

Full wwPDB NMR Structure Validation Report (i)

May 28, 2020 – 07:37 pm BST

PDB ID	:	1H3Z
Title	:	Solution structure of a PWWP domain from Schizosaccharomyces Pombe
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Deposited on	:	2002-09-23

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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

$\operatorname{Cyrange}$:	Kirchner and Güntert (2011)
$\operatorname{NmrClust}$:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
${ m ShiftChecker}$:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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	(# Entries)	(# Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=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 <=5%

Mol	Chain	Length		Quality of chain			
1	A	109	23%	60%	10%	6% •	



2 Ensemble composition and analysis (i)

This entry contains 23 models. Model 7 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) Medoi					
1	A:122-A:222 (101)	0.27	7		

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 3 single-model clusters were found.

Cluster number	Models
1	1, 3, 4, 5, 6, 7, 11, 12, 14, 18, 21, 22
2	2, 16, 23
3	8, 15, 19
4	10, 20
Single-model clusters	9; 13; 17



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1731 atoms, of which 877 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called HYPOTHETICAL 62.8 KDA PROTEIN C215.07C.

Mol	Chain	Residues			Aton	ıs			Trace
1	Δ	108	Total	С	Η	Ν	Ο	S	0
	A	108	1731	553	877	139	157	5	0



4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

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

• Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



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





4.2.2 Score per residue for model 2



IL183 IL183 IL183 IL183 IL184 IL184 IL185 IL18 IL18

4.2.3 Score per residue for model 3

• Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



4.2.4 Score per residue for model 4

• Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



4.2.5 Score per residue for model 5

• Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



4.2.6 Score per residue for model 6





4.2.7 Score per residue for model 7 (medoid)

• Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



4.2.8 Score per residue for model 8



- 4.2.9 Score per residue for model 9
- Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C





4.2.10 Score per residue for model 10

• Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



- 4.2.11 Score per residue for model 11
- Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



- 4.2.12 Score per residue for model 12
- Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



4.2.13 Score per residue for model 13



4.2.14 Score per residue for model 14

• Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



- 4.2.15 Score per residue for model 15
- Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



- 4.2.16 Score per residue for model 16
- Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



4.2.17 Score per residue for model 17



4.2.18 Score per residue for model 18



- 4.2.19 Score per residue for model 19
- Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



- 4.2.20 Score per residue for model 20
- Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



- 4.2.21 Score per residue for model 21
- Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



4.2.22 Score per residue for model 22

• Molecule 1: HYPOTHETICAL 62.8 KDA PROTEIN C215.07C



4.2.23 Score per residue for model 23





5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *DISTANCE GEOMETRY SIMULATED ANNEALING*.

Of the 30 calculated structures, 23 were deposited, based on the following criterion: NO VIOLA-TION GREATER THAN 0.25A AND NO VIOLATIONS GREATER THAN 5 DEGREES.

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

Software name	Classification	Version
X-PLOR	refinement	3.8
ANSIG	structure solution	3.3

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



6 Model quality (i)

6.1 Standard geometry (i)

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

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	А	$0.0{\pm}0.0$	2.8 ± 0.4
All	All	0	65

There are no bond-length outliers.

There are no bond-angle outliers.

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	А	154	ARG	Sidechain	23
1	А	128	ARG	Sidechain	22
1	А	160	ARG	Sidechain	20

6.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	А	800	821	821	105 ± 9
All	All	18400	18883	18883	2426

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 65.

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



1]	H3	Ζ
_		-

Atom 1	A 4 5 575 D		Distance(Å)	Mod	dels
Atom-1	Atom-2	Clash(A)		Worst	Total
1:A:149:MET:HE3	1:A:153:ALA:HB1	1.02	1.27	4	10
1:A:215:THR:HG21	1:A:221:LEU:HD13	1.00	1.32	12	23
1:A:131:THR:CG2	1:A:178:THR:HG21	0.96	1.89	12	13
1:A:123:TYR:HB3	1:A:143:VAL:HG21	0.89	1.44	17	21
1:A:215:THR:CG2	1:A:221:LEU:HD13	0.88	1.97	9	19
1:A:131:THR:HG22	1:A:183:LEU:HD21	0.86	1.43	13	11
1:A:131:THR:HG22	1:A:178:THR:HG21	0.86	1.47	18	17
1:A:153:ALA:HB2	1:A:175:TYR:HB2	0.85	1.47	19	15
1:A:149:MET:HE2	1:A:153:ALA:HB1	0.83	1.51	17	4
1:A:202:THR:HG23	1:A:205:LEU:HB3	0.82	1.50	15	23
1:A:178:THR:HG23	1:A:183:LEU:HD11	0.81	1.50	10	21
1:A:186:LEU:HD11	1:A:191:ILE:HG13	0.81	1.52	10	13
1:A:215:THR:HG21	1:A:221:LEU:CD1	0.80	2.05	7	14
1:A:153:ALA:HB2	1:A:175:TYR:CB	0.80	2.07	12	17
1:A:131:THR:HG22	1:A:183:LEU:CD2	0.79	2.08	13	13
1:A:170:PHE:CG	1:A:212:ALA:HB2	0.76	2.14	3	21
1:A:131:THR:CG2	1:A:183:LEU:HD21	0.76	2.10	19	20
1:A:188:SER:HA	1:A:191:ILE:HD12	0.74	1.59	13	12
1:A:149:MET:CE	1:A:153:ALA:HB1	0.74	2.13	8	10
1:A:148:LYS:HD2	1:A:218:LEU:HD11	0.74	1.58	12	4
1:A:131:THR:HG23	1:A:183:LEU:HD21	0.74	1.58	21	8
1:A:191:ILE:HG23	1:A:213:GLN:CG	0.73	2.14	17	1
1:A:168:ILE:HD13	1:A:168:ILE:C	0.72	2.05	19	14
1:A:168:ILE:C	1:A:168:ILE:HD13	0.72	2.05	8	9
1:A:130:LEU:HD22	1:A:138:TRP:C	0.72	2.05	4	21
1:A:178:THR:HG23	1:A:183:LEU:CD1	0.71	2.15	10	20
1:A:170:PHE:CD2	1:A:212:ALA:HB2	0.70	2.21	16	20
1:A:191:ILE:HG23	1:A:213:GLN:HG2	0.70	1.63	17	1
1:A:205:LEU:O	1:A:208:ALA:HB3	0.70	1.85	1	21
1:A:160:ARG:HD3	1:A:164:PHE:CZ	0.70	2.21	8	5
1:A:168:ILE:HD11	1:A:173:LYS:HA	0.69	1.63	8	18
1:A:194:PHE:CD2	1:A:209:TYR:CD2	0.69	2.81	21	11
1:A:194:PHE:CD1	1:A:209:TYR:CG	0.69	2.81	4	10
1:A:194:PHE:CE1	1:A:209:TYR:CD2	0.68	2.81	4	7
1:A:140:PRO:HG2	1:A:208:ALA:HB1	0.68	1.65	12	19
1:A:194:PHE:CD2	1:A:209:TYR:CG	0.68	2.82	8	12
1:A:160:ARG:CD	1:A:164:PHE:CE1	0.67	2.76	20	3
1:A:130:LEU:HG	1:A:186:LEU:HD13	0.67	1.67	8	4
1:A:144:VAL:HG22	1:A:166:PRO:O	0.67	1.88	2	20
1:A:130:LEU:HD13	1:A:138:TRP:CB	0.67	2.19	11	14
1:A:148:LYS:CD	1:A:218:LEU:HD11	0.66	2.20	12	1
1:A:194:PHE:CE1	1:A:205:LEU:HD23	0.66	2.25	10	11



Atom-1	Atom-2	$Clash(\lambda)$	Distance(Å)	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:186:LEU:HD11	1:A:191:ILE:CG1	0.66	2.20	4	5
1:A:131:THR:HG23	1:A:178:THR:HG21	0.66	1.67	4	1
1:A:130:LEU:HD21	1:A:209:TYR:OH	0.65	1.91	18	5
1:A:139:TRP:CD2	1:A:205:LEU:HD12	0.64	2.27	6	19
1:A:194:PHE:CE1	1:A:205:LEU:CD2	0.64	2.81	14	12
1:A:169:PHE:CZ	1:A:176:LEU:HD22	0.64	2.27	9	23
1:A:160:ARG:CG	1:A:164:PHE:CZ	0.64	2.81	18	8
1:A:149:MET:HE3	1:A:153:ALA:CB	0.64	2.20	18	5
1:A:194:PHE:CE2	1:A:209:TYR:HB2	0.63	2.28	17	13
1:A:160:ARG:NE	1:A:164:PHE:CE1	0.63	2.67	20	1
1:A:194:PHE:CE2	1:A:205:LEU:CD2	0.63	2.81	18	10
1:A:160:ARG:CD	1:A:164:PHE:CZ	0.63	2.81	2	8
1:A:170:PHE:CD2	1:A:212:ALA:CB	0.62	2.82	4	16
1:A:130:LEU:HD13	1:A:138:TRP:HB3	0.62	1.69	11	14
1:A:144:VAL:HG11	1:A:168:ILE:HB	0.62	1.71	14	4
1:A:194:PHE:CE1	1:A:209:TYR:HB2	0.62	2.30	15	10
1:A:158:PRO:CD	1:A:177:TRP:CB	0.62	2.77	10	13
1:A:130:LEU:HD23	1:A:139:TRP:C	0.62	2.14	16	21
1:A:150:THR:HG23	1:A:152:VAL:H	0.62	1.55	20	2
1:A:160:ARG:HD3	1:A:164:PHE:CE1	0.61	2.30	8	2
1:A:160:ARG:CG	1:A:164:PHE:CE1	0.61	2.84	20	5
1:A:130:LEU:HD23	1:A:139:TRP:O	0.60	1.96	11	22
1:A:149:MET:CG	1:A:153:ALA:CB	0.60	2.80	15	1
1:A:169:PHE:CE1	1:A:176:LEU:HD22	0.60	2.31	21	22
1:A:215:THR:HG23	1:A:220:SER:HB3	0.60	1.72	10	1
1:A:191:ILE:HG23	1:A:213:GLN:CD	0.60	2.17	17	1
1:A:194:PHE:CD1	1:A:209:TYR:CB	0.60	2.85	16	10
1:A:131:THR:CG2	1:A:183:LEU:CD2	0.59	2.80	2	17
1:A:194:PHE:CE2	1:A:205:LEU:HD23	0.59	2.32	6	6
1:A:204:SER:O	1:A:207:LYS:HG2	0.59	1.97	5	1
1:A:173:LYS:O	1:A:175:TYR:CE1	0.59	2.55	8	1
1:A:170:PHE:O	1:A:208:ALA:HB1	0.59	1.98	19	3
1:A:173:LYS:O	1:A:175:TYR:CE2	0.59	2.55	16	10
1:A:158:PRO:HD3	1:A:177:TRP:CG	0.59	2.33	19	15
1:A:148:LYS:HE3	1:A:218:LEU:HD21	0.58	1.75	7	1
1:A:194:PHE:CD2	1:A:209:TYR:CB	0.58	2.86	14	13
1:A:158:PRO:CD	1:A:177:TRP:CG	0.58	2.86	21	10
1:A:153:ALA:CB	1:A:175:TYR:CB	0.58	2.82	19	19
1:A:129:VAL:HG21	1:A:183:LEU:HD22	0.58	1.76	23	6
1:A:171:PRO:HG3	1:A:207:LYS:CG	0.58	2.29	18	3
1:A:191:ILE:O	1:A:213:GLN:NE2	0.58	2.37	17	1



A / -1	A 4 5 77 0	$Clash(\lambda)$	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)		Worst	Total	
1:A:131:THR:OG1	1:A:169:PHE:CZ	0.57	2.56	14	9	
1:A:173:LYS:CG	1:A:173:LYS:O	0.57	2.52	1	5	
1:A:194:PHE:CZ	1:A:198:PRO:HB3	0.57	2.35	2	21	
1:A:149:MET:CE	1:A:153:ALA:CB	0.57	2.82	8	1	
1:A:194:PHE:CE2	1:A:209:TYR:CD2	0.57	2.91	22	8	
1:A:160:ARG:HG3	1:A:164:PHE:CZ	0.57	2.35	13	12	
1:A:130:LEU:HD22	1:A:138:TRP:HB3	0.57	1.76	9	10	
1:A:170:PHE:O	1:A:208:ALA:CB	0.57	2.53	10	19	
1:A:126:GLY:N	1:A:218:LEU:HD12	0.56	2.15	17	2	
1:A:195:LEU:CD1	1:A:213:GLN:OE1	0.56	2.53	17	1	
1:A:191:ILE:HG22	1:A:213:GLN:CG	0.56	2.31	9	1	
1:A:169:PHE:CE1	1:A:176:LEU:HB3	0.56	2.35	9	23	
1:A:132:LYS:CE	1:A:138:TRP:CZ2	0.56	2.88	22	1	
1:A:131:THR:HG21	1:A:178:THR:HG21	0.56	1.72	12	3	
1:A:133:MET:HE3	1:A:136:PHE:CD2	0.56	2.36	15	2	
1:A:172:ASN:O	1:A:174:GLU:N	0.56	2.39	22	4	
1:A:139:TRP:CH2	1:A:205:LEU:HB2	0.56	2.35	19	23	
1:A:160:ARG:O	1:A:160:ARG:CZ	0.56	2.53	8	2	
1:A:132:LYS:HE2	1:A:138:TRP:CZ2	0.56	2.35	22	1	
1:A:158:PRO:HD3	1:A:177:TRP:CB	0.56	2.31	7	23	
1:A:202:THR:HG23	1:A:205:LEU:CB	0.55	2.30	2	11	
1:A:165:TYR:CD1	1:A:165:TYR:N	0.55	2.68	11	4	
1:A:131:THR:HG23	1:A:183:LEU:CD2	0.55	2.31	12	5	
1:A:157:LYS:HG3	1:A:177:TRP:CZ2	0.55	2.37	12	4	
1:A:162:GLY:O	1:A:164:PHE:CD1	0.55	2.59	19	15	
1:A:165:TYR:N	1:A:165:TYR:CD1	0.55	2.74	2	9	
1:A:171:PRO:CG	1:A:207:LYS:CD	0.55	2.85	5	1	
1:A:194:PHE:CD1	1:A:209:TYR:CD2	0.55	2.95	16	8	
1:A:194:PHE:CE2	1:A:209:TYR:CB	0.55	2.89	17	11	
1:A:194:PHE:CE1	1:A:205:LEU:HD21	0.55	2.37	8	5	
1:A:133:MET:CE	1:A:176:LEU:HD13	0.55	2.32	8	1	
1:A:149:MET:CG	1:A:153:ALA:HB3	0.55	2.32	17	4	
1:A:160:ARG:O	1:A:160:ARG:NE	0.55	2.40	8	2	
1:A:130:LEU:HB2	1:A:184:THR:CG2	0.55	2.32	14	23	
1:A:130:LEU:CB	1:A:184:THR:CG2	0.55	2.85	14	19	
1:A:132:LYS:HG3	1:A:138:TRP:CE2	0.55	2.37	3	15	
1:A:139:TRP:HB3	1:A:169:PHE:CE2	0.54	2.37	23	5	
1:A:194:PHE:CE2	1:A:205:LEU:HD21	0.54	2.36	18	5	
1:A:194:PHE:CZ	1:A:209:TYR:CD2	0.54	2.95	4	4	
1:A:131:THR:HG23	1:A:141:SER:OG	0.54	2.02	17	4	
1:A:160:ARG:CD	1:A:161:ALA:N	0.54	2.70	19	2	



				Mod	lels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:168:ILE:HA	1:A:174:GLU:O	0.54	2.03	1	23
1:A:209:TYR:O	1:A:213:GLN:CB	0.54	2.56	2	8
1:A:186:LEU:HD11	1:A:191:ILE:HG12	0.54	1.80	16	1
1:A:131:THR:CG2	1:A:141:SER:OG	0.54	2.56	17	4
1:A:168:ILE:HG13	1:A:221:LEU:HD21	0.54	1.77	20	5
1:A:126:GLY:HA2	1:A:218:LEU:CB	0.54	2.33	13	16
1:A:194:PHE:CE2	1:A:198:PRO:HA	0.54	2.38	4	10
1:A:128:ARG:CG	1:A:128:ARG:O	0.54	2.56	7	2
1:A:160:ARG:NE	1:A:160:ARG:O	0.54	2.41	20	1
1:A:194:PHE:CG	1:A:209:TYR:CD2	0.54	2.96	13	5
1:A:186:LEU:HD21	1:A:191:ILE:HD11	0.54	1.79	21	3
1:A:173:LYS:O	1:A:173:LYS:CD	0.53	2.56	1	1
1:A:194:PHE:CD2	1:A:198:PRO:HA	0.53	2.38	18	10
1:A:194:PHE:CZ	1:A:205:LEU:HD23	0.53	2.38	18	9
1:A:138:TRP:CZ3	1:A:184:THR:HB	0.53	2.39	20	23
1:A:132:LYS:CD	1:A:138:TRP:CZ2	0.53	2.92	20	4
1:A:128:ARG:N	1:A:142:MET:SD	0.53	2.82	23	10
1:A:160:ARG:HG2	1:A:164:PHE:CZ	0.53	2.39	4	4
1:A:148:LYS:HG2	1:A:218:LEU:HD21	0.53	1.81	16	1
1:A:194:PHE:CE1	1:A:198:PRO:HA	0.53	2.39	17	13
1:A:128:ARG:O	1:A:128:ARG:CG	0.53	2.57	23	3
1:A:132:LYS:HD2	1:A:138:TRP:CZ2	0.52	2.39	23	3
1:A:192:SER:HA	1:A:195:LEU:HD12	0.52	1.81	3	4
1:A:201:LYS:O	1:A:201:LYS:CD	0.52	2.57	9	3
1:A:165:TYR:HB2	1:A:183:LEU:CD1	0.52	2.34	20	3
1:A:172:ASN:N	1:A:172:ASN:OD1	0.52	2.41	2	2
1:A:194:PHE:CD1	1:A:198:PRO:HA	0.52	2.39	10	13
1:A:215:THR:HG23	1:A:220:SER:CB	0.52	2.35	10	1
1:A:217:ASP:OD2	1:A:219:ASP:CB	0.52	2.58	11	1
1:A:160:ARG:HG3	1:A:164:PHE:CE1	0.52	2.39	13	8
1:A:149:MET:O	1:A:154:ARG:NH1	0.52	2.43	6	1
1:A:132:LYS:CE	1:A:133:MET:O	0.52	2.57	13	6
1:A:172:ASN:ND2	1:A:172:ASN:N	0.52	2.57	11	2
1:A:173:LYS:O	1:A:173:LYS:CG	0.52	2.55	15	3
1:A:209:TYR:O	1:A:213:GLN:HG3	0.52	2.05	17	1
1:A:144:VAL:CG2	1:A:149:MET:SD	0.52	2.98	23	9
1:A:133:MET:HB3	1:A:136:PHE:HB2	0.52	1.82	21	23
1:A:195:LEU:HD11	1:A:213:GLN:HG3	0.52	1.81	8	10
1:A:203:ALA:O	1:A:207:LYS:CG	0.52	2.57	12	4
1:A:123:TYR:OH	1:A:184:THR:HA	0.52	2.05	8	18
1:A:168:ILE:CD1	1:A:168:ILE:C	0.52	2.77	16	13



Atom 1	Atom 0	(1 - 1)	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)		Worst	Total	
1:A:171:PRO:CB	1:A:211:MET:SD	0.52	2.98	3	7	
1:A:128:ARG:CA	1:A:142:MET:SD	0.52	2.98	13	8	
1:A:139:TRP:CD1	1:A:140:PRO:HD2	0.51	2.39	8	23	
1:A:194:PHE:CD2	1:A:195:LEU:HD23	0.51	2.40	17	1	
1:A:172:ASN:O	1:A:173:LYS:C	0.51	2.49	22	21	
1:A:138:TRP:CE3	1:A:184:THR:HG22	0.51	2.40	16	5	
1:A:157:LYS:HE3	1:A:177:TRP:CH2	0.51	2.41	7	2	
1:A:128:ARG:CG	1:A:142:MET:SD	0.51	2.99	12	2	
1:A:149:MET:HG2	1:A:153:ALA:CB	0.51	2.36	15	1	
1:A:168:ILE:C	1:A:168:ILE:CD1	0.51	2.79	23	8	
1:A:146:GLU:O	1:A:154:ARG:NH1	0.51	2.44	6	1	
1:A:171:PRO:CG	1:A:207:LYS:CG	0.51	2.88	18	1	
1:A:132:LYS:HB3	1:A:138:TRP:CD2	0.51	2.41	1	8	
1:A:130:LEU:CD2	1:A:139:TRP:C	0.51	2.79	2	14	
1:A:158:PRO:HD2	1:A:177:TRP:CG	0.51	2.41	10	8	
1:A:202:THR:CG2	1:A:205:LEU:CB	0.51	2.88	2	4	
1:A:133:MET:HB3	1:A:136:PHE:CB	0.51	2.36	21	5	
1:A:149:MET:HE2	1:A:153:ALA:CB	0.51	2.31	8	3	
1:A:129:VAL:HG22	1:A:141:SER:O	0.51	2.06	1	7	
1:A:132:LYS:HB3	1:A:138:TRP:CE2	0.51	2.41	16	6	
1:A:160:ARG:HD2	1:A:164:PHE:CZ	0.51	2.41	20	3	
1:A:202:THR:CG2	1:A:205:LEU:HB3	0.50	2.35	16	18	
1:A:171:PRO:HG3	1:A:207:LYS:CD	0.50	2.35	5	1	
1:A:142:MET:HB3	1:A:168:ILE:CG2	0.50	2.36	14	21	
1:A:173:LYS:HD3	1:A:221:LEU:CD2	0.50	2.36	5	1	
1:A:130:LEU:CB	1:A:184:THR:HG22	0.50	2.37	8	9	
1:A:171:PRO:HB3	1:A:211:MET:CB	0.50	2.37	18	2	
1:A:208:ALA:O	1:A:212:ALA:CB	0.50	2.60	12	3	
1:A:194:PHE:CE1	1:A:209:TYR:CB	0.50	2.95	9	9	
1:A:204:SER:HA	1:A:207:LYS:HG2	0.50	1.83	5	1	
1:A:191:ILE:CG2	1:A:213:GLN:HG2	0.50	2.37	17	1	
1:A:158:PRO:HB2	1:A:160:ARG:CD	0.50	2.37	12	4	
1:A:160:ARG:HD2	1:A:164:PHE:CE1	0.50	2.42	8	3	
1:A:138:TRP:CZ3	1:A:182:SER:O	0.49	2.65	1	3	
1:A:209:TYR:O	1:A:213:GLN:HB2	0.49	2.07	1	19	
1:A:139:TRP:CZ2	1:A:205:LEU:HB2	0.49	2.42	18	6	
1:A:166:PRO:HB3	1:A:177:TRP:CH2	0.49	2.42	9	13	
1:A:129:VAL:CG2	1:A:183:LEU:HD22	0.49	2.37	11	4	
1:A:128:ARG:NE	1:A:216:PRO:O	0.49	2.43	19	2	
1:A:205:LEU:O	1:A:208:ALA:CB	0.49	2.60	1	2	
1:A:166:PRO:HB3	1:A:177:TRP:CZ2	0.49	2.43	9	5	



Atom 1	Atom 2	$Clash(\lambda)$	Distanco(Å)	Mod	dels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:205:LEU:O	1:A:208:ALA:N	0.49	2.46	7	12
1:A:149:MET:HG3	1:A:153:ALA:HB3	0.49	1.85	8	2
1:A:195:LEU:HD11	1:A:213:GLN:OE1	0.49	2.07	17	1
1:A:173:LYS:NZ	1:A:222:SER:O	0.49	2.44	4	1
1:A:138:TRP:CE3	1:A:184:THR:CG2	0.49	2.96	16	3
1:A:174:GLU:O	1:A:175:TYR:CD1	0.49	2.66	1	1
1:A:153:ALA:CB	1:A:175:TYR:HB2	0.49	2.35	17	12
1:A:194:PHE:CE1	1:A:206:ILE:HA	0.48	2.43	2	9
1:A:132:LYS:HE2	1:A:133:MET:N	0.48	2.22	18	4
1:A:158:PRO:CD	1:A:177:TRP:HB3	0.48	2.38	18	7
1:A:131:THR:CG2	1:A:178:THR:CG2	0.48	2.80	12	1
1:A:171:PRO:CG	1:A:207:LYS:HG3	0.48	2.38	18	1
1:A:167:VAL:O	1:A:175:TYR:HA	0.48	2.08	8	22
1:A:193:GLN:HG2	1:A:194:PHE:N	0.48	2.24	21	2
1:A:149:MET:HG3	1:A:153:ALA:CB	0.48	2.38	15	3
1:A:149:MET:HB3	1:A:153:ALA:CB	0.48	2.39	23	4
1:A:165:TYR:CE2	1:A:180:SER:HB2	0.48	2.44	17	1
1:A:160:ARG:HG2	1:A:164:PHE:CE1	0.48	2.44	22	3
1:A:158:PRO:HB2	1:A:160:ARG:NE	0.48	2.24	2	2
1:A:150:THR:HG23	1:A:152:VAL:HB	0.48	1.85	8	4
1:A:132:LYS:HE3	1:A:133:MET:N	0.48	2.24	17	2
1:A:139:TRP:CB	1:A:169:PHE:CE2	0.48	2.96	23	1
1:A:153:ALA:HB2	1:A:175:TYR:CD2	0.48	2.43	9	2
1:A:171:PRO:HG3	1:A:207:LYS:HG3	0.48	1.84	18	1
1:A:129:VAL:O	1:A:141:SER:O	0.48	2.32	5	7
1:A:130:LEU:HD11	1:A:209:TYR:OH	0.48	2.08	7	3
1:A:168:ILE:CD1	1:A:173:LYS:HA	0.48	2.38	19	13
1:A:168:ILE:HD13	1:A:168:ILE:O	0.48	2.07	10	3
1:A:174:GLU:C	1:A:175:TYR:CG	0.47	2.87	1	1
1:A:148:LYS:HG3	1:A:218:LEU:HD21	0.47	1.86	9	2
1:A:191:ILE:CG2	1:A:213:GLN:CG	0.47	2.92	9	2
1:A:173:LYS:CD	1:A:222:SER:O	0.47	2.62	21	1
1:A:191:ILE:HG22	1:A:192:SER:N	0.47	2.23	17	1
1:A:170:PHE:CB	1:A:212:ALA:HB2	0.47	2.40	5	3
1:A:158:PRO:O	1:A:160:ARG:NH2	0.47	2.43	8	1
1:A:158:PRO:HB2	1:A:160:ARG:HG3	0.47	1.86	8	2
1:A:129:VAL:CA	1:A:186:LEU:HB3	0.47	2.39	10	4
1:A:133:MET:CE	1:A:136:PHE:CD2	0.47	2.97	15	1
1:A:140:PRO:CG	1:A:208:ALA:HB1	0.47	2.38	1	5
1:A:191:ILE:HG23	1:A:209:TYR:HD1	0.47	1.70	1	1
1:A:149:MET:O	1:A:150:THR:O	0.47	2.33	7	4



A 4 1		(1 - 1)	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)		Worst	Total	
1:A:194:PHE:C	1:A:194:PHE:CD1	0.47	2.88	9	3	
1:A:150:THR:OG1	1:A:151:SER:N	0.47	2.48	14	8	
1:A:142:MET:HE1	1:A:217:ASP:HA	0.47	1.86	3	1	
1:A:192:SER:OG	1:A:213:GLN:NE2	0.47	2.48	22	1	
1:A:173:LYS:HD3	1:A:221:LEU:HD21	0.47	1.85	5	1	
1:A:149:MET:SD	1:A:177:TRP:CZ2	0.47	3.08	19	4	
1:A:140:PRO:HD3	1:A:209:TYR:CE2	0.47	2.45	18	2	
1:A:160:ARG:NE	1:A:164:PHE:CD1	0.47	2.83	20	1	
1:A:173:LYS:O	1:A:174:GLU:O	0.47	2.33	23	1	
1:A:169:PHE:HB2	1:A:174:GLU:CB	0.47	2.40	12	1	
1:A:186:LEU:HD21	1:A:191:ILE:HG12	0.47	1.87	23	1	
1:A:213:GLN:OE1	1:A:213:GLN:O	0.47	2.33	1	3	
1:A:171:PRO:HG3	1:A:207:LYS:CB	0.47	2.39	12	5	
1:A:131:THR:OG1	1:A:141:SER:OG	0.47	2.32	12	3	
1:A:216:PRO:HG2	1:A:220:SER:CB	0.47	2.40	22	2	
1:A:172:ASN:C	1:A:173:LYS:CD	0.47	2.83	23	1	
1:A:176:LEU:HG	1:A:177:TRP:N	0.46	2.26	8	16	
1:A:173:LYS:HE3	1:A:221:LEU:CD2	0.46	2.40	11	2	
1:A:195:LEU:HD11	1:A:213:GLN:HG2	0.46	1.87	1	4	
1:A:142:MET:SD	1:A:218:LEU:N	0.46	2.89	2	1	
1:A:142:MET:CE	1:A:217:ASP:HA	0.46	2.40	3	1	
1:A:126:GLY:O	1:A:142:MET:SD	0.46	2.74	19	6	
1:A:171:PRO:O	1:A:211:MET:SD	0.46	2.74	22	1	
1:A:173:LYS:O	1:A:173:LYS:HG2	0.46	2.10	1	2	
1:A:149:MET:HB3	1:A:153:ALA:HB3	0.46	1.85	14	4	
1:A:157:LYS:CG	1:A:158:PRO:HD2	0.46	2.41	5	2	
1:A:126:GLY:HA2	1:A:218:LEU:HD12	0.46	1.85	6	1	
1:A:125:PRO:HA	1:A:143:VAL:O	0.46	2.11	7	22	
1:A:219:ASP:N	1:A:219:ASP:OD1	0.46	2.46	2	1	
1:A:173:LYS:CD	1:A:221:LEU:CD2	0.46	2.92	5	1	
1:A:146:GLU:OE2	1:A:146:GLU:O	0.46	2.34	11	1	
1:A:165:TYR:CE2	1:A:180:SER:HB3	0.46	2.45	9	1	
1:A:216:PRO:HD2	1:A:220:SER:CB	0.46	2.41	8	6	
1:A:194:PHE:CZ	1:A:206:ILE:HA	0.46	2.46	23	12	
1:A:171:PRO:O	1:A:172:ASN:HB2	0.46	2.11	21	14	
1:A:178:THR:CG2	1:A:183:LEU:HD11	0.46	2.37	19	3	
1:A:217:ASP:OD1	1:A:217:ASP:N	0.46	2.48	14	4	
1:A:194:PHE:CE2	1:A:206:ILE:HA	0.46	2.46	22	7	
1:A:148:LYS:HD2	1:A:218:LEU:CD2	0.46	2.41	6	1	
1:A:139:TRP:CE2	1:A:205:LEU:HD12	0.46	2.46	6	2	
1:A:213:GLN:OE1	1:A:213:GLN:HA	0.46	2.11	23	4	



Atom 1	A tom 2	$Cleah(\lambda)$	Distance (Å)	Mod	dels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:204:SER:O	1:A:207:LYS:CG	0.46	2.64	5	1
1:A:181:ASP:N	1:A:181:ASP:OD1	0.46	2.48	6	1
1:A:173:LYS:O	1:A:175:TYR:CZ	0.46	2.69	23	3
1:A:173:LYS:CE	1:A:222:SER:O	0.46	2.64	20	1
1:A:186:LEU:CD2	1:A:191:ILE:HD11	0.46	2.41	17	1
1:A:195:LEU:HG	1:A:213:GLN:OE1	0.46	2.11	17	1
1:A:168:ILE:O	1:A:168:ILE:HD13	0.45	2.10	20	3
1:A:132:LYS:CE	1:A:133:MET:N	0.45	2.79	17	1
1:A:209:TYR:HB3	1:A:213:GLN:NE2	0.45	2.26	17	1
1:A:197:LYS:O	1:A:197:LYS:CG	0.45	2.64	20	1
1:A:133:MET:SD	1:A:176:LEU:HD13	0.45	2.51	15	1
1:A:146:GLU:HA	1:A:149:MET:CB	0.45	2.41	15	1
1:A:168:ILE:HD12	1:A:170:PHE:CZ	0.45	2.47	1	1
1:A:126:GLY:O	1:A:217:ASP:OD1	0.45	2.34	22	1
1:A:173:LYS:HG2	1:A:175:TYR:OH	0.45	2.11	2	2
1:A:144:VAL:CG2	1:A:166:PRO:O	0.45	2.62	6	4
1:A:168:ILE:CD1	1:A:221:LEU:HD21	0.45	2.41	6	1
1:A:215:THR:CG2	1:A:221:LEU:CD1	0.45	2.89	7	1
1:A:171:PRO:HB2	1:A:211:MET:SD	0.45	2.51	12	2
1:A:213:GLN:CA	1:A:213:GLN:OE1	0.45	2.64	22	2
1:A:149:MET:SD	1:A:166:PRO:HB2	0.45	2.52	21	9
1:A:129:VAL:CG2	1:A:183:LEU:CD2	0.45	2.94	5	2
1:A:173:LYS:HG2	1:A:173:LYS:O	0.45	2.12	17	4
1:A:137:PRO:HG3	1:A:200:PRO:CD	0.45	2.42	18	1
1:A:173:LYS:NZ	1:A:175:TYR:OH	0.45	2.48	2	1
1:A:191:ILE:HG22	1:A:213:GLN:HG3	0.45	1.88	9	3
1:A:211:MET:SD	1:A:211:MET:O	0.45	2.74	14	2
1:A:149:MET:HE3	1:A:166:PRO:CB	0.45	2.42	11	1
1:A:213:GLN:HA	1:A:213:GLN:OE1	0.45	2.11	3	3
1:A:193:GLN:CG	1:A:194:PHE:N	0.45	2.79	21	5
1:A:194:PHE:CZ	1:A:198:PRO:CB	0.45	3.00	2	5
1:A:123:TYR:OH	1:A:184:THR:CA	0.45	2.64	8	2
1:A:160:ARG:CD	1:A:160:ARG:N	0.45	2.80	20	1
1:A:128:ARG:HG3	1:A:186:LEU:O	0.44	2.12	23	6
1:A:168:ILE:HG13	1:A:173:LYS:HG3	0.44	1.89	14	1
1:A:131:THR:OG1	1:A:141:SER:CB	0.44	2.66	4	2
1:A:124:LYS:CG	1:A:127:MET:HG3	0.44	2.42	10	3
1:A:133:MET:SD	1:A:176:LEU:CD1	0.44	3.05	15	2
1:A:173:LYS:HE2	1:A:221:LEU:CD2	0.44	2.43	21	1
1:A:194:PHE:CD1	1:A:194:PHE:C	0.44	2.90	4	3
1:A:131:THR:HB	1:A:169:PHE:CZ	0.44	2.47	4	1



A 4 1	A 4 9	$Clash(\hat{\lambda})$	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)		Worst	Total	
1:A:173:LYS:CD	1:A:221:LEU:HG	0.44	2.42	4	1	
1:A:158:PRO:HB2	1:A:160:ARG:CG	0.44	2.42	8	2	
1:A:195:LEU:CD1	1:A:213:GLN:HG3	0.44	2.43	8	2	
1:A:168:ILE:HD13	1:A:169:PHE:N	0.44	2.27	21	1	
1:A:203:ALA:O	1:A:207:LYS:HG2	0.44	2.13	22	1	
1:A:129:VAL:HG21	1:A:183:LEU:CD2	0.44	2.41	23	1	
1:A:171:PRO:O	1:A:172:ASN:CB	0.44	2.65	11	2	
1:A:194:PHE:O	1:A:197:LYS:C	0.44	2.55	19	10	
1:A:171:PRO:HB3	1:A:211:MET:SD	0.44	2.52	5	3	
1:A:160:ARG:HG3	1:A:161:ALA:N	0.44	2.26	11	1	
1:A:141:SER:HA	1:A:168:ILE:O	0.44	2.12	23	12	
1:A:130:LEU:HD22	1:A:138:TRP:CB	0.44	2.41	4	4	
1:A:140:PRO:HB2	1:A:212:ALA:CB	0.44	2.43	4	1	
1:A:128:ARG:O	1:A:128:ARG:HG3	0.44	2.13	13	3	
1:A:131:THR:HG21	1:A:167:VAL:HG21	0.44	1.88	13	2	
1:A:149:MET:HE1	1:A:177:TRP:CE2	0.44	2.48	1	2	
1:A:141:SER:HB2	1:A:167:VAL:CG2	0.44	2.43	2	1	
1:A:149:MET:HE2	1:A:175:TYR:HB3	0.44	1.89	11	1	
1:A:191:ILE:CG2	1:A:213:GLN:HB2	0.44	2.43	16	5	
1:A:173:LYS:CG	1:A:175:TYR:OH	0.44	2.66	9	1	
1:A:124:LYS:CG	1:A:127:MET:SD	0.44	3.06	17	1	
1:A:126:GLY:O	1:A:217:ASP:CG	0.44	2.56	21	1	
1:A:160:ARG:NE	1:A:164:PHE:CE2	0.43	2.86	6	1	
1:A:173:LYS:HD3	1:A:222:SER:O	0.43	2.12	21	1	
1:A:196:GLU:CG	1:A:197:LYS:N	0.43	2.81	8	5	
1:A:128:ARG:CG	1:A:186:LEU:O	0.43	2.66	15	1	
1:A:142:MET:O	1:A:167:VAL:HA	0.43	2.14	11	3	
1:A:160:ARG:HD2	1:A:161:ALA:N	0.43	2.28	19	1	
1:A:213:GLN:O	1:A:213:GLN:OE1	0.43	2.36	22	1	
1:A:180:SER:HA	1:A:183:LEU:HB2	0.43	1.90	10	1	
1:A:199:LYS:HA	1:A:200:PRO:C	0.43	2.33	2	8	
1:A:144:VAL:HG21	1:A:149:MET:SD	0.43	2.54	23	6	
1:A:168:ILE:CG1	1:A:173:LYS:HG3	0.43	2.43	5	1	
1:A:201:LYS:CD	1:A:201:LYS:O	0.43	2.67	13	1	
1:A:146:GLU:O	1:A:146:GLU:OE1	0.43	2.37	22	1	
1:A:132:LYS:HD2	1:A:138:TRP:CE2	0.43	2.49	1	2	
1:A:123:TYR:CD1	1:A:129:VAL:HG11	0.43	2.49	11	1	
1:A:124:LYS:HG2	1:A:127:MET:SD	0.43	2.53	17	2	
1:A:195:LEU:CG	1:A:213:GLN:OE1	0.43	2.66	17	1	
1:A:165:TYR:HB2	1:A:183:LEU:HD11	0.43	1.89	20	1	
1:A:128:ARG:O	1:A:128:ARG:HG2	0.42	2.14	5	3	



			Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)		Worst	Total	
1:A:168:ILE:HD12	1:A:221:LEU:HD21	0.42	1.91	6	1	
1:A:146:GLU:CG	1:A:154:ARG:HD2	0.42	2.44	8	3	
1:A:201:LYS:O	1:A:201:LYS:HD2	0.42	2.13	9	1	
1:A:126:GLY:CA	1:A:218:LEU:HB2	0.42	2.44	10	1	
1:A:170:PHE:HE1	1:A:221:LEU:HD11	0.42	1.73	17	1	
1:A:129:VAL:HA	1:A:186:LEU:HB3	0.42	1.91	10	1	
1:A:186:LEU:CD1	1:A:191:ILE:HG13	0.42	2.43	12	1	
1:A:139:TRP:CZ2	1:A:205:LEU:CA	0.42	3.02	20	2	
1:A:158:PRO:HG2	1:A:160:ARG:NH2	0.42	2.28	20	1	
1:A:168:ILE:HG13	1:A:221:LEU:CD2	0.42	2.44	1	4	
1:A:171:PRO:HG3	1:A:207:LYS:HB3	0.42	1.92	23	2	
1:A:216:PRO:O	1:A:217:ASP:OD1	0.42	2.38	15	1	
1:A:191:ILE:O	1:A:195:LEU:HG	0.42	2.14	2	4	
1:A:142:MET:SD	1:A:217:ASP:C	0.42	2.98	2	1	
1:A:132:LYS:HD3	1:A:138:TRP:CZ2	0.42	2.49	20	1	
1:A:126:GLY:HA2	1:A:218:LEU:HB2	0.42	1.91	5	2	
1:A:197:LYS:CG	1:A:197:LYS:O	0.42	2.68	9	1	
1:A:144:VAL:CG2	1:A:149:MET:CG	0.42	2.98	18	1	
1:A:195:LEU:CD1	1:A:213:GLN:HG2	0.42	2.45	18	1	
1:A:164:PHE:N	1:A:164:PHE:CD1	0.42	2.86	23	1	
1:A:130:LEU:HD23	1:A:130:LEU:HA	0.42	1.67	15	6	
1:A:172:ASN:O	1:A:173:LYS:HG2	0.42	2.14	22	12	
1:A:149:MET:HA	1:A:175:TYR:CE2	0.42	2.49	8	1	
1:A:124:LYS:HG3	1:A:127:MET:CG	0.42	2.44	17	1	
1:A:213:GLN:OE1	1:A:213:GLN:CA	0.42	2.67	1	1	
1:A:170:PHE:HB3	1:A:208:ALA:O	0.42	2.14	17	1	
1:A:137:PRO:O	1:A:138:TRP:C	0.42	2.58	15	3	
1:A:207:LYS:O	1:A:211:MET:HB2	0.42	2.15	16	3	
1:A:153:ALA:CB	1:A:175:TYR:HB3	0.42	2.43	12	1	
1:A:173:LYS:O	1:A:173:LYS:HG3	0.42	2.14	12	1	
1:A:213:GLN:OE1	1:A:213:GLN:C	0.42	2.58	8	1	
1:A:157:LYS:HA	1:A:177:TRP:CD1	0.42	2.49	13	1	
1:A:198:PRO:O	1:A:199:LYS:HD3	0.42	2.15	23	1	
1:A:130:LEU:HA	1:A:130:LEU:HD23	0.42	1.68	3	3	
1:A:194:PHE:CE1	1:A:209:TYR:CG	0.42	3.07	4	1	
1:A:178:THR:OG1	1:A:182:SER:OG	0.42	2.38	12	1	
1:A:149:MET:HG2	1:A:153:ALA:HB3	0.42	1.90	15	1	
1:A:149:MET:HE1	1:A:166:PRO:CB	0.41	2.45	17	2	
1:A:184:THR:OG1	1:A:185:PRO:HD2	0.41	2.15	13	2	
1:A:126:GLY:C	1:A:142:MET:SD	0.41	2.98	19	1	
1:A:173:LYS:CE	1:A:221:LEU:HG	0.41	2.45	21	1	



Atom 1	A 4 5 55 0	$Cleart(\hat{\lambda})$	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)		Worst	Total	
1:A:133:MET:CE	1:A:169:PHE:CZ	0.41	3.04	8	1	
1:A:194:PHE:CE1	1:A:198:PRO:CB	0.41	3.03	8	1	
1:A:221:LEU:HD12	1:A:221:LEU:HA	0.41	1.76	10	1	
1:A:131:THR:OG1	1:A:141:SER:HB2	0.41	2.15	4	1	
1:A:160:ARG:HD3	1:A:160:ARG:N	0.41	2.30	20	1	
1:A:171:PRO:HB3	1:A:211:MET:HB2	0.41	1.93	23	1	
1:A:158:PRO:CG	1:A:177:TRP:HB3	0.41	2.46	14	1	
1:A:216:PRO:O	1:A:217:ASP:CG	0.41	2.59	5	1	
1:A:130:LEU:HB2	1:A:184:THR:HG23	0.41	1.91	16	2	
1:A:127:MET:O	1:A:142:MET:CG	0.41	2.68	6	1	
1:A:133:MET:HE1	1:A:176:LEU:HD13	0.41	1.91	8	1	
1:A:165:TYR:O	1:A:167:VAL:HG13	0.41	2.15	10	1	
1:A:160:ARG:CD	1:A:160:ARG:H	0.41	2.29	20	1	
1:A:149:MET:HE1	1:A:153:ALA:HB1	0.41	1.92	14	1	
1:A:158:PRO:HD3	1:A:177:TRP:HB2	0.41	1.91	3	2	
1:A:132:LYS:HB3	1:A:138:TRP:CG	0.41	2.51	5	1	
1:A:203:ALA:O	1:A:207:LYS:HG3	0.41	2.16	14	3	
1:A:166:PRO:HB3	1:A:177:TRP:CZ3	0.41	2.51	15	2	
1:A:126:GLY:CA	1:A:218:LEU:HB3	0.41	2.45	13	1	
1:A:155:LYS:HG3	1:A:155:LYS:O	0.41	2.15	15	1	
1:A:152:VAL:O	1:A:155:LYS:HG2	0.41	2.16	17	1	
1:A:128:ARG:HG3	1:A:186:LEU:HD23	0.41	1.92	23	1	
1:A:132:LYS:O	1:A:132:LYS:HG3	0.41	2.16	2	1	
1:A:126:GLY:CA	1:A:218:LEU:HD12	0.41	2.46	6	1	
1:A:146:GLU:OE2	1:A:157:LYS:HD2	0.41	2.16	9	1	
1:A:217:ASP:OD2	1:A:219:ASP:HB2	0.41	2.16	11	1	
1:A:128:ARG:HG3	1:A:142:MET:SD	0.41	2.56	12	2	
1:A:169:PHE:HB2	1:A:174:GLU:HB2	0.41	1.92	16	1	
1:A:158:PRO:HB2	1:A:160:ARG:HD3	0.41	1.91	20	1	
1:A:131:THR:HG1	1:A:141:SER:CB	0.41	2.28	4	1	
1:A:164:PHE:CD1	1:A:164:PHE:N	0.41	2.88	6	2	
1:A:146:GLU:HG3	1:A:154:ARG:CG	0.41	2.46	7	1	
1:A:124:LYS:HG3	1:A:127:MET:HG3	0.41	1.92	17	1	
1:A:150:THR:CG2	1:A:152:VAL:HB	0.40	2.46	3	1	
1:A:214:SER:O	1:A:216:PRO:HD3	0.40	2.16	9	1	
1:A:216:PRO:HG2	1:A:220:SER:HB2	0.40	1.91	22	1	
1:A:173:LYS:HD3	1:A:175:TYR:OH	0.40	2.16	1	1	
1:A:202:THR:O	1:A:206:ILE:HG13	0.40	2.16	2	2	
1:A:217:ASP:C	1:A:217:ASP:OD1	0.40	2.60	16	1	
1:A:127:MET:C	1:A:142:MET:HG3	0.40	2.37	17	1	
1:A:172:ASN:C	1:A:173:LYS:HD2	0.40	2.37	23	1	



Adams 1	Atom-2	Clash(Å)	Distance (Å)	Models	
Atom-1			Distance(A)	Worst	Total
1:A:129:VAL:CG2	1:A:141:SER:O	0.40	2.69	1	1
1:A:203:ALA:HB1	1:A:207:LYS:HE3	0.40	1.91	16	1
1:A:172:ASN:O	1:A:173:LYS:CG	0.40	2.70	23	1
1:A:209:TYR:O	1:A:213:GLN:HB3	0.40	2.17	2	1
1:A:132:LYS:HE3	1:A:136:PHE:O	0.40	2.17	4	1
1:A:169:PHE:CE1	1:A:176:LEU:CB	0.40	3.05	8	1
1:A:203:ALA:O	1:A:207:LYS:HB3	0.40	2.17	8	1
1:A:126:GLY:HA2	1:A:142:MET:SD	0.40	2.56	20	1
1:A:217:ASP:OD1	1:A:217:ASP:C	0.40	2.60	20	1
1:A:131:THR:OG1	1:A:141:SER:HB3	0.40	2.17	21	1
1:A:190:ALA:O	1:A:193:GLN:HG2	0.40	2.16	21	1
1:A:139:TRP:CE3	1:A:205:LEU:HD12	0.40	2.50	6	1
1:A:146:GLU:OE2	1:A:154:ARG:NE	0.40	2.54	19	1
1:A:127:MET:O	1:A:142:MET:HG3	0.40	2.17	14	1

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	А	101/109~(93%)	93 ± 2 ($92\pm2\%$)	$7\pm2~(7\pm2\%)$	$2\pm1 (2\pm1\%)$	14 59	
All	All	2323/2507~(93%)	2129 (92%)	158 (7%)	36 (2%)	14 59	

All 4 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	150	THR	13
1	А	216	PRO	11
1	А	173	LYS	7
1	А	174	GLU	5



6.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles			
1	А	91/98~(93%)	70 ± 4 (76 $\pm4\%$)	$21 \pm 4 (24 \pm 4\%)$		3	27	
All	All	2093/2254~(93%)	1599~(76%)	494 (24%)		3	27	

All 54 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	\mathbf{Res}	Type	Models (Total)
1	А	168	ILE	23
1	А	202	THR	23
1	А	173	LYS	22
1	А	136	PHE	21
1	А	132	LYS	18
1	А	151	SER	18
1	А	155	LYS	18
1	А	199	LYS	15
1	А	188	SER	15
1	А	176	LEU	15
1	А	160	ARG	15
1	А	197	LYS	14
1	А	154	ARG	13
1	А	128	ARG	12
1	А	149	MET	12
1	А	147	SER	12
1	А	174	GLU	12
1	А	182	SER	12
1	А	220	SER	11
1	А	156	SER	10
1	А	181	ASP	9
1	А	211	MET	9
1	А	222	SER	9
1	А	134	SER	9
1	А	214	SER	9
1	А	159	LYS	8
1	А	218	LEU	8
1	А	201	LYS	8
1	А	180	SER	8



Mol	Chain	Res	Type	Models (Total)
1	А	131	THR	7
1	А	192	SER	7
1	А	204	SER	7
1	А	196	GLU	7
1	А	210	LYS	7
1	А	207	LYS	6
1	А	213	GLN	6
1	А	193	GLN	6
1	А	124	LYS	6
1	А	133	MET	6
1	А	141	SER	5
1	А	217	ASP	5
1	А	219	ASP	5
1	А	205	LEU	4
1	А	189	GLU	4
1	А	215	THR	3
1	А	146	GLU	3
1	А	157	LYS	3
1	А	148	LYS	3
1	А	139	TRP	1
1	А	163	THR	1
1	А	191	ILE	1
1	А	142	MET	1
1	А	167	VAL	1
1	А	186	LEU	1

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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 (i)

No chemical shift data were provided

