



Full wwPDB NMR Structure Validation Report ⓘ

Mar 1, 2026 – 09:40 PM UTC

PDB ID : 2PON / pdb_00002pon
Title : Solution structure of the Bcl-xL/Beclin-1 complex
Authors : Feng, W.; Huang, S.; Wu, H.; Zhang, M.
Deposited on : 2007-04-27

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

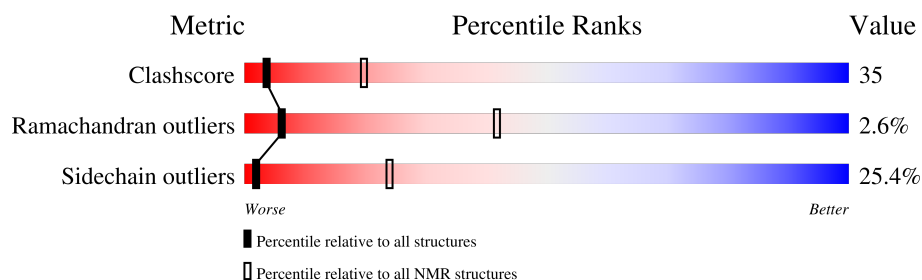
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	23	
2	B	156	

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 18 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:23-A:39, B:60-B:83, B:99-B:212 (155)	0.47	4

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 5 clusters and 5 single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2796 atoms, of which 1360 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Beclin-1.

Mol	Chain	Residues	Atoms						Trace
1	A	23	Total	C	H	N	O	S	0
			347	105	175	31	34	2	

- Molecule 2 is a protein called Apoptosis regulator Bcl-X.

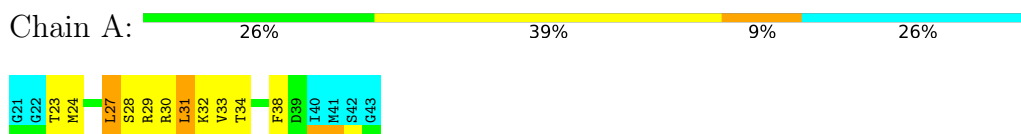
Mol	Chain	Residues	Atoms						Trace
2	B	156	Total	C	H	N	O	S	0
			2449	800	1185	211	249	4	

4 Residue-property plots

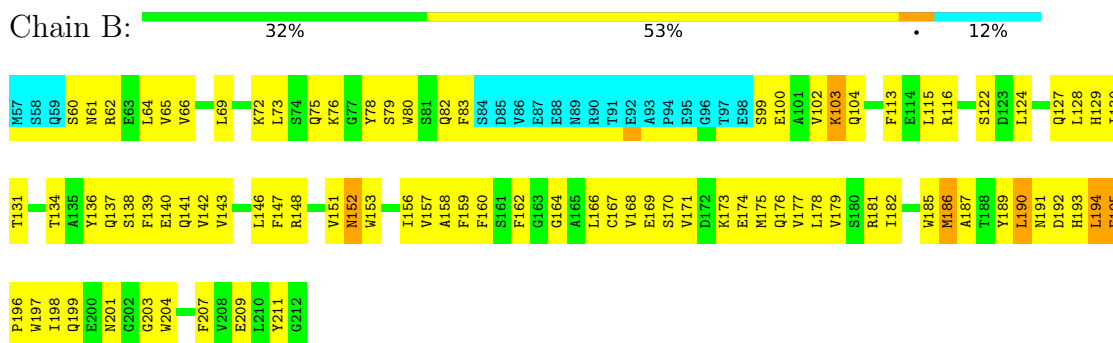
4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Beclin-1



- Molecule 2: Apoptosis regulator Bcl-X



4.2 Scores per residue for each member of the ensemble

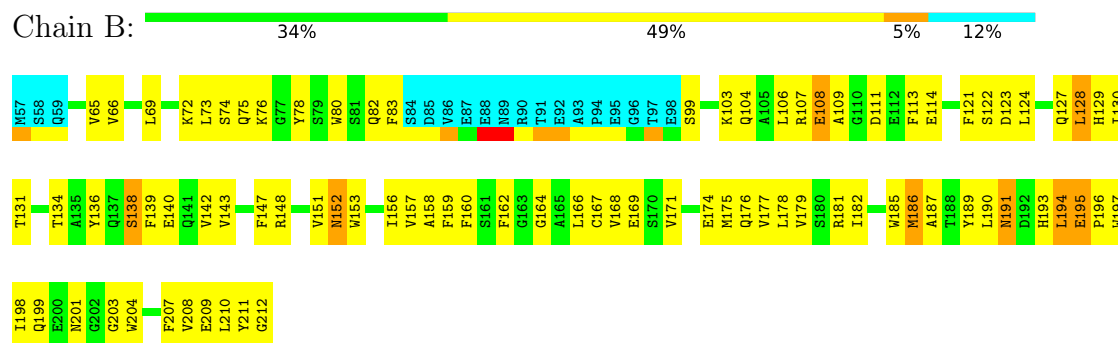
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Beclin-1

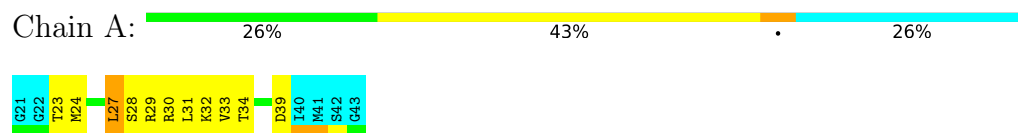


- Molecule 2: Apoptosis regulator Bcl-X

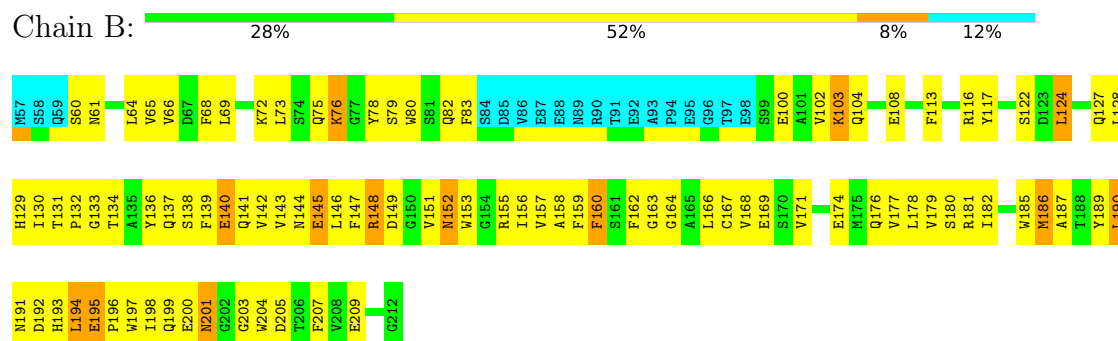


4.2.2 Score per residue for model 2

- Molecule 1: Beclin-1

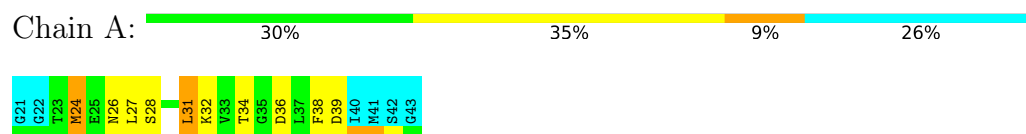


- Molecule 2: Apoptosis regulator Bcl-X

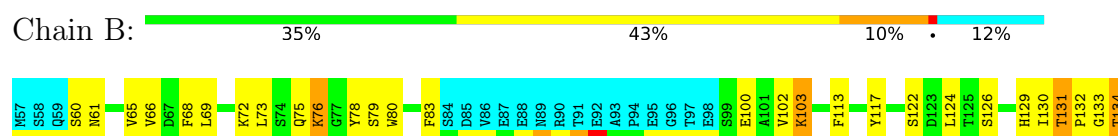


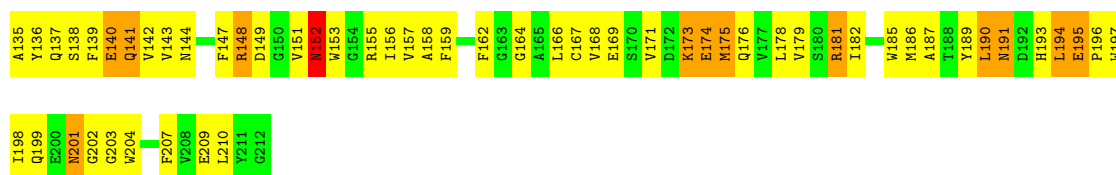
4.2.3 Score per residue for model 3

- Molecule 1: Beclin-1



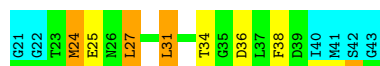
- Molecule 2: Apoptosis regulator Bcl-X



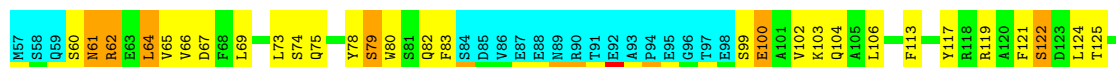


4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Beclin-1

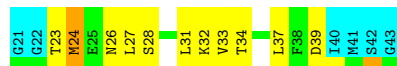


- Molecule 2: Apoptosis regulator Bcl-X



4.2.5 Score per residue for model 5

- Molecule 1: Beclin-1

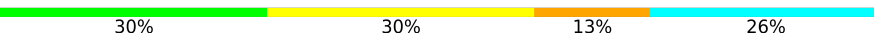


- Molecule 2: Apoptosis regulator Bcl-X



4.2.6 Score per residue for model 6

- Molecule 1: Beclin-1

Chain A: 



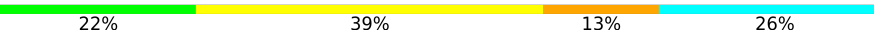
- Molecule 2: Apoptosis regulator Bcl-X

Chain B: 



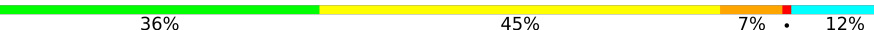
4.2.7 Score per residue for model 7

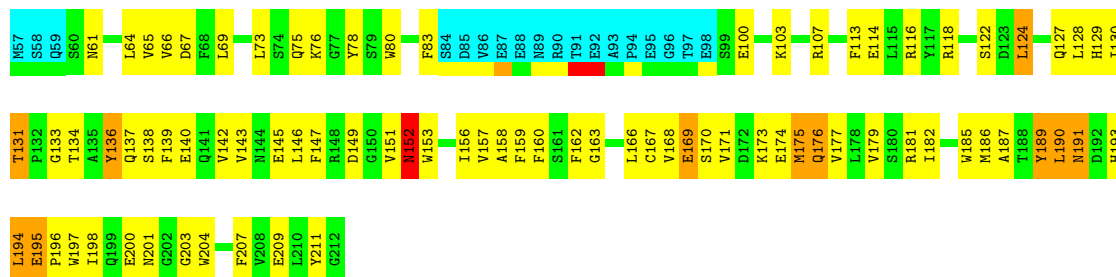
- Molecule 1: Beclin-1

Chain A: 



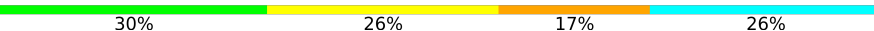
- Molecule 2: Apoptosis regulator Bcl-X

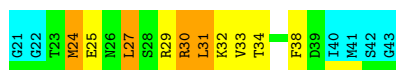
Chain B: 



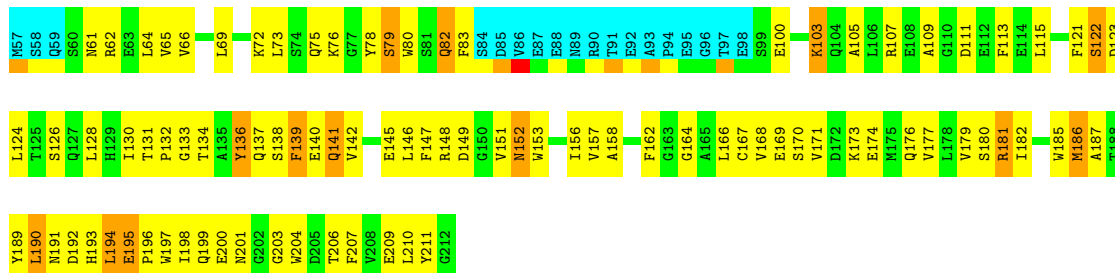
4.2.8 Score per residue for model 8

- Molecule 1: Beclin-1

Chain A: 

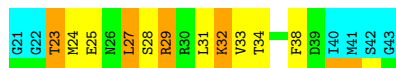
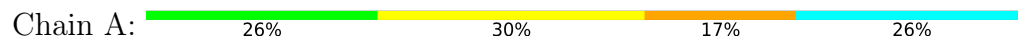


- Molecule 2: Apoptosis regulator Bcl-X



4.2.9 Score per residue for model 9

- Molecule 1: Beclin-1

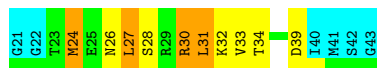
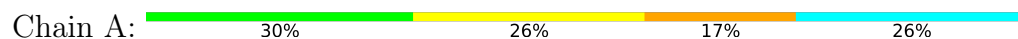


- Molecule 2: Apoptosis regulator Bcl-X

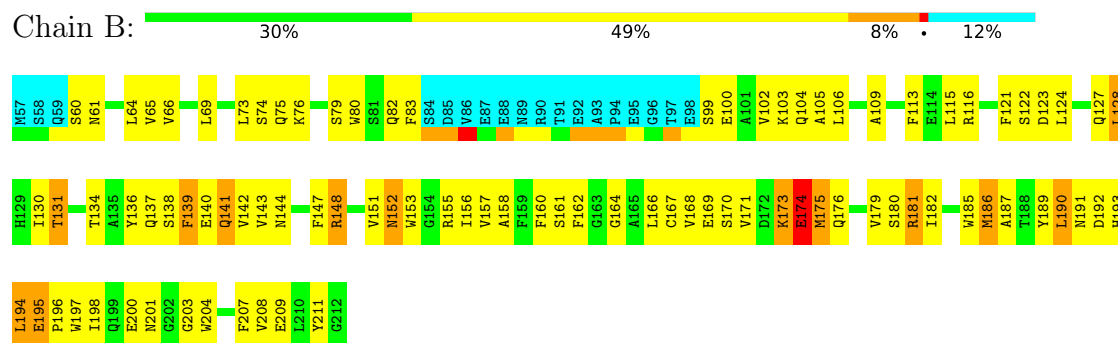


4.2.10 Score per residue for model 10

- Molecule 1: Beclin-1

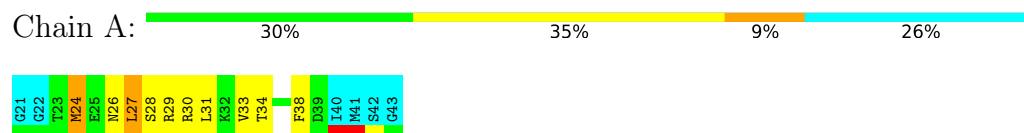


- Molecule 2: Apoptosis regulator Bcl-X

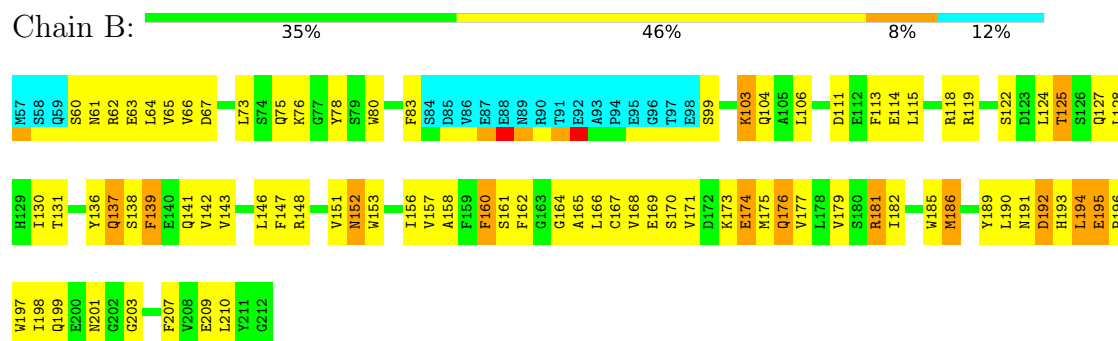


4.2.11 Score per residue for model 11

- Molecule 1: Beclin-1

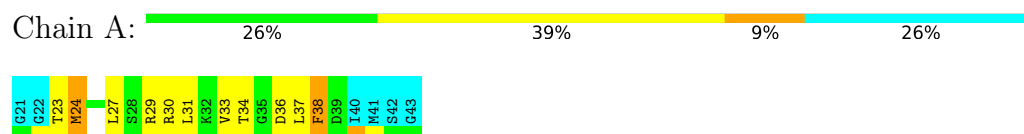


- Molecule 2: Apoptosis regulator Bcl-X

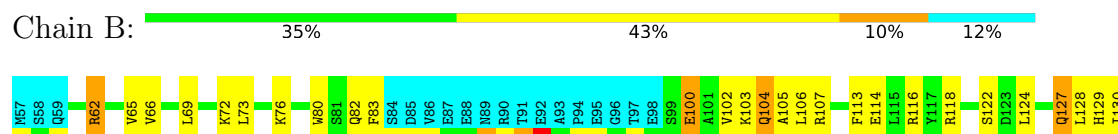


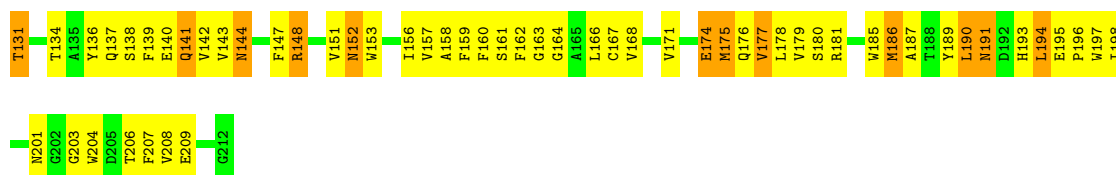
4.2.12 Score per residue for model 12

- Molecule 1: Beclin-1



- Molecule 2: Apoptosis regulator Bcl-X





4.2.13 Score per residue for model 13

- Molecule 1: Beclin-1

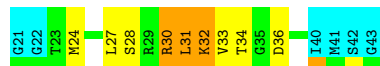


- Molecule 2: Apoptosis regulator Bcl-X

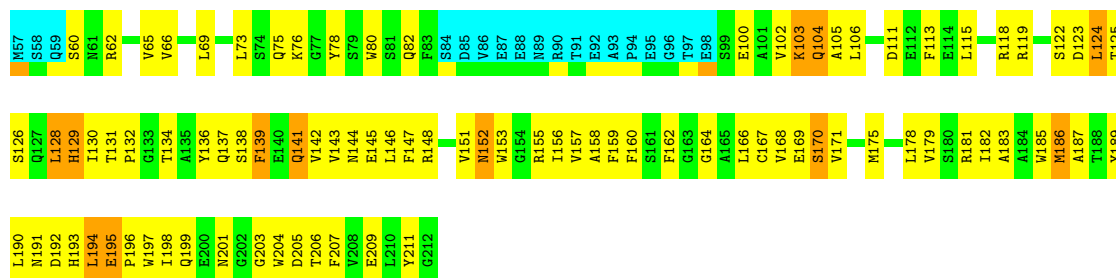


4.2.14 Score per residue for model 14

- Molecule 1: Beclin-1

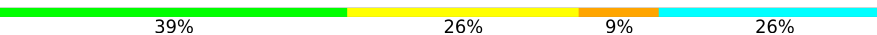


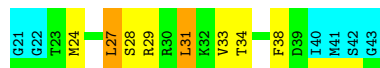
- Molecule 2: Apoptosis regulator Bcl-X



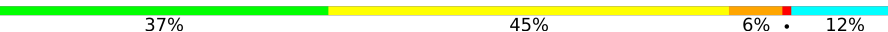
4.2.15 Score per residue for model 15

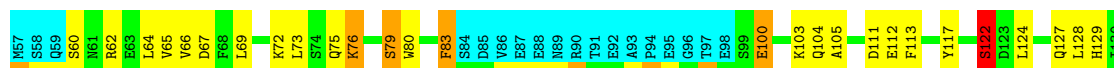
- Molecule 1: Beclin-1

Chain A: 



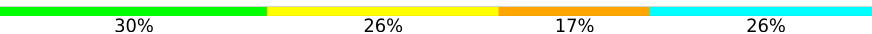
- Molecule 2: Apoptosis regulator Bcl-X

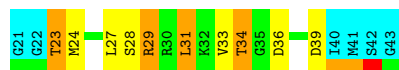
Chain B: 



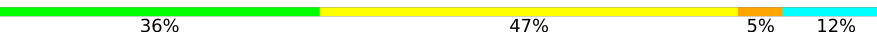
4.2.16 Score per residue for model 16

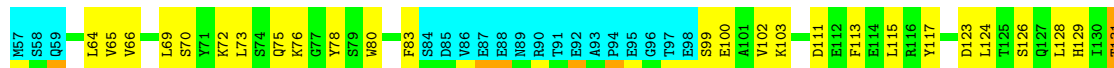
- Molecule 1: Beclin-1

Chain A: 



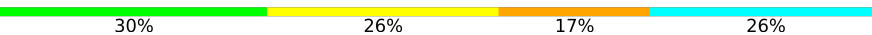
- Molecule 2: Apoptosis regulator Bcl-X

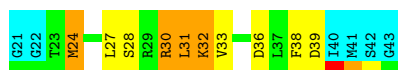
Chain B: 



4.2.17 Score per residue for model 17

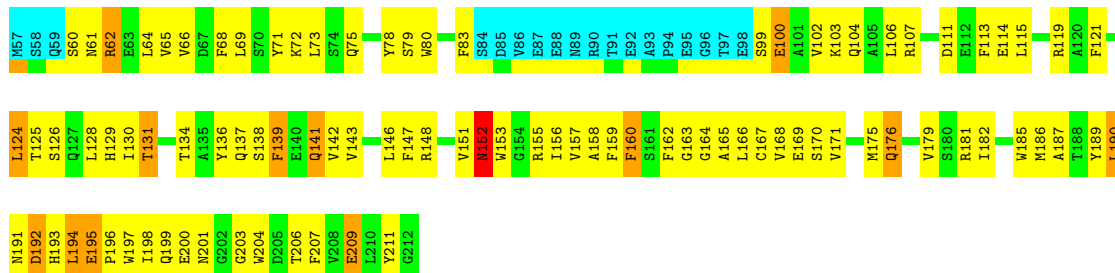
- Molecule 1: Beclin-1

Chain A: 



- Molecule 2: Apoptosis regulator Bcl-X

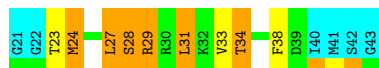
Chain B: 29% 51% 8% 12%



4.2.18 Score per residue for model 18

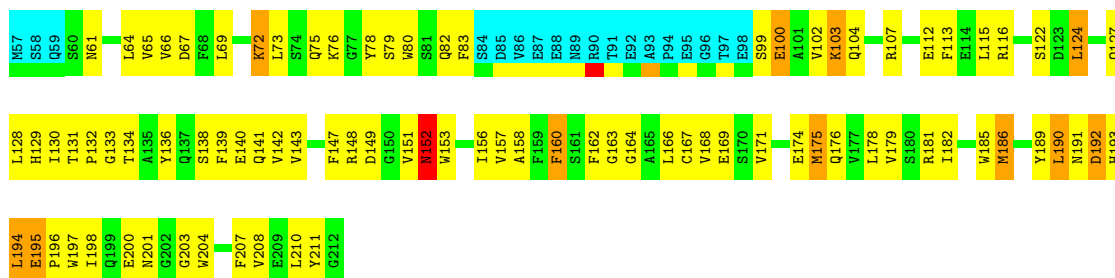
- Molecule 1: Beclin-1

Chain A: 35% 13% 26% 26%



- Molecule 2: Apoptosis regulator Bcl-X

Chain B: 33% 48% 7% 12%



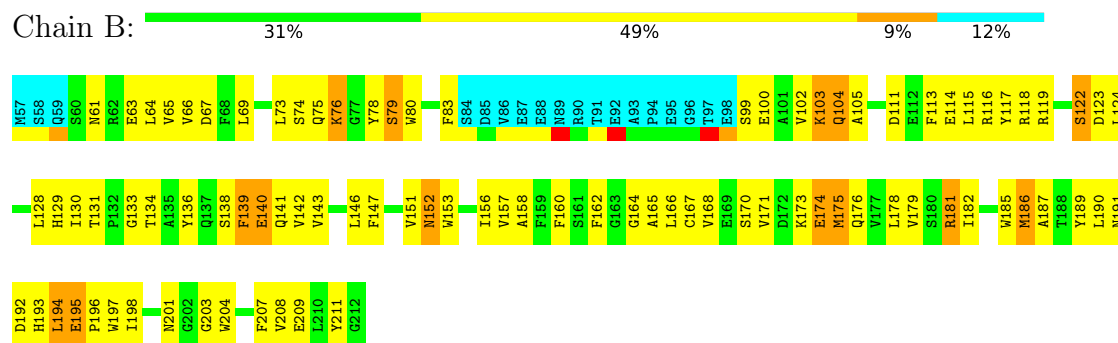
4.2.19 Score per residue for model 19

- Molecule 1: Beclin-1

Chain A: 39% 17% 17% 26%

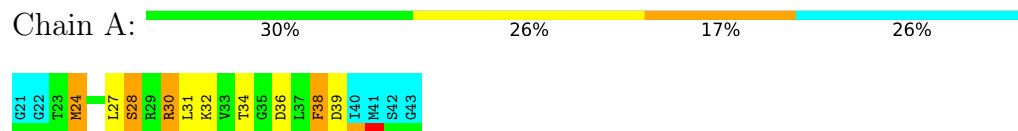


- Molecule 2: Apoptosis regulator Bcl-X

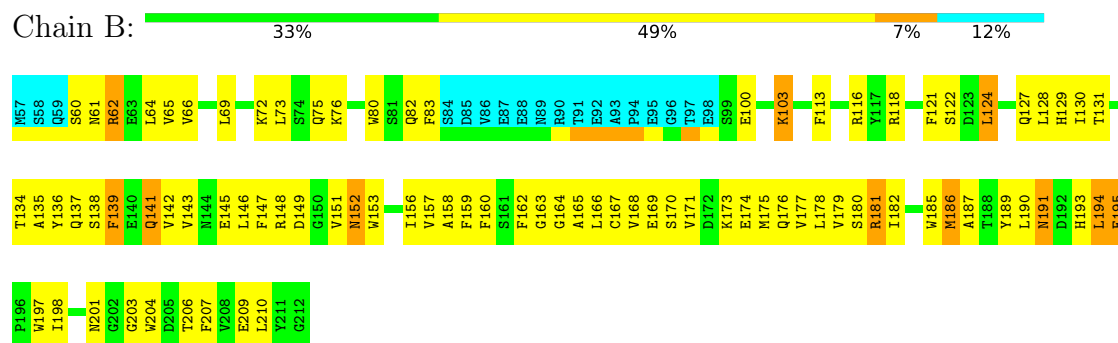


4.2.20 Score per residue for model 20

- Molecule 1: Beclin-1



- Molecule 2: Apoptosis regulator Bcl-X



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.

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	138	141	141	9±3
2	B	1126	1067	1065	84±8
All	All	25280	24160	24120	1729

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 35.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:66:VAL:HG13	2:B:80:TRP:CE2	0.90	2.02	10	20
1:A:31:LEU:HD13	2:B:158:ALA:HB1	0.89	1.42	12	6
2:B:83:PHE:CE1	2:B:179:VAL:HG11	0.87	2.03	3	15
2:B:66:VAL:HG13	2:B:80:TRP:CZ2	0.87	2.04	18	14
2:B:73:LEU:HD23	2:B:168:VAL:HG22	0.87	1.45	10	20
2:B:162:PHE:CE2	2:B:166:LEU:HD11	0.85	2.06	12	11
2:B:153:TRP:O	2:B:157:VAL:HG23	0.84	1.73	4	20
2:B:113:PHE:CE2	2:B:158:ALA:HB2	0.82	2.10	16	2
2:B:162:PHE:CZ	2:B:166:LEU:HD11	0.81	2.09	9	9
2:B:160:PHE:CD1	2:B:186:MET:HE1	0.81	2.10	2	7
2:B:167:CYS:O	2:B:171:VAL:HG23	0.80	1.76	13	20
2:B:198:ILE:HG22	2:B:203:GLY:HA2	0.80	1.53	3	20
2:B:125:THR:HG23	2:B:165:ALA:HB1	0.79	1.54	11	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:MET:HE3	2:B:138:SER:OG	0.79	1.78	15	4
2:B:138:SER:O	2:B:142:VAL:HG23	0.79	1.78	19	19
2:B:128:LEU:HD13	2:B:166:LEU:HD23	0.79	1.53	11	3
2:B:139:PHE:O	2:B:143:VAL:HG23	0.79	1.78	3	6
1:A:23:THR:HG21	2:B:129:HIS:CD2	0.78	2.12	16	1
1:A:29:ARG:O	1:A:33:VAL:HG23	0.78	1.77	18	9
2:B:159:PHE:CD2	2:B:194:LEU:HD11	0.78	2.13	20	4
1:A:27:LEU:HD11	2:B:124:LEU:HD23	0.77	1.57	2	1
2:B:65:VAL:HG21	2:B:187:ALA:CB	0.76	2.09	2	11
2:B:164:GLY:O	2:B:168:VAL:HG23	0.76	1.81	6	19
1:A:27:LEU:HD22	2:B:162:PHE:CE1	0.75	2.16	4	2
2:B:78:TYR:CE2	2:B:168:VAL:HG13	0.75	2.16	7	14
1:A:27:LEU:HD21	2:B:124:LEU:HD11	0.75	1.57	4	3
2:B:142:VAL:HG21	2:B:162:PHE:CZ	0.75	2.16	4	8
2:B:156:ILE:HD13	2:B:198:ILE:HD11	0.74	1.58	8	20
2:B:190:LEU:HD13	2:B:194:LEU:HD12	0.74	1.59	11	5
2:B:83:PHE:CE1	2:B:179:VAL:HG21	0.73	2.18	16	5
1:A:24:MET:HE2	2:B:138:SER:OG	0.72	1.83	5	1
2:B:171:VAL:HG13	2:B:176:GLN:HG3	0.72	1.61	8	5
2:B:66:VAL:HG13	2:B:80:TRP:NE1	0.72	1.99	1	17
2:B:151:VAL:HG13	2:B:197:TRP:CD1	0.72	2.20	18	16
2:B:65:VAL:HG21	2:B:187:ALA:HB2	0.72	1.60	2	3
2:B:113:PHE:CE1	2:B:158:ALA:HB2	0.71	2.20	6	1
2:B:193:HIS:CD2	2:B:194:LEU:HD23	0.71	2.20	9	1
2:B:190:LEU:HD12	2:B:190:LEU:O	0.71	1.86	2	12
2:B:190:LEU:CD1	2:B:194:LEU:HD12	0.71	2.16	11	5
1:A:27:LEU:HD23	1:A:31:LEU:HD21	0.70	1.63	1	2
2:B:175:MET:HG3	2:B:178:LEU:HD12	0.70	1.63	18	4
2:B:194:LEU:HD12	2:B:198:ILE:HD11	0.70	1.61	1	1
2:B:130:ILE:O	2:B:175:MET:HE1	0.70	1.86	5	13
2:B:61:ASN:O	2:B:65:VAL:HG23	0.70	1.87	11	14
2:B:124:LEU:HD11	2:B:165:ALA:CB	0.70	2.15	11	2
2:B:65:VAL:HG21	2:B:187:ALA:HA	0.70	1.64	13	11
2:B:176:GLN:O	2:B:179:VAL:HG23	0.70	1.86	11	18
2:B:128:LEU:HD12	2:B:129:HIS:N	0.70	2.02	18	6
2:B:124:LEU:HD12	2:B:165:ALA:CB	0.70	2.17	20	1
2:B:162:PHE:CE1	2:B:166:LEU:HD21	0.69	2.23	5	7
2:B:65:VAL:HG13	2:B:186:MET:HE3	0.69	1.64	5	7
2:B:61:ASN:HA	2:B:64:LEU:HD12	0.69	1.62	5	11
2:B:162:PHE:CZ	2:B:166:LEU:HD21	0.69	2.22	6	8
2:B:146:LEU:HD21	2:B:155:ARG:O	0.68	1.89	4	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:147:PHE:CE2	2:B:151:VAL:HG23	0.67	2.24	19	12
2:B:124:LEU:HD12	2:B:165:ALA:HB3	0.67	1.65	20	1
2:B:106:LEU:HD13	2:B:160:PHE:CE2	0.67	2.24	4	2
1:A:24:MET:HE2	2:B:138:SER:CB	0.67	2.19	8	10
2:B:175:MET:CB	2:B:178:LEU:HD12	0.66	2.21	1	1
2:B:102:VAL:HG13	2:B:204:TRP:HB3	0.66	1.67	12	7
1:A:31:LEU:HD13	2:B:158:ALA:CB	0.66	2.18	12	2
2:B:175:MET:HB2	2:B:178:LEU:HD12	0.66	1.68	1	1
1:A:24:MET:HE2	2:B:138:SER:HB3	0.66	1.68	4	9
2:B:64:LEU:HD23	2:B:103:LYS:HG3	0.66	1.65	5	4
2:B:156:ILE:HG12	2:B:194:LEU:HD13	0.66	1.68	8	2
2:B:153:TRP:CH2	2:B:207:PHE:HB2	0.65	2.27	16	20
1:A:31:LEU:HB3	2:B:158:ALA:HB1	0.65	1.68	1	8
2:B:73:LEU:CD2	2:B:168:VAL:HG22	0.65	2.22	19	17
2:B:115:LEU:HD21	2:B:119:ARG:CZ	0.65	2.22	14	1
2:B:156:ILE:HD13	2:B:198:ILE:CD1	0.64	2.22	17	12
2:B:111:ASP:O	2:B:115:LEU:HD23	0.64	1.92	17	1
2:B:130:ILE:HG22	2:B:138:SER:OG	0.64	1.92	1	8
2:B:147:PHE:CE2	2:B:194:LEU:HD22	0.64	2.27	13	4
2:B:194:LEU:CD1	2:B:198:ILE:HD11	0.64	2.22	1	1
2:B:83:PHE:CD1	2:B:179:VAL:HG11	0.64	2.28	18	2
2:B:65:VAL:HG12	2:B:69:LEU:HD12	0.64	1.70	8	13
2:B:160:PHE:CD1	2:B:186:MET:HE3	0.63	2.28	4	2
1:A:30:ARG:O	1:A:33:VAL:HG12	0.63	1.94	2	5
2:B:139:PHE:O	2:B:143:VAL:HG12	0.63	1.94	5	8
2:B:171:VAL:HG13	2:B:176:GLN:HB3	0.62	1.70	11	2
2:B:131:THR:HA	2:B:175:MET:HE1	0.62	1.71	19	11
2:B:76:LYS:HG3	2:B:168:VAL:HG21	0.62	1.70	18	11
2:B:175:MET:HB3	2:B:178:LEU:HD12	0.62	1.72	14	1
2:B:147:PHE:CD1	2:B:151:VAL:HG13	0.62	2.30	9	1
1:A:24:MET:HE2	2:B:138:SER:HB2	0.61	1.71	8	4
1:A:31:LEU:CD1	2:B:146:LEU:HD22	0.61	2.24	5	3
2:B:78:TYR:CD1	2:B:171:VAL:HG11	0.61	2.30	7	5
1:A:23:THR:HG22	2:B:128:LEU:HA	0.61	1.72	2	5
2:B:177:VAL:HG22	2:B:181:ARG:CD	0.61	2.26	9	5
1:A:27:LEU:HD11	2:B:124:LEU:CD2	0.61	2.25	3	2
2:B:124:LEU:HD23	2:B:128:LEU:HG	0.60	1.72	14	1
1:A:28:SER:HB3	2:B:142:VAL:HG13	0.60	1.72	11	2
2:B:65:VAL:HG13	2:B:186:MET:SD	0.60	2.37	17	1
1:A:27:LEU:HD12	1:A:28:SER:N	0.60	2.11	14	1
2:B:175:MET:CG	2:B:178:LEU:HD12	0.60	2.27	18	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:64:LEU:HD23	2:B:103:LYS:HB3	0.59	1.74	19	7
2:B:65:VAL:HG12	2:B:69:LEU:CD1	0.59	2.28	6	13
2:B:146:LEU:HD21	2:B:158:ALA:HB3	0.59	1.74	8	6
1:A:27:LEU:HD21	2:B:124:LEU:CD1	0.59	2.27	8	2
1:A:31:LEU:HD12	2:B:146:LEU:HD13	0.59	1.74	11	4
2:B:66:VAL:HG22	2:B:80:TRP:CZ2	0.59	2.32	16	4
2:B:142:VAL:HB	2:B:162:PHE:CE2	0.59	2.33	4	11
2:B:144:ASN:OD1	2:B:145:GLU:N	0.59	2.36	14	3
2:B:197:TRP:CZ3	2:B:201:ASN:OD1	0.59	2.56	2	2
2:B:76:LYS:CD	2:B:168:VAL:HG21	0.59	2.27	3	1
2:B:124:LEU:HD11	2:B:165:ALA:HB3	0.58	1.75	13	1
2:B:65:VAL:HG21	2:B:187:ALA:CA	0.58	2.28	6	8
1:A:23:THR:HG23	2:B:127:GLN:O	0.58	1.99	5	1
2:B:147:PHE:CD2	2:B:151:VAL:HG23	0.58	2.33	19	12
2:B:76:LYS:HG2	2:B:168:VAL:HG11	0.58	1.75	2	2
2:B:153:TRP:CZ3	2:B:198:ILE:HD12	0.58	2.33	11	3
2:B:195:GLU:N	2:B:196:PRO:HD2	0.58	2.14	9	11
2:B:136:TYR:HA	2:B:185:TRP:CZ3	0.57	2.34	8	20
2:B:83:PHE:HE1	2:B:179:VAL:HG11	0.57	1.59	19	5
2:B:130:ILE:C	2:B:175:MET:HE1	0.57	2.24	3	6
2:B:139:PHE:CE2	2:B:143:VAL:HG21	0.57	2.35	18	6
1:A:34:THR:HG21	2:B:117:TYR:HB2	0.57	1.77	16	1
1:A:27:LEU:HD21	2:B:124:LEU:HD21	0.57	1.76	17	2
2:B:65:VAL:HG11	2:B:187:ALA:HB2	0.57	1.76	15	5
1:A:27:LEU:HD12	1:A:27:LEU:C	0.57	2.24	14	2
2:B:197:TRP:CE3	2:B:198:ILE:HD13	0.57	2.35	3	6
2:B:197:TRP:HE3	2:B:198:ILE:HD13	0.57	1.60	3	6
2:B:143:VAL:HG12	2:B:189:TYR:CZ	0.57	2.34	3	1
2:B:147:PHE:CE1	2:B:151:VAL:HG13	0.56	2.35	9	1
2:B:152:ASN:HA	2:B:197:TRP:CE2	0.56	2.35	19	10
1:A:33:VAL:O	1:A:37:LEU:HD23	0.56	2.00	12	2
2:B:69:LEU:HD22	2:B:167:CYS:SG	0.56	2.40	7	4
2:B:76:LYS:HD3	2:B:168:VAL:HG21	0.56	1.76	3	1
2:B:62:ARG:O	2:B:66:VAL:HG23	0.56	2.01	9	8
2:B:162:PHE:O	2:B:166:LEU:HD12	0.56	2.01	7	1
2:B:125:THR:HG23	2:B:165:ALA:CB	0.56	2.28	11	1
2:B:160:PHE:CZ	2:B:190:LEU:HD22	0.56	2.34	19	4
2:B:100:GLU:O	2:B:103:LYS:HG2	0.56	2.01	14	3
2:B:115:LEU:HD21	2:B:119:ARG:NH1	0.56	2.16	14	1
2:B:105:ALA:HB2	2:B:208:VAL:HG22	0.56	1.77	12	5
1:A:31:LEU:HD23	2:B:117:TYR:CE1	0.56	2.35	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:173:LYS:O	2:B:174:GLU:CG	0.56	2.54	7	1
1:A:27:LEU:HD13	2:B:128:LEU:HD23	0.56	1.77	15	1
1:A:27:LEU:HD12	2:B:117:TYR:OH	0.55	2.00	19	1
2:B:152:ASN:HA	2:B:197:TRP:CZ2	0.55	2.36	8	13
2:B:193:HIS:NE2	2:B:194:LEU:HD23	0.55	2.15	9	1
2:B:198:ILE:HG21	2:B:204:TRP:CD1	0.55	2.36	14	2
2:B:128:LEU:HD22	2:B:166:LEU:HD23	0.55	1.77	2	2
1:A:31:LEU:CD1	2:B:146:LEU:HD13	0.55	2.32	5	3
2:B:197:TRP:CH2	2:B:201:ASN:OD1	0.55	2.60	13	2
2:B:124:LEU:C	2:B:124:LEU:HD13	0.55	2.26	12	1
2:B:128:LEU:C	2:B:128:LEU:HD12	0.55	2.27	12	2
2:B:171:VAL:HG22	2:B:176:GLN:HA	0.55	1.80	20	6
1:A:32:LYS:HG3	2:B:146:LEU:HD12	0.55	1.79	17	1
2:B:131:THR:CA	2:B:175:MET:HE1	0.54	2.32	19	3
2:B:167:CYS:HB3	2:B:179:VAL:HG13	0.54	1.79	12	7
1:A:31:LEU:HD13	2:B:146:LEU:HD22	0.54	1.79	5	2
1:A:31:LEU:HD23	1:A:31:LEU:N	0.54	2.18	1	10
2:B:186:MET:O	2:B:190:LEU:HB3	0.54	2.03	17	11
2:B:124:LEU:HD22	2:B:162:PHE:HA	0.54	1.78	18	1
2:B:197:TRP:CE2	2:B:201:ASN:ND2	0.54	2.76	7	18
2:B:113:PHE:CD1	2:B:157:VAL:HG11	0.53	2.38	7	8
2:B:130:ILE:HG21	2:B:166:LEU:HD22	0.53	1.80	1	2
2:B:189:TYR:CZ	2:B:193:HIS:CE1	0.53	2.97	7	8
2:B:124:LEU:HD23	2:B:128:LEU:HD23	0.53	1.80	1	2
2:B:69:LEU:HD11	2:B:186:MET:SD	0.53	2.44	9	1
2:B:113:PHE:CD1	2:B:157:VAL:CG1	0.53	2.92	12	16
2:B:166:LEU:CB	2:B:182:ILE:HD13	0.53	2.33	9	19
2:B:124:LEU:HD21	2:B:162:PHE:HA	0.53	1.78	8	1
1:A:27:LEU:HD21	2:B:124:LEU:HD13	0.53	1.79	11	1
2:B:189:TYR:CE1	2:B:193:HIS:CG	0.53	2.97	2	8
2:B:170:SER:HB3	2:B:178:LEU:HD12	0.53	1.79	4	4
2:B:73:LEU:HD11	2:B:167:CYS:HB3	0.53	1.80	14	1
2:B:128:LEU:HD22	2:B:166:LEU:CD2	0.53	2.34	2	3
2:B:125:THR:HG22	2:B:165:ALA:O	0.52	2.04	17	3
1:A:27:LEU:CD1	2:B:124:LEU:HD23	0.52	2.32	2	1
2:B:189:TYR:CE2	2:B:193:HIS:CG	0.52	2.98	19	7
1:A:32:LYS:HG2	2:B:146:LEU:HD12	0.52	1.81	14	2
2:B:162:PHE:CE1	2:B:166:LEU:HD11	0.52	2.39	18	2
1:A:24:MET:HE3	2:B:138:SER:CB	0.52	2.34	9	2
1:A:24:MET:HE1	2:B:128:LEU:HB2	0.52	1.80	6	1
2:B:125:THR:HA	2:B:128:LEU:HD12	0.52	1.81	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:102:VAL:HG22	2:B:204:TRP:CB	0.52	2.35	19	1
2:B:131:THR:HG23	2:B:134:THR:OG1	0.52	2.04	3	1
2:B:207:PHE:CD1	2:B:211:TYR:CD2	0.52	2.98	13	3
2:B:130:ILE:HD12	2:B:170:SER:OG	0.52	2.03	17	2
2:B:189:TYR:CE2	2:B:193:HIS:CE1	0.52	2.98	12	9
2:B:160:PHE:CE1	2:B:190:LEU:HD22	0.52	2.39	4	4
2:B:73:LEU:HD11	2:B:167:CYS:SG	0.52	2.44	17	1
1:A:24:MET:HE3	2:B:138:SER:HB3	0.52	1.82	6	3
2:B:124:LEU:CD2	2:B:128:LEU:HD23	0.52	2.35	1	1
2:B:124:LEU:C	2:B:124:LEU:HD23	0.52	2.30	15	1
2:B:207:PHE:CE1	2:B:211:TYR:CD2	0.51	2.98	9	4
2:B:69:LEU:HD23	2:B:164:GLY:HA2	0.51	1.82	16	5
2:B:128:LEU:HD12	2:B:128:LEU:C	0.51	2.30	1	2
1:A:27:LEU:HD21	2:B:128:LEU:HD22	0.51	1.82	10	1
2:B:170:SER:O	2:B:175:MET:N	0.51	2.43	14	2
2:B:207:PHE:CE1	2:B:211:TYR:CE2	0.51	2.99	1	1
2:B:159:PHE:CE2	2:B:194:LEU:HD11	0.51	2.39	20	1
2:B:144:ASN:O	2:B:148:ARG:HB3	0.51	2.05	14	6
1:A:31:LEU:CB	2:B:158:ALA:HB1	0.51	2.36	4	4
2:B:181:ARG:O	2:B:185:TRP:CD1	0.51	2.64	18	20
2:B:78:TYR:CD2	2:B:168:VAL:HG13	0.51	2.41	19	2
2:B:73:LEU:HD13	2:B:83:PHE:CE1	0.51	2.40	11	3
2:B:198:ILE:O	2:B:203:GLY:N	0.51	2.44	11	20
2:B:100:GLU:O	2:B:104:GLN:HG2	0.51	2.06	18	2
2:B:73:LEU:HD13	2:B:83:PHE:CZ	0.51	2.41	3	2
2:B:189:TYR:CD2	2:B:193:HIS:CG	0.51	2.98	3	2
2:B:131:THR:O	2:B:133:GLY:N	0.50	2.43	6	9
2:B:124:LEU:HD11	2:B:162:PHE:HD1	0.50	1.66	20	1
2:B:166:LEU:HB3	2:B:182:ILE:HD13	0.50	1.82	16	12
2:B:189:TYR:CD2	2:B:193:HIS:CD2	0.50	2.99	15	3
2:B:105:ALA:CB	2:B:208:VAL:HG22	0.50	2.37	12	1
2:B:171:VAL:HG22	2:B:179:VAL:HG21	0.50	1.83	14	1
2:B:197:TRP:CE3	2:B:197:TRP:C	0.50	2.90	9	19
2:B:143:VAL:CG1	2:B:189:TYR:CZ	0.50	2.94	3	1
2:B:190:LEU:HD11	2:B:204:TRP:CH2	0.50	2.42	18	6
2:B:115:LEU:C	2:B:115:LEU:HD13	0.50	2.32	13	1
2:B:117:TYR:CE2	2:B:124:LEU:HD22	0.49	2.41	5	1
2:B:136:TYR:CD2	2:B:185:TRP:CE2	0.49	3.00	5	2
2:B:207:PHE:CD1	2:B:211:TYR:CD1	0.49	3.00	19	2
2:B:76:LYS:CG	2:B:168:VAL:HG11	0.49	2.36	2	1
2:B:162:PHE:C	2:B:162:PHE:CD1	0.49	2.90	17	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:190:LEU:HD12	2:B:190:LEU:C	0.49	2.32	17	6
2:B:189:TYR:CZ	2:B:193:HIS:CG	0.49	3.00	20	4
2:B:198:ILE:HG21	2:B:204:TRP:CE2	0.49	2.42	8	2
1:A:27:LEU:HD21	2:B:124:LEU:CG	0.49	2.37	1	2
2:B:162:PHE:CD1	2:B:163:GLY:N	0.49	2.81	2	3
2:B:124:LEU:O	2:B:128:LEU:HD23	0.49	2.08	10	1
2:B:139:PHE:CD1	2:B:139:PHE:C	0.49	2.91	14	5
2:B:190:LEU:HD13	2:B:194:LEU:HD11	0.49	1.84	3	4
2:B:113:PHE:CD2	2:B:157:VAL:CG1	0.49	2.96	6	1
2:B:143:VAL:HG22	2:B:162:PHE:CZ	0.49	2.43	3	1
2:B:136:TYR:CE2	2:B:137:GLN:NE2	0.49	2.81	11	1
2:B:175:MET:SD	2:B:178:LEU:HD12	0.49	2.48	14	2
2:B:181:ARG:HB3	2:B:185:TRP:CZ2	0.49	2.43	15	17
2:B:151:VAL:HG22	2:B:152:ASN:N	0.49	2.23	2	13
2:B:130:ILE:HD11	2:B:169:GLU:HG3	0.49	1.83	6	1
2:B:100:GLU:O	2:B:103:LYS:CG	0.49	2.60	15	6
2:B:167:CYS:HB3	2:B:179:VAL:HG22	0.49	1.84	11	1
2:B:189:TYR:CZ	2:B:193:HIS:ND1	0.49	2.81	17	14
1:A:27:LEU:CD2	2:B:124:LEU:HD11	0.49	2.37	8	1
2:B:167:CYS:HB2	2:B:179:VAL:HG22	0.48	1.84	17	1
2:B:100:GLU:HA	2:B:103:LYS:HD3	0.48	1.85	2	2
2:B:198:ILE:HG22	2:B:203:GLY:CA	0.48	2.33	3	8
2:B:175:MET:HE3	2:B:178:LEU:HD12	0.48	1.85	5	3
2:B:113:PHE:CZ	2:B:158:ALA:HB2	0.48	2.43	12	1
2:B:159:PHE:CZ	2:B:186:MET:HG2	0.48	2.43	20	2
1:A:23:THR:HG21	2:B:129:HIS:CE1	0.48	2.43	12	1
2:B:137:GLN:O	2:B:141:GLN:HG2	0.48	2.08	2	1
2:B:109:ALA:HB2	2:B:211:TYR:CD2	0.48	2.44	10	2
2:B:153:TRP:CZ3	2:B:198:ILE:CD1	0.48	2.97	4	4
2:B:190:LEU:HA	2:B:194:LEU:HG	0.48	1.84	16	5
2:B:209:GLU:OE1	2:B:210:LEU:HD23	0.48	2.09	9	1
1:A:28:SER:CB	2:B:142:VAL:HG13	0.48	2.39	11	1
2:B:106:LEU:HD11	2:B:204:TRP:CZ3	0.48	2.44	17	1
2:B:191:ASN:OD1	2:B:192:ASP:N	0.47	2.47	2	14
2:B:160:PHE:CD1	2:B:186:MET:CE	0.47	2.96	4	2
2:B:162:PHE:CE1	2:B:166:LEU:CD2	0.47	2.97	16	3
2:B:76:LYS:HG3	2:B:168:VAL:HG11	0.47	1.86	8	1
1:A:27:LEU:HD11	2:B:124:LEU:HD21	0.47	1.85	3	1
2:B:151:VAL:CG1	2:B:197:TRP:CD1	0.47	2.98	6	4
2:B:207:PHE:CE1	2:B:211:TYR:CG	0.47	3.02	18	2
1:A:27:LEU:HD21	2:B:124:LEU:CD2	0.47	2.40	17	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:156:ILE:HG23	2:B:194:LEU:HD13	0.47	1.86	10	3
2:B:163:GLY:HA3	2:B:186:MET:SD	0.47	2.49	4	4
2:B:147:PHE:CE2	2:B:194:LEU:CD2	0.47	2.98	13	3
2:B:115:LEU:HD23	2:B:118:ARG:HE	0.47	1.70	19	1
2:B:113:PHE:CG	2:B:157:VAL:CG1	0.47	2.97	4	2
1:A:23:THR:HG21	2:B:129:HIS:HD2	0.47	1.65	16	1
2:B:189:TYR:CE1	2:B:193:HIS:CE1	0.47	3.03	1	2
2:B:113:PHE:CG	2:B:157:VAL:HG12	0.47	2.45	20	7
2:B:159:PHE:CE2	2:B:194:LEU:HD21	0.47	2.44	6	1
2:B:125:THR:CG2	2:B:165:ALA:HB1	0.47	2.32	11	1
2:B:128:LEU:HD21	2:B:162:PHE:CE1	0.47	2.45	13	1
2:B:78:TYR:CE1	2:B:168:VAL:HG13	0.47	2.45	14	1
2:B:147:PHE:HD2	2:B:151:VAL:HG22	0.47	1.70	1	3
2:B:147:PHE:CE1	2:B:155:ARG:HB3	0.47	2.45	4	1
2:B:198:ILE:HG21	2:B:204:TRP:NE1	0.47	2.25	20	2
2:B:151:VAL:HG12	2:B:152:ASN:N	0.47	2.25	8	3
2:B:135:ALA:HB2	2:B:178:LEU:HD13	0.47	1.87	5	2
2:B:146:LEU:HD11	2:B:155:ARG:HA	0.47	1.86	9	1
2:B:153:TRP:CE3	2:B:156:ILE:HD12	0.47	2.45	17	1
2:B:128:LEU:HD21	2:B:162:PHE:HE1	0.46	1.71	13	2
2:B:143:VAL:HG22	2:B:189:TYR:CZ	0.46	2.46	17	1
2:B:143:VAL:CG2	2:B:189:TYR:CE1	0.46	2.98	12	6
2:B:100:GLU:O	2:B:104:GLN:CD	0.46	2.58	14	1
2:B:142:VAL:CG2	2:B:162:PHE:CE2	0.46	2.98	18	2
2:B:102:VAL:CG1	2:B:204:TRP:HB3	0.46	2.41	18	1
1:A:30:ARG:HG3	2:B:121:PHE:CG	0.46	2.45	10	3
2:B:141:GLN:HA	2:B:144:ASN:ND2	0.46	2.25	6	2
2:B:141:GLN:O	2:B:144:ASN:OD1	0.46	2.32	14	1
2:B:206:THR:O	2:B:209:GLU:HB2	0.46	2.09	17	1
1:A:31:LEU:CD2	2:B:117:TYR:CE1	0.46	2.99	13	2
2:B:136:TYR:CE2	2:B:185:TRP:NE1	0.46	2.83	6	1
1:A:27:LEU:HD22	2:B:124:LEU:HD21	0.46	1.88	14	1
2:B:187:ALA:O	2:B:191:ASN:ND2	0.46	2.48	20	6
2:B:195:GLU:N	2:B:196:PRO:CD	0.46	2.78	18	7
2:B:159:PHE:HA	2:B:162:PHE:CE2	0.46	2.44	7	3
2:B:186:MET:HG3	2:B:187:ALA:N	0.46	2.26	7	2
2:B:167:CYS:SG	2:B:179:VAL:HG13	0.46	2.51	14	1
1:A:27:LEU:CD2	2:B:162:PHE:CE1	0.46	2.99	11	3
2:B:142:VAL:CB	2:B:162:PHE:CE2	0.46	2.98	4	3
1:A:27:LEU:HD21	2:B:162:PHE:CD1	0.46	2.46	20	1
2:B:189:TYR:O	2:B:193:HIS:HB2	0.46	2.09	1	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:177:VAL:HG22	2:B:181:ARG:HD3	0.46	1.87	9	1
2:B:189:TYR:CE1	2:B:193:HIS:NE2	0.46	2.84	4	3
2:B:124:LEU:HD23	2:B:128:LEU:CD2	0.46	2.41	9	2
2:B:153:TRP:CZ3	2:B:207:PHE:HB2	0.46	2.46	14	3
2:B:68:PHE:CD1	2:B:160:PHE:CD1	0.45	3.04	17	2
2:B:189:TYR:CD1	2:B:193:HIS:CG	0.45	3.04	2	2
2:B:189:TYR:CE2	2:B:193:HIS:ND1	0.45	2.84	3	3
2:B:113:PHE:HE1	2:B:158:ALA:HB2	0.45	1.67	6	1
2:B:204:TRP:O	2:B:208:VAL:HG23	0.45	2.11	12	1
1:A:28:SER:CA	2:B:142:VAL:HG13	0.45	2.42	18	1
2:B:191:ASN:ND2	2:B:191:ASN:N	0.45	2.62	20	1
2:B:137:GLN:O	2:B:141:GLN:NE2	0.45	2.49	8	8
2:B:105:ALA:CB	2:B:207:PHE:CE2	0.45	2.99	14	2
2:B:162:PHE:CE1	2:B:166:LEU:CG	0.45	3.00	18	2
2:B:102:VAL:HG22	2:B:204:TRP:HB3	0.45	1.88	19	1
2:B:143:VAL:CG2	2:B:159:PHE:CE1	0.45	3.00	20	1
2:B:65:VAL:O	2:B:69:LEU:HD12	0.45	2.11	16	2
2:B:102:VAL:CG1	2:B:204:TRP:CE3	0.45	3.00	4	2
2:B:128:LEU:HD11	2:B:169:GLU:HG3	0.45	1.88	7	1
2:B:194:LEU:O	2:B:195:GLU:C	0.45	2.60	20	13
1:A:30:ARG:O	1:A:33:VAL:CG2	0.45	2.65	10	1
1:A:24:MET:HE1	2:B:128:LEU:O	0.45	2.11	11	1
2:B:196:PRO:O	2:B:200:GLU:CG	0.45	2.65	2	1
2:B:139:PHE:CD1	2:B:140:GLU:N	0.45	2.85	19	4
2:B:140:GLU:HA	2:B:143:VAL:HG12	0.45	1.88	1	5
2:B:109:ALA:CB	2:B:211:TYR:CD2	0.45	3.00	10	1
2:B:135:ALA:HB2	2:B:178:LEU:CD1	0.45	2.42	20	1
2:B:170:SER:OG	2:B:178:LEU:HD12	0.45	2.12	20	1
2:B:136:TYR:CA	2:B:185:TRP:CZ3	0.44	3.00	11	5
2:B:190:LEU:CD1	2:B:194:LEU:HD11	0.44	2.42	9	2
2:B:190:LEU:HD11	2:B:204:TRP:CZ2	0.44	2.48	18	3
2:B:189:TYR:CD1	2:B:193:HIS:CD2	0.44	3.05	4	2
2:B:124:LEU:HD22	2:B:165:ALA:CB	0.44	2.43	19	1
1:A:31:LEU:HB2	2:B:158:ALA:HB1	0.44	1.89	5	1
2:B:135:ALA:HB2	2:B:178:LEU:HD11	0.44	1.89	13	1
2:B:175:MET:HE3	2:B:178:LEU:CD1	0.44	2.42	4	1
2:B:62:ARG:HD3	2:B:187:ALA:HB1	0.44	1.89	13	1
1:A:30:ARG:CG	2:B:121:PHE:CD2	0.44	3.01	17	1
2:B:106:LEU:HD22	2:B:160:PHE:CD2	0.44	2.47	1	2
2:B:160:PHE:CE1	2:B:186:MET:HE1	0.44	2.48	11	2
2:B:130:ILE:HD11	2:B:166:LEU:O	0.44	2.12	3	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:140:GLU:HA	2:B:143:VAL:CG1	0.44	2.42	1	1
2:B:113:PHE:CD2	2:B:157:VAL:HG11	0.44	2.48	6	1
2:B:171:VAL:CG2	2:B:179:VAL:CG2	0.44	2.96	15	15
2:B:197:TRP:CE3	2:B:201:ASN:OD1	0.44	2.71	2	1
1:A:34:THR:HG22	2:B:116:ARG:CD	0.44	2.43	18	1
1:A:27:LEU:HD23	1:A:31:LEU:CD2	0.44	2.42	20	1
2:B:178:LEU:HD23	2:B:181:ARG:HD2	0.43	1.89	2	1
2:B:78:TYR:CD1	2:B:171:VAL:CG1	0.43	3.01	19	3
2:B:160:PHE:CE1	2:B:186:MET:HE3	0.43	2.48	18	2
2:B:69:LEU:HD21	2:B:186:MET:SD	0.43	2.53	9	2
2:B:65:VAL:CG2	2:B:190:LEU:HD23	0.43	2.44	1	5
2:B:143:VAL:HG22	2:B:189:TYR:CE1	0.43	2.48	2	3
2:B:143:VAL:CG1	2:B:189:TYR:CE1	0.43	3.01	3	1
2:B:78:TYR:HE2	2:B:168:VAL:HG13	0.43	1.72	9	1
2:B:78:TYR:CD1	2:B:78:TYR:N	0.43	2.86	14	1
2:B:146:LEU:HD11	2:B:155:ARG:HD3	0.43	1.89	6	2
2:B:189:TYR:CE1	2:B:193:HIS:CB	0.43	3.02	5	3
2:B:69:LEU:CB	2:B:80:TRP:CZ3	0.43	3.02	1	1
2:B:148:ARG:CG	2:B:149:ASP:N	0.43	2.82	3	1
2:B:142:VAL:CG1	2:B:162:PHE:CD2	0.43	3.02	7	1
2:B:166:LEU:HB3	2:B:182:ILE:CD1	0.43	2.44	10	5
2:B:117:TYR:CD1	2:B:117:TYR:C	0.43	2.97	15	1
2:B:131:THR:HA	2:B:175:MET:HE3	0.43	1.88	15	2
2:B:62:ARG:NH2	2:B:183:ALA:HB1	0.43	2.28	14	1
2:B:72:LYS:HD2	2:B:72:LYS:N	0.43	2.28	18	1
2:B:156:ILE:HG23	2:B:194:LEU:CD1	0.43	2.43	19	1
2:B:68:PHE:CE1	2:B:72:LYS:HG3	0.43	2.49	3	2
2:B:153:TRP:CZ2	2:B:207:PHE:HB2	0.43	2.49	8	4
2:B:70:SER:OG	2:B:80:TRP:CG	0.43	2.72	16	1
1:A:31:LEU:HB3	2:B:158:ALA:CB	0.42	2.43	4	2
1:A:27:LEU:HD21	2:B:124:LEU:HD23	0.42	1.91	7	1
2:B:69:LEU:HD23	2:B:164:GLY:CA	0.42	2.44	12	1
2:B:73:LEU:HD23	2:B:168:VAL:CG2	0.42	2.33	16	1
2:B:189:TYR:CE2	2:B:193:HIS:CD2	0.42	3.08	20	1
1:A:30:ARG:O	1:A:33:VAL:CG1	0.42	2.67	2	1
2:B:117:TYR:CE1	2:B:122:SER:O	0.42	2.73	2	1
2:B:144:ASN:O	2:B:148:ARG:CB	0.42	2.67	2	1
2:B:173:LYS:O	2:B:174:GLU:CB	0.42	2.66	3	4
2:B:160:PHE:HE1	2:B:190:LEU:HD22	0.42	1.72	4	1
2:B:83:PHE:CD1	2:B:179:VAL:HG21	0.42	2.50	16	1
1:A:31:LEU:HD12	1:A:32:LYS:N	0.42	2.30	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:162:PHE:CD1	2:B:162:PHE:C	0.42	2.97	2	5
2:B:179:VAL:O	2:B:183:ALA:HB2	0.42	2.14	13	2
1:A:27:LEU:HD11	2:B:128:LEU:CA	0.42	2.45	18	1
2:B:198:ILE:HG21	2:B:204:TRP:CD2	0.42	2.49	19	1
2:B:198:ILE:C	2:B:203:GLY:HA2	0.42	2.40	4	3
2:B:71:TYR:CE2	2:B:75:GLN:OE1	0.42	2.73	13	1
2:B:113:PHE:HE2	2:B:158:ALA:HB2	0.42	1.67	16	1
2:B:130:ILE:HD11	2:B:170:SER:HB3	0.42	1.91	8	1
2:B:208:VAL:O	2:B:212:GLY:CA	0.42	2.68	15	1
2:B:130:ILE:CG2	2:B:166:LEU:HD22	0.42	2.45	17	1
2:B:143:VAL:HG21	2:B:189:TYR:CD2	0.42	2.49	19	1
2:B:135:ALA:CB	2:B:178:LEU:HD13	0.42	2.44	3	2
2:B:198:ILE:CG2	2:B:203:GLY:HA2	0.42	2.45	5	1
2:B:136:TYR:CD2	2:B:137:GLN:OE1	0.42	2.73	7	1
2:B:79:SER:O	2:B:82:GLN:HG2	0.42	2.15	8	1
1:A:28:SER:N	2:B:142:VAL:HG13	0.42	2.30	18	1
2:B:159:PHE:CZ	2:B:189:TYR:HB3	0.41	2.50	1	1
2:B:79:SER:O	2:B:83:PHE:CZ	0.41	2.73	15	4
2:B:138:SER:O	2:B:142:VAL:CG2	0.41	2.67	5	1
2:B:106:LEU:CD1	2:B:160:PHE:CE2	0.41	3.04	11	1
2:B:117:TYR:CD2	2:B:122:SER:O	0.41	2.73	3	1
2:B:136:TYR:CD1	2:B:136:TYR:O	0.41	2.73	3	1
2:B:78:TYR:CE1	2:B:171:VAL:HG12	0.41	2.50	6	1
2:B:128:LEU:O	2:B:129:HIS:CG	0.41	2.73	7	2
2:B:191:ASN:C	2:B:195:GLU:HB2	0.41	2.40	7	1
2:B:71:TYR:CD1	2:B:71:TYR:C	0.41	2.98	17	1
1:A:28:SER:HA	1:A:31:LEU:HD21	0.41	1.92	20	1
1:A:27:LEU:O	1:A:31:LEU:HG	0.41	2.16	1	1
2:B:79:SER:O	2:B:83:PHE:CE1	0.41	2.74	10	1
2:B:159:PHE:CD2	2:B:194:LEU:HD21	0.41	2.50	9	1
2:B:106:LEU:CD2	2:B:160:PHE:CD2	0.41	3.03	11	1
2:B:79:SER:O	2:B:83:PHE:CE2	0.41	2.74	19	1
2:B:208:VAL:O	2:B:212:GLY:N	0.41	2.54	1	1
2:B:100:GLU:O	2:B:104:GLN:NE2	0.41	2.54	12	3
1:A:27:LEU:HD13	2:B:128:LEU:HB3	0.41	1.91	2	1
2:B:106:LEU:HD13	2:B:160:PHE:CZ	0.41	2.51	10	1
2:B:141:GLN:OE1	2:B:141:GLN:N	0.41	2.54	17	1
2:B:111:ASP:O	2:B:115:LEU:HD12	0.41	2.14	19	1
2:B:187:ALA:O	2:B:191:ASN:CG	0.41	2.64	3	2
2:B:117:TYR:CE1	2:B:121:PHE:HB2	0.41	2.51	4	1
2:B:151:VAL:O	2:B:152:ASN:CB	0.41	2.69	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:142:VAL:HG21	2:B:162:PHE:CE2	0.41	2.51	15	1
2:B:108:GLU:HG3	2:B:109:ALA:N	0.41	2.31	1	1
2:B:189:TYR:CE1	2:B:193:HIS:ND1	0.41	2.89	2	1
2:B:159:PHE:O	2:B:162:PHE:CD2	0.41	2.74	3	1
2:B:99:SER:O	2:B:103:LYS:CD	0.41	2.69	5	2
1:A:27:LEU:HD12	1:A:31:LEU:HD21	0.41	1.92	12	1
2:B:140:GLU:CG	2:B:141:GLN:OE1	0.40	2.69	8	1
2:B:82:GLN:HG2	2:B:83:PHE:CD2	0.40	2.51	9	1
2:B:186:MET:HE3	2:B:186:MET:HB3	0.40	1.84	13	1
2:B:68:PHE:CG	2:B:160:PHE:CD1	0.40	3.09	17	1
2:B:142:VAL:O	2:B:146:LEU:CB	0.40	2.69	19	2
2:B:197:TRP:C	2:B:197:TRP:CD2	0.40	2.99	9	2
2:B:137:GLN:O	2:B:141:GLN:CD	0.40	2.64	3	1
2:B:191:ASN:OD1	2:B:191:ASN:C	0.40	2.64	15	2
2:B:189:TYR:CE1	2:B:193:HIS:CD2	0.40	3.09	6	1
2:B:65:VAL:HG13	2:B:186:MET:HE2	0.40	1.93	12	1
2:B:128:LEU:HD13	2:B:130:ILE:HG23	0.40	1.94	17	1
2:B:124:LEU:CD2	2:B:165:ALA:CB	0.40	2.99	19	1
2:B:69:LEU:HB3	2:B:80:TRP:CZ3	0.40	2.51	1	1
2:B:211:TYR:N	2:B:211:TYR:CD1	0.40	2.89	7	1
2:B:117:TYR:CD1	2:B:122:SER:O	0.40	2.74	15	1
2:B:190:LEU:O	2:B:190:LEU:HD12	0.40	2.16	15	1
2:B:207:PHE:CE1	2:B:211:TYR:CE1	0.40	3.09	10	1
1:A:27:LEU:CD1	1:A:28:SER:N	0.40	2.84	14	1
2:B:115:LEU:HD12	2:B:119:ARG:CZ	0.40	2.46	17	1
1:A:38:PHE:CZ	2:B:112:GLU:CD	0.40	2.99	18	1
2:B:102:VAL:CG2	2:B:204:TRP:CB	0.40	2.99	18	1
1:A:30:ARG:HG2	2:B:121:PHE:CG	0.40	2.51	20	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	17/23 (74%)	15±1 (91±4%)	2±1 (9±4%)	0±0 (0±0%)	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	137/156 (88%)	123±2 (90±1%)	10±2 (7±1%)	4±1 (3±1%)	5	39
All	All	3080/3580 (86%)	2765 (90%)	236 (8%)	79 (3%)	6	42

All 9 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	174	GLU	17
2	B	152	ASN	17
2	B	122	SER	11
2	B	123	ASP	8
2	B	60	SER	8
2	B	132	PRO	7
2	B	127	GLN	5
2	B	128	LEU	4
2	B	129	HIS	2

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	16/19 (84%)	9±1 (59±8%)	7±1 (41±8%)	0	5
2	B	118/134 (88%)	91±3 (77±3%)	27±3 (23±3%)	2	27
All	All	2680/3060 (88%)	2000 (75%)	680 (25%)	2	24

All 90 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	34	THR	19
2	B	75	GLN	18
2	B	194	LEU	18
2	B	195	GLU	18
2	B	209	GLU	18
2	B	134	THR	17
2	B	169	GLU	17

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Mol	Chain	Res	Type	Models (Total)
2	B	186	MET	16
2	B	103	LYS	15
1	A	27	LEU	14
1	A	31	LEU	14
2	B	148	ARG	14
2	B	141	GLN	14
2	B	190	LEU	13
2	B	82	GLN	12
1	A	28	SER	12
2	B	170	SER	12
1	A	30	ARG	11
2	B	72	LYS	11
2	B	104	GLN	11
2	B	131	THR	11
2	B	139	PHE	11
1	A	24	MET	11
2	B	100	GLU	11
2	B	99	SER	10
2	B	116	ARG	10
2	B	122	SER	10
2	B	180	SER	9
1	A	36	ASP	9
1	A	38	PHE	9
2	B	181	ARG	9
2	B	114	GLU	8
2	B	152	ASN	8
2	B	177	VAL	8
2	B	79	SER	8
2	B	124	LEU	8
2	B	127	GLN	8
2	B	160	PHE	8
1	A	32	LYS	8
2	B	126	SER	8
2	B	175	MET	8
2	B	74	SER	7
2	B	107	ARG	7
2	B	111	ASP	7
1	A	29	ARG	7
2	B	145	GLU	7
2	B	60	SER	7
2	B	62	ARG	7
2	B	67	ASP	7

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Mol	Chain	Res	Type	Models (Total)
2	B	200	GLU	7
2	B	115	LEU	7
1	A	26	ASN	6
2	B	191	ASN	6
2	B	129	HIS	6
2	B	173	LYS	6
2	B	76	LYS	5
2	B	140	GLU	5
2	B	149	ASP	5
2	B	201	ASN	5
2	B	119	ARG	5
2	B	137	GLN	5
2	B	118	ARG	5
2	B	205	ASP	4
2	B	155	ARG	4
1	A	25	GLU	4
2	B	174	GLU	4
2	B	192	ASP	4
1	A	23	THR	4
2	B	176	GLN	4
2	B	206	THR	4
2	B	138	SER	3
2	B	199	GLN	3
2	B	128	LEU	3
2	B	208	VAL	3
2	B	161	SER	3
2	B	108	GLU	2
2	B	136	TYR	2
2	B	189	TYR	2
1	A	39	ASP	2
2	B	106	LEU	2
1	A	33	VAL	1
2	B	61	ASN	1
2	B	64	LEU	1
2	B	123	ASP	1
2	B	193	HIS	1
2	B	63	GLU	1
2	B	125	THR	1
2	B	144	ASN	1
2	B	83	PHE	1
2	B	112	GLU	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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided