



Full wwPDB NMR Structure Validation Report ⓘ

Oct 17, 2021 – 09:20 AM EDT

PDB ID : 1JOR
Title : Ensemble structures for unligated Staphylococcal nuclease-H124L
Authors : Wang, J.; Truckses, D.M.; Abildgaard, F.; Dzakula, Z.; Zolnai, Z.; Markley, J.L.
Deposited on : 2001-07-30

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

MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.23.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

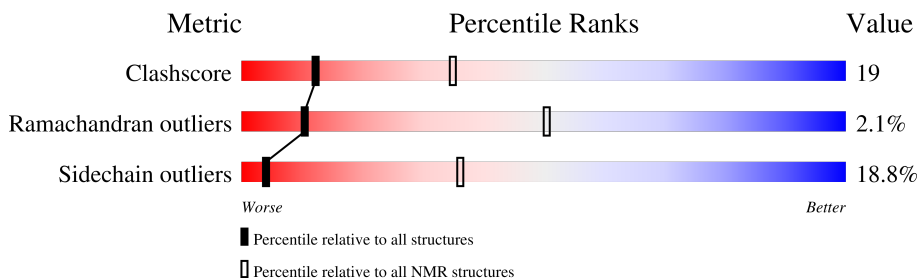
1 Overall quality at a glance

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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

Mol	Chain	Length	Quality of chain
1	A	149	

2 Ensemble composition and analysis

This entry contains 30 models. Model 16 is the overall representative, medoid model (most similar to other models).

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:9-A:41, A:57-A:141 (118)	0.34	16

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 7 clusters and 7 single-model clusters were found.

Cluster number	Models
1	4, 5, 13, 15, 21, 22, 23
2	6, 7, 9, 16, 17, 30
3	2, 14
4	10, 12
5	1, 25
6	8, 29
7	3, 18
Single-model clusters	11; 19; 20; 24; 26; 27; 28

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2397 atoms, of which 1216 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called staphylococcal nuclease.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	149	2397	747	1216	206	224	4	0

There is a discrepancy between the modelled and reference sequences:

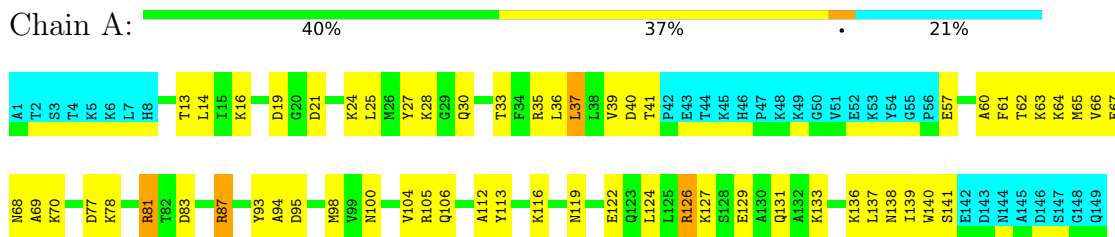
Chain	Residue	Modelled	Actual	Comment	Reference
A	124	LEU	HIS	engineered mutation	UNP P00644

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: staphylococcal nuclease

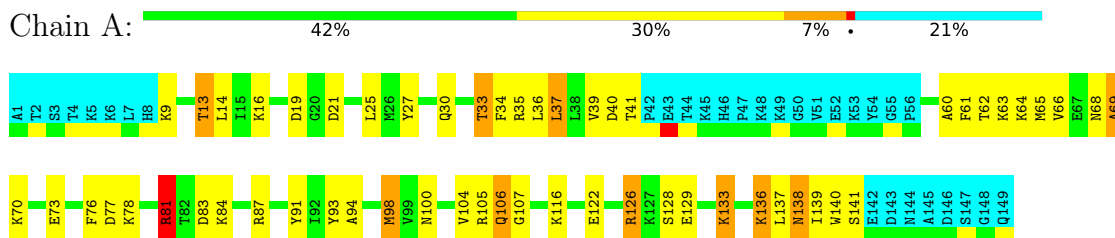


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

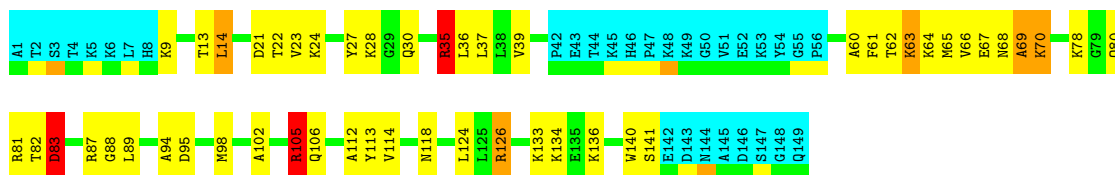
- Molecule 1: staphylococcal nuclease



4.2.2 Score per residue for model 2

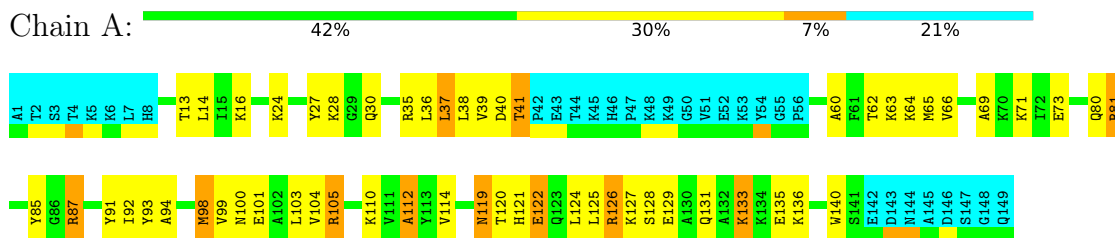
- Molecule 1: staphylococcal nuclease





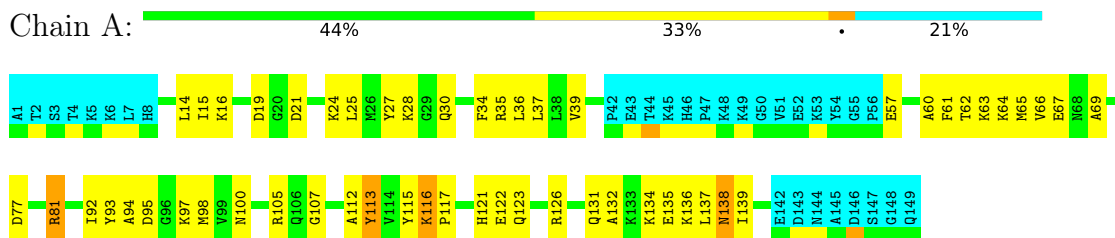
4.2.3 Score per residue for model 3

- Molecule 1: staphylococcal nuclease



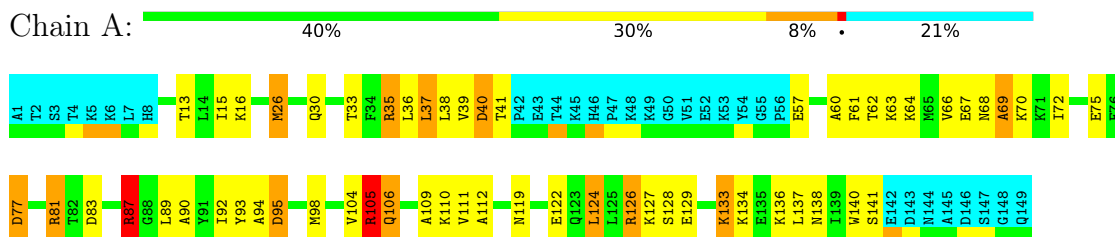
4.2.4 Score per residue for model 4

- Molecule 1: staphylococcal nuclease



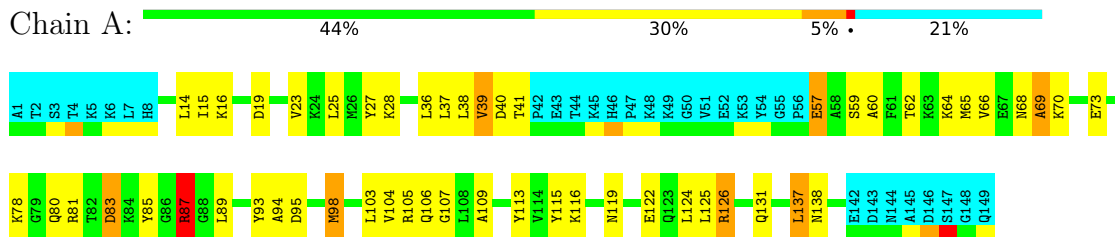
4.2.5 Score per residue for model 5

- Molecule 1: staphylococcal nuclease



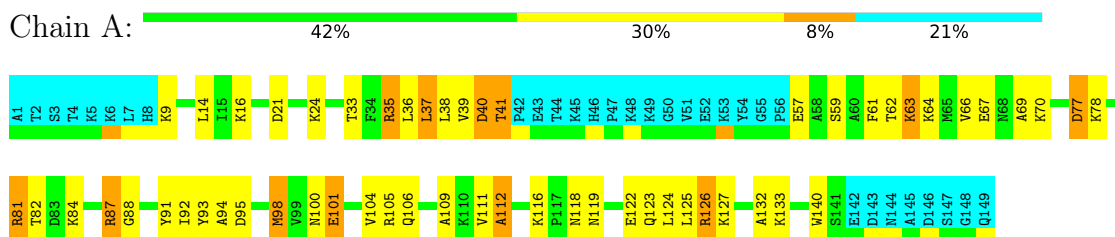
4.2.6 Score per residue for model 6

- Molecule 1: staphylococcal nuclease



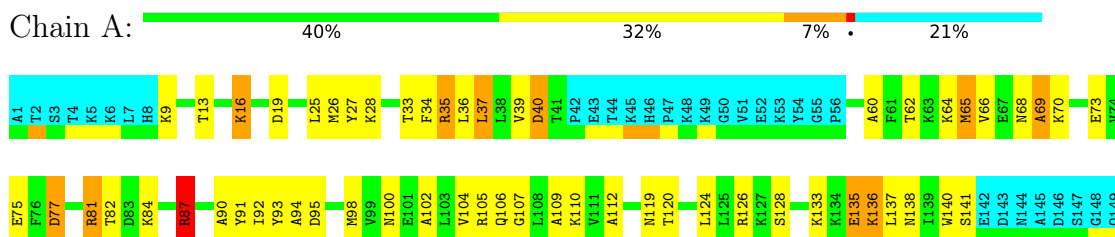
4.2.7 Score per residue for model 7

- Molecule 1: staphylococcal nuclease



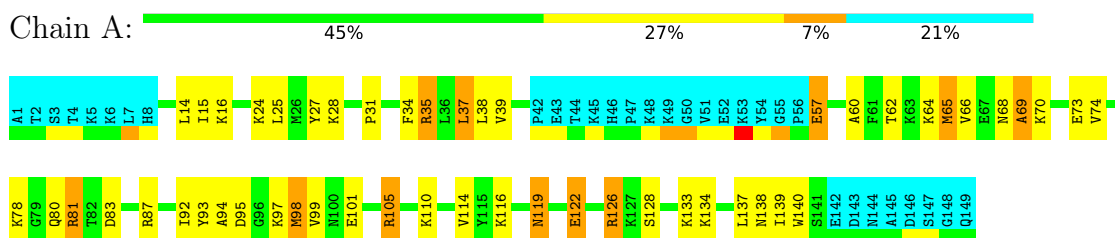
4.2.8 Score per residue for model 8

- Molecule 1: staphylococcal nuclease



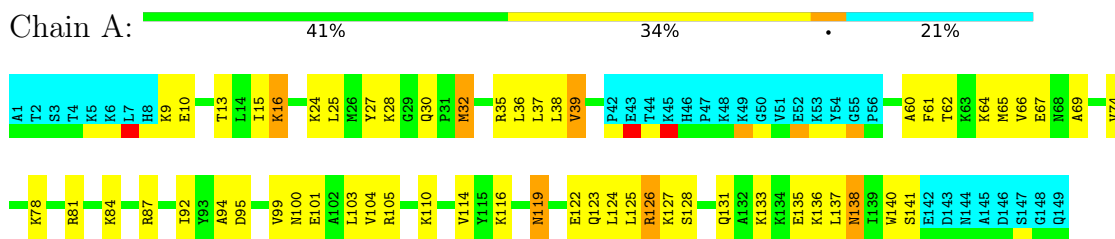
4.2.9 Score per residue for model 9

- Molecule 1: staphylococcal nuclease



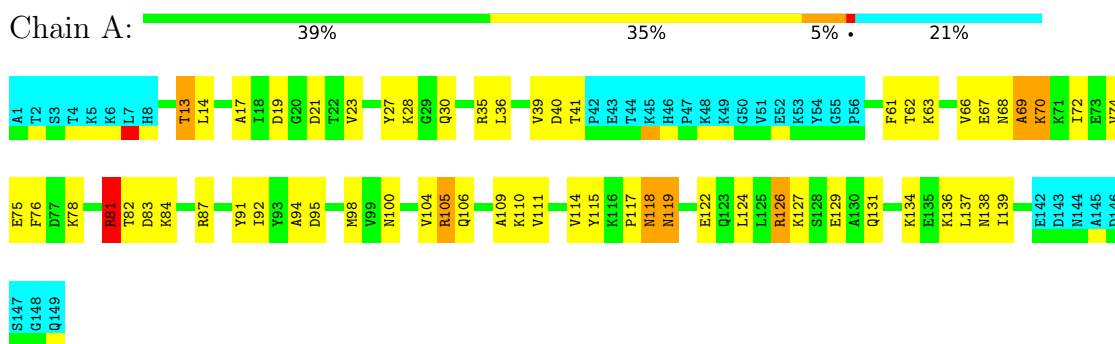
4.2.10 Score per residue for model 10

- Molecule 1: staphylococcal nuclease



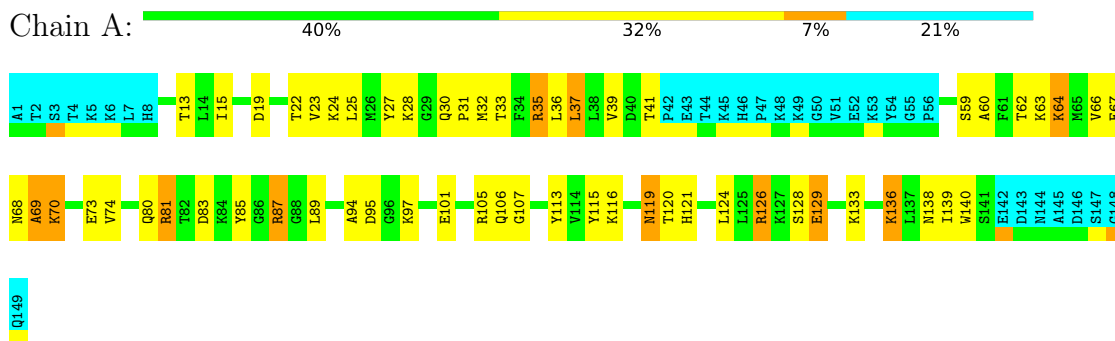
4.2.11 Score per residue for model 11

- Molecule 1: staphylococcal nuclease



4.2.12 Score per residue for model 12

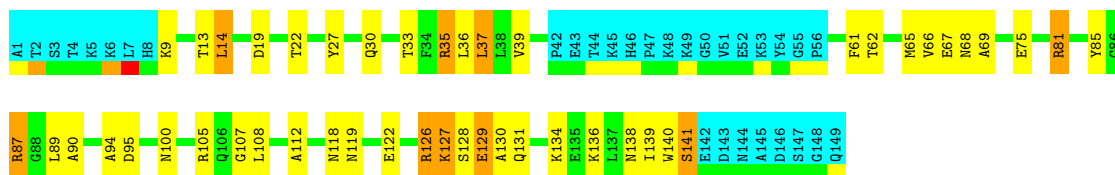
- Molecule 1: staphylococcal nuclease



4.2.13 Score per residue for model 13

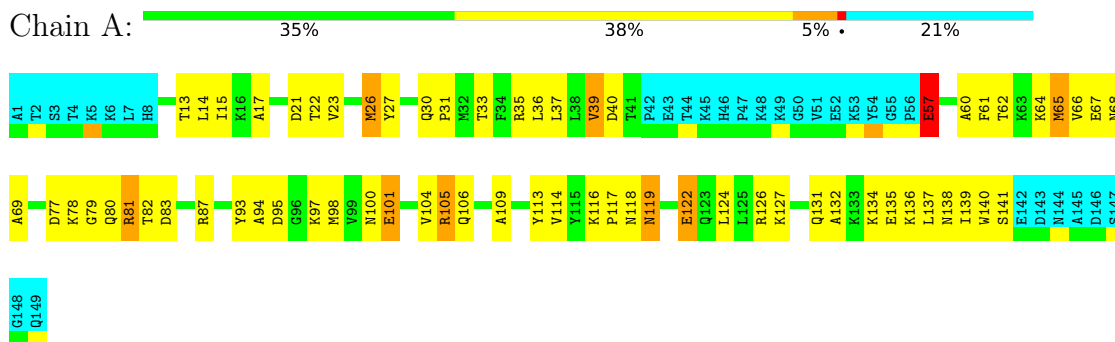
- Molecule 1: staphylococcal nuclease





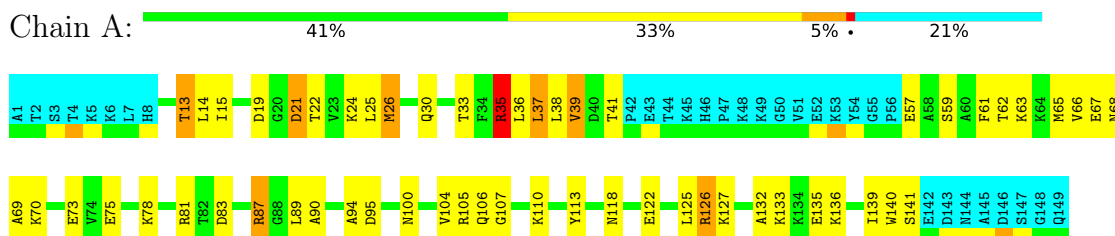
4.2.14 Score per residue for model 14

- Molecule 1: staphylococcal nuclease



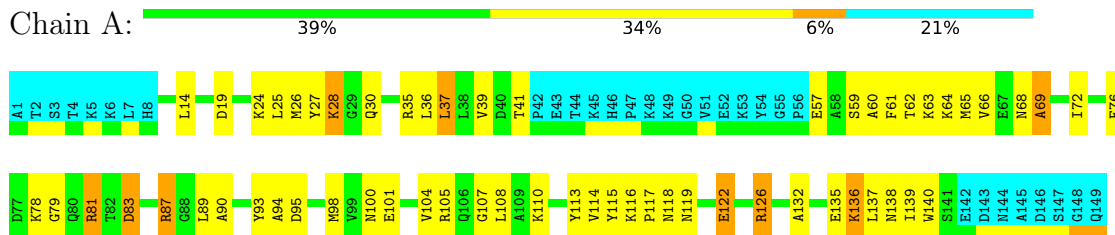
4.2.15 Score per residue for model 15

- Molecule 1: staphylococcal nuclease



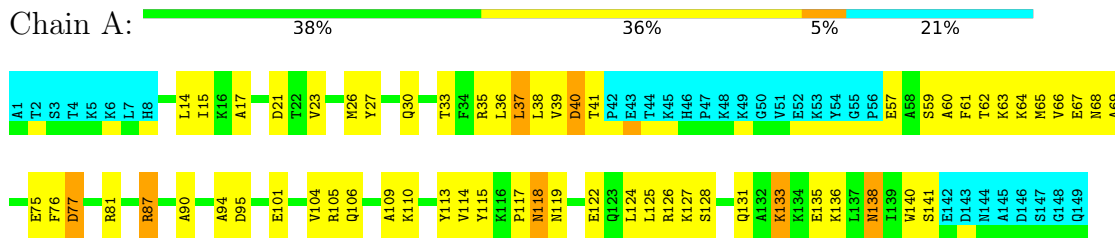
4.2.16 Score per residue for model 16 (medoid)

- Molecule 1: staphylococcal nuclease



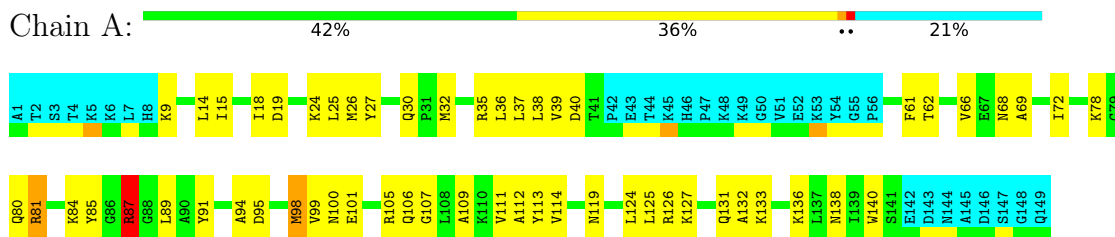
4.2.17 Score per residue for model 17

- Molecule 1: staphylococcal nuclease



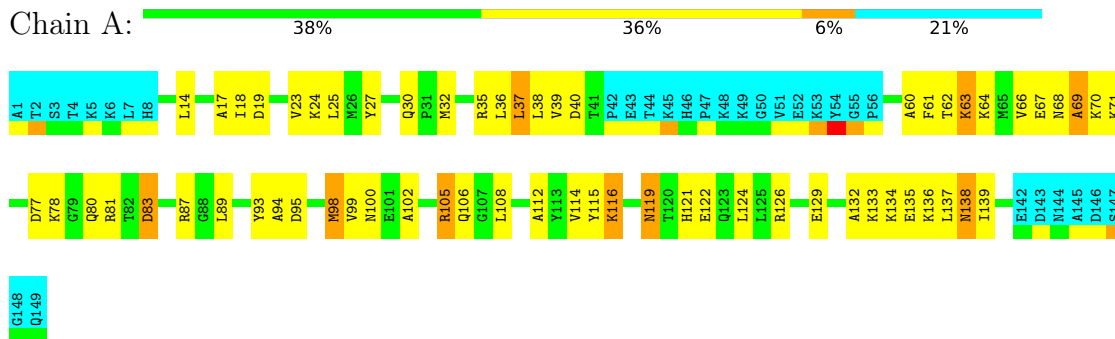
4.2.18 Score per residue for model 18

- Molecule 1: staphylococcal nuclease



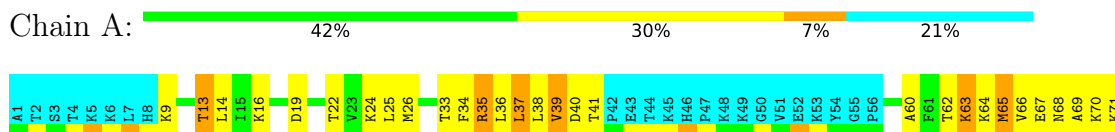
4.2.19 Score per residue for model 19

- Molecule 1: staphylococcal nuclease



4.2.20 Score per residue for model 20

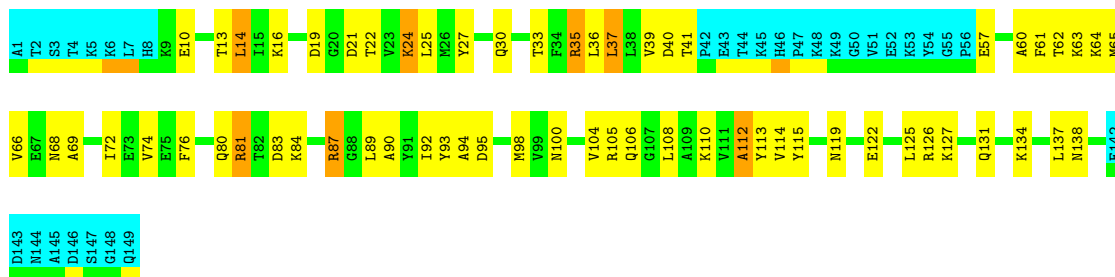
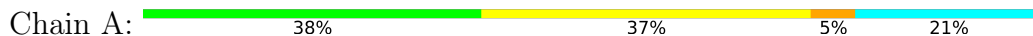
- Molecule 1: staphylococcal nuclease





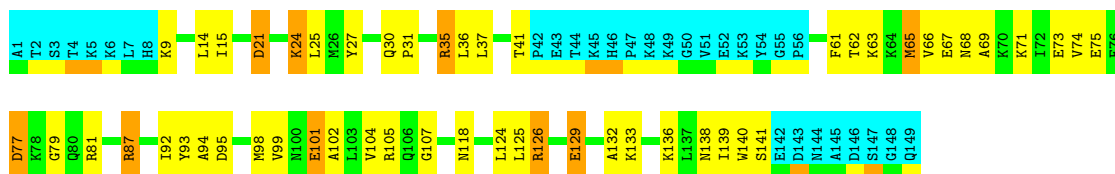
4.2.21 Score per residue for model 21

- Molecule 1: staphylococcal nuclease



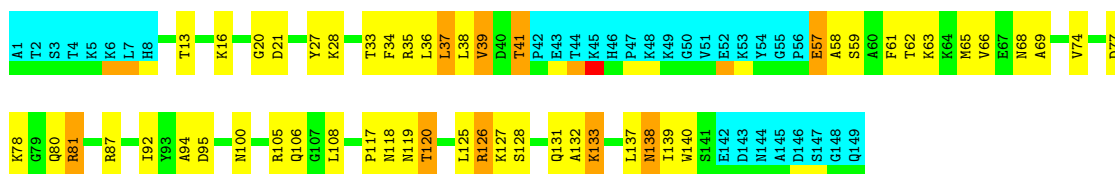
4.2.22 Score per residue for model 22

- Molecule 1: staphylococcal nuclease



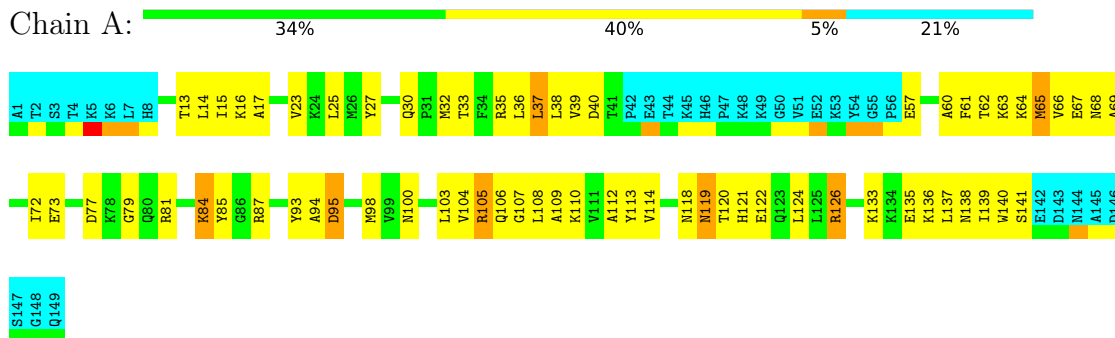
4.2.23 Score per residue for model 23

- Molecule 1: staphylococcal nuclease



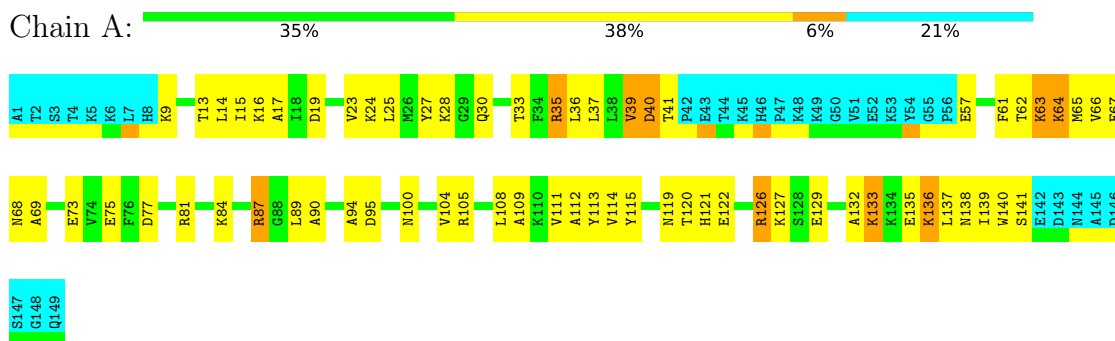
4.2.24 Score per residue for model 24

- Molecule 1: staphylococcal nuclease



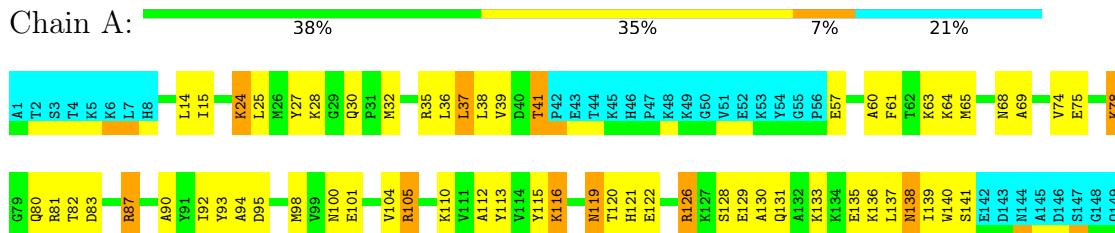
4.2.25 Score per residue for model 25

- Molecule 1: staphylococcal nuclease



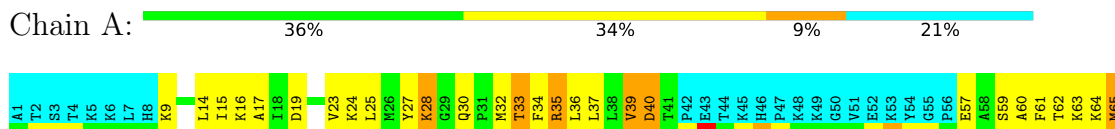
4.2.26 Score per residue for model 26

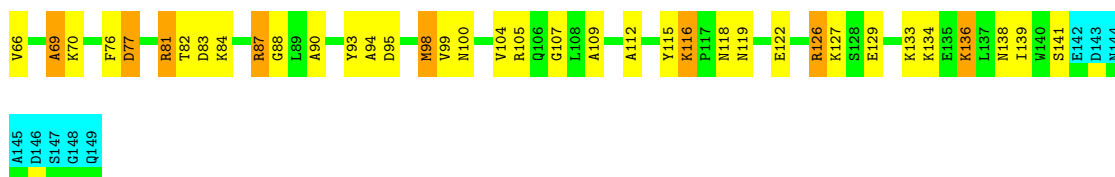
- Molecule 1: staphylococcal nuclease



4.2.27 Score per residue for model 27

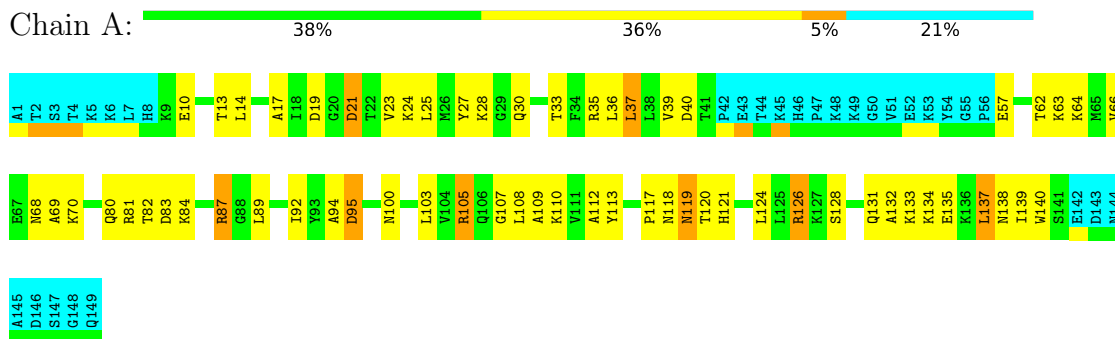
- Molecule 1: staphylococcal nuclease





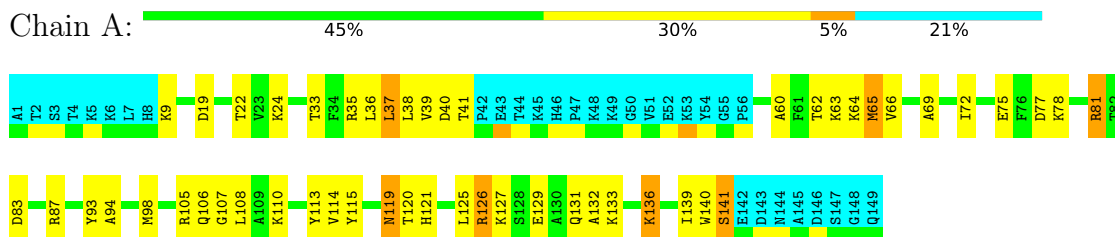
4.2.28 Score per residue for model 28

- Molecule 1: staphylococcal nuclease



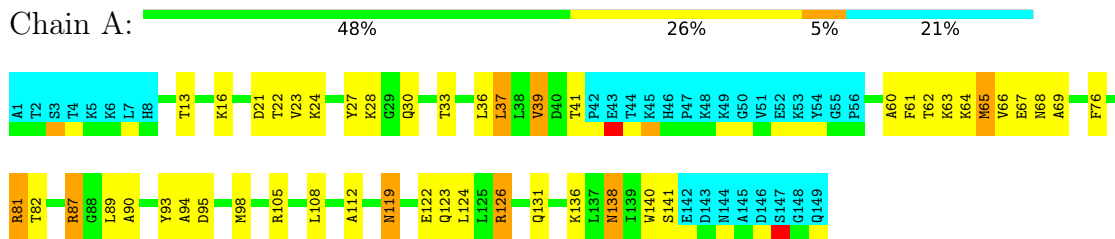
4.2.29 Score per residue for model 29

- Molecule 1: staphylococcal nuclease



4.2.30 Score per residue for model 30

- Molecule 1: staphylococcal nuclease



5 Refinement protocol and experimental data overview

The models were refined using the following method: *Distance, hydrogen bond and torsion angle constraints*.

Of the 90 calculated structures, 30 were deposited, based on the following criterion: *structures with acceptable covalent geometry, structures with the least restraint violations*.

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

Software name	Classification	Version
X-PLOR	structure solution	3.1
Insight II	structure solution	2.3
HBPLUS	structure solution	
X-PLOR	refinement	3.1

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.

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	4.8±0.4
All	All	0	144

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	81	ARG	Sidechain	30
1	A	105	ARG	Sidechain	30
1	A	126	ARG	Sidechain	30
1	A	35	ARG	Sidechain	28
1	A	87	ARG	Sidechain	26

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	943	982	982	37±6
All	All	28290	29460	29460	1101

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 19.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:LEU:HD12	1:A:25:LEU:CD2	0.96	1.89	1	4
1:A:107:GLY:O	1:A:139:ILE:HD12	0.89	1.67	16	8
1:A:135:GLU:HB3	1:A:137:LEU:HD21	0.89	1.45	26	7
1:A:69:ALA:CB	1:A:94:ALA:HB1	0.88	1.99	6	12
1:A:14:LEU:HD12	1:A:25:LEU:HD22	0.84	1.47	1	1
1:A:36:LEU:HD22	1:A:100:ASN:OD1	0.84	1.71	4	10
1:A:83:ASP:OD1	1:A:89:LEU:HD11	0.83	1.73	2	3
1:A:24:LYS:O	1:A:25:LEU:HD23	0.83	1.73	16	8
1:A:14:LEU:HD13	1:A:15:ILE:N	0.82	1.90	26	6
1:A:100:ASN:O	1:A:104:VAL:HG23	0.81	1.75	8	11
1:A:65:MET:O	1:A:69:ALA:HB2	0.81	1.74	13	12
1:A:25:LEU:HD12	1:A:34:PHE:CG	0.79	2.13	27	5
1:A:62:THR:O	1:A:66:VAL:HG22	0.77	1.80	25	21
1:A:124:LEU:HD13	1:A:124:LEU:O	0.76	1.80	17	2
1:A:69:ALA:HB2	1:A:94:ALA:HB1	0.76	1.57	28	13
1:A:62:THR:O	1:A:66:VAL:HG13	0.75	1.81	13	25
1:A:83:ASP:CG	1:A:89:LEU:HD11	0.75	2.02	12	4
1:A:40:ASP:O	1:A:109:ALA:HB1	0.75	1.81	25	12
1:A:105:ARG:O	1:A:137:LEU:HD13	0.74	1.82	5	1
1:A:135:GLU:CB	1:A:137:LEU:HD21	0.72	2.13	26	3
1:A:104:VAL:HG21	1:A:125:LEU:CD2	0.72	2.14	22	2
1:A:104:VAL:HG13	1:A:129:GLU:OE1	0.71	1.85	27	2
1:A:14:LEU:HD22	1:A:66:VAL:O	0.71	1.84	16	2
1:A:25:LEU:HD12	1:A:34:PHE:CD1	0.71	2.20	27	2
1:A:82:THR:HG22	1:A:88:GLY:HA2	0.71	1.59	27	1
1:A:38:LEU:HD22	1:A:114:VAL:HG22	0.71	1.62	17	2
1:A:33:THR:HG21	1:A:87:ARG:CZ	0.69	2.18	28	1
1:A:39:VAL:O	1:A:112:ALA:HB2	0.69	1.88	21	11
1:A:38:LEU:HD23	1:A:114:VAL:HG21	0.69	1.63	18	1
1:A:72:ILE:HD12	1:A:72:ILE:N	0.69	2.03	5	1
1:A:104:VAL:HG21	1:A:125:LEU:HD22	0.68	1.64	6	6
1:A:83:ASP:HB3	1:A:89:LEU:HD11	0.67	1.66	16	3
1:A:21:ASP:OD2	1:A:41:THR:HG23	0.67	1.88	21	2
1:A:33:THR:HG21	1:A:87:ARG:NH2	0.67	2.05	28	1
1:A:14:LEU:C	1:A:14:LEU:HD13	0.67	2.09	4	3
1:A:37:LEU:O	1:A:39:VAL:HG23	0.67	1.88	9	23
1:A:114:VAL:HG11	1:A:122:GLU:HG3	0.67	1.67	14	1
1:A:17:ALA:CB	1:A:23:VAL:HG12	0.67	2.20	19	5
1:A:36:LEU:HB3	1:A:39:VAL:HG21	0.66	1.67	3	24
1:A:114:VAL:HG12	1:A:119:ASN:OD1	0.66	1.91	14	1
1:A:69:ALA:O	1:A:72:ILE:HD11	0.66	1.91	18	3
1:A:74:VAL:HG12	1:A:92:ILE:HD12	0.66	1.67	26	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:108:LEU:HD21	1:A:138:ASN:OD1	0.65	1.90	16	7
1:A:21:ASP:CG	1:A:41:THR:HG23	0.65	2.11	21	2
1:A:14:LEU:HD13	1:A:14:LEU:C	0.65	2.12	22	4
1:A:74:VAL:HG12	1:A:92:ILE:CD1	0.64	2.22	26	4
1:A:106:GLN:HB3	1:A:108:LEU:HD12	0.64	1.69	29	1
1:A:14:LEU:HD13	1:A:66:VAL:HB	0.64	1.70	2	4
1:A:41:THR:O	1:A:41:THR:HG23	0.63	1.92	17	1
1:A:114:VAL:HG21	1:A:122:GLU:OE2	0.63	1.94	21	1
1:A:36:LEU:CB	1:A:39:VAL:HG21	0.62	2.24	11	1
1:A:104:VAL:HG13	1:A:129:GLU:CD	0.62	2.16	5	1
1:A:124:LEU:HD13	1:A:124:LEU:C	0.61	2.15	17	2
1:A:120:THR:HG22	1:A:121:HIS:CE1	0.61	2.31	25	1
1:A:37:LEU:HD12	1:A:89:LEU:C	0.61	2.16	13	1
1:A:17:ALA:HB1	1:A:23:VAL:HG12	0.61	1.73	27	7
1:A:99:VAL:O	1:A:103:LEU:HD12	0.60	1.97	10	2
1:A:33:THR:HG21	1:A:87:ARG:NH1	0.60	2.12	25	2
1:A:101:GLU:OE1	1:A:124:LEU:HD21	0.60	1.97	18	1
1:A:133:LYS:CG	1:A:140:TRP:CD2	0.60	2.84	17	4
1:A:38:LEU:HD11	1:A:119:ASN:HA	0.60	1.74	19	2
1:A:69:ALA:HB1	1:A:95:ASP:N	0.59	2.13	2	1
1:A:36:LEU:CB	1:A:39:VAL:CG2	0.59	2.80	11	2
1:A:133:LYS:CG	1:A:140:TRP:CE3	0.58	2.85	3	5
1:A:15:ILE:HD11	1:A:26:MET:SD	0.58	2.38	14	2
1:A:33:THR:O	1:A:34:PHE:CD1	0.56	2.58	1	1
1:A:23:VAL:HG23	1:A:25:LEU:HD21	0.56	1.77	12	1
1:A:66:VAL:HG23	1:A:67:GLU:N	0.56	2.15	13	7
1:A:75:GLU:O	1:A:90:ALA:HB1	0.56	1.99	8	5
1:A:132:ALA:HB1	1:A:140:TRP:CD1	0.56	2.35	7	8
1:A:101:GLU:HG3	1:A:124:LEU:HD21	0.56	1.77	14	3
1:A:135:GLU:HB2	1:A:137:LEU:HD12	0.56	1.76	28	1
1:A:61:PHE:CZ	1:A:65:MET:SD	0.56	2.99	13	1
1:A:93:TYR:CZ	1:A:98:MET:SD	0.56	2.99	16	7
1:A:114:VAL:HG11	1:A:122:GLU:OE1	0.56	2.01	11	1
1:A:124:LEU:C	1:A:124:LEU:HD23	0.56	2.20	24	1
1:A:14:LEU:HD22	1:A:25:LEU:HD23	0.56	1.75	27	1
1:A:126:ARG:O	1:A:130:ALA:HB2	0.56	1.99	26	1
1:A:133:LYS:HG2	1:A:140:TRP:CD2	0.56	2.35	17	8
1:A:66:VAL:O	1:A:72:ILE:HD11	0.56	2.01	24	3
1:A:133:LYS:HG3	1:A:140:TRP:CD2	0.55	2.36	20	7
1:A:37:LEU:HD12	1:A:90:ALA:HA	0.55	1.78	27	2
1:A:133:LYS:HG2	1:A:140:TRP:CE3	0.55	2.36	3	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:83:ASP:HB3	1:A:89:LEU:HD21	0.55	1.76	15	1
1:A:24:LYS:C	1:A:25:LEU:HD23	0.55	2.22	21	4
1:A:98:MET:SD	1:A:124:LEU:HD21	0.55	2.41	22	1
1:A:114:VAL:HG21	1:A:122:GLU:CG	0.54	2.32	14	1
1:A:65:MET:CE	1:A:94:ALA:HB3	0.54	2.32	21	1
1:A:18:ILE:HG22	1:A:19:ASP:OD1	0.54	2.02	18	2
1:A:72:ILE:HD12	1:A:72:ILE:H	0.54	1.62	5	2
1:A:38:LEU:HD23	1:A:114:VAL:CG2	0.54	2.31	18	1
1:A:132:ALA:C	1:A:140:TRP:CD1	0.54	2.81	7	6
1:A:61:PHE:CD1	1:A:103:LEU:HD21	0.54	2.38	24	1
1:A:136:LYS:O	1:A:141:SER:CB	0.54	2.56	26	8
1:A:27:TYR:O	1:A:30:GLN:CG	0.54	2.56	13	16
1:A:132:ALA:HA	1:A:137:LEU:HD12	0.54	1.80	25	2
1:A:15:ILE:HD12	1:A:25:LEU:O	0.54	2.03	22	5
1:A:76:PHE:CD2	1:A:90:ALA:HB2	0.54	2.37	27	2
1:A:91:TYR:CD1	1:A:91:TYR:N	0.54	2.76	8	4
1:A:38:LEU:HD22	1:A:114:VAL:HG13	0.54	1.79	9	1
1:A:38:LEU:HB3	1:A:125:LEU:HD12	0.54	1.79	20	1
1:A:76:PHE:CD1	1:A:90:ALA:HB2	0.53	2.38	30	3
1:A:62:THR:O	1:A:66:VAL:CG1	0.53	2.56	19	9
1:A:114:VAL:HG13	1:A:119:ASN:HB3	0.53	1.81	29	2
1:A:61:PHE:O	1:A:61:PHE:CD1	0.53	2.61	5	2
1:A:63:LYS:O	1:A:67:GLU:CG	0.53	2.57	17	6
1:A:14:LEU:HD22	1:A:25:LEU:CD2	0.53	2.34	27	3
1:A:68:ASN:O	1:A:70:LYS:N	0.52	2.42	12	9
1:A:37:LEU:O	1:A:39:VAL:CG2	0.52	2.58	25	6
1:A:60:ALA:O	1:A:64:LYS:CB	0.52	2.57	14	8
1:A:65:MET:HE2	1:A:94:ALA:HB3	0.52	1.81	6	1
1:A:83:ASP:OD2	1:A:87:ARG:CZ	0.52	2.57	1	1
1:A:107:GLY:O	1:A:138:ASN:CB	0.52	2.57	24	6
1:A:101:GLU:CG	1:A:128:SER:OG	0.52	2.58	9	1
1:A:21:ASP:OD1	1:A:41:THR:HG23	0.52	2.04	15	2
1:A:40:ASP:O	1:A:109:ALA:CB	0.52	2.57	7	2
1:A:65:MET:O	1:A:69:ALA:CB	0.52	2.56	13	10
1:A:15:ILE:HD12	1:A:25:LEU:C	0.52	2.25	24	2
1:A:61:PHE:C	1:A:61:PHE:CD1	0.52	2.82	19	9
1:A:110:LYS:HD3	1:A:140:TRP:CH2	0.52	2.40	15	1
1:A:61:PHE:CE2	1:A:106:GLN:OE1	0.52	2.63	5	1
1:A:136:LYS:O	1:A:141:SER:CA	0.52	2.58	14	7
1:A:85:TYR:CD1	1:A:85:TYR:N	0.52	2.76	3	1
1:A:92:ILE:C	1:A:93:TYR:CD1	0.52	2.83	4	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:93:TYR:CD1	1:A:98:MET:HA	0.52	2.40	6	2
1:A:64:LYS:O	1:A:68:ASN:ND2	0.52	2.43	1	4
1:A:114:VAL:CG1	1:A:119:ASN:OD1	0.52	2.57	3	2
1:A:106:GLN:O	1:A:138:ASN:ND2	0.52	2.43	24	1
1:A:101:GLU:OE1	1:A:124:LEU:CD2	0.52	2.57	3	1
1:A:133:LYS:HG3	1:A:140:TRP:CE2	0.52	2.39	17	5
1:A:113:TYR:HB3	1:A:115:TYR:CE1	0.52	2.40	17	1
1:A:21:ASP:OD2	1:A:41:THR:CG2	0.51	2.58	21	1
1:A:62:THR:O	1:A:66:VAL:CG2	0.51	2.57	3	8
1:A:114:VAL:HG21	1:A:122:GLU:HG3	0.51	1.82	14	4
1:A:21:ASP:OD1	1:A:22:THR:N	0.51	2.44	14	1
1:A:14:LEU:HA	1:A:25:LEU:HD23	0.51	1.81	20	1
1:A:137:LEU:O	1:A:139:ILE:N	0.51	2.44	23	8
1:A:61:PHE:CD1	1:A:61:PHE:C	0.51	2.83	5	12
1:A:113:TYR:HB3	1:A:115:TYR:CZ	0.51	2.41	17	5
1:A:69:ALA:CB	1:A:95:ASP:OD1	0.51	2.59	27	3
1:A:38:LEU:HB2	1:A:125:LEU:CD1	0.51	2.36	18	5
1:A:10:GLU:CB	1:A:27:TYR:OH	0.51	2.59	28	1
1:A:60:ALA:O	1:A:64:LYS:CG	0.50	2.59	1	5
1:A:81:ARG:O	1:A:82:THR:HG23	0.50	2.06	11	1
1:A:95:ASP:OD1	1:A:95:ASP:N	0.50	2.43	27	1
1:A:40:ASP:OD2	1:A:112:ALA:CB	0.50	2.59	18	2
1:A:14:LEU:C	1:A:14:LEU:CD1	0.50	2.80	22	7
1:A:97:LYS:O	1:A:99:VAL:N	0.50	2.45	9	1
1:A:120:THR:HG23	1:A:121:HIS:N	0.50	2.20	12	3
1:A:100:ASN:O	1:A:104:VAL:CG2	0.50	2.59	24	1
1:A:60:ALA:O	1:A:64:LYS:CD	0.50	2.60	30	2
1:A:119:ASN:OD1	1:A:122:GLU:CB	0.50	2.60	30	6
1:A:30:GLN:NE2	1:A:32:MET:SD	0.50	2.85	12	1
1:A:113:TYR:HB3	1:A:115:TYR:CE2	0.50	2.41	20	4
1:A:124:LEU:CD1	1:A:124:LEU:C	0.50	2.79	5	1
1:A:98:MET:SD	1:A:101:GLU:CB	0.49	3.00	22	2
1:A:27:TYR:CD2	1:A:28:LYS:HG3	0.49	2.42	28	1
1:A:85:TYR:HB2	1:A:87:ARG:CD	0.49	2.37	6	2
1:A:27:TYR:CE2	1:A:28:LYS:CD	0.49	2.96	6	1
1:A:105:ARG:O	1:A:137:LEU:CD1	0.49	2.59	5	1
1:A:85:TYR:CB	1:A:87:ARG:CD	0.49	2.90	6	1
1:A:26:MET:SD	1:A:30:GLN:N	0.49	2.86	15	1
1:A:14:LEU:HD12	1:A:25:LEU:HD23	0.49	1.84	25	1
1:A:85:TYR:CB	1:A:87:ARG:HD2	0.49	2.38	6	1
1:A:66:VAL:CG2	1:A:67:GLU:N	0.49	2.76	13	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:LEU:CD2	1:A:66:VAL:O	0.49	2.59	16	1
1:A:113:TYR:O	1:A:115:TYR:CE1	0.49	2.65	29	1
1:A:36:LEU:HB2	1:A:39:VAL:CG2	0.49	2.37	11	2
1:A:117:PRO:O	1:A:119:ASN:N	0.49	2.45	11	6
1:A:124:LEU:C	1:A:124:LEU:CD1	0.49	2.81	17	1
1:A:133:LYS:HD3	1:A:140:TRP:CE3	0.48	2.43	12	1
1:A:39:VAL:CG1	1:A:104:VAL:CG2	0.48	2.90	15	1
1:A:99:VAL:O	1:A:102:ALA:HB3	0.48	2.08	19	2
1:A:36:LEU:HB3	1:A:39:VAL:CG2	0.48	2.37	11	19
1:A:133:LYS:HA	1:A:140:TRP:CG	0.48	2.42	9	4
1:A:36:LEU:CD2	1:A:92:ILE:HG12	0.48	2.39	7	4
1:A:9:LYS:CG	1:A:75:GLU:OE1	0.48	2.61	29	1
1:A:95:ASP:N	1:A:95:ASP:OD1	0.48	2.47	24	2
1:A:93:TYR:CZ	1:A:98:MET:HG3	0.48	2.43	3	2
1:A:102:ALA:O	1:A:106:GLN:CG	0.48	2.62	2	1
1:A:37:LEU:CD1	1:A:77:ASP:OD2	0.48	2.61	22	3
1:A:98:MET:CE	1:A:121:HIS:ND1	0.48	2.76	19	1
1:A:61:PHE:CD1	1:A:61:PHE:O	0.48	2.66	15	5
1:A:124:LEU:O	1:A:124:LEU:CD1	0.48	2.62	5	1
1:A:21:ASP:CG	1:A:41:THR:CG2	0.48	2.82	21	1
1:A:36:LEU:HB2	1:A:39:VAL:HG23	0.48	1.86	18	1
1:A:57:GLU:CD	1:A:58:ALA:N	0.48	2.67	23	1
1:A:14:LEU:CD2	1:A:25:LEU:CD2	0.47	2.92	27	1
1:A:113:TYR:CD1	1:A:114:VAL:N	0.47	2.82	2	1
1:A:87:ARG:CD	1:A:87:ARG:N	0.47	2.77	5	2
1:A:119:ASN:O	1:A:119:ASN:OD1	0.47	2.32	11	2
1:A:93:TYR:CD1	1:A:93:TYR:N	0.47	2.82	9	1
1:A:114:VAL:HG11	1:A:119:ASN:ND2	0.47	2.24	25	1
1:A:63:LYS:HA	1:A:66:VAL:CG2	0.47	2.40	25	8
1:A:25:LEU:HD12	1:A:34:PHE:CD2	0.47	2.45	4	1
1:A:83:ASP:OD1	1:A:89:LEU:CD1	0.47	2.61	5	1
1:A:68:ASN:ND2	1:A:68:ASN:N	0.47	2.62	17	6
1:A:77:ASP:OD2	1:A:91:TYR:OH	0.47	2.33	7	1
1:A:21:ASP:OD2	1:A:39:VAL:O	0.47	2.32	11	1
1:A:69:ALA:O	1:A:72:ILE:CD1	0.47	2.60	18	1
1:A:22:THR:CG2	1:A:33:THR:CG2	0.47	2.93	21	2
1:A:61:PHE:O	1:A:65:MET:CB	0.47	2.62	27	1
1:A:10:GLU:CG	1:A:27:TYR:OH	0.47	2.63	28	1
1:A:101:GLU:OE1	1:A:124:LEU:HD23	0.47	2.08	3	1
1:A:132:ALA:CB	1:A:140:TRP:CD1	0.47	2.98	7	3
1:A:92:ILE:HG22	1:A:93:TYR:N	0.47	2.24	21	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:83:ASP:OD2	1:A:89:LEU:HD21	0.47	2.10	12	2
1:A:133:LYS:HG2	1:A:140:TRP:CE2	0.46	2.45	22	3
1:A:94:ALA:CB	1:A:99:VAL:HG22	0.46	2.40	27	1
1:A:133:LYS:HE2	1:A:140:TRP:CZ3	0.46	2.46	7	1
1:A:93:TYR:CE2	1:A:98:MET:HB3	0.46	2.45	22	1
1:A:33:THR:HG22	1:A:34:PHE:N	0.46	2.26	23	1
1:A:60:ALA:O	1:A:64:LYS:HB2	0.46	2.11	14	10
1:A:107:GLY:O	1:A:138:ASN:HB2	0.46	2.11	18	7
1:A:27:TYR:CE2	1:A:28:LYS:HG3	0.46	2.45	27	2
1:A:38:LEU:CB	1:A:125:LEU:CD1	0.46	2.93	18	1
1:A:37:LEU:CD2	1:A:89:LEU:HD22	0.46	2.40	25	1
1:A:116:LYS:CB	1:A:117:PRO:HA	0.46	2.41	4	1
1:A:39:VAL:O	1:A:40:ASP:OD1	0.46	2.33	1	2
1:A:21:ASP:OD1	1:A:36:LEU:HD12	0.46	2.11	28	1
1:A:27:TYR:O	1:A:30:GLN:HG2	0.46	2.11	24	12
1:A:77:ASP:OD1	1:A:118:ASN:OD1	0.46	2.34	24	1
1:A:77:ASP:OD2	1:A:118:ASN:OD1	0.46	2.34	7	1
1:A:115:TYR:O	1:A:116:LYS:C	0.45	2.55	16	7
1:A:76:PHE:CD2	1:A:81:ARG:HB3	0.45	2.47	11	1
1:A:136:LYS:HA	1:A:140:TRP:O	0.45	2.11	12	10
1:A:93:TYR:CE1	1:A:98:MET:HB3	0.45	2.46	7	1
1:A:83:ASP:OD1	1:A:87:ARG:O	0.45	2.34	16	1
1:A:104:VAL:HG13	1:A:129:GLU:HB2	0.45	1.87	26	1
1:A:121:HIS:CD2	1:A:121:HIS:N	0.45	2.84	4	1
1:A:133:LYS:HG3	1:A:140:TRP:CE3	0.45	2.46	5	1
1:A:57:GLU:OE1	1:A:108:LEU:HD22	0.45	2.12	23	1
1:A:114:VAL:HG13	1:A:119:ASN:CB	0.45	2.41	29	1
1:A:27:TYR:O	1:A:30:GLN:HG3	0.45	2.12	25	8
1:A:135:GLU:O	1:A:136:LYS:CB	0.45	2.63	4	5
1:A:119:ASN:OD1	1:A:122:GLU:HB3	0.45	2.11	6	2
1:A:38:LEU:CD2	1:A:114:VAL:HB	0.45	2.41	18	1
1:A:73:GLU:OE1	1:A:73:GLU:N	0.45	2.50	24	1
1:A:133:LYS:HD2	1:A:140:TRP:CZ3	0.45	2.46	1	1
1:A:133:LYS:HD2	1:A:140:TRP:CH2	0.45	2.47	1	1
1:A:60:ALA:O	1:A:64:LYS:HB3	0.45	2.12	27	2
1:A:127:LYS:O	1:A:130:ALA:HB3	0.45	2.11	13	1
1:A:57:GLU:OE2	1:A:138:ASN:OD1	0.45	2.34	17	1
1:A:23:VAL:HG11	1:A:62:THR:CG2	0.45	2.42	24	1
1:A:100:ASN:N	1:A:100:ASN:OD1	0.45	2.50	3	3
1:A:128:SER:O	1:A:130:ALA:N	0.45	2.50	13	1
1:A:30:GLN:OE1	1:A:32:MET:CG	0.44	2.65	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:135:GLU:CB	1:A:137:LEU:HD11	0.44	2.41	14	1
1:A:115:TYR:O	1:A:116:LYS:O	0.44	2.35	4	1
1:A:106:GLN:O	1:A:106:GLN:OE1	0.44	2.35	20	1
1:A:136:LYS:HA	1:A:140:TRP:CB	0.44	2.42	13	9
1:A:78:LYS:C	1:A:78:LYS:CD	0.44	2.85	26	1
1:A:101:GLU:HG3	1:A:128:SER:OG	0.44	2.12	9	1
1:A:71:LYS:O	1:A:73:GLU:OE2	0.44	2.34	22	1
1:A:38:LEU:O	1:A:125:LEU:HD13	0.44	2.12	23	1
1:A:132:ALA:HA	1:A:137:LEU:CD1	0.44	2.42	4	1
1:A:87:ARG:N	1:A:87:ARG:HD3	0.44	2.28	5	1
1:A:111:VAL:HG11	1:A:122:GLU:OE2	0.44	2.13	5	1
1:A:27:TYR:CZ	1:A:28:LYS:HG3	0.44	2.48	11	1
1:A:83:ASP:OD1	1:A:83:ASP:N	0.44	2.49	16	1
1:A:93:TYR:OH	1:A:98:MET:SD	0.44	2.75	30	2
1:A:77:ASP:HB3	1:A:118:ASN:OD1	0.44	2.13	27	1
1:A:85:TYR:O	1:A:87:ARG:NH1	0.44	2.50	13	1
1:A:106:GLN:OE1	1:A:106:GLN:CA	0.44	2.65	20	1
1:A:137:LEU:O	1:A:138:ASN:C	0.44	2.56	23	7
1:A:37:LEU:O	1:A:38:LEU:CB	0.44	2.66	6	1
1:A:14:LEU:HD22	1:A:66:VAL:HG23	0.44	1.90	9	1
1:A:13:THR:CB	1:A:26:MET:HB3	0.44	2.43	20	1
1:A:98:MET:SD	1:A:101:GLU:HB2	0.44	2.52	22	1
1:A:69:ALA:HB1	1:A:95:ASP:OD1	0.44	2.13	26	1
1:A:68:ASN:O	1:A:69:ALA:C	0.44	2.57	18	11
1:A:111:VAL:O	1:A:112:ALA:O	0.44	2.35	7	1
1:A:132:ALA:O	1:A:140:TRP:CD1	0.44	2.71	7	1
1:A:37:LEU:HD12	1:A:90:ALA:N	0.44	2.26	13	1
1:A:15:ILE:CD1	1:A:25:LEU:C	0.44	2.86	24	1
1:A:33:THR:HG21	1:A:87:ARG:HH11	0.44	1.70	27	1
1:A:22:THR:HG22	1:A:33:THR:CG2	0.44	2.43	29	1
1:A:76:PHE:CD2	1:A:81:ARG:HG2	0.43	2.47	1	1
1:A:100:ASN:OD1	1:A:100:ASN:N	0.43	2.51	4	3
1:A:141:SER:O	1:A:141:SER:OG	0.43	2.34	15	2
1:A:60:ALA:O	1:A:64:LYS:HD2	0.43	2.13	30	1
1:A:136:LYS:O	1:A:141:SER:HA	0.43	2.13	1	6
1:A:111:VAL:HG23	1:A:129:GLU:OE1	0.43	2.13	11	2
1:A:128:SER:O	1:A:129:GLU:C	0.43	2.55	13	1
1:A:84:LYS:O	1:A:85:TYR:CD1	0.43	2.71	24	1
1:A:108:LEU:CD2	1:A:138:ASN:OD1	0.43	2.63	16	1
1:A:77:ASP:CB	1:A:118:ASN:OD1	0.43	2.65	17	2
1:A:13:THR:O	1:A:14:LEU:C	0.43	2.56	11	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:94:ALA:O	1:A:95:ASP:HB2	0.43	2.12	22	23
1:A:14:LEU:CD2	1:A:67:GLU:HA	0.43	2.44	7	1
1:A:39:VAL:HG21	1:A:100:ASN:ND2	0.43	2.28	21	4
1:A:122:GLU:O	1:A:123:GLN:C	0.43	2.57	4	2
1:A:15:ILE:CD1	1:A:31:PRO:HB3	0.43	2.43	12	3
1:A:35:ARG:O	1:A:36:LEU:C	0.43	2.57	25	5
1:A:20:GLY:HA3	1:A:41:THR:HG21	0.43	1.90	23	1
1:A:106:GLN:O	1:A:107:GLY:C	0.43	2.57	1	2
1:A:69:ALA:CB	1:A:94:ALA:CB	0.43	2.89	2	1
1:A:21:ASP:OD1	1:A:21:ASP:C	0.43	2.57	7	1
1:A:67:GLU:OE1	1:A:67:GLU:CA	0.43	2.67	12	1
1:A:122:GLU:HA	1:A:122:GLU:OE1	0.43	2.14	27	1
1:A:120:THR:HG23	1:A:121:HIS:CD2	0.43	2.49	3	2
1:A:77:ASP:OD1	1:A:120:THR:CG2	0.43	2.66	8	1
1:A:98:MET:O	1:A:99:VAL:C	0.43	2.57	9	3
1:A:33:THR:O	1:A:88:GLY:N	0.43	2.52	7	1
1:A:93:TYR:CE1	1:A:98:MET:HG3	0.43	2.48	19	1
1:A:27:TYR:O	1:A:28:LYS:HB2	0.42	2.14	27	11
1:A:104:VAL:HG13	1:A:129:GLU:OE2	0.42	2.13	5	1
1:A:14:LEU:HG	1:A:15:ILE:N	0.42	2.28	6	1
1:A:102:ALA:O	1:A:106:GLN:HG2	0.42	2.14	8	1
1:A:120:THR:CG2	1:A:121:HIS:N	0.42	2.82	12	1
1:A:69:ALA:HA	1:A:95:ASP:OD1	0.42	2.14	26	1
1:A:108:LEU:HD21	1:A:138:ASN:CG	0.42	2.34	30	1
1:A:136:LYS:HA	1:A:140:TRP:HB2	0.42	1.92	29	1
1:A:93:TYR:OH	1:A:98:MET:CE	0.42	2.68	14	1
1:A:119:ASN:OD1	1:A:119:ASN:C	0.42	2.58	19	2
1:A:119:ASN:O	1:A:119:ASN:CG	0.42	2.58	10	1
1:A:13:THR:HB	1:A:26:MET:CB	0.42	2.44	20	1
1:A:77:ASP:OD1	1:A:120:THR:OG1	0.42	2.37	23	1
1:A:10:GLU:HB2	1:A:74:VAL:CG2	0.42	2.44	10	1
1:A:27:TYR:O	1:A:30:GLN:OE1	0.42	2.38	1	1
1:A:37:LEU:O	1:A:38:LEU:HB2	0.42	2.15	15	4
1:A:136:LYS:O	1:A:141:SER:HB2	0.42	2.15	8	7
1:A:129:GLU:OE2	1:A:133:LYS:CG	0.42	2.68	12	1
1:A:39:VAL:HG12	1:A:104:VAL:CG2	0.42	2.45	15	1
1:A:138:ASN:N	1:A:141:SER:HB2	0.42	2.29	26	1
1:A:113:TYR:CB	1:A:115:TYR:CZ	0.42	3.02	6	1
1:A:63:LYS:O	1:A:67:GLU:CB	0.42	2.67	19	1
1:A:83:ASP:OD2	1:A:89:LEU:HD11	0.42	2.14	6	1
1:A:134:LYS:O	1:A:134:LYS:CG	0.42	2.68	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:TYR:HB3	1:A:87:ARG:CZ	0.42	2.45	13	1
1:A:79:GLY:O	1:A:80:GLN:C	0.42	2.58	14	1
1:A:82:THR:HG22	1:A:87:ARG:O	0.42	2.15	30	1
1:A:27:TYR:O	1:A:28:LYS:C	0.42	2.58	26	1
1:A:72:ILE:N	1:A:72:ILE:CD1	0.41	2.75	5	1
1:A:67:GLU:OE1	1:A:67:GLU:HA	0.41	2.14	12	1
1:A:101:GLU:HG3	1:A:124:LEU:CD2	0.41	2.43	12	1
1:A:74:VAL:HG13	1:A:92:ILE:HD13	0.41	1.91	23	1
1:A:101:GLU:OE2	1:A:128:SER:HB2	0.41	2.15	26	1
1:A:112:ALA:O	1:A:113:TYR:C	0.41	2.57	4	2
1:A:14:LEU:HD22	1:A:66:VAL:C	0.41	2.36	18	1
1:A:111:VAL:O	1:A:112:ALA:C	0.41	2.58	18	1
1:A:9:LYS:HG2	1:A:75:GLU:OE1	0.41	2.15	29	1
1:A:23:VAL:HG23	1:A:23:VAL:O	0.41	2.15	30	1
1:A:35:ARG:HD2	1:A:87:ARG:NH1	0.41	2.30	7	1
1:A:119:ASN:CG	1:A:119:ASN:O	0.41	2.58	12	1
1:A:38:LEU:HB3	1:A:125:LEU:CD1	0.41	2.45	20	1
1:A:115:TYR:O	1:A:118:ASN:HB2	0.41	2.16	11	1
1:A:85:TYR:HB3	1:A:87:ARG:CD	0.41	2.45	18	1
1:A:133:LYS:HE3	1:A:140:TRP:CZ3	0.41	2.50	20	1
1:A:124:LEU:C	1:A:124:LEU:CD2	0.41	2.89	24	1
1:A:13:THR:HG22	1:A:14:LEU:N	0.41	2.31	3	1
1:A:91:TYR:O	1:A:92:ILE:HD13	0.41	2.16	11	1
1:A:37:LEU:CD1	1:A:89:LEU:HB3	0.41	2.46	15	1
1:A:24:LYS:NZ	1:A:31:PRO:HB2	0.41	2.31	22	1
1:A:104:VAL:CG1	1:A:129:GLU:HB2	0.41	2.45	20	2
1:A:10:GLU:OE1	1:A:27:TYR:OH	0.41	2.34	21	1
1:A:114:VAL:CG1	1:A:119:ASN:CB	0.41	2.98	29	1
1:A:63:LYS:HA	1:A:66:VAL:HG22	0.41	1.93	4	2
1:A:114:VAL:CG1	1:A:122:GLU:OE1	0.41	2.68	11	1
1:A:37:LEU:HD12	1:A:77:ASP:OD2	0.41	2.15	22	1
1:A:16:LYS:O	1:A:24:LYS:CB	0.41	2.69	4	1
1:A:38:LEU:HD22	1:A:122:GLU:OE1	0.41	2.16	5	1
1:A:21:ASP:OD1	1:A:21:ASP:O	0.41	2.39	7	1
1:A:14:LEU:HB2	1:A:72:ILE:HD13	0.41	1.93	11	1
1:A:37:LEU:HD13	1:A:118:ASN:OD1	0.41	2.16	22	1
1:A:119:ASN:ND2	1:A:122:GLU:CB	0.41	2.83	3	1
1:A:135:GLU:O	1:A:136:LYS:HB2	0.41	2.16	25	3
1:A:68:ASN:N	1:A:68:ASN:ND2	0.41	2.66	5	1
1:A:85:TYR:HB3	1:A:87:ARG:HD2	0.41	1.93	6	1
1:A:133:LYS:CE	1:A:140:TRP:CZ3	0.41	3.04	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:137:LEU:N	1:A:137:LEU:HD23	0.41	2.31	10	1
1:A:129:GLU:O	1:A:133:LYS:HG3	0.41	2.16	22	1
1:A:61:PHE:O	1:A:65:MET:HB3	0.41	2.16	27	1
1:A:106:GLN:O	1:A:108:LEU:N	0.41	2.54	29	1
1:A:83:ASP:HB2	1:A:87:ARG:CG	0.41	2.46	1	1
1:A:40:ASP:OD2	1:A:112:ALA:HB2	0.41	2.15	18	1
1:A:135:GLU:C	1:A:136:LYS:CG	0.41	2.90	20	1
1:A:105:ARG:O	1:A:105:ARG:CG	0.40	2.70	2	1
1:A:35:ARG:NH2	1:A:85:TYR:CD2	0.40	2.90	12	1
1:A:36:LEU:CD2	1:A:92:ILE:CG1	0.40	3.00	10	1
1:A:14:LEU:CD2	1:A:67:GLU:CD	0.40	2.89	13	1
1:A:37:LEU:HD11	1:A:89:LEU:HB3	0.40	1.94	18	1
1:A:64:LYS:O	1:A:68:ASN:CG	0.40	2.60	25	1
1:A:120:THR:HG22	1:A:121:HIS:ND1	0.40	2.31	28	2
1:A:114:VAL:CG1	1:A:119:ASN:HB3	0.40	2.45	29	1
1:A:65:MET:CE	1:A:97:LYS:NZ	0.40	2.85	14	1
1:A:114:VAL:HG11	1:A:119:ASN:OD1	0.40	2.16	16	1
1:A:60:ALA:O	1:A:64:LYS:HG3	0.40	2.17	20	1
1:A:38:LEU:CD2	1:A:114:VAL:HG13	0.40	2.46	24	1
1:A:124:LEU:HD23	1:A:124:LEU:C	0.40	2.36	28	1
1:A:82:THR:C	1:A:89:LEU:CD1	0.40	2.89	30	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	118/149 (79%)	103±3 (87±2%)	13±3 (11±2%)	2±1 (2±1%)	10	50
All	All	3540/4470 (79%)	3085 (87%)	380 (11%)	75 (2%)	10	50

All 14 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	138	ASN	12

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Mol	Chain	Res	Type	Models (Total)
1	A	119	ASN	12
1	A	69	ALA	11
1	A	118	ASN	9
1	A	57	GLU	9
1	A	98	MET	7
1	A	112	ALA	4
1	A	79	GLY	3
1	A	83	ASP	2
1	A	16	LYS	2
1	A	88	GLY	1
1	A	141	SER	1
1	A	80	GLN	1
1	A	109	ALA	1

6.3.2 Protein sidechains [i](#)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	99/125 (79%)	80±4 (81±4%)	19±4 (19±4%)	4 36
All	All	2970/3750 (79%)	2412 (81%)	558 (19%)	4 36

All 65 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	126	ARG	21
1	A	37	LEU	20
1	A	81	ARG	18
1	A	13	THR	17
1	A	127	LYS	16
1	A	131	GLN	16
1	A	16	LYS	15
1	A	19	ASP	15
1	A	63	LYS	15
1	A	65	MET	15
1	A	78	LYS	15
1	A	106	GLN	14

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Mol	Chain	Res	Type	Models (Total)
1	A	24	LYS	13
1	A	110	LYS	13
1	A	87	ARG	13
1	A	33	THR	12
1	A	9	LYS	11
1	A	41	THR	11
1	A	77	ASP	11
1	A	84	LYS	11
1	A	83	ASP	11
1	A	134	LYS	11
1	A	40	ASP	11
1	A	116	LYS	10
1	A	122	GLU	10
1	A	133	LYS	10
1	A	80	GLN	10
1	A	105	ARG	10
1	A	128	SER	9
1	A	136	LYS	9
1	A	124	LEU	9
1	A	39	VAL	9
1	A	21	ASP	8
1	A	73	GLU	8
1	A	35	ARG	8
1	A	70	LYS	8
1	A	57	GLU	8
1	A	59	SER	8
1	A	129	GLU	7
1	A	113	TYR	7
1	A	26	MET	7
1	A	22	THR	6
1	A	82	THR	6
1	A	119	ASN	6
1	A	98	MET	6
1	A	32	MET	6
1	A	95	ASP	5
1	A	101	GLU	5
1	A	14	LEU	4
1	A	64	LYS	4
1	A	71	LYS	3
1	A	137	LEU	3
1	A	67	GLU	3
1	A	28	LYS	3

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Mol	Chain	Res	Type	Models (Total)
1	A	23	VAL	2
1	A	97	LYS	2
1	A	103	LEU	2
1	A	123	GLN	2
1	A	74	VAL	2
1	A	75	GLU	2
1	A	141	SER	2
1	A	30	GLN	1
1	A	135	GLU	1
1	A	138	ASN	1
1	A	120	THR	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided