



Full wwPDB NMR Structure Validation Report ⓘ

Mar 22, 2026 – 09:25 PM UTC

PDB ID : 3BDO / pdb_00003bdo
Title : SOLUTION STRUCTURE OF APO-BIOTINYL DOMAIN FROM ACETYL COENZYME A CARBOXYLASE OF ESCHERICHIA COLI DETERMINED BY TRIPLE-RESONANCE NMR SPECTROSCOPY
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Deposited on : 1999-03-08

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

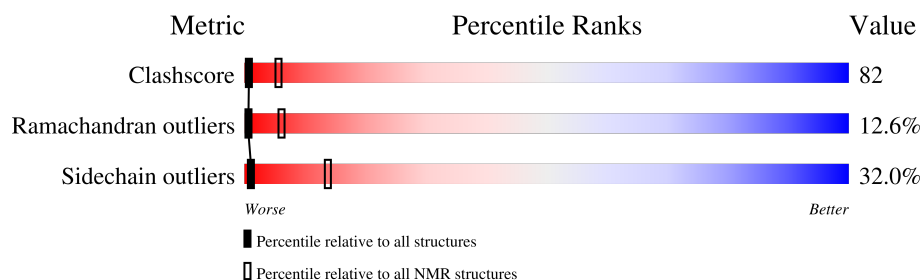
1 Overall quality at a glance

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	82	

2 Ensemble composition and analysis

This entry contains 20 models. Model 8 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:80-A:156 (77)	0.62	8

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

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

The models can be grouped into 4 clusters and 4 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1240 atoms, of which 623 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN (ACETYL-COA CARBOXYLASE).

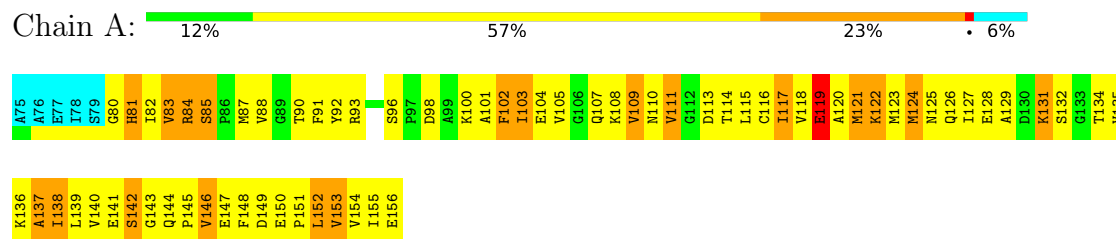
Mol	Chain	Residues	Atoms						Trace
1	A	82	Total	C	H	N	O	S	0
			1240	390	623	100	122	5	

4 Residue-property plots

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: PROTEIN (ACETYL-COA CARBOXYLASE)

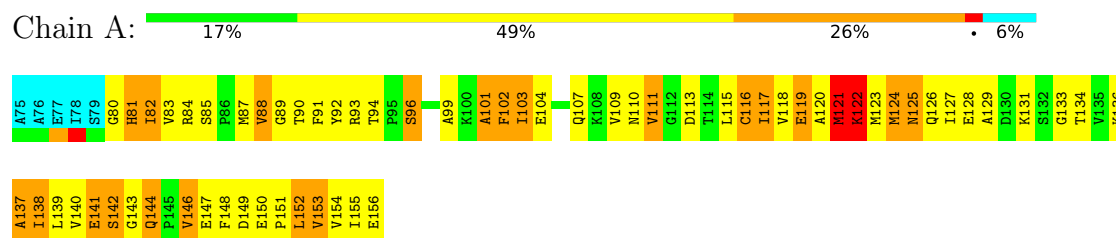


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

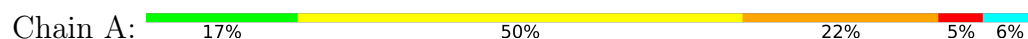
4.2.1 Score per residue for model 1

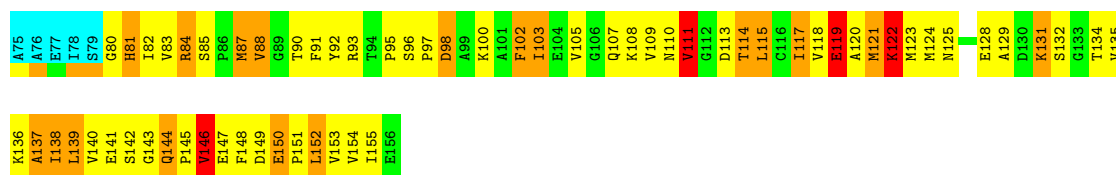
- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)



4.2.2 Score per residue for model 2

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

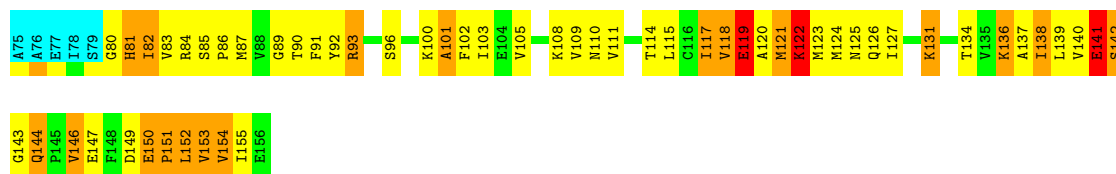




4.2.3 Score per residue for model 3

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

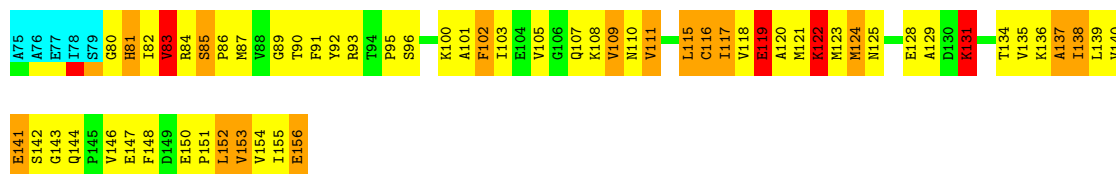
Chain A: 26% 43% 22% 6%



4.2.4 Score per residue for model 4

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

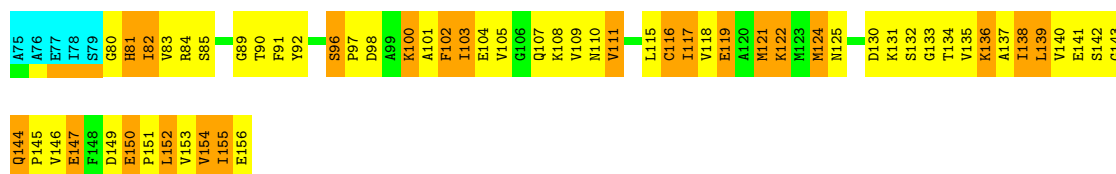
Chain A: 21% 50% 18% 5% 6%



4.2.5 Score per residue for model 5

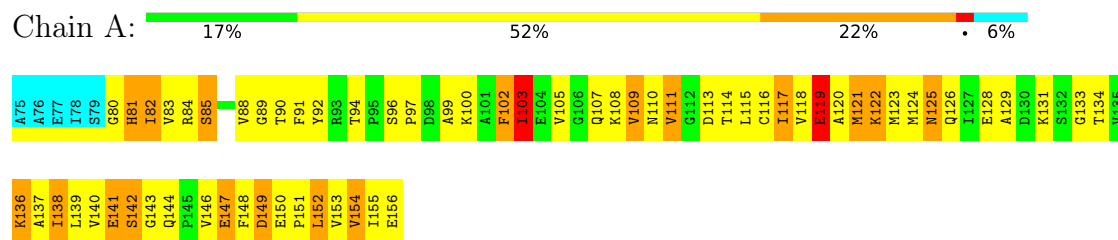
- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

Chain A: 22% 45% 27% 6%



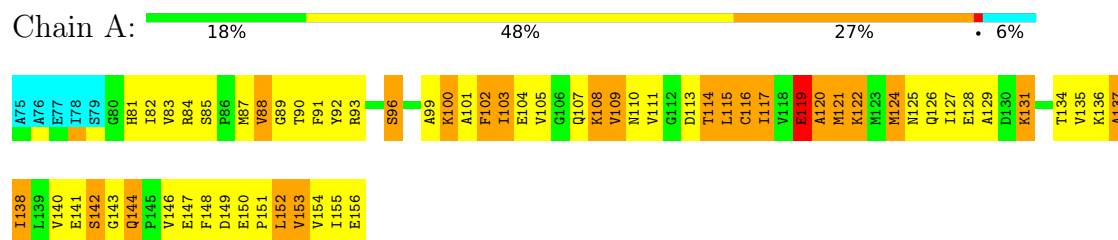
4.2.6 Score per residue for model 6

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)



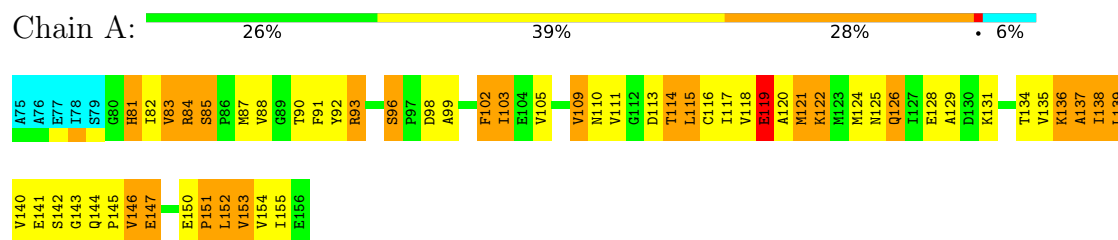
4.2.7 Score per residue for model 7

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)



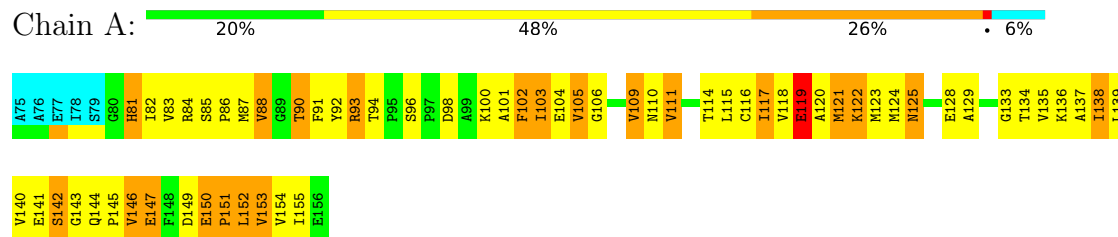
4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)



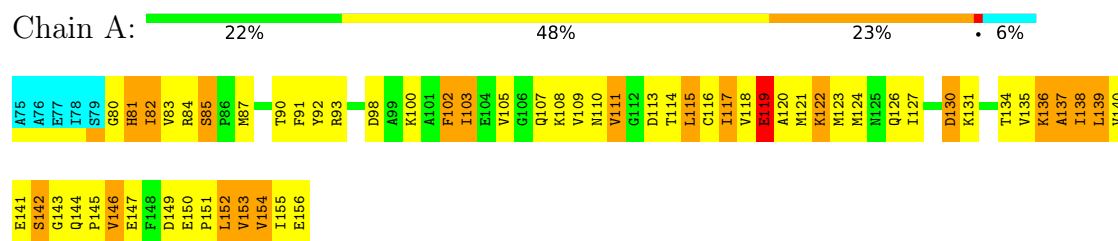
4.2.9 Score per residue for model 9

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)



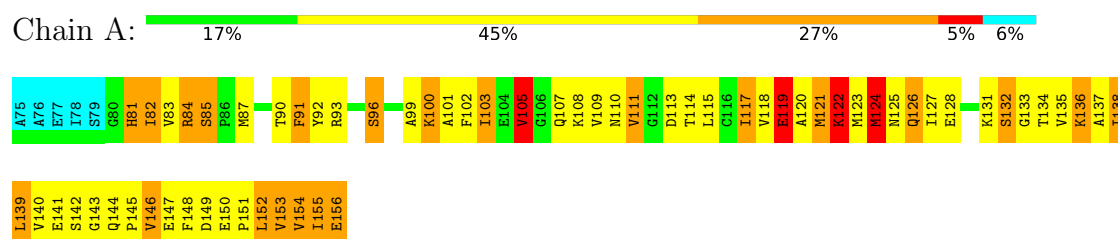
4.2.10 Score per residue for model 10

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)



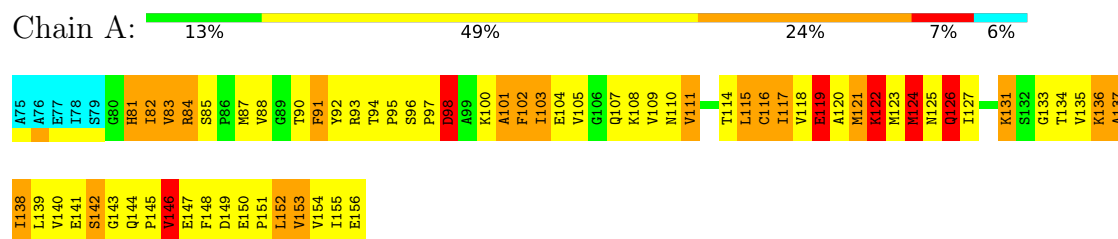
4.2.11 Score per residue for model 11

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)



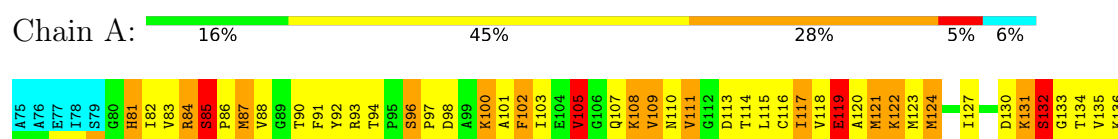
4.2.12 Score per residue for model 12

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)



4.2.13 Score per residue for model 13

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

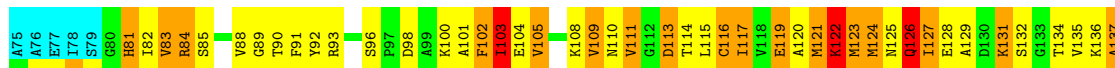




4.2.14 Score per residue for model 14

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

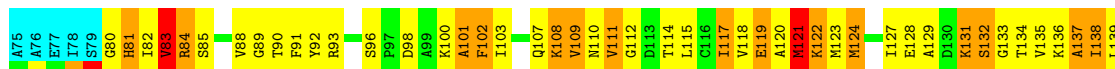
Chain A: 17% 45% 28% 6%



4.2.15 Score per residue for model 15

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

Chain A: 18% 48% 26% 6%



4.2.16 Score per residue for model 16

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

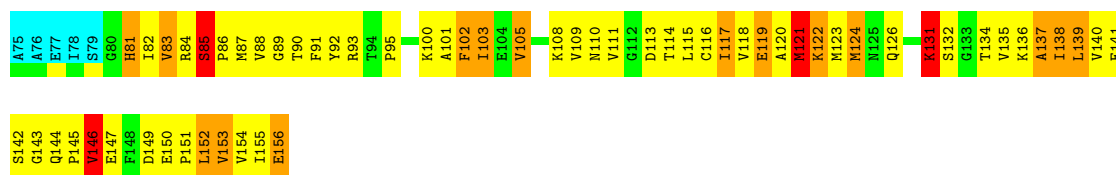
Chain A: 12% 54% 24% 6%



4.2.17 Score per residue for model 17

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

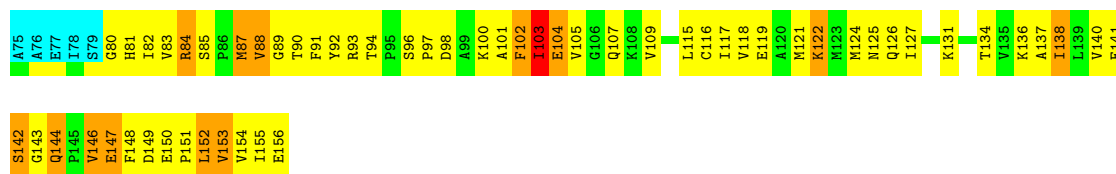
Chain A: 21% 50% 18% 5% 6%



4.2.18 Score per residue for model 18

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

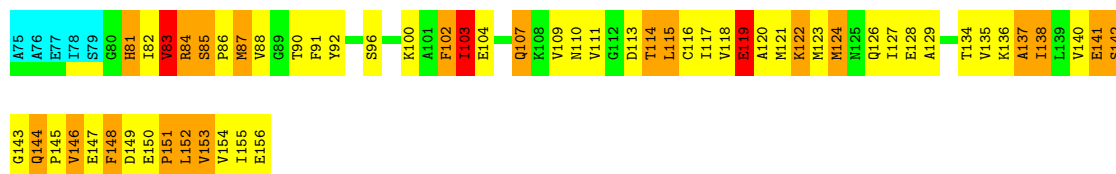
Chain A: 24% 52% 16% 6%



4.2.19 Score per residue for model 19

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

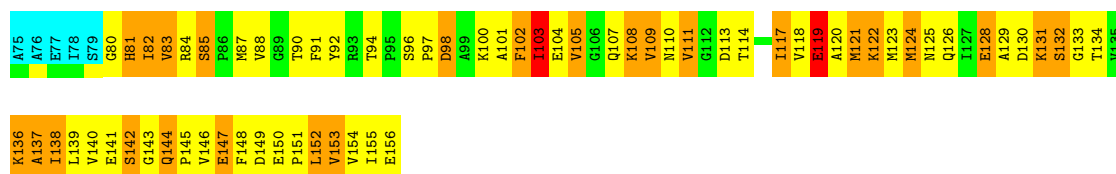
Chain A: 23% 43% 24% 6%



4.2.20 Score per residue for model 20

- Molecule 1: PROTEIN (ACETYL-COA CARBOXYLASE)

Chain A: 13% 48% 30% 6%



5 Refinement protocol and experimental data overview

The models were refined using the following method: ?.

Of the 40 calculated structures, 20 were deposited, based on the following criterion: *LOWEST ENERGY*.

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

Software name	Classification	Version
X-PLOR	refinement	3.1
Azara	structure solution	
ANSIG	structure solution	
XPLOR	structure solution	

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	584	591	593	97±11
All	All	11680	11820	11860	1937

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 82.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:82:ILE:HD12	1:A:154:VAL:HG13	1.08	1.23	20	6
1:A:140:VAL:HG21	1:A:152:LEU:HD23	1.04	1.20	13	19
1:A:146:VAL:HG11	1:A:152:LEU:CD2	1.01	1.86	20	18
1:A:90:THR:HG23	1:A:144:GLN:C	0.95	1.84	3	15
1:A:117:ILE:HG22	1:A:124:MET:CB	0.94	1.92	14	2
1:A:117:ILE:HG22	1:A:119:GLU:OE2	0.91	1.63	15	1
1:A:85:SER:CA	1:A:152:LEU:HD11	0.91	1.96	19	3
1:A:85:SER:OG	1:A:152:LEU:HD21	0.88	1.69	12	2
1:A:102:PHE:O	1:A:103:ILE:HD13	0.86	1.71	1	3
1:A:118:VAL:HG12	1:A:125:ASN:O	0.86	1.71	11	2
1:A:91:PHE:CZ	1:A:138:ILE:HG21	0.85	2.06	11	14
1:A:83:VAL:HG12	1:A:153:VAL:CG1	0.84	2.03	2	2
1:A:109:VAL:HG11	1:A:115:LEU:CD2	0.83	2.01	16	9
1:A:91:PHE:CD2	1:A:152:LEU:HD12	0.83	2.09	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:91:PHE:HB2	1:A:152:LEU:HD22	0.83	1.51	18	15
1:A:134:THR:C	1:A:155:ILE:HG23	0.83	1.98	16	16
1:A:102:PHE:O	1:A:103:ILE:HG23	0.83	1.73	18	16
1:A:82:ILE:CD1	1:A:154:VAL:HG13	0.83	2.03	12	7
1:A:139:LEU:HD11	1:A:154:VAL:HG22	0.83	1.50	5	1
1:A:117:ILE:HD13	1:A:124:MET:HB3	0.82	1.49	18	3
1:A:109:VAL:HG22	1:A:133:GLY:O	0.82	1.74	15	3
1:A:83:VAL:CG2	1:A:153:VAL:HG13	0.82	2.05	20	13
1:A:145:PRO:O	1:A:146:VAL:HG13	0.82	1.73	12	5
1:A:90:THR:HG23	1:A:145:PRO:HA	0.82	1.51	9	6
1:A:140:VAL:HG23	1:A:151:PRO:O	0.81	1.74	1	17
1:A:82:ILE:HG12	1:A:154:VAL:HG13	0.81	1.50	5	12
1:A:117:ILE:HD13	1:A:124:MET:HB2	0.81	1.52	7	4
1:A:140:VAL:CG2	1:A:152:LEU:HD23	0.81	2.01	17	3
1:A:146:VAL:HG11	1:A:152:LEU:HD23	0.81	1.52	2	10
1:A:117:ILE:HG22	1:A:124:MET:HB3	0.80	1.53	14	1
1:A:103:ILE:HG22	1:A:135:VAL:HG21	0.80	1.51	11	3
1:A:91:PHE:CB	1:A:152:LEU:HD22	0.80	2.06	2	12
1:A:103:ILE:HD13	1:A:153:VAL:CG2	0.80	2.05	9	5
1:A:90:THR:HG23	1:A:144:GLN:O	0.80	1.76	16	10
1:A:85:SER:HB3	1:A:152:LEU:HD21	0.79	1.54	19	1
1:A:146:VAL:HG21	1:A:152:LEU:HD21	0.76	1.56	13	5
1:A:83:VAL:HG21	1:A:115:LEU:HD13	0.76	1.55	15	3
1:A:139:LEU:HD21	1:A:154:VAL:HG21	0.76	1.58	20	4
1:A:105:VAL:HG23	1:A:136:LYS:C	0.75	2.05	7	2
1:A:96:SER:OG	1:A:99:ALA:HB2	0.75	1.80	11	1
1:A:82:ILE:N	1:A:82:ILE:HD13	0.75	1.97	1	6
1:A:103:ILE:HG22	1:A:135:VAL:CG2	0.74	2.12	11	2
1:A:104:GLU:O	1:A:135:VAL:HG11	0.74	1.82	19	3
1:A:85:SER:CB	1:A:152:LEU:HD11	0.74	2.13	13	3
1:A:109:VAL:HG11	1:A:115:LEU:HD23	0.73	1.59	2	7
1:A:85:SER:HA	1:A:152:LEU:HD11	0.73	1.58	13	3
1:A:137:ALA:C	1:A:138:ILE:HD13	0.73	2.09	15	12
1:A:96:SER:HB2	1:A:99:ALA:HB2	0.73	1.58	6	3
1:A:83:VAL:HG23	1:A:153:VAL:HG13	0.73	1.59	4	13
1:A:139:LEU:HD12	1:A:151:PRO:HB2	0.72	1.59	17	5
1:A:138:ILE:N	1:A:138:ILE:HD13	0.72	1.99	17	13
1:A:103:ILE:HD13	1:A:153:VAL:HG23	0.72	1.61	8	2
1:A:88:VAL:HG22	1:A:88:VAL:O	0.71	1.85	16	2
1:A:107:GLN:O	1:A:135:VAL:HG12	0.71	1.85	19	3
1:A:83:VAL:HG13	1:A:83:VAL:O	0.71	1.85	11	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:116:CYS:SG	1:A:153:VAL:HG11	0.70	2.25	4	6
1:A:138:ILE:HG23	1:A:153:VAL:HG22	0.70	1.61	3	1
1:A:103:ILE:HD11	1:A:153:VAL:HG21	0.70	1.64	3	1
1:A:118:VAL:HG13	1:A:118:VAL:O	0.69	1.85	11	2
1:A:102:PHE:CZ	1:A:114:THR:HG21	0.69	2.22	15	3
1:A:138:ILE:HD13	1:A:138:ILE:N	0.69	2.02	15	3
1:A:90:THR:HG23	1:A:145:PRO:CA	0.69	2.17	11	6
1:A:117:ILE:HG22	1:A:124:MET:HB2	0.69	1.62	14	1
1:A:86:PRO:HD2	1:A:118:VAL:HG11	0.69	1.64	13	2
1:A:90:THR:HG23	1:A:145:PRO:N	0.69	2.02	17	5
1:A:109:VAL:CG2	1:A:129:ALA:HB2	0.68	2.18	1	2
1:A:103:ILE:HD13	1:A:153:VAL:HG21	0.68	1.65	2	5
1:A:83:VAL:CG2	1:A:115:LEU:HD13	0.68	2.18	5	1
1:A:88:VAL:O	1:A:88:VAL:HG23	0.68	1.87	8	5
1:A:118:VAL:HG12	1:A:118:VAL:O	0.68	1.88	12	2
1:A:82:ILE:HD12	1:A:154:VAL:CG1	0.68	2.12	6	1
1:A:134:THR:N	1:A:155:ILE:HG23	0.67	2.03	20	15
1:A:118:VAL:CG2	1:A:127:ILE:HD11	0.67	2.20	16	1
1:A:91:PHE:CZ	1:A:138:ILE:CG2	0.67	2.78	6	20
1:A:83:VAL:HG12	1:A:153:VAL:HB	0.66	1.67	11	1
1:A:136:LYS:O	1:A:137:ALA:HB2	0.66	1.91	2	16
1:A:83:VAL:HG11	1:A:127:ILE:HG21	0.66	1.67	15	1
1:A:82:ILE:HD13	1:A:154:VAL:HG22	0.66	1.66	19	8
1:A:140:VAL:HG21	1:A:152:LEU:CD2	0.66	2.12	13	9
1:A:90:THR:CG2	1:A:92:TYR:CE1	0.65	2.79	14	1
1:A:85:SER:HB3	1:A:146:VAL:HG21	0.65	1.69	3	1
1:A:93:ARG:O	1:A:101:ALA:HB1	0.65	1.92	15	5
1:A:89:GLY:O	1:A:146:VAL:HG23	0.64	1.93	17	2
1:A:87:MET:HE3	1:A:120:ALA:CB	0.64	2.21	8	2
1:A:146:VAL:HG12	1:A:150:GLU:HG2	0.64	1.70	1	3
1:A:83:VAL:HG12	1:A:153:VAL:HG12	0.64	1.68	2	2
1:A:138:ILE:HG23	1:A:153:VAL:CG2	0.63	2.22	3	1
1:A:115:LEU:HD22	1:A:155:ILE:HD11	0.63	1.67	9	3
1:A:109:VAL:HG11	1:A:115:LEU:HD21	0.63	1.70	16	3
1:A:146:VAL:HG21	1:A:152:LEU:CD2	0.63	2.22	10	1
1:A:103:ILE:HB	1:A:135:VAL:HG21	0.63	1.70	9	1
1:A:139:LEU:CD2	1:A:154:VAL:HG21	0.62	2.23	20	3
1:A:90:THR:HG21	1:A:92:TYR:CZ	0.62	2.29	6	6
1:A:85:SER:CB	1:A:152:LEU:HD21	0.62	2.24	19	2
1:A:103:ILE:CD1	1:A:153:VAL:HG21	0.62	2.24	2	2
1:A:90:THR:CG2	1:A:92:TYR:CZ	0.62	2.82	4	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:118:VAL:HG21	1:A:127:ILE:HD11	0.62	1.70	16	2
1:A:111:VAL:HG12	1:A:131:LYS:N	0.62	2.08	3	3
1:A:90:THR:O	1:A:118:VAL:HG13	0.62	1.95	19	4
1:A:139:LEU:HD12	1:A:154:VAL:CG2	0.61	2.24	13	1
1:A:96:SER:CB	1:A:99:ALA:HB2	0.61	2.26	8	4
1:A:139:LEU:HD12	1:A:154:VAL:HG22	0.61	1.72	13	2
1:A:140:VAL:HG23	1:A:152:LEU:HA	0.60	1.73	3	19
1:A:114:THR:HG21	1:A:126:GLN:OE1	0.60	1.95	17	1
1:A:139:LEU:HD13	1:A:151:PRO:CB	0.60	2.27	12	1
1:A:117:ILE:HG21	1:A:124:MET:HG2	0.60	1.73	4	1
1:A:91:PHE:CD1	1:A:152:LEU:CB	0.60	2.84	18	3
1:A:82:ILE:CG1	1:A:154:VAL:HG22	0.60	2.27	15	2
1:A:85:SER:HB2	1:A:152:LEU:HD21	0.60	1.73	13	3
1:A:109:VAL:HG22	1:A:133:GLY:C	0.60	2.21	15	1
1:A:89:GLY:O	1:A:146:VAL:HG22	0.59	1.96	15	2
1:A:105:VAL:HG22	1:A:137:ALA:HA	0.59	1.74	6	5
1:A:139:LEU:HD13	1:A:151:PRO:HB2	0.59	1.74	12	2
1:A:82:ILE:HG21	1:A:151:PRO:HB3	0.59	1.74	16	5
1:A:83:VAL:CG1	1:A:153:VAL:CG1	0.59	2.81	6	2
1:A:103:ILE:HD13	1:A:109:VAL:HG12	0.59	1.75	5	1
1:A:119:GLU:N	1:A:119:GLU:CD	0.59	2.61	15	1
1:A:134:THR:N	1:A:155:ILE:CG2	0.59	2.66	9	16
1:A:91:PHE:O	1:A:92:TYR:CD1	0.59	2.56	9	19
1:A:96:SER:CB	1:A:97:PRO:CD	0.58	2.81	13	1
1:A:91:PHE:CE2	1:A:138:ILE:CG2	0.58	2.86	14	2
1:A:82:ILE:HG12	1:A:154:VAL:HG22	0.58	1.74	15	2
1:A:81:HIS:CD2	1:A:81:HIS:O	0.58	2.57	1	13
1:A:88:VAL:HG12	1:A:88:VAL:O	0.58	1.98	1	1
1:A:82:ILE:CG1	1:A:154:VAL:HG13	0.58	2.29	18	8
1:A:83:VAL:O	1:A:152:LEU:HD12	0.58	1.99	7	4
1:A:92:TYR:CD2	1:A:119:GLU:OE1	0.58	2.56	15	1
1:A:83:VAL:HG12	1:A:83:VAL:O	0.58	1.99	1	3
1:A:92:TYR:CD1	1:A:143:GLY:HA2	0.57	2.34	6	20
1:A:121:MET:O	1:A:122:LYS:CB	0.57	2.52	16	15
1:A:85:SER:OG	1:A:146:VAL:HG21	0.57	1.98	16	2
1:A:117:ILE:CG2	1:A:124:MET:CB	0.57	2.83	20	16
1:A:91:PHE:CD1	1:A:91:PHE:C	0.57	2.82	11	10
1:A:111:VAL:O	1:A:111:VAL:HG23	0.57	1.98	6	2
1:A:82:ILE:CD1	1:A:154:VAL:HG22	0.57	2.30	15	3
1:A:109:VAL:CG2	1:A:110:ASN:N	0.56	2.68	9	2
1:A:105:VAL:HG23	1:A:136:LYS:HA	0.56	1.77	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:91:PHE:CD2	1:A:152:LEU:CB	0.56	2.89	2	6
1:A:109:VAL:CG1	1:A:115:LEU:HD23	0.56	2.30	16	1
1:A:139:LEU:HD11	1:A:154:VAL:CG2	0.56	2.28	5	1
1:A:139:LEU:HD12	1:A:152:LEU:C	0.56	2.24	5	1
1:A:103:ILE:CG2	1:A:135:VAL:CG2	0.56	2.83	11	1
1:A:111:VAL:HG13	1:A:129:ALA:O	0.56	2.01	19	1
1:A:102:PHE:CE2	1:A:117:ILE:CG1	0.56	2.89	8	7
1:A:120:ALA:O	1:A:121:MET:CB	0.56	2.54	15	9
1:A:139:LEU:HD12	1:A:151:PRO:CB	0.56	2.30	17	3
1:A:102:PHE:CZ	1:A:114:THR:CG2	0.56	2.89	15	2
1:A:109:VAL:HG11	1:A:115:LEU:HD22	0.56	1.77	6	1
1:A:91:PHE:CD2	1:A:141:GLU:O	0.56	2.58	19	1
1:A:105:VAL:O	1:A:105:VAL:HG13	0.55	2.00	3	2
1:A:81:HIS:C	1:A:82:ILE:HD13	0.55	2.25	10	1
1:A:88:VAL:HG22	1:A:147:GLU:HG2	0.55	1.78	19	3
1:A:109:VAL:HG22	1:A:110:ASN:N	0.55	2.17	1	2
1:A:117:ILE:HG22	1:A:119:GLU:CD	0.55	2.24	15	1
1:A:81:HIS:CD2	1:A:155:ILE:CG2	0.55	2.90	11	1
1:A:90:THR:HG22	1:A:92:TYR:CE1	0.55	2.36	14	1
1:A:141:GLU:CB	1:A:144:GLN:CD	0.55	2.80	15	1
1:A:103:ILE:HD12	1:A:103:ILE:O	0.55	2.02	18	1
1:A:91:PHE:CD2	1:A:152:LEU:HB2	0.55	2.37	10	6
1:A:137:ALA:O	1:A:154:VAL:HG23	0.54	2.03	11	6
1:A:91:PHE:CE1	1:A:138:ILE:HG21	0.54	2.36	16	2
1:A:83:VAL:CG2	1:A:153:VAL:CG1	0.54	2.85	14	12
1:A:82:ILE:N	1:A:82:ILE:CD1	0.54	2.67	6	3
1:A:114:THR:HG23	1:A:126:GLN:HB2	0.54	1.79	12	1
1:A:148:PHE:CE2	1:A:149:ASP:OD1	0.54	2.60	1	1
1:A:122:LYS:CD	1:A:122:LYS:O	0.54	2.56	13	10
1:A:105:VAL:HG13	1:A:136:LYS:C	0.54	2.27	16	3
1:A:83:VAL:O	1:A:84:ARG:C	0.54	2.50	16	17
1:A:120:ALA:O	1:A:121:MET:CG	0.54	2.56	17	13
1:A:147:GLU:O	1:A:150:GLU:CB	0.54	2.56	19	12
1:A:148:PHE:CD2	1:A:149:ASP:OD1	0.54	2.60	1	1
1:A:91:PHE:CE2	1:A:153:VAL:HG23	0.54	2.38	3	2
1:A:91:PHE:CD1	1:A:152:LEU:HB3	0.54	2.37	18	2
1:A:139:LEU:CD1	1:A:154:VAL:HG22	0.54	2.32	12	1
1:A:109:VAL:CG1	1:A:115:LEU:CD2	0.54	2.82	16	2
1:A:103:ILE:CG1	1:A:115:LEU:O	0.54	2.56	15	3
1:A:88:VAL:HG22	1:A:147:GLU:CG	0.54	2.32	13	2
1:A:102:PHE:O	1:A:103:ILE:CB	0.54	2.55	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:109:VAL:HG21	1:A:155:ILE:HD13	0.53	1.80	16	2
1:A:84:ARG:O	1:A:84:ARG:CD	0.53	2.57	7	3
1:A:94:THR:O	1:A:117:ILE:HD11	0.53	2.02	12	2
1:A:141:GLU:O	1:A:142:SER:C	0.53	2.50	14	14
1:A:121:MET:CG	1:A:121:MET:O	0.53	2.56	17	1
1:A:138:ILE:N	1:A:138:ILE:CD1	0.53	2.67	17	10
1:A:121:MET:O	1:A:122:LYS:CG	0.53	2.56	18	4
1:A:90:THR:O	1:A:118:VAL:CG1	0.53	2.57	10	2
1:A:102:PHE:CE2	1:A:117:ILE:HG13	0.53	2.39	17	7
1:A:87:MET:SD	1:A:120:ALA:HB1	0.53	2.43	12	5
1:A:103:ILE:HD11	1:A:116:CYS:HB3	0.53	1.78	10	2
1:A:136:LYS:O	1:A:137:ALA:CB	0.53	2.57	8	14
1:A:150:GLU:O	1:A:152:LEU:CD2	0.53	2.57	11	1
1:A:102:PHE:O	1:A:103:ILE:CG2	0.53	2.57	19	13
1:A:105:VAL:HG22	1:A:136:LYS:C	0.53	2.29	2	2
1:A:93:ARG:O	1:A:101:ALA:CB	0.53	2.56	11	3
1:A:122:LYS:O	1:A:122:LYS:CE	0.53	2.57	19	1
1:A:81:HIS:N	1:A:155:ILE:O	0.52	2.42	8	11
1:A:117:ILE:CG2	1:A:124:MET:HB2	0.52	2.35	20	15
1:A:81:HIS:O	1:A:81:HIS:ND1	0.52	2.42	9	7
1:A:147:GLU:O	1:A:150:GLU:CG	0.52	2.57	17	2
1:A:118:VAL:O	1:A:120:ALA:N	0.52	2.42	1	11
1:A:118:VAL:O	1:A:118:VAL:HG12	0.52	2.04	1	3
1:A:146:VAL:HG11	1:A:152:LEU:HD22	0.52	1.81	4	3
1:A:90:THR:N	1:A:119:GLU:O	0.52	2.42	15	3
1:A:104:GLU:O	1:A:135:VAL:CG1	0.52	2.57	19	2
1:A:91:PHE:O	1:A:142:SER:O	0.52	2.27	15	10
1:A:136:LYS:CD	1:A:154:VAL:CG1	0.52	2.88	11	2
1:A:141:GLU:O	1:A:144:GLN:CG	0.52	2.58	10	4
1:A:102:PHE:O	1:A:103:ILE:CD1	0.52	2.57	11	3
1:A:148:PHE:O	1:A:149:ASP:CB	0.52	2.57	16	7
1:A:150:GLU:O	1:A:152:LEU:HD23	0.52	2.03	11	1
1:A:87:MET:SD	1:A:120:ALA:CB	0.52	2.98	9	5
1:A:140:VAL:CG1	1:A:141:GLU:N	0.52	2.72	4	4
1:A:122:LYS:CG	1:A:122:LYS:O	0.52	2.57	7	1
1:A:152:LEU:HD23	1:A:152:LEU:N	0.52	2.18	11	1
1:A:86:PRO:O	1:A:148:PHE:CD1	0.52	2.62	16	1
1:A:92:TYR:O	1:A:116:CYS:CB	0.52	2.58	16	1
1:A:111:VAL:HG12	1:A:130:ASP:C	0.52	2.29	20	1
1:A:146:VAL:HG23	1:A:147:GLU:N	0.52	2.18	13	2
1:A:118:VAL:O	1:A:125:ASN:CB	0.52	2.58	5	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:140:VAL:CG2	1:A:150:GLU:OE2	0.52	2.58	5	1
1:A:107:GLN:O	1:A:109:VAL:N	0.52	2.43	7	3
1:A:109:VAL:N	1:A:133:GLY:O	0.52	2.43	15	6
1:A:97:PRO:O	1:A:98:ASP:CB	0.52	2.57	12	4
1:A:120:ALA:N	1:A:123:MET:O	0.52	2.43	6	2
1:A:89:GLY:O	1:A:146:VAL:CG2	0.52	2.58	15	4
1:A:120:ALA:C	1:A:121:MET:CG	0.52	2.82	19	2
1:A:134:THR:C	1:A:155:ILE:CG2	0.52	2.81	16	1
1:A:91:PHE:CE2	1:A:138:ILE:HG21	0.51	2.41	14	3
1:A:139:LEU:HG	1:A:154:VAL:HG22	0.51	1.81	10	1
1:A:85:SER:OG	1:A:146:VAL:CG2	0.51	2.58	16	2
1:A:102:PHE:C	1:A:103:ILE:CG1	0.51	2.82	19	3
1:A:140:VAL:HG12	1:A:141:GLU:N	0.51	2.19	4	4
1:A:110:ASN:O	1:A:111:VAL:C	0.51	2.52	1	18
1:A:115:LEU:N	1:A:127:ILE:O	0.51	2.43	13	6
1:A:136:LYS:N	1:A:154:VAL:O	0.51	2.42	11	4
1:A:146:VAL:HG11	1:A:152:LEU:HD21	0.51	1.81	6	1
1:A:118:VAL:CG2	1:A:127:ILE:CG1	0.51	2.88	13	2
1:A:119:GLU:OE1	1:A:123:MET:N	0.51	2.43	19	1
1:A:117:ILE:HG21	1:A:124:MET:CG	0.51	2.35	2	4
1:A:100:LYS:O	1:A:101:ALA:HB3	0.51	2.06	13	2
1:A:125:ASN:O	1:A:127:ILE:N	0.51	2.43	14	1
1:A:103:ILE:CD1	1:A:153:VAL:CG2	0.51	2.88	2	1
1:A:136:LYS:HD2	1:A:154:VAL:CG1	0.51	2.36	3	2
1:A:81:HIS:ND1	1:A:155:ILE:HD12	0.51	2.21	6	1
1:A:140:VAL:HG22	1:A:150:GLU:OE2	0.50	2.07	5	1
1:A:89:GLY:CA	1:A:120:ALA:HB2	0.50	2.36	15	1
1:A:104:GLU:N	1:A:104:GLU:OE1	0.50	2.44	20	1
1:A:102:PHE:CD2	1:A:117:ILE:HG12	0.50	2.41	5	6
1:A:141:GLU:N	1:A:144:GLN:OE1	0.50	2.42	8	1
1:A:91:PHE:CE1	1:A:138:ILE:CG2	0.50	2.95	16	3
1:A:81:HIS:CD2	1:A:131:LYS:HE3	0.50	2.41	15	1
1:A:82:ILE:CD1	1:A:82:ILE:N	0.50	2.66	1	2
1:A:93:ARG:O	1:A:101:ALA:CA	0.50	2.59	11	1
1:A:144:GLN:NE2	1:A:145:PRO:O	0.50	2.43	19	1
1:A:139:LEU:N	1:A:139:LEU:HD23	0.50	2.21	15	3
1:A:102:PHE:CE2	1:A:117:ILE:HG12	0.50	2.42	3	6
1:A:104:GLU:O	1:A:106:GLY:N	0.50	2.44	9	1
1:A:122:LYS:O	1:A:123:MET:CG	0.50	2.60	19	2
1:A:109:VAL:O	1:A:110:ASN:ND2	0.50	2.45	15	1
1:A:81:HIS:CD2	1:A:155:ILE:HB	0.50	2.41	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:95:PRO:HG3	1:A:102:PHE:CG	0.50	2.42	17	1
1:A:92:TYR:CE2	1:A:119:GLU:HG2	0.50	2.41	17	4
1:A:139:LEU:N	1:A:152:LEU:O	0.50	2.45	17	1
1:A:83:VAL:HG12	1:A:153:VAL:HG13	0.50	1.78	2	1
1:A:90:THR:HG21	1:A:92:TYR:OH	0.50	2.07	20	3
1:A:105:VAL:HA	1:A:135:VAL:HG12	0.50	1.82	7	6
1:A:116:CYS:SG	1:A:117:ILE:N	0.50	2.84	13	1
1:A:84:ARG:O	1:A:85:SER:C	0.50	2.55	16	16
1:A:96:SER:OG	1:A:99:ALA:CB	0.50	2.57	11	1
1:A:93:ARG:O	1:A:102:PHE:N	0.50	2.44	10	10
1:A:133:GLY:HA3	1:A:155:ILE:HG21	0.50	1.83	20	2
1:A:120:ALA:O	1:A:121:MET:C	0.50	2.54	7	1
1:A:140:VAL:CG2	1:A:152:LEU:HB3	0.50	2.37	11	1
1:A:102:PHE:O	1:A:103:ILE:HB	0.49	2.07	5	1
1:A:111:VAL:O	1:A:111:VAL:CG2	0.49	2.60	6	1
1:A:85:SER:N	1:A:152:LEU:HD21	0.49	2.22	11	1
1:A:85:SER:HB2	1:A:146:VAL:CG2	0.49	2.37	11	1
1:A:91:PHE:HB3	1:A:152:LEU:HD22	0.49	1.83	12	1
1:A:92:TYR:CE1	1:A:143:GLY:HA2	0.49	2.42	8	11
1:A:84:ARG:O	1:A:86:PRO:N	0.49	2.46	13	5
1:A:85:SER:N	1:A:152:LEU:HD11	0.49	2.20	19	3
1:A:93:ARG:CD	1:A:142:SER:HB3	0.49	2.37	10	4
1:A:81:HIS:CE1	1:A:155:ILE:HD12	0.49	2.42	6	1
1:A:93:ARG:HD2	1:A:142:SER:CB	0.49	2.37	9	1
1:A:87:MET:HE3	1:A:120:ALA:HB2	0.49	1.83	16	1
1:A:85:SER:CB	1:A:146:VAL:HG21	0.49	2.37	3	2
1:A:92:TYR:CE2	1:A:119:GLU:HB2	0.49	2.43	2	6
1:A:105:VAL:CG2	1:A:136:LYS:O	0.49	2.61	11	1
1:A:110:ASN:O	1:A:129:ALA:HB3	0.49	2.08	16	1
1:A:90:THR:O	1:A:119:GLU:N	0.48	2.46	8	2
1:A:90:THR:HG21	1:A:92:TYR:CE1	0.48	2.42	14	1
1:A:148:PHE:O	1:A:149:ASP:CG	0.48	2.56	19	1
1:A:131:LYS:NZ	1:A:131:LYS:O	0.48	2.47	20	1
1:A:147:GLU:O	1:A:148:PHE:C	0.48	2.56	14	10
1:A:109:VAL:CG1	1:A:115:LEU:HD22	0.48	2.37	6	1
1:A:110:ASN:O	1:A:113:ASP:CB	0.48	2.61	16	1
1:A:85:SER:HG	1:A:147:GLU:C	0.48	2.17	11	1
1:A:139:LEU:HG	1:A:154:VAL:CG2	0.48	2.39	20	12
1:A:113:ASP:O	1:A:114:THR:C	0.48	2.56	14	11
1:A:109:VAL:O	1:A:110:ASN:CG	0.48	2.57	8	12
1:A:102:PHE:CZ	1:A:117:ILE:HG13	0.48	2.43	19	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:87:MET:CE	1:A:120:ALA:CB	0.48	2.92	16	1
1:A:89:GLY:O	1:A:146:VAL:N	0.48	2.43	4	6
1:A:118:VAL:O	1:A:119:GLU:C	0.48	2.57	13	8
1:A:102:PHE:CE1	1:A:114:THR:CG2	0.48	2.97	9	1
1:A:118:VAL:C	1:A:119:GLU:OE2	0.48	2.57	15	1
1:A:118:VAL:CG1	1:A:125:ASN:HB3	0.48	2.38	11	2
1:A:127:ILE:HG22	1:A:128:GLU:N	0.48	2.23	11	1
1:A:97:PRO:O	1:A:98:ASP:C	0.48	2.57	13	1
1:A:143:GLY:O	1:A:144:GLN:CD	0.48	2.57	4	4
1:A:104:GLU:O	1:A:105:VAL:C	0.48	2.57	12	4
1:A:131:LYS:NZ	1:A:132:SER:O	0.48	2.44	15	1
1:A:91:PHE:CD1	1:A:152:LEU:HB2	0.48	2.44	1	3
1:A:83:VAL:O	1:A:83:VAL:CG1	0.48	2.57	2	2
1:A:145:PRO:O	1:A:146:VAL:CG1	0.48	2.61	10	4
1:A:91:PHE:HB2	1:A:152:LEU:CD1	0.48	2.39	11	1
1:A:114:THR:CG2	1:A:126:GLN:HB3	0.48	2.38	14	1
1:A:113:ASP:O	1:A:115:LEU:N	0.48	2.46	2	3
1:A:128:GLU:O	1:A:129:ALA:C	0.47	2.57	6	9
1:A:135:VAL:N	1:A:155:ILE:HG23	0.47	2.24	12	3
1:A:118:VAL:HG23	1:A:127:ILE:CG1	0.47	2.38	13	2
1:A:83:VAL:HB	1:A:153:VAL:CG1	0.47	2.40	12	15
1:A:136:LYS:CD	1:A:154:VAL:HB	0.47	2.39	3	2
1:A:95:PRO:HG3	1:A:102:PHE:CD1	0.47	2.44	12	2
1:A:93:ARG:HD3	1:A:142:SER:CB	0.47	2.39	8	4
1:A:125:ASN:O	1:A:126:GLN:C	0.47	2.57	12	4
1:A:115:LEU:HD12	1:A:127:ILE:CG2	0.47	2.39	3	1
1:A:115:LEU:HD12	1:A:127:ILE:HG22	0.47	1.84	16	2
1:A:85:SER:OG	1:A:147:GLU:C	0.47	2.58	11	1
1:A:122:LYS:C	1:A:123:MET:CG	0.47	2.87	11	2
1:A:92:TYR:CE1	1:A:143:GLY:CA	0.47	2.98	6	5
1:A:109:VAL:HG21	1:A:129:ALA:HB2	0.47	1.86	1	1
1:A:138:ILE:O	1:A:139:LEU:C	0.47	2.57	11	10
1:A:83:VAL:CB	1:A:153:VAL:HG13	0.47	2.39	4	4
1:A:143:GLY:C	1:A:144:GLN:OE1	0.47	2.57	15	1
1:A:139:LEU:CD2	1:A:154:VAL:CG2	0.47	2.92	20	1
1:A:140:VAL:O	1:A:141:GLU:O	0.47	2.32	3	6
1:A:131:LYS:O	1:A:132:SER:C	0.47	2.57	2	3
1:A:103:ILE:HD11	1:A:153:VAL:CG2	0.47	2.38	3	1
1:A:82:ILE:CG2	1:A:153:VAL:O	0.47	2.62	11	1
1:A:114:THR:CG2	1:A:126:GLN:OE1	0.47	2.63	17	1
1:A:134:THR:O	1:A:156:GLU:N	0.47	2.44	11	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:116:CYS:O	1:A:127:ILE:N	0.47	2.46	7	3
1:A:126:GLN:O	1:A:126:GLN:CG	0.47	2.63	10	1
1:A:83:VAL:O	1:A:84:ARG:O	0.47	2.33	16	1
1:A:111:VAL:HG12	1:A:131:LYS:HA	0.47	1.86	16	1
1:A:117:ILE:CG2	1:A:124:MET:HB3	0.47	2.40	10	4
1:A:88:VAL:O	1:A:88:VAL:CG2	0.47	2.57	16	5
1:A:83:VAL:CG1	1:A:153:VAL:HG12	0.47	2.40	6	2
1:A:117:ILE:HG12	1:A:126:GLN:CA	0.47	2.40	18	4
1:A:108:LYS:O	1:A:109:VAL:O	0.47	2.33	15	3
1:A:122:LYS:CD	1:A:122:LYS:C	0.46	2.88	3	5
1:A:83:VAL:O	1:A:83:VAL:HG12	0.46	2.10	10	1
1:A:96:SER:CB	1:A:97:PRO:HD3	0.46	2.39	13	1
1:A:150:GLU:O	1:A:151:PRO:C	0.46	2.59	9	19
1:A:90:THR:HB	1:A:119:GLU:CG	0.46	2.40	16	3
1:A:87:MET:HE2	1:A:120:ALA:HB1	0.46	1.87	10	1
1:A:81:HIS:CD2	1:A:155:ILE:HG22	0.46	2.45	11	1
1:A:153:VAL:O	1:A:153:VAL:HG12	0.46	2.09	11	1
1:A:136:LYS:HD2	1:A:156:GLU:CA	0.46	2.40	14	2
1:A:140:VAL:HG21	1:A:152:LEU:HB3	0.46	1.88	11	1
1:A:134:THR:O	1:A:135:VAL:C	0.46	2.57	2	6
1:A:109:VAL:HG23	1:A:133:GLY:N	0.46	2.26	11	1
1:A:131:LYS:O	1:A:132:SER:O	0.46	2.33	15	3
1:A:138:ILE:O	1:A:140:VAL:N	0.46	2.48	11	3
1:A:100:LYS:O	1:A:101:ALA:O	0.46	2.33	3	1
1:A:85:SER:OG	1:A:87:MET:O	0.46	2.34	4	1
1:A:93:ARG:CD	1:A:142:SER:HB2	0.46	2.41	9	1
1:A:93:ARG:CD	1:A:142:SER:CB	0.46	2.94	10	2
1:A:103:ILE:HG12	1:A:115:LEU:O	0.46	2.11	11	5
1:A:144:GLN:OE1	1:A:145:PRO:O	0.46	2.33	5	2
1:A:82:ILE:HG23	1:A:153:VAL:O	0.46	2.09	11	1
1:A:84:ARG:HB3	1:A:151:PRO:CD	0.46	2.40	6	5
1:A:138:ILE:C	1:A:140:VAL:N	0.46	2.73	13	13
1:A:85:SER:CB	1:A:146:VAL:CG2	0.46	2.94	3	2
1:A:96:SER:CB	1:A:97:PRO:HD2	0.46	2.40	5	1
1:A:98:ASP:CG	1:A:98:ASP:O	0.46	2.58	8	1
1:A:86:PRO:O	1:A:87:MET:O	0.46	2.33	13	2
1:A:109:VAL:HG11	1:A:155:ILE:HD13	0.46	1.88	9	2
1:A:123:MET:O	1:A:125:ASN:N	0.46	2.49	11	1
1:A:82:ILE:HD13	1:A:139:LEU:CD1	0.46	2.40	13	1
1:A:120:ALA:C	1:A:121:MET:HG2	0.46	2.36	19	2
1:A:122:LYS:O	1:A:122:LYS:NZ	0.46	2.48	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:117:ILE:HG21	1:A:124:MET:CB	0.46	2.40	8	5
1:A:120:ALA:O	1:A:121:MET:HG2	0.46	2.11	10	5
1:A:122:LYS:C	1:A:123:MET:HG3	0.46	2.36	19	2
1:A:89:GLY:HA3	1:A:120:ALA:HB2	0.46	1.87	15	1
1:A:122:LYS:C	1:A:122:LYS:HD3	0.45	2.36	12	3
1:A:103:ILE:CG2	1:A:135:VAL:HG21	0.45	2.32	11	1
1:A:83:VAL:HB	1:A:153:VAL:HG13	0.45	1.88	15	1
1:A:108:LYS:O	1:A:110:ASN:OD1	0.45	2.33	16	1
1:A:140:VAL:CG2	1:A:152:LEU:HA	0.45	2.42	1	16
1:A:147:GLU:O	1:A:150:GLU:HB2	0.45	2.12	1	11
1:A:148:PHE:CZ	1:A:149:ASP:OD1	0.45	2.69	1	1
1:A:135:VAL:HA	1:A:155:ILE:CG1	0.45	2.41	13	3
1:A:118:VAL:O	1:A:125:ASN:HB2	0.45	2.11	5	1
1:A:121:MET:O	1:A:121:MET:SD	0.45	2.74	8	2
1:A:90:THR:CG2	1:A:144:GLN:C	0.45	2.89	17	2
1:A:149:ASP:O	1:A:149:ASP:OD1	0.45	2.34	19	1
1:A:122:LYS:O	1:A:122:LYS:HD2	0.45	2.11	12	8
1:A:120:ALA:O	1:A:121:MET:HG3	0.45	2.12	3	3
1:A:135:VAL:N	1:A:155:ILE:HG13	0.45	2.27	5	2
1:A:102:PHE:CE2	1:A:117:ILE:HD12	0.45	2.46	8	4
1:A:136:LYS:HD3	1:A:154:VAL:HG11	0.45	1.88	11	1
1:A:85:SER:OG	1:A:146:VAL:HG23	0.45	2.11	14	1
1:A:143:GLY:O	1:A:144:GLN:OE1	0.45	2.35	15	1
1:A:109:VAL:CG2	1:A:133:GLY:O	0.45	2.57	15	1
1:A:141:GLU:HB3	1:A:144:GLN:CD	0.45	2.35	15	1
1:A:92:TYR:O	1:A:116:CYS:HB2	0.45	2.11	16	1
1:A:117:ILE:HG21	1:A:124:MET:HB3	0.45	1.87	18	3
1:A:133:GLY:HA3	1:A:155:ILE:CG2	0.45	2.41	6	2
1:A:126:GLN:O	1:A:127:ILE:C	0.45	2.60	14	1
1:A:136:LYS:HG2	1:A:137:ALA:N	0.45	2.27	11	4
1:A:102:PHE:O	1:A:115:LEU:O	0.45	2.35	5	1
1:A:121:MET:O	1:A:122:LYS:HB3	0.45	2.12	17	3
1:A:141:GLU:HB2	1:A:144:GLN:CG	0.45	2.42	15	2
1:A:85:SER:O	1:A:85:SER:OG	0.45	2.34	2	4
1:A:109:VAL:C	1:A:110:ASN:CG	0.45	2.84	3	4
1:A:82:ILE:HG23	1:A:153:VAL:C	0.45	2.37	11	2
1:A:147:GLU:O	1:A:150:GLU:HB3	0.45	2.12	9	1
1:A:81:HIS:O	1:A:155:ILE:N	0.45	2.50	16	1
1:A:87:MET:CE	1:A:125:ASN:OD1	0.45	2.65	16	1
1:A:136:LYS:HD3	1:A:156:GLU:CB	0.45	2.42	17	2
1:A:122:LYS:HD2	1:A:122:LYS:O	0.45	2.12	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:84:ARG:HB3	1:A:151:PRO:CA	0.45	2.42	6	1
1:A:90:THR:O	1:A:118:VAL:CA	0.45	2.65	8	1
1:A:130:ASP:O	1:A:130:ASP:OD1	0.45	2.34	13	1
1:A:148:PHE:CG	1:A:149:ASP:OD1	0.45	2.70	1	1
1:A:108:LYS:O	1:A:110:ASN:ND2	0.45	2.49	2	2
1:A:117:ILE:HG21	1:A:124:MET:HB2	0.45	1.89	8	2
1:A:109:VAL:HG21	1:A:115:LEU:HD21	0.45	1.88	9	1
1:A:131:LYS:O	1:A:131:LYS:CE	0.45	2.65	20	2
1:A:109:VAL:C	1:A:110:ASN:ND2	0.44	2.76	2	1
1:A:90:THR:HG22	1:A:92:TYR:CZ	0.44	2.46	4	1
1:A:97:PRO:O	1:A:98:ASP:HB2	0.44	2.12	12	1
1:A:91:PHE:CZ	1:A:138:ILE:HG23	0.44	2.46	16	1
1:A:136:LYS:CD	1:A:156:GLU:HB3	0.44	2.42	18	1
1:A:141:GLU:O	1:A:144:GLN:HG2	0.44	2.12	17	4
1:A:92:TYR:HH	1:A:119:GLU:CD	0.44	2.19	17	1
1:A:80:GLY:O	1:A:81:HIS:HB2	0.44	2.13	3	8
1:A:80:GLY:CA	1:A:156:GLU:HB2	0.44	2.43	18	1
1:A:105:VAL:CG2	1:A:136:LYS:C	0.44	2.85	7	1
1:A:95:PRO:HD3	1:A:102:PHE:N	0.44	2.28	17	2
1:A:86:PRO:C	1:A:87:MET:HG2	0.44	2.38	13	2
1:A:119:GLU:OE2	1:A:122:LYS:O	0.44	2.36	20	1
1:A:143:GLY:N	1:A:144:GLN:OE1	0.44	2.51	15	2
1:A:136:LYS:CD	1:A:156:GLU:HB2	0.44	2.42	20	3
1:A:102:PHE:C	1:A:103:ILE:HG13	0.44	2.37	5	2
1:A:121:MET:O	1:A:122:LYS:HG3	0.44	2.12	8	4
1:A:118:VAL:O	1:A:118:VAL:CG1	0.44	2.57	11	1
1:A:96:SER:HB2	1:A:97:PRO:CD	0.44	2.42	13	1
1:A:119:GLU:HG3	1:A:124:MET:CA	0.44	2.43	15	1
1:A:156:GLU:OE1	1:A:156:GLU:O	0.44	2.36	1	1
1:A:95:PRO:HB3	1:A:102:PHE:CE1	0.44	2.47	2	1
1:A:121:MET:O	1:A:121:MET:CG	0.44	2.66	11	2
1:A:122:LYS:O	1:A:123:MET:HG2	0.44	2.11	11	2
1:A:93:ARG:CG	1:A:142:SER:HB3	0.44	2.43	13	1
1:A:120:ALA:O	1:A:121:MET:HB3	0.44	2.12	14	1
1:A:105:VAL:O	1:A:105:VAL:CG1	0.43	2.66	3	1
1:A:105:VAL:HA	1:A:135:VAL:CG1	0.43	2.43	7	2
1:A:139:LEU:HD13	1:A:151:PRO:C	0.43	2.38	5	1
1:A:105:VAL:HG22	1:A:137:ALA:CA	0.43	2.43	10	1
1:A:85:SER:OG	1:A:147:GLU:O	0.43	2.34	11	1
1:A:149:ASP:O	1:A:151:PRO:HD3	0.43	2.13	1	1
1:A:84:ARG:O	1:A:84:ARG:HD3	0.43	2.12	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:91:PHE:CG	1:A:152:LEU:HB3	0.43	2.48	2	1
1:A:95:PRO:CD	1:A:101:ALA:C	0.43	2.91	4	1
1:A:156:GLU:OE2	1:A:156:GLU:OXT	0.43	2.35	4	1
1:A:92:TYR:CD1	1:A:143:GLY:CA	0.43	3.01	6	1
1:A:85:SER:HB2	1:A:152:LEU:CD2	0.43	2.42	13	1
1:A:131:LYS:O	1:A:131:LYS:HG3	0.43	2.14	14	1
1:A:91:PHE:CD1	1:A:141:GLU:O	0.43	2.71	15	1
1:A:144:GLN:CD	1:A:145:PRO:O	0.43	2.61	2	2
1:A:105:VAL:HG23	1:A:136:LYS:O	0.43	2.13	3	1
1:A:102:PHE:HE2	1:A:117:ILE:HD12	0.43	1.74	18	5
1:A:90:THR:O	1:A:118:VAL:C	0.43	2.62	8	1
1:A:115:LEU:HD22	1:A:155:ILE:CD1	0.43	2.42	9	1
1:A:131:LYS:CD	1:A:131:LYS:C	0.43	2.91	17	1
1:A:134:THR:HB	1:A:156:GLU:CG	0.43	2.44	1	2
1:A:109:VAL:HG11	1:A:155:ILE:HD11	0.43	1.90	5	1
1:A:111:VAL:HA	1:A:129:ALA:CB	0.43	2.44	19	2
1:A:85:SER:HG	1:A:152:LEU:HD21	0.43	1.70	12	1
1:A:136:LYS:HD3	1:A:156:GLU:CG	0.43	2.44	15	1
1:A:109:VAL:C	1:A:110:ASN:OD1	0.43	2.62	16	3
1:A:84:ARG:O	1:A:86:PRO:CD	0.43	2.66	13	2
1:A:97:PRO:O	1:A:98:ASP:OD1	0.43	2.36	13	1
1:A:122:LYS:O	1:A:122:LYS:HD3	0.43	2.13	15	1
1:A:105:VAL:HG23	1:A:136:LYS:CA	0.43	2.43	17	1
1:A:83:VAL:CG1	1:A:153:VAL:HB	0.43	2.41	11	1
1:A:91:PHE:HB2	1:A:152:LEU:HD13	0.43	1.88	11	1
1:A:119:GLU:OE2	1:A:124:MET:CB	0.43	2.67	15	1
1:A:121:MET:CG	1:A:122:LYS:HG3	0.43	2.44	1	1
1:A:139:LEU:HD12	1:A:152:LEU:O	0.43	2.14	5	1
1:A:134:THR:N	1:A:155:ILE:HG12	0.43	2.29	11	2
1:A:90:THR:HA	1:A:146:VAL:HG22	0.43	1.91	9	1
1:A:100:LYS:N	1:A:100:LYS:CD	0.43	2.81	11	1
1:A:81:HIS:NE2	1:A:131:LYS:HE3	0.43	2.29	15	1
1:A:86:PRO:O	1:A:87:MET:CG	0.43	2.67	19	1
1:A:148:PHE:O	1:A:148:PHE:CG	0.43	2.70	6	1
1:A:136:LYS:HD2	1:A:156:GLU:CB	0.43	2.44	14	2
1:A:82:ILE:HG12	1:A:154:VAL:CG1	0.43	2.42	15	2
1:A:82:ILE:HD13	1:A:139:LEU:HD12	0.43	1.91	13	1
1:A:119:GLU:OE2	1:A:124:MET:HA	0.43	2.14	15	1
1:A:93:ARG:HD3	1:A:142:SER:OG	0.42	2.14	4	1
1:A:125:ASN:O	1:A:126:GLN:O	0.42	2.37	12	1
1:A:96:SER:HB3	1:A:99:ALA:HB2	0.42	1.88	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:105:VAL:CG2	1:A:137:ALA:HA	0.42	2.43	10	1
1:A:90:THR:C	1:A:118:VAL:HG13	0.42	2.38	17	1
1:A:97:PRO:O	1:A:98:ASP:HB3	0.42	2.13	20	2
1:A:148:PHE:O	1:A:149:ASP:OD2	0.42	2.37	19	1
1:A:102:PHE:C	1:A:103:ILE:HG12	0.42	2.37	15	3
1:A:143:GLY:C	1:A:144:GLN:CD	0.42	2.87	1	1
1:A:81:HIS:CD2	1:A:131:LYS:HD2	0.42	2.49	6	1
1:A:111:VAL:CG1	1:A:131:LYS:HA	0.42	2.45	12	1
1:A:111:VAL:CG2	1:A:112:GLY:N	0.42	2.82	15	1
1:A:148:PHE:CD1	1:A:148:PHE:C	0.42	2.96	16	1
1:A:98:ASP:OD1	1:A:98:ASP:O	0.42	2.36	18	1
1:A:122:LYS:O	1:A:122:LYS:HG3	0.42	2.14	7	1
1:A:95:PRO:HG3	1:A:102:PHE:CD2	0.42	2.49	17	1
1:A:103:ILE:HD11	1:A:116:CYS:CB	0.42	2.44	19	1
1:A:122:LYS:C	1:A:122:LYS:HD2	0.42	2.39	19	1
1:A:84:ARG:HA	1:A:151:PRO:HA	0.42	1.90	3	6
1:A:139:LEU:CD1	1:A:154:VAL:CG2	0.42	2.98	5	2
1:A:136:LYS:CE	1:A:156:GLU:HB2	0.42	2.45	16	2
1:A:118:VAL:N	1:A:119:GLU:OE2	0.42	2.53	15	1
1:A:103:ILE:HD11	1:A:116:CYS:SG	0.42	2.54	19	1
1:A:121:MET:C	1:A:122:LYS:HG3	0.42	2.39	1	1
1:A:143:GLY:C	1:A:144:GLN:HG2	0.42	2.40	4	2
1:A:114:THR:CG2	1:A:126:GLN:HB2	0.42	2.45	11	2
1:A:140:VAL:C	1:A:141:GLU:O	0.42	2.62	19	1
1:A:110:ASN:ND2	1:A:132:SER:HB2	0.42	2.29	20	1
1:A:92:TYR:HA	1:A:142:SER:O	0.42	2.15	1	8
1:A:149:ASP:O	1:A:151:PRO:CD	0.42	2.68	1	1
1:A:150:GLU:CD	1:A:150:GLU:C	0.42	2.87	5	1
1:A:121:MET:O	1:A:122:LYS:HB2	0.42	2.14	7	2
1:A:86:PRO:O	1:A:87:MET:C	0.42	2.63	13	2
1:A:103:ILE:HG23	1:A:115:LEU:O	0.42	2.15	8	1
1:A:118:VAL:HG23	1:A:127:ILE:HG12	0.42	1.91	12	2
1:A:121:MET:SD	1:A:123:MET:SD	0.42	3.18	12	1
1:A:136:LYS:CE	1:A:156:GLU:HB3	0.42	2.44	13	1
1:A:103:ILE:HG13	1:A:115:LEU:O	0.42	2.15	15	1
1:A:105:VAL:HG13	1:A:136:LYS:HA	0.42	1.91	8	2
1:A:119:GLU:HA	1:A:123:MET:O	0.42	2.14	14	3
1:A:81:HIS:ND1	1:A:131:LYS:HD3	0.42	2.30	2	1
1:A:102:PHE:O	1:A:103:ILE:HG13	0.42	2.15	5	1
1:A:87:MET:O	1:A:89:GLY:N	0.42	2.52	18	2
1:A:102:PHE:CE2	1:A:117:ILE:HB	0.42	2.49	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:148:PHE:CD1	1:A:149:ASP:N	0.42	2.88	11	1
1:A:91:PHE:CZ	1:A:138:ILE:HG22	0.42	2.50	13	1
1:A:82:ILE:HG12	1:A:154:VAL:CG2	0.42	2.43	15	1
1:A:92:TYR:O	1:A:116:CYS:HB3	0.41	2.15	5	1
1:A:122:LYS:O	1:A:122:LYS:CG	0.41	2.68	15	1
1:A:135:VAL:HA	1:A:155:ILE:HG12	0.41	1.91	14	2
1:A:100:LYS:O	1:A:100:LYS:CG	0.41	2.68	5	1
1:A:111:VAL:HA	1:A:129:ALA:HB3	0.41	1.91	15	1
1:A:136:LYS:CG	1:A:156:GLU:HB3	0.41	2.45	15	1
1:A:83:VAL:N	1:A:153:VAL:O	0.41	2.53	3	1
1:A:131:LYS:O	1:A:131:LYS:HE3	0.41	2.16	20	1
1:A:147:GLU:O	1:A:150:GLU:HG3	0.41	2.15	11	2
1:A:141:GLU:O	1:A:142:SER:O	0.41	2.37	9	2
1:A:93:ARG:HD3	1:A:93:ARG:C	0.41	2.40	12	1
1:A:156:GLU:O	1:A:156:GLU:CD	0.41	2.63	1	1
1:A:122:LYS:O	1:A:122:LYS:CD	0.41	2.69	6	1
1:A:131:LYS:O	1:A:131:LYS:HD3	0.41	2.15	6	1
1:A:147:GLU:O	1:A:150:GLU:HG2	0.41	2.15	6	2
1:A:111:VAL:CG1	1:A:131:LYS:N	0.41	2.81	3	1
1:A:107:GLN:O	1:A:134:THR:HG23	0.41	2.16	5	1
1:A:126:GLN:O	1:A:126:GLN:HG3	0.41	2.16	18	1
1:A:90:THR:O	1:A:118:VAL:HA	0.41	2.15	8	3
1:A:91:PHE:CD2	1:A:152:LEU:HB3	0.41	2.51	2	1
1:A:105:VAL:HG13	1:A:136:LYS:CA	0.41	2.46	8	1
1:A:118:VAL:O	1:A:118:VAL:HG22	0.41	2.16	9	1
1:A:102:PHE:CG	1:A:116:CYS:HA	0.41	2.50	10	2
1:A:85:SER:OG	1:A:85:SER:O	0.41	2.38	11	1
1:A:84:ARG:HB3	1:A:151:PRO:N	0.41	2.31	6	1
1:A:91:PHE:CD2	1:A:116:CYS:SG	0.41	3.14	9	1
1:A:118:VAL:CG1	1:A:125:ASN:CB	0.41	2.99	11	1
1:A:82:ILE:HG23	1:A:154:VAL:HA	0.41	1.93	12	1
1:A:91:PHE:CE2	1:A:141:GLU:O	0.41	2.73	1	2
1:A:93:ARG:O	1:A:101:ALA:HA	0.41	2.16	11	2
1:A:110:ASN:O	1:A:113:ASP:HB2	0.41	2.15	1	2
1:A:138:ILE:HA	1:A:152:LEU:O	0.41	2.16	17	5
1:A:91:PHE:CE2	1:A:153:VAL:CG2	0.41	3.04	3	1
1:A:102:PHE:C	1:A:103:ILE:HG23	0.41	2.41	3	1
1:A:89:GLY:C	1:A:146:VAL:HG22	0.41	2.41	6	1
1:A:91:PHE:O	1:A:143:GLY:HA2	0.41	2.16	6	2
1:A:150:GLU:O	1:A:152:LEU:HG	0.41	2.16	19	1
1:A:140:VAL:HG21	1:A:146:VAL:HG11	0.41	1.93	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:81:HIS:ND1	1:A:131:LYS:HE2	0.41	2.31	11	1
1:A:136:LYS:CG	1:A:156:GLU:HB2	0.41	2.45	12	1
1:A:84:ARG:O	1:A:86:PRO:HD3	0.41	2.16	13	1
1:A:118:VAL:CG2	1:A:127:ILE:HG13	0.41	2.46	13	1
1:A:92:TYR:HB2	1:A:117:ILE:CG1	0.41	2.46	15	1
1:A:84:ARG:O	1:A:84:ARG:HD2	0.40	2.15	7	1
1:A:117:ILE:HD13	1:A:124:MET:SD	0.40	2.56	7	1
1:A:81:HIS:HB3	1:A:155:ILE:O	0.40	2.16	13	2
1:A:139:LEU:HG	1:A:154:VAL:HG21	0.40	1.92	12	1
1:A:85:SER:N	1:A:152:LEU:CD1	0.40	2.84	19	1
1:A:81:HIS:O	1:A:155:ILE:HB	0.40	2.17	1	2
1:A:111:VAL:HG13	1:A:131:LYS:N	0.40	2.31	2	1
1:A:122:LYS:HD3	1:A:122:LYS:C	0.40	2.40	7	1
1:A:133:GLY:C	1:A:155:ILE:CG2	0.40	2.94	9	1
1:A:130:ASP:OD1	1:A:130:ASP:N	0.40	2.52	10	1
1:A:122:LYS:HD2	1:A:122:LYS:C	0.40	2.41	4	1
1:A:88:VAL:O	1:A:88:VAL:HG22	0.40	2.16	9	1
1:A:81:HIS:HD2	1:A:155:ILE:HD12	0.40	1.76	12	1
1:A:95:PRO:HD3	1:A:101:ALA:C	0.40	2.40	12	1
1:A:96:SER:OG	1:A:97:PRO:HD2	0.40	2.16	16	1
1:A:120:ALA:C	1:A:122:LYS:N	0.40	2.78	19	1
1:A:90:THR:CG2	1:A:144:GLN:O	0.40	2.68	12	1
1:A:116:CYS:O	1:A:127:ILE:HG12	0.40	2.15	19	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	76/82 (93%)	42±2 (55±3%)	24±4 (32±5%)	10±3 (13±4%)	1	6
All	All	1520/1640 (93%)	842 (55%)	486 (32%)	192 (13%)	1	6

All 37 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	81	HIS	18
1	A	119	GLU	16
1	A	111	VAL	13
1	A	137	ALA	13
1	A	122	LYS	11
1	A	101	ALA	10
1	A	109	VAL	9
1	A	146	VAL	8
1	A	115	LEU	7
1	A	131	LYS	7
1	A	103	ILE	7
1	A	141	GLU	6
1	A	121	MET	5
1	A	151	PRO	5
1	A	105	VAL	5
1	A	142	SER	5
1	A	88	VAL	4
1	A	114	THR	4
1	A	83	VAL	4
1	A	85	SER	4
1	A	124	MET	4
1	A	132	SER	4
1	A	98	ASP	3
1	A	84	ARG	3
1	A	108	LYS	2
1	A	139	LEU	2
1	A	126	GLN	2
1	A	87	MET	2
1	A	80	GLY	1
1	A	97	PRO	1
1	A	120	ALA	1
1	A	96	SER	1
1	A	127	ILE	1
1	A	143	GLY	1
1	A	86	PRO	1
1	A	149	ASP	1
1	A	148	PHE	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	66/69 (96%)	45±3 (68±4%)	21±3 (32±4%)	1	14
All	All	1320/1380 (96%)	897 (68%)	423 (32%)	1	14

All 52 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	138	ILE	20
1	A	152	LEU	20
1	A	102	PHE	18
1	A	117	ILE	17
1	A	119	GLU	17
1	A	122	LYS	17
1	A	153	VAL	17
1	A	100	LYS	17
1	A	96	SER	16
1	A	121	MET	15
1	A	103	ILE	14
1	A	108	LYS	12
1	A	124	MET	11
1	A	144	GLN	11
1	A	131	LYS	10
1	A	82	ILE	9
1	A	107	GLN	9
1	A	116	CYS	9
1	A	123	MET	9
1	A	142	SER	9
1	A	85	SER	9
1	A	147	GLU	9
1	A	125	ASN	8
1	A	136	LYS	8
1	A	149	ASP	8
1	A	146	VAL	7
1	A	84	ARG	7
1	A	83	VAL	7
1	A	98	ASP	7
1	A	126	GLN	7
1	A	94	THR	6
1	A	87	MET	5
1	A	104	GLU	5
1	A	139	LEU	5

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Mol	Chain	Res	Type	Models (Total)
1	A	93	ARG	5
1	A	154	VAL	5
1	A	156	GLU	5
1	A	88	VAL	4
1	A	150	GLU	4
1	A	128	GLU	3
1	A	105	VAL	3
1	A	111	VAL	2
1	A	141	GLU	2
1	A	130	ASP	2
1	A	155	ILE	2
1	A	109	VAL	2
1	A	91	PHE	2
1	A	132	SER	2
1	A	113	ASP	2
1	A	114	THR	1
1	A	118	VAL	1
1	A	90	THR	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