



# Full wwPDB NMR Structure Validation Report ⓘ

Oct 16, 2021 – 10:17 PM EDT

PDB ID : 1TTE  
Title : The Structure of a Class II ubiquitin-conjugating enzyme, Ubc1.  
Authors : Merkle, N.; Shaw, G.S.  
Deposited on : 2004-06-22

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : 2.23.2  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

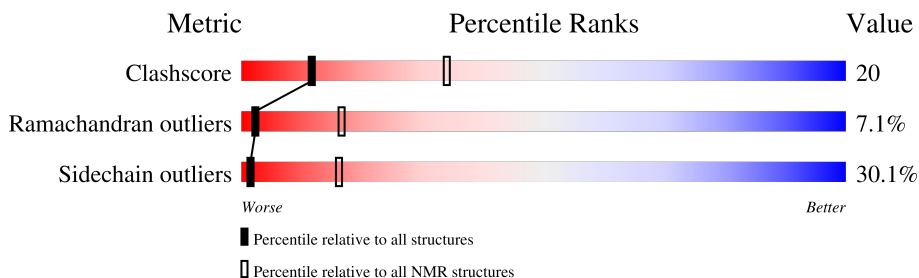
# 1 Overall quality at a glance

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	215	

## 2 Ensemble composition and analysis i

This entry contains 21 models. Model 17 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:2-A:149 (148)	0.97	17
2	A:169-A:195, A:203-A:215 (40)	0.40	2

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 and 1 single-model cluster was found.

Cluster number	Models
1	2, 4, 5, 6, 7, 12, 13, 16, 18, 19
2	8, 10, 11, 15
3	1, 17
4	3, 20
5	9, 14
Single-model clusters	21

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3384 atoms, of which 1680 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ubiquitin-conjugating enzyme E2-24 kDa.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	215	3384	1077	1680	289	334	4	0

There are 2 discrepancies between the modelled and reference sequences:

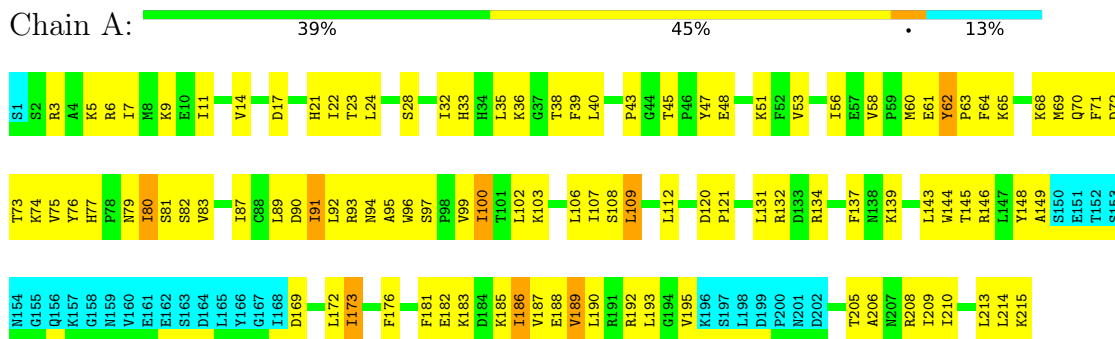
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	MET	engineered mutation	UNP P21734
A	93	ARG	LYS	engineered mutation	UNP P21734

## 4 Residue-property plots [i](#)

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa

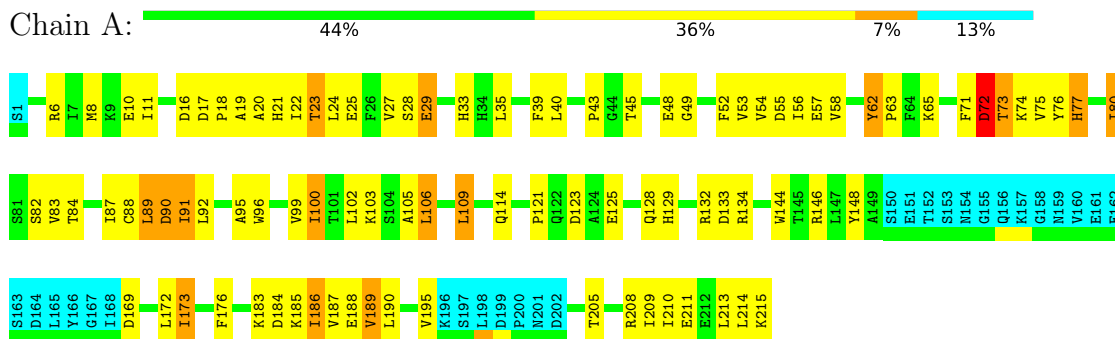


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

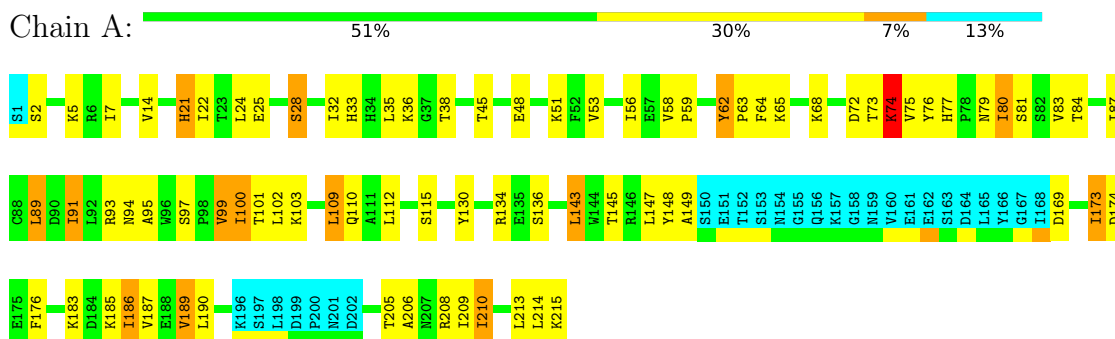
#### 4.2.1 Score per residue for model 1

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



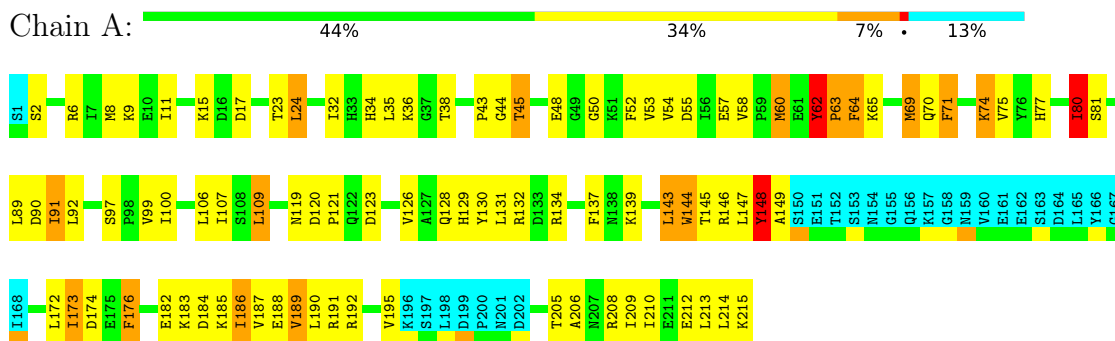
### 4.2.2 Score per residue for model 2

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



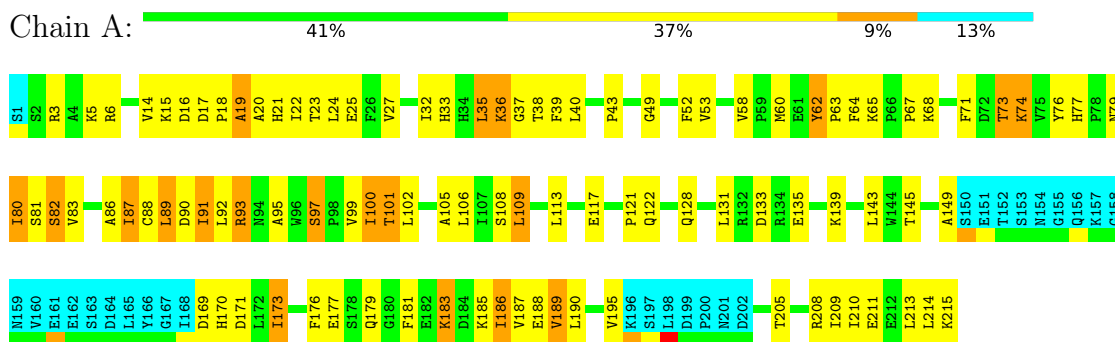
### 4.2.3 Score per residue for model 3

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



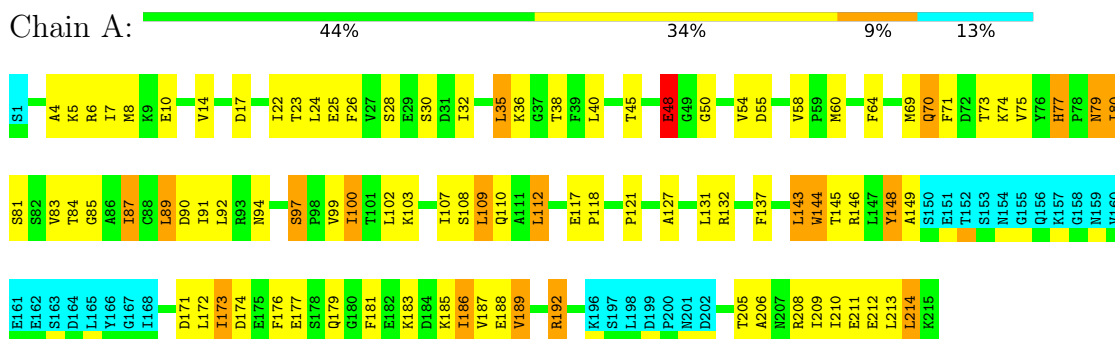
### 4.2.4 Score per residue for model 4

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



### 4.2.5 Score per residue for model 5

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



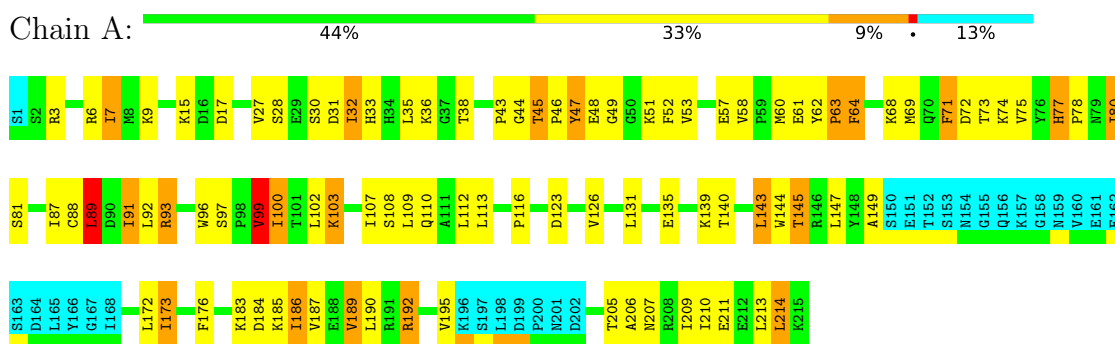
### 4.2.6 Score per residue for model 6

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



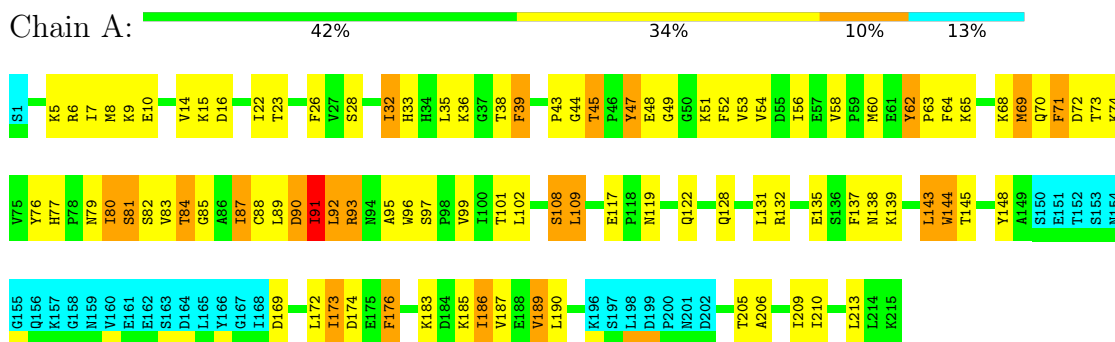
### 4.2.7 Score per residue for model 7

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



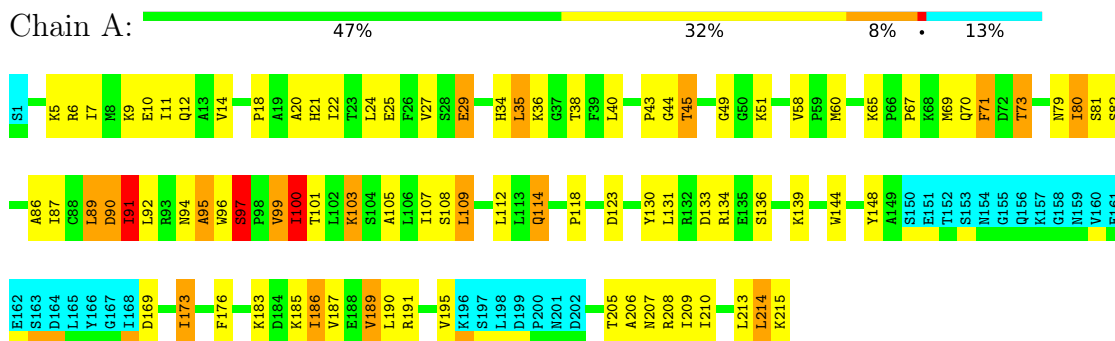
### 4.2.8 Score per residue for model 8

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



### 4.2.9 Score per residue for model 9

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



### 4.2.10 Score per residue for model 10

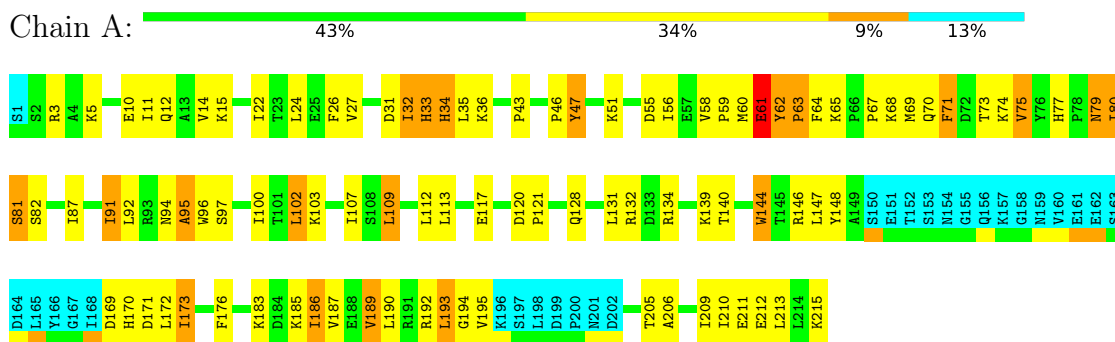
- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa





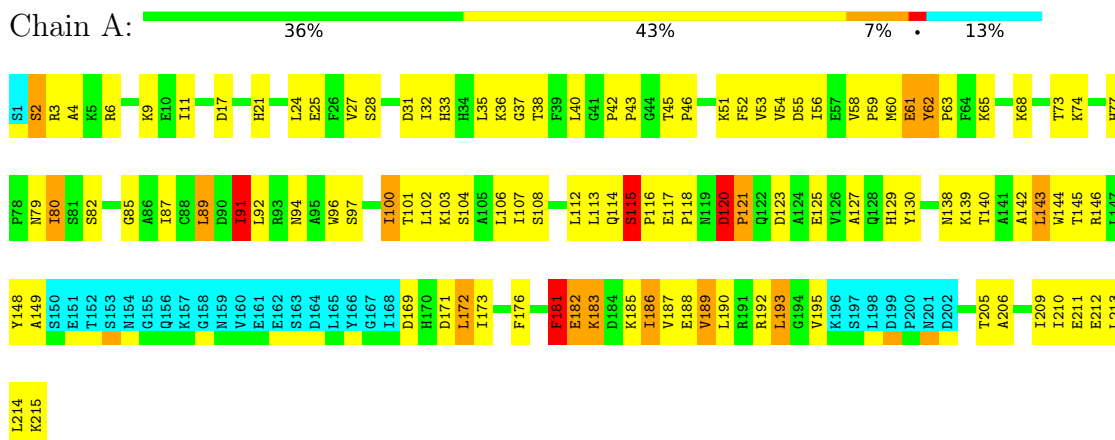
### 4.2.11 Score per residue for model 11

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



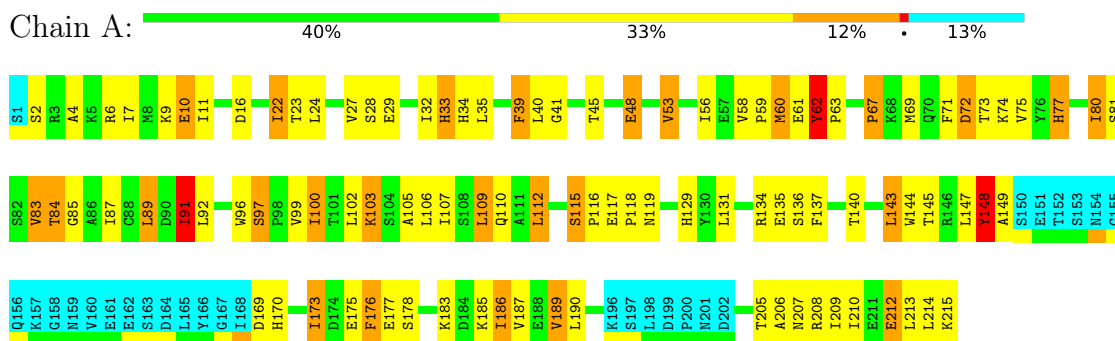
### 4.2.12 Score per residue for model 12

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



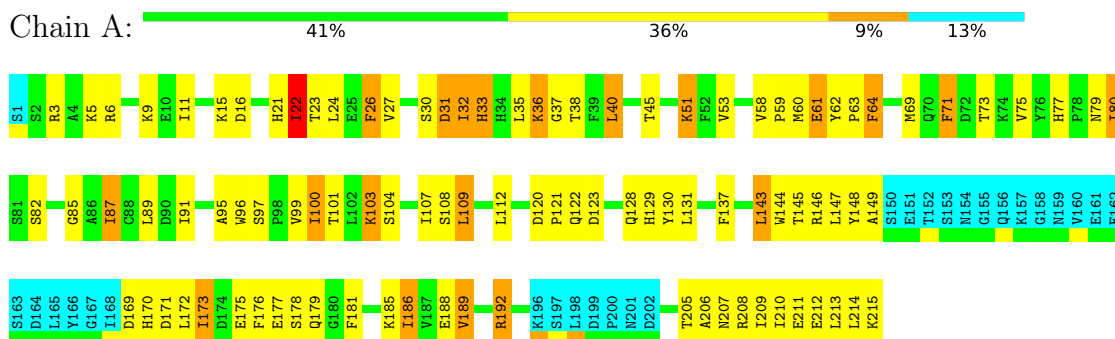
### 4.2.13 Score per residue for model 13

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



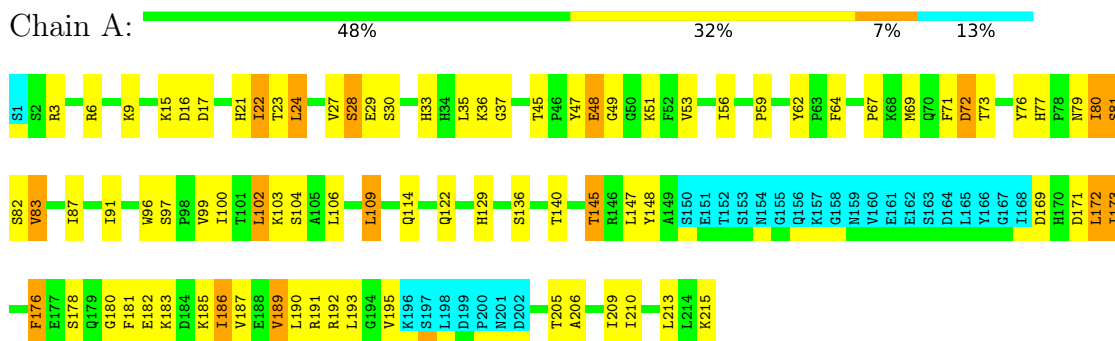
#### 4.2.14 Score per residue for model 14

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



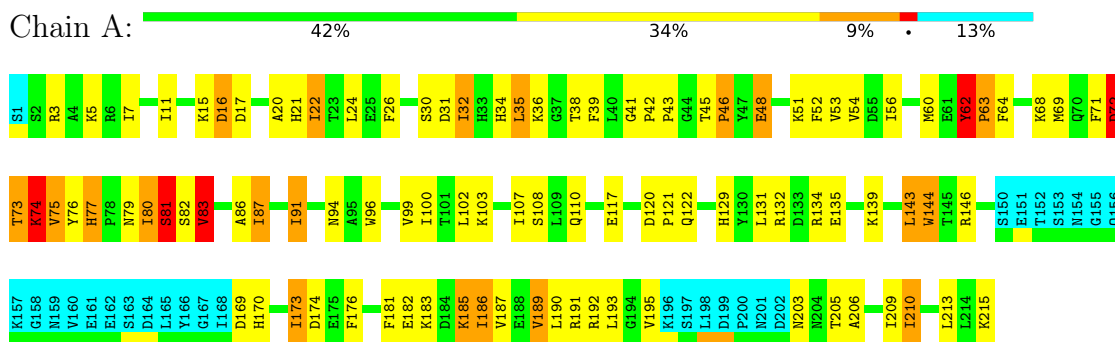
#### 4.2.15 Score per residue for model 15

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



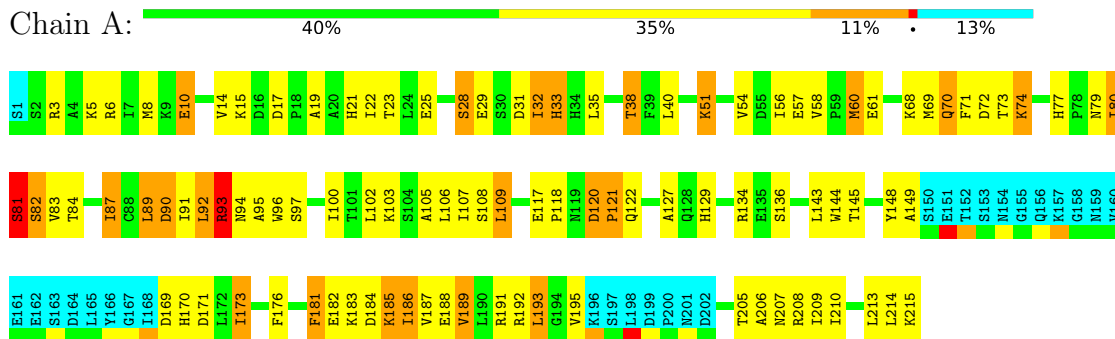
#### 4.2.16 Score per residue for model 16

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



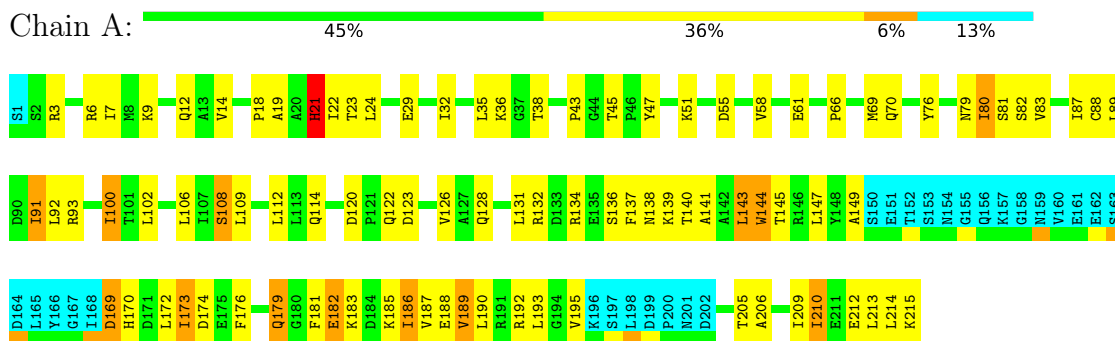
### 4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



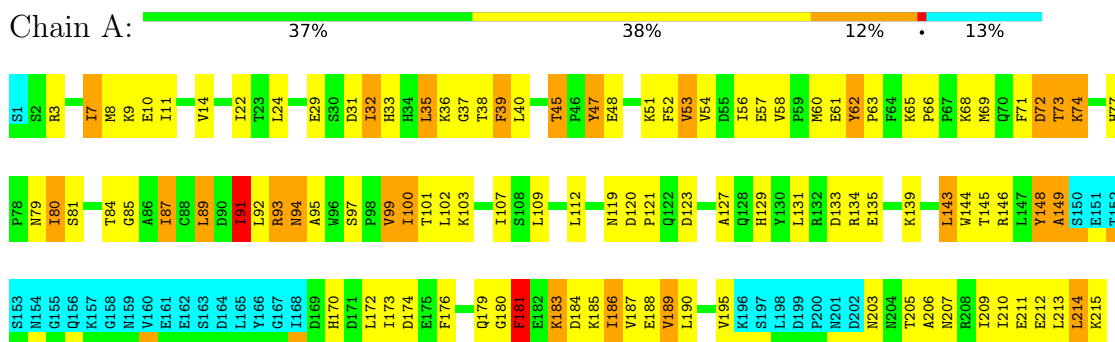
### 4.2.18 Score per residue for model 18

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



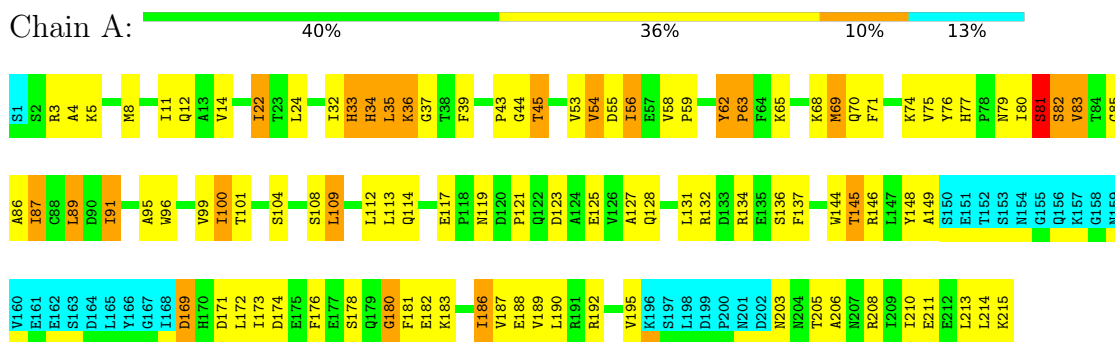
### 4.2.19 Score per residue for model 19

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



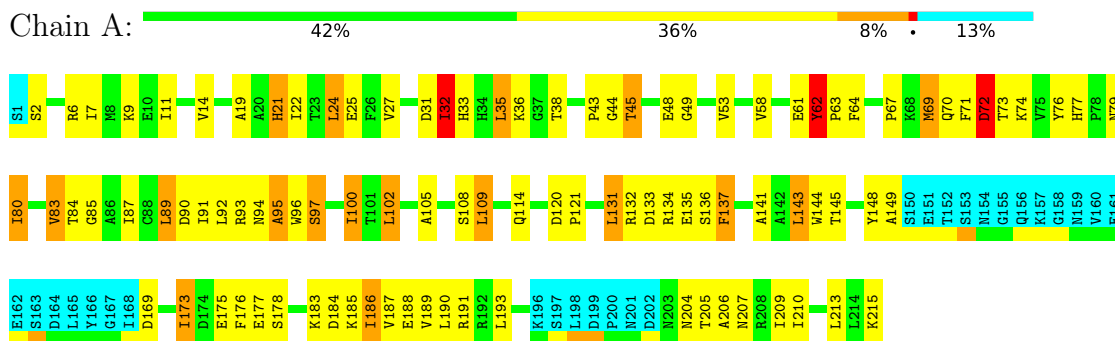
#### 4.2.20 Score per residue for model 20

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



#### 4.2.21 Score per residue for model 21

- Molecule 1: Ubiquitin-conjugating enzyme E2-24 kDa



## 5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 21 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	1503	1497	1500	59±9
All	All	31563	31437	31500	1246

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 20.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:ILE:HD11	1:A:102:LEU:HD12	0.99	1.30	19	1
1:A:176:PHE:CD2	1:A:186:ILE:HG23	0.99	1.91	9	18
1:A:56:ILE:HD13	1:A:102:LEU:HD21	0.96	1.34	11	3
1:A:80:ILE:HG23	1:A:87:ILE:HG23	0.94	1.36	17	14
1:A:189:VAL:HG21	1:A:213:LEU:HD23	0.90	1.41	17	11
1:A:80:ILE:HG23	1:A:87:ILE:HG22	0.89	1.42	21	5
1:A:53:VAL:O	1:A:72:ASP:HA	0.88	1.68	16	6
1:A:91:ILE:HG22	1:A:100:ILE:HD13	0.84	1.47	21	2
1:A:56:ILE:HD11	1:A:106:LEU:HD21	0.83	1.48	12	2
1:A:80:ILE:HG23	1:A:87:ILE:CG2	0.83	2.04	9	11
1:A:11:ILE:HG23	1:A:24:LEU:CD1	0.82	2.04	3	3
1:A:56:ILE:HG21	1:A:102:LEU:HD11	0.82	1.52	1	2
1:A:87:ILE:HG21	1:A:109:LEU:HD21	0.81	1.48	17	11
1:A:92:LEU:HD23	1:A:112:LEU:HD22	0.81	1.51	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:89:LEU:HD12	1:A:112:LEU:HD22	0.80	1.54	12	1
1:A:176:PHE:CD1	1:A:213:LEU:HD11	0.79	2.12	6	6
1:A:183:LYS:O	1:A:187:VAL:HG23	0.78	1.78	15	20
1:A:35:LEU:HD12	1:A:58:VAL:HG21	0.78	1.55	10	1
1:A:176:PHE:CD2	1:A:213:LEU:HD11	0.78	2.14	12	14
1:A:185:LYS:O	1:A:189:VAL:HG23	0.78	1.78	21	20
1:A:32:ILE:HD12	1:A:58:VAL:HG21	0.77	1.54	20	1
1:A:77:HIS:HB3	1:A:80:ILE:HD12	0.77	1.55	2	11
1:A:80:ILE:CG1	1:A:87:ILE:HG22	0.77	2.10	5	7
1:A:87:ILE:HD12	1:A:92:LEU:HD21	0.76	1.56	21	2
1:A:48:GLU:O	1:A:145:THR:HG21	0.76	1.79	15	2
1:A:80:ILE:HG22	1:A:86:ALA:CB	0.76	2.11	16	1
1:A:91:ILE:HD12	1:A:100:ILE:HG21	0.74	1.58	3	2
1:A:7:ILE:HD11	1:A:102:LEU:CD1	0.74	2.11	19	2
1:A:189:VAL:HG11	1:A:209:ILE:HG23	0.74	1.58	12	4
1:A:176:PHE:HB2	1:A:186:ILE:HD13	0.74	1.59	20	6
1:A:89:LEU:HD21	1:A:108:SER:OG	0.74	1.82	18	1
1:A:21:HIS:O	1:A:22:ILE:HD13	0.73	1.83	2	4
1:A:97:SER:HB3	1:A:100:ILE:HD12	0.73	1.61	9	1
1:A:38:THR:HG22	1:A:53:VAL:HA	0.73	1.61	14	8
1:A:80:ILE:CG2	1:A:87:ILE:HG22	0.73	2.14	21	2
1:A:91:ILE:O	1:A:92:LEU:HD22	0.73	1.83	9	5
1:A:189:VAL:HG22	1:A:212:GLU:OE2	0.72	1.84	13	1
1:A:176:PHE:CE2	1:A:209:ILE:HG21	0.72	2.19	1	10
1:A:87:ILE:O	1:A:92:LEU:HD22	0.72	1.83	17	2
1:A:32:ILE:HD11	1:A:35:LEU:HD11	0.72	1.60	19	1
1:A:71:PHE:CE2	1:A:75:VAL:HG13	0.71	2.20	3	2
1:A:176:PHE:CB	1:A:186:ILE:HD12	0.71	2.15	12	1
1:A:11:ILE:HG23	1:A:24:LEU:HB2	0.70	1.63	14	6
1:A:143:LEU:HD23	1:A:144:TRP:N	0.70	2.01	21	11
1:A:89:LEU:HD11	1:A:108:SER:OG	0.70	1.86	4	3
1:A:189:VAL:HG21	1:A:213:LEU:CD2	0.70	2.14	17	16
1:A:40:LEU:HD13	1:A:41:GLY:N	0.70	2.01	13	1
1:A:36:LYS:HD3	1:A:53:VAL:HG13	0.70	1.62	20	2
1:A:56:ILE:HG23	1:A:68:LYS:O	0.70	1.85	16	1
1:A:14:VAL:HG11	1:A:24:LEU:HD12	0.70	1.64	11	9
1:A:186:ILE:N	1:A:186:ILE:HD13	0.70	2.02	12	1
1:A:87:ILE:CD1	1:A:92:LEU:HD21	0.70	2.15	21	2
1:A:45:THR:HG21	1:A:114:GLN:OE1	0.70	1.87	9	1
1:A:173:ILE:HA	1:A:186:ILE:HG21	0.69	1.65	21	7
1:A:56:ILE:CD1	1:A:102:LEU:HD21	0.69	2.17	11	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:79:ASN:ND2	1:A:112:LEU:HD22	0.69	2.03	18	1
1:A:189:VAL:CG1	1:A:209:ILE:HG23	0.68	2.19	4	3
1:A:91:ILE:HD12	1:A:91:ILE:O	0.68	1.88	5	3
1:A:210:ILE:HA	1:A:213:LEU:HD12	0.68	1.66	13	14
1:A:91:ILE:C	1:A:92:LEU:HD22	0.68	2.09	13	5
1:A:176:PHE:HD2	1:A:186:ILE:HG23	0.68	1.47	4	13
1:A:7:ILE:HD11	1:A:102:LEU:HD11	0.68	1.66	13	4
1:A:54:VAL:HG13	1:A:72:ASP:OD2	0.68	1.88	1	1
1:A:89:LEU:HD11	1:A:108:SER:HB3	0.68	1.66	20	4
1:A:82:SER:HB2	1:A:86:ALA:HB3	0.68	1.64	4	1
1:A:189:VAL:HG13	1:A:212:GLU:CD	0.68	2.09	12	2
1:A:91:ILE:O	1:A:91:ILE:HD13	0.67	1.89	11	1
1:A:40:LEU:HD23	1:A:51:LYS:HB3	0.67	1.64	14	1
1:A:44:GLY:O	1:A:45:THR:HG23	0.67	1.90	21	8
1:A:32:ILE:HD12	1:A:58:VAL:CG2	0.67	2.20	20	1
1:A:69:MET:HB3	1:A:87:ILE:HD11	0.67	1.65	20	1
1:A:82:SER:O	1:A:83:VAL:HG13	0.66	1.91	16	1
1:A:67:PRO:HD2	1:A:91:ILE:HD11	0.66	1.67	11	1
1:A:89:LEU:HD21	1:A:108:SER:CB	0.66	2.21	4	4
1:A:91:ILE:CG2	1:A:100:ILE:HD13	0.66	2.21	9	2
1:A:10:GLU:OE2	1:A:102:LEU:HD12	0.66	1.90	13	1
1:A:91:ILE:H	1:A:91:ILE:HD13	0.65	1.51	19	3
1:A:80:ILE:HG22	1:A:86:ALA:HB3	0.65	1.68	16	1
1:A:81:SER:N	1:A:86:ALA:HB1	0.65	2.05	16	1
1:A:176:PHE:CZ	1:A:209:ILE:HG21	0.65	2.27	9	2
1:A:145:THR:HA	1:A:149:ALA:HB2	0.65	1.69	3	3
1:A:10:GLU:O	1:A:14:VAL:HG12	0.65	1.91	19	6
1:A:103:LYS:O	1:A:107:ILE:HG22	0.65	1.92	9	9
1:A:176:PHE:HB3	1:A:186:ILE:HD12	0.65	1.66	12	1
1:A:91:ILE:CG2	1:A:100:ILE:HG21	0.65	2.22	2	4
1:A:89:LEU:HD11	1:A:108:SER:CB	0.65	2.22	21	3
1:A:58:VAL:HG12	1:A:67:PRO:HB3	0.64	1.70	10	3
1:A:56:ILE:HD13	1:A:102:LEU:HD22	0.64	1.67	17	2
1:A:90:ASP:O	1:A:95:ALA:HB1	0.64	1.93	21	1
1:A:195:VAL:HG11	1:A:205:THR:HG21	0.64	1.67	7	3
1:A:32:ILE:HD11	1:A:35:LEU:CD1	0.64	2.23	4	1
1:A:95:ALA:HB1	1:A:100:ILE:HD11	0.64	1.70	10	2
1:A:176:PHE:CE2	1:A:186:ILE:HG23	0.63	2.27	16	5
1:A:89:LEU:HB3	1:A:92:LEU:HD23	0.63	1.68	19	3
1:A:20:ALA:O	1:A:22:ILE:HD13	0.63	1.93	16	1
1:A:195:VAL:HG21	1:A:205:THR:HG23	0.62	1.70	18	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:ASP:O	1:A:32:ILE:HG22	0.62	1.94	19	1
1:A:62:TYR:N	1:A:63:PRO:CD	0.62	2.62	14	7
1:A:87:ILE:HG21	1:A:109:LEU:CD2	0.62	2.23	20	4
1:A:89:LEU:HD11	1:A:108:SER:HB2	0.62	1.70	18	4
1:A:87:ILE:HG21	1:A:109:LEU:HD11	0.62	1.70	6	1
1:A:77:HIS:CB	1:A:80:ILE:HD12	0.62	2.24	16	4
1:A:90:ASP:O	1:A:100:ILE:HD13	0.62	1.95	4	1
1:A:37:GLY:HA3	1:A:106:LEU:HD21	0.62	1.71	15	3
1:A:145:THR:O	1:A:149:ALA:HB2	0.62	1.94	5	6
1:A:97:SER:CB	1:A:100:ILE:HD12	0.62	2.24	9	1
1:A:182:GLU:O	1:A:185:LYS:HG3	0.62	1.95	17	1
1:A:91:ILE:HG21	1:A:100:ILE:HG21	0.61	1.71	21	1
1:A:24:LEU:HD11	1:A:102:LEU:HD13	0.61	1.72	16	1
1:A:87:ILE:CG2	1:A:109:LEU:HD21	0.61	2.25	9	5
1:A:102:LEU:HD22	1:A:102:LEU:C	0.61	2.16	21	1
1:A:11:ILE:HG23	1:A:24:LEU:HD12	0.61	1.73	12	1
1:A:75:VAL:HG21	1:A:80:ILE:HD13	0.61	1.72	13	1
1:A:80:ILE:CG2	1:A:87:ILE:HG23	0.61	2.22	16	2
1:A:172:LEU:HD11	1:A:190:LEU:HD11	0.60	1.70	19	2
1:A:27:VAL:HG13	1:A:36:LYS:HG2	0.60	1.73	14	1
1:A:58:VAL:O	1:A:58:VAL:HG23	0.60	1.97	21	18
1:A:80:ILE:HG13	1:A:87:ILE:HG22	0.60	1.73	15	10
1:A:80:ILE:HD13	1:A:80:ILE:N	0.60	2.12	10	1
1:A:181:PHE:CD2	1:A:213:LEU:HD13	0.59	2.32	6	2
1:A:91:ILE:HG12	1:A:100:ILE:HG21	0.59	1.71	15	1
1:A:118:PRO:HB3	1:A:127:ALA:HB1	0.59	1.72	12	2
1:A:181:PHE:O	1:A:186:ILE:HD11	0.59	1.96	12	1
1:A:105:ALA:O	1:A:109:LEU:HD12	0.59	1.97	17	2
1:A:87:ILE:HD13	1:A:109:LEU:HD11	0.59	1.73	17	2
1:A:91:ILE:HD13	1:A:91:ILE:N	0.59	2.13	7	5
1:A:27:VAL:HG21	1:A:34:HIS:NE2	0.59	2.12	9	1
1:A:32:ILE:HD11	1:A:35:LEU:HD12	0.59	1.75	4	1
1:A:69:MET:CE	1:A:105:ALA:HB3	0.59	2.28	21	1
1:A:205:THR:O	1:A:209:ILE:HG13	0.58	1.97	4	18
1:A:31:ASP:C	1:A:32:ILE:HD13	0.58	2.18	16	1
1:A:89:LEU:HD12	1:A:112:LEU:HD11	0.58	1.75	20	1
1:A:140:THR:HG22	1:A:144:TRP:CE3	0.58	2.33	6	1
1:A:32:ILE:HD13	1:A:32:ILE:N	0.58	2.14	11	2
1:A:22:ILE:HD12	1:A:39:PHE:CE2	0.58	2.32	13	1
1:A:91:ILE:HA	1:A:95:ALA:HB2	0.58	1.76	10	5
1:A:7:ILE:HB	1:A:32:ILE:HG21	0.58	1.73	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:206:ALA:O	1:A:210:ILE:HG12	0.58	1.99	12	18
1:A:79:ASN:OD1	1:A:112:LEU:HD11	0.58	1.98	5	1
1:A:145:THR:O	1:A:149:ALA:HB3	0.58	1.99	18	3
1:A:22:ILE:HD13	1:A:22:ILE:N	0.58	2.13	20	3
1:A:24:LEU:HD12	1:A:24:LEU:O	0.57	1.98	3	3
1:A:21:HIS:HA	1:A:40:LEU:HD12	0.57	1.73	10	1
1:A:80:ILE:HG22	1:A:86:ALA:C	0.57	2.20	10	1
1:A:27:VAL:O	1:A:27:VAL:HG13	0.57	2.00	21	4
1:A:195:VAL:HG21	1:A:205:THR:HG21	0.57	1.77	9	3
1:A:176:PHE:CE2	1:A:213:LEU:HD11	0.57	2.35	17	5
1:A:14:VAL:HG22	1:A:22:ILE:HB	0.57	1.75	11	6
1:A:56:ILE:HG21	1:A:102:LEU:HD22	0.57	1.76	8	1
1:A:123:ASP:HB3	1:A:126:VAL:HG12	0.57	1.77	7	1
1:A:27:VAL:HG23	1:A:34:HIS:CE1	0.57	2.35	11	1
1:A:4:ALA:HA	1:A:32:ILE:HD11	0.57	1.75	12	1
1:A:176:PHE:CD2	1:A:186:ILE:HG21	0.57	2.35	20	2
1:A:52:PHE:CZ	1:A:145:THR:HG23	0.57	2.34	12	1
1:A:210:ILE:HD13	1:A:210:ILE:N	0.56	2.15	16	21
1:A:80:ILE:HG12	1:A:87:ILE:HG22	0.56	1.77	5	1
1:A:181:PHE:O	1:A:182:GLU:CB	0.56	2.53	18	1
1:A:91:ILE:HG23	1:A:100:ILE:HD12	0.56	1.76	18	1
1:A:4:ALA:HA	1:A:32:ILE:HD13	0.56	1.77	5	1
1:A:21:HIS:C	1:A:22:ILE:HD13	0.56	2.21	15	2
1:A:32:ILE:O	1:A:32:ILE:HG23	0.56	2.01	21	3
1:A:89:LEU:HD11	1:A:112:LEU:HD12	0.55	1.78	2	1
1:A:87:ILE:HD11	1:A:92:LEU:HD21	0.55	1.79	11	1
1:A:89:LEU:CD1	1:A:112:LEU:HD12	0.55	2.30	2	1
1:A:176:PHE:CD2	1:A:186:ILE:CG2	0.55	2.90	20	7
1:A:100:ILE:HG22	1:A:104:SER:HB3	0.55	1.77	6	1
1:A:38:THR:HG22	1:A:52:PHE:O	0.55	2.02	7	2
1:A:82:SER:CB	1:A:86:ALA:HB3	0.55	2.32	4	3
1:A:193:LEU:HB2	1:A:195:VAL:HG23	0.55	1.77	11	1
1:A:189:VAL:CG2	1:A:213:LEU:HD23	0.55	2.24	17	1
1:A:32:ILE:C	1:A:32:ILE:HD13	0.54	2.21	21	2
1:A:145:THR:HG22	1:A:149:ALA:HB3	0.54	1.79	20	1
1:A:53:VAL:O	1:A:53:VAL:HG12	0.54	2.02	13	4
1:A:210:ILE:O	1:A:214:LEU:HD12	0.54	2.01	7	3
1:A:69:MET:HB2	1:A:92:LEU:HD11	0.54	1.80	19	2
1:A:169:ASP:O	1:A:173:ILE:HB	0.54	2.02	16	4
1:A:173:ILE:HG12	1:A:186:ILE:HG21	0.54	1.80	16	1
1:A:185:LYS:HE2	1:A:213:LEU:HD22	0.54	1.78	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:38:THR:HG21	1:A:51:LYS:HD3	0.54	1.78	17	1
1:A:189:VAL:HG13	1:A:212:GLU:HB2	0.54	1.80	19	7
1:A:73:THR:HG21	1:A:149:ALA:HB2	0.54	1.79	12	1
1:A:54:VAL:HG13	1:A:70:GLN:O	0.54	2.02	5	2
1:A:210:ILE:HG22	1:A:214:LEU:HD12	0.54	1.78	14	2
1:A:43:PRO:HB2	1:A:45:THR:HG22	0.54	1.79	16	1
1:A:45:THR:HG23	1:A:48:GLU:H	0.54	1.61	1	1
1:A:176:PHE:CD1	1:A:176:PHE:N	0.53	2.74	13	13
1:A:189:VAL:HG11	1:A:209:ILE:HA	0.53	1.80	4	12
1:A:27:VAL:HG23	1:A:27:VAL:O	0.53	2.03	4	1
1:A:97:SER:HB2	1:A:100:ILE:HD11	0.53	1.79	6	1
1:A:69:MET:CE	1:A:105:ALA:HB1	0.53	2.33	13	1
1:A:54:VAL:HG22	1:A:72:ASP:HB3	0.53	1.81	16	2
1:A:131:LEU:HD12	1:A:132:ARG:N	0.53	2.17	21	1
1:A:24:LEU:HD11	1:A:102:LEU:CD1	0.53	2.33	16	1
1:A:173:ILE:HA	1:A:186:ILE:CD1	0.53	2.34	2	15
1:A:32:ILE:O	1:A:32:ILE:HD13	0.53	2.04	7	2
1:A:102:LEU:HD23	1:A:106:LEU:HD12	0.53	1.81	1	1
1:A:73:THR:HG23	1:A:148:TYR:O	0.53	2.03	5	2
1:A:96:TRP:O	1:A:100:ILE:HD11	0.53	2.04	12	2
1:A:89:LEU:N	1:A:92:LEU:HD23	0.53	2.19	21	2
1:A:35:LEU:HD12	1:A:58:VAL:CG2	0.52	2.30	10	1
1:A:7:ILE:HG21	1:A:35:LEU:HD11	0.52	1.80	5	4
1:A:121:PRO:HG3	1:A:127:ALA:HB2	0.52	1.81	5	2
1:A:77:HIS:CD2	1:A:113:LEU:HD23	0.52	2.40	4	1
1:A:40:LEU:HD23	1:A:50:GLY:O	0.52	2.04	5	1
1:A:26:PHE:CZ	1:A:32:ILE:HD12	0.52	2.40	14	1
1:A:189:VAL:HG11	1:A:209:ILE:CG2	0.52	2.35	4	1
1:A:26:PHE:CE2	1:A:32:ILE:HD12	0.52	2.39	14	1
1:A:91:ILE:HG13	1:A:92:LEU:HD22	0.52	1.82	21	1
1:A:89:LEU:HD21	1:A:108:SER:HB3	0.52	1.82	6	1
1:A:89:LEU:HD21	1:A:108:SER:HB2	0.52	1.82	20	2
1:A:91:ILE:HG22	1:A:100:ILE:HG21	0.52	1.81	2	1
1:A:89:LEU:H	1:A:92:LEU:HD23	0.52	1.65	21	2
1:A:11:ILE:HD11	1:A:35:LEU:HD21	0.52	1.81	9	1
1:A:186:ILE:HG22	1:A:190:LEU:HG	0.52	1.82	9	2
1:A:176:PHE:CD1	1:A:213:LEU:CD1	0.51	2.94	5	6
1:A:46:PRO:HB3	1:A:142:ALA:HB2	0.51	1.80	12	1
1:A:186:ILE:HA	1:A:213:LEU:HD21	0.51	1.82	20	1
1:A:189:VAL:CB	1:A:209:ILE:HG23	0.51	2.35	4	2
1:A:176:PHE:HB2	1:A:186:ILE:CD1	0.51	2.36	15	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:80:ILE:HG23	1:A:87:ILE:HA	0.51	1.82	7	1
1:A:56:ILE:HD13	1:A:102:LEU:HD23	0.51	1.81	2	1
1:A:53:VAL:HG12	1:A:53:VAL:O	0.51	2.05	19	1
1:A:7:ILE:HG21	1:A:32:ILE:CD1	0.51	2.36	13	2
1:A:38:THR:HG21	1:A:51:LYS:HE3	0.51	1.82	8	1
1:A:91:ILE:O	1:A:92:LEU:HD13	0.51	2.05	4	1
1:A:173:ILE:O	1:A:186:ILE:CD1	0.51	2.60	7	16
1:A:4:ALA:CB	1:A:32:ILE:HG22	0.51	2.36	10	1
1:A:210:ILE:HA	1:A:213:LEU:HB2	0.50	1.82	13	6
1:A:100:ILE:HG22	1:A:100:ILE:O	0.50	2.07	17	2
1:A:121:PRO:HG2	1:A:127:ALA:HB2	0.50	1.83	20	1
1:A:19:ALA:O	1:A:20:ALA:HB3	0.50	2.07	1	1
1:A:181:PHE:CE1	1:A:214:LEU:HD22	0.50	2.40	4	1
1:A:176:PHE:CD1	1:A:186:ILE:CG2	0.50	2.94	19	1
1:A:176:PHE:CD2	1:A:213:LEU:CD1	0.50	2.94	16	5
1:A:173:ILE:HG23	1:A:186:ILE:HD12	0.50	1.82	5	1
1:A:52:PHE:CD1	1:A:71:PHE:CZ	0.50	2.99	8	1
1:A:91:ILE:HG23	1:A:100:ILE:HD13	0.50	1.82	9	1
1:A:62:TYR:N	1:A:63:PRO:HD3	0.50	2.21	2	1
1:A:143:LEU:O	1:A:147:LEU:HD12	0.50	2.05	2	2
1:A:91:ILE:HD12	1:A:100:ILE:CG2	0.50	2.34	3	2
1:A:144:TRP:CZ2	1:A:148:TYR:CZ	0.50	3.00	11	1
1:A:145:THR:HG23	1:A:149:ALA:CB	0.50	2.37	14	1
1:A:91:ILE:CD1	1:A:105:ALA:HB2	0.50	2.37	4	1
1:A:71:PHE:CE2	1:A:109:LEU:HD22	0.50	2.41	11	2
1:A:181:PHE:HB3	1:A:185:LYS:HG2	0.50	1.83	17	1
1:A:67:PRO:HG3	1:A:102:LEU:HD12	0.50	1.83	15	1
1:A:72:ASP:OD2	1:A:80:ILE:HG21	0.50	2.07	19	1
1:A:73:THR:HG21	1:A:149:ALA:O	0.50	2.07	19	1
1:A:52:PHE:CD1	1:A:71:PHE:CE1	0.50	3.00	8	1
1:A:181:PHE:O	1:A:182:GLU:CG	0.50	2.60	18	1
1:A:99:VAL:O	1:A:100:ILE:HG22	0.49	2.07	9	1
1:A:32:ILE:HD13	1:A:32:ILE:H	0.49	1.66	11	1
1:A:42:PRO:N	1:A:43:PRO:CD	0.49	2.76	12	1
1:A:176:PHE:CB	1:A:186:ILE:CD1	0.49	2.89	12	1
1:A:58:VAL:HG12	1:A:67:PRO:HG3	0.49	1.83	13	1
1:A:31:ASP:O	1:A:32:ILE:CG2	0.49	2.60	19	1
1:A:56:ILE:CD1	1:A:102:LEU:HD11	0.49	2.38	19	1
1:A:73:THR:O	1:A:73:THR:HG22	0.49	2.08	11	3
1:A:75:VAL:HG23	1:A:80:ILE:HB	0.49	1.84	1	1
1:A:8:MET:HA	1:A:11:ILE:HD12	0.49	1.84	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:87:ILE:HG21	1:A:109:LEU:CD1	0.49	2.36	6	1
1:A:91:ILE:HG21	1:A:100:ILE:CB	0.49	2.38	9	1
1:A:193:LEU:HD12	1:A:209:ILE:HG12	0.49	1.83	18	1
1:A:62:TYR:CB	1:A:63:PRO:CD	0.49	2.91	16	5
1:A:102:LEU:CD2	1:A:106:LEU:HD12	0.48	2.37	1	1
1:A:186:ILE:HG22	1:A:190:LEU:HD21	0.48	1.85	18	2
1:A:4:ALA:O	1:A:7:ILE:HG22	0.48	2.09	13	1
1:A:24:LEU:HD21	1:A:106:LEU:HD11	0.48	1.85	13	1
1:A:56:ILE:HD13	1:A:102:LEU:CD2	0.48	2.38	2	3
1:A:186:ILE:HD13	1:A:186:ILE:H	0.48	1.67	12	1
1:A:67:PRO:O	1:A:91:ILE:HD13	0.48	2.08	21	1
1:A:176:PHE:CE2	1:A:209:ILE:CG2	0.48	2.95	9	2
1:A:75:VAL:HG11	1:A:113:LEU:HD11	0.48	1.84	20	1
1:A:74:LYS:O	1:A:75:VAL:HG13	0.48	2.09	2	1
1:A:186:ILE:O	1:A:190:LEU:HG	0.48	2.09	1	13
1:A:73:THR:HG22	1:A:148:TYR:HB3	0.48	1.85	9	1
1:A:90:ASP:O	1:A:91:ILE:HG23	0.48	2.09	6	1
1:A:80:ILE:HG22	1:A:86:ALA:HB1	0.48	1.81	16	1
1:A:95:ALA:HB1	1:A:100:ILE:CD1	0.47	2.39	10	2
1:A:193:LEU:HD22	1:A:193:LEU:N	0.47	2.24	11	1
1:A:91:ILE:HD13	1:A:91:ILE:C	0.47	2.29	11	1
1:A:193:LEU:HD22	1:A:193:LEU:H	0.47	1.69	11	1
1:A:169:ASP:N	1:A:172:LEU:HD23	0.47	2.24	12	1
1:A:21:HIS:O	1:A:40:LEU:HD12	0.47	2.09	17	1
1:A:80:ILE:HG22	1:A:85:GLY:HA2	0.47	1.85	8	1
1:A:69:MET:HE3	1:A:105:ALA:HB1	0.47	1.85	9	1
1:A:52:PHE:CD1	1:A:73:THR:HG21	0.47	2.44	4	1
1:A:11:ILE:HG22	1:A:15:LYS:CD	0.47	2.39	16	1
1:A:173:ILE:HA	1:A:186:ILE:HD12	0.47	1.87	8	2
1:A:52:PHE:N	1:A:52:PHE:CD1	0.47	2.83	16	1
1:A:82:SER:C	1:A:83:VAL:HG22	0.47	2.30	16	1
1:A:75:VAL:HG21	1:A:113:LEU:HD21	0.46	1.87	7	1
1:A:54:VAL:HG11	1:A:69:MET:SD	0.46	2.51	8	1
1:A:181:PHE:CD1	1:A:181:PHE:N	0.46	2.82	14	1
1:A:170:HIS:HA	1:A:173:ILE:HB	0.46	1.86	18	4
1:A:79:ASN:ND2	1:A:112:LEU:HD13	0.46	2.24	10	1
1:A:91:ILE:HG23	1:A:100:ILE:HG21	0.46	1.88	13	2
1:A:90:ASP:HA	1:A:95:ALA:HB1	0.46	1.87	6	1
1:A:24:LEU:HD23	1:A:37:GLY:HA3	0.46	1.85	14	1
1:A:91:ILE:CG1	1:A:100:ILE:HG21	0.46	2.39	15	1
1:A:18:PRO:O	1:A:19:ALA:HB3	0.46	2.11	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:32:ILE:O	1:A:34:HIS:N	0.46	2.49	13	1
1:A:23:THR:HG23	1:A:38:THR:OG1	0.46	2.11	17	1
1:A:45:THR:HG23	1:A:48:GLU:N	0.46	2.26	1	1
1:A:189:VAL:O	1:A:192:ARG:HG2	0.46	2.11	5	2
1:A:90:ASP:O	1:A:100:ILE:HD12	0.46	2.11	6	1
1:A:19:ALA:HB3	1:A:22:ILE:CD1	0.46	2.41	21	1
1:A:210:ILE:CD1	1:A:213:LEU:HD12	0.46	2.41	12	5
1:A:37:GLY:O	1:A:54:VAL:HG23	0.46	2.11	20	3
1:A:79:ASN:CB	1:A:112:LEU:HD21	0.46	2.40	14	1
1:A:47:TYR:CE1	1:A:141:ALA:HB1	0.46	2.46	18	1
1:A:176:PHE:HE2	1:A:209:ILE:HG21	0.46	1.71	12	2
1:A:52:PHE:CE1	1:A:54:VAL:HG22	0.46	2.46	19	1
1:A:15:LYS:O	1:A:17:ASP:N	0.46	2.48	4	1
1:A:45:THR:O	1:A:47:TYR:N	0.46	2.49	6	1
1:A:47:TYR:CD1	1:A:145:THR:CG2	0.46	2.99	8	1
1:A:176:PHE:HB2	1:A:186:ILE:HD12	0.46	1.87	12	1
1:A:72:ASP:O	1:A:74:LYS:N	0.46	2.49	16	1
1:A:66:PRO:CG	1:A:91:ILE:HG22	0.46	2.41	18	1
1:A:173:ILE:HA	1:A:186:ILE:HD13	0.46	1.88	17	4
1:A:91:ILE:HG22	1:A:91:ILE:O	0.46	2.11	15	3
1:A:74:LYS:CE	1:A:148:TYR:CE2	0.46	2.99	19	1
1:A:11:ILE:HG23	1:A:24:LEU:HD11	0.45	1.83	3	1
1:A:177:GLU:CG	1:A:178:SER:N	0.45	2.79	13	3
1:A:41:GLY:O	1:A:43:PRO:CD	0.45	2.64	16	1
1:A:87:ILE:HG21	1:A:109:LEU:CG	0.45	2.42	6	1
1:A:91:ILE:C	1:A:91:ILE:HD13	0.45	2.31	12	1
1:A:115:SER:CB	1:A:116:PRO:CD	0.45	2.94	13	2
1:A:189:VAL:O	1:A:193:LEU:HD12	0.45	2.11	12	3
1:A:73:THR:O	1:A:73:THR:CG2	0.45	2.64	13	1
1:A:79:ASN:HD22	1:A:112:LEU:HD22	0.45	1.70	18	1
1:A:172:LEU:HD11	1:A:190:LEU:CD1	0.45	2.42	19	1
1:A:123:ASP:HB3	1:A:126:VAL:HG23	0.45	1.88	18	3
1:A:189:VAL:HA	1:A:192:ARG:HG2	0.45	1.89	7	1
1:A:22:ILE:CD1	1:A:39:PHE:CE2	0.45	2.99	8	3
1:A:20:ALA:HB1	1:A:22:ILE:HG12	0.45	1.88	9	1
1:A:181:PHE:O	1:A:182:GLU:HB3	0.45	2.12	18	1
1:A:31:ASP:O	1:A:32:ILE:O	0.45	2.34	19	1
1:A:90:ASP:CB	1:A:100:ILE:HD13	0.45	2.42	6	2
1:A:192:ARG:HG3	1:A:193:LEU:HD23	0.45	1.86	6	1
1:A:53:VAL:O	1:A:72:ASP:CA	0.45	2.65	19	2
1:A:52:PHE:CD1	1:A:53:VAL:N	0.45	2.84	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:VAL:HG12	1:A:67:PRO:CB	0.45	2.41	21	1
1:A:90:ASP:C	1:A:95:ALA:HB1	0.45	2.32	4	1
1:A:210:ILE:HG22	1:A:214:LEU:HD23	0.45	1.88	4	1
1:A:172:LEU:HD11	1:A:176:PHE:CZ	0.45	2.47	5	1
1:A:47:TYR:O	1:A:145:THR:HG21	0.45	2.12	6	1
1:A:7:ILE:CG2	1:A:32:ILE:HD13	0.45	2.41	18	1
1:A:176:PHE:CG	1:A:213:LEU:HD11	0.45	2.47	21	3
1:A:22:ILE:CD1	1:A:39:PHE:CZ	0.45	3.00	4	3
1:A:62:TYR:HB2	1:A:63:PRO:CD	0.45	2.41	11	1
1:A:177:GLU:HA	1:A:181:PHE:O	0.45	2.12	14	2
1:A:14:VAL:HG11	1:A:24:LEU:CD1	0.45	2.39	9	2
1:A:92:LEU:O	1:A:93:ARG:CB	0.45	2.65	17	1
1:A:87:ILE:CG1	1:A:89:LEU:HD23	0.45	2.41	6	1
1:A:186:ILE:HG22	1:A:190:LEU:CG	0.45	2.42	9	1
1:A:172:LEU:O	1:A:176:PHE:CD2	0.45	2.70	10	2
1:A:205:THR:O	1:A:209:ILE:HG12	0.45	2.13	13	1
1:A:87:ILE:CG2	1:A:109:LEU:HD11	0.44	2.42	6	1
1:A:11:ILE:HG23	1:A:24:LEU:HD13	0.44	1.86	3	1
1:A:54:VAL:HG22	1:A:71:PHE:CE1	0.44	2.46	3	1
1:A:173:ILE:CA	1:A:186:ILE:HD12	0.44	2.42	8	6
1:A:172:LEU:O	1:A:176:PHE:CE2	0.44	2.70	20	2
1:A:14:VAL:HG21	1:A:22:ILE:HG21	0.44	1.88	6	1
1:A:7:ILE:HG21	1:A:32:ILE:HD13	0.44	1.88	18	2
1:A:75:VAL:HG23	1:A:75:VAL:O	0.44	2.12	16	1
1:A:64:PHE:O	1:A:64:PHE:CD2	0.44	2.71	7	1
1:A:189:VAL:HG12	1:A:209:ILE:HD13	0.44	1.89	13	1
1:A:22:ILE:HG22	1:A:39:PHE:HB3	0.44	1.90	20	2
1:A:77:HIS:HB2	1:A:80:ILE:HD12	0.44	1.89	5	1
1:A:87:ILE:HG12	1:A:89:LEU:HD23	0.44	1.89	6	1
1:A:7:ILE:CG2	1:A:35:LEU:HD11	0.44	2.43	10	2
1:A:100:ILE:HG22	1:A:101:THR:N	0.44	2.28	12	1
1:A:91:ILE:HG23	1:A:100:ILE:CD1	0.44	2.42	18	1
1:A:27:VAL:HG22	1:A:28:SER:N	0.44	2.27	15	1
1:A:97:SER:O	1:A:100:ILE:HD12	0.44	2.13	19	1
1:A:32:ILE:HD12	1:A:32:ILE:O	0.44	2.13	2	1
1:A:181:PHE:CE2	1:A:213:LEU:HD13	0.44	2.48	18	1
1:A:97:SER:O	1:A:100:ILE:HD11	0.44	2.13	21	1
1:A:75:VAL:HG11	1:A:113:LEU:HD21	0.43	1.89	11	1
1:A:38:THR:CG2	1:A:53:VAL:HG22	0.43	2.42	16	1
1:A:83:VAL:HG13	1:A:84:THR:N	0.43	2.28	2	2
1:A:69:MET:CG	1:A:109:LEU:HD11	0.43	2.43	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:209:ILE:HG22	1:A:213:LEU:HG	0.43	1.89	21	1
1:A:180:GLY:O	1:A:181:PHE:CD2	0.43	2.71	10	2
1:A:176:PHE:O	1:A:180:GLY:C	0.43	2.57	20	1
1:A:87:ILE:HD11	1:A:92:LEU:CD2	0.43	2.44	5	1
1:A:60:MET:O	1:A:61:GLU:CB	0.43	2.67	11	1
1:A:34:HIS:CD2	1:A:57:GLU:CG	0.43	3.01	3	1
1:A:53:VAL:N	1:A:73:THR:OG1	0.43	2.52	13	1
1:A:193:LEU:HB3	1:A:195:VAL:HG23	0.43	1.89	18	1
1:A:8:MET:SD	1:A:11:ILE:HD12	0.43	2.54	19	1
1:A:79:ASN:OD1	1:A:112:LEU:HD21	0.43	2.12	19	1
1:A:27:VAL:HG23	1:A:28:SER:N	0.43	2.29	12	1
1:A:81:SER:O	1:A:83:VAL:N	0.43	2.51	20	3
1:A:91:ILE:HG22	1:A:100:ILE:HD12	0.43	1.90	20	1
1:A:195:VAL:HG21	1:A:205:THR:CG2	0.43	2.44	20	1
1:A:91:ILE:HD13	1:A:91:ILE:H	0.43	1.73	8	1
1:A:180:GLY:O	1:A:181:PHE:HB2	0.43	2.14	20	1
1:A:62:TYR:HB3	1:A:63:PRO:HD3	0.43	1.89	6	2
1:A:38:THR:CG2	1:A:53:VAL:HG13	0.43	2.44	10	1
1:A:14:VAL:CG2	1:A:22:ILE:CG2	0.43	2.96	21	1
1:A:62:TYR:N	1:A:63:PRO:HD2	0.43	2.28	14	2
1:A:56:ILE:HD12	1:A:102:LEU:HD21	0.43	1.88	15	1
1:A:62:TYR:CB	1:A:63:PRO:HD3	0.43	2.44	19	1
1:A:87:ILE:HD12	1:A:92:LEU:CD2	0.42	2.37	4	1
1:A:14:VAL:CG2	1:A:22:ILE:HG21	0.42	2.44	6	3
1:A:89:LEU:H	1:A:89:LEU:HD13	0.42	1.74	7	1
1:A:172:LEU:HD12	1:A:172:LEU:O	0.42	2.14	7	1
1:A:79:ASN:HD22	1:A:112:LEU:HD13	0.42	1.72	10	1
1:A:80:ILE:C	1:A:86:ALA:HB1	0.42	2.34	16	1
1:A:23:THR:HG23	1:A:38:THR:CB	0.42	2.44	17	1
1:A:65:LYS:N	1:A:66:PRO:HD3	0.42	2.29	19	1
1:A:143:LEU:HD23	1:A:143:LEU:C	0.42	2.35	7	8
1:A:22:ILE:CG2	1:A:106:LEU:HD13	0.42	2.44	15	1
1:A:169:ASP:O	1:A:173:ILE:CB	0.42	2.67	16	1
1:A:120:ASP:N	1:A:121:PRO:CD	0.42	2.82	6	5
1:A:71:PHE:CE2	1:A:109:LEU:HD13	0.42	2.50	7	1
1:A:195:VAL:CG1	1:A:205:THR:HG21	0.42	2.42	7	1
1:A:24:LEU:HD22	1:A:35:LEU:HD22	0.42	1.91	10	1
1:A:80:ILE:N	1:A:80:ILE:CD1	0.42	2.81	10	1
1:A:79:ASN:CG	1:A:112:LEU:HD21	0.42	2.35	11	1
1:A:190:LEU:HA	1:A:193:LEU:HD21	0.42	1.91	11	1
1:A:181:PHE:CE2	1:A:210:ILE:HG23	0.42	2.49	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:90:ASP:HA	1:A:95:ALA:HB2	0.42	1.90	8	1
1:A:92:LEU:HD22	1:A:92:LEU:N	0.42	2.29	10	1
1:A:92:LEU:N	1:A:92:LEU:CD2	0.42	2.82	10	1
1:A:22:ILE:HD12	1:A:39:PHE:CD2	0.42	2.50	13	1
1:A:189:VAL:HG13	1:A:212:GLU:CG	0.42	2.44	13	1
1:A:94:ASN:O	1:A:95:ALA:HB3	0.42	2.14	19	1
1:A:141:ALA:O	1:A:144:TRP:CD1	0.42	2.72	21	1
1:A:191:ARG:HG3	1:A:192:ARG:N	0.42	2.29	3	1
1:A:46:PRO:O	1:A:47:TYR:CD2	0.42	2.73	6	3
1:A:32:ILE:N	1:A:32:ILE:CD1	0.42	2.83	11	1
1:A:4:ALA:HA	1:A:32:ILE:HG23	0.42	1.92	20	1
1:A:89:LEU:O	1:A:92:LEU:HD23	0.42	2.13	1	1
1:A:87:ILE:HG22	1:A:88:CYS:N	0.42	2.29	7	1
1:A:118:PRO:CG	1:A:131:LEU:HD21	0.42	2.44	9	1
1:A:40:LEU:HD13	1:A:40:LEU:C	0.42	2.35	13	1
1:A:172:LEU:HD11	1:A:190:LEU:HD21	0.42	1.91	15	1
1:A:138:ASN:OD1	1:A:139:LYS:N	0.42	2.52	18	1
1:A:22:ILE:HG22	1:A:23:THR:N	0.42	2.30	8	4
1:A:40:LEU:C	1:A:40:LEU:HD13	0.42	2.35	4	1
1:A:7:ILE:HG13	1:A:32:ILE:HD12	0.42	1.90	5	1
1:A:181:PHE:CG	1:A:185:LYS:HG3	0.42	2.50	10	1
1:A:169:ASP:H	1:A:172:LEU:HD23	0.42	1.74	12	1
1:A:35:LEU:CB	1:A:56:ILE:HD11	0.42	2.43	20	1
1:A:99:VAL:O	1:A:100:ILE:CB	0.42	2.68	7	3
1:A:117:GLU:N	1:A:118:PRO:CD	0.42	2.83	5	1
1:A:192:ARG:CG	1:A:193:LEU:HD23	0.42	2.45	6	1
1:A:147:LEU:O	1:A:148:TYR:CD2	0.42	2.73	13	2
1:A:103:LYS:O	1:A:107:ILE:HD12	0.42	2.15	19	2
1:A:90:ASP:HB3	1:A:100:ILE:HD13	0.41	1.90	1	1
1:A:80:ILE:CG1	1:A:87:ILE:CG2	0.41	2.98	2	2
1:A:181:PHE:HZ	1:A:214:LEU:HD23	0.41	1.75	5	1
1:A:46:PRO:O	1:A:47:TYR:CG	0.41	2.72	7	2
1:A:89:LEU:HD21	1:A:112:LEU:HD23	0.41	1.92	9	1
1:A:176:PHE:O	1:A:181:PHE:N	0.41	2.43	15	1
1:A:89:LEU:HD12	1:A:112:LEU:CD1	0.41	2.44	20	1
1:A:47:TYR:CE1	1:A:145:THR:HG23	0.41	2.50	8	1
1:A:77:HIS:CE1	1:A:113:LEU:O	0.41	2.73	12	1
1:A:91:ILE:HD12	1:A:105:ALA:HB2	0.41	1.90	4	1
1:A:185:LYS:O	1:A:189:VAL:CG2	0.41	2.69	4	1
1:A:192:ARG:CG	1:A:193:LEU:N	0.41	2.82	16	2
1:A:99:VAL:O	1:A:101:THR:HG23	0.41	2.15	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:172:LEU:O	1:A:176:PHE:CD1	0.41	2.73	19	1
1:A:181:PHE:CE2	1:A:214:LEU:HD23	0.41	2.50	19	1
1:A:83:VAL:HG23	1:A:84:THR:N	0.41	2.30	8	4
1:A:89:LEU:O	1:A:91:ILE:N	0.41	2.54	1	1
1:A:97:SER:HB3	1:A:100:ILE:HD11	0.41	1.92	3	1
1:A:189:VAL:HB	1:A:209:ILE:HG23	0.41	1.92	4	1
1:A:172:LEU:CD1	1:A:176:PHE:CE2	0.41	3.03	5	1
1:A:45:THR:HB	1:A:46:PRO:CD	0.41	2.46	6	1
1:A:69:MET:SD	1:A:105:ALA:HB1	0.41	2.54	10	1
1:A:45:THR:HG22	1:A:47:TYR:CD1	0.41	2.50	19	1
1:A:53:VAL:O	1:A:53:VAL:CG1	0.41	2.68	19	1
1:A:32:ILE:O	1:A:58:VAL:HG23	0.41	2.15	2	1
1:A:87:ILE:CG2	1:A:109:LEU:CD2	0.41	2.99	5	1
1:A:192:ARG:HG3	1:A:193:LEU:N	0.41	2.30	17	3
1:A:89:LEU:HD11	1:A:112:LEU:HD13	0.41	1.93	13	1
1:A:14:VAL:HG11	1:A:24:LEU:HD21	0.41	1.91	21	1
1:A:186:ILE:O	1:A:190:LEU:N	0.41	2.48	21	1
1:A:71:PHE:CE2	1:A:75:VAL:CG1	0.41	3.00	3	1
1:A:91:ILE:HG21	1:A:100:ILE:HB	0.41	1.91	9	1
1:A:20:ALA:HB1	1:A:22:ILE:HD11	0.41	1.92	16	1
1:A:45:THR:OG1	1:A:46:PRO:HD2	0.41	2.16	16	1
1:A:91:ILE:CD1	1:A:91:ILE:O	0.41	2.69	17	1
1:A:89:LEU:CB	1:A:92:LEU:HD23	0.41	2.42	19	1
1:A:91:ILE:HG21	1:A:100:ILE:CG2	0.41	2.45	19	1
1:A:91:ILE:HB	1:A:100:ILE:HG21	0.41	1.92	5	2
1:A:190:LEU:O	1:A:194:GLY:N	0.41	2.52	11	1
1:A:120:ASP:N	1:A:121:PRO:HD2	0.41	2.31	12	1
1:A:47:TYR:OH	1:A:77:HIS:CE1	0.41	2.74	7	1
1:A:210:ILE:HD12	1:A:213:LEU:HD12	0.41	1.92	9	1
1:A:186:ILE:N	1:A:186:ILE:CD1	0.41	2.73	12	1
1:A:97:SER:H	1:A:100:ILE:HD11	0.41	1.74	13	1
1:A:65:LYS:N	1:A:66:PRO:CD	0.41	2.84	19	1
1:A:73:THR:HG22	1:A:148:TYR:O	0.41	2.16	1	1
1:A:147:LEU:O	1:A:148:TYR:CG	0.41	2.74	3	1
1:A:90:ASP:O	1:A:95:ALA:CB	0.41	2.69	9	1
1:A:39:PHE:CD1	1:A:39:PHE:O	0.41	2.74	10	1
1:A:107:ILE:HG23	1:A:108:SER:N	0.41	2.30	17	1
1:A:185:LYS:CE	1:A:213:LEU:HD22	0.41	2.45	17	1
1:A:24:LEU:HD23	1:A:37:GLY:HA2	0.41	1.91	19	1
1:A:22:ILE:HD13	1:A:22:ILE:H	0.41	1.73	20	1
1:A:22:ILE:N	1:A:22:ILE:CD1	0.41	2.82	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:145:THR:HG22	1:A:149:ALA:CB	0.41	2.46	20	1
1:A:58:VAL:O	1:A:58:VAL:CG2	0.41	2.68	21	1
1:A:69:MET:CE	1:A:105:ALA:CB	0.41	2.99	21	1
1:A:89:LEU:CD1	1:A:112:LEU:CD1	0.41	2.99	2	1
1:A:99:VAL:O	1:A:100:ILE:HB	0.41	2.16	7	2
1:A:64:PHE:CD2	1:A:64:PHE:O	0.41	2.74	5	1
1:A:206:ALA:O	1:A:209:ILE:HB	0.41	2.16	13	1
1:A:34:HIS:CD2	1:A:56:ILE:O	0.41	2.74	20	1
1:A:50:GLY:O	1:A:52:PHE:CE2	0.40	2.74	3	1
1:A:130:TYR:CZ	1:A:137:PHE:CD1	0.40	3.09	10	1
1:A:81:SER:C	1:A:82:SER:HG	0.40	2.18	17	1
1:A:120:ASP:CB	1:A:121:PRO:HD3	0.40	2.45	17	1
1:A:169:ASP:OD1	1:A:170:HIS:CG	0.40	2.73	18	1
1:A:61:GLU:O	1:A:62:TYR:CD2	0.40	2.74	19	1
1:A:137:PHE:O	1:A:141:ALA:HB2	0.40	2.16	21	1
1:A:21:HIS:O	1:A:39:PHE:CD2	0.40	2.75	1	1
1:A:120:ASP:CB	1:A:121:PRO:CD	0.40	2.99	12	1
1:A:20:ALA:O	1:A:21:HIS:HB2	0.40	2.16	16	1
1:A:181:PHE:CG	1:A:185:LYS:HE3	0.40	2.51	17	1
1:A:99:VAL:O	1:A:101:THR:N	0.40	2.54	19	1
1:A:69:MET:HE2	1:A:105:ALA:HB3	0.40	1.93	21	1
1:A:71:PHE:CD1	1:A:80:ILE:HD11	0.40	2.52	3	1
1:A:39:PHE:CD1	1:A:110:GLN:OE1	0.40	2.75	6	1
1:A:77:HIS:CG	1:A:78:PRO:HD2	0.40	2.51	7	1
1:A:47:TYR:CD1	1:A:145:THR:HG21	0.40	2.51	8	1
1:A:80:ILE:CD1	1:A:109:LEU:CD2	0.40	2.99	9	1
1:A:189:VAL:O	1:A:193:LEU:CD1	0.40	2.70	11	1
1:A:17:ASP:O	1:A:19:ALA:N	0.40	2.54	4	2
1:A:181:PHE:CE1	1:A:213:LEU:O	0.40	2.74	5	1
1:A:52:PHE:CD1	1:A:52:PHE:O	0.40	2.74	8	1
1:A:89:LEU:CD2	1:A:108:SER:CB	0.40	3.00	8	1
1:A:192:ARG:HG3	1:A:193:LEU:HD13	0.40	1.93	11	1
1:A:91:ILE:HG23	1:A:92:LEU:N	0.40	2.31	12	1
1:A:205:THR:O	1:A:209:ILE:CG1	0.40	2.69	14	1
1:A:52:PHE:CD1	1:A:52:PHE:N	0.40	2.90	1	1
1:A:18:PRO:O	1:A:21:HIS:CD2	0.40	2.75	9	1
1:A:181:PHE:O	1:A:182:GLU:O	0.40	2.39	12	1
1:A:32:ILE:HG13	1:A:33:HIS:N	0.40	2.31	13	1
1:A:170:HIS:CE1	1:A:171:ASP:OD1	0.40	2.74	14	1
1:A:172:LEU:HD11	1:A:176:PHE:CE2	0.40	2.52	14	1
1:A:84:THR:HG22	1:A:84:THR:O	0.40	2.16	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:56:ILE:HD11	1:A:102:LEU:HD21	0.40	1.92	19	1
1:A:74:LYS:HE3	1:A:148:TYR:CE2	0.40	2.51	19	1
1:A:176:PHE:O	1:A:181:PHE:O	0.40	2.40	19	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	187/215 (87%)	148±4 (79±2%)	26±3 (14±2%)	13±3 (7±2%)	2	16
All	All	3927/4515 (87%)	3106 (79%)	542 (14%)	279 (7%)	2	16

All 68 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	81	SER	16
1	A	100	ILE	15
1	A	43	PRO	12
1	A	74	LYS	12
1	A	62	TYR	11
1	A	33	HIS	9
1	A	49	GLY	8
1	A	64	PHE	8
1	A	91	ILE	8
1	A	83	VAL	8
1	A	169	ASP	8
1	A	59	PRO	7
1	A	94	ASN	7
1	A	101	THR	7
1	A	93	ARG	7
1	A	85	GLY	7
1	A	182	GLU	7
1	A	48	GLU	6
1	A	97	SER	6

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Mol	Chain	Res	Type	Models (Total)
1	A	95	ALA	6
1	A	71	PHE	5
1	A	72	ASP	5
1	A	121	PRO	5
1	A	63	PRO	5
1	A	82	SER	5
1	A	31	ASP	5
1	A	29	GLU	4
1	A	60	MET	4
1	A	90	ASP	3
1	A	16	ASP	3
1	A	75	VAL	3
1	A	47	TYR	3
1	A	99	VAL	3
1	A	61	GLU	3
1	A	18	PRO	2
1	A	28	SER	2
1	A	148	TYR	2
1	A	19	ALA	2
1	A	20	ALA	2
1	A	67	PRO	2
1	A	2	SER	2
1	A	118	PRO	2
1	A	115	SER	2
1	A	120	ASP	2
1	A	181	PHE	2
1	A	21	HIS	2
1	A	32	ILE	2
1	A	180	GLY	2
1	A	17	ASP	1
1	A	80	ILE	1
1	A	195	VAL	1
1	A	122	GLN	1
1	A	65	LYS	1
1	A	76	TYR	1
1	A	30	SER	1
1	A	89	LEU	1
1	A	116	PRO	1
1	A	96	TRP	1
1	A	132	ARG	1
1	A	86	ALA	1
1	A	123	ASP	1

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Mol	Chain	Res	Type	Models (Total)
1	A	214	LEU	1
1	A	22	ILE	1
1	A	42	PRO	1
1	A	46	PRO	1
1	A	73	THR	1
1	A	179	GLN	1
1	A	149	ALA	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	166/190 (87%)	116±4 (70±2%)	50±4 (30±2%)	<b>1</b> <b>16</b>
All	All	3486/3990 (87%)	2437 (70%)	1049 (30%)	<b>1</b> <b>16</b>

All 140 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	35	LEU	21
1	A	173	ILE	21
1	A	186	ILE	21
1	A	80	ILE	20
1	A	189	VAL	20
1	A	36	LYS	18
1	A	109	LEU	17
1	A	215	LYS	17
1	A	6	ARG	16
1	A	45	THR	16
1	A	143	LEU	16
1	A	89	LEU	14
1	A	99	VAL	14
1	A	134	ARG	14
1	A	131	LEU	14
1	A	91	ILE	13
1	A	51	LYS	13
1	A	79	ASN	13

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Mol	Chain	Res	Type	Models (Total)
1	A	96	TRP	12
1	A	144	TRP	12
1	A	188	GLU	12
1	A	97	SER	12
1	A	9	LYS	12
1	A	69	MET	12
1	A	3	ARG	12
1	A	33	HIS	11
1	A	146	ARG	11
1	A	208	ARG	11
1	A	5	LYS	11
1	A	148	TYR	11
1	A	60	MET	11
1	A	71	PHE	11
1	A	65	LYS	10
1	A	73	THR	10
1	A	76	TYR	10
1	A	129	HIS	10
1	A	214	LEU	10
1	A	68	LYS	10
1	A	74	LYS	10
1	A	70	GLN	10
1	A	139	LYS	10
1	A	25	GLU	9
1	A	28	SER	9
1	A	72	ASP	9
1	A	103	LYS	9
1	A	128	GLN	9
1	A	132	ARG	9
1	A	211	GLU	9
1	A	136	SER	9
1	A	174	ASP	9
1	A	137	PHE	9
1	A	87	ILE	9
1	A	61	GLU	9
1	A	62	TYR	8
1	A	77	HIS	8
1	A	93	ARG	8
1	A	17	ASP	8
1	A	32	ILE	8
1	A	117	GLU	8
1	A	207	ASN	8

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Mol	Chain	Res	Type	Models (Total)
1	A	23	THR	7
1	A	55	ASP	7
1	A	114	GLN	7
1	A	184	ASP	7
1	A	48	GLU	7
1	A	15	LYS	7
1	A	64	PHE	7
1	A	102	LEU	7
1	A	135	GLU	7
1	A	171	ASP	7
1	A	192	ARG	7
1	A	81	SER	7
1	A	122	GLN	7
1	A	8	MET	6
1	A	57	GLU	6
1	A	82	SER	6
1	A	133	ASP	6
1	A	2	SER	6
1	A	21	HIS	6
1	A	110	GLN	6
1	A	38	THR	6
1	A	26	PHE	6
1	A	181	PHE	6
1	A	108	SER	6
1	A	140	THR	6
1	A	22	ILE	6
1	A	16	ASP	5
1	A	29	GLU	5
1	A	40	LEU	5
1	A	106	LEU	5
1	A	123	ASP	5
1	A	169	ASP	5
1	A	130	TYR	5
1	A	119	ASN	5
1	A	179	GLN	5
1	A	30	SER	5
1	A	191	ARG	5
1	A	88	CYS	4
1	A	125	GLU	4
1	A	176	PHE	4
1	A	183	LYS	4
1	A	138	ASN	4

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Mol	Chain	Res	Type	Models (Total)
1	A	147	LEU	4
1	A	193	LEU	4
1	A	145	THR	4
1	A	12	GLN	4
1	A	104	SER	4
1	A	120	ASP	4
1	A	10	GLU	3
1	A	210	ILE	3
1	A	24	LEU	3
1	A	90	ASP	3
1	A	7	ILE	3
1	A	39	PHE	3
1	A	47	TYR	3
1	A	84	THR	3
1	A	94	ASN	3
1	A	178	SER	3
1	A	34	HIS	3
1	A	31	ASP	3
1	A	175	GLU	3
1	A	203	ASN	3
1	A	115	SER	2
1	A	182	GLU	2
1	A	112	LEU	2
1	A	92	LEU	2
1	A	172	LEU	2
1	A	53	VAL	2
1	A	170	HIS	2
1	A	185	LYS	2
1	A	107	ILE	1
1	A	101	THR	1
1	A	177	GLU	1
1	A	100	ILE	1
1	A	195	VAL	1
1	A	212	GLU	1
1	A	83	VAL	1
1	A	54	VAL	1
1	A	56	ILE	1
1	A	204	ASN	1

### 6.3.3 RNA

There are no RNA molecules in this entry.

## 6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided