



Full wwPDB NMR Structure Validation Report ⓘ

Mar 10, 2026 – 10:46 AM UTC

PDB ID : 1BFM / pdb_00001bfm
Title : HISTONE B FROM METHANOTHERMUS FERVIDUS
Authors : Starich, M.R.; Sandman, K.; Reeve, J.N.; Summers, M.F.
Deposited on : 1995-09-28

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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

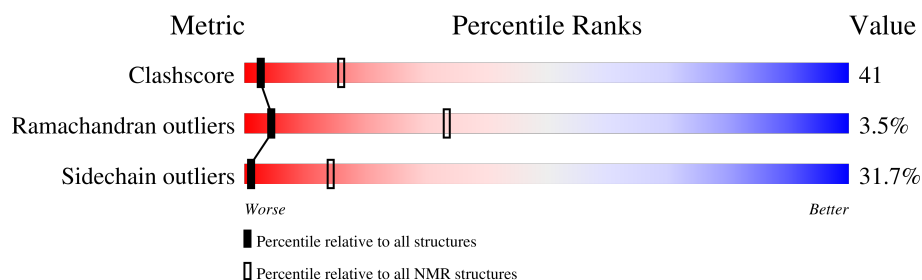
1 Overall quality at a glance

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	69	
1	B	69	

2 Ensemble composition and analysis

This entry contains 33 models. Model 10 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:3-A:67, B:3-B:67 (130)	1.03	10

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 1 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2238 atoms, of which 1164 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called HISTONE B.

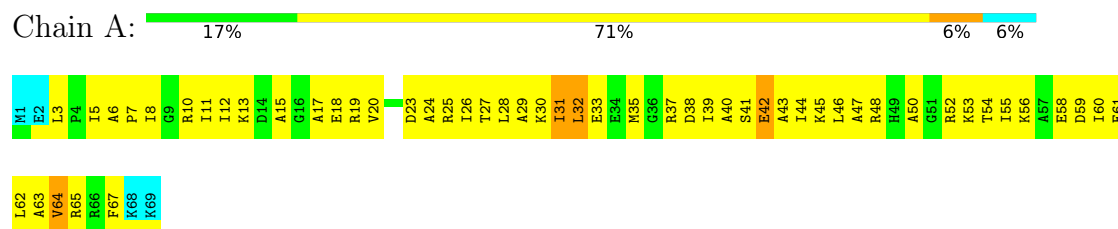
Mol	Chain	Residues	Atoms						Trace
1	A	69	Total	C	H	N	O	S	0
			1119	335	582	102	98	2	
1	B	69	Total	C	H	N	O	S	0
			1119	335	582	102	98	2	

4 Residue-property plots [i](#)

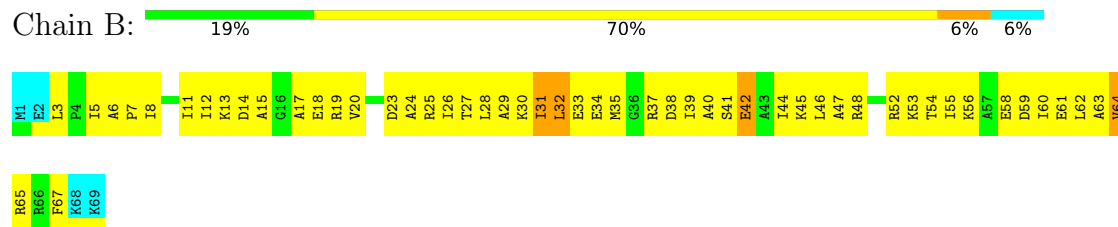
4.1 Average score per residue in the NMR ensemble

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

• Molecule 1: HISTONE B



• Molecule 1: HISTONE B

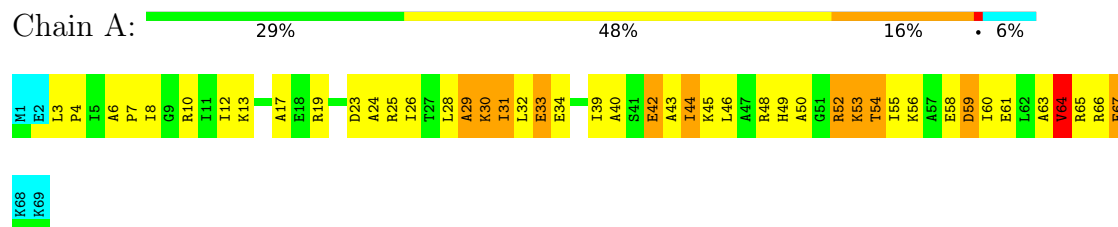


4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

4.2.1 Score per residue for model 1

• Molecule 1: HISTONE B



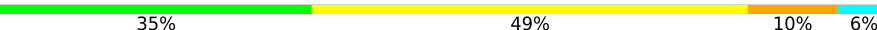
- Molecule 1: HISTONE B

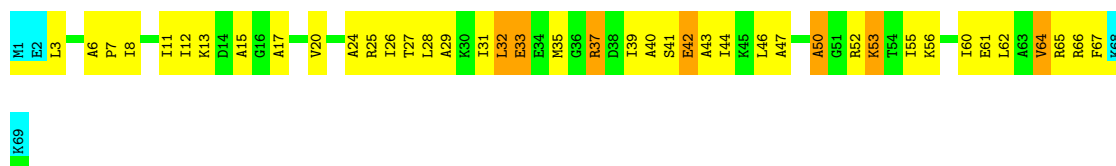
Chain B: 



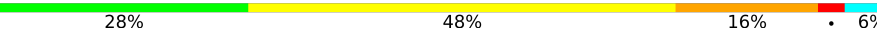
4.2.2 Score per residue for model 2

- Molecule 1: HISTONE B

Chain A: 



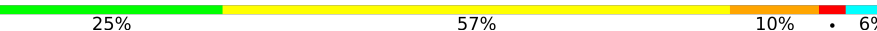
- Molecule 1: HISTONE B

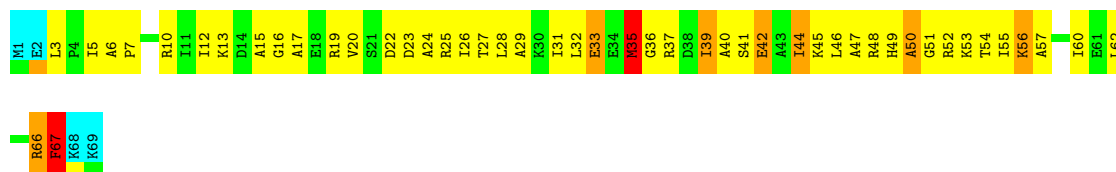
Chain B: 



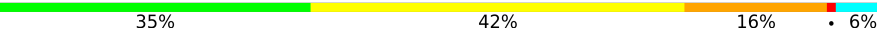
4.2.3 Score per residue for model 3

- Molecule 1: HISTONE B

Chain A: 



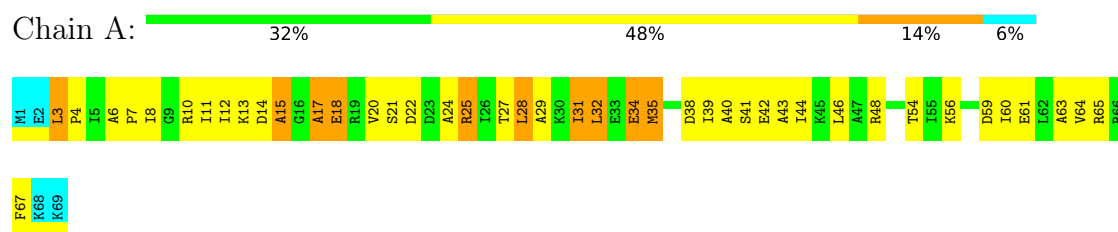
- Molecule 1: HISTONE B

Chain B: 

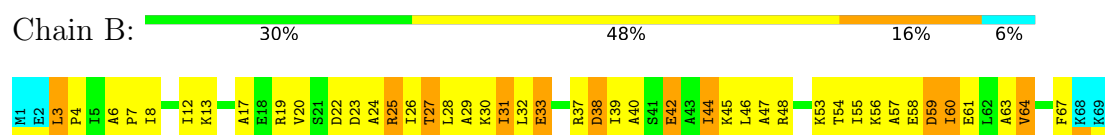


4.2.4 Score per residue for model 4

- Molecule 1: HISTONE B

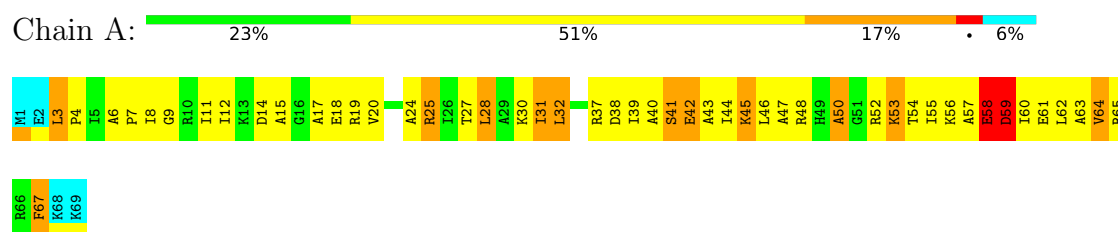


- Molecule 1: HISTONE B

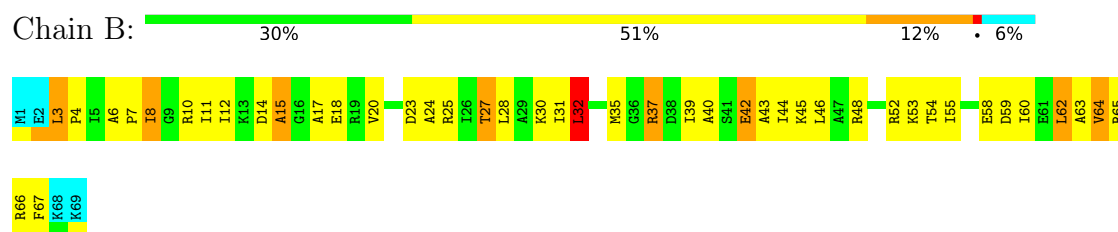


4.2.5 Score per residue for model 5

- Molecule 1: HISTONE B

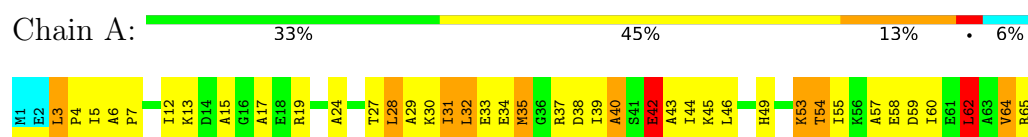


- Molecule 1: HISTONE B



4.2.6 Score per residue for model 6

- Molecule 1: HISTONE B



- Molecule 1: HISTONE B





4.2.7 Score per residue for model 7

- Molecule 1: HISTONE B



- Molecule 1: HISTONE B



4.2.8 Score per residue for model 8

- Molecule 1: HISTONE B



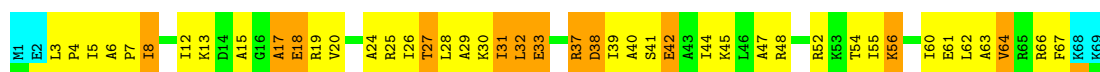
- Molecule 1: HISTONE B



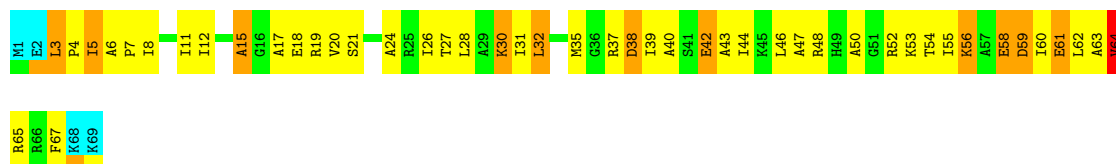
4.2.9 Score per residue for model 9

- Molecule 1: HISTONE B



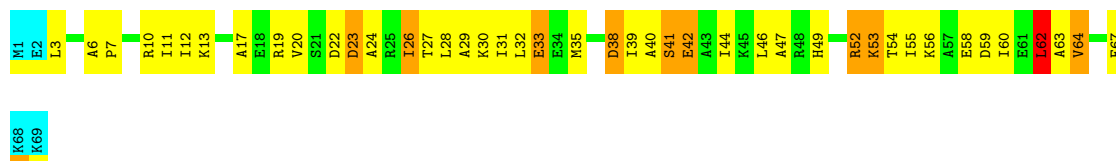


• Molecule 1: HISTONE B

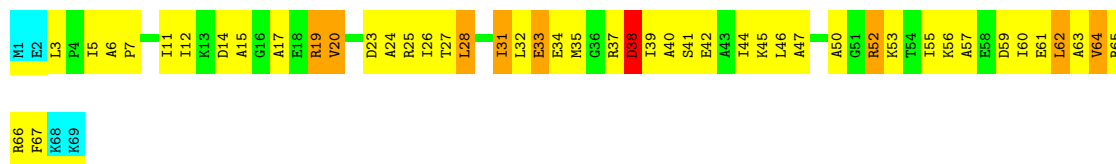


4.2.10 Score per residue for model 10 (medoid)

• Molecule 1: HISTONE B



• Molecule 1: HISTONE B



4.2.11 Score per residue for model 11

• Molecule 1: HISTONE B



• Molecule 1: HISTONE B



R65
R66
F67
K68
K69

4.2.12 Score per residue for model 12

- Molecule 1: HISTONE B

Chain A: 32% 48% 13% • 6%

M1 E2 L3 A6 P7 R10 I11 I12 K13 A17 E18 R19 V20 S21 D22 D23 A24 R25 T26 T27 L28 L29 K30 I31 L32 L33 E33 E34 E35 D38 I39 A40 S41 E42 I43 I44 L45 L46 A47 R48 H49 R52 K53 T54 I55 K56 A57 E58 D59 I60 E61 L62 A63 V64 F67

K68
K69

- Molecule 1: HISTONE B

Chain B: 26% 55% 12% • 6%

M1 E2 L3 P4 A6 A7 P7 I11 I12 K13 D14 A15 G16 A17 E18 R19 V20 D23 A24 R25 T26 T27 L28 I31 L32 E33 E34 E35 G36 R37 D38 I39 A40 S41 E42 I43 I44 K45 L46 A47 A50 G51 R52 K53 T54 I55 K56 A57 E58 D59 I60 E61 L62 A63 V64 R65

R65
R66
F67
K68
K69

4.2.13 Score per residue for model 13

- Molecule 1: HISTONE B

Chain A: 35% 48% 12% 6%

M1 E2 L3 P4 I5 A6 A7 P7 I8 G9 R10 I11 I12 A17 E18 R19 V20 A24 T27 L28 A29 K30 I31 L32 E33 E34 M35 D38 I39 A40 S41 E42 I43 I44 K45 L46 H49 A50 G51 R52 K53 T54 I55 K56 A57 E58 D59 I60 E61 L62 A63 V64 R65 F67 K68

K69

- Molecule 1: HISTONE B

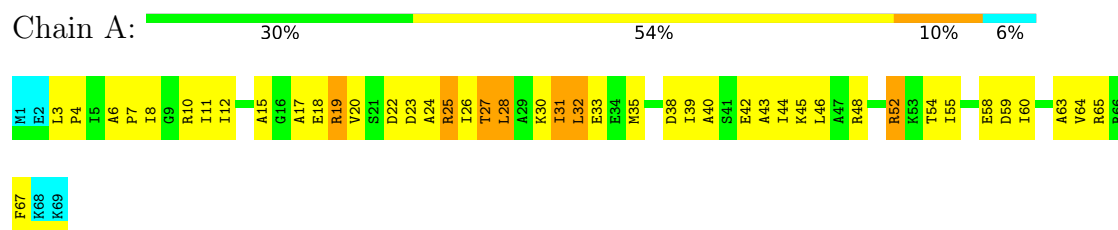
Chain B: 32% 49% 13% 6%

M1 E2 L3 P4 A6 A7 P7 I8 G9 R10 I11 I12 K13 D14 A15 G16 A17 E18 R19 V20 A24 T27 L28 A29 K30 I31 L32 E33 E34 R37 D38 I39 A40 S41 E42 I43 I44 K45 L46 A47 A50 G51 R52 K53 T54 I55 D59 I60 E61 L62 A63 V64

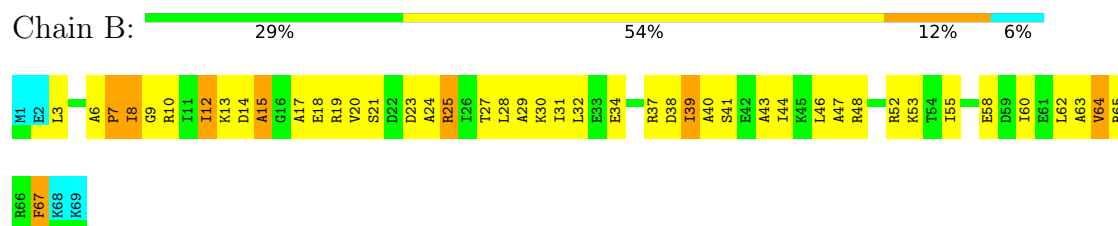
R65
R66
F67
K68
K69

4.2.14 Score per residue for model 14

• Molecule 1: HISTONE B

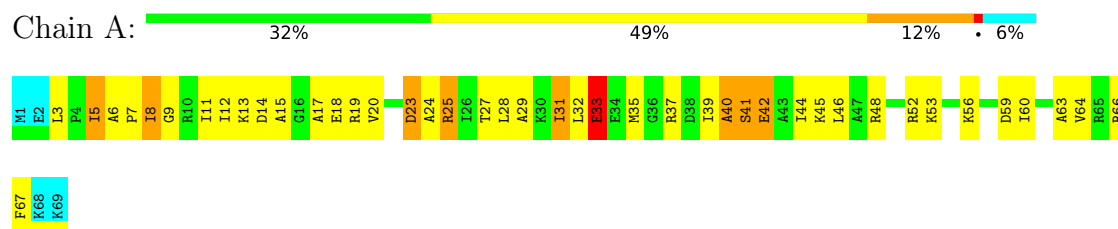


• Molecule 1: HISTONE B

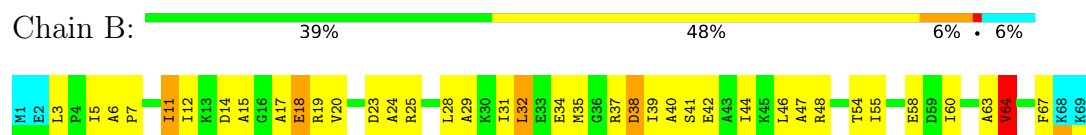


4.2.15 Score per residue for model 15

• Molecule 1: HISTONE B

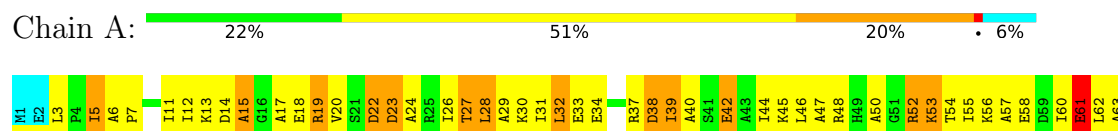


• Molecule 1: HISTONE B



4.2.16 Score per residue for model 16

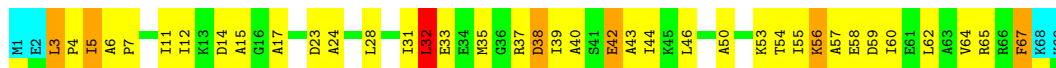
• Molecule 1: HISTONE B





• Molecule 1: HISTONE B

Chain B: 39% 45% 9% • 6%



4.2.17 Score per residue for model 17

• Molecule 1: HISTONE B

Chain A: 25% 57% 12% • 6%



• Molecule 1: HISTONE B

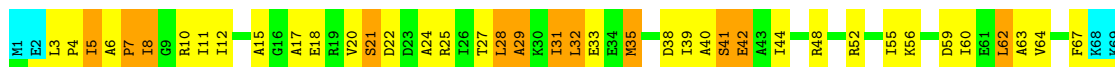
Chain B: 28% 57% 10% 6%



4.2.18 Score per residue for model 18

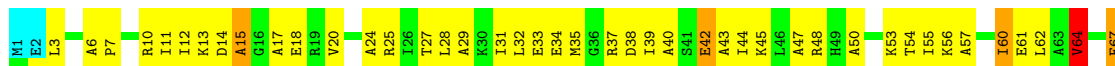
• Molecule 1: HISTONE B

Chain A: 36% 41% 17% 6%



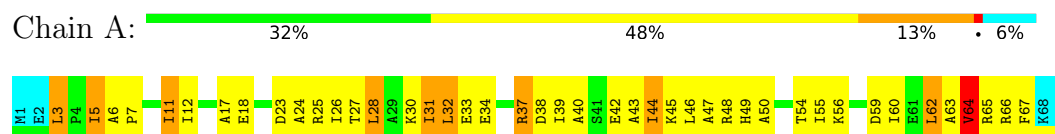
• Molecule 1: HISTONE B

Chain B: 32% 55% 6% • 6%

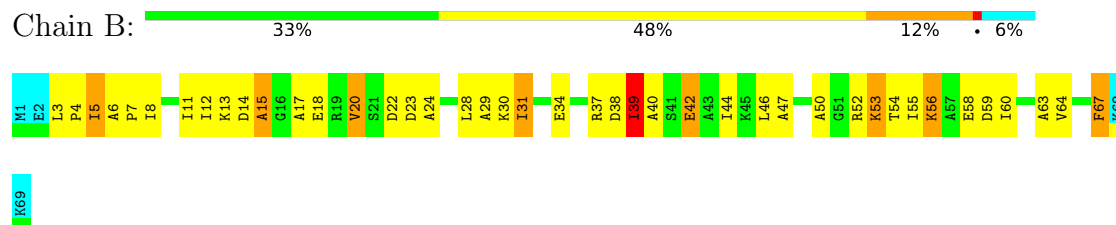


4.2.19 Score per residue for model 19

• Molecule 1: HISTONE B

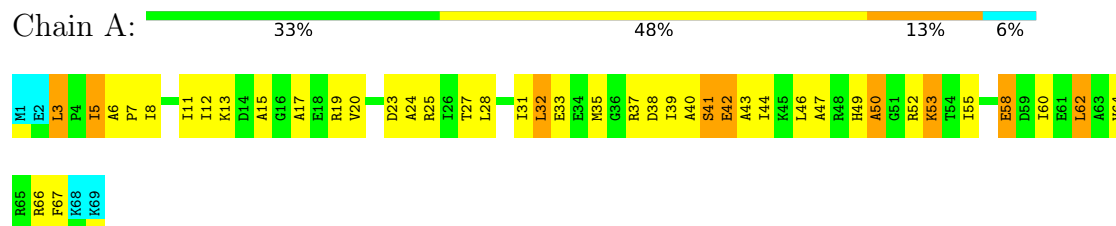


• Molecule 1: HISTONE B

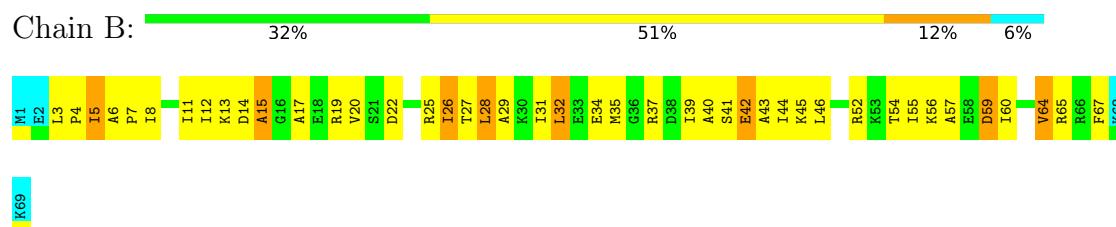


4.2.20 Score per residue for model 20

• Molecule 1: HISTONE B

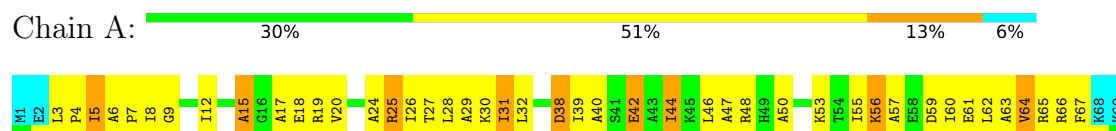


• Molecule 1: HISTONE B

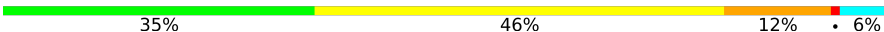


4.2.21 Score per residue for model 21

• Molecule 1: HISTONE B



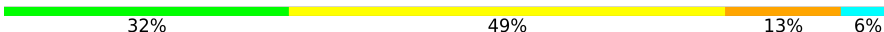
- Molecule 1: HISTONE B

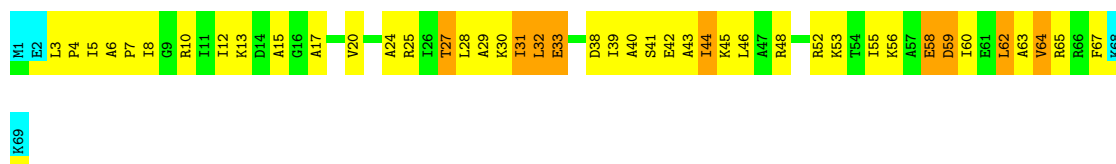
Chain B: 



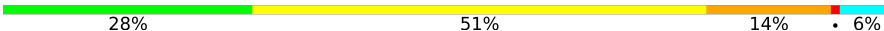
4.2.22 Score per residue for model 22

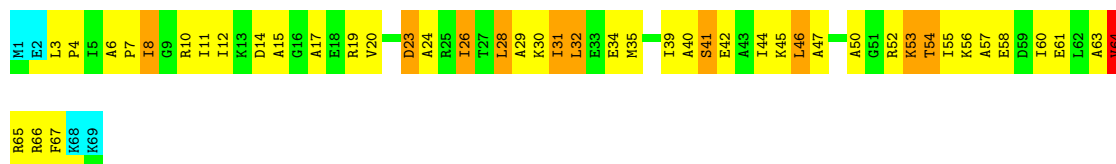
- Molecule 1: HISTONE B

Chain A: 



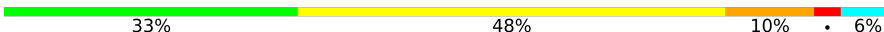
- Molecule 1: HISTONE B

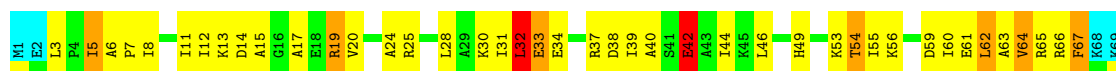
Chain B: 



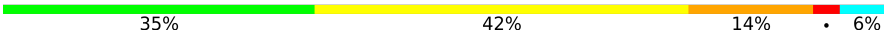
4.2.23 Score per residue for model 23

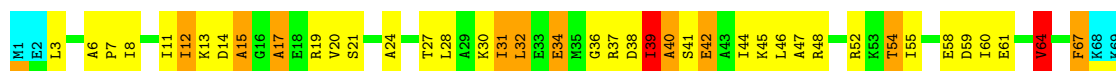
- Molecule 1: HISTONE B

Chain A: 



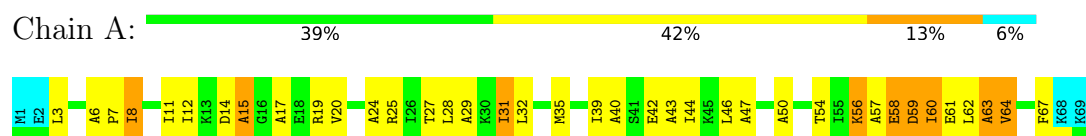
- Molecule 1: HISTONE B

Chain B: 

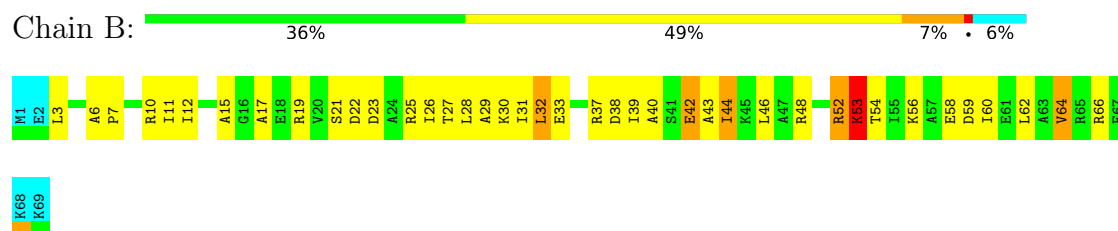


4.2.24 Score per residue for model 24

- Molecule 1: HISTONE B

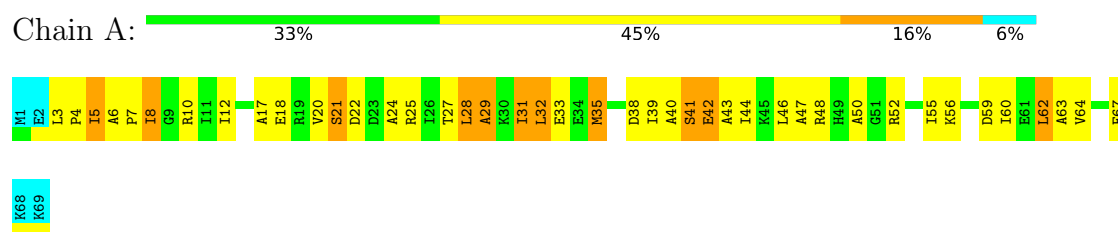


- Molecule 1: HISTONE B

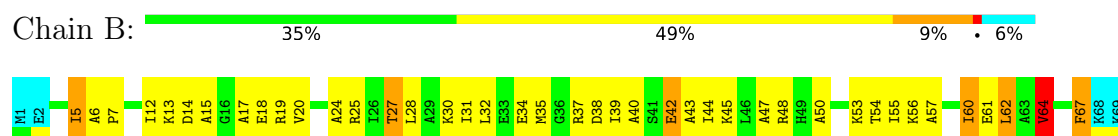


4.2.25 Score per residue for model 25

- Molecule 1: HISTONE B

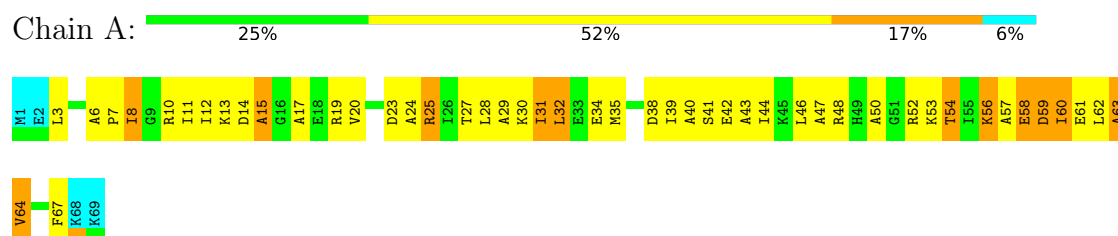


- Molecule 1: HISTONE B



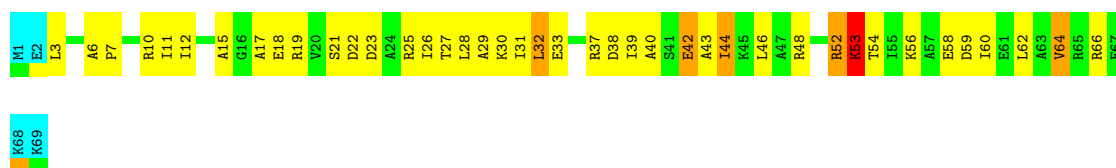
4.2.26 Score per residue for model 26

- Molecule 1: HISTONE B



- Molecule 1: HISTONE B

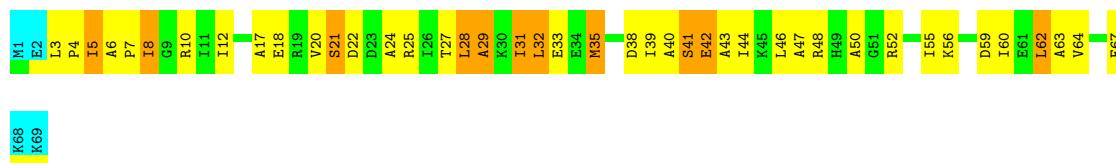




4.2.27 Score per residue for model 27

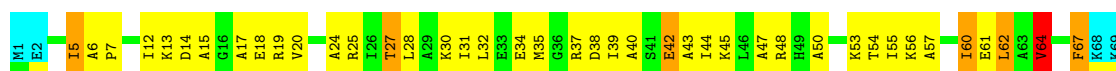
- Molecule 1: HISTONE B

Chain A: 33% 45% 16% 6%



- Molecule 1: HISTONE B

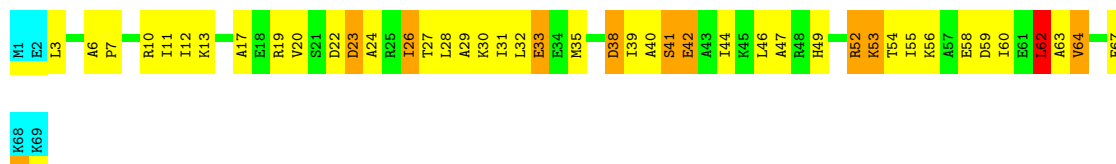
Chain B: 35% 49% 9% 6%



4.2.28 Score per residue for model 28

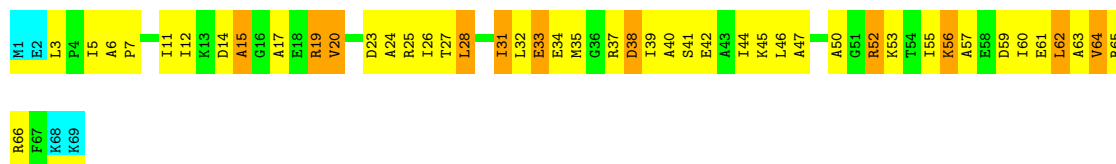
- Molecule 1: HISTONE B

Chain A: 32% 48% 13% 6%



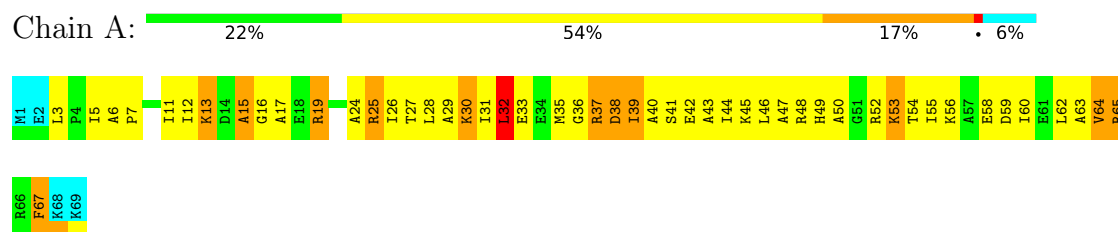
- Molecule 1: HISTONE B

Chain B: 28% 51% 16% 6%

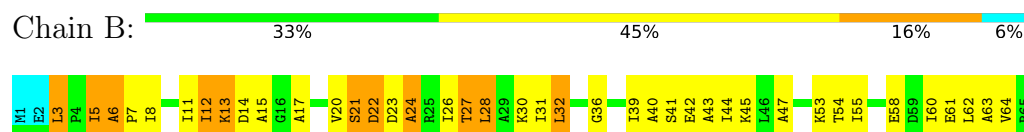


4.2.29 Score per residue for model 29

• Molecule 1: HISTONE B

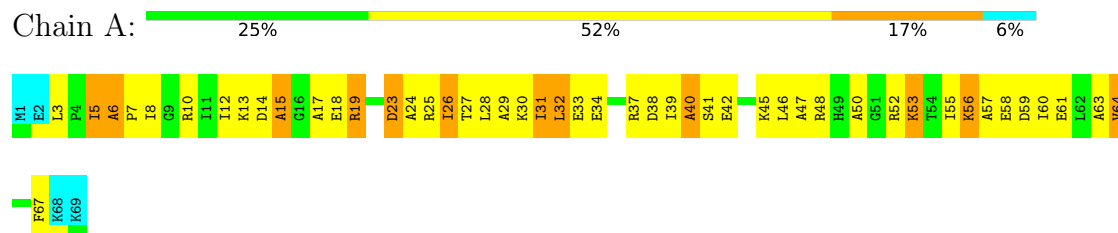


• Molecule 1: HISTONE B

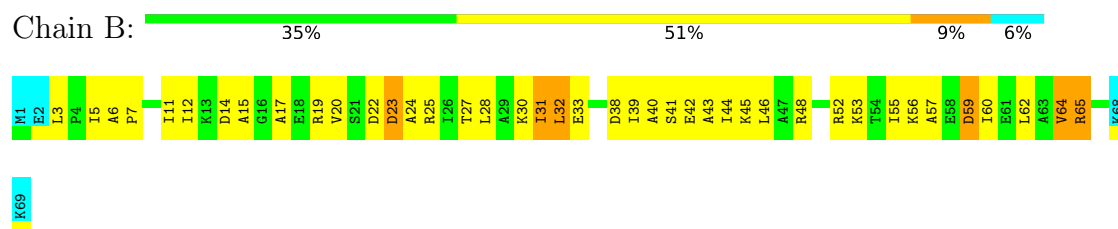


4.2.30 Score per residue for model 30

• Molecule 1: HISTONE B

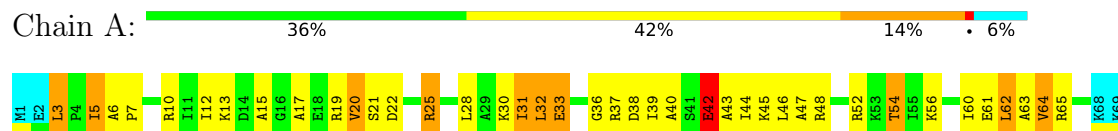


• Molecule 1: HISTONE B

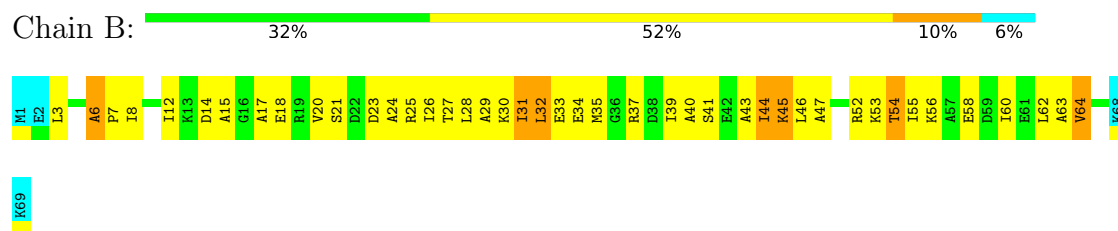


4.2.31 Score per residue for model 31

• Molecule 1: HISTONE B

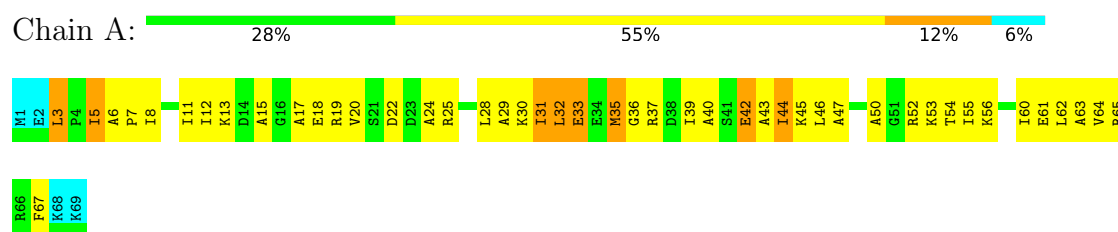


- Molecule 1: HISTONE B

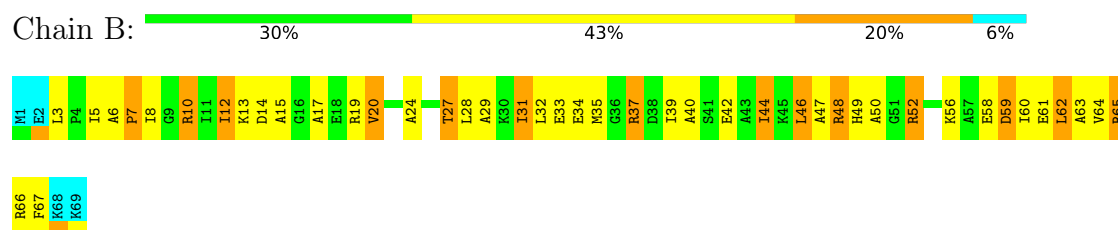


4.2.32 Score per residue for model 32

- Molecule 1: HISTONE B

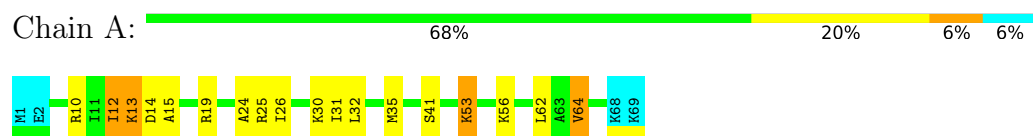


- Molecule 1: HISTONE B

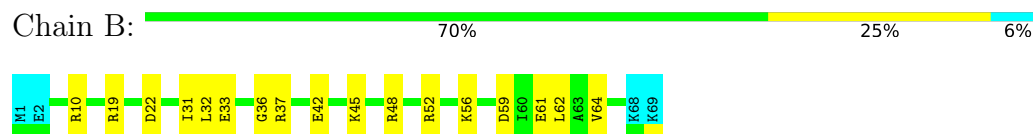


4.2.33 Score per residue for model 33

- Molecule 1: HISTONE B



- Molecule 1: HISTONE B



5 Refinement protocol and experimental data overview ⓘ

Of the ? calculated structures, 33 were deposited, based on the following criterion: ?.

The authors did not provide any information on software used for structure solution, optimization or refinement.

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.70±0.01	0±0/505 (0.0± 0.0%)	1.07±0.02	0±0/677 (0.0± 0.1%)
1	B	0.70±0.01	0±0/505 (0.0± 0.0%)	1.08±0.02	0±0/677 (0.1± 0.1%)
All	All	0.70	0/33293 (0.0%)	1.08	17/44629 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	3.6±2.0
1	B	0.0±0.0	3.7±1.7
All	All	0	239

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	B	64	VAL	CB-CA-C	7.29	117.91	111.71	18	9
1	A	59	ASP	CA-CB-CG	6.32	118.92	112.60	5	1
1	A	64	VAL	CB-CA-C	5.85	118.70	111.80	33	3
1	B	38	ASP	CA-CB-CG	5.64	118.25	112.60	10	3
1	A	23	ASP	CA-CB-CG	5.14	117.74	112.60	15	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	B	14	ASP	Mainchain	26

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group	Models (Total)
1	B	15	ALA	Mainchain	18
1	B	29	ALA	Mainchain	15
1	A	29	ALA	Mainchain	10
1	A	32	LEU	Mainchain	10
1	A	14	ASP	Mainchain	10
1	A	15	ALA	Mainchain	10
1	B	62	LEU	Mainchain	9
1	A	42	GLU	Mainchain	9
1	A	62	LEU	Mainchain	8
1	A	50	ALA	Mainchain	7
1	B	61	GLU	Mainchain	7
1	B	27	THR	Mainchain	7
1	B	32	LEU	Mainchain	7
1	A	28	LEU	Mainchain	7
1	A	63	ALA	Mainchain	7
1	B	8	ILE	Mainchain	6
1	A	8	ILE	Mainchain	6
1	A	13	LYS	Mainchain	4
1	A	35	MET	Mainchain	4
1	A	40	ALA	Mainchain	4
1	B	13	LYS	Mainchain	4
1	A	27	THR	Mainchain	4
1	B	28	LEU	Mainchain	3
1	A	58	GLU	Mainchain	3
1	A	61	GLU	Mainchain	3
1	A	67	PHE	Mainchain	2
1	B	7	PRO	Mainchain	2
1	A	39	ILE	Mainchain	2
1	B	39	ILE	Mainchain	2
1	B	67	PHE	Sidechain	2
1	B	22	ASP	Mainchain	2
1	B	42	GLU	Mainchain	2
1	B	53	LYS	Mainchain	2
1	A	48	ARG	Mainchain	1
1	B	48	ARG	Mainchain	1
1	A	37	ARG	Mainchain	1
1	B	33	GLU	Mainchain	1
1	A	34	GLU	Mainchain	1
1	A	45	LYS	Mainchain	1
1	A	59	ASP	Mainchain	1
1	B	63	ALA	Mainchain	1
1	A	9	GLY	Mainchain	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group	Models (Total)
1	A	33	GLU	Mainchain	1
1	B	43	ALA	Mainchain	1
1	A	7	PRO	Mainchain	1
1	B	12	ILE	Mainchain	1
1	B	34	GLU	Mainchain	1
1	B	40	ALA	Mainchain	1

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	501	539	0	61±14
1	B	501	539	0	61±12
All	All	33066	35574	34432	2798

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 41.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:32:LEU:HD23	1:B:32:LEU:HD23	1.08	1.22	29	7
1:A:31:ILE:HD13	1:B:64:VAL:HG21	1.03	1.17	7	6
1:A:64:VAL:HG21	1:B:31:ILE:HD13	1.03	1.20	4	8
1:A:3:LEU:HD21	1:B:11:ILE:HD11	1.02	1.30	29	3
1:A:64:VAL:HG21	1:B:31:ILE:HG21	0.96	1.37	19	21
1:A:27:THR:HG22	1:B:60:ILE:HG22	0.95	1.35	18	5
1:A:60:ILE:HG22	1:B:27:THR:HG22	0.94	1.38	24	5
1:A:17:ALA:HB2	1:B:44:ILE:HD11	0.91	1.42	29	26
1:A:40:ALA:HB2	1:B:12:ILE:HD12	0.91	1.41	5	26
1:A:20:VAL:HG21	1:A:25:ARG:NH2	0.86	1.84	2	1
1:A:12:ILE:HG22	1:A:17:ALA:HB2	0.86	1.45	4	12
1:A:31:ILE:HG21	1:B:64:VAL:HG21	0.85	1.48	13	26
1:A:11:ILE:HD11	1:B:3:LEU:HD21	0.84	1.46	19	11
1:A:55:ILE:HD12	1:B:20:VAL:HG22	0.84	1.48	23	6
1:A:3:LEU:CB	1:A:29:ALA:HB1	0.83	2.04	6	6
1:A:60:ILE:CG2	1:B:28:LEU:HD13	0.83	2.04	14	7

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:3:LEU:HB2	1:A:29:ALA:HB1	0.83	1.48	13	6
1:B:12:ILE:HG22	1:B:17:ALA:HB2	0.82	1.51	23	17
1:B:12:ILE:HG21	1:B:25:ARG:NH2	0.81	1.88	5	1
1:A:44:ILE:HD11	1:B:17:ALA:HB2	0.81	1.51	18	23
1:B:3:LEU:HB3	1:B:8:ILE:HD12	0.81	1.53	3	1
1:A:17:ALA:CA	1:B:44:ILE:HD11	0.81	2.05	24	5
1:A:64:VAL:CG2	1:B:31:ILE:HD13	0.81	2.06	4	4
1:B:55:ILE:HG23	1:B:59:ASP:HB3	0.81	1.52	9	5
1:B:31:ILE:HG23	1:B:35:MET:HE3	0.81	1.50	32	2
1:A:28:LEU:HD12	1:A:31:ILE:CG2	0.81	2.06	15	2
1:B:12:ILE:HD11	1:B:28:LEU:HD23	0.80	1.51	6	9
1:A:36:GLY:HA2	1:B:32:LEU:HD11	0.80	1.53	3	3
1:A:24:ALA:HB2	1:B:56:LYS:CA	0.79	2.06	4	5
1:B:46:LEU:HD22	1:B:62:LEU:HD23	0.79	1.51	8	4
1:B:39:ILE:HD13	1:B:64:VAL:HG23	0.79	1.52	17	13
1:A:28:LEU:HD13	1:B:60:ILE:HG23	0.79	1.54	20	14
1:A:47:ALA:HB2	1:A:55:ILE:HD13	0.79	1.53	10	10
1:B:12:ILE:HG22	1:B:17:ALA:CB	0.79	2.07	23	3
1:A:60:ILE:HG23	1:B:28:LEU:HD13	0.79	1.54	25	20
1:A:44:ILE:HG12	1:A:55:ILE:HD11	0.79	1.55	5	1
1:A:31:ILE:HG12	1:B:64:VAL:HG11	0.79	1.54	32	4
1:A:24:ALA:HB2	1:B:56:LYS:HA	0.78	1.54	2	4
1:A:5:ILE:HD13	1:A:25:ARG:NH2	0.78	1.93	7	1
1:A:3:LEU:HD13	1:A:33:GLU:CG	0.78	2.08	18	6
1:A:20:VAL:HG22	1:B:55:ILE:CG1	0.78	2.07	21	2
1:A:43:ALA:HB1	1:A:59:ASP:CG	0.78	2.04	5	1
1:A:55:ILE:HG13	1:B:20:VAL:HG22	0.78	1.55	3	2
1:A:31:ILE:HD13	1:B:64:VAL:CG2	0.78	2.07	7	1
1:A:3:LEU:HD13	1:A:33:GLU:CB	0.77	2.09	1	1
1:A:39:ILE:HG21	1:A:64:VAL:HG23	0.77	1.53	25	18
1:B:31:ILE:CG2	1:B:35:MET:HE3	0.77	2.09	9	3
1:A:28:LEU:HD11	1:B:39:ILE:HB	0.77	1.55	28	11
1:A:3:LEU:HD21	1:B:11:ILE:CD1	0.77	2.09	29	2
1:A:32:LEU:HD23	1:B:32:LEU:CD2	0.77	2.07	29	3
1:A:27:THR:CG2	1:B:60:ILE:HG22	0.77	2.10	18	5
1:A:32:LEU:HD12	1:B:32:LEU:HD23	0.77	1.54	7	1
1:A:60:ILE:HG13	1:B:28:LEU:HD22	0.76	1.57	16	5
1:A:11:ILE:HG23	1:B:37:ARG:HG3	0.76	1.57	4	5
1:A:40:ALA:HB1	1:B:12:ILE:HG23	0.76	1.56	1	28
1:A:32:LEU:HD21	1:B:39:ILE:HD12	0.76	1.56	30	3
1:A:44:ILE:HD11	1:B:17:ALA:CA	0.76	2.11	32	10

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:32:LEU:HD11	1:B:39:ILE:HD12	0.76	1.56	19	2
1:A:12:ILE:HG23	1:B:40:ALA:HB1	0.75	1.58	8	26
1:B:3:LEU:HB3	1:B:8:ILE:HD11	0.75	1.56	13	10
1:A:64:VAL:HG21	1:B:31:ILE:CD1	0.75	2.08	4	2
1:A:40:ALA:HB2	1:B:12:ILE:CD1	0.75	2.11	5	28
1:B:12:ILE:HD11	1:B:28:LEU:CD2	0.75	2.12	6	4
1:A:17:ALA:HA	1:B:44:ILE:HD11	0.75	1.58	24	2
1:A:44:ILE:HD11	1:B:17:ALA:N	0.75	1.96	21	8
1:A:55:ILE:HG23	1:A:59:ASP:CG	0.75	2.07	5	1
1:A:60:ILE:HD12	1:B:28:LEU:HD21	0.75	1.58	22	6
1:A:3:LEU:HD13	1:A:33:GLU:HB3	0.74	1.57	1	4
1:A:28:LEU:HD22	1:B:60:ILE:HG13	0.74	1.58	8	6
1:A:28:LEU:HD22	1:B:60:ILE:CG2	0.74	2.13	13	3
1:B:3:LEU:CB	1:B:8:ILE:HD11	0.74	2.12	13	11
1:A:3:LEU:CB	1:A:8:ILE:HD11	0.74	2.11	5	6
1:A:32:LEU:HD12	1:B:32:LEU:HB3	0.74	1.58	2	4
1:B:17:ALA:HB1	1:B:20:VAL:CG2	0.74	2.13	17	2
1:B:39:ILE:HD13	1:B:64:VAL:CG2	0.73	2.12	17	15
1:A:60:ILE:HD12	1:B:28:LEU:CD2	0.73	2.13	20	4
1:A:47:ALA:CB	1:A:55:ILE:HD13	0.73	2.12	17	5
1:A:24:ALA:HB1	1:B:60:ILE:CG1	0.73	2.13	29	12
1:A:60:ILE:CG2	1:B:28:LEU:HD22	0.73	2.13	22	7
1:A:11:ILE:HD11	1:B:3:LEU:CD2	0.73	2.13	19	12
1:A:55:ILE:CG2	1:B:20:VAL:HG13	0.73	2.13	14	2
1:A:32:LEU:HD12	1:B:32:LEU:CB	0.73	2.14	2	2
1:A:17:ALA:N	1:B:44:ILE:HD11	0.73	1.98	31	5
1:A:61:GLU:CG	1:B:31:ILE:HD11	0.73	2.14	24	2
1:B:20:VAL:HG11	1:B:25:ARG:CZ	0.73	2.14	5	1
1:A:15:ALA:HB1	1:B:41:SER:CB	0.72	2.14	6	2
1:A:20:VAL:HG22	1:B:55:ILE:HB	0.72	1.60	16	5
1:A:56:LYS:CA	1:B:24:ALA:HB2	0.72	2.15	16	4
1:A:11:ILE:HD11	1:B:3:LEU:HD22	0.72	1.61	2	2
1:A:60:ILE:CG2	1:B:27:THR:HG22	0.72	2.12	24	10
1:A:19:ARG:NH2	1:B:44:ILE:HG23	0.72	2.00	16	1
1:A:31:ILE:HD12	1:B:60:ILE:HG22	0.72	1.62	19	4
1:A:12:ILE:HD12	1:B:40:ALA:HB2	0.72	1.60	4	25
1:A:55:ILE:HB	1:B:20:VAL:HG13	0.72	1.62	17	11
1:A:39:ILE:HD13	1:A:64:VAL:HG23	0.72	1.61	6	11
1:A:39:ILE:HD13	1:A:64:VAL:CG2	0.71	2.15	6	12
1:A:32:LEU:O	1:B:32:LEU:HD21	0.71	1.84	30	11
1:A:27:THR:O	1:A:31:ILE:HD12	0.71	1.85	16	12

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:32:LEU:HD21	1:B:32:LEU:O	0.71	1.84	31	12
1:B:39:ILE:HG23	1:B:63:ALA:O	0.71	1.85	32	2
1:A:39:ILE:HG23	1:A:63:ALA:O	0.71	1.85	31	1
1:A:57:ALA:HA	1:B:27:THR:HG21	0.71	1.63	3	3
1:B:28:LEU:O	1:B:32:LEU:HD12	0.71	1.85	21	4
1:A:8:ILE:HA	1:A:11:ILE:HD12	0.71	1.62	2	3
1:B:27:THR:O	1:B:31:ILE:HD12	0.71	1.85	32	10
1:A:15:ALA:HB1	1:B:41:SER:OG	0.71	1.86	21	3
1:B:55:ILE:HG23	1:B:59:ASP:HB2	0.71	1.63	5	2
1:A:24:ALA:HB1	1:B:55:ILE:HG22	0.71	1.61	21	6
1:A:15:ALA:HB1	1:B:41:SER:HB3	0.71	1.60	20	1
1:A:61:GLU:HG2	1:B:31:ILE:HD11	0.71	1.59	24	2
1:B:55:ILE:HG23	1:B:59:ASP:CB	0.71	2.15	9	7
1:A:20:VAL:HG22	1:B:55:ILE:HD12	0.71	1.61	18	10
1:A:23:ASP:HB3	1:B:57:ALA:HB2	0.70	1.62	30	1
1:A:47:ALA:O	1:A:50:ALA:HB3	0.70	1.85	7	17
1:A:39:ILE:HB	1:B:28:LEU:HD11	0.70	1.63	8	13
1:A:42:GLU:C	1:A:46:LEU:HD12	0.70	2.11	30	5
1:A:3:LEU:CD2	1:B:11:ILE:HD11	0.70	2.14	29	3
1:A:39:ILE:HG12	1:A:64:VAL:HG23	0.70	1.63	8	3
1:A:20:VAL:HG21	1:A:25:ARG:CD	0.70	2.16	31	1
1:A:60:ILE:CG2	1:B:31:ILE:HD13	0.70	2.16	30	3
1:A:32:LEU:HD23	1:B:32:LEU:HB3	0.70	1.63	18	10
1:A:20:VAL:CG1	1:A:24:ALA:HB3	0.70	2.17	4	10
1:A:32:LEU:HD13	1:B:32:LEU:HG	0.70	1.61	6	2
1:A:33:GLU:O	1:B:11:ILE:HD12	0.70	1.87	15	1
1:A:3:LEU:HB3	1:A:8:ILE:HD11	0.69	1.62	32	14
1:B:3:LEU:CB	1:B:8:ILE:HD12	0.69	2.17	3	1
1:A:3:LEU:HD13	1:A:33:GLU:HG2	0.69	1.63	25	3
1:B:3:LEU:HD21	1:B:33:GLU:CG	0.69	2.17	31	1
1:A:12:ILE:HD11	1:A:28:LEU:HD23	0.69	1.63	3	12
1:A:60:ILE:CG1	1:B:28:LEU:HD22	0.69	2.18	9	6
1:A:43:ALA:HA	1:A:46:LEU:HD12	0.69	1.64	14	6
1:A:24:ALA:CB	1:B:55:ILE:HG22	0.69	2.17	18	8
1:A:32:LEU:CD2	1:B:32:LEU:HD23	0.69	2.17	31	5
1:A:24:ALA:O	1:A:27:THR:HG22	0.69	1.86	5	1
1:B:46:LEU:CD2	1:B:62:LEU:HD23	0.69	2.17	8	2
1:A:27:THR:C	1:A:31:ILE:HD12	0.69	2.13	9	14
1:B:39:ILE:HD13	1:B:64:VAL:HG22	0.69	1.63	7	1
1:A:5:ILE:HG21	1:A:26:ILE:HG12	0.69	1.65	3	1
1:B:28:LEU:HA	1:B:31:ILE:HD12	0.68	1.66	18	9

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:ILE:O	1:A:17:ALA:HB3	0.68	1.89	29	1
1:A:56:LYS:C	1:B:24:ALA:HB2	0.68	2.14	21	6
1:A:12:ILE:CD1	1:A:28:LEU:HD23	0.68	2.19	3	9
1:B:47:ALA:HB2	1:B:55:ILE:HG12	0.68	1.62	4	4
1:A:41:SER:OG	1:B:15:ALA:HB1	0.68	1.88	10	8
1:A:54:THR:HG23	1:B:19:ARG:O	0.68	1.88	1	2
1:A:11:ILE:CD1	1:B:3:LEU:HD21	0.68	2.18	19	5
1:A:40:ALA:HB2	1:B:12:ILE:HD13	0.68	1.63	11	4
1:A:44:ILE:HD11	1:B:17:ALA:HA	0.67	1.66	32	5
1:A:54:THR:HG23	1:B:19:ARG:HG3	0.67	1.65	9	1
1:A:46:LEU:HD22	1:A:62:LEU:CD2	0.67	2.19	21	1
1:B:28:LEU:HD12	1:B:32:LEU:HD11	0.67	1.66	17	7
1:B:47:ALA:HB2	1:B:55:ILE:CD1	0.67	2.19	31	4
1:B:17:ALA:HB1	1:B:20:VAL:HG22	0.67	1.66	22	2
1:A:55:ILE:HG23	1:A:59:ASP:OD2	0.67	1.88	5	1
1:A:28:LEU:HD22	1:B:60:ILE:CG1	0.67	2.19	1	6
1:A:22:ASP:O	1:A:26:ILE:HD12	0.67	1.90	16	3
1:B:46:LEU:HD22	1:B:59:ASP:OD1	0.67	1.88	32	1
1:B:26:ILE:HD13	1:B:26:ILE:O	0.67	1.90	22	4
1:A:60:ILE:HG12	1:B:28:LEU:HD13	0.66	1.64	24	2
1:A:11:ILE:HG23	1:B:37:ARG:HG2	0.66	1.66	32	1
1:B:57:ALA:HB1	1:B:61:GLU:OE2	0.66	1.90	17	1
1:B:42:GLU:C	1:B:46:LEU:HD12	0.66	2.15	23	8
1:A:55:ILE:HD12	1:B:20:VAL:CG2	0.66	2.19	23	1
1:A:42:GLU:O	1:A:46:LEU:HD13	0.66	1.91	32	17
1:A:43:ALA:HB1	1:A:59:ASP:OD2	0.66	1.91	5	1
1:A:46:LEU:HD22	1:A:62:LEU:HD23	0.66	1.68	21	1
1:A:20:VAL:HG13	1:B:55:ILE:HB	0.65	1.67	21	5
1:A:32:LEU:HD11	1:B:32:LEU:O	0.65	1.90	7	5
1:A:6:ALA:HB3	1:A:7:PRO:HD3	0.65	1.69	1	32
1:B:12:ILE:O	1:B:15:ALA:HB3	0.65	1.90	14	28
1:A:15:ALA:HB1	1:B:41:SER:HB2	0.65	1.66	6	3
1:B:39:ILE:HG21	1:B:64:VAL:HG23	0.65	1.69	17	18
1:A:58:GLU:O	1:A:62:LEU:HD23	0.65	1.91	11	4
1:A:28:LEU:HA	1:A:31:ILE:HD12	0.65	1.68	24	3
1:A:3:LEU:HD13	1:A:33:GLU:HB2	0.65	1.69	14	4
1:A:55:ILE:CD1	1:B:20:VAL:HG22	0.65	2.22	23	2
1:B:8:ILE:HA	1:B:11:ILE:HD12	0.64	1.67	22	3
1:B:6:ALA:HB3	1:B:7:PRO:HD3	0.64	1.69	2	32
1:A:31:ILE:HD13	1:B:60:ILE:CG2	0.64	2.22	2	5
1:A:47:ALA:HB2	1:A:55:ILE:CD1	0.64	2.22	9	6

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:ASP:O	1:A:26:ILE:HG22	0.64	1.92	10	3
1:B:58:GLU:C	1:B:62:LEU:HD23	0.64	2.17	29	1
1:A:26:ILE:HD13	1:A:26:ILE:O	0.64	1.91	7	1
1:A:41:SER:CA	1:B:15:ALA:HB1	0.64	2.22	15	1
1:B:43:ALA:HA	1:B:46:LEU:HD12	0.64	1.67	30	7
1:A:3:LEU:HD11	1:B:11:ILE:HD11	0.64	1.70	20	2
1:A:20:VAL:HG13	1:A:24:ALA:HB3	0.64	1.70	24	6
1:B:35:MET:HE2	1:B:39:ILE:HD11	0.63	1.70	20	1
1:A:39:ILE:CG2	1:A:64:VAL:HG23	0.63	2.22	25	22
1:A:3:LEU:HB3	1:A:29:ALA:HB1	0.63	1.69	6	1
1:B:5:ILE:HD12	1:B:25:ARG:HD2	0.63	1.70	15	1
1:A:28:LEU:CD2	1:B:60:ILE:HD12	0.63	2.23	13	2
1:A:60:ILE:HG22	1:B:27:THR:CG2	0.63	2.21	24	2
1:A:27:THR:HG22	1:B:60:ILE:CG2	0.63	2.23	3	9
1:A:55:ILE:HG23	1:A:59:ASP:HB2	0.63	1.70	23	2
1:B:60:ILE:O	1:B:64:VAL:HG23	0.63	1.93	29	4
1:A:23:ASP:HB2	1:B:57:ALA:HB2	0.63	1.69	16	1
1:B:3:LEU:HD21	1:B:33:GLU:HG2	0.63	1.70	31	1
1:B:12:ILE:CD1	1:B:28:LEU:HD23	0.63	2.24	15	9
1:A:60:ILE:HG23	1:B:28:LEU:HD22	0.63	1.71	20	4
1:A:5:ILE:HD13	1:A:25:ARG:NH1	0.63	2.08	3	1
1:A:55:ILE:CG2	1:B:20:VAL:HG12	0.63	2.24	28	3
1:B:58:GLU:C	1:B:62:LEU:HD12	0.63	2.18	14	1
1:A:20:VAL:HG21	1:A:25:ARG:HD2	0.63	1.68	31	1
1:B:28:LEU:HD12	1:B:32:LEU:CD1	0.62	2.24	17	5
1:A:12:ILE:O	1:A:15:ALA:HB3	0.62	1.94	16	21
1:A:3:LEU:HB2	1:A:8:ILE:HD11	0.62	1.70	7	4
1:B:46:LEU:HD21	1:B:66:ARG:NH2	0.62	2.07	1	1
1:A:33:GLU:HG2	1:B:11:ILE:HD13	0.62	1.70	8	1
1:A:26:ILE:O	1:A:29:ALA:HB3	0.62	1.94	9	3
1:A:61:GLU:C	1:A:62:LEU:HD23	0.62	2.20	31	1
1:A:44:ILE:CG1	1:A:55:ILE:HD11	0.62	2.22	5	1
1:A:17:ALA:HB2	1:B:44:ILE:CD1	0.62	2.25	14	21
1:A:3:LEU:HD11	1:A:33:GLU:HB2	0.62	1.71	16	2
1:B:12:ILE:HG21	1:B:20:VAL:HG21	0.62	1.72	11	1
1:A:28:LEU:HD12	1:A:31:ILE:HG22	0.62	1.70	15	2
1:A:28:LEU:HD12	1:A:31:ILE:HG21	0.62	1.69	15	2
1:B:31:ILE:HG22	1:B:32:LEU:HD12	0.62	1.70	18	3
1:A:12:ILE:HG22	1:A:17:ALA:CB	0.61	2.25	4	1
1:B:11:ILE:HG22	1:B:12:ILE:HD13	0.61	1.72	7	2
1:A:32:LEU:HD21	1:B:39:ILE:CD1	0.61	2.25	30	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:39:ILE:HD12	1:B:32:LEU:HD11	0.61	1.71	4	7
1:A:55:ILE:HG22	1:B:24:ALA:HB1	0.61	1.71	30	2
1:A:28:LEU:HD22	1:B:60:ILE:HG21	0.61	1.70	5	3
1:A:32:LEU:HD13	1:B:32:LEU:CG	0.61	2.25	6	1
1:B:47:ALA:O	1:B:50:ALA:HB3	0.61	1.95	32	14
1:A:28:LEU:HD21	1:B:60:ILE:HD12	0.61	1.71	13	3
1:B:12:ILE:O	1:B:17:ALA:HB3	0.61	1.96	32	2
1:A:32:LEU:HD12	1:B:32:LEU:CD2	0.61	2.25	7	1
1:A:58:GLU:O	1:A:62:LEU:HD12	0.61	1.95	10	4
1:A:60:ILE:CG1	1:B:24:ALA:HB1	0.61	2.26	3	10
1:A:58:GLU:O	1:A:62:LEU:HD13	0.61	1.95	22	3
1:A:62:LEU:HD23	1:A:62:LEU:N	0.61	2.11	31	1
1:B:31:ILE:HG22	1:B:35:MET:HE3	0.61	1.70	9	1
1:A:19:ARG:HH22	1:B:44:ILE:HG23	0.61	1.55	16	1
1:A:42:GLU:HB3	1:A:63:ALA:HB1	0.61	1.72	15	8
1:B:39:ILE:CG1	1:B:64:VAL:HG23	0.60	2.26	6	12
1:A:3:LEU:HD21	1:A:33:GLU:CD	0.60	2.21	16	1
1:A:32:LEU:HA	1:A:35:MET:HE3	0.60	1.74	29	1
1:A:64:VAL:HG21	1:B:31:ILE:CG2	0.60	2.26	31	1
1:A:12:ILE:HG23	1:B:40:ALA:CB	0.60	2.27	9	30
1:A:60:ILE:CG1	1:B:28:LEU:HD13	0.60	2.27	24	3
1:A:32:LEU:HD11	1:B:36:GLY:CA	0.60	2.25	29	1
1:B:27:THR:C	1:B:31:ILE:HD12	0.60	2.21	14	9
1:A:31:ILE:HD13	1:B:60:ILE:HG22	0.60	1.74	6	2
1:A:3:LEU:HD21	1:A:33:GLU:OE2	0.60	1.96	15	1
1:B:58:GLU:O	1:B:62:LEU:HD22	0.60	1.97	32	1
1:A:54:THR:HG22	1:A:55:ILE:O	0.60	1.97	32	5
1:A:27:THR:HG23	1:B:60:ILE:HG21	0.60	1.71	5	1
1:A:3:LEU:HD21	1:A:33:GLU:HG3	0.59	1.74	17	1
1:A:5:ILE:HG22	1:A:25:ARG:NH1	0.59	2.12	32	1
1:A:37:ARG:NE	1:B:11:ILE:HG23	0.59	2.11	19	1
1:A:35:MET:HE2	1:A:39:ILE:HD11	0.59	1.74	24	2
1:B:40:ALA:C	1:B:44:ILE:HD12	0.59	2.21	2	13
1:A:31:ILE:HD11	1:B:61:GLU:CG	0.59	2.27	29	1
1:A:41:SER:CB	1:B:15:ALA:HB1	0.59	2.28	15	2
1:A:60:ILE:O	1:A:64:VAL:HG23	0.59	1.96	24	4
1:A:32:LEU:C	1:B:32:LEU:HD21	0.59	2.23	30	2
1:A:64:VAL:HG11	1:B:31:ILE:HD13	0.59	1.72	16	1
1:B:20:VAL:CG1	1:B:24:ALA:HB3	0.59	2.27	7	6
1:A:24:ALA:HB2	1:B:55:ILE:C	0.59	2.22	18	5
1:A:60:ILE:CG2	1:B:31:ILE:HD12	0.58	2.28	16	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:5:ILE:HD12	1:B:25:ARG:HD3	0.58	1.75	13	2
1:A:55:ILE:CB	1:B:20:VAL:HG13	0.58	2.28	14	2
1:B:3:LEU:HD12	1:B:29:ALA:O	0.58	1.99	6	1
1:A:28:LEU:HD12	1:A:32:LEU:CD1	0.58	2.27	11	2
1:B:39:ILE:CD1	1:B:64:VAL:HG23	0.58	2.28	1	13
1:A:31:ILE:HD11	1:B:61:GLU:HG2	0.58	1.74	29	2
1:A:41:SER:HB2	1:B:15:ALA:HB1	0.58	1.74	29	1
1:B:3:LEU:HB2	1:B:8:ILE:HD11	0.58	1.75	5	9
1:A:31:ILE:CD1	1:B:60:ILE:HG22	0.58	2.27	19	8
1:B:47:ALA:HB2	1:B:55:ILE:HD13	0.58	1.75	31	6
1:B:12:ILE:HG21	1:B:25:ARG:CZ	0.58	2.27	5	1
1:A:55:ILE:HB	1:B:20:VAL:HG12	0.58	1.75	19	5
1:A:60:ILE:HG22	1:B:31:ILE:CD1	0.58	2.28	19	5
1:B:27:THR:HG22	1:B:31:ILE:HD11	0.58	1.75	4	8
1:B:46:LEU:HD21	1:B:66:ARG:HH21	0.57	1.59	1	1
1:A:36:GLY:CA	1:B:32:LEU:HD11	0.57	2.28	3	2
1:B:46:LEU:HD22	1:B:62:LEU:HG	0.57	1.75	11	2
1:B:20:VAL:HG11	1:B:25:ARG:NH2	0.57	2.15	5	1
1:A:57:ALA:CA	1:B:27:THR:HG21	0.57	2.29	24	2
1:A:55:ILE:HG23	1:A:59:ASP:OD1	0.57	1.99	5	1
1:A:17:ALA:HB1	1:A:20:VAL:HG23	0.57	1.76	5	1
1:B:21:SER:O	1:B:24:ALA:HB3	0.57	2.00	23	2
1:A:32:LEU:HG	1:B:35:MET:HE2	0.57	1.74	17	1
1:A:32:LEU:O	1:B:32:LEU:HD22	0.57	1.98	22	1
1:A:40:ALA:C	1:A:44:ILE:HD12	0.57	2.25	29	3
1:A:40:ALA:CB	1:B:12:ILE:HG23	0.57	2.30	7	27
1:A:60:ILE:HG13	1:B:24:ALA:HB1	0.57	1.76	3	11
1:A:20:VAL:HG22	1:B:55:ILE:HG13	0.57	1.76	15	2
1:A:28:LEU:HD13	1:B:60:ILE:HG13	0.57	1.75	3	2
1:A:39:ILE:CG1	1:A:64:VAL:HG23	0.57	2.29	8	7
1:B:64:VAL:HG22	1:B:67:PHE:CZ	0.57	2.35	23	1
1:A:47:ALA:HB1	1:A:53:LYS:HB3	0.57	1.74	30	1
1:B:46:LEU:HD11	1:B:63:ALA:HA	0.56	1.75	11	9
1:B:5:ILE:HD12	1:B:25:ARG:CD	0.56	2.30	13	2
1:A:46:LEU:HD22	1:A:63:ALA:HB2	0.56	1.76	24	12
1:A:5:ILE:HD13	1:A:25:ARG:HH22	0.56	1.59	7	1
1:B:50:ALA:HB1	1:B:53:LYS:NZ	0.56	2.16	16	1
1:A:17:ALA:HB1	1:A:20:VAL:CG2	0.56	2.30	21	5
1:B:5:ILE:HG21	1:B:25:ARG:HE	0.56	1.60	21	1
1:A:6:ALA:HB3	1:A:7:PRO:CD	0.56	2.31	10	32
1:A:55:ILE:HG22	1:B:20:VAL:HG13	0.56	1.78	14	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:6:ALA:HB3	1:B:7:PRO:CD	0.56	2.31	11	32
1:A:60:ILE:HG21	1:B:28:LEU:HD22	0.55	1.77	10	8
1:A:28:LEU:HD22	1:B:60:ILE:HG23	0.55	1.78	13	2
1:A:17:ALA:N	1:B:44:ILE:HD13	0.55	2.16	6	7
1:A:55:ILE:HB	1:B:20:VAL:HG22	0.55	1.77	21	4
1:A:28:LEU:HD11	1:B:39:ILE:CB	0.55	2.30	10	6
1:A:31:ILE:HD13	1:B:60:ILE:HG21	0.55	1.78	2	1
1:A:39:ILE:HD13	1:A:64:VAL:HG22	0.55	1.79	32	5
1:A:8:ILE:HD11	1:A:29:ALA:HA	0.55	1.76	30	3
1:A:43:ALA:HA	1:A:46:LEU:HD22	0.55	1.79	24	4
1:A:36:GLY:CA	1:B:32:LEU:HD21	0.55	2.32	8	1
1:A:5:ILE:HG23	1:A:26:ILE:CD1	0.55	2.31	29	1
1:B:46:LEU:HD11	1:B:62:LEU:C	0.55	2.27	30	1
1:B:26:ILE:HG22	1:B:30:LYS:HD2	0.54	1.78	9	1
1:B:46:LEU:HD11	1:B:62:LEU:O	0.54	2.02	30	1
1:B:20:VAL:HG11	1:B:25:ARG:NE	0.54	2.17	5	1
1:B:3:LEU:HD21	1:B:33:GLU:OE1	0.54	2.03	6	2
1:A:11:ILE:HG22	1:A:12:ILE:HD13	0.54	1.77	29	4
1:A:27:THR:HG22	1:A:31:ILE:CD1	0.54	2.32	9	5
1:A:8:ILE:HD11	1:A:29:ALA:CA	0.54	2.31	30	3
1:A:5:ILE:HD13	1:A:5:ILE:H	0.54	1.62	32	11
1:A:44:ILE:HD13	1:B:17:ALA:N	0.54	2.17	16	7
1:B:3:LEU:HD11	1:B:33:GLU:OE1	0.54	2.02	6	1
1:A:50:ALA:HB1	1:A:52:ARG:HB2	0.54	1.80	13	1
1:B:42:GLU:HB3	1:B:63:ALA:HB1	0.54	1.79	3	6
1:A:27:THR:HG22	1:A:31:ILE:HD11	0.54	1.80	24	8
1:B:39:ILE:CG2	1:B:64:VAL:HG23	0.54	2.33	15	24
1:A:28:LEU:O	1:A:32:LEU:HD23	0.54	2.03	2	1
1:A:3:LEU:HD13	1:A:33:GLU:HG3	0.54	1.78	28	3
1:A:44:ILE:HD11	1:B:17:ALA:CB	0.53	2.30	18	7
1:B:58:GLU:O	1:B:62:LEU:HD13	0.53	2.01	9	2
1:A:31:ILE:HG22	1:A:32:LEU:HD22	0.53	1.79	4	2
1:A:3:LEU:CD1	1:A:33:GLU:HB2	0.53	2.33	22	3
1:A:24:ALA:HB2	1:B:56:LYS:C	0.53	2.28	9	6
1:A:60:ILE:HG22	1:B:31:ILE:HD12	0.53	1.80	5	1
1:B:24:ALA:O	1:B:27:THR:HG22	0.53	2.02	14	1
1:A:31:ILE:HD13	1:B:60:ILE:HG23	0.53	1.80	18	5
1:B:43:ALA:N	1:B:63:ALA:HB2	0.53	2.18	31	3
1:A:32:LEU:HD11	1:B:36:GLY:HA2	0.53	1.79	29	1
1:B:26:ILE:O	1:B:29:ALA:HB3	0.53	2.04	6	6
1:A:3:LEU:N	1:A:3:LEU:HD23	0.53	2.18	7	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:LEU:O	1:A:62:LEU:HD13	0.53	2.04	25	3
1:B:39:ILE:HG23	1:B:67:PHE:HE2	0.53	1.64	19	1
1:B:43:ALA:HB1	1:B:55:ILE:CG2	0.53	2.34	30	1
1:A:44:ILE:O	1:A:47:ALA:HB3	0.53	2.04	2	3
1:A:5:ILE:HG22	1:A:25:ARG:HB3	0.53	1.78	15	1
1:A:3:LEU:HD12	1:A:29:ALA:O	0.53	2.04	32	1
1:A:57:ALA:HB2	1:B:23:ASP:HB3	0.53	1.81	6	5
1:B:58:GLU:O	1:B:62:LEU:HG	0.53	2.03	24	3
1:B:8:ILE:HG22	1:B:25:ARG:HH12	0.53	1.64	14	1
1:B:3:LEU:HB2	1:B:29:ALA:HB1	0.52	1.81	1	1
1:A:44:ILE:HA	1:A:55:ILE:HD11	0.52	1.81	23	1
1:A:47:ALA:HB1	1:A:53:LYS:CB	0.52	2.34	30	1
1:A:23:ASP:HA	1:A:26:ILE:HG22	0.52	1.81	19	3
1:A:56:LYS:HA	1:B:24:ALA:HB2	0.52	1.82	1	3
1:A:44:ILE:CD1	1:B:17:ALA:HB2	0.52	2.33	4	7
1:A:24:ALA:HB2	1:B:56:LYS:N	0.52	2.19	4	6
1:B:12:ILE:C	1:B:17:ALA:HB3	0.52	2.29	23	1
1:A:8:ILE:CD1	1:A:29:ALA:HB2	0.52	2.35	30	3
1:A:39:ILE:CD1	1:A:64:VAL:HG23	0.52	2.34	11	9
1:B:22:ASP:O	1:B:26:ILE:HD12	0.52	2.05	1	3
1:A:60:ILE:HG23	1:B:28:LEU:CD2	0.52	2.34	17	4
1:B:20:VAL:HG12	1:B:21:SER:N	0.52	2.20	23	2
1:B:53:LYS:O	1:B:54:THR:HG22	0.52	2.04	21	4
1:B:20:VAL:HG21	1:B:25:ARG:NH2	0.52	2.20	4	1
1:A:57:ALA:HB2	1:B:23:ASP:CB	0.52	2.34	6	2
1:A:27:THR:HG22	1:B:60:ILE:HG21	0.52	1.82	2	2
1:B:39:ILE:HG12	1:B:64:VAL:HG23	0.52	1.82	8	6
1:A:24:ALA:HB2	1:B:55:ILE:O	0.52	2.05	3	1
1:B:35:MET:CG	1:B:39:ILE:HD11	0.52	2.35	6	1
1:A:11:ILE:HG23	1:B:37:ARG:CG	0.52	2.34	4	1
1:B:12:ILE:HD11	1:B:28:LEU:HG	0.52	1.81	31	3
1:B:36:GLY:HA2	1:B:39:ILE:HD12	0.52	1.81	23	1
1:B:23:ASP:HA	1:B:26:ILE:HG22	0.52	1.82	22	2
1:A:60:ILE:HG12	1:B:28:LEU:HD21	0.52	1.80	31	1
1:A:60:ILE:HG21	1:B:28:LEU:N	0.51	2.20	11	6
1:A:52:ARG:NE	1:A:53:LYS:H	0.51	2.04	2	1
1:A:12:ILE:CD1	1:B:40:ALA:HB2	0.51	2.35	5	29
1:B:5:ILE:H	1:B:5:ILE:HD13	0.51	1.65	7	8
1:A:20:VAL:HG12	1:A:24:ALA:HB3	0.51	1.83	13	3
1:B:17:ALA:HB1	1:B:20:VAL:HG21	0.51	1.83	15	2
1:B:5:ILE:HD13	1:B:25:ARG:CZ	0.51	2.36	6	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:LEU:N	1:B:60:ILE:HG21	0.51	2.20	19	8
1:A:20:VAL:HG11	1:A:25:ARG:HH21	0.51	1.65	14	1
1:A:24:ALA:HB1	1:B:60:ILE:HG13	0.51	1.82	22	4
1:A:47:ALA:C	1:A:50:ALA:HB3	0.51	2.31	20	1
1:B:42:GLU:O	1:B:46:LEU:HG	0.51	2.06	30	1
1:A:24:ALA:HB1	1:B:60:ILE:HG12	0.51	1.82	29	1
1:A:28:LEU:HD13	1:B:60:ILE:CG2	0.51	2.30	20	1
1:A:17:ALA:CB	1:B:44:ILE:HD11	0.51	2.32	22	2
1:A:33:GLU:HG3	1:B:11:ILE:HD12	0.50	1.82	16	2
1:B:46:LEU:HD22	1:B:62:LEU:CD2	0.50	2.36	17	4
1:A:20:VAL:HG22	1:B:55:ILE:HG12	0.50	1.82	21	1
1:B:54:THR:HG22	1:B:55:ILE:O	0.50	2.07	16	2
1:B:4:PRO:HG2	1:B:7:PRO:HG2	0.50	1.82	19	1
1:A:28:LEU:HD22	1:B:60:ILE:HG12	0.50	1.83	4	1
1:A:55:ILE:HG22	1:B:24:ALA:CB	0.50	2.36	5	1
1:A:8:ILE:HD11	1:A:29:ALA:CB	0.50	2.37	30	3
1:A:28:LEU:HD11	1:B:39:ILE:HG21	0.50	1.82	29	1
1:B:47:ALA:CB	1:B:55:ILE:HD13	0.50	2.37	15	4
1:A:3:LEU:HD12	1:A:3:LEU:N	0.50	2.22	30	4
1:A:4:PRO:HG2	1:A:7:PRO:HG2	0.50	1.84	22	4
1:A:3:LEU:HD21	1:A:33:GLU:HB2	0.50	1.84	6	1
1:B:39:ILE:HG23	1:B:67:PHE:CE2	0.50	2.42	19	1
1:A:3:LEU:HD11	1:B:11:ILE:CD1	0.50	2.37	20	1
1:B:5:ILE:HD13	1:B:25:ARG:NE	0.50	2.22	8	2
1:A:39:ILE:CG2	1:B:28:LEU:HD11	0.49	2.37	21	8
1:A:20:VAL:HG13	1:A:24:ALA:CB	0.49	2.37	25	5
1:A:39:ILE:HG21	1:B:28:LEU:CD1	0.49	2.37	21	8
1:B:20:VAL:HG21	1:B:25:ARG:HG3	0.49	1.83	31	1
1:A:39:ILE:CB	1:B:28:LEU:HD11	0.49	2.34	8	7
1:B:20:VAL:HG21	1:B:25:ARG:HH21	0.49	1.67	4	1
1:A:32:LEU:CD1	1:B:32:LEU:HD23	0.49	2.37	20	2
1:B:47:ALA:HB2	1:B:55:ILE:HG13	0.49	1.83	22	1
1:A:28:LEU:HD13	1:B:60:ILE:CG1	0.49	2.37	3	1
1:A:46:LEU:HD11	1:A:63:ALA:HA	0.49	1.83	14	3
1:A:42:GLU:O	1:A:46:LEU:HD12	0.49	2.07	30	2
1:A:3:LEU:HD11	1:A:33:GLU:HB3	0.49	1.83	31	1
1:A:4:PRO:HB2	1:A:7:PRO:HG2	0.49	1.85	14	3
1:B:20:VAL:HG12	1:B:24:ALA:HB3	0.49	1.83	11	2
1:B:58:GLU:O	1:B:62:LEU:HD12	0.49	2.07	14	1
1:A:19:ARG:O	1:B:54:THR:HG23	0.49	2.07	15	1
1:A:43:ALA:HB2	1:A:60:ILE:HG13	0.49	1.84	31	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:3:LEU:CD1	1:B:11:ILE:HD11	0.49	2.38	1	5
1:B:4:PRO:HB2	1:B:7:PRO:HD2	0.49	1.83	4	6
1:B:3:LEU:HG	1:B:33:GLU:HB3	0.49	1.84	7	1
1:B:4:PRO:HB2	1:B:7:PRO:HG2	0.48	1.84	2	1
1:A:33:GLU:HG2	1:B:11:ILE:HD12	0.48	1.85	10	3
1:A:47:ALA:HB1	1:A:52:ARG:O	0.48	2.08	31	1
1:A:43:ALA:CA	1:A:63:ALA:HB2	0.48	2.38	29	2
1:A:60:ILE:HG22	1:B:31:ILE:HD13	0.48	1.85	32	1
1:A:64:VAL:HA	1:A:67:PHE:CE1	0.48	2.44	1	4
1:A:27:THR:HG21	1:B:57:ALA:HA	0.48	1.85	18	4
1:A:8:ILE:HG13	1:A:29:ALA:HB2	0.48	1.83	30	1
1:A:28:LEU:HD13	1:B:60:ILE:HG12	0.48	1.85	25	3
1:B:5:ILE:HD13	1:B:5:ILE:N	0.48	2.23	21	1
1:A:39:ILE:HG21	1:B:28:LEU:HD11	0.48	1.86	4	6
1:B:35:MET:HG2	1:B:39:ILE:HD11	0.48	1.84	15	1
1:A:33:GLU:HB2	1:A:37:ARG:NH2	0.48	2.24	19	1
1:B:3:LEU:HD11	1:B:33:GLU:HB2	0.48	1.86	2	5
1:A:5:ILE:C	1:A:5:ILE:HD12	0.48	2.33	7	2
1:A:55:ILE:CG1	1:B:20:VAL:HG22	0.48	2.38	17	2
1:A:32:LEU:HD12	1:B:32:LEU:CG	0.48	2.39	2	2
1:A:54:THR:HG21	1:B:21:SER:OG	0.48	2.09	29	1
1:A:54:THR:HG21	1:B:21:SER:HB2	0.48	1.85	11	2
1:B:42:GLU:O	1:B:46:LEU:HD12	0.48	2.09	16	5
1:B:6:ALA:N	1:B:7:PRO:HD2	0.48	2.23	8	2
1:B:3:LEU:N	1:B:3:LEU:HD23	0.48	2.24	9	2
1:A:4:PRO:HB2	1:A:7:PRO:HD2	0.48	1.84	25	7
1:B:3:LEU:CD1	1:B:33:GLU:HB2	0.47	2.39	30	2
1:B:41:SER:HA	1:B:44:ILE:HD12	0.47	1.85	20	1
1:B:27:THR:HG22	1:B:31:ILE:HD13	0.47	1.85	31	1
1:A:20:VAL:HG12	1:A:21:SER:N	0.47	2.24	4	1
1:B:5:ILE:CD1	1:B:5:ILE:H	0.47	2.22	21	1
1:B:44:ILE:O	1:B:47:ALA:HB3	0.47	2.09	22	3
1:A:12:ILE:HD13	1:B:40:ALA:HB2	0.47	1.87	30	2
1:A:60:ILE:CG2	1:B:27:THR:HG23	0.47	2.40	14	1
1:A:8:ILE:HB	1:A:25:ARG:NH2	0.47	2.23	23	1
1:B:58:GLU:HA	1:B:62:LEU:HD23	0.47	1.86	29	1
1:B:44:ILE:HG12	1:B:55:ILE:HD13	0.47	1.86	3	1
1:A:20:VAL:HG22	1:B:55:ILE:HD13	0.47	1.84	16	1
1:A:20:VAL:HG22	1:B:55:ILE:CB	0.47	2.34	16	1
1:A:12:ILE:C	1:A:17:ALA:HB3	0.47	2.34	4	1
1:A:8:ILE:CG1	1:A:29:ALA:HB2	0.47	2.39	30	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:35:MET:HE3	1:A:67:PHE:HD2	0.47	1.69	32	1
1:B:39:ILE:HG12	1:B:67:PHE:CE2	0.47	2.45	23	5
1:A:11:ILE:HG23	1:B:37:ARG:HD2	0.47	1.86	5	1
1:A:60:ILE:HG21	1:B:27:THR:HG23	0.47	1.86	14	1
1:A:17:ALA:HB1	1:A:20:VAL:HG21	0.47	1.86	21	1
1:A:58:GLU:OE2	1:A:62:LEU:HD11	0.47	2.10	24	2
1:A:21:SER:HB2	1:B:54:THR:HG23	0.47	1.86	18	3
1:B:54:THR:HG22	1:B:55:ILE:N	0.47	2.25	2	4
1:B:5:ILE:HG21	1:B:26:ILE:CG1	0.47	2.40	29	1
1:A:39:ILE:HG12	1:A:67:PHE:CE2	0.46	2.45	4	6
1:A:31:ILE:HG21	1:B:64:VAL:CG2	0.46	2.39	29	2
1:A:6:ALA:N	1:A:7:PRO:HD2	0.46	2.24	19	2
1:A:43:ALA:O	1:A:47:ALA:HB2	0.46	2.10	20	1
1:A:39:ILE:HG21	1:A:64:VAL:CG2	0.46	2.35	25	2
1:A:42:GLU:HG3	1:A:67:PHE:CZ	0.46	2.46	2	1
1:A:39:ILE:O	1:A:63:ALA:HB1	0.46	2.10	11	1
1:B:58:GLU:CA	1:B:62:LEU:HD23	0.46	2.40	29	1
1:A:20:VAL:HG13	1:B:55:ILE:CG2	0.46	2.41	16	2
1:A:39:ILE:HA	1:A:42:GLU:HB2	0.46	1.87	23	2
1:A:3:LEU:O	1:A:29:ALA:HB1	0.46	2.10	29	1
1:B:31:ILE:HD12	1:B:31:ILE:N	0.46	2.26	31	2
1:B:4:PRO:CD	1:B:7:PRO:HG2	0.46	2.40	3	1
1:A:12:ILE:CD1	1:A:28:LEU:HD21	0.46	2.41	19	1
1:B:43:ALA:HB1	1:B:55:ILE:HG21	0.46	1.87	30	1
1:A:32:LEU:CG	1:B:32:LEU:HD23	0.46	2.39	31	1
1:A:39:ILE:HG12	1:A:67:PHE:CZ	0.46	2.46	1	5
1:A:46:LEU:O	1:A:50:ALA:HB2	0.46	2.09	3	1
1:A:32:LEU:HB3	1:B:32:LEU:HD23	0.46	1.88	10	3
1:A:30:LYS:NZ	1:A:30:LYS:HB3	0.46	2.26	29	2
1:A:35:MET:HE3	1:A:35:MET:HA	0.46	1.86	3	4
1:A:60:ILE:HB	1:B:27:THR:HG21	0.46	1.88	31	2
1:A:39:ILE:HA	1:A:67:PHE:CE2	0.46	2.46	24	4
1:B:39:ILE:HA	1:B:67:PHE:CE2	0.46	2.46	7	5
1:A:28:LEU:CA	1:A:31:ILE:HD12	0.46	2.38	17	1
1:A:46:LEU:HD21	1:A:66:ARG:CD	0.46	2.41	3	1
1:A:42:GLU:HG2	1:A:67:PHE:CE1	0.46	2.46	5	2
1:A:28:LEU:O	1:A:32:LEU:HD12	0.46	2.11	8	1
1:A:42:GLU:HG2	1:A:67:PHE:CZ	0.46	2.45	7	6
1:A:20:VAL:HG12	1:A:21:SER:H	0.45	1.69	4	1
1:A:38:ASP:HB3	1:A:67:PHE:CZ	0.45	2.45	23	8
1:B:44:ILE:HA	1:B:55:ILE:HD11	0.45	1.88	20	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:5:ILE:HG21	1:A:25:ARG:HG3	0.45	1.88	29	1
1:A:54:THR:HG22	1:B:21:SER:HB3	0.45	1.88	31	1
1:A:26:ILE:HA	1:A:29:ALA:HB3	0.45	1.88	1	1
1:B:3:LEU:HD12	1:B:29:ALA:HA	0.45	1.88	1	1
1:A:32:LEU:HD11	1:B:36:GLY:N	0.45	2.26	3	1
1:B:42:GLU:HG3	1:B:67:PHE:CZ	0.45	2.47	5	1
1:A:4:PRO:HB2	1:A:7:PRO:CG	0.45	2.42	6	3
1:B:39:ILE:CG2	1:B:63:ALA:HB3	0.45	2.41	14	1
1:A:57:ALA:O	1:B:27:THR:HG21	0.45	2.10	24	2
1:B:18:GLU:HG3	1:B:19:ARG:N	0.45	2.26	25	2
1:A:20:VAL:HG13	1:B:55:ILE:CB	0.45	2.41	4	1
1:B:47:ALA:HB2	1:B:55:ILE:CG1	0.45	2.37	4	1
1:A:13:LYS:HD3	1:A:18:GLU:HB2	0.45	1.86	4	1
1:A:60:ILE:N	1:A:60:ILE:CD1	0.45	2.80	30	2
1:B:39:ILE:CG1	1:B:67:PHE:CE2	0.45	3.00	14	1
1:A:19:ARG:N	1:A:19:ARG:CD	0.45	2.80	16	1
1:A:39:ILE:HD12	1:B:32:LEU:CD1	0.45	2.41	24	2
1:A:3:LEU:HD12	1:B:11:ILE:HD11	0.45	1.89	1	1
1:A:34:GLU:OE2	1:A:35:MET:HE1	0.45	2.12	4	1
1:B:3:LEU:HD23	1:B:3:LEU:N	0.45	2.26	5	2
1:A:32:LEU:HD21	1:B:32:LEU:C	0.45	2.36	16	2
1:A:30:LYS:O	1:A:34:GLU:HB2	0.45	2.12	17	4
1:B:57:ALA:O	1:B:61:GLU:HB2	0.45	2.12	4	6
1:A:48:ARG:CD	1:A:52:ARG:NH1	0.45	2.80	16	1
1:A:54:THR:HG22	1:B:21:SER:N	0.45	2.27	17	1
1:B:20:VAL:CG1	1:B:21:SER:N	0.45	2.80	23	1
1:A:54:THR:CG2	1:B:21:SER:N	0.45	2.80	24	2
1:A:57:ALA:C	1:B:27:THR:HG21	0.45	2.37	24	2
1:A:64:VAL:HG21	1:B:31:ILE:HG12	0.45	1.88	32	1
1:A:32:LEU:HA	1:B:32:LEU:CD2	0.45	2.42	5	1
1:B:64:VAL:CG2	1:B:67:PHE:CZ	0.45	3.00	23	1
1:A:28:LEU:HB2	1:B:60:ILE:HG23	0.45	1.86	32	1
1:B:38:ASP:HB3	1:B:67:PHE:CZ	0.45	2.46	15	7
1:A:3:LEU:CD2	1:A:3:LEU:N	0.45	2.80	6	1
1:B:22:ASP:CA	1:B:25:ARG:NH1	0.45	2.80	20	2
1:A:37:ARG:N	1:B:11:ILE:CG2	0.45	2.80	15	1
1:A:29:ALA:O	1:A:33:GLU:HB2	0.45	2.11	18	3
1:B:54:THR:CG2	1:B:55:ILE:N	0.45	2.80	2	4
1:A:31:ILE:HD12	1:B:60:ILE:CG2	0.45	2.42	3	2
1:B:35:MET:HG3	1:B:39:ILE:HD11	0.45	1.87	6	1
1:B:22:ASP:HA	1:B:25:ARG:NH1	0.45	2.27	7	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:VAL:CG1	1:A:65:ARG:N	0.45	2.80	29	2
1:A:58:GLU:HA	1:A:61:GLU:HB2	0.45	1.88	1	1
1:B:5:ILE:CD1	1:B:25:ARG:NH2	0.45	2.80	2	1
1:B:60:ILE:CD1	1:B:60:ILE:N	0.45	2.80	8	3
1:A:3:LEU:HG	1:A:33:GLU:HB2	0.45	1.89	8	2
1:B:44:ILE:HG12	1:B:55:ILE:HD11	0.45	1.88	14	1
1:A:9:GLY:HA3	1:A:25:ARG:NH1	0.45	2.27	21	1
1:A:52:ARG:NE	1:A:53:LYS:N	0.44	2.64	2	1
1:B:20:VAL:CG2	1:B:25:ARG:NH2	0.44	2.80	4	1
1:B:27:THR:HG22	1:B:31:ILE:CD1	0.44	2.41	23	4
1:B:42:GLU:HG2	1:B:67:PHE:CE1	0.44	2.47	6	2
1:B:39:ILE:CG1	1:B:67:PHE:CZ	0.44	3.00	8	1
1:B:20:VAL:HB	1:B:24:ALA:HB3	0.44	1.89	10	3
1:A:46:LEU:HD11	1:A:63:ALA:CA	0.44	2.42	14	1
1:B:26:ILE:CD1	1:B:26:ILE:N	0.44	2.80	24	2
1:B:38:ASP:HB3	1:B:67:PHE:CE2	0.44	2.48	8	4
1:B:46:LEU:CD1	1:B:63:ALA:N	0.44	2.80	14	3
1:A:44:ILE:CD1	1:B:17:ALA:N	0.44	2.80	17	1
1:A:3:LEU:HG	1:A:33:GLU:HB3	0.44	1.88	19	2
1:A:39:ILE:CG1	1:A:67:PHE:CE2	0.44	3.00	4	2
1:A:31:ILE:CG2	1:B:64:VAL:HG21	0.44	2.34	13	1
1:B:39:ILE:HG12	1:B:67:PHE:CE1	0.44	2.48	18	3
1:A:42:GLU:CG	1:A:67:PHE:CE1	0.44	3.00	5	1
1:B:20:VAL:HG12	1:B:21:SER:H	0.44	1.73	14	2
1:B:42:GLU:HG2	1:B:67:PHE:HB3	0.44	1.90	25	3
1:A:56:LYS:HG3	1:A:59:ASP:HB2	0.44	1.88	24	2
1:A:54:THR:HG22	1:A:56:LYS:NZ	0.44	2.27	3	1
1:A:32:LEU:HD11	1:B:39:ILE:CD1	0.44	2.43	23	2
1:A:40:ALA:CB	1:B:12:ILE:HD12	0.44	2.32	22	1
1:A:27:THR:CG2	1:B:60:ILE:HG21	0.44	2.43	5	1
1:A:57:ALA:HB2	1:B:23:ASP:CG	0.44	2.38	6	1
1:B:3:LEU:CG	1:B:33:GLU:HB3	0.44	2.43	7	1
1:B:5:ILE:HD13	1:B:25:ARG:HE	0.44	1.73	8	1
1:B:39:ILE:HG12	1:B:67:PHE:CZ	0.44	2.48	8	4
1:A:57:ALA:O	1:A:61:GLU:HB2	0.44	2.13	30	2
1:B:4:PRO:HB2	1:B:7:PRO:CD	0.44	2.43	19	4
1:B:29:ALA:O	1:B:33:GLU:HB2	0.44	2.12	3	1
1:A:8:ILE:CG2	1:A:25:ARG:NH2	0.44	2.81	23	1
1:A:37:ARG:N	1:B:11:ILE:HG22	0.44	2.28	29	1
1:B:39:ILE:HG21	1:B:64:VAL:CG2	0.44	2.41	17	2
1:A:60:ILE:HG21	1:B:27:THR:HG22	0.44	1.90	20	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:22:ASP:HB3	1:B:25:ARG:NH1	0.44	2.28	20	1
1:A:43:ALA:HA	1:A:46:LEU:HB2	0.43	1.90	32	5
1:A:60:ILE:HG13	1:B:24:ALA:CB	0.43	2.43	15	6
1:A:42:GLU:C	1:A:46:LEU:HD13	0.43	2.38	31	4
1:A:24:ALA:HA	1:B:60:ILE:HG13	0.43	1.89	21	4
1:B:20:VAL:HG13	1:B:24:ALA:HB3	0.43	1.89	31	1
1:B:48:ARG:HB2	1:B:52:ARG:NE	0.43	2.28	32	1
1:A:41:SER:N	1:B:15:ALA:HB1	0.43	2.27	15	1
1:B:43:ALA:HB2	1:B:60:ILE:HG13	0.43	1.90	18	3
1:A:44:ILE:HG12	1:A:55:ILE:CD1	0.43	2.43	23	1
1:B:58:GLU:O	1:B:62:LEU:HD23	0.43	2.12	29	1
1:A:42:GLU:HG3	1:A:67:PHE:CE2	0.43	2.48	30	1
1:A:60:ILE:N	1:A:60:ILE:HD12	0.43	2.28	30	1
1:A:20:VAL:HG21	1:A:25:ARG:HH22	0.43	1.64	2	1
1:A:20:VAL:HG13	1:B:55:ILE:HG22	0.43	1.88	16	1
1:B:30:LYS:O	1:B:34:GLU:HB2	0.43	2.12	23	2
1:B:35:MET:HB3	1:B:39:ILE:HD11	0.43	1.89	18	3
1:A:60:ILE:HG13	1:B:24:ALA:HA	0.43	1.91	22	2
1:A:5:ILE:HG23	1:A:26:ILE:HD11	0.43	1.89	29	1
1:B:3:LEU:HD21	1:B:33:GLU:HG3	0.43	1.90	30	1
1:B:47:ALA:HB3	1:B:55:ILE:CD1	0.43	2.43	2	1
1:A:55:ILE:CB	1:B:20:VAL:HG12	0.43	2.43	10	3
1:A:20:VAL:HG12	1:A:25:ARG:HG3	0.43	1.88	18	3
1:A:12:ILE:HD12	1:A:28:LEU:CD2	0.43	2.44	23	1
1:A:28:LEU:CD1	1:B:39:ILE:HG21	0.43	2.43	4	3
1:B:3:LEU:HB2	1:B:8:ILE:CD1	0.43	2.44	5	2
1:A:44:ILE:HD13	1:B:17:ALA:CA	0.43	2.43	10	5
1:B:35:MET:HE2	1:B:67:PHE:HZ	0.43	1.73	25	3
1:A:5:ILE:HG21	1:A:25:ARG:HD3	0.43	1.90	19	1
1:A:28:LEU:HD13	1:B:39:ILE:HG21	0.43	1.91	32	1
1:A:55:ILE:HB	1:B:20:VAL:CG1	0.43	2.44	10	4
1:A:8:ILE:HD12	1:A:29:ALA:CB	0.43	2.44	15	1
1:A:31:ILE:HG12	1:B:64:VAL:HG21	0.43	1.90	16	1
1:B:28:LEU:HD12	1:B:32:LEU:HD12	0.43	1.90	31	1
1:A:60:ILE:HG21	1:B:31:ILE:HD13	0.43	1.88	30	1
1:A:4:PRO:HG2	1:A:7:PRO:HG3	0.43	1.91	4	1
1:A:22:ASP:HB3	1:A:25:ARG:NH2	0.43	2.29	4	1
1:A:4:PRO:HB2	1:A:7:PRO:CD	0.43	2.43	18	5
1:B:43:ALA:CA	1:B:63:ALA:HB2	0.43	2.44	9	2
1:B:39:ILE:HG22	1:B:63:ALA:HB3	0.43	1.91	14	1
1:B:26:ILE:CD1	1:B:30:LYS:HD3	0.43	2.43	3	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:SER:HB2	1:B:54:THR:CG2	0.43	2.44	4	1
1:A:5:ILE:HD12	1:A:6:ALA:N	0.43	2.29	7	1
1:A:20:VAL:HG12	1:A:25:ARG:CG	0.43	2.43	18	1
1:A:60:ILE:HG21	1:B:27:THR:CG2	0.43	2.43	14	2
1:A:8:ILE:HD13	1:A:29:ALA:HA	0.43	1.91	8	1
1:A:5:ILE:CG2	1:A:25:ARG:HB3	0.43	2.44	15	1
1:B:42:GLU:HG3	1:B:67:PHE:CE1	0.42	2.49	5	1
1:A:25:ARG:HH21	1:A:28:LEU:HD23	0.42	1.74	8	1
1:A:8:ILE:HG22	1:A:25:ARG:NH1	0.42	2.29	14	1
1:A:3:LEU:CG	1:A:33:GLU:HB3	0.42	2.45	19	1
1:A:43:ALA:HB2	1:A:63:ALA:HB2	0.42	1.90	22	1
1:B:4:PRO:HD2	1:B:7:PRO:HG2	0.42	1.90	3	1
1:A:20:VAL:CG2	1:B:55:ILE:HD13	0.42	2.44	16	1
1:B:26:ILE:N	1:B:26:ILE:HD12	0.42	2.28	24	2
1:A:60:ILE:HG12	1:B:28:LEU:HD22	0.42	1.89	29	1
1:B:28:LEU:CA	1:B:31:ILE:HD12	0.42	2.41	25	4
1:A:44:ILE:HD13	1:B:17:ALA:HA	0.42	1.90	6	1
1:A:5:ILE:CG2	1:A:26:ILE:HG12	0.42	2.43	30	1
1:A:17:ALA:N	1:B:44:ILE:CD1	0.42	2.80	4	1
1:A:8:ILE:HD11	1:A:29:ALA:HB2	0.42	1.90	30	3
1:A:42:GLU:HG3	1:A:67:PHE:CE1	0.42	2.49	24	2
1:B:40:ALA:O	1:B:44:ILE:HD12	0.42	2.15	29	1
1:A:5:ILE:HB	1:A:25:ARG:CB	0.42	2.44	15	2
1:B:35:MET:HE2	1:B:67:PHE:CZ	0.42	2.49	25	3
1:B:5:ILE:HD12	1:B:25:ARG:NH2	0.42	2.30	2	1
1:A:4:PRO:HG2	1:A:7:PRO:CG	0.42	2.45	4	3
1:A:46:LEU:CD1	1:A:63:ALA:N	0.42	2.83	14	1
1:B:17:ALA:CB	1:B:20:VAL:HG22	0.42	2.40	22	1
1:A:43:ALA:HB1	1:A:59:ASP:HB3	0.42	1.89	29	1
1:B:10:ARG:N	1:B:10:ARG:HD3	0.42	2.29	32	1
1:A:16:GLY:C	1:B:44:ILE:HG21	0.42	2.38	3	1
1:A:3:LEU:CD1	1:A:33:GLU:HG3	0.42	2.45	22	1
1:A:43:ALA:O	1:A:55:ILE:HD12	0.42	2.14	32	1
1:B:44:ILE:HG12	1:B:55:ILE:CD1	0.42	2.45	8	2
1:B:5:ILE:HB	1:B:25:ARG:HB3	0.42	1.90	10	3
1:A:38:ASP:O	1:A:42:GLU:HB2	0.42	2.15	20	5
1:B:5:ILE:CG2	1:B:26:ILE:HD13	0.42	2.45	10	3
1:A:24:ALA:CB	1:B:60:ILE:HG13	0.42	2.45	20	2
1:B:38:ASP:O	1:B:42:GLU:HB2	0.42	2.15	9	5
1:B:60:ILE:N	1:B:60:ILE:CD1	0.42	2.83	9	1
1:A:55:ILE:CB	1:B:20:VAL:HG22	0.42	2.44	23	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:4:PRO:HG2	1:B:7:PRO:CG	0.41	2.45	22	6
1:A:9:GLY:HA2	1:A:25:ARG:HG2	0.41	1.92	5	1
1:A:53:LYS:HG2	1:A:54:THR:N	0.41	2.30	6	1
1:B:5:ILE:CG2	1:B:26:ILE:HG13	0.41	2.44	9	1
1:B:64:VAL:CG1	1:B:65:ARG:N	0.41	2.83	30	1
1:A:5:ILE:HA	1:A:25:ARG:NH2	0.41	2.29	32	1
1:A:38:ASP:HB3	1:A:67:PHE:CE1	0.41	2.50	9	1
1:A:32:LEU:CD1	1:B:39:ILE:HD12	0.41	2.44	14	2
1:B:52:ARG:NE	1:B:52:ARG:HA	0.41	2.31	14	1
1:A:46:LEU:CD1	1:A:63:ALA:HA	0.41	2.45	21	2
1:B:5:ILE:HD13	1:B:5:ILE:H	0.41	1.74	21	1
1:B:28:LEU:C	1:B:32:LEU:HD12	0.41	2.39	21	1
1:B:6:ALA:H	1:B:7:PRO:HD2	0.41	1.74	29	3
1:A:59:ASP:O	1:A:63:ALA:HB2	0.41	2.15	1	1
1:A:27:THR:HG21	1:B:57:ALA:CA	0.41	2.45	2	1
1:A:46:LEU:CD2	1:A:63:ALA:N	0.41	2.83	10	3
1:A:52:ARG:HB3	1:A:52:ARG:CZ	0.41	2.46	10	3
1:B:5:ILE:N	1:B:5:ILE:CD1	0.41	2.83	21	1
1:A:60:ILE:HD12	1:A:60:ILE:N	0.41	2.30	29	1
1:A:35:MET:HE3	1:A:67:PHE:CD2	0.41	2.50	32	1
1:A:52:ARG:CD	1:A:53:LYS:N	0.41	2.83	2	1
1:A:55:ILE:HG21	1:B:25:ARG:HH22	0.41	1.76	5	1
1:A:56:LYS:N	1:B:24:ALA:HB2	0.41	2.30	16	1
1:B:20:VAL:HG21	1:B:25:ARG:HE	0.41	1.75	30	1
1:B:65:ARG:HB3	1:B:65:ARG:NH1	0.41	2.30	32	1
1:A:35:MET:N	1:A:35:MET:HE3	0.41	2.31	4	1
1:B:46:LEU:CD1	1:B:63:ALA:HA	0.41	2.45	10	6
1:B:39:ILE:HG13	1:B:67:PHE:CE2	0.41	2.50	8	1
1:A:12:ILE:HG23	1:B:44:ILE:HD11	0.41	1.92	3	1
1:B:64:VAL:HA	1:B:67:PHE:CD2	0.41	2.51	3	1
1:A:46:LEU:HD23	1:A:59:ASP:O	0.41	2.16	24	2
1:B:43:ALA:N	1:B:63:ALA:CB	0.41	2.84	31	1
1:B:64:VAL:HA	1:B:67:PHE:CD1	0.41	2.50	18	4
1:A:42:GLU:O	1:A:46:LEU:HG	0.41	2.15	20	1
1:A:27:THR:HG22	1:A:31:ILE:HD12	0.41	1.91	29	1
1:A:62:LEU:N	1:A:62:LEU:CD2	0.41	2.80	31	1
1:A:44:ILE:CG2	1:A:45:LYS:N	0.41	2.84	32	1
1:A:20:VAL:HG22	1:B:55:ILE:CD1	0.41	2.45	3	1
1:A:33:GLU:HG2	1:B:11:ILE:CD1	0.41	2.45	8	1
1:A:39:ILE:HG12	1:A:67:PHE:CE1	0.41	2.51	13	2
1:B:37:ARG:O	1:B:40:ALA:HB3	0.41	2.16	15	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:LEU:HG	1:A:32:LEU:CD1	0.41	2.46	18	3
1:A:3:LEU:N	1:A:3:LEU:CD1	0.41	2.84	20	3
1:A:5:ILE:HG13	1:A:25:ARG:HD3	0.41	1.92	20	1
1:B:5:ILE:HG21	1:B:26:ILE:HG13	0.41	1.92	29	1
1:A:21:SER:HB3	1:B:54:THR:CG2	0.41	2.46	31	1
1:A:37:ARG:HD3	1:B:15:ALA:HA	0.41	1.92	2	1
1:A:41:SER:O	1:A:44:ILE:HG22	0.41	2.15	22	2
1:B:44:ILE:CG1	1:B:55:ILE:HD13	0.41	2.46	3	1
1:B:8:ILE:HD13	1:B:29:ALA:HA	0.41	1.92	7	1
1:A:54:THR:HB	1:A:56:LYS:NZ	0.41	2.30	28	3
1:A:55:ILE:CG2	1:A:60:ILE:HD11	0.41	2.46	14	1
1:A:33:GLU:HG3	1:B:11:ILE:CD1	0.41	2.46	15	1
1:B:12:ILE:HD12	1:B:28:LEU:HD23	0.41	1.92	15	1
1:B:42:GLU:HG2	1:B:67:PHE:CB	0.41	2.46	25	3
1:A:46:LEU:CD2	1:A:63:ALA:HA	0.41	2.46	19	1
1:A:11:ILE:HG22	1:A:12:ILE:CD1	0.41	2.46	29	1
1:A:11:ILE:HD13	1:B:33:GLU:HG2	0.41	1.93	4	1
1:A:18:GLU:HG3	1:A:19:ARG:NH1	0.41	2.31	7	1
1:A:8:ILE:HD12	1:A:29:ALA:HB2	0.41	1.93	15	1
1:A:24:ALA:CA	1:B:60:ILE:HG13	0.41	2.46	21	2
1:A:5:ILE:HG13	1:A:25:ARG:NE	0.41	2.31	19	1
1:B:43:ALA:HA	1:B:46:LEU:HB2	0.41	1.92	24	2
1:A:6:ALA:H	1:A:7:PRO:HD2	0.41	1.76	30	1
1:A:57:ALA:N	1:B:23:ASP:HB3	0.40	2.31	6	1
1:A:40:ALA:HB1	1:B:12:ILE:CG2	0.40	2.40	14	1
1:B:9:GLY:HA2	1:B:25:ARG:NH1	0.40	2.30	14	1
1:A:27:THR:HG21	1:B:57:ALA:O	0.40	2.16	16	1
1:A:23:ASP:OD1	1:B:57:ALA:HB2	0.40	2.16	20	1
1:B:5:ILE:HG21	1:B:25:ARG:NE	0.40	2.30	21	1
1:A:8:ILE:HB	1:A:25:ARG:HG3	0.40	1.93	24	2
1:A:43:ALA:CB	1:A:60:ILE:HD12	0.40	2.46	24	2
1:B:3:LEU:CG	1:B:33:GLU:HB2	0.40	2.46	8	1
1:B:12:ILE:HG13	1:B:25:ARG:NH2	0.40	2.31	14	1
1:A:54:THR:HB	1:A:56:LYS:HZ3	0.40	1.75	29	1
1:B:39:ILE:O	1:B:63:ALA:HB1	0.40	2.17	31	1
1:A:55:ILE:C	1:B:24:ALA:HB2	0.40	2.41	3	1
1:A:60:ILE:HG13	1:B:24:ALA:CA	0.40	2.45	11	2
1:B:22:ASP:HA	1:B:25:ARG:NE	0.40	2.32	13	1
1:A:3:LEU:CG	1:A:33:GLU:HB2	0.40	2.46	17	1
1:B:44:ILE:CG2	1:B:45:LYS:N	0.40	2.84	31	1
1:B:48:ARG:HD2	1:B:49:HIS:N	0.40	2.31	32	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:60:ILE:HG12	1:B:24:ALA:HB1	0.40	1.94	5	1
1:A:44:ILE:CD1	1:B:17:ALA:HA	0.40	2.47	6	1
1:A:37:ARG:O	1:A:40:ALA:HB3	0.40	2.16	9	1
1:B:28:LEU:HG	1:B:32:LEU:CD1	0.40	2.47	11	1
1:A:60:ILE:CG2	1:B:27:THR:CG2	0.40	3.00	14	1
1:B:42:GLU:CB	1:B:67:PHE:CZ	0.40	3.05	16	1
1:B:12:ILE:CD1	1:B:28:LEU:CD2	0.40	3.00	18	1
1:B:38:ASP:HB3	1:B:67:PHE:CD2	0.40	2.51	18	1
1:A:33:GLU:CD	1:A:34:GLU:N	0.40	2.80	19	1
1:A:64:VAL:CG2	1:B:31:ILE:HG21	0.40	2.47	32	1
1:A:28:LEU:HD11	1:B:39:ILE:CG2	0.40	2.47	1	1
1:A:31:ILE:CD1	1:B:60:ILE:CG2	0.40	3.00	1	1
1:A:40:ALA:CB	1:B:12:ILE:HG12	0.40	2.46	1	1
1:A:5:ILE:HG21	1:A:26:ILE:CG1	0.40	2.40	3	1
1:A:32:LEU:CD1	1:B:32:LEU:CG	0.40	3.00	7	1
1:B:22:ASP:HA	1:B:25:ARG:CZ	0.40	2.47	7	1
1:B:3:LEU:HG	1:B:33:GLU:HB2	0.40	1.94	8	1
1:B:38:ASP:CG	1:B:67:PHE:CZ	0.40	3.00	10	2
1:A:46:LEU:HD21	1:A:63:ALA:N	0.40	2.32	11	1
1:A:60:ILE:CG1	1:B:24:ALA:CB	0.40	3.00	11	1
1:A:28:LEU:CD2	1:B:60:ILE:HG23	0.40	2.46	13	1
1:B:6:ALA:CB	1:B:7:PRO:CD	0.40	3.00	16	1
1:A:57:ALA:N	1:B:24:ALA:HB2	0.40	2.31	21	1
1:A:44:ILE:CG1	1:A:55:ILE:CD1	0.40	3.00	23	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	59/69 (86%)	53±10 (89±17%)	8±4 (14±6%)	2±2 (4±3%)	4	32
1	B	65/69 (94%)	54±10 (83±15%)	7±3 (11±4%)	2±1 (3±2%)	4	34
All	All	4156/4554 (91%)	3517 (85%)	494 (12%)	145 (3%)	4	33

All 38 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	31	ILE	17
1	A	31	ILE	14
1	B	52	ARG	13
1	A	53	LYS	11
1	A	52	ARG	9
1	B	53	LYS	9
1	B	19	ARG	7
1	A	54	THR	6
1	B	54	THR	6
1	A	19	ARG	6
1	A	18	GLU	5
1	B	18	GLU	4
1	A	64	VAL	4
1	B	64	VAL	4
1	A	51	GLY	2
1	A	17	ALA	2
1	B	11	ILE	2
1	A	8	ILE	2
1	B	6	ALA	2
1	B	12	ILE	2
1	A	60	ILE	1
1	A	11	ILE	1
1	A	3	LEU	1
1	B	17	ALA	1
1	A	16	GLY	1
1	A	62	LEU	1
1	B	22	ASP	1
1	B	23	ASP	1
1	B	24	ALA	1
1	A	5	ILE	1
1	A	6	ALA	1
1	A	22	ASP	1
1	A	36	GLY	1
1	B	7	PRO	1
1	B	20	VAL	1
1	A	12	ILE	1
1	A	24	ALA	1
1	B	36	GLY	1

6.3.2 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	46/54 (85%)	32±8 (69±18%)	15±4 (34±9%)	1	11
1	B	50/54 (93%)	34±6 (67±12%)	15±3 (29±7%)	1	18
All	All	3146/3564 (88%)	2150 (68%)	996 (32%)	1	14

All 86 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	42	GLU	26
1	B	37	ARG	23
1	B	64	VAL	23
1	B	53	LYS	23
1	A	19	ARG	22
1	A	53	LYS	22
1	A	56	LYS	22
1	A	42	GLU	21
1	A	13	LYS	20
1	A	64	VAL	20
1	B	38	ASP	20
1	B	59	ASP	20
1	A	30	LYS	19
1	A	59	ASP	19
1	B	34	GLU	19
1	A	10	ARG	18
1	B	30	LYS	18
1	B	56	LYS	18
1	A	48	ARG	18
1	A	38	ASP	18
1	B	19	ARG	17
1	B	48	ARG	17
1	A	32	LEU	16
1	A	45	LYS	16
1	A	65	ARG	16
1	B	45	LYS	16
1	A	41	SER	16
1	A	52	ARG	15

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	35	MET	15
1	B	65	ARG	15
1	A	62	LEU	15
1	A	25	ARG	14
1	B	23	ASP	14
1	A	18	GLU	14
1	A	5	ILE	14
1	A	49	HIS	13
1	B	13	LYS	13
1	A	37	ARG	13
1	B	66	ARG	13
1	B	32	LEU	13
1	B	52	ARG	13
1	A	33	GLU	12
1	B	5	ILE	12
1	B	18	GLU	12
1	B	10	ARG	12
1	B	33	GLU	12
1	A	66	ARG	11
1	A	44	ILE	10
1	B	25	ARG	10
1	B	3	LEU	10
1	A	23	ASP	10
1	B	58	GLU	10
1	B	28	LEU	9
1	A	31	ILE	9
1	B	41	SER	9
1	A	61	GLU	8
1	A	58	GLU	8
1	A	22	ASP	8
1	A	67	PHE	7
1	B	61	GLU	7
1	B	62	LEU	7
1	B	67	PHE	7
1	B	22	ASP	6
1	A	3	LEU	6
1	B	35	MET	6
1	B	60	ILE	5
1	B	44	ILE	5
1	A	34	GLU	5
1	B	20	VAL	5
1	A	26	ILE	5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	B	26	ILE	4
1	A	28	LEU	4
1	B	39	ILE	4
1	B	54	THR	4
1	A	54	THR	3
1	A	21	SER	3
1	B	27	THR	2
1	B	12	ILE	2
1	B	46	LEU	2
1	A	60	ILE	2
1	A	39	ILE	1
1	B	8	ILE	1
1	B	31	ILE	1
1	B	21	SER	1
1	A	20	VAL	1
1	A	12	ILE	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 oligosaccharides 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 ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided