



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 09:29 PM BST

PDB ID : 2JOA  
Title : HtrA1 bound to an optimized peptide: NMR assignment of PDZ domain and ligand resonances  
Authors : Runyon, S.T.; Zhang, Y.; Appleton, B.A.; Sazinksy, S.L.; Wu, P.; Pan, B.; Wiesmann, C.; Skelton, N.J.; Sidhu, S.S.  
Deposited on : 2007-03-01

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : rb-20027457  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

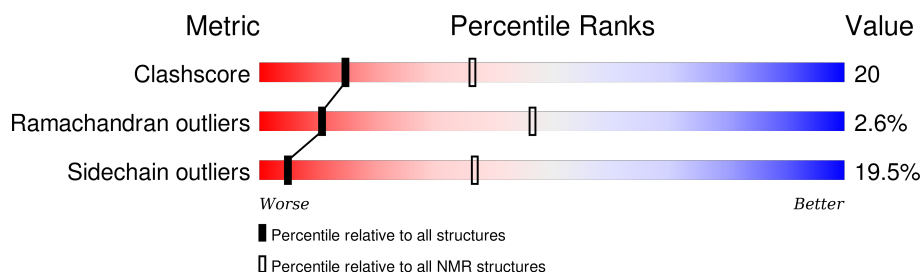
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 87%.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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

Mol	Chain	Length	Quality of chain
1	A	105	
2	B	7	

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 2 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:381-A:477, B:2-B:7 (103)	0.51	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 3 clusters and 5 single-model clusters were found.

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1769 atoms, of which 892 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Serine protease HTRA1.

Mol	Chain	Residues	Atoms						Trace
1	A	105	Total	C	H	N	O	S	0
			1636	501	828	140	162	5	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	376	GLY	-	EXPRESSION TAG	UNP Q92743
A	377	SER	-	EXPRESSION TAG	UNP Q92743
A	378	HIS	-	EXPRESSION TAG	UNP Q92743
A	379	MET	-	EXPRESSION TAG	UNP Q92743

- Molecule 2 is a protein called Peptide H1-C1.

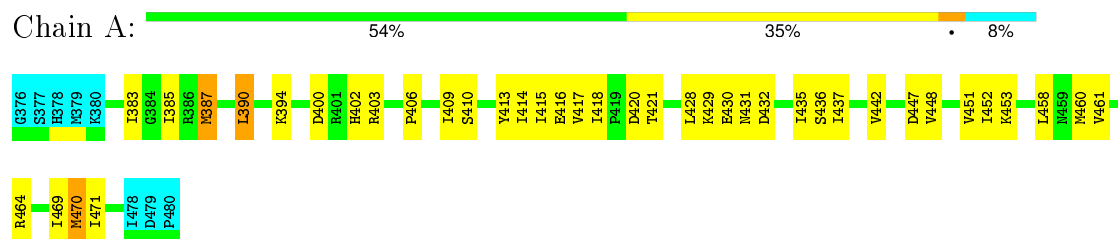
Mol	Chain	Residues	Atoms					Trace
2	B	7	Total	C	H	N	O	0
			133	46	64	12	11	

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

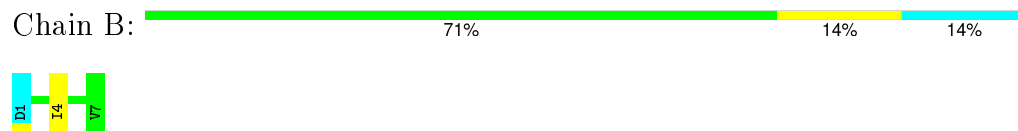
### 4.1 Average score per residue in the NMR ensemble

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: Serine protease HTRA1



- Molecule 2: Peptide H1-C1

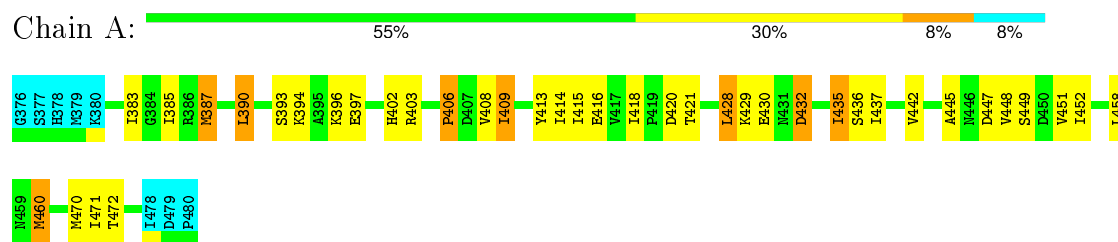


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

- Molecule 1: Serine protease HTRA1

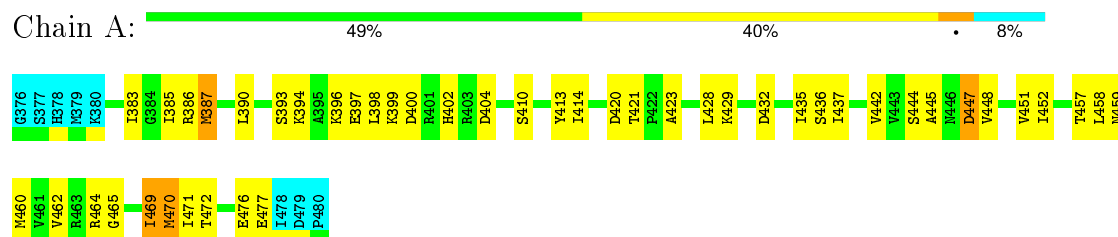


- Molecule 2: Peptide H1-C1

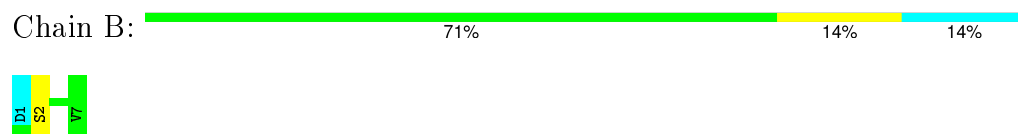


#### 4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Serine protease HTRA1

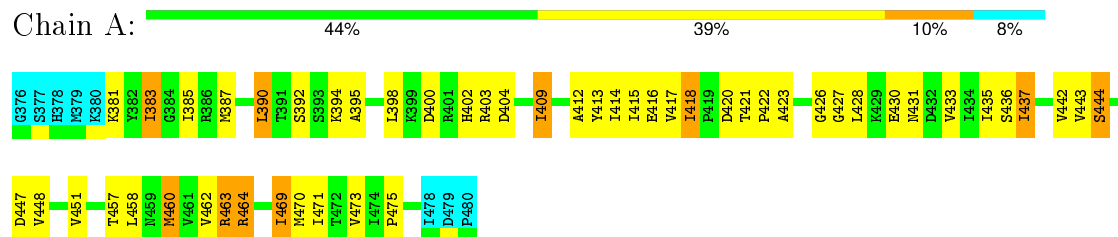


- Molecule 2: Peptide H1-C1



#### 4.2.3 Score per residue for model 3

- Molecule 1: Serine protease HTRA1

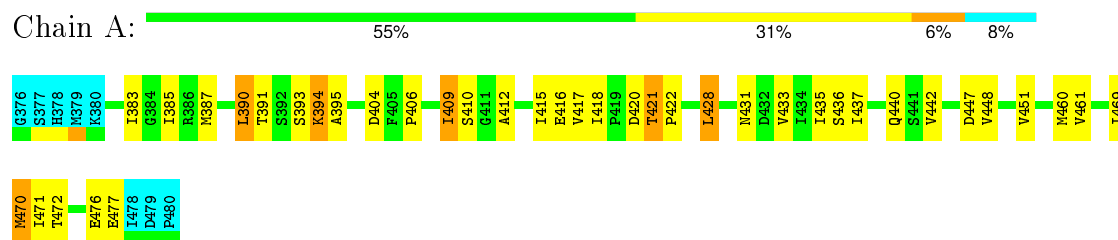


- Molecule 2: Peptide H1-C1

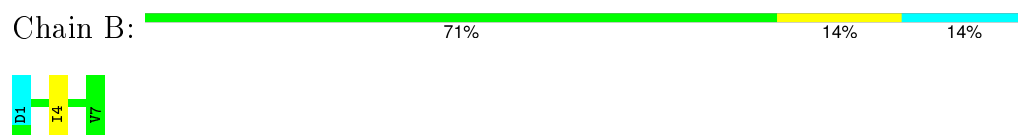


#### 4.2.4 Score per residue for model 4

- Molecule 1: Serine protease HTRA1

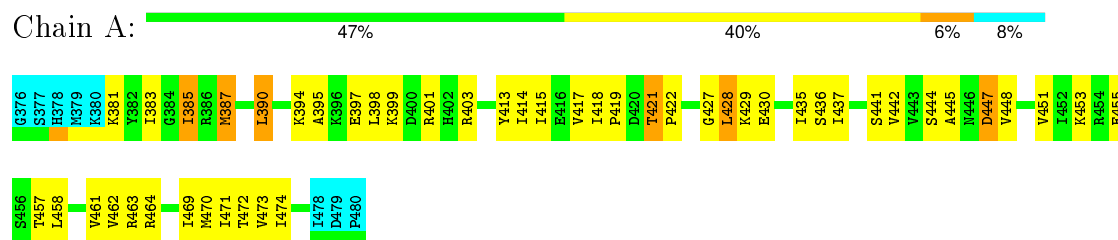


- Molecule 2: Peptide H1-C1



#### 4.2.5 Score per residue for model 5

- Molecule 1: Serine protease HTRA1

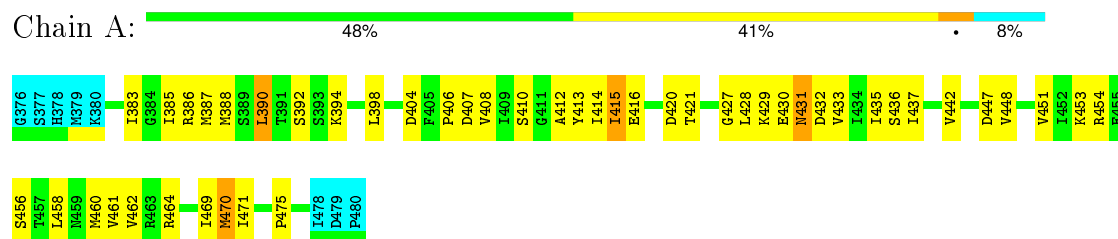


- Molecule 2: Peptide H1-C1

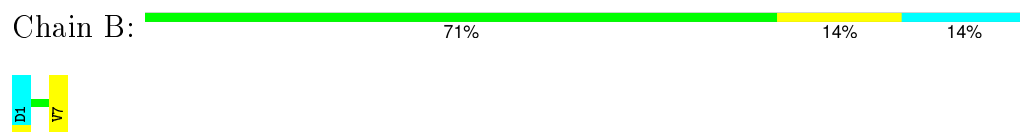


#### 4.2.6 Score per residue for model 6

- Molecule 1: Serine protease HTRA1

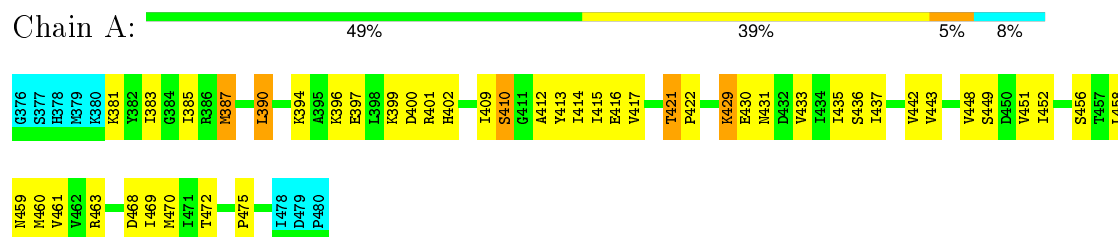


- Molecule 2: Peptide H1-C1



#### 4.2.7 Score per residue for model 7

- Molecule 1: Serine protease HTRA1

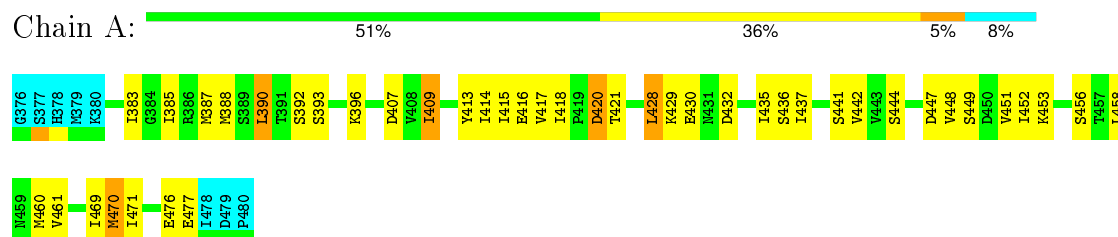


- Molecule 2: Peptide H1-C1

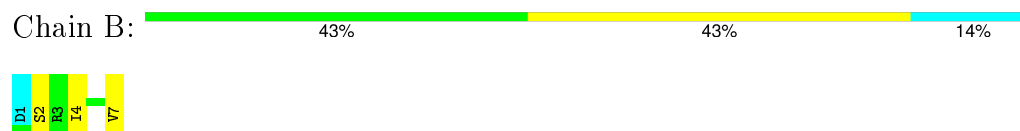


#### 4.2.8 Score per residue for model 8

- Molecule 1: Serine protease HTRA1



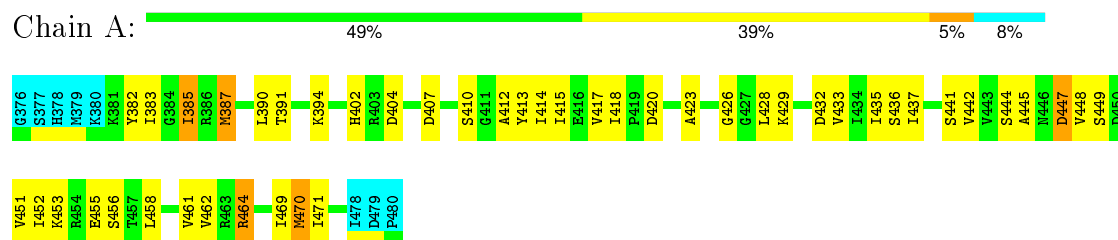
- Molecule 2: Peptide H1-C1



#### 4.2.9 Score per residue for model 9

- Molecule 1: Serine protease HTRA1



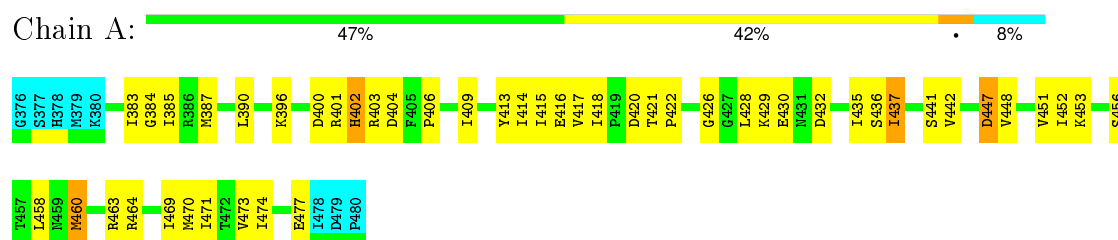


- Molecule 2: Peptide H1-C1



#### 4.2.10 Score per residue for model 10

- Molecule 1: Serine protease HTRA1

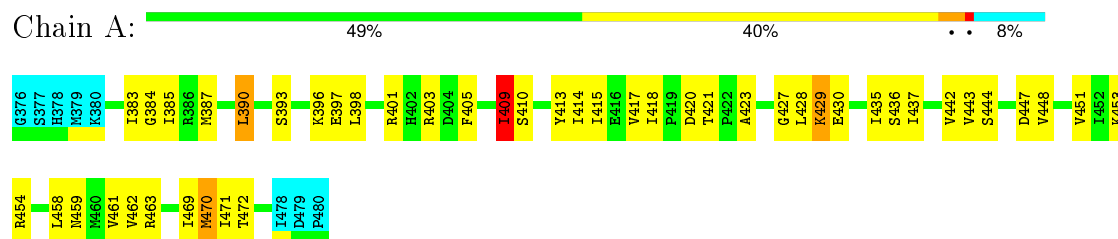


- Molecule 2: Peptide H1-C1

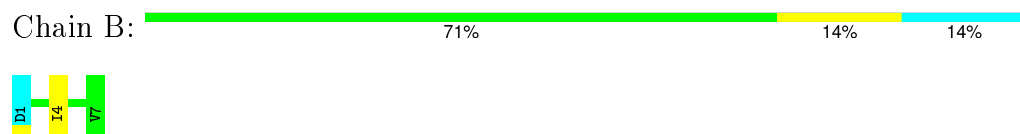


#### 4.2.11 Score per residue for model 11

- Molecule 1: Serine protease HTRA1

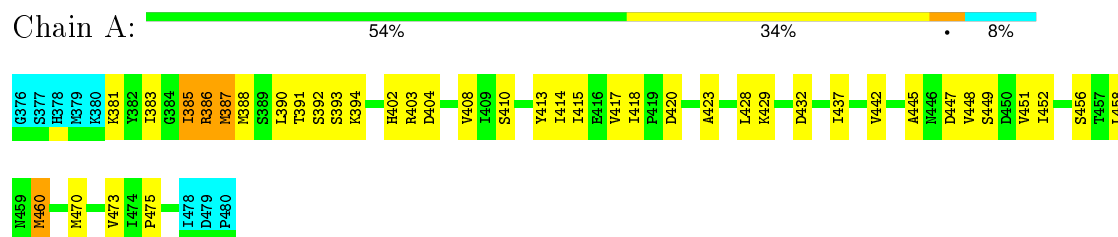


- Molecule 2: Peptide H1-C1

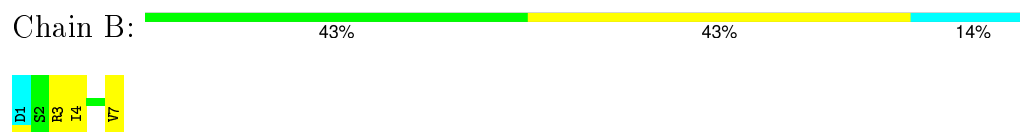


#### 4.2.12 Score per residue for model 12

- Molecule 1: Serine protease HTRA1

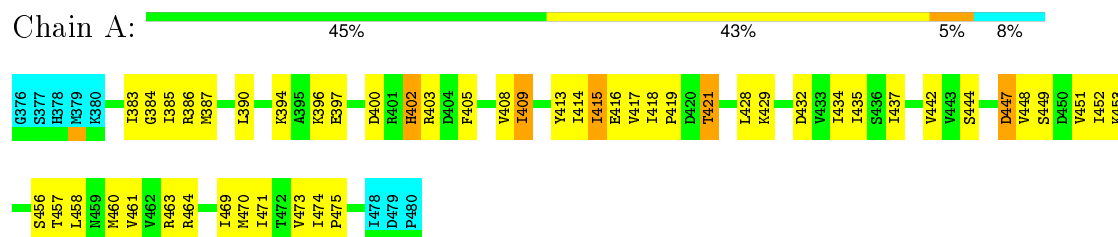


- Molecule 2: Peptide H1-C1

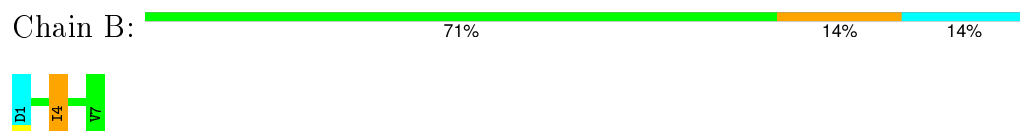


#### 4.2.13 Score per residue for model 13

- Molecule 1: Serine protease HTRA1

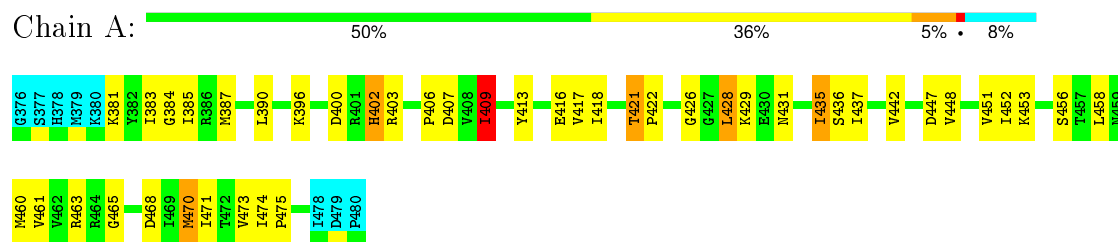


- Molecule 2: Peptide H1-C1

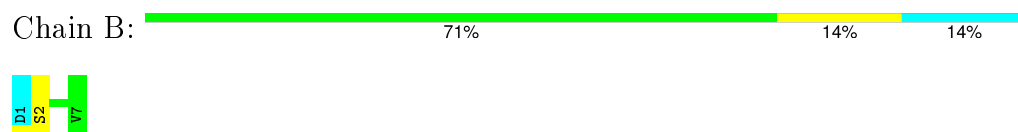


#### 4.2.14 Score per residue for model 14

- Molecule 1: Serine protease HTRA1

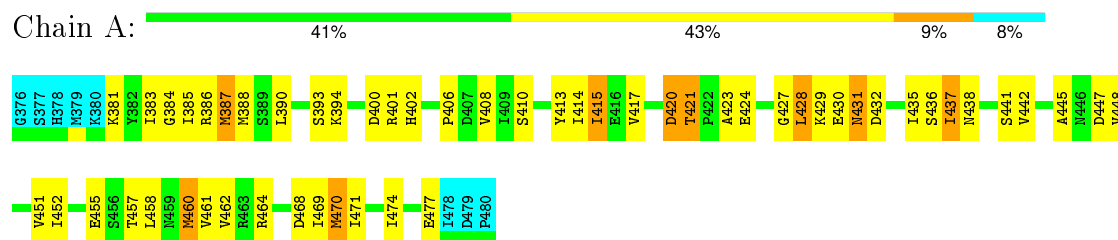


- Molecule 2: Peptide H1-C1



#### 4.2.15 Score per residue for model 15

- Molecule 1: Serine protease HTRA1

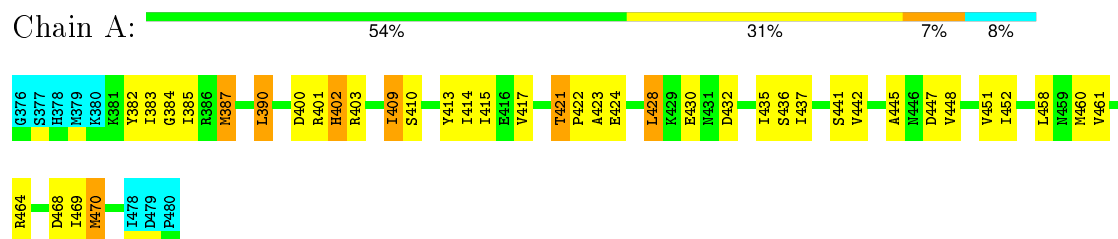


- Molecule 2: Peptide H1-C1



#### 4.2.16 Score per residue for model 16

- Molecule 1: Serine protease HTRA1

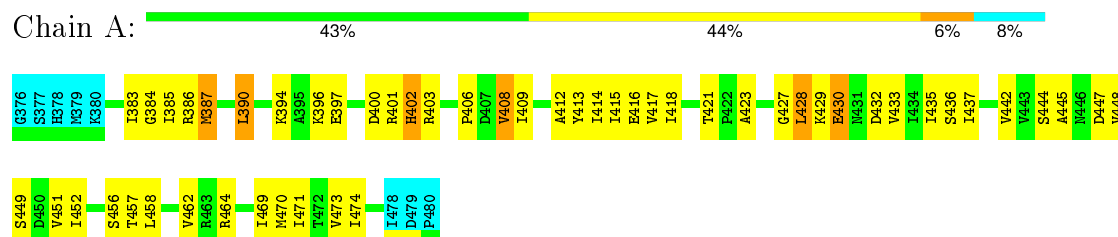


- Molecule 2: Peptide H1-C1



#### 4.2.17 Score per residue for model 17

- Molecule 1: Serine protease HTRA1

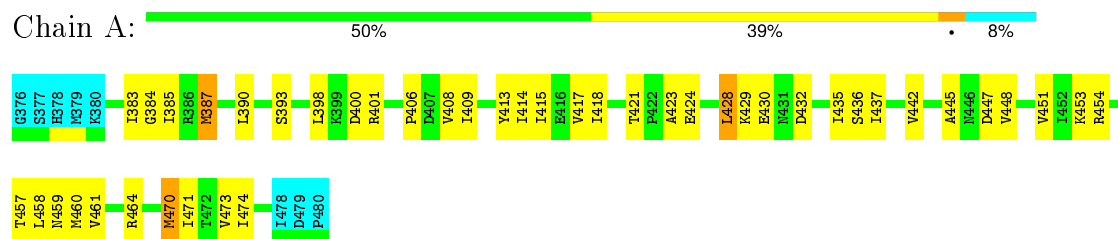


- Molecule 2: Peptide H1-C1

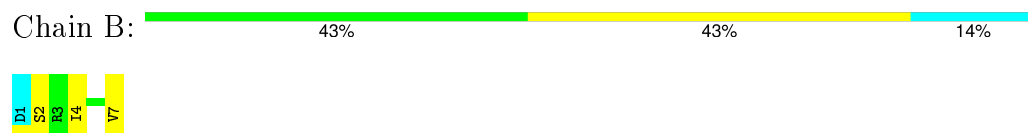


#### 4.2.18 Score per residue for model 18

- Molecule 1: Serine protease HTRA1

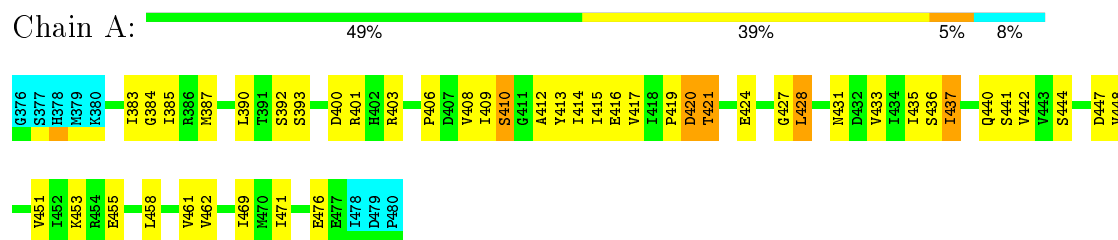


- Molecule 2: Peptide H1-C1

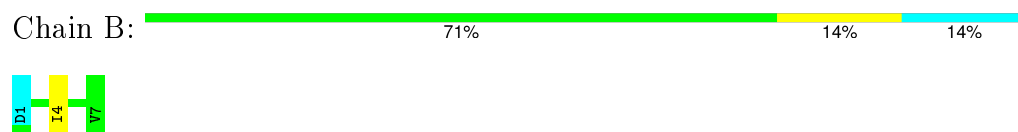


#### 4.2.19 Score per residue for model 19

- Molecule 1: Serine protease HTRA1

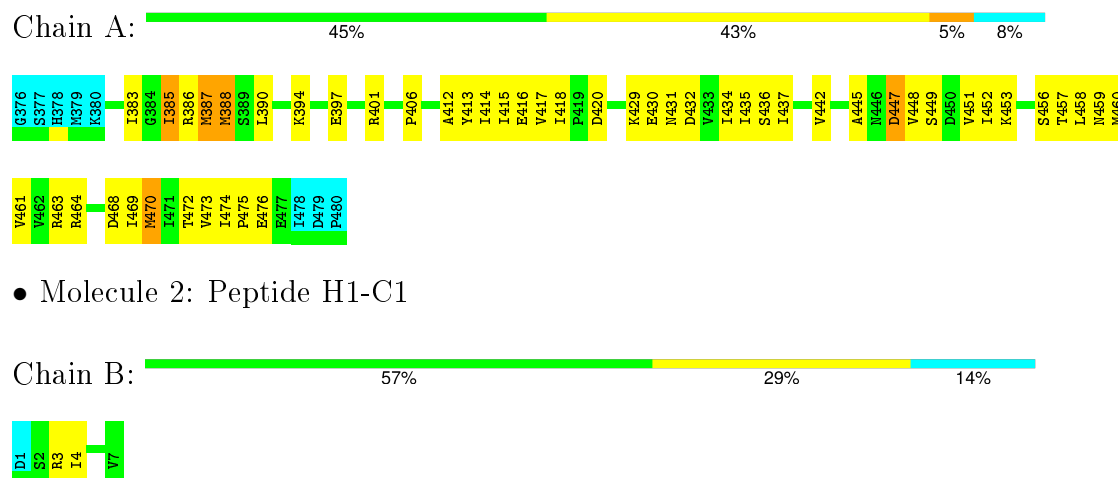


- Molecule 2: Peptide H1-C1



#### 4.2.20 Score per residue for model 20

- Molecule 1: Serine protease HTRA1



- Molecule 2: Peptide H1-C1

## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
CNX	structure solution	2002
CNX	refinement	2002

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 15154
Number of chemical shift lists	1
Total number of shifts	1319
Number of shifts mapped to atoms	1319
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

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

## 6 Model quality ⓘ

### 6.1 Standard geometry ⓘ

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 6.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	747	766	765	32±4
2	B	61	58	58	2±2
All	All	16160	16480	16460	650

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:385:ILE:HD13	1:A:417:VAL:HG22	1.04	1.24	17	10
1:A:437:ILE:HG21	1:A:451:VAL:HG11	0.91	1.43	1	15
1:A:442:VAL:HG11	1:A:448:VAL:HG22	0.90	1.41	12	19
1:A:385:ILE:CD1	1:A:417:VAL:HG22	0.84	2.03	16	9
1:A:442:VAL:HG11	1:A:448:VAL:CG2	0.83	2.04	6	15
1:A:385:ILE:HD11	1:A:414:ILE:HG23	0.83	1.50	12	15
1:A:447:ASP:O	1:A:451:VAL:HG23	0.80	1.77	10	19
1:A:437:ILE:CG2	1:A:451:VAL:HG11	0.79	2.08	1	12
1:A:451:VAL:HG13	1:A:455:GLU:OE2	0.78	1.79	15	3
1:A:414:ILE:HD12	1:A:432:ASP:HB2	0.77	1.55	12	12
1:A:415:ILE:CD1	2:B:4:ILE:HG22	0.77	2.09	4	15
1:A:435:ILE:HD12	1:A:436:SER:N	0.76	1.95	11	18
1:A:385:ILE:HD11	1:A:414:ILE:CG2	0.75	2.12	19	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:409:ILE:O	1:A:409:ILE:HG23	0.74	1.82	14	1
1:A:385:ILE:HD12	1:A:416:GLU:O	0.74	1.80	7	7
1:A:428:LEU:HD23	1:A:471:ILE:HG21	0.73	1.59	3	9
1:A:462:VAL:HG22	1:A:471:ILE:HD13	0.73	1.61	11	2
1:A:462:VAL:HG23	1:A:471:ILE:HD13	0.72	1.61	9	6
1:A:385:ILE:HG12	1:A:417:VAL:HG22	0.72	1.60	20	2
1:A:390:LEU:HD11	1:A:398:LEU:HD11	0.72	1.58	18	3
1:A:390:LEU:HD13	1:A:413:TYR:HB2	0.72	1.59	19	19
1:A:415:ILE:HD13	2:B:4:ILE:HG22	0.71	1.63	11	11
1:A:423:ALA:HB1	1:A:428:LEU:HD12	0.71	1.61	17	4
1:A:414:ILE:HD12	1:A:432:ASP:CB	0.69	2.17	13	8
1:A:387:MET:CE	2:B:7:VAL:HG23	0.69	2.18	7	1
1:A:448:VAL:HG12	1:A:452:ILE:HD11	0.67	1.65	10	7
1:A:437:ILE:HD13	1:A:451:VAL:HG11	0.67	1.67	8	1
1:A:473:VAL:C	1:A:474:ILE:HD12	0.66	2.11	5	6
1:A:462:VAL:HG22	1:A:471:ILE:CD1	0.66	2.21	6	1
1:A:464:ARG:HB3	1:A:469:ILE:HD11	0.66	1.68	6	2
1:A:464:ARG:HB2	1:A:469:ILE:HD11	0.65	1.69	17	5
1:A:464:ARG:HG2	1:A:469:ILE:HD11	0.65	1.68	2	1
1:A:383:ILE:HG22	1:A:422:PRO:HG2	0.64	1.66	3	1
1:A:462:VAL:O	1:A:469:ILE:HD12	0.64	1.91	2	2
1:A:383:ILE:HG13	1:A:385:ILE:HG22	0.64	1.69	7	14
1:A:428:LEU:HD11	1:A:473:VAL:HG21	0.63	1.70	12	2
1:A:459:ASN:OD1	1:A:472:THR:HG23	0.63	1.93	2	2
1:A:437:ILE:HD11	1:A:458:LEU:HB3	0.62	1.71	12	17
1:A:437:ILE:HD12	1:A:460:MET:CG	0.62	2.25	20	4
1:A:461:VAL:HG13	1:A:469:ILE:O	0.61	1.95	6	11
1:A:412:ALA:O	1:A:433:VAL:HG13	0.61	1.96	17	7
1:A:390:LEU:HD11	1:A:398:LEU:CD1	0.61	2.25	6	2
1:A:435:ILE:HD12	1:A:436:SER:HB3	0.60	1.73	7	10
1:A:449:SER:HA	1:A:452:ILE:HD12	0.60	1.72	8	8
1:A:409:ILE:N	1:A:409:ILE:HD13	0.59	2.12	11	4
1:A:461:VAL:HG22	1:A:470:MET:HG3	0.59	1.71	14	8
1:A:473:VAL:O	1:A:474:ILE:HD13	0.59	1.97	10	1
1:A:442:VAL:HG11	1:A:448:VAL:HG23	0.58	1.76	14	5
1:A:415:ILE:HD13	2:B:4:ILE:CG2	0.58	2.29	11	6
1:A:386:ARG:HB3	1:A:415:ILE:HD12	0.58	1.74	13	1
1:A:471:ILE:N	1:A:471:ILE:HD12	0.58	2.14	15	5
1:A:428:LEU:CD2	1:A:471:ILE:HG21	0.57	2.28	14	8
1:A:471:ILE:HD12	1:A:471:ILE:N	0.57	2.13	17	2
1:A:385:ILE:HD13	1:A:417:VAL:CG2	0.57	2.16	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:418:ILE:HG22	1:A:420:ASP:H	0.57	1.59	20	3
1:A:409:ILE:HD13	1:A:409:ILE:N	0.57	2.15	16	2
1:A:452:ILE:HG23	1:A:458:LEU:HD11	0.56	1.76	10	1
1:A:409:ILE:HD13	1:A:409:ILE:H	0.56	1.61	8	4
1:A:437:ILE:HD13	1:A:451:VAL:CG1	0.56	2.30	8	1
1:A:383:ILE:HD12	1:A:385:ILE:CG2	0.56	2.31	13	10
1:A:390:LEU:HD21	1:A:398:LEU:CD1	0.56	2.30	18	1
1:A:406:PRO:HB2	1:A:408:VAL:HG22	0.55	1.78	15	3
1:A:384:GLY:HA3	1:A:421:THR:HG21	0.55	1.78	18	9
1:A:385:ILE:CG1	1:A:417:VAL:HG22	0.55	2.31	20	2
1:A:423:ALA:CB	1:A:428:LEU:HD12	0.55	2.30	3	1
1:A:417:VAL:HG11	1:A:424:GLU:HB2	0.54	1.79	19	1
1:A:383:ILE:HG23	1:A:475:PRO:HB3	0.54	1.78	6	7
1:A:409:ILE:HD12	1:A:410:SER:N	0.54	2.17	7	2
1:A:464:ARG:CG	1:A:469:ILE:HD11	0.54	2.32	2	1
1:A:408:VAL:HG23	1:A:408:VAL:O	0.53	2.03	12	2
1:A:474:ILE:HD12	1:A:474:ILE:N	0.53	2.19	20	3
1:A:418:ILE:N	1:A:418:ILE:CD1	0.52	2.73	20	2
1:A:437:ILE:HG12	1:A:451:VAL:HG11	0.51	1.82	17	1
1:A:437:ILE:HG23	1:A:437:ILE:O	0.51	2.04	14	7
1:A:414:ILE:HG21	1:A:429:LYS:O	0.51	2.05	7	2
1:A:408:VAL:O	1:A:408:VAL:HG23	0.51	2.05	13	3
1:A:437:ILE:O	1:A:437:ILE:HG23	0.51	2.06	17	12
1:A:470:MET:C	1:A:471:ILE:HD12	0.51	2.25	15	2
1:A:385:ILE:HD13	1:A:386:ARG:N	0.51	2.21	20	2
1:A:409:ILE:O	1:A:409:ILE:CG2	0.51	2.53	14	1
1:A:451:VAL:HG13	1:A:455:GLU:CD	0.51	2.25	19	3
1:A:385:ILE:HD13	1:A:385:ILE:C	0.50	2.26	5	2
1:A:383:ILE:HD11	1:A:452:ILE:HD13	0.50	1.84	14	1
1:A:474:ILE:N	1:A:474:ILE:HD12	0.50	2.21	18	3
2:B:7:VAL:O	2:B:7:VAL:HG12	0.50	2.06	6	2
1:A:435:ILE:HD12	1:A:436:SER:CB	0.50	2.37	5	15
1:A:419:PRO:O	1:A:420:ASP:CB	0.50	2.60	19	1
1:A:426:GLY:HA3	1:A:473:VAL:HG22	0.49	1.85	3	1
1:A:417:VAL:CG1	1:A:423:ALA:HB3	0.49	2.38	18	3
1:A:415:ILE:HG22	1:A:416:GLU:H	0.49	1.66	13	2
1:A:418:ILE:HG22	1:A:419:PRO:HD2	0.49	1.84	5	2
1:A:385:ILE:HG13	1:A:417:VAL:HG22	0.49	1.85	13	2
1:A:423:ALA:HA	1:A:428:LEU:HD12	0.49	1.85	12	1
1:A:385:ILE:C	1:A:385:ILE:HD13	0.48	2.29	12	2
1:A:418:ILE:N	1:A:418:ILE:HD12	0.48	2.21	20	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:437:ILE:HD12	1:A:451:VAL:HG11	0.48	1.84	15	1
1:A:388:MET:O	1:A:412:ALA:HB1	0.48	2.08	20	1
1:A:457:THR:C	1:A:458:LEU:HD23	0.48	2.29	2	1
1:A:414:ILE:HD12	1:A:432:ASP:C	0.48	2.29	8	1
1:A:385:ILE:HD12	1:A:417:VAL:HG22	0.47	1.86	18	1
1:A:391:THR:HG23	1:A:394:LYS:H	0.47	1.70	4	1
1:A:461:VAL:HG22	1:A:470:MET:SD	0.47	2.49	8	1
1:A:414:ILE:HD12	1:A:432:ASP:HB3	0.47	1.86	13	1
1:A:383:ILE:HG22	1:A:422:PRO:CG	0.47	2.37	3	1
1:A:406:PRO:HG2	1:A:408:VAL:HG22	0.47	1.86	18	1
1:A:464:ARG:HB2	1:A:469:ILE:HD12	0.46	1.87	16	2
1:A:435:ILE:HD12	1:A:436:SER:OG	0.46	2.09	8	1
1:A:442:VAL:CG1	1:A:448:VAL:HG22	0.46	2.39	5	1
1:A:383:ILE:HD12	1:A:385:ILE:HG21	0.46	1.86	10	3
1:A:383:ILE:CG1	1:A:385:ILE:HG22	0.46	2.41	15	3
1:A:452:ILE:HD13	2:B:7:VAL:C	0.46	2.30	7	1
1:A:418:ILE:CD1	1:A:418:ILE:N	0.46	2.78	9	5
1:A:409:ILE:C	1:A:409:ILE:HD12	0.46	2.31	10	1
2:B:7:VAL:HG12	2:B:7:VAL:O	0.46	2.10	16	1
1:A:474:ILE:CD1	1:A:474:ILE:N	0.46	2.79	20	4
1:A:398:LEU:HD22	1:A:405:PHE:CE2	0.46	2.45	11	1
1:A:387:MET:SD	1:A:445:ALA:HB1	0.46	2.51	15	10
1:A:418:ILE:HD12	1:A:418:ILE:N	0.45	2.25	4	4
1:A:443:VAL:HG22	1:A:447:ASP:OD2	0.45	2.12	11	1
1:A:418:ILE:HB	1:A:421:THR:CG2	0.45	2.42	11	4
2:B:7:VAL:HG12	2:B:7:VAL:OXT	0.45	2.12	8	1
1:A:474:ILE:N	1:A:474:ILE:CD1	0.45	2.80	18	2
1:A:386:ARG:HB2	1:A:415:ILE:HB	0.45	1.89	13	2
1:A:421:THR:HB	1:A:422:PRO:HD2	0.44	1.89	10	4
1:A:457:THR:O	1:A:457:THR:HG23	0.44	2.13	17	1
1:A:385:ILE:HD11	1:A:417:VAL:HG22	0.44	1.85	11	1
1:A:395:ALA:HA	1:A:398:LEU:HD12	0.44	1.88	5	2
1:A:459:ASN:ND2	1:A:472:THR:HG23	0.44	2.27	11	1
2:B:4:ILE:N	2:B:4:ILE:HD13	0.44	2.26	15	1
1:A:414:ILE:HG12	1:A:434:ILE:HD11	0.44	1.89	20	1
1:A:387:MET:HE3	2:B:7:VAL:HG23	0.44	1.89	7	1
1:A:409:ILE:N	1:A:409:ILE:CD1	0.44	2.80	11	1
1:A:415:ILE:HD11	2:B:4:ILE:HG22	0.43	1.90	7	1
1:A:464:ARG:CB	1:A:469:ILE:HD11	0.43	2.41	6	1
1:A:402:HIS:O	1:A:403:ARG:CB	0.43	2.66	17	4
1:A:417:VAL:HG13	1:A:423:ALA:CB	0.43	2.44	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:437:ILE:HD12	1:A:460:MET:HG2	0.43	1.89	20	1
1:A:409:ILE:C	1:A:409:ILE:CD1	0.43	2.87	14	1
1:A:442:VAL:HG12	1:A:443:VAL:N	0.43	2.28	11	3
1:A:437:ILE:HD13	1:A:438:ASN:N	0.43	2.29	15	1
1:A:457:THR:HA	1:A:474:ILE:HD12	0.43	1.90	15	1
1:A:409:ILE:CD1	1:A:409:ILE:N	0.42	2.82	16	3
1:A:452:ILE:HD13	2:B:7:VAL:CG1	0.42	2.44	12	1
1:A:390:LEU:HD22	1:A:433:VAL:CG1	0.42	2.45	17	1
1:A:413:TYR:CE1	1:A:414:ILE:O	0.42	2.71	15	3
1:A:423:ALA:CA	1:A:428:LEU:HD12	0.42	2.44	16	2
1:A:418:ILE:HB	1:A:421:THR:HG23	0.42	1.90	17	1
1:A:383:ILE:CD1	1:A:385:ILE:CG2	0.42	2.96	13	7
1:A:426:GLY:O	1:A:471:ILE:HG23	0.42	2.15	9	1
1:A:386:ARG:NH2	2:B:6:TRP:CZ2	0.42	2.88	17	1
1:A:421:THR:OG1	1:A:422:PRO:HD2	0.42	2.14	7	1
1:A:418:ILE:HG22	1:A:419:PRO:CD	0.42	2.45	5	1
1:A:388:MET:HE2	2:B:2:SER:HA	0.42	1.92	15	1
1:A:442:VAL:HG13	1:A:447:ASP:HB3	0.42	1.92	18	1
1:A:437:ILE:HD13	1:A:437:ILE:C	0.41	2.35	15	1
1:A:387:MET:HE2	2:B:7:VAL:HG23	0.41	1.89	7	1
1:A:428:LEU:N	1:A:428:LEU:CD2	0.41	2.83	19	1
1:A:452:ILE:HD13	2:B:7:VAL:HG11	0.41	1.90	12	1
1:A:417:VAL:CG1	1:A:423:ALA:CB	0.41	2.99	11	2
1:A:409:ILE:H	1:A:409:ILE:HD13	0.41	1.72	11	1
1:A:459:ASN:CG	1:A:472:THR:HG23	0.41	2.36	20	1
1:A:458:LEU:CB	1:A:460:MET:CE	0.41	2.98	15	2
1:A:388:MET:HG2	1:A:415:ILE:HD11	0.41	1.93	15	1
1:A:470:MET:O	1:A:471:ILE:HD13	0.41	2.15	14	1
1:A:415:ILE:CG1	2:B:4:ILE:HG22	0.41	2.46	10	1
1:A:444:SER:O	1:A:448:VAL:HG23	0.41	2.16	3	1
1:A:390:LEU:HG	1:A:395:ALA:HB2	0.41	1.91	4	1
1:A:422:PRO:O	1:A:426:GLY:N	0.41	2.54	14	2
1:A:388:MET:CE	2:B:2:SER:CB	0.41	2.99	8	1
1:A:462:VAL:HG12	1:A:463:ARG:N	0.41	2.31	3	1
1:A:402:HIS:HB2	1:A:405:PHE:CE2	0.41	2.51	13	1
1:A:434:ILE:HG22	1:A:435:ILE:N	0.41	2.30	13	1
1:A:471:ILE:N	1:A:471:ILE:CD1	0.41	2.83	17	1
1:A:386:ARG:O	1:A:415:ILE:HD12	0.40	2.16	12	1
1:A:420:ASP:O	1:A:421:THR:HG22	0.40	2.17	11	1
1:A:418:ILE:O	1:A:421:THR:HG22	0.40	2.16	3	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	97/105 (92%)	81±3 (84±3%)	13±2 (14±3%)	2±2 (2±2%)	11	48
2	B	5/7 (71%)	3±1 (61±22%)	2±1 (33±21%)	0±0 (6±9%)	4	21
All	All	2040/2240 (91%)	1686 (83%)	300 (15%)	54 (3%)	11	47

All 16 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	390	LEU	10
1	A	420	ASP	8
1	A	406	PRO	7
1	A	427	GLY	7
2	B	3	ARG	4
1	A	431	ASN	3
1	A	415	ILE	3
1	A	465	GLY	2
1	A	409	ILE	2
1	A	435	ILE	2
1	A	430	GLU	1
1	A	404	ASP	1
2	B	2	SER	1
1	A	408	VAL	1
2	B	4	ILE	1
1	A	437	ILE	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	86/93 (92%)	68±2 (80±3%)	18±2 (20±3%)	4	34
2	B	6/7 (86%)	6±0 (94±8%)	0±0 (6±8%)	29	75
All	All	1840/2000 (92%)	1481 (80%)	359 (20%)	5	37

All 54 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	387	MET	20
1	A	470	MET	19
1	A	429	LYS	16
1	A	460	MET	14
1	A	430	GLU	13
1	A	394	LYS	13
1	A	428	LEU	13
1	A	402	HIS	12
1	A	421	THR	12
1	A	453	LYS	11
1	A	400	ASP	11
1	A	410	SER	10
1	A	401	ARG	10
1	A	409	ILE	10
1	A	456	SER	10
1	A	396	LYS	9
1	A	444	SER	9
1	A	393	SER	9
1	A	397	GLU	8
1	A	463	ARG	8
1	A	403	ARG	7
1	A	441	SER	7
1	A	431	ASN	7
1	A	381	LYS	6
1	A	447	ASP	6
1	A	404	ASP	6
1	A	457	THR	5
1	A	476	GLU	5
1	A	392	SER	5
1	A	468	ASP	5
1	A	477	GLU	5
1	A	407	ASP	4
1	A	464	ARG	4
1	A	385	ILE	4

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Mol	Chain	Res	Type	Models (Total)
1	A	386	ARG	4
2	B	2	SER	4
1	A	420	ASP	3
1	A	399	LYS	3
1	A	454	ARG	3
1	A	437	ILE	3
1	A	416	GLU	3
1	A	472	THR	3
1	A	388	MET	3
1	A	424	GLU	3
1	A	469	ILE	2
2	B	4	ILE	2
1	A	440	GLN	2
1	A	391	THR	2
2	B	3	ARG	1
1	A	455	GLU	1
1	A	432	ASP	1
1	A	383	ILE	1
1	A	459	ASN	1
1	A	418	ILE	1

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 6.7 Other polymers [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

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 85% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 15154

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 7.1.1 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	1319
Number of shifts mapped to atoms	1319
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	101	$-0.23 \pm 0.12$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	95	$0.11 \pm 0.11$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	95	$-0.02 \pm 0.13$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	96	$0.75 \pm 0.44$	None needed (imprecise)

#### 7.1.3 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 87%, i.e. 1112 atoms were assigned a chemical shift out of a possible 1271. 14 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	485/507 (96%)	202/202 (100%)	190/206 (92%)	93/99 (94%)
Sidechain	599/707 (85%)	373/411 (91%)	217/263 (83%)	9/33 (27%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	28/57 (49%)	23/29 (79%)	5/24 (21%)	0/4 (0%)
Overall	1112/1271 (87%)	598/642 (93%)	412/493 (84%)	102/136 (75%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 85%, i.e. 1164 atoms were assigned a chemical shift out of a possible 1375. 14 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	503/550 (91%)	211/219 (96%)	196/224 (88%)	96/107 (90%)
Sidechain	633/760 (83%)	395/443 (89%)	229/283 (81%)	9/34 (26%)
Aromatic	28/65 (43%)	23/33 (70%)	5/26 (19%)	0/6 (0%)
Overall	1164/1375 (85%)	629/695 (91%)	430/533 (81%)	105/147 (71%)

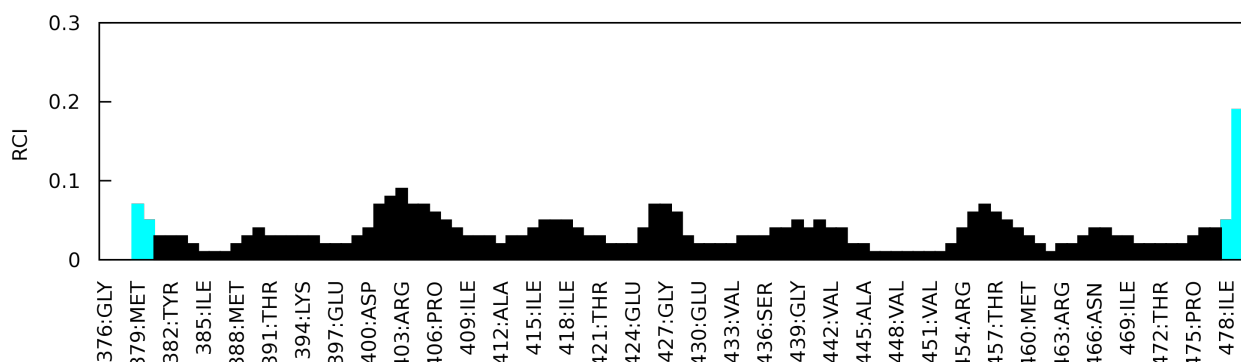
#### 7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

#### 7.1.5 Random Coil Index (RCI) plots [i](#)

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:

