



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 01:16 AM UTC

PDB ID : 1JSP / pdb_00001jsp
Title : NMR Structure of CBP Bromodomain in complex with p53 peptide
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Deposited on : 2001-08-17

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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
Mogul	:	2022.3.0, CSD as543be (2022)
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

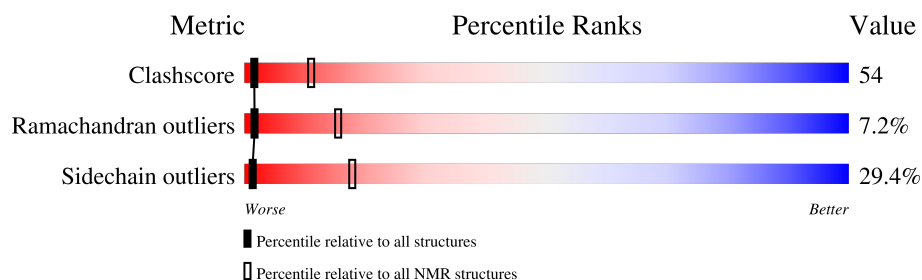
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

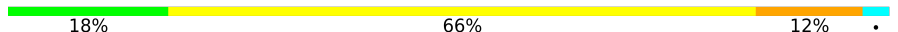
The overall completeness of chemical shifts assignment was not calculated.

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	20	
2	B	121	

2 Ensemble composition and analysis

This entry contains 20 models. Model 3 is the overall representative, medoid model (most similar to other models).

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:383-A:384, B:1081- B:1197 (119)	1.13	3

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 5 clusters and 1 single-model cluster was found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2375 atoms, of which 1192 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called tumor protein p53.

Mol	Chain	Residues	Atoms						Trace
1	A	20	Total	C	H	N	O	S	0
			354	105	186	34	28	1	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	382	ALY	LYS	modified residue	UNP P04637

- Molecule 2 is a protein called CREB-BINDING PROTEIN.

Mol	Chain	Residues	Atoms						Trace
2	B	121	Total	C	H	N	O	S	0
			2021	655	1006	169	185	6	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1077	GLY	-	cloning artifact	UNP Q92793
B	1078	SER	-	cloning artifact	UNP Q92793
B	1079	HIS	-	cloning artifact	UNP Q92793
B	1080	MET	-	cloning artifact	UNP Q92793

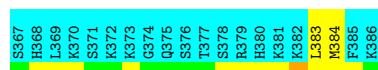
4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

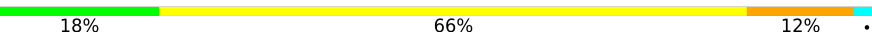
These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for 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.

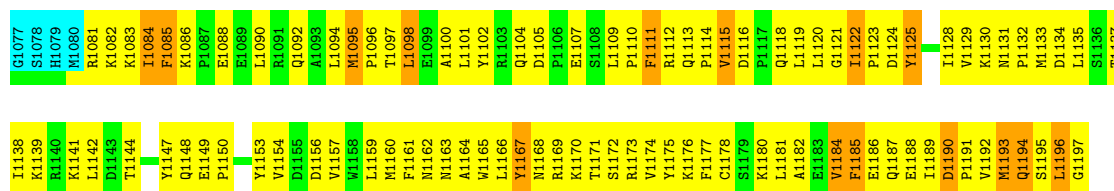
- Molecule 1: tumor protein p53

Chain A:  10% 90%



- Molecule 2: CREB-BINDING PROTEIN

Chain B:  18% 66% 12%



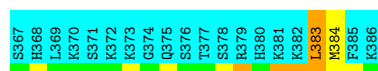
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

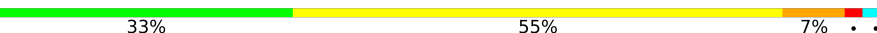
4.2.1 Score per residue for model 1

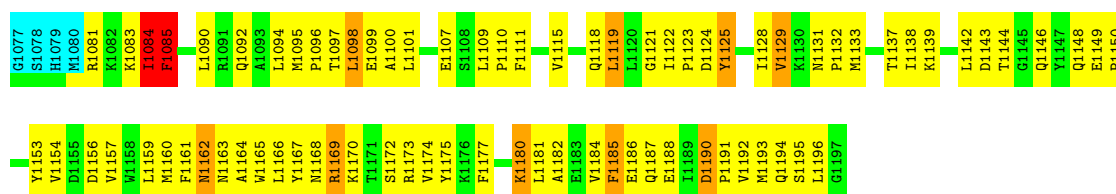
- Molecule 1: tumor protein p53

Chain A:  5% 5% 90%



- Molecule 2: CREB-BINDING PROTEIN

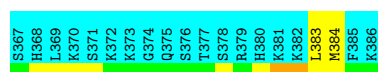
Chain B:  33% 55% 7%



4.2.2 Score per residue for model 2

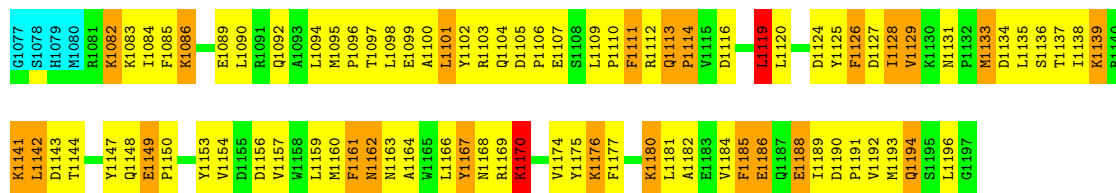
- Molecule 1: tumor protein p53

Chain A: 10% 90%



- Molecule 2: CREB-BINDING PROTEIN

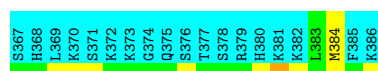
Chain B: 26% 50% 19%



4.2.3 Score per residue for model 3 (medoid)

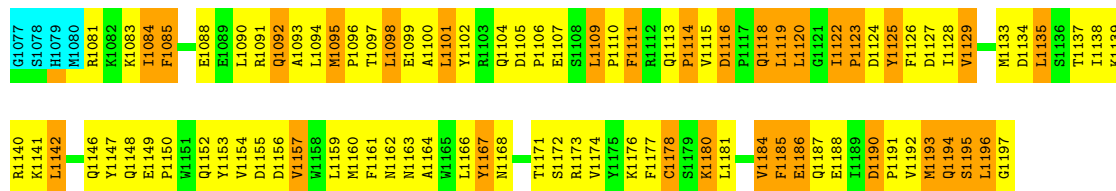
- Molecule 1: tumor protein p53

Chain A: 5% 5% 90%



- Molecule 2: CREB-BINDING PROTEIN

Chain B: 21% 50% 26%



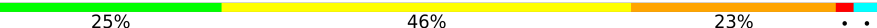
4.2.4 Score per residue for model 4

- Molecule 1: tumor protein p53

Chain A:  90%



- Molecule 2: CREB-BINDING PROTEIN

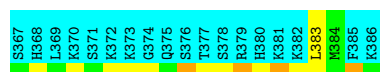
Chain B:  25% 46% 23% . .



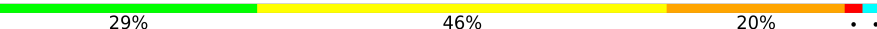
4.2.5 Score per residue for model 5

- Molecule 1: tumor protein p53

Chain A:  90%



- Molecule 2: CREB-BINDING PROTEIN

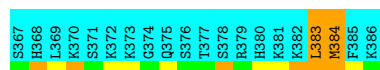
Chain B:  29% 46% 20% . .



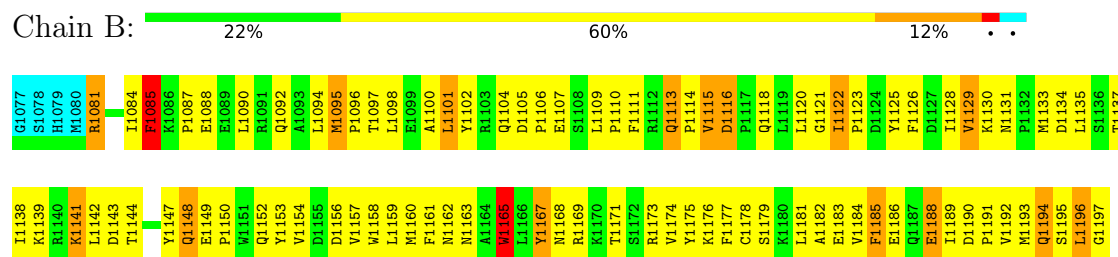
4.2.6 Score per residue for model 6

- Molecule 1: tumor protein p53

Chain A:  10% 90%



- Molecule 2: CREB-BINDING PROTEIN

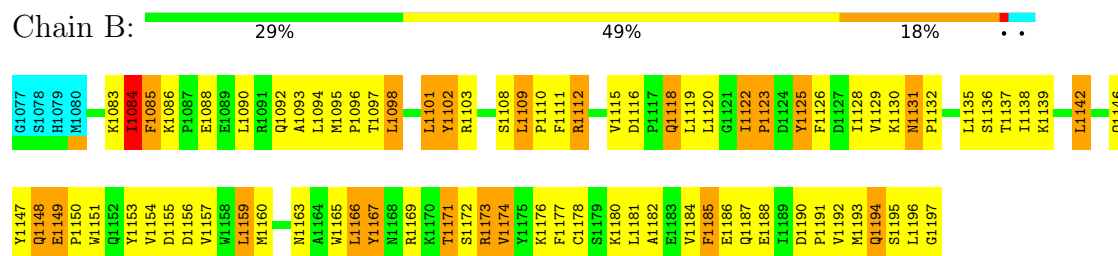


4.2.7 Score per residue for model 7

- Molecule 1: tumor protein p53



- Molecule 2: CREB-BINDING PROTEIN

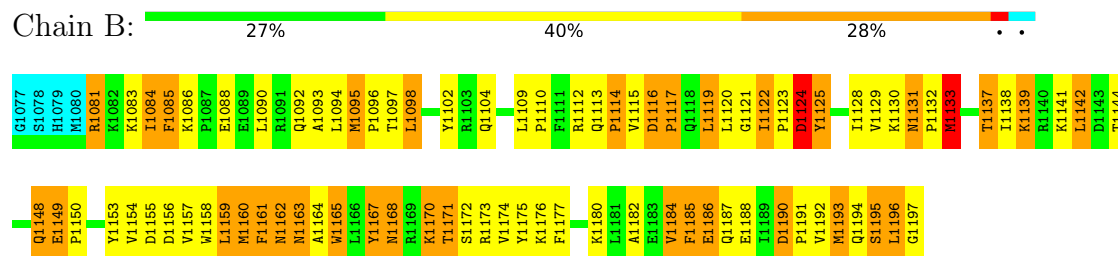


4.2.8 Score per residue for model 8

- Molecule 1: tumor protein p53

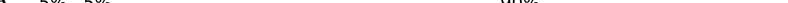


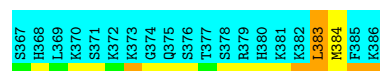
- Molecule 2: CREB-BINDING PROTEIN



4.2.9 Score per residue for model 9

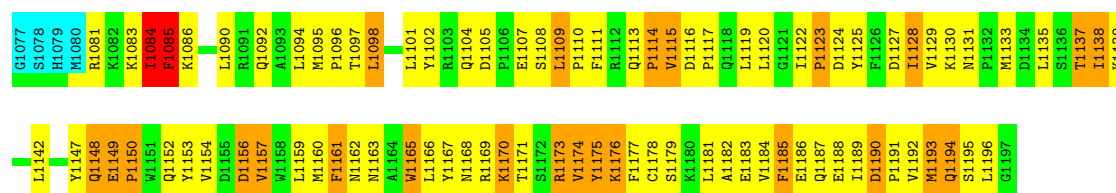
- Molecule 1: tumor protein p53

Chain A:  5% 5% 90%



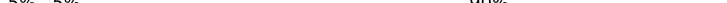
- Molecule 2: CREB-BINDING PROTEIN

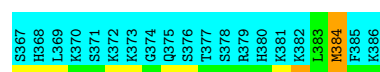
Chain B: 25% 50% 20% 5%



4.2.10 Score per residue for model 10

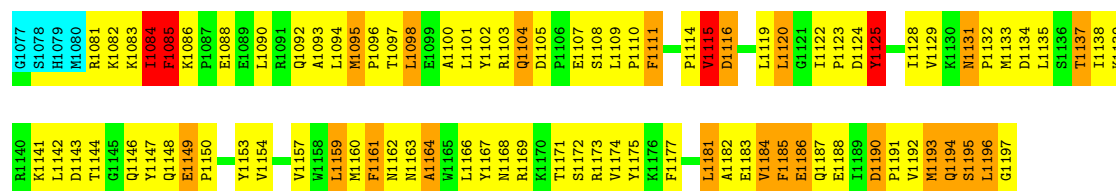
- Molecule 1: tumor protein p53

Chain A:  5% 5% 90%



- Molecule 2: CREB-BINDING PROTEIN

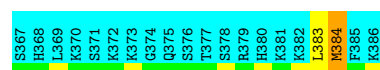
Chain B: 23% 53% 17% ...



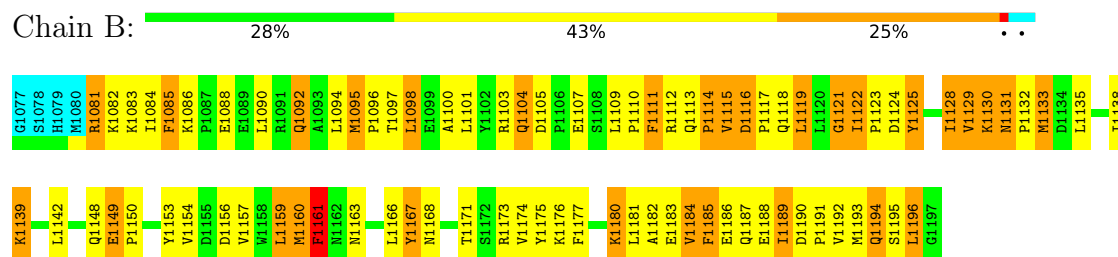
4.2.11 Score per residue for model 11

- Molecule 1: tumor protein p53

Chain A: 5% 5% 90%



- Molecule 2: CREB-BINDING PROTEIN

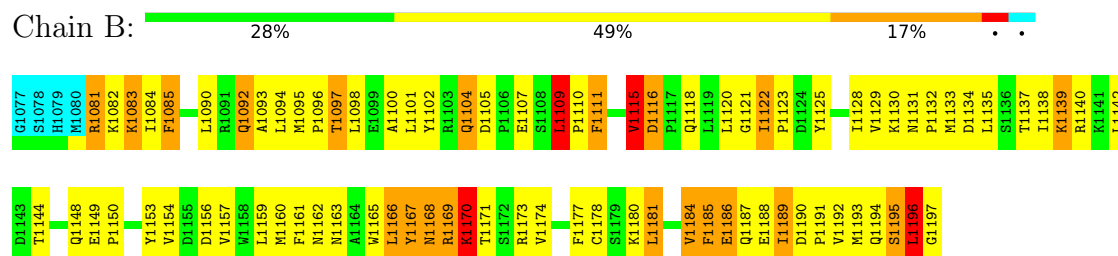


4.2.12 Score per residue for model 12

- Molecule 1: tumor protein p53



- Molecule 2: CREB-BINDING PROTEIN

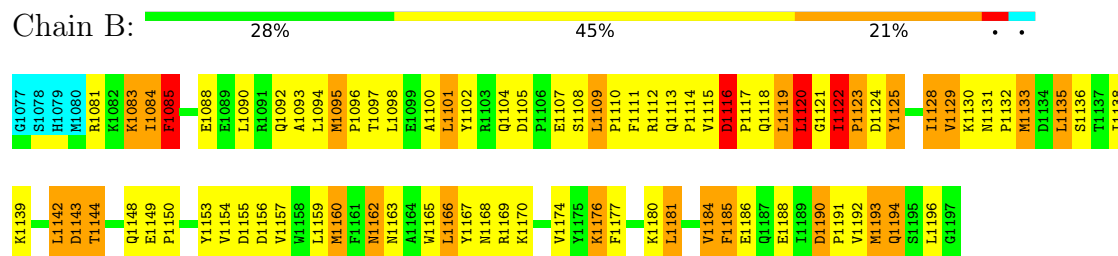


4.2.13 Score per residue for model 13

- Molecule 1: tumor protein p53



- Molecule 2: CREB-BINDING PROTEIN



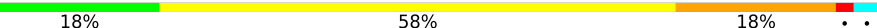
4.2.14 Score per residue for model 14

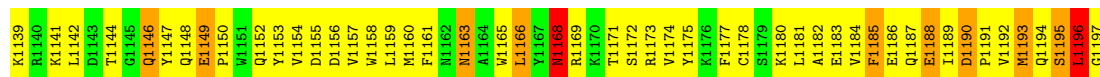
- Molecule 1: tumor protein p53

Chain A:  5% 5% 90%



- Molecule 2: CREB-BINDING PROTEIN

Chain B:  18% 58% 18% . .



4.2.15 Score per residue for model 15

- Molecule 1: tumor protein p53

Chain A:  10% 90%



- Molecule 2: CREB-BINDING PROTEIN

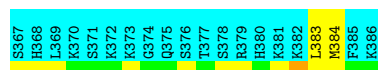
Chain B:  30% 46% 18% . .



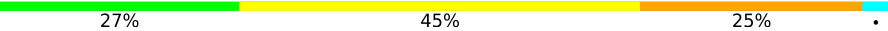
4.2.16 Score per residue for model 16

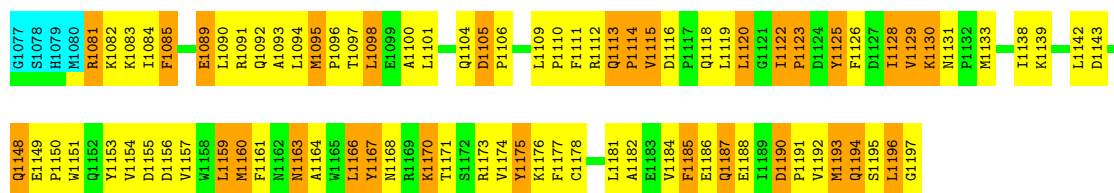
- Molecule 1: tumor protein p53

Chain A:  10% 90%



- Molecule 2: CREB-BINDING PROTEIN

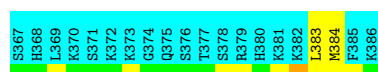
Chain B: 



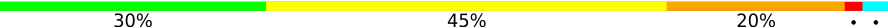
4.2.17 Score per residue for model 17

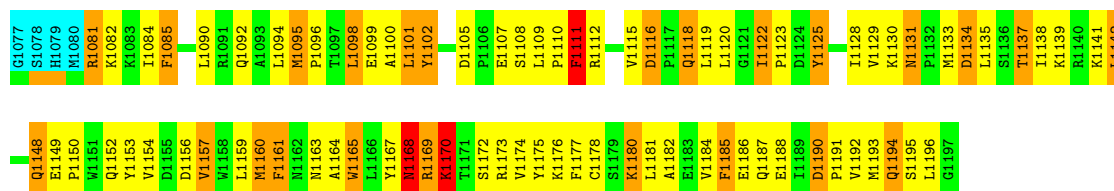
- Molecule 1: tumor protein p53

Chain A: 



- Molecule 2: CREB-BINDING PROTEIN

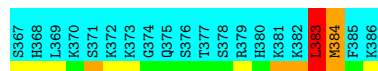
Chain B: 



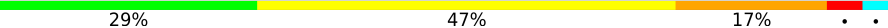
4.2.18 Score per residue for model 18

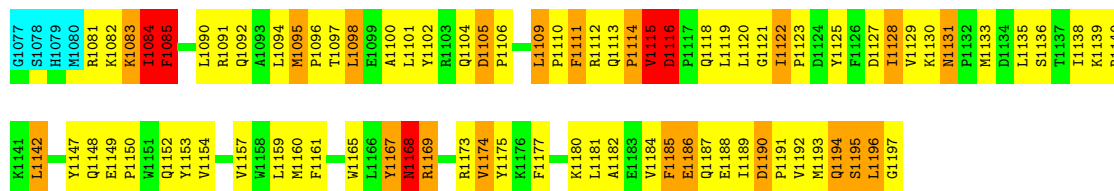
- Molecule 1: tumor protein p53

Chain A: 



- Molecule 2: CREB-BINDING PROTEIN

Chain B: 



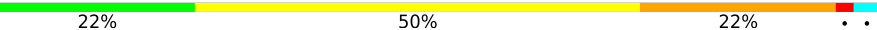
4.2.19 Score per residue for model 19

- Molecule 1: tumor protein p53

Chain A:  5% 5% 90%



- Molecule 2: CREB-BINDING PROTEIN

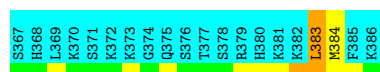
Chain B:  22% 50% 22% . .



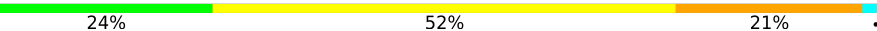
4.2.20 Score per residue for model 20

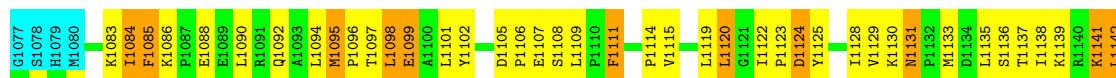
- Molecule 1: tumor protein p53

Chain A:  5% 5% 90%



- Molecule 2: CREB-BINDING PROTEIN

Chain B:  24% 52% 21% .



5 Refinement protocol and experimental data overview ⓘ

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations, structures with the lowest energy*.

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

Software name	Classification	Version
X-PLOR	structure solution	3.1
X-PLOR	refinement	3.1

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ALY

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.17±0.06	0±0/16 (0.0± 0.0%)	1.52±0.16	0±0/21 (0.0± 0.0%)
2	B	1.36±0.01	0±0/1014 (0.0± 0.0%)	1.53±0.01	2±1/1373 (0.1± 0.1%)
All	All	1.36	0/20600 (0.0%)	1.53	39/27880 (0.1%)

There are no bond-length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	1122	ILE	N-CA-CB	-7.21	105.54	111.67	5	1
2	B	1116	ASP	N-CA-CB	-6.44	105.22	111.27	2	3
2	B	1174	VAL	N-CA-CB	-6.01	103.67	111.90	18	2
2	B	1129	VAL	N-CA-CB	-6.00	104.35	111.90	2	2
2	B	1095	MET	N-CA-CB	-5.82	104.86	110.39	16	2
2	B	1109	LEU	N-CA-CB	-5.79	104.89	110.39	12	4
2	B	1157	VAL	N-CA-CB	-5.78	104.55	110.62	17	4
2	B	1142	LEU	N-CA-CB	-5.69	103.02	110.59	5	1
2	B	1084	ILE	N-CA-CB	-5.69	105.94	111.57	5	1
2	B	1082	LYS	N-CA-CB	-5.66	103.54	112.08	4	1
2	B	1161	PHE	CA-CB-CG	-5.62	108.18	113.80	2	5
2	B	1161	PHE	N-CA-CB	-5.49	102.46	110.53	8	1
2	B	1131	ASN	N-CA-CB	-5.45	104.31	111.23	11	3
2	B	1128	ILE	N-CA-CB	-5.35	105.96	112.33	11	3
2	B	1124	ASP	N-CA-CB	-5.20	104.53	112.28	3	1
2	B	1169	ARG	N-CA-CB	-5.15	103.19	110.51	14	1
2	B	1105	ASP	N-CA-CB	-5.14	104.82	111.35	16	1
2	B	1175	TYR	N-CA-CB	-5.10	104.64	110.35	16	1
2	B	1120	LEU	N-CA-CB	-5.06	106.21	113.65	13	1
2	B	1194	GLN	N-CA-C	-5.01	105.82	111.28	6	1

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	16	20	20	3±2
2	B	987	980	980	108±10
All	All	20060	20000	20000	2180

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 54.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1098:LEU:HD21	2:B:1142:LEU:HD23	1.08	1.21	3	4
2:B:1098:LEU:HD11	2:B:1142:LEU:HD13	1.07	1.27	14	5
2:B:1098:LEU:HD21	2:B:1142:LEU:HD21	1.05	1.26	5	1
2:B:1098:LEU:HD21	2:B:1142:LEU:HD13	1.04	1.12	19	2
2:B:1122:ILE:HD11	2:B:1128:ILE:HD11	0.99	1.31	4	8
2:B:1098:LEU:HD11	2:B:1142:LEU:HD23	0.95	1.39	20	5
2:B:1193:MET:HE2	2:B:1196:LEU:HD13	0.93	1.39	6	5
2:B:1133:MET:CE	2:B:1159:LEU:HD12	0.93	1.94	14	1
2:B:1193:MET:HE2	2:B:1196:LEU:HD22	0.90	1.41	11	2
2:B:1100:ALA:HB2	2:B:1188:GLU:OE2	0.87	1.69	5	5
2:B:1098:LEU:CD2	2:B:1142:LEU:HD23	0.86	1.99	3	3
2:B:1189:ILE:HD12	2:B:1190:ASP:N	0.86	1.86	6	4
2:B:1128:ILE:HG21	2:B:1167:TYR:CD1	0.86	2.06	6	8
2:B:1101:LEU:HA	2:B:1181:LEU:HD13	0.86	1.47	13	2
2:B:1117:PRO:CB	2:B:1119:LEU:HD23	0.86	2.01	19	1
2:B:1154:VAL:HG22	2:B:1194:GLN:NE2	0.85	1.85	12	1
2:B:1168:ASN:ND2	2:B:1174:VAL:HG12	0.85	1.85	1	1
2:B:1111:PHE:CG	2:B:1135:LEU:HD12	0.85	2.07	17	6
2:B:1117:PRO:HB2	2:B:1119:LEU:HD23	0.85	1.47	19	1
2:B:1142:LEU:HD21	2:B:1153:TYR:CE1	0.84	2.08	18	9
2:B:1098:LEU:CD1	2:B:1142:LEU:HD23	0.84	2.03	7	1
2:B:1084:ILE:HD13	2:B:1090:LEU:HD11	0.83	1.48	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1128:ILE:HD12	2:B:1167:TYR:CD2	0.83	2.08	10	1
2:B:1098:LEU:HD21	2:B:1142:LEU:CD1	0.83	2.01	19	1
2:B:1111:PHE:CD2	2:B:1135:LEU:HD22	0.83	2.09	7	5
2:B:1168:ASN:OD1	2:B:1174:VAL:HG12	0.83	1.72	6	4
2:B:1115:VAL:HG13	2:B:1125:TYR:CE2	0.82	2.10	19	2
2:B:1094:LEU:HD11	2:B:1148:GLN:O	0.82	1.74	8	11
2:B:1133:MET:N	2:B:1133:MET:HE2	0.81	1.90	8	3
1:A:383:LEU:HD23	1:A:383:LEU:O	0.81	1.74	5	2
2:B:1083:LYS:C	2:B:1084:ILE:HD12	0.81	2.01	15	3
2:B:1184:VAL:HG22	2:B:1188:GLU:OE2	0.81	1.76	6	1
2:B:1101:LEU:HD21	2:B:1135:LEU:HD21	0.80	1.52	10	1
2:B:1128:ILE:HG22	2:B:1166:LEU:HD23	0.80	1.54	14	2
2:B:1142:LEU:HD11	2:B:1153:TYR:CE1	0.80	2.12	1	9
2:B:1108:SER:OG	2:B:1135:LEU:HD23	0.80	1.76	20	1
2:B:1098:LEU:CD1	2:B:1142:LEU:HD13	0.79	2.07	9	1
2:B:1188:GLU:O	2:B:1192:VAL:HG23	0.79	1.76	1	18
2:B:1101:LEU:HD21	2:B:1135:LEU:HD11	0.79	1.54	2	1
2:B:1142:LEU:HD11	2:B:1153:TYR:CD1	0.78	2.13	2	6
2:B:1125:TYR:CE1	2:B:1129:VAL:HG11	0.78	2.13	6	1
2:B:1139:LYS:HD2	2:B:1142:LEU:HD12	0.78	1.56	19	4
2:B:1154:VAL:HG11	2:B:1194:GLN:OE1	0.77	1.78	14	6
2:B:1181:LEU:HD23	2:B:1184:VAL:HG11	0.77	1.53	4	1
1:A:384:MET:HE3	2:B:1172:SER:OG	0.77	1.79	14	1
2:B:1090:LEU:HD22	2:B:1150:PRO:HD3	0.77	1.56	6	10
2:B:1098:LEU:HD22	2:B:1142:LEU:HD13	0.77	1.56	6	1
2:B:1098:LEU:HD11	2:B:1142:LEU:CD2	0.77	2.09	20	4
2:B:1084:ILE:HD12	2:B:1193:MET:HB2	0.76	1.57	3	8
1:A:383:LEU:CD2	2:B:1115:VAL:HG21	0.76	2.10	17	1
2:B:1100:ALA:HB1	2:B:1184:VAL:HG22	0.76	1.57	1	4
2:B:1138:ILE:O	2:B:1142:LEU:HD13	0.76	1.81	20	8
2:B:1133:MET:HE1	2:B:1159:LEU:HD22	0.75	1.58	18	2
2:B:1138:ILE:HD12	2:B:1156:ASP:CB	0.75	2.12	16	13
2:B:1083:LYS:C	2:B:1084:ILE:HD13	0.74	2.07	4	4
2:B:1133:MET:HE1	2:B:1159:LEU:HB3	0.74	1.57	16	5
2:B:1128:ILE:O	2:B:1166:LEU:HD22	0.74	1.82	16	2
2:B:1125:TYR:CE2	2:B:1129:VAL:HG11	0.74	2.18	8	2
2:B:1084:ILE:HG23	2:B:1193:MET:HB2	0.73	1.60	1	11
2:B:1084:ILE:CG1	2:B:1090:LEU:HD21	0.73	2.12	13	20
2:B:1111:PHE:CE1	2:B:1181:LEU:HD12	0.73	2.18	9	1
2:B:1081:ARG:CG	2:B:1196:LEU:HD23	0.73	2.13	18	2
2:B:1180:LYS:O	2:B:1184:VAL:HG22	0.73	1.83	3	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1138:ILE:HD12	2:B:1156:ASP:HB3	0.73	1.59	3	14
2:B:1115:VAL:HG13	2:B:1125:TYR:OH	0.73	1.83	3	4
2:B:1129:VAL:HG22	2:B:1163:ASN:CA	0.73	2.14	20	2
2:B:1138:ILE:HD12	2:B:1156:ASP:HB2	0.73	1.60	11	6
2:B:1100:ALA:HB2	2:B:1188:GLU:OE1	0.72	1.84	2	1
2:B:1119:LEU:HD12	2:B:1119:LEU:O	0.72	1.83	13	10
2:B:1095:MET:O	2:B:1095:MET:HE2	0.72	1.83	5	1
2:B:1133:MET:O	2:B:1160:MET:HE3	0.72	1.84	13	2
1:A:383:LEU:HD23	2:B:1115:VAL:HG23	0.72	1.59	16	1
2:B:1128:ILE:HG22	2:B:1166:LEU:HB3	0.72	1.60	2	1
2:B:1090:LEU:HD13	2:B:1149:GLU:HA	0.72	1.61	6	17
2:B:1154:VAL:HG21	2:B:1194:GLN:OE1	0.72	1.84	19	8
2:B:1122:ILE:HG12	2:B:1128:ILE:HD11	0.71	1.60	18	1
2:B:1131:ASN:O	2:B:1133:MET:HE1	0.71	1.85	20	4
2:B:1098:LEU:HD21	2:B:1142:LEU:CD2	0.71	2.14	2	2
2:B:1131:ASN:O	2:B:1159:LEU:HD21	0.71	1.85	7	4
2:B:1160:MET:HE3	2:B:1160:MET:HA	0.71	1.62	5	8
1:A:384:MET:HE2	2:B:1167:TYR:O	0.71	1.86	16	1
2:B:1129:VAL:HG22	2:B:1163:ASN:CB	0.70	2.17	2	2
2:B:1115:VAL:HG21	2:B:1125:TYR:OH	0.70	1.86	11	1
2:B:1165:TRP:CD1	2:B:1178:CYS:HG	0.70	2.04	17	3
2:B:1098:LEU:HD22	2:B:1142:LEU:HD23	0.70	1.63	13	1
2:B:1128:ILE:HA	2:B:1166:LEU:HD23	0.70	1.62	15	4
2:B:1133:MET:SD	2:B:1160:MET:SD	0.70	2.89	18	1
2:B:1101:LEU:HA	2:B:1181:LEU:HD22	0.70	1.64	4	2
2:B:1138:ILE:HG23	2:B:1139:LYS:HD3	0.69	1.61	19	2
2:B:1139:LYS:HD3	2:B:1142:LEU:HD12	0.69	1.65	9	3
2:B:1098:LEU:HD13	2:B:1139:LYS:HE3	0.69	1.63	12	1
2:B:1138:ILE:HD11	2:B:1157:VAL:HG23	0.69	1.63	3	16
2:B:1119:LEU:HD12	2:B:1120:LEU:N	0.69	2.03	2	2
2:B:1131:ASN:HB3	2:B:1159:LEU:HD11	0.69	1.64	4	2
2:B:1098:LEU:HD13	2:B:1139:LYS:CE	0.69	2.18	12	1
2:B:1129:VAL:HG22	2:B:1163:ASN:HB2	0.68	1.65	2	1
2:B:1122:ILE:HD12	2:B:1123:PRO:O	0.68	1.89	10	5
1:A:384:MET:HB2	2:B:1174:VAL:HG21	0.68	1.65	17	4
2:B:1093:ALA:HB1	2:B:1192:VAL:HG22	0.68	1.63	10	10
2:B:1081:ARG:HG3	2:B:1196:LEU:HD23	0.67	1.64	1	1
2:B:1128:ILE:HD12	2:B:1167:TYR:HB2	0.67	1.65	3	3
2:B:1131:ASN:O	2:B:1159:LEU:HD22	0.67	1.90	11	2
2:B:1115:VAL:HA	2:B:1119:LEU:HD11	0.67	1.66	13	1
2:B:1111:PHE:CE1	2:B:1135:LEU:HD13	0.67	2.24	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1189:ILE:HD13	2:B:1194:GLN:OE1	0.67	1.90	20	1
2:B:1129:VAL:HG22	2:B:1163:ASN:HA	0.66	1.64	20	6
2:B:1128:ILE:HG21	2:B:1167:TYR:CG	0.66	2.25	18	3
2:B:1162:ASN:O	2:B:1166:LEU:HD23	0.66	1.91	2	2
2:B:1109:LEU:O	2:B:1109:LEU:HD23	0.66	1.90	20	1
2:B:1098:LEU:HD11	2:B:1139:LYS:HD2	0.66	1.68	18	2
2:B:1125:TYR:CE1	2:B:1129:VAL:HG21	0.66	2.26	18	4
2:B:1115:VAL:HG11	2:B:1125:TYR:OH	0.66	1.91	11	2
2:B:1162:ASN:OD1	2:B:1166:LEU:HD22	0.66	1.90	15	1
2:B:1193:MET:HE2	2:B:1196:LEU:CD1	0.66	2.19	1	1
2:B:1084:ILE:HD13	2:B:1084:ILE:N	0.66	2.05	10	9
2:B:1142:LEU:HD21	2:B:1153:TYR:CD1	0.66	2.25	10	4
2:B:1129:VAL:HG11	2:B:1132:PRO:HB3	0.66	1.65	7	1
2:B:1132:PRO:HA	2:B:1159:LEU:HD11	0.66	1.68	14	1
2:B:1119:LEU:HD12	2:B:1120:LEU:HB2	0.66	1.67	16	1
2:B:1133:MET:O	2:B:1160:MET:HE1	0.65	1.90	20	3
2:B:1090:LEU:C	2:B:1094:LEU:HD12	0.65	2.15	14	5
2:B:1196:LEU:HD23	2:B:1196:LEU:O	0.65	1.91	13	1
2:B:1159:LEU:HD12	2:B:1159:LEU:O	0.65	1.92	7	3
2:B:1098:LEU:HD11	2:B:1142:LEU:HD22	0.65	1.69	10	1
2:B:1115:VAL:HG21	2:B:1125:TYR:CE2	0.65	2.25	11	1
2:B:1168:ASN:CG	2:B:1174:VAL:HG12	0.65	2.16	2	2
2:B:1084:ILE:HG12	2:B:1090:LEU:HD21	0.65	1.68	9	3
2:B:1133:MET:CE	2:B:1159:LEU:HD22	0.65	2.22	12	2
1:A:383:LEU:HD13	1:A:383:LEU:O	0.65	1.92	19	2
1:A:383:LEU:HD21	2:B:1115:VAL:HG11	0.65	1.68	17	1
2:B:1189:ILE:HD13	2:B:1195:SER:OG	0.65	1.92	6	2
2:B:1168:ASN:HB3	2:B:1174:VAL:HG12	0.64	1.66	8	2
2:B:1160:MET:HE2	2:B:1160:MET:HA	0.64	1.66	15	4
2:B:1181:LEU:HD23	2:B:1181:LEU:N	0.64	2.08	10	1
2:B:1159:LEU:C	2:B:1159:LEU:HD13	0.64	2.17	14	1
2:B:1125:TYR:CD1	2:B:1129:VAL:HG11	0.64	2.27	6	1
1:A:384:MET:HE3	2:B:1167:TYR:O	0.64	1.92	12	1
1:A:383:LEU:HD12	2:B:1173:ARG:NH2	0.64	2.08	8	1
2:B:1101:LEU:HD22	2:B:1135:LEU:HD21	0.64	1.70	3	1
2:B:1084:ILE:HG23	2:B:1192:VAL:O	0.63	1.92	10	3
2:B:1101:LEU:HD23	2:B:1139:LYS:NZ	0.63	2.09	14	2
2:B:1115:VAL:HG22	2:B:1115:VAL:O	0.63	1.93	17	3
2:B:1084:ILE:HG13	2:B:1090:LEU:HD21	0.63	1.69	14	15
2:B:1111:PHE:CD1	2:B:1135:LEU:HD12	0.63	2.29	15	1
1:A:384:MET:CB	2:B:1174:VAL:HG21	0.63	2.24	20	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1124:ASP:O	2:B:1128:ILE:HD11	0.63	1.94	2	2
2:B:1129:VAL:HG11	2:B:1163:ASN:HB2	0.63	1.69	14	2
2:B:1101:LEU:HD13	2:B:1139:LYS:NZ	0.62	2.09	7	2
2:B:1154:VAL:HG11	2:B:1194:GLN:NE2	0.62	2.09	20	2
2:B:1101:LEU:CD2	2:B:1135:LEU:HD21	0.62	2.23	10	1
2:B:1090:LEU:HD22	2:B:1150:PRO:CD	0.62	2.23	4	2
1:A:383:LEU:HD21	2:B:1115:VAL:HG21	0.62	1.72	17	1
2:B:1084:ILE:CB	2:B:1090:LEU:HD21	0.62	2.25	5	14
2:B:1119:LEU:HD12	2:B:1119:LEU:C	0.62	2.20	16	2
2:B:1139:LYS:HD3	2:B:1142:LEU:HD22	0.62	1.71	18	4
2:B:1111:PHE:CG	2:B:1135:LEU:HD22	0.62	2.29	7	2
2:B:1095:MET:HE3	2:B:1095:MET:O	0.62	1.93	16	1
2:B:1128:ILE:HG21	2:B:1167:TYR:CE1	0.62	2.28	1	2
2:B:1193:MET:CE	2:B:1196:LEU:HD22	0.62	2.22	11	1
2:B:1115:VAL:HG21	2:B:1125:TYR:CZ	0.62	2.28	11	1
2:B:1122:ILE:CG1	2:B:1128:ILE:HD11	0.62	2.25	15	2
2:B:1084:ILE:HB	2:B:1090:LEU:HD21	0.62	1.72	5	10
2:B:1098:LEU:C	2:B:1098:LEU:HD12	0.62	2.19	6	2
2:B:1181:LEU:N	2:B:1181:LEU:HD22	0.61	2.09	1	3
2:B:1115:VAL:HG22	2:B:1116:ASP:N	0.61	2.10	12	3
2:B:1122:ILE:HG13	2:B:1128:ILE:HD11	0.61	1.71	15	1
2:B:1129:VAL:HG13	2:B:1163:ASN:HB2	0.61	1.71	20	1
2:B:1154:VAL:HG21	2:B:1194:GLN:HB2	0.61	1.70	4	5
2:B:1115:VAL:HG13	2:B:1115:VAL:O	0.61	1.95	8	3
2:B:1101:LEU:O	2:B:1181:LEU:HD22	0.61	1.94	19	8
2:B:1119:LEU:HD12	2:B:1120:LEU:CB	0.61	2.25	16	1
2:B:1101:LEU:HD13	2:B:1185:PHE:CB	0.61	2.25	18	3
1:A:383:LEU:CD2	2:B:1115:VAL:HG11	0.61	2.24	17	1
2:B:1101:LEU:O	2:B:1181:LEU:HD12	0.61	1.96	1	2
2:B:1142:LEU:HD11	2:B:1153:TYR:HE1	0.61	1.52	1	3
2:B:1128:ILE:HD12	2:B:1167:TYR:CG	0.61	2.30	10	1
2:B:1128:ILE:HD12	2:B:1167:TYR:CB	0.60	2.25	3	1
2:B:1094:LEU:O	2:B:1098:LEU:HD23	0.60	1.97	5	4
2:B:1154:VAL:HG21	2:B:1194:GLN:CD	0.60	2.20	13	4
2:B:1084:ILE:HD12	2:B:1084:ILE:N	0.60	2.10	15	3
2:B:1193:MET:CE	2:B:1196:LEU:HD13	0.60	2.26	15	6
2:B:1100:ALA:HB2	2:B:1188:GLU:CD	0.60	2.22	11	4
2:B:1115:VAL:HG21	2:B:1122:ILE:CG2	0.60	2.27	5	2
1:A:384:MET:HB3	2:B:1174:VAL:HG21	0.60	1.72	20	2
2:B:1134:ASP:HA	2:B:1160:MET:HE3	0.60	1.73	17	1
2:B:1095:MET:HE2	2:B:1095:MET:C	0.60	2.22	5	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1138:ILE:HG23	2:B:1139:LYS:HG2	0.59	1.74	20	4
2:B:1101:LEU:HD11	2:B:1135:LEU:HD21	0.59	1.73	13	1
2:B:1115:VAL:HG21	2:B:1122:ILE:HG23	0.59	1.72	6	3
2:B:1193:MET:HE2	2:B:1196:LEU:CD2	0.59	2.26	12	4
2:B:1171:THR:O	2:B:1171:THR:HG23	0.59	1.97	8	7
2:B:1111:PHE:CD2	2:B:1135:LEU:HD12	0.59	2.32	17	2
2:B:1094:LEU:HD13	2:B:1148:GLN:HA	0.59	1.75	4	1
2:B:1111:PHE:CZ	2:B:1181:LEU:HD12	0.59	2.33	9	1
2:B:1115:VAL:HG23	2:B:1117:PRO:O	0.59	1.96	9	1
2:B:1100:ALA:HB1	2:B:1184:VAL:HG13	0.59	1.73	10	1
1:A:383:LEU:HD22	2:B:1115:VAL:HB	0.59	1.74	12	1
2:B:1161:PHE:CD2	2:B:1185:PHE:CE1	0.59	2.91	2	3
2:B:1139:LYS:CD	2:B:1142:LEU:HD12	0.59	2.27	9	3
2:B:1101:LEU:HD13	2:B:1161:PHE:CZ	0.59	2.32	9	3
2:B:1161:PHE:CE2	2:B:1185:PHE:CD1	0.59	2.91	6	10
2:B:1153:TYR:O	2:B:1157:VAL:HG23	0.59	1.98	6	1
2:B:1159:LEU:C	2:B:1159:LEU:HD23	0.58	2.22	3	7
2:B:1128:ILE:HG13	2:B:1129:VAL:HG12	0.58	1.75	3	2
2:B:1092:GLN:O	2:B:1096:PRO:CD	0.58	2.52	16	20
2:B:1092:GLN:O	2:B:1096:PRO:HD2	0.58	1.98	5	20
2:B:1162:ASN:C	2:B:1166:LEU:HD23	0.58	2.24	2	1
2:B:1100:ALA:HB1	2:B:1184:VAL:HB	0.58	1.75	12	4
1:A:384:MET:HE1	2:B:1169:ARG:CD	0.58	2.28	1	1
2:B:1181:LEU:HD23	2:B:1184:VAL:CG1	0.58	2.29	4	1
2:B:1135:LEU:HD23	2:B:1138:ILE:CG2	0.58	2.28	9	1
2:B:1122:ILE:HD12	2:B:1122:ILE:C	0.58	2.24	16	11
2:B:1144:THR:HG23	2:B:1146:GLN:OE1	0.58	1.99	20	1
2:B:1122:ILE:HD11	2:B:1128:ILE:CD1	0.57	2.20	4	4
2:B:1189:ILE:HD12	2:B:1190:ASP:H	0.57	1.58	15	2
2:B:1101:LEU:CA	2:B:1181:LEU:HD13	0.57	2.25	13	1
2:B:1090:LEU:O	2:B:1094:LEU:HD12	0.57	1.99	14	3
2:B:1111:PHE:CB	2:B:1135:LEU:HD12	0.57	2.28	12	2
2:B:1101:LEU:HD13	2:B:1139:LYS:HZ1	0.57	1.59	7	2
2:B:1101:LEU:HD13	2:B:1161:PHE:CE2	0.57	2.33	12	4
2:B:1189:ILE:HD12	2:B:1195:SER:OG	0.57	1.99	12	2
2:B:1122:ILE:CD1	2:B:1128:ILE:HD12	0.57	2.30	13	1
1:A:383:LEU:HD13	2:B:1115:VAL:HB	0.57	1.77	12	1
2:B:1100:ALA:HB3	2:B:1188:GLU:CD	0.57	2.24	6	1
2:B:1122:ILE:HD12	2:B:1123:PRO:N	0.57	2.14	15	7
2:B:1116:ASP:N	2:B:1117:PRO:HA	0.57	2.14	8	2
2:B:1161:PHE:CE2	2:B:1185:PHE:CD2	0.57	2.92	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1133:MET:HE3	2:B:1159:LEU:HD12	0.57	1.73	14	1
2:B:1128:ILE:HG21	2:B:1167:TYR:HB2	0.56	1.77	13	2
2:B:1114:PRO:O	2:B:1119:LEU:HD21	0.56	2.00	20	1
2:B:1098:LEU:CD2	2:B:1142:LEU:HD13	0.56	2.30	6	2
2:B:1173:ARG:HG2	2:B:1174:VAL:N	0.56	2.15	9	1
2:B:1129:VAL:HG12	2:B:1132:PRO:HD3	0.56	1.78	10	4
2:B:1190:ASP:N	2:B:1191:PRO:CD	0.56	2.69	2	19
2:B:1181:LEU:N	2:B:1181:LEU:CD2	0.56	2.69	17	6
2:B:1170:LYS:C	2:B:1171:THR:HG23	0.56	2.25	20	2
2:B:1122:ILE:HB	2:B:1123:PRO:HD2	0.56	1.78	15	1
2:B:1193:MET:HE3	2:B:1196:LEU:HD13	0.55	1.79	11	1
2:B:1081:ARG:HG2	2:B:1196:LEU:HD23	0.55	1.78	18	1
2:B:1094:LEU:O	2:B:1098:LEU:HD12	0.55	2.01	2	2
2:B:1122:ILE:HD11	2:B:1128:ILE:HD12	0.55	1.77	13	1
2:B:1160:MET:O	2:B:1160:MET:HE2	0.55	2.02	13	1
2:B:1125:TYR:CZ	2:B:1129:VAL:HG21	0.55	2.37	8	5
2:B:1094:LEU:CD2	2:B:1153:TYR:CD2	0.55	2.90	12	18
2:B:1177:PHE:O	2:B:1181:LEU:HD23	0.55	2.01	1	2
2:B:1098:LEU:HD11	2:B:1142:LEU:CD1	0.55	2.25	9	1
2:B:1173:ARG:O	2:B:1175:TYR:N	0.55	2.40	9	1
2:B:1115:VAL:HG13	2:B:1116:ASP:N	0.54	2.17	16	1
2:B:1196:LEU:C	2:B:1196:LEU:HD13	0.54	2.27	14	6
2:B:1125:TYR:HD1	2:B:1128:ILE:HD11	0.54	1.63	10	1
2:B:1084:ILE:HD13	2:B:1090:LEU:HD21	0.54	1.79	18	1
2:B:1161:PHE:CE2	2:B:1185:PHE:CG	0.54	2.95	11	4
2:B:1189:ILE:HD12	2:B:1195:SER:CB	0.54	2.32	12	1
2:B:1164:ALA:N	2:B:1167:TYR:CE1	0.54	2.75	10	1
2:B:1129:VAL:O	2:B:1159:LEU:HD11	0.54	2.02	5	1
2:B:1131:ASN:O	2:B:1133:MET:HE2	0.54	2.03	13	1
2:B:1170:LYS:O	2:B:1171:THR:HG23	0.54	2.02	16	1
2:B:1180:LYS:O	2:B:1184:VAL:HG12	0.54	2.03	1	3
2:B:1125:TYR:CE1	2:B:1129:VAL:CG2	0.54	2.91	18	2
2:B:1153:TYR:CE1	2:B:1157:VAL:HG21	0.53	2.37	9	14
2:B:1102:TYR:CD2	2:B:1139:LYS:CE	0.53	2.92	2	1
2:B:1102:TYR:CD1	2:B:1139:LYS:CE	0.53	2.91	5	2
2:B:1094:LEU:O	2:B:1098:LEU:HD13	0.53	2.03	10	3
2:B:1111:PHE:HB3	2:B:1135:LEU:HD12	0.53	1.80	12	2
2:B:1181:LEU:HA	2:B:1184:VAL:HG12	0.53	1.81	7	6
2:B:1160:MET:HE2	2:B:1163:ASN:OD1	0.53	2.02	8	1
2:B:1098:LEU:HD21	2:B:1142:LEU:HB3	0.53	1.79	10	1
2:B:1167:TYR:N	2:B:1167:TYR:CD1	0.53	2.76	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1084:ILE:CD1	2:B:1090:LEU:HD21	0.53	2.33	18	1
2:B:1122:ILE:CG1	2:B:1125:TYR:CD1	0.53	2.91	16	9
2:B:1129:VAL:HG22	2:B:1163:ASN:O	0.53	2.03	8	1
2:B:1135:LEU:HD23	2:B:1138:ILE:HG21	0.53	1.78	9	1
2:B:1185:PHE:CD1	2:B:1186:GLU:N	0.53	2.77	11	9
2:B:1161:PHE:CE1	2:B:1182:ALA:N	0.53	2.77	2	8
2:B:1185:PHE:CG	2:B:1186:GLU:N	0.53	2.76	12	8
2:B:1153:TYR:CE1	2:B:1157:VAL:CG2	0.53	2.92	15	14
2:B:1157:VAL:HG11	2:B:1185:PHE:CE2	0.53	2.39	1	7
2:B:1111:PHE:CE2	2:B:1160:MET:CG	0.53	2.92	2	1
2:B:1163:ASN:O	2:B:1164:ALA:HB2	0.53	2.01	10	1
2:B:1157:VAL:CG1	2:B:1185:PHE:CE1	0.53	2.91	15	2
2:B:1125:TYR:CD1	2:B:1129:VAL:CG1	0.53	2.92	6	1
2:B:1111:PHE:CD1	2:B:1135:LEU:CD1	0.53	2.92	15	1
2:B:1116:ASP:N	2:B:1117:PRO:HD2	0.53	2.19	19	1
2:B:1101:LEU:HD22	2:B:1139:LYS:CE	0.53	2.34	20	1
2:B:1100:ALA:HB2	2:B:1188:GLU:HG3	0.53	1.80	10	1
1:A:384:MET:HE1	2:B:1169:ARG:HD2	0.53	1.79	1	1
2:B:1109:LEU:N	2:B:1110:PRO:CD	0.53	2.71	16	6
2:B:1157:VAL:CG1	2:B:1185:PHE:CE2	0.53	2.92	8	9
2:B:1111:PHE:HD2	2:B:1135:LEU:HD22	0.53	1.64	2	1
2:B:1138:ILE:CD1	2:B:1157:VAL:HG23	0.52	2.34	16	8
2:B:1116:ASP:N	2:B:1117:PRO:CA	0.52	2.72	9	2
2:B:1121:GLY:O	2:B:1122:ILE:O	0.52	2.26	12	2
2:B:1122:ILE:HD11	2:B:1125:TYR:HD1	0.52	1.64	14	5
2:B:1177:PHE:CD1	2:B:1178:CYS:N	0.52	2.77	20	5
2:B:1122:ILE:N	2:B:1123:PRO:CA	0.52	2.72	7	2
2:B:1170:LYS:C	2:B:1171:THR:HG22	0.52	2.29	15	1
2:B:1105:ASP:N	2:B:1106:PRO:HA	0.52	2.19	20	1
2:B:1167:TYR:CD1	2:B:1168:ASN:N	0.52	2.77	4	3
2:B:1161:PHE:CE1	2:B:1182:ALA:HB2	0.52	2.39	10	3
2:B:1141:LYS:CB	2:B:1147:TYR:CE2	0.52	2.93	6	1
2:B:1098:LEU:HD12	2:B:1142:LEU:HD23	0.52	1.78	7	1
2:B:1113:GLN:CB	2:B:1114:PRO:CA	0.52	2.88	19	1
2:B:1129:VAL:HG21	2:B:1163:ASN:HD22	0.52	1.64	19	1
2:B:1133:MET:HE1	2:B:1159:LEU:HD13	0.52	1.80	4	3
2:B:1128:ILE:C	2:B:1129:VAL:HG23	0.52	2.28	11	10
2:B:1129:VAL:HG11	2:B:1132:PRO:HG3	0.52	1.81	5	1
2:B:1113:GLN:N	2:B:1114:PRO:CD	0.52	2.73	11	5
2:B:1167:TYR:C	2:B:1167:TYR:CD1	0.52	2.86	3	3
1:A:384:MET:CA	2:B:1174:VAL:CG2	0.52	2.88	18	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1161:PHE:CE2	2:B:1185:PHE:CE1	0.52	2.98	9	7
2:B:1187:GLN:O	2:B:1191:PRO:CD	0.52	2.58	5	17
2:B:1129:VAL:CG2	2:B:1167:TYR:CE1	0.52	2.92	10	1
2:B:1100:ALA:HB3	2:B:1188:GLU:OE1	0.52	2.04	6	1
2:B:1128:ILE:CG2	2:B:1167:TYR:CD1	0.52	2.92	15	4
2:B:1102:TYR:CE1	2:B:1139:LYS:CB	0.52	2.92	20	1
2:B:1195:SER:O	2:B:1197:GLY:N	0.51	2.43	6	13
2:B:1105:ASP:O	2:B:1109:LEU:HD13	0.51	2.06	9	1
2:B:1141:LYS:O	2:B:1144:THR:HG22	0.51	2.05	20	1
2:B:1128:ILE:HG22	2:B:1166:LEU:HD22	0.51	1.82	12	1
2:B:1142:LEU:HD21	2:B:1153:TYR:HE1	0.51	1.63	17	5
2:B:1101:LEU:CD1	2:B:1161:PHE:CZ	0.51	2.93	15	5
2:B:1122:ILE:HD11	2:B:1125:TYR:CD1	0.51	2.40	14	4
2:B:1101:LEU:CD1	2:B:1161:PHE:CE2	0.51	2.93	12	3
2:B:1098:LEU:HD12	2:B:1153:TYR:OH	0.51	2.06	8	1
2:B:1125:TYR:OH	2:B:1129:VAL:HG11	0.51	2.06	20	2
2:B:1168:ASN:ND2	2:B:1175:TYR:CD1	0.51	2.79	15	4
2:B:1122:ILE:N	2:B:1123:PRO:HA	0.51	2.21	17	2
2:B:1164:ALA:HA	2:B:1167:TYR:CE1	0.51	2.41	8	4
2:B:1163:ASN:O	2:B:1167:TYR:CD1	0.51	2.64	3	2
2:B:1162:ASN:OD1	2:B:1166:LEU:HD13	0.51	2.06	15	2
2:B:1098:LEU:HD21	2:B:1139:LYS:HE3	0.50	1.83	8	1
2:B:1097:THR:O	2:B:1100:ALA:HB3	0.50	2.05	13	1
2:B:1122:ILE:C	2:B:1122:ILE:CD1	0.50	2.85	17	2
2:B:1168:ASN:ND2	2:B:1175:TYR:CE2	0.50	2.80	11	1
2:B:1102:TYR:CD1	2:B:1139:LYS:CG	0.50	2.94	20	1
2:B:1159:LEU:HD23	2:B:1159:LEU:O	0.50	2.05	17	4
2:B:1153:TYR:CZ	2:B:1157:VAL:HG21	0.50	2.41	6	4
2:B:1106:PRO:HA	2:B:1109:LEU:HD12	0.50	1.82	6	2
1:A:384:MET:CB	2:B:1174:VAL:CG2	0.50	2.90	18	1
2:B:1160:MET:HE2	2:B:1163:ASN:HB3	0.50	1.83	19	1
2:B:1090:LEU:HD13	2:B:1150:PRO:HD3	0.50	1.82	2	4
2:B:1114:PRO:C	2:B:1119:LEU:HD21	0.50	2.31	13	1
2:B:1125:TYR:CZ	2:B:1163:ASN:OD1	0.50	2.65	13	1
2:B:1101:LEU:C	2:B:1101:LEU:HD23	0.50	2.32	20	1
1:A:384:MET:CA	2:B:1174:VAL:HG21	0.49	2.37	7	6
2:B:1102:TYR:CD1	2:B:1139:LYS:HG3	0.49	2.42	20	2
1:A:384:MET:HA	2:B:1174:VAL:CG2	0.49	2.37	4	5
1:A:383:LEU:HD11	2:B:1114:PRO:C	0.49	2.31	18	1
2:B:1094:LEU:HD11	2:B:1148:GLN:HA	0.49	1.84	1	1
2:B:1167:TYR:CE1	2:B:1168:ASN:OD1	0.49	2.66	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1143:ASP:C	2:B:1144:THR:HG23	0.49	2.32	10	1
2:B:1116:ASP:CB	2:B:1117:PRO:CD	0.49	2.90	14	2
2:B:1178:CYS:O	2:B:1182:ALA:HB2	0.49	2.06	20	2
2:B:1139:LYS:HA	2:B:1142:LEU:HD22	0.49	1.84	20	1
2:B:1107:GLU:O	2:B:1181:LEU:HD12	0.49	2.08	5	3
1:A:384:MET:HE2	2:B:1169:ARG:HB2	0.49	1.83	6	1
2:B:1189:ILE:CG2	2:B:1194:GLN:NE2	0.49	2.76	12	1
2:B:1108:SER:HB3	2:B:1181:LEU:HD11	0.49	1.85	7	2
2:B:1083:LYS:O	2:B:1084:ILE:C	0.49	2.55	18	3
2:B:1181:LEU:N	2:B:1181:LEU:HD23	0.49	2.21	13	1
2:B:1138:ILE:HD11	2:B:1157:VAL:CG2	0.49	2.37	18	4
2:B:1173:ARG:O	2:B:1177:PHE:CD2	0.49	2.66	17	5
2:B:1129:VAL:HG21	2:B:1132:PRO:HB3	0.49	1.85	19	1
2:B:1111:PHE:CD1	2:B:1135:LEU:HD22	0.49	2.43	20	1
2:B:1173:ARG:O	2:B:1177:PHE:CE2	0.49	2.66	11	5
2:B:1097:THR:HG23	2:B:1098:LEU:N	0.49	2.23	13	2
2:B:1125:TYR:CD1	2:B:1128:ILE:HD11	0.49	2.43	10	1
2:B:1168:ASN:CG	2:B:1175:TYR:CD2	0.49	2.91	11	1
2:B:1115:VAL:O	2:B:1125:TYR:CD2	0.49	2.66	14	1
2:B:1122:ILE:HD11	2:B:1128:ILE:HD13	0.49	1.84	15	1
2:B:1125:TYR:CE2	2:B:1163:ASN:ND2	0.49	2.80	16	1
2:B:1119:LEU:O	2:B:1119:LEU:CD1	0.49	2.60	19	2
2:B:1175:TYR:O	2:B:1175:TYR:CG	0.49	2.66	17	8
2:B:1102:TYR:CD2	2:B:1139:LYS:HE3	0.48	2.43	2	1
2:B:1111:PHE:CE2	2:B:1181:LEU:HD12	0.48	2.43	16	3
2:B:1184:VAL:CG1	2:B:1185:PHE:N	0.48	2.76	4	4
2:B:1102:TYR:CD1	2:B:1139:LYS:HE2	0.48	2.43	5	3
2:B:1159:LEU:HD12	2:B:1159:LEU:C	0.48	2.31	10	3
2:B:1168:ASN:CB	2:B:1174:VAL:HG12	0.48	2.38	9	2
2:B:1193:MET:HE2	2:B:1196:LEU:HD21	0.48	1.85	12	1
2:B:1161:PHE:CE1	2:B:1182:ALA:CA	0.48	2.96	18	11
2:B:1097:THR:HG22	2:B:1098:LEU:N	0.48	2.21	12	1
2:B:1133:MET:CE	2:B:1159:LEU:CD2	0.48	2.91	12	1
2:B:1132:PRO:CB	2:B:1163:ASN:ND2	0.48	2.77	13	1
2:B:1111:PHE:CE2	2:B:1181:LEU:CD1	0.48	2.96	15	1
2:B:1185:PHE:CD2	2:B:1186:GLU:N	0.48	2.80	15	1
2:B:1184:VAL:HG13	2:B:1185:PHE:N	0.48	2.23	14	5
2:B:1143:ASP:O	2:B:1144:THR:HG23	0.48	2.09	13	2
2:B:1157:VAL:HG11	2:B:1185:PHE:CD2	0.48	2.43	14	3
2:B:1105:ASP:N	2:B:1106:PRO:CA	0.48	2.76	20	1
2:B:1113:GLN:N	2:B:1114:PRO:HD3	0.48	2.24	11	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1137:THR:HG22	2:B:1138:ILE:N	0.48	2.23	10	5
2:B:1150:PRO:O	2:B:1154:VAL:HG23	0.48	2.08	9	15
2:B:1174:VAL:O	2:B:1177:PHE:CZ	0.48	2.67	2	6
2:B:1196:LEU:C	2:B:1196:LEU:CD1	0.48	2.85	4	5
2:B:1146:GLN:C	2:B:1147:TYR:CD1	0.48	2.92	7	2
2:B:1081:ARG:O	2:B:1083:LYS:N	0.48	2.46	12	1
2:B:1109:LEU:CB	2:B:1110:PRO:CD	0.48	2.92	11	9
1:A:383:LEU:HD23	1:A:383:LEU:C	0.48	2.34	5	1
2:B:1167:TYR:CD1	2:B:1167:TYR:C	0.48	2.91	11	2
2:B:1167:TYR:O	2:B:1167:TYR:CG	0.48	2.67	3	2
2:B:1150:PRO:CB	2:B:1194:GLN:CB	0.48	2.91	12	1
2:B:1159:LEU:O	2:B:1159:LEU:HD23	0.48	2.09	18	1
2:B:1161:PHE:CD1	2:B:1182:ALA:HB2	0.48	2.43	2	1
2:B:1125:TYR:CZ	2:B:1129:VAL:HG11	0.48	2.44	18	5
2:B:1194:GLN:CG	2:B:1195:SER:N	0.48	2.76	6	2
2:B:1111:PHE:CE2	2:B:1181:LEU:HD13	0.48	2.44	15	1
2:B:1160:MET:HE2	2:B:1160:MET:O	0.48	2.09	19	1
2:B:1133:MET:O	2:B:1137:THR:HG22	0.48	2.09	2	1
2:B:1164:ALA:C	2:B:1167:TYR:CE1	0.48	2.91	8	3
2:B:1107:GLU:C	2:B:1181:LEU:HD11	0.48	2.33	14	1
2:B:1102:TYR:CG	2:B:1139:LYS:HE2	0.48	2.44	15	1
2:B:1102:TYR:CD2	2:B:1135:LEU:O	0.48	2.67	4	1
2:B:1081:ARG:CD	2:B:1196:LEU:CB	0.48	2.91	19	1
2:B:1115:VAL:HG22	2:B:1121:GLY:HA2	0.47	1.86	1	1
2:B:1161:PHE:CE1	2:B:1181:LEU:C	0.47	2.92	2	1
2:B:1194:GLN:HG3	2:B:1195:SER:N	0.47	2.23	6	1
2:B:1094:LEU:HD22	2:B:1153:TYR:CD2	0.47	2.44	13	1
2:B:1125:TYR:CZ	2:B:1163:ASN:ND2	0.47	2.82	16	1
2:B:1098:LEU:HD11	2:B:1139:LYS:CE	0.47	2.39	1	1
2:B:1122:ILE:CD1	2:B:1128:ILE:HD11	0.47	2.39	7	2
2:B:1115:VAL:O	2:B:1125:TYR:CE2	0.47	2.67	14	2
2:B:1182:ALA:O	2:B:1185:PHE:CD1	0.47	2.67	20	1
2:B:1137:THR:CG2	2:B:1138:ILE:N	0.47	2.77	9	4
2:B:1095:MET:CB	2:B:1096:PRO:CD	0.47	2.92	4	2
2:B:1165:TRP:N	2:B:1168:ASN:ND2	0.47	2.61	9	2
2:B:1181:LEU:HA	2:B:1184:VAL:HG23	0.47	1.85	13	1
1:A:383:LEU:CD2	2:B:1115:VAL:CG2	0.47	2.90	17	1
2:B:1084:ILE:O	2:B:1085:PHE:CG	0.47	2.68	8	6
2:B:1108:SER:HA	2:B:1181:LEU:HD11	0.47	1.85	9	1
1:A:383:LEU:CG	2:B:1115:VAL:HG21	0.47	2.39	17	1
2:B:1159:LEU:HD23	2:B:1159:LEU:C	0.47	2.34	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1133:MET:CG	2:B:1134:ASP:N	0.47	2.77	14	5
2:B:1084:ILE:O	2:B:1085:PHE:CD2	0.47	2.67	6	4
2:B:1113:GLN:CB	2:B:1114:PRO:HA	0.47	2.39	19	1
2:B:1154:VAL:CG1	2:B:1194:GLN:OE1	0.47	2.61	6	1
2:B:1117:PRO:O	2:B:1119:LEU:N	0.47	2.48	8	1
2:B:1174:VAL:O	2:B:1176:LYS:N	0.47	2.46	9	1
2:B:1159:LEU:C	2:B:1159:LEU:HD12	0.47	2.34	19	1
2:B:1084:ILE:N	2:B:1084:ILE:CD1	0.47	2.76	4	6
2:B:1122:ILE:CG1	2:B:1125:TYR:CE1	0.47	2.98	1	2
2:B:1150:PRO:O	2:B:1154:VAL:N	0.47	2.46	12	12
2:B:1182:ALA:HA	2:B:1185:PHE:CD1	0.47	2.45	1	4
2:B:1177:PHE:CD1	2:B:1177:PHE:C	0.47	2.92	12	5
2:B:1110:PRO:O	2:B:1177:PHE:CD1	0.47	2.68	14	2
2:B:1175:TYR:O	2:B:1175:TYR:CD2	0.47	2.68	1	3
2:B:1138:ILE:HG23	2:B:1139:LYS:N	0.47	2.24	7	3
2:B:1196:LEU:HD23	2:B:1196:LEU:C	0.47	2.34	13	1
2:B:1169:ARG:CG	2:B:1170:LYS:N	0.47	2.78	17	1
2:B:1094:LEU:HA	2:B:1097:THR:CG2	0.47	2.40	20	17
2:B:1122:ILE:HG13	2:B:1125:TYR:CD1	0.47	2.45	6	4
2:B:1122:ILE:HG12	2:B:1125:TYR:CD1	0.47	2.44	5	2
2:B:1150:PRO:HB3	2:B:1194:GLN:CB	0.47	2.40	18	10
2:B:1115:VAL:HG13	2:B:1116:ASP:H	0.46	1.70	5	5
2:B:1137:THR:HG23	2:B:1138:ILE:N	0.46	2.25	2	1
2:B:1108:SER:CA	2:B:1181:LEU:HD11	0.46	2.41	9	1
2:B:1115:VAL:HG11	2:B:1167:TYR:CE2	0.46	2.45	3	1
2:B:1157:VAL:HG11	2:B:1185:PHE:CE1	0.46	2.46	3	2
2:B:1116:ASP:O	2:B:1118:GLN:N	0.46	2.47	19	3
2:B:1172:SER:O	2:B:1174:VAL:N	0.46	2.48	7	1
2:B:1107:GLU:CB	2:B:1181:LEU:HD21	0.46	2.40	10	1
2:B:1164:ALA:O	2:B:1168:ASN:N	0.46	2.48	10	1
2:B:1081:ARG:CD	2:B:1081:ARG:C	0.46	2.88	11	1
2:B:1122:ILE:O	2:B:1124:ASP:N	0.46	2.48	14	2
2:B:1116:ASP:CB	2:B:1117:PRO:HD3	0.46	2.41	14	1
2:B:1141:LYS:HD2	2:B:1147:TYR:CZ	0.46	2.45	14	1
2:B:1102:TYR:CG	2:B:1139:LYS:CE	0.46	2.99	15	1
2:B:1129:VAL:HG13	2:B:1129:VAL:O	0.46	2.10	19	1
2:B:1187:GLN:HG2	2:B:1188:GLU:N	0.46	2.25	20	1
2:B:1129:VAL:CG1	2:B:1163:ASN:ND2	0.46	2.78	4	1
2:B:1094:LEU:HD11	2:B:1149:GLU:N	0.46	2.25	6	1
2:B:1165:TRP:HA	2:B:1168:ASN:ND2	0.46	2.26	12	1
1:A:383:LEU:HD22	2:B:1173:ARG:NH1	0.46	2.25	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1148:GLN:CD	2:B:1149:GLU:N	0.46	2.73	16	2
2:B:1129:VAL:HG21	2:B:1163:ASN:ND2	0.46	2.25	19	1
2:B:1190:ASP:N	2:B:1191:PRO:HD2	0.46	2.25	16	15
2:B:1098:LEU:CD2	2:B:1139:LYS:NZ	0.46	2.79	11	1
2:B:1101:LEU:HD13	2:B:1185:PHE:HB3	0.46	1.87	18	1
2:B:1110:PRO:HG3	2:B:1177:PHE:CG	0.46	2.46	19	1
2:B:1116:ASP:CB	2:B:1117:PRO:C	0.46	2.89	8	1
2:B:1168:ASN:O	2:B:1169:ARG:CG	0.46	2.64	18	2
2:B:1133:MET:O	2:B:1134:ASP:CB	0.46	2.64	17	2
2:B:1157:VAL:HG12	2:B:1185:PHE:CE2	0.46	2.46	2	1
2:B:1135:LEU:O	2:B:1139:LYS:CG	0.46	2.64	3	4
2:B:1094:LEU:CD1	2:B:1148:GLN:O	0.46	2.63	14	2
2:B:1121:GLY:O	2:B:1122:ILE:HG13	0.46	2.10	13	2
2:B:1135:LEU:O	2:B:1139:LYS:HG2	0.46	2.11	18	1
2:B:1116:ASP:N	2:B:1117:PRO:CD	0.46	2.79	19	1
2:B:1094:LEU:CD1	2:B:1148:GLN:HA	0.46	2.41	20	6
2:B:1192:VAL:O	2:B:1193:MET:CB	0.46	2.63	17	13
2:B:1173:ARG:HG3	2:B:1174:VAL:HG23	0.46	1.88	8	1
2:B:1150:PRO:CB	2:B:1194:GLN:HB2	0.46	2.41	12	2
2:B:1111:PHE:CZ	2:B:1178:CYS:SG	0.45	3.10	16	2
2:B:1159:LEU:C	2:B:1159:LEU:CD1	0.45	2.89	14	1
1:A:384:MET:O	1:A:384:MET:CG	0.45	2.64	20	2
2:B:1115:VAL:HG13	2:B:1125:TYR:CZ	0.45	2.45	19	1
2:B:1174:VAL:HA	2:B:1177:PHE:CE2	0.45	2.46	9	14
2:B:1125:TYR:O	2:B:1126:PHE:CB	0.45	2.64	3	2
2:B:1147:TYR:CD1	2:B:1152:GLN:CD	0.45	2.94	3	1
2:B:1122:ILE:HD12	2:B:1124:ASP:N	0.45	2.26	8	1
2:B:1115:VAL:CG2	2:B:1125:TYR:CE2	0.45	2.99	11	1
2:B:1118:GLN:O	2:B:1120:LEU:N	0.45	2.49	19	2
2:B:1107:GLU:O	2:B:1111:PHE:CE1	0.45	2.69	5	1
2:B:1102:TYR:CB	2:B:1139:LYS:CE	0.45	2.94	6	2
2:B:1115:VAL:HG21	2:B:1122:ILE:HG21	0.45	1.88	12	1
2:B:1169:ARG:O	2:B:1175:TYR:CD2	0.45	2.69	15	1
2:B:1083:LYS:O	2:B:1085:PHE:N	0.45	2.49	15	6
2:B:1138:ILE:O	2:B:1142:LEU:CB	0.45	2.65	5	1
2:B:1084:ILE:CG1	2:B:1150:PRO:HG2	0.45	2.41	5	9
2:B:1095:MET:CB	2:B:1096:PRO:HD3	0.45	2.42	13	13
2:B:1125:TYR:CE2	2:B:1129:VAL:CG1	0.45	2.96	8	1
2:B:1169:ARG:O	2:B:1171:THR:N	0.45	2.49	9	1
2:B:1122:ILE:HB	2:B:1123:PRO:CD	0.45	2.41	12	3
2:B:1163:ASN:O	2:B:1163:ASN:CG	0.45	2.60	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1093:ALA:O	2:B:1097:THR:HG22	0.45	2.12	16	2
2:B:1160:MET:O	2:B:1160:MET:CE	0.45	2.65	19	2
2:B:1081:ARG:HD3	2:B:1196:LEU:HD23	0.45	1.87	17	1
2:B:1161:PHE:CE2	2:B:1185:PHE:CE2	0.45	3.04	19	1
2:B:1094:LEU:O	2:B:1097:THR:HG22	0.45	2.11	1	3
2:B:1100:ALA:CB	2:B:1184:VAL:HG22	0.45	2.36	1	1
2:B:1175:TYR:CD2	2:B:1175:TYR:O	0.45	2.69	16	1
2:B:1102:TYR:CD2	2:B:1139:LYS:HG3	0.45	2.47	4	4
2:B:1151:TRP:C	2:B:1151:TRP:CD1	0.45	2.94	16	2
2:B:1149:GLU:CG	2:B:1149:GLU:O	0.45	2.64	9	1
2:B:1117:PRO:O	2:B:1118:GLN:CB	0.45	2.64	14	1
2:B:1098:LEU:HD11	2:B:1142:LEU:CG	0.45	2.42	16	1
2:B:1096:PRO:O	2:B:1099:GLU:CG	0.45	2.65	20	1
2:B:1194:GLN:C	2:B:1194:GLN:NE2	0.45	2.75	16	5
2:B:1101:LEU:HD11	2:B:1157:VAL:HG13	0.45	1.88	17	2
2:B:1109:LEU:N	2:B:1110:PRO:HD2	0.45	2.27	19	4
2:B:1139:LYS:HD2	2:B:1142:LEU:HD23	0.45	1.88	5	1
2:B:1189:ILE:HD12	2:B:1195:SER:HB2	0.45	1.89	12	1
2:B:1116:ASP:HB3	2:B:1117:PRO:CD	0.45	2.42	14	1
1:A:383:LEU:CD2	2:B:1115:VAL:HG23	0.45	2.38	16	1
2:B:1095:MET:HE3	2:B:1095:MET:HA	0.45	1.89	16	1
2:B:1082:LYS:O	2:B:1084:ILE:CD1	0.44	2.65	12	6
2:B:1111:PHE:CE1	2:B:1160:MET:SD	0.44	3.10	4	1
2:B:1128:ILE:CD1	2:B:1167:TYR:CD2	0.44	3.00	9	1
2:B:1150:PRO:HA	2:B:1153:TYR:HB3	0.44	1.88	9	1
2:B:1115:VAL:CG2	2:B:1116:ASP:N	0.44	2.80	12	1
2:B:1133:MET:HE1	2:B:1159:LEU:CD2	0.44	2.42	12	1
2:B:1111:PHE:CE1	2:B:1178:CYS:SG	0.44	3.10	14	1
2:B:1107:GLU:HB3	2:B:1181:LEU:HD21	0.44	1.87	1	1
2:B:1159:LEU:C	2:B:1159:LEU:CD2	0.44	2.90	9	8
2:B:1147:TYR:C	2:B:1148:GLN:CG	0.44	2.89	4	1
2:B:1157:VAL:O	2:B:1161:PHE:N	0.44	2.51	11	3
2:B:1194:GLN:NE2	2:B:1194:GLN:C	0.44	2.75	20	2
2:B:1116:ASP:HB3	2:B:1117:PRO:HD3	0.44	1.88	14	1
2:B:1133:MET:HB2	2:B:1137:THR:HG21	0.44	1.88	17	1
2:B:1165:TRP:CD1	2:B:1178:CYS:SG	0.44	3.10	17	2
2:B:1125:TYR:OH	2:B:1163:ASN:ND2	0.44	2.50	16	6
2:B:1107:GLU:O	2:B:1181:LEU:HD11	0.44	2.11	2	2
2:B:1109:LEU:CB	2:B:1110:PRO:HD3	0.44	2.43	9	9
2:B:1094:LEU:CD2	2:B:1153:TYR:CE2	0.44	2.99	9	2
2:B:1129:VAL:O	2:B:1130:LYS:CB	0.44	2.66	16	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1157:VAL:HG12	2:B:1161:PHE:HD2	0.44	1.72	11	1
2:B:1190:ASP:HB2	2:B:1191:PRO:HD3	0.44	1.88	12	1
2:B:1110:PRO:HG2	2:B:1177:PHE:CD1	0.44	2.47	19	2
2:B:1181:LEU:HA	2:B:1184:VAL:CG2	0.44	2.42	12	2
2:B:1170:LYS:O	2:B:1171:THR:CG2	0.44	2.65	15	1
2:B:1129:VAL:HG23	2:B:1163:ASN:HB2	0.44	1.89	3	1
2:B:1090:LEU:CB	2:B:1148:GLN:O	0.44	2.66	7	6
2:B:1115:VAL:HG22	2:B:1117:PRO:HB3	0.44	1.88	11	1
2:B:1115:VAL:HA	2:B:1119:LEU:HD21	0.44	1.90	16	1
2:B:1084:ILE:HD12	2:B:1193:MET:CB	0.44	2.42	1	1
2:B:1128:ILE:C	2:B:1129:VAL:CG2	0.44	2.91	11	8
2:B:1168:ASN:OD1	2:B:1174:VAL:CG1	0.44	2.66	9	2
2:B:1094:LEU:O	2:B:1098:LEU:CD2	0.44	2.66	6	3
2:B:1169:ARG:O	2:B:1170:LYS:CG	0.44	2.66	12	2
2:B:1165:TRP:CD1	2:B:1165:TRP:N	0.44	2.84	13	1
2:B:1108:SER:OG	2:B:1109:LEU:N	0.44	2.50	17	1
2:B:1141:LYS:HB3	2:B:1147:TYR:CE2	0.44	2.47	6	1
2:B:1190:ASP:HB3	2:B:1191:PRO:HD3	0.44	1.90	11	1
2:B:1122:ILE:CG1	2:B:1128:ILE:CD1	0.44	2.96	15	1
2:B:1150:PRO:O	2:B:1154:VAL:CB	0.43	2.66	11	5
2:B:1111:PHE:CE1	2:B:1181:LEU:HG	0.43	2.48	7	1
2:B:1116:ASP:HB2	2:B:1117:PRO:HD2	0.43	1.90	13	1
2:B:1123:PRO:O	2:B:1125:TYR:N	0.43	2.51	20	2
2:B:1131:ASN:CB	2:B:1159:LEU:HD11	0.43	2.42	18	1
2:B:1116:ASP:OD1	2:B:1132:PRO:CG	0.43	2.66	19	1
2:B:1084:ILE:HG13	2:B:1090:LEU:CD2	0.43	2.43	13	6
2:B:1133:MET:O	2:B:1137:THR:CG2	0.43	2.66	2	1
2:B:1095:MET:O	2:B:1098:LEU:CB	0.43	2.66	9	5
2:B:1081:ARG:NH2	2:B:1195:SER:O	0.43	2.51	6	2
2:B:1102:TYR:CB	2:B:1139:LYS:HE3	0.43	2.43	6	2
2:B:1129:VAL:HG11	2:B:1163:ASN:CB	0.43	2.43	13	1
2:B:1105:ASP:CG	2:B:1106:PRO:CD	0.43	2.92	14	1
2:B:1129:VAL:CG2	2:B:1163:ASN:O	0.43	2.67	8	3
2:B:1098:LEU:O	2:B:1102:TYR:N	0.43	2.51	10	9
2:B:1188:GLU:O	2:B:1192:VAL:CG2	0.43	2.66	16	10
2:B:1100:ALA:CB	2:B:1188:GLU:CD	0.43	2.92	11	3
2:B:1107:GLU:HB3	2:B:1181:LEU:CD2	0.43	2.43	12	2
2:B:1164:ALA:O	2:B:1168:ASN:CB	0.43	2.67	10	1
2:B:1193:MET:HB3	2:B:1196:LEU:HD23	0.43	1.91	14	1
2:B:1114:PRO:O	2:B:1115:VAL:C	0.43	2.61	16	1
2:B:1142:LEU:CD1	2:B:1153:TYR:CD1	0.43	3.01	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:383:LEU:O	1:A:384:MET:CG	0.43	2.66	18	1
2:B:1092:GLN:O	2:B:1095:MET:N	0.43	2.50	7	8
2:B:1150:PRO:O	2:B:1154:VAL:CG2	0.43	2.66	12	12
2:B:1099:GLU:O	2:B:1103:ARG:CG	0.43	2.66	2	3
2:B:1102:TYR:CE2	2:B:1135:LEU:O	0.43	2.71	4	1
2:B:1102:TYR:HB2	2:B:1139:LYS:CE	0.43	2.43	15	3
2:B:1112:ARG:O	2:B:1112:ARG:CG	0.43	2.66	7	1
2:B:1115:VAL:O	2:B:1115:VAL:CG1	0.43	2.67	8	1
2:B:1158:TRP:O	2:B:1162:ASN:N	0.43	2.51	8	1
2:B:1105:ASP:OD2	2:B:1108:SER:N	0.43	2.51	13	1
2:B:1122:ILE:HD12	2:B:1123:PRO:CD	0.43	2.44	15	1
2:B:1098:LEU:CD1	2:B:1139:LYS:CE	0.43	2.96	1	1
2:B:1190:ASP:CB	2:B:1191:PRO:CD	0.43	2.97	12	2
2:B:1131:ASN:O	2:B:1159:LEU:CD2	0.43	2.67	12	5
2:B:1159:LEU:CD2	2:B:1159:LEU:C	0.43	2.91	4	1
2:B:1121:GLY:C	2:B:1122:ILE:CG2	0.43	2.92	19	3
2:B:1101:LEU:O	2:B:1181:LEU:CD1	0.43	2.67	12	2
2:B:1167:TYR:CD2	2:B:1167:TYR:O	0.43	2.71	13	1
2:B:1119:LEU:O	2:B:1119:LEU:CG	0.43	2.66	19	1
2:B:1125:TYR:HA	2:B:1128:ILE:CG1	0.43	2.43	20	2
2:B:1126:PHE:CD1	2:B:1126:PHE:C	0.43	2.96	4	1
2:B:1155:ASP:O	2:B:1159:LEU:CB	0.43	2.66	5	3
2:B:1163:ASN:ND2	2:B:1163:ASN:C	0.43	2.76	8	1
2:B:1163:ASN:ND2	2:B:1167:TYR:OH	0.43	2.51	10	1
2:B:1185:PHE:O	2:B:1189:ILE:CG1	0.43	2.67	20	2
2:B:1164:ALA:O	2:B:1168:ASN:ND2	0.43	2.52	1	3
2:B:1105:ASP:CB	2:B:1106:PRO:CD	0.43	2.96	14	3
2:B:1138:ILE:O	2:B:1142:LEU:HB2	0.43	2.14	16	2
2:B:1101:LEU:C	2:B:1101:LEU:CD2	0.43	2.92	20	1
2:B:1084:ILE:HD12	2:B:1193:MET:C	0.43	2.38	1	1
2:B:1169:ARG:O	2:B:1175:TYR:CB	0.43	2.67	6	1
2:B:1154:VAL:O	2:B:1158:TRP:CB	0.43	2.67	8	2
2:B:1111:PHE:O	2:B:1113:GLN:N	0.43	2.52	15	3
2:B:1129:VAL:HG22	2:B:1166:LEU:HG	0.43	1.90	13	1
2:B:1118:GLN:O	2:B:1119:LEU:HB2	0.43	2.14	14	1
2:B:1107:GLU:O	2:B:1177:PHE:CA	0.43	2.67	17	1
2:B:1107:GLU:CD	2:B:1180:LYS:CB	0.43	2.92	20	1
2:B:1169:ARG:CG	2:B:1169:ARG:O	0.43	2.67	20	1
2:B:1180:LYS:O	2:B:1184:VAL:CG1	0.43	2.66	7	3
2:B:1106:PRO:O	2:B:1110:PRO:CD	0.43	2.67	18	3
2:B:1136:SER:O	2:B:1140:ARG:CG	0.43	2.67	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1128:ILE:HG13	2:B:1129:VAL:HG23	0.43	1.91	5	1
2:B:1147:TYR:O	2:B:1149:GLU:N	0.43	2.51	6	1
2:B:1111:PHE:CD2	2:B:1135:LEU:CD1	0.43	3.01	9	1
2:B:1173:ARG:O	2:B:1174:VAL:C	0.43	2.62	9	1
2:B:1168:ASN:ND2	2:B:1168:ASN:C	0.43	2.76	12	1
2:B:1177:PHE:CE1	2:B:1178:CYS:SG	0.43	3.09	16	1
2:B:1116:ASP:OD1	2:B:1118:GLN:N	0.43	2.51	18	1
2:B:1156:ASP:O	2:B:1160:MET:CB	0.43	2.67	1	1
2:B:1107:GLU:O	2:B:1181:LEU:CD1	0.43	2.67	2	3
2:B:1128:ILE:O	2:B:1129:VAL:CG2	0.43	2.67	8	2
2:B:1125:TYR:CE2	2:B:1129:VAL:HG21	0.43	2.48	5	1
2:B:1168:ASN:ND2	2:B:1175:TYR:CD2	0.43	2.87	11	1
1:A:383:LEU:CD2	1:A:383:LEU:O	0.42	2.67	1	1
2:B:1094:LEU:O	2:B:1097:THR:CG2	0.42	2.67	1	1
2:B:1168:ASN:ND2	2:B:1174:VAL:O	0.42	2.52	3	1
2:B:1129:VAL:CG2	2:B:1163:ASN:CG	0.42	2.92	6	1
2:B:1138:ILE:O	2:B:1142:LEU:N	0.42	2.52	11	1
2:B:1114:PRO:C	2:B:1119:LEU:CD2	0.42	2.92	13	1
2:B:1114:PRO:O	2:B:1119:LEU:CD2	0.42	2.67	13	1
1:A:384:MET:O	2:B:1173:ARG:NH2	0.42	2.52	20	1
2:B:1102:TYR:CD1	2:B:1139:LYS:CD	0.42	3.02	20	1
2:B:1172:SER:OG	2:B:1173:ARG:NH2	0.42	2.52	20	1
2:B:1190:ASP:CB	2:B:1191:PRO:HD3	0.42	2.44	1	8
2:B:1194:GLN:NE2	2:B:1194:GLN:O	0.42	2.52	15	2
2:B:1163:ASN:O	2:B:1164:ALA:CB	0.42	2.67	10	1
2:B:1168:ASN:ND2	2:B:1168:ASN:N	0.42	2.67	14	1
2:B:1192:VAL:HG12	2:B:1192:VAL:O	0.42	2.14	14	1
2:B:1170:LYS:C	2:B:1171:THR:CG2	0.42	2.92	15	1
2:B:1116:ASP:N	2:B:1125:TYR:OH	0.42	2.52	18	1
2:B:1147:TYR:CD1	2:B:1147:TYR:N	0.42	2.87	18	1
2:B:1194:GLN:CD	2:B:1194:GLN:C	0.42	2.88	10	8
2:B:1115:VAL:O	2:B:1115:VAL:CG2	0.42	2.67	7	3
2:B:1112:ARG:O	2:B:1112:ARG:NH1	0.42	2.52	8	1
2:B:1142:LEU:CD2	2:B:1147:TYR:O	0.42	2.67	9	1
2:B:1119:LEU:O	2:B:1120:LEU:CB	0.42	2.67	19	2
2:B:1100:ALA:O	2:B:1184:VAL:CG1	0.42	2.67	16	1
2:B:1141:LYS:HB3	2:B:1147:TYR:CD2	0.42	2.50	6	2
2:B:1150:PRO:O	2:B:1154:VAL:HB	0.42	2.14	11	4
1:A:384:MET:HA	2:B:1174:VAL:HG21	0.42	1.92	6	1
2:B:1092:GLN:O	2:B:1096:PRO:HD3	0.42	2.14	6	2
2:B:1131:ASN:O	2:B:1159:LEU:CD1	0.42	2.67	6	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1189:ILE:CD1	2:B:1195:SER:OG	0.42	2.66	12	2
2:B:1192:VAL:O	2:B:1193:MET:HB2	0.42	2.13	11	3
2:B:1122:ILE:O	2:B:1123:PRO:C	0.42	2.63	16	3
2:B:1101:LEU:HD23	2:B:1139:LYS:CE	0.42	2.45	4	1
2:B:1102:TYR:CD1	2:B:1139:LYS:HE3	0.42	2.49	7	1
2:B:1122:ILE:HD11	2:B:1125:TYR:CE1	0.42	2.49	7	1
2:B:1154:VAL:CG1	2:B:1194:GLN:NE2	0.42	2.83	11	1
2:B:1081:ARG:NE	2:B:1196:LEU:CB	0.42	2.83	12	1
2:B:1081:ARG:CB	2:B:1196:LEU:HD23	0.42	2.45	18	1
2:B:1102:TYR:CD2	2:B:1139:LYS:HG2	0.42	2.50	19	1
2:B:1102:TYR:CD2	2:B:1139:LYS:HE2	0.42	2.50	19	1
2:B:1165:TRP:HA	2:B:1168:ASN:OD1	0.42	2.15	19	1
2:B:1181:LEU:HA	2:B:1184:VAL:CG1	0.42	2.45	1	2
2:B:1101:LEU:O	2:B:1181:LEU:CD2	0.42	2.66	2	5
2:B:1170:LYS:O	2:B:1172:SER:N	0.42	2.52	8	2
2:B:1154:VAL:CG2	2:B:1194:GLN:OE1	0.42	2.67	5	2
2:B:1196:LEU:HG	2:B:1197:GLY:N	0.42	2.30	6	1
2:B:1148:GLN:NE2	2:B:1148:GLN:C	0.42	2.78	8	1
2:B:1156:ASP:O	2:B:1159:LEU:CB	0.42	2.68	8	1
2:B:1179:SER:O	2:B:1183:GLU:CB	0.42	2.67	9	1
1:A:384:MET:O	2:B:1173:ARG:NE	0.42	2.53	11	2
2:B:1118:GLN:O	2:B:1122:ILE:HG23	0.42	2.14	14	1
2:B:1129:VAL:CG2	2:B:1163:ASN:HA	0.42	2.44	16	1
2:B:1102:TYR:CE1	2:B:1139:LYS:HG3	0.42	2.49	20	1
2:B:1129:VAL:O	2:B:1131:ASN:N	0.42	2.52	5	2
2:B:1111:PHE:CD1	2:B:1160:MET:SD	0.42	3.13	4	1
2:B:1087:PRO:CB	2:B:1148:GLN:OE1	0.42	2.67	6	1
2:B:1133:MET:N	2:B:1133:MET:CE	0.42	2.76	8	1
2:B:1123:PRO:O	2:B:1124:ASP:C	0.42	2.63	9	1
2:B:1189:ILE:HB	2:B:1194:GLN:CD	0.42	2.40	12	1
2:B:1170:LYS:O	2:B:1171:THR:C	0.42	2.63	15	1
2:B:1178:CYS:O	2:B:1182:ALA:CB	0.42	2.67	15	1
2:B:1108:SER:N	2:B:1181:LEU:HD11	0.42	2.29	20	1
2:B:1122:ILE:HG12	2:B:1125:TYR:CE1	0.42	2.50	1	2
2:B:1133:MET:O	2:B:1160:MET:CE	0.42	2.67	1	2
2:B:1170:LYS:HA	2:B:1175:TYR:CD2	0.42	2.50	2	1
2:B:1132:PRO:HB3	2:B:1163:ASN:ND2	0.42	2.30	12	2
2:B:1094:LEU:O	2:B:1098:LEU:CD1	0.42	2.67	10	1
2:B:1184:VAL:O	2:B:1188:GLU:CG	0.42	2.67	11	1
2:B:1090:LEU:CD1	2:B:1149:GLU:OE2	0.42	2.67	17	1
2:B:1101:LEU:HD11	2:B:1161:PHE:CZ	0.42	2.50	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1086:LYS:CB	2:B:1089:GLU:OE1	0.42	2.67	2	1
2:B:1189:ILE:HB	2:B:1194:GLN:HG2	0.42	1.91	2	1
2:B:1090:LEU:O	2:B:1094:LEU:CG	0.42	2.68	17	2
2:B:1115:VAL:O	2:B:1116:ASP:O	0.42	2.38	18	2
2:B:1105:ASP:O	2:B:1109:LEU:CD1	0.42	2.67	9	1
2:B:1139:LYS:HA	2:B:1142:LEU:HB2	0.42	1.92	15	1
2:B:1095:MET:HB3	2:B:1096:PRO:CD	0.42	2.45	16	1
2:B:1141:LYS:HB2	2:B:1147:TYR:CE2	0.42	2.50	20	1
1:A:384:MET:CE	2:B:1169:ARG:CD	0.42	2.97	1	1
2:B:1110:PRO:HD2	2:B:1177:PHE:CD2	0.42	2.50	4	1
2:B:1163:ASN:O	2:B:1163:ASN:ND2	0.42	2.52	5	1
2:B:1149:GLU:O	2:B:1150:PRO:C	0.42	2.63	9	1
2:B:1098:LEU:HD23	2:B:1139:LYS:NZ	0.42	2.30	10	1
2:B:1160:MET:HE3	2:B:1160:MET:CA	0.42	2.43	11	1
2:B:1111:PHE:CD2	2:B:1181:LEU:HD12	0.42	2.49	16	2
2:B:1119:LEU:C	2:B:1119:LEU:CD1	0.42	2.92	16	1
2:B:1139:LYS:N	2:B:1139:LYS:HD2	0.42	2.29	16	1
2:B:1173:ARG:HG3	2:B:1174:VAL:N	0.41	2.30	14	2
2:B:1081:ARG:CZ	2:B:1195:SER:O	0.41	2.68	4	1
2:B:1165:TRP:O	2:B:1167:TYR:N	0.41	2.52	4	1
2:B:1192:VAL:C	2:B:1193:MET:CG	0.41	2.91	17	2
2:B:1090:LEU:HB3	2:B:1148:GLN:O	0.41	2.15	9	1
2:B:1143:ASP:O	2:B:1144:THR:CG2	0.41	2.68	10	1
2:B:1138:ILE:CG2	2:B:1139:LYS:N	0.41	2.83	13	1
2:B:1159:LEU:O	2:B:1163:ASN:N	0.41	2.49	16	2
2:B:1163:ASN:OD1	2:B:1164:ALA:N	0.41	2.53	2	1
2:B:1102:TYR:CG	2:B:1139:LYS:HG2	0.41	2.50	6	1
2:B:1128:ILE:O	2:B:1129:VAL:HG23	0.41	2.15	8	1
2:B:1148:GLN:CD	2:B:1148:GLN:C	0.41	2.88	9	1
2:B:1098:LEU:O	2:B:1102:TYR:CB	0.41	2.67	15	2
2:B:1116:ASP:HB2	2:B:1117:PRO:CD	0.41	2.44	13	1
2:B:1125:TYR:CD2	2:B:1129:VAL:HB	0.41	2.50	17	1
1:A:384:MET:O	1:A:384:MET:HG3	0.41	2.15	3	1
2:B:1128:ILE:HD13	2:B:1167:TYR:CG	0.41	2.50	6	1
2:B:1161:PHE:O	2:B:1165:TRP:CD1	0.41	2.73	8	1
2:B:1110:PRO:O	2:B:1113:GLN:CG	0.41	2.68	13	1
2:B:1133:MET:HE1	2:B:1156:ASP:HA	0.41	1.93	14	1
2:B:1091:ARG:NH1	2:B:1143:ASP:O	0.41	2.53	16	1
2:B:1116:ASP:OD1	2:B:1118:GLN:CB	0.41	2.69	3	1
2:B:1173:ARG:CG	2:B:1174:VAL:N	0.41	2.83	14	3
2:B:1157:VAL:O	2:B:1160:MET:N	0.41	2.54	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1161:PHE:O	2:B:1165:TRP:CB	0.41	2.69	6	1
2:B:1116:ASP:OD1	2:B:1117:PRO:N	0.41	2.53	13	1
1:A:384:MET:O	1:A:384:MET:HE2	0.41	2.15	14	1
2:B:1109:LEU:C	2:B:1109:LEU:HD12	0.41	2.41	14	1
2:B:1117:PRO:C	2:B:1118:GLN:CG	0.41	2.92	14	1
2:B:1112:ARG:O	2:B:1113:GLN:CG	0.41	2.69	16	1
2:B:1168:ASN:O	2:B:1169:ARG:HG2	0.41	2.15	20	1
2:B:1189:ILE:O	2:B:1192:VAL:N	0.41	2.53	20	1
2:B:1147:TYR:O	2:B:1148:GLN:C	0.41	2.63	4	1
2:B:1097:THR:CG2	2:B:1098:LEU:N	0.41	2.83	6	1
2:B:1182:ALA:O	2:B:1185:PHE:CD2	0.41	2.74	10	1
2:B:1156:ASP:O	2:B:1160:MET:N	0.41	2.52	12	1
2:B:1094:LEU:HD23	2:B:1153:TYR:CD2	0.41	2.50	14	1
2:B:1084:ILE:HG12	2:B:1090:LEU:CD2	0.41	2.46	15	1
2:B:1173:ARG:HG2	2:B:1174:VAL:HG23	0.41	1.92	15	1
2:B:1089:GLU:N	2:B:1089:GLU:OE1	0.41	2.53	16	1
2:B:1112:ARG:HB3	2:B:1112:ARG:CZ	0.41	2.45	16	1
2:B:1187:GLN:O	2:B:1191:PRO:CG	0.41	2.68	5	2
2:B:1158:TRP:O	2:B:1158:TRP:CD1	0.41	2.74	6	1
2:B:1133:MET:SD	2:B:1156:ASP:CB	0.41	3.09	9	2
2:B:1161:PHE:CZ	2:B:1182:ALA:HA	0.41	2.51	10	1
2:B:1133:MET:O	2:B:1134:ASP:OD1	0.41	2.39	17	1
2:B:1111:PHE:CE1	2:B:1160:MET:HG3	0.41	2.51	18	1
2:B:1106:PRO:O	2:B:1107:GLU:C	0.41	2.63	20	1
2:B:1189:ILE:O	2:B:1192:VAL:HB	0.41	2.15	2	1
2:B:1102:TYR:CG	2:B:1139:LYS:HG3	0.41	2.51	9	1
2:B:1107:GLU:OE1	2:B:1107:GLU:CA	0.41	2.67	13	1
2:B:1196:LEU:C	2:B:1196:LEU:CD2	0.41	2.92	13	1
2:B:1110:PRO:HB2	2:B:1177:PHE:CE1	0.41	2.51	16	1
2:B:1134:ASP:O	2:B:1137:THR:N	0.41	2.53	3	4
2:B:1138:ILE:HD11	2:B:1153:TYR:CD1	0.41	2.51	11	1
2:B:1159:LEU:O	2:B:1163:ASN:CB	0.41	2.69	11	1
2:B:1094:LEU:O	2:B:1098:LEU:CG	0.41	2.69	13	1
1:A:383:LEU:HD22	1:A:383:LEU:N	0.41	2.31	16	1
2:B:1116:ASP:C	2:B:1118:GLN:N	0.41	2.79	19	1
2:B:1133:MET:HE3	2:B:1160:MET:HB2	0.41	1.92	2	1
2:B:1095:MET:HB3	2:B:1096:PRO:HD3	0.41	1.92	3	2
2:B:1098:LEU:HD13	2:B:1102:TYR:HB2	0.41	1.93	3	1
2:B:1168:ASN:ND2	2:B:1175:TYR:CG	0.41	2.88	4	1
2:B:1095:MET:N	2:B:1096:PRO:HD2	0.41	2.31	5	1
2:B:1173:ARG:C	2:B:1174:VAL:HG23	0.41	2.41	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1154:VAL:CG2	2:B:1194:GLN:CD	0.41	2.93	11	1
1:A:383:LEU:CD2	1:A:383:LEU:N	0.41	2.84	16	1
1:A:383:LEU:O	1:A:383:LEU:CD1	0.41	2.65	19	1
1:A:383:LEU:O	1:A:383:LEU:CD2	0.41	2.68	20	1
2:B:1169:ARG:HB2	2:B:1175:TYR:CD2	0.41	2.50	20	1
2:B:1094:LEU:HD21	2:B:1153:TYR:CD2	0.41	2.50	10	1
2:B:1129:VAL:HG11	2:B:1163:ASN:HD22	0.41	1.75	10	1
2:B:1142:LEU:CD2	2:B:1153:TYR:CE1	0.41	3.04	11	1
2:B:1154:VAL:HG21	2:B:1194:GLN:CG	0.41	2.46	13	1
2:B:1141:LYS:CG	2:B:1146:GLN:HB3	0.41	2.45	14	1
2:B:1189:ILE:HD12	2:B:1194:GLN:HE21	0.41	1.76	14	1
2:B:1111:PHE:CD1	2:B:1135:LEU:HG	0.41	2.51	15	1
2:B:1134:ASP:OD1	2:B:1134:ASP:C	0.41	2.63	17	1
2:B:1095:MET:CE	2:B:1099:GLU:OE1	0.40	2.69	3	1
2:B:1161:PHE:CE1	2:B:1182:ALA:HA	0.40	2.52	4	1
2:B:1131:ASN:O	2:B:1131:ASN:ND2	0.40	2.53	8	1
2:B:1157:VAL:HG12	2:B:1161:PHE:CD2	0.40	2.51	11	1
2:B:1081:ARG:HG2	2:B:1196:LEU:CD2	0.40	2.46	1	1
2:B:1157:VAL:O	2:B:1161:PHE:CD2	0.40	2.75	2	1
2:B:1189:ILE:HB	2:B:1194:GLN:CG	0.40	2.46	2	1
2:B:1081:ARG:NH2	2:B:1197:GLY:OXT	0.40	2.54	4	1
2:B:1115:VAL:O	2:B:1116:ASP:C	0.40	2.64	7	1
2:B:1116:ASP:CB	2:B:1117:PRO:HD2	0.40	2.47	13	1
2:B:1090:LEU:O	2:B:1091:ARG:C	0.40	2.63	14	1
2:B:1149:GLU:O	2:B:1149:GLU:CG	0.40	2.69	14	1
2:B:1094:LEU:C	2:B:1097:THR:HG22	0.40	2.42	15	1
2:B:1111:PHE:CD1	2:B:1135:LEU:CG	0.40	3.04	15	1
2:B:1115:VAL:CA	2:B:1119:LEU:HD21	0.40	2.47	16	1
2:B:1167:TYR:O	2:B:1168:ASN:C	0.40	2.63	17	1
2:B:1110:PRO:CG	2:B:1177:PHE:CG	0.40	3.04	19	1
2:B:1125:TYR:O	2:B:1127:ASP:N	0.40	2.52	2	1
2:B:1141:LYS:HB3	2:B:1147:TYR:CD1	0.40	2.52	19	2
2:B:1133:MET:N	2:B:1133:MET:SD	0.40	2.95	6	1
1:A:383:LEU:CD2	2:B:1119:LEU:CD1	0.40	2.99	9	1
2:B:1185:PHE:O	2:B:1189:ILE:HG12	0.40	2.16	11	1
2:B:1124:ASP:N	2:B:1124:ASP:OD1	0.40	2.54	13	1
2:B:1117:PRO:O	2:B:1118:GLN:CD	0.40	2.64	14	1
2:B:1084:ILE:N	2:B:1084:ILE:HD13	0.40	2.31	16	1
2:B:1194:GLN:C	2:B:1194:GLN:CD	0.40	2.90	16	1
2:B:1173:ARG:O	2:B:1173:ARG:CG	0.40	2.67	5	1
2:B:1131:ASN:O	2:B:1133:MET:CE	0.40	2.70	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:1115:VAL:O	2:B:1115:VAL:HG22	0.40	2.15	14	1
2:B:1117:PRO:O	2:B:1118:GLN:HB3	0.40	2.16	14	1
2:B:1141:LYS:CD	2:B:1147:TYR:CZ	0.40	3.04	14	1
2:B:1107:GLU:N	2:B:1107:GLU:OE1	0.40	2.55	17	1
2:B:1168:ASN:OD1	2:B:1168:ASN:N	0.40	2.53	17	1
2:B:1102:TYR:HD2	2:B:1135:LEU:HD22	0.40	1.76	18	1
2:B:1101:LEU:HD23	2:B:1102:TYR:N	0.40	2.32	2	1
2:B:1185:PHE:O	2:B:1188:GLU:N	0.40	2.55	5	1
2:B:1101:LEU:O	2:B:1101:LEU:HD12	0.40	2.17	13	1
2:B:1090:LEU:CD1	2:B:1149:GLU:CD	0.40	2.95	17	1
2:B:1102:TYR:CB	2:B:1139:LYS:HE2	0.40	2.46	19	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	2/20 (10%)	1±1 (50±27%)	1±1 (45±31%)	0±0 (5±15%)	3	24
2	B	116/121 (96%)	86±4 (75±3%)	21±3 (18±3%)	8±2 (7±2%)	1	15
All	All	2360/2820 (84%)	1750 (74%)	439 (19%)	171 (7%)	2	15

All 42 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	1085	PHE	20
2	B	1104	GLN	12
2	B	1196	LEU	10
2	B	1114	PRO	9
2	B	1176	LYS	8
2	B	1123	PRO	7
2	B	1171	THR	7
2	B	1115	VAL	7
2	B	1084	ILE	6
2	B	1129	VAL	6

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Mol	Chain	Res	Type	Models (Total)
2	B	1170	LYS	6
2	B	1120	LEU	6
2	B	1116	ASP	6
2	B	1121	GLY	6
2	B	1124	ASP	5
2	B	1111	PHE	4
2	B	1169	ARG	4
2	B	1168	ASN	4
2	B	1118	GLN	3
2	B	1122	ILE	3
2	B	1081	ARG	3
2	B	1119	LEU	2
2	B	1157	VAL	2
1	A	383	LEU	2
2	B	1126	PHE	2
2	B	1173	ARG	2
2	B	1117	PRO	2
2	B	1125	TYR	2
2	B	1105	ASP	2
2	B	1148	GLN	1
2	B	1167	TYR	1
2	B	1165	TRP	1
2	B	1132	PRO	1
2	B	1133	MET	1
2	B	1150	PRO	1
2	B	1174	VAL	1
2	B	1175	TYR	1
2	B	1134	ASP	1
2	B	1164	ALA	1
2	B	1112	ARG	1
2	B	1127	ASP	1
2	B	1130	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	2/18 (11%)	1±1 (42±36%)	1±1 (57±36%)	0 0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	110/113 (97%)	78±4 (71±4%)	32±4 (29±4%)	1	18
All	All	2240/2620 (85%)	1581 (71%)	659 (29%)	1	18

All 90 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)
2	B	1185	PHE	19
2	B	1085	PHE	17
2	B	1098	LEU	16
2	B	1095	MET	15
1	A	383	LEU	14
2	B	1190	ASP	14
2	B	1120	LEU	14
2	B	1105	ASP	13
2	B	1194	GLN	13
2	B	1088	GLU	13
2	B	1084	ILE	12
2	B	1118	GLN	12
2	B	1119	LEU	12
2	B	1081	ARG	12
2	B	1166	LEU	12
2	B	1193	MET	12
2	B	1130	LYS	12
2	B	1162	ASN	11
2	B	1165	TRP	11
2	B	1086	LYS	11
2	B	1167	TYR	11
2	B	1122	ILE	11
2	B	1111	PHE	10
2	B	1125	TYR	10
2	B	1137	THR	10
2	B	1195	SER	10
2	B	1083	LYS	10
2	B	1160	MET	10
2	B	1184	VAL	10
2	B	1144	THR	9
2	B	1112	ARG	9
2	B	1176	LYS	9
2	B	1196	LEU	9
1	A	384	MET	9
2	B	1173	ARG	8

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Mol	Chain	Res	Type	Models (Total)
2	B	1180	LYS	8
2	B	1142	LEU	8
2	B	1104	GLN	8
2	B	1148	GLN	8
2	B	1143	ASP	7
2	B	1170	LYS	7
2	B	1101	LEU	7
2	B	1139	LYS	7
2	B	1149	GLU	7
2	B	1131	ASN	7
2	B	1159	LEU	7
2	B	1168	ASN	7
2	B	1169	ARG	6
2	B	1172	SER	6
2	B	1082	LYS	6
2	B	1128	ILE	6
2	B	1136	SER	6
2	B	1141	LYS	6
2	B	1186	GLU	6
2	B	1155	ASP	6
2	B	1109	LEU	6
2	B	1152	GLN	6
2	B	1113	GLN	5
2	B	1092	GLN	5
2	B	1163	ASN	5
2	B	1115	VAL	5
2	B	1116	ASP	5
2	B	1099	GLU	4
2	B	1146	GLN	4
2	B	1133	MET	4
2	B	1091	ARG	4
2	B	1127	ASP	4
2	B	1135	LEU	4
2	B	1140	ARG	4
2	B	1124	ASP	4
2	B	1183	GLU	4
2	B	1103	ARG	4
2	B	1189	ILE	4
2	B	1126	PHE	3
2	B	1188	GLU	3
2	B	1178	CYS	3
2	B	1102	TYR	3

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Mol	Chain	Res	Type	Models (Total)
2	B	1161	PHE	3
2	B	1181	LEU	3
2	B	1187	GLN	2
2	B	1107	GLU	2
2	B	1134	ASP	2
2	B	1179	SER	1
2	B	1138	ILE	1
2	B	1156	ASP	1
2	B	1108	SER	1
2	B	1097	THR	1
2	B	1089	GLU	1
2	B	1117	PRO	1
2	B	1171	THR	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	ALY	A	382	1	10,11,12	0.91±0.06	0±0 (1±4%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	ALY	A	382	1	7,12,14	1.27±0.12	1±1 (13±8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	ALY	A	382	1	-	0±0,9,10,12	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	382	ALY	CH3-CH	2.04	1.54	1.50	15	1
1	A	382	ALY	CE-NZ	2.03	1.50	1.46	15	2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	382	ALY	CD-CE-NZ	2.69	104.65	112.20	8	16
1	A	382	ALY	CE-NZ-CH	2.13	119.41	122.56	9	3

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided