Full wwPDB NMR Structure Validation Report (i)

Apr 20, 2024 – 03:20 PM EDT

PDB ID	:	1Q53
Title	:	SOLUTION STRUCTURE OF HYPOTHETICAL ARABIDOPSIS THALIANA PROTEIN AT3G17210. CENTER FOR EUKARYOTIC STRUCTURAL GENOMICS TARGET 13081
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Deposited on	:	2003-08-06

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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

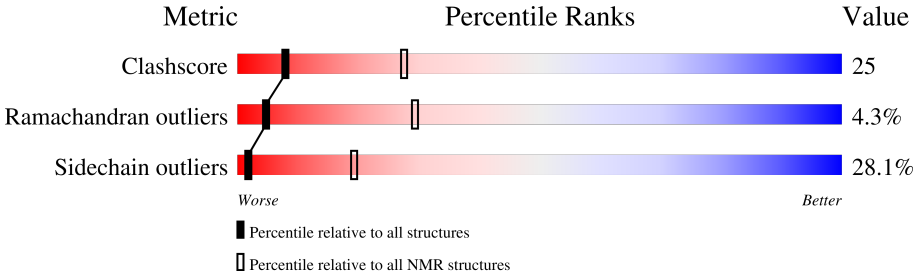
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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	Whole archive (#Entries)	NMR archive (#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	112	40% 48% • 8%
1	B	112	33% 54% • 8%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:10-A:112, B:10-B:112 (206)	1.37	6

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 3521 atoms, of which 1759 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called expressed protein: At3g17210.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	112	1761	573	880	141	165	2	0
1	B	112	1760	573	879	141	165	2	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q9LUV2
A	2	SER	-	cloning artifact	UNP Q9LUV2
A	3	HIS	-	cloning artifact	UNP Q9LUV2
B	1	GLY	-	cloning artifact	UNP Q9LUV2
B	2	SER	-	cloning artifact	UNP Q9LUV2
B	3	HIS	-	cloning artifact	UNP Q9LUV2

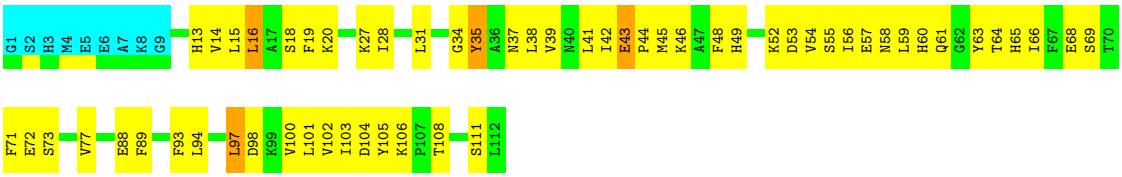
4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

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

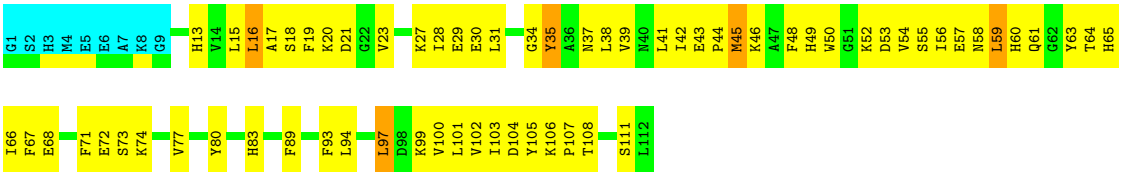
• Molecule 1: expressed protein: At3g17210

Chain A: 40% 48% • 8%



• Molecule 1: expressed protein: At3g17210

Chain B: 33% 54% • 8%



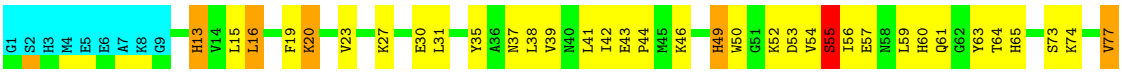
4.2 Scores per residue for each member of the ensemble

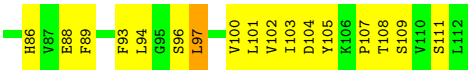
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: expressed protein: At3g17210

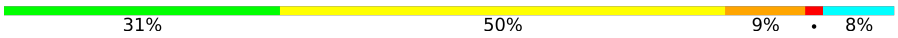
Chain A: 46% 40% 5% • 8%

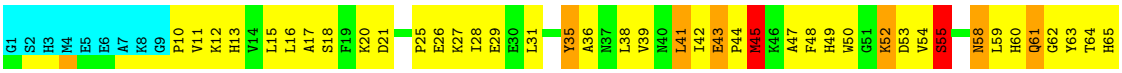


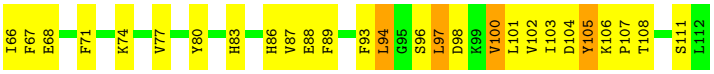


• Molecule 1: expressed protein: At3g17210

Chain B:



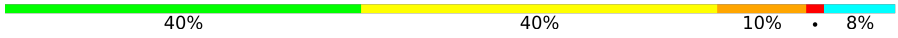


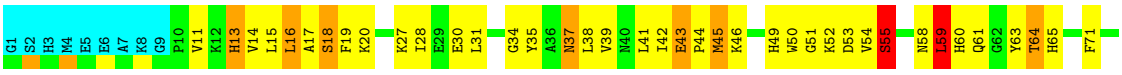


4.2.2 Score per residue for model 2

• Molecule 1: expressed protein: At3g17210

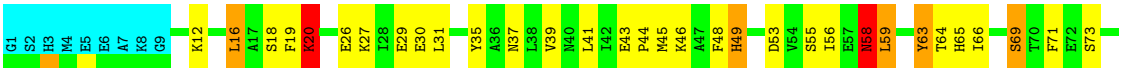
Chain A:

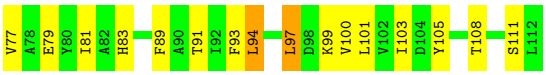




• Molecule 1: expressed protein: At3g17210

Chain B:

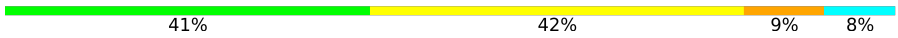


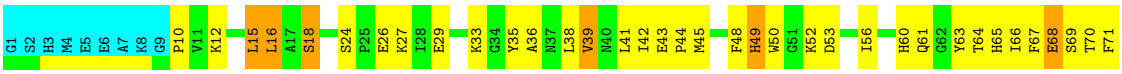


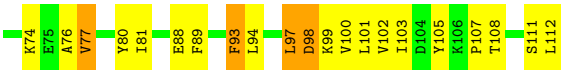
4.2.3 Score per residue for model 3

• Molecule 1: expressed protein: At3g17210

Chain A:

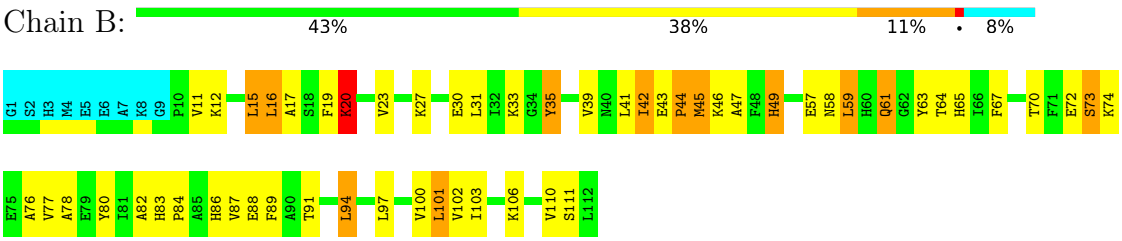






• Molecule 1: expressed protein: At3g17210

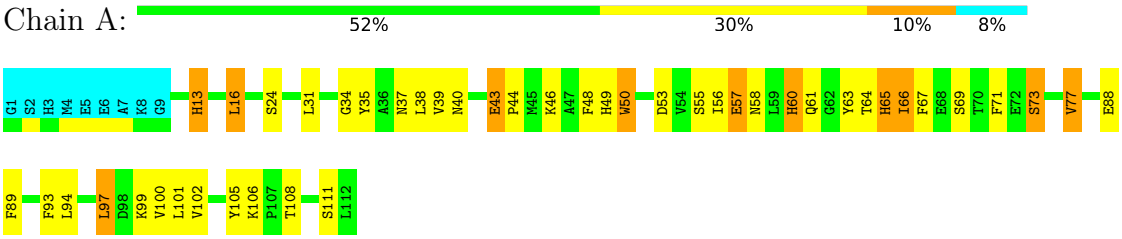
Chain B:



4.2.4 Score per residue for model 4

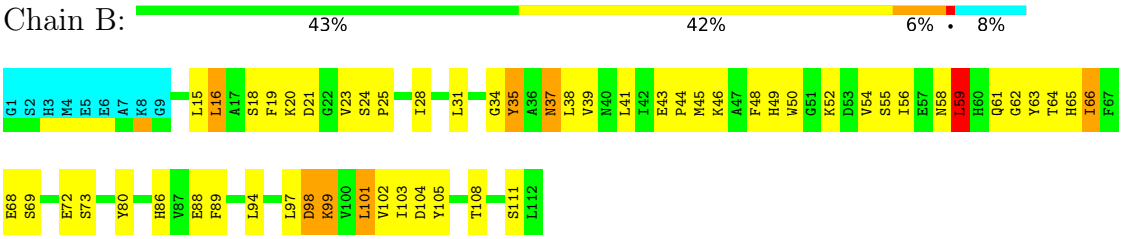
- Molecule 1: expressed protein: At3g17210

Chain A:



- Molecule 1: expressed protein: At3g17210

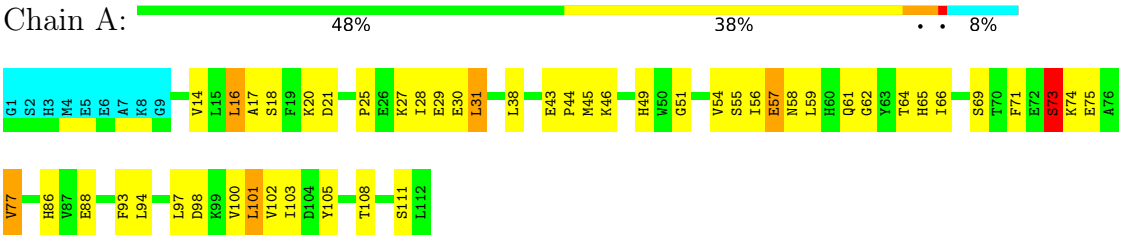
Chain B:



4.2.5 Score per residue for model 5

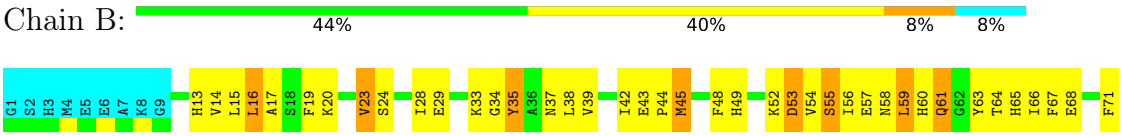
- Molecule 1: expressed protein: At3g17210

Chain A:



- Molecule 1: expressed protein: At3g17210

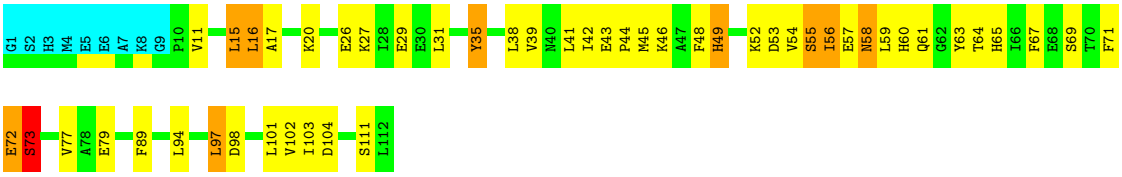
Chain B:



4.2.6 Score per residue for model 6 (medoid)

• Molecule 1: expressed protein: At3g17210

Chain A:



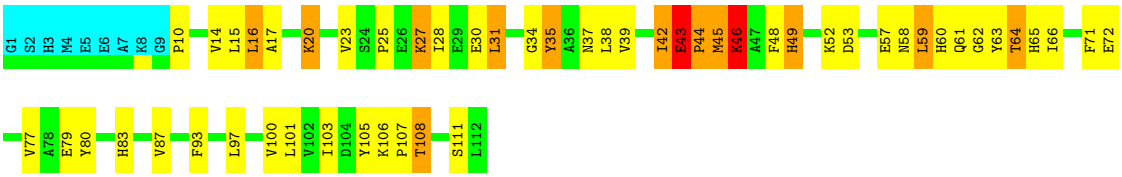
• Molecule 1: expressed protein: At3g17210

Chain B:

4.2.7 Score per residue for model 7

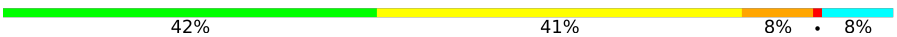
• Molecule 1: expressed protein: At3g17210

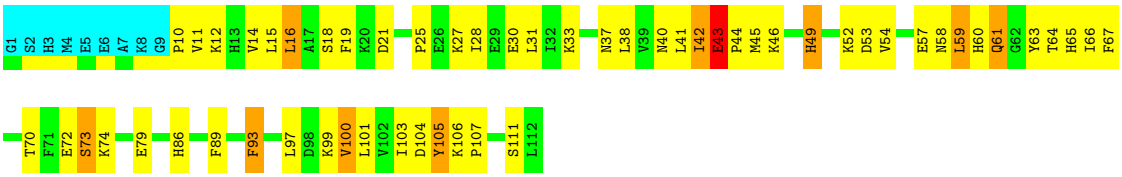
Chain A:



• Molecule 1: expressed protein: At3g17210

Chain B:

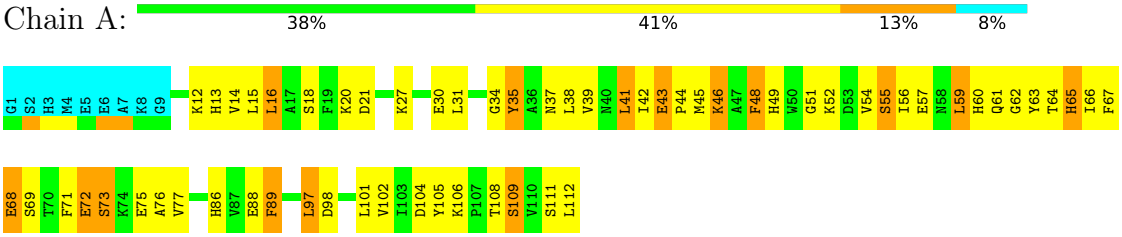




4.2.8 Score per residue for model 8

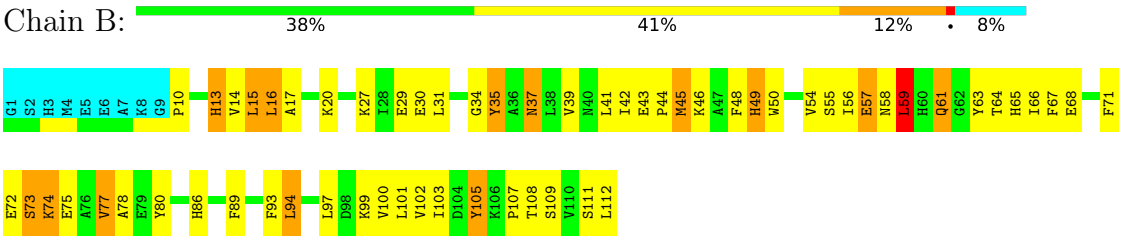
- Molecule 1: expressed protein: At3g17210

Chain A:



- Molecule 1: expressed protein: At3g17210

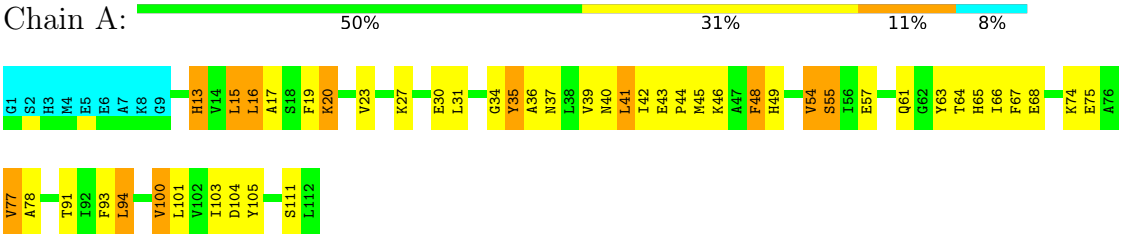
Chain B:



4.2.9 Score per residue for model 9

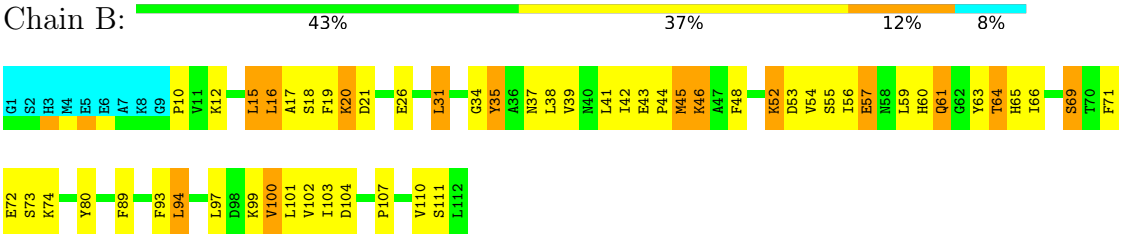
- Molecule 1: expressed protein: At3g17210

Chain A:



- Molecule 1: expressed protein: At3g17210

Chain B:



4.2.10 Score per residue for model 10

- Molecule 1: expressed protein: At3g17210

Chain A: 49% 33% 10% 8%

G1 S2 H3 M4 E5 E6 A7 K8 G9 P10 V11 K12 H13 V14 L15 L16 A17 S18 F19 K20 E29 E30 L31 I32 K33 G34 Y35 A36 N37 L38 V39 N40 L41 I42 E43 P44 M45 K46 A47 F48 H49 K52 D53 V54 E57 H60 Q61 G62 Y63 T64 H65 F71 K74

V77 A78 E79 Y80 H83 E88 F89 F93 L97 V100 L101 V102 Y105 K106 P107 T108 S111 L112

• Molecule 1: expressed protein: At3g17210

Chain B: 39% 42% 11% 8%

G1 S2 H3 M4 E5 E6 A7 K8 G9 P10 V11 K12 H13 V14 L15 L16 D21 G22 V23 S24 K27 I28 E29 E30 L31 I32 K33 G34 Y35 A36 N37 L38 V39 I42 E43 P44 M45 K46 H49 W50 S55 I56 E57 N58 L59 H60 Q61 G62 Y63 T64 H65 I66 F67 E68

F71 E72 S73 K74 V77 A78 E79 Y80 H86 F89 A90 F93 L94 L97 V100 L101 V102 I103 D104 Y105 K106 P107 S111 L112

4.2.11 Score per residue for model 11

• Molecule 1: expressed protein: At3g17210

Chain A: 38% 43% 11% 8%

G1 S2 H3 M4 E5 E6 A7 K8 G9 P10 V14 L15 L16 A17 S18 F19 K20 D21 S24 I28 E29 E30 L31 I32 K33 G34 Y35 A36 N37 L38 V39 E43 P44 M45 F48 H49 K52 S55 I56 E57 N58 L59 H60 Q61 G62 Y63 T64 H65 I66 F67 E68 S69 T70

F71 E72 S73 K74 E75 A76 V77 Y80 I81 V87 E88 F89 F93 L94 L97 D98 K99 V100 L101 V102 I103 D104 T108 S111 L112

• Molecule 1: expressed protein: At3g17210

Chain B: 38% 40% 13% 8%

G1 S2 H3 M4 E5 E6 A7 K8 G9 P10 H13 V14 L15 L16 A17 S18 F19 K20 D21 G22 V23 S24 K27 I28 E29 E30 L31 Y35 V39 N40 L41 I42 E43 P44 M45 K46 A47 F48 H49 K52 D53 V54 S55 I56 E57 N58 L59 H60 Q61 G62 Y63 T64 H65 I66 F67

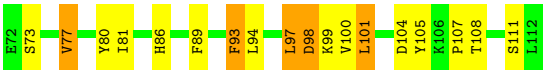
E68 F71 E72 S73 A76 V77 F89 F93 L94 L97 D98 K99 V100 L101 V102 I103 D104 Y105 K106 P107 T108 S111 L112

4.2.12 Score per residue for model 12

• Molecule 1: expressed protein: At3g17210

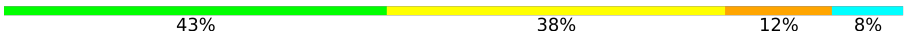
Chain A: 45% 32% 14% • 8%

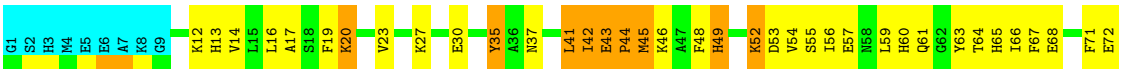
G1 S2 H3 M4 E5 E6 A7 K8 G9 K12 H13 V14 L15 L16 A17 S18 F19 K20 D21 P25 I28 L31 Y35 A36 N37 L38 V39 N40 L41 I42 E43 P44 M45 K46 A47 F48 H49 D53 E57 N58 L59 H60 Q61 G62 Y63 T64 H65 I66 F67 E68 S69 T70 F71



• Molecule 1: expressed protein: At3g17210

Chain B:

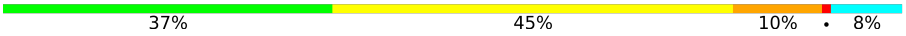


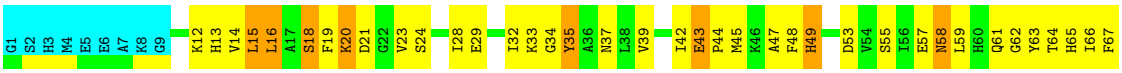


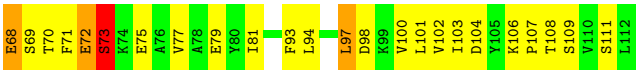
4.2.13 Score per residue for model 13

• Molecule 1: expressed protein: At3g17210

Chain A:

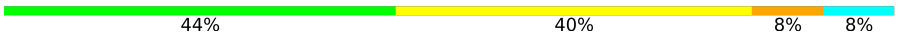


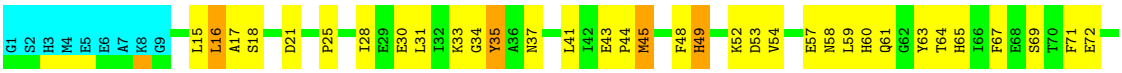


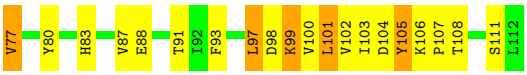


• Molecule 1: expressed protein: At3g17210

Chain B:



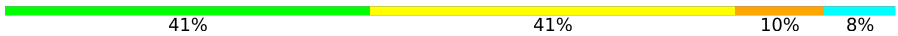


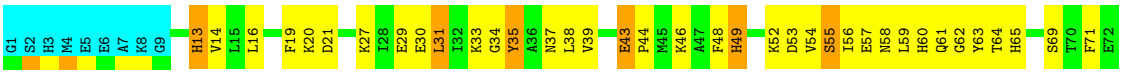


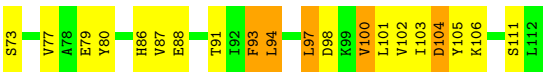
4.2.14 Score per residue for model 14

• Molecule 1: expressed protein: At3g17210

Chain A:







• Molecule 1: expressed protein: At3g17210

Chain B: 37% 43% 12% • 8%

G1 S2 H3 M4 E5 E6 A7 K8 G9 P10 V14 L15 L16 A17 S18 F19 K20 D21 G22 V23 S24 P25 E26 K27 I28 E29 E30 L31 I32 K33 G34 Y35 A36 N37 L38 V39 N40 L41 I42 E43 P44 M45 K46 A47 F48 H49 W50 G51 K52 D53 V54 S55 I56 E57 H60 Q61 G62 Y63

T64 H65 I66 F67 E68 S69 A76 E79 H83 H86 V87 E88 F89 F93 L97 D98 K99 V100 L101 V102 I103 D104 Y105 K106 P107 T108 S111 L112

4.2.15 Score per residue for model 15

- Molecule 1: expressed protein: At3g17210

Chain A: 48% 31% 11% • 8%

G1 S2 H3 M4 E5 E6 A7 K8 G9 V14 L15 L16 A17 S18 F19 K20 V23 S24 P25 E26 K27 I28 E29 E30 L31 Y35 A36 N37 L38 V39 I42 E43 P44 M45 K46 H49 V54 S55 I56 E57 N58 L59 H60 Q61 G62 Y63 T64 H65 I66 F67 E68 F71 E72

S73 K74 V77 E88 F89 F93 L97 V100 L101 Y105 K106 P107 S111 L112

- Molecule 1: expressed protein: At3g17210

Chain B: 41% 40% 11% 8%

G1 S2 H3 M4 E5 E6 A7 K8 G9 P10 V11 K12 H13 V14 L15 L16 A17 S18 F19 K20 V23 E29 E30 L31 G34 Y35 A36 N37 L38 V39 N40 L41 I42 E43 P44 M45 K46 A47 F48 H49 V54 S55 I56 E57 N58 L59 H60 Y63 T64 H65 I66 F67 E68 F71

E72 S73 K74 V77 A78 E79 H83 F89 A90 T91 L94 G95 S96 L97 D98 K99 V100 L101 V102 I103 D104 Y105 K106 P107 T108 L112

4.2.16 Score per residue for model 16

- Molecule 1: expressed protein: At3g17210

Chain A: 37% 48% 6% • 8%

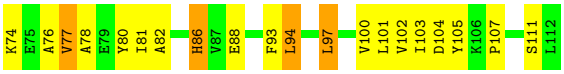
G1 S2 H3 M4 E5 E6 A7 K8 G9 P10 V11 K12 H13 V14 L15 L16 A17 S18 D21 K27 E30 L31 I32 K33 G34 Y35 A36 N37 L38 V39 N40 L41 I42 E43 P44 M45 K46 A47 F48 H49 K52 D53 V54 S55 I56 E57 N58 L59 H60 Q61 G62 Y63 T64 H65 I66 F67

E68 S69 T70 F71 E72 S73 K74 E75 A76 V77 A78 E79 A82 V87 E88 F89 L97 V100 L101 V102 I103 D104 Y105 K106 P107 T108 S111 L112

- Molecule 1: expressed protein: At3g17210

Chain B: 41% 39% 12% 8%

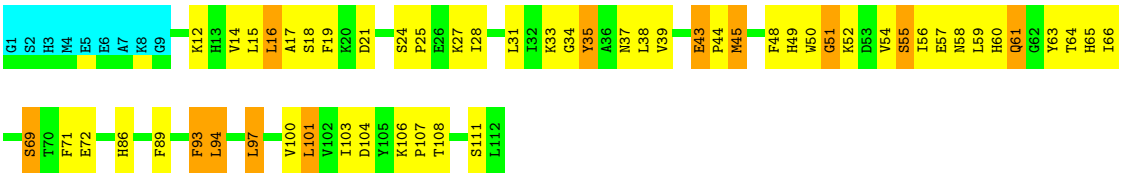
G1 S2 H3 M4 E5 E6 A7 K8 G9 K12 H13 V14 L15 L16 A17 K20 D21 G22 V23 K27 I28 E29 E30 G34 Y35 L38 E43 P44 M45 K46 H49 W50 D53 V54 E57 N58 L59 H60 Q61 G62 Y63 T64 H65 I66 F67 E68 S69 T70 F71 E72 S73



4.2.17 Score per residue for model 17

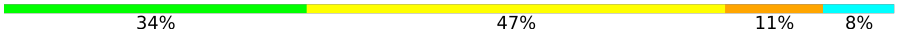
- Molecule 1: expressed protein: At3g17210

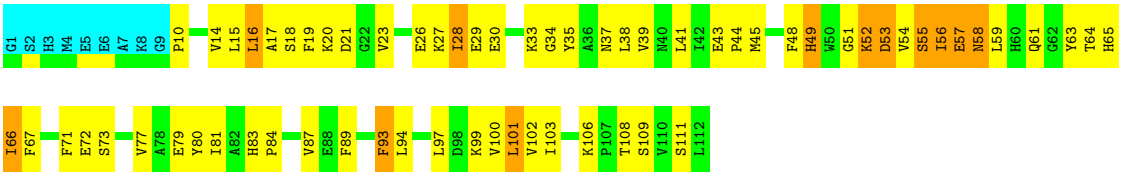
Chain A:



- Molecule 1: expressed protein: At3g17210

Chain B:

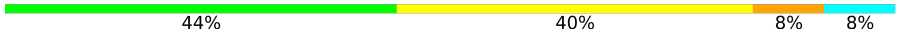


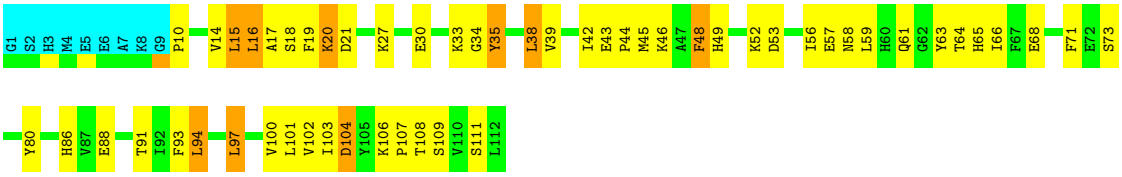


4.2.18 Score per residue for model 18

- Molecule 1: expressed protein: At3g17210

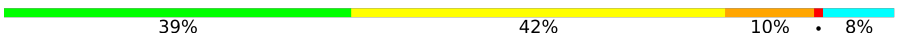
Chain A:

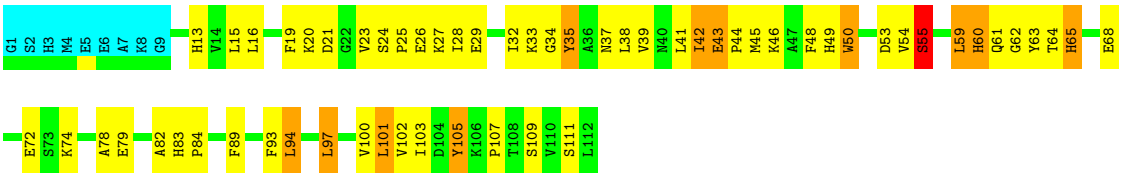




- Molecule 1: expressed protein: At3g17210

Chain B:

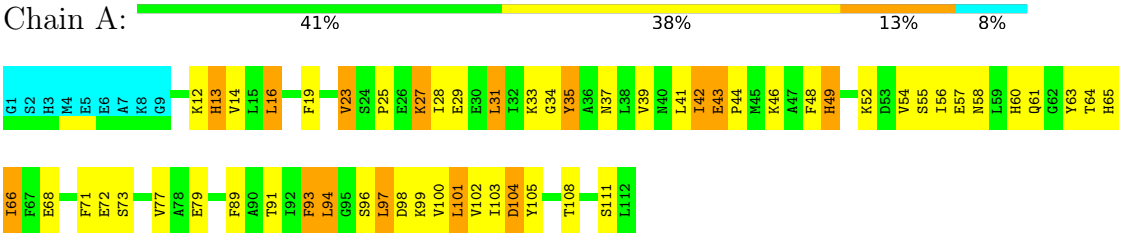




4.2.19 Score per residue for model 19

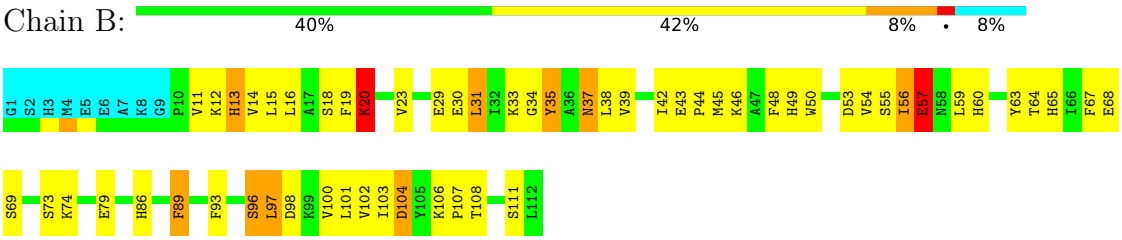
- Molecule 1: expressed protein: At3g17210

Chain A:



- Molecule 1: expressed protein: At3g17210

Chain B:



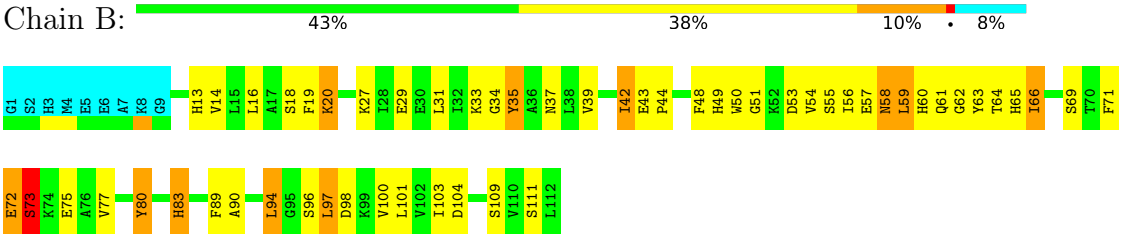
4.2.20 Score per residue for model 20

- Molecule 1: expressed protein: At3g17210

Chain A:

- Molecule 1: expressed protein: At3g17210

Chain B:



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *LOWEST TARGET FUNCTION*.

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

Software name	Classification	Version
CYANA	refinement	1.0.6
XwinNMR	structure solution	3.0
NMRPipe	structure solution	97.027.12.56
XEASY	structure solution	1.4
CYANA	structure solution	1.0.6

No chemical shift data was provided.

6 Model quality (i)

6.1 Standard geometry (i)

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts (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	A	817	822	816	48±7
1	B	817	822	816	48±9
All	All	32680	32880	32640	1640

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 25.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:64:THR:HG22	1:A:65:HIS:CE1	1.00	1.91	4	7
1:B:71:PHE:CD1	1:B:77:VAL:HG23	0.99	1.92	6	2
1:B:16:LEU:HD11	1:B:63:TYR:CD2	0.98	1.94	4	1
1:B:16:LEU:HD11	1:B:63:TYR:CE2	0.96	1.96	4	1
1:A:63:TYR:CZ	1:B:16:LEU:HD13	0.94	1.98	4	2
1:B:64:THR:HG22	1:B:65:HIS:CE1	0.92	2.00	2	10
1:A:63:TYR:CZ	1:B:16:LEU:HD21	0.92	2.00	18	4
1:A:97:LEU:O	1:A:97:LEU:HD13	0.92	1.64	14	3
1:B:71:PHE:CD1	1:B:77:VAL:HG22	0.91	2.00	10	1
1:A:35:TYR:O	1:A:39:VAL:HG23	0.90	1.65	1	9
1:A:16:LEU:HD12	1:A:101:LEU:HD12	0.90	1.42	6	1
1:B:54:VAL:O	1:B:56:ILE:HG23	0.89	1.67	4	1
1:A:102:VAL:C	1:A:103:ILE:HD12	0.89	1.88	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:63:TYR:CE2	1:B:16:LEU:HD21	0.88	2.04	2	3
1:B:16:LEU:O	1:B:16:LEU:HD13	0.87	1.67	11	1
1:A:16:LEU:HD12	1:A:101:LEU:CD1	0.87	1.99	6	1
1:B:102:VAL:O	1:B:103:ILE:HD13	0.87	1.70	15	7
1:B:17:ALA:HB1	1:B:97:LEU:HD21	0.85	1.48	9	3
1:A:101:LEU:HD11	1:B:61:GLN:NE2	0.84	1.87	10	10
1:A:16:LEU:HD22	1:A:17:ALA:N	0.84	1.88	7	5
1:B:97:LEU:HD13	1:B:97:LEU:O	0.84	1.72	19	1
1:A:61:GLN:NE2	1:B:101:LEU:HD11	0.83	1.89	18	9
1:A:71:PHE:CD2	1:A:77:VAL:HG22	0.82	2.08	8	6
1:B:71:PHE:CG	1:B:77:VAL:HG22	0.81	2.10	11	4
1:A:16:LEU:HD11	1:B:63:TYR:OH	0.81	1.75	3	1
1:A:61:GLN:NE2	1:B:101:LEU:HD23	0.81	1.91	6	5
1:A:19:PHE:CE1	1:A:28:ILE:HG23	0.81	2.11	19	1
1:A:93:PHE:O	1:A:97:LEU:HD13	0.80	1.76	5	1
1:B:35:TYR:CE1	1:B:48:PHE:CE1	0.80	2.68	15	5
1:B:16:LEU:HD22	1:B:17:ALA:N	0.80	1.91	8	4
1:B:19:PHE:CZ	1:B:93:PHE:CZ	0.80	2.69	17	3
1:A:15:LEU:HD12	1:A:102:VAL:HG22	0.80	1.51	1	2
1:A:71:PHE:CG	1:A:77:VAL:HG22	0.80	2.11	8	3
1:A:104:ASP:HB2	1:B:54:VAL:HG22	0.80	1.53	8	2
1:A:16:LEU:HA	1:A:66:ILE:HG22	0.79	1.55	20	2
1:A:16:LEU:HD13	1:A:16:LEU:O	0.79	1.75	7	4
1:B:35:TYR:CD1	1:B:48:PHE:CZ	0.79	2.71	20	5
1:A:101:LEU:O	1:A:101:LEU:HD13	0.78	1.77	17	1
1:B:100:VAL:C	1:B:101:LEU:HD12	0.78	1.97	5	1
1:A:35:TYR:CD2	1:A:48:PHE:CZ	0.78	2.72	7	2
1:A:39:VAL:HG11	1:A:48:PHE:CD2	0.78	2.14	14	1
1:A:71:PHE:CD1	1:A:80:TYR:CE2	0.77	2.72	3	3
1:A:25:PRO:HA	1:A:28:ILE:HD12	0.77	1.54	15	7
1:B:71:PHE:CD2	1:B:77:VAL:HG22	0.77	2.15	2	5
1:A:16:LEU:C	1:A:16:LEU:HD13	0.77	1.99	9	3
1:A:93:PHE:CD2	1:A:97:LEU:HD11	0.77	2.14	11	1
1:A:103:ILE:HG23	1:B:53:ASP:HB2	0.77	1.56	16	2
1:A:19:PHE:CE1	1:A:93:PHE:CZ	0.76	2.73	14	2
1:A:101:LEU:HD21	1:B:61:GLN:NE2	0.76	1.94	18	2
1:A:16:LEU:HD13	1:A:63:TYR:CE1	0.76	2.15	15	1
1:A:35:TYR:CE1	1:A:48:PHE:CE1	0.76	2.73	11	4
1:A:35:TYR:CE2	1:A:48:PHE:CZ	0.76	2.73	12	1
1:B:97:LEU:HD11	1:B:100:VAL:CG1	0.75	2.11	5	1
1:A:16:LEU:HD13	1:B:63:TYR:CZ	0.75	2.17	1	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:97:LEU:N	1:A:97:LEU:HD13	0.74	1.97	2	1
1:B:35:TYR:O	1:B:39:VAL:HG13	0.74	1.81	2	1
1:B:16:LEU:HD22	1:B:63:TYR:CE1	0.74	2.17	13	4
1:A:56:ILE:HG21	1:B:103:ILE:CD1	0.74	2.12	3	1
1:A:16:LEU:C	1:A:16:LEU:HD22	0.74	2.02	5	1
1:B:16:LEU:HA	1:B:66:ILE:HG22	0.74	1.59	9	1
1:A:16:LEU:HD21	1:A:63:TYR:HA	0.74	1.59	17	1
1:B:35:TYR:CD1	1:B:48:PHE:CE2	0.74	2.76	1	3
1:A:16:LEU:HD22	1:A:63:TYR:CE1	0.74	2.16	2	4
1:A:35:TYR:CE1	1:A:48:PHE:CZ	0.74	2.75	11	3
1:A:15:LEU:C	1:A:15:LEU:HD13	0.74	2.03	9	1
1:A:14:VAL:HG22	1:A:68:GLU:HG2	0.74	1.57	11	1
1:A:38:LEU:HD13	1:A:89:PHE:CE1	0.73	2.19	17	3
1:A:16:LEU:HD13	1:B:63:TYR:OH	0.73	1.84	1	3
1:A:16:LEU:HD13	1:A:63:TYR:HA	0.73	1.61	2	1
1:B:39:VAL:HG13	1:B:45:MET:SD	0.73	2.24	4	2
1:B:94:LEU:HA	1:B:97:LEU:HD23	0.73	1.60	2	4
1:B:39:VAL:HG21	1:B:48:PHE:HB3	0.73	1.61	8	2
1:A:102:VAL:O	1:B:59:LEU:HD12	0.73	1.84	20	1
1:A:19:PHE:CZ	1:A:93:PHE:CE2	0.72	2.77	13	1
1:A:101:LEU:HD12	1:B:60:HIS:HA	0.72	1.60	13	4
1:A:103:ILE:HG23	1:B:53:ASP:CB	0.72	2.15	19	3
1:A:35:TYR:CD1	1:A:48:PHE:CD1	0.72	2.77	7	1
1:B:42:ILE:HG22	1:B:44:PRO:HD2	0.72	1.61	7	3
1:A:61:GLN:HE21	1:B:101:LEU:HD21	0.71	1.45	7	4
1:B:97:LEU:C	1:B:97:LEU:HD12	0.71	2.05	1	3
1:A:66:ILE:C	1:A:66:ILE:HD12	0.71	2.06	4	1
1:B:15:LEU:HD11	1:B:102:VAL:HG12	0.71	1.61	16	1
1:A:100:VAL:O	1:A:101:LEU:HD13	0.71	1.85	10	3
1:B:16:LEU:HD13	1:B:16:LEU:C	0.71	2.05	11	1
1:A:19:PHE:CZ	1:A:28:ILE:HG23	0.71	2.21	19	1
1:A:16:LEU:HD22	1:A:63:TYR:CD1	0.70	2.20	2	2
1:B:35:TYR:CZ	1:B:48:PHE:CE1	0.70	2.79	13	4
1:A:31:LEU:HD22	1:A:93:PHE:CD1	0.70	2.22	5	3
1:A:61:GLN:NE2	1:B:101:LEU:HD21	0.70	2.01	7	4
1:A:101:LEU:HD11	1:B:60:HIS:HA	0.70	1.64	5	4
1:A:108:THR:CG2	1:B:50:TRP:CD1	0.70	2.74	1	1
1:A:66:ILE:HD11	1:B:105:TYR:HB2	0.70	1.63	8	1
1:A:97:LEU:HD22	1:A:97:LEU:C	0.70	2.07	6	3
1:B:39:VAL:HG21	1:B:48:PHE:CB	0.70	2.17	8	3
1:B:16:LEU:HB2	1:B:66:ILE:HG22	0.69	1.65	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:16:LEU:C	1:B:16:LEU:HD13	0.69	2.08	3	2
1:A:19:PHE:CZ	1:A:93:PHE:CZ	0.69	2.80	17	2
1:A:63:TYR:C	1:A:64:THR:HG23	0.69	2.08	18	7
1:A:71:PHE:CD2	1:A:77:VAL:HG23	0.69	2.22	12	2
1:B:35:TYR:O	1:B:39:VAL:HG22	0.69	1.88	3	1
1:B:97:LEU:HD13	1:B:100:VAL:HG11	0.69	1.64	10	1
1:B:17:ALA:HB1	1:B:97:LEU:HD11	0.69	1.63	17	2
1:A:63:TYR:OH	1:B:16:LEU:HD21	0.69	1.87	18	1
1:B:35:TYR:O	1:B:39:VAL:HG23	0.69	1.88	5	6
1:B:97:LEU:C	1:B:97:LEU:HD22	0.68	2.08	19	1
1:B:64:THR:HG22	1:B:65:HIS:ND1	0.68	2.02	8	3
1:A:27:LYS:O	1:A:31:LEU:HD12	0.68	1.88	7	2
1:A:103:ILE:HG23	1:B:53:ASP:HB3	0.68	1.65	19	2
1:B:65:HIS:CD2	1:B:67:PHE:CZ	0.68	2.81	11	6
1:A:100:VAL:C	1:A:101:LEU:HD22	0.68	2.09	9	8
1:A:56:ILE:O	1:A:59:LEU:HD12	0.67	1.89	16	1
1:A:16:LEU:HD12	1:A:101:LEU:HD23	0.67	1.67	9	1
1:B:17:ALA:HB1	1:B:97:LEU:HD22	0.67	1.66	15	1
1:B:52:LYS:O	1:B:54:VAL:HG23	0.67	1.90	12	3
1:B:19:PHE:CD1	1:B:28:ILE:HD11	0.67	2.24	18	2
1:A:16:LEU:HD12	1:A:66:ILE:HG22	0.67	1.65	18	1
1:B:94:LEU:HD23	1:B:97:LEU:CD2	0.67	2.19	20	1
1:B:35:TYR:CZ	1:B:48:PHE:CZ	0.67	2.82	12	1
1:B:25:PRO:HA	1:B:28:ILE:HD12	0.67	1.65	7	4
1:A:101:LEU:HD11	1:B:61:GLN:HE21	0.67	1.49	16	3
1:A:63:TYR:O	1:A:66:ILE:HG23	0.67	1.90	20	1
1:A:66:ILE:HD11	1:B:105:TYR:CD2	0.67	2.24	4	1
1:A:35:TYR:CE1	1:A:48:PHE:CD1	0.67	2.82	7	2
1:B:16:LEU:HD22	1:B:17:ALA:H	0.67	1.48	8	1
1:B:20:LYS:O	1:B:23:VAL:HG23	0.66	1.90	12	3
1:B:35:TYR:CE1	1:B:48:PHE:CE2	0.66	2.83	9	1
1:B:35:TYR:CE1	1:B:48:PHE:CZ	0.66	2.83	15	5
1:B:16:LEU:CD1	1:B:63:TYR:CE2	0.66	2.78	4	1
1:B:32:ILE:HD13	1:B:50:TRP:CH2	0.66	2.25	18	1
1:B:15:LEU:CD1	1:B:102:VAL:HG12	0.66	2.20	16	2
1:A:60:HIS:HA	1:B:101:LEU:HD21	0.66	1.65	17	4
1:A:71:PHE:CD1	1:A:77:VAL:HG22	0.66	2.25	13	2
1:B:63:TYR:C	1:B:64:THR:HG23	0.66	2.10	10	2
1:B:16:LEU:HB3	1:B:66:ILE:HG22	0.66	1.67	1	2
1:A:42:ILE:HG22	1:A:44:PRO:HD2	0.66	1.65	15	3
1:B:74:LYS:O	1:B:77:VAL:HG12	0.66	1.89	6	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:36:ALA:HB1	1:B:110:VAL:HG11	0.66	1.67	9	1
1:A:16:LEU:HB2	1:A:66:ILE:HG22	0.66	1.66	5	5
1:A:63:TYR:OH	1:B:16:LEU:HD22	0.66	1.91	4	1
1:A:102:VAL:O	1:A:103:ILE:HD13	0.65	1.92	19	9
1:A:53:ASP:OD2	1:B:103:ILE:HD13	0.65	1.91	2	1
1:A:108:THR:O	1:A:108:THR:HG22	0.65	1.91	17	11
1:A:104:ASP:CB	1:B:54:VAL:HG22	0.65	2.22	16	4
1:B:71:PHE:CE1	1:B:77:VAL:HG23	0.65	2.27	6	1
1:B:97:LEU:HD13	1:B:100:VAL:CG1	0.65	2.22	10	1
1:A:61:GLN:CG	1:B:101:LEU:HD21	0.65	2.22	14	1
1:A:63:TYR:O	1:A:65:HIS:N	0.65	2.29	8	14
1:B:83:HIS:O	1:B:87:VAL:HG23	0.65	1.92	13	5
1:B:15:LEU:C	1:B:15:LEU:HD23	0.65	2.12	18	4
1:B:16:LEU:HD13	1:B:16:LEU:O	0.65	1.92	3	1
1:A:43:GLU:N	1:A:44:PRO:CD	0.65	2.60	20	17
1:A:53:ASP:CB	1:B:103:ILE:HG23	0.64	2.21	18	2
1:A:101:LEU:HD21	1:B:60:HIS:CA	0.64	2.22	19	1
1:A:35:TYR:CG	1:A:48:PHE:CZ	0.64	2.84	7	1
1:A:39:VAL:HG23	1:A:45:MET:SD	0.64	2.31	16	1
1:B:93:PHE:CD1	1:B:97:LEU:HD13	0.64	2.27	17	1
1:B:16:LEU:CB	1:B:66:ILE:HG22	0.64	2.21	1	1
1:B:108:THR:HG22	1:B:108:THR:O	0.64	1.91	15	10
1:B:71:PHE:CE2	1:B:77:VAL:HG23	0.64	2.28	8	1
1:B:97:LEU:HD13	1:B:100:VAL:HG13	0.64	1.68	18	2
1:A:65:HIS:CD2	1:A:67:PHE:CZ	0.64	2.86	6	2
1:A:35:TYR:O	1:A:39:VAL:HG22	0.64	1.91	18	2
1:B:23:VAL:HG21	1:B:96:SER:HB3	0.64	1.69	19	1
1:A:101:LEU:HD11	1:A:103:ILE:HG13	0.64	1.70	17	1
1:A:93:PHE:CD1	1:A:97:LEU:HD11	0.64	2.28	12	1
1:A:53:ASP:HB2	1:B:103:ILE:HG23	0.63	1.69	20	3
1:A:60:HIS:HA	1:B:101:LEU:HD12	0.63	1.69	19	7
1:B:100:VAL:O	1:B:101:LEU:HD13	0.63	1.92	18	4
1:A:101:LEU:HD21	1:B:61:GLN:HE21	0.63	1.51	18	3
1:A:97:LEU:C	1:A:97:LEU:HD12	0.63	2.14	4	2
1:A:16:LEU:HD22	1:A:63:TYR:HE1	0.63	1.53	12	1
1:B:100:VAL:O	1:B:101:LEU:HD22	0.63	1.92	20	1
1:A:53:ASP:HB2	1:B:103:ILE:HD12	0.63	1.70	12	3
1:A:76:ALA:HB1	1:A:80:TYR:CE2	0.63	2.28	3	1
1:A:71:PHE:CE1	1:A:80:TYR:CD2	0.63	2.86	3	2
1:A:15:LEU:HD12	1:A:67:PHE:HB2	0.63	1.71	9	1
1:B:42:ILE:N	1:B:42:ILE:HD13	0.63	2.08	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:74:LYS:O	1:A:77:VAL:HG12	0.62	1.94	9	5
1:A:64:THR:O	1:A:65:HIS:CG	0.62	2.52	5	9
1:A:35:TYR:C	1:A:35:TYR:CD1	0.62	2.72	14	3
1:A:93:PHE:CD2	1:A:97:LEU:CD1	0.62	2.82	11	2
1:A:16:LEU:HD22	1:A:17:ALA:H	0.62	1.53	6	2
1:A:39:VAL:HG21	1:A:48:PHE:HB3	0.62	1.71	8	2
1:A:101:LEU:HD23	1:B:61:GLN:NE2	0.62	2.09	11	2
1:A:97:LEU:HD22	1:A:98:ASP:N	0.62	2.10	13	3
1:A:15:LEU:C	1:A:15:LEU:HD23	0.62	2.15	12	2
1:A:94:LEU:C	1:A:94:LEU:HD12	0.62	2.15	14	2
1:B:66:ILE:C	1:B:66:ILE:HD13	0.62	2.14	17	1
1:B:19:PHE:CE2	1:B:28:ILE:HG23	0.62	2.29	4	1
1:A:101:LEU:HD13	1:A:101:LEU:C	0.62	2.13	17	1
1:B:39:VAL:HG11	1:B:48:PHE:HB2	0.62	1.71	19	2
1:A:34:GLY:O	1:A:38:LEU:HD12	0.62	1.95	18	1
1:A:101:LEU:HD21	1:B:61:GLN:HE22	0.62	1.54	9	1
1:A:35:TYR:CZ	1:A:48:PHE:CE1	0.62	2.87	7	4
1:A:15:LEU:HD12	1:A:102:VAL:HG12	0.61	1.73	20	2
1:B:35:TYR:C	1:B:35:TYR:CD1	0.61	2.73	15	1
1:B:15:LEU:C	1:B:15:LEU:HD13	0.61	2.16	17	1
1:B:15:LEU:HD12	1:B:102:VAL:HG22	0.61	1.72	8	3
1:A:97:LEU:HD21	1:A:100:VAL:CG1	0.61	2.26	1	3
1:A:15:LEU:CD1	1:A:102:VAL:HG22	0.61	2.25	10	2
1:A:16:LEU:CB	1:A:66:ILE:HG22	0.61	2.26	3	4
1:B:97:LEU:HD21	1:B:100:VAL:HB	0.61	1.72	16	2
1:B:14:VAL:HG13	1:B:66:ILE:HD11	0.61	1.71	17	1
1:A:63:TYR:CE1	1:B:63:TYR:OH	0.61	2.54	20	2
1:B:16:LEU:CD1	1:B:63:TYR:CD2	0.61	2.81	4	1
1:B:19:PHE:CZ	1:B:28:ILE:HG23	0.61	2.31	5	2
1:A:91:THR:HA	1:A:94:LEU:HD23	0.61	1.72	19	3
1:B:19:PHE:CZ	1:B:93:PHE:CE1	0.60	2.88	17	2
1:B:19:PHE:CE1	1:B:93:PHE:CE1	0.60	2.89	11	1
1:A:97:LEU:HD13	1:A:97:LEU:C	0.60	2.17	14	2
1:B:35:TYR:CD1	1:B:48:PHE:CE1	0.60	2.89	20	1
1:A:107:PRO:HA	1:B:49:HIS:CD2	0.60	2.30	18	9
1:A:60:HIS:HA	1:B:101:LEU:HD11	0.60	1.72	12	4
1:B:97:LEU:HD21	1:B:100:VAL:HG11	0.60	1.74	5	1
1:A:38:LEU:HD13	1:A:89:PHE:CZ	0.60	2.31	17	1
1:A:71:PHE:CD1	1:A:80:TYR:CD2	0.60	2.90	7	2
1:B:64:THR:O	1:B:65:HIS:CG	0.60	2.54	4	8
1:A:97:LEU:HD11	1:A:100:VAL:HB	0.60	1.73	7	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:63:TYR:O	1:B:65:HIS:N	0.60	2.34	19	10
1:B:16:LEU:HD12	1:B:17:ALA:N	0.60	2.12	13	2
1:A:64:THR:HG22	1:A:65:HIS:ND1	0.60	2.11	9	4
1:B:80:TYR:CE1	1:B:86:HIS:CG	0.60	2.90	4	2
1:A:101:LEU:HD21	1:B:60:HIS:HA	0.60	1.74	19	3
1:B:23:VAL:HG13	1:B:28:ILE:HD11	0.59	1.72	10	1
1:A:39:VAL:HG22	1:A:45:MET:CE	0.59	2.27	2	2
1:A:51:GLY:N	1:B:105:TYR:CE2	0.59	2.70	2	1
1:A:101:LEU:N	1:A:101:LEU:HD22	0.59	2.11	10	2
1:B:19:PHE:CZ	1:B:97:LEU:HD21	0.59	2.33	4	1
1:A:71:PHE:CE1	1:A:77:VAL:HG21	0.59	2.33	5	1
1:A:16:LEU:HD11	1:A:101:LEU:HD23	0.59	1.74	15	1
1:A:56:ILE:HG21	1:B:103:ILE:HD11	0.59	1.73	3	1
1:A:63:TYR:CE1	1:B:16:LEU:HD13	0.59	2.32	4	1
1:B:71:PHE:CG	1:B:77:VAL:HG23	0.59	2.33	6	1
1:B:42:ILE:CD1	1:B:83:HIS:CE1	0.59	2.85	15	2
1:B:16:LEU:HD22	1:B:63:TYR:HE2	0.59	1.58	17	1
1:A:101:LEU:HD21	1:B:61:GLN:HG2	0.59	1.73	20	1
1:B:105:TYR:C	1:B:105:TYR:CD1	0.59	2.76	13	7
1:A:16:LEU:HD22	1:A:16:LEU:C	0.59	2.18	7	1
1:A:19:PHE:CE2	1:A:28:ILE:HG23	0.59	2.33	13	1
1:A:63:TYR:OH	1:B:63:TYR:CE1	0.59	2.54	16	3
1:A:93:PHE:O	1:A:97:LEU:HD12	0.59	1.97	11	1
1:B:16:LEU:HD22	1:B:63:TYR:CE2	0.59	2.33	17	1
1:A:49:HIS:CD2	1:B:107:PRO:HA	0.58	2.33	12	14
1:A:51:GLY:N	1:B:105:TYR:CZ	0.58	2.71	2	1
1:B:16:LEU:HD22	1:B:63:TYR:CD1	0.58	2.33	13	2
1:B:16:LEU:HD12	1:B:63:TYR:CD1	0.58	2.32	15	2
1:B:35:TYR:OH	1:B:48:PHE:CD1	0.58	2.55	15	1
1:B:35:TYR:CE2	1:B:48:PHE:CZ	0.58	2.90	12	1
1:A:108:THR:HG23	1:A:108:THR:O	0.58	1.97	1	1
1:A:108:THR:O	1:B:50:TRP:CD1	0.58	2.56	8	5
1:A:16:LEU:HD12	1:A:16:LEU:N	0.58	2.13	1	2
1:A:16:LEU:HD21	1:B:63:TYR:CE2	0.58	2.33	13	2
1:B:32:ILE:HG21	1:B:50:TRP:CE3	0.58	2.33	14	1
1:B:58:ASN:O	1:B:60:HIS:CD2	0.58	2.56	1	2
1:A:63:TYR:OH	1:B:16:LEU:HD13	0.58	1.99	4	1
1:B:73:SER:O	1:B:77:VAL:HG23	0.58	1.98	10	2
1:A:35:TYR:CE1	1:A:48:PHE:CE2	0.58	2.91	9	1
1:A:97:LEU:HD21	1:A:100:VAL:HG12	0.58	1.76	16	5
1:B:19:PHE:CE1	1:B:93:PHE:CZ	0.58	2.92	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:101:LEU:HD21	1:B:61:GLN:CG	0.58	2.28	20	1
1:A:14:VAL:HG22	1:A:68:GLU:CG	0.58	2.29	11	1
1:A:16:LEU:HB3	1:A:66:ILE:HG22	0.58	1.76	15	2
1:B:16:LEU:HD23	1:B:101:LEU:HD22	0.57	1.75	5	1
1:B:14:VAL:HG23	1:B:105:TYR:HB2	0.57	1.76	12	1
1:B:94:LEU:HD23	1:B:97:LEU:HD23	0.57	1.74	20	1
1:B:63:TYR:O	1:B:66:ILE:HG23	0.57	1.99	16	1
1:B:31:LEU:HD13	1:B:89:PHE:CZ	0.57	2.35	19	1
1:A:13:HIS:CD2	1:A:103:ILE:O	0.57	2.57	13	1
1:A:48:PHE:C	1:A:48:PHE:CD1	0.57	2.77	9	1
1:A:68:GLU:OE2	1:B:105:TYR:CE2	0.57	2.57	11	2
1:B:101:LEU:HD13	1:B:101:LEU:C	0.57	2.19	11	1
1:B:97:LEU:HD22	1:B:98:ASP:N	0.57	2.14	19	1
1:B:101:LEU:HD22	1:B:101:LEU:N	0.57	2.14	18	1
1:B:19:PHE:CG	1:B:28:ILE:CG1	0.57	2.88	17	1
1:A:105:TYR:CD2	1:B:66:ILE:HD11	0.56	2.35	7	4
1:A:15:LEU:CD1	1:A:102:VAL:HG12	0.56	2.29	18	1
1:A:94:LEU:HB2	1:A:100:VAL:HG11	0.56	1.77	18	1
1:A:20:LYS:O	1:A:23:VAL:HG23	0.56	1.99	15	4
1:A:19:PHE:CZ	1:A:97:LEU:HD21	0.56	2.35	11	1
1:A:39:VAL:HG13	1:A:45:MET:SD	0.56	2.40	17	1
1:B:31:LEU:HD12	1:B:93:PHE:CD2	0.56	2.35	9	1
1:A:16:LEU:HD21	1:B:63:TYR:CZ	0.56	2.35	13	2
1:A:69:SER:OG	1:A:71:PHE:CE1	0.56	2.56	4	1
1:A:35:TYR:OH	1:A:48:PHE:CD1	0.56	2.57	11	2
1:A:35:TYR:CE2	1:A:48:PHE:CE1	0.56	2.94	7	2
1:A:16:LEU:HD12	1:A:65:HIS:O	0.56	2.01	10	1
1:B:13:HIS:CE1	1:B:102:VAL:HG23	0.56	2.36	18	1
1:B:97:LEU:HD21	1:B:100:VAL:CB	0.56	2.31	16	2
1:B:64:THR:OG1	1:B:65:HIS:N	0.56	2.39	19	2
1:A:48:PHE:CE2	1:A:69:SER:OG	0.56	2.59	14	1
1:A:31:LEU:HD22	1:A:93:PHE:CE1	0.56	2.35	11	1
1:A:63:TYR:O	1:A:64:THR:OG1	0.56	2.23	19	8
1:A:16:LEU:C	1:A:16:LEU:CD1	0.56	2.74	9	2
1:A:62:GLY:O	1:A:64:THR:HG23	0.56	2.01	13	3
1:A:105:TYR:CG	1:B:66:ILE:HD11	0.56	2.36	9	1
1:B:35:TYR:CD2	1:B:48:PHE:CZ	0.55	2.95	2	2
1:A:39:VAL:HG22	1:A:45:MET:HG2	0.55	1.77	3	1
1:A:80:TYR:OH	1:A:86:HIS:CE1	0.55	2.59	18	1
1:A:68:GLU:OE1	1:B:105:TYR:CZ	0.55	2.60	13	1
1:B:32:ILE:HG21	1:B:50:TRP:CD2	0.55	2.36	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:60:HIS:CA	1:B:101:LEU:HD21	0.55	2.31	17	2
1:B:16:LEU:HD21	1:B:63:TYR:HA	0.55	1.78	4	2
1:B:56:ILE:CD1	1:B:59:LEU:N	0.55	2.70	4	1
1:B:19:PHE:CZ	1:B:93:PHE:CE2	0.55	2.95	18	1
1:A:16:LEU:HD13	1:A:16:LEU:C	0.55	2.21	7	1
1:A:64:THR:OG1	1:A:65:HIS:N	0.55	2.38	13	9
1:B:35:TYR:CG	1:B:48:PHE:CZ	0.55	2.95	4	1
1:B:86:HIS:CD2	1:B:86:HIS:C	0.55	2.80	16	1
1:A:14:VAL:HG23	1:A:105:TYR:HB2	0.55	1.76	10	2
1:A:105:TYR:CD1	1:B:66:ILE:HD11	0.54	2.37	4	1
1:B:43:GLU:CB	1:B:44:PRO:HD3	0.54	2.32	7	3
1:A:16:LEU:HD13	1:A:63:TYR:HD2	0.54	1.61	10	1
1:A:61:GLN:HG2	1:B:101:LEU:HD21	0.54	1.79	14	1
1:B:97:LEU:HD21	1:B:100:VAL:CG1	0.54	2.33	16	4
1:A:64:THR:C	1:A:65:HIS:CG	0.54	2.81	5	6
1:A:93:PHE:CG	1:A:97:LEU:CD2	0.54	2.91	20	1
1:B:17:ALA:HB1	1:B:97:LEU:CD2	0.54	2.31	15	3
1:B:17:ALA:CB	1:B:97:LEU:HD21	0.54	2.29	9	1
1:B:39:VAL:HG21	1:B:48:PHE:CG	0.54	2.38	18	2
1:A:39:VAL:HG21	1:A:48:PHE:HB2	0.54	1.78	6	2
1:A:103:ILE:HD12	1:B:53:ASP:HB3	0.54	1.78	6	1
1:B:42:ILE:CD1	1:B:83:HIS:ND1	0.54	2.70	20	1
1:A:35:TYR:CD1	1:A:48:PHE:CE1	0.54	2.96	7	1
1:A:16:LEU:HD13	1:A:63:TYR:CD2	0.54	2.37	10	3
1:A:103:ILE:HD13	1:B:53:ASP:HB3	0.54	1.80	17	1
1:A:63:TYR:C	1:A:64:THR:CG2	0.53	2.77	11	4
1:B:56:ILE:O	1:B:56:ILE:HG23	0.53	2.03	17	1
1:A:81:ILE:O	1:A:87:VAL:HG23	0.53	2.02	11	1
1:A:97:LEU:N	1:A:97:LEU:CD2	0.53	2.71	18	1
1:B:13:HIS:HE1	1:B:102:VAL:HG13	0.53	1.63	12	4
1:A:38:LEU:HD22	1:A:89:PHE:CE2	0.53	2.39	8	1
1:B:93:PHE:CD2	1:B:97:LEU:HD23	0.53	2.38	8	1
1:B:16:LEU:HD23	1:B:16:LEU:O	0.53	2.04	9	1
1:B:52:LYS:CE	1:B:53:ASP:O	0.53	2.57	9	1
1:A:101:LEU:HD11	1:B:61:GLN:HG2	0.53	1.80	20	1
1:B:19:PHE:CD2	1:B:97:LEU:HD11	0.53	2.38	4	1
1:A:16:LEU:HD22	1:B:63:TYR:OH	0.53	2.03	10	1
1:A:39:VAL:HG11	1:A:48:PHE:HB2	0.53	1.80	13	1
1:A:103:ILE:HD12	1:A:103:ILE:N	0.53	2.17	16	1
1:A:16:LEU:HD13	1:B:63:TYR:CE1	0.53	2.39	19	1
1:B:52:LYS:CB	1:B:65:HIS:CD2	0.53	2.92	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:54:VAL:HG22	1:B:104:ASP:HB2	0.53	1.79	10	2
1:A:16:LEU:CG	1:A:66:ILE:HG22	0.53	2.33	4	1
1:B:64:THR:C	1:B:65:HIS:CG	0.53	2.81	18	8
1:B:35:TYR:CE2	1:B:67:PHE:CD1	0.53	2.97	16	1
1:B:39:VAL:HG21	1:B:48:PHE:CD2	0.53	2.39	18	1
1:B:94:LEU:HD12	1:B:94:LEU:O	0.53	2.03	11	3
1:A:11:VAL:HG22	1:A:106:LYS:HG2	0.53	1.80	2	1
1:A:96:SER:HB3	1:A:97:LEU:HD13	0.53	1.80	2	1
1:B:64:THR:C	1:B:65:HIS:ND1	0.53	2.62	20	7
1:A:71:PHE:CG	1:A:77:VAL:HG23	0.53	2.38	10	1
1:A:19:PHE:CE1	1:A:28:ILE:CG2	0.53	2.92	19	1
1:A:43:GLU:CB	1:A:44:PRO:HD3	0.52	2.34	15	8
1:B:80:TYR:CE2	1:B:86:HIS:CE1	0.52	2.96	8	2
1:B:25:PRO:O	1:B:28:ILE:HG22	0.52	2.05	18	2
1:B:18:SER:O	1:B:97:LEU:HD23	0.52	2.04	11	2
1:B:11:VAL:HG22	1:B:106:LYS:CE	0.52	2.34	1	1
1:B:39:VAL:HG13	1:B:45:MET:CE	0.52	2.35	5	1
1:B:16:LEU:H	1:B:16:LEU:HD12	0.52	1.63	14	1
1:B:38:LEU:HD23	1:B:42:ILE:HD11	0.52	1.82	18	1
1:A:58:ASN:O	1:A:59:LEU:CB	0.52	2.57	11	1
1:A:93:PHE:CE2	1:A:97:LEU:HD12	0.52	2.39	10	1
1:B:39:VAL:HG23	1:B:45:MET:CE	0.52	2.35	11	2
1:A:18:SER:HB3	1:A:64:THR:HG21	0.52	1.80	13	1
1:B:63:TYR:O	1:B:64:THR:OG1	0.52	2.28	19	1
1:A:16:LEU:HG	1:A:66:ILE:HG22	0.52	1.80	4	1
1:A:64:THR:CG2	1:A:65:HIS:CE1	0.52	2.82	4	2
1:B:17:ALA:HB1	1:B:97:LEU:CD1	0.52	2.35	16	1
1:B:38:LEU:HD13	1:B:89:PHE:CE1	0.52	2.40	18	2
1:A:50:TRP:CE3	1:A:67:PHE:CE2	0.52	2.98	4	1
1:A:71:PHE:CD1	1:A:77:VAL:HG23	0.52	2.39	10	2
1:B:80:TYR:CZ	1:B:86:HIS:CE1	0.52	2.98	4	1
1:A:35:TYR:CG	1:A:48:PHE:CE2	0.52	2.98	7	1
1:A:16:LEU:CD1	1:A:66:ILE:HG22	0.52	2.36	18	1
1:B:16:LEU:C	1:B:16:LEU:CD1	0.51	2.78	11	2
1:A:104:ASP:O	1:B:53:ASP:CB	0.51	2.59	14	1
1:A:68:GLU:OE1	1:B:105:TYR:CE2	0.51	2.64	15	1
1:A:101:LEU:HD12	1:B:59:LEU:O	0.51	2.04	20	1
1:B:101:LEU:HD12	1:B:101:LEU:N	0.51	2.20	5	1
1:B:35:TYR:CG	1:B:48:PHE:CE2	0.51	2.98	12	1
1:A:101:LEU:HD12	1:A:103:ILE:HD11	0.51	1.81	19	1
1:B:94:LEU:HD12	1:B:94:LEU:C	0.51	2.26	8	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:LEU:C	1:A:16:LEU:CD2	0.51	2.76	5	2
1:A:71:PHE:CD1	1:A:77:VAL:HG21	0.51	2.39	5	1
1:A:19:PHE:CD2	1:A:28:ILE:HD11	0.51	2.40	11	1
1:A:108:THR:CG2	1:A:108:THR:O	0.51	2.59	1	1
1:A:43:GLU:N	1:A:44:PRO:HD2	0.51	2.20	20	2
1:A:63:TYR:OH	1:B:63:TYR:CE2	0.51	2.62	17	1
1:A:71:PHE:CE1	1:A:77:VAL:HG23	0.51	2.41	4	1
1:A:103:ILE:HG23	1:B:53:ASP:CG	0.51	2.26	9	1
1:B:35:TYR:CE1	1:B:48:PHE:CD1	0.51	2.98	15	2
1:B:71:PHE:CZ	1:B:80:TYR:CG	0.51	2.98	13	2
1:A:63:TYR:OH	1:B:16:LEU:HD11	0.51	2.05	18	1
1:A:39:VAL:HG13	1:A:45:MET:HG3	0.51	1.82	11	1
1:B:16:LEU:HD23	1:B:16:LEU:N	0.51	2.21	15	1
1:A:66:ILE:HD11	1:B:105:TYR:CE2	0.51	2.40	4	1
1:A:50:TRP:CD1	1:B:108:THR:O	0.51	2.64	1	2
1:B:43:GLU:N	1:B:44:PRO:CD	0.51	2.74	19	19
1:B:15:LEU:HD12	1:B:101:LEU:O	0.51	2.06	3	1
1:A:38:LEU:O	1:A:42:ILE:CD1	0.51	2.59	15	1
1:A:53:ASP:OD2	1:A:56:ILE:HD12	0.51	2.06	1	1
1:B:97:LEU:C	1:B:97:LEU:CD1	0.51	2.80	1	3
1:A:63:TYR:OH	1:B:16:LEU:CD1	0.51	2.59	15	3
1:B:15:LEU:CB	1:B:67:PHE:O	0.51	2.59	10	1
1:B:12:LYS:HB2	1:B:105:TYR:CD2	0.51	2.41	12	1
1:B:56:ILE:O	1:B:57:GLU:CB	0.51	2.57	19	1
1:B:100:VAL:C	1:B:101:LEU:HD22	0.51	2.25	7	7
1:A:100:VAL:O	1:A:101:LEU:HD22	0.51	2.06	9	1
1:B:71:PHE:CG	1:B:77:VAL:HG21	0.51	2.41	20	1
1:A:71:PHE:CE1	1:A:80:TYR:CE2	0.50	2.99	3	1
1:A:66:ILE:HD12	1:A:66:ILE:O	0.50	2.05	4	1
1:B:53:ASP:HB2	1:B:56:ILE:HG22	0.50	1.84	11	2
1:A:101:LEU:HD21	1:A:103:ILE:CG1	0.50	2.36	17	1
1:A:15:LEU:C	1:A:15:LEU:CD1	0.50	2.78	9	1
1:A:97:LEU:HD21	1:A:100:VAL:HG13	0.50	1.82	1	1
1:A:15:LEU:HD23	1:A:16:LEU:N	0.50	2.22	8	1
1:A:61:GLN:CD	1:B:101:LEU:HD21	0.50	2.27	10	1
1:B:39:VAL:HG21	1:B:48:PHE:HB2	0.50	1.83	11	1
1:B:15:LEU:C	1:B:15:LEU:CD2	0.50	2.79	18	1
1:A:16:LEU:HD12	1:A:17:ALA:N	0.50	2.22	2	1
1:A:94:LEU:CD2	1:A:100:VAL:HG11	0.50	2.37	5	1
1:B:14:VAL:HG23	1:B:105:TYR:HB3	0.50	1.83	8	2
1:A:42:ILE:HD13	1:A:45:MET:SD	0.50	2.47	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:19:PHE:CD1	1:B:28:ILE:HG13	0.50	2.41	17	1
1:A:61:GLN:HE22	1:B:101:LEU:HD11	0.50	1.62	18	1
1:A:64:THR:O	1:A:65:HIS:ND1	0.50	2.45	17	7
1:B:54:VAL:HG23	1:B:56:ILE:HG12	0.50	1.83	20	1
1:B:97:LEU:HD12	1:B:97:LEU:O	0.50	2.06	20	2
1:B:19:PHE:CD1	1:B:28:ILE:CD1	0.50	2.94	14	1
1:A:16:LEU:HD21	1:A:101:LEU:HB2	0.50	1.82	16	2
1:A:51:GLY:O	1:A:65:HIS:CB	0.50	2.60	8	1
1:B:97:LEU:HD11	1:B:100:VAL:HG11	0.49	1.79	5	1
1:A:16:LEU:CD2	1:A:63:TYR:O	0.49	2.60	6	2
1:A:16:LEU:CD1	1:A:63:TYR:O	0.49	2.59	8	1
1:A:103:ILE:HG21	1:B:53:ASP:OD2	0.49	2.06	14	1
1:A:101:LEU:HD11	1:A:103:ILE:CG1	0.49	2.37	17	1
1:A:13:HIS:C	1:A:13:HIS:CD2	0.49	2.85	1	4
1:A:52:LYS:HA	1:A:65:HIS:CD2	0.49	2.42	1	3
1:B:64:THR:O	1:B:65:HIS:ND1	0.49	2.45	18	4
1:B:13:HIS:CE1	1:B:102:VAL:HG13	0.49	2.42	11	3
1:B:102:VAL:O	1:B:103:ILE:CD1	0.49	2.60	12	3
1:B:16:LEU:HG	1:B:63:TYR:CD2	0.49	2.42	12	1
1:B:11:VAL:CG1	1:B:104:ASP:OD2	0.49	2.60	7	1
1:A:103:ILE:HD12	1:B:53:ASP:HB2	0.49	1.83	13	1
1:A:63:TYR:CZ	1:B:63:TYR:OH	0.49	2.63	17	1
1:A:105:TYR:HD2	1:B:66:ILE:HD11	0.49	1.67	8	1
1:B:53:ASP:OD1	1:B:53:ASP:C	0.49	2.50	16	1
1:B:36:ALA:O	1:B:39:VAL:HG12	0.49	2.07	1	1
1:B:42:ILE:O	1:B:43:GLU:CB	0.49	2.60	10	2
1:A:67:PHE:CE2	1:A:93:PHE:CZ	0.49	3.00	12	1
1:B:52:LYS:HB2	1:B:65:HIS:CD2	0.49	2.42	17	1
1:A:15:LEU:HD12	1:A:16:LEU:N	0.49	2.22	6	1
1:B:13:HIS:O	1:B:68:GLU:CG	0.49	2.60	8	3
1:A:63:TYR:CD1	1:B:63:TYR:OH	0.49	2.60	9	1
1:A:40:ASN:ND2	1:A:41:LEU:N	0.49	2.60	9	1
1:B:42:ILE:HG22	1:B:44:PRO:CD	0.49	2.38	10	1
1:B:97:LEU:CD2	1:B:100:VAL:CG1	0.49	2.90	16	1
1:A:77:VAL:O	1:A:81:ILE:CG1	0.49	2.60	3	1
1:B:23:VAL:CG1	1:B:23:VAL:O	0.49	2.60	5	4
1:A:35:TYR:HB3	1:A:48:PHE:CD2	0.49	2.43	7	1
1:A:102:VAL:HG23	1:B:59:LEU:HD12	0.49	1.84	8	1
1:B:65:HIS:NE2	1:B:67:PHE:CZ	0.49	2.80	11	1
1:A:101:LEU:CD1	1:B:59:LEU:O	0.49	2.61	20	1
1:A:19:PHE:CE2	1:A:28:ILE:HG12	0.49	2.43	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:69:SER:HB3	1:B:71:PHE:CZ	0.49	2.43	16	2
1:A:35:TYR:CD2	1:A:48:PHE:CE1	0.49	3.00	7	1
1:A:58:ASN:O	1:A:59:LEU:CD2	0.49	2.61	2	1
1:B:93:PHE:CZ	1:B:97:LEU:HD21	0.49	2.43	6	1
1:B:93:PHE:CD2	1:B:97:LEU:CD2	0.49	2.95	8	1
1:A:38:LEU:CD1	1:A:89:PHE:CE1	0.49	2.96	12	2
1:A:73:SER:O	1:A:77:VAL:HG23	0.49	2.07	15	1
1:B:23:VAL:O	1:B:23:VAL:HG13	0.48	2.08	4	1
1:A:15:LEU:HD23	1:A:16:LEU:H	0.48	1.68	8	1
1:A:64:THR:C	1:A:65:HIS:ND1	0.48	2.67	13	8
1:A:102:VAL:O	1:B:56:ILE:CG2	0.48	2.61	10	1
1:B:63:TYR:C	1:B:64:THR:CG2	0.48	2.79	10	1
1:B:54:VAL:CG1	1:B:54:VAL:O	0.48	2.60	11	1
1:B:15:LEU:C	1:B:15:LEU:CD1	0.48	2.81	17	1
1:A:39:VAL:HG21	1:A:48:PHE:CD2	0.48	2.43	20	1
1:A:60:HIS:CG	1:A:64:THR:OG1	0.48	2.65	2	1
1:A:47:ALA:O	1:A:70:THR:HG22	0.48	2.08	13	1
1:B:51:GLY:O	1:B:66:ILE:HG22	0.48	2.09	17	1
1:A:93:PHE:CD2	1:A:97:LEU:HG	0.48	2.43	20	1
1:B:72:GLU:O	1:B:73:SER:CB	0.48	2.60	3	3
1:B:57:GLU:CG	1:B:57:GLU:O	0.48	2.60	5	2
1:B:73:SER:HB3	1:B:76:ALA:HB3	0.48	1.84	16	1
1:B:42:ILE:HG21	1:B:80:TYR:CD1	0.48	2.43	20	1
1:A:51:GLY:HA3	1:B:105:TYR:CD2	0.48	2.44	2	1
1:B:56:ILE:HG22	1:B:56:ILE:O	0.48	2.08	12	1
1:A:63:TYR:OH	1:B:63:TYR:CD1	0.48	2.66	15	1
1:A:108:THR:O	1:A:108:THR:CG2	0.48	2.61	17	3
1:B:63:TYR:O	1:B:64:THR:CB	0.48	2.62	3	6
1:A:71:PHE:CD2	1:A:77:VAL:CG2	0.48	2.95	2	4
1:A:71:PHE:CG	1:A:77:VAL:CG2	0.48	2.93	8	3
1:B:16:LEU:HD23	1:B:66:ILE:HG21	0.48	1.84	7	1
1:A:18:SER:HA	1:A:64:THR:HG21	0.48	1.86	11	1
1:B:19:PHE:CE2	1:B:28:ILE:HG12	0.48	2.44	11	1
1:B:93:PHE:CE1	1:B:97:LEU:HD21	0.48	2.44	6	1
1:B:16:LEU:HD23	1:B:16:LEU:C	0.48	2.29	9	1
1:A:16:LEU:HD13	1:A:63:TYR:CD1	0.48	2.44	15	1
1:A:60:HIS:CE1	1:A:64:THR:HG1	0.48	2.27	3	1
1:A:66:ILE:C	1:A:66:ILE:CD1	0.48	2.80	4	1
1:A:101:LEU:HD21	1:B:61:GLN:HB2	0.48	1.84	6	1
1:A:38:LEU:O	1:A:42:ILE:HD12	0.48	2.08	15	1
1:B:13:HIS:C	1:B:13:HIS:CD2	0.48	2.86	19	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:19:PHE:CE1	1:B:28:ILE:HG23	0.48	2.43	5	1
1:B:56:ILE:O	1:B:56:ILE:CG2	0.48	2.62	12	2
1:A:103:ILE:CG2	1:B:53:ASP:OD2	0.48	2.62	14	1
1:A:61:GLN:CD	1:B:101:LEU:HD11	0.48	2.28	16	1
1:B:15:LEU:HD23	1:B:16:LEU:N	0.47	2.24	1	2
1:B:37:ASN:O	1:B:41:LEU:HD23	0.47	2.09	2	1
1:B:90:ALA:O	1:B:94:LEU:HD12	0.47	2.09	12	3
1:A:53:ASP:HA	1:B:103:ILE:HG23	0.47	1.86	13	1
1:A:56:ILE:HD12	1:B:102:VAL:HG23	0.47	1.86	16	1
1:B:39:VAL:HG11	1:B:48:PHE:HB3	0.47	1.86	18	1
1:A:71:PHE:CE2	1:A:77:VAL:CG2	0.47	2.98	2	1
1:B:93:PHE:CE2	1:B:97:LEU:CD1	0.47	2.98	16	1
1:B:11:VAL:HG22	1:B:106:LYS:HE2	0.47	1.86	1	1
1:A:15:LEU:O	1:A:67:PHE:N	0.47	2.47	16	3
1:B:47:ALA:HB3	1:B:70:THR:HB	0.47	1.85	3	1
1:B:98:ASP:CG	1:B:99:LYS:N	0.47	2.67	15	2
1:B:13:HIS:O	1:B:68:GLU:CB	0.47	2.62	5	2
1:A:13:HIS:NE2	1:A:102:VAL:HG13	0.47	2.23	10	1
1:B:16:LEU:HD12	1:B:16:LEU:N	0.47	2.25	14	1
1:A:53:ASP:CG	1:B:103:ILE:HD12	0.47	2.30	4	1
1:A:109:SER:OG	1:B:49:HIS:CD2	0.47	2.66	13	1
1:B:20:LYS:O	1:B:21:ASP:CB	0.47	2.62	14	1
1:A:71:PHE:CE2	1:A:77:VAL:HG22	0.47	2.44	16	1
1:B:93:PHE:CD2	1:B:97:LEU:HD13	0.47	2.45	16	1
1:A:17:ALA:HB1	1:A:97:LEU:HD12	0.47	1.86	18	1
1:B:78:ALA:O	1:B:82:ALA:CB	0.47	2.62	3	2
1:B:13:HIS:CD2	1:B:13:HIS:C	0.47	2.88	8	1
1:B:91:THR:HA	1:B:94:LEU:HD23	0.47	1.87	3	3
1:B:83:HIS:O	1:B:87:VAL:CG2	0.47	2.62	3	1
1:A:35:TYR:CG	1:A:48:PHE:CE1	0.47	3.02	7	1
1:A:63:TYR:CE2	1:B:16:LEU:HD13	0.47	2.45	7	1
1:B:15:LEU:HD12	1:B:15:LEU:C	0.47	2.30	15	1
1:A:34:GLY:O	1:A:37:ASN:N	0.47	2.48	14	13
1:A:56:ILE:CD1	1:A:56:ILE:O	0.47	2.63	6	1
1:B:15:LEU:CD2	1:B:100:VAL:HG23	0.47	2.40	9	1
1:A:68:GLU:CD	1:B:105:TYR:CE1	0.47	2.88	13	1
1:B:29:GLU:OE2	1:B:30:GLU:N	0.47	2.48	10	1
1:B:19:PHE:CD2	1:B:28:ILE:HG12	0.47	2.45	11	2
1:A:39:VAL:HG13	1:A:45:MET:HG2	0.47	1.86	13	1
1:B:35:TYR:CG	1:B:36:ALA:N	0.47	2.82	15	1
1:A:61:GLN:HE21	1:B:101:LEU:HD11	0.46	1.70	8	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:53:ASP:OD2	1:B:64:THR:HG22	0.46	2.10	9	1
1:A:35:TYR:CZ	1:A:48:PHE:CZ	0.46	3.02	12	1
1:B:63:TYR:O	1:B:64:THR:C	0.46	2.52	15	3
1:B:11:VAL:HG22	1:B:106:LYS:HG2	0.46	1.86	15	1
1:A:101:LEU:HD22	1:B:63:TYR:CE2	0.46	2.44	16	1
1:A:31:LEU:HD23	1:A:89:PHE:CE1	0.46	2.45	19	1
1:B:93:PHE:CE2	1:B:97:LEU:HB2	0.46	2.45	2	1
1:A:97:LEU:HD22	1:A:98:ASP:C	0.46	2.31	13	3
1:A:69:SER:HB3	1:A:71:PHE:CZ	0.46	2.44	17	2
1:A:101:LEU:HD22	1:A:101:LEU:N	0.46	2.24	13	1
1:A:63:TYR:OH	1:B:16:LEU:CD2	0.46	2.62	4	1
1:B:58:ASN:O	1:B:59:LEU:CB	0.46	2.62	7	2
1:B:31:LEU:HD12	1:B:93:PHE:CE1	0.46	2.45	14	1
1:B:93:PHE:CE1	1:B:97:LEU:HD13	0.46	2.45	17	1
1:A:16:LEU:HD21	1:A:63:TYR:O	0.46	2.11	6	1
1:A:16:LEU:HD23	1:A:66:ILE:HG21	0.46	1.88	12	1
1:B:19:PHE:CD1	1:B:28:ILE:HG12	0.46	2.46	4	1
1:B:54:VAL:O	1:B:56:ILE:N	0.46	2.49	20	3
1:B:44:PRO:HG3	1:B:80:TYR:CE1	0.46	2.46	10	1
1:B:105:TYR:CD1	1:B:105:TYR:C	0.46	2.89	18	1
1:B:18:SER:O	1:B:98:ASP:CB	0.46	2.63	20	2
1:B:108:THR:O	1:B:108:THR:HG22	0.46	2.10	1	1
1:B:34:GLY:O	1:B:37:ASN:N	0.46	2.49	14	12
1:A:54:VAL:O	1:A:56:ILE:N	0.46	2.49	8	3
1:B:16:LEU:HD12	1:B:101:LEU:HB3	0.46	1.87	11	1
1:A:35:TYR:CD1	1:A:48:PHE:CE2	0.46	3.03	9	1
1:B:49:HIS:CE1	1:B:68:GLU:OE2	0.46	2.69	10	1
1:B:80:TYR:N	1:B:80:TYR:CD1	0.46	2.79	16	1
1:A:108:THR:HG21	1:B:50:TRP:NE1	0.46	2.24	1	1
1:A:13:HIS:CD2	1:A:13:HIS:C	0.46	2.89	19	4
1:A:14:VAL:N	1:A:103:ILE:O	0.46	2.48	16	6
1:B:65:HIS:CD2	1:B:67:PHE:CE2	0.46	3.03	5	2
1:A:35:TYR:CB	1:A:48:PHE:CE2	0.46	2.98	7	1
1:A:13:HIS:NE2	1:A:103:ILE:O	0.46	2.49	13	1
1:A:103:ILE:CG2	1:B:53:ASP:HB3	0.46	2.41	14	1
1:B:49:HIS:CE1	1:B:68:GLU:OE1	0.46	2.69	1	1
1:A:35:TYR:CD1	1:A:48:PHE:CG	0.46	3.03	7	1
1:A:42:ILE:O	1:A:43:GLU:CB	0.46	2.64	7	2
1:B:71:PHE:CZ	1:B:80:TYR:CE2	0.46	3.04	12	1
1:A:101:LEU:HG	1:B:63:TYR:CE1	0.46	2.46	17	1
1:A:39:VAL:HG22	1:A:45:MET:HE2	0.46	1.88	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:67:PHE:N	1:A:67:PHE:CD1	0.46	2.79	8	1
1:A:93:PHE:O	1:A:97:LEU:HD23	0.46	2.11	20	1
1:A:51:GLY:HA3	1:B:105:TYR:CD1	0.45	2.46	5	1
1:B:15:LEU:O	1:B:67:PHE:N	0.45	2.49	13	5
1:B:93:PHE:CZ	1:B:97:LEU:HB2	0.45	2.46	19	1
1:A:50:TRP:CD1	1:B:110:VAL:HG23	0.45	2.46	3	1
1:B:60:HIS:CG	1:B:64:THR:HG23	0.45	2.47	9	1
1:A:73:SER:O	1:A:76:ALA:N	0.45	2.50	11	1
1:B:17:ALA:HB1	1:B:93:PHE:CZ	0.45	2.46	1	1
1:A:18:SER:O	1:A:98:ASP:N	0.45	2.49	5	5
1:A:71:PHE:HD2	1:A:77:VAL:HG22	0.45	1.70	7	1
1:A:61:GLN:HG2	1:B:101:LEU:HD23	0.45	1.89	12	1
1:A:94:LEU:HA	1:A:97:LEU:HD12	0.45	1.88	13	1
1:B:64:THR:HG22	1:B:65:HIS:NE2	0.45	2.23	18	1
1:A:54:VAL:O	1:A:55:SER:CB	0.45	2.64	1	1
1:B:83:HIS:CG	1:B:84:PRO:HD2	0.45	2.47	3	3
1:B:57:GLU:O	1:B:59:LEU:N	0.45	2.50	9	1
1:B:42:ILE:CG2	1:B:44:PRO:HD2	0.45	2.40	10	1
1:A:97:LEU:H	1:A:97:LEU:HD22	0.45	1.70	2	1
1:A:16:LEU:CA	1:A:66:ILE:HG22	0.45	2.41	3	1
1:A:71:PHE:CD1	1:A:77:VAL:CG2	0.45	2.99	5	2
1:B:14:VAL:N	1:B:103:ILE:O	0.45	2.50	7	6
1:A:53:ASP:OD2	1:B:103:ILE:CD1	0.45	2.64	2	1
1:A:23:VAL:CG1	1:A:23:VAL:O	0.45	2.65	13	2
1:B:98:ASP:OD1	1:B:99:LYS:N	0.45	2.49	14	1
1:B:56:ILE:O	1:B:58:ASN:N	0.45	2.49	17	2
1:B:97:LEU:HD21	1:B:100:VAL:HG12	0.45	1.89	13	3
1:B:31:LEU:HD13	1:B:89:PHE:CE2	0.45	2.47	3	1
1:A:56:ILE:O	1:A:58:ASN:N	0.45	2.50	19	2
1:A:72:GLU:HB2	1:A:76:ALA:HB2	0.45	1.89	8	1
1:A:63:TYR:C	1:A:65:HIS:N	0.45	2.70	2	3
1:B:43:GLU:CB	1:B:44:PRO:CD	0.45	2.94	7	1
1:B:58:ASN:O	1:B:60:HIS:N	0.45	2.50	1	1
1:B:105:TYR:CD1	1:B:106:LYS:N	0.45	2.85	1	1
1:B:78:ALA:O	1:B:82:ALA:HB3	0.45	2.11	3	1
1:B:18:SER:O	1:B:98:ASP:N	0.45	2.46	14	2
1:B:59:LEU:O	1:B:60:HIS:C	0.45	2.54	18	2
1:B:97:LEU:HD11	1:B:100:VAL:HB	0.45	1.88	8	2
1:B:44:PRO:O	1:B:45:MET:C	0.45	2.55	12	1
1:B:97:LEU:CD2	1:B:100:VAL:HG12	0.45	2.42	16	1
1:B:71:PHE:CB	1:B:77:VAL:HG22	0.45	2.42	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:LEU:HD22	1:A:16:LEU:N	0.45	2.27	18	1
1:A:50:TRP:CA	1:B:105:TYR:OH	0.44	2.65	2	1
1:A:53:ASP:HB3	1:B:103:ILE:HD12	0.44	1.89	4	1
1:A:52:LYS:HB2	1:A:65:HIS:CD2	0.44	2.46	7	3
1:A:101:LEU:C	1:A:101:LEU:CD1	0.44	2.86	17	1
1:B:108:THR:O	1:B:108:THR:CG2	0.44	2.61	15	2
1:B:15:LEU:HD21	1:B:100:VAL:HG23	0.44	1.89	7	1
1:A:14:VAL:HG23	1:A:105:TYR:HB3	0.44	1.89	14	1
1:A:49:HIS:O	1:A:68:GLU:N	0.44	2.49	15	1
1:B:34:GLY:O	1:B:38:LEU:HD23	0.44	2.11	16	1
1:B:19:PHE:CD2	1:B:28:ILE:HG13	0.44	2.47	18	1
1:B:63:TYR:C	1:B:65:HIS:N	0.44	2.70	14	4
1:B:98:ASP:O	1:B:99:LYS:CG	0.44	2.65	15	1
1:A:101:LEU:HD13	1:B:63:TYR:HE2	0.44	1.72	16	1
1:A:39:VAL:HG21	1:A:48:PHE:CB	0.44	2.42	4	1
1:B:37:ASN:O	1:B:40:ASN:ND2	0.44	2.50	7	1
1:A:44:PRO:O	1:A:45:MET:CB	0.44	2.65	9	1
1:B:31:LEU:HD22	1:B:93:PHE:CE2	0.44	2.47	10	1
1:A:32:ILE:HD11	1:A:67:PHE:CZ	0.44	2.46	13	1
1:A:101:LEU:HD22	1:B:63:TYR:CD2	0.44	2.48	16	1
1:B:15:LEU:HD13	1:B:16:LEU:N	0.44	2.27	17	1
1:B:15:LEU:HD12	1:B:102:VAL:HG12	0.44	1.90	3	1
1:A:40:ASN:O	1:A:40:ASN:ND2	0.44	2.51	4	1
1:A:41:LEU:O	1:A:43:GLU:N	0.44	2.51	6	2
1:A:72:GLU:CB	1:A:76:ALA:HB2	0.44	2.43	8	1
1:B:37:ASN:O	1:B:41:LEU:N	0.44	2.50	12	1
1:A:51:GLY:O	1:A:66:ILE:CG1	0.44	2.65	17	1
1:A:104:ASP:HB3	1:B:54:VAL:HG22	0.44	1.89	18	1
1:A:53:ASP:CG	1:A:54:VAL:N	0.44	2.71	20	1
1:B:54:VAL:O	1:B:55:SER:CB	0.44	2.64	1	2
1:A:16:LEU:CD1	1:A:101:LEU:HD12	0.44	2.31	6	1
1:A:101:LEU:HD12	1:B:60:HIS:CA	0.44	2.37	13	2
1:A:61:GLN:NE2	1:B:101:LEU:CD1	0.44	2.80	16	1
1:B:54:VAL:O	1:B:55:SER:C	0.44	2.56	17	1
1:B:13:HIS:NE2	1:B:102:VAL:HG13	0.44	2.27	1	1
1:A:63:TYR:O	1:A:64:THR:C	0.44	2.56	2	1
1:A:57:GLU:O	1:A:58:ASN:CB	0.44	2.65	4	1
1:A:75:GLU:O	1:A:78:ALA:HB3	0.44	2.11	9	2
1:A:42:ILE:O	1:A:43:GLU:C	0.44	2.56	12	1
1:A:66:ILE:CG2	1:A:68:GLU:CD	0.44	2.86	19	1
1:A:63:TYR:CE1	1:B:63:TYR:CZ	0.44	3.05	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:36:ALA:O	1:A:39:VAL:HG12	0.44	2.13	3	1
1:B:71:PHE:CE2	1:B:77:VAL:HA	0.44	2.47	6	1
1:A:16:LEU:HD12	1:A:101:LEU:HB2	0.44	1.90	7	1
1:A:13:HIS:CE1	1:A:102:VAL:HG23	0.44	2.48	4	1
1:A:63:TYR:O	1:A:64:THR:HG23	0.44	2.13	18	3
1:A:15:LEU:HD12	1:A:102:VAL:HA	0.44	1.89	10	1
1:A:16:LEU:HD11	1:A:63:TYR:O	0.44	2.12	10	1
1:B:87:VAL:O	1:B:91:THR:CB	0.44	2.66	13	1
1:A:19:PHE:CD2	1:A:28:ILE:HG12	0.43	2.48	2	1
1:A:66:ILE:HD11	1:B:105:TYR:HD2	0.43	1.68	4	1
1:B:93:PHE:CE2	1:B:97:LEU:CD2	0.43	3.01	8	1
1:B:38:LEU:O	1:B:42:ILE:HD12	0.43	2.13	9	1
1:B:36:ALA:O	1:B:39:VAL:HG22	0.43	2.13	10	1
1:A:15:LEU:HD22	1:A:67:PHE:HB2	0.43	1.90	12	1
1:A:105:TYR:HH	1:B:49:HIS:CE1	0.43	2.31	15	1
1:B:45:MET:HE2	1:B:48:PHE:HD2	0.43	1.73	15	1
1:A:45:MET:O	1:A:47:ALA:N	0.43	2.49	16	1
1:A:54:VAL:HG22	1:B:104:ASP:CB	0.43	2.42	20	1
1:A:53:ASP:OD1	1:B:103:ILE:CG2	0.43	2.65	4	1
1:A:94:LEU:HD22	1:A:100:VAL:HG11	0.43	1.90	5	1
1:A:72:GLU:O	1:A:73:SER:CB	0.43	2.66	6	1
1:A:39:VAL:HG13	1:A:45:MET:HB3	0.43	1.89	15	1
1:B:53:ASP:OD1	1:B:54:VAL:N	0.43	2.51	16	1
1:A:93:PHE:CG	1:A:97:LEU:HD21	0.43	2.48	20	1
1:A:108:THR:CG2	1:B:50:TRP:NE1	0.43	2.81	1	1
1:A:54:VAL:O	1:A:55:SER:C	0.43	2.56	2	4
1:A:48:PHE:CD1	1:A:48:PHE:C	0.43	2.92	8	2
1:A:78:ALA:O	1:A:82:ALA:N	0.43	2.52	16	1
1:A:51:GLY:CA	1:B:105:TYR:CE2	0.43	3.01	2	1
1:A:35:TYR:CD1	1:A:48:PHE:CZ	0.43	3.05	3	1
1:B:58:ASN:O	1:B:59:LEU:HD12	0.43	2.13	7	1
1:A:80:TYR:CE1	1:A:86:HIS:CE1	0.43	3.06	12	1
1:B:16:LEU:HD23	1:B:101:LEU:HB2	0.43	1.90	13	1
1:A:34:GLY:O	1:A:38:LEU:N	0.43	2.49	14	1
1:A:73:SER:O	1:A:75:GLU:N	0.43	2.51	5	3
1:B:45:MET:SD	1:B:71:PHE:CZ	0.43	3.11	6	1
1:B:69:SER:HB3	1:B:71:PHE:CE2	0.43	2.49	9	1
1:A:63:TYR:CD1	1:B:101:LEU:HG	0.43	2.48	11	1
1:B:23:VAL:HG21	1:B:96:SER:CB	0.43	2.42	19	1
1:A:15:LEU:HD23	1:A:15:LEU:O	0.43	2.14	20	1
1:B:97:LEU:HD22	1:B:100:VAL:HG11	0.43	1.91	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:72:GLU:OE1	1:B:72:GLU:N	0.43	2.52	10	1
1:A:87:VAL:O	1:A:91:THR:CB	0.43	2.67	14	1
1:B:42:ILE:HD13	1:B:83:HIS:CE1	0.43	2.48	15	1
1:A:65:HIS:C	1:A:66:ILE:CG2	0.43	2.87	16	1
1:B:14:VAL:HG13	1:B:66:ILE:CD1	0.43	2.42	17	1
1:B:19:PHE:CE2	1:B:93:PHE:CZ	0.43	3.07	18	1
1:A:97:LEU:N	1:A:97:LEU:CD1	0.43	2.69	2	1
1:A:71:PHE:CE1	1:A:77:VAL:CG2	0.43	3.02	5	1
1:B:35:TYR:O	1:B:39:VAL:CG2	0.43	2.64	5	1
1:B:13:HIS:CE1	1:B:102:VAL:CG1	0.43	3.02	1	1
1:B:42:ILE:HG22	1:B:45:MET:N	0.43	2.29	3	1
1:A:16:LEU:HD12	1:A:101:LEU:HD13	0.43	1.86	6	1
1:A:45:MET:HG2	1:A:80:TYR:CD1	0.43	2.49	10	1
1:B:14:VAL:HG23	1:B:105:TYR:CB	0.43	2.43	12	1
1:A:31:LEU:HD22	1:A:93:PHE:CD2	0.43	2.49	14	1
1:A:43:GLU:CB	1:A:44:PRO:CD	0.43	2.97	15	1
1:B:101:LEU:HD12	1:B:103:ILE:HD11	0.43	1.91	17	1
1:B:77:VAL:HG12	1:B:81:ILE:HD12	0.43	1.91	2	1
1:A:16:LEU:HD11	1:B:63:TYR:CZ	0.43	2.49	3	1
1:A:16:LEU:HD23	1:A:101:LEU:HD23	0.43	1.89	10	1
1:B:73:SER:O	1:B:76:ALA:N	0.43	2.52	11	1
1:B:101:LEU:CD1	1:B:103:ILE:HD11	0.43	2.43	12	1
1:A:68:GLU:OE1	1:B:105:TYR:CE1	0.43	2.72	13	1
1:B:45:MET:O	1:B:47:ALA:N	0.42	2.48	1	1
1:A:97:LEU:C	1:A:97:LEU:CD1	0.42	2.85	4	3
1:B:53:ASP:CG	1:B:54:VAL:N	0.42	2.72	9	1
1:A:63:TYR:O	1:A:64:THR:CB	0.42	2.67	10	1
1:A:107:PRO:HB3	1:B:49:HIS:CD2	0.42	2.49	15	1
1:A:101:LEU:HD21	1:B:60:HIS:N	0.42	2.29	19	1
1:A:19:PHE:O	1:A:20:LYS:O	0.42	2.37	1	2
1:A:83:HIS:O	1:A:87:VAL:HG23	0.42	2.14	7	1
1:A:109:SER:HB2	1:B:49:HIS:CD2	0.42	2.48	8	1
1:A:44:PRO:O	1:A:45:MET:O	0.42	2.37	12	1
1:A:20:LYS:O	1:A:21:ASP:CB	0.42	2.67	13	1
1:B:16:LEU:HD22	1:B:63:TYR:HE1	0.42	1.63	13	1
1:A:103:ILE:HD13	1:B:53:ASP:CB	0.42	2.43	17	1
1:B:53:ASP:HB2	1:B:56:ILE:CG2	0.42	2.45	17	1
1:B:51:GLY:O	1:B:66:ILE:CG1	0.42	2.67	20	1
1:B:18:SER:HA	1:B:64:THR:HG21	0.42	1.92	2	1
1:A:14:VAL:O	1:A:103:ILE:O	0.42	2.38	17	8
1:A:31:LEU:CD2	1:A:93:PHE:CD1	0.42	3.01	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:75:GLU:O	1:B:78:ALA:HB3	0.42	2.14	6	2
1:A:102:VAL:O	1:A:103:ILE:CD1	0.42	2.67	14	1
1:A:11:VAL:HG22	1:A:106:LYS:HE3	0.42	1.89	16	1
1:A:56:ILE:HD11	1:B:102:VAL:HB	0.42	1.91	17	1
1:A:103:ILE:CD1	1:B:53:ASP:OD1	0.42	2.67	17	1
1:A:58:ASN:O	1:A:59:LEU:HD23	0.42	2.14	2	1
1:B:32:ILE:HG21	1:B:50:TRP:CD1	0.42	2.49	10	1
1:B:44:PRO:O	1:B:45:MET:CB	0.42	2.68	10	1
1:A:37:ASN:O	1:A:40:ASN:ND2	0.42	2.53	12	1
1:A:71:PHE:CE2	1:A:77:VAL:HG23	0.42	2.49	2	1
1:A:101:LEU:N	1:A:101:LEU:CD2	0.42	2.81	10	1
1:B:76:ALA:O	1:B:79:GLU:N	0.42	2.52	14	1
1:A:19:PHE:CE1	1:A:93:PHE:CE1	0.42	3.08	15	1
1:A:69:SER:HB3	1:A:71:PHE:CE2	0.42	2.50	16	1
1:B:73:SER:O	1:B:75:GLU:N	0.42	2.48	20	1
1:A:60:HIS:ND1	1:A:64:THR:OG1	0.42	2.51	2	1
1:A:71:PHE:CG	1:A:77:VAL:HG21	0.42	2.50	6	1
1:B:15:LEU:HD21	1:B:100:VAL:CG2	0.42	2.45	7	1
1:A:18:SER:OG	1:A:64:THR:CG2	0.42	2.68	8	1
1:A:62:GLY:O	1:A:64:THR:CG2	0.42	2.67	13	2
1:A:93:PHE:O	1:A:97:LEU:CB	0.42	2.67	19	1
1:A:93:PHE:CD2	1:A:97:LEU:CD2	0.42	3.02	20	1
1:B:97:LEU:CD1	1:B:100:VAL:CG1	0.42	2.96	10	1
1:B:49:HIS:CD2	1:B:49:HIS:O	0.42	2.73	15	1
1:A:93:PHE:CD2	1:A:97:LEU:HD21	0.42	2.49	20	1
1:A:16:LEU:CD1	1:A:101:LEU:CD1	0.42	2.88	6	1
1:A:97:LEU:C	1:A:97:LEU:CD2	0.42	2.80	6	2
1:B:16:LEU:HG	1:B:63:TYR:CD1	0.42	2.50	8	1
1:A:16:LEU:HG	1:A:63:TYR:CD2	0.42	2.50	17	1
1:A:16:LEU:HD23	1:B:63:TYR:CZ	0.42	2.49	18	1
1:A:49:HIS:N	1:A:68:GLU:O	0.42	2.50	3	1
1:A:54:VAL:O	1:A:54:VAL:HG13	0.42	2.15	5	1
1:B:14:VAL:O	1:B:103:ILE:O	0.42	2.37	16	5
1:B:101:LEU:N	1:B:101:LEU:CD1	0.42	2.82	5	1
1:B:56:ILE:HD12	1:B:56:ILE:O	0.42	2.15	8	1
1:A:15:LEU:HD22	1:A:16:LEU:N	0.42	2.30	9	1
1:B:52:LYS:O	1:B:53:ASP:C	0.42	2.57	12	2
1:B:15:LEU:HD22	1:B:67:PHE:HB2	0.42	1.92	13	1
1:B:15:LEU:HD23	1:B:67:PHE:HB2	0.42	1.91	14	1
1:B:66:ILE:HG22	1:B:68:GLU:OE1	0.42	2.15	15	1
1:A:39:VAL:HG21	1:A:48:PHE:CD1	0.42	2.49	17	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:19:PHE:O	1:B:20:LYS:C	0.41	2.58	12	2
1:B:56:ILE:O	1:B:57:GLU:C	0.41	2.58	8	4
1:A:60:HIS:CA	1:B:101:LEU:HD12	0.41	2.43	7	1
1:B:18:SER:OG	1:B:99:LYS:CG	0.41	2.68	7	1
1:A:61:GLN:HG3	1:B:101:LEU:HD21	0.41	1.90	14	1
1:A:25:PRO:HA	1:A:28:ILE:CD1	0.41	2.42	19	1
1:B:59:LEU:N	1:B:59:LEU:HD23	0.41	2.29	20	1
1:A:16:LEU:HG	1:A:66:ILE:CG2	0.41	2.46	4	1
1:A:101:LEU:HD21	1:B:61:GLN:N	0.41	2.30	5	1
1:A:14:VAL:HG23	1:A:105:TYR:CB	0.41	2.45	8	1
1:A:13:HIS:CE1	1:A:102:VAL:HG13	0.41	2.50	10	1
1:A:63:TYR:CE2	1:B:63:TYR:OH	0.41	2.53	17	2
1:A:89:PHE:CZ	1:A:93:PHE:CE1	0.41	3.08	11	1
1:A:52:LYS:HD2	1:A:65:HIS:CE1	0.41	2.50	20	1
1:A:76:ALA:O	1:A:80:TYR:CD2	0.41	2.73	3	1
1:B:15:LEU:CD1	1:B:102:VAL:HG22	0.41	2.44	8	1
1:A:104:ASP:CB	1:B:54:VAL:CG2	0.41	2.98	13	1
1:B:93:PHE:CD1	1:B:97:LEU:HD12	0.41	2.51	7	1
1:B:16:LEU:HG	1:B:63:TYR:CE1	0.41	2.50	8	1
1:A:13:HIS:CE1	1:A:102:VAL:CG1	0.41	3.04	10	1
1:B:103:ILE:CG2	1:B:104:ASP:N	0.41	2.83	11	1
1:B:31:LEU:CD1	1:B:89:PHE:CZ	0.41	3.02	19	1
1:A:101:LEU:CD2	1:B:61:GLN:HG2	0.41	2.46	20	1
1:B:15:LEU:CD2	1:B:100:VAL:CG2	0.41	2.98	9	1
1:B:57:GLU:HA	1:B:60:HIS:CD2	0.41	2.51	14	1
1:A:53:ASP:CB	1:B:103:ILE:HD12	0.41	2.46	18	1
1:A:35:TYR:HB3	1:A:48:PHE:CE2	0.41	2.50	7	1
1:A:15:LEU:C	1:A:15:LEU:CD2	0.41	2.88	12	1
1:B:104:ASP:OD1	1:B:105:TYR:N	0.41	2.54	16	1
1:A:56:ILE:O	1:A:57:GLU:C	0.41	2.59	14	2
1:A:105:TYR:CD1	1:A:105:TYR:C	0.41	2.94	2	2
1:A:17:ALA:HB1	1:A:97:LEU:HD23	0.41	1.92	5	1
1:A:97:LEU:HD12	1:A:98:ASP:N	0.41	2.30	8	1
1:A:16:LEU:HD13	1:A:63:TYR:CE2	0.41	2.50	16	1
1:B:39:VAL:HG21	1:B:48:PHE:CD1	0.41	2.50	17	1
1:B:97:LEU:HD13	1:B:97:LEU:C	0.41	2.36	19	1
1:A:90:ALA:O	1:A:94:LEU:N	0.41	2.53	2	1
1:B:19:PHE:O	1:B:20:LYS:O	0.41	2.39	19	4
1:B:46:LYS:CD	1:B:72:GLU:OE2	0.41	2.68	8	1
1:A:37:ASN:O	1:A:40:ASN:OD1	0.41	2.39	9	1
1:B:16:LEU:HD22	1:B:16:LEU:C	0.41	2.35	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:LEU:O	1:A:60:HIS:O	0.41	2.39	16	1
1:B:26:GLU:O	1:B:29:GLU:CG	0.41	2.69	17	1
1:A:53:ASP:OD2	1:A:56:ILE:CG1	0.41	2.69	1	1
1:A:54:VAL:HG12	1:B:103:ILE:HA	0.41	1.92	5	1
1:A:71:PHE:HB3	1:A:77:VAL:CG2	0.41	2.46	6	1
1:A:15:LEU:HD13	1:A:15:LEU:O	0.41	2.16	9	1
1:A:16:LEU:CD1	1:A:101:LEU:HD23	0.41	2.42	9	1
1:B:89:PHE:CD1	1:B:89:PHE:C	0.41	2.94	9	1
1:A:59:LEU:O	1:A:60:HIS:C	0.41	2.59	11	1
1:A:71:PHE:CZ	1:A:80:TYR:CD2	0.41	3.09	14	1
1:B:19:PHE:CD1	1:B:28:ILE:CG1	0.41	3.04	14	1
1:B:19:PHE:CG	1:B:28:ILE:HG13	0.41	2.50	14	2
1:A:14:VAL:HG13	1:A:66:ILE:HD13	0.41	1.92	15	1
1:A:16:LEU:HD21	1:A:63:TYR:CA	0.41	2.40	17	1
1:A:80:TYR:CZ	1:A:86:HIS:CE1	0.41	3.09	18	1
1:B:50:TRP:CD1	1:B:50:TRP:N	0.41	2.89	18	1
1:B:19:PHE:CD2	1:B:97:LEU:CD1	0.41	3.04	4	1
1:B:35:TYR:HB3	1:B:48:PHE:CE2	0.41	2.51	4	1
1:A:56:ILE:O	1:A:56:ILE:HD13	0.41	2.14	6	1
1:A:13:HIS:O	1:A:68:GLU:CD	0.41	2.59	16	2
1:B:35:TYR:O	1:B:39:VAL:HG12	0.41	2.16	14	1
1:A:101:LEU:HG	1:B:63:TYR:CD1	0.41	2.51	17	1
1:A:39:VAL:HA	1:A:42:ILE:HD12	0.41	1.93	19	1
1:B:53:ASP:O	1:B:53:ASP:OD1	0.41	2.39	19	1
1:B:41:LEU:O	1:B:43:GLU:N	0.40	2.54	1	1
1:B:39:VAL:HG22	1:B:45:MET:CE	0.40	2.45	8	1
1:B:97:LEU:HD11	1:B:99:LYS:O	0.40	2.17	13	1
1:A:35:TYR:O	1:A:39:VAL:N	0.40	2.50	17	1
1:A:39:VAL:HG11	1:A:48:PHE:CE1	0.40	2.51	19	1
1:A:105:TYR:HH	1:B:68:GLU:CD	0.40	2.18	19	1
1:A:105:TYR:OH	1:B:49:HIS:C	0.40	2.60	3	1
1:B:45:MET:HE2	1:B:80:TYR:CE1	0.40	2.51	9	1
1:A:16:LEU:HD11	1:A:63:TYR:CA	0.40	2.46	10	1
1:B:53:ASP:OD1	1:B:64:THR:O	0.40	2.39	13	1
1:A:63:TYR:OH	1:B:63:TYR:CG	0.40	2.74	15	1
1:B:66:ILE:HD13	1:B:67:PHE:N	0.40	2.31	17	1
1:B:13:HIS:CE1	1:B:102:VAL:CG2	0.40	3.04	18	1
1:B:78:ALA:O	1:B:82:ALA:N	0.40	2.54	18	1
1:A:97:LEU:HD11	1:A:100:VAL:HG11	0.40	1.92	1	1
1:B:76:ALA:HB1	1:B:80:TYR:CZ	0.40	2.51	3	1
1:A:16:LEU:HD13	1:A:17:ALA:N	0.40	2.31	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:42:ILE:CG2	1:A:44:PRO:HD2	0.40	2.44	7	1
1:A:19:PHE:O	1:A:20:LYS:C	0.40	2.60	9	1
1:B:101:LEU:HD22	1:B:102:VAL:N	0.40	2.32	11	1
1:B:16:LEU:HD13	1:B:63:TYR:HD1	0.40	1.77	13	1
1:A:105:TYR:OH	1:B:49:HIS:NE2	0.40	2.54	15	1
1:A:104:ASP:HB3	1:B:54:VAL:CG2	0.40	2.46	18	1
1:B:57:GLU:O	1:B:58:ASN:O	0.40	2.39	20	1
1:A:52:LYS:O	1:A:53:ASP:C	0.40	2.58	6	1
1:B:54:VAL:HG12	1:B:55:SER:N	0.40	2.32	6	1
1:B:45:MET:O	1:B:46:LYS:C	0.40	2.59	10	1
1:A:73:SER:C	1:A:75:GLU:N	0.40	2.72	11	1
1:B:52:LYS:HA	1:B:65:HIS:CB	0.40	2.47	11	1
1:A:19:PHE:CG	1:A:97:LEU:HD23	0.40	2.51	12	1
1:A:105:TYR:OH	1:B:68:GLU:CD	0.40	2.60	12	2
1:A:16:LEU:CB	1:B:63:TYR:OH	0.40	2.70	18	1
1:A:17:ALA:HB1	1:A:97:LEU:CB	0.40	2.47	2	1
1:A:45:MET:O	1:A:46:LYS:C	0.40	2.59	7	1
1:A:39:VAL:HG11	1:B:112:LEU:HD22	0.40	1.93	12	1
1:B:66:ILE:C	1:B:66:ILE:CD1	0.40	2.87	17	1
1:A:19:PHE:CG	1:A:28:ILE:HG12	0.40	2.52	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	102/112 (91%)	85±3 (83±3%)	13±3 (13±3%)	4±2 (4±2%)	5	31
1	B	102/112 (91%)	84±3 (82±3%)	14±2 (13±2%)	5±2 (5±2%)	4	28
All	All	4080/4480 (91%)	3374 (83%)	531 (13%)	175 (4%)	5	29

All 36 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	42	ILE	13

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Mol	Chain	Res	Type	Models (Total)
1	B	42	ILE	13
1	A	20	LYS	10
1	B	58	ASN	10
1	B	59	LEU	10
1	A	57	GLU	9
1	A	58	ASN	9
1	B	55	SER	7
1	B	20	LYS	7
1	B	73	SER	7
1	A	73	SER	7
1	A	55	SER	5
1	B	45	MET	5
1	B	62	GLY	5
1	A	59	LEU	5
1	B	57	GLU	5
1	B	53	ASP	4
1	A	62	GLY	4
1	A	45	MET	4
1	B	64	THR	4
1	A	98	ASP	3
1	B	44	PRO	3
1	B	46	LYS	3
1	B	43	GLU	3
1	A	64	THR	2
1	A	10	PRO	2
1	B	21	ASP	2
1	A	72	GLU	2
1	A	43	GLU	2
1	A	44	PRO	2
1	A	46	LYS	2
1	B	10	PRO	2
1	A	60	HIS	1
1	A	51	GLY	1
1	B	60	HIS	1
1	B	72	GLU	1

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	A	90/96 (94%)	65±3 (72±3%)	25±3 (28±3%)	2 19
1	B	90/96 (94%)	65±3 (72±4%)	25±3 (28±4%)	2 19
All	All	3600/3840 (94%)	2587 (72%)	1013 (28%)	2 19

All 141 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	111	SER	19
1	B	111	SER	19
1	A	16	LEU	18
1	B	35	TYR	18
1	A	31	LEU	17
1	A	35	TYR	17
1	A	46	LYS	15
1	A	55	SER	15
1	A	97	LEU	15
1	B	55	SER	15
1	A	27	LYS	14
1	A	49	HIS	14
1	B	41	LEU	14
1	B	45	MET	14
1	B	16	LEU	14
1	B	49	HIS	14
1	B	20	LYS	13
1	B	27	LYS	13
1	B	31	LEU	13
1	B	89	PHE	13
1	B	94	LEU	13
1	B	46	LYS	13
1	B	59	LEU	13
1	A	38	LEU	12
1	A	59	LEU	12
1	A	88	GLU	12
1	A	93	PHE	12
1	B	29	GLU	12
1	B	30	GLU	12
1	A	73	SER	11
1	A	94	LEU	11
1	A	57	GLU	11
1	A	30	GLU	10
1	B	21	ASP	10

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Mol	Chain	Res	Type	Models (Total)
1	B	97	LEU	10
1	A	43	GLU	10
1	A	45	MET	10
1	A	15	LEU	10
1	A	33	LYS	10
1	B	106	LYS	10
1	A	41	LEU	9
1	A	104	ASP	9
1	B	12	LYS	9
1	B	52	LYS	9
1	B	74	LYS	9
1	B	100	VAL	9
1	A	18	SER	9
1	B	79	GLU	9
1	A	29	GLU	9
1	B	33	LYS	9
1	A	106	LYS	9
1	A	21	ASP	9
1	A	13	HIS	8
1	A	77	VAL	8
1	A	89	PHE	8
1	B	38	LEU	8
1	B	105	TYR	8
1	A	20	LYS	8
1	A	52	LYS	8
1	A	12	LYS	8
1	B	15	LEU	8
1	B	57	GLU	8
1	B	101	LEU	8
1	B	72	GLU	8
1	A	79	GLU	8
1	A	72	GLU	8
1	B	61	GLN	7
1	B	86	HIS	7
1	B	88	GLU	7
1	B	104	ASP	7
1	A	100	VAL	7
1	B	69	SER	7
1	B	99	LYS	7
1	A	69	SER	7
1	A	101	LEU	7
1	B	93	PHE	7

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Mol	Chain	Res	Type	Models (Total)
1	A	86	HIS	6
1	A	99	LYS	6
1	B	66	ILE	6
1	B	73	SER	6
1	B	24	SER	6
1	B	23	VAL	6
1	B	18	SER	6
1	B	43	GLU	5
1	A	74	LYS	5
1	B	53	ASP	5
1	A	24	SER	5
1	A	56	ILE	5
1	A	66	ILE	5
1	B	56	ILE	5
1	B	109	SER	5
1	A	37	ASN	4
1	A	109	SER	4
1	B	26	GLU	4
1	B	96	SER	4
1	B	83	HIS	4
1	A	68	GLU	4
1	B	37	ASN	4
1	B	98	ASP	4
1	A	61	GLN	4
1	B	77	VAL	4
1	A	96	SER	3
1	B	58	ASN	3
1	A	26	GLU	3
1	A	112	LEU	3
1	B	68	GLU	3
1	A	53	ASP	3
1	A	64	THR	3
1	A	48	PHE	3
1	B	13	HIS	3
1	A	58	ASN	3
1	A	105	TYR	2
1	B	80	TYR	2
1	B	63	TYR	2
1	A	39	VAL	2
1	B	11	VAL	2
1	A	65	HIS	2
1	A	11	VAL	2

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Mol	Chain	Res	Type	Models (Total)
1	B	54	VAL	2
1	B	112	LEU	2
1	A	81	ILE	2
1	B	28	ILE	2
1	B	50	TRP	2
1	B	81	ILE	2
1	A	70	THR	1
1	A	50	TRP	1
1	A	60	HIS	1
1	B	102	VAL	1
1	A	102	VAL	1
1	B	39	VAL	1
1	A	108	THR	1
1	A	54	VAL	1
1	A	83	HIS	1
1	B	64	THR	1
1	A	28	ILE	1
1	A	63	TYR	1
1	B	48	PHE	1
1	A	87	VAL	1
1	B	87	VAL	1
1	B	65	HIS	1
1	A	23	VAL	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no monosaccharides 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