



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 07:26 pm GMT

PDB ID : 1PRL  
Title : TWO BINDING ORIENTATIONS FOR PEPTIDES TO SRC SH3 DOMAIN:  
DEVELOPMENT OF A GENERAL MODEL FOR SH3-LIGAND INTERAC-  
TIONS  
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Deposited on : 1994-10-10

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

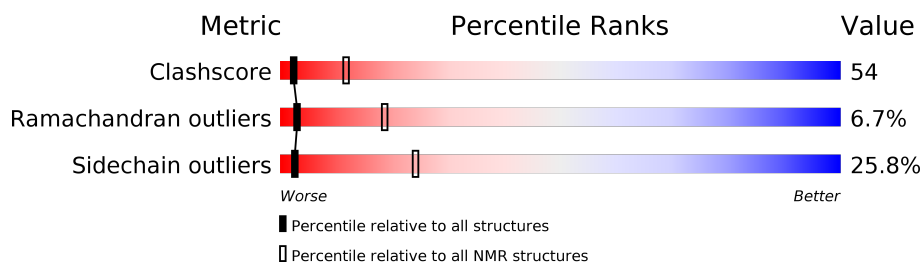
# 1 Overall quality at a glance

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	C	64	
2	A	9	

## 2 Ensemble composition and analysis

This entry contains 16 models. The atoms present in the NMR models are not consistent. Some calculations may have failed as a result. All residues are included in the validation scores. Model 6 is the overall representative, medoid model (most similar to other models).

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	C:9-C:64, A:71-A:79 (65)	0.75	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 1 single-model cluster was found.

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

### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1025 atoms, of which 500 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called C-SRC TYROSINE KINASE SH3 DOMAIN.

Mol	Chain	Residues	Atoms					Trace
1	C	56	Total	C	H	N	O	0
			873	287	421	73	92	

- Molecule 2 is a protein called PROLINE-RICH LIGAND PLR1 (AFAPPLPRR).

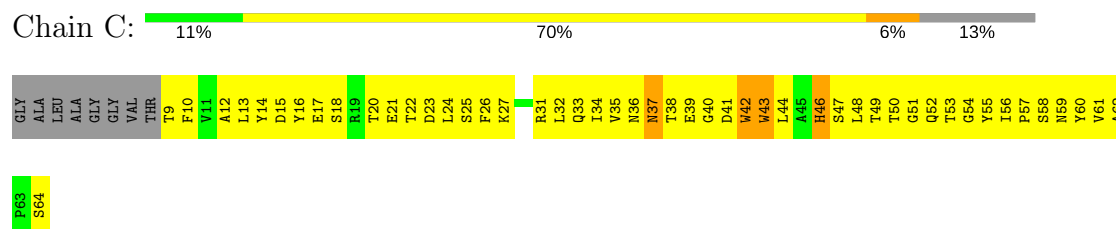
Mol	Chain	Residues	Atoms					Trace
2	A	9	Total	C	H	N	O	0
			152	48	79	15	10	

## 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: C-SRC TYROSINE KINASE SH3 DOMAIN



- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

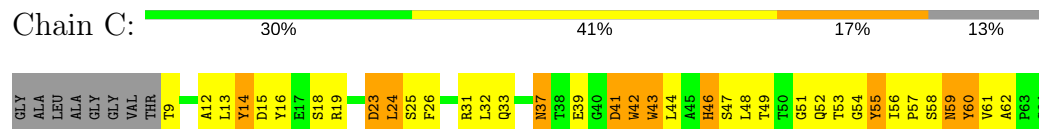


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN




- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)



A71  
F72  
A73  
P74  
P75  
L76  
P77  
R78  
R79

#### 4.2.2 Score per residue for model 2

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

Chain C: 

GLY  
ALA  
LEU  
ALA  
GLY  
GLY  
VAL  
THR  
T9  
F10  
V11  
A12  
L13  
Y14  
D15  
Y16  
E17  
S18  
R19  
T20  
E21  
T22  
S25  
F26  
K27  
R28  
G29  
E30  
R31  
L32  
Q33  
I34  
V35  
N36  
N37  
T38  
E39  
G40  
D41  
W42  
W43  
L44  
L45  
H46  
S47  
L48  
T49  
T50  
Q51  
Q52  
T53  
Y54  
Y55  
I56  
P57  
S58  
N59  
Y60  
V61

A62  
P63  
S64

- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

Chain A: 

A71  
F72  
A73  
P74  
P75  
L76  
P77  
R78  
R79

#### 4.2.3 Score per residue for model 3

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

Chain C: 

GLY  
ALA  
LEU  
ALA  
GLY  
GLY  
VAL  
THR  
T9  
F10  
V11  
A12  
L13  
Y14  
D15  
Y16  
R19  
T20  
E21  
T22  
D23  
L24  
S25  
F26  
R31  
L32  
Q33  
I34  
V35  
N36  
N37  
T38  
E39  
G40  
D41  
W42  
W43  
L44  
A45  
H46  
S47  
L48  
T49  
T50  
Q51  
Q52  
T53  
Y54  
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I56  
P57  
S58  
N59  
Y60  
V61  
A62  
P63  
S64

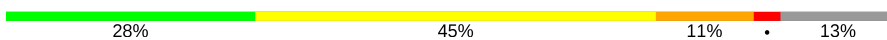
- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

Chain A: 

A71  
F72  
A73  
P74  
R79

#### 4.2.4 Score per residue for model 4

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

Chain C: 

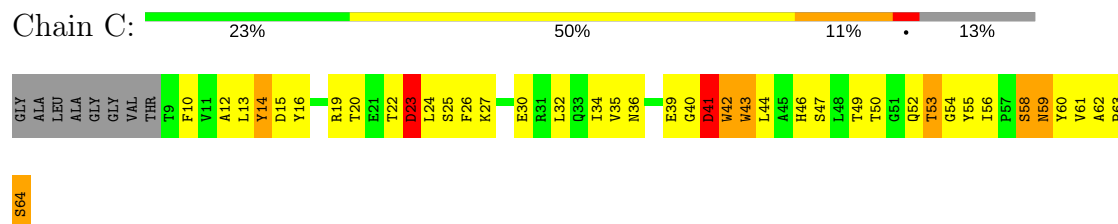
GLY  
ALA  
LEU  
ALA  
GLY  
GLY  
VAL  
THR  
T9  
F10  
V11  
A12  
L13  
Y14  
D15  
Y16  
E17  
S18  
R19  
T20  
D23  
L24  
S25  
F26  
Q33  
I34  
V35  
N36  
N37  
T38  
E39  
G40  
D41  
W42  
W43  
L44  
A45  
H46  
T50  
Q51  
Q52  
T53  
Y54  
Y55  
I56  
P57  
S58  
N59  
Y60  
V61  
A62  
P63  
S64

- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

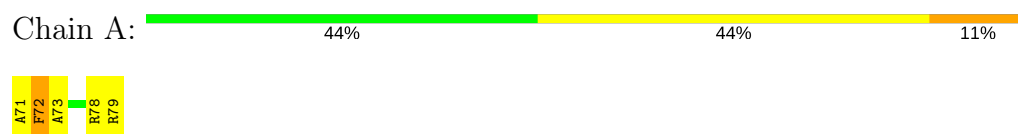


#### 4.2.5 Score per residue for model 5

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

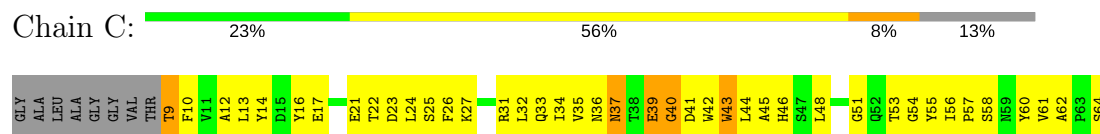


- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

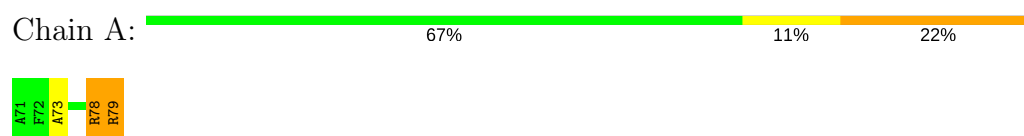


#### 4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

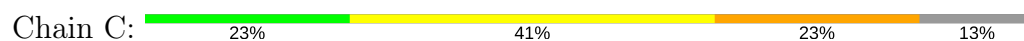


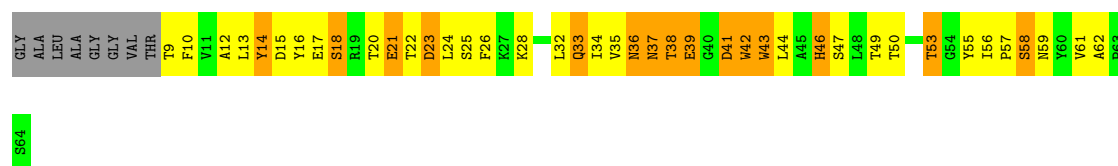
- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)



#### 4.2.7 Score per residue for model 7

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN





- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

Chain A: 33% 44% 22%



#### 4.2.8 Score per residue for model 8

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

Chain C: 19% 44% 23% 13%



- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

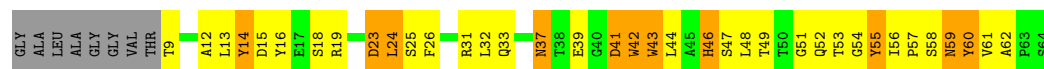
Chain A: 11% 33% 44% 11%



#### 4.2.9 Score per residue for model 9

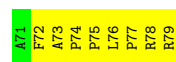
- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

Chain C: 30% 41% 17% 13%



- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

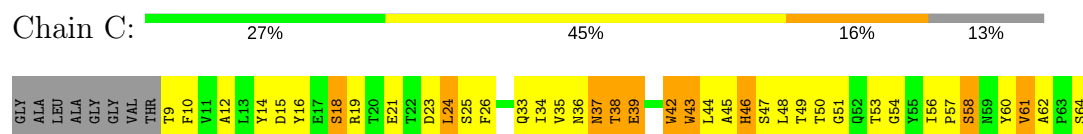
Chain A: 11% 89%



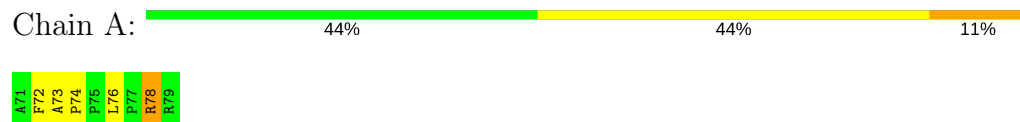


### 4.2.10 Score per residue for model 10

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

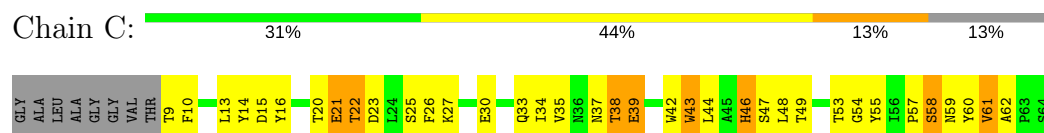


- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)



### 4.2.11 Score per residue for model 11

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

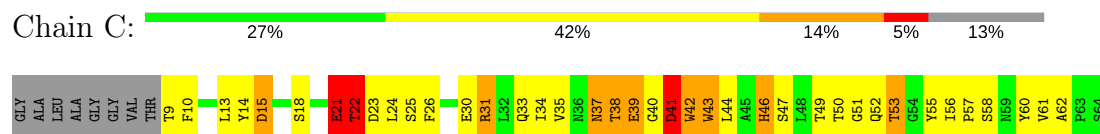


- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

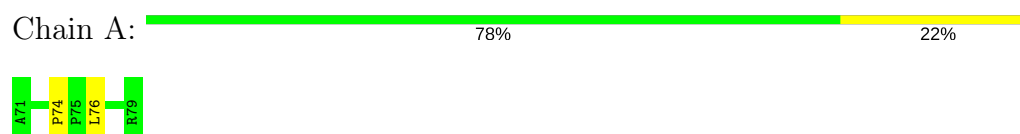


### 4.2.12 Score per residue for model 12

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN



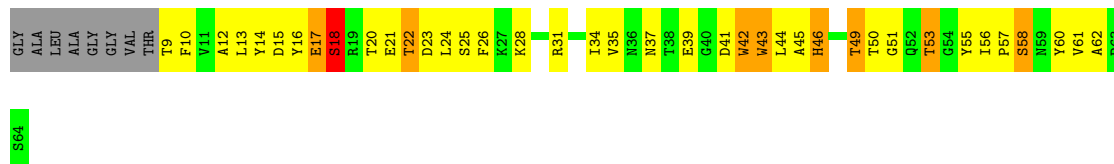
- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)



### 4.2.13 Score per residue for model 13

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

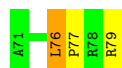
Chain C: 27% 47% 13% 13%



S64

- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

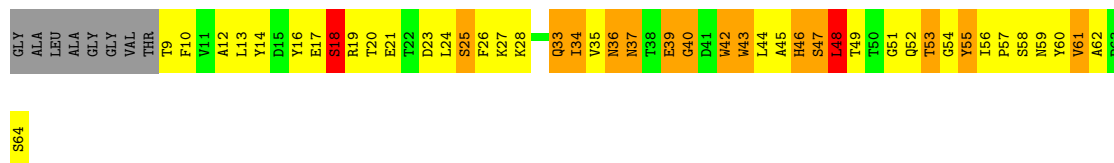
Chain A: 67% 22% 11%



### 4.2.14 Score per residue for model 14

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

Chain C: 17% 45% 22% 13%



S64

- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

Chain A: 22% 44% 33%



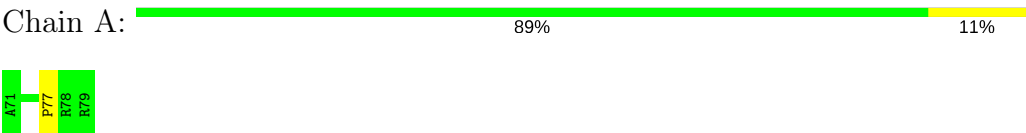
### 4.2.15 Score per residue for model 15

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN

Chain C: 25% 45% 17% 13%

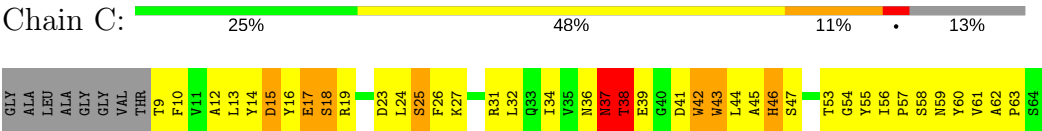


- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)

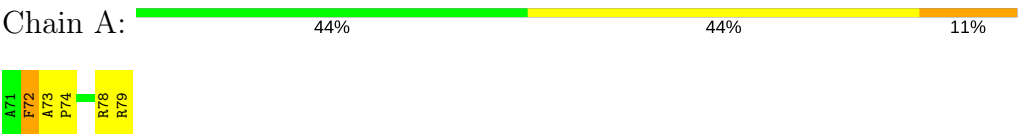


4.2.16 Score per residue for model 16

- Molecule 1: C-SRC TYROSINE KINASE SH3 DOMAIN



- Molecule 2: PROLINE-RICH LIGAND PLR1 (AFAPPLPRR)



## 5 Refinement protocol and experimental data overview

Of the ? calculated structures, 16 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
X-PLOR	refinement	

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](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	C	1.12±0.00	3±0/464 (0.6±0.0%)	1.24±0.01	8±0/632 (1.3±0.0%)
2	A	0.94±0.00	0±0/76 (0.0±0.0%)	0.95±0.01	0±0/102 (0.0±0.0%)
All	All	1.10	48/8640 (0.6%)	1.21	129/11744 (1.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	C	43	TRP	CG-CD2	-6.07	1.33	1.43	2	16
1	C	42	TRP	CG-CD2	-6.03	1.33	1.43	3	16
1	C	46	HIS	CG-ND1	-5.29	1.27	1.38	5	16

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	C	43	TRP	NE1-CE2-CZ2	8.17	139.38	130.40	7	16
1	C	42	TRP	NE1-CE2-CZ2	8.09	139.29	130.40	7	16
1	C	43	TRP	CD1-NE1-CE2	6.91	115.22	109.00	13	16
1	C	42	TRP	CD1-NE1-CE2	6.85	115.17	109.00	8	16
1	C	43	TRP	CG-CD1-NE1	-6.61	103.49	110.10	15	16
1	C	42	TRP	CG-CD1-NE1	-6.58	103.52	110.10	3	16
1	C	43	TRP	NE1-CE2-CD2	-6.52	100.78	107.30	14	16
1	C	42	TRP	NE1-CE2-CD2	-6.46	100.84	107.30	7	16
1	C	43	TRP	CG-CD2-CE3	-5.04	129.37	133.90	15	1

There are no chirality outliers.

There are no planarity outliers.

## 6.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	C	452	422	421	52±10
2	A	73	79	76	5±4
All	All	8400	8015	7952	878

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 54.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:13:LEU:HD11	1:C:62:ALA:HB2	1.04	1.24	6	11
1:C:34:ILE:HD11	1:C:56:ILE:HD11	1.04	1.25	10	1
1:C:56:ILE:HD12	1:C:61:VAL:HG11	1.02	1.28	10	3
1:C:36:ASN:O	1:C:38:THR:HG22	0.98	1.58	2	1
1:C:34:ILE:HD11	1:C:56:ILE:CD1	0.97	1.88	10	1
2:A:73:ALA:HB1	2:A:74:PRO:HD2	0.94	1.38	8	4
1:C:13:LEU:HD11	1:C:62:ALA:CB	0.94	1.92	2	15
1:C:44:LEU:HD21	1:C:53:THR:CG2	0.86	2.01	4	2
1:C:13:LEU:CD1	1:C:62:ALA:HB2	0.84	2.01	14	8
1:C:44:LEU:HD21	1:C:53:THR:HG21	0.84	1.47	4	3
1:C:44:LEU:HD12	1:C:55:TYR:CE1	0.83	2.08	14	2
1:C:56:ILE:CD1	1:C:61:VAL:HG11	0.80	2.04	10	6
1:C:44:LEU:HD13	1:C:55:TYR:CD2	0.79	2.13	4	1
1:C:12:ALA:HB1	1:C:26:PHE:CE1	0.78	2.13	7	8
1:C:24:LEU:N	1:C:24:LEU:HD13	0.78	1.92	3	1
1:C:44:LEU:HD13	1:C:55:TYR:CE1	0.77	2.14	12	6
1:C:24:LEU:HD13	1:C:53:THR:O	0.77	1.80	15	1
1:C:13:LEU:HD11	1:C:62:ALA:HB3	0.77	1.57	16	2
1:C:44:LEU:HD11	1:C:53:THR:HG22	0.76	1.56	1	3
1:C:56:ILE:HD12	1:C:56:ILE:O	0.76	1.81	14	1
1:C:12:ALA:HB1	1:C:26:PHE:CD1	0.72	2.19	1	11
1:C:44:LEU:O	1:C:44:LEU:HD23	0.71	1.84	10	2
1:C:56:ILE:HD12	1:C:61:VAL:CG1	0.71	2.14	10	1
1:C:42:TRP:CZ2	2:A:76:LEU:HD22	0.71	2.21	13	6
2:A:73:ALA:HB1	2:A:74:PRO:CD	0.71	2.14	8	2
1:C:61:VAL:HG13	1:C:62:ALA:N	0.71	2.00	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:44:LEU:HD13	1:C:55:TYR:CE2	0.71	2.21	4	1
1:C:24:LEU:HD22	1:C:54:GLY:HA3	0.70	1.61	3	1
1:C:44:LEU:HD11	1:C:53:THR:CG2	0.70	2.16	1	4
1:C:44:LEU:C	1:C:44:LEU:HD23	0.69	2.08	10	3
1:C:34:ILE:HD13	1:C:45:ALA:HB2	0.68	1.64	10	3
1:C:14:TYR:CD1	1:C:14:TYR:N	0.68	2.61	8	6
1:C:56:ILE:H	1:C:56:ILE:HD13	0.68	1.48	2	1
1:C:24:LEU:HD11	1:C:53:THR:O	0.68	1.89	7	5
1:C:44:LEU:HD13	1:C:55:TYR:CD1	0.67	2.23	12	6
1:C:20:THR:CG2	1:C:22:THR:HG22	0.67	2.20	5	2
1:C:16:TYR:CB	1:C:26:PHE:CE2	0.66	2.79	7	8
1:C:44:LEU:HD23	1:C:44:LEU:C	0.66	2.11	8	2
1:C:14:TYR:N	1:C:14:TYR:CD1	0.66	2.62	10	8
1:C:56:ILE:HD11	1:C:61:VAL:HG11	0.66	1.68	6	1
1:C:22:THR:HG23	1:C:23:ASP:N	0.65	2.06	5	1
1:C:56:ILE:HD12	1:C:57:PRO:O	0.65	1.90	4	1
1:C:33:GLN:OE1	1:C:48:LEU:HD21	0.64	1.92	8	3
1:C:12:ALA:CB	1:C:26:PHE:CD1	0.64	2.81	1	11
1:C:42:TRP:HZ2	2:A:76:LEU:HD22	0.64	1.52	13	3
1:C:16:TYR:CD1	1:C:57:PRO:CG	0.64	2.81	14	4
1:C:16:TYR:CB	1:C:26:PHE:CZ	0.63	2.81	15	11
1:C:55:TYR:CD1	1:C:55:TYR:N	0.63	2.66	7	2
1:C:49:THR:HG22	1:C:50:THR:N	0.63	2.07	13	5
1:C:57:PRO:CB	2:A:76:LEU:HD21	0.62	2.25	8	1
1:C:59:ASN:O	1:C:60:TYR:CB	0.62	2.47	1	2
1:C:35:VAL:HG21	1:C:44:LEU:CD2	0.62	2.25	7	3
1:C:44:LEU:CD1	1:C:55:TYR:CE1	0.62	2.82	14	2
1:C:61:VAL:O	1:C:62:ALA:HB2	0.62	1.94	8	1
1:C:44:LEU:HD12	1:C:55:TYR:CD1	0.62	2.29	14	4
1:C:37:ASN:O	1:C:39:GLU:N	0.61	2.32	2	2
1:C:46:HIS:O	1:C:47:SER:CB	0.61	2.47	14	1
1:C:59:ASN:O	1:C:60:TYR:CG	0.61	2.54	1	2
1:C:56:ILE:C	1:C:56:ILE:HD12	0.61	2.14	14	2
1:C:10:PHE:CD2	1:C:34:ILE:HD11	0.61	2.31	12	1
1:C:35:VAL:HG21	1:C:44:LEU:HD22	0.61	1.72	6	3
1:C:34:ILE:CD1	1:C:56:ILE:HD11	0.61	2.16	10	2
1:C:44:LEU:CD1	1:C:55:TYR:CD1	0.61	2.83	16	5
1:C:33:GLN:HG3	1:C:48:LEU:HD21	0.60	1.73	6	1
1:C:56:ILE:N	1:C:56:ILE:HD13	0.60	2.12	2	1
1:C:46:HIS:NE2	1:C:51:GLY:HA2	0.60	2.11	14	1
1:C:26:PHE:CE2	1:C:56:ILE:HG22	0.59	2.32	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:55:TYR:N	1:C:55:TYR:CD1	0.59	2.67	8	1
1:C:16:TYR:HB2	1:C:26:PHE:CZ	0.59	2.33	15	11
1:C:61:VAL:HG22	1:C:62:ALA:N	0.58	2.13	6	15
1:C:37:ASN:O	1:C:43:TRP:CD1	0.58	2.56	14	2
1:C:10:PHE:CD2	1:C:34:ILE:CD1	0.58	2.86	12	1
1:C:56:ILE:CD1	1:C:61:VAL:CG1	0.58	2.81	6	1
1:C:26:PHE:CE2	1:C:56:ILE:CG2	0.58	2.87	14	1
1:C:26:PHE:CD1	1:C:26:PHE:O	0.58	2.57	11	6
1:C:11:VAL:HG23	1:C:64:SER:OXT	0.58	1.99	2	1
1:C:42:TRP:CZ3	1:C:57:PRO:N	0.58	2.72	10	6
1:C:26:PHE:O	1:C:26:PHE:CD1	0.58	2.56	5	4
1:C:61:VAL:CG2	1:C:62:ALA:N	0.57	2.67	2	14
1:C:46:HIS:CD2	1:C:47:SER:O	0.57	2.56	2	8
1:C:53:THR:CG2	1:C:54:GLY:N	0.57	2.67	10	5
1:C:24:LEU:HD22	1:C:24:LEU:H	0.57	1.57	3	1
1:C:24:LEU:HD11	1:C:52:GLN:O	0.57	1.99	12	1
1:C:53:THR:HG23	1:C:54:GLY:N	0.57	2.13	5	1
1:C:57:PRO:CG	2:A:76:LEU:HD21	0.57	2.30	8	1
1:C:45:ALA:HB2	1:C:56:ILE:HG12	0.57	1.75	13	1
1:C:13:LEU:C	1:C:14:TYR:CD1	0.57	2.78	16	9
1:C:16:TYR:HB3	1:C:26:PHE:CZ	0.56	2.35	1	7
1:C:37:ASN:OD1	1:C:43:TRP:CH2	0.56	2.57	3	1
1:C:16:TYR:HB3	1:C:26:PHE:CE2	0.56	2.36	15	10
1:C:10:PHE:CG	1:C:34:ILE:CG1	0.56	2.89	6	4
1:C:20:THR:HG23	1:C:22:THR:HG22	0.56	1.78	5	1
1:C:16:TYR:CD1	1:C:57:PRO:HG3	0.55	2.35	15	5
1:C:14:TYR:HB2	1:C:60:TYR:CD2	0.55	2.36	3	4
1:C:46:HIS:CE1	1:C:52:GLN:N	0.55	2.74	14	1
1:C:20:THR:CG2	1:C:21:GLU:N	0.55	2.69	11	1
1:C:36:ASN:O	1:C:37:ASN:CB	0.55	2.55	7	2
1:C:44:LEU:HD13	1:C:55:TYR:CZ	0.55	2.36	1	4
1:C:16:TYR:HB2	1:C:26:PHE:CE1	0.55	2.37	8	1
1:C:12:ALA:CB	1:C:26:PHE:CE1	0.55	2.89	8	4
1:C:44:LEU:HD11	1:C:53:THR:HG23	0.55	1.78	12	2
1:C:44:LEU:HD23	1:C:45:ALA:N	0.55	2.17	3	2
1:C:16:TYR:CD2	1:C:26:PHE:CE2	0.55	2.94	8	3
1:C:44:LEU:CD1	1:C:55:TYR:CD2	0.55	2.89	4	1
1:C:61:VAL:HG22	1:C:62:ALA:H	0.54	1.62	15	1
1:C:56:ILE:HD13	1:C:61:VAL:HG11	0.54	1.79	1	3
1:C:13:LEU:HB3	1:C:14:TYR:CE1	0.54	2.38	6	3
1:C:35:VAL:HG23	1:C:44:LEU:O	0.54	2.02	4	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:32:LEU:HD22	1:C:56:ILE:HG21	0.54	1.80	6	2
1:C:26:PHE:CE2	1:C:56:ILE:HB	0.54	2.37	8	3
1:C:32:LEU:N	1:C:32:LEU:HD12	0.54	2.17	16	1
1:C:21:GLU:O	1:C:23:ASP:N	0.54	2.41	12	1
1:C:46:HIS:CE1	1:C:51:GLY:HA2	0.53	2.38	3	6
1:C:37:ASN:HB3	1:C:43:TRP:CD1	0.53	2.38	7	4
1:C:36:ASN:O	1:C:38:THR:N	0.53	2.41	2	1
1:C:37:ASN:CB	1:C:43:TRP:CD1	0.53	2.91	6	1
1:C:24:LEU:N	1:C:24:LEU:CD1	0.53	2.66	3	1
1:C:34:ILE:HG22	1:C:37:ASN:OD1	0.53	2.03	2	1
1:C:22:THR:O	1:C:23:ASP:C	0.53	2.46	5	1
1:C:41:ASP:O	1:C:42:TRP:CD1	0.53	2.62	8	3
1:C:16:TYR:CD1	1:C:57:PRO:CD	0.53	2.91	14	3
1:C:60:TYR:CZ	2:A:73:ALA:HB1	0.53	2.38	6	1
1:C:13:LEU:O	1:C:28:LYS:CD	0.53	2.56	15	1
1:C:10:PHE:CD2	1:C:34:ILE:HG13	0.53	2.38	13	9
1:C:53:THR:HG22	1:C:54:GLY:N	0.53	2.19	11	3
1:C:46:HIS:CD2	1:C:46:HIS:O	0.53	2.62	8	1
1:C:44:LEU:HD12	1:C:54:GLY:C	0.53	2.24	4	1
1:C:13:LEU:CD1	1:C:62:ALA:CB	0.53	2.87	16	6
1:C:56:ILE:HD13	1:C:56:ILE:H	0.53	1.64	8	1
1:C:34:ILE:HG22	1:C:35:VAL:N	0.53	2.19	14	2
1:C:38:THR:O	1:C:38:THR:HG23	0.53	2.04	7	1
1:C:16:TYR:CE1	1:C:57:PRO:HG3	0.52	2.38	14	4
1:C:35:VAL:CG2	1:C:44:LEU:O	0.52	2.57	2	3
2:A:73:ALA:CB	2:A:74:PRO:CD	0.52	2.84	8	2
1:C:20:THR:CG2	1:C:22:THR:OG1	0.52	2.57	7	1
1:C:24:LEU:N	1:C:24:LEU:HD23	0.52	2.19	1	1
1:C:24:LEU:CD1	1:C:53:THR:O	0.52	2.58	16	8
1:C:24:LEU:HD23	1:C:24:LEU:N	0.52	2.19	9	1
2:A:71:ALA:O	2:A:72:PHE:CB	0.52	2.58	8	2
1:C:34:ILE:HD11	1:C:56:ILE:CG1	0.52	2.35	10	1
1:C:40:GLY:O	1:C:41:ASP:CB	0.52	2.56	12	1
1:C:18:SER:CB	1:C:23:ASP:O	0.52	2.58	4	2
1:C:37:ASN:HA	1:C:43:TRP:CD1	0.52	2.39	12	3
1:C:10:PHE:HB3	1:C:61:VAL:CG2	0.52	2.35	3	9
1:C:11:VAL:CG2	1:C:64:SER:OXT	0.52	2.58	2	1
1:C:42:TRP:CD1	2:A:79:ARG:HB3	0.52	2.40	13	1
1:C:46:HIS:NE2	1:C:47:SER:O	0.52	2.43	12	8
1:C:10:PHE:CD1	1:C:34:ILE:HG12	0.52	2.39	15	1
1:C:23:ASP:N	1:C:23:ASP:OD1	0.52	2.43	4	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:43:TRP:CH2	1:C:58:SER:HB3	0.52	2.40	8	1
1:C:48:LEU:HD21	1:C:52:GLN:O	0.52	2.04	14	1
1:C:41:ASP:OD2	2:A:77:PRO:CG	0.52	2.57	7	1
1:C:12:ALA:CB	1:C:30:GLU:OE2	0.52	2.58	15	1
1:C:60:TYR:CE2	2:A:76:LEU:HD21	0.51	2.41	4	3
1:C:10:PHE:CG	1:C:34:ILE:HG13	0.51	2.41	2	4
1:C:61:VAL:CG1	1:C:62:ALA:N	0.51	2.71	8	1
1:C:47:SER:O	1:C:48:LEU:C	0.51	2.48	14	2
1:C:37:ASN:O	1:C:38:THR:C	0.51	2.49	2	4
1:C:13:LEU:N	1:C:60:TYR:O	0.51	2.43	8	2
1:C:44:LEU:HD21	1:C:53:THR:HG23	0.51	1.82	3	1
1:C:59:ASN:OD1	1:C:60:TYR:CD1	0.51	2.63	14	1
1:C:43:TRP:CE2	1:C:58:SER:HB2	0.51	2.41	1	3
1:C:20:THR:HG22	1:C:21:GLU:N	0.51	2.19	11	1
1:C:29:GLY:O	1:C:31:ARG:NH1	0.51	2.44	2	1
1:C:38:THR:HG23	1:C:39:GLU:N	0.51	2.20	11	2
1:C:59:ASN:O	1:C:60:TYR:HB2	0.51	2.06	1	2
1:C:16:TYR:CE2	1:C:57:PRO:HD3	0.51	2.41	3	5
1:C:51:GLY:O	1:C:52:GLN:CG	0.51	2.59	2	1
1:C:37:ASN:O	1:C:38:THR:CG2	0.51	2.58	12	1
1:C:9:THR:HG22	1:C:32:LEU:O	0.51	2.06	6	1
1:C:38:THR:O	1:C:39:GLU:C	0.50	2.49	12	1
1:C:29:GLY:O	1:C:31:ARG:CZ	0.50	2.59	2	1
1:C:37:ASN:O	1:C:43:TRP:CG	0.50	2.65	6	1
1:C:43:TRP:CH2	1:C:58:SER:HB2	0.50	2.40	14	1
1:C:13:LEU:HD12	1:C:61:VAL:C	0.50	2.26	16	1
1:C:37:ASN:OD1	1:C:37:ASN:N	0.50	2.43	14	2
1:C:15:ASP:OD1	1:C:15:ASP:N	0.50	2.44	2	4
1:C:37:ASN:HA	1:C:43:TRP:CG	0.50	2.41	2	1
1:C:44:LEU:HD12	1:C:55:TYR:HE1	0.50	1.67	6	2
2:A:71:ALA:O	2:A:72:PHE:CD2	0.50	2.65	8	1
1:C:41:ASP:O	1:C:42:TRP:CG	0.50	2.64	8	5
1:C:14:TYR:HB2	1:C:60:TYR:CD1	0.50	2.42	12	2
1:C:37:ASN:HB2	1:C:43:TRP:CD1	0.50	2.42	6	4
1:C:37:ASN:HB2	1:C:43:TRP:CE2	0.50	2.42	11	1
2:A:71:ALA:C	2:A:72:PHE:CD1	0.50	2.85	5	1
1:C:23:ASP:OD1	2:A:79:ARG:NH2	0.50	2.44	5	1
1:C:16:TYR:CB	1:C:26:PHE:CE1	0.50	2.95	8	1
1:C:16:TYR:CZ	1:C:18:SER:OG	0.50	2.62	1	2
1:C:38:THR:CG2	1:C:39:GLU:N	0.50	2.74	10	2
1:C:16:TYR:CD2	1:C:57:PRO:HD3	0.50	2.42	13	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:33:GLN:N	1:C:33:GLN:CD	0.50	2.65	14	1
1:C:33:GLN:CD	1:C:48:LEU:HD21	0.50	2.26	1	2
1:C:16:TYR:CE2	1:C:18:SER:HB3	0.49	2.42	13	1
2:A:72:PHE:CD1	2:A:72:PHE:N	0.49	2.78	7	1
1:C:16:TYR:HB2	1:C:26:PHE:CE2	0.49	2.42	7	2
1:C:54:GLY:O	1:C:56:ILE:HG23	0.49	2.08	14	3
1:C:44:LEU:CD2	1:C:44:LEU:C	0.49	2.81	7	3
1:C:38:THR:HG23	1:C:39:GLU:H	0.49	1.67	2	1
1:C:34:ILE:HG21	1:C:37:ASN:HB3	0.49	1.83	2	1
2:A:71:ALA:O	2:A:72:PHE:CD1	0.49	2.66	5	1
1:C:16:TYR:HB3	1:C:26:PHE:CD2	0.49	2.43	7	2
1:C:35:VAL:HG21	1:C:44:LEU:HD23	0.49	1.85	15	1
1:C:44:LEU:HD21	1:C:53:THR:OG1	0.49	2.07	14	1
2:A:73:ALA:CB	2:A:74:PRO:HD2	0.49	2.24	8	1
1:C:42:TRP:CD1	2:A:79:ARG:HA	0.48	2.43	1	3
1:C:10:PHE:CE1	1:C:63:PRO:HB3	0.48	2.43	16	1
1:C:14:TYR:CD2	2:A:73:ALA:HB1	0.48	2.43	8	1
1:C:46:HIS:CD2	1:C:47:SER:N	0.48	2.81	14	1
1:C:46:HIS:O	1:C:46:HIS:CD2	0.48	2.66	1	2
1:C:37:ASN:HA	1:C:43:TRP:CE2	0.48	2.42	16	2
1:C:22:THR:OG1	1:C:23:ASP:N	0.48	2.45	13	1
1:C:16:TYR:CD2	1:C:57:PRO:CD	0.48	2.96	13	3
1:C:39:GLU:O	1:C:40:GLY:O	0.48	2.31	14	2
1:C:42:TRP:O	1:C:43:TRP:CD1	0.48	2.66	5	1
1:C:46:HIS:CE1	1:C:47:SER:O	0.48	2.66	12	2
1:C:24:LEU:N	1:C:24:LEU:CD2	0.48	2.77	10	1
1:C:13:LEU:HD12	1:C:62:ALA:HB2	0.48	1.86	12	2
1:C:16:TYR:CD2	1:C:26:PHE:CD2	0.47	3.02	8	1
1:C:16:TYR:CE1	1:C:57:PRO:HD3	0.47	2.43	4	5
1:C:21:GLU:O	1:C:22:THR:C	0.47	2.52	12	2
1:C:38:THR:O	1:C:39:GLU:O	0.47	2.32	12	1
1:C:46:HIS:HD2	1:C:47:SER:N	0.47	2.06	14	1
1:C:33:GLN:HB2	1:C:46:HIS:O	0.47	2.09	14	1
1:C:10:PHE:CZ	1:C:63:PRO:HB3	0.47	2.44	2	1
2:A:77:PRO:O	2:A:78:ARG:C	0.47	2.52	1	5
1:C:46:HIS:CD2	1:C:48:LEU:HD23	0.47	2.44	10	1
1:C:43:TRP:CZ2	1:C:58:SER:HB2	0.47	2.43	6	4
1:C:61:VAL:O	1:C:62:ALA:CB	0.47	2.59	8	1
1:C:33:GLN:O	1:C:34:ILE:O	0.47	2.32	14	1
1:C:44:LEU:CD2	1:C:53:THR:CG2	0.47	2.86	4	1
1:C:51:GLY:O	1:C:52:GLN:O	0.47	2.32	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:44:LEU:HB2	1:C:55:TYR:CE1	0.47	2.45	4	2
1:C:44:LEU:HD12	1:C:55:TYR:N	0.47	2.25	4	1
1:C:34:ILE:CD1	1:C:56:ILE:CD1	0.47	2.93	16	1
1:C:14:TYR:CB	1:C:60:TYR:CD2	0.47	2.97	3	2
1:C:10:PHE:CG	1:C:34:ILE:HG12	0.47	2.45	6	3
1:C:20:THR:HG23	1:C:21:GLU:N	0.47	2.24	7	1
1:C:60:TYR:OH	2:A:74:PRO:O	0.47	2.33	3	5
1:C:10:PHE:CD2	1:C:34:ILE:CG1	0.47	2.98	12	5
1:C:13:LEU:HB2	1:C:14:TYR:CD1	0.47	2.45	2	1
1:C:34:ILE:CG2	1:C:37:ASN:OD1	0.47	2.62	2	1
1:C:42:TRP:CZ3	1:C:57:PRO:HD3	0.47	2.45	2	1
1:C:42:TRP:CZ2	2:A:76:LEU:CD2	0.47	2.96	13	1
2:A:72:PHE:O	2:A:73:ALA:O	0.47	2.32	8	1
1:C:17:GLU:O	1:C:18:SER:O	0.47	2.33	7	2
1:C:34:ILE:CG2	1:C:36:ASN:O	0.47	2.63	16	1
1:C:14:TYR:CE2	1:C:59:ASN:O	0.47	2.68	7	1
1:C:24:LEU:CD1	1:C:53:THR:C	0.47	2.84	8	3
1:C:15:ASP:N	1:C:15:ASP:OD1	0.46	2.46	9	1
1:C:27:LYS:O	1:C:30:GLU:OE1	0.46	2.33	15	1
1:C:33:GLN:HB2	1:C:47:SER:CB	0.46	2.40	14	1
2:A:77:PRO:O	2:A:78:ARG:O	0.46	2.32	7	1
2:A:78:ARG:O	2:A:79:ARG:O	0.46	2.33	14	1
1:C:33:GLN:HG2	1:C:47:SER:CB	0.46	2.39	14	1
1:C:14:TYR:O	1:C:15:ASP:O	0.46	2.33	4	1
1:C:24:LEU:HD12	1:C:53:THR:C	0.46	2.31	16	2
1:C:46:HIS:CE1	1:C:51:GLY:C	0.46	2.89	14	1
1:C:37:ASN:OD1	1:C:43:TRP:CD1	0.46	2.68	7	1
1:C:57:PRO:HG2	1:C:60:TYR:CD2	0.46	2.46	14	2
1:C:9:THR:O	1:C:64:SER:O	0.46	2.34	6	1
1:C:37:ASN:O	1:C:43:TRP:NE1	0.46	2.49	14	1
1:C:13:LEU:O	1:C:28:LYS:HD2	0.46	2.11	15	1
1:C:27:LYS:O	1:C:30:GLU:OE2	0.46	2.34	15	1
1:C:35:VAL:CB	1:C:44:LEU:O	0.46	2.64	2	2
1:C:35:VAL:HB	1:C:44:LEU:O	0.46	2.11	2	11
1:C:20:THR:HG22	1:C:22:THR:HG22	0.46	1.87	11	1
2:A:78:ARG:O	2:A:79:ARG:OXT	0.46	2.34	6	3
1:C:58:SER:O	1:C:58:SER:OG	0.45	2.33	11	1
1:C:42:TRP:CE3	1:C:57:PRO:HA	0.45	2.46	1	2
1:C:44:LEU:HD12	1:C:55:TYR:HD1	0.45	1.70	15	1
1:C:16:TYR:OH	1:C:23:ASP:OD2	0.45	2.34	5	2
1:C:17:GLU:O	1:C:18:SER:C	0.45	2.55	14	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:13:LEU:CB	1:C:14:TYR:CE1	0.45	3.00	11	2
1:C:37:ASN:C	1:C:38:THR:HG22	0.45	2.31	12	1
1:C:44:LEU:HD11	1:C:53:THR:HG21	0.45	1.87	14	1
1:C:43:TRP:CD1	1:C:43:TRP:N	0.45	2.83	4	1
1:C:24:LEU:HD23	1:C:54:GLY:HA2	0.45	1.88	10	1
1:C:13:LEU:HB2	1:C:14:TYR:CE1	0.45	2.46	2	1
1:C:16:TYR:CD2	1:C:25:SER:HA	0.45	2.47	8	1
2:A:71:ALA:O	2:A:72:PHE:O	0.45	2.35	7	1
1:C:24:LEU:HD23	1:C:54:GLY:CA	0.45	2.42	10	1
1:C:54:GLY:O	1:C:56:ILE:N	0.45	2.50	14	1
1:C:57:PRO:O	1:C:61:VAL:HG12	0.45	2.12	14	3
1:C:26:PHE:CE2	1:C:56:ILE:CB	0.45	3.00	14	1
1:C:44:LEU:HD11	1:C:55:TYR:CE1	0.45	2.46	16	1
1:C:36:ASN:C	1:C:37:ASN:CG	0.45	2.75	2	1
1:C:44:LEU:HD13	1:C:55:TYR:CG	0.44	2.47	11	1
2:A:72:PHE:O	2:A:73:ALA:C	0.44	2.55	7	4
1:C:16:TYR:CZ	1:C:18:SER:HB2	0.44	2.47	10	2
1:C:13:LEU:C	1:C:14:TYR:CG	0.44	2.91	11	2
1:C:40:GLY:O	1:C:41:ASP:C	0.44	2.55	2	1
1:C:16:TYR:CG	1:C:57:PRO:CG	0.44	3.00	13	1
1:C:36:ASN:C	1:C:37:ASN:OD1	0.44	2.56	2	1
1:C:10:PHE:CE2	1:C:34:ILE:HG13	0.44	2.48	3	3
1:C:56:ILE:CD1	1:C:56:ILE:O	0.44	2.60	14	1
1:C:36:ASN:O	1:C:37:ASN:CG	0.44	2.56	2	1
1:C:37:ASN:C	1:C:38:THR:CG2	0.44	2.86	12	1
1:C:33:GLN:O	1:C:34:ILE:C	0.44	2.56	4	5
1:C:13:LEU:O	1:C:14:TYR:CG	0.44	2.71	11	1
1:C:56:ILE:HD13	1:C:56:ILE:N	0.44	2.27	8	1
1:C:18:SER:OG	1:C:25:SER:N	0.44	2.50	14	1
1:C:33:GLN:OE1	1:C:48:LEU:CD2	0.44	2.64	8	1
1:C:56:ILE:CD1	1:C:57:PRO:O	0.44	2.65	4	1
1:C:44:LEU:C	1:C:44:LEU:CD2	0.44	2.82	3	2
1:C:37:ASN:O	1:C:39:GLU:O	0.44	2.36	2	1
1:C:16:TYR:CZ	1:C:42:TRP:CH2	0.44	3.06	2	1
1:C:15:ASP:OD1	1:C:27:LYS:CB	0.44	2.66	8	1
1:C:44:LEU:O	1:C:44:LEU:CD2	0.44	2.64	10	1
1:C:49:THR:CG2	1:C:50:THR:N	0.44	2.76	13	2
1:C:38:THR:OG1	1:C:39:GLU:N	0.44	2.49	16	1
1:C:41:ASP:OD2	2:A:77:PRO:HG3	0.44	2.13	7	1
1:C:18:SER:OG	1:C:24:LEU:C	0.43	2.56	15	1
1:C:20:THR:OG1	1:C:21:GLU:OE2	0.43	2.35	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:16:TYR:CE1	1:C:57:PRO:CG	0.43	3.01	8	2
1:C:15:ASP:OD1	1:C:26:PHE:O	0.43	2.36	7	1
1:C:32:LEU:HD12	1:C:32:LEU:N	0.43	2.28	8	3
1:C:57:PRO:HB3	2:A:76:LEU:HD21	0.43	1.89	13	1
1:C:31:ARG:C	1:C:32:LEU:HD12	0.43	2.33	1	2
1:C:41:ASP:O	1:C:58:SER:HB3	0.43	2.14	5	1
1:C:18:SER:CB	1:C:23:ASP:HB2	0.43	2.43	13	1
1:C:48:LEU:HD23	1:C:48:LEU:H	0.43	1.73	14	1
1:C:13:LEU:CD1	1:C:62:ALA:N	0.43	2.82	16	1
1:C:60:TYR:CD1	1:C:60:TYR:N	0.43	2.86	12	1
1:C:23:ASP:OD1	1:C:55:TYR:CD2	0.43	2.71	8	1
1:C:46:HIS:O	1:C:47:SER:OG	0.43	2.33	14	1
1:C:33:GLN:HB2	1:C:47:SER:HB2	0.43	1.91	14	1
2:A:75:PRO:O	2:A:76:LEU:C	0.43	2.57	1	3
1:C:46:HIS:C	1:C:46:HIS:CD2	0.43	2.92	1	2
1:C:37:ASN:HA	1:C:43:TRP:NE1	0.43	2.29	10	1
2:A:78:ARG:O	2:A:79:ARG:C	0.43	2.57	5	3
1:C:46:HIS:CD2	1:C:46:HIS:C	0.43	2.92	9	1
1:C:51:GLY:O	1:C:52:GLN:HG2	0.43	2.12	2	1
1:C:40:GLY:O	1:C:41:ASP:CG	0.43	2.57	12	2
1:C:40:GLY:C	1:C:41:ASP:OD1	0.43	2.57	5	1
1:C:41:ASP:O	1:C:58:SER:CB	0.43	2.67	5	1
1:C:36:ASN:O	1:C:37:ASN:HB2	0.43	2.14	14	1
1:C:37:ASN:ND2	1:C:43:TRP:CE3	0.43	2.87	3	1
1:C:41:ASP:O	1:C:58:SER:OG	0.42	2.37	4	1
1:C:59:ASN:O	1:C:60:TYR:CD1	0.42	2.72	5	1
1:C:47:SER:N	1:C:51:GLY:O	0.42	2.52	15	1
1:C:37:ASN:HB2	1:C:43:TRP:NE1	0.42	2.29	11	1
1:C:33:GLN:HB2	1:C:47:SER:OG	0.42	2.15	14	1
1:C:17:GLU:O	1:C:19:ARG:N	0.42	2.52	14	1
2:A:71:ALA:O	2:A:72:PHE:HB2	0.42	2.14	8	1
1:C:36:ASN:OD1	1:C:38:THR:HG22	0.42	2.15	8	1
1:C:24:LEU:CD2	1:C:52:GLN:HB3	0.42	2.44	14	1
1:C:36:ASN:O	1:C:37:ASN:C	0.42	2.57	4	1
1:C:45:ALA:HB2	1:C:56:ILE:CG2	0.42	2.45	16	1
1:C:10:PHE:CD1	1:C:63:PRO:HA	0.42	2.49	16	1
1:C:48:LEU:O	1:C:49:THR:C	0.42	2.58	15	2
1:C:17:GLU:N	1:C:17:GLU:CD	0.42	2.73	4	1
1:C:12:ALA:O	1:C:28:LYS:HG2	0.42	2.14	14	1
1:C:24:LEU:N	1:C:24:LEU:HD12	0.42	2.30	14	2
1:C:24:LEU:O	1:C:25:SER:C	0.42	2.57	8	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:71:ALA:O	2:A:72:PHE:C	0.42	2.57	2	1
1:C:14:TYR:CD2	2:A:73:ALA:CB	0.42	3.03	8	1
1:C:44:LEU:CD2	1:C:53:THR:HG21	0.41	2.42	11	1
1:C:23:ASP:OD1	1:C:23:ASP:N	0.41	2.51	1	1
1:C:47:SER:O	1:C:49:THR:N	0.41	2.53	10	1
1:C:13:LEU:HD12	1:C:61:VAL:CA	0.41	2.45	16	1
1:C:30:GLU:HG3	1:C:31:ARG:N	0.41	2.30	12	1
1:C:42:TRP:NE1	2:A:79:ARG:HB3	0.41	2.29	13	1
1:C:16:TYR:N	1:C:26:PHE:O	0.41	2.53	8	1
1:C:56:ILE:CD1	1:C:56:ILE:H	0.41	2.28	8	1
1:C:42:TRP:CD1	2:A:79:ARG:HG2	0.41	2.50	2	1
1:C:20:THR:HG23	1:C:22:THR:H	0.41	1.75	2	1
1:C:57:PRO:O	1:C:58:SER:C	0.41	2.56	1	2
1:C:44:LEU:HD12	1:C:55:TYR:CA	0.41	2.45	4	1
1:C:41:ASP:C	1:C:58:SER:OG	0.41	2.58	4	1
1:C:21:GLU:HG2	1:C:22:THR:N	0.41	2.29	2	1
1:C:56:ILE:N	1:C:56:ILE:CD1	0.41	2.83	2	1
1:C:10:PHE:CD1	1:C:34:ILE:HG13	0.41	2.51	12	1
1:C:24:LEU:HD11	1:C:53:THR:N	0.41	2.30	13	1
1:C:45:ALA:CB	1:C:56:ILE:HG12	0.41	2.45	3	1
1:C:15:ASP:OD1	1:C:15:ASP:C	0.41	2.59	7	1
1:C:22:THR:C	1:C:23:ASP:OD1	0.41	2.59	7	1
1:C:42:TRP:CZ3	1:C:56:ILE:C	0.41	2.94	7	2
1:C:63:PRO:O	1:C:64:SER:C	0.41	2.57	3	1
1:C:18:SER:HB3	1:C:24:LEU:O	0.41	2.16	15	1
1:C:47:SER:O	1:C:48:LEU:HD23	0.41	2.16	3	1
1:C:56:ILE:O	1:C:56:ILE:HD12	0.41	2.15	4	1
1:C:11:VAL:O	1:C:61:VAL:HA	0.41	2.16	8	1
1:C:42:TRP:CH2	2:A:76:LEU:HD22	0.41	2.51	8	3
1:C:19:ARG:O	1:C:20:THR:HB	0.41	2.15	5	1
1:C:59:ASN:OD1	2:A:74:PRO:HG2	0.40	2.16	1	2
1:C:53:THR:HG22	1:C:53:THR:O	0.40	2.16	15	1
1:C:46:HIS:CE1	1:C:51:GLY:CA	0.40	3.05	10	1
1:C:26:PHE:CG	1:C:26:PHE:O	0.40	2.74	12	1
1:C:20:THR:OG1	1:C:21:GLU:N	0.40	2.54	3	1
1:C:33:GLN:CG	1:C:47:SER:CB	0.40	2.99	14	1
2:A:73:ALA:O	2:A:75:PRO:HD3	0.40	2.16	1	2
1:C:42:TRP:CZ3	1:C:57:PRO:CA	0.40	3.04	15	1
1:C:63:PRO:O	1:C:64:SER:HB3	0.40	2.15	2	1
1:C:57:PRO:HB3	2:A:76:LEU:CD2	0.40	2.46	8	1
1:C:16:TYR:CE1	1:C:57:PRO:CD	0.40	3.04	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:36:ASN:O	1:C:43:TRP:HB3	0.40	2.17	10	1
1:C:35:VAL:O	1:C:36:ASN:HB2	0.40	2.16	14	1
1:C:46:HIS:NE2	1:C:52:GLN:N	0.40	2.69	14	1
1:C:31:ARG:O	1:C:32:LEU:HG	0.40	2.17	15	1
1:C:44:LEU:HB2	1:C:55:TYR:CD1	0.40	2.51	15	1
1:C:63:PRO:O	1:C:64:SER:HB2	0.40	2.17	5	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	C	54/64 (84%)	41±2 (77±4%)	9±2 (17±3%)	4±2 (6±3%)	3	19
2	A	7/9 (78%)	5±1 (72±15%)	1±1 (20±16%)	1±1 (8±12%)	2	14
All	All	976/1168 (84%)	743 (76%)	168 (17%)	65 (7%)	3	18

All 24 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	C	37	ASN	7
1	C	38	THR	6
1	C	18	SER	6
1	C	49	THR	4
1	C	39	GLU	3
1	C	51	GLY	3
1	C	34	ILE	3
1	C	40	GLY	3
2	A	77	PRO	3
2	A	72	PHE	3
1	C	55	TYR	3
1	C	41	ASP	2
2	A	78	ARG	2
1	C	36	ASN	2
1	C	60	TYR	2

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Mol	Chain	Res	Type	Models (Total)
1	C	22	THR	2
1	C	15	ASP	2
1	C	52	GLN	2
1	C	47	SER	2
1	C	62	ALA	1
1	C	48	LEU	1
1	C	21	GLU	1
1	C	23	ASP	1
2	A	73	ALA	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	C	49/52 (94%)	36±2 (73±4%)	13±2 (27±4%)	2	22
2	A	7/7 (100%)	6±1 (83±14%)	1±1 (17±14%)	6	41
All	All	896/944 (95%)	665 (74%)	231 (26%)	2	24

All 41 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	C	25	SER	16
1	C	9	THR	12
1	C	58	SER	12
1	C	23	ASP	11
1	C	41	ASP	10
1	C	39	GLU	10
1	C	21	GLU	9
1	C	53	THR	8
1	C	31	ARG	8
1	C	27	LYS	7
2	A	72	PHE	7
1	C	33	GLN	7
1	C	50	THR	6
1	C	18	SER	6
2	A	79	ARG	6

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Mol	Chain	Res	Type	Models (Total)
1	C	15	ASP	6
1	C	64	SER	6
1	C	59	ASN	6
2	A	78	ARG	5
1	C	19	ARG	5
1	C	36	ASN	5
1	C	14	TYR	5
1	C	24	LEU	5
1	C	49	THR	5
1	C	52	GLN	5
1	C	20	THR	5
1	C	61	VAL	5
1	C	37	ASN	4
1	C	22	THR	4
1	C	17	GLU	4
1	C	28	LYS	3
1	C	38	THR	3
1	C	32	LEU	3
1	C	46	HIS	2
1	C	30	GLU	2
1	C	56	ILE	2
1	C	47	SER	2
1	C	48	LEU	1
1	C	63	PRO	1
2	A	76	LEU	1
1	C	44	LEU	1

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.6 Ligand geometry

There are no ligands in this entry.

## 6.7 Other polymers

There are no such molecules in this entry.

## 6.8 Polymer linkage issues

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided