Full wwPDB NMR Structure Validation Report (i)

Apr 21, 2024 – 05:01 PM EDT

PDB ID	:	2K8M
Title	:	S100A13-C2A binary complex structure
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Deposited on	:	2008-09-14

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

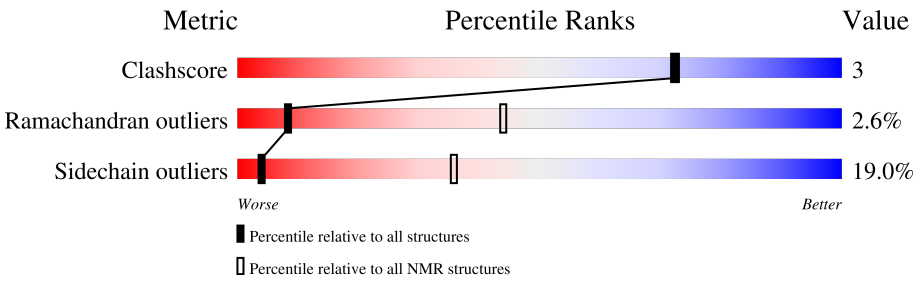
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Mol	Chain	Length	Quality of chain
1	A	128	77% 22% •
1	D	128	75% 24% •
2	B	98	80% 17% • •
2	C	98	83% 16% •

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 8 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:1-A:128, B:1-B:96, C:2-C:98, D:1-D:128 (449)	0.64	8

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 2 single-model clusters were found.

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

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7451 atoms, of which 3750 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Putative uncharacterized protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	128	2086	677	1042	169	195	3	0
1	D	128	2086	677	1042	169	195	3	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLU	-	expression tag	UNP Q6AI31
A	2	LYS	-	expression tag	UNP Q6AI31
D	1	GLU	-	expression tag	UNP Q6AI31
D	2	LYS	-	expression tag	UNP Q6AI31

- Molecule 2 is a protein called Protein S100-A13.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	B	98	1640	512	834	136	156	2	0
2	C	98	1639	512	832	136	157	2	0

4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

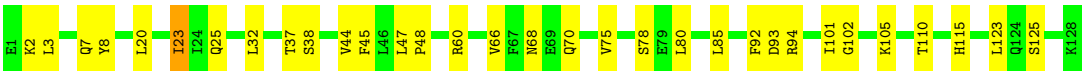
These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for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

• Molecule 1: Putative uncharacterized protein

Chain A:

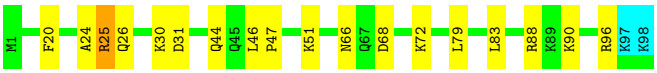
• Molecule 1: Putative uncharacterized protein

Chain D:



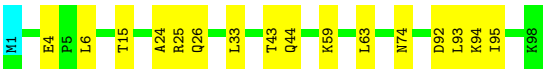
• Molecule 2: Protein S100-A13

Chain B:



• Molecule 2: Protein S100-A13

Chain C:



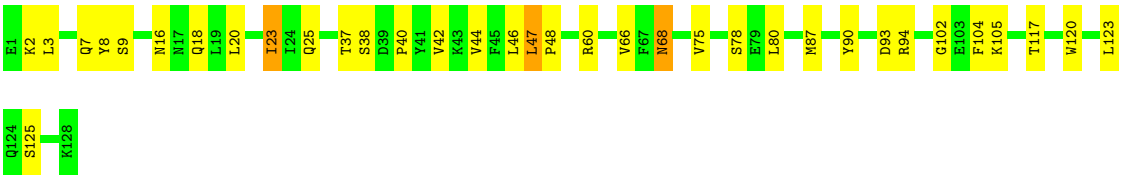
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

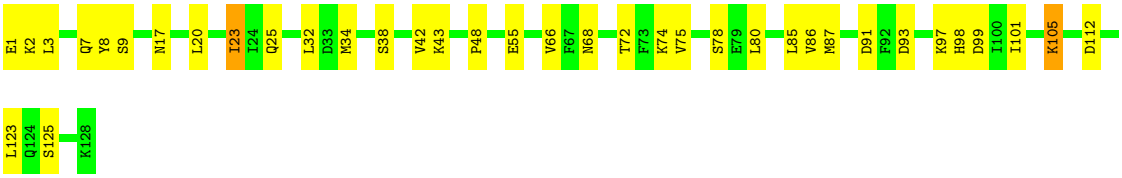
• Molecule 1: Putative uncharacterized protein

Chain A: 73% 25%



- Molecule 1: Putative uncharacterized protein

Chain D: 71% 27%

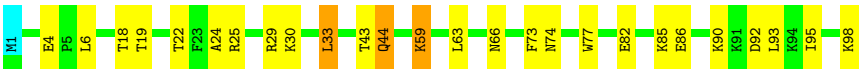


- Molecule 2: Protein S100-A13

Chain B: 77% 20%

- Molecule 2: Protein S100-A13

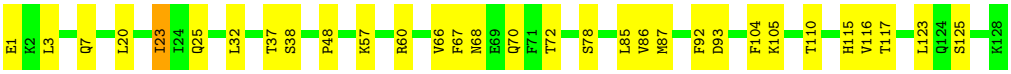
Chain C: 72% 23%



4.2.2 Score per residue for model 2

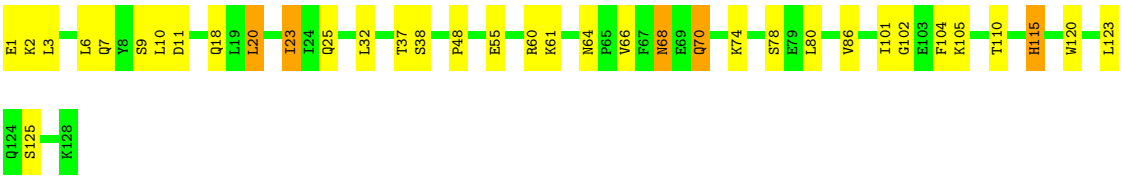
- Molecule 1: Putative uncharacterized protein

Chain A: 76% 23%



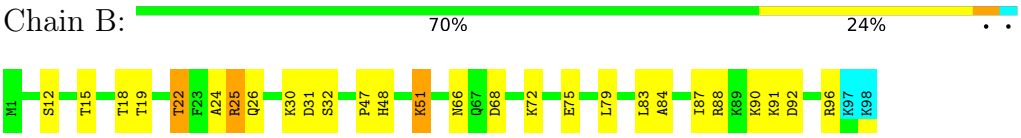
- Molecule 1: Putative uncharacterized protein

Chain D: 72% 24%



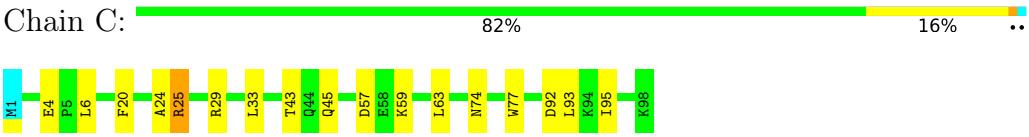
• Molecule 2: Protein S100-A13

Chain B:



• Molecule 2: Protein S100-A13

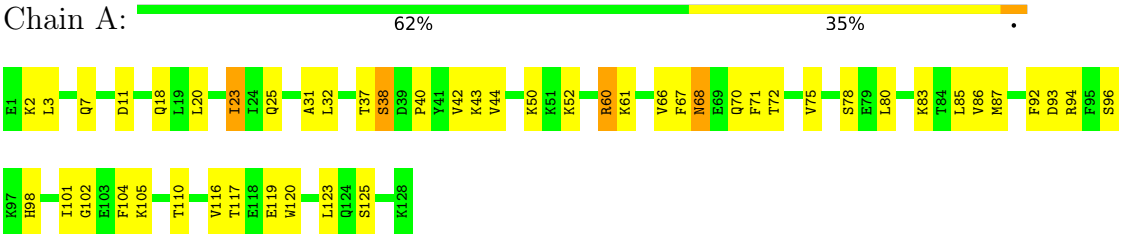
Chain C:



4.2.3 Score per residue for model 3

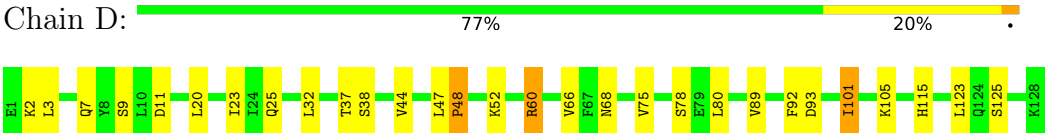
• Molecule 1: Putative uncharacterized protein

Chain A:



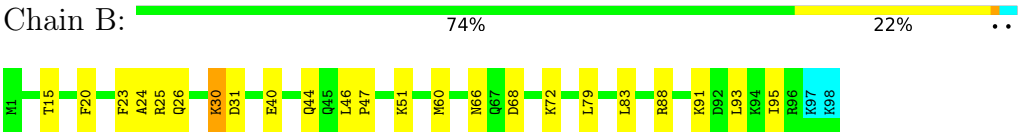
• Molecule 1: Putative uncharacterized protein

Chain D:



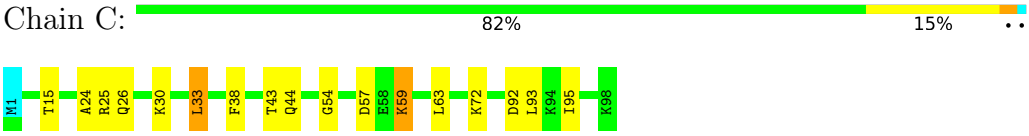
• Molecule 2: Protein S100-A13

Chain B:



• Molecule 2: Protein S100-A13

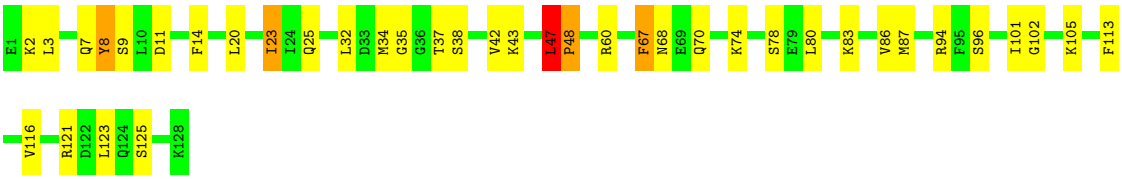
Chain C:



4.2.4 Score per residue for model 4

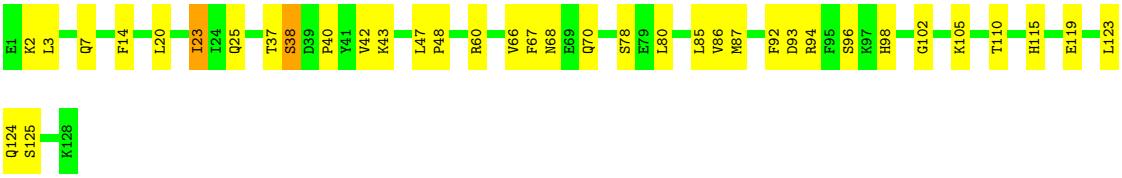
• Molecule 1: Putative uncharacterized protein

Chain A: 70% 27%



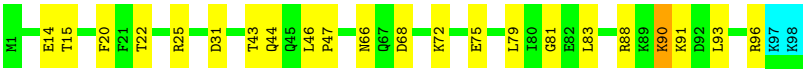
• Molecule 1: Putative uncharacterized protein

Chain D: 71% 27%



• Molecule 2: Protein S100-A13

Chain B: 76% 21%



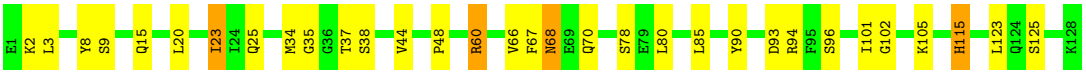
• Molecule 2: Protein S100-A13

Chain C: 80% 15%

4.2.5 Score per residue for model 5

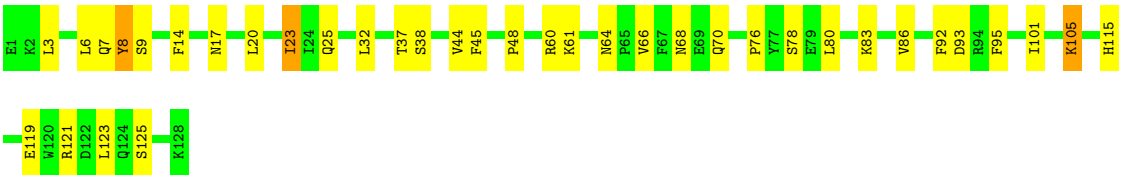
• Molecule 1: Putative uncharacterized protein

Chain A: 75% 22%



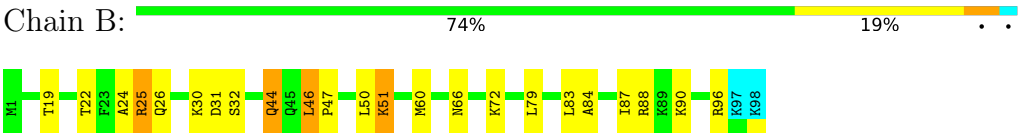
• Molecule 1: Putative uncharacterized protein

Chain D: 71% 27%



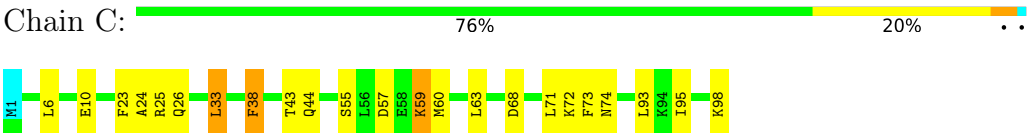
• Molecule 2: Protein S100-A13

Chain B:



• Molecule 2: Protein S100-A13

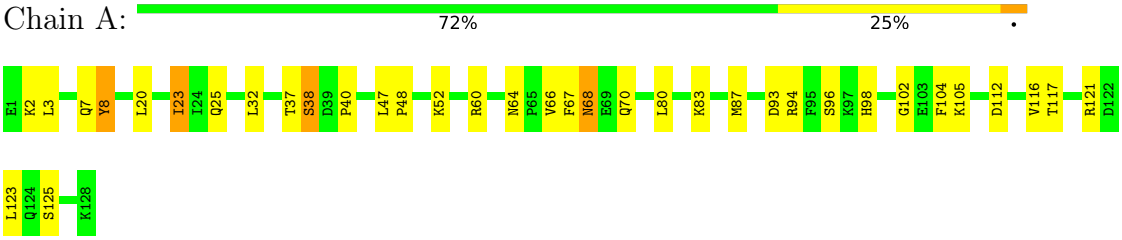
Chain C:



4.2.6 Score per residue for model 6

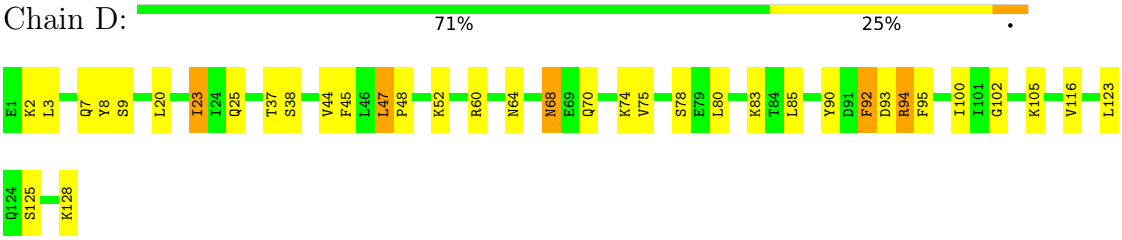
• Molecule 1: Putative uncharacterized protein

Chain A:



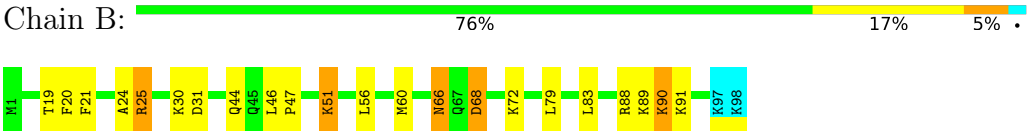
• Molecule 1: Putative uncharacterized protein

Chain D:



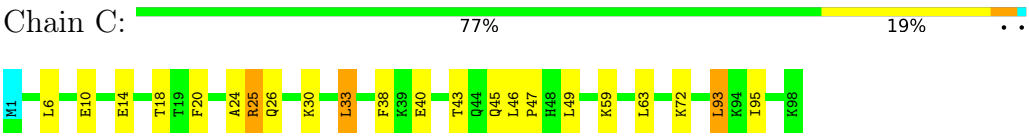
• Molecule 2: Protein S100-A13

Chain B:



• Molecule 2: Protein S100-A13

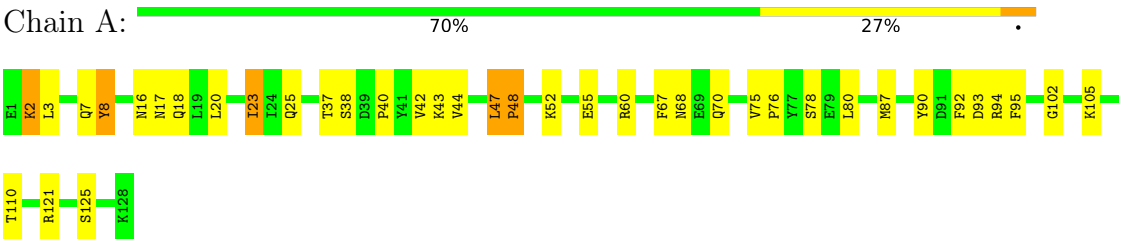
Chain C:



4.2.7 Score per residue for model 7

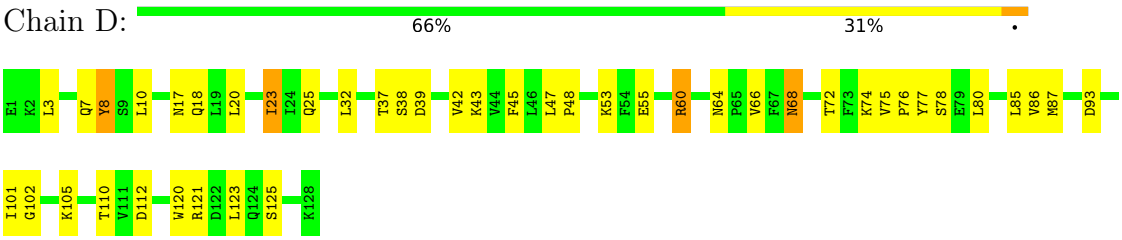
- Molecule 1: Putative uncharacterized protein

Chain A:



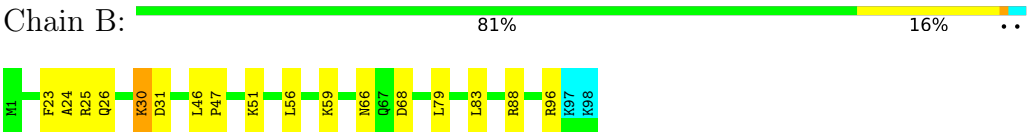
- Molecule 1: Putative uncharacterized protein

Chain D:



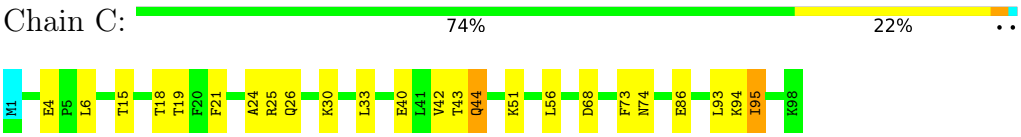
- Molecule 2: Protein S100-A13

Chain B:



- Molecule 2: Protein S100-A13

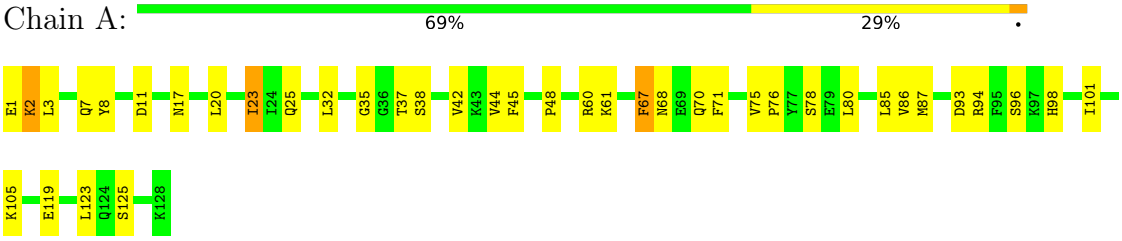
Chain C:



4.2.8 Score per residue for model 8 (medoid)

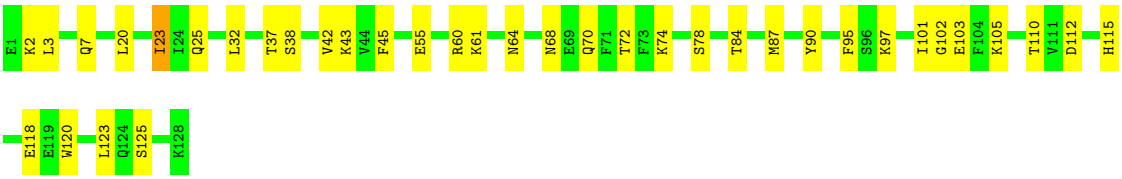
- Molecule 1: Putative uncharacterized protein

Chain A:



- Molecule 1: Putative uncharacterized protein

Chain D: 71% 28%

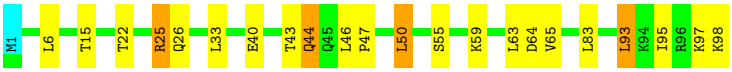


• Molecule 2: Protein S100-A13

Chain B: 68% 27%

• Molecule 2: Protein S100-A13

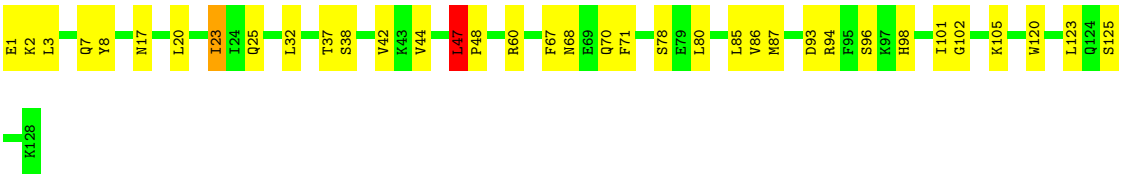
Chain C: 77% 18%



4.2.9 Score per residue for model 9

• Molecule 1: Putative uncharacterized protein

Chain A: 72% 27%

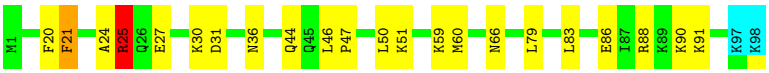


• Molecule 1: Putative uncharacterized protein

Chain D: 74% 24%

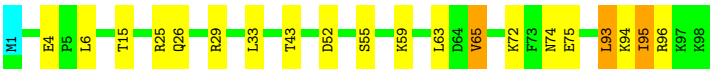
• Molecule 2: Protein S100-A13

Chain B: 76% 20%



• Molecule 2: Protein S100-A13

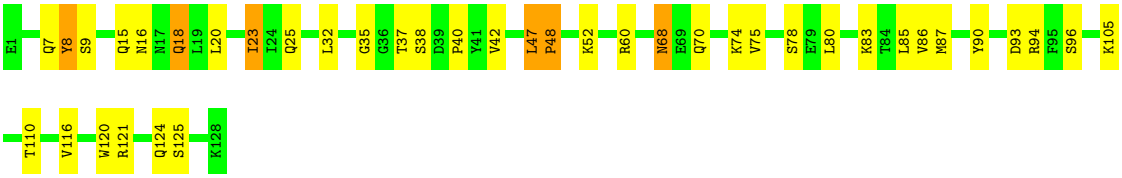
Chain C: 79% 17%



4.2.10 Score per residue for model 10

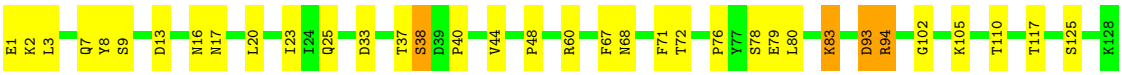
- Molecule 1: Putative uncharacterized protein

Chain A: 69% 27% 5%



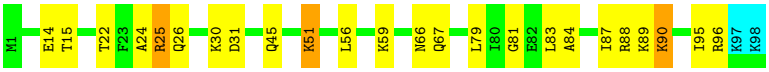
- Molecule 1: Putative uncharacterized protein

Chain D: 73% 24%



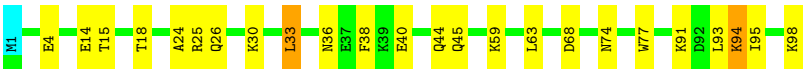
- Molecule 2: Protein S100-A13

Chain B: 73% 21%



- Molecule 2: Protein S100-A13

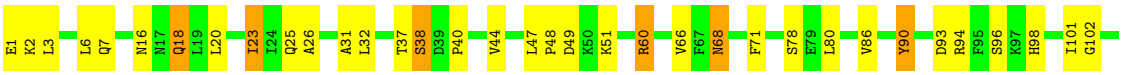
Chain C: 74% 22%

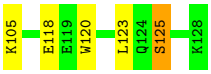


4.2.11 Score per residue for model 11

- Molecule 1: Putative uncharacterized protein

Chain A: 69% 26% 5%



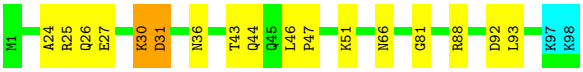


• Molecule 1: Putative uncharacterized protein

Chain D:

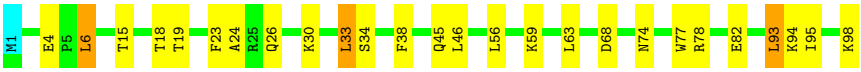
• Molecule 2: Protein S100-A13

Chain B:



• Molecule 2: Protein S100-A13

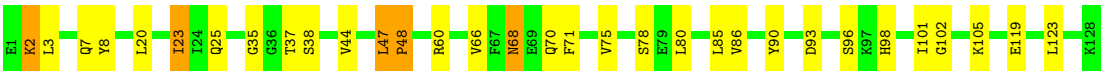
Chain C:



4.2.12 Score per residue for model 12

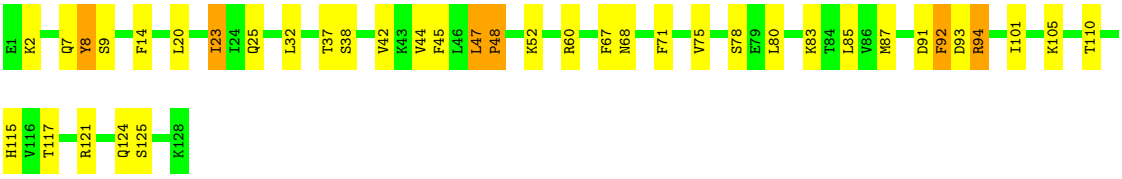
• Molecule 1: Putative uncharacterized protein

Chain A:



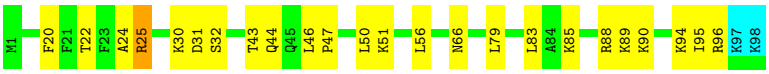
• Molecule 1: Putative uncharacterized protein

Chain D:



• Molecule 2: Protein S100-A13

Chain B:



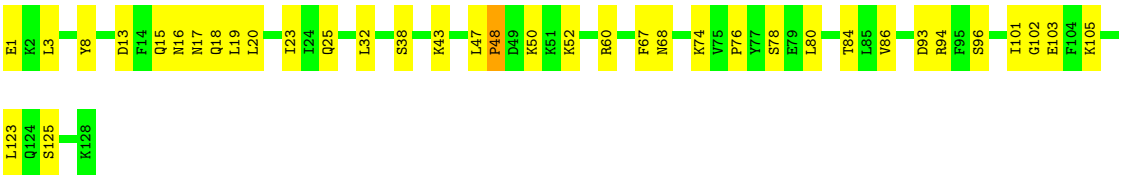
• Molecule 2: Protein S100-A13

Chain C:

4.2.13 Score per residue for model 13

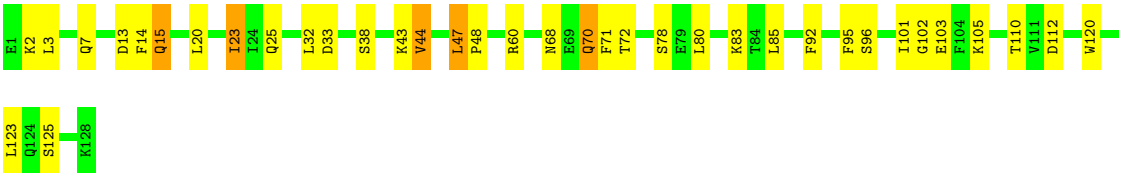
• Molecule 1: Putative uncharacterized protein

Chain A:



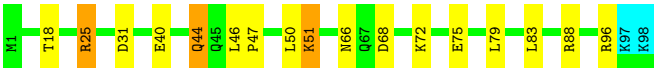
• Molecule 1: Putative uncharacterized protein

Chain D:



• Molecule 2: Protein S100-A13

Chain B:



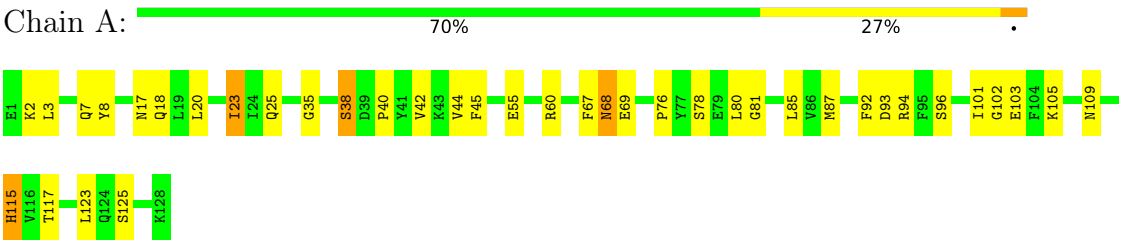
• Molecule 2: Protein S100-A13

Chain C:

4.2.14 Score per residue for model 14

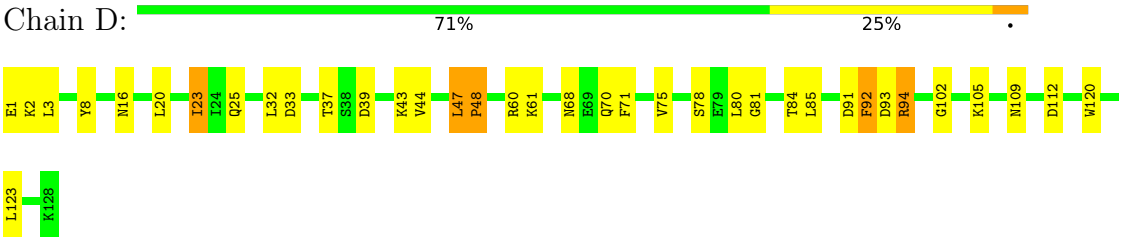
• Molecule 1: Putative uncharacterized protein

Chain A:



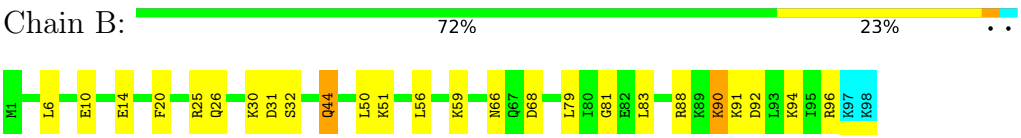
• Molecule 1: Putative uncharacterized protein

Chain D:



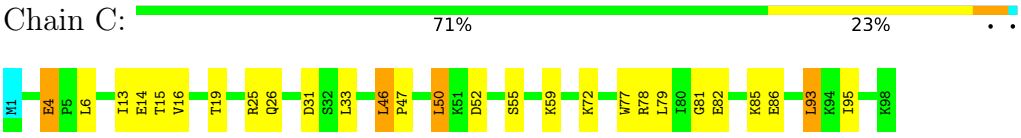
• Molecule 2: Protein S100-A13

Chain B:



• Molecule 2: Protein S100-A13

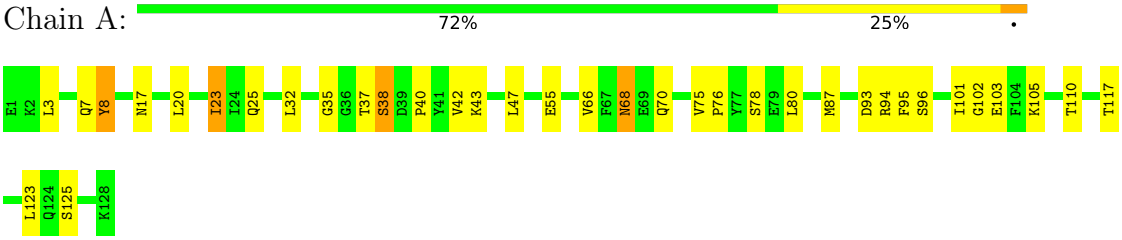
Chain C:



4.2.15 Score per residue for model 15

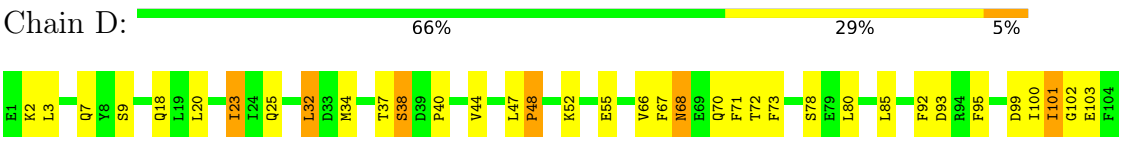
• Molecule 1: Putative uncharacterized protein

Chain A:



• Molecule 1: Putative uncharacterized protein

Chain D:



• Molecule 2: Protein S100-A13

Chain B:

• Molecule 2: Protein S100-A13

Chain C:

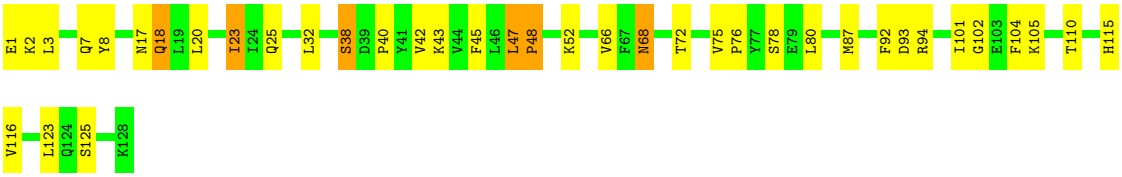
4.2.16 Score per residue for model 16

• Molecule 1: Putative uncharacterized protein

Chain A:

• Molecule 1: Putative uncharacterized protein

Chain D:

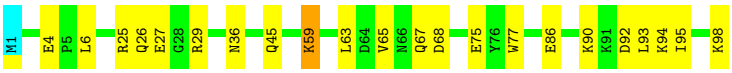


• Molecule 2: Protein S100-A13

Chain B:

• Molecule 2: Protein S100-A13

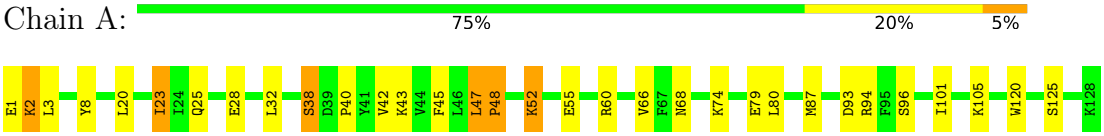
Chain C:



4.2.17 Score per residue for model 17

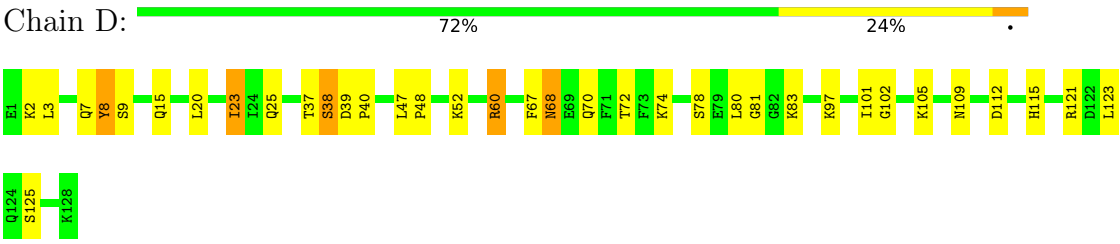
- Molecule 1: Putative uncharacterized protein

Chain A:



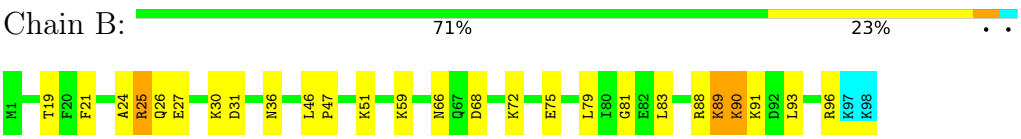
- Molecule 1: Putative uncharacterized protein

Chain D:



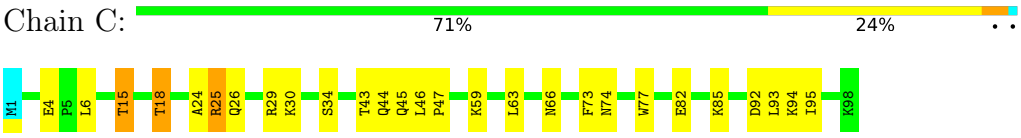
- Molecule 2: Protein S100-A13

Chain B:



- Molecule 2: Protein S100-A13

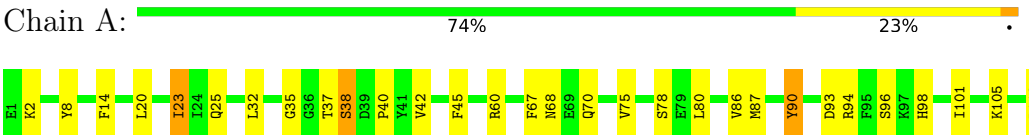
Chain C:



4.2.18 Score per residue for model 18

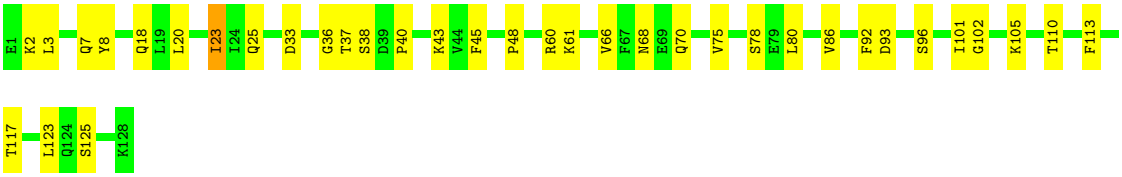
- Molecule 1: Putative uncharacterized protein

Chain A:



- Molecule 1: Putative uncharacterized protein

Chain D:

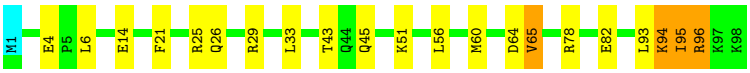


• Molecule 2: Protein S100-A13

Chain B:

• Molecule 2: Protein S100-A13

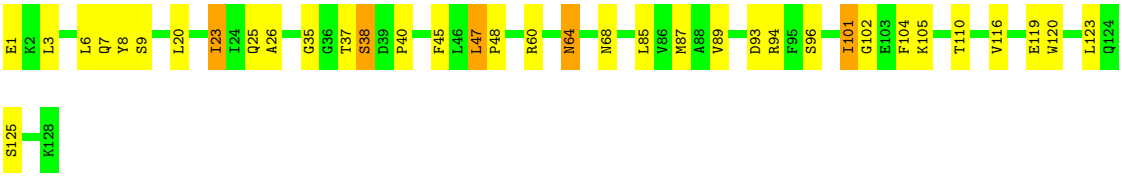
Chain C:



4.2.19 Score per residue for model 19

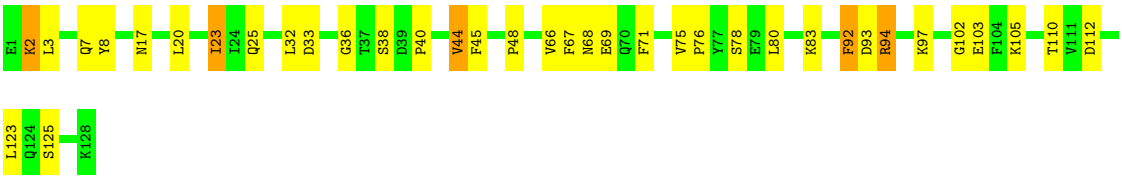
• Molecule 1: Putative uncharacterized protein

Chain A:



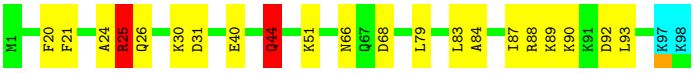
• Molecule 1: Putative uncharacterized protein

Chain D:



• Molecule 2: Protein S100-A13

Chain B:



• Molecule 2: Protein S100-A13

Chain C: 76% 22%

M1 T15 T22 R25 Q26 L33 T43 Q44 Q45 L50 K51 D52 D64 V65 N66 Q67 K72 F73 N74 E75 R78 E82 K85 L93 K94 I95 K98

4.2.20 Score per residue for model 20

- Molecule 1: Putative uncharacterized protein

Chain A: 66% 30%

E1 K2 L3 Q7 Y8 S9 N17 L20 I23 I24 Q25 L32 G35 G36 T37 S38 D39 P40 Y41 V42 K43 V44 F45 R60 N68 E69 Q70 F71 T72 V75 P76 Y77 S78 E79 L80 L85 V86 M87 F92 D93 R94 F95 S96 K97 H98 G102 K105

T110 T117 E118 E119 W120 L123 Q124 S125 K128

- Molecule 1: Putative uncharacterized protein

Chain D: 73% 25%

E1 K2 L3 Q7 L20 I23 L32 T37 S38 K43 V44 F45 L46 L47 P48 K52 E55 R60 N64 P65 V66 F67 N68 E69 Q70 F71 T72 S78 E79 L80 L85 D93 R94 F95 S96 K97 G102 K105 T110 H115 W120

L123 Q124 S125 K128

- Molecule 2: Protein S100-A13

Chain B: 72% 24%

M1 E14 R25 Q26 D31 N36 T43 L46 P47 L50 K51 L56 K59 N66 K72 L79 I80 G81 E82 L83 A84 I87 R88 K89 K90 K91 D92 L93 R96 K97 K98

- Molecule 2: Protein S100-A13

Chain C: 74% 21%

M1 P5 L6 E10 I13 V16 T19 F20 F21 R25 Q26 L33 T43 Q44 D52 S55 K59 L63 F73 N74 W77 D92 L93 K94 I95 K98

5 Refinement protocol and experimental data overview (i)

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

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

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

Software name	Classification	Version
CNS	structure solution	1.2
CNS	refinement	1.2
ARIA	structure solution	1.2 & 2.2

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	1044	1042	1039	8±2
1	D	1044	1042	1039	7±2
2	B	788	808	807	6±1
2	C	799	823	822	5±2
All	All	73500	74300	74140	505

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:D:3:LEU:HD23	1:D:123:LEU:HB3	0.75	1.59	9	18
1:A:3:LEU:HD23	1:A:123:LEU:HB3	0.75	1.58	11	16
1:D:3:LEU:HD22	1:D:102:GLY:HA3	0.68	1.65	18	16
1:A:23:ILE:O	1:A:68:ASN:HA	0.66	1.89	12	19
1:D:23:ILE:O	1:D:68:ASN:HA	0.66	1.91	6	20
1:A:52:LYS:HE2	1:A:75:VAL:HG23	0.65	1.66	7	2
2:C:24:ALA:O	2:C:30:LYS:HA	0.64	1.93	1	8
2:C:24:ALA:HB2	2:C:33:LEU:HD22	0.63	1.69	1	9
2:B:24:ALA:O	2:B:30:LYS:HA	0.62	1.95	19	15
2:B:79:LEU:O	2:B:83:LEU:HG	0.62	1.95	19	19
2:C:4:GLU:O	2:C:6:LEU:HG	0.61	1.95	15	11

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:47:LEU:HB2	1:A:48:PRO:CD	0.60	2.26	1	6
1:D:47:LEU:HB2	1:D:48:PRO:CD	0.59	2.27	11	2
1:D:92:PHE:O	1:D:94:ARG:HD3	0.58	1.99	6	4
1:D:13:ASP:OD1	1:D:15:GLN:HG2	0.58	1.98	13	1
2:C:50:LEU:HG	2:C:83:LEU:HD21	0.57	1.76	8	1
1:A:42:VAL:HB	1:A:87:MET:SD	0.56	2.40	17	12
2:C:59:LYS:O	2:C:63:LEU:HG	0.56	1.98	11	14
2:C:42:VAL:HG21	2:C:56:LEU:HG	0.56	1.75	7	2
1:A:3:LEU:HD22	1:A:102:GLY:HA3	0.55	1.78	11	15
2:B:81:GLY:HA2	2:C:77:TRP:CH2	0.55	2.37	4	6
2:B:46:LEU:N	2:B:47:PRO:HD3	0.55	2.16	7	16
2:C:51:LYS:HB3	1:D:36:GLY:N	0.54	2.17	18	2
1:A:47:LEU:HB2	1:A:48:PRO:HD2	0.54	1.79	1	10
1:D:100:ILE:HD12	1:D:128:LYS:HG3	0.53	1.79	15	2
2:B:40:GLU:O	2:B:44:GLN:HB2	0.53	2.03	13	2
1:A:35:GLY:O	2:B:94:LYS:HB2	0.52	2.04	8	4
2:C:40:GLU:O	2:C:44:GLN:HB3	0.52	2.03	8	1
1:D:52:LYS:HE2	1:D:75:VAL:HG23	0.52	1.82	6	1
2:B:21:PHE:O	2:B:25:ARG:HG2	0.52	2.05	19	5
1:D:86:VAL:HG12	1:D:105:LYS:HB3	0.51	1.80	5	2
1:D:42:VAL:HB	1:D:87:MET:SD	0.51	2.46	9	7
1:A:44:VAL:HG21	1:A:71:PHE:CE1	0.51	2.41	9	6
1:D:47:LEU:HB2	1:D:48:PRO:HD2	0.51	1.82	11	5
2:B:84:ALA:O	2:B:87:ILE:HG22	0.51	2.05	19	9
2:B:72:LYS:HB2	2:B:75:GLU:OE1	0.51	2.06	8	5
1:A:17:ASN:OD1	1:A:76:PRO:HA	0.50	2.07	7	6
1:D:38:SER:C	1:D:40:PRO:HD3	0.50	2.26	19	5
1:A:8:TYR:CE1	1:A:121:ARG:HB2	0.50	2.42	10	4
1:D:60:ARG:O	1:D:60:ARG:HD3	0.49	2.07	3	1
2:C:46:LEU:N	2:C:47:PRO:HD3	0.49	2.22	17	5
1:A:52:LYS:HE2	1:A:74:LYS:O	0.49	2.07	17	1
1:A:60:ARG:O	1:A:60:ARG:HD2	0.49	2.06	5	1
2:B:51:LYS:O	2:B:51:LYS:HD3	0.48	2.09	2	7
2:B:18:THR:O	2:B:22:THR:HB	0.48	2.08	2	1
2:B:12:SER:O	2:B:15:THR:HG22	0.48	2.09	18	2
2:C:82:GLU:O	2:C:85:LYS:HG2	0.48	2.08	1	4
2:C:72:LYS:HB2	2:C:75:GLU:OE1	0.47	2.09	9	1
1:A:13:ASP:OD1	1:A:15:GLN:HG2	0.47	2.09	13	1
2:C:64:ASP:O	2:C:65:VAL:HG22	0.47	2.09	18	1
1:A:23:ILE:H	1:A:23:ILE:HD13	0.47	1.69	1	1
2:B:27:GLU:OE2	2:B:36:ASN:HB3	0.47	2.09	16	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:13:ILE:O	2:C:16:VAL:HG22	0.47	2.09	20	2
2:B:89:LYS:HG2	2:B:90:LYS:N	0.47	2.24	17	1
2:C:64:ASP:OD2	2:C:67:GLN:HA	0.47	2.08	19	1
1:A:45:PHE:O	1:A:86:VAL:HB	0.47	2.09	18	1
1:A:38:SER:C	1:A:40:PRO:HD3	0.47	2.30	15	10
1:D:17:ASN:OD1	1:D:76:PRO:HA	0.47	2.10	19	5
2:B:23:PHE:HA	2:B:26:GLN:NE2	0.47	2.25	7	2
1:A:75:VAL:HG21	1:A:83:LYS:HG2	0.47	1.85	10	1
1:A:40:PRO:HA	1:A:90:TYR:O	0.47	2.10	11	5
1:D:3:LEU:O	1:D:3:LEU:HG	0.46	2.10	8	4
2:B:90:LYS:C	2:B:91:LYS:HD2	0.46	2.31	9	1
1:D:44:VAL:HG21	1:D:71:PHE:CE1	0.46	2.45	15	2
2:C:40:GLU:O	2:C:44:GLN:HB2	0.46	2.09	12	4
1:D:75:VAL:HG21	1:D:83:LYS:HG2	0.46	1.87	6	1
1:D:8:TYR:CE1	1:D:121:ARG:HB2	0.46	2.46	17	3
1:A:16:ASN:OD1	1:A:18:GLN:HG3	0.46	2.11	1	4
2:C:15:THR:O	2:C:18:THR:HG22	0.46	2.10	11	2
1:D:81:GLY:O	1:D:109:ASN:HB2	0.45	2.12	17	2
1:A:34:MET:O	2:B:91:LYS:HG3	0.45	2.12	4	1
2:C:94:LYS:O	2:C:95:ILE:HG12	0.45	2.12	20	5
2:C:52:ASP:OD2	2:C:55:SER:HB2	0.45	2.11	20	3
1:A:3:LEU:O	1:A:3:LEU:HG	0.45	2.12	9	4
2:C:78:ARG:O	2:C:82:GLU:HG2	0.45	2.11	14	5
1:A:81:GLY:O	1:A:109:ASN:HB2	0.44	2.12	14	1
1:A:39:ASP:CG	1:A:60:ARG:HA	0.44	2.32	20	2
2:C:6:LEU:HB3	2:C:10:GLU:CB	0.44	2.42	5	4
1:A:87:MET:HB3	1:A:104:PHE:CE2	0.44	2.48	6	1
1:D:11:ASP:OD2	1:D:20:LEU:HB3	0.44	2.12	2	1
1:D:89:VAL:HG13	1:D:101:ILE:HG12	0.44	1.89	3	1
1:A:2:LYS:O	1:A:2:LYS:HD3	0.44	2.13	17	5
1:A:89:VAL:HG13	1:A:101:ILE:HG12	0.44	1.89	19	1
1:A:60:ARG:O	1:A:60:ARG:HD3	0.44	2.12	3	2
2:C:93:LEU:O	2:C:94:LYS:HB2	0.44	2.13	11	1
2:C:65:VAL:HG23	2:C:66:ASN:H	0.44	1.72	19	1
2:B:66:ASN:OD1	2:B:68:ASP:HB3	0.44	2.13	6	1
2:B:86:GLU:O	2:B:90:LYS:HD2	0.44	2.12	9	1
1:D:20:LEU:HD11	1:D:70:GLN:HG3	0.43	1.89	2	1
2:C:75:GLU:HA	2:C:78:ARG:NH1	0.43	2.28	19	1
1:D:2:LYS:O	1:D:2:LYS:HD3	0.43	2.12	19	1
1:D:44:VAL:HG11	1:D:71:PHE:CE2	0.43	2.49	10	1
1:D:24:ILE:HA	1:D:68:ASN:OD1	0.43	2.13	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:ALA:HA	1:A:38:SER:OG	0.43	2.14	3	2
1:D:39:ASP:CG	1:D:60:ARG:HA	0.43	2.33	17	2
1:D:93:ASP:O	1:D:94:ARG:HB2	0.43	2.13	20	3
2:C:38:PHE:CE2	2:C:71:LEU:HG	0.43	2.49	5	1
1:D:91:ASP:HB2	1:D:101:ILE:HD11	0.43	1.88	11	2
2:C:91:LYS:HZ1	1:D:33:ASP:CG	0.43	2.17	10	1
1:A:16:ASN:OD1	1:A:18:GLN:HG2	0.43	2.13	11	1
2:B:72:LYS:HE2	2:B:75:GLU:OE2	0.43	2.13	4	1
1:A:1:GLU:HB3	1:A:125:SER:H	0.43	1.74	11	1
2:B:30:LYS:O	2:B:31:ASP:HB2	0.43	2.14	11	1
1:D:38:SER:O	1:D:40:PRO:HD3	0.42	2.12	15	4
1:A:87:MET:HB3	1:A:104:PHE:CE1	0.42	2.49	2	2
1:A:38:SER:O	1:A:40:PRO:HD3	0.42	2.14	3	3
1:D:18:GLN:OE1	1:D:72:THR:HG23	0.42	2.14	16	2
2:B:92:ASP:OD1	2:B:96:ARG:HD3	0.42	2.14	8	1
2:C:50:LEU:HD11	2:C:79:LEU:HD11	0.42	1.91	14	1
2:B:90:LYS:NZ	2:B:90:LYS:HB2	0.42	2.30	12	1
1:D:44:VAL:HG21	1:D:71:PHE:CD1	0.42	2.49	13	1
1:D:39:ASP:O	1:D:91:ASP:HA	0.42	2.14	14	1
1:D:8:TYR:CZ	1:D:121:ARG:HB2	0.42	2.50	5	1
2:C:81:GLY:O	2:C:85:LYS:HE3	0.42	2.15	14	1
1:D:44:VAL:HG11	1:D:71:PHE:CD2	0.42	2.48	14	1
2:C:45:GLN:C	2:C:47:PRO:HD3	0.42	2.35	17	1
1:A:3:LEU:HB3	1:A:123:LEU:CB	0.42	2.45	2	1
1:A:47:LEU:CB	1:A:48:PRO:HD2	0.42	2.44	13	3
1:A:35:GLY:HA2	2:B:95:ILE:O	0.42	2.14	10	1
1:A:26:ALA:O	1:A:64:ASN:HA	0.42	2.15	19	1
1:A:8:TYR:N	1:A:8:TYR:CD1	0.41	2.88	15	1
1:D:13:ASP:HB3	1:D:16:ASN:OD1	0.41	2.15	10	1
1:D:79:GLU:O	1:D:83:LYS:HE2	0.41	2.15	10	1
1:D:18:GLN:HB2	1:D:73:PHE:O	0.41	2.15	15	1
2:B:6:LEU:HB3	2:B:10:GLU:OE1	0.41	2.16	14	1
2:B:81:GLY:HA2	2:C:77:TRP:CZ2	0.41	2.50	17	1
1:D:44:VAL:HG21	1:D:71:PHE:CG	0.41	2.51	19	1
2:C:21:PHE:O	2:C:25:ARG:HG2	0.41	2.15	13	1
2:C:27:GLU:OE2	2:C:36:ASN:HB3	0.41	2.16	16	1
2:C:96:ARG:HD2	2:C:96:ARG:O	0.41	2.16	18	1
2:C:90:LYS:HB3	2:C:92:ASP:OD1	0.41	2.16	4	1
1:A:49:ASP:O	1:A:51:LYS:HG3	0.41	2.16	11	1
2:C:34:SER:O	2:C:38:PHE:HB2	0.41	2.15	11	1
1:D:47:LEU:CB	1:D:48:PRO:CD	0.41	2.99	13	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:70:GLU:O	2:C:72:LYS:HD2	0.41	2.16	13	1
2:C:64:ASP:O	2:C:66:ASN:N	0.41	2.54	19	1
1:D:47:LEU:CB	1:D:48:PRO:HD2	0.41	2.46	3	1
2:B:85:LYS:O	2:B:89:LYS:HB3	0.41	2.16	12	1
1:A:44:VAL:HG21	1:A:71:PHE:CD1	0.40	2.51	3	1
2:B:51:LYS:HD3	2:B:51:LYS:O	0.40	2.16	5	1
1:D:3:LEU:CD2	1:D:123:LEU:HB3	0.40	2.46	11	1
1:D:70:GLN:HG2	1:D:71:PHE:N	0.40	2.31	13	1
1:A:23:ILE:HD13	1:A:23:ILE:H	0.40	1.76	4	1
1:A:6:LEU:HD12	1:A:26:ALA:HB2	0.40	1.92	11	1
1:A:95:PHE:CG	2:B:51:LYS:HB2	0.40	2.51	15	1
2:C:59:LYS:HE2	1:D:34:MET:SD	0.40	2.57	15	1
1:D:32:LEU:HG	1:D:101:ILE:HD12	0.40	1.94	15	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	126/128 (98%)	106±2 (84±2%)	18±2 (14±2%)	2±1 (2±1%)	14	59
1	D	126/128 (98%)	108±2 (85±2%)	16±3 (13±2%)	2±1 (2±1%)	12	54
2	B	95/98 (97%)	77±2 (81±2%)	14±2 (15±2%)	4±1 (4±1%)	6	34
2	C	96/98 (98%)	79±2 (82±2%)	14±2 (14±2%)	4±1 (4±1%)	5	32
All	All	8860/9040 (98%)	7383 (83%)	1248 (14%)	229 (3%)	8	44

All 39 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	31	ASP	20
2	C	95	ILE	20
1	D	48	PRO	17
2	B	25	ARG	14
2	B	44	GLN	13

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Mol	Chain	Res	Type	Models (Total)
2	C	74	ASN	11
1	A	48	PRO	11
1	D	47	LEU	10
1	A	47	LEU	9
2	C	44	GLN	9
2	B	93	LEU	8
2	C	29	ARG	7
2	C	93	LEU	7
2	C	25	ARG	6
1	A	35	GLY	6
1	D	67	PHE	6
2	B	30	LYS	5
1	D	61	LYS	5
1	A	67	PHE	5
2	B	90	LYS	5
1	D	74	LYS	4
2	B	92	ASP	4
2	C	65	VAL	4
2	C	5	PRO	3
1	A	115	HIS	3
1	D	115	HIS	2
1	A	61	LYS	2
2	C	90	LYS	2
2	B	47	PRO	1
2	B	48	HIS	1
2	C	54	GLY	1
1	A	74	LYS	1
1	D	95	PHE	1
1	A	95	PHE	1
2	C	96	ARG	1
2	C	94	LYS	1
1	A	28	GLU	1
2	C	34	SER	1
2	C	52	ASP	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	115/115 (100%)	89±4 (77±3%)	26±4 (23±3%)	3 28
1	D	115/115 (100%)	88±3 (77±2%)	27±3 (23±2%)	3 27
2	B	89/91 (98%)	77±3 (86±3%)	12±3 (14±3%)	7 47
2	C	90/91 (99%)	78±2 (86±3%)	12±2 (14±3%)	7 47
All	All	8180/8240 (99%)	6627 (81%)	1553 (19%)	4 36

All 225 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	20	LEU	20
1	A	105	LYS	20
2	B	66	ASN	20
2	C	93	LEU	20
1	D	20	LEU	20
1	D	78	SER	20
1	D	105	LYS	20
1	A	23	ILE	19
1	A	25	GLN	19
1	A	38	SER	19
1	A	60	ARG	19
1	A	93	ASP	19
1	A	125	SER	19
2	B	51	LYS	19
2	B	88	ARG	19
1	D	7	GLN	19
1	D	25	GLN	19
1	D	80	LEU	19
1	D	125	SER	19
1	A	80	LEU	18
1	A	94	ARG	18
2	B	25	ARG	18
1	D	2	LYS	18
1	D	23	ILE	18
1	A	37	THR	17
1	A	78	SER	17
2	C	33	LEU	17
1	D	38	SER	17
2	C	25	ARG	17
1	A	96	SER	17
2	C	26	GLN	17
1	A	7	GLN	16

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Mol	Chain	Res	Type	Models (Total)
1	A	8	TYR	16
1	D	37	THR	16
1	D	60	ARG	16
1	A	2	LYS	15
2	C	43	THR	15
1	D	32	LEU	14
1	A	70	GLN	14
2	B	90	LYS	13
2	B	96	ARG	13
1	D	8	TYR	13
1	A	32	LEU	13
1	A	101	ILE	13
1	D	66	VAL	12
1	D	93	ASP	12
1	D	101	ILE	12
1	D	70	GLN	12
1	D	110	THR	12
2	B	20	PHE	11
2	B	26	GLN	11
1	D	85	LEU	11
2	B	68	ASP	11
1	D	92	PHE	11
1	D	45	PHE	11
2	C	92	ASP	10
1	D	9	SER	10
1	D	43	LYS	10
1	D	75	VAL	10
1	A	85	LEU	10
1	D	115	HIS	10
1	A	66	VAL	9
1	A	68	ASN	9
1	D	112	ASP	9
1	A	86	VAL	9
1	D	68	ASN	9
1	A	98	HIS	9
2	C	15	THR	9
2	B	59	LYS	9
1	A	117	THR	8
1	A	120	TRP	8
1	D	72	THR	8
1	A	67	PHE	8
1	A	43	LYS	8

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Mol	Chain	Res	Type	Models (Total)
1	A	75	VAL	7
2	B	22	THR	7
2	B	32	SER	7
2	B	72	LYS	7
2	C	73	PHE	7
2	C	98	LYS	7
1	D	55	GLU	7
1	A	1	GLU	7
1	A	110	THR	7
2	B	91	LYS	7
2	C	45	GLN	7
1	D	120	TRP	7
2	C	72	LYS	7
2	B	14	GLU	7
1	D	94	ARG	7
2	B	50	LEU	7
1	D	83	LYS	7
2	B	56	LEU	7
2	C	94	LYS	7
1	A	9	SER	6
2	C	59	LYS	6
1	D	1	GLU	6
1	D	97	LYS	6
1	A	92	PHE	6
1	A	116	VAL	6
1	D	64	ASN	6
2	B	60	MET	6
1	D	44	VAL	6
1	D	52	LYS	6
1	A	45	PHE	6
1	A	90	TYR	5
2	C	6	LEU	5
2	C	18	THR	5
2	C	19	THR	5
2	C	22	THR	5
2	C	86	GLU	5
1	D	86	VAL	5
2	B	15	THR	5
2	B	43	THR	5
1	D	14	PHE	5
2	C	68	ASP	5
2	B	21	PHE	5

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Mol	Chain	Res	Type	Models (Total)
2	C	14	GLU	5
1	D	95	PHE	5
1	A	44	VAL	4
2	C	4	GLU	4
2	C	66	ASN	4
1	A	115	HIS	4
2	B	19	THR	4
2	C	20	PHE	4
1	A	18	GLN	4
1	A	52	LYS	4
1	A	119	GLU	4
2	C	38	PHE	4
1	A	47	LEU	4
1	D	96	SER	4
2	B	44	GLN	4
2	B	89	LYS	4
1	A	55	GLU	4
1	D	103	GLU	4
1	D	117	THR	4
1	A	103	GLU	4
1	D	33	ASP	4
2	C	77	TRP	3
1	A	72	THR	3
2	C	57	ASP	3
1	D	6	LEU	3
1	D	18	GLN	3
1	D	74	LYS	3
1	A	11	ASP	3
1	A	83	LYS	3
2	C	55	SER	3
1	D	90	TYR	3
2	C	21	PHE	3
2	B	18	THR	3
2	C	50	LEU	3
1	D	84	THR	3
2	C	56	LEU	3
1	A	104	PHE	2
2	C	44	GLN	2
2	C	90	LYS	2
1	D	98	HIS	2
1	D	99	ASP	2
1	D	10	LEU	2

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Mol	Chain	Res	Type	Models (Total)
1	D	104	PHE	2
1	A	50	LYS	2
2	B	95	ILE	2
1	A	14	PHE	2
2	C	36	ASN	2
1	D	67	PHE	2
1	D	119	GLU	2
1	D	124	GLN	2
1	A	15	GLN	2
2	C	23	PHE	2
2	C	60	MET	2
1	A	64	ASN	2
1	A	112	ASP	2
1	D	116	VAL	2
2	C	65	VAL	2
1	A	74	LYS	2
1	A	124	GLN	2
1	A	118	GLU	2
2	C	46	LEU	2
2	C	31	ASP	2
1	D	15	GLN	2
2	B	12	SER	2
1	A	40	PRO	1
1	A	46	LEU	1
1	D	17	ASN	1
1	D	34	MET	1
1	D	91	ASP	1
1	A	57	LYS	1
2	B	40	GLU	1
1	D	11	ASP	1
1	A	113	PHE	1
2	C	47	PRO	1
1	A	34	MET	1
2	B	46	LEU	1
2	C	40	GLU	1
2	C	49	LEU	1
2	C	51	LYS	1
1	D	53	LYS	1
1	D	77	TYR	1
2	C	64	ASP	1
2	C	97	LYS	1
1	D	118	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	17	ASN	1
2	B	45	GLN	1
2	B	67	GLN	1
2	C	30	LYS	1
1	D	46	LEU	1
2	C	34	SER	1
2	C	91	LYS	1
1	A	19	LEU	1
1	A	84	THR	1
1	A	69	GLU	1
2	B	92	ASP	1
1	D	16	ASN	1
2	B	9	LEU	1
2	B	4	GLU	1
2	C	67	GLN	1
2	C	75	GLU	1
1	A	3	LEU	1
1	A	79	GLU	1
2	B	7	THR	1
2	B	31	ASP	1
2	C	96	ARG	1
1	D	113	PHE	1
1	A	6	LEU	1
1	D	69	GLU	1
2	B	36	ASN	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

No chemical shift data were provided