Full wwPDB NMR Structure Validation Report (i)

Oct 31, 2021 – 12:13 PM EDT

PDB ID	:	1F3Y
Title	:	SOLUTION STRUCTURE OF THE NUDIX ENZYME DIADENOSINE TETRAPHOSPHATE HYDROLASE FROM LUPINUS ANGUSTIFOLIUS L.
Authors	:	Swarbrick, J.D.; Bashtannyk, T.; Maksel, D.; Zhang, X.R.; Blackburn, G.M.; Gayler, K.R.; Gooley, P.R.
Deposited on	:	2000-06-06

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 (i) symbol.

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

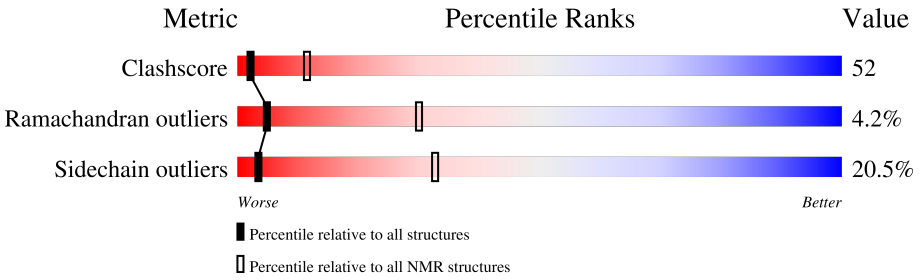
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.23.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al.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

1 Overall quality at a glance (i)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	165	14% 53% 7% 26%

2 Ensemble composition and analysis (i)

This entry contains 25 models. Model 20 is the overall representative, medoid model (most similar to other models). The authors have identified model 3 as representative, based on the following criterion: *lowest energy*.

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:6-A:7, A:15-A:80, A:104-A:121, A:130-A:165 (122)	0.23	20

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 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2617 atoms, of which 1286 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	165	2617	855	1286	220	252	4	0

There are 4 discrepancies between the modelled and reference sequences:

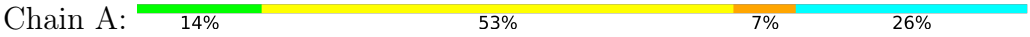
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	TYR	engineered mutation	UNP O04841
A	2	PRO	CYS	engineered mutation	UNP O04841
A	3	LEU	HIS	engineered mutation	UNP O04841
A	4	GLY	SER	engineered mutation	UNP O04841

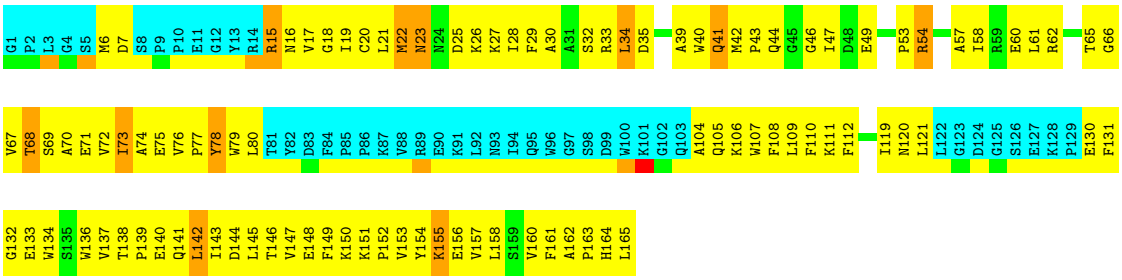
4 Residue-property plots

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: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

Chain A: 

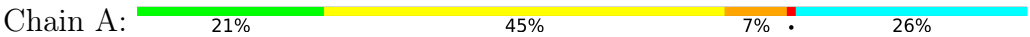


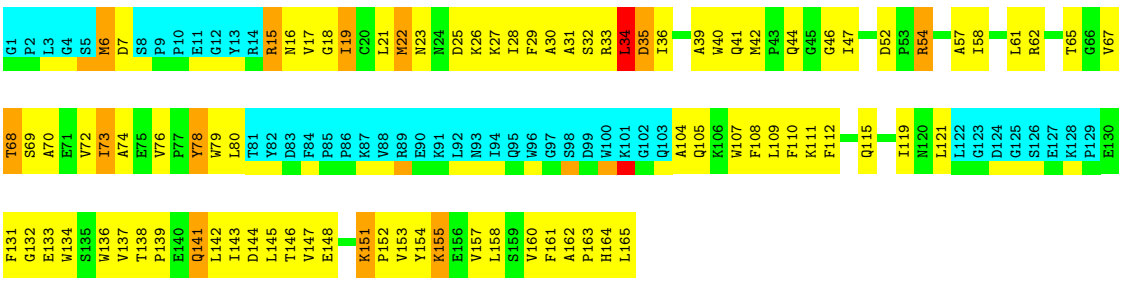
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

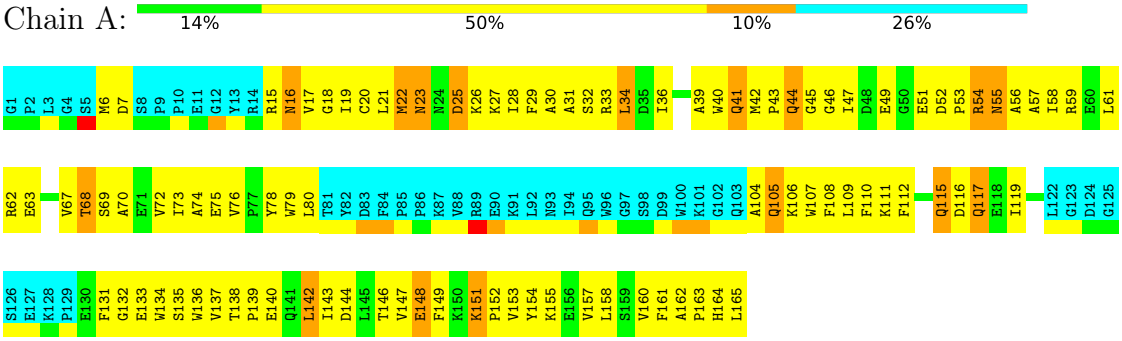
Chain A: 



4.2.2 Score per residue for model 2

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

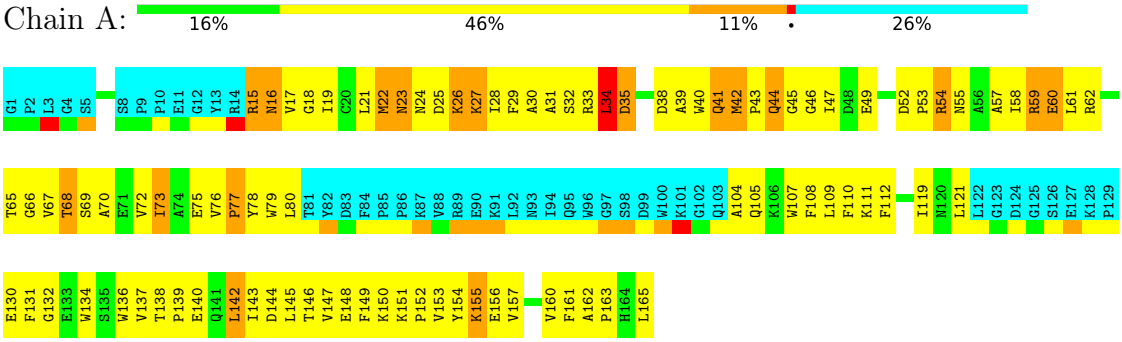
Chain A:



4.2.3 Score per residue for model 3

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

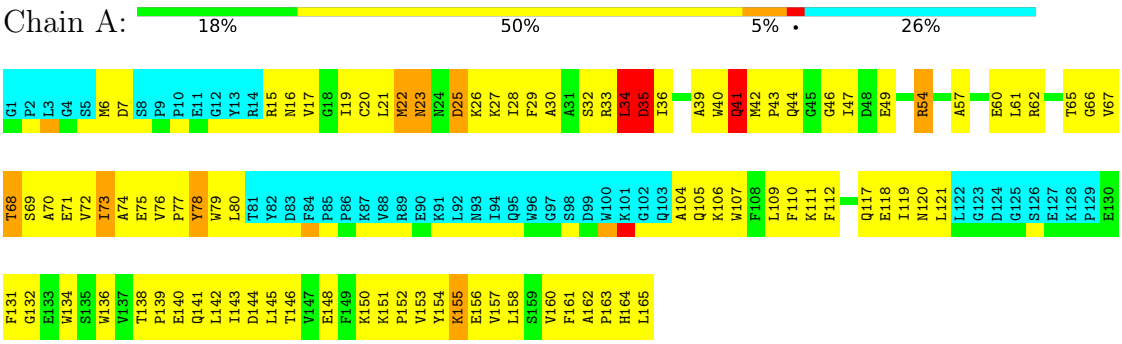
Chain A:



4.2.4 Score per residue for model 4

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

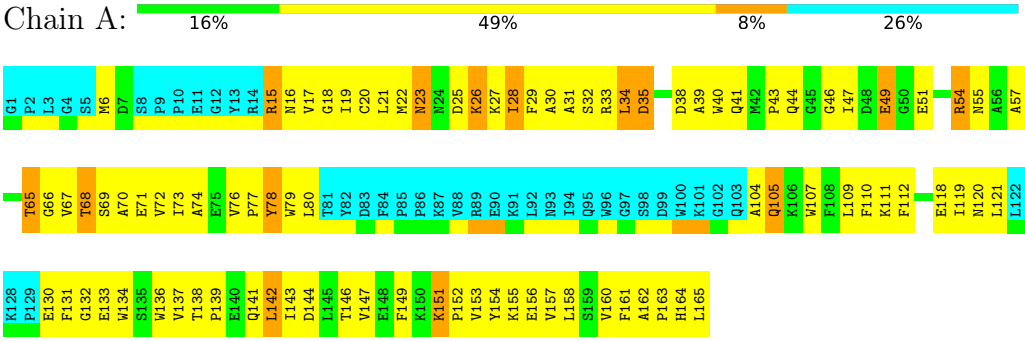
Chain A:



4.2.5 Score per residue for model 5

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

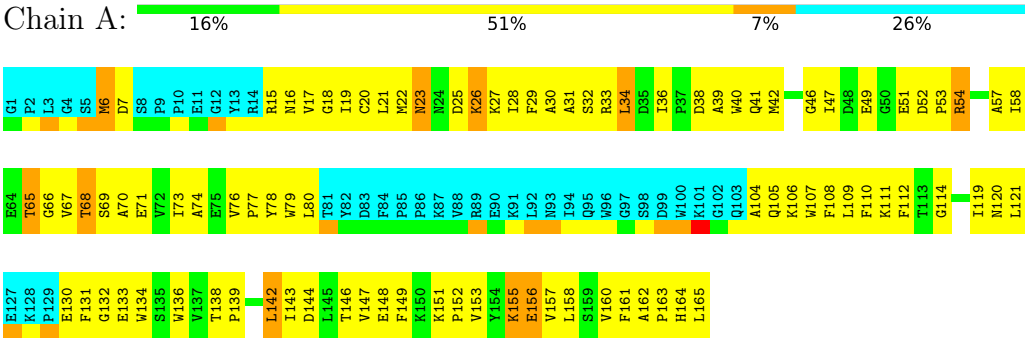
Chain A:



4.2.6 Score per residue for model 6

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

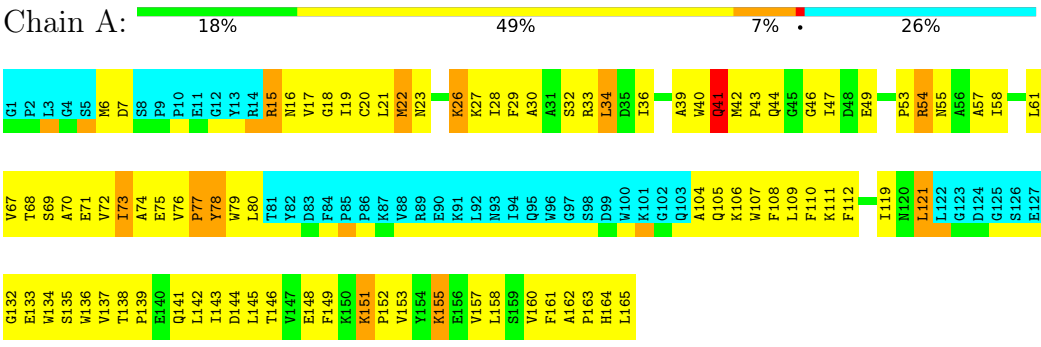
Chain A:



4.2.7 Score per residue for model 7

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

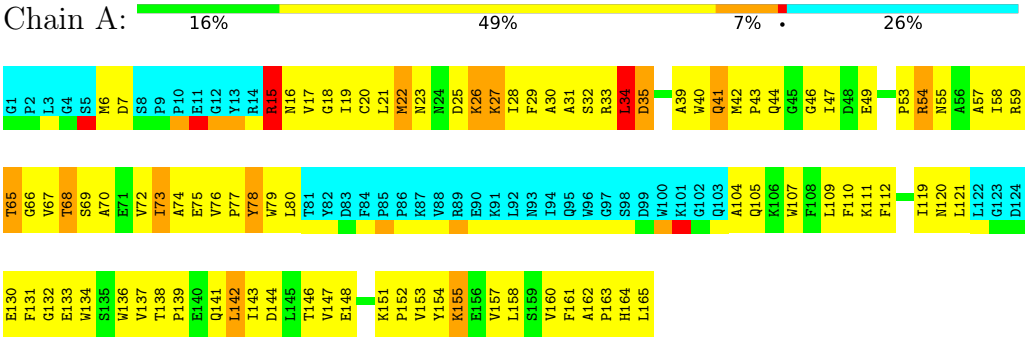
Chain A:



4.2.8 Score per residue for model 8

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

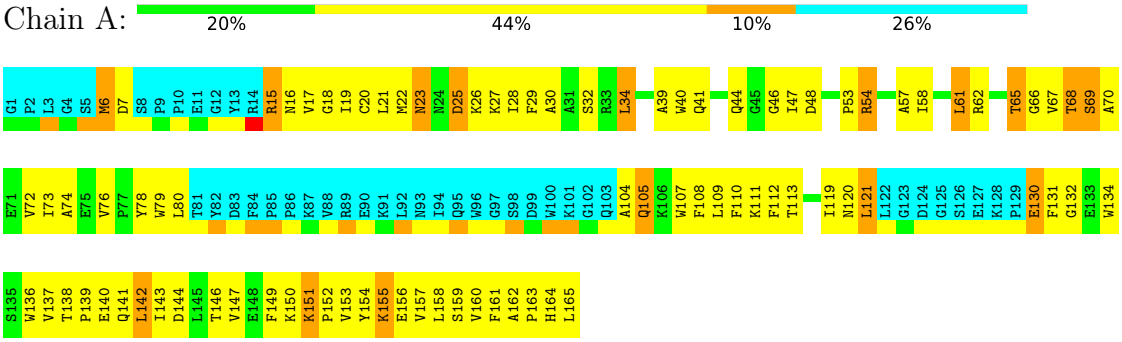
Chain A:



4.2.9 Score per residue for model 9

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

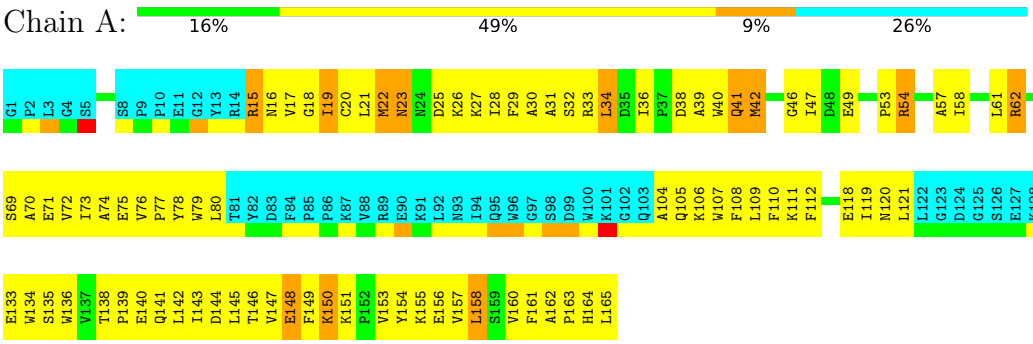
Chain A:



4.2.10 Score per residue for model 10

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

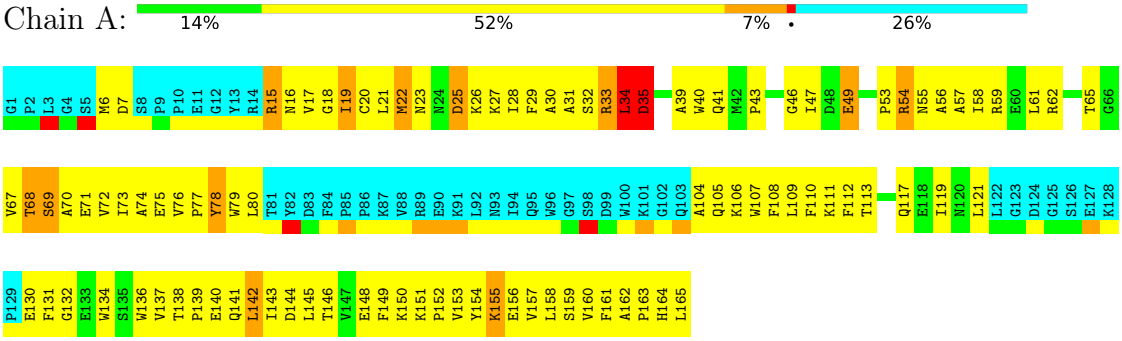
Chain A:



4.2.11 Score per residue for model 11

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

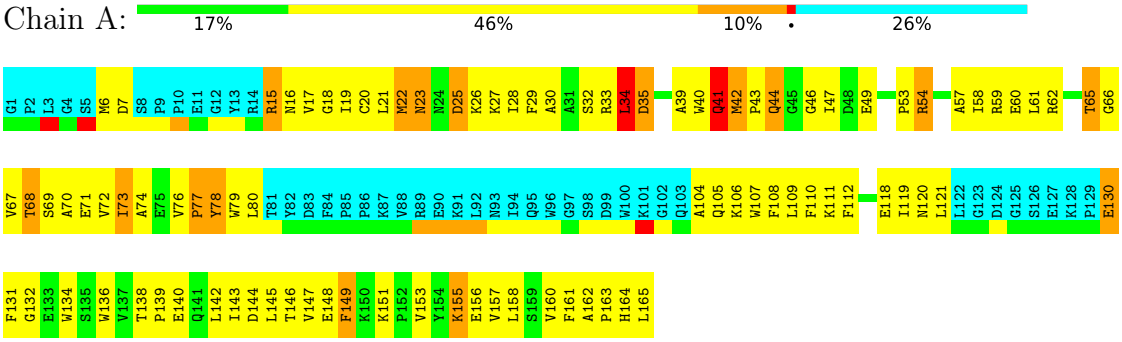
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

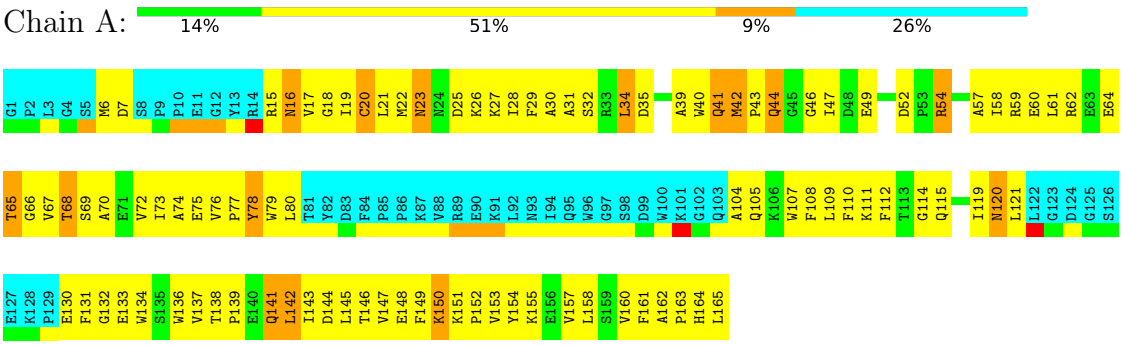
Chain A:



4.2.13 Score per residue for model 13

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

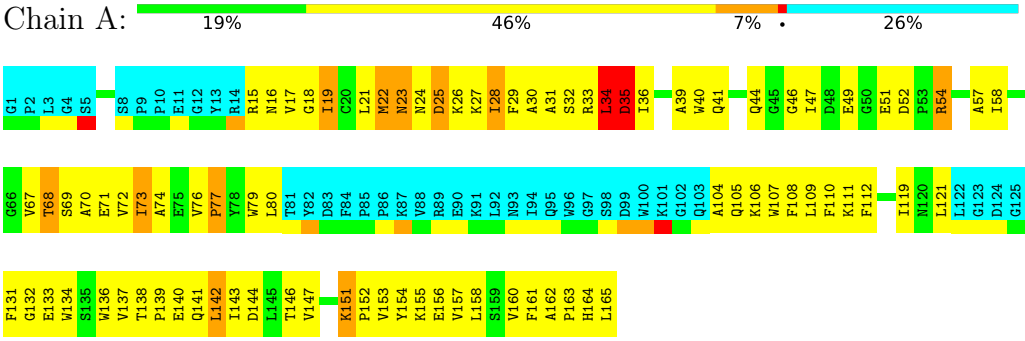
Chain A:



4.2.14 Score per residue for model 14

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

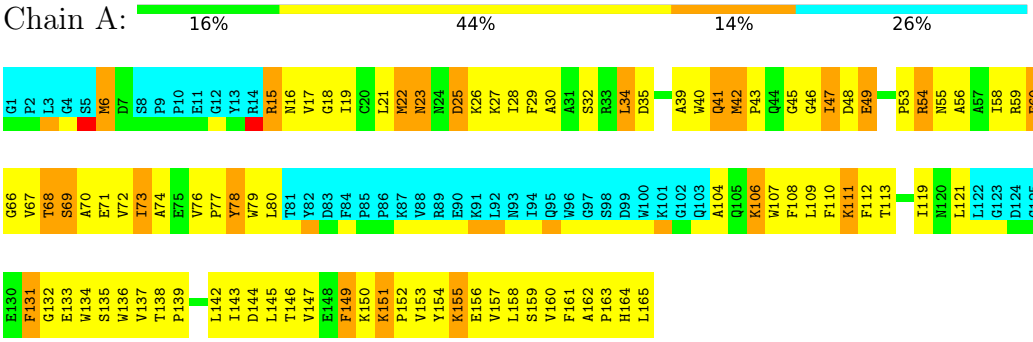
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

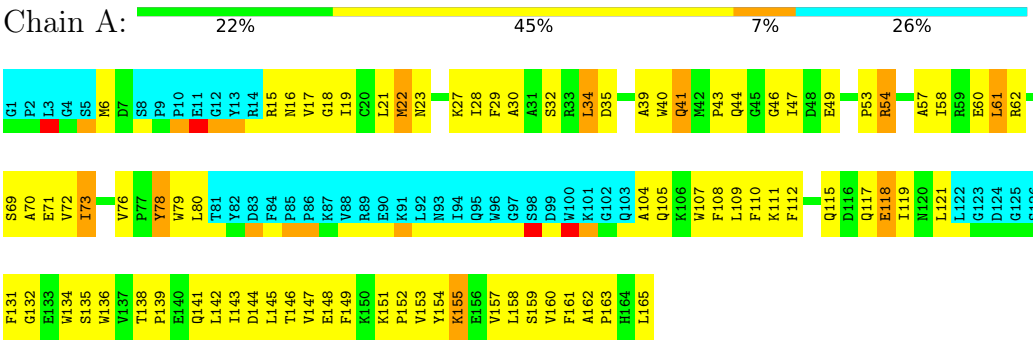
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

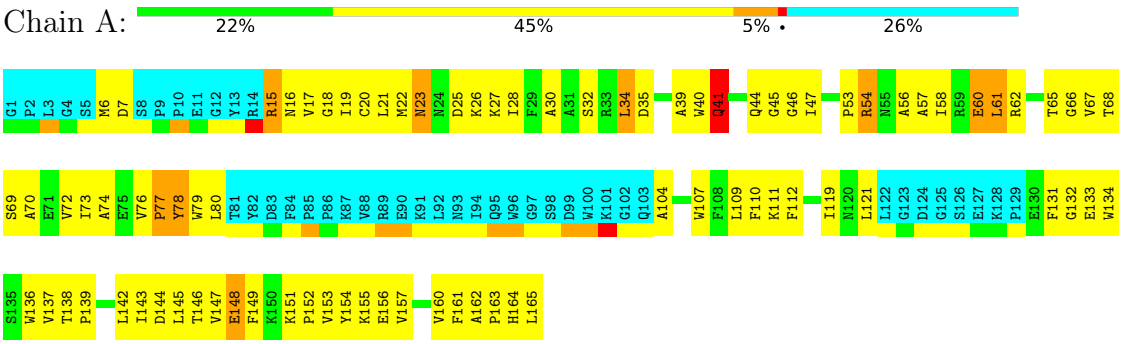
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

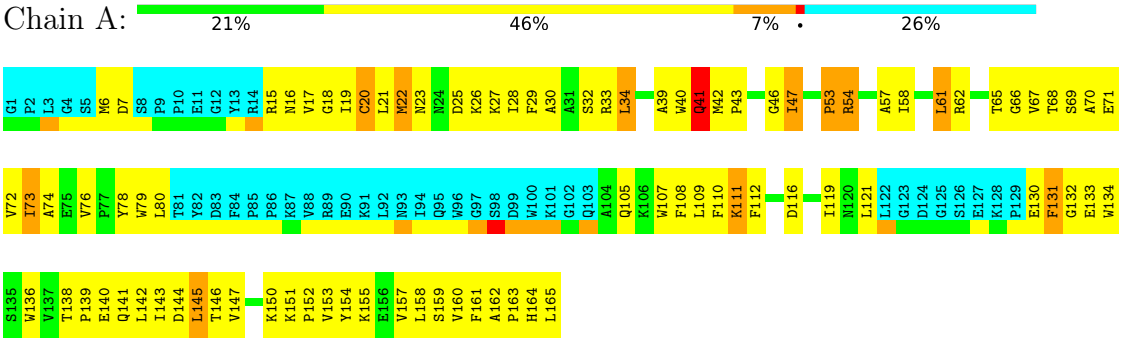
Chain A:



4.2.18 Score per residue for model 18

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

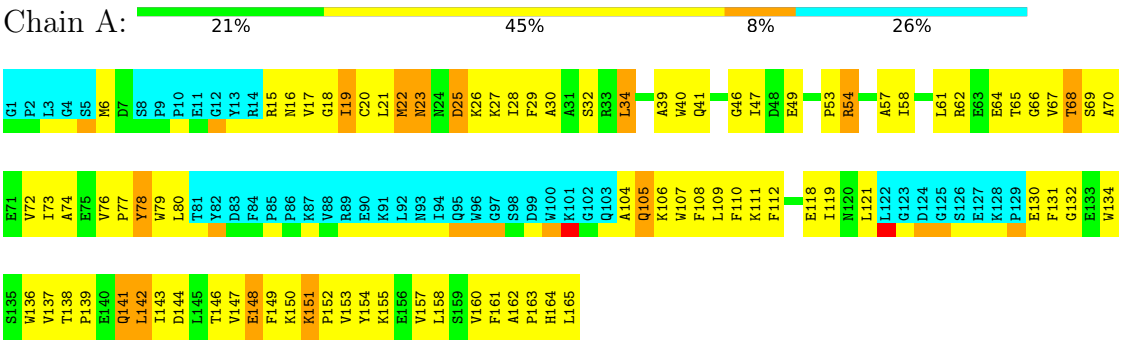
Chain A:



4.2.19 Score per residue for model 19

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

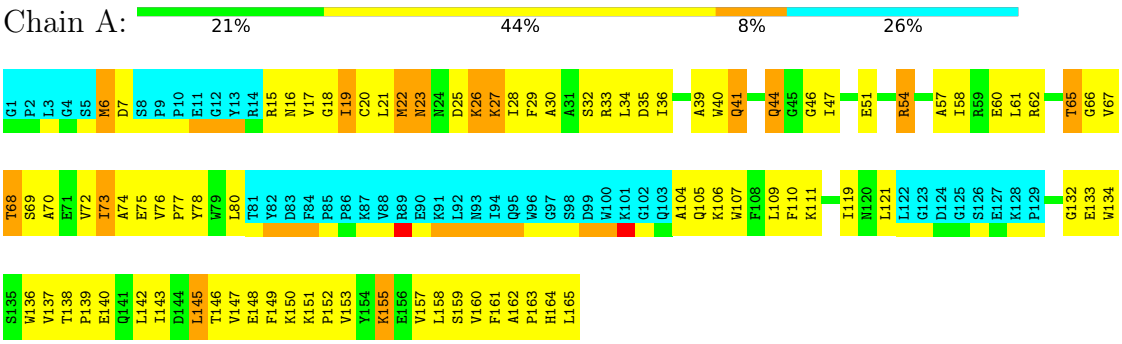
Chain A:



4.2.20 Score per residue for model 20 (medoid)

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

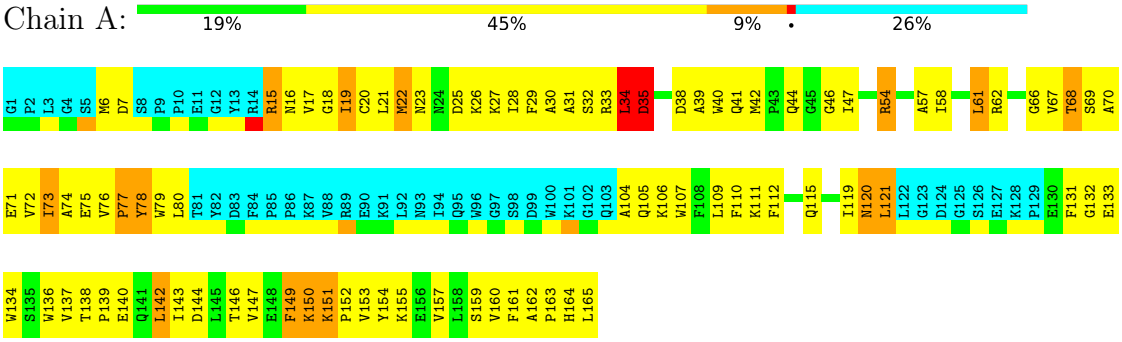
Chain A:



4.2.21 Score per residue for model 21

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

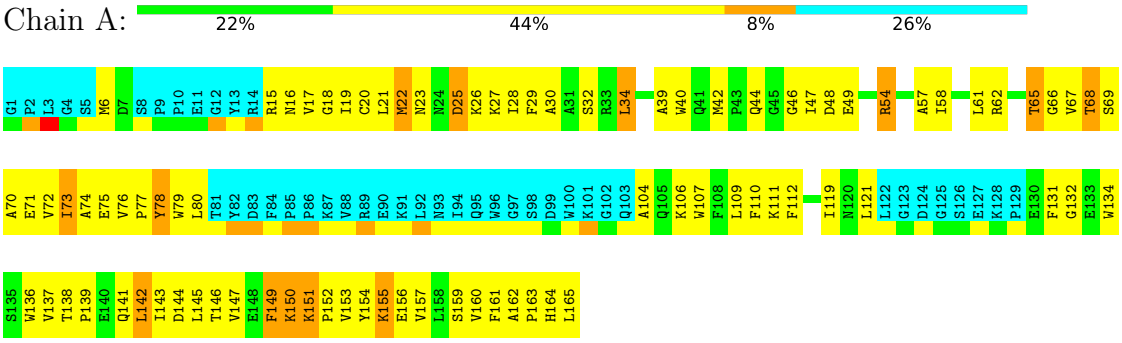
Chain A:



4.2.22 Score per residue for model 22

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

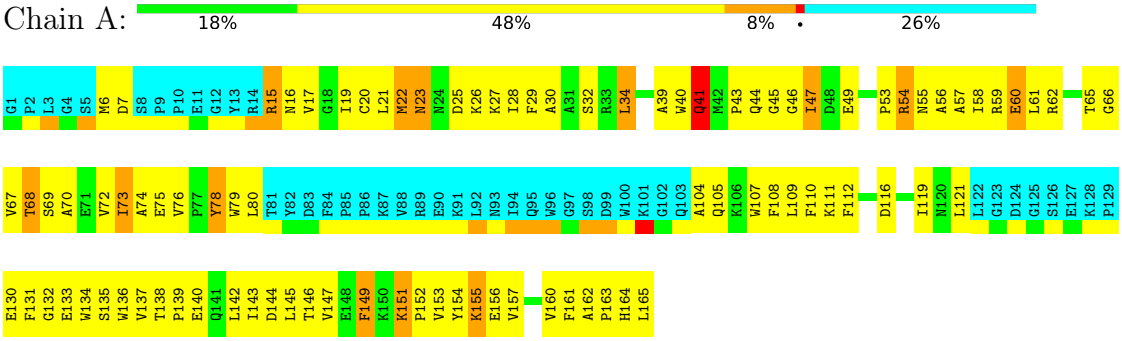
Chain A:



4.2.23 Score per residue for model 23

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

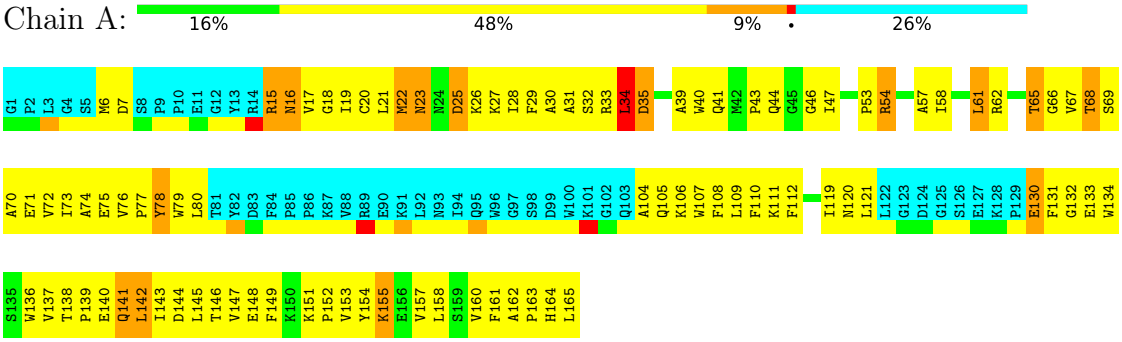
Chain A:



4.2.24 Score per residue for model 24

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

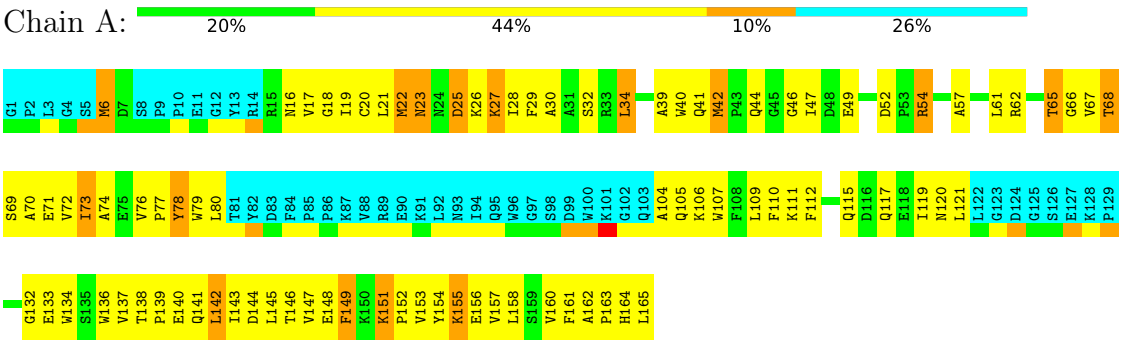
Chain A:



4.2.25 Score per residue for model 25

• Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 25 were deposited, based on the following criterion: *structures with favorable non-bond energy,structures with the least restraint violations,target function.*

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

Software name	Classification	Version
DYANA	refinement	1.5,1.4
CNS	refinement	0.9

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

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	993	964	963	102±14
All	All	24825	24100	24075	2545

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 52.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:ILE:HG21	1:A:61:LEU:HD22	0.97	1.35	22	12
1:A:19:ILE:HG23	1:A:57:ALA:HB1	0.93	1.40	10	7
1:A:19:ILE:HG21	1:A:61:LEU:HD13	0.90	1.41	23	5
1:A:19:ILE:HG22	1:A:110:PHE:CE1	0.89	2.02	19	6
1:A:143:ILE:HG21	1:A:155:LYS:HD3	0.89	1.44	1	5
1:A:139:PRO:HB2	1:A:158:LEU:HD21	0.87	1.44	10	1
1:A:34:LEU:H	1:A:34:LEU:HD23	0.87	1.28	19	3
1:A:72:VAL:HG22	1:A:110:PHE:CE2	0.85	2.05	11	16
1:A:30:ALA:HB2	1:A:142:LEU:HD12	0.84	1.49	3	16
1:A:61:LEU:HD11	1:A:67:VAL:HB	0.83	1.48	18	4
1:A:61:LEU:HD21	1:A:67:VAL:HB	0.81	1.53	10	4
1:A:80:LEU:HD12	1:A:107:TRP:CD1	0.81	2.11	13	4
1:A:54:ARG:CZ	1:A:72:VAL:HG21	0.81	2.05	13	10
1:A:39:ALA:HB1	1:A:147:VAL:CG1	0.81	2.06	2	17

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:ILE:HG23	1:A:110:PHE:CE2	0.80	2.10	3	4
1:A:16:ASN:HB2	1:A:105:GLN:HG2	0.79	1.52	3	11
1:A:21:LEU:HD22	1:A:67:VAL:HG11	0.77	1.56	6	25
1:A:146:THR:HG23	1:A:151:LYS:HG3	0.76	1.57	12	4
1:A:73:ILE:N	1:A:73:ILE:HD13	0.75	1.95	4	2
1:A:62:ARG:HG2	1:A:68:THR:HG23	0.75	1.58	6	4
1:A:19:ILE:HB	1:A:61:LEU:HD12	0.75	1.56	1	6
1:A:17:VAL:O	1:A:44:GLN:HG2	0.74	1.82	2	4
1:A:43:PRO:HG2	1:A:61:LEU:HD12	0.74	1.56	23	1
1:A:43:PRO:HG3	1:A:61:LEU:HD13	0.74	1.59	18	6
1:A:65:THR:HG22	1:A:121:LEU:HD23	0.74	1.59	16	13
1:A:54:ARG:NH2	1:A:72:VAL:HG11	0.74	1.97	4	3
1:A:62:ARG:HG3	1:A:68:THR:HG23	0.73	1.61	16	18
1:A:19:ILE:CG2	1:A:61:LEU:HD13	0.73	2.14	23	1
1:A:153:VAL:O	1:A:157:VAL:HG23	0.73	1.82	17	24
1:A:32:SER:HA	1:A:39:ALA:O	0.73	1.83	7	25
1:A:121:LEU:HD11	1:A:134:TRP:HB3	0.72	1.60	21	1
1:A:18:GLY:HA3	1:A:107:TRP:CD2	0.72	2.19	7	21
1:A:27:LYS:C	1:A:28:ILE:HD12	0.72	2.04	21	4
1:A:21:LEU:HD11	1:A:112:PHE:HB2	0.72	1.62	18	13
1:A:15:ARG:HG2	1:A:47:ILE:HD12	0.71	1.61	10	7
1:A:19:ILE:HG23	1:A:110:PHE:CE1	0.71	2.20	16	3
1:A:23:ASN:OD1	1:A:136:TRP:CE3	0.71	2.43	12	19
1:A:72:VAL:HG22	1:A:110:PHE:CE1	0.71	2.21	18	5
1:A:54:ARG:CZ	1:A:72:VAL:HG11	0.71	2.16	22	3
1:A:121:LEU:HD13	1:A:131:PHE:HB2	0.71	1.61	21	4
1:A:17:VAL:HG13	1:A:47:ILE:CG1	0.71	2.15	18	25
1:A:34:LEU:HG	1:A:132:GLY:CA	0.70	2.17	3	22
1:A:23:ASN:ND2	1:A:27:LYS:HB2	0.70	2.02	3	9
1:A:61:LEU:HD12	1:A:61:LEU:O	0.69	1.87	18	1
1:A:28:ILE:HD11	1:A:139:PRO:HG3	0.69	1.65	5	17
1:A:21:LEU:HD21	1:A:112:PHE:CD1	0.69	2.23	12	16
1:A:19:ILE:HG23	1:A:110:PHE:CD2	0.69	2.21	12	4
1:A:21:LEU:HD21	1:A:112:PHE:CD2	0.69	2.22	16	3
1:A:19:ILE:HG13	1:A:57:ALA:HB1	0.69	1.65	17	10
1:A:16:ASN:O	1:A:105:GLN:HA	0.68	1.88	25	20
1:A:54:ARG:NH1	1:A:72:VAL:HG21	0.68	2.03	22	7
1:A:20:CYS:O	1:A:109:LEU:HD12	0.68	1.88	5	17
1:A:72:VAL:HG22	1:A:110:PHE:CZ	0.68	2.24	9	10
1:A:139:PRO:CB	1:A:158:LEU:HD21	0.68	2.17	10	1
1:A:115:GLN:O	1:A:118:GLU:HG2	0.68	1.89	16	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:54:ARG:NE	1:A:58:ILE:HD11	0.67	2.02	20	13
1:A:21:LEU:CD2	1:A:67:VAL:HG11	0.67	2.19	11	13
1:A:28:ILE:N	1:A:28:ILE:HD12	0.67	2.05	18	8
1:A:61:LEU:CD2	1:A:67:VAL:HB	0.67	2.19	11	3
1:A:22:MET:HE2	1:A:73:ILE:HD13	0.67	1.65	9	4
1:A:76:VAL:HA	1:A:160:VAL:HG11	0.66	1.67	7	25
1:A:19:ILE:HG23	1:A:110:PHE:CD1	0.66	2.24	24	8
1:A:33:ARG:O	1:A:35:ASP:N	0.66	2.27	1	10
1:A:22:MET:HB3	1:A:27:LYS:O	0.66	1.91	7	6
1:A:19:ILE:CB	1:A:61:LEU:HD12	0.66	2.21	1	5
1:A:22:MET:CG	1:A:109:LEU:HD11	0.66	2.21	4	2
1:A:22:MET:SD	1:A:109:LEU:HD11	0.66	2.30	16	13
1:A:58:ILE:HG12	1:A:110:PHE:CE2	0.66	2.25	11	10
1:A:54:ARG:HE	1:A:72:VAL:HG21	0.66	1.49	11	10
1:A:34:LEU:HD22	1:A:132:GLY:N	0.65	2.05	9	3
1:A:80:LEU:HB2	1:A:105:GLN:HG2	0.65	1.67	9	1
1:A:62:ARG:HD3	1:A:68:THR:HG23	0.65	1.65	2	3
1:A:143:ILE:HG21	1:A:155:LYS:HG2	0.65	1.68	23	10
1:A:72:VAL:C	1:A:73:ILE:HD13	0.65	2.12	4	2
1:A:67:VAL:HG13	1:A:112:PHE:CE1	0.65	2.26	7	14
1:A:34:LEU:HD23	1:A:34:LEU:N	0.65	2.06	19	3
1:A:42:MET:SD	1:A:142:LEU:HD21	0.65	2.31	13	2
1:A:65:THR:HG22	1:A:121:LEU:CD2	0.65	2.22	1	20
1:A:157:VAL:HG12	1:A:161:PHE:CE2	0.65	2.27	7	23
1:A:143:ILE:HG21	1:A:155:LYS:CD	0.64	2.19	1	2
1:A:19:ILE:HB	1:A:43:PRO:HB2	0.64	1.67	2	4
1:A:147:VAL:HG21	1:A:149:PHE:CZ	0.64	2.27	5	11
1:A:30:ALA:HA	1:A:41:GLN:O	0.64	1.93	18	7
1:A:40:TRP:O	1:A:146:THR:HA	0.64	1.93	3	25
1:A:80:LEU:CD1	1:A:157:VAL:HG22	0.64	2.23	13	5
1:A:54:ARG:HH11	1:A:58:ILE:HG13	0.64	1.53	6	1
1:A:22:MET:HA	1:A:27:LYS:O	0.64	1.93	10	22
1:A:148:GLU:HG2	1:A:149:PHE:N	0.64	2.08	19	2
1:A:119:ILE:HD12	1:A:134:TRP:CZ2	0.64	2.28	5	22
1:A:19:ILE:HD12	1:A:57:ALA:O	0.63	1.92	11	6
1:A:17:VAL:HG13	1:A:47:ILE:HD11	0.63	1.71	7	10
1:A:30:ALA:CB	1:A:142:LEU:HD13	0.63	2.24	10	5
1:A:143:ILE:CG2	1:A:151:LYS:HG3	0.63	2.23	11	6
1:A:34:LEU:H	1:A:34:LEU:CD2	0.63	2.07	13	3
1:A:34:LEU:HD21	1:A:131:PHE:N	0.63	2.08	13	3
1:A:67:VAL:HG13	1:A:112:PHE:CE2	0.63	2.29	16	3

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:143:ILE:O	1:A:146:THR:HG22	0.62	1.94	10	22
1:A:19:ILE:HG13	1:A:61:LEU:HB2	0.62	1.71	10	6
1:A:62:ARG:CG	1:A:68:THR:HG23	0.62	2.23	21	5
1:A:54:ARG:HE	1:A:58:ILE:HD11	0.62	1.52	7	6
1:A:21:LEU:HD21	1:A:112:PHE:HD2	0.62	1.54	11	4
1:A:54:ARG:O	1:A:58:ILE:CD1	0.62	2.48	23	3
1:A:28:ILE:HD12	1:A:28:ILE:N	0.61	2.10	12	3
1:A:28:ILE:HG21	1:A:42:MET:SD	0.61	2.35	8	4
1:A:34:LEU:HD21	1:A:130:GLU:C	0.61	2.16	13	3
1:A:139:PRO:HB2	1:A:158:LEU:CD2	0.61	2.23	10	1
1:A:139:PRO:HB3	1:A:158:LEU:HD22	0.61	1.73	24	16
1:A:17:VAL:CG1	1:A:47:ILE:HD11	0.61	2.25	21	17
1:A:54:ARG:O	1:A:58:ILE:HD13	0.61	1.95	16	3
1:A:143:ILE:O	1:A:151:LYS:HG2	0.61	1.95	12	8
1:A:72:VAL:HG22	1:A:110:PHE:CD1	0.61	2.30	3	5
1:A:65:THR:HG23	1:A:131:PHE:CE2	0.60	2.30	22	7
1:A:45:GLY:HA3	1:A:60:GLU:HG2	0.60	1.71	23	3
1:A:22:MET:HE1	1:A:73:ILE:HD13	0.60	1.73	3	2
1:A:31:ALA:HB1	1:A:131:PHE:CB	0.60	2.26	5	9
1:A:147:VAL:CG2	1:A:150:LYS:HD2	0.60	2.27	3	1
1:A:30:ALA:HB2	1:A:142:LEU:HD13	0.60	1.74	18	6
1:A:28:ILE:N	1:A:137:VAL:O	0.60	2.33	13	15
1:A:54:ARG:NH1	1:A:57:ALA:HB3	0.60	2.11	6	1
1:A:17:VAL:HG13	1:A:47:ILE:CD1	0.60	2.26	9	10
1:A:16:ASN:HA	1:A:46:GLY:HA2	0.60	1.73	13	24
1:A:28:ILE:HG13	1:A:139:PRO:HA	0.60	1.72	3	12
1:A:26:LYS:HE2	1:A:165:LEU:HA	0.60	1.73	7	1
1:A:22:MET:HE3	1:A:73:ILE:HD13	0.60	1.74	11	2
1:A:29:PHE:CE1	1:A:119:ILE:HD13	0.59	2.32	2	17
1:A:51:GLU:OE1	1:A:56:ALA:HB2	0.59	1.96	2	1
1:A:28:ILE:HD13	1:A:139:PRO:N	0.59	2.12	20	8
1:A:80:LEU:HD11	1:A:156:GLU:OE1	0.59	1.97	15	1
1:A:7:ASP:HA	1:A:78:TYR:HA	0.59	1.71	2	16
1:A:157:VAL:CG1	1:A:161:PHE:CE2	0.59	2.86	3	25
1:A:139:PRO:O	1:A:143:ILE:HG12	0.59	1.98	10	16
1:A:54:ARG:NH1	1:A:58:ILE:HG13	0.59	2.13	6	1
1:A:27:LYS:HB3	1:A:137:VAL:O	0.59	1.98	7	4
1:A:29:PHE:CE2	1:A:65:THR:HG21	0.59	2.32	1	10
1:A:16:ASN:CB	1:A:46:GLY:HA2	0.59	2.28	18	7
1:A:34:LEU:CD2	1:A:34:LEU:N	0.58	2.67	9	2
1:A:34:LEU:N	1:A:34:LEU:CD2	0.58	2.65	19	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:79:TRP:O	1:A:80:LEU:HD23	0.58	1.98	1	10
1:A:21:LEU:HD21	1:A:112:PHE:HD1	0.58	1.58	1	5
1:A:161:PHE:O	1:A:165:LEU:HG	0.58	1.97	19	25
1:A:16:ASN:OD1	1:A:105:GLN:HG2	0.58	1.99	2	1
1:A:73:ILE:HD11	1:A:111:LYS:HB2	0.58	1.74	9	20
1:A:67:VAL:HG22	1:A:119:ILE:HG12	0.58	1.76	19	8
1:A:30:ALA:HB2	1:A:142:LEU:CD1	0.57	2.27	3	14
1:A:19:ILE:HD13	1:A:61:LEU:HB2	0.57	1.74	15	1
1:A:54:ARG:CZ	1:A:58:ILE:HD11	0.57	2.29	5	7
1:A:43:PRO:HG3	1:A:61:LEU:HD12	0.57	1.74	16	1
1:A:15:ARG:CG	1:A:47:ILE:HD12	0.57	2.30	10	5
1:A:148:GLU:HA	1:A:151:LYS:HD3	0.57	1.76	12	2
1:A:41:GLN:O	1:A:142:LEU:HD11	0.57	1.99	20	3
1:A:19:ILE:N	1:A:19:ILE:HD13	0.57	2.14	11	6
1:A:70:ALA:HA	1:A:111:LYS:O	0.57	2.00	1	25
1:A:41:GLN:HG3	1:A:146:THR:OG1	0.57	1.99	18	2
1:A:16:ASN:HB3	1:A:45:GLY:O	0.57	1.99	15	2
1:A:17:VAL:HG21	1:A:57:ALA:N	0.57	2.14	11	19
1:A:109:LEU:HD22	1:A:161:PHE:CG	0.57	2.35	23	3
1:A:23:ASN:OD1	1:A:136:TRP:CD2	0.56	2.58	11	12
1:A:43:PRO:CG	1:A:61:LEU:HD13	0.56	2.31	18	6
1:A:23:ASN:ND2	1:A:112:PHE:HB3	0.56	2.15	11	2
1:A:55:ASN:HA	1:A:58:ILE:HD12	0.56	1.77	8	4
1:A:33:ARG:NE	1:A:36:ILE:HD12	0.56	2.16	1	1
1:A:162:ALA:N	1:A:163:PRO:HD2	0.56	2.15	16	20
1:A:16:ASN:CB	1:A:105:GLN:HG2	0.56	2.30	11	3
1:A:40:TRP:O	1:A:146:THR:OG1	0.56	2.22	20	3
1:A:61:LEU:HD12	1:A:61:LEU:C	0.56	2.21	18	1
1:A:65:THR:O	1:A:119:ILE:HA	0.56	2.01	3	2
1:A:54:ARG:CZ	1:A:57:ALA:HB3	0.56	2.31	6	1
1:A:61:LEU:HD23	1:A:67:VAL:O	0.56	2.01	21	1
1:A:54:ARG:NE	1:A:72:VAL:HG21	0.56	2.16	12	9
1:A:148:GLU:HG2	1:A:149:PHE:H	0.56	1.61	10	2
1:A:39:ALA:HB1	1:A:147:VAL:HG12	0.55	1.77	2	1
1:A:18:GLY:HA3	1:A:107:TRP:CE2	0.55	2.36	6	14
1:A:22:MET:HG2	1:A:109:LEU:HD11	0.55	1.76	4	2
1:A:21:LEU:HD11	1:A:112:PHE:CB	0.55	2.30	18	8
1:A:62:ARG:HD2	1:A:66:GLY:HA2	0.55	1.77	19	1
1:A:15:ARG:HB2	1:A:79:TRP:CZ3	0.55	2.36	23	2
1:A:15:ARG:HG3	1:A:79:TRP:CH2	0.55	2.35	2	4
1:A:107:TRP:CZ2	1:A:154:TYR:CE1	0.55	2.94	3	15

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:ASN:HB2	1:A:105:GLN:CG	0.55	2.32	23	2
1:A:19:ILE:CG2	1:A:57:ALA:HB1	0.55	2.28	1	2
1:A:73:ILE:HB	1:A:109:LEU:HD23	0.55	1.79	4	2
1:A:23:ASN:N	1:A:23:ASN:OD1	0.55	2.40	23	4
1:A:18:GLY:C	1:A:19:ILE:HD13	0.55	2.22	20	3
1:A:23:ASN:OD1	1:A:136:TRP:CZ3	0.55	2.60	4	9
1:A:19:ILE:CG1	1:A:57:ALA:HB1	0.55	2.32	6	4
1:A:143:ILE:HG22	1:A:151:LYS:HG3	0.55	1.79	23	6
1:A:29:PHE:HB2	1:A:136:TRP:CZ3	0.55	2.37	3	2
1:A:19:ILE:HD13	1:A:19:ILE:N	0.55	2.16	20	1
1:A:80:LEU:HB2	1:A:105:GLN:O	0.54	2.03	4	3
1:A:77:PRO:HD2	1:A:160:VAL:HG21	0.54	1.78	17	2
1:A:54:ARG:O	1:A:58:ILE:HD12	0.54	2.03	3	1
1:A:74:ALA:CB	1:A:164:HIS:CD2	0.54	2.90	21	23
1:A:162:ALA:HB3	1:A:163:PRO:HD3	0.54	1.78	14	5
1:A:29:PHE:HE2	1:A:65:THR:HG21	0.54	1.62	1	2
1:A:62:ARG:CD	1:A:68:THR:HG23	0.54	2.32	2	2
1:A:119:ILE:HD12	1:A:134:TRP:CE2	0.54	2.37	19	3
1:A:17:VAL:HG12	1:A:47:ILE:HD11	0.54	1.78	6	1
1:A:18:GLY:HA3	1:A:107:TRP:CE3	0.54	2.38	15	4
1:A:22:MET:CE	1:A:73:ILE:HD13	0.54	2.32	11	7
1:A:6:MET:N	1:A:6:MET:HE2	0.54	2.18	25	2
1:A:34:LEU:HD12	1:A:130:GLU:O	0.54	2.03	12	6
1:A:34:LEU:HD22	1:A:131:PHE:C	0.54	2.23	19	3
1:A:19:ILE:HG21	1:A:61:LEU:CD1	0.54	2.27	23	1
1:A:21:LEU:HD23	1:A:29:PHE:HB2	0.54	1.79	23	1
1:A:43:PRO:HB3	1:A:61:LEU:HA	0.54	1.80	23	1
1:A:25:ASP:O	1:A:26:LYS:HB2	0.53	2.03	15	23
1:A:51:GLU:OE2	1:A:56:ALA:HB2	0.53	2.02	2	1
1:A:42:MET:HG3	1:A:107:TRP:CZ3	0.53	2.39	10	1
1:A:32:SER:HA	1:A:33:ARG:NH2	0.53	2.19	11	1
1:A:19:ILE:HD11	1:A:60:GLU:CD	0.53	2.23	15	1
1:A:17:VAL:HG13	1:A:47:ILE:HG13	0.53	1.79	6	10
1:A:138:THR:HB	1:A:139:PRO:CD	0.53	2.33	7	24
1:A:139:PRO:CB	1:A:158:LEU:HD13	0.53	2.34	7	3
1:A:143:ILE:HG21	1:A:155:LYS:CE	0.53	2.34	19	2
1:A:16:ASN:HB3	1:A:105:GLN:HG2	0.53	1.80	13	1
1:A:146:THR:HG23	1:A:151:LYS:HG2	0.53	1.81	8	2
1:A:160:VAL:O	1:A:163:PRO:HD2	0.53	2.04	7	4
1:A:16:ASN:N	1:A:104:ALA:O	0.53	2.37	23	1
1:A:46:GLY:C	1:A:47:ILE:HG13	0.53	2.23	11	3

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:107:TRP:CH2	1:A:154:TYR:CE1	0.53	2.97	19	3
1:A:45:GLY:N	1:A:60:GLU:OE2	0.53	2.42	15	1
1:A:62:ARG:O	1:A:66:GLY:N	0.53	2.40	13	18
1:A:29:PHE:CZ	1:A:65:THR:HG21	0.53	2.38	16	7
1:A:109:LEU:HD13	1:A:161:PHE:CD2	0.52	2.38	23	3
1:A:138:THR:HB	1:A:139:PRO:HD2	0.52	1.80	10	23
1:A:79:TRP:CD1	1:A:106:LYS:HD3	0.52	2.39	11	3
1:A:53:PRO:HB2	1:A:108:PHE:CZ	0.52	2.40	7	4
1:A:54:ARG:HH21	1:A:72:VAL:HG11	0.52	1.63	9	1
1:A:54:ARG:C	1:A:54:ARG:HD2	0.52	2.23	20	5
1:A:16:ASN:ND2	1:A:17:VAL:N	0.52	2.57	13	1
1:A:51:GLU:CD	1:A:56:ALA:HB2	0.52	2.25	2	1
1:A:34:LEU:CD2	1:A:131:PHE:CA	0.52	2.87	19	3
1:A:15:ARG:HG3	1:A:79:TRP:CZ3	0.52	2.40	11	9
1:A:43:PRO:CB	1:A:61:LEU:HD12	0.52	2.35	24	1
1:A:33:ARG:NE	1:A:36:ILE:HD13	0.52	2.19	14	1
1:A:148:GLU:O	1:A:152:PRO:HD2	0.52	2.03	11	15
1:A:39:ALA:HB1	1:A:147:VAL:HG13	0.52	1.81	12	1
1:A:40:TRP:O	1:A:41:GLN:HG3	0.52	2.05	20	6
1:A:19:ILE:HD12	1:A:44:GLN:HA	0.51	1.82	22	8
1:A:73:ILE:N	1:A:73:ILE:CD1	0.51	2.67	4	1
1:A:30:ALA:CB	1:A:142:LEU:HD12	0.51	2.32	6	3
1:A:15:ARG:HA	1:A:104:ALA:O	0.51	2.06	7	3
1:A:33:ARG:HE	1:A:36:ILE:HD12	0.51	1.64	6	1
1:A:34:LEU:HD12	1:A:130:GLU:C	0.51	2.26	12	3
1:A:22:MET:SD	1:A:109:LEU:HD21	0.51	2.45	7	4
1:A:79:TRP:CE2	1:A:106:LYS:HE2	0.51	2.40	2	2
1:A:80:LEU:HD11	1:A:157:VAL:HG22	0.51	1.82	8	4
1:A:17:VAL:HG13	1:A:47:ILE:HG12	0.51	1.82	15	4
1:A:40:TRP:C	1:A:41:GLN:HG3	0.51	2.25	3	3
1:A:134:TRP:CZ3	1:A:136:TRP:CE2	0.51	2.99	15	11
1:A:54:ARG:CZ	1:A:110:PHE:CE1	0.51	2.93	6	1
1:A:73:ILE:HD11	1:A:111:LYS:N	0.51	2.21	14	9
1:A:23:ASN:OD1	1:A:136:TRP:CE2	0.51	2.64	18	3
1:A:58:ILE:O	1:A:61:LEU:HB3	0.51	2.06	15	1
1:A:151:LYS:N	1:A:152:PRO:HD2	0.50	2.21	22	15
1:A:76:VAL:HG12	1:A:78:TYR:O	0.50	2.06	18	16
1:A:54:ARG:HH21	1:A:108:PHE:HB2	0.50	1.66	6	1
1:A:55:ASN:OD1	1:A:56:ALA:N	0.50	2.44	23	2
1:A:79:TRP:O	1:A:80:LEU:CD2	0.50	2.59	1	7
1:A:74:ALA:HB2	1:A:164:HIS:CD2	0.50	2.42	14	9

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:MET:CB	1:A:27:LYS:O	0.50	2.59	18	6
1:A:19:ILE:HG12	1:A:57:ALA:O	0.50	2.07	3	4
1:A:54:ARG:NH2	1:A:57:ALA:CB	0.50	2.74	6	1
1:A:16:ASN:HB3	1:A:46:GLY:HA2	0.50	1.83	18	3
1:A:61:LEU:HD12	1:A:65:THR:OG1	0.50	2.06	18	3
1:A:121:LEU:HD11	1:A:134:TRP:HD1	0.50	1.65	10	8
1:A:73:ILE:HD12	1:A:109:LEU:HG	0.50	1.84	14	2
1:A:31:ALA:O	1:A:33:ARG:NH2	0.50	2.42	11	1
1:A:29:PHE:CE1	1:A:134:TRP:CD2	0.50	2.99	7	1
1:A:54:ARG:HD2	1:A:58:ILE:CD1	0.50	2.36	16	3
1:A:54:ARG:HG2	1:A:108:PHE:CD1	0.50	2.42	15	3
1:A:16:ASN:OD1	1:A:105:GLN:HB3	0.50	2.07	2	1
1:A:30:ALA:O	1:A:134:TRP:HB2	0.50	2.07	7	16
1:A:42:MET:HE2	1:A:154:TYR:CD2	0.50	2.42	22	1
1:A:68:THR:O	1:A:70:ALA:N	0.50	2.45	9	24
1:A:30:ALA:HB1	1:A:40:TRP:CE3	0.50	2.41	7	7
1:A:17:VAL:HG11	1:A:53:PRO:HA	0.50	1.84	18	6
1:A:150:LYS:HG2	1:A:154:TYR:CZ	0.50	2.42	21	2
1:A:31:ALA:HB1	1:A:131:PHE:HB3	0.49	1.83	13	4
1:A:54:ARG:CD	1:A:58:ILE:HD11	0.49	2.37	20	8
1:A:19:ILE:HD13	1:A:43:PRO:HB2	0.49	1.83	4	3
1:A:54:ARG:O	1:A:58:ILE:HG13	0.49	2.07	11	3
1:A:108:PHE:HB2	1:A:110:PHE:HE1	0.49	1.67	11	5
1:A:33:ARG:NH1	1:A:41:GLN:HG2	0.49	2.23	10	1
1:A:31:ALA:HB1	1:A:131:PHE:CG	0.49	2.43	5	5
1:A:40:TRP:CZ3	1:A:134:TRP:HA	0.49	2.43	3	10
1:A:20:CYS:O	1:A:110:PHE:N	0.49	2.46	6	4
1:A:44:GLN:HG3	1:A:107:TRP:CZ2	0.49	2.43	12	1
1:A:19:ILE:HG21	1:A:61:LEU:CD2	0.49	2.36	18	2
1:A:24:ASN:HA	1:A:111:LYS:HE2	0.49	1.85	3	1
1:A:76:VAL:HG13	1:A:77:PRO:HD2	0.49	1.85	8	10
1:A:43:PRO:CG	1:A:61:LEU:HD12	0.49	2.37	16	1
1:A:22:MET:CA	1:A:27:LYS:O	0.49	2.61	9	11
1:A:73:ILE:HD11	1:A:111:LYS:CB	0.49	2.37	18	11
1:A:23:ASN:OD1	1:A:23:ASN:N	0.49	2.46	6	2
1:A:161:PHE:O	1:A:165:LEU:N	0.49	2.45	7	1
1:A:79:TRP:CD2	1:A:106:LYS:HB2	0.49	2.43	11	2
1:A:79:TRP:O	1:A:80:LEU:HG	0.49	2.07	22	7
1:A:43:PRO:CB	1:A:61:LEU:HA	0.49	2.38	23	1
1:A:151:LYS:O	1:A:155:LYS:HB2	0.49	2.08	9	6
1:A:54:ARG:HG3	1:A:108:PHE:CE2	0.49	2.43	3	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:ARG:HD2	1:A:79:TRP:CH2	0.49	2.43	19	2
1:A:19:ILE:CG2	1:A:110:PHE:CD2	0.49	2.95	3	2
1:A:121:LEU:HD11	1:A:134:TRP:CD1	0.48	2.42	19	2
1:A:40:TRP:CD1	1:A:145:LEU:HB3	0.48	2.42	18	2
1:A:23:ASN:OD1	1:A:136:TRP:CH2	0.48	2.66	1	5
1:A:42:MET:HB3	1:A:107:TRP:CZ3	0.48	2.43	22	3
1:A:28:ILE:CG1	1:A:139:PRO:HA	0.48	2.38	16	3
1:A:147:VAL:HB	1:A:149:PHE:CE1	0.48	2.43	23	7
1:A:17:VAL:HA	1:A:106:LYS:O	0.48	2.09	15	4
1:A:6:MET:C	1:A:78:TYR:HB2	0.48	2.29	15	1
1:A:41:GLN:HG3	1:A:146:THR:HG1	0.48	1.69	23	3
1:A:17:VAL:HG11	1:A:53:PRO:CA	0.48	2.38	2	2
1:A:58:ILE:CD1	1:A:110:PHE:CZ	0.48	2.96	23	3
1:A:119:ILE:HD12	1:A:134:TRP:CH2	0.48	2.44	8	2
1:A:19:ILE:HG12	1:A:61:LEU:HB2	0.48	1.85	23	1
1:A:67:VAL:HG13	1:A:112:PHE:CD1	0.48	2.43	7	6
1:A:130:GLU:HG3	1:A:131:PHE:CE1	0.48	2.42	7	1
1:A:19:ILE:HG22	1:A:110:PHE:CD1	0.48	2.42	20	2
1:A:52:ASP:HB2	1:A:55:ASN:OD1	0.48	2.09	2	1
1:A:42:MET:HB2	1:A:43:PRO:HD2	0.48	1.85	18	3
1:A:146:THR:CG2	1:A:151:LYS:HG2	0.48	2.38	8	4
1:A:120:ASN:O	1:A:121:LEU:HB2	0.48	2.09	25	3
1:A:61:LEU:CD1	1:A:67:VAL:HB	0.48	2.33	18	2
1:A:30:ALA:HB2	1:A:137:VAL:HG22	0.48	1.85	7	1
1:A:19:ILE:CG1	1:A:61:LEU:HD12	0.48	2.39	20	1
1:A:19:ILE:CG2	1:A:61:LEU:HD22	0.48	2.29	3	3
1:A:150:LYS:HB3	1:A:154:TYR:CZ	0.48	2.43	11	2
1:A:134:TRP:CZ3	1:A:136:TRP:NE1	0.47	2.82	19	7
1:A:23:ASN:HD22	1:A:112:PHE:HB3	0.47	1.69	11	1
1:A:65:THR:HG23	1:A:131:PHE:CE1	0.47	2.44	18	3
1:A:54:ARG:HD2	1:A:58:ILE:HD11	0.47	1.85	3	3
1:A:109:LEU:HD22	1:A:161:PHE:HB3	0.47	1.86	3	1
1:A:17:VAL:O	1:A:44:GLN:HG3	0.47	2.08	23	1
1:A:27:LYS:C	1:A:28:ILE:HD13	0.47	2.30	4	3
1:A:33:ARG:NH2	1:A:41:GLN:HG3	0.47	2.24	11	1
1:A:108:PHE:HB2	1:A:110:PHE:CE1	0.47	2.44	19	2
1:A:54:ARG:HG2	1:A:108:PHE:CD2	0.47	2.45	10	2
1:A:19:ILE:HG13	1:A:61:LEU:HD12	0.47	1.85	20	1
1:A:21:LEU:CD1	1:A:112:PHE:HB2	0.47	2.39	18	1
1:A:22:MET:HE1	1:A:26:LYS:HE2	0.47	1.85	24	1
1:A:26:LYS:NZ	1:A:165:LEU:HA	0.47	2.25	3	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:LEU:HD11	1:A:112:PHE:CA	0.47	2.40	22	5
1:A:32:SER:O	1:A:131:PHE:HA	0.47	2.10	14	1
1:A:16:ASN:HB2	1:A:45:GLY:O	0.47	2.10	2	1
1:A:19:ILE:HD11	1:A:60:GLU:CG	0.47	2.40	12	1
1:A:54:ARG:NH1	1:A:72:VAL:HG11	0.47	2.24	12	1
1:A:21:LEU:HD12	1:A:110:PHE:O	0.47	2.10	21	1
1:A:28:ILE:N	1:A:28:ILE:CD1	0.47	2.76	18	8
1:A:54:ARG:NH1	1:A:110:PHE:CZ	0.47	2.83	6	1
1:A:54:ARG:HG2	1:A:108:PHE:CE1	0.47	2.46	15	5
1:A:28:ILE:HD13	1:A:139:PRO:CA	0.47	2.40	21	2
1:A:58:ILE:HD12	1:A:58:ILE:H	0.46	1.70	3	1
1:A:138:THR:OG1	1:A:141:GLN:HB2	0.46	2.10	9	10
1:A:18:GLY:HA2	1:A:44:GLN:CG	0.46	2.40	2	2
1:A:47:ILE:HG23	1:A:51:GLU:OE1	0.46	2.10	2	1
1:A:16:ASN:CA	1:A:46:GLY:HA2	0.46	2.41	3	5
1:A:6:MET:O	1:A:78:TYR:HB2	0.46	2.09	25	1
1:A:162:ALA:N	1:A:163:PRO:CD	0.46	2.79	12	12
1:A:47:ILE:HG12	1:A:53:PRO:HA	0.46	1.86	3	1
1:A:154:TYR:O	1:A:157:VAL:HB	0.46	2.10	10	1
1:A:143:ILE:O	1:A:151:LYS:CG	0.46	2.63	14	2
1:A:56:ALA:O	1:A:60:GLU:HB2	0.46	2.11	17	1
1:A:54:ARG:N	1:A:108:PHE:CZ	0.46	2.84	16	3
1:A:33:ARG:CD	1:A:41:GLN:NE2	0.46	2.79	8	1
1:A:19:ILE:HD11	1:A:60:GLU:OE2	0.46	2.11	15	1
1:A:19:ILE:HD12	1:A:57:ALA:CA	0.46	2.41	20	1
1:A:28:ILE:HD11	1:A:139:PRO:CG	0.46	2.40	5	2
1:A:47:ILE:HG21	1:A:51:GLU:O	0.46	2.11	14	4
1:A:77:PRO:HD3	1:A:160:VAL:CG1	0.46	2.40	7	2
1:A:16:ASN:ND2	1:A:104:ALA:O	0.45	2.49	2	1
1:A:147:VAL:HG23	1:A:150:LYS:HB2	0.45	1.86	22	1
1:A:39:ALA:CB	1:A:147:VAL:CG1	0.45	2.94	1	4
1:A:7:ASP:HA	1:A:78:TYR:CA	0.45	2.41	2	2
1:A:42:MET:HG3	1:A:142:LEU:HD11	0.45	1.87	2	1
1:A:155:LYS:HA	1:A:155:LYS:HE2	0.45	1.86	15	2
1:A:134:TRP:CE3	1:A:135:SER:N	0.45	2.84	23	5
1:A:79:TRP:CE3	1:A:106:LYS:HB2	0.45	2.46	15	1
1:A:79:TRP:C	1:A:80:LEU:HG	0.45	2.32	9	4
1:A:72:VAL:HG22	1:A:110:PHE:CD2	0.45	2.47	19	2
1:A:119:ILE:HB	1:A:134:TRP:NE1	0.45	2.27	21	1
1:A:143:ILE:CG2	1:A:151:LYS:CG	0.45	2.95	23	5
1:A:65:THR:O	1:A:120:ASN:N	0.45	2.50	4	3

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:41:GLN:N	1:A:142:LEU:HD11	0.45	2.27	10	1
1:A:142:LEU:O	1:A:146:THR:HB	0.45	2.11	21	8
1:A:121:LEU:HD22	1:A:131:PHE:CD2	0.45	2.46	1	2
1:A:39:ALA:CB	1:A:147:VAL:HG12	0.45	2.41	2	1
1:A:121:LEU:HD21	1:A:134:TRP:CD1	0.45	2.47	3	2
1:A:19:ILE:CG2	1:A:110:PHE:CD1	0.45	3.00	9	3
1:A:79:TRP:CD2	1:A:106:LYS:HD3	0.45	2.46	15	1
1:A:109:LEU:C	1:A:110:PHE:CD1	0.45	2.90	19	1
1:A:62:ARG:NE	1:A:66:GLY:HA2	0.45	2.27	10	1
1:A:147:VAL:HG21	1:A:149:PHE:CE1	0.45	2.47	5	1
1:A:21:LEU:HD23	1:A:29:PHE:CB	0.45	2.42	23	1
1:A:80:LEU:N	1:A:105:GLN:O	0.45	2.50	8	3
1:A:108:PHE:HB3	1:A:110:PHE:CE1	0.45	2.46	12	3
1:A:148:GLU:HA	1:A:151:LYS:HE2	0.45	1.87	4	1
1:A:146:THR:HG23	1:A:151:LYS:CG	0.45	2.42	16	5
1:A:30:ALA:CB	1:A:40:TRP:CE3	0.45	3.01	7	2
1:A:139:PRO:HB2	1:A:158:LEU:HD13	0.44	1.89	7	1
1:A:143:ILE:C	1:A:146:THR:HG22	0.44	2.32	23	2
1:A:139:PRO:CG	1:A:158:LEU:HD21	0.44	2.41	10	1
1:A:143:ILE:CD1	1:A:154:TYR:HB2	0.44	2.42	1	1
1:A:15:ARG:CD	1:A:79:TRP:CH2	0.44	3.00	19	1
1:A:33:ARG:NH1	1:A:36:ILE:HD12	0.44	2.28	7	1
1:A:42:MET:CE	1:A:154:TYR:CG	0.44	3.01	15	1
1:A:34:LEU:HG	1:A:132:GLY:N	0.44	2.26	5	4
1:A:115:GLN:HG3	1:A:117:GLN:CG	0.44	2.42	2	1
1:A:44:GLN:OE1	1:A:150:LYS:NZ	0.44	2.50	4	1
1:A:80:LEU:HD12	1:A:107:TRP:HD1	0.44	1.66	13	2
1:A:41:GLN:HG2	1:A:154:TYR:OH	0.44	2.12	18	1
1:A:47:ILE:HG22	1:A:51:GLU:O	0.44	2.12	2	1
1:A:43:PRO:CB	1:A:61:LEU:HD13	0.44	2.42	5	3
1:A:119:ILE:HG21	1:A:134:TRP:CD1	0.44	2.47	19	2
1:A:109:LEU:HD12	1:A:110:PHE:H	0.44	1.73	13	1
1:A:31:ALA:N	1:A:41:GLN:O	0.44	2.48	10	4
1:A:67:VAL:HG13	1:A:112:PHE:HE1	0.44	1.67	7	1
1:A:54:ARG:CA	1:A:108:PHE:CZ	0.44	3.01	16	1
1:A:158:LEU:O	1:A:162:ALA:N	0.44	2.51	11	6
1:A:34:LEU:CD2	1:A:131:PHE:C	0.44	2.86	19	3
1:A:73:ILE:HD11	1:A:111:LYS:CA	0.44	2.43	14	10
1:A:80:LEU:CD1	1:A:157:VAL:CG2	0.44	2.95	13	3
1:A:31:ALA:HA	1:A:133:GLU:O	0.44	2.13	13	1
1:A:16:ASN:HA	1:A:47:ILE:HG13	0.43	1.88	2	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:29:PHE:CZ	1:A:134:TRP:HB2	0.43	2.48	2	1
1:A:142:LEU:O	1:A:146:THR:N	0.43	2.51	7	5
1:A:143:ILE:HA	1:A:146:THR:HG22	0.43	1.89	20	5
1:A:15:ARG:HD3	1:A:79:TRP:CH2	0.43	2.48	5	1
1:A:17:VAL:HG21	1:A:57:ALA:CA	0.43	2.43	6	1
1:A:19:ILE:HD11	1:A:57:ALA:O	0.43	2.13	25	2
1:A:54:ARG:CG	1:A:108:PHE:CE2	0.43	3.01	16	3
1:A:61:LEU:C	1:A:61:LEU:HD23	0.43	2.34	11	2
1:A:149:PHE:CD2	1:A:150:LYS:HG3	0.43	2.48	19	2
1:A:29:PHE:CE2	1:A:43:PRO:HD3	0.43	2.48	18	1
1:A:55:ASN:O	1:A:59:ARG:HB2	0.43	2.13	3	2
1:A:156:GLU:O	1:A:160:VAL:HG23	0.43	2.13	3	2
1:A:19:ILE:N	1:A:19:ILE:CD1	0.43	2.80	20	5
1:A:33:ARG:HD2	1:A:41:GLN:NE2	0.43	2.27	21	1
1:A:18:GLY:HA2	1:A:44:GLN:HG2	0.43	1.88	2	1
1:A:23:ASN:ND2	1:A:136:TRP:CE3	0.43	2.86	2	1
1:A:116:ASP:HB3	1:A:134:TRP:CH2	0.43	2.48	2	1
1:A:16:ASN:HB2	1:A:105:GLN:HB3	0.43	1.91	5	1
1:A:134:TRP:HE3	1:A:135:SER:N	0.43	2.11	10	2
1:A:58:ILE:HG12	1:A:110:PHE:HE2	0.43	1.72	2	1
1:A:54:ARG:NH1	1:A:58:ILE:HD11	0.43	2.28	5	1
1:A:54:ARG:NH1	1:A:110:PHE:HZ	0.43	2.12	6	1
1:A:54:ARG:HG2	1:A:108:PHE:CE2	0.43	2.49	6	3
1:A:70:ALA:CA	1:A:111:LYS:O	0.43	2.66	17	6
1:A:21:LEU:HA	1:A:110:PHE:O	0.43	2.13	4	2
1:A:29:PHE:HE1	1:A:134:TRP:CD2	0.43	2.32	12	3
1:A:30:ALA:HB1	1:A:142:LEU:HD13	0.43	1.88	10	1
1:A:33:ARG:CZ	1:A:41:GLN:OE1	0.43	2.67	10	1
1:A:40:TRP:HZ3	1:A:134:TRP:HA	0.43	1.73	11	1
1:A:146:THR:CG2	1:A:151:LYS:HG3	0.43	2.43	14	2
1:A:151:LYS:CB	1:A:152:PRO:CD	0.43	2.95	14	4
1:A:18:GLY:N	1:A:106:LYS:O	0.43	2.51	15	1
1:A:19:ILE:CG2	1:A:110:PHE:CE1	0.43	2.99	20	1
1:A:155:LYS:HE2	1:A:158:LEU:HD12	0.43	1.91	15	2
1:A:19:ILE:HG12	1:A:43:PRO:O	0.43	2.13	11	1
1:A:150:LYS:HG2	1:A:154:TYR:CE1	0.43	2.48	22	1
1:A:143:ILE:HG13	1:A:155:LYS:CD	0.43	2.44	7	3
1:A:148:GLU:CG	1:A:149:PHE:N	0.43	2.81	7	1
1:A:120:ASN:O	1:A:121:LEU:C	0.43	2.57	13	1
1:A:130:GLU:CG	1:A:131:PHE:CE1	0.43	3.02	7	1
1:A:19:ILE:CD1	1:A:57:ALA:O	0.43	2.66	18	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:147:VAL:CG2	1:A:150:LYS:HD3	0.43	2.43	18	1
1:A:47:ILE:CG2	1:A:51:GLU:O	0.43	2.67	2	1
1:A:109:LEU:O	1:A:110:PHE:CD1	0.43	2.72	3	1
1:A:157:VAL:HG12	1:A:161:PHE:CD2	0.43	2.49	10	3
1:A:73:ILE:HB	1:A:109:LEU:CD2	0.43	2.44	4	1
1:A:23:ASN:ND2	1:A:136:TRP:CH2	0.43	2.87	11	1
1:A:134:TRP:HZ3	1:A:136:TRP:NE1	0.42	2.12	14	2
1:A:119:ILE:CG2	1:A:134:TRP:CD1	0.42	3.02	21	2
1:A:30:ALA:CB	1:A:142:LEU:CD1	0.42	2.97	15	2
1:A:19:ILE:HG22	1:A:110:PHE:CZ	0.42	2.47	19	1
1:A:142:LEU:HD21	1:A:154:TYR:CD2	0.42	2.48	21	1
1:A:154:TYR:CD1	1:A:154:TYR:N	0.42	2.87	3	2
1:A:154:TYR:N	1:A:154:TYR:CD1	0.42	2.87	15	5
1:A:29:PHE:CD2	1:A:43:PRO:HD3	0.42	2.49	7	1
1:A:54:ARG:NH1	1:A:108:PHE:CE1	0.42	2.87	9	1
1:A:26:LYS:HE3	1:A:164:HIS:O	0.42	2.14	10	1
1:A:138:THR:CB	1:A:139:PRO:CD	0.42	2.98	10	1
1:A:19:ILE:CD1	1:A:60:GLU:OE2	0.42	2.67	15	1
1:A:143:ILE:HG23	1:A:151:LYS:HG3	0.42	1.91	19	1
1:A:40:TRP:O	1:A:146:THR:CB	0.42	2.68	12	4
1:A:78:TYR:CE1	1:A:80:LEU:HD21	0.42	2.49	12	1
1:A:16:ASN:ND2	1:A:46:GLY:CA	0.42	2.82	14	1
1:A:19:ILE:N	1:A:107:TRP:CZ3	0.42	2.88	23	1
1:A:77:PRO:HD2	1:A:160:VAL:HG11	0.42	1.92	11	1
1:A:46:GLY:O	1:A:47:ILE:O	0.42	2.37	15	1
1:A:21:LEU:O	1:A:29:PHE:N	0.42	2.51	7	1
1:A:26:LYS:O	1:A:26:LYS:HG3	0.42	2.14	7	1
1:A:121:LEU:HG	1:A:134:TRP:HD1	0.42	1.73	21	1
1:A:22:MET:SD	1:A:165:LEU:CD2	0.42	3.08	9	2
1:A:77:PRO:CD	1:A:160:VAL:HG11	0.42	2.45	6	1
1:A:31:ALA:O	1:A:41:GLN:N	0.42	2.52	8	1
1:A:69:SER:O	1:A:113:THR:N	0.42	2.53	9	3
1:A:20:CYS:CB	1:A:161:PHE:CE2	0.42	3.03	7	2
1:A:29:PHE:CD2	1:A:43:PRO:CD	0.42	3.03	16	1
1:A:109:LEU:CD2	1:A:164:HIS:CB	0.42	2.98	8	1
1:A:15:ARG:CG	1:A:79:TRP:CH2	0.41	3.03	2	1
1:A:34:LEU:HG	1:A:132:GLY:HA2	0.41	1.90	3	1
1:A:151:LYS:HB2	1:A:152:PRO:CD	0.41	2.44	4	3
1:A:30:ALA:HB1	1:A:40:TRP:HE3	0.41	1.73	7	1
1:A:58:ILE:HG12	1:A:110:PHE:CZ	0.41	2.49	9	1
1:A:33:ARG:CZ	1:A:41:GLN:HG3	0.41	2.45	11	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:56:ALA:O	1:A:60:GLU:CG	0.41	2.68	15	1
1:A:109:LEU:HB2	1:A:161:PHE:CZ	0.41	2.50	3	1
1:A:15:ARG:HB2	1:A:79:TRP:HZ3	0.41	1.74	12	1
1:A:19:ILE:HD12	1:A:57:ALA:HA	0.41	1.92	20	1
1:A:147:VAL:CG2	1:A:150:LYS:HB2	0.41	2.45	22	1
1:A:58:ILE:HD12	1:A:58:ILE:N	0.41	2.30	3	1
1:A:53:PRO:HB2	1:A:108:PHE:HZ	0.41	1.73	7	1
1:A:54:ARG:HH11	1:A:72:VAL:HG11	0.41	1.75	12	1
1:A:28:ILE:HG13	1:A:139:PRO:CA	0.41	2.45	17	1
1:A:16:ASN:OD1	1:A:16:ASN:N	0.41	2.53	3	1
1:A:61:LEU:CD2	1:A:67:VAL:O	0.41	2.68	19	2
1:A:30:ALA:N	1:A:135:SER:O	0.41	2.53	2	1
1:A:36:ILE:HB	1:A:39:ALA:HB3	0.41	1.92	4	1
1:A:26:LYS:O	1:A:26:LYS:CG	0.41	2.67	7	1
1:A:147:VAL:HB	1:A:149:PHE:CE2	0.41	2.51	13	1
1:A:40:TRP:O	1:A:146:THR:CA	0.41	2.69	15	1
1:A:54:ARG:HD2	1:A:54:ARG:O	0.41	2.16	21	1
1:A:47:ILE:CD1	1:A:79:TRP:CZ3	0.41	3.03	3	1
1:A:54:ARG:HG3	1:A:108:PHE:CD2	0.41	2.50	3	1
1:A:150:LYS:HG3	1:A:154:TYR:CE1	0.41	2.49	13	1
1:A:116:ASP:HB2	1:A:134:TRP:CH2	0.41	2.50	18	2
1:A:6:MET:SD	1:A:6:MET:N	0.41	2.94	22	1
1:A:17:VAL:N	1:A:45:GLY:O	0.41	2.44	2	1
1:A:42:MET:HB3	1:A:107:TRP:CH2	0.41	2.51	21	2
1:A:16:ASN:CG	1:A:46:GLY:HA2	0.41	2.36	6	1
1:A:17:VAL:CG1	1:A:47:ILE:CG1	0.41	2.99	6	1
1:A:61:LEU:HD21	1:A:67:VAL:CB	0.41	2.39	11	1
1:A:35:ASP:N	1:A:35:ASP:OD1	0.41	2.54	1	1
1:A:138:THR:OG1	1:A:141:GLN:HG3	0.41	2.16	1	1
1:A:33:ARG:O	1:A:36:ILE:N	0.41	2.53	2	3
1:A:46:GLY:C	1:A:47:ILE:CG1	0.41	2.89	9	1
1:A:42:MET:HG3	1:A:107:TRP:HZ3	0.41	1.76	15	1
1:A:151:LYS:N	1:A:152:PRO:CD	0.41	2.84	15	1
1:A:58:ILE:HG13	1:A:110:PHE:CE2	0.41	2.51	16	1
1:A:54:ARG:HG3	1:A:58:ILE:HD11	0.41	1.93	22	1
1:A:143:ILE:CD1	1:A:154:TYR:CB	0.41	2.99	1	1
1:A:23:ASN:HD22	1:A:27:LYS:HB2	0.41	1.76	3	1
1:A:26:LYS:NZ	1:A:165:LEU:HD23	0.41	2.31	3	2
1:A:21:LEU:HD23	1:A:29:PHE:CD2	0.41	2.51	5	1
1:A:28:ILE:HD13	1:A:138:THR:C	0.41	2.36	6	3
1:A:59:ARG:HG3	1:A:60:GLU:N	0.41	2.31	6	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:ASN:HA	1:A:47:ILE:H	0.41	1.76	7	1
1:A:74:ALA:HB2	1:A:164:HIS:CG	0.41	2.50	17	2
1:A:150:LYS:CG	1:A:154:TYR:CE1	0.41	3.04	13	2
1:A:46:GLY:O	1:A:47:ILE:HG13	0.41	2.15	11	1
1:A:54:ARG:HH11	1:A:54:ARG:HB3	0.41	1.76	11	1
1:A:33:ARG:HG3	1:A:41:GLN:NE2	0.41	2.30	3	1
1:A:143:ILE:HG22	1:A:151:LYS:CG	0.41	2.44	23	1
1:A:54:ARG:CB	1:A:108:PHE:CE2	0.40	3.04	16	1
1:A:80:LEU:O	1:A:105:GLN:N	0.40	2.52	6	1
1:A:116:ASP:HB2	1:A:134:TRP:CZ2	0.40	2.51	18	1
1:A:16:ASN:N	1:A:16:ASN:ND2	0.40	2.69	24	1
1:A:79:TRP:NE1	1:A:106:LYS:HE2	0.40	2.30	25	1
1:A:112:PHE:CE2	1:A:114:GLY:C	0.40	2.94	6	2
1:A:79:TRP:CE2	1:A:106:LYS:HD3	0.40	2.51	14	1
1:A:21:LEU:HD11	1:A:112:PHE:N	0.40	2.32	22	1
1:A:54:ARG:CG	1:A:108:PHE:CD2	0.40	3.05	3	1
1:A:22:MET:HE2	1:A:26:LYS:HE2	0.40	1.93	4	1
1:A:31:ALA:CB	1:A:131:PHE:CG	0.40	3.05	5	1
1:A:42:MET:HE3	1:A:107:TRP:CZ3	0.40	2.50	6	1
1:A:74:ALA:HB3	1:A:109:LEU:HB3	0.40	1.94	8	1
1:A:54:ARG:HD3	1:A:108:PHE:CD1	0.40	2.52	9	1
1:A:138:THR:OG1	1:A:141:GLN:CG	0.40	2.70	16	1
1:A:64:GLU:HB3	1:A:131:PHE:CE2	0.40	2.51	19	1
1:A:67:VAL:CG2	1:A:119:ILE:HG12	0.40	2.46	19	1
1:A:23:ASN:C	1:A:25:ASP:N	0.40	2.75	24	1
1:A:23:ASN:C	1:A:25:ASP:H	0.40	2.20	24	1
1:A:18:GLY:HA2	1:A:44:GLN:CB	0.40	2.47	9	1
1:A:41:GLN:HB3	1:A:154:TYR:OH	0.40	2.17	13	1
1:A:79:TRP:O	1:A:80:LEU:CG	0.40	2.70	15	2
1:A:112:PHE:CE1	1:A:115:GLN:O	0.40	2.75	16	1
1:A:16:ASN:OD1	1:A:46:GLY:CA	0.40	2.70	17	1
1:A:146:THR:CG2	1:A:151:LYS:CG	0.40	3.00	17	1
1:A:110:PHE:CD1	1:A:110:PHE:N	0.40	2.89	19	1
1:A:65:THR:HB	1:A:119:ILE:HG23	0.40	1.92	23	1
1:A:72:VAL:CG2	1:A:110:PHE:CE2	0.40	3.00	24	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	121/165 (73%)	99±2 (82±2%)	17±2 (14±2%)	5±2 (4±1%)	5 30
All	All	3025/4125 (73%)	2485 (82%)	413 (14%)	127 (4%)	5 30

All 13 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	69	SER	25
1	A	6	MET	16
1	A	49	GLU	14
1	A	77	PRO	12
1	A	15	ARG	11
1	A	34	LEU	10
1	A	35	ASP	10
1	A	41	GLN	8
1	A	53	PRO	8
1	A	149	PHE	7
1	A	47	ILE	3
1	A	121	LEU	2
1	A	117	GLN	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	106/142 (75%)	84±4 (79±3%)	22±4 (21±3%)	3 33
All	All	2650/3550 (75%)	2106 (79%)	544 (21%)	3 33

All 59 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	54	ARG	25
1	A	144	ASP	24
1	A	34	LEU	23
1	A	155	LYS	23
1	A	68	THR	22
1	A	22	MET	20
1	A	41	GLN	20
1	A	78	TYR	18
1	A	145	LEU	17
1	A	23	ASN	17
1	A	133	GLU	16
1	A	73	ILE	15
1	A	71	GLU	15
1	A	140	GLU	14
1	A	142	LEU	14
1	A	65	THR	14
1	A	75	GLU	13
1	A	15	ARG	12
1	A	151	LYS	12
1	A	156	GLU	12
1	A	25	ASP	11
1	A	44	GLN	10
1	A	141	GLN	10
1	A	60	GLU	10
1	A	35	ASP	9
1	A	59	ARG	8
1	A	130	GLU	8
1	A	159	SER	8
1	A	19	ILE	7
1	A	42	MET	7
1	A	49	GLU	7
1	A	52	ASP	6
1	A	26	LYS	6
1	A	149	PHE	6
1	A	118	GLU	6
1	A	61	LEU	6
1	A	150	LYS	6
1	A	115	GLN	5
1	A	38	ASP	5
1	A	6	MET	5
1	A	16	ASN	4
1	A	105	GLN	4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	117	GLN	4
1	A	148	GLU	4
1	A	27	LYS	4
1	A	120	ASN	4
1	A	106	LYS	4
1	A	63	GLU	3
1	A	48	ASP	3
1	A	20	CYS	3
1	A	131	PHE	3
1	A	28	ILE	2
1	A	62	ARG	2
1	A	33	ARG	2
1	A	111	LYS	2
1	A	55	ASN	1
1	A	121	LEU	1
1	A	158	LEU	1
1	A	24	ASN	1

6.3.3 RNA

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates

There are no monosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation (i)

No chemical shift data were provided