Full wwPDB NMR Structure Validation Report (i)

May 28, 2020 – 10:25 pm BST

PDB ID	:	2JW1
Title	:	Structural characterization of the type III pilotin-secretin interaction in Shigella flexneri by NMR spectroscopy
Authors	:	Okon, M.S.; Lario, P.I.; Creagh, L.; Jung, Y.M.T.; Maurelli, A.T.; Strynadka, N.C.J.; McIntosh, L.P.
Deposited on	:	2007-10-02

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

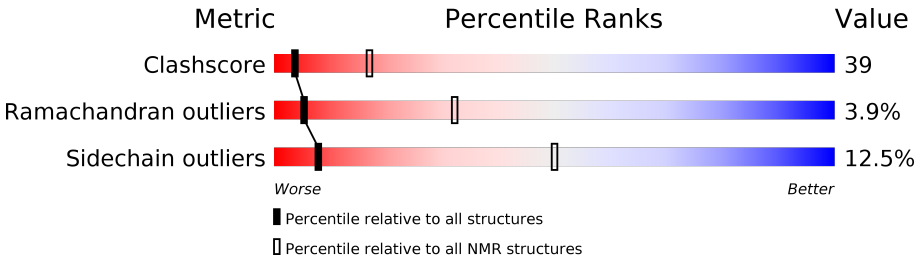
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 is 88%.

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	115	37% 43% 8% 12%
2	B	19	21% 53% 16% 11%

2 Ensemble composition and analysis

This entry contains 15 models. Model 15 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *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:34-A:119, A:125-A:139, B:554-B:570 (118)	0.22	15

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters and 3 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2123 atoms, of which 1066 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Lipoprotein mxiM.

Mol	Chain	Residues	Atoms						Trace
1	A	115	Total	C	H	N	O	S	0
			1828	582	922	148	171	5	

- Molecule 2 is a protein called Outer membrane protein mxiD.

Mol	Chain	Residues	Atoms					Trace
2	B	19	Total	C	H	N	O	0
			295	95	144	20	36	

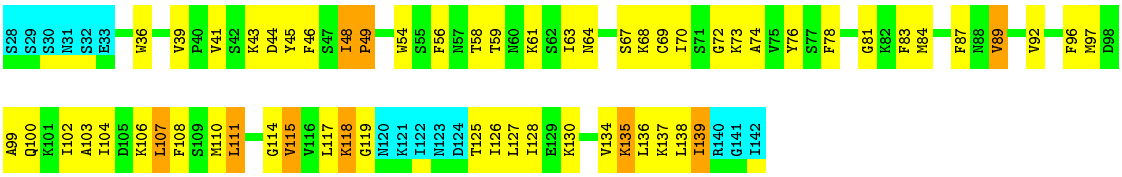
4 Residue-property plots

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: Lipoprotein mxiM

Chain A:



• Molecule 2: Outer membrane protein mxiD

Chain B:

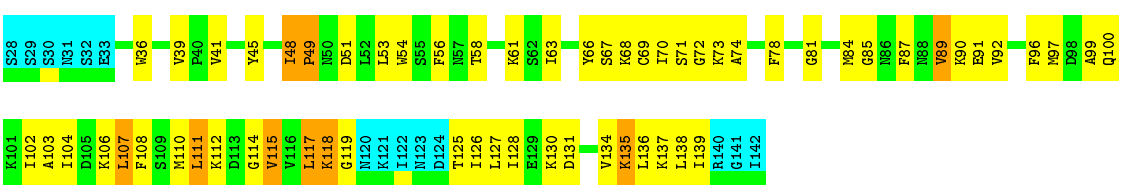
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

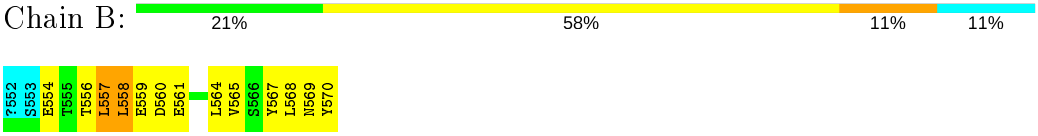
• Molecule 1: Lipoprotein mxiM

Chain A:



• Molecule 2: Outer membrane protein mxiD

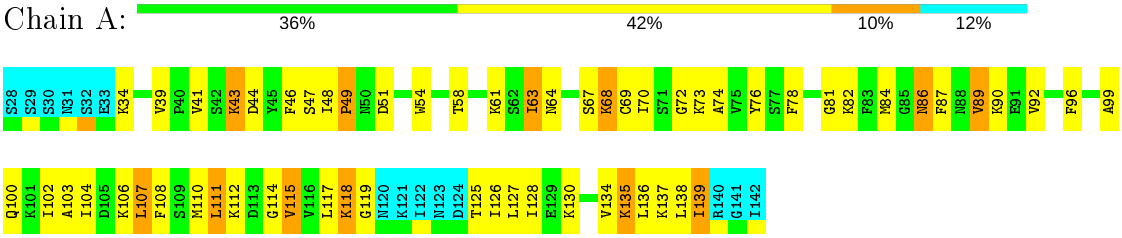
Chain B:



4.2.2 Score per residue for model 2

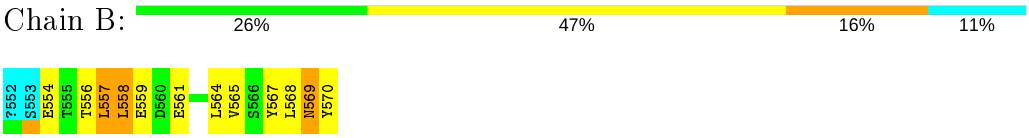
- Molecule 1: Lipoprotein mxiM

Chain A:



- Molecule 2: Outer membrane protein mxiD

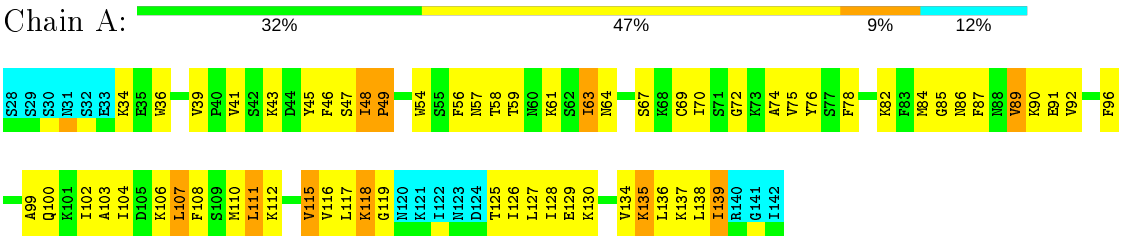
Chain B:



4.2.3 Score per residue for model 3

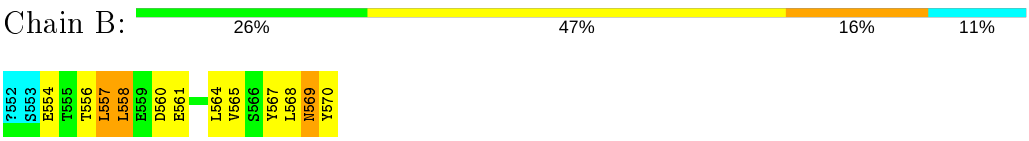
- Molecule 1: Lipoprotein mxiM

Chain A:



- Molecule 2: Outer membrane protein mxiD

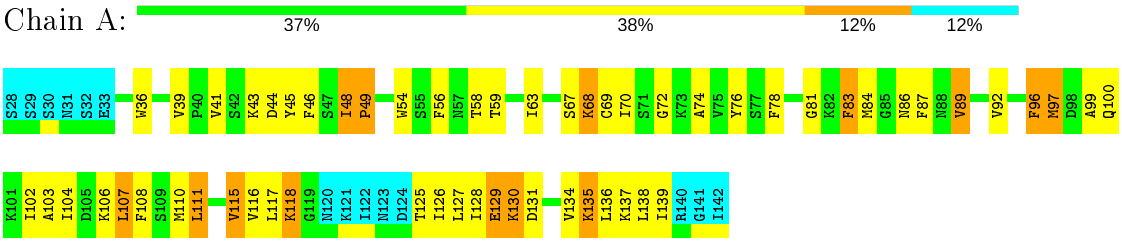
Chain B:



4.2.4 Score per residue for model 4

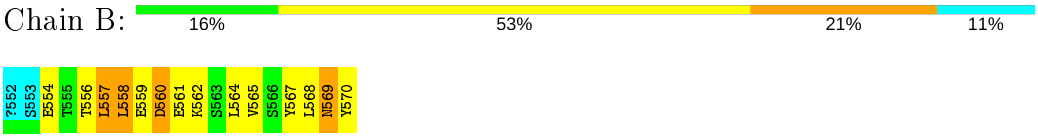
- Molecule 1: Lipoprotein mxiM

Chain A:



- Molecule 2: Outer membrane protein mxiD

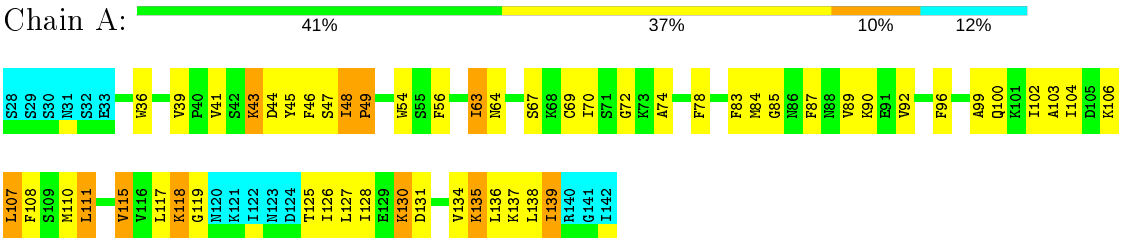
Chain B:



4.2.5 Score per residue for model 5

- Molecule 1: Lipoprotein mxiM

Chain A:



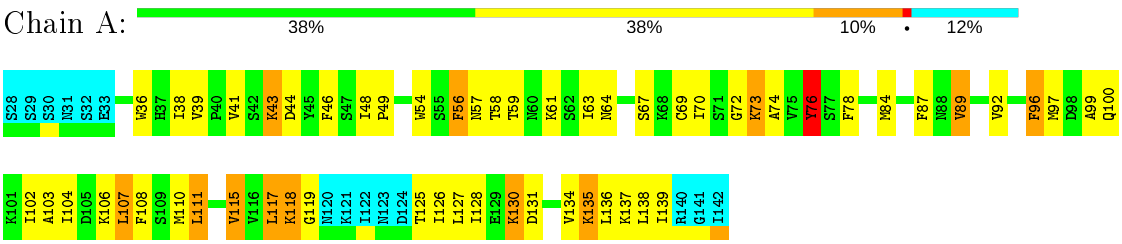
- Molecule 2: Outer membrane protein mxiD

Chain B:

4.2.6 Score per residue for model 6

- Molecule 1: Lipoprotein mxiM

Chain A:



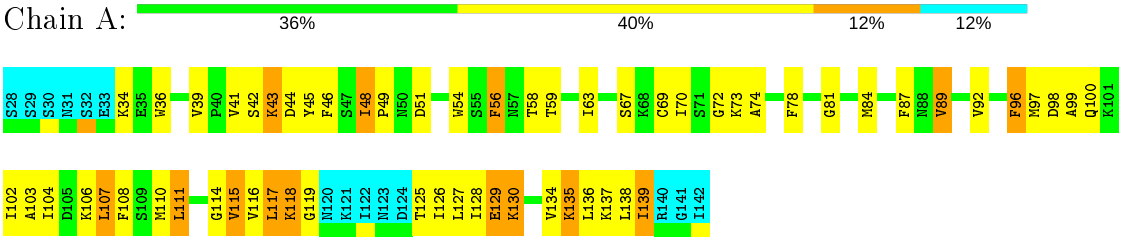
- Molecule 2: Outer membrane protein mxiD

Chain B:

4.2.7 Score per residue for model 7

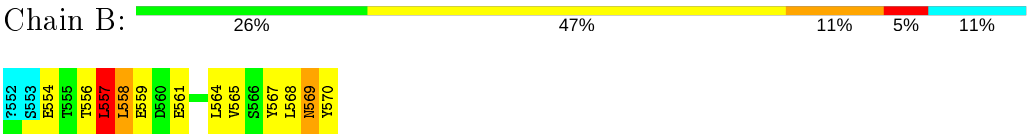
- Molecule 1: Lipoprotein mxiM

Chain A:



- Molecule 2: Outer membrane protein mxiD

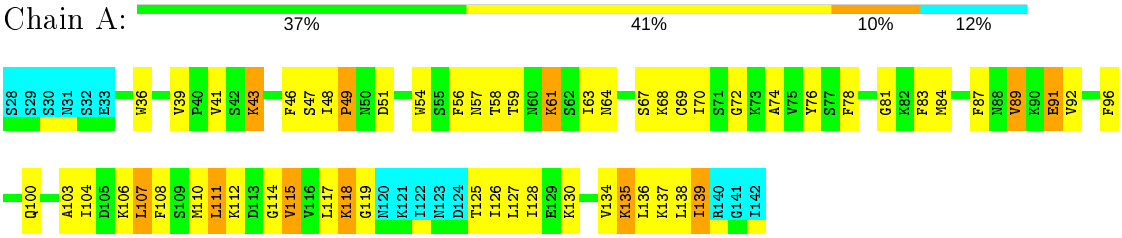
Chain B:



4.2.8 Score per residue for model 8

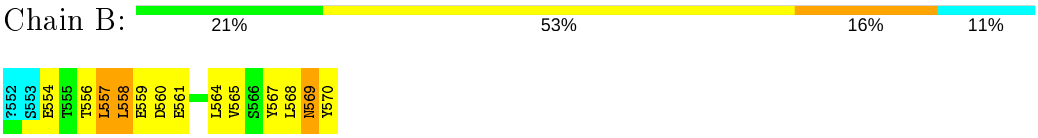
- Molecule 1: Lipoprotein mxiM

Chain A:



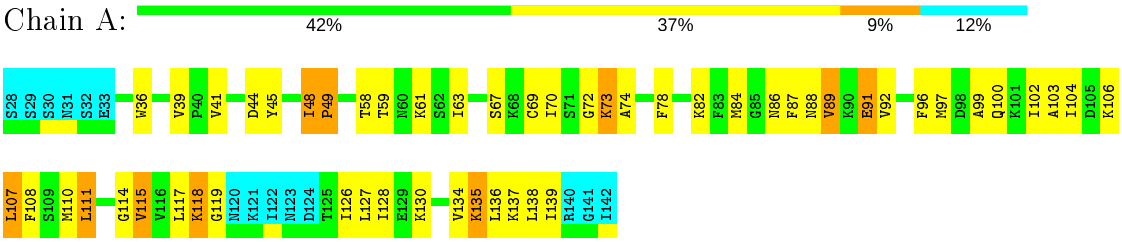
- Molecule 2: Outer membrane protein mxiD

Chain B:



4.2.9 Score per residue for model 9

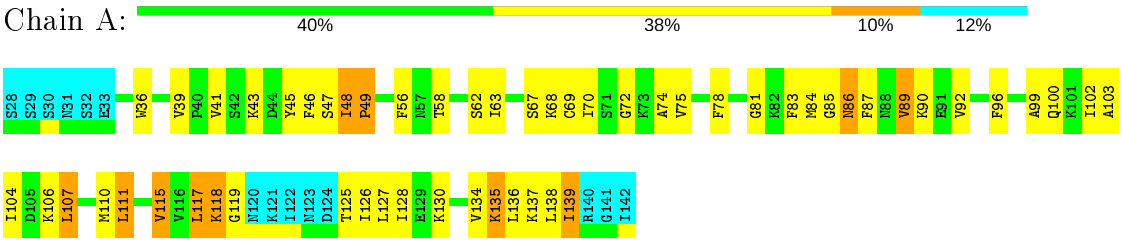
- Molecule 1: Lipoprotein mxiM



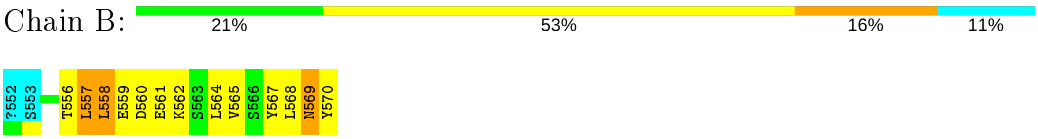
- Molecule 2: Outer membrane protein mxiD

4.2.10 Score per residue for model 10

- Molecule 1: Lipoprotein mxiM

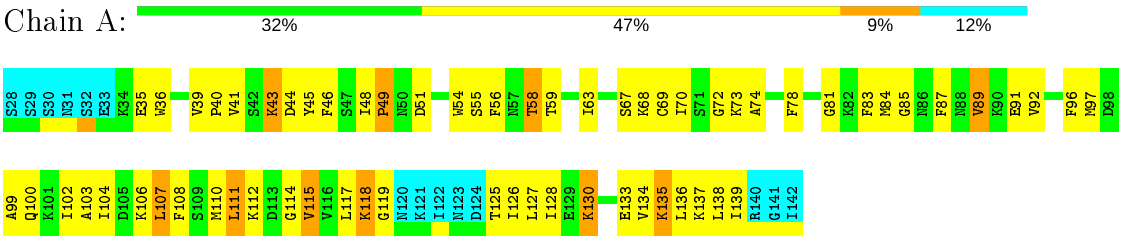


- Molecule 2: Outer membrane protein mxiD



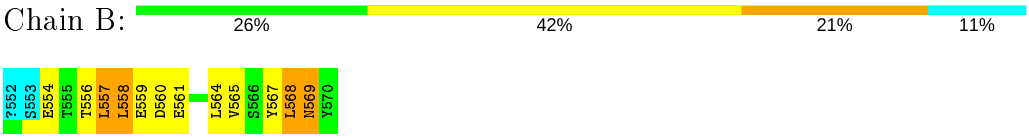
4.2.11 Score per residue for model 11

- Molecule 1: Lipoprotein mxiM



- Molecule 2: Outer membrane protein mxiD

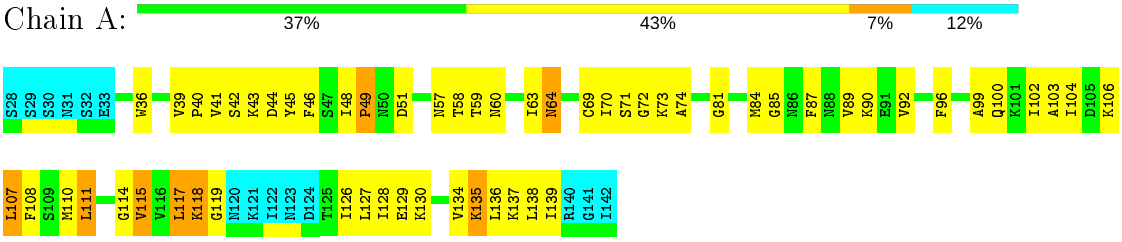
Chain B:



4.2.12 Score per residue for model 12

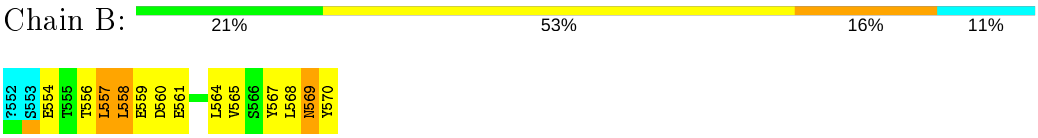
- Molecule 1: Lipoprotein mxiM

Chain A:



- Molecule 2: Outer membrane protein mxiD

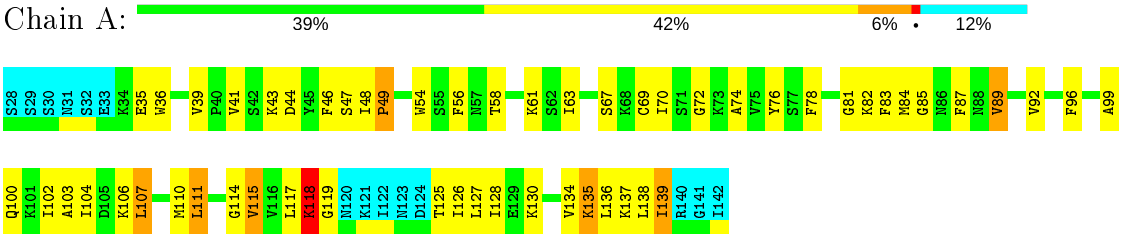
Chain B:



4.2.13 Score per residue for model 13

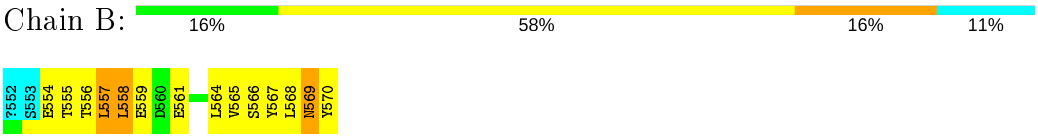
- Molecule 1: Lipoprotein mxiM

Chain A:



- Molecule 2: Outer membrane protein mxiD

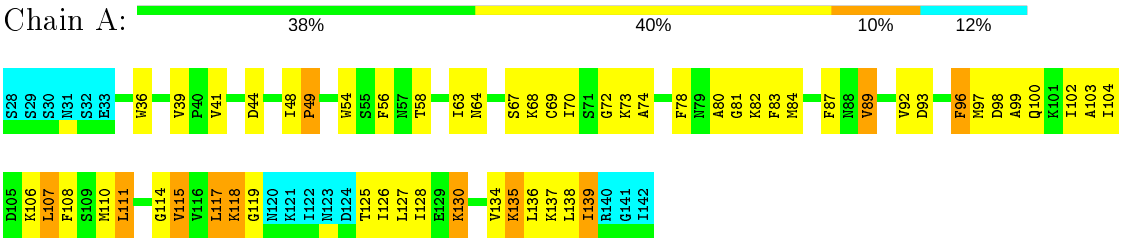
Chain B:



4.2.14 Score per residue for model 14

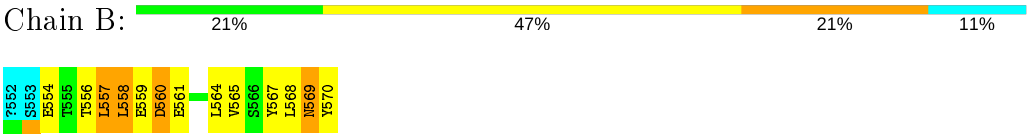
- Molecule 1: Lipoprotein mxiM

Chain A:



- Molecule 2: Outer membrane protein mxiD

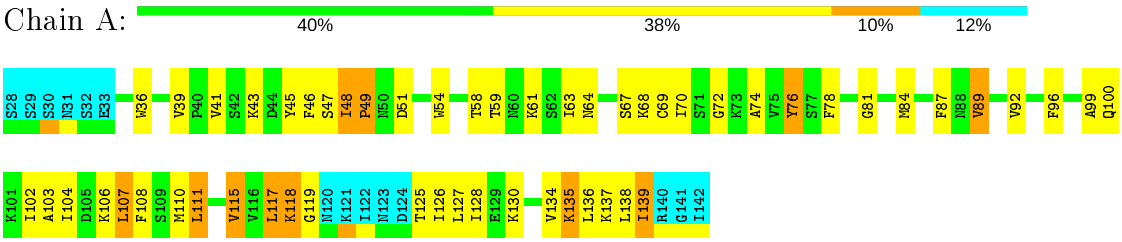
Chain B:



4.2.15 Score per residue for model 15 (medoid)

- Molecule 1: Lipoprotein mxiM

Chain A:



- Molecule 2: Outer membrane protein mxiD

Chain B:

5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing, molecular dynamics, torsion angle dynamics.*

Of the 200 calculated structures, 15 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
ARIA	refinement	2.1

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1561
Number of shifts mapped to atoms	1558
Number of unparsed shifts	0
Number of shifts with mapping errors	3
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

5.1 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	800	821	820	61±4
2	B	142	136	136	20±3
All	All	14130	14355	14340	1102

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 39.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:558:LEU:HG	2:B:564:LEU:HA	1.01	1.33	14	15
1:A:48:ILE:HG12	1:A:103:ALA:HB1	0.98	1.33	12	15
1:A:63:ILE:HB	1:A:74:ALA:HB3	0.93	1.38	4	15
1:A:70:ILE:HB	1:A:96:PHE:CZ	0.87	2.05	5	15
1:A:78:PHE:HZ	2:B:564:LEU:HD12	0.84	1.33	5	13
1:A:49:PRO:HG3	1:A:104:ILE:HD11	0.78	1.55	14	14
1:A:127:LEU:HD22	1:A:137:LYS:HD2	0.77	1.57	6	14
1:A:119:GLY:HA3	1:A:127:LEU:HD12	0.76	1.56	14	14
1:A:128:ILE:HB	1:A:136:LEU:HB3	0.76	1.55	12	15
1:A:39:VAL:HG11	1:A:137:LYS:HE2	0.72	1.61	2	13
2:B:558:LEU:HB3	2:B:564:LEU:HG	0.71	1.60	10	15
1:A:58:THR:HG21	2:B:565:VAL:HG12	0.71	1.61	7	9
1:A:54:TRP:HH2	1:A:111:LEU:HG	0.70	1.45	14	12
1:A:126:ILE:HG12	2:B:567:TYR:HE2	0.70	1.46	9	11
1:A:87:PHE:H	1:A:112:LYS:HE2	0.69	1.45	3	2
1:A:63:ILE:HD11	1:A:76:TYR:HB3	0.69	1.64	15	3
1:A:118:LYS:HA	2:B:556:THR:HB	0.69	1.63	9	15
1:A:117:LEU:HA	1:A:127:LEU:O	0.69	1.88	13	15
1:A:110:MET:SD	1:A:135:LYS:HG3	0.69	2.28	13	10
1:A:36:TRP:HB3	1:A:138:LEU:HB3	0.68	1.65	4	12
1:A:78:PHE:CZ	2:B:564:LEU:HD12	0.67	2.22	5	14
1:A:43:LYS:HA	1:A:46:PHE:CD2	0.67	2.25	11	11
2:B:554:GLU:HB2	2:B:557:LEU:HG	0.66	1.65	8	4
2:B:558:LEU:HD11	2:B:567:TYR:CB	0.66	2.20	13	15
1:A:41:VAL:HG21	1:A:134:VAL:HG22	0.65	1.69	8	15
1:A:81:GLY:HA2	2:B:559:GLU:HB3	0.64	1.68	13	11
1:A:70:ILE:HB	1:A:96:PHE:HZ	0.64	1.52	10	11
1:A:41:VAL:HB	1:A:135:LYS:HA	0.63	1.69	12	7
1:A:49:PRO:HA	1:A:100:GLN:NE2	0.63	2.09	4	7
2:B:558:LEU:HD11	2:B:567:TYR:CG	0.63	2.29	4	15
1:A:85:GLY:O	1:A:112:LYS:HG2	0.63	1.93	11	2
1:A:39:VAL:HB	1:A:137:LYS:HG2	0.63	1.70	2	1
1:A:96:PHE:O	1:A:100:GLN:HB2	0.63	1.93	3	15
1:A:84:MET:HA	1:A:111:LEU:O	0.62	1.94	3	15
1:A:118:LYS:HD3	2:B:554:GLU:HG2	0.62	1.71	4	10
1:A:69:CYS:HB3	1:A:92:VAL:CG2	0.62	2.24	11	15
1:A:48:ILE:HG23	1:A:49:PRO:HD2	0.62	1.72	12	15
1:A:69:CYS:HB3	1:A:92:VAL:HG22	0.62	1.72	8	6
1:A:130:LYS:O	1:A:135:LYS:HE2	0.61	1.96	11	2
1:A:115:VAL:HG11	1:A:128:ILE:HG23	0.60	1.71	2	15
1:A:64:ASN:HA	1:A:72:GLY:O	0.60	1.95	5	3
1:A:41:VAL:HG11	1:A:134:VAL:HG13	0.60	1.74	1	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:558:LEU:HG	2:B:564:LEU:CA	0.60	2.19	13	7
1:A:117:LEU:HG	1:A:126:ILE:CG2	0.60	2.27	12	4
1:A:72:GLY:HA3	1:A:89:VAL:HG13	0.59	1.73	14	12
1:A:96:PHE:HA	1:A:100:GLN:HE21	0.59	1.56	5	8
1:A:99:ALA:HA	1:A:102:ILE:HD12	0.59	1.73	14	14
1:A:72:GLY:HA3	1:A:89:VAL:HA	0.59	1.73	2	4
1:A:115:VAL:CG1	1:A:128:ILE:HG23	0.59	2.27	3	15
1:A:127:LEU:CD2	1:A:137:LYS:HD2	0.59	2.26	6	3
2:B:558:LEU:CG	2:B:564:LEU:HA	0.58	2.17	13	14
1:A:106:LYS:O	1:A:110:MET:HG3	0.58	1.98	6	14
2:B:557:LEU:O	2:B:558:LEU:HB2	0.58	1.97	15	15
1:A:126:ILE:HB	1:A:138:LEU:HB2	0.58	1.75	11	15
1:A:125:THR:HG23	1:A:139:ILE:HB	0.58	1.76	14	8
2:B:564:LEU:HD22	2:B:568:LEU:HD22	0.58	1.76	11	11
1:A:92:VAL:HG22	1:A:96:PHE:CE1	0.57	2.33	14	7
1:A:49:PRO:HG2	1:A:104:ILE:HD11	0.57	1.73	13	1
1:A:49:PRO:CG	1:A:104:ILE:HD11	0.57	2.29	13	7
1:A:70:ILE:HB	1:A:96:PHE:CE2	0.57	2.34	7	13
2:B:561:GLU:O	2:B:565:VAL:HG13	0.56	2.01	7	14
1:A:72:GLY:CA	1:A:89:VAL:HG13	0.56	2.31	15	5
1:A:67:SER:OG	1:A:70:ILE:HG22	0.55	2.01	14	14
1:A:39:VAL:O	1:A:136:LEU:HA	0.55	2.01	11	14
1:A:45:TYR:CZ	1:A:106:LYS:HB3	0.55	2.36	11	3
1:A:74:ALA:HA	1:A:86:ASN:O	0.55	2.00	4	5
2:B:558:LEU:CB	2:B:564:LEU:HG	0.55	2.32	2	9
1:A:118:LYS:HG3	2:B:557:LEU:H	0.55	1.61	13	2
1:A:44:ASP:OD2	1:A:106:LYS:HE2	0.55	2.01	14	7
1:A:45:TYR:O	1:A:48:ILE:HG13	0.55	2.02	9	7
1:A:56:PHE:CD1	2:B:568:LEU:HD21	0.54	2.37	6	5
1:A:87:PHE:CE1	1:A:111:LEU:HD23	0.54	2.38	12	6
1:A:42:SER:HB3	1:A:45:TYR:CD1	0.54	2.38	7	1
1:A:87:PHE:CE2	1:A:111:LEU:HD23	0.53	2.37	4	6
1:A:71:SER:HB2	1:A:90:LYS:HE2	0.53	1.80	12	1
1:A:126:ILE:HG12	2:B:567:TYR:CE2	0.53	2.36	9	7
1:A:63:ILE:O	1:A:73:LYS:HA	0.53	2.04	6	3
1:A:117:LEU:O	1:A:118:LYS:HG3	0.53	2.03	12	4
1:A:56:PHE:HE2	1:A:83:PHE:CZ	0.53	2.22	10	5
1:A:51:ASP:HB3	1:A:68:LYS:HE2	0.52	1.82	2	1
1:A:108:PHE:HA	1:A:111:LEU:CD2	0.52	2.35	15	12
1:A:103:ALA:HA	1:A:106:LYS:HD2	0.52	1.80	2	10
1:A:48:ILE:CG2	1:A:49:PRO:HD2	0.52	2.34	3	14

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:57:ASN:O	1:A:61:LYS:HA	0.52	2.05	8	1
1:A:92:VAL:HG22	1:A:96:PHE:HE1	0.52	1.65	14	3
1:A:87:PHE:HE2	1:A:111:LEU:HD23	0.52	1.63	14	6
2:B:560:ASP:O	2:B:564:LEU:HB2	0.51	2.04	14	10
1:A:97:MET:HG3	1:A:100:GLN:OE1	0.51	2.04	14	7
1:A:43:LYS:HA	1:A:46:PHE:CD1	0.51	2.40	5	1
1:A:107:LEU:HD13	1:A:136:LEU:HD21	0.51	1.81	2	14
1:A:54:TRP:CH2	1:A:111:LEU:HG	0.51	2.39	2	3
1:A:42:SER:HB3	1:A:45:TYR:HD1	0.51	1.65	7	1
1:A:107:LEU:HD13	1:A:136:LEU:CD2	0.51	2.36	10	13
2:B:558:LEU:HD11	2:B:567:TYR:HB3	0.50	1.82	8	5
1:A:58:THR:CG2	2:B:565:VAL:HG12	0.50	2.37	2	12
1:A:47:SER:O	1:A:100:GLN:HA	0.50	2.06	13	6
1:A:119:GLY:HA3	1:A:127:LEU:CD1	0.50	2.36	10	6
1:A:72:GLY:CA	1:A:89:VAL:HA	0.50	2.37	13	7
1:A:70:ILE:HB	1:A:96:PHE:CE1	0.50	2.40	12	1
1:A:118:LYS:HE2	2:B:554:GLU:HG2	0.50	1.84	13	1
1:A:82:LYS:HD2	1:A:114:GLY:O	0.49	2.07	9	4
1:A:74:ALA:HB2	1:A:87:PHE:CD2	0.49	2.42	7	3
1:A:76:TYR:HA	1:A:84:MET:O	0.49	2.06	13	2
1:A:69:CYS:HB3	1:A:92:VAL:HG21	0.49	1.85	7	5
1:A:116:VAL:HG13	1:A:129:GLU:HB3	0.49	1.85	3	3
1:A:115:VAL:HG21	1:A:128:ILE:CG2	0.48	2.38	6	10
1:A:86:ASN:HA	1:A:112:LYS:HE2	0.48	1.84	2	1
2:B:564:LEU:CD2	2:B:568:LEU:HD22	0.48	2.39	2	3
1:A:41:VAL:HB	1:A:135:LYS:CA	0.48	2.38	12	2
1:A:74:ALA:HB2	1:A:87:PHE:CD1	0.48	2.44	2	4
1:A:63:ILE:CB	1:A:74:ALA:HB3	0.48	2.26	4	4
1:A:47:SER:O	1:A:100:GLN:HG2	0.48	2.08	15	4
1:A:49:PRO:HD3	1:A:100:GLN:HB3	0.48	1.86	5	2
1:A:36:TRP:CZ3	1:A:139:ILE:HD11	0.48	2.44	5	4
1:A:48:ILE:HG12	1:A:103:ALA:CB	0.47	2.24	12	1
2:B:567:TYR:O	2:B:570:TYR:CD1	0.47	2.68	12	11
1:A:107:LEU:HA	1:A:110:MET:HE2	0.47	1.86	9	1
1:A:45:TYR:CE2	1:A:106:LYS:HB3	0.47	2.44	1	2
1:A:57:ASN:OD1	1:A:59:THR:HB	0.47	2.09	6	1
2:B:566:SER:HA	2:B:569:ASN:ND2	0.47	2.24	13	1
1:A:100:GLN:O	1:A:104:ILE:HG13	0.47	2.10	13	3
1:A:133:GLU:HG3	1:A:135:LYS:HD2	0.46	1.87	11	1
1:A:128:ILE:CB	1:A:136:LEU:HB3	0.46	2.38	15	8
1:A:61:LYS:HG3	1:A:76:TYR:OH	0.46	2.09	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:96:PHE:CD2	1:A:104:ILE:HD12	0.46	2.45	10	6
1:A:48:ILE:CG1	1:A:103:ALA:HB1	0.45	2.41	6	2
1:A:70:ILE:HD11	1:A:89:VAL:HG11	0.45	1.88	15	5
1:A:119:GLY:O	2:B:555:THR:HG21	0.45	2.10	15	2
1:A:110:MET:SD	1:A:135:LYS:HE3	0.45	2.51	11	1
1:A:73:LYS:HG3	1:A:88:ASN:HB2	0.45	1.87	9	1
1:A:39:VAL:CG1	1:A:137:LYS:HE2	0.45	2.41	12	5
1:A:57:ASN:HB3	1:A:60:ASN:OD1	0.45	2.11	12	1
2:B:555:THR:HG23	2:B:556:THR:H	0.45	1.71	15	1
1:A:75:VAL:O	1:A:85:GLY:HA2	0.45	2.12	3	2
1:A:115:VAL:HG23	1:A:130:LYS:CG	0.45	2.42	6	2
1:A:127:LEU:HA	1:A:137:LYS:HB2	0.45	1.88	2	1
1:A:118:LYS:O	1:A:127:LEU:HB2	0.45	2.11	11	4
1:A:73:LYS:HG2	1:A:74:ALA:N	0.45	2.26	2	1
1:A:118:LYS:HD3	2:B:554:GLU:CG	0.45	2.42	7	4
1:A:70:ILE:HG13	1:A:91:GLU:HB3	0.45	1.86	8	2
1:A:107:LEU:O	1:A:110:MET:HB2	0.44	2.11	8	5
1:A:126:ILE:HB	1:A:138:LEU:HD23	0.44	1.89	2	3
1:A:40:PRO:HA	1:A:136:LEU:HD12	0.44	1.90	12	1
1:A:71:SER:HB2	1:A:90:LYS:CG	0.44	2.43	1	1
1:A:63:ILE:CD1	1:A:85:GLY:HA3	0.44	2.42	5	3
1:A:38:ILE:HA	1:A:137:LYS:O	0.43	2.13	6	1
1:A:78:PHE:CE1	1:A:83:PHE:HB2	0.43	2.48	13	1
1:A:108:PHE:HA	1:A:111:LEU:HD22	0.43	1.90	15	1
1:A:117:LEU:HG	1:A:126:ILE:HG22	0.43	1.90	2	2
1:A:34:LYS:HE2	2:B:568:LEU:O	0.43	2.14	3	1
2:B:565:VAL:O	2:B:569:ASN:ND2	0.43	2.52	15	9
1:A:126:ILE:HA	2:B:556:THR:CG2	0.43	2.44	6	4
1:A:56:PHE:CE2	1:A:83:PHE:CZ	0.43	3.06	5	1
2:B:565:VAL:HA	2:B:568:LEU:HB2	0.43	1.91	11	1
1:A:56:PHE:CZ	1:A:117:LEU:HD21	0.43	2.49	13	1
1:A:119:GLY:H	2:B:555:THR:CG2	0.43	2.26	13	1
1:A:39:VAL:HB	1:A:137:LYS:CG	0.43	2.41	2	1
1:A:111:LEU:HA	1:A:115:VAL:HB	0.43	1.90	13	2
2:B:566:SER:HA	2:B:569:ASN:HD21	0.42	1.73	13	1
1:A:68:LYS:N	1:A:68:LYS:CD	0.42	2.82	4	1
1:A:84:MET:HG2	1:A:114:GLY:HA2	0.42	1.91	8	8
1:A:90:LYS:HG3	1:A:90:LYS:O	0.42	2.13	3	1
1:A:56:PHE:HE1	1:A:83:PHE:CZ	0.42	2.33	11	1
2:B:554:GLU:HG3	2:B:555:THR:HG22	0.42	1.91	13	1
1:A:126:ILE:HA	2:B:556:THR:HG21	0.42	1.91	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:110:MET:HE1	1:A:136:LEU:HD22	0.42	1.91	4	2
1:A:87:PHE:HB3	1:A:89:VAL:CG2	0.42	2.44	13	1
1:A:100:GLN:O	1:A:103:ALA:HB3	0.42	2.14	6	5
2:B:557:LEU:HA	2:B:557:LEU:HD23	0.42	1.71	7	1
2:B:557:LEU:HD23	2:B:557:LEU:HA	0.42	1.73	6	3
1:A:135:LYS:HB3	1:A:135:LYS:NZ	0.41	2.30	1	1
1:A:63:ILE:HD13	1:A:83:PHE:CZ	0.41	2.50	5	1
1:A:42:SER:OG	1:A:135:LYS:HB2	0.41	2.15	12	1
1:A:96:PHE:CD1	1:A:104:ILE:HD12	0.41	2.50	12	1
1:A:43:LYS:HA	1:A:46:PHE:CE2	0.41	2.49	7	1
1:A:130:LYS:O	1:A:131:ASP:HB2	0.41	2.16	5	3
1:A:68:LYS:HD2	1:A:68:LYS:H	0.41	1.75	8	1
1:A:111:LEU:HD13	1:A:111:LEU:N	0.41	2.31	15	2
1:A:110:MET:SD	1:A:135:LYS:CG	0.41	3.09	10	2
1:A:107:LEU:HG	1:A:108:PHE:N	0.41	2.29	1	4
1:A:126:ILE:CG2	1:A:138:LEU:HD23	0.41	2.46	6	1
1:A:92:VAL:HG22	1:A:96:PHE:CE2	0.41	2.50	12	1
1:A:61:LYS:CB	1:A:76:TYR:OH	0.41	2.69	6	1
1:A:82:LYS:HD3	1:A:116:VAL:HB	0.41	1.92	3	1
1:A:36:TRP:CE3	1:A:55:SER:HA	0.41	2.51	11	1
2:B:558:LEU:HD21	2:B:567:TYR:CD2	0.41	2.51	13	1
1:A:87:PHE:HE1	1:A:111:LEU:HD23	0.41	1.73	12	2
1:A:62:SER:HA	1:A:74:ALA:O	0.41	2.16	10	1
1:A:53:LEU:HB2	1:A:66:TYR:O	0.40	2.16	1	1
1:A:96:PHE:C	1:A:100:GLN:HB2	0.40	2.36	15	2
1:A:96:PHE:CD2	1:A:104:ILE:CD1	0.40	3.04	2	1
1:A:102:ILE:HG22	1:A:106:LYS:HE3	0.40	1.92	7	1
1:A:40:PRO:HB3	1:A:45:TYR:O	0.40	2.16	11	1

5.2 Torsion angles (i)

5.2.1 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	101/115 (88%)	89±2 (88±2%)	8±2 (8±2%)	3±1 (3±1%)	6	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	16/19 (84%)	13±0 (81±2%)	2±0 (12±3%)	1±0 (7±2%)	2 18
All	All	1755/2010 (87%)	1531 (87%)	156 (9%)	68 (4%)	5 32

All 9 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	558	LEU	15
1	A	118	LYS	15
1	A	139	ILE	15
1	A	49	PRO	13
1	A	51	ASP	6
1	A	80	ALA	1
2	B	557	LEU	1
1	A	97	MET	1
1	A	61	LYS	1

5.2.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	90/103 (87%)	79±2 (88±2%)	11±2 (12±2%)	8 50
2	B	17/18 (94%)	15±1 (86±4%)	2±1 (14±4%)	7 47
All	All	1605/1815 (88%)	1404 (87%)	201 (13%)	8 50

All 33 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)
2	B	557	LEU	15
1	A	135	LYS	15
1	A	115	VAL	15
1	A	130	LYS	15
1	A	111	LEU	15
1	A	107	LEU	15
2	B	569	ASN	15

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Mol	Chain	Res	Type	Models (Total)
1	A	89	VAL	13
1	A	48	ILE	8
1	A	117	LEU	7
1	A	68	LYS	7
1	A	43	LYS	6
1	A	64	ASN	6
1	A	61	LYS	5
1	A	73	LYS	5
1	A	91	GLU	5
1	A	96	PHE	4
1	A	63	ILE	3
1	A	90	LYS	3
1	A	129	GLU	3
1	A	44	ASP	3
2	B	560	ASP	2
1	A	56	PHE	2
2	B	562	LYS	2
1	A	98	ASP	2
1	A	86	ASN	2
1	A	35	GLU	2
1	A	131	ASP	1
2	B	568	LEU	1
1	A	83	PHE	1
1	A	93	ASP	1
1	A	58	THR	1
1	A	118	LYS	1

5.2.3 RNA

There are no RNA molecules in this entry.

5.3 Non-standard residues in protein, DNA, RNA chains

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

5.4 Carbohydrates

There are no carbohydrates in this entry.

5.5 Ligand geometry

There are no ligands in this entry.

5.6 Other polymers

There are no such molecules in this entry.

5.7 Polymer linkage issues

There are no chain breaks in this entry.

6 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 88% for the well-defined parts and 84% for the entire structure.

6.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

6.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1561
Number of shifts mapped to atoms	1558
Number of unparsed shifts	0
Number of shifts with mapping errors	3
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	7

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. All 3 occurences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
B	19	ACE	H23	2.05	0.02	1
B	19	ACE	H21	2.05	0.02	1
B	19	ACE	H22	2.05	0.02	1

6.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	110	0.11 ± 0.12	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	102	0.11 ± 0.08	None needed (< 0.5 ppm)
$^{13}C'$	104	0.22 ± 0.08	None needed (< 0.5 ppm)
^{15}N	105	0.11 ± 0.45	None needed (< 0.5 ppm)

6.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 88%, i.e. 1289 atoms were assigned a chemical shift out of a possible 1463. 0 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	527/586 (90%)	232/234 (99%)	198/236 (84%)	97/116 (84%)
Sidechain	646/742 (87%)	419/432 (97%)	219/286 (77%)	8/24 (33%)
Aromatic	116/135 (86%)	65/71 (92%)	49/60 (82%)	2/4 (50%)
Overall	1289/1463 (88%)	716/737 (97%)	466/582 (80%)	107/144 (74%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 84%, i.e. 1379 atoms were assigned a chemical shift out of a possible 1634. 0 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	571/661 (86%)	252/264 (95%)	214/266 (80%)	105/131 (80%)
Sidechain	692/838 (83%)	447/489 (91%)	236/318 (74%)	9/31 (29%)
Aromatic	116/135 (86%)	65/71 (92%)	49/60 (82%)	2/4 (50%)
Overall	1379/1634 (84%)	764/824 (93%)	499/644 (77%)	116/166 (70%)

6.1.4 Statistically unusual chemical shifts

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

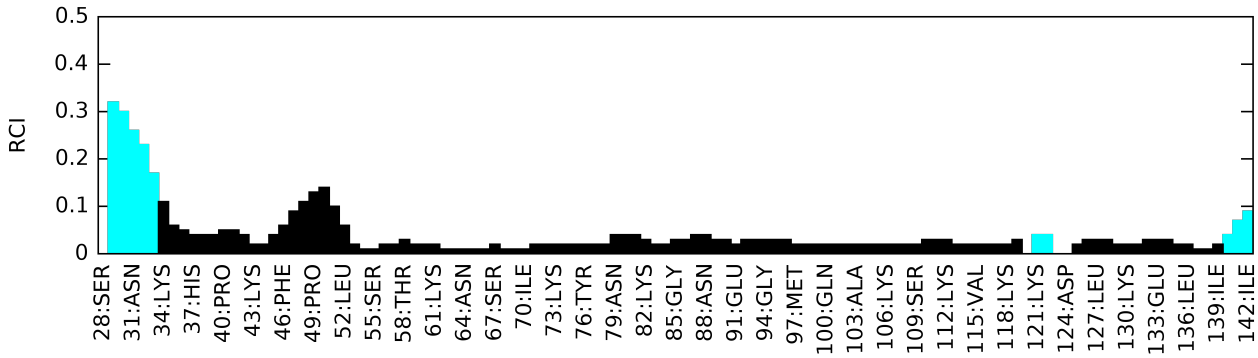
Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	54	TRP	HE1	5.53	12.85 – 7.35	-8.3
1	A	74	ALA	HB1	-0.46	2.61 – 0.11	-7.3
1	A	74	ALA	HB2	-0.46	2.61 – 0.11	-7.3
1	A	74	ALA	HB3	-0.46	2.61 – 0.11	-7.3
1	A	138	LEU	HD22	-1.00	2.14 – -0.66	-6.2
1	A	138	LEU	HD21	-1.00	2.14 – -0.66	-6.2
1	A	138	LEU	HD23	-1.00	2.14 – -0.66	-6.2

6.1.5 Random Coil Index (RCI) plots

The images below report *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-

defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:



Random coil index (RCI) for chain B: