



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 04:06 PM BST

PDB ID : 1JOQ
Title : Ensemble structures for Staphylococcal nuclease-H124L in ternary complex with Ca²⁺ and thymidine-3',5'-bisphosphate
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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
<http://wwpdb.org/validation/2016/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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

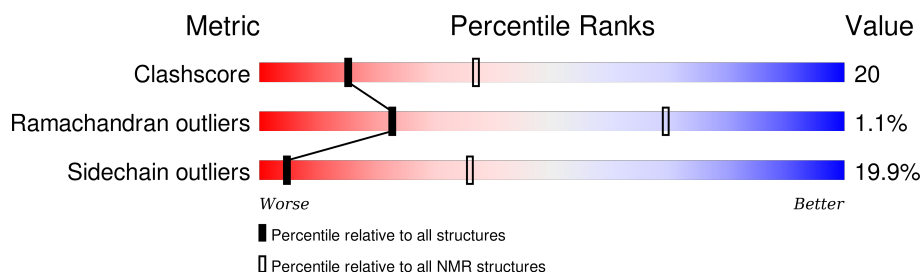
1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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 14 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:8-A:41, A:57-A:140 (118)	0.31	14

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 6 single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2432 atoms, of which 1226 are hydrogens and 0 are deuteriums.

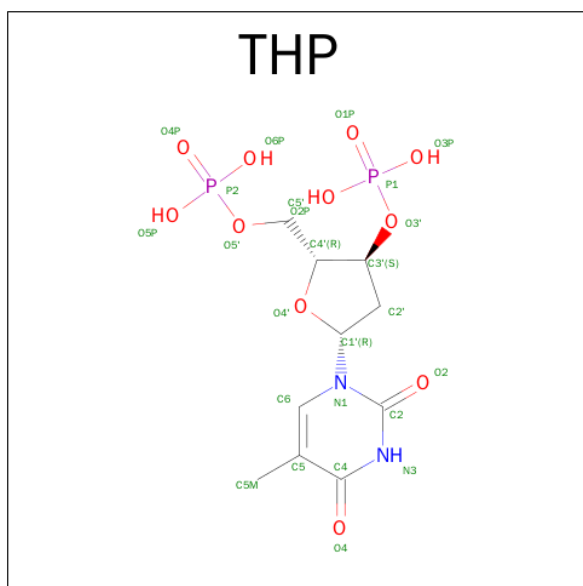
- Molecule 1 is a protein called staphylococcal nuclease.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 2 is THYMIDINE-3',5'-DIPHOSPHATE (three-letter code: THP) (formula: $C_{10}H_{16}N_2O_{11}P_2$).



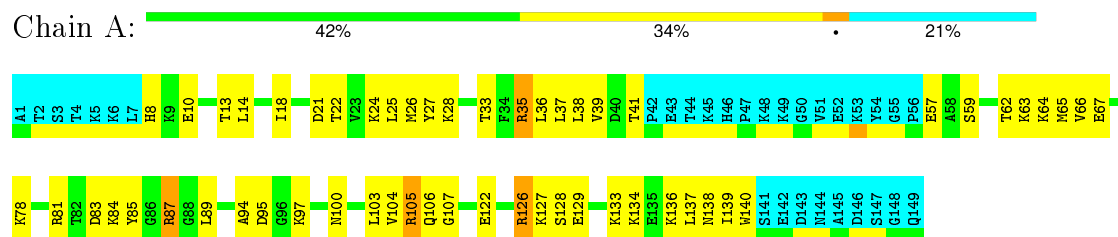
Mol	Chain	Residues	Atoms					
2	A	1	Total	C	H	N	O	P
			35	10	10	2	11	2

4 Residue-property plots

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: staphylococcal nuclease

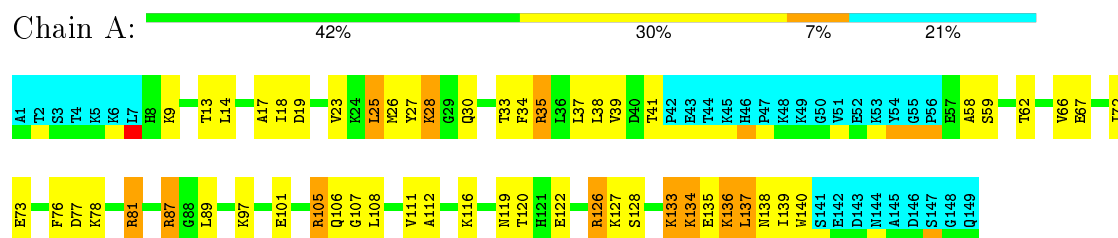


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

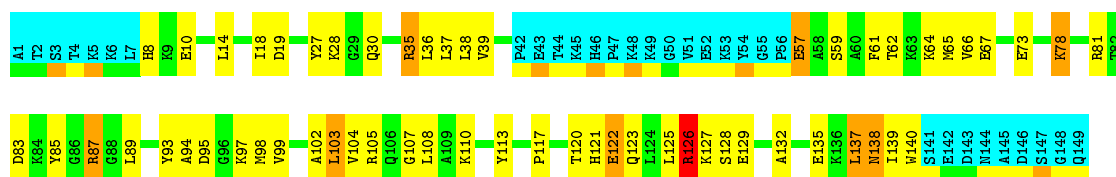
- Molecule 1: staphylococcal nuclease



4.2.2 Score per residue for model 2

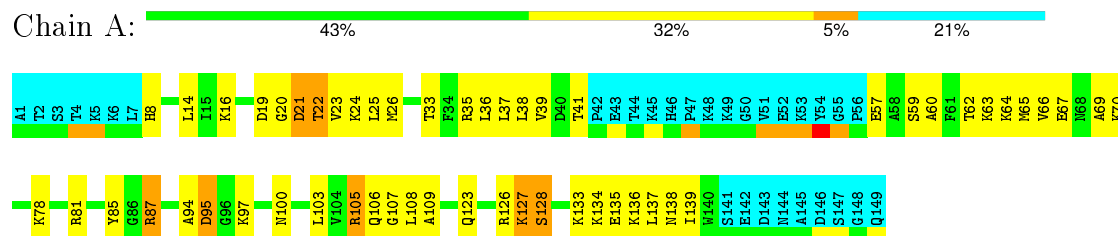
- Molecule 1: staphylococcal nuclease





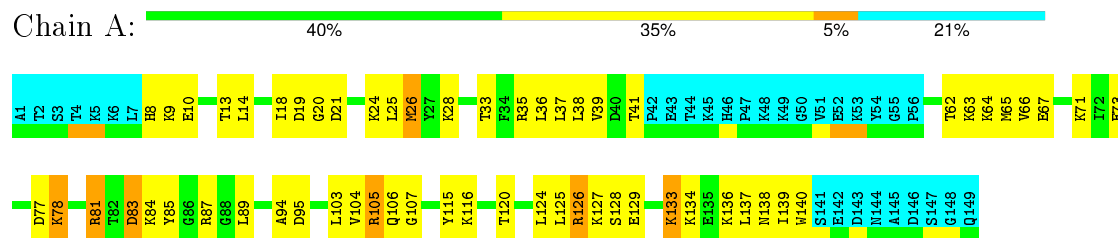
4.2.3 Score per residue for model 3

- Molecule 1: staphylococcal nuclease



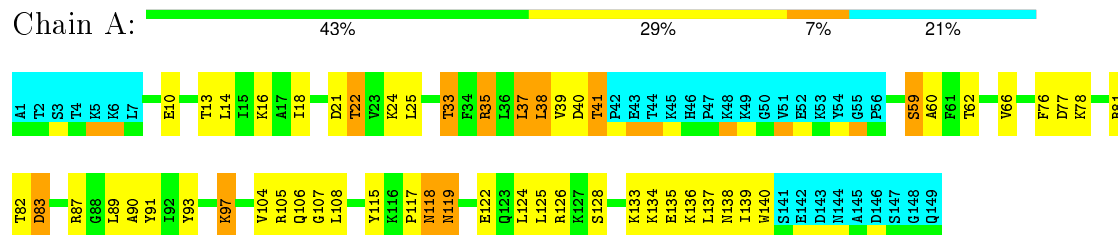
4.2.4 Score per residue for model 4

- Molecule 1: staphylococcal nuclease



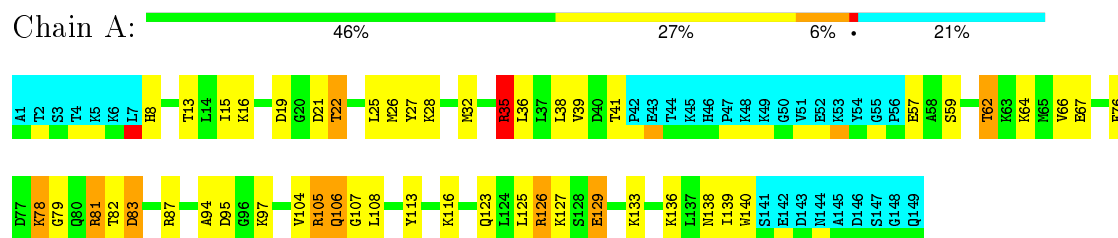
4.2.5 Score per residue for model 5

- Molecule 1: staphylococcal nuclease



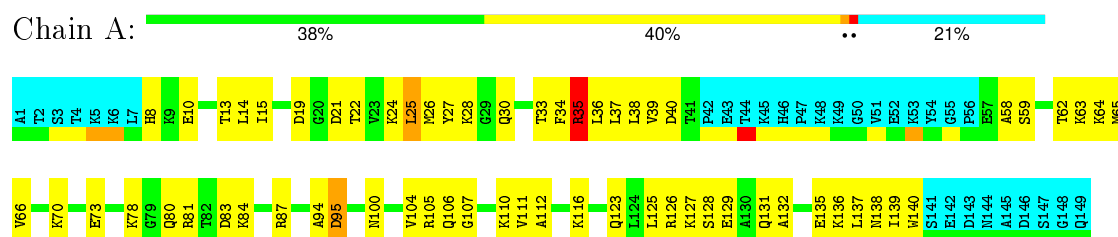
4.2.6 Score per residue for model 6

- Molecule 1: staphylococcal nuclease



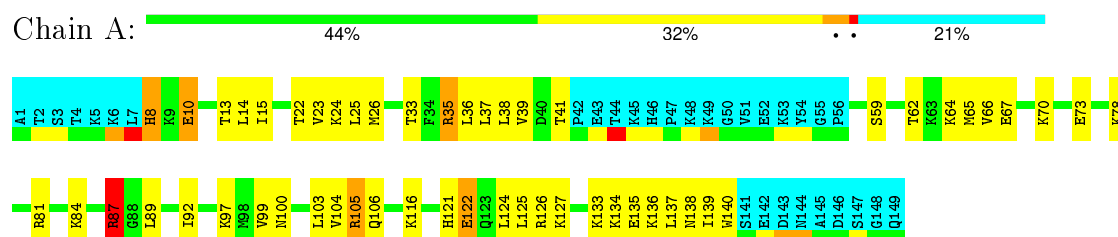
4.2.7 Score per residue for model 7

- Molecule 1: staphylococcal nuclease



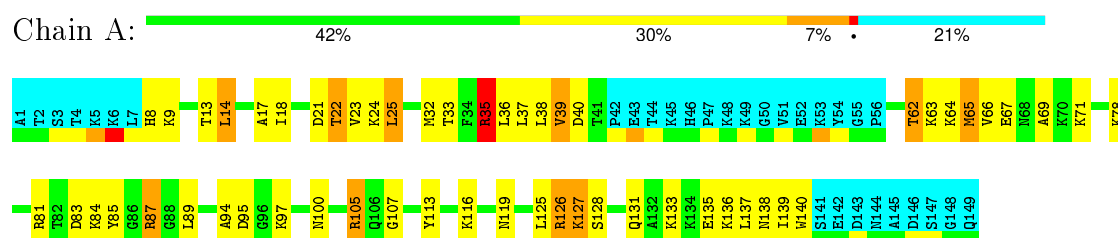
4.2.8 Score per residue for model 8

- Molecule 1: staphylococcal nuclease



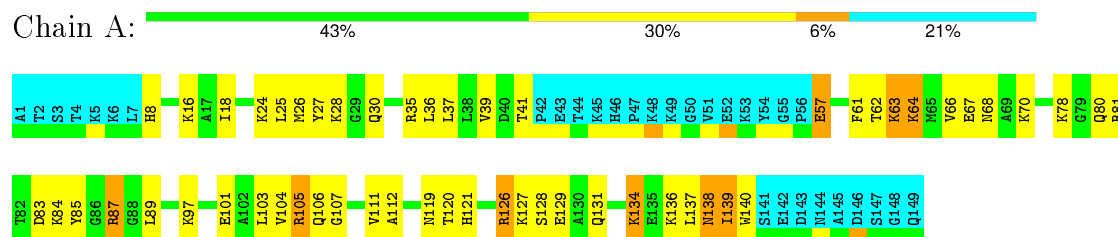
4.2.9 Score per residue for model 9

- Molecule 1: staphylococcal nuclease



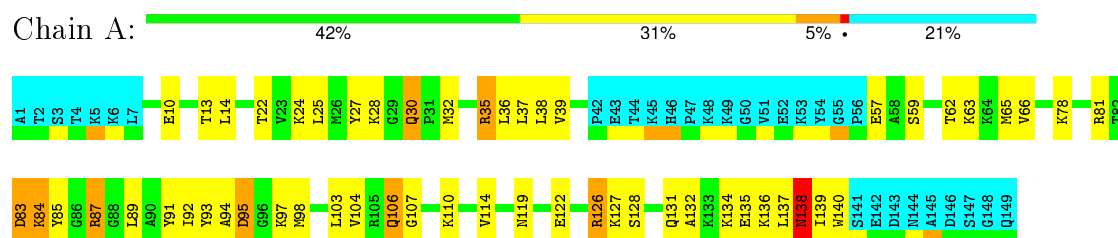
4.2.10 Score per residue for model 10

- Molecule 1: staphylococcal nuclease



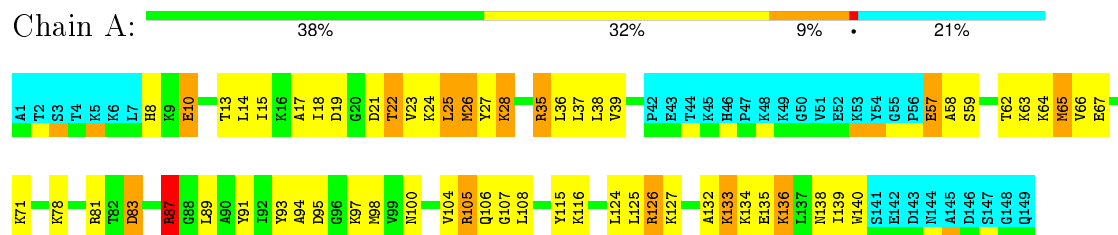
4.2.11 Score per residue for model 11

- Molecule 1: staphylococcal nuclease



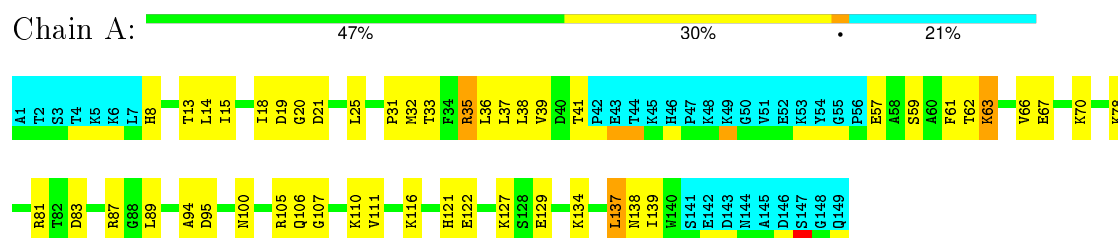
4.2.12 Score per residue for model 12

- Molecule 1: staphylococcal nuclease



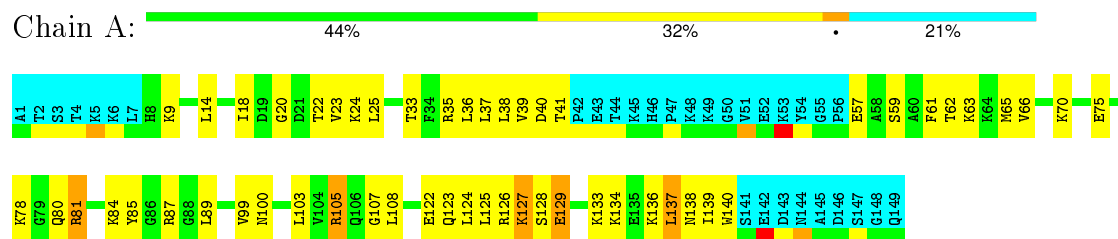
4.2.13 Score per residue for model 13

- Molecule 1: staphylococcal nuclease



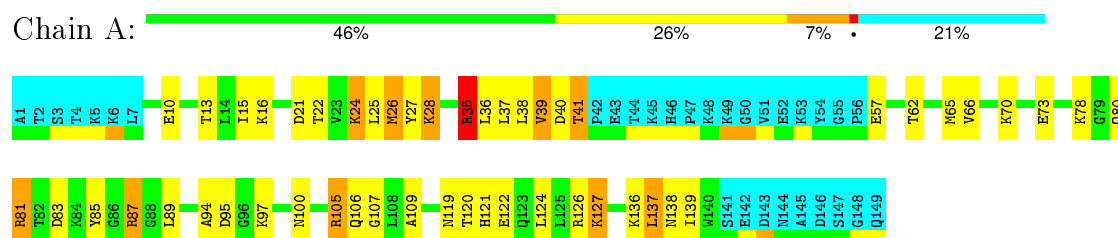
4.2.14 Score per residue for model 14 (medoid)

- Molecule 1: staphylococcal nuclease



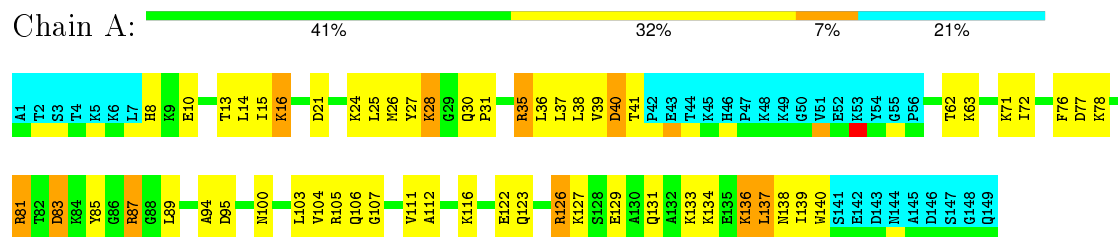
4.2.15 Score per residue for model 15

- Molecule 1: staphylococcal nuclease



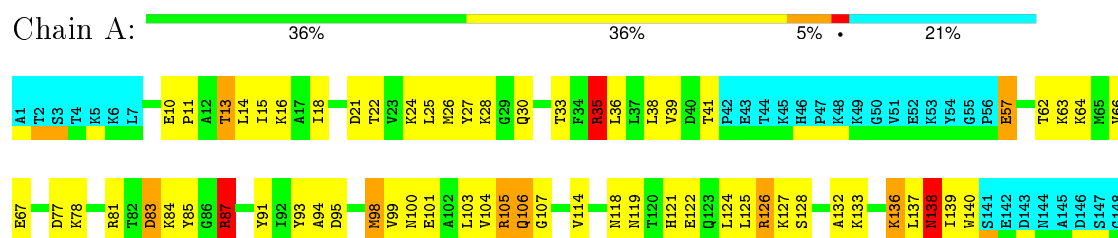
4.2.16 Score per residue for model 16

- Molecule 1: staphylococcal nuclease



4.2.17 Score per residue for model 17

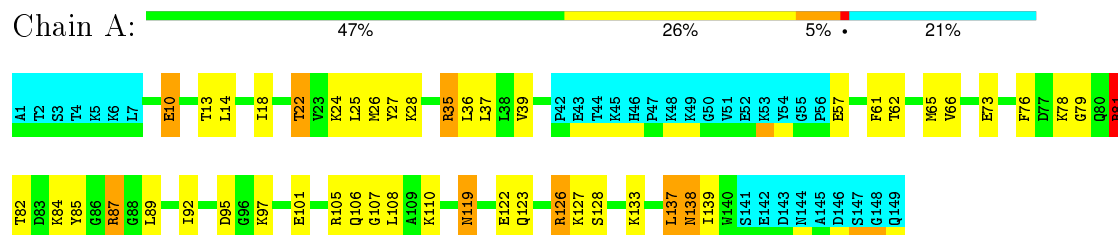
- Molecule 1: staphylococcal nuclease



Q149

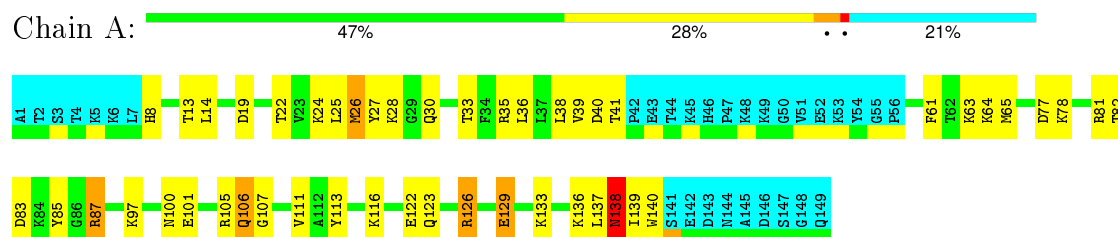
4.2.18 Score per residue for model 18

- Molecule 1: staphylococcal nuclease



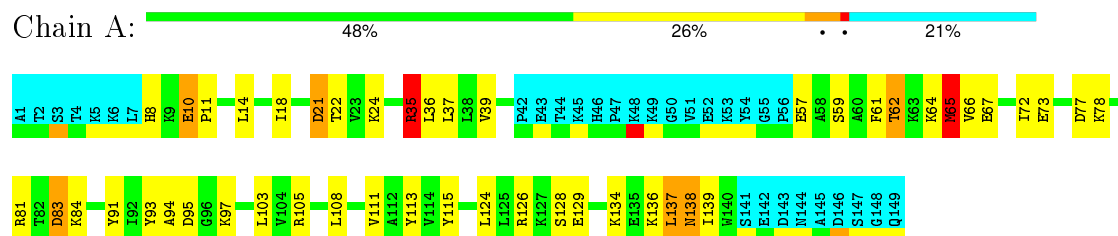
4.2.19 Score per residue for model 19

- Molecule 1: staphylococcal nuclease



4.2.20 Score per residue for model 20

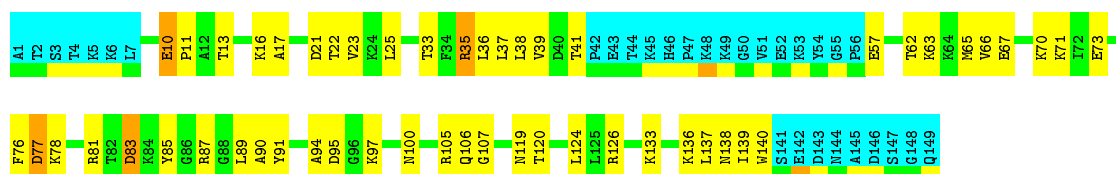
- Molecule 1: staphylococcal nuclease



4.2.21 Score per residue for model 21

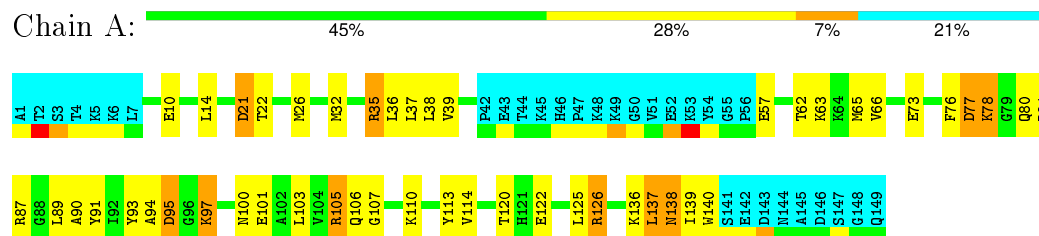
- Molecule 1: staphylococcal nuclease





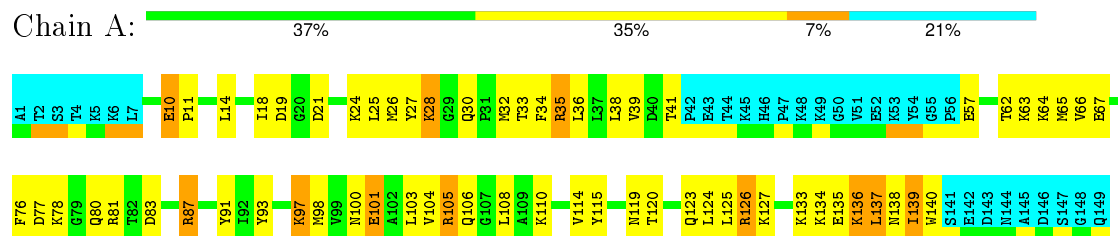
4.2.22 Score per residue for model 22

- Molecule 1: staphylococcal nuclease



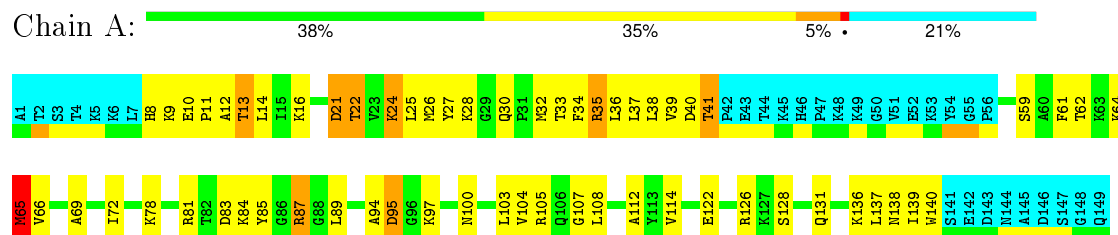
4.2.23 Score per residue for model 23

- Molecule 1: staphylococcal nuclease



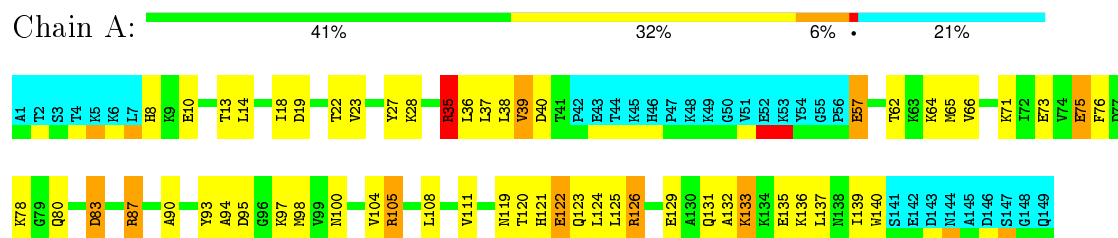
4.2.24 Score per residue for model 24

- Molecule 1: staphylococcal nuclease



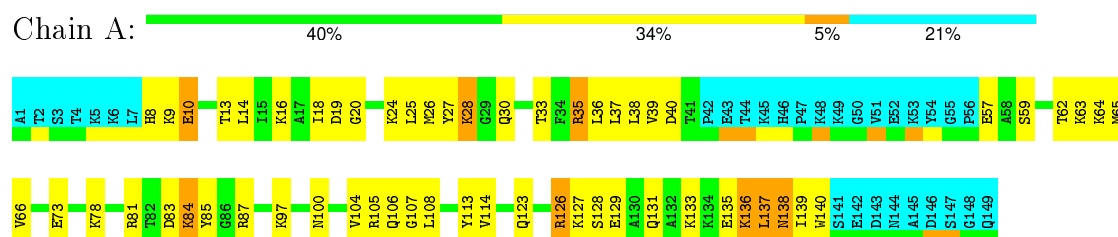
4.2.25 Score per residue for model 25

- Molecule 1: staphylococcal nuclease



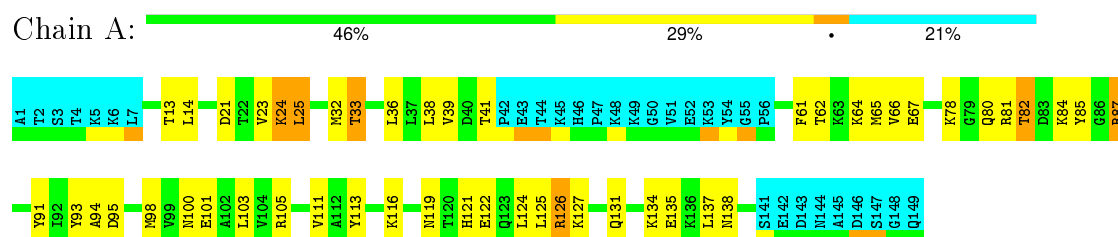
4.2.26 Score per residue for model 26

- Molecule 1: staphylococcal nuclease



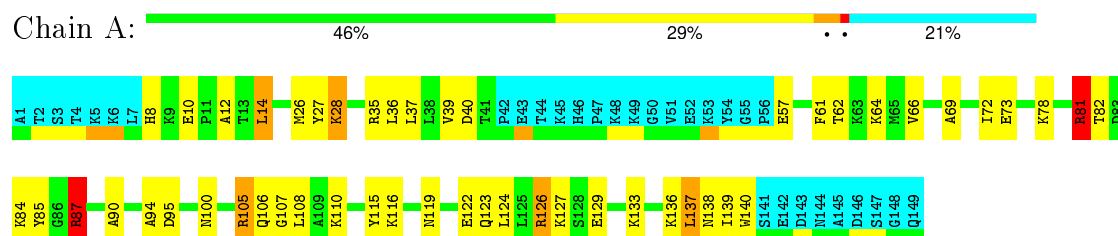
4.2.27 Score per residue for model 27

- Molecule 1: staphylococcal nuclease



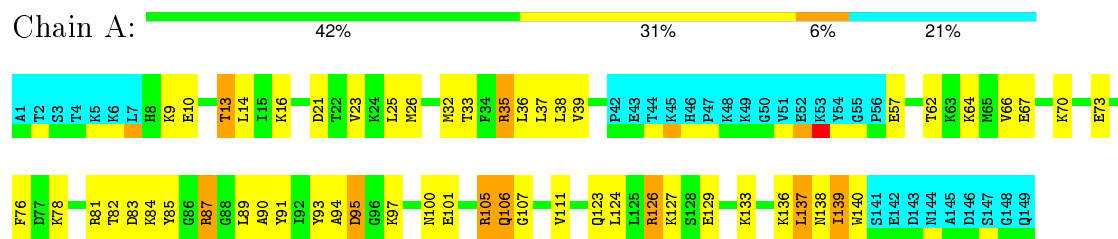
4.2.28 Score per residue for model 28

- Molecule 1: staphylococcal nuclease



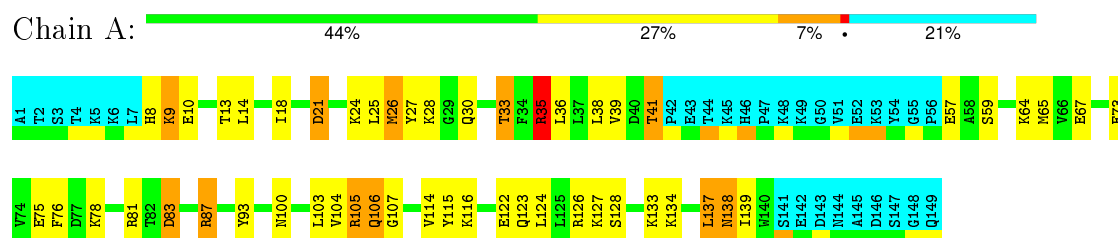
4.2.29 Score per residue for model 29

- 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
INSIGHTII	structure solution	2.3
HBPLUS	structure solution	
X-PLOR	refinement	3.1

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

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: THP

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	4.6±0.5
All	All	0	139

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	29
1	A	126	ARG	Sidechain	29
1	A	87	ARG	Sidechain	29
1	A	105	ARG	Sidechain	28
1	A	35	ARG	Sidechain	24

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	A	947	984	984	38±6
2	A	25	10	12	4±3
All	All	29160	29820	29880	1152

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 20.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:THR:O	1:A:66:VAL:HG22	0.93	1.64	25	27
1:A:21:ASP:OD1	1:A:36:LEU:HD12	0.89	1.67	17	5
1:A:107:GLY:O	1:A:139:ILE:HD12	0.89	1.66	7	22
1:A:14:LEU:HD13	1:A:15:ILE:N	0.88	1.83	7	2
1:A:36:LEU:HD22	1:A:100:ASN:OD1	0.87	1.69	17	17
1:A:40:ASP:OD2	1:A:112:ALA:HB3	0.87	1.70	16	1
1:A:108:LEU:HD21	1:A:138:ASN:OD1	0.82	1.75	2	1
1:A:38:LEU:CD2	1:A:114:VAL:HG22	0.82	2.04	24	3
1:A:121:HIS:O	1:A:125:LEU:HD12	0.79	1.76	17	1
1:A:38:LEU:HD23	1:A:114:VAL:HG22	0.78	1.53	24	3
1:A:89:LEU:HD22	2:A:150:THP:H52	0.78	1.54	4	1
1:A:101:GLU:OE1	1:A:124:LEU:HD21	0.76	1.80	27	1
1:A:14:LEU:HD22	1:A:25:LEU:HD22	0.76	1.58	12	2
1:A:104:VAL:HG21	1:A:125:LEU:HD22	0.75	1.57	23	4
1:A:57:GLU:OE2	1:A:108:LEU:HD21	0.75	1.79	18	1
1:A:57:GLU:CD	1:A:108:LEU:HD21	0.75	2.02	18	1
1:A:24:LYS:O	1:A:25:LEU:HD23	0.74	1.83	3	16
1:A:120:THR:HG22	1:A:121:HIS:CE1	0.74	2.17	10	1
1:A:24:LYS:C	1:A:25:LEU:HD23	0.74	2.02	12	4
1:A:37:LEU:HD11	1:A:89:LEU:HB3	0.73	1.59	14	14
1:A:40:ASP:OD1	1:A:112:ALA:HB3	0.73	1.84	24	1
1:A:18:ILE:HD11	1:A:24:LYS:CG	0.73	2.13	17	7
1:A:83:ASP:OD2	1:A:89:LEU:HD21	0.72	1.85	10	2
1:A:39:VAL:HG13	1:A:125:LEU:HD13	0.72	1.62	5	1
1:A:21:ASP:CG	1:A:41:THR:HG23	0.71	2.06	21	3
1:A:38:LEU:HD12	1:A:122:GLU:OE1	0.71	1.84	22	1
1:A:18:ILE:HD11	1:A:24:LYS:HE2	0.71	1.61	20	2
1:A:22:THR:HG23	1:A:35:ARG:HG2	0.71	1.61	9	1
1:A:17:ALA:CB	1:A:23:VAL:HG12	0.69	2.17	12	4
1:A:14:LEU:C	1:A:14:LEU:HD13	0.69	2.08	22	7
1:A:18:ILE:HD11	1:A:24:LYS:HG2	0.69	1.64	9	3
1:A:22:THR:HG23	1:A:35:ARG:HD2	0.68	1.66	18	2
1:A:14:LEU:HD13	1:A:14:LEU:C	0.67	2.09	18	9
1:A:99:VAL:O	1:A:103:LEU:HD12	0.67	1.89	17	3
1:A:36:LEU:CB	1:A:39:VAL:HG21	0.67	2.19	29	11
1:A:18:ILE:HD12	1:A:22:THR:HG22	0.67	1.66	25	1
1:A:23:VAL:HG21	1:A:92:ILE:CD1	0.66	2.21	8	1
1:A:37:LEU:HD13	1:A:77:ASP:OD2	0.66	1.90	21	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:THR:HG22	1:A:33:THR:CG2	0.65	2.22	3	2
1:A:25:LEU:HD12	1:A:34:PHE:CD2	0.65	2.25	7	1
1:A:115:TYR:CD2	2:A:150:THP:N3	0.64	2.65	4	1
1:A:18:ILE:HG22	1:A:19:ASP:OD1	0.63	1.92	13	4
1:A:22:THR:HG22	1:A:33:THR:HG22	0.63	1.68	3	1
1:A:38:LEU:O	1:A:111:VAL:HG13	0.63	1.94	7	4
1:A:35:ARG:NH2	2:A:150:THP:P2	0.63	2.72	6	2
1:A:36:LEU:HB3	1:A:39:VAL:HG21	0.63	1.70	29	7
1:A:135:GLU:HB3	1:A:137:LEU:HD12	0.62	1.70	2	1
1:A:85:TYR:CG	1:A:87:ARG:NH1	0.62	2.68	28	1
1:A:21:ASP:CG	1:A:41:THR:HG22	0.62	2.14	30	2
1:A:38:LEU:CD1	1:A:125:LEU:HD12	0.62	2.24	5	1
1:A:85:TYR:CG	1:A:87:ARG:CZ	0.62	2.83	29	1
1:A:133:LYS:CG	1:A:140:TRP:CZ3	0.61	2.83	1	2
1:A:14:LEU:HD12	1:A:25:LEU:CD2	0.61	2.25	11	1
1:A:36:LEU:HB3	1:A:39:VAL:HG13	0.61	1.72	25	3
1:A:83:ASP:CG	1:A:89:LEU:HD11	0.61	2.15	21	5
1:A:104:VAL:O	1:A:132:ALA:HB2	0.60	1.96	2	5
1:A:36:LEU:CB	1:A:39:VAL:CG2	0.60	2.80	3	24
1:A:124:LEU:C	1:A:124:LEU:HD13	0.60	2.16	15	1
1:A:38:LEU:HD12	1:A:125:LEU:HD12	0.60	1.72	5	2
1:A:18:ILE:HD11	1:A:24:LYS:HD3	0.60	1.71	23	1
1:A:21:ASP:OD2	1:A:39:VAL:HG23	0.60	1.96	22	2
1:A:20:GLY:O	1:A:62:THR:HG21	0.59	1.97	13	1
1:A:36:LEU:CD1	1:A:103:LEU:CD1	0.59	2.80	27	7
1:A:104:VAL:HG11	1:A:128:SER:OG	0.59	1.96	2	4
1:A:85:TYR:CZ	2:A:150:THP:O3P	0.59	2.55	29	6
1:A:21:ASP:OD1	1:A:41:THR:HG23	0.58	1.97	21	3
1:A:77:ASP:OD1	1:A:91:TYR:CE2	0.58	2.57	22	1
1:A:120:THR:CG2	1:A:121:HIS:N	0.58	2.67	2	3
1:A:37:LEU:O	1:A:39:VAL:HG13	0.57	1.98	26	3
1:A:25:LEU:HD12	1:A:34:PHE:HD2	0.57	1.59	7	1
1:A:33:THR:O	1:A:33:THR:HG23	0.57	1.99	1	3
1:A:57:GLU:OE1	1:A:108:LEU:HD21	0.57	1.99	20	1
1:A:39:VAL:CG2	1:A:40:ASP:N	0.57	2.67	9	3
1:A:133:LYS:CG	1:A:140:TRP:CE3	0.57	2.87	1	4
1:A:77:ASP:OD1	1:A:91:TYR:CE1	0.57	2.57	21	1
1:A:14:LEU:CD2	1:A:25:LEU:CD2	0.57	2.81	29	2
1:A:91:TYR:O	1:A:93:TYR:CE1	0.57	2.57	23	4
1:A:23:VAL:CG2	1:A:92:ILE:CD1	0.57	2.82	8	1
1:A:38:LEU:HD22	1:A:122:GLU:OE2	0.57	2.00	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:GLY:C	1:A:41:THR:HG21	0.57	2.20	3	1
1:A:93:TYR:CZ	1:A:98:MET:SD	0.57	2.98	27	3
1:A:36:LEU:HD22	1:A:100:ASN:CG	0.57	2.20	12	3
1:A:35:ARG:NH1	1:A:87:ARG:NH2	0.56	2.52	25	1
1:A:33:THR:HG23	1:A:33:THR:O	0.56	2.00	29	1
1:A:14:LEU:HD22	1:A:25:LEU:CD2	0.56	2.30	17	4
1:A:85:TYR:CE1	2:A:150:THP:O3P	0.56	2.58	16	5
1:A:110:LYS:CD	1:A:140:TRP:CZ2	0.56	2.88	2	1
1:A:133:LYS:HG3	1:A:140:TRP:CE3	0.56	2.35	1	3
1:A:76:PHE:CD2	1:A:90:ALA:HB2	0.56	2.36	22	1
1:A:76:PHE:CD1	1:A:90:ALA:HB2	0.56	2.35	29	4
1:A:100:ASN:O	1:A:104:VAL:HG23	0.56	1.99	30	4
1:A:36:LEU:CD1	1:A:103:LEU:HD13	0.56	2.30	23	5
1:A:69:ALA:HB2	1:A:94:ALA:HB1	0.56	1.76	28	4
1:A:14:LEU:HD13	1:A:66:VAL:HB	0.56	1.78	8	2
1:A:38:LEU:HD13	1:A:122:GLU:HA	0.55	1.77	17	4
1:A:129:GLU:OE2	1:A:140:TRP:CZ2	0.55	2.59	29	4
1:A:38:LEU:HD22	1:A:114:VAL:HG13	0.55	1.79	17	1
1:A:23:VAL:HG23	1:A:25:LEU:HD11	0.55	1.77	9	2
1:A:22:THR:O	1:A:23:VAL:HG13	0.55	2.01	21	4
1:A:91:TYR:CD1	1:A:121:HIS:ND1	0.55	2.74	27	1
1:A:103:LEU:HB3	1:A:109:ALA:HB2	0.55	1.79	3	1
1:A:85:TYR:CE2	2:A:150:THP:O3P	0.54	2.60	15	2
1:A:39:VAL:O	1:A:39:VAL:HG23	0.54	2.02	24	1
1:A:69:ALA:CB	1:A:94:ALA:HB1	0.54	2.33	28	3
1:A:104:VAL:HG21	1:A:125:LEU:CD2	0.54	2.32	23	2
1:A:129:GLU:OE2	1:A:140:TRP:CH2	0.54	2.60	29	1
1:A:137:LEU:O	1:A:139:ILE:N	0.54	2.41	19	10
1:A:87:ARG:CZ	2:A:150:THP:O4P	0.54	2.56	9	7
1:A:106:GLN:O	1:A:137:LEU:HD22	0.54	2.02	18	2
1:A:27:TYR:CE1	1:A:28:LYS:HG2	0.54	2.38	23	3
1:A:17:ALA:HB1	1:A:23:VAL:HG12	0.54	1.77	12	3
1:A:38:LEU:HD11	1:A:91:TYR:OH	0.54	2.02	17	1
1:A:14:LEU:HD22	1:A:66:VAL:O	0.53	2.03	13	2
1:A:35:ARG:NH1	2:A:150:THP:O5'	0.53	2.41	25	1
1:A:91:TYR:CG	1:A:121:HIS:CE1	0.53	2.96	27	1
1:A:85:TYR:CD1	1:A:87:ARG:NH1	0.53	2.76	29	1
1:A:72:ILE:N	1:A:72:ILE:HD12	0.53	2.19	16	1
1:A:35:ARG:NH2	2:A:150:THP:O5P	0.53	2.42	6	2
1:A:63:LYS:O	1:A:67:GLU:CG	0.53	2.57	21	2
1:A:36:LEU:HB3	1:A:39:VAL:CG2	0.53	2.34	28	14

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:136:LYS:CA	1:A:140:TRP:O	0.53	2.56	12	8
1:A:27:TYR:CE1	1:A:28:LYS:CG	0.53	2.91	23	2
1:A:61:PHE:CD2	1:A:108:LEU:CD1	0.53	2.91	28	1
1:A:77:ASP:OD1	1:A:77:ASP:N	0.53	2.42	22	2
1:A:39:VAL:HG23	1:A:39:VAL:O	0.53	2.03	16	1
1:A:15:ILE:HD12	1:A:25:LEU:O	0.53	2.03	6	1
1:A:115:TYR:CD2	2:A:150:THP:C4	0.53	2.91	4	1
1:A:110:LYS:HD3	1:A:140:TRP:CZ2	0.53	2.39	2	1
1:A:87:ARG:NH1	2:A:150:THP:O6P	0.53	2.42	16	1
1:A:35:ARG:NH1	2:A:150:THP:O6P	0.53	2.42	1	1
1:A:87:ARG:NH2	2:A:150:THP:O4P	0.53	2.42	28	3
1:A:85:TYR:OH	2:A:150:THP:P1	0.53	2.67	16	6
1:A:104:VAL:HG13	1:A:129:GLU:OE1	0.53	2.04	16	1
1:A:137:LEU:HD22	1:A:138:ASN:ND2	0.53	2.18	1	1
1:A:111:VAL:O	1:A:111:VAL:HG13	0.53	2.04	20	1
1:A:36:LEU:HB2	1:A:39:VAL:CG2	0.52	2.34	27	22
1:A:87:ARG:NH2	2:A:150:THP:O6P	0.52	2.42	18	3
1:A:35:ARG:CZ	2:A:150:THP:O4P	0.52	2.57	5	6
1:A:100:ASN:HA	1:A:103:LEU:HD12	0.52	1.81	3	1
1:A:8:HIS:CE1	1:A:10:GLU:CG	0.52	2.93	7	1
1:A:19:ASP:OD1	1:A:22:THR:N	0.52	2.42	7	1
1:A:14:LEU:HA	1:A:25:LEU:HD23	0.52	1.82	9	1
1:A:83:ASP:OD2	2:A:150:THP:C2	0.52	2.58	20	5
1:A:108:LEU:C	1:A:139:ILE:HD11	0.52	2.25	28	2
1:A:21:ASP:OD2	1:A:39:VAL:CG2	0.52	2.58	22	2
1:A:35:ARG:NH2	2:A:150:THP:O4P	0.52	2.42	20	3
1:A:95:ASP:OD1	1:A:95:ASP:N	0.52	2.43	3	2
1:A:35:ARG:NE	2:A:150:THP:O5P	0.52	2.43	1	4
1:A:119:ASN:OD1	1:A:122:GLU:CB	0.52	2.57	18	2
1:A:39:VAL:HG22	1:A:40:ASP:H	0.52	1.65	19	1
1:A:21:ASP:OD2	1:A:41:THR:N	0.52	2.43	13	1
1:A:131:GLN:O	1:A:135:GLU:CG	0.52	2.57	27	1
1:A:83:ASP:OD2	1:A:87:ARG:NH2	0.52	2.43	11	1
1:A:38:LEU:HD11	1:A:119:ASN:HA	0.51	1.80	27	2
1:A:22:THR:OG1	1:A:35:ARG:NH1	0.51	2.43	17	1
1:A:37:LEU:CD1	1:A:77:ASP:OD2	0.51	2.58	21	1
1:A:35:ARG:CZ	2:A:150:THP:O6P	0.51	2.58	10	4
1:A:61:PHE:CZ	1:A:106:GLN:OE1	0.51	2.64	13	1
1:A:38:LEU:CD1	1:A:122:GLU:OE1	0.51	2.58	22	1
1:A:38:LEU:HD21	1:A:114:VAL:HG13	0.51	1.83	26	1
1:A:138:ASN:O	1:A:140:TRP:N	0.51	2.44	10	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:TYR:CB	1:A:87:ARG:NE	0.51	2.74	29	1
1:A:36:LEU:HB2	1:A:39:VAL:CG1	0.51	2.36	19	1
1:A:35:ARG:CD	2:A:150:THP:O4P	0.51	2.59	16	2
1:A:37:LEU:O	1:A:39:VAL:HG12	0.51	2.06	15	3
1:A:78:LYS:CD	1:A:117:PRO:O	0.51	2.58	2	1
1:A:25:LEU:CD1	1:A:34:PHE:CD1	0.51	2.94	1	1
1:A:84:LYS:HG3	1:A:85:TYR:CD1	0.50	2.41	28	3
1:A:18:ILE:HD11	1:A:24:LYS:HG3	0.50	1.82	30	2
1:A:133:LYS:HG2	1:A:140:TRP:CE3	0.50	2.41	4	5
1:A:91:TYR:O	1:A:93:TYR:CD1	0.50	2.65	23	1
1:A:111:VAL:HG23	1:A:129:GLU:OE2	0.50	2.05	16	1
1:A:35:ARG:NE	2:A:150:THP:P2	0.50	2.84	10	2
1:A:35:ARG:NH1	2:A:150:THP:P2	0.50	2.85	26	1
1:A:8:HIS:CE1	1:A:10:GLU:OE2	0.50	2.65	20	1
1:A:104:VAL:HG13	1:A:129:GLU:HA	0.50	1.81	25	2
1:A:122:GLU:OE2	1:A:126:ARG:CD	0.50	2.59	27	1
1:A:36:LEU:CB	1:A:39:VAL:HG13	0.50	2.37	9	2
1:A:136:LYS:CB	1:A:140:TRP:O	0.50	2.60	4	6
1:A:115:TYR:CE2	2:A:150:THP:C2	0.50	2.95	28	2
1:A:35:ARG:NH1	2:A:150:THP:O4P	0.50	2.44	2	2
1:A:107:GLY:C	1:A:139:ILE:HD12	0.50	2.27	28	2
1:A:8:HIS:ND1	1:A:10:GLU:OE2	0.50	2.45	20	1
1:A:32:MET:HE2	1:A:34:PHE:CZ	0.50	2.41	24	2
1:A:39:VAL:HG22	1:A:40:ASP:N	0.50	2.22	9	3
1:A:98:MET:CE	1:A:124:LEU:CD2	0.50	2.89	12	1
1:A:85:TYR:OH	2:A:150:THP:O1P	0.50	2.30	18	8
1:A:85:TYR:CE2	2:A:150:THP:O1P	0.49	2.65	19	3
1:A:135:GLU:C	1:A:136:LYS:CG	0.49	2.80	23	1
1:A:83:ASP:OD2	1:A:89:LEU:HD11	0.49	2.07	29	2
1:A:24:LYS:HG2	1:A:33:THR:HG23	0.49	1.82	5	1
1:A:14:LEU:C	1:A:14:LEU:CD1	0.49	2.81	2	7
1:A:14:LEU:CD1	1:A:14:LEU:C	0.49	2.81	30	9
1:A:8:HIS:CE1	1:A:10:GLU:CD	0.49	2.86	7	1
1:A:10:GLU:O	1:A:73:GLU:CB	0.49	2.61	20	5
1:A:85:TYR:OH	2:A:150:THP:O3P	0.49	2.30	3	7
1:A:18:ILE:HD11	1:A:24:LYS:CD	0.49	2.37	17	1
1:A:19:ASP:OD1	1:A:22:THR:CB	0.49	2.60	7	2
1:A:120:THR:HG23	1:A:121:HIS:N	0.49	2.22	2	3
1:A:83:ASP:CB	1:A:89:LEU:HD11	0.49	2.37	21	1
1:A:23:VAL:HG23	1:A:23:VAL:O	0.49	2.06	29	1
1:A:138:ASN:O	1:A:139:ILE:C	0.49	2.51	10	15

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:83:ASP:OD2	2:A:150:THP:C1'	0.49	2.61	21	1
1:A:135:GLU:HB3	1:A:137:LEU:HD23	0.49	1.85	8	1
1:A:83:ASP:OD1	2:A:150:THP:C2	0.49	2.60	12	1
1:A:111:VAL:HG23	1:A:129:GLU:HG3	0.49	1.84	19	1
1:A:127:LYS:CG	1:A:128:SER:N	0.49	2.76	30	3
1:A:38:LEU:HB2	1:A:125:LEU:HD12	0.49	1.84	14	3
1:A:83:ASP:HB3	1:A:89:LEU:HD11	0.49	1.84	4	1
1:A:91:TYR:HB2	1:A:93:TYR:CE1	0.49	2.42	20	2
1:A:83:ASP:OD2	2:A:150:THP:N3	0.49	2.46	20	1
1:A:27:TYR:CZ	1:A:28:LYS:CE	0.48	2.96	18	1
1:A:24:LYS:HG2	1:A:33:THR:HG22	0.48	1.84	4	2
1:A:93:TYR:OH	1:A:121:HIS:NE2	0.48	2.46	17	1
1:A:127:LYS:HG3	1:A:128:SER:N	0.48	2.23	30	5
1:A:36:LEU:HB3	1:A:39:VAL:CG1	0.48	2.37	9	2
1:A:18:ILE:HD11	1:A:24:LYS:HD2	0.48	1.85	4	1
1:A:61:PHE:C	1:A:61:PHE:CD1	0.48	2.87	24	2
1:A:81:ARG:C	1:A:82:THR:CG2	0.48	2.82	18	1
1:A:91:TYR:CE1	1:A:121:HIS:HB2	0.48	2.43	27	1
1:A:27:TYR:CE2	1:A:28:LYS:HG3	0.48	2.44	7	2
1:A:93:TYR:CE2	1:A:98:MET:SD	0.48	3.07	25	3
1:A:104:VAL:HG13	1:A:129:GLU:CD	0.48	2.29	16	1
1:A:38:LEU:HD12	1:A:125:LEU:CD1	0.48	2.38	5	1
1:A:8:HIS:CE1	1:A:9:LYS:O	0.48	2.67	9	1
1:A:18:ILE:HD12	1:A:22:THR:CG2	0.48	2.38	25	1
1:A:62:THR:O	1:A:66:VAL:CG2	0.48	2.57	1	2
1:A:38:LEU:HB2	1:A:125:LEU:CD1	0.48	2.39	2	6
1:A:106:GLN:O	1:A:138:ASN:OD1	0.48	2.32	17	4
1:A:35:ARG:CZ	2:A:150:THP:P2	0.48	3.02	10	2
1:A:36:LEU:HD21	1:A:92:ILE:HD12	0.48	1.85	18	2
1:A:27:TYR:CZ	1:A:28:LYS:HD3	0.48	2.43	28	1
1:A:136:LYS:CG	1:A:140:TRP:O	0.48	2.62	26	1
1:A:106:GLN:O	1:A:137:LEU:HD12	0.48	2.09	16	1
1:A:23:VAL:CG2	1:A:25:LEU:HD11	0.48	2.38	27	1
1:A:61:PHE:O	1:A:65:MET:CB	0.48	2.62	27	1
1:A:27:TYR:CE2	1:A:28:LYS:HE2	0.47	2.44	17	1
1:A:84:LYS:HG3	1:A:85:TYR:CD2	0.47	2.44	14	1
1:A:35:ARG:NE	2:A:150:THP:O6P	0.47	2.46	2	1
1:A:10:GLU:CB	1:A:11:PRO:CD	0.47	2.92	23	4
1:A:15:ILE:CD1	1:A:31:PRO:HB3	0.47	2.39	16	2
1:A:124:LEU:CD1	1:A:124:LEU:C	0.47	2.82	15	1
1:A:12:ALA:HB3	1:A:72:ILE:HG22	0.47	1.86	24	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:84:LYS:CE	2:A:150:THP:O3P	0.47	2.62	20	1
1:A:108:LEU:O	1:A:139:ILE:CD1	0.47	2.62	23	1
1:A:84:LYS:HZ1	2:A:150:THP:P1	0.47	2.33	22	1
1:A:14:LEU:HD21	1:A:67:GLU:HG2	0.47	1.86	27	1
1:A:137:LEU:O	1:A:138:ASN:OD1	0.47	2.32	17	3
1:A:38:LEU:HB2	1:A:125:LEU:HD13	0.47	1.86	17	2
1:A:87:ARG:NH1	1:A:87:ARG:CB	0.47	2.78	17	1
1:A:76:PHE:CE1	1:A:81:ARG:HG2	0.47	2.44	16	1
1:A:111:VAL:CG1	1:A:111:VAL:O	0.47	2.62	20	1
1:A:33:THR:O	1:A:33:THR:CG2	0.47	2.63	1	2
1:A:21:ASP:OD1	1:A:35:ARG:CZ	0.47	2.62	15	1
1:A:136:LYS:HA	1:A:140:TRP:O	0.47	2.10	4	18
1:A:32:MET:CE	1:A:34:PHE:CZ	0.47	2.97	23	1
1:A:104:VAL:CG1	1:A:129:GLU:CA	0.47	2.93	10	1
1:A:36:LEU:HD11	1:A:103:LEU:CD1	0.47	2.40	30	2
1:A:103:LEU:HB3	1:A:109:ALA:CB	0.47	2.40	3	1
1:A:110:LYS:HE3	1:A:140:TRP:CH2	0.47	2.45	22	1
1:A:131:GLN:O	1:A:134:LYS:CG	0.47	2.63	10	1
1:A:39:VAL:CG2	1:A:39:VAL:O	0.47	2.62	16	1
1:A:84:LYS:HE2	1:A:85:TYR:CZ	0.46	2.45	26	1
1:A:35:ARG:NH1	2:A:150:THP:O5P	0.46	2.49	15	3
1:A:35:ARG:CD	2:A:150:THP:O5P	0.46	2.63	21	1
1:A:27:TYR:CE2	1:A:28:LYS:HD2	0.46	2.44	1	1
1:A:35:ARG:CZ	2:A:150:THP:O5P	0.46	2.63	1	2
1:A:124:LEU:O	1:A:124:LEU:HD13	0.46	2.09	15	1
1:A:59:SER:OG	1:A:60:ALA:N	0.46	2.47	5	2
1:A:85:TYR:CD1	1:A:87:ARG:CZ	0.46	2.99	29	1
1:A:38:LEU:HB3	1:A:125:LEU:HD12	0.46	1.86	22	1
1:A:27:TYR:CD1	1:A:27:TYR:C	0.46	2.88	23	1
1:A:91:TYR:HB2	1:A:93:TYR:CE2	0.46	2.45	11	1
1:A:61:PHE:CE2	1:A:103:LEU:HG	0.46	2.45	2	1
1:A:19:ASP:OD2	1:A:22:THR:OG1	0.46	2.33	6	1
1:A:83:ASP:OD1	1:A:87:ARG:O	0.46	2.33	16	1
1:A:13:THR:HB	1:A:26:MET:CB	0.46	2.41	19	10
1:A:114:VAL:O	1:A:114:VAL:HG12	0.46	2.10	22	1
1:A:110:LYS:CD	1:A:140:TRP:CH2	0.46	2.99	2	1
1:A:27:TYR:CE2	1:A:28:LYS:CD	0.46	2.99	16	1
1:A:10:GLU:O	1:A:73:GLU:HA	0.46	2.11	7	6
1:A:40:ASP:HB2	1:A:112:ALA:HB3	0.46	1.88	7	1
1:A:108:LEU:O	1:A:139:ILE:HD11	0.46	2.11	1	4
1:A:98:MET:CE	1:A:121:HIS:ND1	0.46	2.79	27	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:39:VAL:HG11	1:A:100:ASN:HB3	0.46	1.88	15	1
1:A:37:LEU:HD11	1:A:89:LEU:CB	0.45	2.40	22	2
1:A:10:GLU:OE1	1:A:11:PRO:HD2	0.45	2.11	17	1
1:A:14:LEU:HB2	1:A:72:ILE:HD13	0.45	1.87	1	2
1:A:22:THR:CG2	1:A:33:THR:CG2	0.45	2.94	21	2
1:A:21:ASP:OD1	1:A:41:THR:HG22	0.45	2.11	30	1
1:A:33:THR:HG23	1:A:87:ARG:HG2	0.45	1.88	30	1
1:A:14:LEU:O	1:A:14:LEU:HD13	0.45	2.11	22	1
1:A:38:LEU:HD13	1:A:122:GLU:CA	0.45	2.42	17	2
1:A:37:LEU:CD1	1:A:89:LEU:HB3	0.45	2.40	15	2
1:A:93:TYR:OH	1:A:98:MET:SD	0.45	2.74	17	2
1:A:22:THR:O	1:A:23:VAL:CG1	0.45	2.64	21	3
1:A:104:VAL:HG11	1:A:128:SER:CB	0.45	2.41	24	1
1:A:84:LYS:HG3	1:A:85:TYR:CE2	0.45	2.46	11	1
1:A:100:ASN:OD1	1:A:100:ASN:N	0.45	2.48	17	1
1:A:84:LYS:NZ	2:A:150:THP:O3'	0.45	2.48	27	3
1:A:65:MET:HE2	1:A:99:VAL:HG22	0.45	1.88	14	1
1:A:84:LYS:HE2	2:A:150:THP:O3'	0.45	2.12	9	1
1:A:85:TYR:CB	1:A:87:ARG:CZ	0.45	2.95	29	1
1:A:21:ASP:OD1	1:A:41:THR:CG2	0.45	2.65	27	1
1:A:10:GLU:O	1:A:73:GLU:CA	0.45	2.65	15	4
1:A:35:ARG:NE	2:A:150:THP:O4P	0.45	2.50	7	2
1:A:38:LEU:N	1:A:38:LEU:CD2	0.45	2.79	22	1
1:A:14:LEU:HA	1:A:25:LEU:HD22	0.45	1.88	11	1
1:A:66:VAL:HG23	1:A:67:GLU:N	0.45	2.27	23	1
1:A:104:VAL:CG1	1:A:129:GLU:HA	0.45	2.42	6	2
1:A:134:LYS:HG3	1:A:135:GLU:N	0.45	2.26	1	1
1:A:27:TYR:O	1:A:28:LYS:HB2	0.45	2.12	11	8
1:A:39:VAL:HG13	1:A:40:ASP:N	0.45	2.27	19	1
1:A:27:TYR:CZ	1:A:28:LYS:HE2	0.45	2.46	26	1
1:A:89:LEU:CD2	2:A:150:THP:H52	0.44	2.34	4	1
1:A:78:LYS:HD3	1:A:79:GLY:N	0.44	2.28	6	1
1:A:61:PHE:CD1	1:A:61:PHE:C	0.44	2.91	27	2
1:A:122:GLU:OE1	1:A:123:GLN:N	0.44	2.50	2	2
1:A:38:LEU:C	1:A:39:VAL:CG1	0.44	2.86	16	2
1:A:91:TYR:CG	1:A:121:HIS:ND1	0.44	2.85	27	1
1:A:61:PHE:CE2	1:A:65:MET:SD	0.44	3.10	20	1
1:A:21:ASP:HB3	1:A:35:ARG:NE	0.44	2.27	6	1
1:A:101:GLU:OE1	1:A:105:ARG:NH2	0.44	2.50	22	1
1:A:113:TYR:HB3	2:A:150:THP:C4	0.44	2.42	6	3
1:A:133:LYS:HG3	1:A:140:TRP:CZ3	0.44	2.48	25	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:124:LEU:O	1:A:127:LYS:HG2	0.44	2.12	17	1
1:A:27:TYR:O	1:A:30:GLN:HG3	0.44	2.13	7	3
1:A:119:ASN:O	1:A:119:ASN:OD1	0.44	2.36	9	2
1:A:64:LYS:O	1:A:68:ASN:ND2	0.44	2.50	10	1
1:A:76:PHE:CD1	1:A:81:ARG:CG	0.44	3.00	16	1
1:A:41:THR:HG23	1:A:109:ALA:CB	0.44	2.43	15	1
1:A:9:LYS:HE2	1:A:93:TYR:CG	0.44	2.48	30	1
1:A:25:LEU:HD12	1:A:34:PHE:HD1	0.44	1.72	1	1
1:A:84:LYS:CG	1:A:85:TYR:CE2	0.44	3.01	11	1
1:A:104:VAL:O	1:A:132:ALA:CB	0.44	2.66	11	2
1:A:22:THR:OG1	1:A:35:ARG:CZ	0.44	2.66	5	1
1:A:133:LYS:HG2	1:A:140:TRP:CZ3	0.44	2.48	1	1
1:A:40:ASP:O	1:A:41:THR:C	0.44	2.55	5	1
1:A:63:LYS:O	1:A:67:GLU:HG3	0.44	2.13	17	1
1:A:129:GLU:OE2	1:A:133:LYS:CD	0.44	2.66	14	1
1:A:25:LEU:HD12	1:A:34:PHE:CD1	0.44	2.47	1	1
1:A:37:LEU:HD12	1:A:90:ALA:N	0.44	2.28	5	1
1:A:57:GLU:OE2	1:A:138:ASN:ND2	0.43	2.51	18	1
1:A:82:THR:HG22	1:A:87:ARG:O	0.43	2.12	27	1
1:A:135:GLU:O	1:A:136:LYS:C	0.43	2.56	5	8
1:A:115:TYR:O	1:A:116:LYS:C	0.43	2.56	12	3
1:A:83:ASP:OD2	1:A:89:LEU:CD2	0.43	2.66	12	1
1:A:122:GLU:CD	1:A:126:ARG:NH1	0.43	2.71	2	1
1:A:76:PHE:CE2	1:A:81:ARG:HD3	0.43	2.48	18	1
1:A:94:ALA:O	1:A:95:ASP:HB2	0.43	2.14	6	20
1:A:131:GLN:O	1:A:134:LYS:HG3	0.43	2.13	10	1
1:A:38:LEU:HD22	1:A:122:GLU:OE1	0.43	2.13	1	2
1:A:10:GLU:HB3	1:A:11:PRO:HD2	0.43	1.90	21	1
1:A:36:LEU:HB2	1:A:39:VAL:HG21	0.43	1.90	20	4
1:A:119:ASN:O	1:A:120:THR:C	0.43	2.57	1	4
1:A:35:ARG:O	1:A:36:LEU:C	0.43	2.56	14	2
1:A:28:LYS:CE	1:A:28:LYS:HA	0.43	2.44	12	1
1:A:20:GLY:N	1:A:59:SER:HA	0.43	2.28	26	2
1:A:104:VAL:CG1	1:A:129:GLU:N	0.43	2.82	10	1
1:A:76:PHE:CD1	1:A:81:ARG:HG2	0.43	2.49	16	1
1:A:77:ASP:OD2	1:A:91:TYR:OH	0.43	2.35	5	2
1:A:83:ASP:OD1	1:A:89:LEU:HD11	0.43	2.14	22	1
1:A:136:LYS:HA	1:A:140:TRP:CB	0.43	2.44	9	3
1:A:9:LYS:CG	1:A:75:GLU:OE1	0.43	2.67	14	1
1:A:58:ALA:O	1:A:59:SER:C	0.43	2.57	1	3
1:A:100:ASN:N	1:A:100:ASN:OD1	0.43	2.52	19	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:137:LEU:O	1:A:138:ASN:C	0.43	2.57	2	3
1:A:111:VAL:HG23	1:A:129:GLU:OE1	0.43	2.14	13	1
1:A:122:GLU:OE1	1:A:122:GLU:C	0.43	2.57	8	1
1:A:137:LEU:O	1:A:138:ASN:CB	0.43	2.66	29	1
1:A:14:LEU:HD22	1:A:25:LEU:HD23	0.43	1.90	29	1
1:A:99:VAL:O	1:A:102:ALA:HB3	0.43	2.14	2	1
1:A:93:TYR:CE1	1:A:98:MET:SD	0.43	3.12	2	1
1:A:85:TYR:CG	1:A:87:ARG:NH2	0.43	2.87	18	1
1:A:14:LEU:HD23	1:A:66:VAL:HB	0.43	1.91	4	1
1:A:25:LEU:N	1:A:25:LEU:HD23	0.43	2.29	12	1
1:A:10:GLU:OE1	1:A:10:GLU:N	0.43	2.52	2	1
1:A:10:GLU:OE1	1:A:11:PRO:CD	0.43	2.66	17	1
1:A:91:TYR:HB2	1:A:93:TYR:CZ	0.43	2.49	20	1
1:A:15:ILE:CD1	1:A:25:LEU:O	0.43	2.67	15	2
1:A:107:GLY:C	1:A:138:ASN:OD1	0.43	2.56	17	4
1:A:106:GLN:O	1:A:137:LEU:HB3	0.43	2.14	17	3
1:A:27:TYR:CE2	1:A:28:LYS:HD3	0.43	2.49	19	1
1:A:127:LYS:O	1:A:128:SER:C	0.43	2.57	9	2
1:A:104:VAL:HG13	1:A:129:GLU:CA	0.43	2.44	10	1
1:A:119:ASN:OD1	1:A:122:GLU:HB2	0.43	2.13	18	2
1:A:91:TYR:CD2	1:A:121:HIS:CE1	0.43	3.07	27	1
1:A:85:TYR:HB2	1:A:87:ARG:NE	0.43	2.29	27	1
1:A:113:TYR:HB3	2:A:150:THP:H53	0.42	1.90	26	1
1:A:131:GLN:O	1:A:135:GLU:HG3	0.42	2.14	25	1
1:A:61:PHE:CE1	1:A:106:GLN:HG2	0.42	2.49	18	1
1:A:137:LEU:C	1:A:138:ASN:OD1	0.42	2.58	19	2
1:A:38:LEU:CD2	1:A:114:VAL:HG13	0.42	2.43	26	2
1:A:129:GLU:CD	1:A:140:TRP:CZ2	0.42	2.93	4	1
1:A:57:GLU:O	1:A:61:PHE:HB2	0.42	2.14	10	1
1:A:93:TYR:CD1	1:A:98:MET:HA	0.42	2.50	11	1
1:A:39:VAL:O	1:A:39:VAL:CG2	0.42	2.67	24	1
1:A:21:ASP:OD1	1:A:21:ASP:N	0.42	2.51	30	1
1:A:59:SER:O	1:A:63:LYS:HB2	0.42	2.14	13	1
1:A:37:LEU:O	1:A:38:LEU:CB	0.42	2.66	25	4
1:A:27:TYR:CZ	1:A:28:LYS:HE3	0.42	2.48	18	1
1:A:119:ASN:OD1	1:A:119:ASN:C	0.42	2.57	27	2
1:A:106:GLN:NE2	1:A:108:LEU:HD11	0.42	2.28	6	1
1:A:85:TYR:CD2	1:A:87:ARG:NH1	0.42	2.88	11	1
1:A:101:GLU:CG	1:A:128:SER:OG	0.42	2.67	17	1
1:A:81:ARG:HG2	1:A:81:ARG:NH1	0.42	2.30	28	1
1:A:10:GLU:O	1:A:73:GLU:HB2	0.42	2.15	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:38:LEU:CB	1:A:125:LEU:CD1	0.42	2.98	27	1
1:A:19:ASP:OD1	1:A:22:THR:HB	0.42	2.14	6	1
1:A:13:THR:O	1:A:25:LEU:HA	0.42	2.15	26	10
1:A:111:VAL:O	1:A:112:ALA:HB2	0.42	2.13	10	2
1:A:15:ILE:HD11	1:A:26:MET:SD	0.42	2.54	12	1
1:A:106:GLN:O	1:A:107:GLY:C	0.42	2.58	3	3
1:A:36:LEU:CB	1:A:39:VAL:HG11	0.42	2.45	19	1
1:A:119:ASN:OD1	1:A:119:ASN:O	0.42	2.38	23	1
1:A:107:GLY:HA3	1:A:132:ALA:HB1	0.42	1.90	12	1
1:A:114:VAL:HG11	1:A:122:GLU:HG3	0.42	1.91	30	1
1:A:107:GLY:O	1:A:139:ILE:CD1	0.42	2.67	5	1
1:A:38:LEU:HD13	1:A:121:HIS:O	0.42	2.15	8	1
1:A:120:THR:HG23	1:A:121:HIS:CG	0.42	2.50	25	1
1:A:27:TYR:O	1:A:28:LYS:C	0.42	2.58	30	3
1:A:87:ARG:NH1	2:A:150:THP:O4P	0.42	2.53	2	1
1:A:91:TYR:CE1	1:A:121:HIS:CG	0.42	3.08	27	1
1:A:38:LEU:HB3	1:A:125:LEU:CD1	0.42	2.44	27	1
1:A:91:TYR:HB2	1:A:93:TYR:OH	0.42	2.15	20	1
1:A:115:TYR:N	1:A:115:TYR:CD1	0.42	2.87	30	1
1:A:37:LEU:O	1:A:38:LEU:HB2	0.42	2.15	12	10
1:A:13:THR:CB	1:A:26:MET:HB3	0.42	2.45	19	2
1:A:35:ARG:HG2	2:A:150:THP:O4P	0.42	2.15	22	1
1:A:114:VAL:C	1:A:115:TYR:CG	0.42	2.93	23	1
1:A:35:ARG:NH2	2:A:150:THP:O6P	0.42	2.53	11	1
1:A:110:LYS:HD3	1:A:140:TRP:CH2	0.42	2.49	2	1
1:A:38:LEU:O	1:A:39:VAL:CG1	0.42	2.68	16	2
1:A:117:PRO:O	1:A:119:ASN:N	0.42	2.53	5	1
1:A:85:TYR:CE1	2:A:150:THP:P1	0.42	3.12	16	2
1:A:10:GLU:CB	1:A:11:PRO:HD2	0.41	2.45	20	2
1:A:78:LYS:HD3	1:A:120:THR:OG1	0.41	2.15	4	2
1:A:36:LEU:HB3	1:A:100:ASN:ND2	0.41	2.29	13	2
1:A:85:TYR:HB2	1:A:87:ARG:CD	0.41	2.45	11	1
1:A:81:ARG:O	1:A:82:THR:HG22	0.41	2.15	18	1
1:A:40:ASP:OD1	1:A:40:ASP:C	0.41	2.59	26	1
1:A:10:GLU:OE1	1:A:27:TYR:OH	0.41	2.37	12	1
1:A:119:ASN:ND2	1:A:122:GLU:OE1	0.41	2.53	11	1
1:A:38:LEU:C	1:A:39:VAL:HG13	0.41	2.36	16	1
1:A:24:LYS:CD	1:A:33:THR:HG23	0.41	2.45	27	1
1:A:36:LEU:CB	1:A:39:VAL:CG1	0.41	2.99	19	1
1:A:35:ARG:HD3	2:A:150:THP:O4P	0.41	2.15	16	3
1:A:93:TYR:HA	1:A:97:LYS:O	0.41	2.16	5	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:91:TYR:CD1	1:A:91:TYR:N	0.41	2.89	11	1
1:A:107:GLY:O	1:A:138:ASN:OD1	0.41	2.38	17	1
1:A:28:LYS:N	1:A:28:LYS:HD2	0.41	2.31	28	1
1:A:63:LYS:O	1:A:67:GLU:HB2	0.41	2.16	3	4
1:A:15:ILE:CD1	1:A:25:LEU:C	0.41	2.89	16	2
1:A:120:THR:HG22	1:A:121:HIS:ND1	0.41	2.28	10	1
1:A:64:LYS:N	1:A:64:LYS:CD	0.41	2.84	10	1
1:A:10:GLU:O	1:A:73:GLU:HB3	0.41	2.16	21	2
1:A:127:LYS:CE	1:A:127:LYS:HA	0.41	2.45	15	1
1:A:37:LEU:HD12	1:A:90:ALA:CA	0.41	2.45	28	1
1:A:114:VAL:C	1:A:115:TYR:CD1	0.41	2.94	23	1
1:A:19:ASP:OD1	1:A:22:THR:OG1	0.41	2.38	6	1
1:A:101:GLU:OE2	1:A:124:LEU:CD2	0.41	2.69	23	1
1:A:115:TYR:CE2	2:A:150:THP:N3	0.41	2.88	4	1
1:A:106:GLN:O	1:A:138:ASN:ND2	0.41	2.53	29	1
1:A:14:LEU:HD12	1:A:25:LEU:HD22	0.41	1.92	11	1
1:A:13:THR:O	1:A:25:LEU:HB3	0.41	2.16	21	2
1:A:13:THR:HB	1:A:26:MET:HB3	0.41	1.93	19	2
1:A:136:LYS:HG2	1:A:140:TRP:O	0.41	2.16	22	1
1:A:137:LEU:O	1:A:138:ASN:HB2	0.41	2.16	23	2
1:A:136:LYS:HA	1:A:140:TRP:HB2	0.41	1.93	1	2
1:A:20:GLY:O	1:A:62:THR:OG1	0.41	2.37	4	1
1:A:35:ARG:NH1	1:A:87:ARG:CZ	0.41	2.84	25	1
1:A:119:ASN:CG	1:A:122:GLU:OE1	0.41	2.60	11	1
1:A:37:LEU:HD23	2:A:150:THP:H52	0.41	1.92	16	1
1:A:16:LYS:O	1:A:16:LYS:HG3	0.41	2.16	16	1
1:A:136:LYS:HB3	1:A:140:TRP:O	0.41	2.16	14	1
1:A:85:TYR:CE2	2:A:150:THP:P1	0.41	3.14	15	1
1:A:41:THR:HG23	1:A:109:ALA:HB2	0.41	1.92	15	1
1:A:33:THR:CG2	1:A:87:ARG:HG2	0.41	2.46	30	1
1:A:106:GLN:HA	1:A:137:LEU:HD13	0.41	1.92	28	1
1:A:40:ASP:C	1:A:40:ASP:OD1	0.41	2.59	28	1
1:A:38:LEU:HD22	1:A:38:LEU:N	0.41	2.29	22	1
1:A:135:GLU:HB3	1:A:137:LEU:CD2	0.41	2.46	8	1
1:A:40:ASP:OD1	1:A:41:THR:O	0.41	2.39	14	1
1:A:113:TYR:HD1	1:A:115:TYR:HH	0.41	1.56	20	1
1:A:21:ASP:OD1	1:A:35:ARG:NE	0.41	2.54	15	1
1:A:19:ASP:OD1	1:A:19:ASP:C	0.40	2.58	7	1
1:A:35:ARG:HG3	1:A:36:LEU:N	0.40	2.29	2	1
1:A:98:MET:CE	1:A:124:LEU:HD23	0.40	2.46	25	1
1:A:94:ALA:O	1:A:95:ASP:CB	0.40	2.68	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:MET:CE	1:A:94:ALA:HB3	0.40	2.46	24	1
1:A:41:THR:CG2	1:A:109:ALA:HB2	0.40	2.47	15	1
1:A:38:LEU:HA	1:A:112:ALA:O	0.40	2.16	1	1
1:A:115:TYR:O	1:A:118:ASN:HB2	0.40	2.16	5	1
1:A:101:GLU:CG	1:A:128:SER:HB3	0.40	2.47	1	1
1:A:21:ASP:O	1:A:35:ARG:HD3	0.40	2.17	12	1
1:A:18:ILE:CG1	1:A:24:LYS:HE2	0.40	2.45	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%)	102±3 (86±2%)	15±3 (13±2%)	1±1 (1±1%)	23	69
All	All	3540/4470 (79%)	3050 (86%)	451 (13%)	39 (1%)	23	69

All 12 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	13
1	A	57	GLU	6
1	A	65	MET	4
1	A	139	ILE	3
1	A	113	TYR	3
1	A	14	LEU	2
1	A	118	ASN	2
1	A	80	GLN	2
1	A	79	GLY	1
1	A	38	LEU	1
1	A	61	PHE	1
1	A	16	LYS	1

6.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	99/125 (79%)	79±4 (80±4%)	20±4 (20±4%)	5 36
All	All	2970/3750 (79%)	2379 (80%)	591 (20%)	5 36

All 64 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	78	LYS	30
1	A	137	LEU	23
1	A	97	LYS	21
1	A	64	LYS	20
1	A	65	MET	19
1	A	83	ASP	19
1	A	127	LYS	18
1	A	126	ARG	18
1	A	105	ARG	17
1	A	133	LYS	17
1	A	57	GLU	16
1	A	106	GLN	16
1	A	26	MET	15
1	A	8	HIS	15
1	A	134	LYS	15
1	A	10	GLU	12
1	A	22	THR	12
1	A	123	GLN	12
1	A	63	LYS	11
1	A	41	THR	10
1	A	16	LYS	10
1	A	116	LYS	10
1	A	30	GLN	10
1	A	124	LEU	9
1	A	33	THR	9
1	A	67	GLU	9
1	A	70	LYS	9
1	A	21	ASP	8
1	A	28	LYS	8

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Mol	Chain	Res	Type	Models (Total)
1	A	136	LYS	8
1	A	35	ARG	8
1	A	59	SER	8
1	A	77	ASP	8
1	A	84	LYS	7
1	A	32	MET	7
1	A	82	THR	7
1	A	87	ARG	7
1	A	129	GLU	7
1	A	13	THR	7
1	A	81	ARG	7
1	A	110	LYS	6
1	A	71	LYS	6
1	A	122	GLU	6
1	A	131	GLN	6
1	A	9	LYS	6
1	A	80	GLN	6
1	A	19	ASP	6
1	A	95	ASP	6
1	A	101	GLU	5
1	A	25	LEU	5
1	A	138	ASN	4
1	A	103	LEU	4
1	A	62	THR	4
1	A	24	LYS	4
1	A	128	SER	3
1	A	39	VAL	3
1	A	119	ASN	3
1	A	73	GLU	3
1	A	98	MET	1
1	A	14	LEU	1
1	A	121	HIS	1
1	A	37	LEU	1
1	A	75	GLU	1
1	A	40	ASP	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	THP	A	150	-	19,26,26	1.14±0.01	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	THP	A	150	-	28,40,40	1.06±0.01	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	THP	A	150	-	-	0±0,11,27,27	0±0,2,2,2

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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