



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 07:49 pm GMT

PDB ID : 1RSO  
Title : Hetero-tetrameric L27 (Lin-2, Lin-7) domain complexes as organization platforms of supra-molecular assemblies  
Authors : Feng, W.; Long, J.-F.; Fan, J.-S.; Suetake, T.; Zhang, M.  
Deposited on : 2003-12-09

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : trunk28760  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

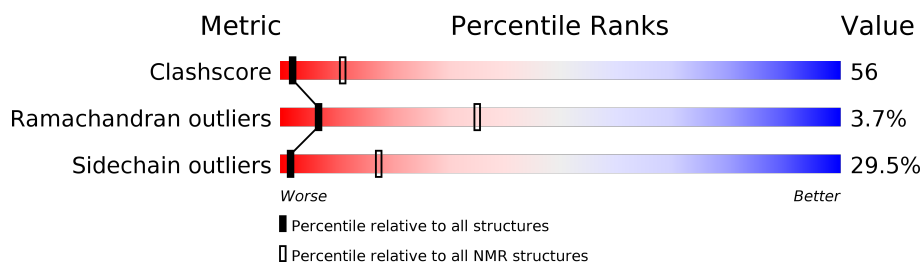
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

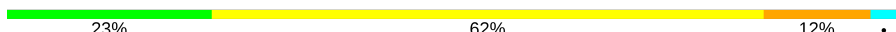
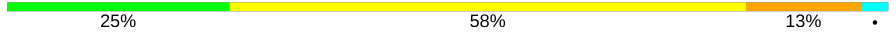
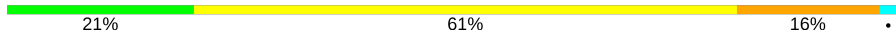
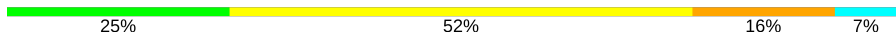
The overall completeness of chemical shifts assignment was not calculated.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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  $\geq 3$ , 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	60	 23% 62% 12% .
1	C	60	 25% 58% 13% .
2	B	56	 21% 61% 16% .
2	D	56	 25% 52% 16% 7%

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 11 as representative, based on the following criterion: *minimized average structure*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:7-A:64, B:82-B:136, C:7-C:64, D:82-D:133 (223)	0.39	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. No single-model clusters were found.

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

### 3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3802 atoms, of which 1894 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Presynaptic protein SAP97.

Mol	Chain	Residues	Atoms					Trace
1	A	60	Total	C	H	N	O	0
			1019	318	510	91	100	
1	C	60	Total	C	H	N	O	0
			1019	318	510	91	100	

- Molecule 2 is a protein called Peripheral plasma membrane protein CASK.

Mol	Chain	Residues	Atoms					Trace
2	B	56	Total	C	H	N	O	0
			882	279	437	74	92	
2	D	56	Total	C	H	N	O	0
			882	279	437	74	92	

There are 2 discrepancies between the modelled and reference sequences:

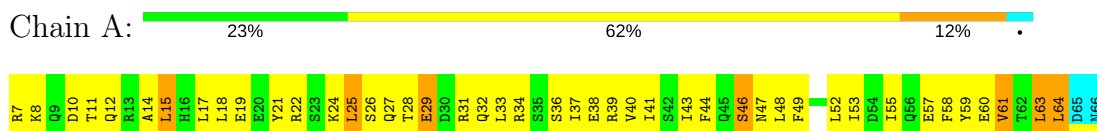
Chain	Residue	Modelled	Actual	Comment	Reference
B	105	SER	CYS	ENGINEERED	UNP Q62915
D	105	SER	CYS	ENGINEERED	UNP Q62915

## 4 Residue-property plots [i](#)

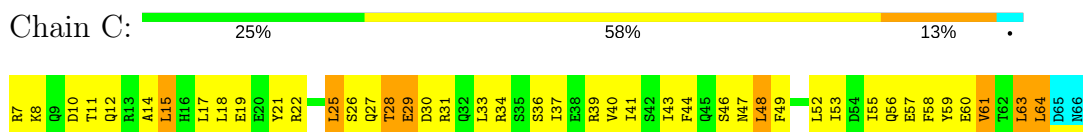
### 4.1 Average score per residue in the NMR ensemble

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

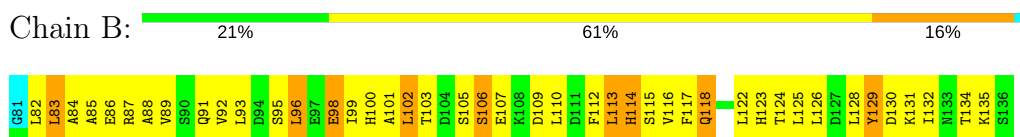
#### • Molecule 1: Presynaptic protein SAP97



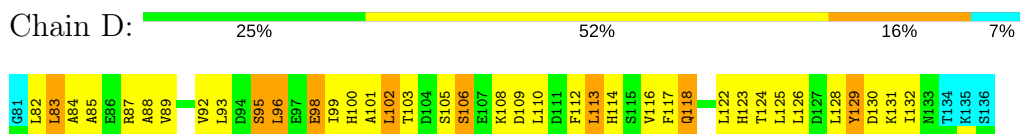
#### • Molecule 1: Presynaptic protein SAP97



#### • Molecule 2: Peripheral plasma membrane protein CASK



#### • Molecule 2: Peripheral plasma membrane protein CASK

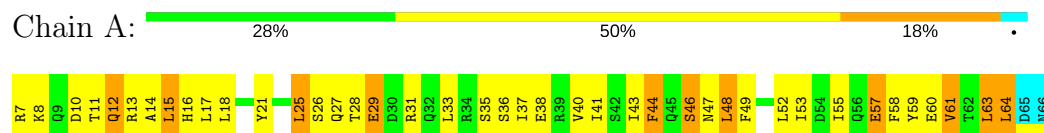


### 4.2 Scores per residue for each member of the ensemble

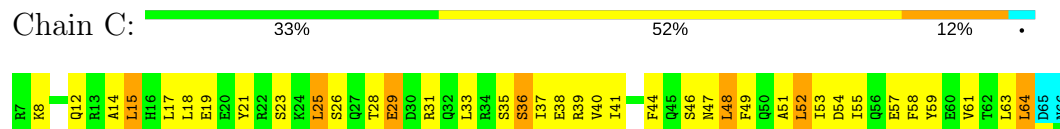
Colouring as in section 4.1 above.

### 4.2.1 Score per residue for model 1

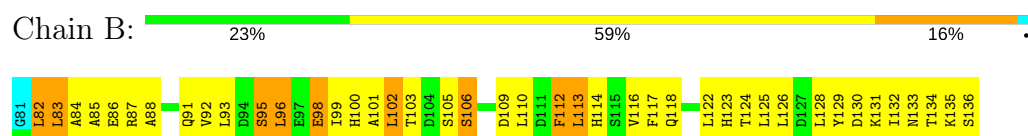
- Molecule 1: Presynaptic protein SAP97



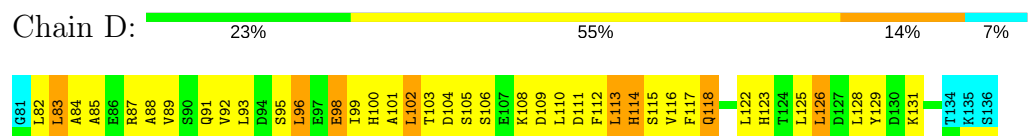
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK

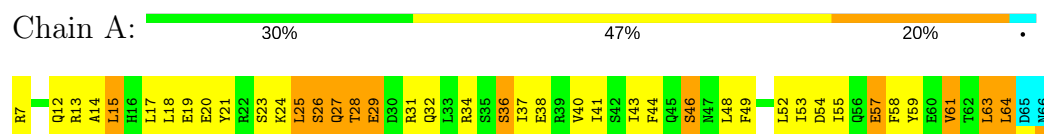


- Molecule 2: Peripheral plasma membrane protein CASK

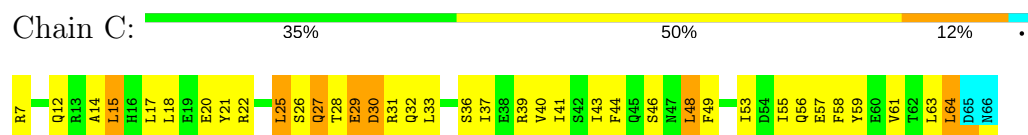


### 4.2.2 Score per residue for model 2

- Molecule 1: Presynaptic protein SAP97



- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK





- Molecule 2: Peripheral plasma membrane protein CASK

Chain D: 21% 52% 18% 7%



#### 4.2.3 Score per residue for model 3 (medoid)

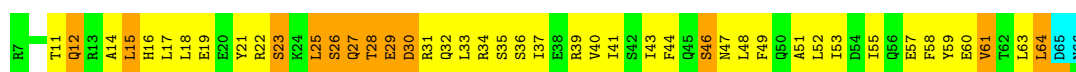
- Molecule 1: Presynaptic protein SAP97

Chain A: 32% 50% 15%



- Molecule 1: Presynaptic protein SAP97

Chain C: 23% 53% 20%



- Molecule 2: Peripheral plasma membrane protein CASK

Chain B: 21% 57% 20%



- Molecule 2: Peripheral plasma membrane protein CASK

Chain D: 23% 48% 21% 7%



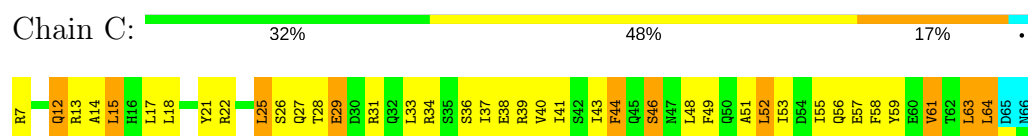
#### 4.2.4 Score per residue for model 4

- Molecule 1: Presynaptic protein SAP97

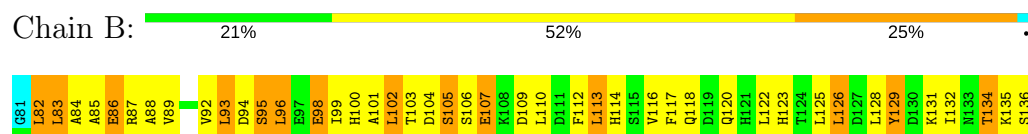
Chain A: 38% 47% 12%



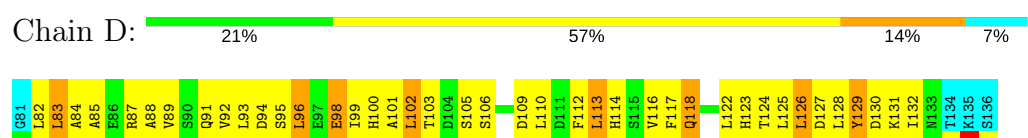
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK

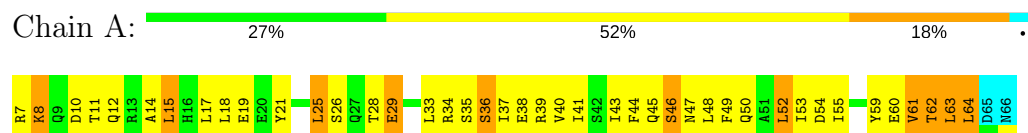


- Molecule 2: Peripheral plasma membrane protein CASK

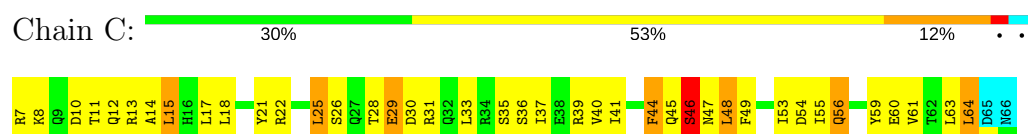


#### 4.2.5 Score per residue for model 5

- Molecule 1: Presynaptic protein SAP97



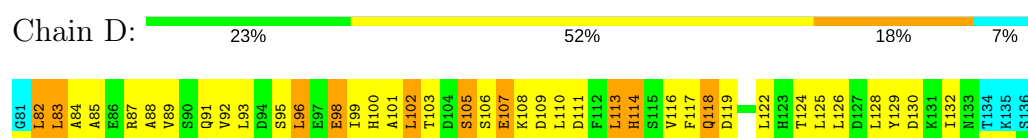
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK



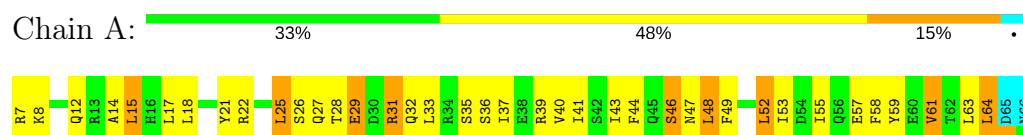
- Molecule 2: Peripheral plasma membrane protein CASK



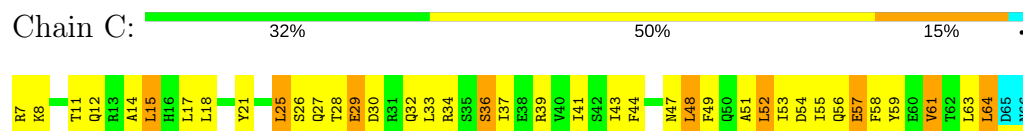


### 4.2.6 Score per residue for model 6

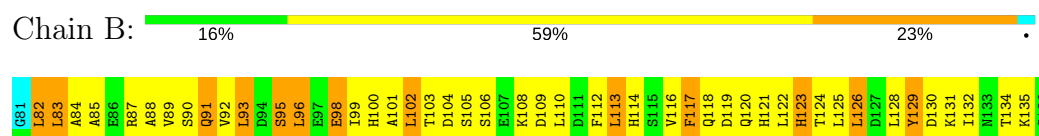
#### • Molecule 1: Presynaptic protein SAP97



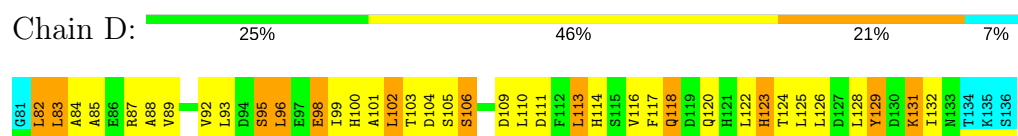
#### • Molecule 1: Presynaptic protein SAP97



#### • Molecule 2: Peripheral plasma membrane protein CASK

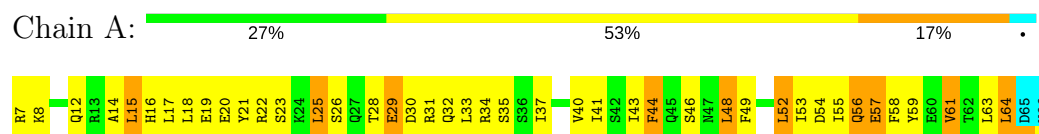


#### • Molecule 2: Peripheral plasma membrane protein CASK

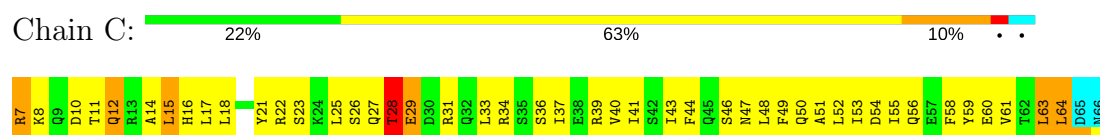


### 4.2.7 Score per residue for model 7

#### • Molecule 1: Presynaptic protein SAP97



#### • Molecule 1: Presynaptic protein SAP97



#### • Molecule 2: Peripheral plasma membrane protein CASK





- Molecule 2: Peripheral plasma membrane protein CASK

Chain D: 18% 57% 18% 7%



#### 4.2.8 Score per residue for model 8

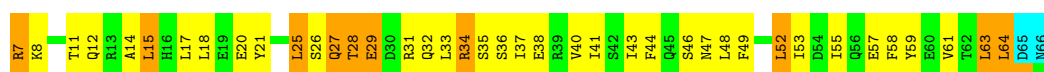
- Molecule 1: Presynaptic protein SAP97

Chain A: 28% 55% 13%



- Molecule 1: Presynaptic protein SAP97

Chain C: 30% 50% 17%



- Molecule 2: Peripheral plasma membrane protein CASK

Chain B: 18% 54% 27%



- Molecule 2: Peripheral plasma membrane protein CASK

Chain D: 23% 50% 20% 7%



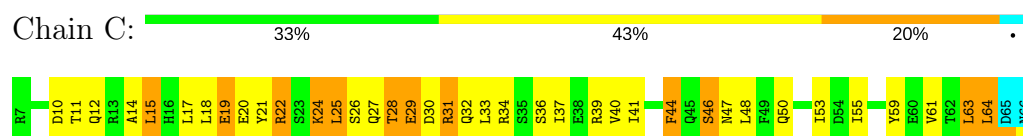
#### 4.2.9 Score per residue for model 9

- Molecule 1: Presynaptic protein SAP97

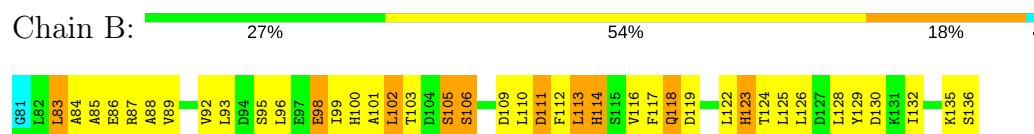
Chain A: 27% 52% 18%



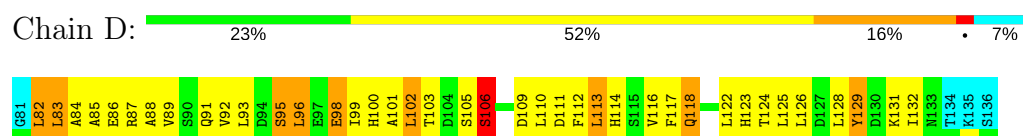
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK

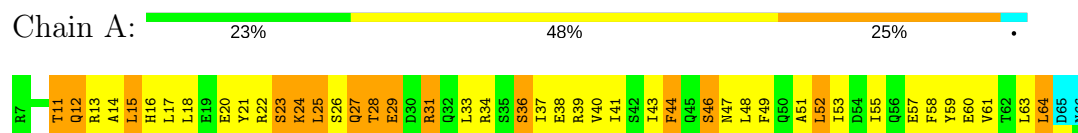


- Molecule 2: Peripheral plasma membrane protein CASK

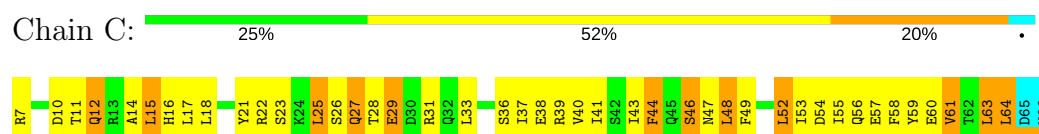


#### 4.2.10 Score per residue for model 10

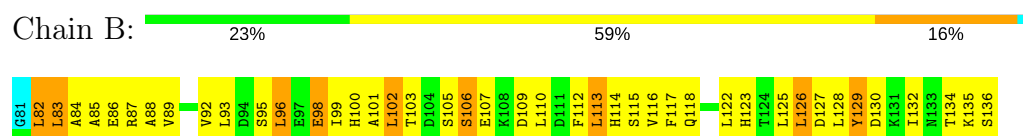
- Molecule 1: Presynaptic protein SAP97



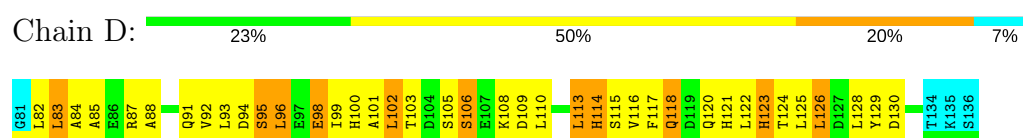
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK

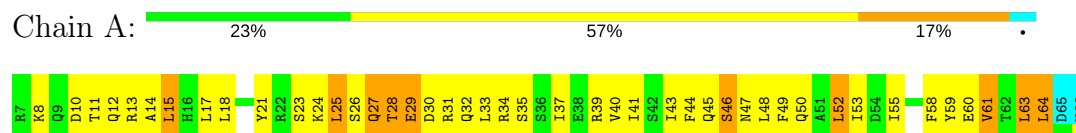


- Molecule 2: Peripheral plasma membrane protein CASK

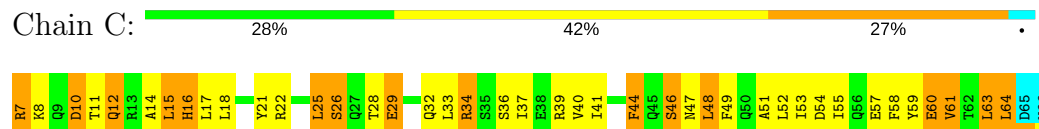


### 4.2.11 Score per residue for model 11

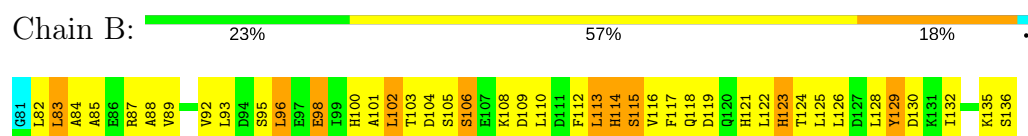
- Molecule 1: Presynaptic protein SAP97



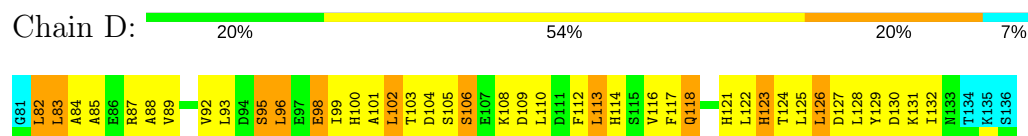
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK

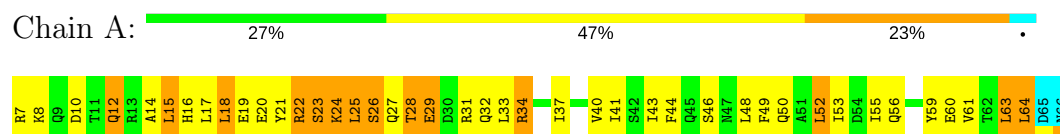


- Molecule 2: Peripheral plasma membrane protein CASK

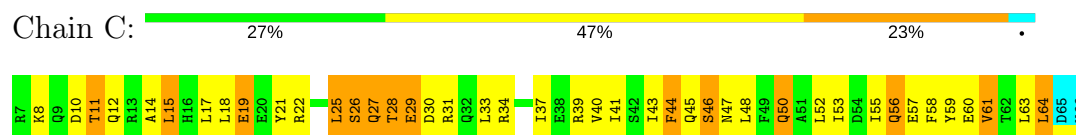


### 4.2.12 Score per residue for model 12

- Molecule 1: Presynaptic protein SAP97



- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK





- Molecule 2: Peripheral plasma membrane protein CASK

Chain D: 20% 55% 18% 7%



#### 4.2.13 Score per residue for model 13

- Molecule 1: Presynaptic protein SAP97

Chain A: 25% 52% 20% .



- Molecule 1: Presynaptic protein SAP97

Chain C: 33% 47% 17% .



- Molecule 2: Peripheral plasma membrane protein CASK

Chain B: 25% 54% 20% .



- Molecule 2: Peripheral plasma membrane protein CASK

Chain D: 20% 57% 16% 7%



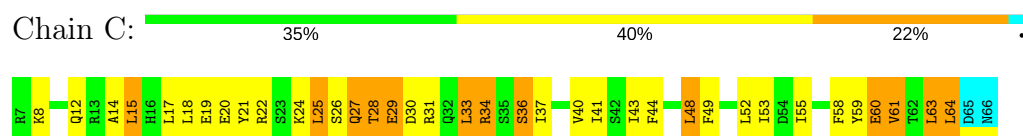
#### 4.2.14 Score per residue for model 14

- Molecule 1: Presynaptic protein SAP97

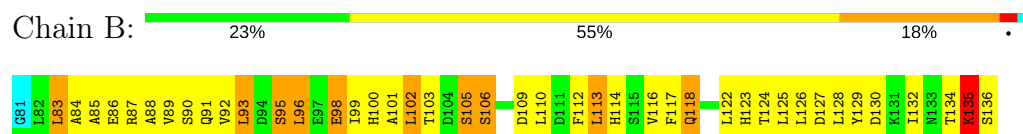
Chain A: 25% 50% 20% . .



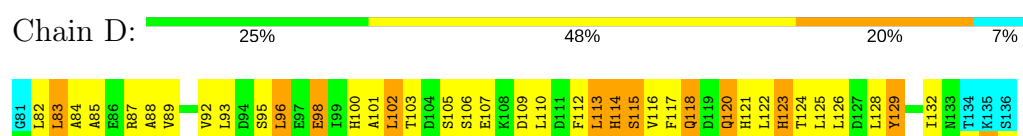
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK

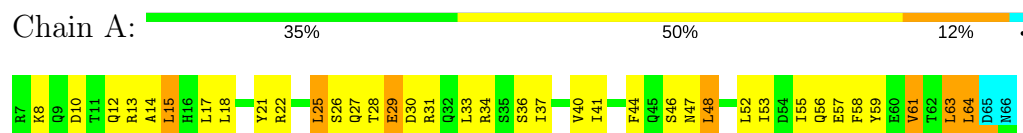


- Molecule 2: Peripheral plasma membrane protein CASK

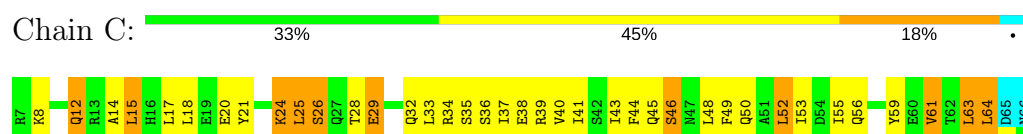


#### 4.2.15 Score per residue for model 15

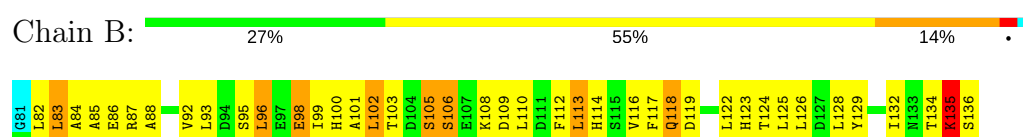
- Molecule 1: Presynaptic protein SAP97



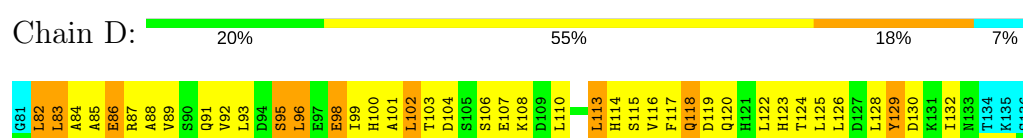
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK

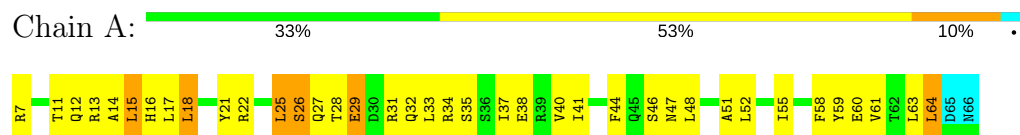


- Molecule 2: Peripheral plasma membrane protein CASK

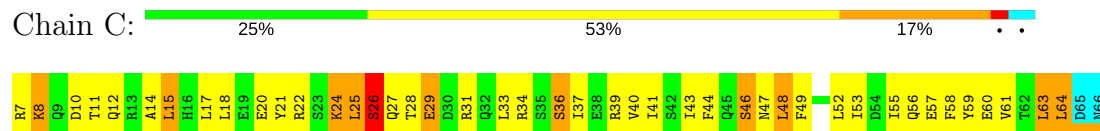


### 4.2.16 Score per residue for model 16

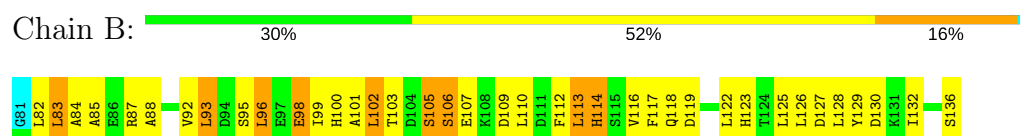
- Molecule 1: Presynaptic protein SAP97



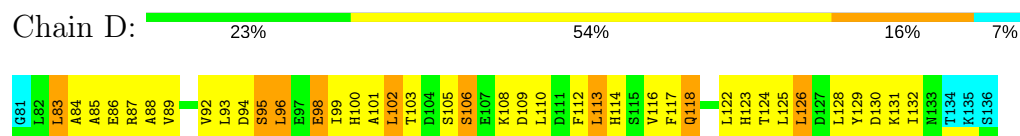
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK

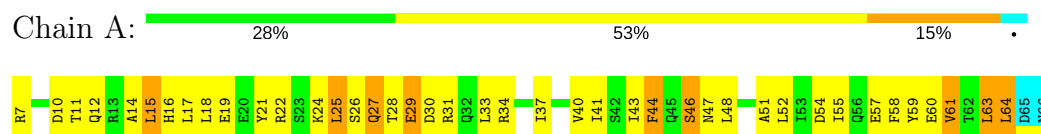


- Molecule 2: Peripheral plasma membrane protein CASK

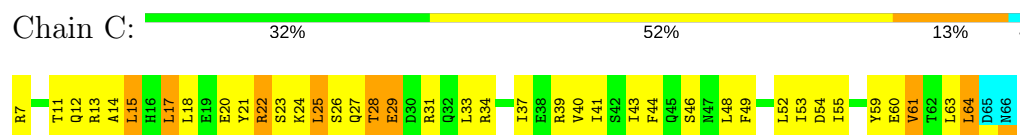


### 4.2.17 Score per residue for model 17

- Molecule 1: Presynaptic protein SAP97



- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK





- Molecule 2: Peripheral plasma membrane protein CASK

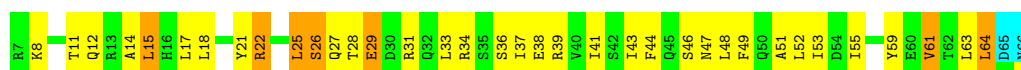
Chain D: 27% 45% 21% 7%



#### 4.2.18 Score per residue for model 18

- Molecule 1: Presynaptic protein SAP97

Chain A: 37% 48% 12%



- Molecule 1: Presynaptic protein SAP97

Chain C: 33% 45% 18%



- Molecule 2: Peripheral plasma membrane protein CASK

Chain B: 21% 61% 16%



- Molecule 2: Peripheral plasma membrane protein CASK

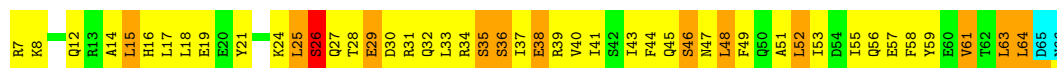
Chain D: 23% 52% 18% 7%



#### 4.2.19 Score per residue for model 19

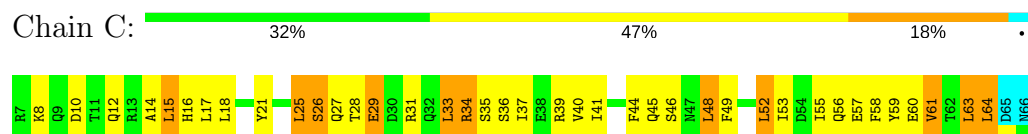
- Molecule 1: Presynaptic protein SAP97

Chain A: 20% 55% 20%

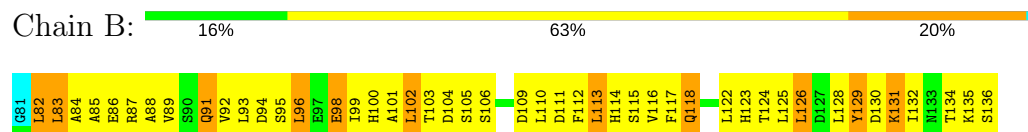




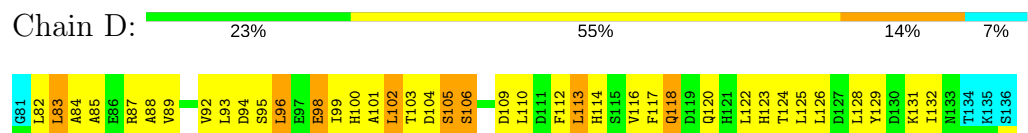
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK

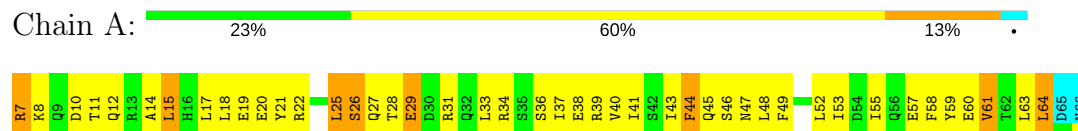


- Molecule 2: Peripheral plasma membrane protein CASK

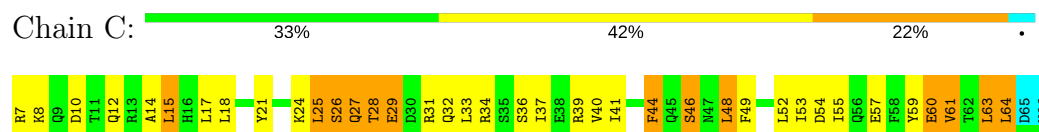


#### 4.2.20 Score per residue for model 20

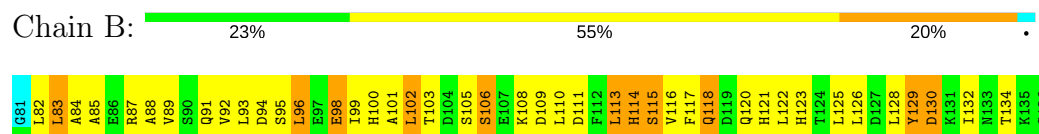
- Molecule 1: Presynaptic protein SAP97



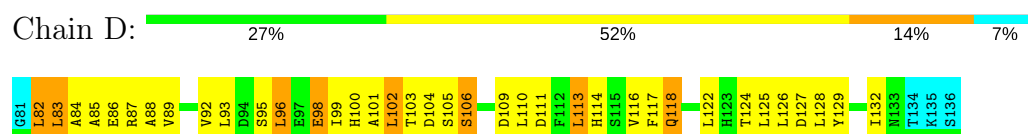
- Molecule 1: Presynaptic protein SAP97



- Molecule 2: Peripheral plasma membrane protein CASK



- Molecule 2: Peripheral plasma membrane protein CASK



## 5 Refinement protocol and experimental data overview ⓘ

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

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

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

Software name	Classification	Version
CNS	structure solution	1.1
CNS	refinement	1.1

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

## 6 Model quality (i)

### 6.1 Standard geometry (i)

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

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	493	500	498	64±7
1	C	493	500	498	65±6
2	B	441	434	430	67±6
2	D	419	409	405	67±5
All	All	36920	36860	36620	4138

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 56.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:84:ALA:HB1	2:B:88:ALA:HB2	1.00	1.33	18	19
2:D:84:ALA:HB1	2:D:88:ALA:HB2	0.99	1.29	16	19
1:A:52:LEU:HD11	2:B:125:LEU:HA	0.94	1.38	12	2
2:B:83:LEU:HD23	2:B:84:ALA:H	0.93	1.22	2	20
1:A:18:LEU:HD22	2:B:92:VAL:HG11	0.92	1.38	12	17
1:C:52:LEU:HD11	2:D:125:LEU:HA	0.90	1.41	8	1
2:D:83:LEU:HD23	2:D:84:ALA:H	0.89	1.27	4	20
1:A:17:LEU:HD22	1:A:21:TYR:CE1	0.89	2.03	8	18
1:A:25:LEU:HD12	1:A:37:ILE:HD11	0.88	1.45	14	20
2:B:96:LEU:HD22	2:B:110:LEU:HD22	0.88	1.45	5	16
2:D:123:HIS:HA	2:D:126:LEU:HD12	0.88	1.44	6	17

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:18:LEU:HD22	1:A:37:ILE:HG23	0.88	1.45	14	7
1:C:18:LEU:HD22	1:C:37:ILE:HG23	0.88	1.42	19	10
2:D:85:ALA:HB1	2:D:126:LEU:CB	0.87	2.00	4	17
1:C:49:PHE:CE2	1:C:53:ILE:HD11	0.87	2.04	11	11
2:B:128:LEU:HD21	1:C:59:TYR:CD2	0.87	2.05	12	20
1:A:59:TYR:CD2	2:D:128:LEU:HD21	0.86	2.05	20	18
1:C:49:PHE:O	1:C:52:LEU:HD23	0.86	1.69	8	1
2:B:82:LEU:HD23	2:B:82:LEU:N	0.86	1.84	7	5
2:D:96:LEU:HD12	2:D:114:HIS:CD2	0.86	2.06	11	7
1:C:18:LEU:HD22	2:D:92:VAL:HG11	0.85	1.45	15	13
1:C:25:LEU:HD11	1:C:33:LEU:HG	0.85	1.45	19	3
1:C:17:LEU:HD22	1:C:21:TYR:CE1	0.85	2.06	6	14
2:B:96:LEU:HD12	2:B:114:HIS:CD2	0.85	2.07	1	2
1:A:43:ILE:HG23	2:B:129:TYR:CE2	0.84	2.07	19	13
2:B:83:LEU:HD23	2:B:84:ALA:N	0.84	1.88	1	20
2:B:123:HIS:HA	2:B:126:LEU:HD12	0.83	1.49	12	19
1:A:49:PHE:O	1:A:52:LEU:HD23	0.83	1.72	12	1
1:A:14:ALA:CB	2:B:116:VAL:HG11	0.83	2.03	19	20
1:A:18:LEU:CD2	2:B:92:VAL:HG11	0.83	2.04	10	14
1:C:18:LEU:CD2	2:D:92:VAL:HG11	0.83	2.04	11	13
1:C:17:LEU:HD22	1:C:21:TYR:CZ	0.83	2.09	11	16
1:C:14:ALA:CB	2:D:116:VAL:HG11	0.82	2.05	16	20
2:D:82:LEU:N	2:D:82:LEU:HD23	0.82	1.88	6	4
2:D:100:HIS:HB2	2:D:110:LEU:HD11	0.82	1.52	7	20
1:C:25:LEU:HD12	1:C:37:ILE:HD11	0.82	1.50	4	19
1:A:49:PHE:CE2	1:A:53:ILE:HD11	0.82	2.09	7	6
2:B:85:ALA:HB1	2:B:126:LEU:HB3	0.81	1.50	11	15
2:D:122:LEU:O	2:D:126:LEU:HD12	0.81	1.76	13	4
1:C:64:LEU:HD23	1:C:64:LEU:N	0.81	1.91	19	15
2:D:83:LEU:HD23	2:D:84:ALA:N	0.81	1.90	19	20
2:B:85:ALA:HB1	2:B:126:LEU:HB2	0.81	1.52	17	7
2:B:82:LEU:O	2:B:82:LEU:HD12	0.80	1.75	1	1
2:B:96:LEU:HD22	2:B:110:LEU:CD2	0.80	2.07	17	11
1:A:33:LEU:HD21	2:B:95:SER:HB2	0.80	1.53	5	4
1:A:63:LEU:HD11	1:C:59:TYR:CE2	0.80	2.11	7	8
2:D:96:LEU:HD22	2:D:110:LEU:HD22	0.80	1.53	3	20
2:B:100:HIS:HB2	2:B:110:LEU:HD11	0.79	1.52	18	18
2:B:85:ALA:HB1	2:B:126:LEU:CB	0.79	2.08	19	10
1:C:43:ILE:HG23	2:D:129:TYR:CE2	0.79	2.11	4	8
1:A:41:ILE:HG22	1:A:45:GLN:NE2	0.79	1.92	11	5
2:B:85:ALA:HB2	2:B:130:ASP:OD2	0.79	1.77	3	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:D:82:LEU:HD23	2:D:82:LEU:N	0.79	1.93	5	4
2:B:132:ILE:HG23	1:C:51:ALA:HB1	0.78	1.52	4	3
1:A:25:LEU:HD12	1:A:37:ILE:CD1	0.78	2.07	14	12
2:B:82:LEU:N	2:B:82:LEU:HD23	0.78	1.93	2	3
2:D:85:ALA:HB1	2:D:126:LEU:HB3	0.78	1.55	15	13
2:D:116:VAL:O	2:D:122:LEU:HD22	0.78	1.79	8	20
1:A:17:LEU:HD22	1:A:21:TYR:CZ	0.78	2.13	10	16
2:D:85:ALA:O	2:D:126:LEU:HD13	0.78	1.77	7	15
1:C:37:ILE:HD11	2:D:99:ILE:CD1	0.77	2.08	19	1
1:C:37:ILE:HD11	2:D:99:ILE:HD13	0.77	1.54	19	1
2:B:116:VAL:O	2:B:122:LEU:HD22	0.77	1.79	8	20
1:A:59:TYR:CE2	1:C:63:LEU:HD11	0.77	2.15	17	6
2:D:85:ALA:HB1	2:D:126:LEU:HB2	0.77	1.55	13	12
1:A:48:LEU:O	1:A:48:LEU:HD12	0.77	1.79	15	7
2:D:84:ALA:HB1	2:D:88:ALA:CB	0.77	2.09	16	11
2:D:89:VAL:HG13	2:D:117:PHE:CD1	0.76	2.15	4	12
1:A:48:LEU:HD12	1:A:48:LEU:O	0.76	1.80	16	9
2:B:83:LEU:O	2:B:87:ARG:HB3	0.76	1.80	7	20
1:C:48:LEU:HD12	1:C:48:LEU:O	0.76	1.81	17	7
1:C:52:LEU:H	1:C:52:LEU:HD13	0.76	1.41	1	2
2:B:85:ALA:O	2:B:126:LEU:HD13	0.76	1.81	19	18
1:A:55:ILE:HD11	2:D:132:ILE:CG1	0.75	2.09	8	4
1:C:18:LEU:HB3	1:C:37:ILE:HG23	0.75	1.56	14	4
2:B:112:PHE:O	2:B:116:VAL:HG23	0.75	1.82	19	15
1:C:7:ARG:O	1:C:11:THR:HG23	0.75	1.82	16	3
2:B:82:LEU:HD22	2:B:130:ASP:OD1	0.75	1.80	1	2
1:C:48:LEU:O	1:C:48:LEU:HD12	0.74	1.82	16	4
2:D:98:GLU:O	2:D:101:ALA:HB3	0.74	1.82	11	20
1:A:15:LEU:O	1:A:41:ILE:HD12	0.74	1.82	17	16
2:B:88:ALA:O	2:B:92:VAL:HG23	0.74	1.80	14	4
1:C:25:LEU:HD11	2:D:99:ILE:HG12	0.74	1.58	7	4
2:B:98:GLU:O	2:B:101:ALA:HB3	0.74	1.82	1	20
2:D:83:LEU:O	2:D:87:ARG:HB3	0.73	1.83	10	17
1:A:48:LEU:HD12	2:B:129:TYR:HA	0.73	1.58	6	4
2:D:85:ALA:HB2	2:D:130:ASP:OD2	0.73	1.81	15	2
1:C:18:LEU:CB	1:C:41:ILE:HD11	0.73	2.13	5	17
2:D:82:LEU:O	2:D:82:LEU:HD23	0.72	1.84	1	3
2:D:84:ALA:HA	2:D:87:ARG:HB2	0.72	1.61	17	3
1:A:7:ARG:O	1:A:11:THR:HG23	0.72	1.85	20	4
1:A:25:LEU:CD1	1:A:37:ILE:HD11	0.72	2.15	7	10
1:A:25:LEU:HD11	2:B:99:ILE:HG12	0.71	1.61	14	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:98:GLU:OE2	2:B:102:LEU:HD21	0.71	1.84	8	7
2:B:100:HIS:CB	2:B:110:LEU:HD11	0.71	2.16	13	13
2:B:132:ILE:CG1	1:C:55:ILE:HD11	0.71	2.14	11	5
1:C:41:ILE:HG22	1:C:45:GLN:NE2	0.71	2.01	19	3
2:D:98:GLU:OE2	2:D:102:LEU:HD21	0.71	1.85	6	13
1:C:15:LEU:HD22	1:C:44:PHE:HB3	0.71	1.61	5	20
2:B:96:LEU:HD13	2:B:110:LEU:HB3	0.71	1.63	3	7
1:A:18:LEU:CB	1:A:41:ILE:HD11	0.70	2.16	14	16
1:A:15:LEU:HD22	1:A:44:PHE:HB3	0.70	1.61	19	20
1:C:25:LEU:O	1:C:28:THR:HG22	0.70	1.86	8	9
1:A:49:PHE:CE1	1:A:53:ILE:HD11	0.70	2.21	5	2
1:C:33:LEU:HD21	2:D:95:SER:HB3	0.70	1.63	20	12
2:D:122:LEU:HD12	2:D:125:LEU:HD12	0.70	1.62	18	16
1:C:15:LEU:O	1:C:41:ILE:HD12	0.70	1.87	18	15
1:C:53:ILE:HG12	2:D:125:LEU:HD13	0.70	1.63	8	9
2:B:84:ALA:O	2:B:88:ALA:HB3	0.70	1.86	11	20
1:C:10:ASP:OD2	2:D:116:VAL:HG22	0.70	1.85	11	1
2:B:128:LEU:O	2:B:132:ILE:HD12	0.70	1.86	20	19
1:A:11:THR:HG23	1:A:44:PHE:CD1	0.70	2.22	1	1
1:C:33:LEU:HD11	2:D:95:SER:OG	0.70	1.86	13	2
1:A:64:LEU:N	1:A:64:LEU:HD23	0.70	2.01	12	12
1:A:18:LEU:HB3	1:A:37:ILE:HG23	0.70	1.63	16	7
1:A:14:ALA:HB2	2:B:116:VAL:HG11	0.70	1.62	5	16
2:D:109:ASP:O	2:D:113:LEU:HD12	0.70	1.87	5	18
1:A:63:LEU:HD12	2:B:124:THR:HG23	0.70	1.64	12	1
1:A:33:LEU:HD21	2:B:95:SER:HB3	0.69	1.63	18	12
1:A:64:LEU:HD23	1:A:64:LEU:N	0.69	2.02	4	8
2:D:100:HIS:CB	2:D:110:LEU:HD11	0.69	2.17	1	15
2:D:96:LEU:HD22	2:D:110:LEU:CD2	0.69	2.17	9	10
2:D:93:LEU:HD21	2:D:114:HIS:HA	0.69	1.62	17	20
1:A:55:ILE:HG22	1:A:59:TYR:HB2	0.69	1.63	15	18
1:A:53:ILE:HG12	2:B:125:LEU:HD13	0.69	1.64	15	10
1:C:64:LEU:N	1:C:64:LEU:HD23	0.69	2.02	15	5
1:A:25:LEU:HD11	1:A:33:LEU:CD2	0.69	2.17	9	3
1:A:49:PHE:HA	1:A:52:LEU:HD23	0.69	1.64	6	1
2:D:128:LEU:O	2:D:132:ILE:HD12	0.69	1.87	2	13
1:C:25:LEU:HD12	1:C:37:ILE:CD1	0.69	2.17	8	14
2:B:82:LEU:HD23	2:B:82:LEU:O	0.69	1.87	11	7
1:A:17:LEU:CD1	2:B:113:LEU:HD11	0.69	2.18	16	20
1:C:52:LEU:HD13	2:D:125:LEU:O	0.69	1.88	20	9
1:C:40:VAL:HG12	1:C:44:PHE:CE2	0.69	2.22	12	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:TYR:CE2	2:D:128:LEU:HD21	0.69	2.23	10	16
2:B:96:LEU:HD12	2:B:114:HIS:CE1	0.69	2.22	10	1
1:A:56:GLN:NE2	2:B:125:LEU:HD21	0.69	2.03	13	2
2:B:84:ALA:HB1	2:B:88:ALA:CB	0.68	2.15	18	9
2:B:122:LEU:HD12	2:B:125:LEU:HD12	0.68	1.65	5	17
2:D:96:LEU:HD13	2:D:110:LEU:HB3	0.68	1.65	2	7
1:A:15:LEU:HA	1:A:18:LEU:HD12	0.68	1.64	19	9
1:A:18:LEU:HD22	2:B:92:VAL:CG1	0.68	2.17	12	3
2:D:84:ALA:O	2:D:88:ALA:HB3	0.68	1.88	1	17
1:C:55:ILE:HG22	1:C:59:TYR:HB2	0.68	1.65	3	20
1:A:18:LEU:HB3	1:A:41:ILE:HD11	0.68	1.65	4	16
1:C:15:LEU:HA	1:C:18:LEU:HD12	0.68	1.66	20	11
1:A:40:VAL:HG11	2:B:117:PHE:CZ	0.68	2.23	16	3
2:B:89:VAL:HG13	2:B:117:PHE:CD1	0.68	2.23	17	8
2:B:122:LEU:O	2:B:126:LEU:HD12	0.67	1.89	6	3
2:B:132:ILE:HG21	1:C:48:LEU:HD13	0.67	1.67	13	1
1:C:18:LEU:CD2	1:C:37:ILE:HG23	0.67	2.19	19	3
1:C:18:LEU:HD11	2:D:117:PHE:CZ	0.67	2.25	8	11
1:C:56:GLN:NE2	2:D:125:LEU:HD21	0.67	2.04	12	4
1:C:26:SER:OG	1:C:34:ARG:HB3	0.67	1.89	11	1
1:A:36:SER:HB3	2:B:91:GLN:NE2	0.67	2.05	14	4
1:C:25:LEU:HD11	1:C:33:LEU:CD2	0.67	2.20	12	3
1:C:36:SER:OG	2:D:92:VAL:HG22	0.67	1.89	7	1
1:C:25:LEU:HD23	2:D:102:LEU:HD13	0.66	1.64	14	13
1:C:52:LEU:N	1:C:52:LEU:HD13	0.66	2.05	6	1
1:C:40:VAL:HG12	1:C:44:PHE:CD2	0.66	2.24	10	8
2:B:93:LEU:CD1	2:B:117:PHE:HB2	0.66	2.20	14	1
2:B:132:ILE:HG12	1:C:55:ILE:HD11	0.66	1.67	11	1
2:B:82:LEU:CD2	2:B:82:LEU:N	0.66	2.57	7	3
1:C:48:LEU:HD12	2:D:129:TYR:HA	0.65	1.67	10	7
2:D:89:VAL:HG12	2:D:117:PHE:HB3	0.65	1.67	7	7
1:A:40:VAL:HG12	1:A:44:PHE:CE2	0.65	2.26	13	5
2:D:82:LEU:N	2:D:82:LEU:CD2	0.65	2.60	6	1
2:B:128:LEU:CD2	1:C:55:ILE:HG23	0.65	2.22	20	4
2:B:82:LEU:N	2:B:82:LEU:CD2	0.65	2.58	8	5
1:A:59:TYR:CZ	1:C:63:LEU:HD11	0.65	2.26	14	8
2:B:132:ILE:HG23	1:C:51:ALA:CB	0.65	2.22	4	2
2:B:96:LEU:HD22	2:B:110:LEU:HD23	0.65	1.67	3	2
1:A:40:VAL:HG12	1:A:44:PHE:CD2	0.65	2.26	1	8
1:C:14:ALA:HB2	2:D:116:VAL:HG11	0.65	1.68	1	9
1:C:33:LEU:HD21	2:D:95:SER:HB2	0.65	1.67	5	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:18:LEU:HB3	1:C:41:ILE:HD11	0.65	1.69	18	16
1:C:25:LEU:CD1	1:C:37:ILE:HD11	0.64	2.22	6	8
1:A:18:LEU:CD2	1:A:37:ILE:HG23	0.64	2.19	14	2
1:C:25:LEU:C	1:C:25:LEU:HD22	0.64	2.12	14	2
1:A:11:THR:HG23	1:A:44:PHE:CE1	0.64	2.27	1	1
2:B:82:LEU:C	2:B:82:LEU:HD12	0.64	2.12	1	1
1:C:25:LEU:HD11	1:C:33:LEU:HD23	0.64	1.68	12	2
2:B:83:LEU:O	2:B:87:ARG:CB	0.64	2.45	7	15
1:C:21:TYR:O	1:C:25:LEU:HB2	0.64	1.93	15	17
1:C:17:LEU:CD1	2:D:113:LEU:HD11	0.64	2.23	8	20
1:A:25:LEU:HD23	2:B:102:LEU:HD13	0.64	1.70	13	16
1:A:48:LEU:O	1:A:48:LEU:HD13	0.64	1.93	6	1
2:B:82:LEU:O	2:B:82:LEU:HD23	0.64	1.93	20	1
2:D:112:PHE:O	2:D:116:VAL:HG23	0.64	1.92	18	7
1:A:18:LEU:HD11	2:B:117:PHE:HZ	0.63	1.52	14	9
1:C:48:LEU:CD1	1:C:52:LEU:HD12	0.63	2.23	19	4
2:B:88:ALA:HA	2:B:91:GLN:NE2	0.63	2.08	14	3
1:C:8:LYS:HG2	1:C:53:ILE:HG21	0.63	1.71	5	3
1:C:48:LEU:O	1:C:51:ALA:HB3	0.63	1.93	6	5
2:B:89:VAL:HG13	2:B:117:PHE:CD2	0.63	2.28	14	3
1:C:48:LEU:O	1:C:48:LEU:HD13	0.63	1.94	5	4
1:C:36:SER:O	1:C:40:VAL:HG23	0.63	1.92	7	3
1:A:21:TYR:O	1:A:25:LEU:HB2	0.63	1.93	17	19
1:C:52:LEU:HD22	1:C:53:ILE:N	0.62	2.09	1	1
2:D:82:LEU:HD12	2:D:82:LEU:N	0.62	2.08	13	2
1:A:28:THR:HG23	1:A:29:GLU:H	0.62	1.54	1	15
1:C:48:LEU:HD13	1:C:48:LEU:O	0.62	1.95	1	5
1:A:34:ARG:HA	1:A:37:ILE:HD12	0.62	1.71	4	7
2:D:83:LEU:O	2:D:87:ARG:CB	0.62	2.47	10	14
1:C:48:LEU:HD21	2:D:132:ILE:HB	0.62	1.70	2	9
1:C:25:LEU:HD23	2:D:102:LEU:CD1	0.62	2.24	14	8
2:B:109:ASP:O	2:B:113:LEU:HD12	0.62	1.94	13	20
1:A:52:LEU:HD13	2:B:125:LEU:O	0.62	1.95	5	9
1:A:43:ILE:HG23	2:B:129:TYR:CD2	0.62	2.30	19	9
2:B:128:LEU:HD21	1:C:59:TYR:CE2	0.62	2.30	18	15
2:B:93:LEU:HD21	2:B:114:HIS:HA	0.61	1.71	20	17
1:A:48:LEU:HD21	2:B:132:ILE:HB	0.61	1.72	1	12
1:A:48:LEU:HD13	1:A:48:LEU:O	0.61	1.95	19	3
1:C:25:LEU:HD12	1:C:37:ILE:HD12	0.61	1.72	7	1
1:A:18:LEU:HB2	1:A:41:ILE:HD11	0.61	1.72	16	6
1:C:48:LEU:HD23	2:D:129:TYR:O	0.61	1.95	4	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:48:LEU:HD13	2:D:132:ILE:CG2	0.61	2.25	5	1
1:A:39:ARG:HG3	2:B:88:ALA:HB1	0.61	1.72	18	7
1:A:24:LYS:O	2:B:103:THR:HG22	0.61	1.96	11	2
2:D:107:GLU:HA	2:D:110:LEU:HD12	0.60	1.72	15	4
2:D:96:LEU:HD12	2:D:114:HIS:NE2	0.60	2.11	12	2
2:D:88:ALA:O	2:D:92:VAL:HG23	0.60	1.95	3	5
2:D:82:LEU:CD2	2:D:82:LEU:N	0.60	2.63	8	7
1:C:25:LEU:CD2	1:C:25:LEU:C	0.60	2.69	14	6
1:C:11:THR:HG23	1:C:44:PHE:CD2	0.60	2.31	17	4
2:B:123:HIS:HA	2:B:126:LEU:CD1	0.60	2.26	4	7
1:C:48:LEU:HD12	1:C:51:ALA:HB3	0.60	1.74	4	1
1:C:37:ILE:O	1:C:41:ILE:HG12	0.60	1.96	13	19
1:A:25:LEU:HD11	1:A:33:LEU:HD23	0.60	1.73	9	2
2:B:114:HIS:O	2:B:118:GLN:HG2	0.60	1.97	6	4
1:A:49:PHE:CE1	2:B:126:LEU:HD23	0.59	2.32	1	7
1:A:10:ASP:HB3	2:B:116:VAL:HG22	0.59	1.72	13	8
1:A:11:THR:HG22	1:A:44:PHE:CE1	0.59	2.32	17	3
1:C:18:LEU:O	1:C:37:ILE:HG21	0.59	1.97	19	8
2:B:128:LEU:CD2	1:C:55:ILE:HD12	0.59	2.28	19	1
1:A:33:LEU:HD11	2:B:95:SER:OG	0.59	1.97	9	2
1:A:61:VAL:CG1	1:C:61:VAL:HG13	0.59	2.28	6	4
2:B:83:LEU:CD2	2:B:84:ALA:N	0.59	2.66	2	20
2:B:134:THR:HG22	2:B:134:THR:O	0.58	1.98	20	5
1:C:39:ARG:HG3	2:D:88:ALA:HB1	0.58	1.74	18	10
1:C:30:ASP:OD2	1:C:33:LEU:HD23	0.58	1.96	14	1
1:C:61:VAL:CG2	2:D:124:THR:HG21	0.58	2.29	6	6
1:C:8:LYS:CB	1:C:53:ILE:HG21	0.58	2.28	16	1
1:A:18:LEU:HD21	2:B:92:VAL:HG11	0.58	1.75	4	2
2:D:85:ALA:O	2:D:126:LEU:HD22	0.58	1.99	19	9
1:C:49:PHE:CE1	2:D:126:LEU:HD23	0.58	2.34	2	2
2:B:89:VAL:HG13	2:B:117:PHE:CG	0.58	2.33	14	1
1:C:43:ILE:HG23	2:D:129:TYR:CD2	0.58	2.33	14	7
2:B:93:LEU:CD2	2:B:114:HIS:HA	0.58	2.29	19	9
1:A:59:TYR:CE1	1:C:63:LEU:HD12	0.58	2.33	1	2
1:C:33:LEU:HD21	2:D:95:SER:CB	0.58	2.29	11	4
2:D:96:LEU:HD12	2:D:114:HIS:CE1	0.58	2.33	20	2
2:D:82:LEU:N	2:D:82:LEU:CD1	0.58	2.66	9	2
1:C:18:LEU:HD21	2:D:92:VAL:HG11	0.58	1.75	5	6
2:D:84:ALA:CB	2:D:88:ALA:HB2	0.58	2.19	16	5
1:A:18:LEU:HD11	2:B:117:PHE:CZ	0.58	2.34	10	13
1:C:28:THR:HG23	1:C:29:GLU:N	0.58	2.14	8	16

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:14:ALA:O	2:D:113:LEU:HD21	0.58	1.99	5	16
1:A:59:TYR:CE1	2:D:128:LEU:HD21	0.58	2.34	1	2
1:C:17:LEU:HD12	2:D:113:LEU:HD11	0.58	1.74	19	17
2:D:123:HIS:HA	2:D:126:LEU:CD1	0.58	2.29	16	8
1:A:33:LEU:HD21	2:B:95:SER:CB	0.58	2.25	5	4
1:C:14:ALA:HB1	2:D:113:LEU:HD23	0.57	1.74	15	17
1:A:48:LEU:HD13	2:D:132:ILE:HG23	0.57	1.76	5	1
1:A:18:LEU:O	1:A:37:ILE:HG21	0.57	2.00	13	11
1:C:64:LEU:N	1:C:64:LEU:CD2	0.57	2.64	19	3
2:B:107:GLU:HA	2:B:110:LEU:HD12	0.57	1.75	4	6
1:C:25:LEU:HD11	1:C:33:LEU:CG	0.57	2.26	19	2
2:B:134:THR:O	2:B:134:THR:HG22	0.57	1.99	5	3
2:D:85:ALA:HB2	2:D:130:ASP:OD1	0.57	1.99	2	1
1:C:28:THR:HG23	1:C:29:GLU:H	0.57	1.60	5	12
2:B:93:LEU:HD11	2:B:117:PHE:HB2	0.57	1.76	6	3
2:B:89:VAL:HG12	2:B:117:PHE:HB3	0.57	1.76	4	7
2:B:98:GLU:CD	2:B:102:LEU:HD21	0.57	2.20	10	2
1:A:63:LEU:CD1	2:B:124:THR:HG23	0.57	2.29	1	1
1:C:18:LEU:HB2	1:C:41:ILE:HD11	0.57	1.75	15	7
1:A:28:THR:HG23	1:A:29:GLU:N	0.57	2.15	10	18
1:A:40:VAL:HG21	2:B:92:VAL:HG21	0.57	1.75	1	3
1:C:18:LEU:HD11	2:D:117:PHE:HZ	0.57	1.59	17	12
2:D:82:LEU:N	2:D:82:LEU:HD12	0.57	2.15	9	2
1:C:56:GLN:HG3	2:D:125:LEU:HD21	0.57	1.76	4	1
2:D:83:LEU:O	2:D:87:ARG:HB2	0.57	2.00	13	3
1:A:11:THR:HG23	1:A:44:PHE:CD2	0.57	2.35	11	2
2:D:82:LEU:C	2:D:82:LEU:HD12	0.57	2.21	4	1
1:A:61:VAL:HG12	1:C:61:VAL:HG13	0.56	1.76	6	2
2:B:85:ALA:O	2:B:126:LEU:HD22	0.56	1.99	13	12
1:A:37:ILE:O	1:A:41:ILE:HG12	0.56	2.00	8	20
1:A:26:SER:HB2	1:A:31:ARG:HA	0.56	1.76	10	2
1:C:48:LEU:O	1:C:52:LEU:HD13	0.56	2.01	1	1
1:A:63:LEU:HD11	1:C:59:TYR:CZ	0.56	2.36	20	4
1:C:36:SER:HB2	2:D:92:VAL:HG22	0.56	1.78	14	1
1:C:7:ARG:NH2	2:D:122:LEU:HD13	0.56	2.16	7	1
1:C:18:LEU:HD22	2:D:92:VAL:CG1	0.56	2.28	15	1
2:D:124:THR:HG22	2:D:128:LEU:HD11	0.56	1.76	5	7
1:C:52:LEU:HA	1:C:55:ILE:HD12	0.56	1.78	8	1
2:D:83:LEU:CD2	2:D:84:ALA:N	0.56	2.69	4	20
1:C:25:LEU:HD22	1:C:25:LEU:C	0.56	2.20	9	2
2:B:85:ALA:HB2	2:B:130:ASP:OD1	0.55	2.02	20	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:49:PHE:CD2	1:C:53:ILE:HD11	0.55	2.36	20	2
2:D:82:LEU:HD21	2:D:131:LYS:HG2	0.55	1.78	13	1
2:D:87:ARG:O	2:D:91:GLN:HG3	0.55	2.01	4	5
2:B:82:LEU:HD13	2:B:82:LEU:O	0.55	2.01	5	1
1:A:52:LEU:HD11	2:B:125:LEU:CA	0.55	2.25	12	1
1:A:25:LEU:CD2	1:A:25:LEU:C	0.55	2.75	13	7
2:B:134:THR:HG22	2:B:135:LYS:HD3	0.55	1.77	17	1
1:A:61:VAL:CG2	2:B:124:THR:HG21	0.55	2.31	1	7
1:C:21:TYR:O	1:C:25:LEU:CB	0.55	2.55	9	4
1:A:55:ILE:HD11	2:D:132:ILE:HG12	0.55	1.79	8	3
1:A:55:ILE:HG22	1:A:59:TYR:CB	0.55	2.31	15	3
1:A:40:VAL:CG2	2:B:92:VAL:HG21	0.55	2.32	1	5
1:A:21:TYR:O	1:A:25:LEU:CB	0.55	2.55	13	4
1:A:17:LEU:HD12	2:B:113:LEU:HD11	0.55	1.79	8	18
2:B:84:ALA:CB	2:B:88:ALA:HB2	0.55	2.21	9	3
2:B:132:ILE:CG2	1:C:48:LEU:HD13	0.55	2.31	13	2
1:C:36:SER:HB3	2:D:91:GLN:NE2	0.55	2.17	13	2
1:A:11:THR:HG23	1:A:44:PHE:CE2	0.54	2.37	11	2
1:C:49:PHE:O	1:C:52:LEU:HD22	0.54	2.02	1	2
2:B:93:LEU:HD13	2:B:117:PHE:CB	0.54	2.33	14	1
1:A:19:GLU:CD	1:A:41:ILE:HG21	0.54	2.23	20	2
2:B:87:ARG:O	2:B:91:GLN:HG3	0.54	2.03	19	6
1:C:48:LEU:HD23	2:D:133:ASN:HB2	0.54	1.79	2	1
1:C:48:LEU:HD12	1:C:52:LEU:HD12	0.54	1.78	10	2
1:C:11:THR:HG23	1:C:44:PHE:CE2	0.54	2.36	13	3
1:A:48:LEU:HD23	2:B:129:TYR:O	0.54	2.03	18	10
2:B:83:LEU:HD11	2:B:87:ARG:NH1	0.54	2.18	19	2
1:C:25:LEU:C	1:C:25:LEU:CD2	0.54	2.77	16	5
2:B:114:HIS:C	2:B:114:HIS:CD2	0.54	2.81	11	2
1:A:63:LEU:HD11	2:B:124:THR:HG23	0.54	1.79	1	1
2:D:114:HIS:CD2	2:D:114:HIS:C	0.54	2.80	10	1
1:A:25:LEU:C	1:A:25:LEU:HD22	0.54	2.24	12	2
1:A:59:TYR:CD1	2:D:128:LEU:HD21	0.54	2.37	16	2
1:A:8:LYS:HB3	1:A:53:ILE:HG21	0.54	1.80	5	1
1:C:26:SER:HB2	1:C:31:ARG:HD2	0.54	1.80	7	4
1:C:11:THR:HG22	1:C:44:PHE:CE1	0.53	2.37	9	2
1:C:10:ASP:HB3	2:D:116:VAL:HG22	0.53	1.79	7	4
1:C:56:GLN:HE22	2:D:125:LEU:HD21	0.53	1.62	5	1
1:A:49:PHE:HE1	1:A:53:ILE:HD11	0.53	1.63	10	1
1:A:33:LEU:HD11	2:B:95:SER:CB	0.53	2.33	9	11
2:B:99:ILE:HG23	2:B:103:THR:HG21	0.53	1.78	17	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:17:LEU:HD22	1:C:21:TYR:CE2	0.53	2.38	14	1
1:A:40:VAL:HG13	1:A:44:PHE:CE1	0.53	2.39	12	1
1:C:15:LEU:O	1:C:41:ILE:HD13	0.53	2.03	12	1
1:C:15:LEU:HB3	1:C:44:PHE:CD2	0.53	2.38	13	11
1:A:36:SER:O	1:A:40:VAL:HG23	0.53	2.02	4	3
1:C:40:VAL:O	1:C:44:PHE:HB2	0.53	2.03	8	7
1:A:24:LYS:HE2	2:B:103:THR:HG22	0.53	1.80	10	1
1:A:21:TYR:HA	1:A:24:LYS:HE2	0.53	1.79	3	2
1:A:17:LEU:HD22	1:A:21:TYR:CE2	0.53	2.39	10	1
2:B:114:HIS:CD2	2:B:114:HIS:C	0.53	2.82	7	2
1:C:40:VAL:HG21	2:D:92:VAL:HG21	0.53	1.80	15	1
2:D:123:HIS:CA	2:D:126:LEU:HD12	0.53	2.30	7	12
1:A:25:LEU:HD23	2:B:102:LEU:CD1	0.53	2.34	13	5
1:A:25:LEU:O	1:A:28:THR:HG22	0.53	2.04	11	14
2:D:88:ALA:HA	2:D:91:GLN:NE2	0.53	2.18	4	4
1:A:49:PHE:HE2	1:A:53:ILE:HD11	0.53	1.58	7	1
1:C:33:LEU:HD11	2:D:95:SER:CB	0.52	2.34	1	13
1:C:56:GLN:OE1	2:D:125:LEU:HD21	0.52	2.04	15	1
1:C:61:VAL:HG23	2:D:124:THR:HG21	0.52	1.81	12	10
1:A:36:SER:CB	2:B:91:GLN:NE2	0.52	2.72	14	6
2:B:82:LEU:HD13	2:B:131:LYS:HD2	0.52	1.80	19	1
1:A:55:ILE:HG23	2:D:128:LEU:CD2	0.52	2.35	6	2
2:B:128:LEU:HD22	1:C:55:ILE:CG2	0.52	2.34	20	1
1:A:21:TYR:O	1:A:25:LEU:N	0.52	2.42	17	15
1:A:51:ALA:CB	2:D:132:ILE:HG23	0.52	2.35	17	3
1:C:17:LEU:HD22	1:C:21:TYR:OH	0.52	2.04	7	1
1:A:40:VAL:O	1:A:44:PHE:HB2	0.52	2.04	15	8
1:A:15:LEU:HB3	1:A:44:PHE:CD2	0.52	2.39	11	6
1:A:61:VAL:HG23	2:B:124:THR:HG21	0.52	1.82	9	10
1:A:52:LEU:HD13	2:B:128:LEU:HB2	0.52	1.82	12	1
1:A:40:VAL:HG12	1:A:44:PHE:CD1	0.52	2.39	3	5
2:D:99:ILE:HG23	2:D:103:THR:HG21	0.52	1.81	4	3
1:C:10:ASP:HB2	2:D:116:VAL:HG22	0.52	1.82	16	1
1:C:52:LEU:HD13	2:D:128:LEU:HB2	0.52	1.80	8	1
1:A:48:LEU:C	1:A:48:LEU:HD12	0.52	2.24	1	4
2:D:99:ILE:O	2:D:103:THR:HG23	0.52	2.04	3	12
2:D:84:ALA:HA	2:D:87:ARG:CB	0.52	2.35	17	3
1:C:49:PHE:HA	1:C:52:LEU:CD2	0.52	2.34	8	1
1:A:26:SER:HB2	1:A:31:ARG:HD2	0.52	1.80	14	1
1:C:48:LEU:CD1	1:C:48:LEU:C	0.51	2.78	18	5
1:C:52:LEU:HD22	1:C:53:ILE:H	0.51	1.65	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:52:LEU:HD23	2:D:125:LEU:HD22	0.51	1.81	1	1
2:D:96:LEU:O	2:D:99:ILE:HB	0.51	2.05	2	8
1:A:61:VAL:HG13	1:C:61:VAL:CG1	0.51	2.35	18	3
2:B:82:LEU:H	2:B:82:LEU:HD23	0.51	1.64	2	1
1:A:18:LEU:CD1	1:A:40:VAL:HG11	0.51	2.34	7	2
2:B:82:LEU:HD22	2:B:130:ASP:HB2	0.51	1.82	5	2
2:B:134:THR:HG22	2:B:135:LYS:HG2	0.51	1.82	14	1
2:B:99:ILE:O	2:B:103:THR:HG23	0.51	2.05	13	11
1:A:8:LYS:HG2	1:A:53:ILE:HG21	0.51	1.83	4	2
2:D:99:ILE:O	2:D:103:THR:OG1	0.51	2.27	10	18
1:A:26:SER:HB3	1:A:34:ARG:HB2	0.51	1.83	10	2
2:D:82:LEU:HA	2:D:130:ASP:CG	0.51	2.26	2	1
1:A:48:LEU:CD1	2:B:129:TYR:HA	0.51	2.36	19	3
1:C:26:SER:HB2	1:C:31:ARG:HA	0.51	1.81	17	4
2:D:96:LEU:HD13	2:D:110:LEU:CB	0.51	2.34	15	5
2:B:93:LEU:CD1	2:B:117:PHE:CB	0.51	2.89	14	1
2:B:82:LEU:CD1	2:B:82:LEU:O	0.51	2.54	1	1
1:C:18:LEU:CD1	1:C:40:VAL:HG11	0.51	2.36	7	3
1:A:48:LEU:HD23	2:B:133:ASN:HB2	0.51	1.81	1	1
1:C:40:VAL:CG2	2:D:92:VAL:HG21	0.51	2.36	15	1
1:A:14:ALA:O	2:B:113:LEU:HD21	0.51	2.06	19	14
1:A:48:LEU:C	1:A:48:LEU:CD1	0.51	2.79	19	4
1:C:48:LEU:C	1:C:48:LEU:CD1	0.51	2.79	6	4
1:A:8:LYS:CB	1:A:53:ILE:HG21	0.51	2.35	5	1
1:C:56:GLN:CG	2:D:125:LEU:HD21	0.51	2.35	4	1
1:C:7:ARG:HG3	1:C:11:THR:HG23	0.51	1.81	8	1
1:C:45:GLN:O	1:C:46:SER:C	0.51	2.50	15	1
2:D:100:HIS:HB2	2:D:110:LEU:CD1	0.51	2.33	7	17
1:C:36:SER:CB	2:D:91:GLN:NE2	0.51	2.73	4	5
2:D:93:LEU:CD2	2:D:114:HIS:HA	0.51	2.36	18	12
1:A:25:LEU:C	1:A:25:LEU:CD2	0.51	2.79	11	1
2:B:123:HIS:CA	2:B:126:LEU:HD12	0.50	2.31	3	12
1:C:10:ASP:OD1	1:C:11:THR:N	0.50	2.44	5	3
2:B:96:LEU:HD11	2:B:113:LEU:HB2	0.50	1.83	19	2
1:A:21:TYR:HA	1:A:24:LYS:HZ3	0.50	1.66	13	1
1:A:59:TYR:OH	1:C:63:LEU:HD11	0.50	2.06	15	1
2:B:82:LEU:CD1	2:B:82:LEU:C	0.50	2.80	1	1
1:C:63:LEU:HD22	2:D:123:HIS:NE2	0.50	2.21	6	1
2:D:82:LEU:HD23	2:D:82:LEU:H	0.50	1.64	8	2
1:A:14:ALA:HB1	2:B:113:LEU:HD23	0.50	1.83	5	17
2:B:131:LYS:O	2:B:134:THR:HG22	0.50	2.07	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:D:96:LEU:HD13	2:D:110:LEU:CD2	0.50	2.36	9	1
2:D:96:LEU:HD12	2:D:114:HIS:ND1	0.50	2.22	17	3
2:B:132:ILE:HD11	1:C:55:ILE:HD11	0.50	1.84	20	1
1:A:21:TYR:HA	1:A:24:LYS:NZ	0.50	2.21	13	1
1:A:22:ARG:HA	1:A:37:ILE:HD12	0.50	1.83	15	2
1:C:21:TYR:O	1:C:25:LEU:N	0.50	2.45	15	13
2:D:96:LEU:HD11	2:D:113:LEU:HB2	0.50	1.83	1	2
1:A:40:VAL:CG1	1:A:44:PHE:CE2	0.50	2.95	7	6
2:B:134:THR:HG22	2:B:135:LYS:CD	0.50	2.36	17	1
1:C:40:VAL:HG21	2:D:92:VAL:CG2	0.50	2.37	20	1
2:B:124:THR:HG22	2:B:128:LEU:HD11	0.50	1.84	18	3
1:A:59:TYR:CD2	1:C:63:LEU:HD11	0.50	2.41	6	1
1:A:52:LEU:HD21	2:B:125:LEU:HB3	0.50	1.84	6	1
2:B:96:LEU:HD13	2:B:110:LEU:CD2	0.50	2.37	10	2
1:A:46:SER:CB	2:B:129:TYR:CE1	0.50	2.95	19	11
1:C:26:SER:CB	1:C:34:ARG:HB2	0.50	2.37	20	4
1:A:61:VAL:HG13	1:C:61:VAL:HG12	0.50	1.84	19	1
1:C:48:LEU:HB3	2:D:129:TYR:CD1	0.49	2.42	14	5
1:C:14:ALA:HB2	2:D:116:VAL:HG21	0.49	1.83	12	2
2:D:82:LEU:HD23	2:D:82:LEU:O	0.49	2.07	14	2
1:C:48:LEU:C	1:C:48:LEU:HD12	0.49	2.27	16	3
1:C:49:PHE:O	1:C:52:LEU:CD2	0.49	2.60	4	2
1:C:39:ARG:HB3	2:D:88:ALA:HB1	0.49	1.83	17	1
1:A:36:SER:O	1:A:39:ARG:HG2	0.49	2.07	14	9
1:C:46:SER:CB	2:D:129:TYR:CE1	0.49	2.96	4	8
1:C:64:LEU:CD2	1:C:64:LEU:N	0.49	2.75	14	4
1:A:56:GLN:HE22	2:B:125:LEU:HD21	0.49	1.66	13	1
1:A:48:LEU:HD12	1:A:48:LEU:C	0.49	2.27	5	9
1:C:40:VAL:HG11	2:D:117:PHE:CE1	0.49	2.43	12	1
1:C:19:GLU:N	1:C:41:ILE:HD11	0.49	2.23	12	1
2:D:102:LEU:HD12	2:D:103:THR:HG23	0.49	1.84	5	19
1:A:33:LEU:HD22	2:B:98:GLU:OE2	0.49	2.08	14	2
1:A:24:LYS:O	1:A:24:LYS:HG2	0.49	2.07	13	1
2:B:82:LEU:HA	2:B:130:ASP:CG	0.49	2.29	20	3
1:A:48:LEU:C	1:A:48:LEU:HD13	0.49	2.28	6	1
1:C:26:SER:HB3	1:C:34:ARG:CD	0.49	2.38	17	4
1:C:43:ILE:HG21	2:D:126:LEU:HD23	0.49	1.84	13	2
1:C:25:LEU:HD22	1:C:30:ASP:CB	0.48	2.38	2	4
1:A:64:LEU:N	1:A:64:LEU:CD2	0.48	2.71	12	6
1:C:28:THR:CG2	1:C:29:GLU:N	0.48	2.76	7	20
1:C:55:ILE:HG22	1:C:59:TYR:CB	0.48	2.38	3	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:36:SER:O	1:C:39:ARG:CG	0.48	2.62	18	9
1:C:49:PHE:HA	1:C:52:LEU:HD21	0.48	1.86	4	1
2:B:102:LEU:HD12	2:B:103:THR:HG23	0.48	1.85	17	18
1:C:48:LEU:HD12	1:C:48:LEU:C	0.48	2.29	17	4
1:A:48:LEU:HG	2:B:129:TYR:O	0.48	2.08	6	3
2:D:82:LEU:CD1	2:D:82:LEU:N	0.48	2.76	13	2
2:D:95:SER:O	2:D:98:GLU:N	0.48	2.46	6	6
1:A:37:ILE:HG12	2:B:92:VAL:HG13	0.48	1.85	19	1
2:D:85:ALA:CB	2:D:126:LEU:HB3	0.48	2.38	3	5
1:A:26:SER:HB3	1:A:34:ARG:CD	0.48	2.39	14	2
2:D:82:LEU:HD12	2:D:130:ASP:HB3	0.48	1.85	18	2
2:B:96:LEU:HD13	2:B:110:LEU:HD22	0.48	1.83	10	1
2:B:129:TYR:CD1	2:B:129:TYR:C	0.48	2.86	7	1
1:A:28:THR:CG2	1:A:29:GLU:N	0.48	2.76	14	18
2:B:95:SER:O	2:B:98:GLU:N	0.48	2.47	5	7
2:B:96:LEU:CD2	2:B:110:LEU:HD23	0.48	2.39	17	2
2:B:118:GLN:N	2:B:118:GLN:NE2	0.48	2.61	14	1
1:A:49:PHE:HA	1:A:52:LEU:CD2	0.48	2.38	12	2
1:A:11:THR:HG22	1:A:44:PHE:HE1	0.48	1.67	17	2
1:A:17:LEU:HD13	2:B:113:LEU:HD11	0.48	1.86	16	5
1:A:37:ILE:HA	2:B:92:VAL:HG21	0.48	1.86	3	2
1:A:40:VAL:HG21	2:B:92:VAL:CG2	0.48	2.39	10	3
2:D:82:LEU:O	2:D:85:ALA:HB3	0.48	2.09	15	1
1:C:48:LEU:CD2	2:D:129:TYR:O	0.48	2.62	4	6
1:C:25:LEU:HD12	2:D:99:ILE:CD1	0.48	2.39	6	2
1:A:11:THR:CG2	1:A:44:PHE:CD1	0.48	2.96	1	1
2:D:89:VAL:HG13	2:D:117:PHE:CG	0.47	2.43	15	2
1:A:40:VAL:O	1:A:44:PHE:CD1	0.47	2.67	11	5
2:D:96:LEU:CB	2:D:114:HIS:CE1	0.47	2.97	19	1
1:C:39:ARG:CD	2:D:88:ALA:HB2	0.47	2.39	4	1
2:B:117:PHE:N	2:B:117:PHE:CD1	0.47	2.82	6	1
2:D:129:TYR:CD1	2:D:129:TYR:C	0.47	2.87	6	2
2:B:84:ALA:HA	2:B:87:ARG:HB3	0.47	1.86	16	1
1:A:26:SER:OG	1:A:34:ARG:CG	0.47	2.63	19	1
1:C:26:SER:HB3	1:C:34:ARG:HB2	0.47	1.85	17	4
1:C:35:SER:O	1:C:38:GLU:HG3	0.47	2.09	1	1
1:A:35:SER:HA	1:A:38:GLU:CG	0.47	2.39	19	1
1:A:18:LEU:CB	1:A:37:ILE:HG23	0.47	2.38	16	1
1:A:55:ILE:HD11	2:D:132:ILE:HG13	0.47	1.86	8	1
2:B:114:HIS:CD2	2:B:118:GLN:OE1	0.47	2.68	8	1
2:B:100:HIS:HB2	2:B:110:LEU:CD1	0.47	2.37	9	13

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:TYR:CE2	1:C:63:LEU:CD1	0.47	2.97	8	11
2:B:117:PHE:CD1	2:B:117:PHE:N	0.47	2.82	12	1
1:C:26:SER:OG	1:C:34:ARG:CD	0.47	2.63	7	4
1:C:25:LEU:CD2	2:D:102:LEU:CD1	0.47	2.92	7	4
1:C:40:VAL:O	1:C:44:PHE:CD1	0.47	2.68	15	6
1:C:52:LEU:HD21	2:D:128:LEU:CB	0.47	2.40	15	1
2:B:93:LEU:CD1	2:B:118:GLN:NE2	0.47	2.78	4	8
1:C:43:ILE:O	1:C:49:PHE:CG	0.47	2.68	17	7
1:C:36:SER:O	1:C:39:ARG:HG2	0.47	2.10	19	6
1:C:50:GLN:OE1	1:C:50:GLN:CA	0.47	2.62	18	1
1:A:22:ARG:HB3	1:A:37:ILE:HD13	0.47	1.87	16	3
1:C:52:LEU:CD1	1:C:52:LEU:N	0.47	2.77	6	1
2:D:114:HIS:O	2:D:118:GLN:NE2	0.47	2.48	17	10
1:C:40:VAL:CG1	1:C:44:PHE:CE2	0.47	2.98	20	3
1:A:21:TYR:HA	1:A:24:LYS:CE	0.47	2.39	13	2
1:C:36:SER:CB	2:D:92:VAL:HG22	0.47	2.39	14	2
1:A:64:LEU:CD2	1:A:64:LEU:N	0.47	2.72	4	5
1:C:22:ARG:HG3	1:C:23:SER:N	0.47	2.25	17	1
2:B:96:LEU:HD13	2:B:110:LEU:CB	0.47	2.40	8	7
2:B:96:LEU:CB	2:B:114:HIS:CE1	0.47	2.97	19	2
2:B:114:HIS:CD2	2:B:115:SER:N	0.47	2.83	7	4
1:C:26:SER:OG	1:C:34:ARG:CG	0.47	2.63	16	2
1:A:22:ARG:HA	1:A:37:ILE:HD13	0.47	1.87	7	3
1:C:41:ILE:CG2	1:C:45:GLN:NE2	0.46	2.76	15	1
1:A:63:LEU:CD1	1:C:59:TYR:CE2	0.46	2.98	14	10
2:D:89:VAL:CG1	2:D:117:PHE:HB3	0.46	2.40	17	9
2:B:93:LEU:HD11	2:B:118:GLN:NE2	0.46	2.25	2	6
1:C:40:VAL:HG12	1:C:44:PHE:CD1	0.46	2.45	2	2
1:C:48:LEU:HG	2:D:129:TYR:O	0.46	2.10	10	3
1:A:18:LEU:HD13	1:A:40:VAL:HB	0.46	1.87	15	1
1:C:53:ILE:HG23	1:C:56:GLN:NE2	0.46	2.25	15	1
1:A:25:LEU:CD1	2:B:99:ILE:HG12	0.46	2.41	4	6
2:B:124:THR:HG22	2:B:128:LEU:CD1	0.46	2.41	1	1
1:A:43:ILE:HD11	2:B:84:ALA:HB3	0.46	1.88	20	1
2:D:114:HIS:CE1	2:D:118:GLN:NE2	0.46	2.84	15	3
1:C:49:PHE:CE1	1:C:53:ILE:HD11	0.46	2.45	16	2
2:D:85:ALA:CB	2:D:126:LEU:CB	0.46	2.94	20	5
1:A:48:LEU:O	1:A:51:ALA:HB3	0.46	2.09	18	4
1:C:25:LEU:HD13	1:C:37:ILE:HD11	0.46	1.86	6	1
1:C:14:ALA:HA	2:D:113:LEU:HD21	0.46	1.87	13	15
1:C:52:LEU:CD1	2:D:129:TYR:N	0.46	2.79	12	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:85:ALA:HB1	2:B:126:LEU:HD22	0.46	1.87	14	1
1:C:21:TYR:CE1	2:D:105:SER:CB	0.46	2.97	13	3
1:C:43:ILE:HD11	2:D:84:ALA:HB3	0.46	1.87	2	1
2:B:82:LEU:HD23	2:B:82:LEU:C	0.46	2.31	12	3
1:A:59:TYR:CZ	1:C:63:LEU:CD1	0.46	2.98	5	1
1:C:34:ARG:HA	1:C:37:ILE:HD12	0.46	1.86	6	1
1:C:40:VAL:CG1	1:C:44:PHE:CD1	0.46	2.98	2	3
1:C:48:LEU:CD1	2:D:129:TYR:HA	0.46	2.41	11	6
1:A:14:ALA:HA	2:B:113:LEU:HD21	0.46	1.87	1	11
1:C:11:THR:HG22	1:C:44:PHE:HE1	0.46	1.68	9	2
2:D:96:LEU:HD13	2:D:110:LEU:HD22	0.46	1.85	9	2
1:A:59:TYR:CG	2:D:128:LEU:HD21	0.46	2.45	20	1
1:A:48:LEU:CD2	2:B:129:TYR:O	0.46	2.64	5	4
2:B:89:VAL:CG1	2:B:117:PHE:CD1	0.46	2.99	3	1
2:D:96:LEU:HD13	2:D:110:LEU:HA	0.46	1.88	18	1
2:D:124:THR:HG22	2:D:128:LEU:CD1	0.46	2.41	6	1
1:A:59:TYR:CE2	1:C:63:LEU:HD12	0.46	2.46	10	1
1:A:26:SER:OG	1:A:34:ARG:CD	0.46	2.64	14	2
2:B:96:LEU:HB3	2:B:114:HIS:CE1	0.46	2.46	12	2
2:D:114:HIS:CD2	2:D:118:GLN:NE2	0.46	2.84	5	2
2:B:82:LEU:HD23	2:B:130:ASP:HB3	0.46	1.87	10	1
2:B:120:GLN:O	2:B:123:HIS:CD2	0.46	2.68	13	2
1:A:52:LEU:HD21	2:B:128:LEU:HB3	0.45	1.88	8	2
2:D:120:GLN:O	2:D:123:HIS:CD2	0.45	2.70	14	1
1:A:15:LEU:CD1	1:A:41:ILE:HG23	0.45	2.42	11	1
2:B:85:ALA:CB	2:B:126:LEU:CB	0.45	2.94	6	2
2:B:128:LEU:HD22	1:C:55:ILE:HG23	0.45	1.85	20	1
1:A:22:ARG:HB3	1:A:37:ILE:HD12	0.45	1.89	3	1
2:B:84:ALA:O	2:B:88:ALA:CB	0.45	2.64	19	4
2:B:110:LEU:O	2:B:114:HIS:CD2	0.45	2.69	12	3
1:A:63:LEU:HD11	1:C:59:TYR:OH	0.45	2.10	12	1
1:A:20:GLU:O	1:A:24:LYS:HG3	0.45	2.12	12	1
1:C:49:PHE:HA	1:C:52:LEU:HD11	0.45	1.89	1	1
1:A:48:LEU:HD13	1:A:48:LEU:C	0.45	2.32	19	1
1:C:33:LEU:HD22	2:D:98:GLU:OE2	0.45	2.12	17	1
1:A:21:TYR:CZ	2:B:105:SER:CB	0.45	2.99	4	2
2:D:93:LEU:HD11	2:D:118:GLN:NE2	0.45	2.26	6	2
2:B:89:VAL:CG1	2:B:117:PHE:HB3	0.45	2.41	14	3
1:A:59:TYR:CE1	1:C:63:LEU:CD1	0.45	2.99	1	2
1:C:10:ASP:O	1:C:14:ALA:HB2	0.45	2.12	5	1
2:D:110:LEU:O	2:D:114:HIS:CD2	0.45	2.70	16	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:45:GLN:O	1:A:46:SER:C	0.45	2.55	11	1
1:C:40:VAL:CG1	1:C:44:PHE:CE1	0.45	2.99	17	2
2:B:134:THR:O	2:B:135:LYS:CB	0.45	2.63	4	2
2:B:96:LEU:HD12	2:B:114:HIS:HD2	0.45	1.71	17	1
2:B:99:ILE:O	2:B:103:THR:OG1	0.45	2.34	15	12
2:D:122:LEU:HG	2:D:126:LEU:HD11	0.45	1.88	13	4
1:A:40:VAL:CG1	1:A:44:PHE:CD1	0.45	2.99	5	4
2:D:129:TYR:C	2:D:129:TYR:CD1	0.45	2.90	14	1
1:C:63:LEU:CD2	2:D:123:HIS:CE1	0.45	3.00	6	1
2:B:128:LEU:CD2	1:C:59:TYR:CE2	0.45	3.00	6	2
2:D:96:LEU:HB3	2:D:114:HIS:CE1	0.45	2.47	16	2
1:A:50:GLN:OE1	1:A:53:ILE:HD12	0.45	2.11	5	1
2:B:128:LEU:HD23	1:C:55:ILE:HD12	0.45	1.88	19	1
1:C:33:LEU:O	1:C:33:LEU:HD12	0.45	2.12	19	1
1:C:26:SER:CB	1:C:34:ARG:CD	0.45	2.95	7	5
1:A:26:SER:CB	1:A:34:ARG:HB2	0.45	2.41	2	2
1:A:43:ILE:HD13	2:B:85:ALA:HA	0.45	1.89	1	1
1:C:36:SER:O	1:C:39:ARG:HB2	0.45	2.12	1	1
1:C:49:PHE:HE1	1:C:53:ILE:HD11	0.45	1.71	16	1
1:A:18:LEU:CB	1:A:41:ILE:CD1	0.45	2.95	15	6
1:A:52:LEU:CD1	2:B:129:TYR:N	0.45	2.80	1	10
1:A:14:ALA:O	1:A:18:LEU:HD12	0.45	2.12	17	3
1:A:43:ILE:HG23	2:B:129:TYR:HE2	0.45	1.69	11	2
1:A:11:THR:CG2	1:A:44:PHE:CD2	0.45	2.99	11	1
1:C:11:THR:CG2	1:C:44:PHE:CD2	0.45	2.99	17	4
2:D:84:ALA:O	2:D:88:ALA:CB	0.45	2.64	15	4
1:A:40:VAL:CG1	1:A:44:PHE:CE1	0.45	3.00	12	2
1:A:26:SER:CB	1:A:34:ARG:CD	0.45	2.95	14	5
2:D:89:VAL:CG1	2:D:117:PHE:CG	0.45	3.00	7	2
1:C:48:LEU:C	1:C:48:LEU:HD13	0.45	2.32	5	4
2:B:83:LEU:HD11	2:B:87:ARG:HH11	0.45	1.72	6	2
2:D:122:LEU:HA	2:D:125:LEU:HD12	0.45	1.89	6	1
1:C:20:GLU:O	1:C:24:LYS:HG3	0.44	2.12	16	3
1:A:15:LEU:CD2	1:A:44:PHE:HB3	0.44	2.41	7	8
1:C:25:LEU:HD21	2:D:102:LEU:CD1	0.44	2.42	17	3
2:D:96:LEU:CD1	2:D:114:HIS:CE1	0.44	2.99	20	1
2:D:83:LEU:HD12	2:D:87:ARG:HH11	0.44	1.71	11	3
1:C:15:LEU:O	1:C:41:ILE:CD1	0.44	2.66	12	1
1:C:15:LEU:HD12	1:C:41:ILE:HG23	0.44	1.90	1	1
1:A:26:SER:CB	1:A:31:ARG:HA	0.44	2.42	10	1
2:B:105:SER:O	2:B:106:SER:CB	0.44	2.65	10	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:40:VAL:HG13	1:C:44:PHE:CE1	0.44	2.48	1	2
2:D:113:LEU:O	2:D:117:PHE:CD2	0.44	2.71	13	9
1:C:27:GLN:OE1	1:C:31:ARG:NH1	0.44	2.51	12	11
1:A:22:ARG:CA	1:A:37:ILE:HD13	0.44	2.42	7	2
1:C:26:SER:OG	1:C:27:GLN:OE1	0.44	2.30	7	4
1:A:48:LEU:CD1	1:A:52:LEU:HD12	0.44	2.42	7	1
2:D:123:HIS:CD2	2:D:124:THR:N	0.44	2.86	3	4
1:A:25:LEU:CD2	2:B:102:LEU:CD1	0.44	2.95	10	3
1:A:25:LEU:HD22	1:A:25:LEU:O	0.44	2.12	12	1
1:A:36:SER:HB2	2:B:91:GLN:NE2	0.44	2.28	1	1
1:C:56:GLN:HE21	2:D:125:LEU:HD11	0.44	1.72	4	1
2:D:82:LEU:HD12	2:D:83:LEU:N	0.44	2.28	4	1
2:D:93:LEU:CD2	2:D:114:HIS:ND1	0.44	2.79	17	1
2:B:123:HIS:CD2	2:B:124:THR:N	0.44	2.86	9	3
2:D:82:LEU:HD23	2:D:130:ASP:HB3	0.44	1.90	3	1
2:D:98:GLU:CD	2:D:102:LEU:HD21	0.44	2.33	6	6
2:D:100:HIS:CD2	2:D:100:HIS:O	0.44	2.71	14	9
2:B:118:GLN:CA	2:B:118:GLN:NE2	0.44	2.79	14	1
2:D:114:HIS:O	2:D:118:GLN:N	0.44	2.51	7	5
1:A:44:PHE:O	1:A:49:PHE:CD1	0.44	2.71	5	1
2:D:83:LEU:CG	2:D:84:ALA:N	0.44	2.81	3	4
1:A:27:GLN:OE1	1:A:31:ARG:NH1	0.44	2.51	2	11
1:C:18:LEU:HB2	1:C:41:ILE:CD1	0.44	2.43	11	5
2:D:127:ASP:OD1	2:D:128:LEU:N	0.44	2.51	12	1
2:B:100:HIS:CD2	2:B:100:HIS:O	0.44	2.71	18	5
2:D:100:HIS:CB	2:D:110:LEU:CD1	0.44	2.95	19	3
1:C:46:SER:CB	2:D:129:TYR:OH	0.44	2.66	20	1
1:C:15:LEU:CD1	1:C:41:ILE:HG23	0.44	2.43	18	3
1:A:59:TYR:HE1	1:C:63:LEU:HD12	0.44	1.70	1	1
1:A:43:ILE:HD13	2:B:85:ALA:CA	0.44	2.43	1	1
2:B:96:LEU:HD12	2:B:114:HIS:NE2	0.43	2.28	10	2
2:B:96:LEU:O	2:B:110:LEU:HD13	0.43	2.13	5	1
2:B:129:TYR:CD2	2:B:130:ASP:OD1	0.43	2.71	5	3
1:C:26:SER:HB2	1:C:34:ARG:HB2	0.43	1.90	3	1
2:D:85:ALA:HB1	2:D:126:LEU:C	0.43	2.33	3	1
2:B:93:LEU:HD13	2:B:118:GLN:NE2	0.43	2.28	16	1
1:C:49:PHE:HZ	2:D:122:LEU:HD11	0.43	1.73	6	1
1:C:18:LEU:HD13	1:C:40:VAL:CG1	0.43	2.43	8	1
2:B:100:HIS:O	2:B:100:HIS:CD2	0.43	2.72	12	8
2:B:113:LEU:O	2:B:117:PHE:CD2	0.43	2.71	18	4
1:C:22:ARG:HB2	1:C:37:ILE:HG21	0.43	1.90	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:TYR:CE1	2:B:105:SER:CB	0.43	3.02	10	1
1:A:56:GLN:HE22	2:B:125:LEU:HD11	0.43	1.73	7	1
1:C:61:VAL:HG11	2:D:128:LEU:HD11	0.43	1.90	15	1
1:A:57:GLU:O	1:A:58:PHE:CD1	0.43	2.71	9	7
1:A:39:ARG:HB3	2:B:88:ALA:CB	0.43	2.43	13	2
1:A:22:ARG:CB	1:A:37:ILE:HD13	0.43	2.43	16	1
2:B:96:LEU:CD1	2:B:114:HIS:CE1	0.43	3.00	10	1
1:C:46:SER:OG	2:D:129:TYR:CE1	0.43	2.71	12	1
2:D:96:LEU:HD13	2:D:110:LEU:CA	0.43	2.43	18	1
2:D:91:GLN:CG	2:D:92:VAL:N	0.43	2.82	1	2
1:C:31:ARG:O	1:C:34:ARG:HG2	0.43	2.14	19	1
2:D:105:SER:O	2:D:106:SER:C	0.43	2.56	10	1
1:C:46:SER:OG	1:C:49:PHE:HB2	0.43	2.14	8	1
2:B:114:HIS:O	2:B:118:GLN:NE2	0.43	2.51	19	3
2:B:82:LEU:HD22	2:B:130:ASP:CG	0.43	2.33	8	1
1:A:39:ARG:CB	2:B:88:ALA:CB	0.43	2.96	13	1
1:C:52:LEU:HD21	2:D:128:LEU:HB3	0.43	1.90	12	3
1:C:50:GLN:OE1	1:C:53:ILE:HD12	0.43	2.14	9	1
1:A:43:ILE:O	1:A:49:PHE:CG	0.43	2.72	10	3
1:A:25:LEU:HD22	1:A:30:ASP:CB	0.43	2.44	14	2
1:A:38:GLU:HA	1:A:41:ILE:HG12	0.43	1.90	19	2
1:A:21:TYR:CE1	2:B:105:SER:HB3	0.43	2.49	10	1
1:A:52:LEU:HD22	2:B:128:LEU:HD12	0.43	1.91	17	1
2:D:96:LEU:HD23	2:D:99:ILE:HD12	0.43	1.90	7	2
1:A:63:LEU:C	1:A:64:LEU:HD23	0.43	2.34	1	1
1:A:40:VAL:O	1:A:44:PHE:CD2	0.43	2.71	13	4
1:C:26:SER:OG	1:C:34:ARG:HD2	0.43	2.13	8	3
1:A:26:SER:OG	1:A:34:ARG:HD2	0.43	2.14	14	1
2:B:83:LEU:CG	2:B:84:ALA:N	0.43	2.82	2	3
1:A:46:SER:OG	2:B:129:TYR:CE1	0.43	2.71	12	4
1:A:49:PHE:CE1	2:B:126:LEU:CD2	0.43	3.02	1	1
2:B:129:TYR:CE2	2:B:130:ASP:OD2	0.43	2.72	19	2
2:B:96:LEU:O	2:B:99:ILE:HB	0.43	2.14	8	4
1:C:22:ARG:CG	1:C:34:ARG:HG2	0.43	2.44	4	1
1:C:39:ARG:CD	2:D:88:ALA:CB	0.43	2.97	4	1
2:B:93:LEU:HG	2:B:117:PHE:CD2	0.43	2.49	6	1
2:B:111:ASP:O	2:B:114:HIS:ND1	0.43	2.49	8	1
2:D:100:HIS:O	2:D:100:HIS:CD2	0.43	2.72	16	6
1:A:48:LEU:HD12	1:A:52:LEU:HD12	0.43	1.91	14	1
1:C:17:LEU:HD13	2:D:113:LEU:HD11	0.43	1.91	1	3
2:D:85:ALA:O	2:D:126:LEU:CD1	0.43	2.66	18	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:25:LEU:HD22	1:C:30:ASP:HB2	0.43	1.90	5	1
2:D:129:TYR:CE2	2:D:130:ASP:OD2	0.43	2.72	7	2
1:A:18:LEU:CD1	1:A:40:VAL:CG1	0.42	2.97	7	3
1:A:36:SER:O	1:A:39:ARG:CG	0.42	2.67	10	2
1:C:24:LYS:O	2:D:103:THR:HG22	0.42	2.14	14	2
2:B:114:HIS:O	2:B:118:GLN:N	0.42	2.52	13	1
1:C:26:SER:O	1:C:31:ARG:HD2	0.42	2.13	7	1
1:C:19:GLU:O	1:C:22:ARG:CG	0.42	2.67	9	3
1:C:12:GLN:O	1:C:16:HIS:CG	0.42	2.72	10	3
2:B:96:LEU:HD23	2:B:99:ILE:HD12	0.42	1.90	14	1
1:C:50:GLN:CA	1:C:50:GLN:OE1	0.42	2.66	12	1
1:C:22:ARG:CG	1:C:34:ARG:CG	0.42	2.97	4	1
2:B:89:VAL:O	2:B:93:LEU:HB2	0.42	2.14	20	2
2:D:93:LEU:HD11	2:D:117:PHE:HB2	0.42	1.91	13	2
1:A:49:PHE:CA	1:A:52:LEU:HD23	0.42	2.41	6	1
1:A:26:SER:O	1:A:31:ARG:HD2	0.42	2.14	14	1
1:A:22:ARG:HB2	1:A:34:ARG:CG	0.42	2.44	14	1
1:A:25:LEU:HD21	2:B:102:LEU:CD1	0.42	2.44	14	2
2:B:125:LEU:O	2:B:129:TYR:CB	0.42	2.67	14	1
1:C:25:LEU:CD1	2:D:99:ILE:HG12	0.42	2.44	5	3
1:A:18:LEU:CD2	2:B:92:VAL:CG1	0.42	2.95	6	1
1:A:22:ARG:CG	1:A:34:ARG:HG2	0.42	2.45	15	1
1:A:19:GLU:O	1:A:22:ARG:CG	0.42	2.67	12	3
2:B:111:ASP:O	2:B:114:HIS:CD2	0.42	2.72	5	2
2:D:105:SER:O	2:D:106:SER:CB	0.42	2.67	3	6
1:C:57:GLU:O	1:C:58:PHE:CD2	0.42	2.73	1	8
1:A:57:GLU:O	1:A:58:PHE:CG	0.42	2.73	1	5
1:C:18:LEU:CB	1:C:41:ILE:CD1	0.42	2.97	2	3
1:C:25:LEU:CD2	1:C:30:ASP:CB	0.42	2.97	2	2
1:C:48:LEU:HD13	1:C:48:LEU:C	0.42	2.34	18	1
2:D:82:LEU:CD2	2:D:130:ASP:HB3	0.42	2.44	5	1
1:C:39:ARG:HD3	2:D:88:ALA:HB2	0.42	1.90	17	1
1:A:57:GLU:O	1:A:58:PHE:CD2	0.42	2.73	15	2
2:D:111:ASP:O	2:D:114:HIS:CD2	0.42	2.72	1	2
2:D:114:HIS:ND1	2:D:118:GLN:OE1	0.42	2.53	14	1
2:D:114:HIS:CD2	2:D:115:SER:N	0.42	2.88	10	2
1:C:21:TYR:CE1	2:D:105:SER:HB3	0.42	2.49	19	4
2:D:93:LEU:HD21	2:D:114:HIS:CA	0.42	2.40	2	2
1:C:23:SER:O	1:C:27:GLN:CG	0.42	2.68	3	1
2:B:93:LEU:CD2	2:B:118:GLN:NE2	0.42	2.82	14	1
1:C:52:LEU:HD22	1:C:52:LEU:N	0.42	2.30	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:39:ARG:NH1	2:B:91:GLN:OE1	0.42	2.53	6	2
2:D:84:ALA:HA	2:D:87:ARG:HB3	0.42	1.90	10	1
1:C:26:SER:OG	1:C:34:ARG:CB	0.42	2.67	9	1
1:C:26:SER:CB	1:C:31:ARG:HA	0.42	2.45	13	1
1:A:21:TYR:CZ	2:B:105:SER:HB2	0.42	2.50	15	1
1:A:22:ARG:CG	1:A:34:ARG:CG	0.42	2.98	18	3
2:D:114:HIS:C	2:D:114:HIS:CD2	0.42	2.91	14	1
2:B:127:ASP:O	2:B:130:ASP:OD1	0.42	2.37	8	1
1:C:56:GLN:CD	2:D:125:LEU:HD21	0.42	2.35	13	1
2:B:114:HIS:C	2:B:114:HIS:ND1	0.42	2.73	9	2
1:C:21:TYR:CE1	2:D:105:SER:HB2	0.42	2.50	14	2
1:A:22:ARG:HG3	1:A:23:SER:N	0.42	2.30	10	1
1:A:25:LEU:HD21	2:B:102:LEU:HD11	0.42	1.91	10	1
2:D:93:LEU:O	2:D:114:HIS:CE1	0.42	2.73	17	1
2:B:100:HIS:CB	2:B:110:LEU:CD1	0.41	2.96	9	5
2:D:93:LEU:CD1	2:D:118:GLN:NE2	0.41	2.83	1	8
1:C:49:PHE:O	1:C:53:ILE:HG13	0.41	2.15	4	1
1:A:61:VAL:HG12	1:C:59:TYR:HB3	0.41	1.91	20	1
1:C:21:TYR:CE1	2:D:105:SER:OG	0.41	2.73	7	1
1:C:12:GLN:HA	1:C:15:LEU:HD23	0.41	1.91	15	2
1:C:46:SER:OG	2:D:129:TYR:CZ	0.41	2.73	13	2
2:D:114:HIS:C	2:D:114:HIS:ND1	0.41	2.73	1	1
1:A:35:SER:O	1:A:38:GLU:HG2	0.41	2.15	5	1
1:C:12:GLN:O	1:C:16:HIS:HB2	0.41	2.14	11	1
2:B:85:ALA:CB	2:B:126:LEU:HB3	0.41	2.39	2	1
1:A:21:TYR:CE1	2:B:105:SER:OG	0.41	2.73	12	2
1:A:52:LEU:HD21	2:B:128:LEU:CB	0.41	2.45	11	1
2:D:93:LEU:CD2	2:D:114:HIS:CG	0.41	3.02	17	1
1:A:53:ILE:O	1:A:56:GLN:CG	0.41	2.69	8	1
1:A:56:GLN:NE2	2:B:125:LEU:HD11	0.41	2.31	7	1
1:C:17:LEU:CD1	2:D:113:LEU:CD1	0.41	2.97	15	4
2:B:116:VAL:O	2:B:122:LEU:CD2	0.41	2.65	12	1
1:C:37:ILE:O	1:C:41:ILE:CG1	0.41	2.68	12	1
1:A:62:THR:HG22	1:C:60:GLU:HB2	0.41	1.91	5	1
2:D:87:ARG:O	2:D:91:GLN:N	0.41	2.52	5	1
1:C:8:LYS:HB3	1:C:53:ILE:HG21	0.41	1.90	16	1
2:B:84:ALA:C	2:B:86:GLU:H	0.41	2.18	4	1
1:C:63:LEU:CD1	2:D:124:THR:HG23	0.41	2.45	4	1
1:A:43:ILE:O	1:A:49:PHE:CD2	0.41	2.73	10	1
2:B:86:GLU:O	2:B:90:SER:CB	0.41	2.69	8	1
1:C:15:LEU:CD2	1:C:44:PHE:HB3	0.41	2.46	1	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:48:LEU:HD22	2:D:132:ILE:CG2	0.41	2.45	14	1
1:A:62:THR:HG22	1:C:60:GLU:CG	0.41	2.45	5	1
2:B:122:LEU:O	2:B:126:LEU:CD1	0.41	2.69	17	1
1:A:18:LEU:HB2	1:A:41:ILE:CD1	0.41	2.46	1	2
1:C:52:LEU:H	1:C:52:LEU:CD1	0.41	2.22	1	1
1:A:46:SER:HB3	2:B:129:TYR:CE1	0.41	2.50	6	3
1:A:50:GLN:OE1	1:A:50:GLN:N	0.41	2.54	11	1
1:C:63:LEU:CD2	2:D:123:HIS:NE2	0.41	2.84	6	1
2:B:114:HIS:ND1	2:B:118:GLN:OE1	0.41	2.54	20	1
1:C:28:THR:CG2	1:C:29:GLU:H	0.41	2.28	13	1
1:A:63:LEU:HD21	1:C:59:TYR:OH	0.41	2.15	1	1
1:C:25:LEU:O	1:C:28:THR:CG2	0.41	2.69	19	1
1:A:17:LEU:HD22	1:A:21:TYR:OH	0.41	2.16	11	1
2:D:82:LEU:HB3	2:D:130:ASP:CB	0.41	2.46	4	1
1:A:39:ARG:HG3	2:B:88:ALA:CB	0.41	2.46	20	1
2:B:128:LEU:O	2:B:132:ILE:CD1	0.41	2.69	8	1
1:C:46:SER:OG	1:C:49:PHE:CB	0.41	2.68	15	1
1:C:40:VAL:O	1:C:44:PHE:CD2	0.41	2.73	12	1
1:C:39:ARG:HB3	2:D:88:ALA:CB	0.41	2.46	12	1
2:B:124:THR:O	2:B:128:LEU:HG	0.41	2.16	18	1
2:D:116:VAL:O	2:D:122:LEU:CD2	0.41	2.64	5	1
2:D:129:TYR:CE2	2:D:130:ASP:OD1	0.41	2.73	16	2
2:B:89:VAL:CG2	2:B:126:LEU:HD22	0.41	2.46	6	1
1:A:10:ASP:O	1:A:14:ALA:HB2	0.41	2.16	17	1
2:B:129:TYR:CE2	2:B:130:ASP:OD1	0.41	2.74	17	1
1:A:40:VAL:CG2	2:B:88:ALA:HB1	0.41	2.45	20	1
1:A:48:LEU:HB3	2:B:129:TYR:CD1	0.41	2.51	7	1
1:C:39:ARG:NH1	2:D:91:GLN:OE1	0.41	2.54	15	1
1:A:17:LEU:O	1:A:21:TYR:CD1	0.41	2.74	3	1
2:B:114:HIS:ND1	2:B:114:HIS:C	0.41	2.74	3	1
1:A:26:SER:OG	1:A:27:GLN:OE1	0.41	2.31	14	2
1:A:18:LEU:HB3	1:A:37:ILE:CG2	0.41	2.46	14	1
1:C:39:ARG:HG3	2:D:88:ALA:CB	0.41	2.46	2	1
1:A:12:GLN:O	1:A:16:HIS:CD2	0.41	2.74	12	2
1:A:23:SER:O	1:A:27:GLN:CG	0.41	2.69	12	1
1:A:52:LEU:HA	1:A:55:ILE:HD12	0.41	1.92	12	1
1:C:52:LEU:CD2	1:C:53:ILE:N	0.41	2.84	1	1
1:A:17:LEU:O	1:A:21:TYR:CG	0.41	2.73	5	2
1:C:22:ARG:HA	1:C:37:ILE:HD12	0.41	1.93	4	1
2:D:82:LEU:C	2:D:82:LEU:CD1	0.41	2.89	4	1
1:C:48:LEU:O	1:C:51:ALA:CB	0.41	2.67	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:52:LEU:HB2	2:D:125:LEU:HD22	0.41	1.93	6	1
1:C:18:LEU:HD11	2:D:117:PHE:CE1	0.41	2.51	8	1
1:C:49:PHE:HA	1:C:52:LEU:HD23	0.41	1.91	8	1
1:A:39:ARG:CB	2:B:88:ALA:HB1	0.41	2.46	13	1
1:A:54:ASP:O	1:A:57:GLU:CG	0.41	2.68	7	1
2:B:134:THR:O	2:B:135:LYS:HG2	0.41	2.16	15	1
1:A:41:ILE:O	1:A:45:GLN:HG3	0.41	2.16	3	1
2:D:114:HIS:ND1	2:D:114:HIS:C	0.41	2.74	3	1
2:B:128:LEU:HD21	1:C:59:TYR:CG	0.41	2.50	14	1
1:C:57:GLU:O	1:C:58:PHE:CD1	0.41	2.73	18	2
2:B:96:LEU:HD13	2:B:110:LEU:HA	0.41	1.92	19	1
1:C:21:TYR:CZ	2:D:105:SER:HB2	0.41	2.51	19	1
1:C:18:LEU:CD1	1:C:40:VAL:CG1	0.41	2.99	7	2
1:A:21:TYR:CZ	2:B:105:SER:HB3	0.41	2.51	4	1
2:B:117:PHE:HA	2:B:122:LEU:CD2	0.41	2.46	6	1
1:A:12:GLN:O	1:A:16:HIS:CG	0.41	2.74	10	1
2:D:114:HIS:CD2	2:D:118:GLN:OE1	0.41	2.74	10	1
2:D:86:GLU:OE1	2:D:123:HIS:CG	0.40	2.75	15	1
1:C:41:ILE:O	1:C:45:GLN:HG2	0.40	2.16	12	1
2:B:128:LEU:HD22	1:C:55:ILE:HD13	0.40	1.93	1	1
2:D:89:VAL:O	2:D:93:LEU:HB2	0.40	2.16	1	1
1:C:57:GLU:O	1:C:58:PHE:CG	0.40	2.73	19	4
1:C:52:LEU:HD11	2:D:128:LEU:C	0.40	2.36	19	1
2:D:129:TYR:CD2	2:D:130:ASP:OD2	0.40	2.74	11	1
1:A:52:LEU:HD11	2:B:129:TYR:N	0.40	2.32	16	1
1:C:8:LYS:CD	1:C:8:LYS:C	0.40	2.90	16	1
2:D:122:LEU:HA	2:D:125:LEU:CD1	0.40	2.47	20	1
1:A:33:LEU:CD2	2:B:95:SER:OG	0.40	2.70	8	1
1:C:63:LEU:C	1:C:64:LEU:HD23	0.40	2.36	15	1
2:D:93:LEU:HG	2:D:117:PHE:CB	0.40	2.46	9	1
2:B:122:LEU:HG	2:B:126:LEU:HD11	0.40	1.93	6	1
1:A:17:LEU:CD1	2:B:113:LEU:CD1	0.40	2.98	8	2
1:C:52:LEU:HD11	2:D:129:TYR:N	0.40	2.31	17	1
1:C:49:PHE:C	1:C:52:LEU:HD23	0.40	2.36	8	1
1:C:25:LEU:CD2	2:D:102:LEU:HD13	0.40	2.46	7	1
1:C:33:LEU:HD11	2:D:95:SER:HB3	0.40	1.92	14	1
2:B:128:LEU:HD22	1:C:55:ILE:HD12	0.40	1.94	19	1
1:A:35:SER:HA	1:A:38:GLU:HG2	0.40	1.92	4	1
1:C:54:ASP:O	1:C:57:GLU:CG	0.40	2.70	6	1
2:B:134:THR:O	2:B:134:THR:CG2	0.40	2.68	20	1
2:D:114:HIS:ND1	2:D:118:GLN:NE2	0.40	2.70	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:D:114:HIS:O	2:D:118:GLN:HG2	0.40	2.16	13	1
1:A:56:GLN:OE1	2:B:121:HIS:CG	0.40	2.74	7	1
2:D:122:LEU:O	2:D:125:LEU:N	0.40	2.55	9	1
1:C:50:GLN:N	1:C:50:GLN:OE1	0.40	2.55	18	1
2:D:96:LEU:CD1	2:D:110:LEU:O	0.40	2.69	1	1
1:A:17:LEU:HD13	2:B:113:LEU:CD1	0.40	2.46	16	1
1:A:55:ILE:CG2	2:D:128:LEU:CD2	0.40	2.99	6	1
1:A:40:VAL:CG2	2:B:92:VAL:CG2	0.40	2.99	17	1
1:A:12:GLN:O	1:A:16:HIS:HB2	0.40	2.16	14	1
2:B:112:PHE:CE1	2:B:116:VAL:CG2	0.40	3.05	14	1
1:A:46:SER:CB	2:B:129:TYR:CZ	0.40	3.04	11	1
1:A:26:SER:CB	1:A:34:ARG:HD3	0.40	2.47	16	1
1:A:25:LEU:HD13	1:A:37:ILE:HD11	0.40	1.92	4	1
1:C:37:ILE:HG12	2:D:92:VAL:HG13	0.40	1.94	13	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	57/60 (95%)	48±1 (85±2%)	6±1 (11±2%)	3±1 (5±1%)	5	29
1	C	57/60 (95%)	48±1 (84±2%)	7±1 (12±2%)	2±0 (4±1%)	6	30
2	B	54/56 (96%)	49±1 (90±3%)	4±1 (7±3%)	2±1 (3±1%)	9	42
2	D	52/56 (93%)	48±1 (92±2%)	3±1 (5±2%)	1±0 (3±1%)	9	44
All	All	4400/4640 (95%)	3852 (88%)	386 (9%)	162 (4%)	7	35

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

Mol	Chain	Res	Type	Models (Total)
1	A	29	GLU	20
1	C	29	GLU	20
2	D	106	SER	20
2	B	106	SER	19

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Mol	Chain	Res	Type	Models (Total)
1	A	26	SER	14
1	C	26	SER	11
1	C	28	THR	9
2	B	105	SER	9
2	D	105	SER	9
1	A	60	GLU	8
1	C	60	GLU	6
1	A	28	THR	6
1	A	46	SER	4
2	B	135	LYS	3
1	C	46	SER	3
2	B	86	GLU	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	56/58 (97%)	40±3 (71±6%)	16±3 (29±6%)	2	18
1	C	56/58 (97%)	40±2 (72±3%)	16±2 (28±3%)	2	19
2	B	51/51 (100%)	35±3 (68±5%)	16±3 (32±5%)	1	14
2	D	48/51 (94%)	34±2 (71±3%)	14±2 (29±3%)	2	19
All	All	4220/4360 (97%)	2977 (71%)	1243 (29%)	2	17

All 148 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	64	LEU	20
2	B	98	GLU	20
2	B	102	LEU	20
2	B	83	LEU	20
1	C	64	LEU	20
2	D	102	LEU	20
2	D	96	LEU	20
2	D	113	LEU	20
2	B	96	LEU	20

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Mol	Chain	Res	Type	Models (Total)
1	C	61	VAL	20
2	D	98	GLU	20
1	A	61	VAL	20
1	C	15	LEU	20
2	D	83	LEU	20
1	A	12	GLN	20
1	C	12	GLN	20
1	A	15	LEU	20
2	B	113	LEU	20
1	A	25	LEU	20
2	D	118	GLN	19
1	C	25	LEU	19
1	A	63	LEU	18
2	B	118	GLN	16
1	C	63	LEU	16
2	B	129	TYR	14
1	C	46	SER	14
1	A	47	ASN	14
1	A	8	LYS	14
2	B	135	LYS	13
1	A	46	SER	13
1	C	47	ASN	13
2	B	114	HIS	12
1	A	7	ARG	12
2	D	131	LYS	12
1	C	27	GLN	12
1	C	48	LEU	11
2	D	129	TYR	11
1	A	32	GLN	11
2	B	86	GLU	11
1	C	7	ARG	11
2	D	108	LYS	11
1	C	8	LYS	10
2	D	95	SER	10
2	D	82	LEU	10
2	B	82	LEU	10
2	B	106	SER	10
2	B	136	SER	10
1	C	32	GLN	9
1	A	38	GLU	9
1	A	36	SER	9
1	C	22	ARG	9

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Mol	Chain	Res	Type	Models (Total)
2	B	108	LYS	9
1	A	27	GLN	9
2	D	86	GLU	8
1	A	44	PHE	8
1	C	60	GLU	8
1	C	44	PHE	8
1	C	52	LEU	8
2	B	119	ASP	8
2	B	131	LYS	8
2	D	126	LEU	8
1	A	30	ASP	8
1	C	56	GLN	8
2	D	123	HIS	8
2	B	112	PHE	8
2	D	114	HIS	7
2	D	120	GLN	7
2	B	120	GLN	7
2	D	94	ASP	7
1	C	36	SER	7
1	A	31	ARG	7
2	B	127	ASP	7
1	C	54	ASP	7
1	A	48	LEU	7
2	D	119	ASP	7
1	A	52	LEU	7
2	D	104	ASP	7
1	A	56	GLN	7
2	B	130	ASP	7
2	B	95	SER	7
2	B	115	SER	6
2	B	123	HIS	6
1	C	19	GLU	6
1	A	13	ARG	6
2	D	106	SER	6
2	B	105	SER	6
2	D	111	ASP	6
1	A	19	GLU	6
2	B	107	GLU	6
1	A	23	SER	6
1	A	35	SER	6
1	A	24	LYS	6
2	B	126	LEU	6

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Mol	Chain	Res	Type	Models (Total)
2	D	112	PHE	6
2	D	121	HIS	6
1	A	20	GLU	5
2	B	93	LEU	5
1	C	30	ASP	5
1	A	54	ASP	5
2	B	111	ASP	5
1	A	10	ASP	5
1	A	26	SER	5
1	C	35	SER	5
1	C	50	GLN	5
2	B	121	HIS	5
1	A	22	ARG	5
2	B	104	ASP	5
1	C	31	ARG	5
2	D	127	ASP	4
1	C	38	GLU	4
1	C	26	SER	4
1	C	20	GLU	4
1	C	24	LYS	4
1	A	16	HIS	4
2	B	94	ASP	4
1	C	23	SER	4
1	C	34	ARG	4
1	A	34	ARG	3
2	D	115	SER	3
2	B	91	GLN	3
1	C	13	ARG	3
1	C	16	HIS	3
1	A	57	GLU	3
1	C	10	ASP	3
2	B	90	SER	3
2	D	87	ARG	3
1	A	60	GLU	3
2	D	107	GLU	3
1	C	11	THR	2
2	D	130	ASP	2
1	C	33	LEU	2
2	D	105	SER	2
2	B	117	PHE	2
1	C	57	GLU	2
1	A	18	LEU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	62	THR	1
1	A	9	GLN	1
2	B	133	ASN	1
2	B	109	ASP	1
1	A	11	THR	1
1	C	17	LEU	1
2	B	134	THR	1
2	D	90	SER	1
1	C	28	THR	1
1	A	28	THR	1
2	D	93	LEU	1
1	A	50	GLN	1
1	A	17	LEU	1

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 6.7 Other polymers [i](#)

There are no such molecules in this entry.

### 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided