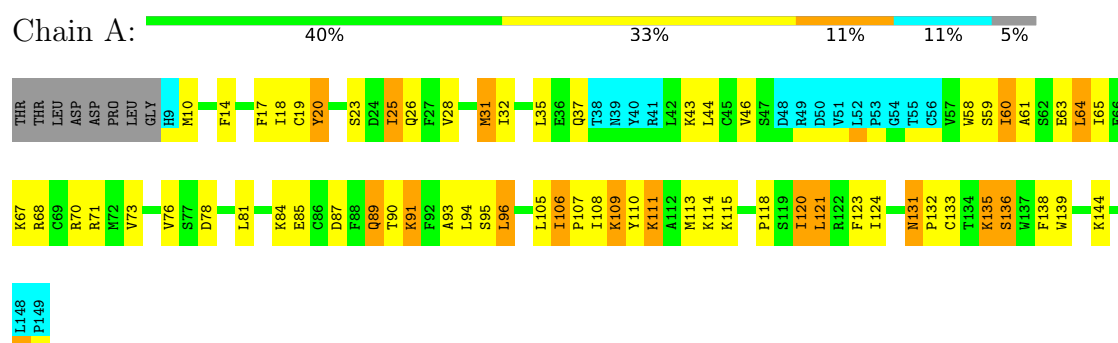
4.2.6 Score per residue for model 6

- Molecule 1: Myeloid differentiation primary response protein MyD88



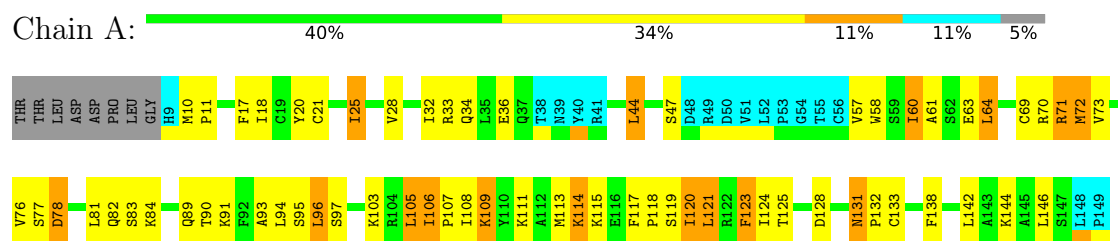
4.2.7 Score per residue for model 7

- Molecule 1: Myeloid differentiation primary response protein MyD88



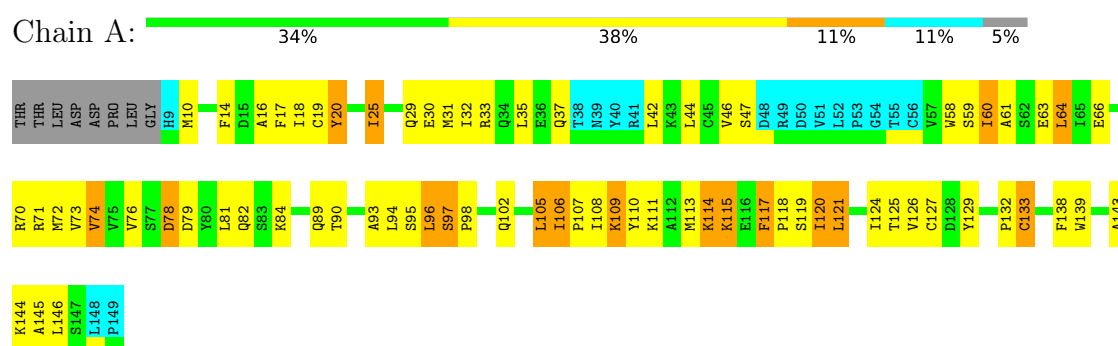
4.2.11 Score per residue for model 11

- Molecule 1: Myeloid differentiation primary response protein MyD88



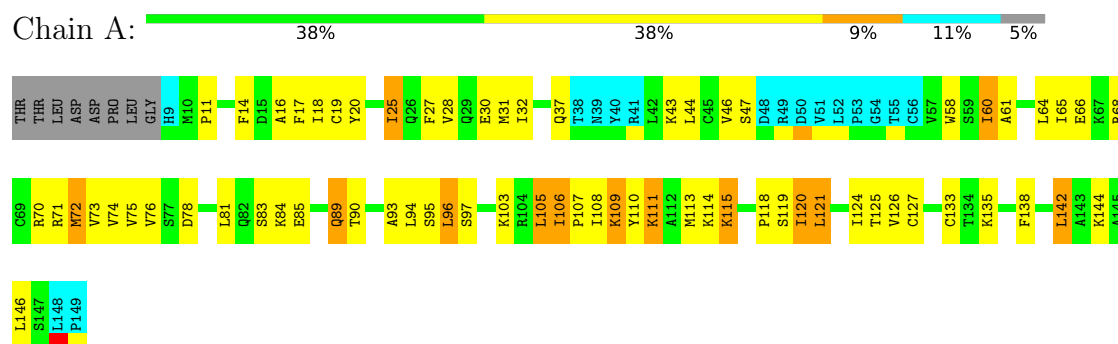
4.2.12 Score per residue for model 12

- Molecule 1: Myeloid differentiation primary response protein MyD88



4.2.13 Score per residue for model 13

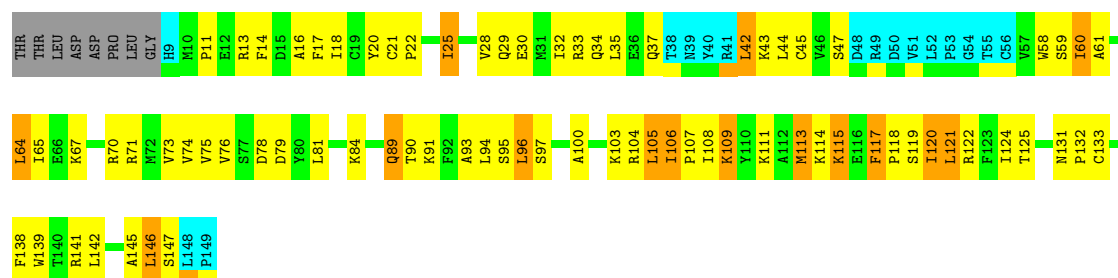
- Molecule 1: Myeloid differentiation primary response protein MyD88



4.2.14 Score per residue for model 14

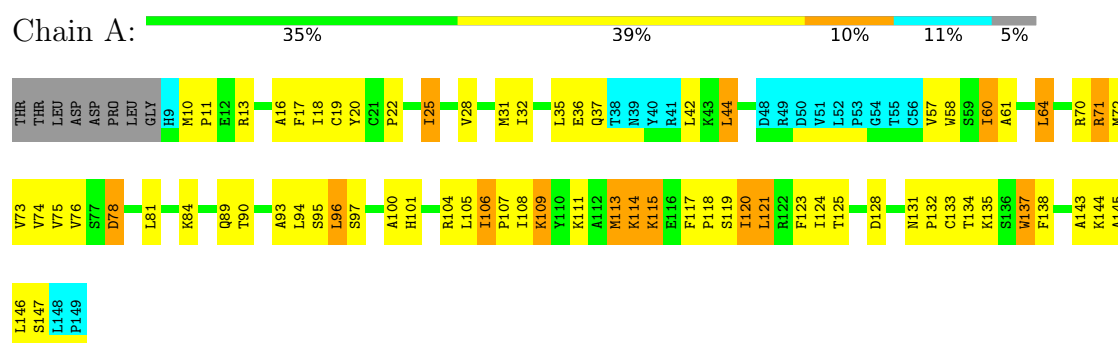
- Molecule 1: Myeloid differentiation primary response protein MyD88





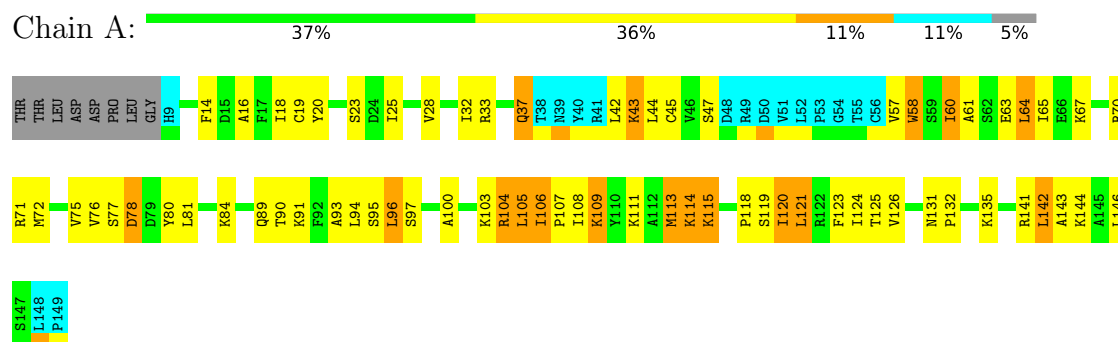
4.2.15 Score per residue for model 15 (medoid)

- Molecule 1: Myeloid differentiation primary response protein MyD88



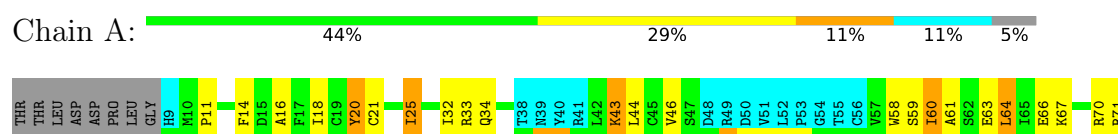
4.2.16 Score per residue for model 16

- Molecule 1: Myeloid differentiation primary response protein MyD88



4.2.17 Score per residue for model 17

- Molecule 1: Myeloid differentiation primary response protein MyD88

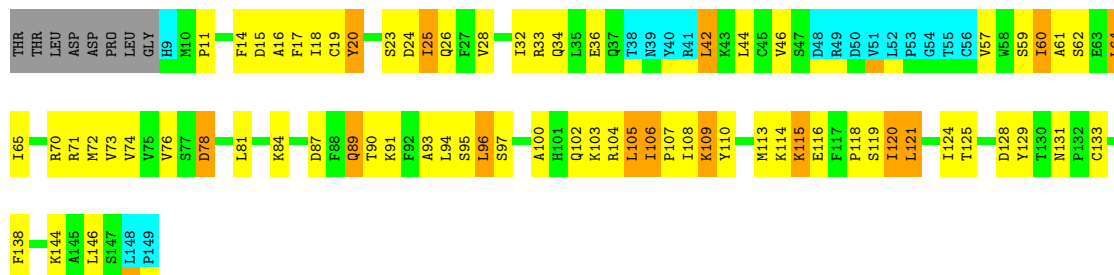




4.2.18 Score per residue for model 18

- Molecule 1: Myeloid differentiation primary response protein MyD88

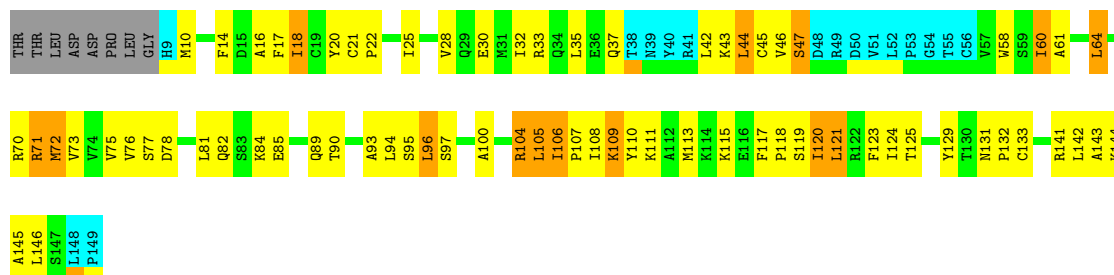
Chain A: 36% 39% 9% 11% 5%



4.2.19 Score per residue for model 19

- Molecule 1: Myeloid differentiation primary response protein MyD88

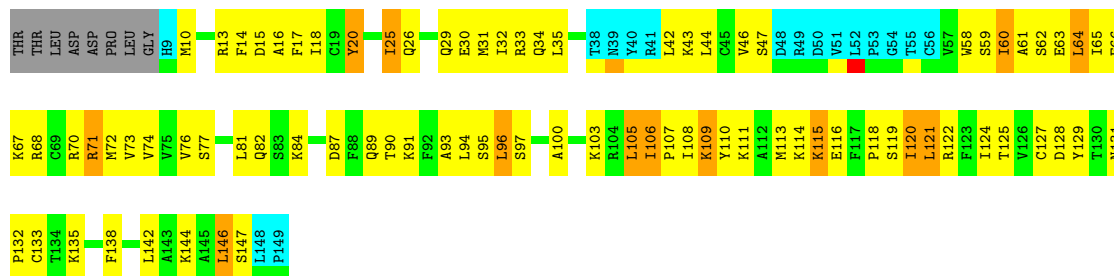
Chain A: 35% 40% 9% 11% 5%



4.2.20 Score per residue for model 20

- Molecule 1: Myeloid differentiation primary response protein MyD88

Chain A: 28% 48% 9% 11% 5%



5 Refinement protocol and experimental data overview

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	refinement	1.1

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.

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 [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	1029	1053	1053	66±4
All	All	20580	21060	21060	1328

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:90:THR:HG22	1:A:94:LEU:HD23	1.12	1.22	20	20
1:A:90:THR:HG23	1:A:120:ILE:HD11	1.02	1.23	13	7
1:A:65:ILE:HG22	1:A:72:MET:HE2	1.00	1.32	3	7
1:A:81:LEU:HD11	1:A:113:MET:HE3	0.99	1.33	17	17
1:A:32:ILE:HG23	1:A:44:LEU:HD13	0.96	1.31	3	16
1:A:16:ALA:HB3	1:A:44:LEU:CD2	0.89	1.98	16	10
1:A:90:THR:HG22	1:A:94:LEU:CD2	0.88	1.98	14	20
1:A:94:LEU:HD12	1:A:95:SER:N	0.86	1.86	17	20
1:A:76:VAL:HG22	1:A:113:MET:HE1	0.85	1.48	20	1
1:A:90:THR:CG2	1:A:120:ILE:HD11	0.84	2.02	13	2
1:A:90:THR:CG2	1:A:94:LEU:HD23	0.83	2.00	14	20
1:A:90:THR:HG23	1:A:120:ILE:HG12	0.83	1.50	17	12
1:A:18:ILE:CD1	1:A:44:LEU:HD22	0.82	2.04	6	10
1:A:71:ARG:O	1:A:72:MET:HE3	0.81	1.76	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:ILE:CG2	1:A:72:MET:HE2	0.79	2.07	3	6
1:A:81:LEU:CD1	1:A:113:MET:HE3	0.79	2.06	19	16
1:A:44:LEU:HD11	1:A:146:LEU:HD21	0.79	1.53	14	1
1:A:18:ILE:HD11	1:A:44:LEU:HD22	0.77	1.57	8	7
1:A:90:THR:HG23	1:A:120:ILE:CG1	0.77	2.09	10	12
1:A:90:THR:HA	1:A:120:ILE:HD11	0.76	1.57	6	6
1:A:81:LEU:HD12	1:A:115:LYS:CD	0.75	2.12	18	1
1:A:90:THR:HG23	1:A:120:ILE:CD1	0.74	2.10	13	2
1:A:25:ILE:HD13	1:A:25:ILE:O	0.74	1.83	2	14
1:A:102:GLN:OE1	1:A:124:ILE:HG22	0.73	1.83	18	3
1:A:61:ALA:HB3	1:A:64:LEU:HG	0.72	1.62	5	20
1:A:44:LEU:HD11	1:A:146:LEU:HD23	0.71	1.62	18	1
1:A:104:ARG:HG3	1:A:105:LEU:HD23	0.71	1.61	14	7
1:A:20:TYR:CD2	1:A:28:VAL:HG21	0.71	2.21	5	10
1:A:60:ILE:HG12	1:A:64:LEU:HD12	0.70	1.62	19	20
1:A:20:TYR:CD1	1:A:25:ILE:HD13	0.69	2.22	11	1
1:A:31:MET:HE3	1:A:32:ILE:CD1	0.69	2.18	6	4
1:A:42:LEU:HD21	1:A:44:LEU:HD12	0.69	1.64	8	4
1:A:100:ALA:O	1:A:105:LEU:HD21	0.68	1.88	14	8
1:A:18:ILE:HD11	1:A:44:LEU:HD13	0.68	1.64	1	3
1:A:90:THR:O	1:A:94:LEU:HG	0.68	1.88	20	20
1:A:73:VAL:HG21	1:A:146:LEU:HD11	0.68	1.64	11	3
1:A:32:ILE:HG22	1:A:36:GLU:OE2	0.68	1.89	9	1
1:A:130:THR:HG23	1:A:135:LYS:HD3	0.67	1.66	4	1
1:A:16:ALA:HB3	1:A:44:LEU:HD21	0.67	1.66	16	6
1:A:16:ALA:HB3	1:A:44:LEU:HD23	0.67	1.67	17	7
1:A:76:VAL:HG22	1:A:113:MET:SD	0.66	2.31	9	12
1:A:18:ILE:HD13	1:A:73:VAL:HB	0.65	1.65	9	9
1:A:16:ALA:CB	1:A:146:LEU:HD22	0.65	2.21	13	5
1:A:107:PRO:C	1:A:108:ILE:HD12	0.65	2.17	12	19
1:A:121:LEU:N	1:A:121:LEU:HD13	0.65	2.07	18	14
1:A:76:VAL:HG11	1:A:121:LEU:HG	0.64	1.66	2	15
1:A:118:PRO:O	1:A:120:ILE:N	0.64	2.31	18	20
1:A:16:ALA:HB2	1:A:71:ARG:HG2	0.64	1.68	19	4
1:A:42:LEU:HD11	1:A:146:LEU:CB	0.63	2.23	1	3
1:A:18:ILE:HB	1:A:46:VAL:HG12	0.63	1.69	7	8
1:A:17:PHE:CB	1:A:72:MET:HE2	0.63	2.24	11	1
1:A:73:VAL:CG2	1:A:146:LEU:HD21	0.62	2.24	12	4
1:A:96:LEU:HD21	1:A:105:LEU:HD11	0.62	1.71	3	8
1:A:107:PRO:HG2	1:A:126:VAL:HG22	0.62	1.69	6	1
1:A:32:ILE:HG23	1:A:44:LEU:CD1	0.62	2.24	5	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:32:ILE:CG2	1:A:44:LEU:HD13	0.62	2.22	5	4
1:A:73:VAL:HG13	1:A:108:ILE:HD13	0.62	1.70	20	5
1:A:76:VAL:HG21	1:A:121:LEU:HD11	0.62	1.70	20	9
1:A:76:VAL:O	1:A:76:VAL:HG13	0.62	1.95	20	19
1:A:44:LEU:HD21	1:A:146:LEU:HD21	0.62	1.72	4	2
1:A:142:LEU:HD13	1:A:142:LEU:O	0.61	1.95	20	1
1:A:81:LEU:HD12	1:A:115:LYS:HD3	0.61	1.72	18	1
1:A:32:ILE:HG23	1:A:44:LEU:HD12	0.61	1.72	16	1
1:A:96:LEU:HD22	1:A:105:LEU:HD21	0.61	1.72	9	6
1:A:96:LEU:HD13	1:A:100:ALA:O	0.60	1.96	20	4
1:A:74:VAL:HG13	1:A:89:GLN:OE1	0.60	1.95	1	2
1:A:20:TYR:OH	1:A:46:VAL:HG11	0.60	1.97	18	2
1:A:17:PHE:HB3	1:A:72:MET:HE2	0.60	1.73	11	1
1:A:120:ILE:O	1:A:124:ILE:HD13	0.60	1.97	17	18
1:A:16:ALA:HB2	1:A:71:ARG:CG	0.59	2.27	19	4
1:A:73:VAL:CG2	1:A:146:LEU:HD11	0.59	2.28	20	4
1:A:96:LEU:HD21	1:A:105:LEU:CD2	0.59	2.28	15	2
1:A:109:LYS:HE2	1:A:126:VAL:HG21	0.59	1.75	9	4
1:A:10:MET:HE2	1:A:60:ILE:HA	0.59	1.73	15	3
1:A:81:LEU:HD13	1:A:116:GLU:O	0.59	1.98	17	2
1:A:106:ILE:O	1:A:108:ILE:HD12	0.59	1.97	17	20
1:A:19:CYS:CB	1:A:74:VAL:HG12	0.58	2.28	18	3
1:A:81:LEU:HD21	1:A:118:PRO:HD3	0.57	1.76	7	16
1:A:94:LEU:HD12	1:A:95:SER:CB	0.57	2.30	11	20
1:A:17:PHE:HB3	1:A:72:MET:HE3	0.57	1.74	19	1
1:A:81:LEU:CB	1:A:115:LYS:HE3	0.57	2.29	15	4
1:A:35:LEU:HD22	1:A:143:ALA:HB2	0.57	1.77	19	5
1:A:118:PRO:HD2	1:A:121:LEU:HD21	0.57	1.77	5	18
1:A:44:LEU:HD11	1:A:146:LEU:CD2	0.56	2.30	1	1
1:A:96:LEU:CD2	1:A:105:LEU:HD21	0.56	2.30	9	3
1:A:73:VAL:HG22	1:A:146:LEU:HD11	0.56	1.75	20	1
1:A:35:LEU:HD11	1:A:139:TRP:CE3	0.56	2.35	5	1
1:A:42:LEU:HD21	1:A:146:LEU:HD23	0.56	1.78	14	1
1:A:89:GLN:NE2	1:A:93:ALA:HB2	0.56	2.15	12	3
1:A:65:ILE:HG21	1:A:72:MET:HE1	0.56	1.78	10	2
1:A:94:LEU:HD12	1:A:95:SER:HB3	0.56	1.78	12	9
1:A:42:LEU:HD21	1:A:146:LEU:CD2	0.56	2.31	14	1
1:A:76:VAL:HG13	1:A:109:LYS:HD2	0.55	1.78	19	4
1:A:18:ILE:HG13	1:A:32:ILE:HG21	0.55	1.75	7	4
1:A:142:LEU:HD23	1:A:146:LEU:HD13	0.55	1.78	4	1
1:A:74:VAL:HG23	1:A:107:PRO:HA	0.55	1.77	5	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:106:ILE:HG13	1:A:142:LEU:HD11	0.55	1.78	1	2
1:A:76:VAL:HG13	1:A:76:VAL:O	0.55	2.01	19	1
1:A:81:LEU:HD13	1:A:115:LYS:HE2	0.55	1.79	14	10
1:A:73:VAL:HG21	1:A:146:LEU:HD21	0.55	1.77	18	3
1:A:42:LEU:HD11	1:A:146:LEU:HB3	0.54	1.80	1	3
1:A:124:ILE:O	1:A:126:VAL:HG23	0.53	2.02	2	2
1:A:35:LEU:HD21	1:A:139:TRP:CD1	0.53	2.39	7	1
1:A:76:VAL:HG21	1:A:121:LEU:CD1	0.53	2.33	20	7
1:A:25:ILE:HD13	1:A:25:ILE:C	0.53	2.28	2	13
1:A:90:THR:O	1:A:94:LEU:N	0.53	2.36	14	12
1:A:89:GLN:HE21	1:A:93:ALA:HB2	0.53	1.64	12	4
1:A:14:PHE:CD2	1:A:60:ILE:HD12	0.52	2.39	8	9
1:A:44:LEU:HD11	1:A:146:LEU:CD1	0.52	2.34	13	1
1:A:91:LYS:HE2	1:A:94:LEU:HD21	0.52	1.81	7	1
1:A:17:PHE:O	1:A:72:MET:HE2	0.51	2.05	19	1
1:A:42:LEU:HD21	1:A:44:LEU:CD1	0.51	2.35	20	3
1:A:20:TYR:CE2	1:A:75:VAL:CG2	0.51	2.93	16	1
1:A:110:TYR:CE1	1:A:129:TYR:CE2	0.51	2.98	20	1
1:A:107:PRO:HD3	1:A:124:ILE:HD11	0.51	1.82	4	17
1:A:109:LYS:HE3	1:A:126:VAL:HG21	0.51	1.82	13	2
1:A:76:VAL:CG2	1:A:121:LEU:HD11	0.51	2.34	20	10
1:A:96:LEU:CD2	1:A:105:LEU:HD22	0.51	2.36	17	3
1:A:61:ALA:HB3	1:A:64:LEU:CG	0.51	2.35	2	17
1:A:91:LYS:CE	1:A:94:LEU:HD21	0.51	2.36	7	1
1:A:25:ILE:HD12	1:A:28:VAL:HB	0.51	1.82	16	1
1:A:16:ALA:HB2	1:A:146:LEU:HD22	0.51	1.83	13	3
1:A:81:LEU:HD21	1:A:118:PRO:HG3	0.50	1.81	5	19
1:A:20:TYR:HA	1:A:75:VAL:HG12	0.50	1.83	16	1
1:A:94:LEU:HD12	1:A:95:SER:HB2	0.50	1.83	19	6
1:A:24:ASP:O	1:A:28:VAL:HG23	0.50	2.07	18	1
1:A:20:TYR:CD1	1:A:75:VAL:HB	0.50	2.41	13	10
1:A:18:ILE:HD12	1:A:32:ILE:CD1	0.50	2.37	4	5
1:A:27:PHE:CZ	1:A:110:TYR:CZ	0.50	2.99	13	1
1:A:113:MET:HB3	1:A:115:LYS:CE	0.50	2.36	18	1
1:A:31:MET:HE3	1:A:32:ILE:HD11	0.50	1.83	6	2
1:A:142:LEU:CD2	1:A:146:LEU:HD13	0.49	2.36	4	1
1:A:35:LEU:HD21	1:A:139:TRP:CB	0.49	2.37	8	2
1:A:138:PHE:CE1	1:A:142:LEU:HD23	0.49	2.42	13	1
1:A:28:VAL:HG13	1:A:31:MET:HE2	0.49	1.83	10	4
1:A:81:LEU:HD12	1:A:115:LYS:CE	0.49	2.37	18	1
1:A:20:TYR:CG	1:A:25:ILE:HD13	0.49	2.41	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:81:LEU:HD22	1:A:118:PRO:HD3	0.49	1.83	18	1
1:A:110:TYR:CE2	1:A:129:TYR:CE2	0.49	3.00	19	2
1:A:35:LEU:HD22	1:A:139:TRP:O	0.49	2.07	6	1
1:A:138:PHE:CE1	1:A:139:TRP:CD1	0.49	3.00	6	2
1:A:110:TYR:CD2	1:A:129:TYR:CE1	0.49	3.01	19	2
1:A:142:LEU:HD13	1:A:142:LEU:C	0.49	2.33	20	1
1:A:89:GLN:O	1:A:93:ALA:N	0.49	2.45	20	18
1:A:35:LEU:HD21	1:A:139:TRP:HB3	0.49	1.83	5	3
1:A:25:ILE:HD12	1:A:25:ILE:O	0.49	2.07	11	1
1:A:65:ILE:HG21	1:A:72:MET:HE2	0.49	1.81	13	1
1:A:20:TYR:CE1	1:A:25:ILE:HD13	0.49	2.43	11	1
1:A:18:ILE:HD12	1:A:44:LEU:HD22	0.49	1.85	19	1
1:A:131:ASN:N	1:A:132:PRO:HD3	0.49	2.23	6	3
1:A:20:TYR:CD2	1:A:28:VAL:CG2	0.48	2.96	14	11
1:A:73:VAL:HG22	1:A:146:LEU:HD21	0.48	1.85	10	4
1:A:20:TYR:CG	1:A:28:VAL:HG11	0.48	2.43	16	1
1:A:94:LEU:CD1	1:A:95:SER:N	0.48	2.72	7	18
1:A:18:ILE:CG2	1:A:20:TYR:CD2	0.48	2.97	20	6
1:A:16:ALA:CB	1:A:44:LEU:HD23	0.48	2.38	18	3
1:A:90:THR:CB	1:A:120:ILE:HD11	0.48	2.39	13	2
1:A:20:TYR:CZ	1:A:25:ILE:HD11	0.48	2.43	20	1
1:A:14:PHE:CE2	1:A:60:ILE:CD1	0.47	2.97	18	13
1:A:35:LEU:HD21	1:A:139:TRP:CG	0.47	2.45	7	2
1:A:100:ALA:HB1	1:A:104:ARG:HD2	0.47	1.87	15	1
1:A:18:ILE:HG22	1:A:20:TYR:CD2	0.47	2.45	7	6
1:A:74:VAL:HG11	1:A:89:GLN:NE2	0.47	2.25	12	1
1:A:110:TYR:CD2	1:A:111:LYS:CG	0.47	2.98	4	2
1:A:78:ASP:OD1	1:A:114:LYS:N	0.47	2.48	4	7
1:A:93:ALA:HB3	1:A:120:ILE:CD1	0.46	2.40	2	4
1:A:90:THR:CA	1:A:120:ILE:HD11	0.46	2.39	19	4
1:A:110:TYR:CE2	1:A:111:LYS:CG	0.46	2.99	7	2
1:A:94:LEU:HD12	1:A:95:SER:OG	0.46	2.11	13	5
1:A:35:LEU:HD13	1:A:142:LEU:HD12	0.46	1.88	20	1
1:A:93:ALA:HA	1:A:96:LEU:HD23	0.46	1.86	12	18
1:A:93:ALA:O	1:A:96:LEU:HD11	0.46	2.10	20	1
1:A:42:LEU:HD11	1:A:146:LEU:HB2	0.46	1.87	1	1
1:A:131:ASN:N	1:A:132:PRO:CD	0.46	2.79	6	12
1:A:60:ILE:CG1	1:A:64:LEU:HD12	0.46	2.40	11	5
1:A:75:VAL:CG1	1:A:75:VAL:O	0.46	2.64	16	1
1:A:108:ILE:CG2	1:A:109:LYS:N	0.46	2.79	9	19
1:A:31:MET:HE3	1:A:32:ILE:HD13	0.46	1.88	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:135:LYS:O	1:A:138:PHE:CD2	0.45	2.69	3	3
1:A:14:PHE:CD2	1:A:60:ILE:CD1	0.45	3.00	10	2
1:A:75:VAL:O	1:A:75:VAL:HG13	0.45	2.11	16	1
1:A:43:LYS:CD	1:A:58:TRP:CH2	0.45	2.99	17	3
1:A:93:ALA:CB	1:A:120:ILE:HD12	0.45	2.40	2	2
1:A:17:PHE:CE2	1:A:65:ILE:HD11	0.45	2.47	7	2
1:A:75:VAL:CG1	1:A:80:TYR:CE2	0.45	2.99	1	1
1:A:46:VAL:HG22	1:A:58:TRP:O	0.45	2.11	19	3
1:A:97:SER:CB	1:A:98:PRO:HD2	0.45	2.42	12	2
1:A:17:PHE:CE2	1:A:65:ILE:CD1	0.45	3.00	18	4
1:A:110:TYR:CE1	1:A:129:TYR:CZ	0.45	3.04	2	1
1:A:75:VAL:HA	1:A:108:ILE:O	0.45	2.12	8	2
1:A:121:LEU:CD2	1:A:121:LEU:C	0.45	2.90	14	12
1:A:135:LYS:CG	1:A:138:PHE:CD1	0.45	3.00	5	1
1:A:141:ARG:O	1:A:145:ALA:HB2	0.45	2.12	19	1
1:A:17:PHE:CD1	1:A:18:ILE:N	0.45	2.85	11	5
1:A:96:LEU:HD21	1:A:105:LEU:HD22	0.45	1.89	17	1
1:A:129:TYR:HB3	1:A:132:PRO:CG	0.44	2.42	1	2
1:A:16:ALA:C	1:A:44:LEU:HD23	0.44	2.37	4	2
1:A:107:PRO:CG	1:A:126:VAL:HG22	0.44	2.40	6	1
1:A:46:VAL:HG22	1:A:59:SER:HA	0.44	1.89	5	1
1:A:18:ILE:HD13	1:A:44:LEU:HD22	0.44	1.86	6	1
1:A:25:ILE:HG23	1:A:26:GLN:N	0.44	2.28	10	3
1:A:138:PHE:CZ	1:A:142:LEU:HD23	0.44	2.48	13	1
1:A:81:LEU:HD21	1:A:118:PRO:CD	0.44	2.42	7	5
1:A:108:ILE:HG22	1:A:109:LYS:N	0.44	2.28	7	18
1:A:120:ILE:HB	1:A:121:LEU:HD13	0.44	1.89	18	1
1:A:93:ALA:HB3	1:A:120:ILE:HD12	0.44	1.89	2	2
1:A:78:ASP:OD2	1:A:114:LYS:N	0.44	2.51	12	3
1:A:117:PHE:CD1	1:A:117:PHE:N	0.44	2.86	14	2
1:A:73:VAL:HG21	1:A:146:LEU:CD1	0.44	2.40	15	1
1:A:32:ILE:N	1:A:32:ILE:CD1	0.44	2.81	5	1
1:A:81:LEU:CD2	1:A:118:PRO:HD3	0.43	2.43	11	15
1:A:17:PHE:CE1	1:A:18:ILE:O	0.43	2.72	8	5
1:A:14:PHE:CE1	1:A:60:ILE:HD11	0.43	2.48	7	1
1:A:17:PHE:C	1:A:17:PHE:CD1	0.43	2.96	10	2
1:A:74:VAL:O	1:A:107:PRO:HA	0.43	2.13	14	3
1:A:110:TYR:CE2	1:A:111:LYS:HG2	0.43	2.48	7	3
1:A:65:ILE:HG22	1:A:72:MET:CE	0.43	2.43	2	1
1:A:121:LEU:N	1:A:121:LEU:CD1	0.43	2.78	18	2
1:A:90:THR:HA	1:A:120:ILE:CD1	0.43	2.41	3	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:107:PRO:CD	1:A:124:ILE:HD11	0.43	2.43	9	3
1:A:96:LEU:HD21	1:A:105:LEU:CD1	0.43	2.44	19	1
1:A:80:TYR:CD1	1:A:80:TYR:N	0.43	2.86	2	2
1:A:20:TYR:CD1	1:A:75:VAL:O	0.43	2.72	5	1
1:A:17:PHE:CE1	1:A:65:ILE:HD11	0.43	2.49	14	1
1:A:110:TYR:O	1:A:110:TYR:CG	0.43	2.72	13	1
1:A:101:HIS:O	1:A:105:LEU:HD11	0.43	2.13	15	1
1:A:20:TYR:CD1	1:A:25:ILE:HG12	0.43	2.48	17	3
1:A:42:LEU:CD2	1:A:44:LEU:HD12	0.43	2.43	3	2
1:A:36:GLU:HG2	1:A:42:LEU:HD23	0.43	1.90	2	1
1:A:31:MET:CE	1:A:32:ILE:HD11	0.43	2.44	7	1
1:A:105:LEU:HD12	1:A:105:LEU:O	0.43	2.14	15	1
1:A:18:ILE:N	1:A:45:CYS:O	0.42	2.51	16	3
1:A:105:LEU:HD23	1:A:105:LEU:N	0.42	2.28	3	4
1:A:20:TYR:CD2	1:A:75:VAL:HB	0.42	2.49	16	1
1:A:45:CYS:HB3	1:A:60:ILE:HG22	0.42	1.91	16	2
1:A:121:LEU:HD13	1:A:121:LEU:H	0.42	1.75	9	1
1:A:96:LEU:HD22	1:A:105:LEU:HD22	0.42	1.91	20	1
1:A:42:LEU:HD11	1:A:146:LEU:HD23	0.42	1.90	4	1
1:A:132:PRO:O	1:A:133:CYS:C	0.42	2.63	12	1
1:A:44:LEU:HD21	1:A:73:VAL:HG21	0.42	1.91	19	1
1:A:14:PHE:CD1	1:A:45:CYS:SG	0.42	3.13	5	1
1:A:11:PRO:O	1:A:14:PHE:CZ	0.42	2.73	9	2
1:A:109:LYS:CE	1:A:126:VAL:HG21	0.42	2.43	9	1
1:A:123:PHE:O	1:A:123:PHE:CG	0.42	2.73	19	2
1:A:76:VAL:HG21	1:A:121:LEU:HG	0.42	1.91	18	1
1:A:17:PHE:CD1	1:A:17:PHE:C	0.42	2.97	19	1
1:A:64:LEU:HD13	1:A:68:ARG:NH1	0.42	2.29	20	1
1:A:110:TYR:CD2	1:A:111:LYS:HG2	0.42	2.50	4	1
1:A:138:PHE:CD1	1:A:138:PHE:C	0.42	2.97	12	2
1:A:35:LEU:HD11	1:A:139:TRP:CD2	0.42	2.50	5	1
1:A:25:ILE:CG2	1:A:26:GLN:N	0.42	2.83	20	2
1:A:73:VAL:CG1	1:A:108:ILE:HD13	0.42	2.42	20	1
1:A:76:VAL:HG13	1:A:109:LYS:HE2	0.42	1.91	15	2
1:A:89:GLN:O	1:A:93:ALA:CB	0.41	2.67	5	3
1:A:76:VAL:O	1:A:76:VAL:CG1	0.41	2.69	1	3
1:A:90:THR:HG23	1:A:120:ILE:HG13	0.41	1.89	10	3
1:A:20:TYR:HB3	1:A:28:VAL:HG11	0.41	1.91	11	1
1:A:110:TYR:CE2	1:A:129:TYR:CZ	0.41	3.08	18	1
1:A:81:LEU:HD21	1:A:118:PRO:CG	0.41	2.44	4	2
1:A:32:ILE:N	1:A:32:ILE:HD12	0.41	2.31	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:PHE:CZ	1:A:46:VAL:C	0.41	2.98	8	2
1:A:78:ASP:OD1	1:A:113:MET:HB3	0.41	2.16	15	1
1:A:14:PHE:CE2	1:A:60:ILE:HD11	0.41	2.51	17	1
1:A:16:ALA:HA	1:A:71:ARG:O	0.41	2.15	15	2
1:A:106:ILE:HD11	1:A:146:LEU:HD21	0.41	1.93	5	1
1:A:43:LYS:HD3	1:A:58:TRP:CZ2	0.41	2.51	9	1
1:A:71:ARG:CD	1:A:71:ARG:N	0.41	2.84	10	1
1:A:17:PHE:CE2	1:A:18:ILE:O	0.41	2.74	13	1
1:A:14:PHE:CD2	1:A:45:CYS:SG	0.41	3.14	19	1
1:A:90:THR:O	1:A:93:ALA:N	0.41	2.54	17	6
1:A:134:THR:O	1:A:137:TRP:CE2	0.41	2.74	15	2
1:A:20:TYR:CD1	1:A:20:TYR:C	0.41	2.99	11	1
1:A:110:TYR:CD1	1:A:129:TYR:CE2	0.41	3.09	12	1
1:A:139:TRP:CE3	1:A:139:TRP:HA	0.41	2.51	5	1
1:A:20:TYR:CE1	1:A:75:VAL:CG1	0.41	3.04	10	1
1:A:69:CYS:HB3	1:A:72:MET:HE1	0.41	1.91	11	1
1:A:32:ILE:HG13	1:A:44:LEU:HD13	0.41	1.93	14	1
1:A:76:VAL:HG21	1:A:121:LEU:CG	0.41	2.46	16	1
1:A:134:THR:OG1	1:A:137:TRP:CH2	0.41	2.74	10	1
1:A:25:ILE:C	1:A:25:ILE:CD1	0.41	2.94	3	2
1:A:109:LYS:CE	1:A:126:VAL:HG11	0.41	2.46	2	1
1:A:93:ALA:HA	1:A:96:LEU:CD2	0.41	2.46	4	4
1:A:110:TYR:CD2	1:A:111:LYS:HG3	0.41	2.50	9	1
1:A:121:LEU:HD13	1:A:121:LEU:N	0.41	2.30	13	2
1:A:44:LEU:O	1:A:58:TRP:CD1	0.41	2.74	14	1
1:A:75:VAL:O	1:A:80:TYR:CD2	0.41	2.74	16	1
1:A:74:VAL:HG23	1:A:107:PRO:CA	0.41	2.45	5	1
1:A:17:PHE:CE2	1:A:46:VAL:C	0.41	2.99	9	1
1:A:121:LEU:C	1:A:121:LEU:CD2	0.41	2.93	15	1
1:A:76:VAL:HG13	1:A:109:LYS:CE	0.41	2.46	16	1
1:A:94:LEU:N	1:A:120:ILE:HD11	0.40	2.31	2	1
1:A:97:SER:CB	1:A:98:PRO:CD	0.40	2.99	3	2
1:A:107:PRO:HD3	1:A:124:ILE:CD1	0.40	2.46	8	2
1:A:30:GLU:O	1:A:33:ARG:HG3	0.40	2.16	9	1
1:A:72:MET:O	1:A:106:ILE:HD13	0.40	2.15	12	1
1:A:76:VAL:O	1:A:109:LYS:HG2	0.40	2.16	13	1
1:A:121:LEU:O	1:A:122:ARG:C	0.40	2.64	20	1
1:A:11:PRO:O	1:A:14:PHE:CE2	0.40	2.74	2	1
1:A:76:VAL:O	1:A:109:LYS:CG	0.40	2.69	2	1
1:A:14:PHE:CG	1:A:45:CYS:SG	0.40	3.15	4	1
1:A:19:CYS:HB3	1:A:74:VAL:HG12	0.40	1.91	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:77:SER:CB	1:A:80:TYR:CD1	0.40	3.05	1	1
1:A:94:LEU:O	1:A:101:HIS:CE1	0.40	2.75	5	1
1:A:43:LYS:CD	1:A:58:TRP:CZ2	0.40	3.04	16	1
1:A:18:ILE:CD1	1:A:32:ILE:CD1	0.40	3.00	19	1
1:A:142:LEU:HD12	1:A:146:LEU:CD1	0.40	2.46	16	1
1:A:43:LYS:HD3	1:A:58:TRP:CH2	0.40	2.51	2	1
1:A:134:THR:O	1:A:137:TRP:CD2	0.40	2.74	10	1
1:A:29:GLN:O	1:A:33:ARG:CG	0.40	2.69	14	1
1:A:100:ALA:HB1	1:A:104:ARG:NE	0.40	2.32	16	1
1:A:16:ALA:CB	1:A:44:LEU:CD2	0.40	2.96	17	1
1:A:78:ASP:CG	1:A:115:LYS:HG3	0.40	2.42	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	125/149 (84%)	102±2 (82±2%)	20±2 (16±2%)	3±1 (3±1%)	6	41
All	All	2500/2980 (84%)	2042 (82%)	390 (16%)	68 (3%)	6	41

All 9 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	120	ILE	19
1	A	125	THR	16
1	A	11	PRO	11
1	A	123	PHE	7
1	A	119	SER	7
1	A	111	LYS	3
1	A	136	SER	2
1	A	99	GLY	2
1	A	47	SER	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	117/139 (84%)	81±3 (69±3%)	36±3 (31±3%)	1	16
All	All	2340/2780 (84%)	1624 (69%)	716 (31%)	1	16

All 79 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	60	ILE	20
1	A	71	ARG	20
1	A	96	LEU	20
1	A	106	ILE	20
1	A	109	LYS	20
1	A	115	LYS	20
1	A	121	LEU	20
1	A	70	ARG	19
1	A	105	LEU	19
1	A	111	LYS	19
1	A	64	LEU	18
1	A	78	ASP	18
1	A	84	LYS	18
1	A	114	LYS	18
1	A	97	SER	18
1	A	25	ILE	17
1	A	133	CYS	16
1	A	144	LYS	16
1	A	33	ARG	15
1	A	58	TRP	13
1	A	43	LYS	13
1	A	59	SER	12
1	A	103	LYS	11
1	A	117	PHE	11
1	A	135	LYS	11
1	A	30	GLU	10
1	A	72	MET	10
1	A	91	LYS	10
1	A	37	GLN	9

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Mol	Chain	Res	Type	Models (Total)
1	A	113	MET	9
1	A	19	CYS	9
1	A	147	SER	9
1	A	67	LYS	9
1	A	142	LEU	9
1	A	20	TYR	8
1	A	77	SER	8
1	A	119	SER	8
1	A	21	CYS	8
1	A	34	GLN	8
1	A	63	GLU	8
1	A	138	PHE	8
1	A	47	SER	8
1	A	13	ARG	8
1	A	31	MET	8
1	A	89	GLN	7
1	A	128	ASP	7
1	A	42	LEU	6
1	A	87	ASP	6
1	A	141	ARG	6
1	A	36	GLU	6
1	A	44	LEU	6
1	A	66	GLU	6
1	A	10	MET	6
1	A	15	ASP	5
1	A	116	GLU	5
1	A	83	SER	5
1	A	62	SER	5
1	A	23	SER	4
1	A	127	CYS	4
1	A	104	ARG	4
1	A	85	GLU	4
1	A	82	GLN	4
1	A	86	CYS	3
1	A	29	GLN	3
1	A	146	LEU	3
1	A	74	VAL	3
1	A	123	PHE	3
1	A	131	ASN	3
1	A	101	HIS	2
1	A	136	SER	2
1	A	26	GLN	2

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Mol	Chain	Res	Type	Models (Total)
1	A	68	ARG	2
1	A	79	ASP	2
1	A	12	GLU	1
1	A	92	PHE	1
1	A	110	TYR	1
1	A	122	ARG	1
1	A	137	TRP	1
1	A	18	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