



# Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 10:58 pm BST

PDB ID : 2KOD  
Title : A high-resolution NMR structure of the dimeric C-terminal domain of HIV-1 CA  
Authors : Byeon, I.-J.L.; Jung, J.; Ahn, J.; concel, J.; Gronenborn, A.M.  
Deposited on : 2009-09-18

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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  
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

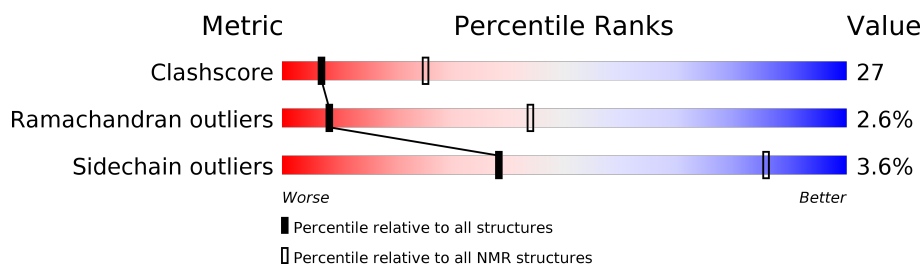
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment was not calculated.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	88	
1	B	88	

## 2 Ensemble composition and analysis i

This entry contains 30 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:145-A:221, B:145-B:221 (154)	0.26	1

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 4 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 4, 7, 10, 11, 12, 14, 17, 20, 21, 23, 24, 26, 28, 30
2	3, 5, 13, 16, 18, 27
3	6, 9, 25, 29
4	2, 15, 19, 22
Single-model clusters	8

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2762 atoms, of which 1388 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called HIV-1 CA C-terminal domain.

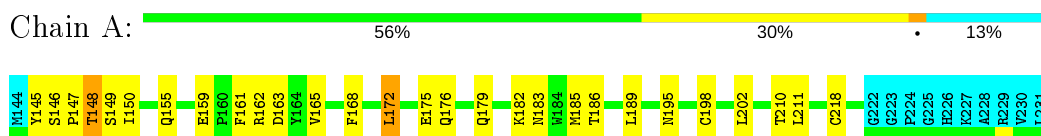
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	88	1381	431	694	120	130	6	0
1	B	88	1381	431	694	120	130	6	0

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

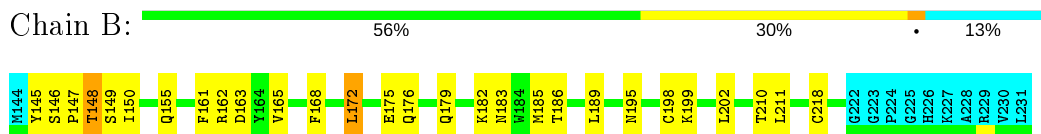
### 4.1 Average score per residue in the NMR ensemble

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: HIV-1 CA C-terminal domain



- Molecule 1: HIV-1 CA C-terminal domain

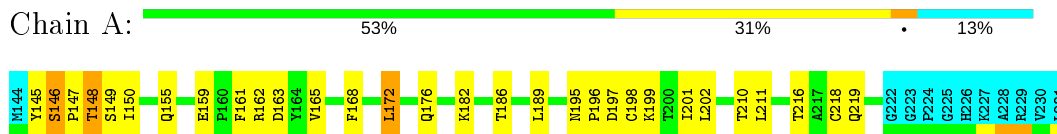


### 4.2 Scores per residue for each member of the ensemble

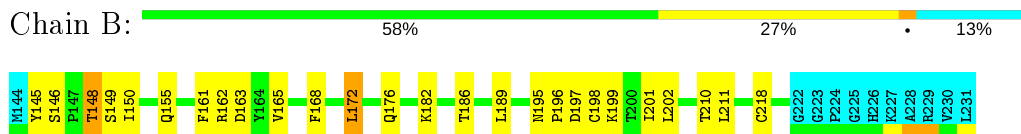
Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: HIV-1 CA C-terminal domain

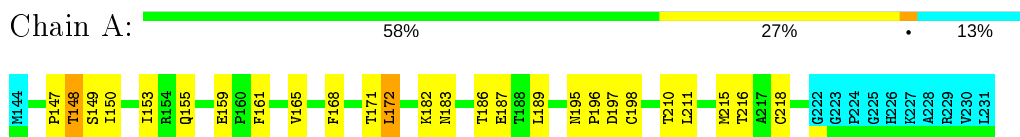


- Molecule 1: HIV-1 CA C-terminal domain

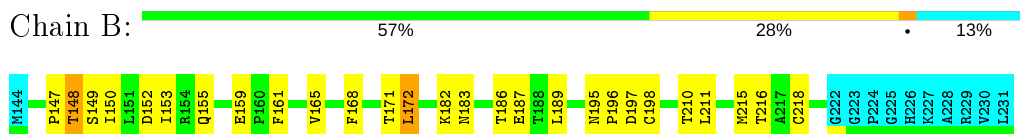


### 4.2.2 Score per residue for model 2

- Molecule 1: HIV-1 CA C-terminal domain

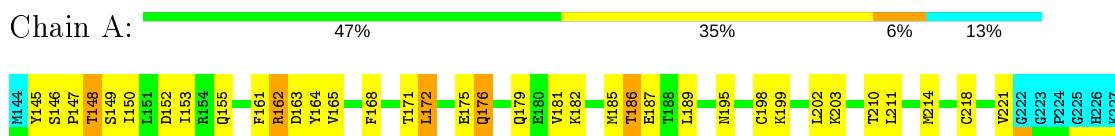


- Molecule 1: HIV-1 CA C-terminal domain

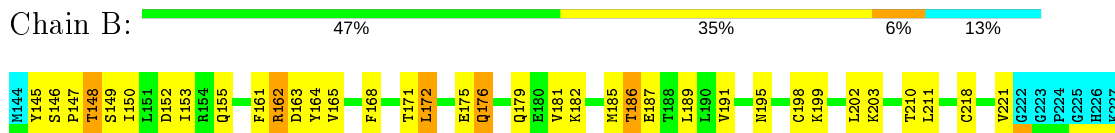


### 4.2.3 Score per residue for model 3

- Molecule 1: HIV-1 CA C-terminal domain

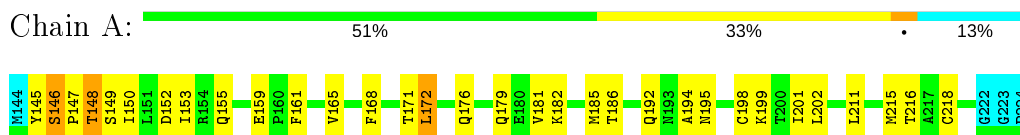


- Molecule 1: HIV-1 CA C-terminal domain

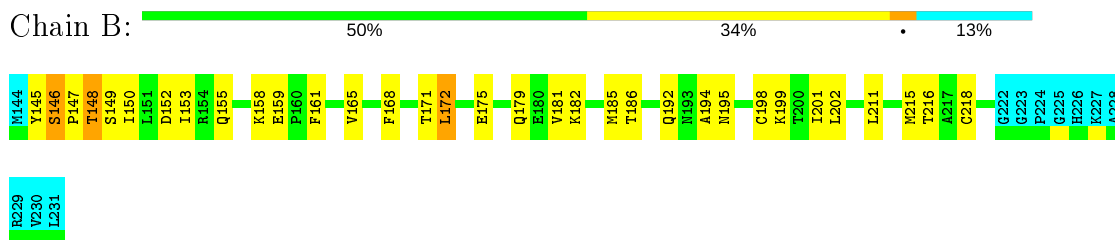


### 4.2.4 Score per residue for model 4

- Molecule 1: HIV-1 CA C-terminal domain

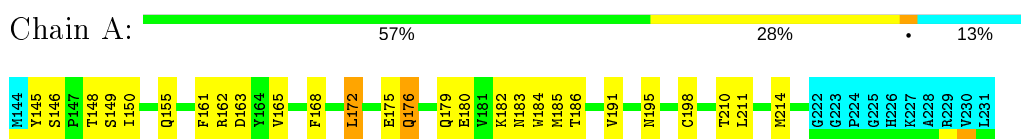


- Molecule 1: HIV-1 CA C-terminal domain

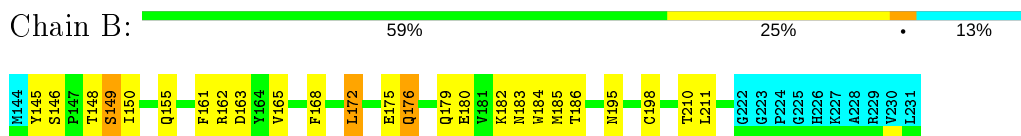


#### 4.2.5 Score per residue for model 5

- Molecule 1: HIV-1 CA C-terminal domain

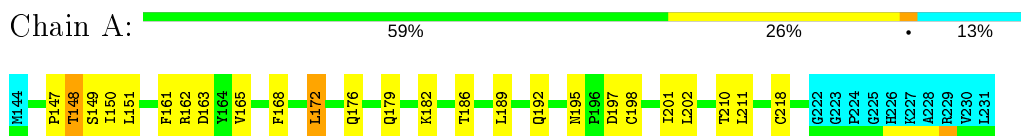


- Molecule 1: HIV-1 CA C-terminal domain

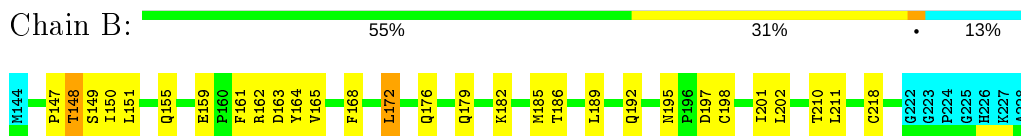


#### 4.2.6 Score per residue for model 6

- Molecule 1: HIV-1 CA C-terminal domain



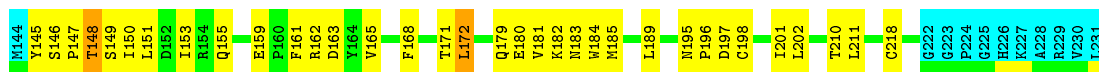
- Molecule 1: HIV-1 CA C-terminal domain



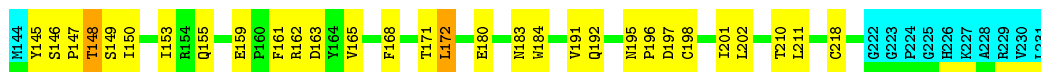
#### 4.2.7 Score per residue for model 7

- Molecule 1: HIV-1 CA C-terminal domain





- Molecule 1: HIV-1 CA C-terminal domain



#### 4.2.8 Score per residue for model 8

- Molecule 1: HIV-1 CA C-terminal domain

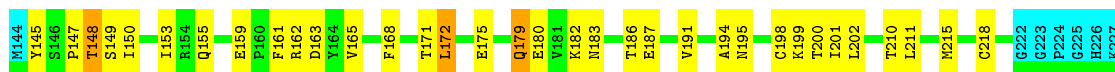


- Molecule 1: HIV-1 CA C-terminal domain

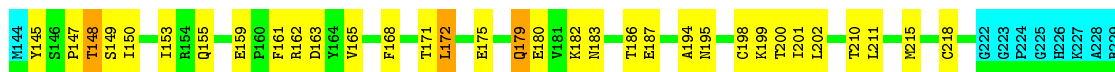


#### 4.2.9 Score per residue for model 9

- Molecule 1: HIV-1 CA C-terminal domain



- Molecule 1: HIV-1 CA C-terminal domain



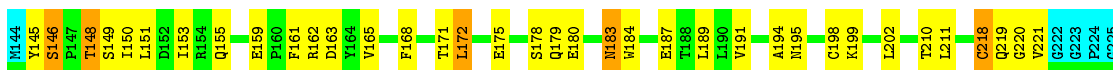


V230  
L231

#### 4.2.10 Score per residue for model 10

- Molecule 1: HIV-1 CA C-terminal domain

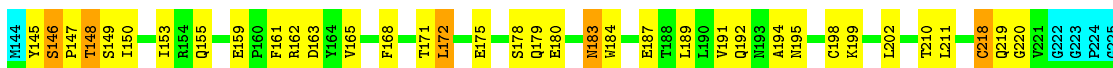
Chain A: 



H226  
K227  
A228  
R229  
V230  
L231

- Molecule 1: HIV-1 CA C-terminal domain

Chain B: 

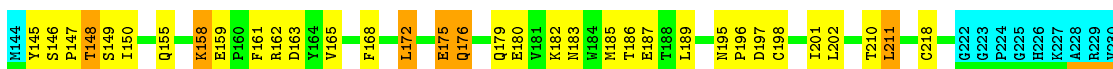


H226  
K227  
A228  
R229  
V230  
L231

#### 4.2.11 Score per residue for model 11

- Molecule 1: HIV-1 CA C-terminal domain

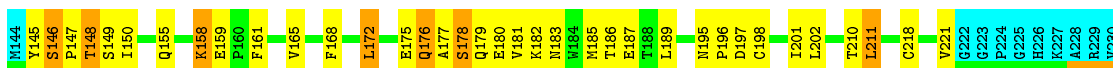
Chain A: 



L231

- Molecule 1: HIV-1 CA C-terminal domain

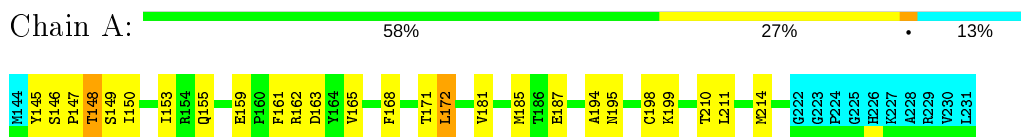
Chain B: 



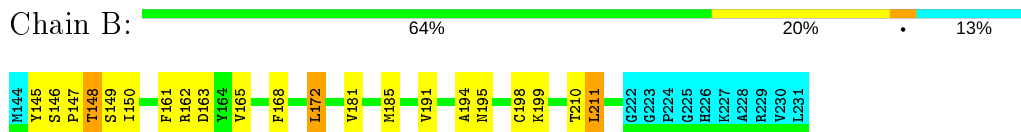
L231

#### 4.2.12 Score per residue for model 12

- Molecule 1: HIV-1 CA C-terminal domain

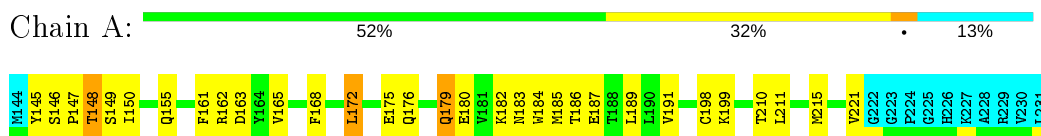


- Molecule 1: HIV-1 CA C-terminal domain

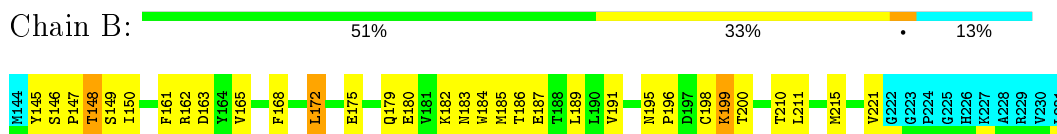


#### 4.2.13 Score per residue for model 13

- Molecule 1: HIV-1 CA C-terminal domain

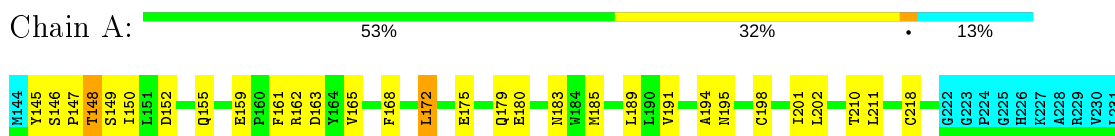


- Molecule 1: HIV-1 CA C-terminal domain

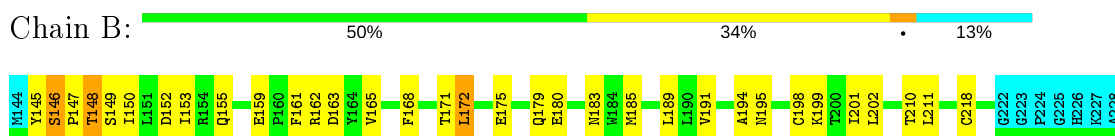


#### 4.2.14 Score per residue for model 14

- Molecule 1: HIV-1 CA C-terminal domain



- Molecule 1: HIV-1 CA C-terminal domain

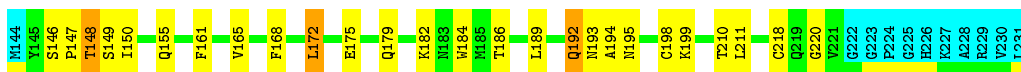


R229  
V230  
L231

#### 4.2.15 Score per residue for model 15

- Molecule 1: HIV-1 CA C-terminal domain

Chain A: 58% 26% 13%



- Molecule 1: HIV-1 CA C-terminal domain

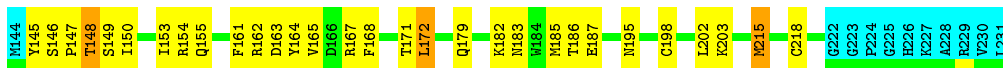
Chain B: 53% 31% 13%



#### 4.2.16 Score per residue for model 16

- Molecule 1: HIV-1 CA C-terminal domain

Chain A: 53% 31% 13%



- Molecule 1: HIV-1 CA C-terminal domain

Chain B: 51% 31% 6% 13%



#### 4.2.17 Score per residue for model 17

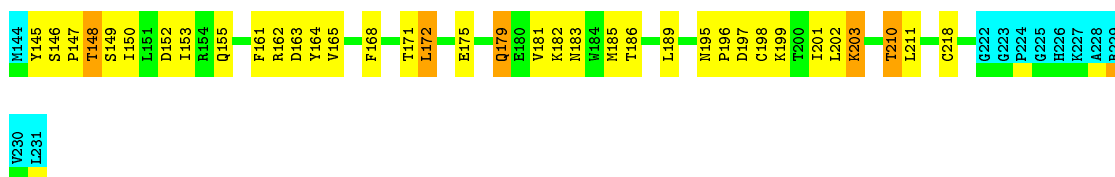
- Molecule 1: HIV-1 CA C-terminal domain

Chain A: 51% 31% 6% 13%



- Molecule 1: HIV-1 CA C-terminal domain

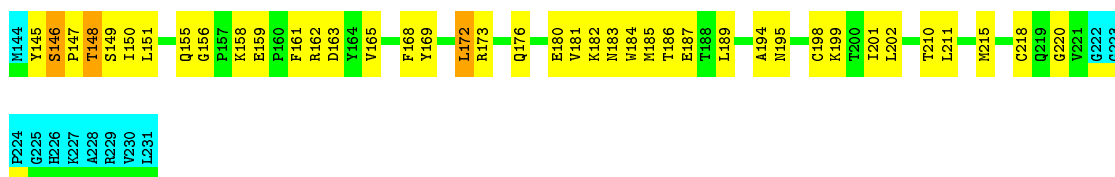
Chain B: 47% 35% 6% 13%



#### 4.2.18 Score per residue for model 18

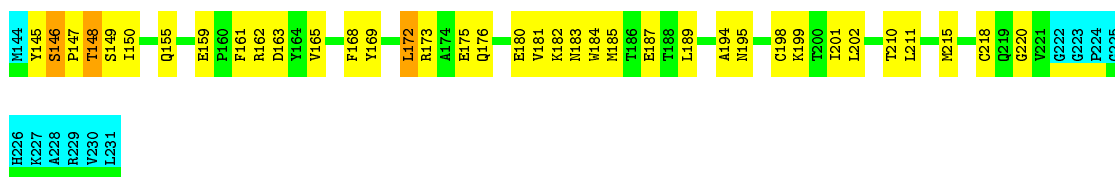
- Molecule 1: HIV-1 CA C-terminal domain

Chain A: 42% 42% 13%



- Molecule 1: HIV-1 CA C-terminal domain

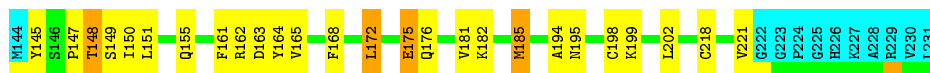
Chain B: 45% 39% 13%



#### 4.2.19 Score per residue for model 19

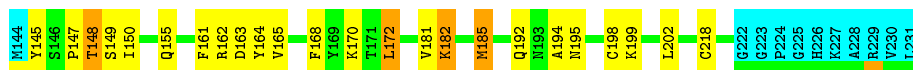
- Molecule 1: HIV-1 CA C-terminal domain

Chain A: 58% 25% 5% 13%



- Molecule 1: HIV-1 CA C-terminal domain

Chain B: 60% 23% 5% 13%



#### 4.2.20 Score per residue for model 20

- Molecule 1: HIV-1 CA C-terminal domain

Chain A: 



- Molecule 1: HIV-1 CA C-terminal domain

Chain B: 



#### 4.2.21 Score per residue for model 21

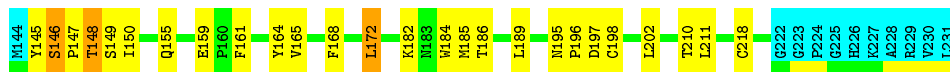
- Molecule 1: HIV-1 CA C-terminal domain

Chain A: 



- Molecule 1: HIV-1 CA C-terminal domain

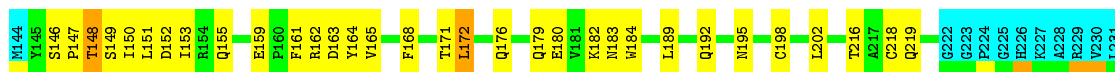
Chain B: 



#### 4.2.22 Score per residue for model 22

- Molecule 1: HIV-1 CA C-terminal domain

Chain A: 



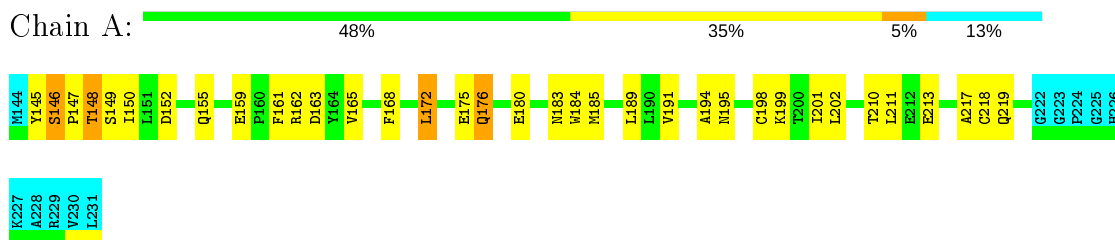
- Molecule 1: HIV-1 CA C-terminal domain

Chain B: 

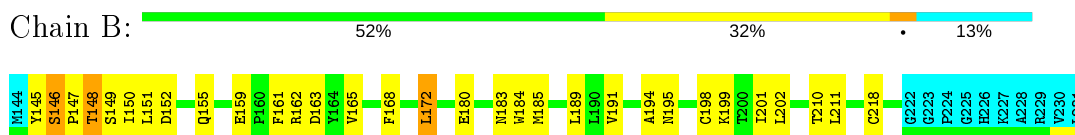


### 4.2.23 Score per residue for model 23

- Molecule 1: HIV-1 CA C-terminal domain



- Molecule 1: HIV-1 CA C-terminal domain

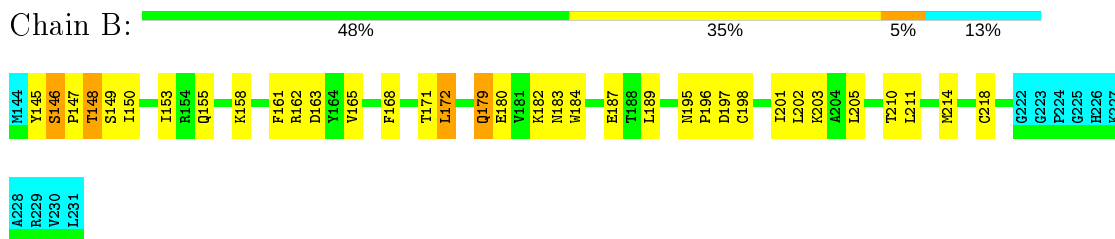


### 4.2.24 Score per residue for model 24

- Molecule 1: HIV-1 CA C-terminal domain

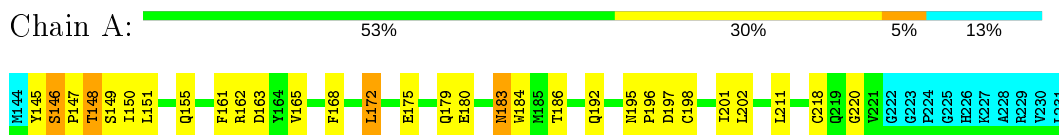


- Molecule 1: HIV-1 CA C-terminal domain

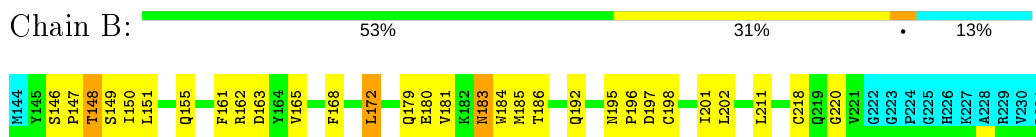


### 4.2.25 Score per residue for model 25

- Molecule 1: HIV-1 CA C-terminal domain

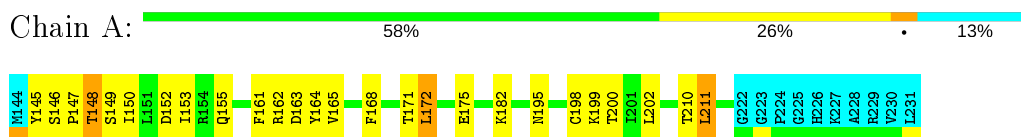


- Molecule 1: HIV-1 CA C-terminal domain

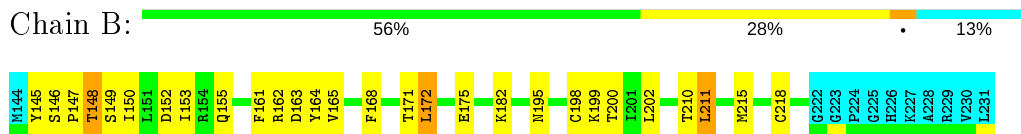


#### 4.2.26 Score per residue for model 26

- Molecule 1: HIV-1 CA C-terminal domain

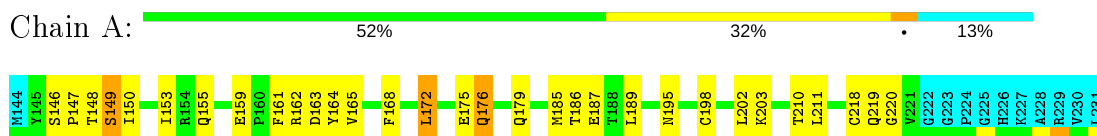


- Molecule 1: HIV-1 CA C-terminal domain

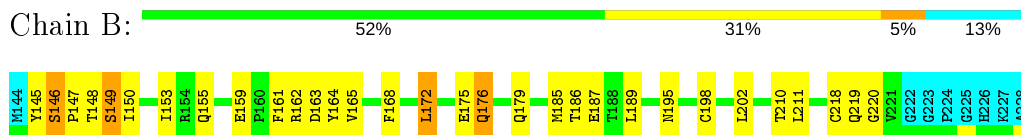


#### 4.2.27 Score per residue for model 27

- Molecule 1: HIV-1 CA C-terminal domain

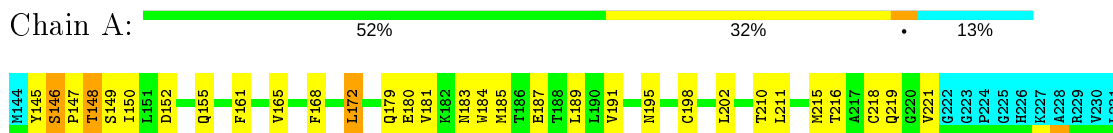


- Molecule 1: HIV-1 CA C-terminal domain

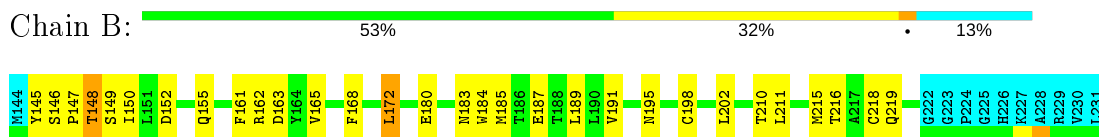


#### 4.2.28 Score per residue for model 28

- Molecule 1: HIV-1 CA C-terminal domain

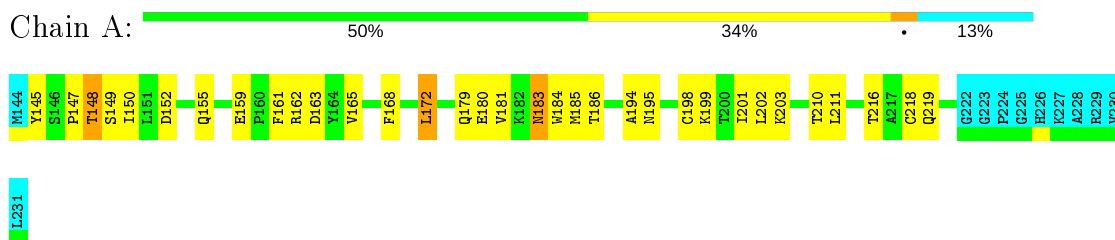


- Molecule 1: HIV-1 CA C-terminal domain

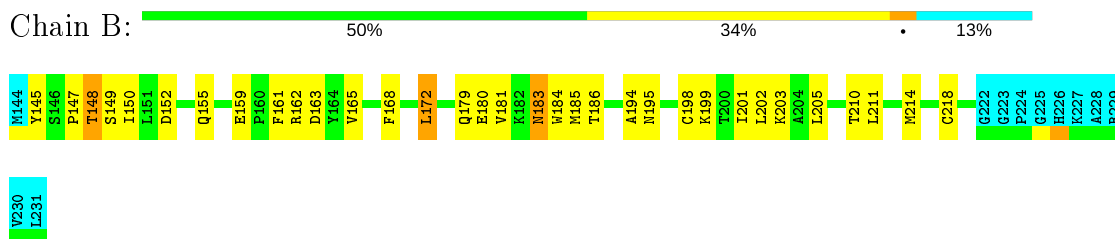


#### 4.2.29 Score per residue for model 29

- Molecule 1: HIV-1 CA C-terminal domain

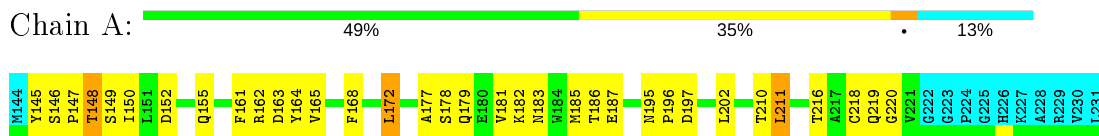


- Molecule 1: HIV-1 CA C-terminal domain

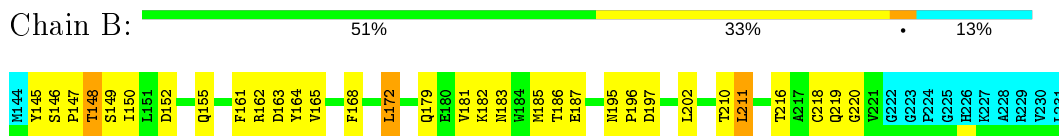


#### 4.2.30 Score per residue for model 30

- Molecule 1: HIV-1 CA C-terminal domain



- Molecule 1: HIV-1 CA C-terminal domain





## 5 Refinement protocol and experimental data overview

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

Of the 500 calculated structures, 30 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
X-PLOR NIH	refinement	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality 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	609	608	608	34±7
1	B	609	608	608	34±7
All	All	36540	36480	36480	1979

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 27.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:194:ALA:HB1	1:B:198:CYS:SG	0.81	2.16	9	11
1:A:194:ALA:HB1	1:A:198:CYS:SG	0.80	2.16	14	11
1:B:202:LEU:HD21	1:B:218:CYS:SG	0.79	2.17	29	17
1:A:172:LEU:HD12	1:A:172:LEU:O	0.79	1.78	18	14
1:A:202:LEU:HD21	1:A:218:CYS:SG	0.78	2.18	29	17
1:B:172:LEU:HD12	1:B:172:LEU:O	0.78	1.78	18	12
1:B:150:ILE:HD12	1:B:168:PHE:CE2	0.78	2.14	28	4
1:B:150:ILE:HD11	1:B:168:PHE:CE2	0.77	2.15	17	20
1:A:150:ILE:HD11	1:A:168:PHE:CE2	0.77	2.15	26	23
1:A:172:LEU:O	1:A:172:LEU:HD12	0.77	1.80	24	16
1:B:172:LEU:O	1:B:172:LEU:HD12	0.77	1.79	24	18
1:A:172:LEU:CD2	1:A:182:LYS:HZ3	0.75	1.95	18	1
1:A:150:ILE:HD12	1:A:168:PHE:CE2	0.73	2.18	28	3

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:172:LEU:CD2	1:B:182:LYS:HZ3	0.71	1.98	18	2
1:A:150:ILE:HD11	1:A:168:PHE:CD2	0.71	2.21	27	21
1:B:150:ILE:HD11	1:B:168:PHE:CD2	0.67	2.24	3	18
1:B:180:GLU:O	1:B:183:ASN:ND2	0.67	2.28	25	5
1:A:198:CYS:SG	1:A:202:LEU:HD11	0.65	2.32	3	4
1:A:180:GLU:O	1:A:183:ASN:ND2	0.65	2.29	29	3
1:A:155:GLN:NE2	1:A:195:ASN:ND2	0.65	2.45	3	18
1:B:195:ASN:OD1	1:B:195:ASN:N	0.64	2.30	16	3
1:B:198:CYS:HG	1:B:218:CYS:HG	0.64	1.33	21	1
1:A:161:PHE:CE2	1:A:165:VAL:CG2	0.64	2.81	20	30
1:B:153:ILE:HD11	1:B:171:THR:OG1	0.64	1.92	8	13
1:A:155:GLN:NE2	1:A:195:ASN:HD21	0.64	1.90	16	1
1:B:186:THR:O	1:B:186:THR:HG22	0.64	1.91	27	3
1:A:186:THR:HG22	1:A:186:THR:O	0.64	1.92	27	4
1:A:195:ASN:N	1:A:195:ASN:OD1	0.64	2.30	16	1
1:B:155:GLN:NE2	1:B:195:ASN:ND2	0.64	2.46	24	19
1:B:161:PHE:CE2	1:B:165:VAL:CG2	0.63	2.81	23	30
1:A:172:LEU:HD22	1:A:182:LYS:HZ2	0.63	1.54	26	1
1:B:172:LEU:HD22	1:B:182:LYS:HZ2	0.63	1.53	26	1
1:B:155:GLN:NE2	1:B:195:ASN:HD21	0.63	1.91	16	2
1:A:179:GLN:HE22	1:A:183:ASN:ND2	0.62	1.92	17	4
1:B:179:GLN:HE22	1:B:183:ASN:ND2	0.62	1.92	30	4
1:A:153:ILE:HD11	1:A:171:THR:OG1	0.62	1.95	8	14
1:A:202:LEU:HD21	1:A:218:CYS:HG	0.61	1.54	24	1
1:A:184:TRP:CH2	1:B:185:MET:SD	0.61	2.93	23	6
1:B:158:LYS:CD	1:B:158:LYS:H	0.61	2.08	11	1
1:A:172:LEU:CD2	1:A:182:LYS:HZ2	0.61	2.08	26	1
1:A:185:MET:SD	1:B:184:TRP:CH2	0.61	2.94	23	7
1:B:198:CYS:SG	1:B:202:LEU:HD11	0.61	2.35	26	3
1:B:183:ASN:ND2	1:B:184:TRP:N	0.60	2.49	10	4
1:A:183:ASN:HD22	1:A:183:ASN:C	0.60	2.00	25	2
1:B:195:ASN:N	1:B:195:ASN:OD1	0.60	2.33	27	1
1:A:210:THR:HG22	1:A:211:LEU:N	0.60	2.12	6	22
1:B:201:ILE:HG23	1:B:202:LEU:N	0.60	2.12	18	15
1:B:183:ASN:HD22	1:B:184:TRP:N	0.60	1.95	25	4
1:B:172:LEU:C	1:B:172:LEU:HD12	0.60	2.17	9	17
1:B:210:THR:HG22	1:B:211:LEU:N	0.59	2.12	29	23
1:A:172:LEU:HD12	1:A:172:LEU:C	0.59	2.16	18	15
1:B:172:LEU:CD2	1:B:182:LYS:HZ2	0.59	2.10	26	1
1:A:185:MET:CE	1:B:184:TRP:CZ2	0.59	2.86	28	1
1:A:153:ILE:HG22	1:A:164:TYR:CE1	0.59	2.33	27	1

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:172:LEU:HD12	1:B:172:LEU:C	0.59	2.17	24	13
1:A:198:CYS:SG	1:A:218:CYS:SG	0.59	3.01	22	2
1:B:155:GLN:NE2	1:B:195:ASN:OD1	0.58	2.37	27	2
1:A:172:LEU:C	1:A:172:LEU:HD12	0.58	2.18	24	15
1:A:183:ASN:ND2	1:A:184:TRP:N	0.58	2.51	10	4
1:B:195:ASN:OD1	1:B:198:CYS:N	0.58	2.36	14	15
1:A:201:ILE:HG23	1:A:202:LEU:N	0.57	2.13	18	14
1:B:148:THR:OG1	1:B:149:SER:N	0.57	2.36	18	30
1:A:202:LEU:CD1	1:A:218:CYS:SG	0.57	2.92	10	2
1:B:202:LEU:CD1	1:B:218:CYS:SG	0.57	2.92	10	2
1:A:148:THR:OG1	1:A:149:SER:N	0.57	2.37	18	30
1:A:195:ASN:OD1	1:A:198:CYS:N	0.57	2.36	14	17
1:A:172:LEU:CD2	1:A:182:LYS:NZ	0.57	2.68	26	2
1:B:198:CYS:SG	1:B:218:CYS:SG	0.57	3.02	22	3
1:B:181:VAL:HG12	1:B:185:MET:SD	0.57	2.40	17	4
1:B:153:ILE:HG22	1:B:164:TYR:CE1	0.57	2.35	27	1
1:B:202:LEU:HD21	1:B:218:CYS:HG	0.56	1.56	24	1
1:A:184:TRP:CZ2	1:B:185:MET:CE	0.56	2.87	28	1
1:B:148:THR:HG1	1:B:175:GLU:CD	0.56	2.03	17	4
1:A:198:CYS:SG	1:A:202:LEU:HD13	0.56	2.41	27	3
1:A:155:GLN:NE2	1:A:195:ASN:OD1	0.56	2.39	22	1
1:B:172:LEU:CD2	1:B:182:LYS:NZ	0.56	2.68	26	2
1:B:201:ILE:CG2	1:B:202:LEU:N	0.56	2.69	18	2
1:A:150:ILE:CG1	1:A:168:PHE:CE2	0.56	2.89	25	19
1:A:201:ILE:CG2	1:A:202:LEU:N	0.55	2.69	18	2
1:A:191:VAL:HG11	1:B:145:TYR:CE1	0.55	2.37	23	8
1:A:179:GLN:NE2	1:A:179:GLN:O	0.55	2.39	25	5
1:B:198:CYS:SG	1:B:202:LEU:HD13	0.55	2.41	27	3
1:B:159:GLU:OE1	1:B:167:ARG:NH2	0.55	2.40	20	1
1:B:175:GLU:O	1:B:176:GLN:CB	0.55	2.53	5	1
1:A:145:TYR:CE1	1:B:191:VAL:HG11	0.55	2.35	14	7
1:A:179:GLN:O	1:A:179:GLN:NE2	0.55	2.39	5	5
1:B:179:GLN:O	1:B:179:GLN:NE2	0.55	2.39	5	7
1:B:179:GLN:NE2	1:B:179:GLN:O	0.55	2.39	25	3
1:B:145:TYR:CD2	1:B:146:SER:N	0.55	2.74	16	20
1:B:195:ASN:OD1	1:B:198:CYS:SG	0.55	2.65	9	17
1:B:155:GLN:NE2	1:B:198:CYS:SG	0.55	2.80	25	8
1:A:195:ASN:OD1	1:A:195:ASN:N	0.55	2.37	22	1
1:B:202:LEU:CD2	1:B:218:CYS:SG	0.55	2.95	6	15
1:A:202:LEU:CD2	1:A:218:CYS:SG	0.54	2.95	18	17
1:B:180:GLU:CD	1:B:183:ASN:HD21	0.54	2.06	28	1

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:198:CYS:SG	1:B:199:LYS:N	0.54	2.80	12	11
1:A:195:ASN:OD1	1:A:198:CYS:SG	0.54	2.65	23	17
1:B:179:GLN:C	1:B:179:GLN:NE2	0.54	2.61	17	1
1:A:155:GLN:NE2	1:A:198:CYS:SG	0.54	2.80	7	12
1:B:183:ASN:C	1:B:183:ASN:ND2	0.54	2.61	20	4
1:A:154:ARG:C	1:A:167:ARG:NH2	0.54	2.61	16	1
1:B:165:VAL:CG1	1:B:211:LEU:HD21	0.54	2.33	21	5
1:A:145:TYR:CD2	1:A:146:SER:N	0.54	2.76	30	16
1:A:199:LYS:NZ	1:A:203:LYS:NZ	0.54	2.56	3	1
1:B:155:GLN:CD	1:B:195:ASN:ND2	0.54	2.62	18	21
1:A:179:GLN:C	1:A:179:GLN:NE2	0.54	2.61	17	2
1:A:159:GLU:OE1	1:A:167:ARG:NH2	0.54	2.40	20	1
1:B:183:ASN:OD1	1:B:184:TRP:N	0.54	2.41	24	8
1:A:183:ASN:HD22	1:A:184:TRP:N	0.53	2.01	10	4
1:B:211:LEU:HD23	1:B:211:LEU:C	0.53	2.23	17	6
1:B:150:ILE:CG1	1:B:168:PHE:CE2	0.53	2.91	25	18
1:B:165:VAL:CG1	1:B:211:LEU:HD11	0.53	2.34	2	3
1:A:198:CYS:SG	1:A:202:LEU:CD1	0.53	2.97	26	5
1:A:183:ASN:OD1	1:A:184:TRP:N	0.53	2.42	28	8
1:B:149:SER:O	1:B:152:ASP:N	0.53	2.41	23	9
1:A:181:VAL:HG12	1:A:185:MET:SD	0.53	2.44	29	2
1:B:154:ARG:C	1:B:167:ARG:NH2	0.53	2.62	16	1
1:A:155:GLN:CD	1:A:195:ASN:ND2	0.53	2.62	18	17
1:B:155:GLN:NE2	1:B:159:GLU:O	0.53	2.42	2	6
1:A:192:GLN:NE2	1:A:193:ASN:OD1	0.53	2.41	15	1
1:B:192:GLN:NE2	1:B:193:ASN:OD1	0.53	2.42	15	1
1:A:183:ASN:ND2	1:A:183:ASN:C	0.53	2.62	20	3
1:A:165:VAL:CG1	1:A:211:LEU:HD21	0.52	2.34	21	5
1:A:155:GLN:CD	1:A:195:ASN:HD22	0.52	2.06	4	2
1:B:211:LEU:HD23	1:B:211:LEU:O	0.52	2.04	23	4
1:A:211:LEU:O	1:A:211:LEU:HD23	0.52	2.04	17	6
1:A:219:GLN:CG	1:A:220:GLY:N	0.52	2.73	30	3
1:A:165:VAL:CG1	1:A:211:LEU:HD11	0.52	2.34	2	3
1:B:179:GLN:NE2	1:B:179:GLN:C	0.52	2.63	9	1
1:B:195:ASN:O	1:B:197:ASP:N	0.52	2.41	30	9
1:B:175:GLU:O	1:B:176:GLN:C	0.52	2.48	20	5
1:A:199:LYS:NZ	1:B:145:TYR:OH	0.52	2.42	29	3
1:A:195:ASN:O	1:A:197:ASP:N	0.52	2.43	17	10
1:A:211:LEU:HD23	1:A:211:LEU:C	0.52	2.25	25	4
1:B:158:LYS:CG	1:B:158:LYS:O	0.52	2.58	24	1
1:A:155:GLN:NE2	1:A:159:GLU:O	0.52	2.43	2	6

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:149:SER:O	1:A:152:ASP:N	0.52	2.43	23	8
1:A:198:CYS:SG	1:A:199:LYS:N	0.52	2.83	12	10
1:B:158:LYS:CD	1:B:158:LYS:N	0.52	2.72	11	1
1:A:189:LEU:HD12	1:A:189:LEU:N	0.52	2.20	23	7
1:B:189:LEU:HD12	1:B:189:LEU:N	0.51	2.20	20	8
1:B:211:LEU:C	1:B:211:LEU:HD23	0.51	2.24	2	3
1:B:218:CYS:SG	1:B:218:CYS:O	0.51	2.68	2	2
1:A:211:LEU:C	1:A:211:LEU:HD23	0.51	2.26	24	5
1:B:219:GLN:CG	1:B:220:GLY:N	0.51	2.74	30	3
1:B:177:ALA:O	1:B:181:VAL:CG2	0.51	2.59	11	1
1:B:194:ALA:HB1	1:B:198:CYS:HG	0.51	1.64	29	1
1:B:214:MET:O	1:B:218:CYS:SG	0.51	2.69	24	2
1:A:211:LEU:CD2	1:A:215:MET:SD	0.51	2.99	2	1
1:A:175:GLU:O	1:A:176:GLN:C	0.51	2.49	23	6
1:A:155:GLN:OE1	1:A:198:CYS:SG	0.51	2.67	15	1
1:B:179:GLN:HE22	1:B:183:ASN:HD21	0.51	1.48	9	1
1:A:145:TYR:OH	1:B:199:LYS:NZ	0.51	2.44	29	3
1:B:198:CYS:SG	1:B:202:LEU:CD1	0.51	2.98	26	4
1:B:185:MET:C	1:B:187:GLU:H	0.50	2.10	3	6
1:A:191:VAL:CG1	1:B:145:TYR:CE1	0.50	2.94	14	6
1:A:211:LEU:HD23	1:A:211:LEU:O	0.50	2.06	9	3
1:A:218:CYS:SG	1:A:218:CYS:O	0.50	2.68	2	1
1:A:214:MET:O	1:A:218:CYS:SG	0.50	2.70	24	2
1:A:183:ASN:OD1	1:A:183:ASN:C	0.50	2.50	22	6
1:B:211:LEU:O	1:B:211:LEU:HD23	0.50	2.06	25	5
1:B:179:GLN:HE22	1:B:182:LYS:HD3	0.50	1.67	22	2
1:A:179:GLN:NE2	1:A:183:ASN:ND2	0.50	2.58	30	1
1:A:189:LEU:N	1:A:189:LEU:HD12	0.50	2.21	8	10
1:A:195:ASN:ND2	1:A:198:CYS:SG	0.50	2.83	2	8
1:B:155:GLN:CD	1:B:195:ASN:HD22	0.50	2.10	18	2
1:B:145:TYR:CD1	1:B:145:TYR:N	0.50	2.80	20	4
1:B:189:LEU:N	1:B:189:LEU:HD12	0.50	2.20	28	9
1:A:145:TYR:CE1	1:B:191:VAL:CG1	0.50	2.94	14	8
1:A:210:THR:HG22	1:A:211:LEU:H	0.50	1.67	29	6
1:B:183:ASN:C	1:B:183:ASN:OD1	0.50	2.50	22	7
1:B:155:GLN:OE1	1:B:198:CYS:SG	0.50	2.69	15	3
1:A:181:VAL:O	1:A:185:MET:N	0.50	2.40	3	6
1:A:186:THR:O	1:A:186:THR:HG22	0.50	2.07	20	2
1:A:195:ASN:OD1	1:A:198:CYS:CB	0.49	2.60	3	9
1:B:181:VAL:O	1:B:185:MET:N	0.49	2.39	3	5
1:B:199:LYS:NZ	1:B:203:LYS:NZ	0.49	2.60	3	1

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:178:SER:CB	1:B:180:GLU:OE2	0.49	2.60	10	1
1:B:176:GLN:OE1	1:B:176:GLN:N	0.49	2.45	1	1
1:B:195:ASN:OD1	1:B:198:CYS:CB	0.49	2.61	21	9
1:A:154:ARG:C	1:A:167:ARG:HH22	0.49	2.09	16	1
1:B:211:LEU:O	1:B:211:LEU:HD13	0.49	2.06	26	1
1:B:145:TYR:O	1:B:146:SER:OG	0.49	2.28	18	3
1:B:211:LEU:CD2	1:B:215:MET:SD	0.49	3.00	2	1
1:A:172:LEU:CD1	1:A:172:LEU:C	0.49	2.78	18	10
1:A:189:LEU:N	1:A:189:LEU:CD1	0.49	2.75	20	7
1:A:179:GLN:HE22	1:A:182:LYS:HD3	0.49	1.66	22	2
1:B:195:ASN:ND2	1:B:198:CYS:SG	0.49	2.86	11	9
1:A:185:MET:C	1:A:187:GLU:H	0.49	2.10	3	8
1:A:180:GLU:OE2	1:B:178:SER:CB	0.49	2.61	10	1
1:A:211:LEU:HD13	1:A:211:LEU:O	0.49	2.08	26	1
1:A:183:ASN:C	1:A:183:ASN:OD1	0.48	2.52	24	3
1:A:145:TYR:N	1:A:145:TYR:CD1	0.48	2.81	20	6
1:B:155:GLN:OE1	1:B:159:GLU:O	0.48	2.31	27	7
1:B:210:THR:HG22	1:B:211:LEU:H	0.48	1.67	23	9
1:A:169:TYR:CE2	1:A:182:LYS:NZ	0.48	2.81	18	1
1:B:195:ASN:C	1:B:197:ASP:H	0.48	2.11	30	9
1:B:154:ARG:C	1:B:167:ARG:HH22	0.48	2.11	16	1
1:A:177:ALA:O	1:A:181:VAL:CG2	0.48	2.61	30	1
1:A:182:LYS:O	1:A:186:THR:CB	0.48	2.62	3	13
1:A:150:ILE:CD1	1:A:168:PHE:CE2	0.48	2.96	22	13
1:A:147:PRO:O	1:A:148:THR:C	0.48	2.52	18	26
1:A:183:ASN:C	1:A:183:ASN:ND2	0.48	2.66	10	1
1:B:183:ASN:OD1	1:B:183:ASN:C	0.48	2.52	7	2
1:A:192:GLN:OE1	1:B:151:LEU:HD13	0.48	2.08	22	1
1:B:182:LYS:O	1:B:186:THR:CB	0.47	2.62	3	12
1:A:155:GLN:OE1	1:A:161:PHE:N	0.47	2.47	7	2
1:B:148:THR:OG1	1:B:175:GLU:CD	0.47	2.51	11	4
1:A:176:GLN:CD	1:A:176:GLN:N	0.47	2.67	22	2
1:B:186:THR:O	1:B:186:THR:CG2	0.47	2.62	27	3
1:B:165:VAL:HG11	1:B:211:LEU:HD11	0.47	1.85	2	3
1:B:169:TYR:CE2	1:B:182:LYS:NZ	0.47	2.82	18	1
1:A:145:TYR:CD1	1:A:145:TYR:N	0.47	2.82	3	11
1:A:155:GLN:OE1	1:A:159:GLU:O	0.47	2.33	22	9
1:B:189:LEU:CD1	1:B:189:LEU:N	0.47	2.77	20	7
1:B:145:TYR:N	1:B:145:TYR:CD1	0.47	2.82	3	11
1:A:195:ASN:O	1:A:195:ASN:OD1	0.47	2.33	23	9
1:B:150:ILE:CD1	1:B:168:PHE:CE2	0.47	2.97	22	9

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:172:LEU:C	1:B:172:LEU:CD1	0.47	2.82	9	12
1:A:199:LYS:CG	1:A:200:THR:N	0.47	2.77	26	2
1:A:215:MET:O	1:A:218:CYS:SG	0.47	2.64	28	2
1:B:182:LYS:O	1:B:186:THR:OG1	0.47	2.33	16	7
1:B:165:VAL:HG11	1:B:211:LEU:HD21	0.47	1.87	21	5
1:B:180:GLU:O	1:B:183:ASN:OD1	0.47	2.33	23	6
1:B:179:GLN:NE2	1:B:183:ASN:ND2	0.47	2.63	30	1
1:A:180:GLU:O	1:A:183:ASN:OD1	0.46	2.33	22	8
1:B:215:MET:O	1:B:218:CYS:SG	0.46	2.64	28	3
1:B:175:GLU:CG	1:B:175:GLU:O	0.46	2.63	11	1
1:A:172:LEU:C	1:A:172:LEU:CD1	0.46	2.82	23	7
1:B:183:ASN:O	1:B:187:GLU:CG	0.46	2.63	9	2
1:A:195:ASN:C	1:A:197:ASP:H	0.46	2.13	17	8
1:A:165:VAL:HG11	1:A:211:LEU:HD11	0.46	1.86	2	3
1:B:148:THR:OG1	1:B:175:GLU:OE2	0.46	2.33	9	7
1:B:155:GLN:OE1	1:B:195:ASN:OD1	0.46	2.34	16	2
1:B:172:LEU:CD1	1:B:172:LEU:C	0.46	2.84	12	7
1:B:203:LYS:NZ	1:B:203:LYS:CB	0.46	2.78	24	1
1:B:215:MET:CG	1:B:216:THR:N	0.46	2.78	2	2
1:A:215:MET:CG	1:A:216:THR:N	0.46	2.79	4	2
1:B:179:GLN:HE22	1:B:182:LYS:CD	0.46	2.23	22	2
1:A:176:GLN:N	1:A:176:GLN:OE1	0.46	2.46	1	1
1:B:210:THR:CG2	1:B:211:LEU:N	0.46	2.78	30	17
1:A:162:ARG:CG	1:A:163:ASP:N	0.46	2.79	16	25
1:A:183:ASN:O	1:A:187:GLU:CG	0.46	2.63	9	2
1:B:199:LYS:CG	1:B:200:THR:N	0.46	2.78	9	2
1:A:179:GLN:HE22	1:A:182:LYS:CE	0.46	2.24	15	1
1:A:218:CYS:O	1:A:221:VAL:HG23	0.46	2.11	28	2
1:A:148:THR:OG1	1:A:175:GLU:OE2	0.45	2.34	9	6
1:B:189:LEU:N	1:B:189:LEU:CD1	0.45	2.78	28	5
1:A:210:THR:CG2	1:A:211:LEU:N	0.45	2.80	26	17
1:A:181:VAL:HG12	1:A:185:MET:HG2	0.45	1.88	19	1
1:A:186:THR:CG2	1:A:186:THR:O	0.45	2.62	27	3
1:A:180:GLU:OE1	1:B:180:GLU:OE1	0.45	2.35	9	3
1:A:167:ARG:CG	1:A:168:PHE:N	0.45	2.80	16	1
1:B:167:ARG:CG	1:B:168:PHE:N	0.45	2.79	16	1
1:B:162:ARG:CG	1:B:163:ASP:N	0.45	2.79	19	26
1:A:216:THR:O	1:A:219:GLN:CG	0.45	2.65	22	6
1:A:182:LYS:O	1:A:186:THR:OG1	0.45	2.34	3	5
1:B:147:PRO:O	1:B:148:THR:C	0.45	2.55	7	26
1:B:195:ASN:O	1:B:195:ASN:OD1	0.45	2.35	18	8

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:155:GLN:OE1	1:A:195:ASN:OD1	0.45	2.34	16	1
1:A:219:GLN:CG	1:A:219:GLN:O	0.45	2.65	20	3
1:B:195:ASN:OD1	1:B:195:ASN:O	0.45	2.34	10	10
1:B:181:VAL:HG12	1:B:185:MET:HG2	0.45	1.88	19	1
1:A:164:TYR:C	1:A:164:TYR:CD1	0.45	2.90	22	4
1:B:155:GLN:OE1	1:B:161:PHE:N	0.45	2.49	7	2
1:A:195:ASN:OD1	1:A:195:ASN:O	0.45	2.35	20	9
1:A:201:ILE:HG23	1:A:202:LEU:H	0.45	1.71	24	4
1:B:221:VAL:HG13	1:B:221:VAL:O	0.45	2.10	8	2
1:A:184:TRP:CH2	1:B:185:MET:CE	0.45	2.99	29	4
1:B:210:THR:OG1	1:B:211:LEU:N	0.45	2.50	17	1
1:A:180:GLU:OE2	1:B:180:GLU:OE1	0.45	2.35	25	1
1:B:146:SER:N	1:B:147:PRO:HD3	0.45	2.26	26	1
1:B:158:LYS:H	1:B:158:LYS:HD3	0.45	1.71	11	1
1:B:152:ASP:O	1:B:152:ASP:OD1	0.45	2.35	8	4
1:B:148:THR:OG1	1:B:175:GLU:CG	0.45	2.65	20	1
1:B:186:THR:HG22	1:B:186:THR:O	0.45	2.12	17	2
1:A:185:MET:SD	1:A:189:LEU:HD12	0.45	2.52	18	2
1:B:216:THR:O	1:B:219:GLN:CG	0.44	2.66	22	4
1:A:161:PHE:O	1:A:164:TYR:N	0.44	2.50	16	8
1:B:164:TYR:CD1	1:B:164:TYR:C	0.44	2.90	17	4
1:A:189:LEU:HD22	1:A:189:LEU:N	0.44	2.26	15	1
1:A:185:MET:CE	1:B:184:TRP:CH2	0.44	3.01	29	2
1:A:211:LEU:O	1:A:211:LEU:HD13	0.44	2.12	11	1
1:A:210:THR:OG1	1:A:211:LEU:N	0.44	2.50	17	1
1:A:219:GLN:O	1:A:219:GLN:CG	0.44	2.65	22	1
1:B:201:ILE:HG23	1:B:202:LEU:H	0.44	1.73	17	4
1:A:146:SER:N	1:A:147:PRO:HD3	0.44	2.27	26	2
1:B:175:GLU:CD	1:B:175:GLU:O	0.44	2.56	16	2
1:B:159:GLU:OE2	1:B:167:ARG:NH2	0.44	2.51	20	1
1:A:152:ASP:O	1:A:152:ASP:OD1	0.44	2.36	4	4
1:A:185:MET:CG	1:A:186:THR:N	0.44	2.80	4	1
1:B:218:CYS:O	1:B:221:VAL:HG23	0.44	2.13	20	1
1:B:175:GLU:OE2	1:B:175:GLU:O	0.44	2.36	11	1
1:B:161:PHE:O	1:B:164:TYR:N	0.44	2.51	26	7
1:A:172:LEU:HG	1:A:173:ARG:N	0.44	2.28	18	1
1:A:202:LEU:HD23	1:A:205:LEU:HD12	0.44	1.88	24	1
1:B:175:GLU:O	1:B:176:GLN:O	0.44	2.36	3	2
1:B:168:PHE:CD1	1:B:168:PHE:C	0.44	2.91	27	3
1:A:165:VAL:HG11	1:A:211:LEU:HD21	0.43	1.88	21	4
1:B:195:ASN:C	1:B:197:ASP:N	0.43	2.71	30	5

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:152:ASP:OD1	1:A:152:ASP:O	0.43	2.35	30	2
1:B:150:ILE:C	1:B:152:ASP:H	0.43	2.15	28	2
1:A:145:TYR:O	1:A:146:SER:CB	0.43	2.66	18	2
1:A:218:CYS:C	1:A:220:GLY:H	0.43	2.16	25	1
1:B:211:LEU:HD13	1:B:211:LEU:O	0.43	2.13	11	1
1:A:176:GLN:N	1:A:176:GLN:CD	0.43	2.72	4	2
1:A:150:ILE:C	1:A:152:ASP:H	0.43	2.15	28	2
1:A:151:LEU:CD2	1:B:192:GLN:OE1	0.43	2.66	6	2
1:A:148:THR:OG1	1:A:175:GLU:OE1	0.43	2.36	14	1
1:B:179:GLN:HE22	1:B:182:LYS:CE	0.43	2.27	15	1
1:A:175:GLU:OE1	1:A:175:GLU:O	0.43	2.36	11	1
1:B:147:PRO:O	1:B:148:THR:O	0.43	2.36	14	4
1:A:199:LYS:O	1:A:203:LYS:CG	0.43	2.66	17	1
1:B:219:GLN:O	1:B:219:GLN:CG	0.43	2.66	20	2
1:B:202:LEU:HD23	1:B:205:LEU:HD12	0.43	1.91	29	2
1:B:183:ASN:O	1:B:187:GLU:CD	0.43	2.57	30	6
1:B:218:CYS:C	1:B:220:GLY:H	0.43	2.16	25	1
1:A:145:TYR:O	1:A:146:SER:OG	0.43	2.33	28	3
1:A:161:PHE:CD2	1:A:165:VAL:CG2	0.43	3.02	13	1
1:A:180:GLU:O	1:A:183:ASN:CG	0.43	2.57	18	7
1:A:179:GLN:HE22	1:A:182:LYS:CD	0.43	2.27	22	3
1:A:151:LEU:HD13	1:B:192:GLN:OE1	0.43	2.13	19	4
1:A:192:GLN:OE1	1:A:192:GLN:O	0.43	2.36	15	1
1:A:179:GLN:OE1	1:A:183:ASN:ND2	0.43	2.52	16	1
1:B:175:GLU:O	1:B:175:GLU:CD	0.43	2.56	20	1
1:A:175:GLU:CG	1:A:175:GLU:O	0.43	2.66	5	1
1:A:181:VAL:O	1:A:184:TRP:N	0.43	2.46	8	1
1:A:189:LEU:CD1	1:A:189:LEU:N	0.43	2.81	23	2
1:A:221:VAL:O	1:A:221:VAL:HG13	0.42	2.13	10	1
1:B:146:SER:C	1:B:148:THR:H	0.42	2.18	15	1
1:B:189:LEU:HD22	1:B:189:LEU:N	0.42	2.28	15	1
1:B:192:GLN:O	1:B:192:GLN:OE1	0.42	2.37	15	1
1:B:164:TYR:C	1:B:164:TYR:CD1	0.42	2.92	22	2
1:B:161:PHE:CD2	1:B:165:VAL:CG2	0.42	3.02	13	2
1:B:159:GLU:OE2	1:B:163:ASP:OD1	0.42	2.37	29	1
1:A:168:PHE:CD1	1:A:168:PHE:C	0.42	2.92	27	4
1:B:175:GLU:O	1:B:175:GLU:CG	0.42	2.66	27	1
1:A:147:PRO:O	1:A:148:THR:O	0.42	2.37	4	6
1:B:185:MET:CG	1:B:186:THR:N	0.42	2.82	4	1
1:A:183:ASN:O	1:A:187:GLU:CD	0.42	2.58	28	6
1:A:189:LEU:N	1:A:189:LEU:CD2	0.42	2.81	15	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:179:GLN:CD	1:A:179:GLN:O	0.42	2.58	22	2
1:A:211:LEU:O	1:A:214:MET:N	0.42	2.53	5	1
1:B:180:GLU:O	1:B:183:ASN:CG	0.42	2.57	23	6
1:B:176:GLN:N	1:B:176:GLN:CD	0.42	2.73	18	1
1:A:146:SER:C	1:A:148:THR:H	0.42	2.18	15	1
1:B:185:MET:SD	1:B:189:LEU:HD12	0.42	2.54	18	1
1:B:179:GLN:O	1:B:179:GLN:CD	0.42	2.58	22	1
1:B:155:GLN:NE2	1:B:161:PHE:N	0.42	2.68	2	1
1:B:199:LYS:O	1:B:203:LYS:CG	0.42	2.67	17	1
1:B:180:GLU:O	1:B:180:GLU:OE1	0.42	2.36	14	1
1:A:168:PHE:C	1:A:168:PHE:CD1	0.42	2.93	19	1
1:A:218:CYS:O	1:A:218:CYS:SG	0.42	2.77	22	1
1:B:195:ASN:OD1	1:B:195:ASN:C	0.42	2.59	3	1
1:B:145:TYR:O	1:B:146:SER:CB	0.42	2.68	18	1
1:B:175:GLU:O	1:B:175:GLU:OE1	0.42	2.38	20	1
1:B:181:VAL:C	1:B:185:MET:SD	0.42	2.98	17	1
1:B:189:LEU:CD2	1:B:189:LEU:N	0.41	2.83	15	1
1:A:168:PHE:CE1	1:A:186:THR:HG23	0.41	2.50	13	1
1:B:179:GLN:CD	1:B:179:GLN:O	0.41	2.58	24	1
1:A:180:GLU:OE1	1:A:180:GLU:O	0.41	2.38	29	2
1:A:148:THR:OG1	1:A:175:GLU:CD	0.41	2.58	13	2
1:B:152:ASP:OD1	1:B:152:ASP:O	0.41	2.39	26	1
1:A:192:GLN:OE1	1:B:151:LEU:CD2	0.41	2.68	25	2
1:A:195:ASN:C	1:A:197:ASP:N	0.41	2.73	17	3
1:B:198:CYS:CB	1:B:218:CYS:HG	0.41	2.29	8	1
1:B:179:GLN:OE1	1:B:179:GLN:O	0.41	2.39	24	1
1:A:195:ASN:O	1:A:198:CYS:SG	0.41	2.67	4	1
1:B:182:LYS:C	1:B:182:LYS:CD	0.41	2.88	19	1
1:B:168:PHE:C	1:B:168:PHE:CD1	0.41	2.94	25	2
1:B:216:THR:O	1:B:219:GLN:CD	0.41	2.59	30	1
1:A:150:ILE:CG2	1:A:151:LEU:N	0.41	2.83	18	1
1:A:185:MET:C	1:A:187:GLU:N	0.41	2.74	3	1
1:A:156:GLY:O	1:A:158:LYS:N	0.41	2.53	18	1
1:A:211:LEU:HD22	1:A:211:LEU:N	0.41	2.31	18	1
1:A:175:GLU:OE1	1:A:176:GLN:N	0.41	2.53	19	1
1:A:175:GLU:CD	1:A:175:GLU:O	0.41	2.59	11	1
1:B:185:MET:C	1:B:187:GLU:N	0.41	2.74	3	1
1:A:213:GLU:O	1:A:217:ALA:HB3	0.41	2.15	23	1
1:B:180:GLU:C	1:B:180:GLU:OE1	0.41	2.59	29	1
1:B:177:ALA:O	1:B:178:SER:O	0.41	2.39	11	1
1:B:168:PHE:CE1	1:B:186:THR:HG23	0.41	2.51	13	1

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:216:THR:O	1:A:219:GLN:CD	0.41	2.60	30	1
1:A:158:LYS:CD	1:A:158:LYS:C	0.41	2.90	11	1
1:A:179:GLN:HE22	1:A:183:ASN:HD21	0.40	1.56	9	1
1:B:176:GLN:CD	1:B:176:GLN:N	0.40	2.74	22	1
1:B:151:LEU:N	1:B:151:LEU:HD12	0.40	2.31	23	1
1:A:162:ARG:HG2	1:A:163:ASP:N	0.40	2.31	24	1
1:B:150:ILE:C	1:B:152:ASP:N	0.40	2.74	28	1
1:A:185:MET:HE2	1:B:184:TRP:CH2	0.40	2.51	29	1
1:B:150:ILE:HD12	1:B:153:ILE:HD12	0.40	1.92	17	1
1:A:211:LEU:CD2	1:A:211:LEU:N	0.40	2.84	18	1
1:A:150:ILE:C	1:A:152:ASP:N	0.40	2.75	28	1
1:B:185:MET:HG3	1:B:186:THR:N	0.40	2.30	6	1
1:B:172:LEU:HG	1:B:173:ARG:N	0.40	2.31	18	1
1:A:145:TYR:CG	1:A:146:SER:N	0.40	2.89	24	1
1:A:159:GLU:OE2	1:A:163:ASP:OD2	0.40	2.39	29	1
1:B:191:VAL:O	1:B:191:VAL:HG12	0.40	2.16	12	1
1:B:199:LYS:HG3	1:B:200:THR:N	0.40	2.31	13	1
1:A:172:LEU:HD22	1:A:182:LYS:HZ3	0.40	1.75	18	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	77/88 (88%)	68±2 (88±3%)	7±2 (10±2%)	2±1 (3±1%)	8	44
1	B	77/88 (88%)	68±2 (88±3%)	7±2 (9±2%)	2±1 (3±1%)	8	43
All	All	4620/5280 (88%)	4056 (88%)	442 (10%)	122 (3%)	8	44

All 20 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	B	148	THR	27
1	A	148	THR	27
1	A	146	SER	11

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	B	146	SER	11
1	B	196	PRO	10
1	A	196	PRO	7
1	B	176	GLN	6
1	A	176	GLN	6
1	A	149	SER	3
1	B	149	SER	3
1	B	145	TYR	2
1	B	178	SER	1
1	B	220	GLY	1
1	A	145	TYR	1
1	A	186	THR	1
1	A	221	VAL	1
1	A	220	GLY	1
1	B	221	VAL	1
1	A	178	SER	1
1	B	186	THR	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	67/74 (91%)	65±1 (96±1%)	2±1 (4±1%)	37	85
1	B	67/74 (91%)	65±1 (96±1%)	2±1 (4±1%)	38	86
All	All	4020/4440 (91%)	3874 (96%)	146 (4%)	38	86

All 36 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	B	172	LEU	30
1	A	172	LEU	30
1	A	179	GLN	9
1	B	179	GLN	8
1	B	183	ASN	4
1	B	215	MET	4
1	A	211	LEU	4

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	183	ASN	4
1	B	211	LEU	4
1	A	215	MET	4
1	A	203	LYS	3
1	A	210	THR	3
1	A	182	LYS	2
1	B	185	MET	2
1	B	175	GLU	2
1	A	175	GLU	2
1	A	185	MET	2
1	B	218	CYS	2
1	B	158	LYS	2
1	B	199	LYS	2
1	B	203	LYS	2
1	A	192	GLN	2
1	B	210	THR	2
1	B	182	LYS	2
1	A	199	LYS	2
1	A	218	CYS	2
1	B	192	GLN	2
1	B	162	ARG	1
1	A	158	LYS	1
1	A	178	SER	1
1	A	176	GLN	1
1	A	214	MET	1
1	B	170	LYS	1
1	B	176	GLN	1
1	A	162	ARG	1
1	B	214	MET	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 carbohydrates in this entry.

## 6.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

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

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided