



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 09:48 pm GMT

PDB ID : 2EV8
Title : Solution structure of the erythroid p55 PDZ domain
Authors : Kusunoki, H.; Kohno, T.
Deposited on : 2005-10-31

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
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

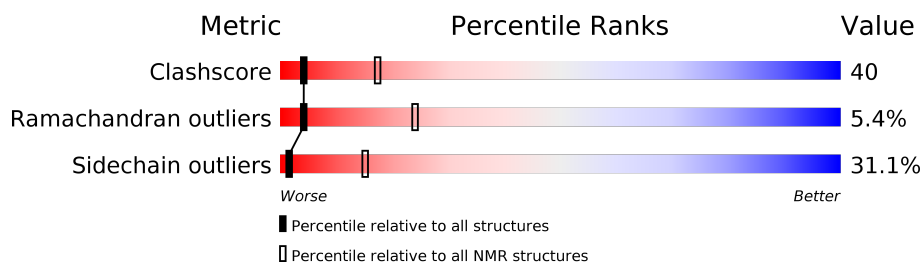
1 Overall quality at a glance

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	97	

2 Ensemble composition and analysis

This entry contains 20 models. Model 19 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:69-A:75, A:83-A:100, A:105-A:151 (72)	0.28	19

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 2 clusters and 1 single-model cluster was found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1357 atoms, of which 694 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called 55 kDa erythrocyte membrane protein.

Mol	Chain	Residues	Atoms						Trace
1	A	85	Total	C	H	N	O	S	0
			1357	411	694	121	126	5	

There are 12 discrepancies between the modelled and reference sequences:

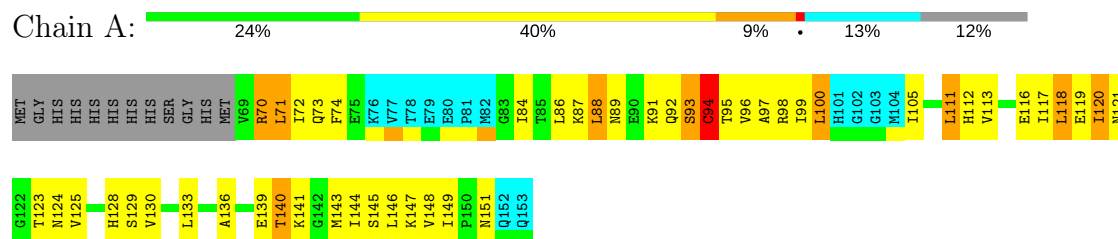
Chain	Residue	Modelled	Actual	Comment	Reference
A	57	MET	-	EXPRESSION TAG	UNP Q00013
A	58	GLY	-	EXPRESSION TAG	UNP Q00013
A	59	HIS	-	EXPRESSION TAG	UNP Q00013
A	60	HIS	-	EXPRESSION TAG	UNP Q00013
A	61	HIS	-	EXPRESSION TAG	UNP Q00013
A	62	HIS	-	EXPRESSION TAG	UNP Q00013
A	63	HIS	-	EXPRESSION TAG	UNP Q00013
A	64	HIS	-	EXPRESSION TAG	UNP Q00013
A	65	SER	-	EXPRESSION TAG	UNP Q00013
A	66	GLY	-	EXPRESSION TAG	UNP Q00013
A	67	HIS	-	EXPRESSION TAG	UNP Q00013
A	68	MET	-	EXPRESSION TAG	UNP Q00013

4 Residue-property plots

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: 55 kDa erythrocyte membrane protein

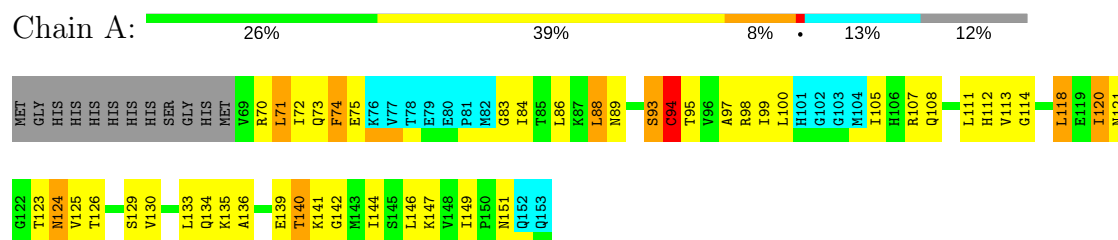


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

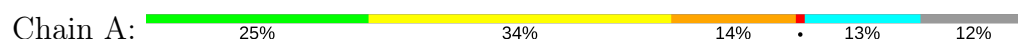
4.2.1 Score per residue for model 1

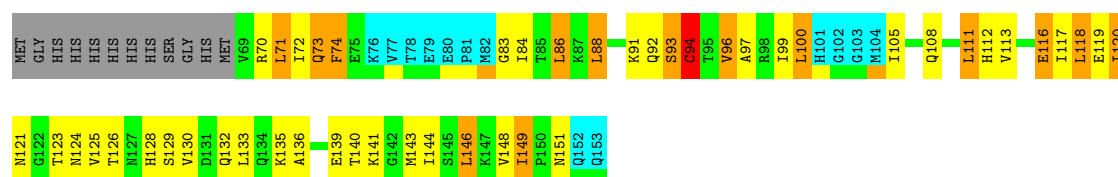
- Molecule 1: 55 kDa erythrocyte membrane protein



4.2.2 Score per residue for model 2

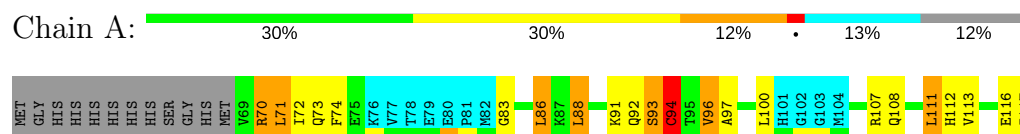
- Molecule 1: 55 kDa erythrocyte membrane protein





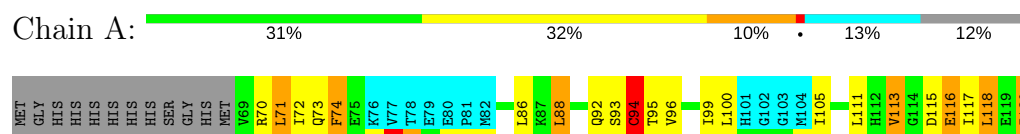
4.2.3 Score per residue for model 3

- Molecule 1: 55 kDa erythrocyte membrane protein



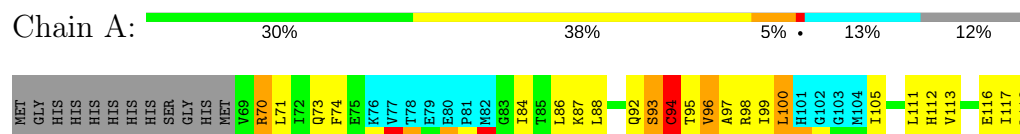
4.2.4 Score per residue for model 4

- Molecule 1: 55 kDa erythrocyte membrane protein



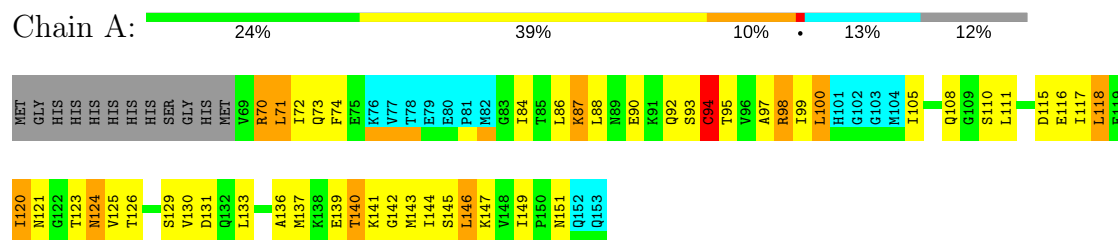
4.2.5 Score per residue for model 5

- Molecule 1: 55 kDa erythrocyte membrane protein



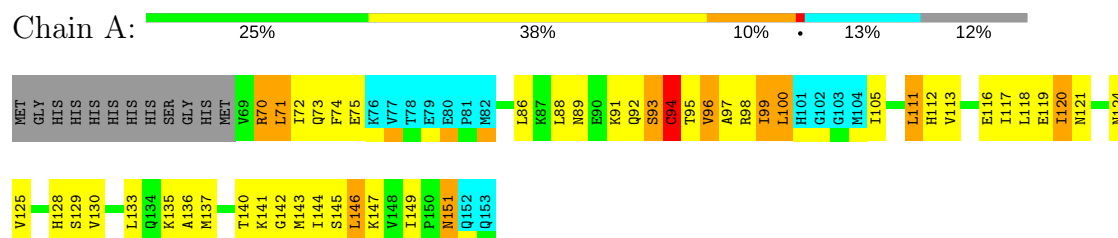
4.2.6 Score per residue for model 6

- Molecule 1: 55 kDa erythrocyte membrane protein



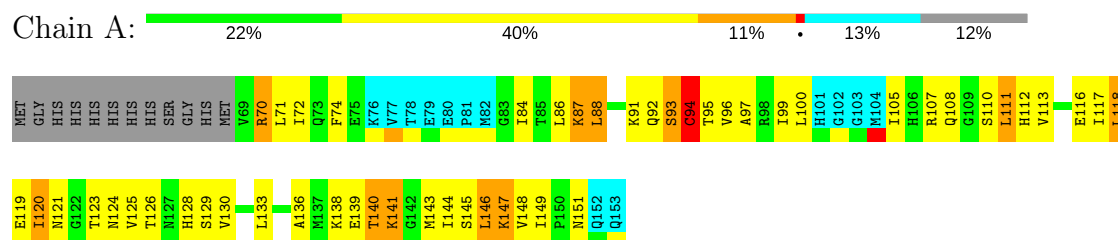
4.2.7 Score per residue for model 7

- Molecule 1: 55 kDa erythrocyte membrane protein



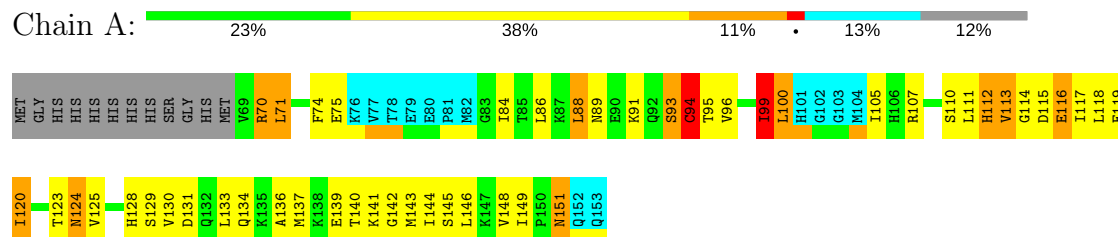
4.2.8 Score per residue for model 8

- Molecule 1: 55 kDa erythrocyte membrane protein



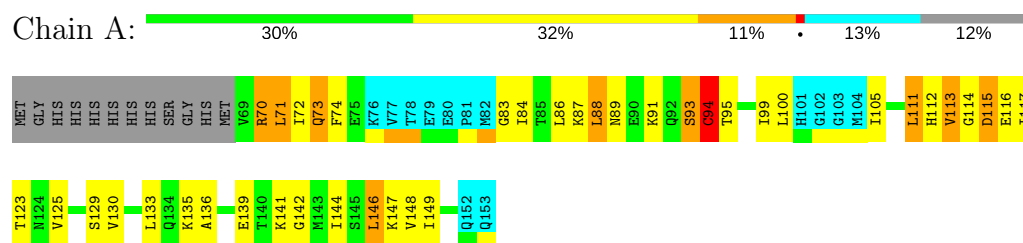
4.2.9 Score per residue for model 9

- Molecule 1: 55 kDa erythrocyte membrane protein



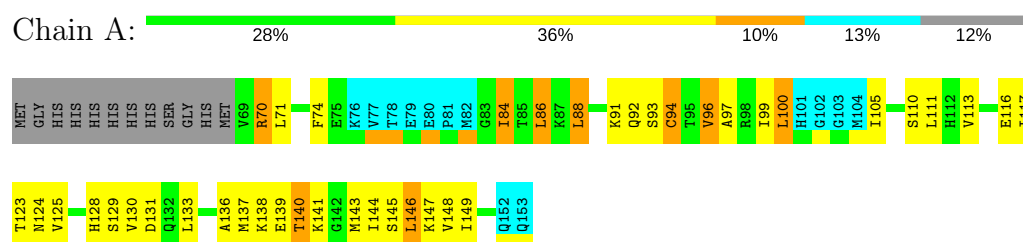
4.2.10 Score per residue for model 10

- Molecule 1: 55 kDa erythrocyte membrane protein



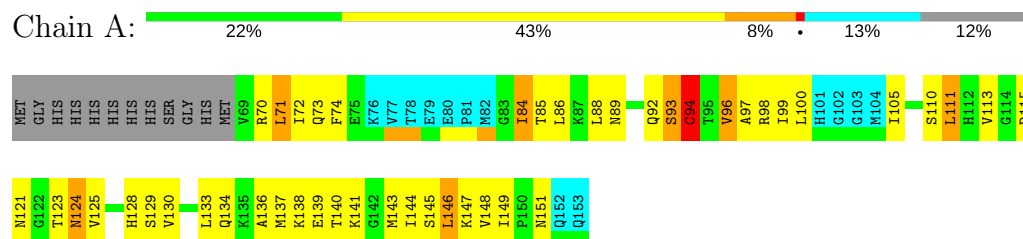
4.2.11 Score per residue for model 11

- Molecule 1: 55 kDa erythrocyte membrane protein



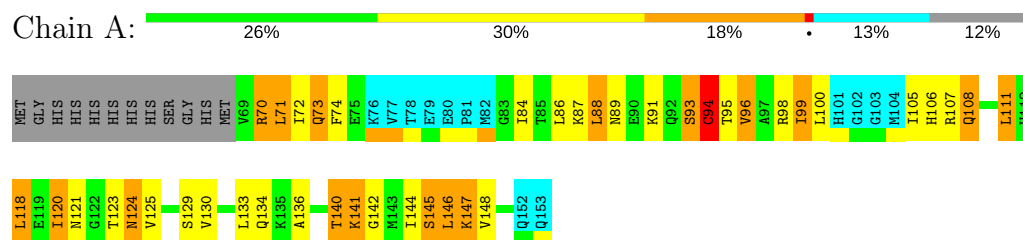
4.2.12 Score per residue for model 12

- Molecule 1: 55 kDa erythrocyte membrane protein



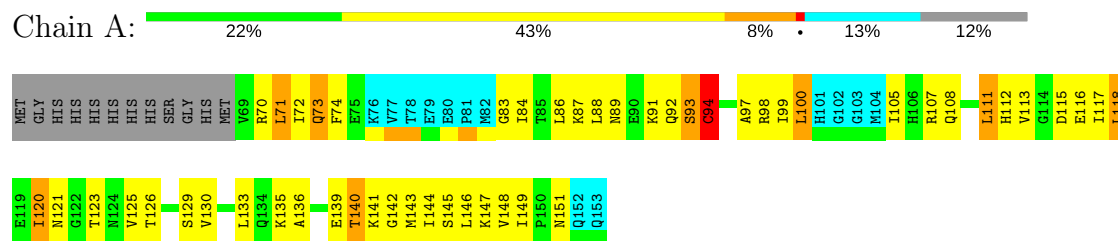
4.2.13 Score per residue for model 13

- Molecule 1: 55 kDa erythrocyte membrane protein



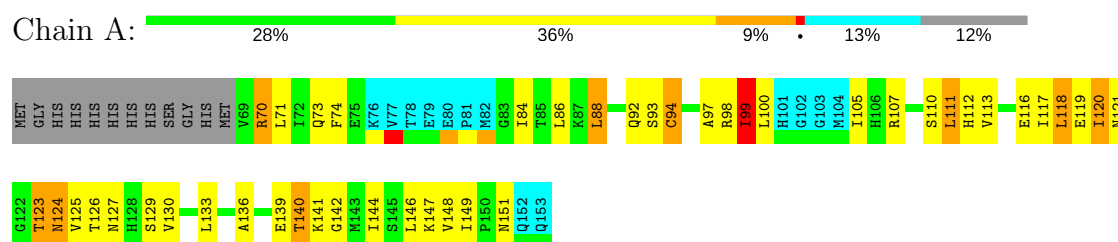
4.2.14 Score per residue for model 14

- Molecule 1: 55 kDa erythrocyte membrane protein



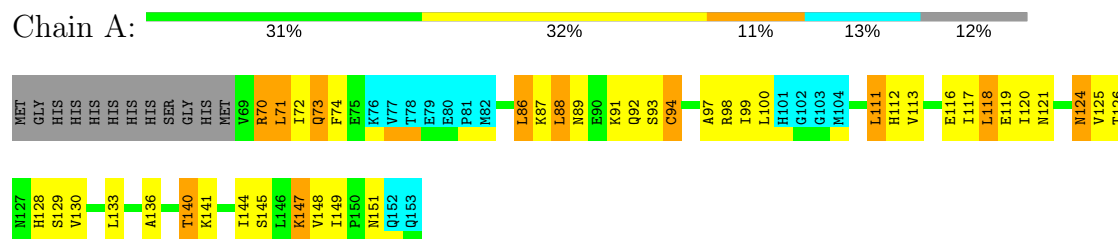
4.2.15 Score per residue for model 15

- Molecule 1: 55 kDa erythrocyte membrane protein



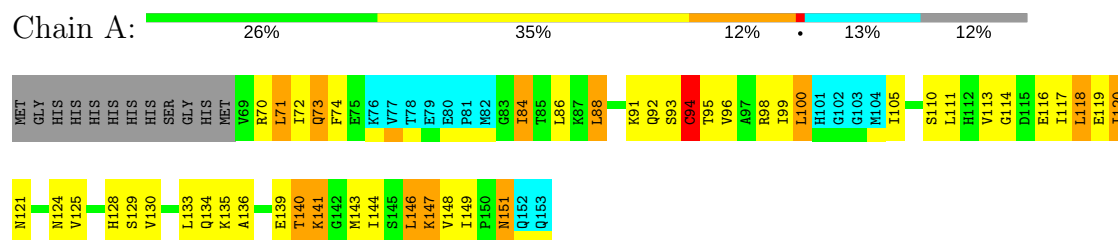
4.2.16 Score per residue for model 16

- Molecule 1: 55 kDa erythrocyte membrane protein



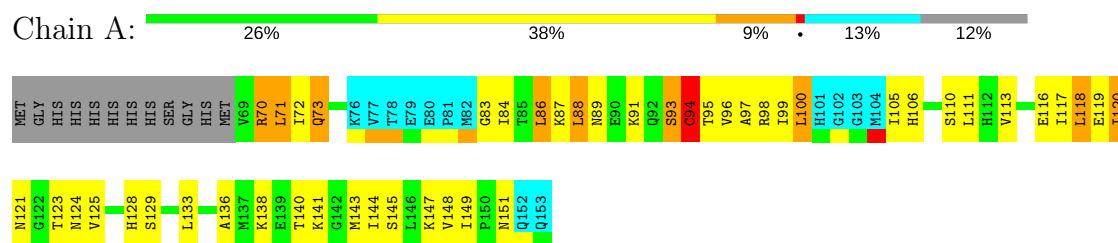
4.2.17 Score per residue for model 17

- Molecule 1: 55 kDa erythrocyte membrane protein



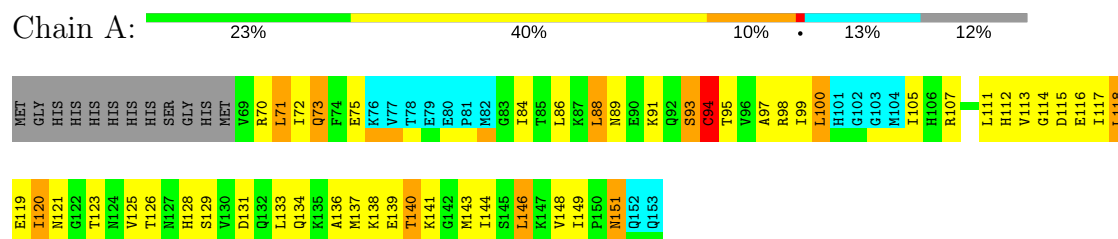
4.2.18 Score per residue for model 18

- Molecule 1: 55 kDa erythrocyte membrane protein



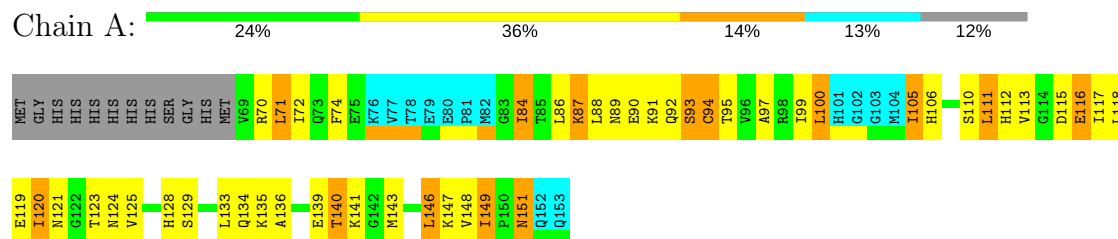
4.2.19 Score per residue for model 19 (medoid)

- Molecule 1: 55 kDa erythrocyte membrane protein



4.2.20 Score per residue for model 20

- Molecule 1: 55 kDa erythrocyte membrane protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 100 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	structure solution	1.1
CNS	refinement	1.1

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	562	598	594	46±6
All	All	11240	11960	11880	922

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 40.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:86:LEU:HD21	1:A:130:VAL:HG21	0.95	1.34	2	3
1:A:120:ILE:CG2	1:A:146:LEU:HD23	0.89	1.98	4	12
1:A:120:ILE:HG21	1:A:146:LEU:HD23	0.86	1.48	4	9
1:A:105:ILE:HG23	1:A:111:LEU:HD13	0.84	1.50	11	1
1:A:99:ILE:HD13	1:A:113:VAL:HG22	0.82	1.51	15	1
1:A:105:ILE:HG23	1:A:111:LEU:HD12	0.82	1.50	18	6
1:A:119:GLU:HA	1:A:125:VAL:HG12	0.82	1.52	12	13
1:A:120:ILE:HD13	1:A:120:ILE:O	0.81	1.74	6	11
1:A:88:LEU:HD12	1:A:92:GLN:HA	0.81	1.52	15	4
1:A:71:LEU:O	1:A:71:LEU:HD13	0.80	1.76	6	5
1:A:125:VAL:HG12	1:A:133:LEU:CD1	0.79	2.07	1	6
1:A:86:LEU:CD2	1:A:130:VAL:HG21	0.79	2.06	2	4
1:A:86:LEU:HD21	1:A:130:VAL:CG2	0.78	2.08	2	5
1:A:71:LEU:HD13	1:A:71:LEU:O	0.78	1.77	7	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:125:VAL:HG23	1:A:133:LEU:HG	0.77	1.56	3	13
1:A:117:ILE:HG22	1:A:125:VAL:HG11	0.77	1.57	9	13
1:A:88:LEU:HD13	1:A:92:GLN:HA	0.76	1.57	5	8
1:A:86:LEU:HD11	1:A:130:VAL:CG2	0.76	2.11	3	4
1:A:120:ILE:O	1:A:120:ILE:HD13	0.76	1.79	7	5
1:A:121:ASN:HB2	1:A:144:ILE:HG23	0.74	1.60	6	8
1:A:88:LEU:HD22	1:A:94:CYS:HA	0.73	1.59	4	2
1:A:120:ILE:HB	1:A:146:LEU:HD23	0.73	1.59	12	7
1:A:84:ILE:HD11	1:A:96:VAL:HG13	0.73	1.59	11	1
1:A:137:MET:CE	1:A:146:LEU:HD21	0.73	2.14	19	1
1:A:71:LEU:HD22	1:A:72:ILE:N	0.72	1.99	19	8
1:A:118:LEU:N	1:A:118:LEU:HD13	0.72	2.00	4	1
1:A:99:ILE:HD12	1:A:113:VAL:HG22	0.72	1.62	7	1
1:A:87:LYS:O	1:A:95:THR:HB	0.71	1.85	6	4
1:A:105:ILE:HG23	1:A:111:LEU:CD1	0.70	2.15	18	5
1:A:84:ILE:HD11	1:A:96:VAL:CG1	0.70	2.15	11	1
1:A:84:ILE:HD11	1:A:137:MET:CE	0.70	2.16	6	1
1:A:143:MET:O	1:A:144:ILE:HD13	0.69	1.86	11	7
1:A:117:ILE:HG12	1:A:148:VAL:HG12	0.69	1.64	14	15
1:A:71:LEU:HD22	1:A:71:LEU:C	0.69	2.08	17	5
1:A:88:LEU:HD12	1:A:92:GLN:C	0.69	2.09	16	1
1:A:88:LEU:HD13	1:A:88:LEU:N	0.69	2.03	9	4
1:A:88:LEU:N	1:A:88:LEU:HD13	0.68	2.04	8	3
1:A:121:ASN:HB3	1:A:144:ILE:HG23	0.68	1.64	7	1
1:A:99:ILE:HD12	1:A:113:VAL:HG12	0.67	1.67	9	3
1:A:121:ASN:ND2	1:A:140:THR:HG21	0.66	2.06	13	11
1:A:119:GLU:CA	1:A:125:VAL:HG12	0.66	2.21	16	13
1:A:120:ILE:HD12	1:A:121:ASN:ND2	0.66	2.06	18	1
1:A:72:ILE:HG13	1:A:111:LEU:HD21	0.66	1.65	12	5
1:A:117:ILE:C	1:A:118:LEU:HD13	0.65	2.10	4	1
1:A:72:ILE:HB	1:A:146:LEU:HD12	0.65	1.67	13	4
1:A:125:VAL:HG12	1:A:133:LEU:HD12	0.65	1.68	4	6
1:A:100:LEU:O	1:A:100:LEU:HD23	0.65	1.90	14	3
1:A:86:LEU:C	1:A:86:LEU:HD22	0.65	2.12	2	4
1:A:137:MET:O	1:A:144:ILE:HD11	0.65	1.92	9	2
1:A:88:LEU:HD12	1:A:94:CYS:HA	0.64	1.68	1	7
1:A:71:LEU:C	1:A:71:LEU:HD22	0.64	2.12	19	3
1:A:84:ILE:HG22	1:A:99:ILE:CG1	0.64	2.23	2	3
1:A:99:ILE:CD1	1:A:113:VAL:HG12	0.63	2.24	4	2
1:A:100:LEU:HD22	1:A:100:LEU:C	0.63	2.14	18	1
1:A:96:VAL:HG12	1:A:113:VAL:HG13	0.63	1.68	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:121:ASN:ND2	1:A:144:ILE:HD13	0.63	2.08	8	3
1:A:120:ILE:CB	1:A:146:LEU:HD23	0.63	2.23	6	9
1:A:118:LEU:O	1:A:126:THR:HG23	0.63	1.94	15	3
1:A:99:ILE:HD12	1:A:113:VAL:CG1	0.63	2.24	10	3
1:A:97:ALA:O	1:A:113:VAL:HG11	0.62	1.94	2	4
1:A:88:LEU:H	1:A:88:LEU:HD23	0.62	1.55	16	1
1:A:88:LEU:N	1:A:88:LEU:HD23	0.62	2.10	15	1
1:A:86:LEU:O	1:A:86:LEU:HD22	0.62	1.94	3	2
1:A:105:ILE:HG23	1:A:111:LEU:HG	0.62	1.71	8	3
1:A:74:PHE:CE2	1:A:146:LEU:HD11	0.61	2.30	4	7
1:A:74:PHE:CZ	1:A:146:LEU:HD11	0.61	2.29	17	7
1:A:71:LEU:O	1:A:72:ILE:HD13	0.61	1.94	1	8
1:A:120:ILE:HG23	1:A:125:VAL:HG11	0.61	1.72	15	5
1:A:100:LEU:C	1:A:100:LEU:HD22	0.61	2.16	2	2
1:A:70:ARG:HG3	1:A:148:VAL:HG22	0.61	1.72	10	6
1:A:99:ILE:HD11	1:A:111:LEU:HD12	0.60	1.73	7	2
1:A:123:THR:HG21	1:A:133:LEU:HD12	0.60	1.73	14	1
1:A:86:LEU:HD23	1:A:86:LEU:N	0.60	2.12	18	7
1:A:84:ILE:HD11	1:A:137:MET:HE1	0.60	1.74	6	1
1:A:88:LEU:HD21	1:A:130:VAL:HB	0.60	1.73	4	1
1:A:86:LEU:HD22	1:A:86:LEU:O	0.60	1.97	2	2
1:A:96:VAL:HG22	1:A:117:ILE:HD11	0.59	1.75	18	4
1:A:88:LEU:HD23	1:A:88:LEU:N	0.59	2.13	4	2
1:A:95:THR:HG23	1:A:114:GLY:O	0.59	1.97	19	5
1:A:84:ILE:HG21	1:A:105:ILE:HG13	0.58	1.75	14	6
1:A:84:ILE:HG22	1:A:99:ILE:HA	0.58	1.76	8	7
1:A:95:THR:HG23	1:A:115:ASP:O	0.58	1.99	13	3
1:A:98:ARG:O	1:A:99:ILE:HD12	0.58	1.99	15	2
1:A:88:LEU:O	1:A:88:LEU:HD22	0.57	1.98	8	4
1:A:74:PHE:HE2	1:A:146:LEU:HD11	0.57	1.58	13	5
1:A:118:LEU:HD22	1:A:118:LEU:H	0.57	1.60	4	1
1:A:88:LEU:HD12	1:A:92:GLN:CA	0.57	2.29	4	3
1:A:86:LEU:HD13	1:A:86:LEU:N	0.57	2.14	16	3
1:A:86:LEU:H	1:A:86:LEU:HD23	0.57	1.60	5	3
1:A:140:THR:HB	1:A:144:ILE:HD11	0.57	1.77	2	1
1:A:71:LEU:HA	1:A:146:LEU:O	0.57	2.00	6	10
1:A:123:THR:CG2	1:A:133:LEU:HD12	0.56	2.30	14	1
1:A:88:LEU:HD12	1:A:89:ASN:O	0.56	2.00	14	4
1:A:120:ILE:HD12	1:A:125:VAL:CG1	0.56	2.31	4	7
1:A:86:LEU:N	1:A:86:LEU:HD23	0.56	2.16	15	5
1:A:118:LEU:HD12	1:A:119:GLU:OE2	0.56	1.99	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:86:LEU:HD11	1:A:130:VAL:HG23	0.56	1.76	8	2
1:A:84:ILE:HD12	1:A:99:ILE:CG1	0.56	2.29	11	1
1:A:88:LEU:HD22	1:A:88:LEU:O	0.56	2.00	9	3
1:A:86:LEU:HD23	1:A:86:LEU:H	0.56	1.61	15	8
1:A:118:LEU:HA	1:A:126:THR:HG23	0.55	1.77	4	3
1:A:117:ILE:HG23	1:A:147:LYS:O	0.55	2.02	6	1
1:A:70:ARG:NE	1:A:72:ILE:HD11	0.55	2.17	10	1
1:A:97:ALA:O	1:A:113:VAL:HG13	0.54	2.01	19	2
1:A:99:ILE:CD1	1:A:113:VAL:HG22	0.54	2.33	13	4
1:A:73:GLN:HA	1:A:144:ILE:O	0.54	2.03	10	13
1:A:86:LEU:H	1:A:86:LEU:HD13	0.54	1.62	2	4
1:A:133:LEU:HA	1:A:136:ALA:HB3	0.54	1.79	6	20
1:A:140:THR:HG22	1:A:141:LYS:HE2	0.54	1.79	17	1
1:A:118:LEU:HD12	1:A:147:LYS:O	0.53	2.04	18	2
1:A:86:LEU:CD1	1:A:130:VAL:HG21	0.53	2.32	3	3
1:A:121:ASN:HD21	1:A:140:THR:HG21	0.53	1.63	6	7
1:A:117:ILE:HG22	1:A:125:VAL:HG21	0.53	1.79	13	2
1:A:117:ILE:HG22	1:A:125:VAL:CG1	0.53	2.32	16	6
1:A:137:MET:HE2	1:A:146:LEU:HD21	0.53	1.80	19	1
1:A:88:LEU:HB3	1:A:94:CYS:N	0.53	2.18	19	7
1:A:137:MET:SD	1:A:146:LEU:HD21	0.53	2.44	9	2
1:A:120:ILE:HD13	1:A:120:ILE:C	0.53	2.24	6	1
1:A:120:ILE:HD13	1:A:123:THR:HB	0.53	1.81	15	13
1:A:125:VAL:CG2	1:A:133:LEU:HG	0.53	2.34	19	7
1:A:125:VAL:HG12	1:A:133:LEU:HG	0.52	1.80	14	1
1:A:96:VAL:HG23	1:A:114:GLY:H	0.52	1.63	13	1
1:A:86:LEU:HG	1:A:130:VAL:HG21	0.52	1.81	14	6
1:A:117:ILE:CG2	1:A:125:VAL:HG11	0.51	2.34	12	5
1:A:86:LEU:HD11	1:A:130:VAL:HG21	0.51	1.79	2	2
1:A:86:LEU:N	1:A:86:LEU:HD13	0.51	2.20	11	1
1:A:99:ILE:HG22	1:A:99:ILE:O	0.51	2.05	12	2
1:A:118:LEU:C	1:A:125:VAL:HG22	0.51	2.26	14	7
1:A:86:LEU:CD1	1:A:130:VAL:CG2	0.51	2.87	11	3
1:A:86:LEU:CD2	1:A:130:VAL:CG2	0.51	2.88	16	2
1:A:99:ILE:HG22	1:A:100:LEU:HD13	0.51	1.81	5	1
1:A:120:ILE:HG22	1:A:146:LEU:HD23	0.51	1.82	10	4
1:A:125:VAL:HB	1:A:133:LEU:HG	0.51	1.82	10	6
1:A:133:LEU:HD22	1:A:133:LEU:N	0.51	2.21	19	7
1:A:72:ILE:CG1	1:A:111:LEU:HD21	0.51	2.36	12	1
1:A:88:LEU:HB3	1:A:94:CYS:HA	0.51	1.83	2	4
1:A:116:GLU:OE2	1:A:149:ILE:HD12	0.50	2.06	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:74:PHE:CE2	1:A:105:ILE:HD11	0.50	2.41	4	1
1:A:129:SER:O	1:A:133:LEU:CD2	0.50	2.60	19	20
1:A:137:MET:CE	1:A:144:ILE:HG21	0.50	2.37	7	1
1:A:74:PHE:CD2	1:A:105:ILE:HD11	0.50	2.40	4	2
1:A:125:VAL:O	1:A:125:VAL:HG22	0.50	2.06	8	4
1:A:99:ILE:HG12	1:A:105:ILE:HG21	0.49	1.82	4	8
1:A:88:LEU:CD1	1:A:88:LEU:N	0.49	2.75	8	4
1:A:100:LEU:HD23	1:A:100:LEU:O	0.49	2.07	15	1
1:A:129:SER:O	1:A:133:LEU:HD22	0.49	2.08	19	14
1:A:94:CYS:SG	1:A:125:VAL:HG22	0.49	2.48	17	2
1:A:71:LEU:C	1:A:71:LEU:HD13	0.49	2.29	3	6
1:A:105:ILE:N	1:A:105:ILE:HD12	0.48	2.23	13	1
1:A:140:THR:HG22	1:A:141:LYS:HD3	0.48	1.85	8	1
1:A:96:VAL:HG23	1:A:115:ASP:OD1	0.48	2.08	4	1
1:A:112:HIS:CG	1:A:151:ASN:ND2	0.48	2.81	2	7
1:A:88:LEU:HD23	1:A:88:LEU:H	0.48	1.69	17	1
1:A:121:ASN:OD1	1:A:140:THR:HG21	0.48	2.09	16	1
1:A:86:LEU:C	1:A:86:LEU:CD2	0.48	2.82	2	3
1:A:84:ILE:C	1:A:84:ILE:HD13	0.48	2.29	17	1
1:A:71:LEU:HD21	1:A:73:GLN:HG3	0.47	1.85	6	2
1:A:86:LEU:HD12	1:A:94:CYS:CB	0.47	2.38	14	2
1:A:105:ILE:HD12	1:A:105:ILE:N	0.47	2.24	8	1
1:A:86:LEU:CD1	1:A:86:LEU:N	0.47	2.77	16	1
1:A:118:LEU:O	1:A:125:VAL:HG22	0.47	2.09	14	2
1:A:86:LEU:N	1:A:86:LEU:CD1	0.47	2.78	3	3
1:A:125:VAL:HG22	1:A:125:VAL:O	0.47	2.10	12	4
1:A:74:PHE:CE2	1:A:146:LEU:CD1	0.47	2.98	9	7
1:A:117:ILE:HG21	1:A:120:ILE:HG22	0.47	1.86	6	2
1:A:70:ARG:O	1:A:147:LYS:HA	0.47	2.10	18	9
1:A:133:LEU:N	1:A:133:LEU:HD22	0.47	2.25	20	4
1:A:100:LEU:C	1:A:100:LEU:HD23	0.47	2.30	14	4
1:A:137:MET:HE3	1:A:146:LEU:HD21	0.47	1.87	19	1
1:A:105:ILE:CG2	1:A:111:LEU:HD12	0.47	2.40	9	1
1:A:88:LEU:CD2	1:A:88:LEU:N	0.47	2.78	16	1
1:A:118:LEU:HD12	1:A:119:GLU:HG2	0.47	1.87	15	1
1:A:86:LEU:HD23	1:A:94:CYS:CB	0.47	2.39	6	1
1:A:128:HIS:CB	1:A:133:LEU:HD21	0.47	2.40	19	1
1:A:97:ALA:O	1:A:113:VAL:CG1	0.46	2.64	12	12
1:A:98:ARG:C	1:A:99:ILE:HD12	0.46	2.31	1	3
1:A:72:ILE:HD12	1:A:111:LEU:CD2	0.46	2.40	2	3
1:A:120:ILE:HD12	1:A:125:VAL:HG11	0.46	1.86	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:88:LEU:CD1	1:A:92:GLN:HA	0.46	2.40	11	1
1:A:125:VAL:CG1	1:A:133:LEU:HG	0.46	2.40	14	1
1:A:88:LEU:N	1:A:88:LEU:CD1	0.46	2.75	18	3
1:A:99:ILE:HD11	1:A:111:LEU:HD13	0.46	1.87	9	1
1:A:130:VAL:HG22	1:A:134:GLN:NE2	0.46	2.25	9	2
1:A:111:LEU:HD13	1:A:112:HIS:H	0.46	1.71	3	4
1:A:112:HIS:CD2	1:A:151:ASN:ND2	0.46	2.84	8	2
1:A:135:LYS:O	1:A:139:GLU:N	0.46	2.48	20	1
1:A:118:LEU:HD22	1:A:147:LYS:O	0.46	2.11	4	1
1:A:124:ASN:O	1:A:128:HIS:CD2	0.46	2.69	3	12
1:A:118:LEU:O	1:A:126:THR:HG22	0.46	2.11	2	2
1:A:120:ILE:CG2	1:A:146:LEU:HD22	0.46	2.41	3	1
1:A:71:LEU:CD2	1:A:71:LEU:C	0.45	2.80	17	4
1:A:120:ILE:C	1:A:120:ILE:HD13	0.45	2.31	7	1
1:A:140:THR:CB	1:A:144:ILE:HD11	0.45	2.41	2	1
1:A:105:ILE:HD13	1:A:105:ILE:N	0.45	2.26	20	1
1:A:86:LEU:CD2	1:A:134:GLN:NE2	0.45	2.79	12	6
1:A:120:ILE:HG22	1:A:146:LEU:HD22	0.45	1.88	3	1
1:A:137:MET:HE2	1:A:144:ILE:HG21	0.45	1.88	7	1
1:A:100:LEU:HD22	1:A:100:LEU:O	0.45	2.11	18	1
1:A:116:GLU:OE2	1:A:149:ILE:HD13	0.45	2.12	20	2
1:A:99:ILE:O	1:A:99:ILE:HG22	0.45	2.11	9	1
1:A:133:LEU:O	1:A:136:ALA:HB3	0.45	2.12	3	5
1:A:74:PHE:CD2	1:A:105:ILE:CD1	0.44	3.00	9	2
1:A:88:LEU:HD13	1:A:88:LEU:H	0.44	1.69	18	3
1:A:120:ILE:HA	1:A:145:SER:O	0.44	2.12	18	1
1:A:100:LEU:HD23	1:A:100:LEU:C	0.44	2.33	15	2
1:A:70:ARG:CG	1:A:148:VAL:HG22	0.44	2.40	10	1
1:A:84:ILE:HG22	1:A:99:ILE:HG12	0.44	1.88	2	1
1:A:72:ILE:CD1	1:A:111:LEU:CD2	0.44	2.96	13	3
1:A:99:ILE:HD12	1:A:113:VAL:CG2	0.44	2.42	12	1
1:A:120:ILE:HG21	1:A:137:MET:HE2	0.44	1.89	12	1
1:A:118:LEU:HD12	1:A:119:GLU:CD	0.44	2.33	3	1
1:A:88:LEU:H	1:A:88:LEU:HD13	0.44	1.70	9	1
1:A:84:ILE:HG22	1:A:99:ILE:HG23	0.44	1.90	5	1
1:A:120:ILE:O	1:A:120:ILE:HG13	0.44	2.13	3	2
1:A:117:ILE:HG21	1:A:120:ILE:CG2	0.43	2.42	6	1
1:A:93:SER:O	1:A:94:CYS:C	0.43	2.56	3	14
1:A:99:ILE:CG2	1:A:100:LEU:N	0.43	2.80	6	1
1:A:72:ILE:HG23	1:A:108:GLN:OE1	0.43	2.14	3	1
1:A:98:ARG:N	1:A:98:ARG:CD	0.43	2.82	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:86:LEU:HD21	1:A:130:VAL:HG23	0.43	1.89	15	5
1:A:125:VAL:HG23	1:A:133:LEU:CG	0.43	2.39	2	1
1:A:100:LEU:N	1:A:100:LEU:CD1	0.43	2.82	5	1
1:A:84:ILE:HG22	1:A:99:ILE:HG13	0.43	1.90	6	1
1:A:120:ILE:HG22	1:A:146:LEU:CD2	0.43	2.44	3	1
1:A:128:HIS:HB3	1:A:133:LEU:HD21	0.43	1.90	19	1
1:A:116:GLU:O	1:A:148:VAL:HG13	0.43	2.13	4	1
1:A:100:LEU:CD1	1:A:100:LEU:N	0.43	2.82	2	2
1:A:125:VAL:HG12	1:A:133:LEU:HD11	0.42	1.90	6	2
1:A:95:THR:O	1:A:96:VAL:C	0.42	2.57	13	3
1:A:86:LEU:HA	1:A:97:ALA:N	0.42	2.29	2	2
1:A:120:ILE:HG13	1:A:120:ILE:O	0.42	2.14	16	1
1:A:74:PHE:CE1	1:A:144:ILE:CG1	0.42	3.02	3	1
1:A:120:ILE:O	1:A:123:THR:N	0.42	2.53	15	9
1:A:112:HIS:CG	1:A:151:ASN:OD1	0.42	2.73	3	1
1:A:88:LEU:CB	1:A:94:CYS:N	0.42	2.83	8	1
1:A:96:VAL:CG2	1:A:117:ILE:HD11	0.42	2.43	18	1
1:A:105:ILE:HG22	1:A:111:LEU:HG	0.42	1.91	2	1
1:A:71:LEU:C	1:A:71:LEU:CD2	0.42	2.86	3	1
1:A:99:ILE:CD1	1:A:113:VAL:CG1	0.42	2.98	17	1
1:A:70:ARG:HE	1:A:72:ILE:HD11	0.42	1.73	10	1
1:A:121:ASN:HD22	1:A:144:ILE:HD12	0.42	1.73	18	1
1:A:71:LEU:HD13	1:A:71:LEU:C	0.42	2.33	13	1
1:A:84:ILE:O	1:A:84:ILE:HD13	0.41	2.15	20	1
1:A:123:THR:O	1:A:125:VAL:N	0.41	2.54	6	1
1:A:70:ARG:CG	1:A:148:VAL:CG2	0.41	2.98	10	1
1:A:120:ILE:CG2	1:A:146:LEU:CD2	0.41	2.98	3	1
1:A:117:ILE:HG12	1:A:148:VAL:HG22	0.41	1.92	4	1
1:A:111:LEU:O	1:A:112:HIS:CG	0.41	2.73	5	3
1:A:86:LEU:HD21	1:A:134:GLN:NE2	0.41	2.30	17	1
1:A:125:VAL:HA	1:A:133:LEU:HG	0.41	1.93	2	2
1:A:105:ILE:O	1:A:108:GLN:N	0.41	2.53	13	2
1:A:74:PHE:CZ	1:A:144:ILE:HB	0.41	2.50	8	4
1:A:121:ASN:ND2	1:A:144:ILE:CD1	0.41	2.83	1	5
1:A:100:LEU:CD2	1:A:100:LEU:C	0.41	2.86	18	1
1:A:111:LEU:O	1:A:112:HIS:CD2	0.41	2.74	14	2
1:A:120:ILE:CD1	1:A:121:ASN:ND2	0.41	2.83	18	1
1:A:121:ASN:N	1:A:145:SER:O	0.41	2.54	13	1
1:A:88:LEU:N	1:A:88:LEU:CD2	0.41	2.80	15	1
1:A:87:LYS:CD	1:A:97:ALA:CB	0.41	2.99	6	1
1:A:121:ASN:ND2	1:A:140:THR:CG2	0.41	2.82	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:ARG:N	1:A:148:VAL:O	0.41	2.54	15	1
1:A:130:VAL:HG13	1:A:131:ASP:N	0.41	2.31	6	1
1:A:110:SER:O	1:A:112:HIS:CE1	0.40	2.74	15	1
1:A:133:LEU:O	1:A:136:ALA:N	0.40	2.55	15	1
1:A:86:LEU:N	1:A:86:LEU:CD2	0.40	2.84	15	1
1:A:118:LEU:HD23	1:A:147:LYS:O	0.40	2.16	14	1
1:A:151:ASN:CG	1:A:151:ASN:O	0.40	2.60	20	1
1:A:87:LYS:CD	1:A:97:ALA:HB1	0.40	2.46	6	1
1:A:96:VAL:HG23	1:A:114:GLY:N	0.40	2.31	13	1
1:A:125:VAL:O	1:A:125:VAL:CG2	0.40	2.69	8	1
1:A:74:PHE:CZ	1:A:146:LEU:CD1	0.40	3.05	20	1
1:A:84:ILE:HD12	1:A:99:ILE:HG13	0.40	1.94	11	1
1:A:123:THR:O	1:A:125:VAL:HG13	0.40	2.15	1	1
1:A:94:CYS:SG	1:A:125:VAL:HG23	0.40	2.56	15	1
1:A:99:ILE:CD1	1:A:113:VAL:CG2	0.40	2.99	5	1
1:A:85:THR:OG1	1:A:98:ARG:HB2	0.40	2.15	12	1
1:A:128:HIS:HD2	1:A:133:LEU:HD11	0.40	1.77	11	1
1:A:83:GLY:N	1:A:100:LEU:HD22	0.40	2.32	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	71/97 (73%)	56±2 (79±3%)	11±2 (16±4%)	4±2 (5±3%)	4	24
All	All	1420/1940 (73%)	1116 (79%)	227 (16%)	77 (5%)	4	24

All 13 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	94	CYS	19
1	A	96	VAL	9
1	A	142	GLY	8
1	A	124	ASN	6

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Mol	Chain	Res	Type	Models (Total)
1	A	151	ASN	6
1	A	89	ASN	6
1	A	115	ASP	6
1	A	83	GLY	5
1	A	141	LYS	4
1	A	113	VAL	3
1	A	99	ILE	3
1	A	112	HIS	1
1	A	126	THR	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	65/86 (76%)	45±2 (69±3%)	20±2 (31±3%)	1	15
All	All	1300/1720 (76%)	896 (69%)	404 (31%)	1	15

All 47 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	93	SER	20
1	A	70	ARG	20
1	A	118	LEU	20
1	A	71	LEU	20
1	A	116	GLU	19
1	A	140	THR	18
1	A	149	ILE	18
1	A	94	CYS	17
1	A	120	ILE	17
1	A	141	LYS	16
1	A	88	LEU	14
1	A	91	LYS	14
1	A	139	GLU	13
1	A	100	LEU	13
1	A	111	LEU	13
1	A	146	LEU	12

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Mol	Chain	Res	Type	Models (Total)
1	A	73	GLN	11
1	A	147	LYS	10
1	A	145	SER	10
1	A	87	LYS	8
1	A	151	ASN	8
1	A	107	ARG	8
1	A	110	SER	8
1	A	98	ARG	8
1	A	124	ASN	7
1	A	135	LYS	7
1	A	143	MET	6
1	A	138	LYS	6
1	A	86	LEU	5
1	A	131	ASP	5
1	A	108	GLN	5
1	A	84	ILE	4
1	A	99	ILE	4
1	A	74	PHE	3
1	A	75	GLU	3
1	A	90	GLU	2
1	A	106	HIS	2
1	A	126	THR	1
1	A	132	GLN	1
1	A	148	VAL	1
1	A	92	GLN	1
1	A	123	THR	1
1	A	127	ASN	1
1	A	115	ASP	1
1	A	105	ILE	1
1	A	128	HIS	1
1	A	89	ASN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no carbohydrates 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