



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 08:03 PM BST

PDB ID : 2E30  
Title : Solution structure of the cytoplasmic region of Na<sup>+</sup>/H<sup>+</sup> exchanger 1 complexed with essential cofactor calcineurin B homologous protein 1  
Authors : Mishima, M.; Wakabayashi, S.; Kojima, C.  
Deposited on : 2006-11-19

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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 : unknown  
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

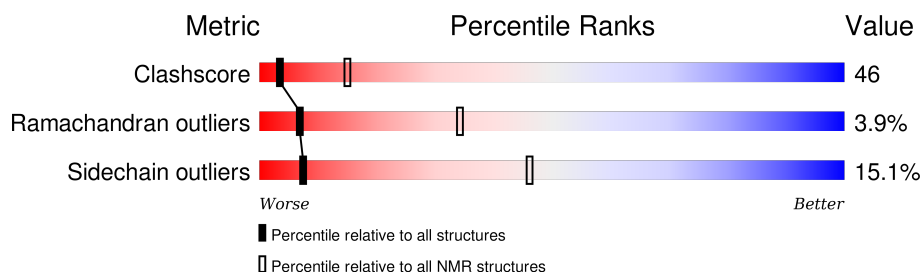
# 1 Overall quality at a glance

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	195	
2	B	43	

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 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:11-A:22, A:26-A:39, A:44-A:71, A:75-A:92, A:108-A:191, B:517-B:538 (178)	0.31	12

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 3 clusters and 4 single-model clusters were found.

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

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

There are 3 unique types of molecules in this entry. The entry contains 3843 atoms, of which 1908 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Calcium-binding protein p22.

Mol	Chain	Residues	Atoms						Trace
1	A	195	Total	C	H	N	O	S	0
			3135	983	1555	279	313	5	

- Molecule 2 is a protein called Sodium/hydrogen exchanger 1.

Mol	Chain	Residues	Atoms						Trace
2	B	43	Total	C	H	N	O	S	0
			706	221	353	65	66	1	

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

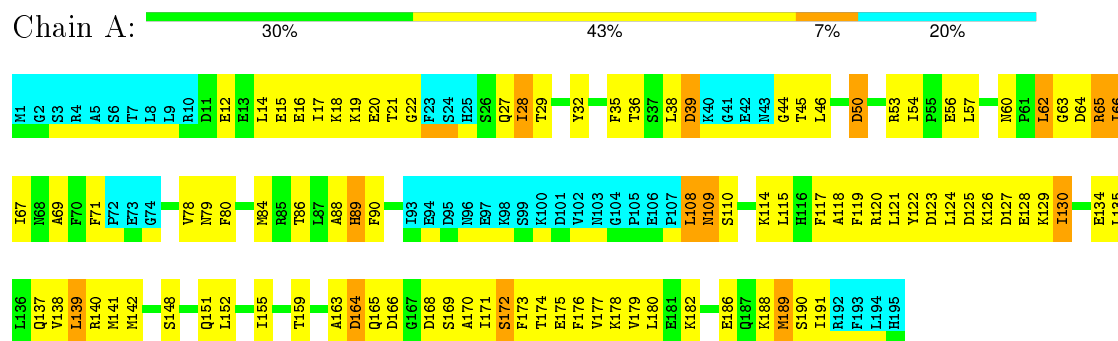
Mol	Chain	Residues	Atoms	
3	A	2	Total	Ca
			2	2

## 4 Residue-property plots

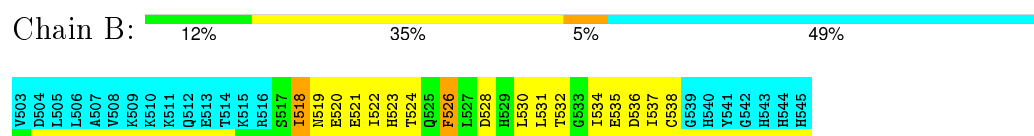
### 4.1 Average score per residue in the NMR ensemble

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: Calcium-binding protein p22



- Molecule 2: Sodium/hydrogen exchanger 1

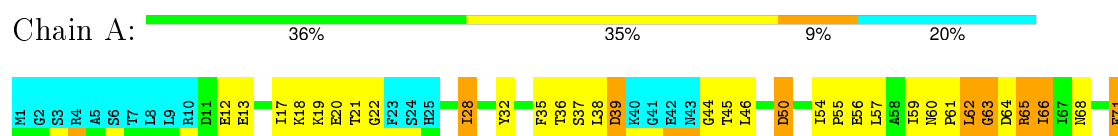


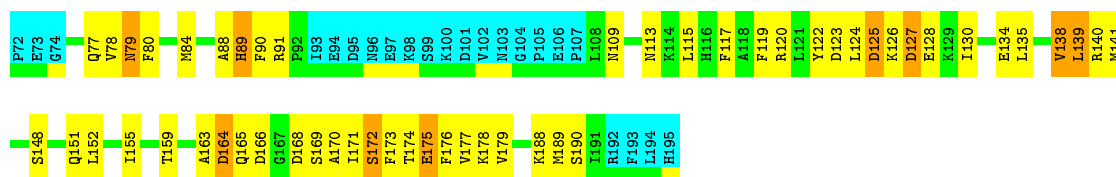
### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

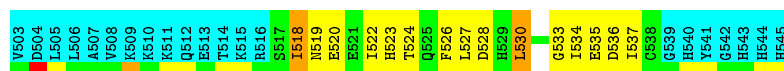
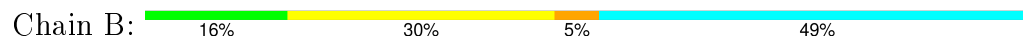
#### 4.2.1 Score per residue for model 1

- Molecule 1: Calcium-binding protein p22



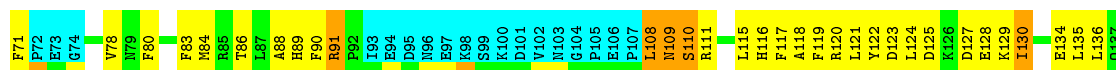
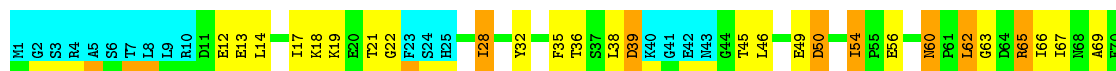


- Molecule 2: Sodium/hydrogen exchanger 1

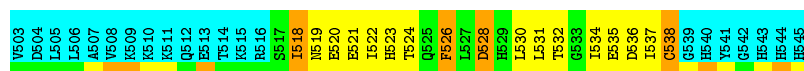


## 4.2.2 Score per residue for model 2

- Molecule 1: Calcium-binding protein p22



- Molecule 2: Sodium/hydrogen exchanger 1



## 4.2.3 Score per residue for model 3

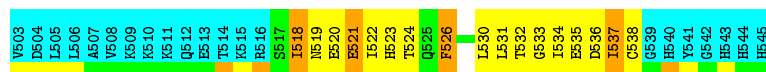
- Molecule 1: Calcium-binding protein p22





- Molecule 2: Sodium/hydrogen exchanger 1

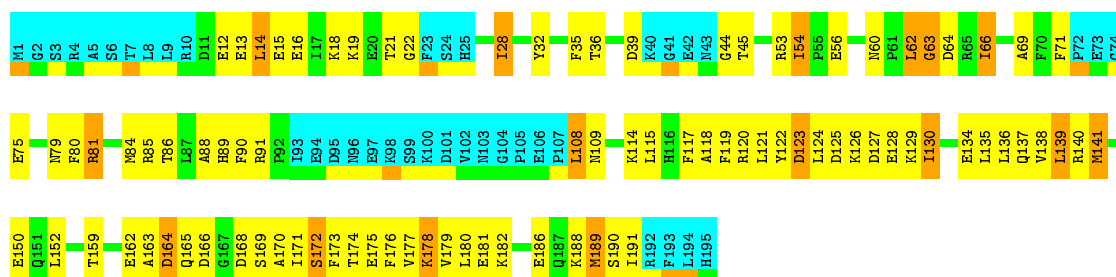
Chain B: 12% 30% 9% 49%



#### 4.2.4 Score per residue for model 4

- Molecule 1: Calcium-binding protein p22

Chain A: 33% 38% 8% 20%



- Molecule 2: Sodium/hydrogen exchanger 1

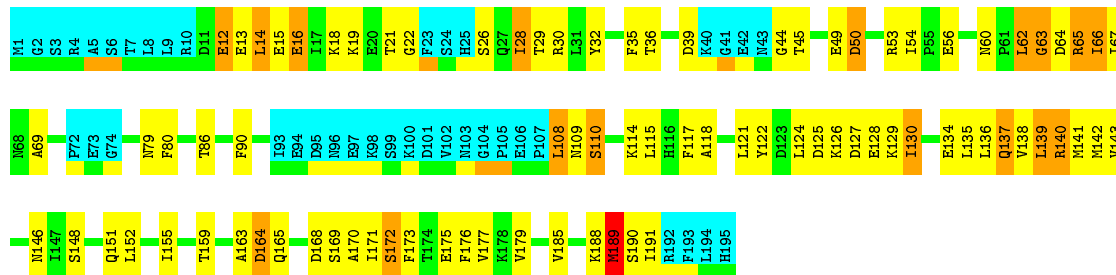
Chain B: 7% 35% 9% 49%



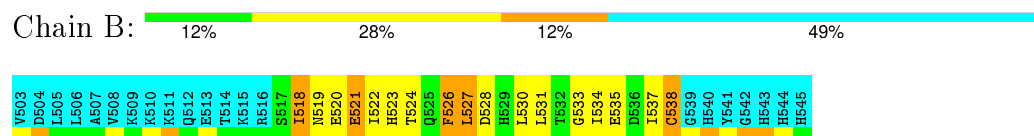
#### 4.2.5 Score per residue for model 5

- Molecule 1: Calcium-binding protein p22

Chain A: 36% 35% 9% 20%

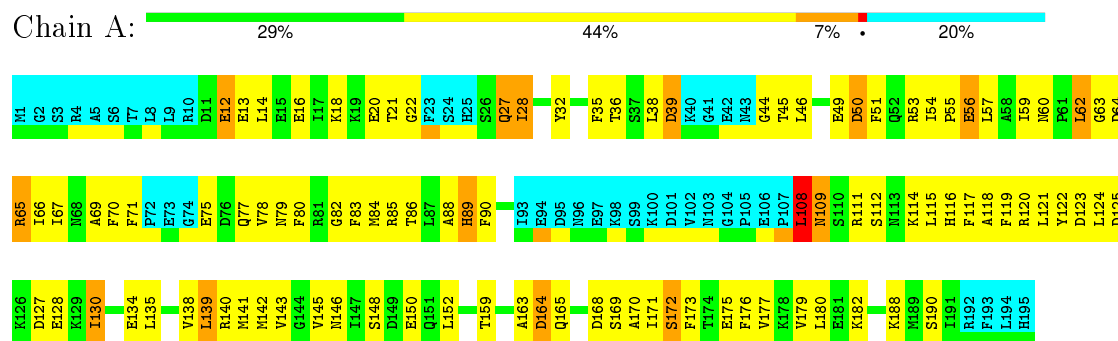


- Molecule 2: Sodium/hydrogen exchanger 1

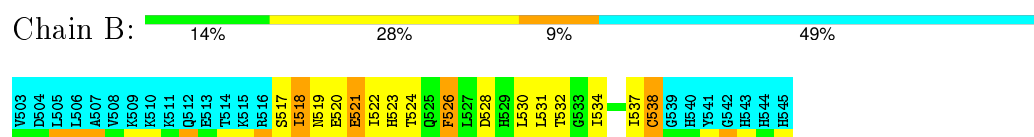


#### 4.2.6 Score per residue for model 6

- Molecule 1: Calcium-binding protein p22



- Molecule 2: Sodium/hydrogen exchanger 1

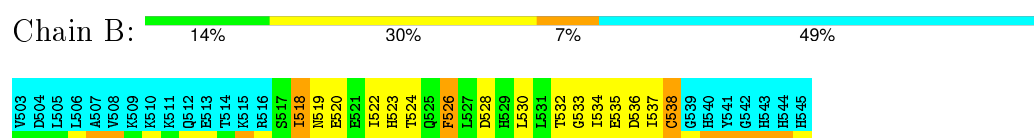


#### 4.2.7 Score per residue for model 7

- Molecule 1: Calcium-binding protein p22



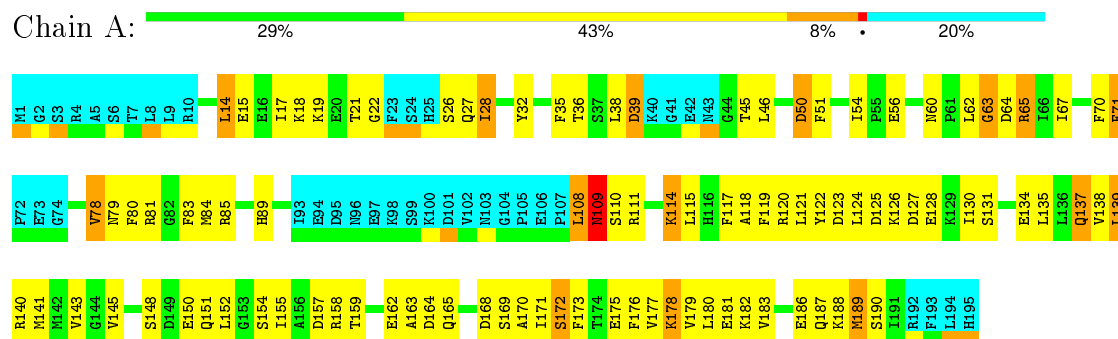
- Molecule 2: Sodium/hydrogen exchanger 1



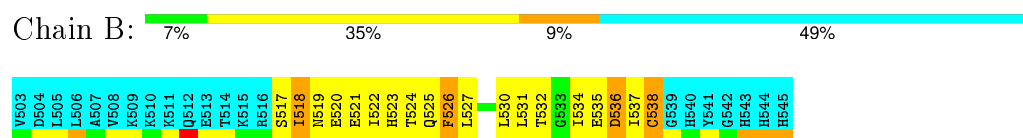


### 4.2.8 Score per residue for model 8

- Molecule 1: Calcium-binding protein p22

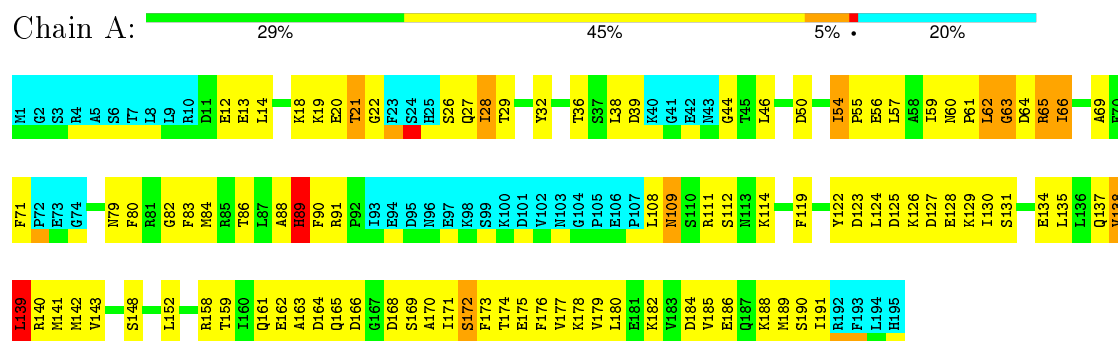


- Molecule 2: Sodium/hydrogen exchanger 1

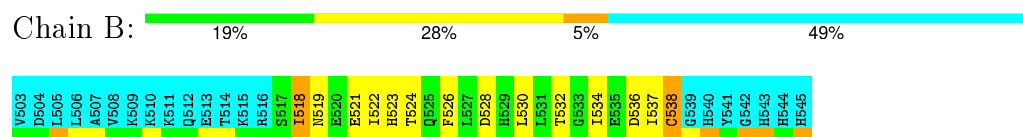


### 4.2.9 Score per residue for model 9

- Molecule 1: Calcium-binding protein p22

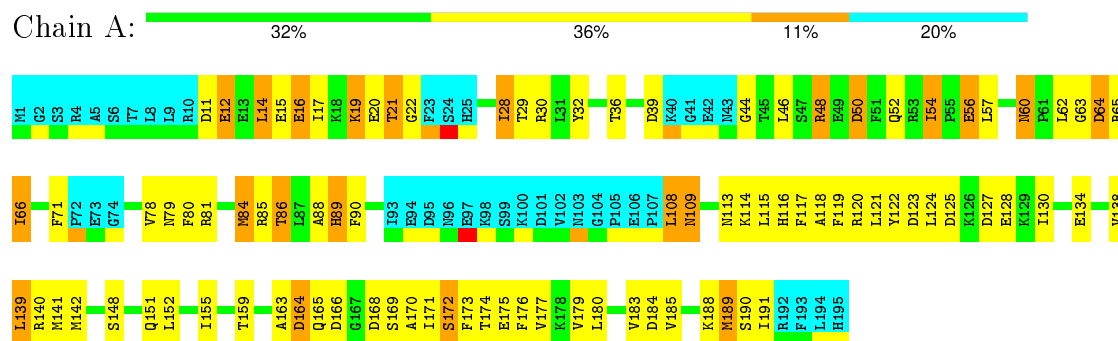


- Molecule 2: Sodium/hydrogen exchanger 1

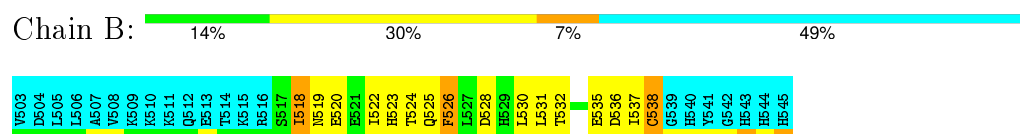


### 4.2.10 Score per residue for model 10

- Molecule 1: Calcium-binding protein p22

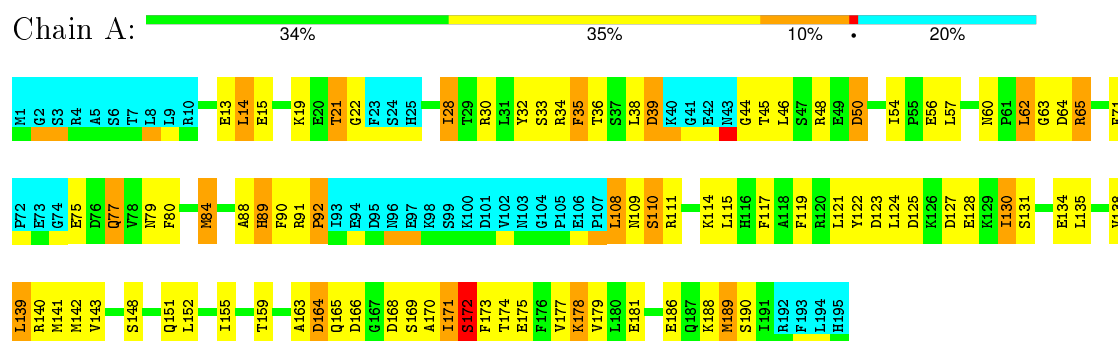


- Molecule 2: Sodium/hydrogen exchanger 1

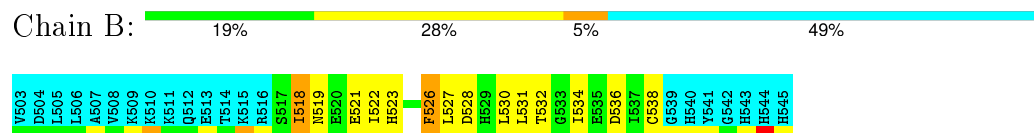


#### 4.2.11 Score per residue for model 11

- Molecule 1: Calcium-binding protein p22

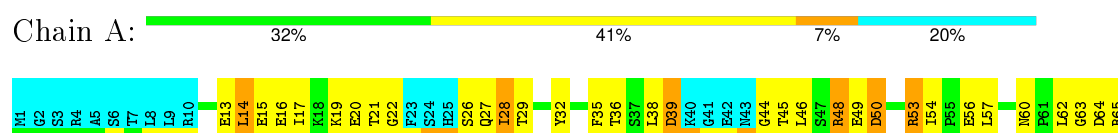


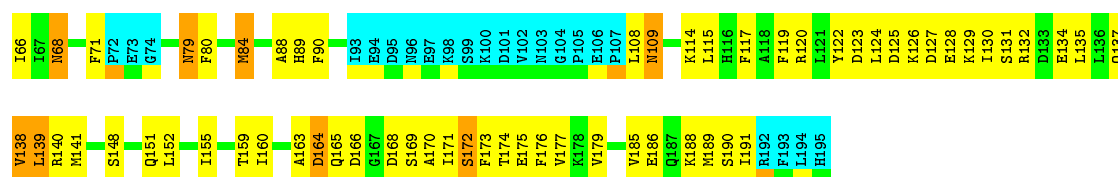
- Molecule 2: Sodium/hydrogen exchanger 1



#### 4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: Calcium-binding protein p22



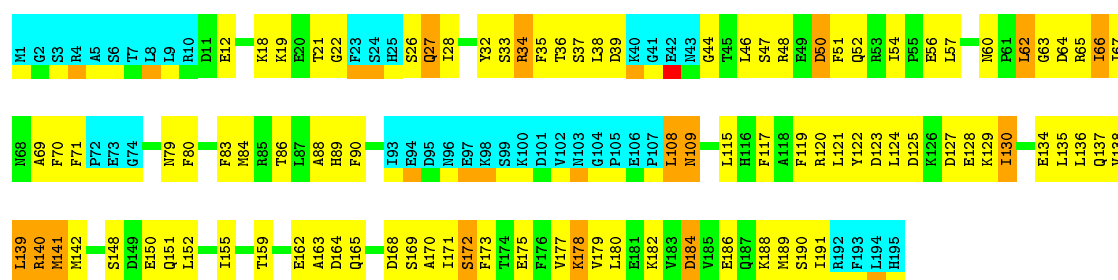


- Molecule 2: Sodium/hydrogen exchanger 1

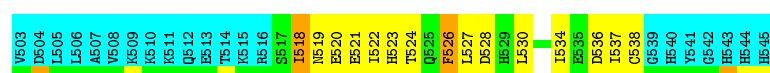


#### 4.2.13 Score per residue for model 13

- Molecule 1: Calcium-binding protein p22

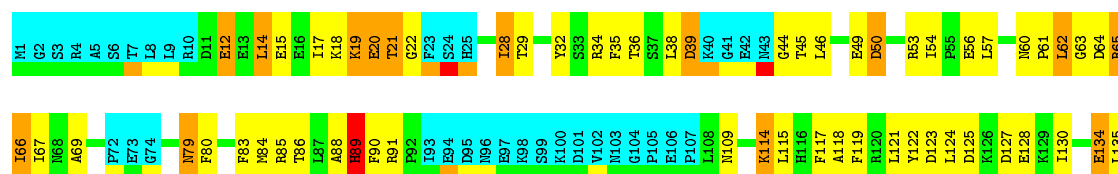


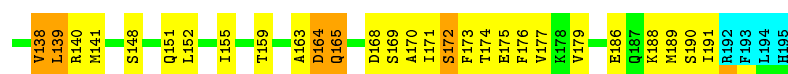
- Molecule 2: Sodium/hydrogen exchanger 1



#### 4.2.14 Score per residue for model 14

- Molecule 1: Calcium-binding protein p22



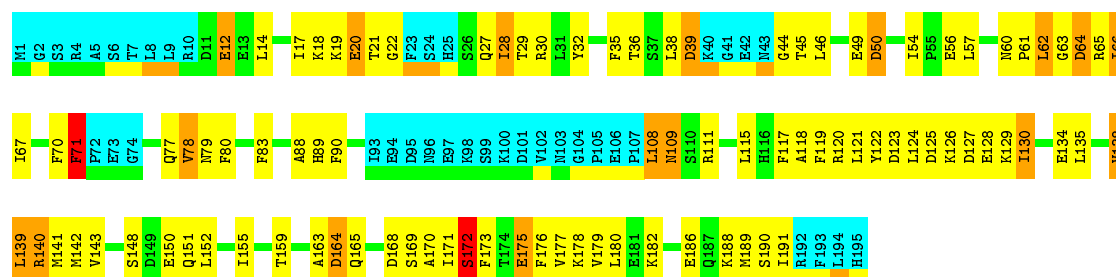


- Molecule 2: Sodium/hydrogen exchanger 1



#### 4.2.15 Score per residue for model 15

- Molecule 1: Calcium-binding protein p22

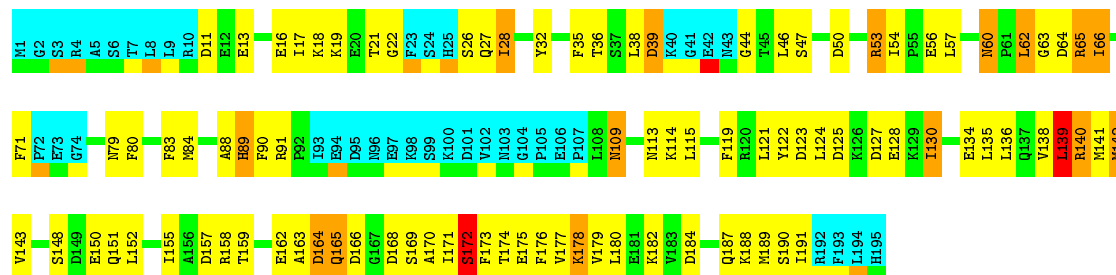


- Molecule 2: Sodium/hydrogen exchanger 1

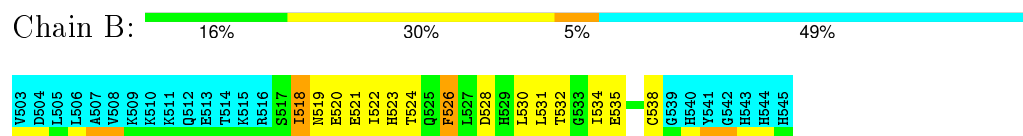


#### 4.2.16 Score per residue for model 16

- Molecule 1: Calcium-binding protein p22

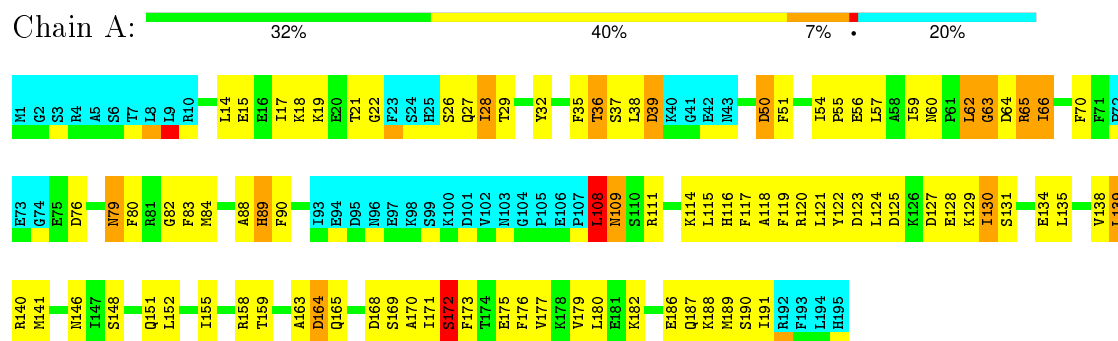


- Molecule 2: Sodium/hydrogen exchanger 1

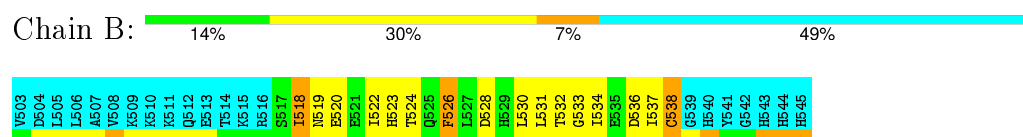


#### 4.2.17 Score per residue for model 17

- Molecule 1: Calcium-binding protein p22

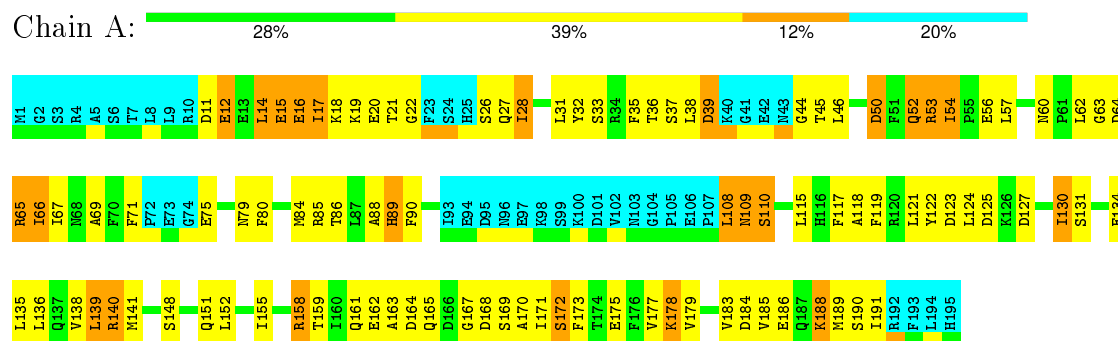


- Molecule 2: Sodium/hydrogen exchanger 1

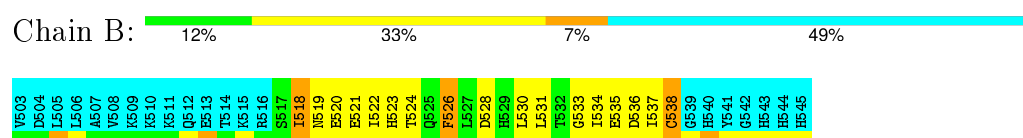


#### 4.2.18 Score per residue for model 18

- Molecule 1: Calcium-binding protein p22

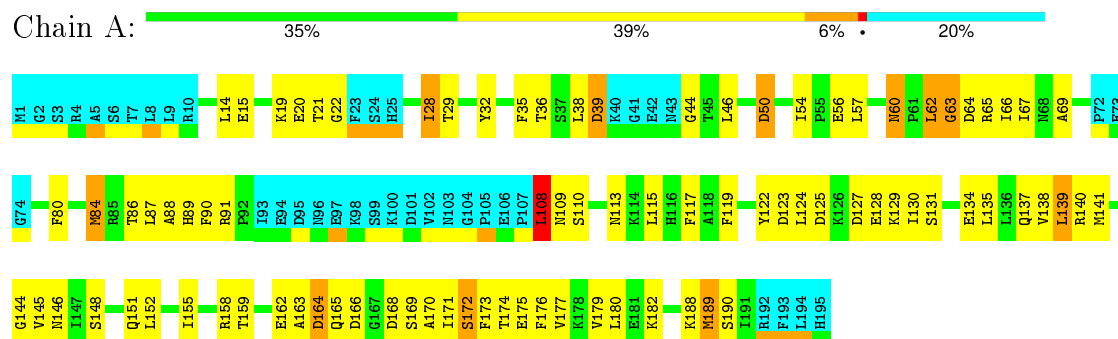


- Molecule 2: Sodium/hydrogen exchanger 1

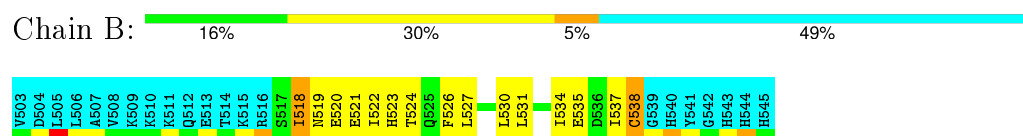


### 4.2.19 Score per residue for model 19

- Molecule 1: Calcium-binding protein p22

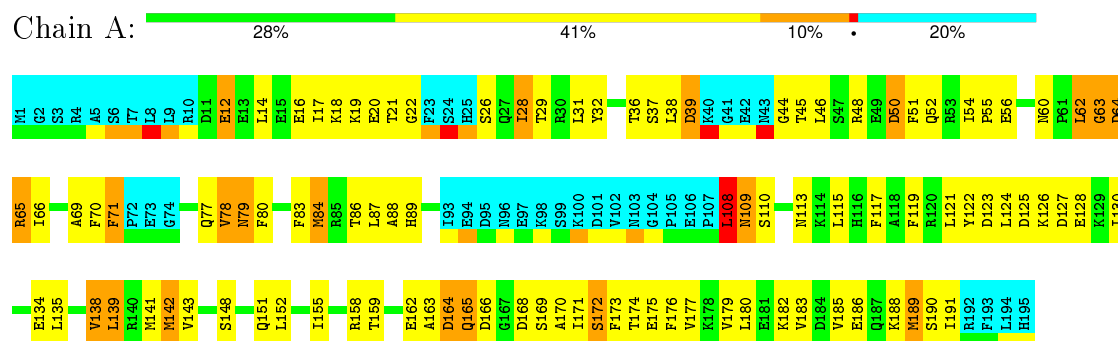


- Molecule 2: Sodium/hydrogen exchanger 1

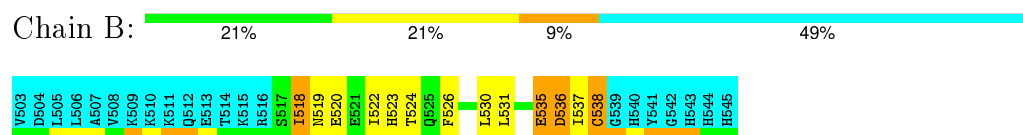


### 4.2.20 Score per residue for model 20

- Molecule 1: Calcium-binding protein p22



- Molecule 2: Sodium/hydrogen exchanger 1



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *Simulated annealing*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
XPLOR-NIH	refinement	2.9.6

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: CA

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	1272	1258	1256	117±9
2	B	177	169	167	23±5
All	All	29020	28540	28453	2624

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 46.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:527:LEU:HD13	2:B:528:ASP:N	0.94	1.78	5	1
1:A:138:VAL:HG11	2:B:526:PHE:CZ	0.93	1.98	8	14
1:A:163:ALA:O	1:A:175:GLU:OE1	0.88	1.92	10	13
2:B:527:LEU:O	2:B:527:LEU:HD22	0.83	1.72	5	1
1:A:32:TYR:O	1:A:36:THR:HG22	0.83	1.74	13	20
1:A:28:ILE:H	1:A:28:ILE:HD13	0.83	1.34	7	8
1:A:138:VAL:HG12	1:A:142:MET:SD	0.82	2.15	16	6
1:A:130:ILE:HD13	1:A:130:ILE:N	0.81	1.90	17	11
1:A:165:GLN:N	1:A:175:GLU:OE1	0.81	2.13	8	13
1:A:130:ILE:N	1:A:130:ILE:HD13	0.81	1.88	11	9
1:A:28:ILE:HD13	1:A:28:ILE:H	0.78	1.39	8	10

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:175:GLU:O	1:A:179:VAL:HG23	0.77	1.78	1	20
1:A:171:ILE:HG22	1:A:172:SER:N	0.76	1.94	20	19
2:B:530:LEU:O	2:B:534:ILE:HG22	0.75	1.81	7	17
1:A:28:ILE:N	1:A:28:ILE:HD13	0.74	1.96	7	6
1:A:139:LEU:C	1:A:139:LEU:HD13	0.74	2.02	16	12
1:A:28:ILE:HD13	1:A:28:ILE:N	0.74	1.97	10	10
2:B:520:GLU:O	2:B:524:THR:HG23	0.74	1.83	16	15
1:A:139:LEU:HD13	1:A:140:ARG:N	0.73	1.97	19	18
1:A:117:PHE:CZ	1:A:121:LEU:HD11	0.73	2.18	11	5
1:A:46:LEU:HD22	1:A:50:ASP:OD2	0.72	1.83	9	3
1:A:35:PHE:CE2	1:A:46:LEU:HD12	0.72	2.19	2	2
1:A:139:LEU:HD13	1:A:139:LEU:C	0.72	2.04	15	8
1:A:130:ILE:HG12	1:A:171:ILE:O	0.71	1.85	14	17
1:A:122:TYR:CE1	2:B:526:PHE:CZ	0.70	2.78	10	18
1:A:122:TYR:CE1	2:B:526:PHE:CE2	0.70	2.80	7	9
2:B:518:ILE:O	2:B:522:ILE:HG22	0.69	1.86	4	20
2:B:527:LEU:C	2:B:527:LEU:HD22	0.68	2.09	5	1
2:B:523:HIS:O	2:B:527:LEU:HD23	0.68	1.89	19	2
1:A:35:PHE:CD2	1:A:83:PHE:CE1	0.68	2.82	13	4
1:A:51:PHE:CG	1:A:70:PHE:CE2	0.67	2.83	8	1
1:A:171:ILE:CG2	1:A:172:SER:N	0.66	2.58	19	19
1:A:60:ASN:ND2	1:A:63:GLY:H	0.66	1.87	6	2
1:A:136:LEU:HD13	1:A:136:LEU:C	0.66	2.11	16	1
1:A:51:PHE:CD1	1:A:70:PHE:CE2	0.66	2.84	8	2
1:A:188:LYS:NZ	2:B:524:THR:HG22	0.66	2.05	6	1
1:A:124:LEU:HD13	1:A:124:LEU:C	0.65	2.12	2	12
1:A:124:LEU:C	1:A:124:LEU:HD13	0.65	2.11	15	8
2:B:527:LEU:HD12	2:B:527:LEU:C	0.65	2.11	1	3
1:A:48:ARG:NH1	1:A:57:LEU:HD13	0.65	2.06	12	1
1:A:163:ALA:O	1:A:175:GLU:OE2	0.65	2.15	5	7
1:A:35:PHE:CE1	1:A:83:PHE:CD1	0.65	2.85	8	3
1:A:176:PHE:CE1	2:B:523:HIS:NE2	0.65	2.64	14	14
2:B:519:ASN:ND2	2:B:523:HIS:NE2	0.65	2.45	4	1
1:A:35:PHE:CE2	1:A:83:PHE:CD1	0.65	2.84	2	2
1:A:117:PHE:CE2	1:A:121:LEU:HD11	0.64	2.26	8	4
1:A:66:ILE:HD12	1:A:66:ILE:O	0.64	1.92	1	2
1:A:122:TYR:CE1	2:B:526:PHE:CE1	0.64	2.86	1	6
1:A:35:PHE:CE1	1:A:46:LEU:HD12	0.64	2.27	8	3
1:A:79:ASN:ND2	1:A:79:ASN:H	0.64	1.90	17	2
1:A:171:ILE:HG21	1:A:175:GLU:HG2	0.63	1.68	4	18
1:A:46:LEU:HD13	1:A:50:ASP:OD2	0.63	1.93	9	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:66:ILE:O	1:A:66:ILE:HD12	0.63	1.93	17	1
1:A:51:PHE:CE1	1:A:70:PHE:CD2	0.63	2.86	20	4
1:A:122:TYR:CD1	2:B:526:PHE:CE2	0.63	2.86	7	6
1:A:65:ARG:CD	1:A:65:ARG:N	0.63	2.62	20	3
1:A:116:HIS:NE2	1:A:120:ARG:NH1	0.63	2.46	6	2
1:A:137:GLN:NE2	1:A:140:ARG:NH1	0.63	2.47	8	1
1:A:89:HIS:CD2	1:A:117:PHE:CG	0.63	2.86	1	6
1:A:60:ASN:ND2	1:A:63:GLY:N	0.63	2.46	2	2
1:A:170:ALA:C	1:A:171:ILE:HD12	0.63	2.14	9	9
1:A:130:ILE:N	1:A:130:ILE:CD1	0.62	2.62	4	7
1:A:176:PHE:CE1	2:B:523:HIS:CE1	0.62	2.87	19	12
1:A:91:ARG:N	1:A:109:ASN:ND2	0.62	2.47	4	1
1:A:116:HIS:CD2	1:A:120:ARG:NH1	0.62	2.67	6	1
1:A:137:GLN:NE2	1:A:140:ARG:NH2	0.62	2.47	5	1
2:B:519:ASN:ND2	2:B:523:HIS:CE1	0.62	2.67	4	1
1:A:119:PHE:CE2	1:A:120:ARG:NH2	0.62	2.67	4	1
1:A:168:ASP:N	1:A:168:ASP:OD1	0.62	2.32	7	7
1:A:27:GLN:NE2	1:A:27:GLN:N	0.62	2.48	13	1
1:A:65:ARG:NH1	2:B:534:ILE:N	0.62	2.48	12	1
1:A:57:LEU:HD23	1:A:57:LEU:C	0.62	2.15	14	4
1:A:65:ARG:HH21	2:B:534:ILE:N	0.62	1.93	5	2
1:A:139:LEU:O	1:A:143:VAL:HG22	0.62	1.95	16	9
1:A:188:LYS:HZ3	2:B:524:THR:HG22	0.62	1.55	6	1
1:A:57:LEU:C	1:A:57:LEU:HD23	0.61	2.15	11	7
1:A:20:GLU:CB	1:A:28:ILE:HG21	0.61	2.23	10	3
1:A:116:HIS:CE1	1:A:120:ARG:NH1	0.61	2.68	7	1
1:A:51:PHE:CE2	1:A:70:PHE:CD2	0.61	2.88	8	1
1:A:60:ASN:ND2	1:A:65:ARG:NH1	0.61	2.47	5	2
1:A:65:ARG:NH2	2:B:534:ILE:N	0.61	2.48	5	3
1:A:57:LEU:HD12	1:A:66:ILE:HD11	0.61	1.72	16	5
1:A:51:PHE:CD1	1:A:70:PHE:CZ	0.61	2.89	8	1
1:A:138:VAL:HG11	2:B:526:PHE:CE2	0.61	2.31	6	13
2:B:530:LEU:C	2:B:530:LEU:HD12	0.61	2.15	12	14
1:A:108:LEU:O	1:A:109:ASN:ND2	0.60	2.34	2	9
1:A:130:ILE:CD1	1:A:130:ILE:N	0.60	2.64	17	2
1:A:176:PHE:CZ	2:B:523:HIS:CE1	0.60	2.88	15	11
1:A:81:ARG:NH1	1:A:85:ARG:NH1	0.60	2.49	4	1
2:B:519:ASN:O	2:B:523:HIS:CG	0.60	2.55	15	18
2:B:534:ILE:HG23	2:B:535:GLU:OE1	0.60	1.96	15	1
1:A:60:ASN:ND2	1:A:62:LEU:H	0.60	1.94	2	2
1:A:31:LEU:C	1:A:31:LEU:HD13	0.60	2.16	20	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:168:ASP:OD1	1:A:168:ASP:N	0.60	2.35	10	13
1:A:51:PHE:CZ	1:A:70:PHE:CG	0.60	2.90	8	1
1:A:80:PHE:CE2	1:A:84:MET:SD	0.60	2.95	11	6
1:A:53:ARG:N	1:A:53:ARG:NE	0.60	2.50	12	1
1:A:164:ASP:OD2	1:A:169:SER:N	0.60	2.35	14	20
1:A:115:LEU:HD22	1:A:115:LEU:N	0.59	2.12	1	7
1:A:63:GLY:O	1:A:65:ARG:N	0.59	2.35	20	9
1:A:63:GLY:O	1:A:66:ILE:N	0.59	2.35	10	7
1:A:176:PHE:CZ	2:B:523:HIS:NE2	0.59	2.70	7	4
1:A:139:LEU:O	1:A:139:LEU:HD22	0.59	1.98	19	11
1:A:80:PHE:CZ	1:A:84:MET:SD	0.59	2.95	19	7
1:A:188:LYS:O	1:A:190:SER:N	0.59	2.35	8	20
2:B:528:ASP:O	2:B:532:THR:HG22	0.59	1.98	11	10
1:A:140:ARG:NH1	1:A:141:MET:SD	0.59	2.75	7	1
1:A:54:ILE:HG22	1:A:56:GLU:H	0.59	1.58	7	17
1:A:163:ALA:O	1:A:165:GLN:N	0.58	2.36	7	15
1:A:30:ARG:NH2	1:A:34:ARG:NH2	0.58	2.51	11	1
1:A:65:ARG:HE	1:A:66:ILE:CG2	0.58	2.11	16	1
1:A:60:ASN:ND2	1:A:65:ARG:HH22	0.58	1.96	13	2
1:A:66:ILE:C	1:A:66:ILE:HD12	0.58	2.19	17	5
1:A:32:TYR:O	1:A:36:THR:CG2	0.58	2.52	18	16
2:B:527:LEU:HD13	2:B:527:LEU:C	0.58	2.18	5	1
1:A:165:GLN:CB	1:A:175:GLU:OE1	0.58	2.51	18	12
1:A:62:LEU:O	1:A:64:ASP:N	0.58	2.36	18	16
1:A:125:ASP:N	1:A:134:GLU:OE2	0.58	2.37	12	8
1:A:51:PHE:CE1	1:A:70:PHE:CE2	0.58	2.91	20	2
1:A:171:ILE:HG21	1:A:175:GLU:CG	0.58	2.29	11	17
1:A:173:PHE:O	1:A:177:VAL:HG23	0.58	1.99	1	20
2:B:530:LEU:HD12	2:B:530:LEU:C	0.58	2.19	6	6
1:A:17:ILE:O	1:A:21:THR:HG22	0.58	1.98	10	2
1:A:46:LEU:HD22	1:A:50:ASP:CG	0.58	2.19	10	4
1:A:89:HIS:CE1	1:A:117:PHE:CB	0.58	2.87	17	2
1:A:28:ILE:CD1	1:A:28:ILE:H	0.57	2.12	19	8
1:A:28:ILE:H	1:A:28:ILE:CD1	0.57	2.07	20	5
1:A:18:LYS:O	1:A:22:GLY:N	0.57	2.37	9	7
1:A:65:ARG:HG2	1:A:66:ILE:N	0.57	2.14	14	2
1:A:89:HIS:CE1	1:A:113:ASN:HD22	0.57	2.18	19	1
1:A:48:ARG:CD	1:A:48:ARG:H	0.57	2.13	10	1
1:A:53:ARG:N	1:A:53:ARG:HE	0.57	1.97	12	1
1:A:179:VAL:HG21	2:B:519:ASN:CB	0.57	2.29	5	1
1:A:158:ARG:CZ	1:A:161:GLN:NE2	0.57	2.68	18	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:GLU:N	1:A:12:GLU:OE1	0.57	2.38	15	6
1:A:60:ASN:ND2	1:A:65:ARG:HH21	0.57	1.97	9	1
1:A:89:HIS:ND1	1:A:113:ASN:ND2	0.56	2.52	19	1
1:A:79:ASN:HD22	1:A:79:ASN:N	0.56	1.96	20	1
1:A:115:LEU:N	1:A:115:LEU:HD22	0.56	2.16	12	12
1:A:115:LEU:CD2	1:A:115:LEU:N	0.56	2.68	6	7
2:B:519:ASN:O	2:B:523:HIS:ND1	0.56	2.39	5	4
1:A:70:PHE:O	1:A:71:PHE:CD1	0.56	2.58	15	2
1:A:60:ASN:HD22	1:A:62:LEU:H	0.56	1.44	2	2
1:A:35:PHE:CE1	1:A:83:PHE:CE1	0.56	2.94	8	3
1:A:55:PRO:O	1:A:59:ILE:HD12	0.56	2.00	1	4
1:A:27:GLN:NE2	1:A:30:ARG:HH21	0.56	1.99	15	1
1:A:53:ARG:NE	1:A:53:ARG:N	0.56	2.54	18	2
1:A:35:PHE:CZ	1:A:83:PHE:CE1	0.56	2.93	8	1
1:A:122:TYR:CD1	1:A:122:TYR:N	0.56	2.72	14	5
1:A:62:LEU:HD22	1:A:138:VAL:HG13	0.56	1.76	8	2
1:A:189:MET:CE	2:B:527:LEU:HD23	0.56	2.31	5	1
1:A:90:PHE:CD1	1:A:90:PHE:N	0.56	2.74	11	4
1:A:171:ILE:CG2	1:A:175:GLU:HG2	0.56	2.30	4	19
1:A:127:ASP:N	1:A:127:ASP:OD1	0.56	2.39	1	4
1:A:66:ILE:HD12	1:A:66:ILE:C	0.56	2.21	1	3
1:A:65:ARG:CG	1:A:66:ILE:N	0.56	2.69	14	4
1:A:139:LEU:HD22	1:A:139:LEU:O	0.56	2.01	14	7
1:A:79:ASN:N	1:A:79:ASN:ND2	0.56	2.53	20	2
1:A:151:GLN:O	1:A:155:ILE:HD13	0.55	2.02	17	16
1:A:122:TYR:N	1:A:122:TYR:CD1	0.55	2.73	13	4
1:A:175:GLU:OE1	1:A:175:GLU:N	0.55	2.40	11	5
1:A:89:HIS:O	1:A:109:ASN:ND2	0.55	2.38	1	3
1:A:178:LYS:NZ	1:A:182:LYS:NZ	0.55	2.54	8	1
1:A:62:LEU:C	1:A:64:ASP:H	0.55	2.05	9	13
1:A:109:ASN:H	1:A:113:ASN:ND2	0.55	1.99	19	2
1:A:60:ASN:HD22	1:A:62:LEU:N	0.55	1.99	2	1
1:A:65:ARG:HH21	2:B:534:ILE:CA	0.55	2.15	5	1
1:A:125:ASP:OD1	1:A:125:ASP:N	0.55	2.39	1	1
1:A:71:PHE:CD1	1:A:75:GLU:O	0.55	2.60	4	3
1:A:50:ASP:OD1	1:A:50:ASP:N	0.55	2.40	14	6
1:A:60:ASN:OD1	1:A:65:ARG:NH2	0.55	2.39	19	1
1:A:12:GLU:OE1	1:A:12:GLU:N	0.55	2.40	20	2
1:A:125:ASP:OD1	1:A:127:ASP:N	0.54	2.40	2	13
1:A:122:TYR:HB2	1:A:130:ILE:HD12	0.54	1.77	2	11
1:A:186:GLU:N	1:A:186:GLU:OE1	0.54	2.40	20	4

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:ARG:CD	1:A:66:ILE:H	0.54	2.15	14	1
2:B:519:ASN:OD1	2:B:523:HIS:NE2	0.54	2.40	12	1
1:A:116:HIS:CE1	1:A:120:ARG:HE	0.54	2.20	17	1
1:A:51:PHE:CZ	1:A:70:PHE:CD2	0.54	2.94	20	2
1:A:60:ASN:OD1	1:A:63:GLY:N	0.54	2.40	9	10
1:A:172:SER:O	1:A:176:PHE:CD2	0.54	2.60	4	12
1:A:20:GLU:HB2	1:A:28:ILE:HG21	0.54	1.78	20	3
1:A:91:ARG:O	1:A:109:ASN:ND2	0.54	2.40	1	2
2:B:537:ILE:O	2:B:538:CYS:SG	0.54	2.65	9	4
1:A:28:ILE:O	1:A:31:LEU:N	0.54	2.41	7	1
1:A:109:ASN:O	1:A:109:ASN:ND2	0.54	2.40	9	2
1:A:85:ARG:O	1:A:89:HIS:CD2	0.54	2.60	3	1
1:A:175:GLU:N	1:A:175:GLU:OE1	0.54	2.39	1	2
1:A:68:ASN:O	1:A:120:ARG:NH1	0.54	2.41	1	1
1:A:84:MET:O	1:A:88:ALA:HB3	0.54	2.02	10	17
1:A:168:ASP:C	1:A:170:ALA:N	0.54	2.57	11	20
1:A:171:ILE:HG23	1:A:175:GLU:OE2	0.54	2.03	3	4
1:A:91:ARG:N	1:A:109:ASN:HD22	0.54	2.01	1	1
2:B:535:GLU:O	2:B:537:ILE:N	0.54	2.40	20	8
1:A:90:PHE:N	1:A:90:PHE:CD1	0.54	2.76	10	2
1:A:127:ASP:OD1	1:A:127:ASP:N	0.54	2.40	10	5
1:A:109:ASN:ND2	1:A:110:SER:N	0.54	2.55	2	1
2:B:522:ILE:HG23	2:B:523:HIS:N	0.54	2.17	2	13
1:A:91:ARG:NH2	1:A:108:LEU:O	0.54	2.41	2	1
1:A:129:LYS:NZ	1:A:168:ASP:OD2	0.54	2.40	17	2
1:A:127:ASP:O	1:A:128:GLU:CB	0.54	2.56	19	19
1:A:191:ILE:HG23	1:A:191:ILE:O	0.54	2.02	14	2
1:A:137:GLN:HE22	1:A:140:ARG:HH21	0.54	1.46	5	1
1:A:119:PHE:CD1	1:A:123:ASP:OD1	0.54	2.60	7	1
1:A:19:LYS:O	1:A:22:GLY:N	0.54	2.36	8	6
1:A:109:ASN:O	1:A:114:LYS:NZ	0.54	2.41	4	1
1:A:56:GLU:O	1:A:60:ASN:ND2	0.54	2.41	19	3
1:A:50:ASP:OD1	1:A:51:PHE:N	0.54	2.40	13	1
1:A:91:ARG:N	1:A:109:ASN:OD1	0.53	2.41	9	2
1:A:56:GLU:OE2	1:A:60:ASN:ND2	0.53	2.42	18	4
1:A:60:ASN:OD1	1:A:62:LEU:N	0.53	2.40	20	3
1:A:171:ILE:O	1:A:172:SER:CB	0.53	2.55	11	1
1:A:119:PHE:CZ	1:A:123:ASP:OD2	0.53	2.62	1	9
1:A:85:ARG:O	1:A:89:HIS:ND1	0.53	2.41	18	4
1:A:28:ILE:CD1	1:A:28:ILE:N	0.53	2.68	9	4
1:A:171:ILE:CG2	1:A:175:GLU:CG	0.53	2.86	11	7

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:63:GLY:C	1:A:65:ARG:N	0.53	2.61	15	13
1:A:65:ARG:HH21	1:A:138:VAL:CG2	0.53	2.16	15	1
2:B:530:LEU:HD12	2:B:531:LEU:N	0.53	2.19	16	16
1:A:115:LEU:N	1:A:115:LEU:CD2	0.53	2.72	20	11
2:B:519:ASN:O	2:B:523:HIS:CD2	0.53	2.62	14	10
1:A:80:PHE:CD1	1:A:80:PHE:O	0.53	2.62	19	2
2:B:521:GLU:OE1	2:B:522:ILE:N	0.53	2.42	3	3
1:A:16:GLU:OE1	1:A:16:GLU:N	0.53	2.42	18	2
1:A:65:ARG:CG	1:A:66:ILE:H	0.53	2.16	7	1
1:A:51:PHE:CD2	1:A:70:PHE:CD2	0.53	2.97	8	1
1:A:124:LEU:HD13	1:A:124:LEU:O	0.53	2.04	12	8
1:A:124:LEU:N	1:A:134:GLU:OE2	0.53	2.41	7	5
1:A:172:SER:OG	1:A:173:PHE:N	0.53	2.42	5	2
1:A:68:ASN:OD1	1:A:126:LYS:NZ	0.53	2.42	12	1
1:A:121:LEU:CD1	2:B:530:LEU:HD13	0.53	2.33	4	8
1:A:124:LEU:O	1:A:124:LEU:HD13	0.53	2.04	20	12
1:A:89:HIS:O	1:A:89:HIS:ND1	0.53	2.42	16	1
1:A:49:GLU:O	1:A:53:ARG:NH1	0.53	2.42	5	3
1:A:60:ASN:HD21	1:A:65:ARG:NH1	0.53	2.02	14	1
1:A:111:ARG:NH1	1:A:186:GLU:OE2	0.53	2.42	15	1
1:A:65:ARG:HE	1:A:65:ARG:CA	0.53	2.16	20	1
2:B:535:GLU:OE1	2:B:536:ASP:N	0.53	2.41	8	2
1:A:28:ILE:N	1:A:28:ILE:CD1	0.53	2.67	10	4
1:A:118:ALA:O	1:A:122:TYR:CD2	0.53	2.62	5	4
1:A:61:PRO:O	1:A:141:MET:SD	0.53	2.67	14	4
1:A:122:TYR:O	1:A:124:LEU:N	0.52	2.41	4	3
1:A:108:LEU:O	1:A:110:SER:N	0.52	2.41	8	1
1:A:150:GLU:CD	1:A:150:GLU:H	0.52	2.08	6	4
1:A:88:ALA:O	1:A:90:PHE:N	0.52	2.42	18	12
1:A:89:HIS:O	1:A:89:HIS:CG	0.52	2.62	1	3
2:B:535:GLU:O	2:B:538:CYS:SG	0.52	2.67	3	1
1:A:110:SER:O	1:A:113:ASN:N	0.52	2.42	3	1
1:A:122:TYR:OH	2:B:530:LEU:CD2	0.52	2.58	14	5
1:A:150:GLU:H	1:A:150:GLU:CD	0.52	2.08	4	3
1:A:50:ASP:N	1:A:50:ASP:OD1	0.52	2.42	18	7
1:A:137:GLN:OE1	1:A:140:ARG:NH1	0.52	2.42	13	2
1:A:138:VAL:O	1:A:141:MET:N	0.52	2.42	16	19
1:A:124:LEU:N	1:A:134:GLU:OE1	0.52	2.42	11	4
1:A:66:ILE:O	1:A:69:ALA:HB3	0.52	2.05	4	1
1:A:70:PHE:N	1:A:70:PHE:CD1	0.52	2.72	20	1
1:A:119:PHE:O	1:A:123:ASP:N	0.52	2.42	14	14

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:520:GLU:OE1	2:B:521:GLU:N	0.52	2.42	19	3
1:A:54:ILE:CG2	1:A:56:GLU:H	0.52	2.17	4	9
1:A:157:ASP:N	1:A:157:ASP:OD1	0.52	2.41	8	1
1:A:178:LYS:O	1:A:182:LYS:NZ	0.52	2.43	15	1
1:A:165:GLN:O	1:A:165:GLN:NE2	0.52	2.38	14	1
1:A:164:ASP:CG	1:A:169:SER:H	0.51	2.08	11	17
1:A:20:GLU:OE2	1:A:84:MET:SD	0.51	2.68	6	2
1:A:46:LEU:O	1:A:78:VAL:HG12	0.51	2.05	8	5
1:A:186:GLU:H	1:A:186:GLU:CD	0.51	2.08	7	8
1:A:137:GLN:O	1:A:141:MET:SD	0.51	2.68	7	3
1:A:57:LEU:O	1:A:57:LEU:HD23	0.51	2.05	1	5
1:A:80:PHE:C	1:A:80:PHE:CD1	0.51	2.84	13	14
1:A:89:HIS:CG	1:A:89:HIS:O	0.51	2.62	7	5
1:A:129:LYS:HA	1:A:172:SER:OG	0.51	2.04	15	1
1:A:119:PHE:CE1	1:A:123:ASP:CG	0.51	2.83	7	12
1:A:125:ASP:N	1:A:134:GLU:OE1	0.51	2.39	11	5
1:A:168:ASP:OD1	1:A:170:ALA:O	0.51	2.28	2	9
1:A:132:ARG:HA	1:A:160:ILE:HD13	0.51	1.82	12	1
1:A:35:PHE:O	1:A:46:LEU:HD11	0.51	2.06	2	2
1:A:109:ASN:HD22	1:A:110:SER:N	0.51	2.04	2	1
1:A:57:LEU:HD23	1:A:57:LEU:O	0.51	2.05	9	5
1:A:117:PHE:CE1	1:A:121:LEU:HD11	0.51	2.41	11	1
1:A:119:PHE:CZ	1:A:123:ASP:CG	0.51	2.84	14	14
1:A:186:GLU:OE1	1:A:186:GLU:N	0.51	2.43	17	3
1:A:163:ALA:HB1	2:B:519:ASN:HD21	0.51	1.66	8	3
1:A:108:LEU:O	1:A:109:ASN:OD1	0.51	2.28	12	2
1:A:127:ASP:O	1:A:128:GLU:CG	0.51	2.59	1	2
1:A:33:SER:OG	1:A:34:ARG:NH1	0.51	2.43	11	1
1:A:168:ASP:CG	1:A:170:ALA:O	0.51	2.49	2	19
1:A:53:ARG:HE	1:A:53:ARG:N	0.51	2.03	18	1
1:A:139:LEU:CD1	1:A:139:LEU:C	0.51	2.80	20	11
1:A:28:ILE:O	1:A:29:THR:C	0.51	2.48	7	4
1:A:178:LYS:NZ	1:A:181:GLU:OE2	0.50	2.44	11	1
1:A:69:ALA:O	1:A:86:THR:OG1	0.50	2.27	9	12
1:A:48:ARG:CD	1:A:48:ARG:N	0.50	2.74	10	1
1:A:109:ASN:ND2	1:A:109:ASN:C	0.50	2.64	2	1
1:A:14:LEU:O	1:A:16:GLU:N	0.50	2.42	18	1
1:A:125:ASP:OD2	1:A:127:ASP:OD1	0.50	2.30	1	1
1:A:45:THR:HG22	1:A:79:ASN:HA	0.50	1.84	7	10
1:A:68:ASN:ND2	1:A:68:ASN:O	0.50	2.41	12	1
1:A:163:ALA:CB	2:B:519:ASN:HD21	0.50	2.19	8	2

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:80:PHE:O	1:A:80:PHE:CD1	0.50	2.64	11	3
1:A:48:ARG:NH2	1:A:52:GLN:NE2	0.50	2.59	13	1
1:A:17:ILE:O	1:A:20:GLU:N	0.50	2.44	18	1
1:A:35:PHE:CZ	1:A:83:PHE:CD1	0.50	3.00	8	1
1:A:137:GLN:O	1:A:141:MET:CE	0.50	2.60	4	3
1:A:109:ASN:H	1:A:113:ASN:HD22	0.50	1.48	19	1
2:B:521:GLU:CD	2:B:522:ILE:N	0.50	2.66	12	3
1:A:163:ALA:HB1	2:B:519:ASN:ND2	0.50	2.22	8	2
2:B:525:GLN:O	2:B:529:HIS:CD2	0.49	2.64	4	1
1:A:165:GLN:OE1	1:A:174:THR:CG2	0.49	2.60	14	1
1:A:114:LYS:HZ1	1:A:185:VAL:HG11	0.49	1.66	12	2
1:A:79:ASN:OD1	1:A:79:ASN:N	0.49	2.43	15	1
1:A:65:ARG:CA	1:A:65:ARG:NE	0.49	2.75	20	1
1:A:122:TYR:CD1	2:B:526:PHE:CZ	0.49	3.00	7	5
1:A:86:THR:O	1:A:90:PHE:CE1	0.49	2.65	2	2
1:A:121:LEU:HD13	2:B:530:LEU:HD13	0.49	1.83	11	8
1:A:88:ALA:C	1:A:90:PHE:N	0.49	2.65	18	13
1:A:138:VAL:O	1:A:142:MET:SD	0.49	2.70	20	1
1:A:173:PHE:CD1	1:A:173:PHE:O	0.49	2.66	5	3
1:A:111:ARG:CG	1:A:112:SER:N	0.49	2.75	9	3
1:A:71:PHE:CD1	1:A:71:PHE:N	0.49	2.81	1	1
1:A:171:ILE:CG2	1:A:175:GLU:CD	0.49	2.80	11	1
1:A:165:GLN:N	1:A:175:GLU:OE2	0.49	2.38	5	5
1:A:175:GLU:O	1:A:179:VAL:CG2	0.49	2.61	3	15
1:A:30:ARG:CD	1:A:30:ARG:N	0.49	2.76	5	1
2:B:538:CYS:SG	2:B:538:CYS:O	0.49	2.70	8	1
1:A:64:ASP:OD1	1:A:65:ARG:N	0.49	2.45	9	3
1:A:166:ASP:OD2	1:A:174:THR:OG1	0.49	2.31	19	9
1:A:66:ILE:CD1	2:B:537:ILE:HD11	0.49	2.37	2	1
1:A:53:ARG:CA	1:A:53:ARG:NE	0.49	2.75	12	2
1:A:17:ILE:CG2	1:A:18:LYS:N	0.49	2.75	18	1
1:A:149:ASP:OD1	1:A:150:GLU:N	0.49	2.44	7	1
1:A:65:ARG:NH1	2:B:526:PHE:CE1	0.49	2.81	8	1
1:A:173:PHE:O	1:A:177:VAL:CG2	0.49	2.61	2	15
1:A:139:LEU:C	1:A:139:LEU:CD1	0.49	2.79	5	7
1:A:65:ARG:NH2	2:B:533:GLY:C	0.49	2.66	17	2
1:A:114:LYS:NZ	1:A:185:VAL:CG1	0.49	2.75	12	3
1:A:119:PHE:CZ	1:A:120:ARG:NH2	0.49	2.81	4	1
1:A:120:ARG:NH2	1:A:123:ASP:OD2	0.49	2.42	15	2
1:A:136:LEU:O	1:A:140:ARG:CG	0.49	2.61	2	5
1:A:79:ASN:N	1:A:79:ASN:OD1	0.49	2.45	14	4

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:29:THR:OG1	1:A:30:ARG:NH1	0.49	2.42	5	1
1:A:49:GLU:CD	1:A:49:GLU:H	0.49	2.11	12	1
1:A:180:LEU:O	1:A:182:LYS:N	0.49	2.46	9	6
1:A:80:PHE:CD1	1:A:80:PHE:C	0.48	2.87	15	5
1:A:108:LEU:O	1:A:109:ASN:CB	0.48	2.61	12	7
1:A:66:ILE:HD11	2:B:537:ILE:HD11	0.48	1.84	2	2
1:A:47:SER:N	1:A:50:ASP:OD2	0.48	2.42	16	1
1:A:109:ASN:CG	1:A:114:LYS:NZ	0.48	2.66	4	1
1:A:110:SER:O	1:A:114:LYS:N	0.48	2.43	8	3
1:A:14:LEU:O	1:A:15:GLU:C	0.48	2.52	4	10
1:A:171:ILE:N	1:A:171:ILE:HD12	0.48	2.23	4	3
1:A:89:HIS:CE1	1:A:113:ASN:OD1	0.48	2.65	1	2
1:A:89:HIS:CE1	1:A:117:PHE:CG	0.48	3.00	17	1
2:B:535:GLU:C	2:B:537:ILE:N	0.48	2.66	20	10
1:A:79:ASN:ND2	1:A:80:PHE:H	0.48	2.06	10	1
1:A:180:LEU:C	1:A:182:LYS:N	0.48	2.67	20	11
1:A:16:GLU:O	1:A:28:ILE:CG2	0.48	2.61	20	4
1:A:49:GLU:H	1:A:49:GLU:CD	0.48	2.11	2	1
1:A:35:PHE:CD2	1:A:46:LEU:CD1	0.48	2.96	13	1
1:A:184:ASP:N	1:A:184:ASP:OD1	0.48	2.46	13	2
1:A:65:ARG:N	1:A:65:ARG:CD	0.48	2.75	15	1
2:B:522:ILE:CG2	2:B:523:HIS:N	0.48	2.77	18	13
1:A:138:VAL:O	1:A:140:ARG:N	0.48	2.46	16	3
1:A:53:ARG:N	1:A:53:ARG:CD	0.48	2.76	12	2
1:A:85:ARG:HH21	1:A:120:ARG:NH1	0.48	2.06	8	1
1:A:174:THR:HG22	1:A:175:GLU:N	0.48	2.23	20	3
1:A:168:ASP:O	1:A:170:ALA:N	0.48	2.47	11	4
1:A:63:GLY:O	1:A:64:ASP:C	0.48	2.51	20	7
1:A:129:LYS:CE	1:A:168:ASP:OD2	0.48	2.62	4	3
1:A:71:PHE:CE2	1:A:77:GLN:O	0.48	2.66	20	1
1:A:123:ASP:OD1	1:A:130:ILE:CD1	0.48	2.62	7	1
1:A:34:ARG:O	1:A:37:SER:OG	0.48	2.27	7	1
1:A:62:LEU:C	1:A:64:ASP:N	0.48	2.67	9	10
1:A:115:LEU:CD2	1:A:115:LEU:H	0.48	2.21	11	3
1:A:186:GLU:N	1:A:186:GLU:OE2	0.48	2.44	9	1
1:A:109:ASN:C	1:A:109:ASN:ND2	0.48	2.67	20	1
1:A:79:ASN:CG	1:A:80:PHE:N	0.48	2.67	9	4
2:B:520:GLU:O	2:B:524:THR:CG2	0.48	2.62	7	3
1:A:114:LYS:NZ	1:A:185:VAL:HG11	0.48	2.24	7	1
1:A:111:ARG:CZ	1:A:186:GLU:OE2	0.48	2.62	8	1
1:A:129:LYS:CA	1:A:172:SER:OG	0.48	2.62	15	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:56:GLU:OE1	2:B:536:ASP:CB	0.48	2.62	20	1
1:A:39:ASP:OD2	1:A:45:THR:O	0.48	2.31	15	6
1:A:18:LYS:NZ	1:A:191:ILE:O	0.47	2.42	4	3
1:A:150:GLU:OE1	1:A:150:GLU:N	0.47	2.42	8	1
1:A:38:LEU:O	1:A:39:ASP:O	0.47	2.32	19	5
1:A:108:LEU:HD23	1:A:109:ASN:N	0.47	2.24	3	5
1:A:35:PHE:CE2	1:A:83:PHE:CE1	0.47	3.02	2	3
1:A:12:GLU:CD	1:A:12:GLU:H	0.47	2.13	3	3
1:A:17:ILE:HD12	1:A:20:GLU:HB3	0.47	1.86	12	2
1:A:117:PHE:O	1:A:119:PHE:N	0.47	2.47	8	2
2:B:521:GLU:H	2:B:521:GLU:CD	0.47	2.12	6	1
1:A:71:PHE:O	1:A:120:ARG:NH2	0.47	2.42	13	1
1:A:65:ARG:NH1	2:B:526:PHE:CZ	0.47	2.83	8	1
1:A:116:HIS:CD2	1:A:120:ARG:HE	0.47	2.27	10	1
1:A:149:ASP:OD1	1:A:149:ASP:N	0.47	2.48	7	1
1:A:154:SER:O	1:A:157:ASP:OD1	0.47	2.33	8	1
1:A:125:ASP:OD1	1:A:127:ASP:OD1	0.47	2.33	19	9
1:A:115:LEU:HD12	1:A:172:SER:O	0.47	2.10	2	1
1:A:178:LYS:C	1:A:178:LYS:CD	0.47	2.83	13	3
1:A:49:GLU:O	1:A:53:ARG:CZ	0.47	2.62	6	2
1:A:91:ARG:H	1:A:109:ASN:ND2	0.47	2.08	4	1
1:A:65:ARG:N	1:A:65:ARG:NE	0.47	2.63	20	2
1:A:178:LYS:CD	1:A:178:LYS:C	0.47	2.83	18	4
1:A:88:ALA:C	1:A:90:PHE:H	0.47	2.13	14	13
1:A:178:LYS:NZ	1:A:181:GLU:CD	0.47	2.68	11	1
1:A:19:LYS:CD	1:A:19:LYS:N	0.47	2.77	15	4
1:A:191:ILE:CG2	1:A:191:ILE:O	0.47	2.62	14	2
1:A:13:GLU:OE1	2:B:538:CYS:SG	0.47	2.72	4	1
1:A:150:GLU:N	1:A:150:GLU:OE2	0.47	2.44	4	2
1:A:48:ARG:NH1	1:A:57:LEU:CD1	0.47	2.78	12	1
1:A:183:VAL:O	1:A:185:VAL:N	0.47	2.48	20	2
1:A:130:ILE:HD11	1:A:172:SER:OG	0.47	2.10	20	1
1:A:124:LEU:CD1	1:A:124:LEU:C	0.47	2.83	15	12
2:B:537:ILE:O	2:B:538:CYS:C	0.47	2.53	18	12
2:B:528:ASP:O	2:B:532:THR:HG23	0.47	2.10	10	1
1:A:130:ILE:CG1	1:A:171:ILE:O	0.47	2.59	14	3
1:A:136:LEU:CD1	1:A:136:LEU:C	0.47	2.83	16	1
1:A:53:ARG:CD	1:A:53:ARG:N	0.47	2.76	18	3
1:A:173:PHE:CD1	1:A:173:PHE:C	0.47	2.87	20	3
1:A:60:ASN:HD21	1:A:65:ARG:NH2	0.47	2.08	9	1
1:A:140:ARG:CG	1:A:141:MET:N	0.46	2.77	10	6

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:52:GLN:CD	1:A:57:LEU:HD22	0.46	2.30	7	3
2:B:537:ILE:C	2:B:538:CYS:SG	0.46	2.93	17	1
1:A:138:VAL:C	1:A:142:MET:SD	0.46	2.93	15	7
1:A:138:VAL:O	1:A:139:LEU:C	0.46	2.53	4	19
1:A:119:PHE:CE1	1:A:123:ASP:OD1	0.46	2.68	7	1
1:A:124:LEU:C	1:A:124:LEU:CD1	0.46	2.84	2	6
1:A:16:GLU:OE1	1:A:27:GLN:O	0.46	2.34	12	2
1:A:27:GLN:NE2	1:A:30:ARG:NH2	0.46	2.63	15	1
1:A:13:GLU:O	2:B:538:CYS:SG	0.46	2.73	7	1
1:A:189:MET:N	1:A:189:MET:SD	0.46	2.86	17	1
1:A:63:GLY:O	1:A:67:ILE:HD12	0.46	2.11	8	1
1:A:27:GLN:H	1:A:27:GLN:NE2	0.46	2.06	13	1
1:A:60:ASN:ND2	1:A:65:ARG:NH2	0.46	2.63	13	1
1:A:127:ASP:OD2	1:A:131:SER:OG	0.46	2.34	12	4
1:A:127:ASP:OD1	1:A:129:LYS:O	0.46	2.34	3	7
1:A:16:GLU:CA	1:A:16:GLU:OE1	0.46	2.63	18	1
1:A:122:TYR:CE1	2:B:526:PHE:CD2	0.46	3.04	7	2
1:A:117:PHE:C	1:A:119:PHE:N	0.46	2.67	8	4
1:A:168:ASP:OD2	1:A:170:ALA:O	0.46	2.33	12	14
1:A:127:ASP:OD1	1:A:129:LYS:N	0.46	2.48	5	4
1:A:34:ARG:N	1:A:34:ARG:CD	0.46	2.78	13	1
1:A:137:GLN:HE22	1:A:140:ARG:NH2	0.46	2.04	5	1
1:A:138:VAL:HG11	2:B:526:PHE:CE1	0.46	2.42	8	3
1:A:62:LEU:HD11	1:A:65:ARG:NH2	0.46	2.26	6	1
2:B:521:GLU:CG	2:B:522:ILE:N	0.46	2.79	13	6
1:A:34:ARG:CD	1:A:34:ARG:N	0.46	2.78	11	1
1:A:125:ASP:OD1	1:A:127:ASP:OD2	0.46	2.33	4	2
1:A:65:ARG:NE	1:A:121:LEU:O	0.46	2.49	3	2
1:A:111:ARG:CG	1:A:112:SER:H	0.46	2.23	9	2
1:A:171:ILE:O	1:A:172:SER:OG	0.46	2.34	15	1
1:A:182:LYS:CB	1:A:182:LYS:NZ	0.46	2.79	19	1
1:A:115:LEU:H	1:A:115:LEU:HD22	0.46	1.71	10	1
1:A:165:GLN:HE21	1:A:165:GLN:C	0.46	2.12	14	1
1:A:115:LEU:HD22	1:A:115:LEU:H	0.45	1.71	11	1
1:A:12:GLU:H	1:A:12:GLU:CD	0.45	2.14	6	4
1:A:65:ARG:HG3	1:A:66:ILE:N	0.45	2.26	13	2
1:A:178:LYS:HZ2	1:A:182:LYS:NZ	0.45	2.08	8	1
1:A:57:LEU:HD21	1:A:66:ILE:HD11	0.45	1.88	15	1
1:A:122:TYR:CB	1:A:130:ILE:HD12	0.45	2.40	11	1
1:A:118:ALA:HB1	1:A:122:TYR:CE2	0.45	2.46	5	3
1:A:119:PHE:CE1	1:A:123:ASP:OD2	0.45	2.69	7	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:191:ILE:O	1:A:191:ILE:CG2	0.45	2.64	17	3
1:A:171:ILE:C	1:A:172:SER:OG	0.45	2.55	15	1
1:A:126:LYS:NZ	1:A:126:LYS:CB	0.45	2.79	15	1
1:A:64:ASP:HA	1:A:67:ILE:HD12	0.45	1.89	19	9
2:B:527:LEU:C	2:B:527:LEU:CD1	0.45	2.84	13	1
1:A:108:LEU:C	1:A:110:SER:N	0.45	2.67	8	1
1:A:165:GLN:NE2	1:A:165:GLN:C	0.45	2.70	14	1
1:A:79:ASN:ND2	1:A:79:ASN:N	0.45	2.64	17	1
1:A:79:ASN:ND2	1:A:81:ARG:CG	0.45	2.79	8	1
1:A:65:ARG:CD	1:A:65:ARG:H	0.45	2.25	20	1
1:A:125:ASP:OD2	1:A:134:GLU:OE2	0.45	2.35	11	5
1:A:118:ALA:HA	1:A:121:LEU:HD12	0.45	1.88	18	4
1:A:19:LYS:C	1:A:21:THR:N	0.45	2.69	9	4
1:A:131:SER:N	1:A:134:GLU:OE1	0.45	2.45	3	1
1:A:145:VAL:O	1:A:146:ASN:OD1	0.45	2.35	19	2
2:B:521:GLU:O	2:B:524:THR:OG1	0.45	2.35	2	7
1:A:191:ILE:O	1:A:191:ILE:HG23	0.45	2.11	17	7
1:A:163:ALA:O	1:A:175:GLU:CD	0.45	2.53	9	3
1:A:35:PHE:CE2	1:A:46:LEU:CD1	0.45	3.00	12	3
1:A:48:ARG:CZ	1:A:57:LEU:HD13	0.45	2.41	12	1
1:A:109:ASN:C	1:A:109:ASN:OD1	0.45	2.55	12	1
1:A:26:SER:O	1:A:29:THR:N	0.45	2.50	17	1
1:A:76:ASP:N	1:A:76:ASP:OD1	0.45	2.50	17	1
1:A:60:ASN:CG	1:A:65:ARG:HH12	0.45	2.15	7	2
1:A:186:GLU:N	1:A:186:GLU:CD	0.45	2.69	15	1
1:A:108:LEU:C	1:A:110:SER:H	0.45	2.15	8	5
1:A:116:HIS:NE2	1:A:120:ARG:NE	0.45	2.65	10	2
1:A:47:SER:OG	1:A:48:ARG:N	0.45	2.49	13	2
1:A:89:HIS:NE2	1:A:117:PHE:CB	0.45	2.80	12	2
1:A:27:GLN:HE22	1:A:30:ARG:NH2	0.45	2.10	15	1
1:A:91:ARG:O	1:A:109:ASN:OD1	0.45	2.35	16	6
1:A:109:ASN:OD1	1:A:109:ASN:O	0.45	2.34	13	4
1:A:60:ASN:HD21	1:A:65:ARG:HH21	0.45	1.55	9	1
1:A:166:ASP:OD1	1:A:174:THR:OG1	0.44	2.36	19	6
1:A:90:PHE:O	1:A:189:MET:O	0.44	2.35	10	2
1:A:125:ASP:C	1:A:125:ASP:OD1	0.44	2.56	6	9
2:B:517:SER:O	2:B:520:GLU:N	0.44	2.49	4	2
1:A:35:PHE:CD1	1:A:83:PHE:CE1	0.44	3.04	15	2
1:A:91:ARG:O	1:A:92:PRO:O	0.44	2.35	11	1
1:A:56:GLU:O	1:A:60:ASN:OD1	0.44	2.36	18	4
1:A:122:TYR:CZ	2:B:526:PHE:CD2	0.44	3.05	8	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:126:LYS:CD	1:A:126:LYS:N	0.44	2.80	20	2
1:A:39:ASP:HB2	1:A:46:LEU:HD23	0.44	1.88	10	2
1:A:108:LEU:O	1:A:109:ASN:CG	0.44	2.56	3	8
1:A:183:VAL:O	1:A:184:ASP:C	0.44	2.56	10	1
1:A:48:ARG:NH1	1:A:71:PHE:CD2	0.44	2.85	11	1
1:A:179:VAL:HG21	2:B:519:ASN:HB2	0.44	1.89	5	2
1:A:21:THR:OG1	1:A:90:PHE:O	0.44	2.36	11	1
1:A:168:ASP:O	1:A:169:SER:C	0.44	2.53	11	16
1:A:165:GLN:OE1	1:A:165:GLN:O	0.44	2.36	16	1
1:A:12:GLU:O	1:A:16:GLU:OE2	0.44	2.36	18	2
1:A:35:PHE:CD1	1:A:46:LEU:CD1	0.44	3.01	7	2
1:A:19:LYS:C	1:A:22:GLY:H	0.44	2.16	20	3
2:B:527:LEU:CD1	2:B:527:LEU:C	0.44	2.82	1	2
1:A:16:GLU:O	1:A:28:ILE:HG23	0.44	2.12	10	1
1:A:178:LYS:CD	1:A:178:LYS:O	0.44	2.66	3	3
1:A:114:LYS:HZ3	1:A:186:GLU:HA	0.44	1.71	14	1
1:A:57:LEU:CD1	1:A:66:ILE:HD11	0.44	2.42	12	1
1:A:79:ASN:H	1:A:79:ASN:ND2	0.44	2.09	1	1
1:A:109:ASN:O	1:A:110:SER:O	0.44	2.36	18	3
1:A:125:ASP:OD2	1:A:134:GLU:OE1	0.44	2.36	12	5
1:A:79:ASN:OD1	1:A:80:PHE:N	0.44	2.50	13	1
2:B:536:ASP:OD1	2:B:536:ASP:O	0.44	2.35	9	2
2:B:533:GLY:O	2:B:536:ASP:OD1	0.44	2.36	1	1
1:A:89:HIS:O	1:A:109:ASN:OD1	0.43	2.35	16	2
1:A:33:SER:O	1:A:37:SER:OG	0.43	2.35	18	2
1:A:168:ASP:O	1:A:169:SER:OG	0.43	2.35	14	1
1:A:68:ASN:OD1	1:A:120:ARG:O	0.43	2.36	12	1
1:A:163:ALA:HB2	2:B:518:ILE:HD12	0.43	1.89	20	1
2:B:530:LEU:C	2:B:530:LEU:CD1	0.43	2.84	12	5
1:A:173:PHE:C	1:A:173:PHE:CD1	0.43	2.90	14	2
1:A:20:GLU:OE1	1:A:20:GLU:O	0.43	2.37	14	2
1:A:122:TYR:OH	2:B:526:PHE:CD1	0.43	2.64	1	1
1:A:26:SER:O	1:A:27:GLN:C	0.43	2.56	13	6
1:A:109:ASN:CG	1:A:114:LYS:HZ1	0.43	2.15	4	1
1:A:37:SER:C	1:A:39:ASP:N	0.43	2.70	17	3
1:A:51:PHE:CE1	1:A:70:PHE:CZ	0.43	3.07	8	1
1:A:57:LEU:C	1:A:57:LEU:CD2	0.43	2.86	11	7
1:A:13:GLU:CD	2:B:538:CYS:SG	0.43	2.96	11	1
1:A:139:LEU:HD22	1:A:139:LEU:C	0.43	2.32	19	1
1:A:87:LEU:HD22	2:B:538:CYS:SG	0.43	2.54	19	1
1:A:109:ASN:O	1:A:109:ASN:OD1	0.43	2.36	10	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:184:ASP:O	1:A:186:GLU:N	0.43	2.52	18	1
1:A:126:LYS:C	1:A:128:GLU:H	0.43	2.16	7	1
1:A:26:SER:O	1:A:28:ILE:N	0.43	2.50	9	1
2:B:519:ASN:OD1	2:B:520:GLU:N	0.43	2.52	16	2
1:A:75:GLU:CD	1:A:76:ASP:H	0.43	2.17	3	1
1:A:11:ASP:O	1:A:15:GLU:OE1	0.43	2.37	18	1
1:A:183:VAL:O	1:A:184:ASP:OD1	0.43	2.36	10	1
1:A:130:ILE:HD13	1:A:130:ILE:H	0.43	1.72	4	1
1:A:65:ARG:HH12	2:B:533:GLY:C	0.43	2.17	12	1
1:A:52:GLN:NE2	1:A:57:LEU:CD2	0.43	2.81	18	1
1:A:184:ASP:C	1:A:186:GLU:N	0.43	2.72	18	1
1:A:37:SER:O	1:A:39:ASP:N	0.43	2.52	17	1
1:A:157:ASP:OD1	1:A:158:ARG:N	0.43	2.52	8	1
1:A:79:ASN:CG	1:A:80:PHE:H	0.43	2.17	10	3
2:B:532:THR:O	2:B:536:ASP:OD2	0.43	2.37	12	4
1:A:158:ARG:O	1:A:162:GLU:OE1	0.43	2.37	16	3
1:A:60:ASN:CG	1:A:65:ARG:HH22	0.43	2.17	13	1
1:A:189:MET:SD	1:A:189:MET:N	0.43	2.91	13	1
1:A:122:TYR:CZ	2:B:526:PHE:CE1	0.43	3.07	1	1
1:A:125:ASP:OD1	1:A:125:ASP:C	0.43	2.56	8	7
1:A:29:THR:HG23	1:A:30:ARG:N	0.43	2.29	7	2
1:A:65:ARG:NE	1:A:66:ILE:CG2	0.43	2.81	16	1
1:A:17:ILE:HG23	1:A:18:LYS:N	0.43	2.29	14	6
1:A:53:ARG:NE	1:A:53:ARG:CA	0.43	2.82	16	1
1:A:178:LYS:O	1:A:181:GLU:CG	0.43	2.66	4	3
2:B:517:SER:O	2:B:521:GLU:OE2	0.43	2.37	6	1
1:A:180:LEU:O	1:A:183:VAL:O	0.43	2.37	8	1
1:A:140:ARG:CD	1:A:140:ARG:C	0.43	2.87	15	1
1:A:56:GLU:OE1	2:B:536:ASP:OD2	0.43	2.37	1	1
1:A:122:TYR:O	1:A:134:GLU:OE1	0.43	2.37	14	1
1:A:163:ALA:CB	2:B:519:ASN:ND2	0.43	2.81	8	1
2:B:530:LEU:CD1	2:B:530:LEU:C	0.43	2.87	9	1
1:A:127:ASP:C	1:A:127:ASP:OD1	0.43	2.56	11	1
1:A:56:GLU:OE1	1:A:57:LEU:N	0.43	2.52	16	1
2:B:524:THR:O	2:B:528:ASP:OD2	0.43	2.37	13	2
1:A:89:HIS:ND1	1:A:117:PHE:CG	0.43	2.87	17	1
1:A:89:HIS:O	1:A:109:ASN:CG	0.43	2.57	9	1
2:B:536:ASP:OD1	2:B:537:ILE:N	0.43	2.52	1	1
1:A:75:GLU:OE2	1:A:77:GLN:O	0.42	2.37	11	1
1:A:158:ARG:HH21	1:A:161:GLN:CD	0.42	2.16	9	1
1:A:169:SER:O	1:A:169:SER:OG	0.42	2.37	19	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:180:LEU:O	1:A:184:ASP:N	0.42	2.40	10	1
1:A:13:GLU:OE1	2:B:538:CYS:O	0.42	2.37	16	1
1:A:85:ARG:O	1:A:89:HIS:CG	0.42	2.72	3	1
1:A:125:ASP:OD1	1:A:134:GLU:OE2	0.42	2.37	1	1
2:B:523:HIS:O	2:B:524:THR:C	0.42	2.56	5	2
1:A:57:LEU:CD2	1:A:57:LEU:C	0.42	2.87	7	2
1:A:127:ASP:OD2	1:A:129:LYS:O	0.42	2.38	19	2
1:A:180:LEU:C	1:A:182:LYS:H	0.42	2.17	15	9
1:A:78:VAL:HG13	1:A:78:VAL:O	0.42	2.14	10	1
1:A:149:ASP:CG	1:A:150:GLU:N	0.42	2.72	7	1
1:A:89:HIS:CE1	1:A:113:ASN:ND2	0.42	2.87	19	1
1:A:56:GLU:OE1	1:A:60:ASN:OD1	0.42	2.37	10	1
1:A:65:ARG:NH2	2:B:534:ILE:CA	0.42	2.83	5	1
1:A:186:GLU:CD	1:A:186:GLU:H	0.42	2.18	4	1
1:A:56:GLU:OE2	2:B:533:GLY:O	0.42	2.37	12	3
1:A:26:SER:C	1:A:28:ILE:N	0.42	2.73	9	1
1:A:63:GLY:C	1:A:65:ARG:H	0.42	2.18	15	1
1:A:111:ARG:O	1:A:114:LYS:N	0.42	2.53	11	2
1:A:117:PHE:O	1:A:118:ALA:C	0.42	2.58	6	7
1:A:140:ARG:O	1:A:144:GLY:N	0.42	2.50	19	1
1:A:115:LEU:O	1:A:119:PHE:CB	0.42	2.68	10	4
1:A:57:LEU:HD12	1:A:66:ILE:CD1	0.42	2.44	16	1
2:B:527:LEU:HD12	2:B:528:ASP:N	0.42	2.30	13	3
1:A:48:ARG:HH12	1:A:57:LEU:HD13	0.42	1.72	12	1
1:A:35:PHE:CG	1:A:83:PHE:CE1	0.42	3.08	17	1
1:A:65:ARG:NH1	1:A:121:LEU:O	0.42	2.52	10	1
1:A:84:MET:O	1:A:88:ALA:CB	0.42	2.68	18	3
1:A:11:ASP:N	1:A:11:ASP:OD1	0.42	2.49	16	1
1:A:65:ARG:HH21	2:B:533:GLY:C	0.42	2.18	7	2
2:B:520:GLU:OE1	2:B:521:GLU:OE1	0.42	2.37	6	1
1:A:46:LEU:CD1	1:A:50:ASP:OD2	0.42	2.67	9	1
1:A:89:HIS:CD2	1:A:117:PHE:CD1	0.42	3.08	1	1
2:B:535:GLU:CD	2:B:535:GLU:O	0.42	2.58	2	2
1:A:110:SER:O	1:A:111:ARG:C	0.42	2.57	3	1
1:A:59:ILE:HG22	1:A:59:ILE:O	0.42	2.15	17	1
1:A:19:LYS:O	1:A:20:GLU:C	0.42	2.58	14	4
1:A:11:ASP:OD1	1:A:11:ASP:N	0.41	2.50	10	1
1:A:191:ILE:HD12	2:B:535:GLU:OE1	0.41	2.15	5	1
1:A:47:SER:O	1:A:50:ASP:OD1	0.41	2.37	3	1
1:A:45:THR:HG22	1:A:79:ASN:CA	0.41	2.45	18	1
1:A:122:TYR:CZ	2:B:526:PHE:CE2	0.41	3.08	8	1

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:119:PHE:C	1:A:121:LEU:N	0.41	2.72	11	1
1:A:115:LEU:H	1:A:115:LEU:CD2	0.41	2.26	10	3
1:A:60:ASN:CG	1:A:65:ARG:HH21	0.41	2.17	2	1
1:A:114:LYS:HZ1	1:A:185:VAL:CG1	0.41	2.27	12	1
1:A:163:ALA:HB1	2:B:519:ASN:OD1	0.41	2.14	18	1
1:A:155:ILE:HD12	1:A:158:ARG:HH21	0.41	1.75	17	1
1:A:63:GLY:O	1:A:66:ILE:HG13	0.41	2.14	20	1
1:A:165:GLN:C	1:A:167:GLY:N	0.41	2.74	2	2
1:A:17:ILE:O	1:A:18:LYS:C	0.41	2.58	14	6
1:A:126:LYS:N	1:A:126:LYS:CD	0.41	2.83	4	1
1:A:51:PHE:CE1	1:A:70:PHE:CE1	0.41	3.08	8	1
1:A:138:VAL:CG1	1:A:142:MET:SD	0.41	3.00	15	1
1:A:13:GLU:OE2	2:B:538:CYS:SG	0.41	2.70	5	1
2:B:532:THR:O	2:B:536:ASP:OD1	0.41	2.38	3	1
1:A:149:ASP:CG	1:A:150:GLU:H	0.41	2.16	7	1
1:A:178:LYS:O	1:A:178:LYS:CD	0.41	2.68	7	1
2:B:536:ASP:O	2:B:538:CYS:SG	0.41	2.70	17	1
1:A:173:PHE:O	1:A:173:PHE:CD2	0.41	2.74	15	1
1:A:83:PHE:CZ	1:A:87:LEU:CD1	0.41	3.04	20	1
1:A:184:ASP:OD1	1:A:184:ASP:N	0.41	2.51	7	1
1:A:49:GLU:OE2	1:A:49:GLU:O	0.41	2.38	15	1
1:A:35:PHE:CE1	1:A:46:LEU:CD1	0.41	3.03	14	2
1:A:85:ARG:NH2	1:A:120:ARG:NH1	0.41	2.69	3	1
1:A:109:ASN:HD21	1:A:189:MET:CB	0.41	2.28	11	1
1:A:15:GLU:OE1	1:A:19:LYS:NZ	0.41	2.43	19	2
2:B:535:GLU:C	2:B:537:ILE:H	0.41	2.19	20	2
1:A:56:GLU:O	1:A:60:ASN:CG	0.41	2.60	7	3
1:A:63:GLY:O	1:A:66:ILE:CG2	0.41	2.69	4	1
1:A:125:ASP:CG	1:A:134:GLU:OE2	0.41	2.59	14	1
1:A:129:LYS:HZ3	1:A:170:ALA:HB3	0.41	1.76	12	1
2:B:532:THR:O	2:B:536:ASP:CG	0.41	2.59	7	1
1:A:126:LYS:C	1:A:128:GLU:N	0.41	2.74	7	1
1:A:82:GLY:O	1:A:83:PHE:C	0.41	2.59	17	3
1:A:37:SER:C	1:A:39:ASP:H	0.41	2.19	17	1
1:A:38:LEU:CB	1:A:50:ASP:OD1	0.41	2.69	9	1
1:A:166:ASP:CG	1:A:174:THR:OG1	0.41	2.59	20	3
1:A:21:THR:OG1	1:A:90:PHE:C	0.41	2.59	10	1
1:A:66:ILE:HG23	1:A:67:ILE:N	0.41	2.31	2	1
1:A:173:PHE:O	1:A:173:PHE:CD1	0.41	2.74	9	1
1:A:48:ARG:HH12	1:A:52:GLN:CD	0.41	2.17	20	1
1:A:172:SER:O	1:A:176:PHE:CG	0.40	2.74	3	1

*Continued on next page...*



Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:109:ASN:OD1	1:A:109:ASN:C	0.40	2.60	6	1
1:A:31:LEU:HD13	1:A:31:LEU:O	0.40	2.16	20	1
1:A:171:ILE:HD12	1:A:171:ILE:N	0.40	2.31	10	1
2:B:525:GLN:O	2:B:526:PHE:C	0.40	2.59	8	2
1:A:125:ASP:OD2	1:A:134:GLU:CG	0.40	2.69	4	1
1:A:56:GLU:CD	1:A:60:ASN:ND2	0.40	2.74	12	1
1:A:13:GLU:O	1:A:17:ILE:HG22	0.40	2.17	1	1
1:A:91:ARG:O	1:A:109:ASN:CG	0.40	2.60	19	1
1:A:81:ARG:CG	1:A:85:ARG:HH22	0.40	2.30	10	1
1:A:114:LYS:HZ2	1:A:185:VAL:HB	0.40	1.76	10	1
1:A:136:LEU:O	1:A:137:GLN:C	0.40	2.60	4	1
1:A:119:PHE:CE2	1:A:120:ARG:CZ	0.40	3.03	4	1
1:A:36:THR:HA	1:A:46:LEU:HD21	0.40	1.93	7	1
1:A:19:LYS:O	1:A:21:THR:N	0.40	2.54	9	1
2:B:522:ILE:HG23	2:B:523:HIS:ND1	0.40	2.31	1	1
1:A:125:ASP:OD1	1:A:127:ASP:CG	0.40	2.60	20	1
2:B:526:PHE:O	2:B:527:LEU:C	0.40	2.60	11	3
2:B:520:GLU:O	2:B:521:GLU:C	0.40	2.58	5	1
1:A:49:GLU:N	1:A:49:GLU:CD	0.40	2.73	12	1
1:A:68:ASN:CB	1:A:120:ARG:O	0.40	2.70	7	1
1:A:108:LEU:C	1:A:109:ASN:ND2	0.40	2.75	17	1
1:A:143:VAL:C	1:A:145:VAL:N	0.40	2.75	8	1
2:B:534:ILE:CG2	2:B:535:GLU:OE1	0.40	2.69	15	1
1:A:125:ASP:OD1	1:A:134:GLU:CD	0.40	2.60	1	1
1:A:19:LYS:N	1:A:19:LYS:CD	0.40	2.83	11	1
1:A:184:ASP:OD1	1:A:184:ASP:O	0.40	2.39	16	1
1:A:14:LEU:C	1:A:16:GLU:N	0.40	2.75	18	1
1:A:20:GLU:O	1:A:88:ALA:CB	0.40	2.69	9	1

## 6.3 Torsion angles ⓘ

### 6.3.1 Protein backbone ⓘ

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	156/195 (80%)	124±3 (79±2%)	26±3 (17±2%)	6±2 (4±1%)	7	35

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	22/43 (51%)	18±1 (82±6%)	3±1 (14±7%)	1±1 (4±3%)	6	31
All	All	3560/4760 (75%)	2839 (80%)	582 (16%)	139 (4%)	7	34

All 22 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	172	SER	18
1	A	189	MET	16
1	A	39	ASP	15
1	A	164	ASP	15
2	B	538	CYS	12
1	A	44	GLY	11
1	A	108	LEU	10
1	A	63	GLY	8
1	A	89	HIS	8
2	B	536	ASP	6
1	A	110	SER	4
1	A	131	SER	3
1	A	64	ASP	3
1	A	139	LEU	2
1	A	15	GLU	1
1	A	109	ASN	1
1	A	123	ASP	1
1	A	71	PHE	1
1	A	184	ASP	1
1	A	55	PRO	1
2	B	537	ILE	1
1	A	92	PRO	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	142/176 (81%)	120±3 (84±2%)	22±3 (16±2%)	7	45
2	B	21/39 (54%)	19±1 (88±4%)	3±1 (12±4%)	11	53

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3260/4300 (76%)	2769 (85%)	491 (15%)	7 46

All 87 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	28	ILE	20
1	A	159	THR	20
1	A	139	LEU	20
1	A	152	LEU	20
1	A	21	THR	20
2	B	518	ILE	20
1	A	135	LEU	19
1	A	148	SER	19
1	A	14	LEU	17
1	A	50	ASP	16
1	A	62	LEU	16
1	A	109	ASN	15
2	B	526	PHE	15
1	A	66	ILE	14
1	A	65	ARG	13
1	A	12	GLU	12
1	A	178	LYS	10
1	A	130	ILE	10
1	A	138	VAL	8
1	A	189	MET	8
1	A	108	LEU	8
1	A	35	PHE	8
1	A	84	MET	7
1	A	89	HIS	7
1	A	172	SER	7
1	A	54	ILE	7
1	A	162	GLU	6
1	A	140	ARG	6
1	A	53	ARG	5
1	A	142	MET	5
1	A	79	ASN	5
1	A	126	LYS	5
1	A	187	GLN	4
1	A	114	LYS	4
1	A	71	PHE	4
1	A	77	GLN	4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	141	MET	4
1	A	78	VAL	4
1	A	60	ASN	4
1	A	16	GLU	4
2	B	521	GLU	4
1	A	19	LYS	3
1	A	137	GLN	3
2	B	535	GLU	3
1	A	113	ASN	3
1	A	56	GLU	3
1	A	165	GLN	3
1	A	175	GLU	2
1	A	52	GLN	2
2	B	519	ASN	2
1	A	146	ASN	2
1	A	20	GLU	2
2	B	528	ASP	2
1	A	27	GLN	2
1	A	48	ARG	2
2	B	530	LEU	2
1	A	45	THR	1
1	A	166	ASP	1
1	A	125	ASP	1
1	A	30	ARG	1
1	A	68	ASN	1
1	A	111	ARG	1
1	A	75	GLU	1
1	A	36	THR	1
1	A	131	SER	1
1	A	188	LYS	1
1	A	123	ASP	1
1	A	120	ARG	1
1	A	158	ARG	1
1	A	191	ILE	1
1	A	17	ILE	1
2	B	523	HIS	1
1	A	184	ASP	1
1	A	47	SER	1
1	A	171	ILE	1
1	A	128	GLU	1
1	A	134	GLU	1
1	A	86	THR	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	34	ARG	1
2	B	527	LEU	1
1	A	127	ASP	1
1	A	91	ARG	1
1	A	31	LEU	1
1	A	64	ASP	1
1	A	81	ARG	1
1	A	157	ASP	1
1	A	129	LYS	1

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided