



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 08:47 PM BST

PDB ID : 2I3E
Title : Solution structure of catalytic domain of goldfish RICH protein
Authors : Denisov, A.Y.; Kozlov, G.; Gehring, K.
Deposited on : 2006-08-18

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

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

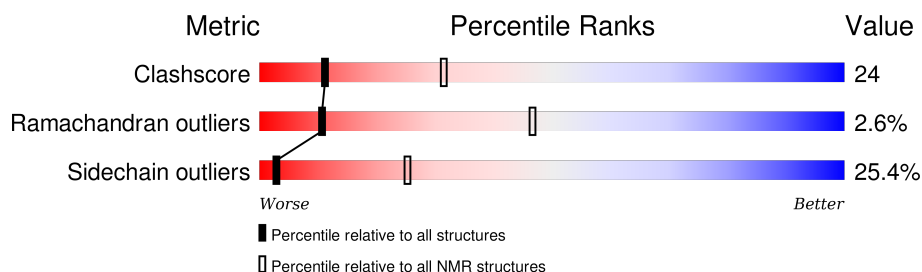
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 68%.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 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	222	

2 Ensemble composition and analysis

This entry contains 10 models. Model 9 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:7-A:40, A:61-A:219 (193)	0.51	9

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

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

The models can be grouped into 2 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 4, 5, 6, 7, 8
2	2, 3, 9, 10

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3432 atoms, of which 1701 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called G-RICH.

Mol	Chain	Residues	Atoms						Trace
1	A	222	Total	C	H	N	O	S	0
			3432	1105	1701	274	345	7	

There are 4 discrepancies between the modelled and reference sequences:

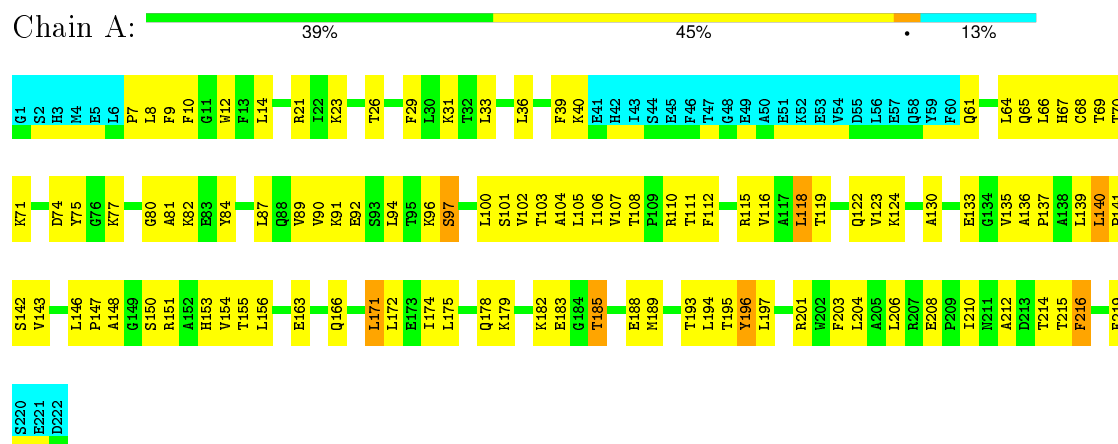
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	CLONING ARTIFACT	UNP Q90306
A	2	SER	-	CLONING ARTIFACT	UNP Q90306
A	3	HIS	-	CLONING ARTIFACT	UNP Q90306
A	4	MET	-	CLONING ARTIFACT	UNP Q90306

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: G-RICH

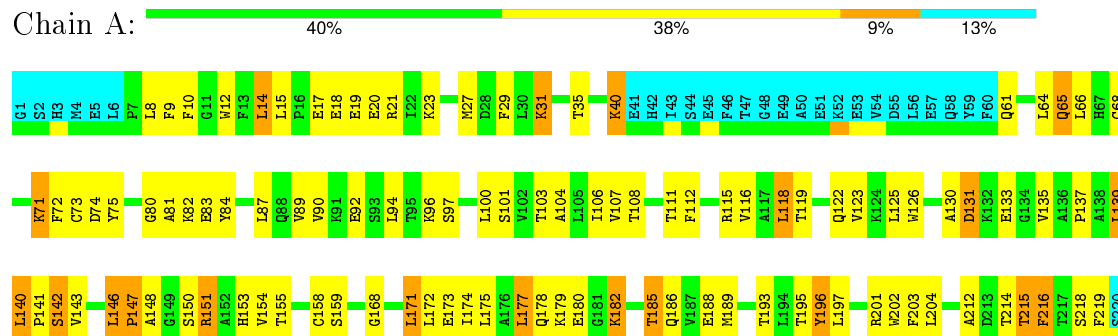


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

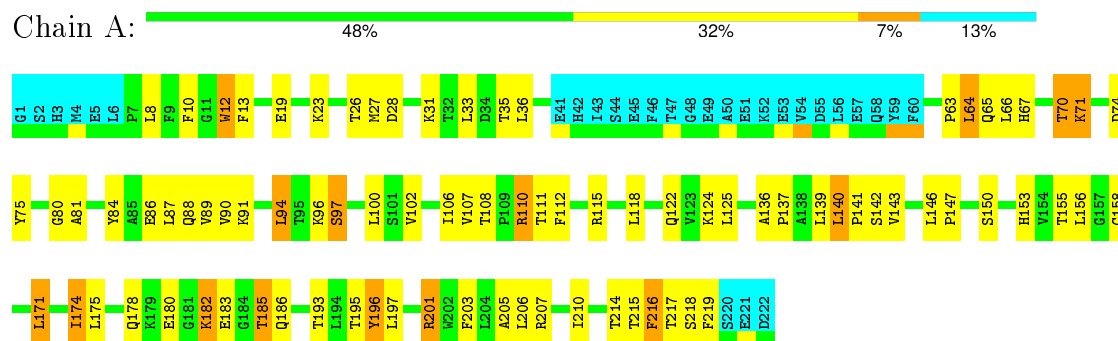
- Molecule 1: G-RICH





4.2.2 Score per residue for model 2

- Molecule 1: G-RICH



4.2.3 Score per residue for model 3

- Molecule 1: G-RICH



4.2.4 Score per residue for model 4

- Molecule 1: G-RICH



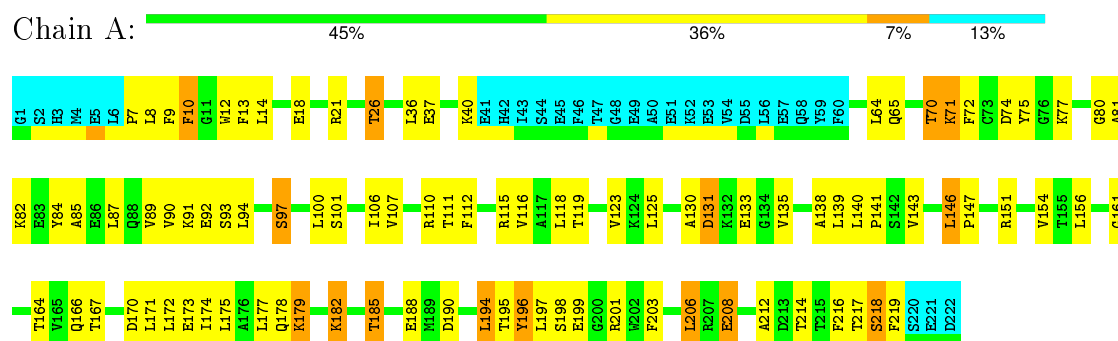
4.2.8 Score per residue for model 8

• Molecule 1: G-RICH



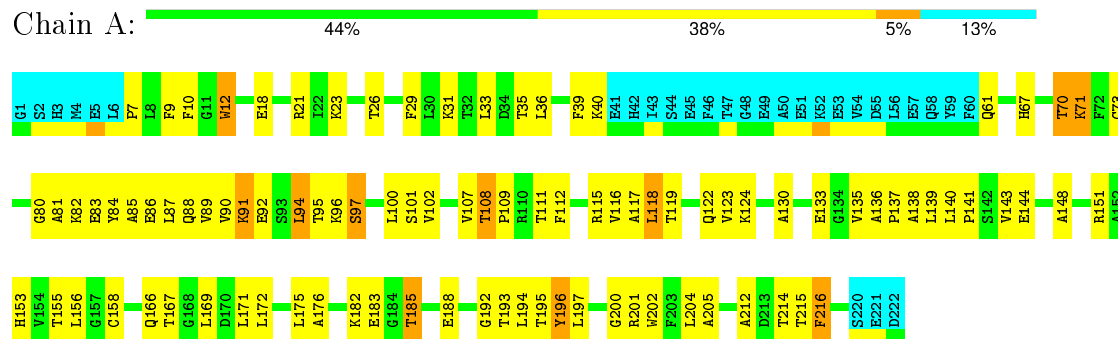
4.2.9 Score per residue for model 9 (medoid)

• Molecule 1: G-RICH



4.2.10 Score per residue for model 10

• Molecule 1: G-RICH



5 Refinement protocol and experimental data overview

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

Of the 150 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy and the least restraint violations*.

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

Software name	Classification	Version
CNS	refinement	1.1

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

Chemical shift file(s)	BMRB entry 7167
Number of chemical shift lists	1
Total number of shifts	1932
Number of shifts mapped to atoms	1932
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	68%

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

6 Model quality ⓘ

6.1 Standard geometry ⓘ

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1493	1497	1497	71±6
All	All	14930	14970	14970	707

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 24.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:135:VAL:HG23	1:A:175:LEU:HD13	1.07	1.23	10	2
1:A:81:ALA:HB2	1:A:130:ALA:HB2	1.04	1.13	9	1
1:A:135:VAL:HG13	1:A:143:VAL:HG22	0.86	1.45	6	1
1:A:140:LEU:O	1:A:143:VAL:HG22	0.85	1.71	10	1
1:A:139:LEU:O	1:A:143:VAL:HG13	0.85	1.72	10	1
1:A:136:ALA:HB3	1:A:139:LEU:HD13	0.83	1.50	10	6
1:A:107:VAL:HG22	1:A:112:PHE:CE2	0.82	2.09	8	6
1:A:143:VAL:CG1	1:A:148:ALA:HB2	0.82	2.04	6	3
1:A:191:LEU:HD23	1:A:206:LEU:HD22	0.82	1.48	8	1
1:A:81:ALA:HB2	1:A:130:ALA:CB	0.81	2.04	9	1
1:A:150:SER:OG	1:A:175:LEU:HD12	0.80	1.77	3	2
1:A:137:PRO:O	1:A:140:LEU:HD23	0.80	1.77	7	1
1:A:135:VAL:HG22	1:A:146:LEU:HD12	0.80	1.50	1	1
1:A:118:LEU:HD11	1:A:123:VAL:HG13	0.80	1.53	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:29:PHE:CZ	1:A:33:LEU:HD13	0.80	2.12	6	1
1:A:153:HIS:CG	1:A:171:LEU:HD13	0.80	2.12	3	2
1:A:107:VAL:HG22	1:A:112:PHE:CD1	0.80	2.10	2	2
1:A:81:ALA:CB	1:A:130:ALA:HB2	0.79	2.05	9	1
1:A:12:TRP:CH2	1:A:118:LEU:HD21	0.79	2.13	5	4
1:A:29:PHE:CD2	1:A:204:LEU:HD22	0.79	2.11	5	2
1:A:135:VAL:HG22	1:A:146:LEU:CD1	0.79	2.07	1	1
1:A:135:VAL:CG2	1:A:175:LEU:HD13	0.79	2.07	10	2
1:A:135:VAL:CG2	1:A:146:LEU:HD11	0.79	2.07	9	1
1:A:107:VAL:HG22	1:A:112:PHE:CE1	0.78	2.13	9	4
1:A:131:ASP:OD2	1:A:138:ALA:HB3	0.78	1.79	9	1
1:A:119:THR:O	1:A:123:VAL:HG23	0.78	1.79	1	3
1:A:143:VAL:HG21	1:A:148:ALA:HB2	0.78	1.52	7	3
1:A:115:ARG:NH1	1:A:175:LEU:HD21	0.78	1.92	4	2
1:A:174:ILE:HD11	1:A:197:LEU:HD11	0.78	1.53	2	1
1:A:174:ILE:HD11	1:A:203:PHE:CE1	0.77	2.14	6	1
1:A:29:PHE:CD1	1:A:204:LEU:HD22	0.77	2.14	3	1
1:A:14:LEU:HD11	1:A:100:LEU:HD21	0.77	1.57	9	1
1:A:7:PRO:HG2	1:A:85:ALA:HB1	0.77	1.56	9	2
1:A:150:SER:OG	1:A:172:LEU:HD23	0.77	1.79	5	1
1:A:31:LYS:O	1:A:35:THR:HG23	0.76	1.80	1	2
1:A:143:VAL:CG2	1:A:148:ALA:HB2	0.76	2.10	7	3
1:A:112:PHE:CD1	1:A:156:LEU:HD11	0.75	2.16	8	1
1:A:143:VAL:HG11	1:A:148:ALA:HB2	0.75	1.58	6	3
1:A:102:VAL:HG13	1:A:115:ARG:O	0.75	1.82	10	4
1:A:147:PRO:O	1:A:175:LEU:HD13	0.74	1.81	3	5
1:A:140:LEU:O	1:A:143:VAL:HG12	0.74	1.82	7	3
1:A:133:GLU:CG	1:A:172:LEU:HD21	0.74	2.12	8	4
1:A:12:TRP:CE3	1:A:214:THR:HG21	0.74	2.17	8	1
1:A:87:LEU:HD23	1:A:89:VAL:CG1	0.74	2.12	2	9
1:A:150:SER:HB3	1:A:175:LEU:HD12	0.74	1.57	5	2
1:A:84:TYR:CE2	1:A:90:VAL:HG11	0.74	2.17	8	8
1:A:100:LEU:HD11	1:A:214:THR:HG21	0.74	1.60	5	2
1:A:13:PHE:CD1	1:A:217:THR:HG21	0.73	2.18	9	3
1:A:118:LEU:HD21	1:A:137:PRO:CG	0.73	2.13	8	3
1:A:118:LEU:CD1	1:A:123:VAL:HG13	0.73	2.13	8	1
1:A:87:LEU:O	1:A:90:VAL:HG22	0.73	1.83	6	10
1:A:139:LEU:O	1:A:143:VAL:HG23	0.72	1.84	2	3
1:A:12:TRP:CZ3	1:A:70:THR:HG23	0.72	2.19	10	1
1:A:102:VAL:HG23	1:A:115:ARG:O	0.72	1.84	5	3
1:A:175:LEU:HD12	1:A:176:ALA:N	0.72	2.00	6	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:105:LEU:HD13	1:A:206:LEU:HD11	0.72	1.62	7	2
1:A:171:LEU:HA	1:A:174:ILE:HD12	0.71	1.62	1	2
1:A:150:SER:OG	1:A:175:LEU:HD23	0.71	1.85	6	1
1:A:143:VAL:HG23	1:A:146:LEU:HD11	0.71	1.62	4	1
1:A:106:ILE:HD13	1:A:107:VAL:N	0.71	2.01	3	1
1:A:150:SER:HA	1:A:171:LEU:HD22	0.70	1.62	1	2
1:A:22:ILE:HD13	1:A:22:ILE:O	0.70	1.86	7	1
1:A:133:GLU:OE1	1:A:172:LEU:HD13	0.69	1.86	7	1
1:A:150:SER:CB	1:A:175:LEU:HD12	0.69	2.17	7	1
1:A:111:THR:OG1	1:A:167:THR:HG23	0.69	1.87	9	1
1:A:104:ALA:HB3	1:A:115:ARG:NH1	0.69	2.02	7	1
1:A:177:LEU:HG	1:A:197:LEU:HD13	0.69	1.65	1	1
1:A:135:VAL:CG1	1:A:143:VAL:HG22	0.69	2.17	6	1
1:A:174:ILE:HG23	1:A:175:LEU:HD23	0.69	1.65	2	1
1:A:139:LEU:O	1:A:143:VAL:HG12	0.68	1.88	9	2
1:A:100:LEU:HD12	1:A:100:LEU:O	0.68	1.89	1	2
1:A:150:SER:HB2	1:A:172:LEU:HD23	0.68	1.66	7	1
1:A:153:HIS:HB3	1:A:171:LEU:HD22	0.68	1.65	2	3
1:A:147:PRO:HB2	1:A:175:LEU:HD22	0.67	1.64	9	7
1:A:188:GLU:HA	1:A:193:THR:HG22	0.67	1.67	7	3
1:A:135:VAL:HG23	1:A:175:LEU:CD1	0.67	2.12	10	2
1:A:111:THR:HG22	1:A:158:CYS:HA	0.67	1.64	7	3
1:A:135:VAL:HG13	1:A:143:VAL:CG2	0.67	2.20	4	2
1:A:68:CYS:SG	1:A:116:VAL:HG21	0.66	2.30	3	2
1:A:94:LEU:HD21	1:A:218:SER:HB3	0.66	1.66	1	1
1:A:174:ILE:HD11	1:A:203:PHE:CD1	0.66	2.25	6	1
1:A:142:SER:O	1:A:146:LEU:HD12	0.66	1.90	3	2
1:A:135:VAL:HG13	1:A:143:VAL:HG21	0.66	1.65	9	2
1:A:118:LEU:HD13	1:A:122:GLN:CG	0.66	2.20	4	1
1:A:135:VAL:HG11	1:A:148:ALA:HA	0.65	1.68	1	5
1:A:91:LYS:O	1:A:94:LEU:HD12	0.65	1.92	5	1
1:A:174:ILE:CD1	1:A:197:LEU:HD11	0.65	2.20	2	1
1:A:118:LEU:HD13	1:A:122:GLN:HB3	0.65	1.67	6	1
1:A:106:ILE:HD12	1:A:174:ILE:HG21	0.64	1.68	7	1
1:A:168:GLY:O	1:A:172:LEU:HD22	0.64	1.92	4	1
1:A:7:PRO:CG	1:A:85:ALA:HB1	0.64	2.22	9	2
1:A:150:SER:HB2	1:A:175:LEU:HD12	0.64	1.69	4	1
1:A:118:LEU:HD13	1:A:122:GLN:HB2	0.64	1.67	10	3
1:A:71:LYS:NZ	1:A:85:ALA:HB2	0.64	2.07	7	1
1:A:36:LEU:HD13	1:A:194:LEU:HD22	0.64	1.68	10	1
1:A:173:GLU:O	1:A:177:LEU:HD13	0.63	1.92	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:33:LEU:HD23	1:A:39:PHE:CE1	0.63	2.29	6	1
1:A:182:LYS:HB3	1:A:197:LEU:HD23	0.63	1.69	2	1
1:A:33:LEU:HD11	1:A:39:PHE:CD1	0.63	2.28	3	1
1:A:118:LEU:HD21	1:A:137:PRO:CB	0.63	2.24	8	3
1:A:100:LEU:CD1	1:A:212:ALA:HB3	0.63	2.24	4	1
1:A:169:LEU:HA	1:A:172:LEU:HD12	0.63	1.71	10	1
1:A:135:VAL:CG1	1:A:143:VAL:HG21	0.62	2.24	9	2
1:A:131:ASP:OD2	1:A:139:LEU:HD12	0.62	1.93	1	1
1:A:100:LEU:HD22	1:A:116:VAL:CG1	0.62	2.25	7	1
1:A:18:GLU:HG3	1:A:212:ALA:HB1	0.62	1.72	1	1
1:A:71:LYS:HD3	1:A:81:ALA:HB1	0.62	1.71	10	1
1:A:100:LEU:HD23	1:A:212:ALA:O	0.62	1.93	6	1
1:A:133:GLU:HB3	1:A:172:LEU:HD22	0.62	1.71	5	2
1:A:115:ARG:HD3	1:A:175:LEU:HD21	0.62	1.72	2	1
1:A:100:LEU:CD1	1:A:214:THR:HG21	0.61	2.25	5	4
1:A:12:TRP:CZ3	1:A:118:LEU:HD21	0.61	2.28	5	1
1:A:150:SER:HA	1:A:171:LEU:HD12	0.61	1.71	8	1
1:A:197:LEU:HD13	1:A:201:ARG:HB2	0.61	1.73	10	2
1:A:71:LYS:HZ3	1:A:85:ALA:HB2	0.61	1.54	7	1
1:A:155:THR:HG21	1:A:164:THR:HB	0.61	1.70	7	1
1:A:70:THR:HG22	1:A:71:LYS:HE3	0.61	1.72	9	1
1:A:146:LEU:HD12	1:A:147:PRO:O	0.61	1.96	2	2
1:A:96:LYS:O	1:A:215:THR:HG23	0.60	1.96	8	6
1:A:123:VAL:HG12	1:A:137:PRO:HB2	0.60	1.74	8	1
1:A:153:HIS:CE1	1:A:171:LEU:HD13	0.60	2.30	6	1
1:A:143:VAL:HG13	1:A:148:ALA:HB2	0.60	1.71	1	2
1:A:118:LEU:HD11	1:A:123:VAL:CG1	0.60	2.24	8	1
1:A:29:PHE:CZ	1:A:33:LEU:HD22	0.60	2.31	3	2
1:A:101:SER:O	1:A:117:ALA:HB3	0.60	1.97	5	3
1:A:194:LEU:HG	1:A:204:LEU:HD12	0.60	1.72	8	1
1:A:30:LEU:HD21	1:A:112:PHE:CE2	0.60	2.32	4	1
1:A:18:GLU:CG	1:A:212:ALA:HB1	0.60	2.25	1	1
1:A:7:PRO:HG3	1:A:85:ALA:HB1	0.60	1.71	7	1
1:A:12:TRP:CD1	1:A:214:THR:HG21	0.59	2.32	7	1
1:A:133:GLU:HG3	1:A:172:LEU:HD21	0.59	1.74	8	1
1:A:100:LEU:HD13	1:A:116:VAL:CG1	0.59	2.28	1	1
1:A:70:THR:HG21	1:A:216:PHE:CZ	0.59	2.32	10	1
1:A:153:HIS:CD2	1:A:171:LEU:HD13	0.59	2.32	10	2
1:A:135:VAL:HG13	1:A:143:VAL:HG12	0.59	1.74	10	1
1:A:115:ARG:HD2	1:A:175:LEU:HD21	0.59	1.75	9	1
1:A:68:CYS:HA	1:A:154:VAL:HG23	0.59	1.73	6	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:106:ILE:HG22	1:A:203:PHE:CB	0.59	2.28	2	2
1:A:106:ILE:HG21	1:A:171:LEU:HD11	0.59	1.74	5	1
1:A:135:VAL:CG2	1:A:146:LEU:HD12	0.59	2.27	1	1
1:A:27:MET:HA	1:A:30:LEU:HD12	0.58	1.74	5	1
1:A:106:ILE:HD13	1:A:174:ILE:CD1	0.58	2.28	8	1
1:A:106:ILE:HG22	1:A:203:PHE:HB3	0.58	1.73	2	3
1:A:175:LEU:HD23	1:A:175:LEU:N	0.58	2.14	1	2
1:A:197:LEU:HD22	1:A:201:ARG:HD2	0.58	1.74	7	1
1:A:146:LEU:N	1:A:146:LEU:HD22	0.58	2.14	5	1
1:A:197:LEU:HD13	1:A:201:ARG:CB	0.58	2.28	2	1
1:A:135:VAL:HG21	1:A:146:LEU:HD11	0.58	1.76	9	1
1:A:115:ARG:CZ	1:A:175:LEU:HD21	0.57	2.28	5	3
1:A:153:HIS:CG	1:A:171:LEU:HD22	0.57	2.34	6	1
1:A:105:LEU:CD1	1:A:206:LEU:HD11	0.57	2.29	4	1
1:A:116:VAL:HG23	1:A:153:HIS:HA	0.57	1.76	3	2
1:A:98:TYR:CE2	1:A:100:LEU:HD11	0.57	2.34	7	1
1:A:104:ALA:HB3	1:A:115:ARG:CZ	0.57	2.29	6	3
1:A:206:LEU:HD13	1:A:210:ILE:CD1	0.57	2.30	2	3
1:A:172:LEU:N	1:A:172:LEU:HD13	0.57	2.15	4	1
1:A:185:THR:O	1:A:195:THR:HG23	0.57	1.99	10	1
1:A:153:HIS:HB3	1:A:171:LEU:HD13	0.57	1.76	1	1
1:A:29:PHE:CE1	1:A:204:LEU:HD22	0.57	2.35	1	1
1:A:104:ALA:HB3	1:A:115:ARG:NE	0.56	2.15	6	2
1:A:9:PHE:CE1	1:A:69:THR:HG22	0.56	2.35	6	1
1:A:118:LEU:HD22	1:A:122:GLN:HB3	0.56	1.76	10	1
1:A:63:PRO:HB3	1:A:66:LEU:HD11	0.56	1.76	2	1
1:A:123:VAL:HG22	1:A:137:PRO:HB3	0.56	1.77	1	1
1:A:70:THR:HG21	1:A:216:PHE:CE1	0.56	2.36	10	2
1:A:194:LEU:HD23	1:A:195:THR:N	0.56	2.15	7	1
1:A:187:VAL:O	1:A:193:THR:HG23	0.56	2.01	5	1
1:A:206:LEU:HD21	1:A:210:ILE:CD1	0.56	2.30	3	1
1:A:167:THR:O	1:A:171:LEU:HD12	0.56	2.01	10	2
1:A:197:LEU:HD22	1:A:201:ARG:CD	0.56	2.31	7	1
1:A:94:LEU:HD11	1:A:218:SER:HB2	0.56	1.76	9	1
1:A:18:GLU:HB3	1:A:212:ALA:HB1	0.56	1.78	10	2
1:A:145:ALA:C	1:A:146:LEU:HD13	0.56	2.21	5	1
1:A:84:TYR:CD2	1:A:90:VAL:HG11	0.55	2.37	4	4
1:A:97:SER:HA	1:A:214:THR:O	0.55	2.00	2	10
1:A:15:LEU:HD23	1:A:17:GLU:HB2	0.55	1.77	1	1
1:A:13:PHE:CG	1:A:217:THR:HG21	0.55	2.36	9	1
1:A:96:LYS:O	1:A:215:THR:HG22	0.55	2.01	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:191:LEU:HD12	1:A:208:GLU:OE2	0.55	2.01	3	1
1:A:115:ARG:HG2	1:A:171:LEU:HD21	0.55	1.76	1	1
1:A:107:VAL:HG22	1:A:112:PHE:CZ	0.55	2.37	8	2
1:A:70:THR:HG22	1:A:71:LYS:HE2	0.55	1.77	6	1
1:A:87:LEU:HD23	1:A:89:VAL:HG11	0.55	1.78	3	7
1:A:118:LEU:HD21	1:A:137:PRO:HB3	0.55	1.79	10	2
1:A:66:LEU:CD2	1:A:156:LEU:HD23	0.55	2.32	6	1
1:A:118:LEU:HD13	1:A:122:GLN:CB	0.54	2.33	10	2
1:A:71:LYS:CD	1:A:81:ALA:HB1	0.54	2.32	10	1
1:A:100:LEU:HD23	1:A:118:LEU:HA	0.54	1.79	7	1
1:A:36:LEU:HD13	1:A:194:LEU:CD2	0.54	2.32	10	1
1:A:100:LEU:HD22	1:A:116:VAL:HG12	0.54	1.79	7	1
1:A:14:LEU:HD12	1:A:19:GLU:HB3	0.53	1.79	1	1
1:A:12:TRP:CE3	1:A:70:THR:HG23	0.53	2.38	10	1
1:A:140:LEU:N	1:A:141:PRO:HD2	0.53	2.18	6	10
1:A:206:LEU:HD21	1:A:210:ILE:HD11	0.53	1.80	3	1
1:A:196:TYR:O	1:A:196:TYR:CD1	0.53	2.62	6	4
1:A:106:ILE:HD13	1:A:171:LEU:HG	0.53	1.80	1	1
1:A:66:LEU:HD13	1:A:67:HIS:H	0.53	1.64	5	1
1:A:183:GLU:HB3	1:A:195:THR:HG21	0.53	1.79	3	2
1:A:12:TRP:CZ2	1:A:216:PHE:CZ	0.53	2.97	2	2
1:A:170:ASP:O	1:A:174:ILE:HG22	0.53	2.04	5	1
1:A:162:VAL:HG11	1:A:166:GLN:CD	0.52	2.24	7	1
1:A:63:PRO:CB	1:A:66:LEU:HD11	0.52	2.35	2	1
1:A:100:LEU:HD13	1:A:116:VAL:HG11	0.52	1.81	10	2
1:A:154:VAL:O	1:A:156:LEU:HD12	0.52	2.04	9	1
1:A:14:LEU:HD12	1:A:14:LEU:O	0.52	2.05	5	1
1:A:174:ILE:CG2	1:A:175:LEU:HD23	0.52	2.33	2	1
1:A:196:TYR:CD1	1:A:196:TYR:O	0.52	2.63	3	4
1:A:84:TYR:CZ	1:A:90:VAL:HG11	0.52	2.39	6	4
1:A:193:THR:O	1:A:205:ALA:HB3	0.52	2.03	3	2
1:A:26:THR:HG21	1:A:156:LEU:CD2	0.51	2.35	2	1
1:A:118:LEU:HD21	1:A:137:PRO:HG2	0.51	1.79	2	2
1:A:104:ALA:HB1	1:A:204:LEU:O	0.51	2.05	3	2
1:A:68:CYS:HB2	1:A:154:VAL:HG22	0.51	1.80	1	1
1:A:84:TYR:O	1:A:90:VAL:HG21	0.51	2.05	7	3
1:A:115:ARG:HD2	1:A:175:LEU:HD11	0.51	1.83	2	1
1:A:94:LEU:HD21	1:A:218:SER:CB	0.51	2.36	1	2
1:A:139:LEU:C	1:A:143:VAL:HG13	0.51	2.26	10	1
1:A:22:ILE:HD13	1:A:22:ILE:C	0.51	2.27	7	1
1:A:182:LYS:CB	1:A:197:LEU:HD23	0.51	2.36	10	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:193:THR:O	1:A:204:LEU:HD12	0.51	2.06	6	2
1:A:12:TRP:CZ3	1:A:216:PHE:CZ	0.50	2.99	3	1
1:A:107:VAL:HG13	1:A:112:PHE:CD2	0.50	2.42	3	2
1:A:196:TYR:CD2	1:A:202:TRP:CE2	0.50	3.00	1	1
1:A:33:LEU:HD21	1:A:39:PHE:CE2	0.50	2.42	5	1
1:A:115:ARG:CD	1:A:175:LEU:HD11	0.50	2.37	2	1
1:A:100:LEU:HD13	1:A:116:VAL:HG13	0.50	1.83	1	1
1:A:115:ARG:CG	1:A:171:LEU:HD21	0.49	2.37	1	1
1:A:106:ILE:HD13	1:A:106:ILE:C	0.49	2.28	3	1
1:A:108:THR:HG22	1:A:109:PRO:HD2	0.49	1.84	10	1
1:A:183:GLU:CB	1:A:195:THR:HG21	0.49	2.37	3	1
1:A:29:PHE:CE2	1:A:204:LEU:HD22	0.49	2.43	4	1
1:A:100:LEU:HD23	1:A:214:THR:HG21	0.49	1.85	1	1
1:A:66:LEU:N	1:A:66:LEU:HD12	0.49	2.23	6	1
1:A:26:THR:HG21	1:A:156:LEU:HD21	0.49	1.83	2	1
1:A:10:PHE:CZ	1:A:216:PHE:CD1	0.49	3.01	1	1
1:A:174:ILE:HA	1:A:197:LEU:HD11	0.49	1.83	1	1
1:A:79:GLU:O	1:A:81:ALA:N	0.49	2.46	8	1
1:A:143:VAL:HG21	1:A:148:ALA:CB	0.48	2.38	5	2
1:A:114:ALA:HB3	1:A:154:VAL:CG1	0.48	2.38	8	2
1:A:142:SER:O	1:A:146:LEU:HD23	0.48	2.08	1	1
1:A:118:LEU:HD13	1:A:122:GLN:HG2	0.48	1.84	4	1
1:A:126:TRP:CE3	1:A:151:ARG:NH2	0.48	2.81	1	1
1:A:66:LEU:HD13	1:A:67:HIS:N	0.48	2.22	5	1
1:A:143:VAL:O	1:A:146:LEU:O	0.48	2.31	2	6
1:A:9:PHE:HE2	1:A:69:THR:HG22	0.48	1.68	7	1
1:A:118:LEU:HD11	1:A:137:PRO:HB3	0.48	1.85	8	2
1:A:18:GLU:CD	1:A:212:ALA:HB1	0.48	2.29	9	1
1:A:123:VAL:HG22	1:A:137:PRO:CB	0.48	2.38	1	1
1:A:29:PHE:CE1	1:A:107:VAL:HG21	0.48	2.44	10	2
1:A:135:VAL:CG1	1:A:143:VAL:HG23	0.48	2.39	5	1
1:A:9:PHE:CE1	1:A:69:THR:HG21	0.48	2.44	3	1
1:A:188:GLU:HG3	1:A:193:THR:HG22	0.48	1.85	1	1
1:A:203:PHE:CD1	1:A:203:PHE:N	0.48	2.81	8	2
1:A:197:LEU:N	1:A:197:LEU:HD12	0.48	2.23	4	1
1:A:155:THR:CG2	1:A:164:THR:HG23	0.48	2.38	6	1
1:A:136:ALA:HB3	1:A:139:LEU:CD1	0.48	2.35	3	2
1:A:14:LEU:CD2	1:A:100:LEU:HD21	0.48	2.39	6	1
1:A:71:LYS:CE	1:A:81:ALA:HB1	0.47	2.38	1	1
1:A:33:LEU:HA	1:A:36:LEU:HD12	0.47	1.86	2	2
1:A:133:GLU:CD	1:A:172:LEU:HD11	0.47	2.29	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:170:ASP:OD1	1:A:174:ILE:HD11	0.47	2.09	9	1
1:A:143:VAL:HG23	1:A:146:LEU:CD1	0.47	2.37	4	1
1:A:135:VAL:HG13	1:A:143:VAL:HG23	0.47	1.85	5	2
1:A:84:TYR:CE2	1:A:90:VAL:CG1	0.47	2.97	7	8
1:A:115:ARG:CD	1:A:171:LEU:HD21	0.47	2.39	1	1
1:A:29:PHE:CE1	1:A:204:LEU:HD13	0.47	2.44	3	1
1:A:125:LEU:C	1:A:125:LEU:HD12	0.47	2.30	1	1
1:A:29:PHE:CE1	1:A:194:LEU:HD21	0.47	2.44	8	1
1:A:206:LEU:HD22	1:A:208:GLU:O	0.47	2.09	9	1
1:A:94:LEU:HA	1:A:216:PHE:HB3	0.47	1.86	4	9
1:A:115:ARG:NH2	1:A:203:PHE:CD2	0.47	2.82	3	1
1:A:140:LEU:HG	1:A:141:PRO:CD	0.47	2.39	7	1
1:A:146:LEU:HD22	1:A:146:LEU:H	0.47	1.68	5	1
1:A:29:PHE:O	1:A:32:THR:HG22	0.47	2.10	7	1
1:A:9:PHE:CE2	1:A:69:THR:HG22	0.46	2.45	7	1
1:A:102:VAL:HG12	1:A:210:ILE:HB	0.46	1.86	5	3
1:A:12:TRP:HE1	1:A:70:THR:HG23	0.46	1.71	8	1
1:A:100:LEU:HB2	1:A:116:VAL:HG13	0.46	1.87	4	1
1:A:10:PHE:CE2	1:A:216:PHE:CE1	0.46	3.03	1	1
1:A:182:LYS:HB2	1:A:197:LEU:HD23	0.46	1.87	10	1
1:A:106:ILE:HG23	1:A:115:ARG:HD2	0.46	1.86	6	1
1:A:115:ARG:HD2	1:A:171:LEU:HD21	0.46	1.88	1	1
1:A:143:VAL:HB	1:A:148:ALA:HB2	0.46	1.87	10	1
1:A:84:TYR:CZ	1:A:90:VAL:CG1	0.46	2.99	9	4
1:A:89:VAL:HG13	1:A:90:VAL:N	0.46	2.26	6	8
1:A:33:LEU:HD11	1:A:39:PHE:CD2	0.46	2.46	7	1
1:A:172:LEU:HA	1:A:175:LEU:HD21	0.46	1.87	6	1
1:A:106:ILE:HD13	1:A:174:ILE:HD13	0.46	1.88	8	1
1:A:118:LEU:HD22	1:A:122:GLN:HG2	0.46	1.87	4	1
1:A:33:LEU:CD2	1:A:39:PHE:CE2	0.46	2.99	10	1
1:A:173:GLU:O	1:A:177:LEU:HD12	0.45	2.11	7	1
1:A:111:THR:HG23	1:A:162:VAL:HG21	0.45	1.88	5	1
1:A:163:GLU:HB3	1:A:165:VAL:HG12	0.45	1.88	3	2
1:A:100:LEU:HD12	1:A:100:LEU:C	0.45	2.30	1	1
1:A:13:PHE:CE1	1:A:217:THR:HG21	0.45	2.47	2	1
1:A:112:PHE:CD1	1:A:113:GLY:N	0.45	2.85	3	2
1:A:133:GLU:HG2	1:A:172:LEU:HD21	0.45	1.88	3	2
1:A:33:LEU:CD2	1:A:39:PHE:CE1	0.45	3.00	6	1
1:A:196:TYR:C	1:A:196:TYR:CD1	0.45	2.90	1	3
1:A:100:LEU:HD22	1:A:214:THR:CG2	0.45	2.42	6	1
1:A:12:TRP:CE2	1:A:100:LEU:HD13	0.45	2.47	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:106:ILE:HG21	1:A:171:LEU:CD1	0.45	2.40	5	1
1:A:112:PHE:CE2	1:A:156:LEU:HD22	0.45	2.47	2	1
1:A:197:LEU:HD12	1:A:197:LEU:N	0.45	2.27	3	1
1:A:9:PHE:CE1	1:A:69:THR:CG2	0.44	3.00	3	2
1:A:115:ARG:HG3	1:A:171:LEU:HD11	0.44	1.88	8	2
1:A:98:TYR:O	1:A:214:THR:HG22	0.44	2.13	4	1
1:A:33:LEU:CD1	1:A:39:PHE:CD1	0.44	3.00	3	1
1:A:123:VAL:HG13	1:A:138:ALA:HA	0.44	1.89	10	1
1:A:118:LEU:HD13	1:A:123:VAL:N	0.44	2.27	6	1
1:A:197:LEU:HD22	1:A:201:ARG:HG3	0.44	1.89	5	1
1:A:106:ILE:HG22	1:A:113:GLY:O	0.44	2.12	4	1
1:A:130:ALA:HB1	1:A:151:ARG:HE	0.44	1.72	10	2
1:A:15:LEU:HD22	1:A:213:ASP:HB3	0.44	1.88	8	1
1:A:171:LEU:O	1:A:174:ILE:HG22	0.44	2.11	6	1
1:A:70:THR:HG22	1:A:71:LYS:CE	0.44	2.43	6	1
1:A:29:PHE:CE2	1:A:105:LEU:CB	0.44	2.99	7	1
1:A:100:LEU:HD12	1:A:214:THR:CG2	0.44	2.42	7	1
1:A:10:PHE:HZ	1:A:94:LEU:HD11	0.44	1.73	7	1
1:A:14:LEU:C	1:A:14:LEU:HD12	0.44	2.33	5	1
1:A:185:THR:HB	1:A:196:TYR:CD1	0.44	2.47	3	6
1:A:91:LYS:HA	1:A:94:LEU:HD12	0.44	1.87	8	1
1:A:105:LEU:HD22	1:A:114:ALA:CB	0.44	2.43	6	1
1:A:12:TRP:CZ2	1:A:100:LEU:HD13	0.44	2.47	8	1
1:A:182:LYS:HG2	1:A:197:LEU:HD21	0.44	1.88	8	1
1:A:33:LEU:CD2	1:A:39:PHE:CD1	0.44	3.01	6	1
1:A:194:LEU:HD12	1:A:204:LEU:HB2	0.44	1.90	6	1
1:A:174:ILE:HG23	1:A:175:LEU:N	0.44	2.28	5	1
1:A:206:LEU:HD13	1:A:210:ILE:HD11	0.44	1.88	2	1
1:A:33:LEU:CD1	1:A:39:PHE:CD2	0.44	3.00	7	1
1:A:203:PHE:N	1:A:203:PHE:CD1	0.44	2.85	7	1
1:A:116:VAL:CG2	1:A:154:VAL:HG23	0.44	2.43	9	1
1:A:93:SER:O	1:A:96:LYS:HB2	0.44	2.13	8	1
1:A:123:VAL:HG21	1:A:138:ALA:HA	0.43	1.89	4	1
1:A:13:PHE:CD2	1:A:217:THR:HG21	0.43	2.48	4	1
1:A:196:TYR:CD1	1:A:196:TYR:C	0.43	2.90	2	5
1:A:12:TRP:O	1:A:12:TRP:CD1	0.43	2.71	7	2
1:A:153:HIS:CE1	1:A:167:THR:CG2	0.43	3.00	10	1
1:A:170:ASP:O	1:A:174:ILE:HD12	0.43	2.12	4	1
1:A:12:TRP:NE1	1:A:100:LEU:HD11	0.43	2.28	3	1
1:A:142:SER:O	1:A:146:LEU:HD22	0.43	2.13	5	1
1:A:12:TRP:CH2	1:A:118:LEU:HD22	0.43	2.48	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:140:LEU:CA	1:A:143:VAL:HG12	0.43	2.43	9	2
1:A:74:ASP:O	1:A:76:GLY:N	0.43	2.51	4	1
1:A:63:PRO:O	1:A:64:LEU:CB	0.43	2.66	8	1
1:A:146:LEU:HB3	1:A:179:LYS:HB2	0.43	1.88	9	1
1:A:36:LEU:HD13	1:A:194:LEU:CD1	0.43	2.43	9	1
1:A:13:PHE:CD1	1:A:217:THR:CG2	0.43	2.98	2	1
1:A:118:LEU:HD22	1:A:122:GLN:NE2	0.43	2.28	1	1
1:A:12:TRP:CZ3	1:A:70:THR:CG2	0.43	2.99	10	1
1:A:193:THR:C	1:A:204:LEU:HD12	0.43	2.34	6	1
1:A:71:LYS:HD2	1:A:81:ALA:HB1	0.43	1.89	2	1
1:A:66:LEU:HD12	1:A:154:VAL:HG21	0.43	1.90	3	1
1:A:123:VAL:HG12	1:A:137:PRO:CB	0.43	2.41	8	1
1:A:63:PRO:O	1:A:64:LEU:HD23	0.43	2.14	7	1
1:A:12:TRP:CE3	1:A:216:PHE:CZ	0.43	3.06	3	1
1:A:140:LEU:C	1:A:140:LEU:HD13	0.43	2.34	8	1
1:A:126:TRP:CE3	1:A:151:ARG:CZ	0.43	3.01	1	1
1:A:12:TRP:CE2	1:A:216:PHE:CZ	0.43	3.07	2	1
1:A:197:LEU:HD12	1:A:201:ARG:O	0.43	2.14	2	1
1:A:130:ALA:HB1	1:A:151:ARG:NE	0.42	2.29	7	1
1:A:135:VAL:CG1	1:A:143:VAL:CG2	0.42	2.94	9	1
1:A:195:THR:O	1:A:203:PHE:CD1	0.42	2.72	9	1
1:A:140:LEU:HA	1:A:143:VAL:CG1	0.42	2.44	9	2
1:A:9:PHE:CE1	1:A:72:PHE:CZ	0.42	3.07	1	1
1:A:163:GLU:OE1	1:A:165:VAL:HG23	0.42	2.14	7	1
1:A:130:ALA:HB1	1:A:151:ARG:HH21	0.42	1.74	9	1
1:A:29:PHE:HE2	1:A:204:LEU:HD13	0.42	1.74	5	1
1:A:170:ASP:C	1:A:174:ILE:HD12	0.42	2.35	4	1
1:A:182:LYS:O	1:A:197:LEU:HD22	0.42	2.15	9	1
1:A:133:GLU:CD	1:A:172:LEU:HD21	0.42	2.34	9	1
1:A:174:ILE:CG2	1:A:175:LEU:N	0.42	2.81	2	1
1:A:70:THR:HG21	1:A:216:PHE:HE1	0.42	1.73	2	1
1:A:29:PHE:CE1	1:A:107:VAL:CG2	0.42	3.03	7	1
1:A:12:TRP:CE3	1:A:70:THR:OG1	0.42	2.72	7	2
1:A:150:SER:CA	1:A:171:LEU:HD22	0.42	2.40	1	1
1:A:154:VAL:HG13	1:A:154:VAL:O	0.42	2.14	7	1
1:A:177:LEU:CG	1:A:197:LEU:HD13	0.42	2.39	1	1
1:A:33:LEU:HD21	1:A:39:PHE:CE1	0.42	2.50	3	1
1:A:91:LYS:HG3	1:A:92:GLU:N	0.42	2.30	10	1
1:A:200:GLY:O	1:A:202:TRP:CD1	0.42	2.73	10	1
1:A:150:SER:HA	1:A:171:LEU:HD23	0.42	1.91	6	1
1:A:106:ILE:HD11	1:A:171:LEU:CD2	0.42	2.45	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:29:PHE:CE2	1:A:204:LEU:HD13	0.42	2.50	5	1
1:A:26:THR:HG22	1:A:105:LEU:HD21	0.42	1.90	5	1
1:A:159:SER:HB2	1:A:162:VAL:HG21	0.42	1.90	4	1
1:A:153:HIS:CB	1:A:171:LEU:HD13	0.42	2.45	1	1
1:A:107:VAL:CG2	1:A:112:PHE:CE2	0.42	2.99	7	1
1:A:98:TYR:HE2	1:A:100:LEU:HD11	0.42	1.74	7	1
1:A:153:HIS:CE1	1:A:168:GLY:CA	0.42	3.03	1	1
1:A:10:PHE:CE2	1:A:216:PHE:CD1	0.42	3.08	1	1
1:A:185:THR:OG1	1:A:196:TYR:HB2	0.41	2.14	4	1
1:A:79:GLU:O	1:A:130:ALA:N	0.41	2.53	8	1
1:A:10:PHE:CE1	1:A:94:LEU:HD21	0.41	2.50	8	1
1:A:174:ILE:HD12	1:A:197:LEU:HD21	0.41	1.92	3	1
1:A:36:LEU:CD1	1:A:194:LEU:HD22	0.41	2.40	10	1
1:A:72:PHE:O	1:A:72:PHE:CD2	0.41	2.73	3	1
1:A:104:ALA:CB	1:A:115:ARG:NH1	0.41	2.84	8	1
1:A:12:TRP:CH2	1:A:118:LEU:HD11	0.41	2.49	9	1
1:A:12:TRP:NE1	1:A:100:LEU:CD1	0.41	2.83	5	2
1:A:133:GLU:O	1:A:134:GLY:C	0.41	2.58	8	1
1:A:64:LEU:C	1:A:64:LEU:HD12	0.41	2.35	8	1
1:A:146:LEU:HD12	1:A:179:LYS:HB3	0.41	1.90	5	1
1:A:133:GLU:CG	1:A:172:LEU:CD2	0.41	2.99	3	1
1:A:91:LYS:O	1:A:94:LEU:HD13	0.41	2.15	10	2
1:A:26:THR:HG21	1:A:156:LEU:HD22	0.41	1.90	9	1
1:A:94:LEU:HA	1:A:216:PHE:O	0.41	2.16	4	1
1:A:7:PRO:O	1:A:8:LEU:HD23	0.41	2.16	3	1
1:A:197:LEU:N	1:A:197:LEU:CD1	0.41	2.84	5	2
1:A:177:LEU:HD22	1:A:182:LYS:HE3	0.41	1.92	7	1
1:A:30:LEU:HD21	1:A:112:PHE:HE2	0.41	1.72	4	1
1:A:74:ASP:O	1:A:75:TYR:CD2	0.41	2.73	4	1
1:A:185:THR:CG2	1:A:196:TYR:CD1	0.41	3.04	3	2
1:A:115:ARG:NH1	1:A:175:LEU:HD22	0.41	2.30	1	1
1:A:126:TRP:CZ2	1:A:130:ALA:CB	0.41	3.04	1	1
1:A:72:PHE:O	1:A:72:PHE:CD1	0.41	2.75	4	2
1:A:150:SER:O	1:A:153:HIS:CE1	0.41	2.74	3	1
1:A:112:PHE:CD1	1:A:156:LEU:CD1	0.41	2.99	8	1
1:A:114:ALA:HB3	1:A:154:VAL:HG12	0.41	1.92	8	1
1:A:153:HIS:CG	1:A:171:LEU:CD2	0.41	3.03	6	1
1:A:123:VAL:HG23	1:A:137:PRO:HB2	0.41	1.93	6	1
1:A:113:GLY:CA	1:A:156:LEU:HD12	0.41	2.46	5	1
1:A:12:TRP:CD1	1:A:100:LEU:HD11	0.40	2.52	3	1
1:A:195:THR:O	1:A:203:PHE:CE1	0.40	2.74	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:192:GLY:HA3	1:A:205:ALA:O	0.40	2.16	10	1
1:A:29:PHE:CD1	1:A:29:PHE:C	0.40	2.94	7	1
1:A:12:TRP:CE3	1:A:98:TYR:OH	0.40	2.74	7	1
1:A:146:LEU:N	1:A:146:LEU:CD2	0.40	2.83	5	1
1:A:146:LEU:N	1:A:146:LEU:HD13	0.40	2.31	5	1
1:A:147:PRO:CB	1:A:175:LEU:HD22	0.40	2.46	4	1
1:A:120:GLU:O	1:A:123:VAL:HG12	0.40	2.16	4	1
1:A:178:GLN:OE1	1:A:203:PHE:CG	0.40	2.74	4	1
1:A:174:ILE:HD12	1:A:197:LEU:CD2	0.40	2.46	3	1
1:A:182:LYS:O	1:A:197:LEU:HG	0.40	2.17	3	1
1:A:9:PHE:CE1	1:A:10:PHE:O	0.40	2.74	9	1
1:A:74:ASP:OD1	1:A:75:TYR:CE2	0.40	2.75	4	1
1:A:146:LEU:HB3	1:A:179:LYS:CB	0.40	2.47	4	1
1:A:84:TYR:CD1	1:A:84:TYR:C	0.40	2.95	3	2
1:A:140:LEU:HA	1:A:143:VAL:HG12	0.40	1.92	4	1
1:A:170:ASP:OD2	1:A:174:ILE:HD11	0.40	2.16	4	1
1:A:81:ALA:N	1:A:127:PRO:CB	0.40	2.85	8	1
1:A:70:THR:CG2	1:A:71:LYS:NZ	0.40	2.84	6	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	193/222 (87%)	175±4 (91±2%)	13±3 (7±2%)	5±2 (3±1%)	11	47
All	All	1930/2220 (87%)	1749 (91%)	130 (7%)	51 (3%)	11	47

All 16 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	80	GLY	10
1	A	75	TYR	8
1	A	74	ASP	6
1	A	201	ARG	5

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Mol	Chain	Res	Type	Models (Total)
1	A	118	LEU	4
1	A	200	GLY	3
1	A	64	LEU	3
1	A	110	ARG	3
1	A	65	GLN	2
1	A	206	LEU	1
1	A	63	PRO	1
1	A	147	PRO	1
1	A	76	GLY	1
1	A	161	GLY	1
1	A	182	LYS	1
1	A	132	LYS	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	160/186 (86%)	119±4 (75±3%)	41±4 (25±3%)	3	25
All	All	1600/1860 (86%)	1194 (75%)	406 (25%)	3	25

All 111 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	216	PHE	10
1	A	185	THR	10
1	A	196	TYR	9
1	A	10	PHE	9
1	A	71	LYS	8
1	A	108	THR	8
1	A	178	GLN	8
1	A	155	THR	7
1	A	182	LYS	7
1	A	97	SER	7
1	A	183	GLU	6
1	A	189	MET	6
1	A	31	LYS	6

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Mol	Chain	Res	Type	Models (Total)
1	A	64	LEU	6
1	A	124	LYS	6
1	A	171	LEU	6
1	A	119	THR	6
1	A	77	LYS	6
1	A	179	LYS	6
1	A	219	PHE	6
1	A	110	ARG	6
1	A	61	GLN	5
1	A	142	SER	5
1	A	82	LYS	5
1	A	140	LEU	5
1	A	92	GLU	5
1	A	103	THR	5
1	A	23	LYS	5
1	A	66	LEU	5
1	A	26	THR	5
1	A	67	HIS	5
1	A	101	SER	5
1	A	40	LYS	5
1	A	21	ARG	5
1	A	146	LEU	4
1	A	207	ARG	4
1	A	215	THR	4
1	A	111	THR	4
1	A	65	GLN	4
1	A	86	GLU	4
1	A	91	LYS	4
1	A	88	GLN	4
1	A	194	LEU	4
1	A	180	GLU	4
1	A	9	PHE	4
1	A	144	GLU	4
1	A	73	CYS	4
1	A	8	LEU	4
1	A	198	SER	4
1	A	208	GLU	4
1	A	166	GLN	4
1	A	83	GLU	4
1	A	70	THR	4
1	A	12	TRP	4
1	A	188	GLU	3

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Mol	Chain	Res	Type	Models (Total)
1	A	95	THR	3
1	A	93	SER	3
1	A	14	LEU	3
1	A	96	LYS	3
1	A	156	LEU	3
1	A	28	ASP	3
1	A	186	GLN	3
1	A	151	ARG	3
1	A	100	LEU	3
1	A	199	GLU	3
1	A	190	ASP	3
1	A	143	VAL	3
1	A	150	SER	3
1	A	94	LEU	3
1	A	195	THR	3
1	A	206	LEU	3
1	A	69	THR	3
1	A	118	LEU	3
1	A	201	ARG	2
1	A	27	MET	2
1	A	87	LEU	2
1	A	173	GLU	2
1	A	159	SER	2
1	A	35	THR	2
1	A	164	THR	2
1	A	163	GLU	2
1	A	131	ASP	2
1	A	37	GLU	2
1	A	197	LEU	2
1	A	30	LEU	2
1	A	122	GLN	2
1	A	20	GLU	2
1	A	133	GLU	2
1	A	125	LEU	2
1	A	128	GLU	2
1	A	106	ILE	1
1	A	36	LEU	1
1	A	218	SER	1
1	A	105	LEU	1
1	A	115	ARG	1
1	A	204	LEU	1
1	A	158	CYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	177	LEU	1
1	A	170	ASP	1
1	A	15	LEU	1
1	A	172	LEU	1
1	A	203	PHE	1
1	A	75	TYR	1
1	A	17	GLU	1
1	A	139	LEU	1
1	A	193	THR	1
1	A	132	LYS	1
1	A	22	ILE	1
1	A	213	ASP	1
1	A	174	ILE	1
1	A	19	GLU	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 68% for the well-defined parts and 67% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 7167

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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

Total number of shifts	1932
Number of shifts mapped to atoms	1932
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	220	-0.19 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	205	0.24 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	208	-0.74 ± 0.12	Should be applied
^{15}N	209	0.15 ± 0.34	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 68%, i.e. 1562 atoms were assigned a chemical shift out of a possible 2306. 0 out of 40 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	935/947 (99%)	375/377 (99%)	377/386 (98%)	183/184 (99%)
Sidechain	621/1187 (52%)	442/689 (64%)	179/459 (39%)	0/39 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	6/172 (3%)	3/92 (3%)	0/75 (0%)	3/5 (60%)
Overall	1562/2306 (68%)	820/1158 (71%)	556/920 (60%)	186/228 (82%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 67%, i.e. 1782 atoms were assigned a chemical shift out of a possible 2649. 0 out of 43 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	1061/1092 (97%)	424/435 (97%)	428/444 (96%)	209/213 (98%)
Sidechain	715/1345 (53%)	510/781 (65%)	205/523 (39%)	0/41 (0%)
Aromatic	6/212 (3%)	3/114 (3%)	0/91 (0%)	3/7 (43%)
Overall	1782/2649 (67%)	937/1330 (70%)	633/1058 (60%)	212/261 (81%)

7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

