



# Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 1E8L  
Title : NMR SOLUTION STRUCTURE OF HEN LYSOZYME  
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Redfield, C.; Smith, L.J.  
Deposited on : 2000-09-27

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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

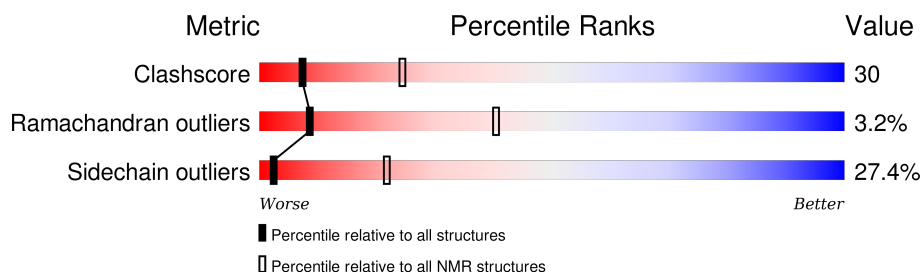
# 1 Overall quality at a glance

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  $\geq 3$ , 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	129	

## 2 Ensemble composition and analysis

This entry contains 50 models. Model 24 is the overall representative, medoid model (most similar to other models). The authors have identified model 49 as representative.

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:1-A:129 (129)	0.34	24

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, 2, 3, 4, 5, 6, 7, 8, 9, 10, 14, 15, 16, 17, 18, 19, 21, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37
2	40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50
3	11, 12, 13
4	20, 22
5	38, 39

### 3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1961 atoms, of which 960 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called LYSOZYME.

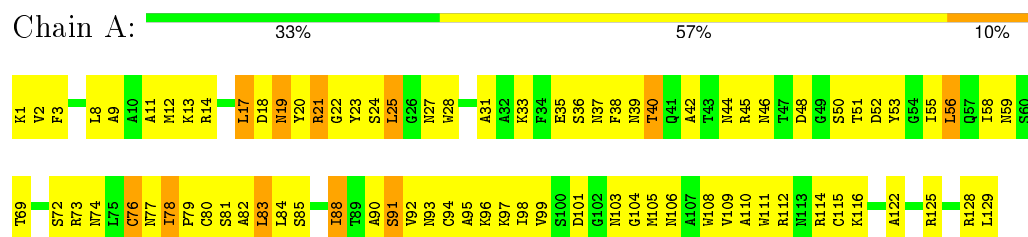
Mol	Chain	Residues	Atoms						Trace
1	A	129	Total	C	H	N	O	S	0
			1961	613	960	193	185	10	

## 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: LYSOZYME

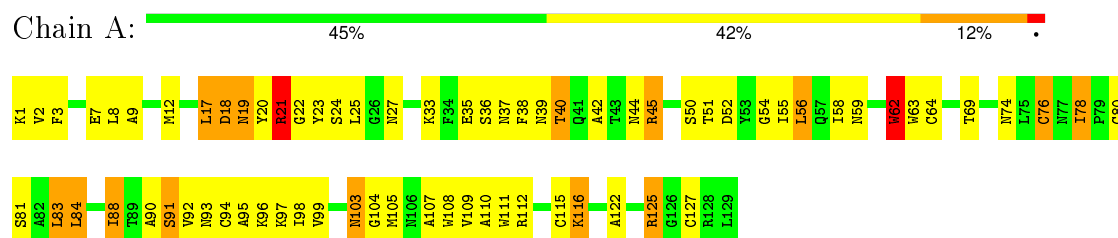


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

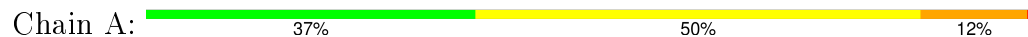
#### 4.2.1 Score per residue for model 1

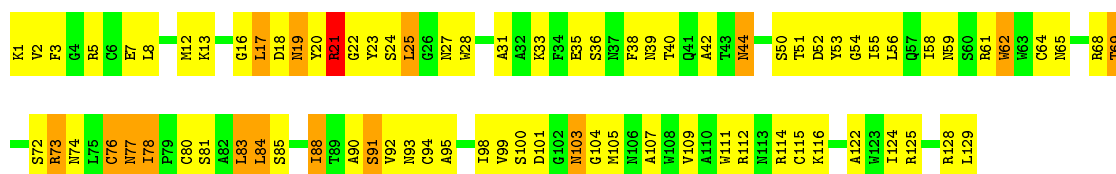
#### • Molecule 1: LYSOZYME



#### 4.2.2 Score per residue for model 2

#### • Molecule 1: LYSOZYME

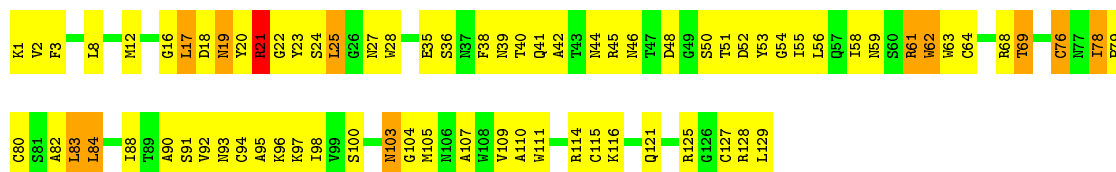




### 4.2.3 Score per residue for model 3

- Molecule 1: LYSOZYME

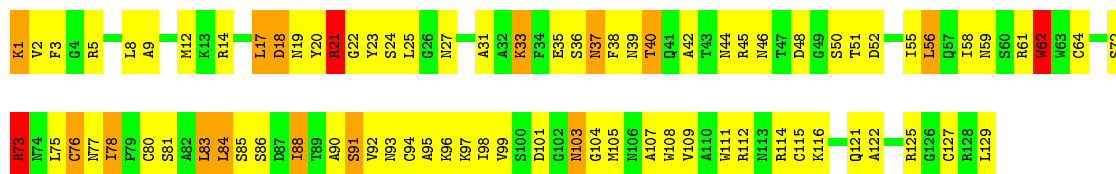
Chain A: 41% 50% 9%



### 4.2.4 Score per residue for model 4

- Molecule 1: LYSOZYME

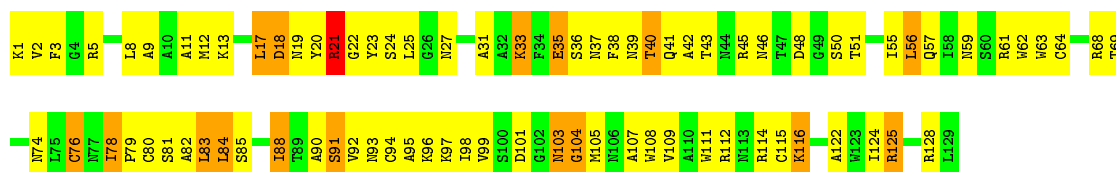
Chain A: 37% 50% 11%



### 4.2.5 Score per residue for model 5

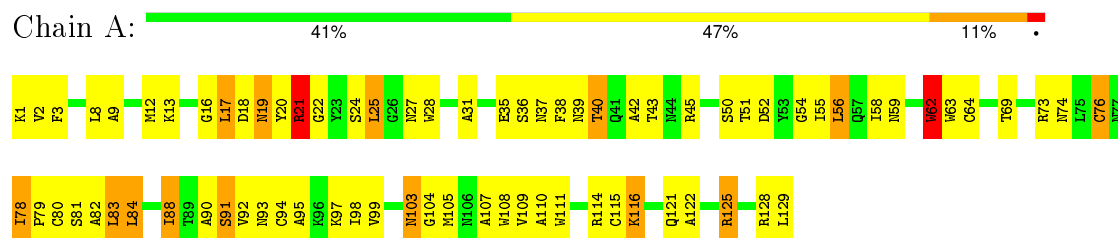
- Molecule 1: LYSOZYME

Chain A: 36% 50% 12%



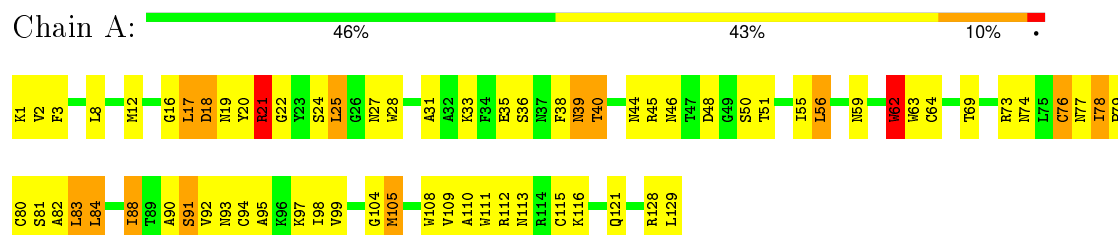
### 4.2.6 Score per residue for model 6

- Molecule 1: LYSOZYME



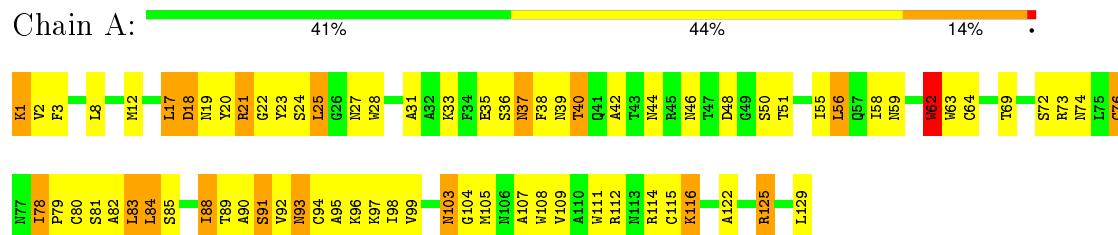
#### 4.2.7 Score per residue for model 7

- Molecule 1: LYSOZYME



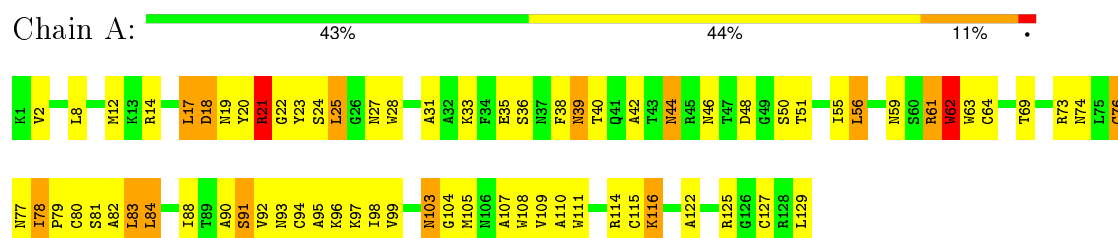
#### 4.2.8 Score per residue for model 8

- Molecule 1: LYSOZYME



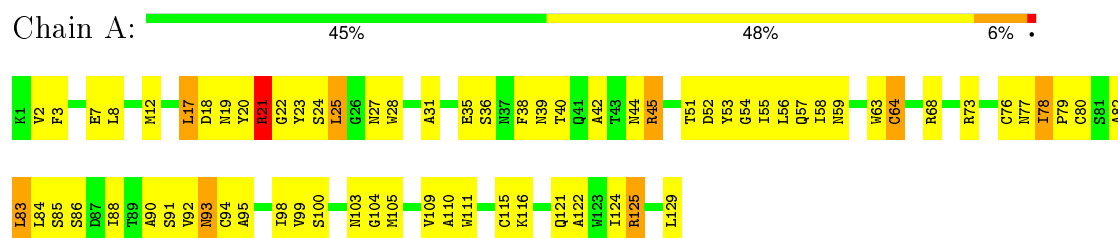
#### 4.2.9 Score per residue for model 9

- Molecule 1: LYSOZYME



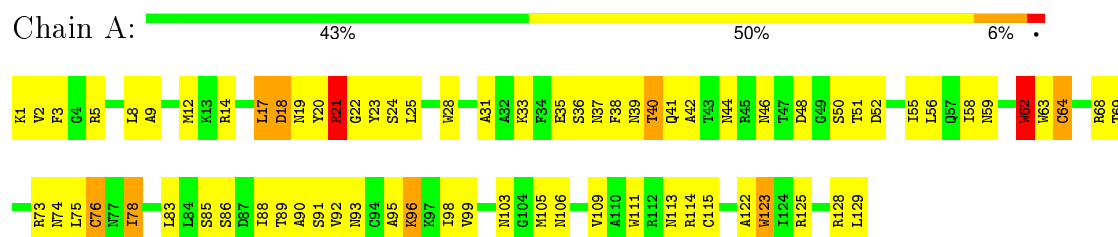
## 4.2.10 Score per residue for model 10

- Molecule 1: LYSOZYME



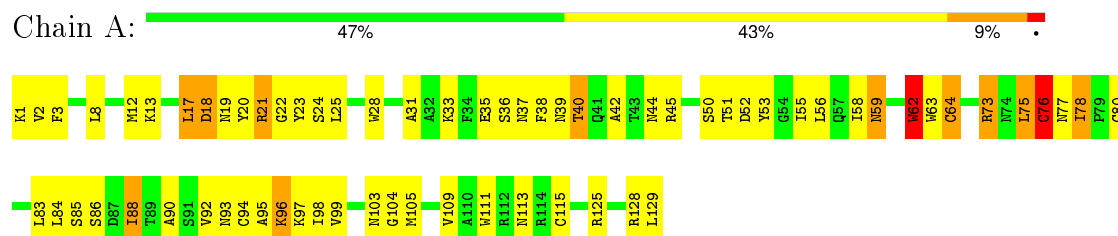
## 4.2.11 Score per residue for model 11

- Molecule 1: LYSOZYME



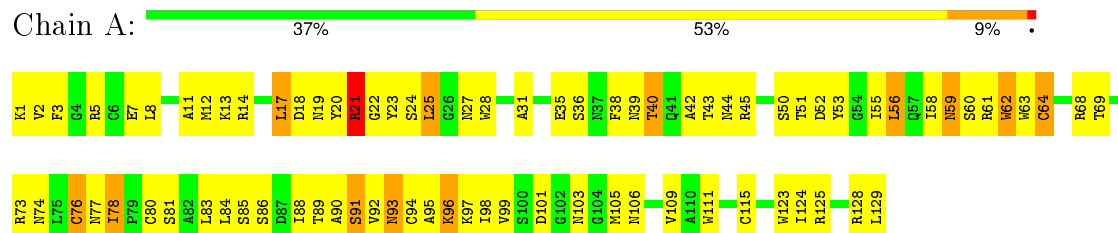
## 4.2.12 Score per residue for model 12

- Molecule 1: LYSOZYME



## 4.2.13 Score per residue for model 13

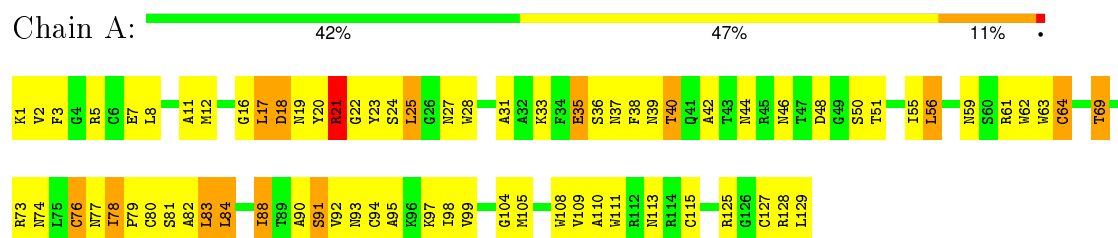
- Molecule 1: LYSOZYME





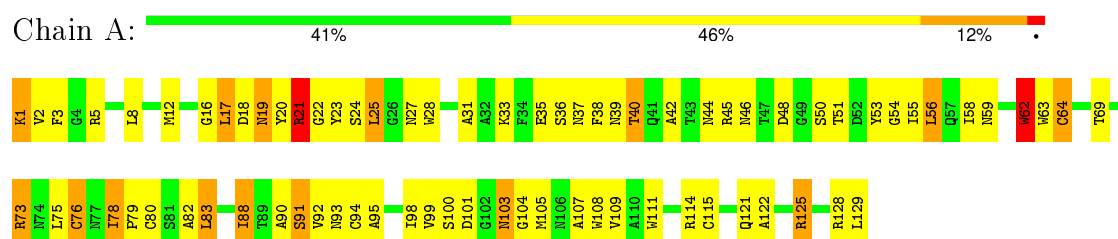
## 4.2.14 Score per residue for model 14

- Molecule 1: LYSOZYME



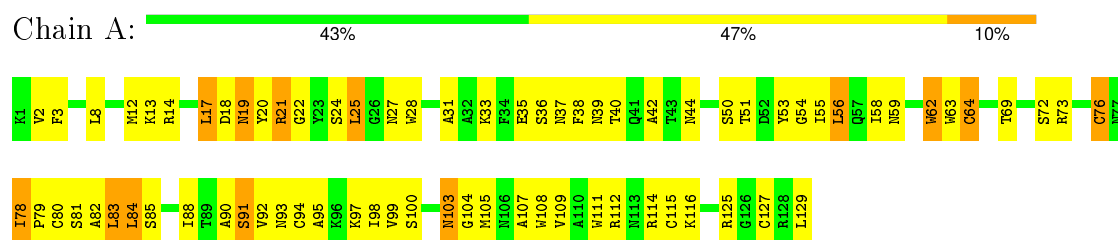
## 4.2.15 Score per residue for model 15

- Molecule 1: LYSOZYME



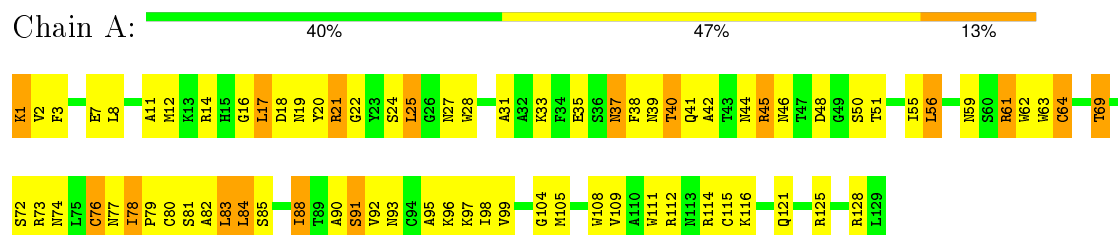
## 4.2.16 Score per residue for model 16

- Molecule 1: LYSOZYME



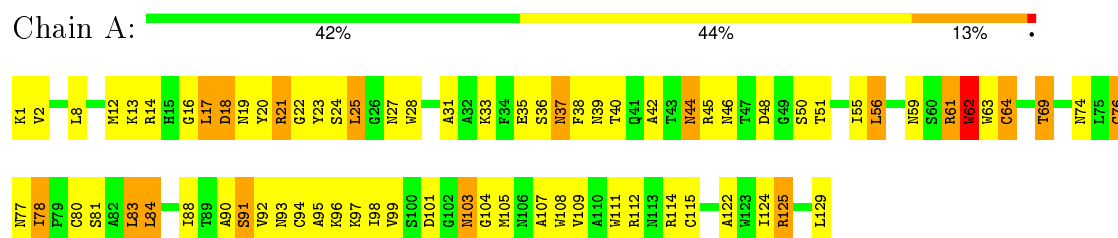
## 4.2.17 Score per residue for model 17

- Molecule 1: LYSOZYME



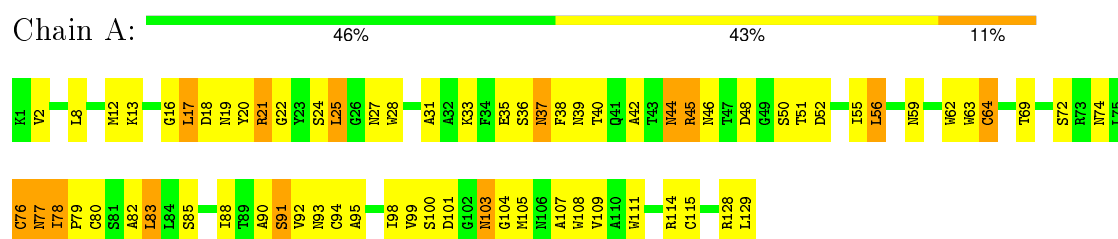
## 4.2.18 Score per residue for model 18

- Molecule 1: LYSOZYME



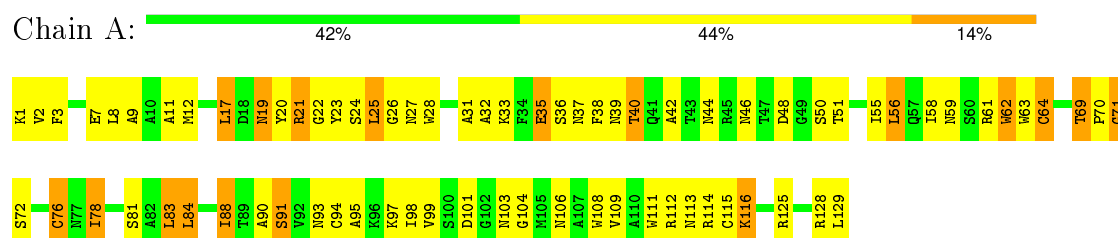
## 4.2.19 Score per residue for model 19

- Molecule 1: LYSOZYME



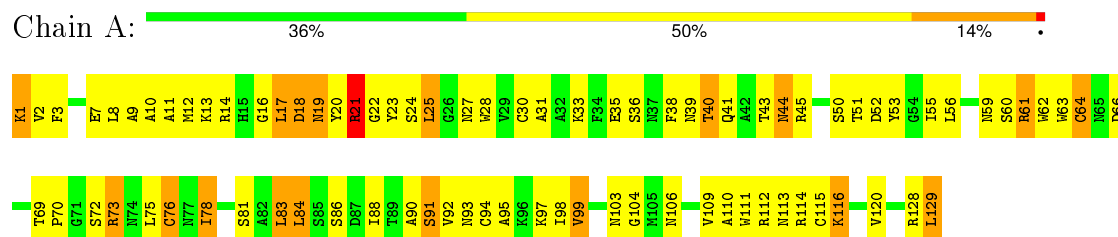
## 4.2.20 Score per residue for model 20

- Molecule 1: LYSOZYME



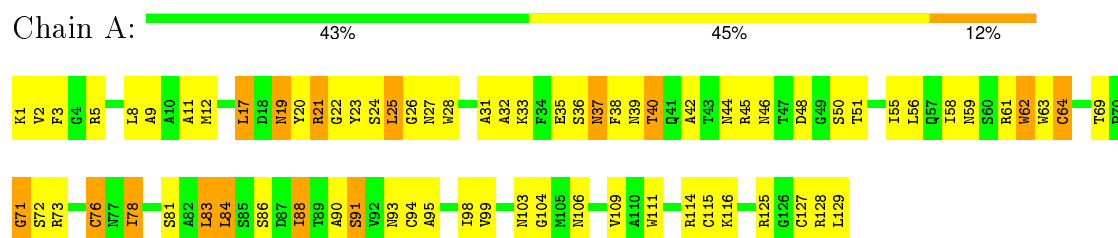
## 4.2.21 Score per residue for model 21

- Molecule 1: LYSOZYME



### 4.2.22 Score per residue for model 22

- Molecule 1: LYSOZYME



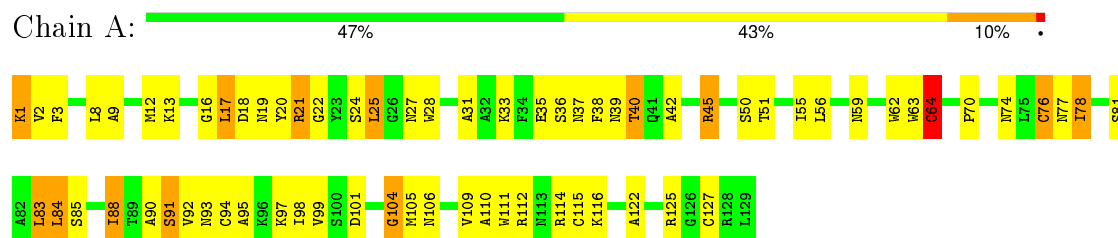
### 4.2.23 Score per residue for model 23

- Molecule 1: LYSOZYME



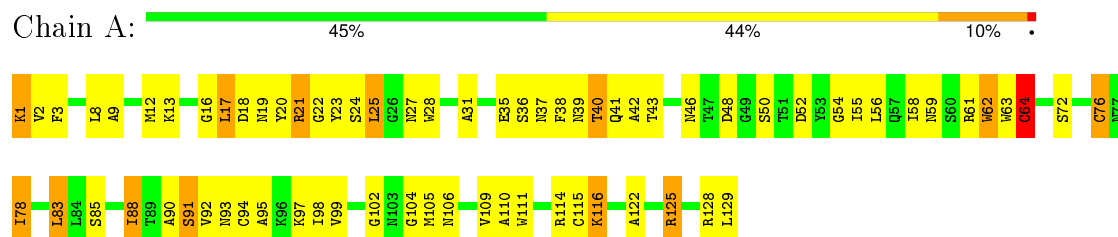
### 4.2.24 Score per residue for model 24 (medoid)

- Molecule 1: LYSOZYME



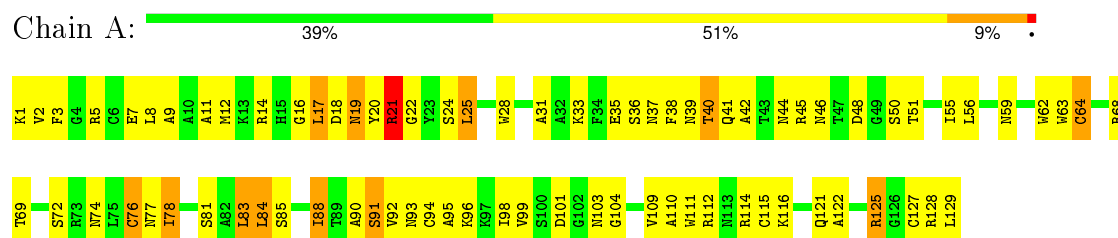
### 4.2.25 Score per residue for model 25

- Molecule 1: LYSOZYME



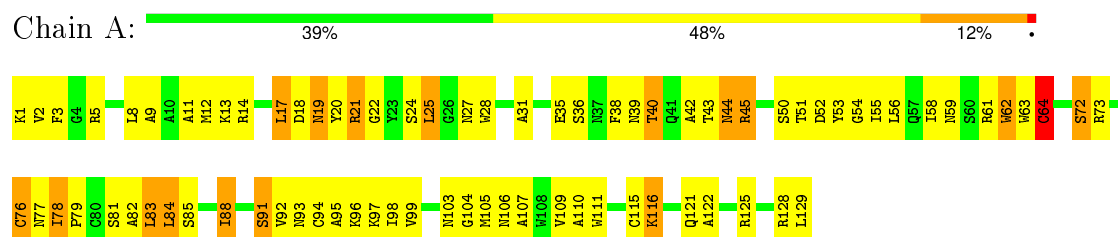
## 4.2.26 Score per residue for model 26

- Molecule 1: LYSOZYME



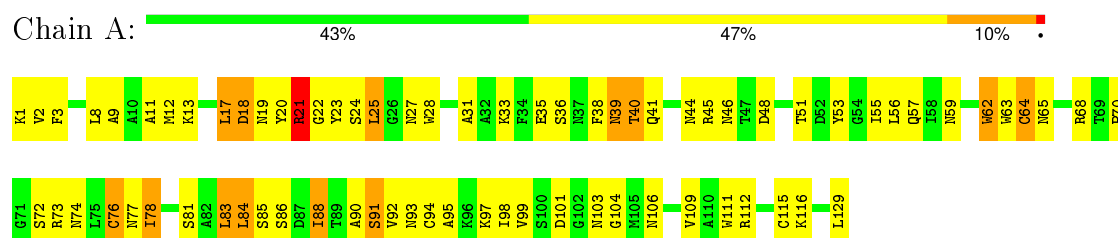
## 4.2.27 Score per residue for model 27

- Molecule 1: LYSOZYME



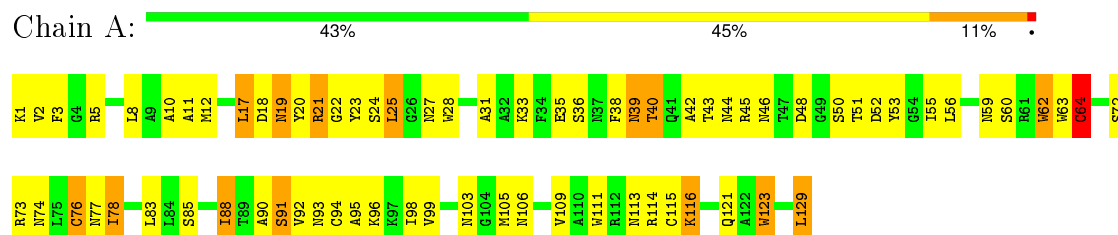
## 4.2.28 Score per residue for model 28

- Molecule 1: LYSOZYME



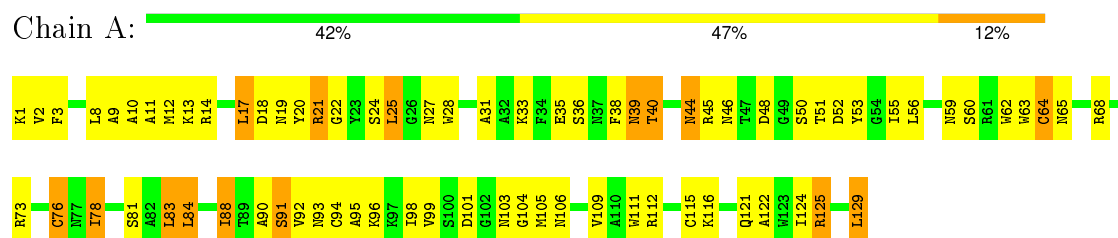
## 4.2.29 Score per residue for model 29

- Molecule 1: LYSOZYME



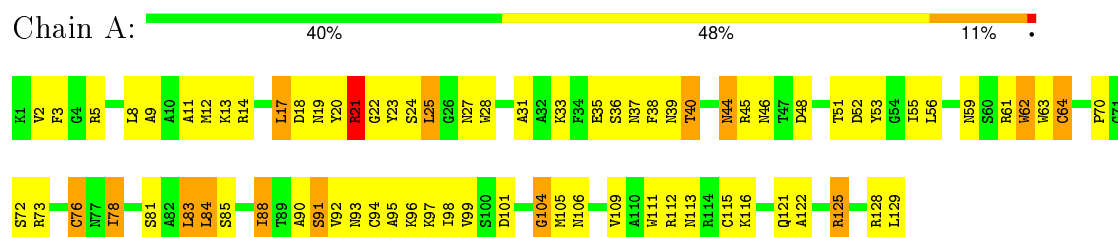
## 4.2.30 Score per residue for model 30

- Molecule 1: LYSOZYME



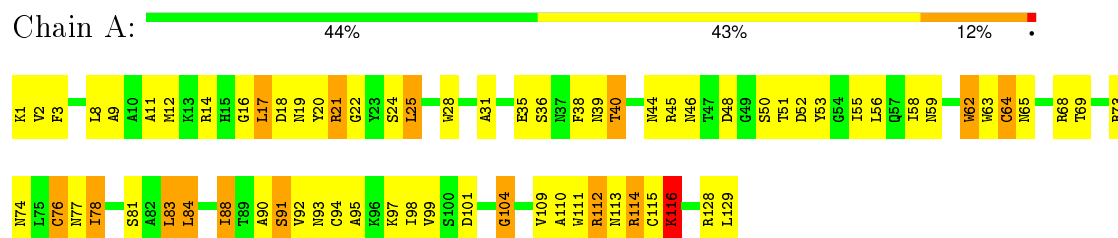
## 4.2.31 Score per residue for model 31

- Molecule 1: LYSOZYME



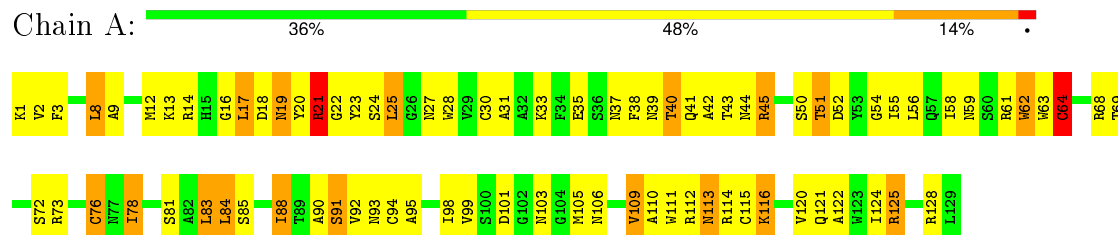
## 4.2.32 Score per residue for model 32

- Molecule 1: LYSOZYME



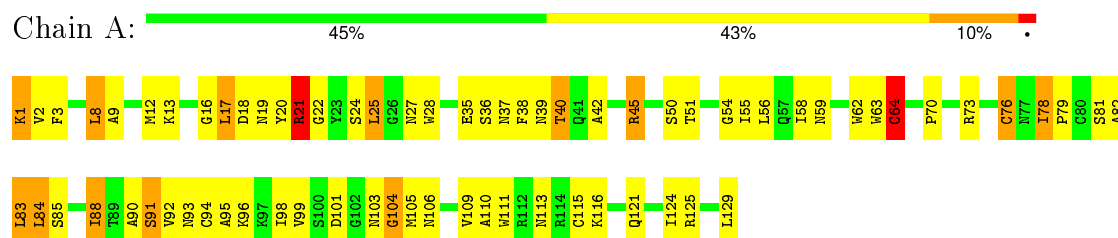
## 4.2.33 Score per residue for model 33

- Molecule 1: LYSOZYME



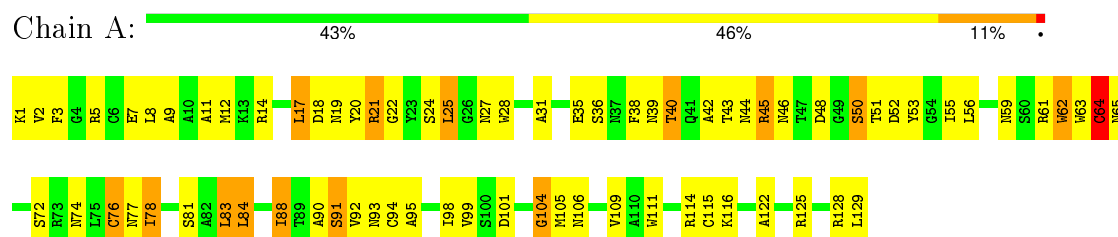
## 4.2.34 Score per residue for model 34

- Molecule 1: LYSOZYME



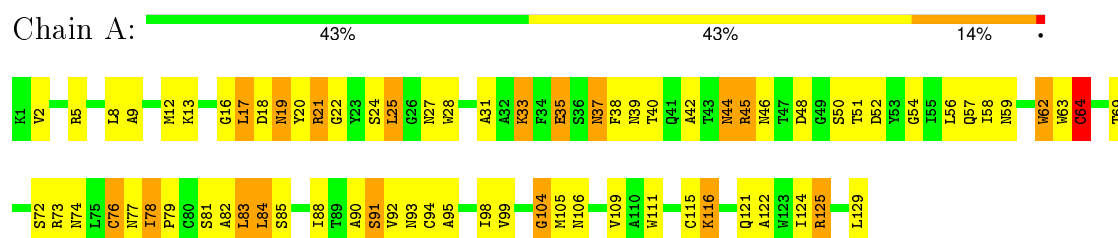
## 4.2.35 Score per residue for model 35

- Molecule 1: LYSOZYME



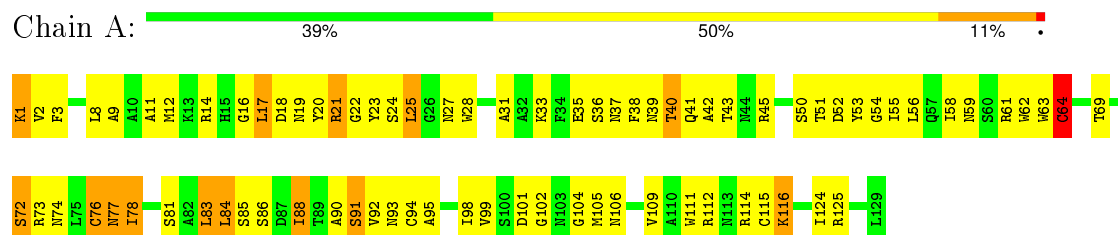
## 4.2.36 Score per residue for model 36

- Molecule 1: LYSOZYME



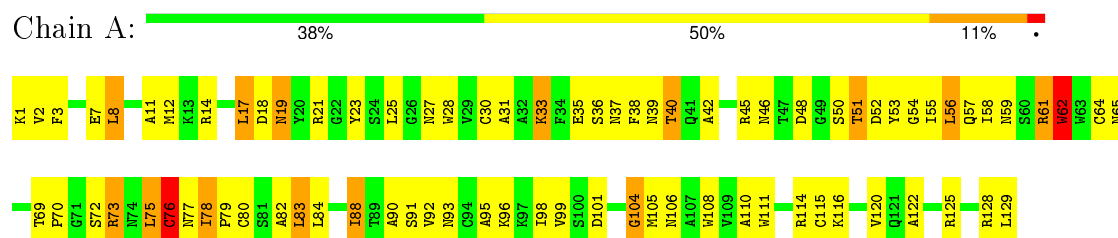
## 4.2.37 Score per residue for model 37

- Molecule 1: LYSOZYME



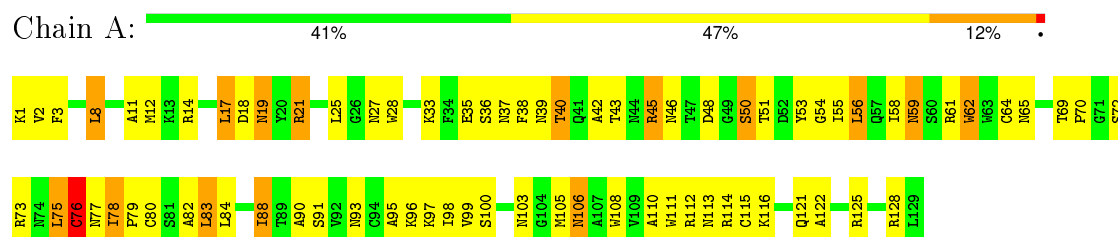
## 4.2.38 Score per residue for model 38

- Molecule 1: LYSOZYME



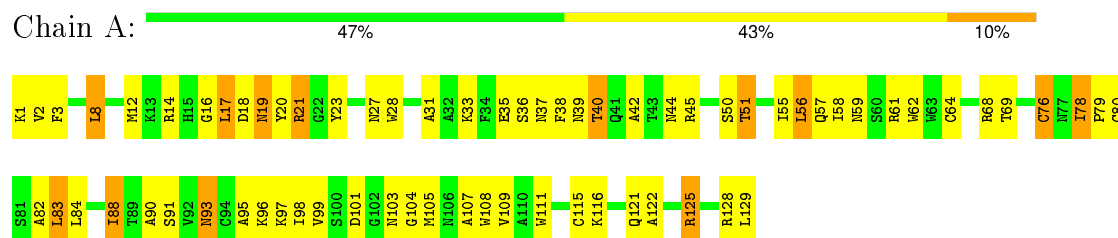
## 4.2.39 Score per residue for model 39

- Molecule 1: LYSOZYME



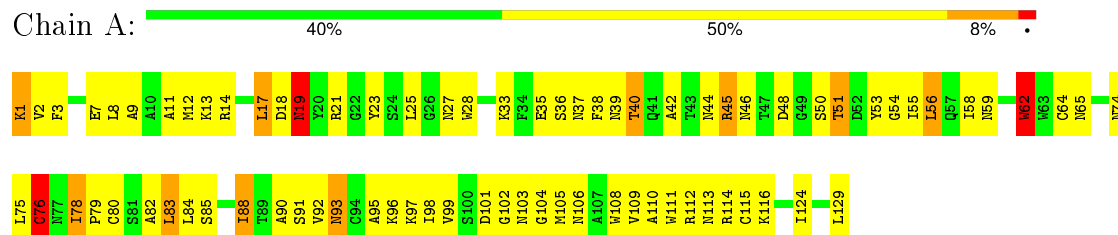
## 4.2.40 Score per residue for model 40

- Molecule 1: LYSOZYME



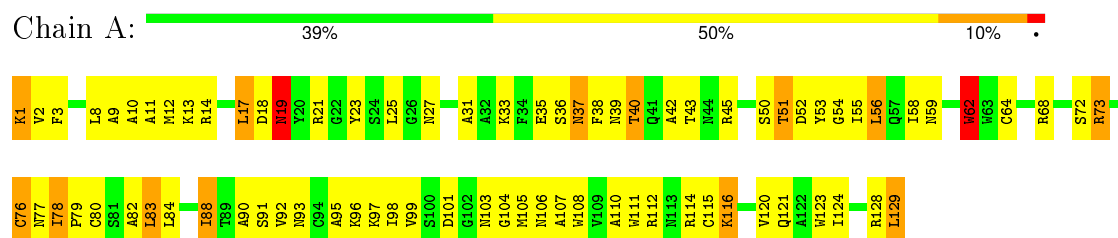
## 4.2.41 Score per residue for model 41

- Molecule 1: LYSOZYME



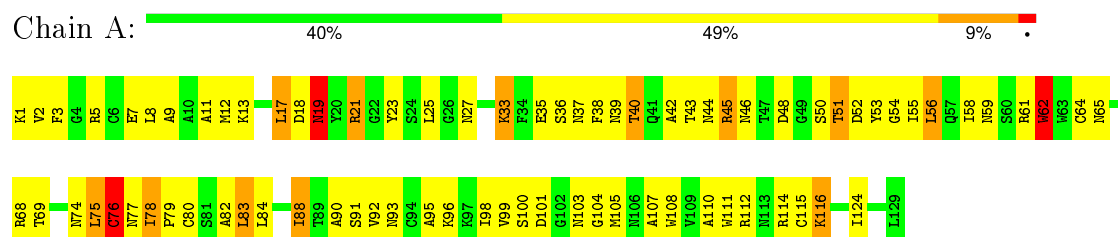
## 4.2.42 Score per residue for model 42

- Molecule 1: LYSOZYME



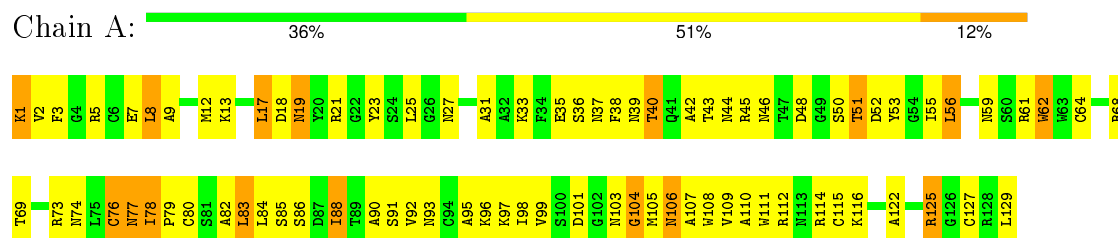
## 4.2.43 Score per residue for model 43

- Molecule 1: LYSOZYME



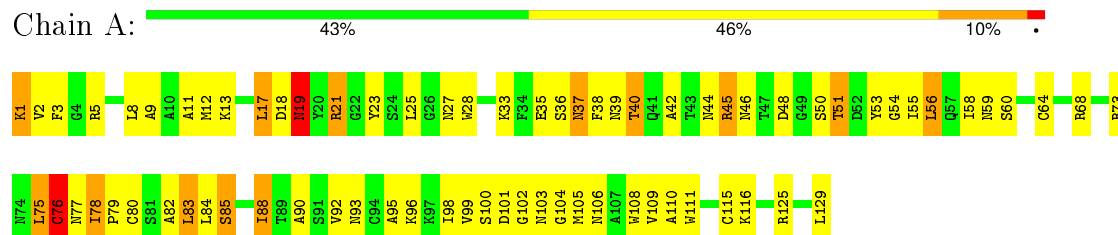
## 4.2.44 Score per residue for model 44

- Molecule 1: LYSOZYME



## 4.2.45 Score per residue for model 45

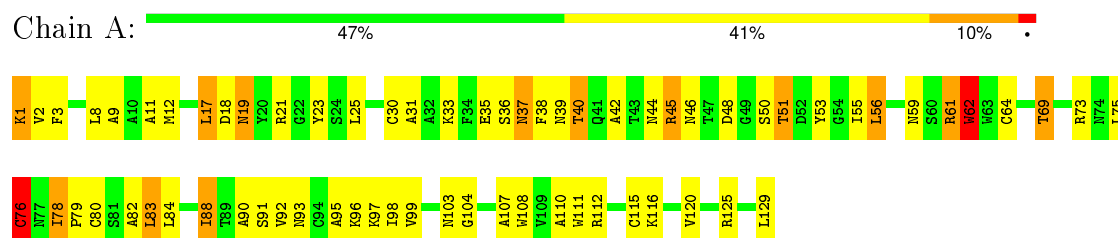
- Molecule 1: LYSOZYME





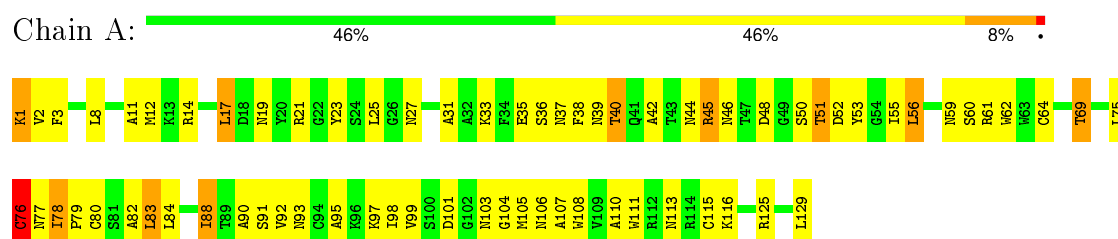
## 4.2.46 Score per residue for model 46

- Molecule 1: LYSOZYME



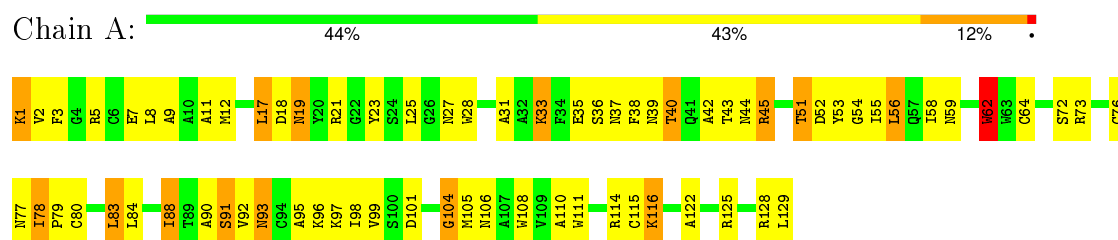
## 4.2.47 Score per residue for model 47

- Molecule 1: LYSOZYME



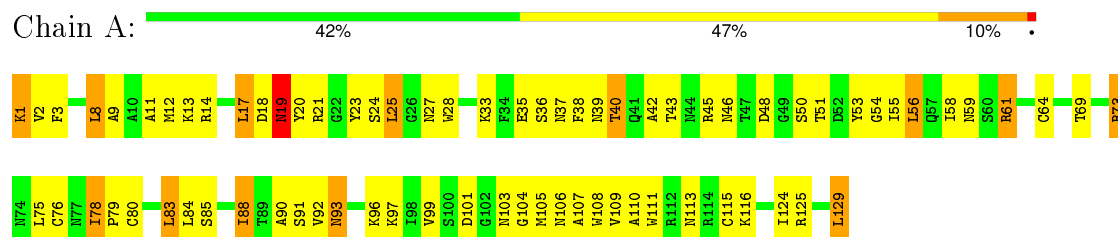
## 4.2.48 Score per residue for model 48

- Molecule 1: LYSOZYME



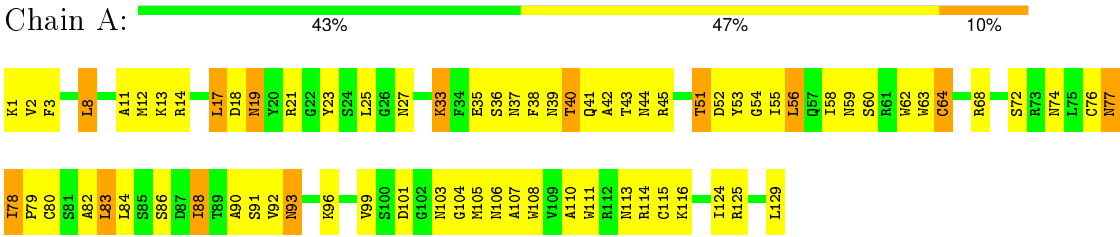
## 4.2.49 Score per residue for model 49

- Molecule 1: LYSOZYME



4.2.50 Score per residue for model 50

● Molecule 1: LYSOZYME



## 5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *SIMULATED ANNEALING*.

Of the 300 calculated structures, 50 were deposited, based on the following criterion: *LOWEST ENERGY*.

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

Software name	Classification	Version
X-PLOR	refinement	
XPLOR	structure solution	

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	1001	960	959	60±4
All	All	50050	48000	47950	2980

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 30.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:39:ASN:HB3	1:A:42:ALA:HB2	0.94	1.39	46	38
1:A:99:VAL:HG23	1:A:104:GLY:HA2	0.87	1.46	34	42
1:A:58:ILE:HD11	1:A:91:SER:HA	0.87	1.44	13	2
1:A:19:ASN:H	1:A:24:SER:HA	0.85	1.31	8	38
1:A:80:CYS:HA	1:A:83:LEU:HD23	0.85	1.49	46	25
1:A:12:MET:HE3	1:A:17:LEU:HD12	0.84	1.45	27	46
1:A:83:LEU:HD23	1:A:90:ALA:HB1	0.81	1.50	50	3
1:A:79:PRO:HB2	1:A:82:ALA:HB3	0.78	1.54	47	12
1:A:17:LEU:HD23	1:A:17:LEU:N	0.77	1.94	40	18
1:A:17:LEU:N	1:A:17:LEU:HD23	0.77	1.94	39	32
1:A:54:GLY:HA3	1:A:58:ILE:HD12	0.76	1.55	48	1
1:A:58:ILE:HG21	1:A:83:LEU:HD13	0.75	1.57	50	3
1:A:8:LEU:O	1:A:12:MET:HG2	0.74	1.83	50	43
1:A:19:ASN:N	1:A:24:SER:HA	0.73	1.99	25	37

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2:VAL:HG13	1:A:38:PHE:C	0.73	2.04	15	50
1:A:2:VAL:HG22	1:A:39:ASN:HA	0.73	1.60	5	50
1:A:8:LEU:HD12	1:A:88:ILE:HD13	0.73	1.61	40	24
1:A:69:THR:N	1:A:70:PRO:HD2	0.72	1.98	38	2
1:A:83:LEU:HD22	1:A:90:ALA:HB2	0.72	1.61	11	1
1:A:27:ASN:HB3	1:A:105:MET:HG3	0.72	1.62	48	39
1:A:64:CYS:HB3	1:A:78:ILE:HD13	0.71	1.61	3	7
1:A:18:ASP:HB2	1:A:25:LEU:HG	0.71	1.62	46	7
1:A:10:ALA:HB2	1:A:129:LEU:HD22	0.70	1.64	42	3
1:A:9:ALA:HA	1:A:12:MET:HG3	0.70	1.64	6	7
1:A:103:ASN:HB3	1:A:107:ALA:HB2	0.69	1.62	42	15
1:A:12:MET:CE	1:A:17:LEU:HD12	0.69	2.18	48	50
1:A:38:PHE:HD1	1:A:55:ILE:HD11	0.69	1.47	4	37
1:A:83:LEU:HB3	1:A:90:ALA:HB3	0.68	1.66	18	23
1:A:25:LEU:HD23	1:A:25:LEU:H	0.68	1.48	21	1
1:A:64:CYS:HB3	1:A:78:ILE:HG22	0.68	1.65	49	3
1:A:83:LEU:HD13	1:A:91:SER:HB3	0.67	1.66	23	31
1:A:20:TYR:O	1:A:22:GLY:N	0.67	2.28	31	37
1:A:12:MET:HB2	1:A:25:LEU:HD21	0.67	1.66	7	39
1:A:55:ILE:HG21	1:A:88:ILE:HG22	0.66	1.67	49	16
1:A:12:MET:HE2	1:A:17:LEU:HD12	0.66	1.66	45	2
1:A:64:CYS:HB2	1:A:78:ILE:O	0.65	1.91	15	49
1:A:27:ASN:HB3	1:A:105:MET:SD	0.65	2.31	7	1
1:A:35:GLU:HG3	1:A:110:ALA:HB3	0.65	1.68	44	25
1:A:3:PHE:CE2	1:A:88:ILE:HG23	0.65	2.27	38	27
1:A:76:CYS:HB3	1:A:78:ILE:HG23	0.63	1.69	43	41
1:A:12:MET:HE3	1:A:17:LEU:CD1	0.63	2.23	27	33
1:A:12:MET:HE2	1:A:28:TRP:HB3	0.63	1.69	29	4
1:A:3:PHE:CE1	1:A:88:ILE:HG23	0.62	2.29	45	1
1:A:103:ASN:ND2	1:A:107:ALA:HB2	0.62	2.09	2	1
1:A:111:TRP:O	1:A:115:CYS:HB2	0.62	1.95	13	23
1:A:8:LEU:O	1:A:12:MET:HG3	0.61	1.94	44	6
1:A:44:ASN:HB2	1:A:52:ASP:HB2	0.61	1.72	44	14
1:A:56:LEU:HD12	1:A:108:TRP:NE1	0.61	2.10	5	13
1:A:9:ALA:HA	1:A:12:MET:HG2	0.61	1.72	22	17
1:A:17:LEU:HD11	1:A:92:VAL:HG13	0.61	1.72	3	31
1:A:56:LEU:HB2	1:A:91:SER:HB3	0.61	1.72	13	1
1:A:83:LEU:HD22	1:A:90:ALA:HB1	0.60	1.74	45	1
1:A:2:VAL:HG22	1:A:39:ASN:CA	0.60	2.27	6	50
1:A:83:LEU:HA	1:A:90:ALA:HB3	0.60	1.72	49	12
1:A:17:LEU:CD2	1:A:17:LEU:N	0.60	2.65	40	29

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:ARG:HG3	1:A:69:THR:HG21	0.60	1.73	44	9
1:A:79:PRO:HG2	1:A:82:ALA:HB3	0.59	1.73	50	9
1:A:58:ILE:HG13	1:A:83:LEU:HD13	0.59	1.73	10	2
1:A:81:SER:HA	1:A:84:LEU:HD12	0.59	1.75	27	28
1:A:78:ILE:HD12	1:A:94:CYS:HB2	0.59	1.72	23	5
1:A:45:ARG:HA	1:A:51:THR:HG23	0.59	1.72	48	27
1:A:44:ASN:HB3	1:A:52:ASP:HB2	0.59	1.73	32	4
1:A:83:LEU:HD13	1:A:90:ALA:HB2	0.59	1.74	12	1
1:A:17:LEU:N	1:A:17:LEU:CD2	0.59	2.64	39	21
1:A:83:LEU:HD13	1:A:90:ALA:HB1	0.58	1.74	45	2
1:A:51:THR:O	1:A:59:ASN:HA	0.58	1.99	30	46
1:A:63:TRP:O	1:A:76:CYS:HB3	0.57	1.98	10	5
1:A:63:TRP:CZ3	1:A:75:LEU:HB3	0.57	2.33	21	1
1:A:2:VAL:HG13	1:A:38:PHE:O	0.57	1.99	40	49
1:A:3:PHE:CE1	1:A:40:THR:HG21	0.57	2.35	13	5
1:A:76:CYS:SG	1:A:78:ILE:HD13	0.57	2.40	48	4
1:A:64:CYS:CB	1:A:78:ILE:HG22	0.57	2.30	49	4
1:A:58:ILE:HD11	1:A:91:SER:HB2	0.57	1.77	11	1
1:A:83:LEU:CB	1:A:90:ALA:HB2	0.57	2.30	13	1
1:A:3:PHE:HE2	1:A:88:ILE:HG23	0.56	1.60	26	11
1:A:93:ASN:HA	1:A:96:LYS:HD3	0.56	1.75	49	4
1:A:54:GLY:HA3	1:A:58:ILE:HG12	0.56	1.75	50	15
1:A:39:ASN:HB3	1:A:42:ALA:CB	0.56	2.28	41	9
1:A:83:LEU:O	1:A:83:LEU:HD12	0.56	2.00	39	7
1:A:59:ASN:ND2	1:A:62:TRP:HB2	0.56	2.16	25	33
1:A:69:THR:N	1:A:70:PRO:CD	0.56	2.68	39	2
1:A:112:ARG:HG2	1:A:116:LYS:HD2	0.56	1.76	21	2
1:A:20:TYR:O	1:A:21:ARG:C	0.55	2.44	5	37
1:A:60:SER:HA	1:A:64:CYS:SG	0.55	2.41	50	3
1:A:78:ILE:HD11	1:A:93:ASN:OD1	0.55	2.02	10	2
1:A:92:VAL:O	1:A:96:LYS:N	0.55	2.38	13	10
1:A:99:VAL:HA	1:A:103:ASN:O	0.55	2.01	8	23
1:A:21:ARG:HD2	1:A:100:SER:HA	0.55	1.79	39	2
1:A:36:SER:OG	1:A:55:ILE:HA	0.55	2.01	12	41
1:A:20:TYR:C	1:A:22:GLY:N	0.55	2.59	31	37
1:A:76:CYS:HB3	1:A:78:ILE:CG2	0.55	2.32	12	7
1:A:17:LEU:HD21	1:A:92:VAL:HG11	0.55	1.78	11	15
1:A:2:VAL:HG11	1:A:37:ASN:O	0.54	2.03	46	30
1:A:78:ILE:HD11	1:A:83:LEU:HD22	0.54	1.78	46	9
1:A:11:ALA:HB1	1:A:88:ILE:HD11	0.54	1.79	21	12
1:A:62:TRP:HA	1:A:73:ARG:HB2	0.54	1.77	39	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:78:ILE:HB	1:A:93:ASN:HD21	0.54	1.62	23	1
1:A:3:PHE:CD2	1:A:40:THR:HG22	0.54	2.37	44	14
1:A:103:ASN:HB2	1:A:107:ALA:HB2	0.54	1.79	40	3
1:A:80:CYS:O	1:A:84:LEU:HG	0.53	2.03	39	14
1:A:83:LEU:HD12	1:A:83:LEU:O	0.53	2.03	47	4
1:A:3:PHE:CZ	1:A:40:THR:HG21	0.53	2.39	7	12
1:A:80:CYS:O	1:A:83:LEU:HG	0.53	2.04	10	1
1:A:31:ALA:O	1:A:35:GLU:HB2	0.53	2.04	17	40
1:A:44:ASN:C	1:A:51:THR:HG23	0.53	2.24	22	14
1:A:3:PHE:CD1	1:A:40:THR:HG22	0.53	2.39	45	1
1:A:12:MET:CE	1:A:28:TRP:HB3	0.53	2.33	6	4
1:A:36:SER:HB2	1:A:42:ALA:HB3	0.53	1.81	45	13
1:A:63:TRP:O	1:A:64:CYS:O	0.53	2.26	20	19
1:A:94:CYS:O	1:A:98:ILE:HG13	0.53	2.04	3	34
1:A:58:ILE:N	1:A:58:ILE:HD12	0.53	2.17	32	3
1:A:111:TRP:O	1:A:115:CYS:HB3	0.52	2.04	2	27
1:A:78:ILE:HG13	1:A:83:LEU:HG	0.52	1.80	45	1
1:A:78:ILE:HB	1:A:93:ASN:ND2	0.52	2.19	23	1
1:A:83:LEU:CB	1:A:90:ALA:HB3	0.52	2.34	19	32
1:A:12:MET:HE1	1:A:17:LEU:HD12	0.52	1.80	48	5
1:A:83:LEU:HD13	1:A:91:SER:CB	0.52	2.35	18	16
1:A:8:LEU:CD2	1:A:88:ILE:HD13	0.52	2.35	48	14
1:A:122:ALA:HA	1:A:125:ARG:HB2	0.52	1.82	30	24
1:A:99:VAL:HG23	1:A:104:GLY:CA	0.52	2.32	17	4
1:A:74:ASN:ND2	1:A:77:ASN:HA	0.52	2.20	17	11
1:A:17:LEU:HB3	1:A:28:TRP:CE2	0.52	2.40	21	28
1:A:64:CYS:CB	1:A:78:ILE:HD13	0.52	2.35	16	5
1:A:58:ILE:HG21	1:A:78:ILE:HD11	0.51	1.81	40	7
1:A:3:PHE:HD2	1:A:55:ILE:HD12	0.51	1.65	1	8
1:A:39:ASN:CB	1:A:42:ALA:HB2	0.51	2.35	16	17
1:A:38:PHE:CD1	1:A:55:ILE:HD11	0.51	2.39	5	9
1:A:103:ASN:OD1	1:A:107:ALA:HB2	0.51	2.06	3	2
1:A:60:SER:HB2	1:A:64:CYS:SG	0.51	2.46	45	2
1:A:111:TRP:HA	1:A:115:CYS:SG	0.51	2.45	18	7
1:A:12:MET:HE1	1:A:28:TRP:HB3	0.51	1.83	20	7
1:A:83:LEU:HG	1:A:84:LEU:HG	0.51	1.81	3	8
1:A:1:LYS:O	1:A:40:THR:HG23	0.50	2.06	47	28
1:A:54:GLY:HA3	1:A:58:ILE:HD13	0.50	1.82	36	6
1:A:3:PHE:CD2	1:A:8:LEU:HD23	0.50	2.41	11	8
1:A:40:THR:HG22	1:A:55:ILE:HB	0.50	1.82	13	6
1:A:56:LEU:O	1:A:108:TRP:NE1	0.50	2.45	49	13

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:92:VAL:HG12	1:A:96:LYS:HG3	0.50	1.83	38	4
1:A:12:MET:CB	1:A:25:LEU:HD22	0.50	2.36	4	5
1:A:1:LYS:HD2	1:A:86:SER:HB2	0.50	1.81	28	1
1:A:69:THR:HG22	1:A:71:GLY:H	0.50	1.66	22	1
1:A:45:ARG:N	1:A:51:THR:HG23	0.50	2.22	37	3
1:A:83:LEU:HD22	1:A:89:THR:HB	0.50	1.82	13	1
1:A:36:SER:HB3	1:A:57:GLN:HE22	0.50	1.67	40	1
1:A:95:ALA:HA	1:A:98:ILE:HB	0.50	1.84	13	48
1:A:2:VAL:HG22	1:A:39:ASN:CB	0.50	2.37	2	13
1:A:2:VAL:HA	1:A:38:PHE:O	0.50	2.07	13	14
1:A:31:ALA:HB2	1:A:111:TRP:HB2	0.50	1.82	14	6
1:A:127:CYS:HB3	1:A:129:LEU:HD23	0.50	1.84	14	9
1:A:69:THR:HA	1:A:72:SER:HB2	0.49	1.84	39	2
1:A:17:LEU:HD11	1:A:92:VAL:CG1	0.49	2.37	3	20
1:A:45:ARG:HG2	1:A:51:THR:HG23	0.49	1.84	42	1
1:A:1:LYS:H3	1:A:41:GLN:HB2	0.49	1.66	28	1
1:A:2:VAL:CG1	1:A:38:PHE:HB2	0.49	2.38	34	10
1:A:58:ILE:HD12	1:A:58:ILE:N	0.49	2.23	27	4
1:A:51:THR:HB	1:A:53:TYR:CE1	0.49	2.43	21	3
1:A:21:ARG:HG3	1:A:99:VAL:HG13	0.49	1.84	39	1
1:A:43:THR:HA	1:A:52:ASP:O	0.49	2.07	37	11
1:A:83:LEU:HD12	1:A:84:LEU:HG	0.49	1.83	10	1
1:A:11:ALA:CB	1:A:88:ILE:HD11	0.49	2.37	48	23
1:A:21:ARG:HG2	1:A:99:VAL:O	0.49	2.08	50	2
1:A:51:THR:HB	1:A:53:TYR:CE2	0.49	2.43	13	18
1:A:1:LYS:H2	1:A:41:GLN:HB2	0.49	1.68	21	1
1:A:8:LEU:CD1	1:A:88:ILE:HD13	0.48	2.38	43	12
1:A:3:PHE:HD2	1:A:8:LEU:HD23	0.48	1.68	7	3
1:A:12:MET:HB2	1:A:25:LEU:CD2	0.48	2.39	13	26
1:A:83:LEU:HD13	1:A:90:ALA:CB	0.48	2.38	11	2
1:A:23:TYR:CE2	1:A:104:GLY:HA3	0.48	2.43	48	12
1:A:104:GLY:O	1:A:105:MET:CB	0.48	2.61	7	11
1:A:33:LYS:O	1:A:37:ASN:HA	0.48	2.08	47	28
1:A:12:MET:HE2	1:A:28:TRP:CB	0.48	2.38	26	4
1:A:103:ASN:CG	1:A:107:ALA:HB2	0.48	2.28	3	2
1:A:12:MET:HE3	1:A:28:TRP:HB3	0.48	1.84	45	1
1:A:35:GLU:OE2	1:A:108:TRP:HB3	0.48	2.09	14	1
1:A:58:ILE:HD11	1:A:91:SER:HB3	0.48	1.86	48	2
1:A:110:ALA:O	1:A:114:ARG:HB2	0.48	2.09	32	1
1:A:44:ASN:O	1:A:51:THR:HG23	0.47	2.08	22	6
1:A:64:CYS:HB2	1:A:78:ILE:HG12	0.47	1.86	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:TYR:HB3	1:A:27:ASN:ND2	0.47	2.24	29	15
1:A:23:TYR:HB2	1:A:105:MET:SD	0.47	2.49	37	6
1:A:63:TRP:O	1:A:74:ASN:HA	0.47	2.09	18	11
1:A:78:ILE:HG12	1:A:78:ILE:O	0.47	2.09	11	1
1:A:83:LEU:HD22	1:A:90:ALA:CB	0.47	2.38	45	1
1:A:65:ASN:HB2	1:A:74:ASN:ND2	0.47	2.23	32	6
1:A:18:ASP:HB2	1:A:25:LEU:HD12	0.47	1.85	8	6
1:A:1:LYS:HE2	1:A:86:SER:HB2	0.47	1.86	37	1
1:A:53:TYR:O	1:A:58:ILE:HB	0.47	2.09	13	7
1:A:64:CYS:CB	1:A:78:ILE:HG12	0.47	2.40	45	2
1:A:12:MET:HB2	1:A:25:LEU:HD22	0.47	1.87	12	1
1:A:13:LYS:HD3	1:A:129:LEU:HD12	0.47	1.86	49	1
1:A:16:GLY:O	1:A:20:TYR:HB2	0.47	2.10	17	20
1:A:95:ALA:O	1:A:98:ILE:N	0.47	2.48	3	29
1:A:12:MET:HE1	1:A:28:TRP:HB2	0.47	1.85	40	1
1:A:46:ASN:HB2	1:A:48:ASP:OD1	0.46	2.10	39	32
1:A:39:ASN:CG	1:A:42:ALA:HB2	0.46	2.31	13	5
1:A:23:TYR:HE2	1:A:104:GLY:HA3	0.46	1.70	49	8
1:A:73:ARG:HG2	1:A:75:LEU:HG	0.46	1.88	12	3
1:A:78:ILE:HD11	1:A:93:ASN:HD21	0.46	1.70	49	1
1:A:8:LEU:O	1:A:8:LEU:HD22	0.46	2.11	45	4
1:A:61:ARG:HD3	1:A:69:THR:HG21	0.46	1.88	2	1
1:A:83:LEU:HD23	1:A:83:LEU:N	0.46	2.26	45	1
1:A:38:PHE:HA	1:A:55:ILE:HG13	0.46	1.87	42	4
1:A:3:PHE:CZ	1:A:88:ILE:HG23	0.46	2.45	45	4
1:A:8:LEU:HD22	1:A:8:LEU:O	0.46	2.10	11	7
1:A:104:GLY:O	1:A:105:MET:HB2	0.46	2.10	7	5
1:A:45:ARG:CA	1:A:51:THR:HG23	0.46	2.41	24	9
1:A:30:CYS:HB2	1:A:120:VAL:HG12	0.46	1.88	33	4
1:A:71:GLY:O	1:A:72:SER:HB3	0.46	2.10	20	2
1:A:79:PRO:O	1:A:83:LEU:HG	0.46	2.11	48	3
1:A:112:ARG:HA	1:A:116:LYS:HB2	0.46	1.88	32	1
1:A:23:TYR:HB3	1:A:27:ASN:OD1	0.45	2.11	23	6
1:A:35:GLU:HG2	1:A:57:GLN:HG3	0.45	1.87	23	3
1:A:25:LEU:HG	1:A:26:GLY:N	0.45	2.26	20	3
1:A:18:ASP:O	1:A:19:ASN:HB2	0.45	2.11	39	2
1:A:98:ILE:O	1:A:102:GLY:N	0.45	2.50	37	4
1:A:1:LYS:HZ2	1:A:41:GLN:HG3	0.45	1.70	37	1
1:A:99:VAL:HA	1:A:103:ASN:HB2	0.45	1.89	5	2
1:A:89:THR:O	1:A:93:ASN:HB3	0.45	2.11	13	2
1:A:17:LEU:O	1:A:28:TRP:NE1	0.45	2.50	49	25

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:73:ARG:HD3	1:A:75:LEU:HG	0.45	1.89	4	1
1:A:69:THR:HG22	1:A:70:PRO:HD2	0.45	1.89	20	1
1:A:75:LEU:O	1:A:77:ASN:N	0.45	2.50	38	5
1:A:1:LYS:N	1:A:41:GLN:HB2	0.45	2.27	21	2
1:A:106:ASN:HA	1:A:112:ARG:HG3	0.45	1.89	39	2
1:A:22:GLY:HA3	1:A:99:VAL:HG21	0.44	1.88	36	8
1:A:63:TRP:HB3	1:A:94:CYS:SG	0.44	2.52	12	5
1:A:22:GLY:HA3	1:A:99:VAL:CG2	0.44	2.42	32	10
1:A:50:SER:HB2	1:A:59:ASN:OD1	0.44	2.11	39	1
1:A:76:CYS:O	1:A:77:ASN:C	0.44	2.55	50	2
1:A:53:TYR:O	1:A:83:LEU:HD11	0.44	2.12	30	3
1:A:50:SER:HA	1:A:61:ARG:HD3	0.44	1.88	35	1
1:A:2:VAL:CG1	1:A:37:ASN:O	0.44	2.66	46	16
1:A:33:LYS:HB2	1:A:38:PHE:CZ	0.44	2.48	36	13
1:A:95:ALA:HA	1:A:98:ILE:HD12	0.44	1.88	13	28
1:A:78:ILE:HD12	1:A:83:LEU:HD12	0.44	1.90	45	1
1:A:103:ASN:CB	1:A:107:ALA:HB2	0.44	2.43	4	9
1:A:60:SER:HB2	1:A:66:ASP:HB3	0.44	1.88	21	1
1:A:78:ILE:HG12	1:A:83:LEU:HD21	0.44	1.90	48	1
1:A:18:ASP:HB2	1:A:25:LEU:HD22	0.43	1.90	21	1
1:A:83:LEU:HB2	1:A:91:SER:OG	0.43	2.13	10	1
1:A:32:ALA:HB1	1:A:55:ILE:HG12	0.43	1.91	23	3
1:A:93:ASN:O	1:A:96:LYS:HB2	0.43	2.14	50	4
1:A:103:ASN:O	1:A:106:ASN:HB2	0.43	2.13	41	1
1:A:9:ALA:CA	1:A:12:MET:HG2	0.43	2.41	22	3
1:A:97:LYS:O	1:A:101:ASP:HB2	0.43	2.12	23	1
1:A:59:ASN:OD1	1:A:62:TRP:HB2	0.43	2.14	27	5
1:A:79:PRO:HB2	1:A:82:ALA:CB	0.43	2.44	9	8
1:A:61:ARG:HA	1:A:72:SER:OG	0.43	2.13	38	2
1:A:10:ALA:N	1:A:129:LEU:HD22	0.43	2.29	30	1
1:A:109:VAL:O	1:A:113:ASN:HB2	0.43	2.14	33	2
1:A:123:TRP:HA	1:A:123:TRP:CE3	0.43	2.49	29	2
1:A:21:ARG:HD3	1:A:100:SER:HA	0.43	1.90	45	1
1:A:3:PHE:CE2	1:A:40:THR:HG21	0.43	2.49	30	4
1:A:35:GLU:OE2	1:A:110:ALA:HB3	0.43	2.14	14	2
1:A:12:MET:HB3	1:A:25:LEU:HD22	0.43	1.91	4	2
1:A:83:LEU:HB3	1:A:90:ALA:HB2	0.43	1.91	13	1
1:A:95:ALA:HA	1:A:98:ILE:CG1	0.42	2.44	10	4
1:A:84:LEU:HD23	1:A:84:LEU:N	0.42	2.29	50	1
1:A:11:ALA:HB3	1:A:88:ILE:HD11	0.42	1.91	48	4
1:A:60:SER:O	1:A:64:CYS:O	0.42	2.37	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:ARG:O	1:A:73:ARG:HB2	0.42	2.14	21	1
1:A:78:ILE:HG13	1:A:79:PRO:CD	0.42	2.44	48	2
1:A:80:CYS:HA	1:A:83:LEU:CD1	0.42	2.45	50	1
1:A:43:THR:HB	1:A:53:TYR:CD1	0.42	2.49	44	6
1:A:80:CYS:HA	1:A:83:LEU:HD12	0.42	1.92	48	1
1:A:9:ALA:HA	1:A:12:MET:CG	0.42	2.44	49	7
1:A:10:ALA:HB2	1:A:129:LEU:HD13	0.42	1.90	21	1
1:A:61:ARG:O	1:A:61:ARG:HD2	0.42	2.14	4	1
1:A:18:ASP:O	1:A:19:ASN:CB	0.42	2.67	38	12
1:A:17:LEU:HA	1:A:20:TYR:HB2	0.42	1.92	49	1
1:A:83:LEU:HD13	1:A:91:SER:OG	0.42	2.15	8	1
1:A:56:LEU:HD12	1:A:108:TRP:CE2	0.42	2.50	20	1
1:A:63:TRP:CZ3	1:A:75:LEU:HD13	0.42	2.50	11	1
1:A:55:ILE:HG21	1:A:88:ILE:CG2	0.42	2.45	33	3
1:A:74:ASN:OD1	1:A:77:ASN:HA	0.42	2.15	14	4
1:A:20:TYR:C	1:A:22:GLY:H	0.41	2.18	31	1
1:A:52:ASP:HB3	1:A:57:GLN:HB3	0.41	1.92	36	2
1:A:51:THR:H	1:A:59:ASN:ND2	0.41	2.12	24	1
1:A:64:CYS:HB3	1:A:78:ILE:CG2	0.41	2.44	48	1
1:A:25:LEU:HA	1:A:28:TRP:CD1	0.41	2.50	22	3
1:A:3:PHE:HE2	1:A:88:ILE:HG12	0.41	1.75	27	2
1:A:123:TRP:CE3	1:A:123:TRP:HA	0.41	2.50	11	1
1:A:17:LEU:HD21	1:A:92:VAL:CG1	0.41	2.45	12	1
1:A:2:VAL:HG12	1:A:3:PHE:O	0.41	2.16	15	3
1:A:31:ALA:HB2	1:A:111:TRP:CD1	0.41	2.51	48	2
1:A:23:TYR:CD1	1:A:105:MET:HG2	0.41	2.51	23	1
1:A:54:GLY:HA3	1:A:58:ILE:CD1	0.41	2.46	45	1
1:A:58:ILE:HG13	1:A:83:LEU:HD22	0.40	1.93	20	3
1:A:122:ALA:O	1:A:125:ARG:HG2	0.40	2.16	33	1
1:A:25:LEU:O	1:A:28:TRP:N	0.40	2.54	21	1
1:A:83:LEU:CD1	1:A:90:ALA:HB1	0.40	2.46	45	1
1:A:79:PRO:O	1:A:83:LEU:HB3	0.40	2.15	46	1
1:A:112:ARG:O	1:A:116:LYS:HB3	0.40	2.15	32	1
1:A:120:VAL:HA	1:A:123:TRP:CD1	0.40	2.51	42	1
1:A:3:PHE:CE2	1:A:40:THR:HG22	0.40	2.52	46	2
1:A:56:LEU:O	1:A:57:GLN:HB2	0.40	2.16	5	1
1:A:41:GLN:O	1:A:43:THR:HG23	0.40	2.17	5	1
1:A:56:LEU:HA	1:A:56:LEU:HD13	0.40	1.82	18	1
1:A:53:TYR:HB2	1:A:58:ILE:O	0.40	2.17	12	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	127/129 (98%)	108±2 (85±2%)	15±3 (12±2%)	4±1 (3±1%)	8	40
All	All	6350/6450 (98%)	5395 (85%)	754 (12%)	201 (3%)	8	40

All 17 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	116	LYS	41
1	A	21	ARG	37
1	A	62	TRP	27
1	A	64	CYS	19
1	A	19	ASN	13
1	A	104	GLY	13
1	A	103	ASN	12
1	A	75	LEU	8
1	A	76	CYS	8
1	A	72	SER	7
1	A	70	PRO	5
1	A	73	ARG	3
1	A	59	ASN	2
1	A	127	CYS	2
1	A	71	GLY	2
1	A	105	MET	1
1	A	85	SER	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	105/105 (100%)	76±4 (73±4%)	29±4 (27±4%)	2	22
All	All	5250/5250 (100%)	3810 (73%)	1440 (27%)	2	22

All 61 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	56	LEU	50
1	A	40	THR	50
1	A	93	ASN	50
1	A	17	LEU	50
1	A	78	ILE	50
1	A	88	ILE	48
1	A	76	CYS	46
1	A	91	SER	46
1	A	83	LEU	46
1	A	50	SER	45
1	A	109	VAL	41
1	A	18	ASP	34
1	A	73	ARG	34
1	A	129	LEU	33
1	A	25	LEU	33
1	A	114	ARG	33
1	A	97	LYS	31
1	A	125	ARG	31
1	A	21	ARG	31
1	A	101	ASP	30
1	A	1	LYS	30
1	A	62	TRP	29
1	A	45	ARG	28
1	A	128	ARG	28
1	A	84	LEU	28
1	A	106	ASN	27
1	A	85	SER	27
1	A	69	THR	26
1	A	13	LYS	25
1	A	14	ARG	25
1	A	112	ARG	21
1	A	44	ASN	21
1	A	64	CYS	20
1	A	19	ASN	20
1	A	61	ARG	19
1	A	5	ARG	18

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Mol	Chain	Res	Type	Models (Total)
1	A	121	GLN	18
1	A	116	LYS	18
1	A	96	LYS	18
1	A	68	ARG	18
1	A	7	GLU	16
1	A	72	SER	15
1	A	124	ILE	15
1	A	113	ASN	15
1	A	37	ASN	14
1	A	51	THR	14
1	A	77	ASN	13
1	A	33	LYS	10
1	A	86	SER	9
1	A	41	GLN	8
1	A	8	LEU	8
1	A	100	SER	6
1	A	39	ASN	5
1	A	35	GLU	5
1	A	65	ASN	3
1	A	103	ASN	2
1	A	123	TRP	2
1	A	59	ASN	1
1	A	52	ASP	1
1	A	99	VAL	1
1	A	89	THR	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