wwPDB EM Map/Model Validation Report (i)

Oct 17, 2016 – 08:30 PM EDT

PDB ID	:	5TAX
EMDB ID:	:	EMD-8388
Title	:	Structure of rabbit RyR1 (ryanodine dataset, class 1)
Authors	:	Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.; Frank, J.
Deposited on	:	2016-09-10
Resolution	:	6.60 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

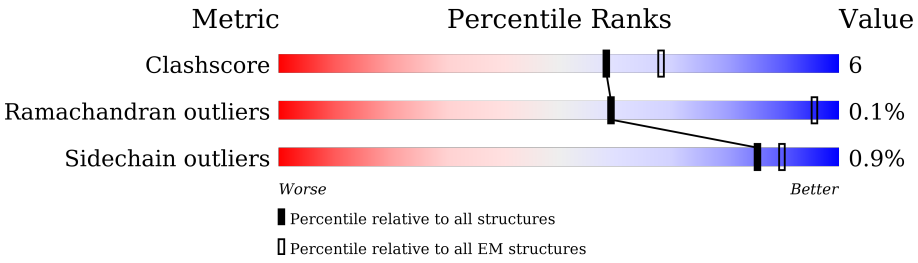
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027939

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 6.60 Å.

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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	108	80% 19% .
1	F	108	78% 21% .
1	H	108	79% 20% .
1	J	108	76% 23% .
2	B	4416	83% 12% 5%
2	E	4416	83% 12% 5%
2	G	4416	83% 12% 5%
2	I	4416	83% 12% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 121276 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	A	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	H	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	J	107	Total	C	N	O	S	0	0
			818	516	144	154	4		

- Molecule 2 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		
2	I	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		
2	G	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		
2	E	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	G	1	Total	Zn	0
			1	1	
3	B	1	Total	Zn	0
			1	1	
3	I	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

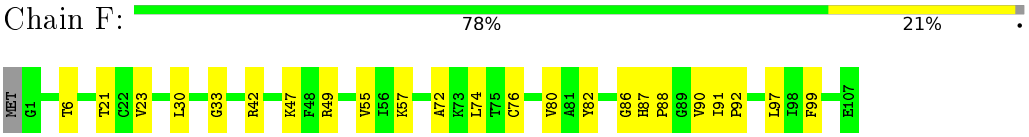
Mol	Chain	Residues	Atoms	AltConf
4	G	1	Total Ca 1 1	0
4	B	1	Total Ca 1 1	0
4	I	1	Total Ca 1 1	0
4	E	1	Total Ca 1 1	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-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 outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

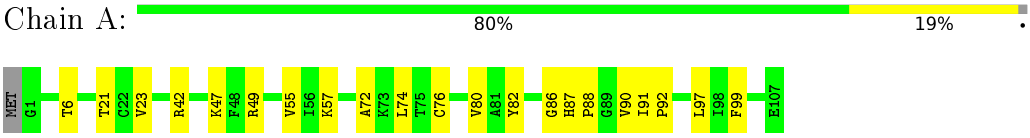
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain F:



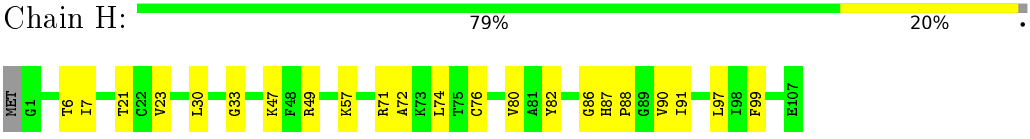
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain A:



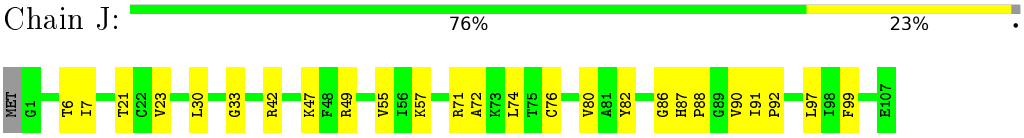
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain H:



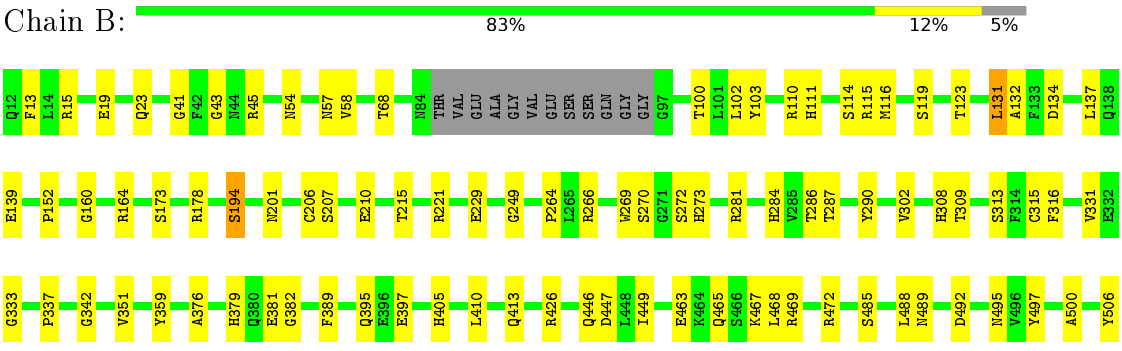
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

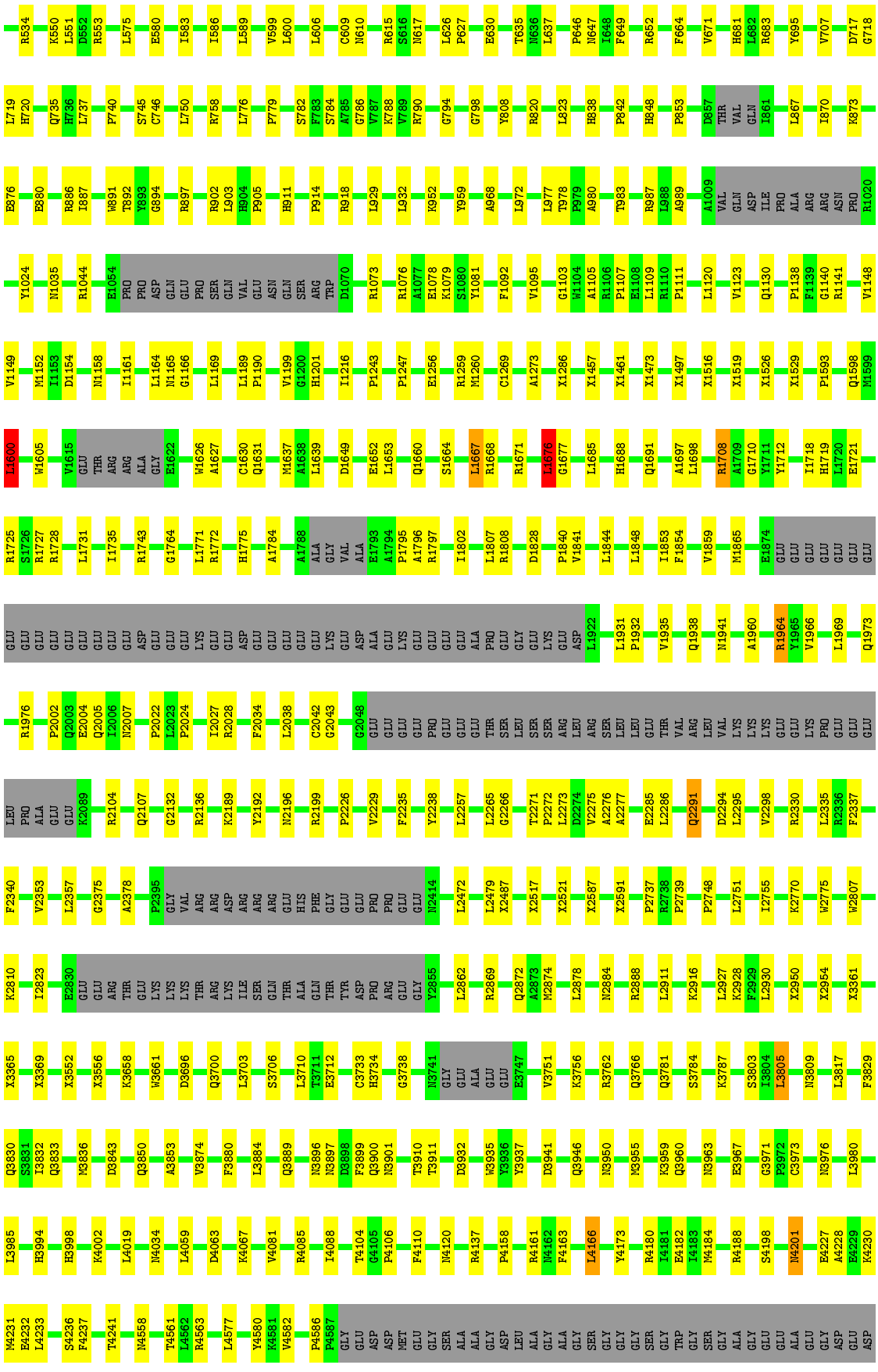
Chain J:

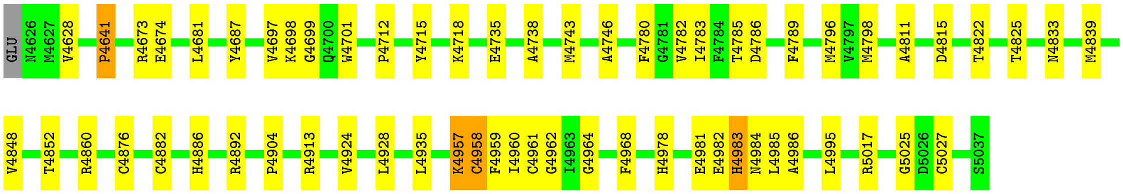


- Molecule 2: Ryanodine receptor 1

Chain B:

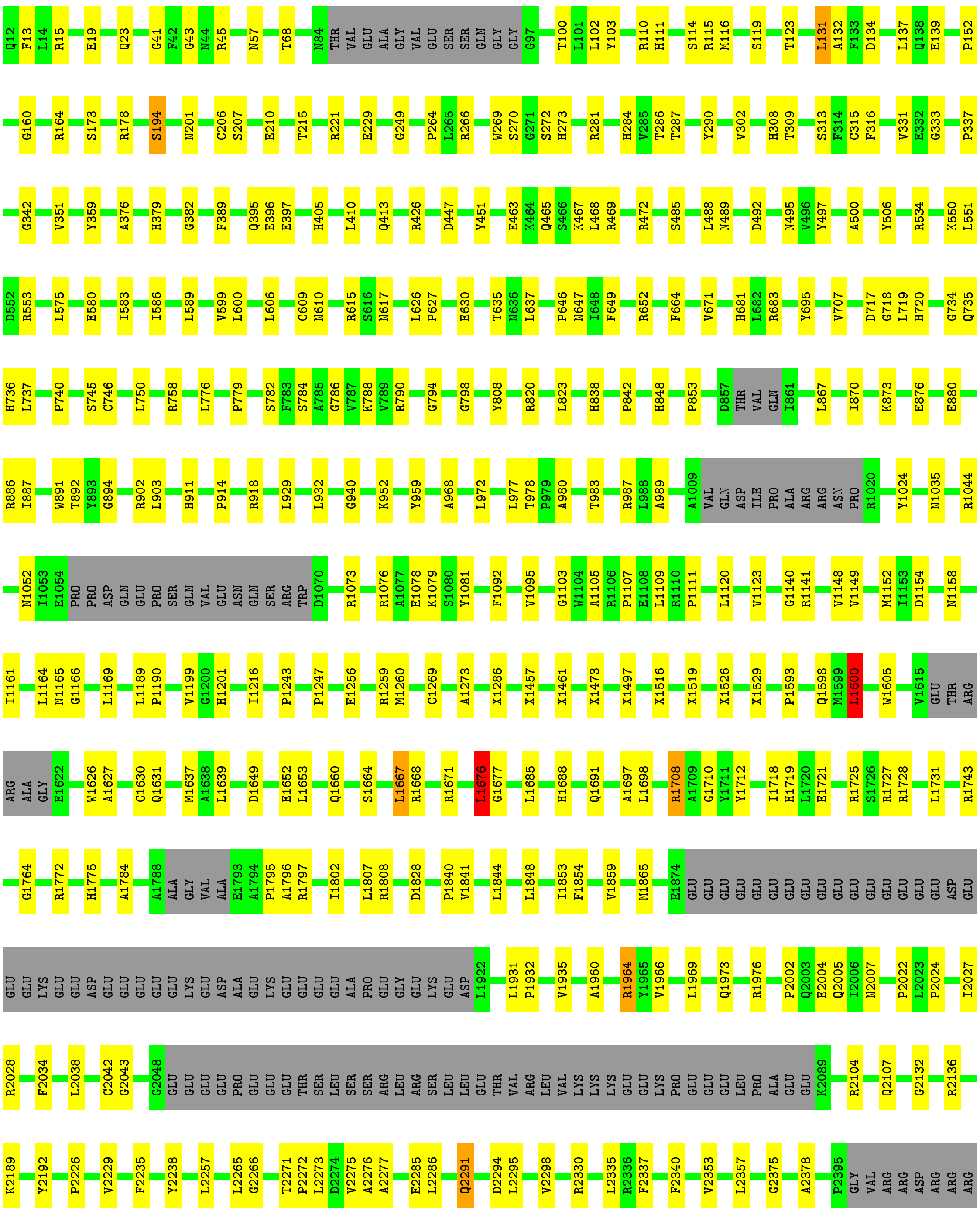


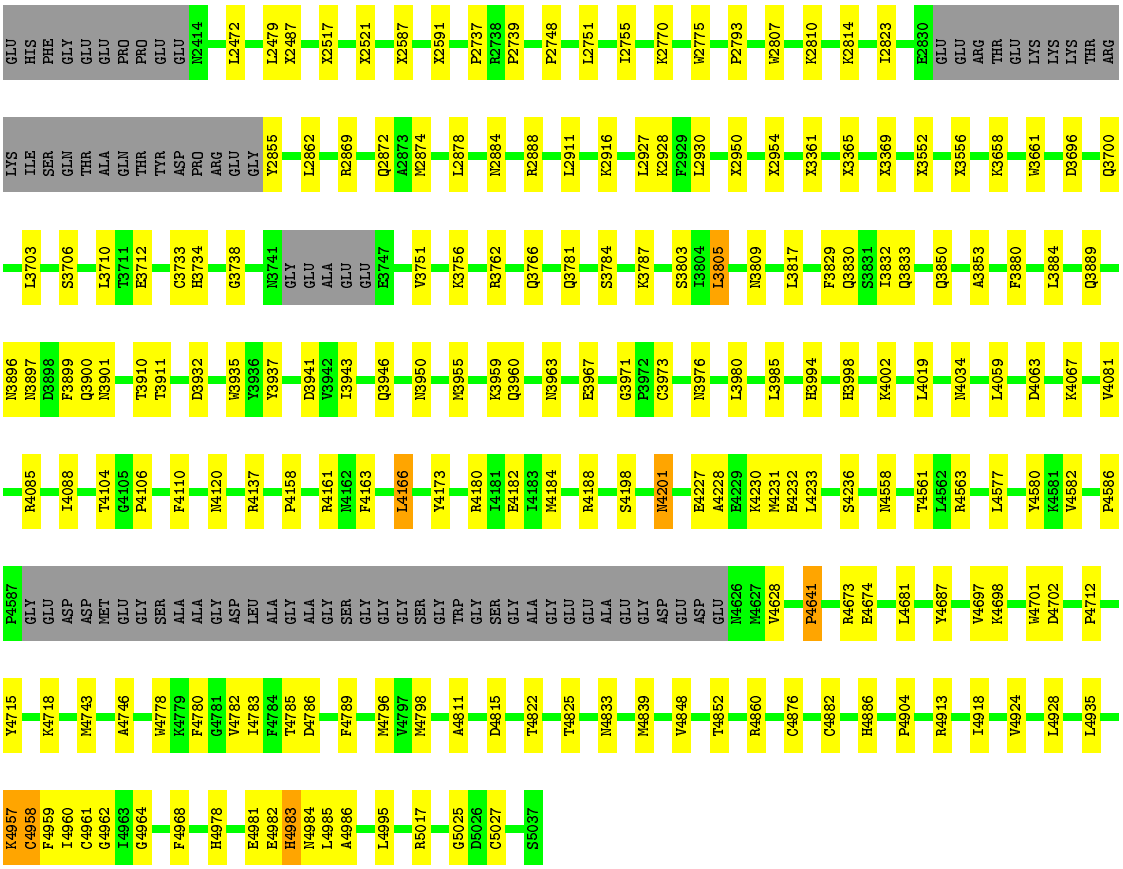




• Molecule 2: Ryanodine receptor 1

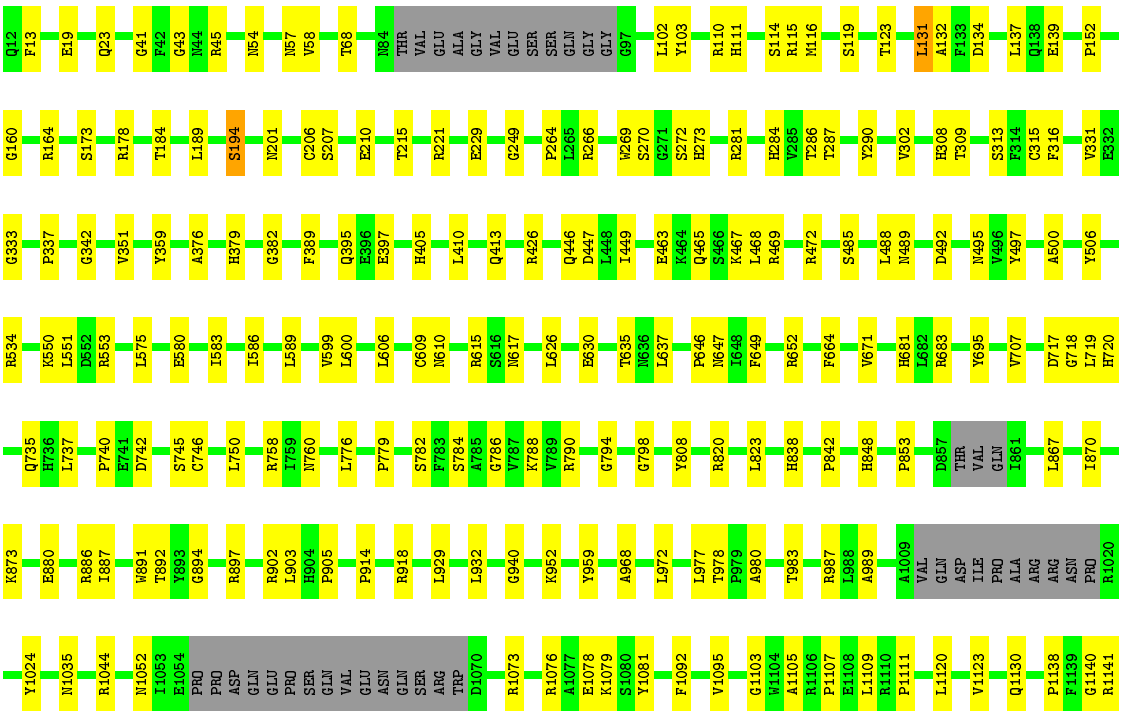
Chain I:

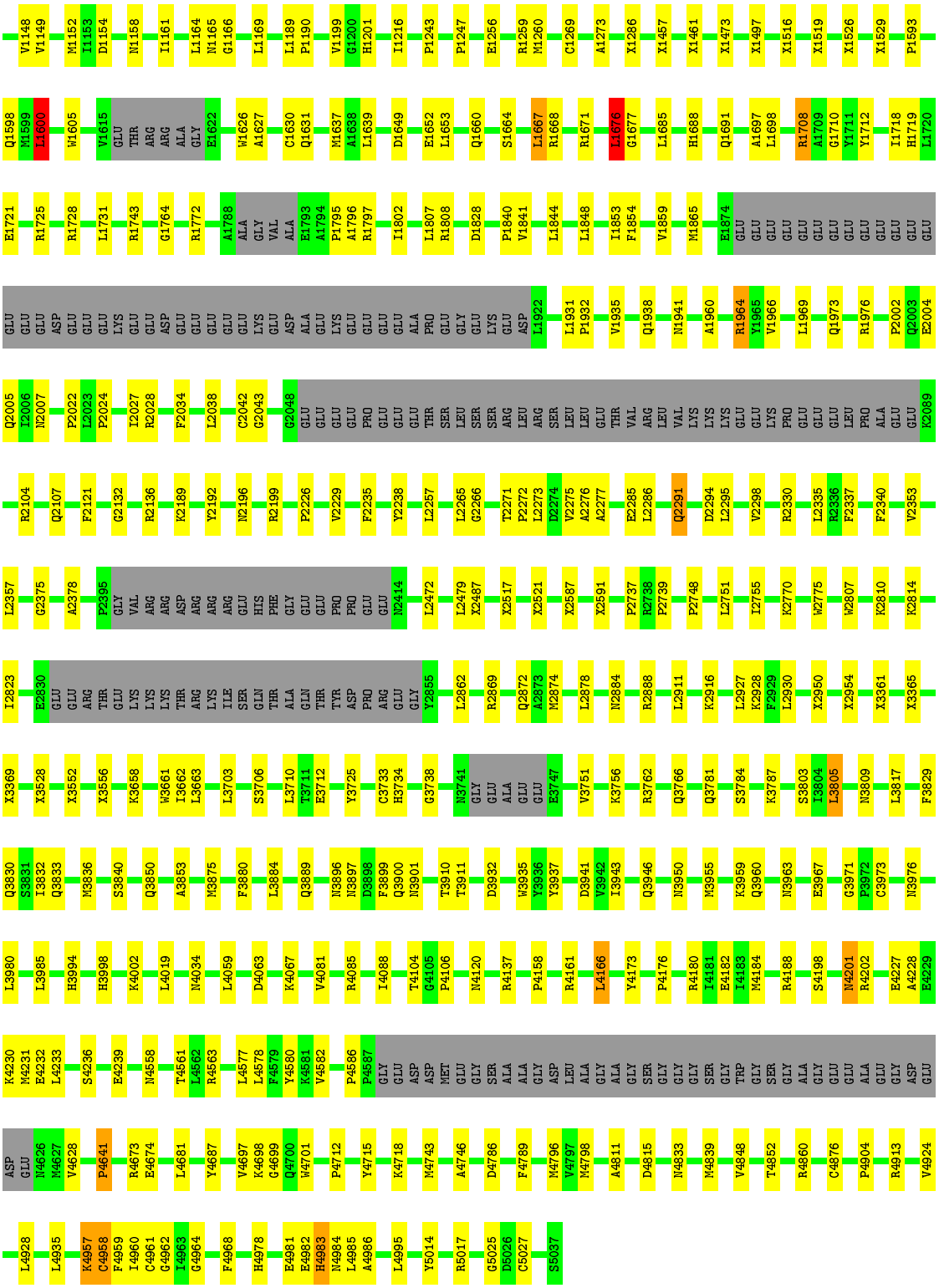




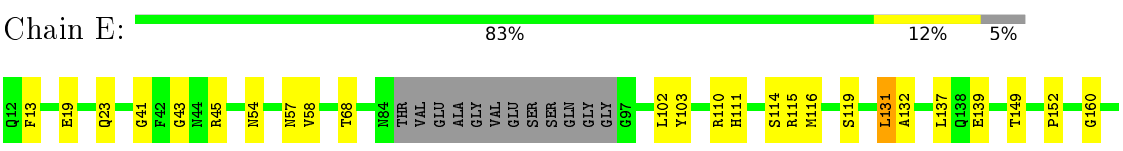
• Molecule 2: Ryanodine receptor 1

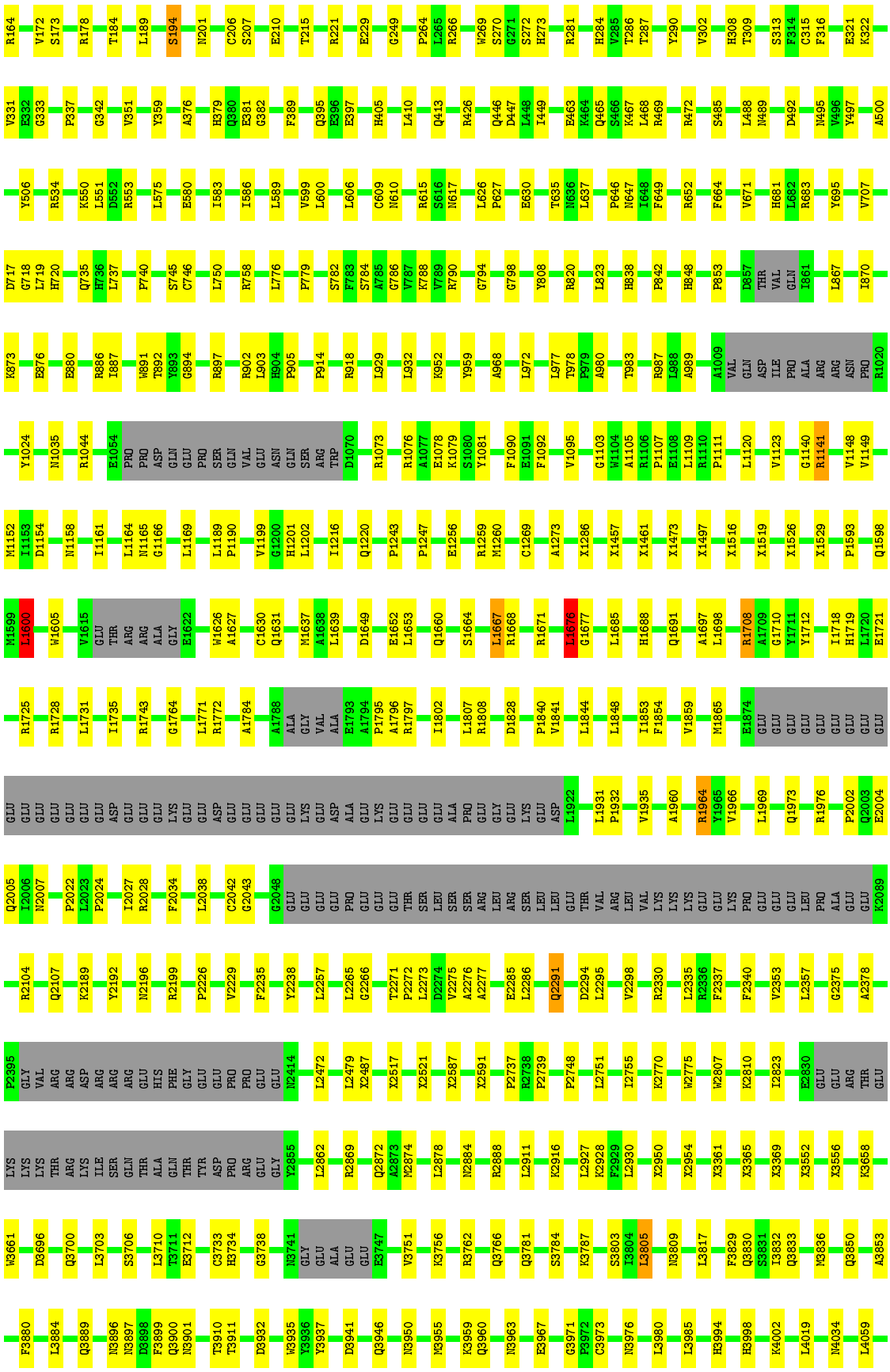
Chain G:

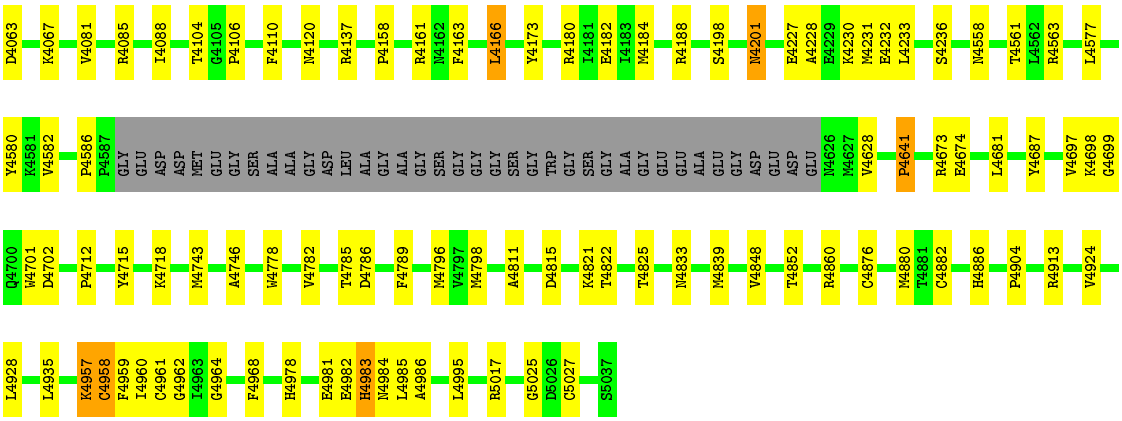




• Molecule 2: Ryanodine receptor 1






D4063 K4067 V4081 R4085 I4088 T4104 G4105 P4106 F4110 N4120 R4137 P4158 R4161 N4162 F4163 L4166 Y4173 R4180 I4181 E4182 I4183 M4184 R4188 S4198 N4201 E4227 A4228 E4229 K4230 M4231 E4232 L4233 S4236 M4558 T4561 L4562 R4563 L4577
Y4580 K4581 V4582 P4586 P4587 GLY GLU ASP ASP MET GLU GLY SER ALA ALA GLY ASP LEU ALA GLY ALA GLY SER GLY GLY GLY SER GLY TRP GLY SER GLY ALA GLY GLU GLU ALA GLU GLY ASP GLU ASP GLU N4626 M4627 V4628 P4641 R4673 E4674 L4681 Y4687 V4697 K4698 G4699
Q4700 W4701 D4702 P4712 Y4715 K4718 M4743 A4746 W4778 V4782 T4785 D4786 F4789 M4796 V4797 M4798 A4811 D4815 K4821 T4822 T4825 N4833 M4839 V4848 T4852 R4860 C4876 M4880 T4881 C4882 H4886 P4904 R4913 V4924
L4928 L4935 K4957 C4958 F4959 I4960 C4961 G4962 I4963 G4964 F4968 H4978 E4981 E4982 H4983 N4984 L4985 A4986 L4995 R5017 G5025 D5026 C5027 S5037

4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	55564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>2$	RMSZ	#$\|Z\|>2$
1	A	0.29	0/834	0.53	0/1123
1	F	0.29	0/834	0.53	0/1123
1	H	0.29	0/834	0.53	0/1123
1	J	0.29	0/834	0.53	0/1123
2	B	0.29	0/25428	0.54	7/34534 (0.0%)
2	E	0.29	0/25428	0.54	7/34534 (0.0%)
2	G	0.29	0/25428	0.54	7/34534 (0.0%)
2	I	0.29	0/25428	0.54	7/34534 (0.0%)
All	All	0.29	0/105048	0.54	28/142628 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	11
2	E	0	11
2	G	0	11
2	I	0	11
All	All	0	44

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	131	LEU	CA-CB-CG	8.10	133.93	115.30
2	I	131	LEU	CA-CB-CG	8.09	133.90	115.30
2	B	131	LEU	CA-CB-CG	8.08	133.88	115.30
2	G	131	LEU	CA-CB-CG	8.07	133.87	115.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	4985	LEU	CA-CB-CG	7.05	131.51	115.30
2	B	4985	LEU	CA-CB-CG	7.04	131.49	115.30
2	I	4985	LEU	CA-CB-CG	7.04	131.48	115.30
2	G	4985	LEU	CA-CB-CG	7.03	131.47	115.30
2	I	1140	GLY	C-N-CA	6.89	138.93	121.70
2	B	1140	GLY	C-N-CA	6.89	138.93	121.70
2	E	1140	GLY	C-N-CA	6.89	138.93	121.70
2	G	1140	GLY	C-N-CA	6.88	138.90	121.70
2	E	1676	LEU	CA-CB-CG	6.50	130.25	115.30
2	G	1676	LEU	CA-CB-CG	6.50	130.24	115.30
2	B	1676	LEU	CA-CB-CG	6.49	130.23	115.30
2	I	1676	LEU	CA-CB-CG	6.48	130.21	115.30
2	E	1600	LEU	CA-CB-CG	6.40	130.02	115.30
2	B	1600	LEU	CA-CB-CG	6.39	130.00	115.30
2	G	1600	LEU	CA-CB-CG	6.38	129.99	115.30
2	I	1600	LEU	CA-CB-CG	6.38	129.98	115.30
2	I	977	LEU	CA-CB-CG	5.36	127.63	115.30
2	G	977	LEU	CA-CB-CG	5.36	127.62	115.30
2	E	977	LEU	CA-CB-CG	5.35	127.60	115.30
2	B	977	LEU	CA-CB-CG	5.35	127.60	115.30
2	B	1667	LEU	CA-CB-CG	5.07	126.96	115.30
2	I	1667	LEU	CA-CB-CG	5.07	126.95	115.30
2	E	1667	LEU	CA-CB-CG	5.06	126.93	115.30
2	G	1667	LEU	CA-CB-CG	5.06	126.93	115.30

There are no chirality outliers.

All (44) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	139	GLU	Peptide
2	B	1676	LEU	Peptide
2	B	1795	PRO	Peptide
2	B	1828	ASP	Peptide
2	B	194	SER	Peptide
2	B	2291	GLN	Peptide
2	B	2472	LEU	Peptide
2	B	2807	TRP	Peptide
2	B	3971	GLY	Peptide
2	B	4641	PRO	Peptide
2	B	808	TYR	Peptide
2	E	139	GLU	Peptide
2	E	1676	LEU	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
2	E	1795	PRO	Peptide
2	E	1828	ASP	Peptide
2	E	194	SER	Peptide
2	E	2291	GLN	Peptide
2	E	2472	LEU	Peptide
2	E	2807	TRP	Peptide
2	E	3971	GLY	Peptide
2	E	4641	PRO	Peptide
2	E	808	TYR	Peptide
2	G	139	GLU	Peptide
2	G	1676	LEU	Peptide
2	G	1795	PRO	Peptide
2	G	1828	ASP	Peptide
2	G	194	SER	Peptide
2	G	2291	GLN	Peptide
2	G	2472	LEU	Peptide
2	G	2807	TRP	Peptide
2	G	3971	GLY	Peptide
2	G	4641	PRO	Peptide
2	G	808	TYR	Peptide
2	I	139	GLU	Peptide
2	I	1676	LEU	Peptide
2	I	1795	PRO	Peptide
2	I	1828	ASP	Peptide
2	I	194	SER	Peptide
2	I	2291	GLN	Peptide
2	I	2472	LEU	Peptide
2	I	2807	TRP	Peptide
2	I	3971	GLY	Peptide
2	I	4641	PRO	Peptide
2	I	808	TYR	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	818	0	824	13	0
1	F	818	0	824	14	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	818	0	824	12	0
1	J	818	0	824	15	0
2	B	29499	0	24741	329	0
2	E	29499	0	24742	325	0
2	G	29499	0	24741	322	0
2	I	29499	0	24742	324	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
4	B	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
All	All	121276	0	102262	1338	0

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 6.

All (1338) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:4182:GLU:OE2	2:I:4983:HIS:NE2	1.64	1.31
2:E:4182:GLU:OE2	2:E:4983:HIS:NE2	1.64	1.29
2:G:4182:GLU:OE2	2:G:4983:HIS:NE2	1.64	1.29
2:B:4182:GLU:OE2	2:B:4983:HIS:NE2	1.64	1.27
2:G:4982:GLU:OE1	2:G:5027:CYS:SG	1.98	1.22
2:I:4982:GLU:OE1	2:I:5027:CYS:SG	1.98	1.21
2:B:4982:GLU:OE1	2:B:5027:CYS:SG	1.98	1.21
2:E:4982:GLU:OE1	2:E:5027:CYS:SG	1.98	1.20
2:E:4230:LYS:HG3	2:E:4959:PHE:CZ	1.89	1.07
2:G:4230:LYS:HG3	2:G:4959:PHE:CZ	1.89	1.06
2:B:4230:LYS:HG3	2:B:4959:PHE:CZ	1.89	1.06
2:I:4230:LYS:HG3	2:I:4959:PHE:CZ	1.89	1.06
2:G:4968:PHE:CZ	2:G:4978:HIS:CE1	2.50	1.00
2:I:4968:PHE:CZ	2:I:4978:HIS:CE1	2.50	1.00
2:E:4968:PHE:CZ	2:E:4978:HIS:CE1	2.50	0.99
2:B:4968:PHE:CZ	2:B:4978:HIS:CE1	2.50	0.99
2:I:4230:LYS:HG3	2:I:4959:PHE:HZ	1.30	0.96
2:B:4230:LYS:HG3	2:B:4959:PHE:HZ	1.30	0.94
2:G:4230:LYS:HG3	2:G:4959:PHE:HZ	1.30	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:4230:LYS:HG3	2:E:4959:PHE:HZ	1.30	0.92
2:G:4230:LYS:HD2	2:G:4959:PHE:CZ	2.06	0.91
2:I:4230:LYS:HD2	2:I:4959:PHE:CZ	2.06	0.90
2:E:4230:LYS:HD2	2:E:4959:PHE:CZ	2.06	0.90
2:B:4230:LYS:HD2	2:B:4959:PHE:CZ	2.06	0.89
2:B:4230:LYS:CG	2:B:4959:PHE:CZ	2.59	0.85
2:I:4230:LYS:CG	2:I:4959:PHE:CZ	2.59	0.85
2:G:4230:LYS:CG	2:G:4959:PHE:CZ	2.59	0.84
2:E:4230:LYS:CG	2:E:4959:PHE:CZ	2.59	0.84
2:E:4978:HIS:HA	2:E:4982:GLU:HB2	1.61	0.83
2:B:4978:HIS:HA	2:B:4982:GLU:HB2	1.61	0.82
2:G:4968:PHE:CZ	2:G:4978:HIS:ND1	2.48	0.82
2:B:4968:PHE:CZ	2:B:4978:HIS:ND1	2.48	0.82
2:I:4978:HIS:HA	2:I:4982:GLU:HB2	1.61	0.82
2:I:4968:PHE:CZ	2:I:4978:HIS:ND1	2.48	0.82
2:G:4978:HIS:HA	2:G:4982:GLU:HB2	1.61	0.81
2:E:4230:LYS:CD	2:E:4959:PHE:CZ	2.63	0.81
2:G:4230:LYS:CD	2:G:4959:PHE:CZ	2.63	0.81
2:E:4968:PHE:CZ	2:E:4978:HIS:ND1	2.48	0.81
2:I:4230:LYS:CD	2:I:4959:PHE:CZ	2.63	0.81
2:B:4230:LYS:CD	2:B:4959:PHE:CZ	2.63	0.81
2:G:4957:LYS:HZ3	2:G:4957:LYS:HB2	1.55	0.72
2:E:1259:ARG:HH12	2:E:1593:PRO:HA	1.56	0.71
2:G:1259:ARG:HH12	2:G:1593:PRO:HA	1.56	0.71
2:G:4957:LYS:HG3	2:G:4964:GLY:CA	2.22	0.70
2:I:1260:MET:HB2	2:I:1269:CYS:H	1.56	0.70
2:B:1260:MET:HB2	2:B:1269:CYS:H	1.56	0.70
2:B:4957:LYS:HG3	2:B:4964:GLY:CA	2.22	0.70
2:G:1260:MET:HB2	2:G:1269:CYS:H	1.56	0.70
2:B:1259:ARG:HH12	2:B:1593:PRO:HA	1.56	0.69
2:E:4957:LYS:HG3	2:E:4964:GLY:CA	2.22	0.69
2:I:4957:LYS:HG3	2:I:4964:GLY:CA	2.22	0.69
2:E:1260:MET:HB2	2:E:1269:CYS:H	1.56	0.69
2:I:788:LYS:HG2	2:I:1630:CYS:H	1.58	0.69
2:G:788:LYS:HG2	2:G:1630:CYS:H	1.58	0.69
2:I:1259:ARG:HH12	2:I:1593:PRO:HA	1.56	0.69
2:B:4957:LYS:HG3	2:B:4964:GLY:HA2	1.75	0.69
2:G:4957:LYS:HG3	2:G:4964:GLY:HA2	1.76	0.68
2:B:788:LYS:HG2	2:B:1630:CYS:H	1.58	0.68
2:E:788:LYS:HG2	2:E:1630:CYS:H	1.58	0.67
2:I:4957:LYS:HG3	2:I:4964:GLY:HA2	1.75	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:4968:PHE:CZ	2:I:4978:HIS:HE1	2.09	0.67
2:G:2291:GLN:HB2	2:G:2295:LEU:HG	1.76	0.67
2:E:2291:GLN:HB2	2:E:2295:LEU:HG	1.76	0.67
2:B:2291:GLN:HB2	2:B:2295:LEU:HG	1.76	0.66
2:G:4968:PHE:CZ	2:G:4978:HIS:HE1	2.09	0.66
2:I:2291:GLN:HB2	2:I:2295:LEU:HG	1.76	0.66
2:E:4968:PHE:CZ	2:E:4978:HIS:HE1	2.09	0.66
2:I:2291:GLN:HB3	2:I:2294:ASP:H	1.60	0.66
2:E:4957:LYS:HG3	2:E:4964:GLY:HA2	1.76	0.66
2:B:646:PRO:HD2	2:B:779:PRO:HB2	1.77	0.66
2:B:2291:GLN:HB3	2:B:2294:ASP:H	1.60	0.66
2:B:4230:LYS:HD2	2:B:4959:PHE:CE1	2.31	0.65
2:E:2291:GLN:HB3	2:E:2294:ASP:H	1.60	0.65
2:E:646:PRO:HD2	2:E:779:PRO:HB2	1.77	0.65
2:G:379:HIS:HD2	2:G:382:GLY:H	1.44	0.65
2:E:379:HIS:HD2	2:E:382:GLY:H	1.44	0.65
2:G:4230:LYS:HD2	2:G:4959:PHE:CE1	2.31	0.65
2:G:2291:GLN:HB3	2:G:2294:ASP:H	1.60	0.65
2:I:4230:LYS:HD2	2:I:4959:PHE:CE1	2.31	0.65
2:I:646:PRO:HD2	2:I:779:PRO:HB2	1.77	0.65
2:E:4230:LYS:HD2	2:E:4959:PHE:CE1	2.31	0.65
2:B:626:LEU:HD23	2:B:630:GLU:H	1.62	0.64
2:B:4968:PHE:CZ	2:B:4978:HIS:HE1	2.09	0.64
2:G:626:LEU:HD23	2:G:630:GLU:H	1.62	0.64
2:G:646:PRO:HD2	2:G:779:PRO:HB2	1.78	0.64
2:E:626:LEU:HD23	2:E:630:GLU:H	1.62	0.64
2:I:379:HIS:HD2	2:I:382:GLY:H	1.44	0.64
2:B:379:HIS:HD2	2:B:382:GLY:H	1.44	0.64
2:E:1667:LEU:HD23	2:E:1671:ARG:HH12	1.63	0.64
2:G:1667:LEU:HD23	2:G:1671:ARG:HH12	1.63	0.64
2:B:426:ARG:HB2	2:B:506:TYR:HA	1.80	0.63
2:I:426:ARG:HB2	2:I:506:TYR:HA	1.80	0.63
2:G:426:ARG:HB2	2:G:506:TYR:HA	1.80	0.63
2:I:626:LEU:HD23	2:I:630:GLU:H	1.62	0.63
2:E:4957:LYS:CG	2:E:4964:GLY:HA2	2.29	0.63
2:B:4957:LYS:CG	2:B:4964:GLY:HA2	2.29	0.62
2:G:745:SER:HB2	2:G:758:ARG:HB3	1.81	0.62
2:E:111:HIS:HD2	2:E:114:SER:H	1.47	0.62
2:E:426:ARG:HB2	2:E:506:TYR:HA	1.80	0.62
2:E:745:SER:HB2	2:E:758:ARG:HB3	1.82	0.62
2:I:1667:LEU:HD23	2:I:1671:ARG:HH12	1.63	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:331:VAL:HG12	2:I:333:GLY:H	1.64	0.62
2:B:497:TYR:HB3	2:B:500:ALA:HB2	1.82	0.62
2:B:745:SER:HB2	2:B:758:ARG:HB3	1.82	0.62
2:I:4063:ASP:OD2	2:I:4067:LYS:NZ	2.33	0.62
2:I:497:TYR:HB3	2:I:500:ALA:HB2	1.82	0.62
2:I:745:SER:HB2	2:I:758:ARG:HB3	1.82	0.62
2:I:4957:LYS:CG	2:I:4964:GLY:HA2	2.29	0.62
2:E:4063:ASP:OD2	2:E:4067:LYS:NZ	2.33	0.62
2:G:4957:LYS:CG	2:G:4964:GLY:HA2	2.29	0.62
2:B:331:VAL:HG12	2:B:333:GLY:H	1.64	0.62
2:G:1653:LEU:HB3	2:G:1660:GLN:HB2	1.81	0.62
2:I:1079:LYS:NZ	2:I:1107:PRO:O	2.33	0.62
2:B:1667:LEU:HD23	2:B:1671:ARG:HH12	1.63	0.61
2:B:4063:ASP:OD2	2:B:4067:LYS:NZ	2.33	0.61
2:G:497:TYR:HB3	2:G:500:ALA:HB2	1.82	0.61
2:B:1653:LEU:HB3	2:B:1660:GLN:HB2	1.81	0.61
2:E:1079:LYS:NZ	2:E:1107:PRO:O	2.33	0.61
2:G:331:VAL:HG12	2:G:333:GLY:H	1.64	0.61
1:F:87:HIS:H	1:F:91:ILE:HB	1.65	0.61
2:B:1079:LYS:NZ	2:B:1107:PRO:O	2.33	0.61
2:B:111:HIS:HD2	2:B:114:SER:H	1.47	0.61
2:E:497:TYR:HB3	2:E:500:ALA:HB2	1.82	0.61
2:G:4063:ASP:OD2	2:G:4067:LYS:NZ	2.33	0.61
2:B:132:ALA:HA	2:B:194:SER:HB2	1.83	0.61
2:G:1079:LYS:NZ	2:G:1107:PRO:O	2.33	0.61
2:B:4198:SER:HB3	2:B:4201:ASN:HB2	1.83	0.61
2:E:331:VAL:HG12	2:E:333:GLY:H	1.64	0.61
1:A:87:HIS:H	1:A:91:ILE:HB	1.66	0.61
2:E:132:ALA:HA	2:E:194:SER:HB2	1.83	0.61
1:H:87:HIS:H	1:H:91:ILE:HB	1.66	0.61
2:B:4957:LYS:HZ3	2:B:4957:LYS:HB2	1.65	0.61
2:E:4198:SER:HB3	2:E:4201:ASN:HB2	1.83	0.61
2:G:111:HIS:HD2	2:G:114:SER:H	1.47	0.61
2:E:465:GLN:HG3	2:E:3710:LEU:HB3	1.83	0.60
2:G:465:GLN:HG3	2:G:3710:LEU:HB3	1.83	0.60
2:E:683:ARG:HB2	2:E:782:SER:HB3	1.83	0.60
2:G:4198:SER:HB3	2:G:4201:ASN:HB2	1.83	0.60
2:I:111:HIS:HD2	2:I:114:SER:H	1.47	0.60
2:I:1653:LEU:HB3	2:I:1660:GLN:HB2	1.81	0.60
1:J:87:HIS:H	1:J:91:ILE:HB	1.66	0.60
2:G:3937:TYR:O	2:G:4002:LYS:NZ	2.35	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:132:ALA:HA	2:I:194:SER:HB2	1.83	0.60
2:I:3937:TYR:O	2:I:4002:LYS:NZ	2.35	0.60
2:B:683:ARG:HB2	2:B:782:SER:HB3	1.83	0.60
2:E:1653:LEU:HB3	2:E:1660:GLN:HB2	1.81	0.60
2:E:3937:TYR:O	2:E:4002:LYS:NZ	2.35	0.60
2:E:4957:LYS:HB2	2:E:4957:LYS:HZ3	1.66	0.60
2:G:132:ALA:HA	2:G:194:SER:HB2	1.83	0.60
2:I:2755:ILE:HD13	2:I:2810:LYS:HG2	1.83	0.60
2:I:469:ARG:HH21	2:I:3712:GLU:HB3	1.67	0.60
2:I:4198:SER:HB3	2:I:4201:ASN:HB2	1.83	0.60
2:B:3937:TYR:O	2:B:4002:LYS:NZ	2.35	0.60
2:G:210:GLU:HG3	2:G:337:PRO:HG3	1.84	0.60
2:G:469:ARG:HH21	2:G:3712:GLU:HB3	1.67	0.60
2:I:210:GLU:HG3	2:I:337:PRO:HG3	1.84	0.60
2:E:210:GLU:HG3	2:E:337:PRO:HG3	1.84	0.60
2:G:463:GLU:OE2	2:G:467:LYS:NZ	2.35	0.60
2:E:463:GLU:OE2	2:E:467:LYS:NZ	2.35	0.60
2:G:683:ARG:HB2	2:G:782:SER:HB3	1.83	0.60
2:I:4674:GLU:HB3	2:I:4715:TYR:HB2	1.84	0.60
2:B:2755:ILE:HD13	2:B:2810:LYS:HG2	1.83	0.59
2:E:2755:ILE:HD13	2:E:2810:LYS:HG2	1.83	0.59
2:I:463:GLU:OE2	2:I:467:LYS:NZ	2.35	0.59
2:G:4674:GLU:HB3	2:G:4715:TYR:HB2	1.84	0.59
2:I:683:ARG:NH1	2:I:707:VAL:O	2.36	0.59
2:B:210:GLU:HG3	2:B:337:PRO:HG3	1.84	0.59
2:B:465:GLN:HG3	2:B:3710:LEU:HB3	1.83	0.59
2:I:281:ARG:NH2	2:I:309:THR:OG1	2.36	0.59
2:I:465:GLN:HG3	2:I:3710:LEU:HB3	1.83	0.59
2:B:1671:ARG:NH2	2:B:1710:GLY:O	2.36	0.59
2:B:469:ARG:HH21	2:B:3712:GLU:HB3	1.67	0.59
2:B:4674:GLU:HB3	2:B:4715:TYR:HB2	1.84	0.59
2:E:281:ARG:NH2	2:E:309:THR:OG1	2.36	0.59
2:E:1671:ARG:NH2	2:E:1710:GLY:O	2.36	0.59
2:I:1671:ARG:NH2	2:I:1710:GLY:O	2.36	0.59
2:E:1685:LEU:HA	2:E:1688:HIS:HD2	1.68	0.59
2:G:1685:LEU:HA	2:G:1688:HIS:HD2	1.68	0.59
2:G:2755:ILE:HD13	2:G:2810:LYS:HG2	1.83	0.59
2:E:315:CYS:SG	2:E:316:PHE:N	2.77	0.58
2:E:469:ARG:HH21	2:E:3712:GLU:HB3	1.67	0.58
2:E:683:ARG:NH1	2:E:707:VAL:O	2.36	0.58
2:B:315:CYS:SG	2:B:316:PHE:N	2.77	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:463:GLU:OE2	2:B:467:LYS:NZ	2.35	0.58
2:I:683:ARG:HB2	2:I:782:SER:HB3	1.83	0.58
2:B:683:ARG:NH1	2:B:707:VAL:O	2.36	0.58
2:E:1152:MET:HB2	2:E:1161:ILE:HB	1.85	0.58
2:B:4860:ARG:HD2	2:E:4582:VAL:HG11	1.84	0.58
2:E:4674:GLU:HB3	2:E:4715:TYR:HB2	1.84	0.58
2:G:1671:ARG:NH2	2:G:1710:GLY:O	2.36	0.58
2:G:315:CYS:SG	2:G:316:PHE:N	2.77	0.58
2:I:315:CYS:SG	2:I:316:PHE:N	2.77	0.58
2:I:1092:PHE:HB3	2:I:1149:VAL:HB	1.85	0.58
2:I:1152:MET:HB2	2:I:1161:ILE:HB	1.85	0.58
2:B:3889:GLN:OE1	2:B:3960:GLN:NE2	2.37	0.58
2:B:3955:MET:HG3	2:B:4019:LEU:HD22	1.85	0.58
2:B:1247:PRO:HA	2:B:1598:GLN:HA	1.86	0.58
2:E:4983:HIS:H	2:E:4983:HIS:CD2	2.22	0.58
2:I:2911:LEU:HB2	2:I:2916:LYS:HE3	1.86	0.58
2:I:3955:MET:HG3	2:I:4019:LEU:HD22	1.85	0.58
2:I:3889:GLN:OE1	2:I:3960:GLN:NE2	2.37	0.58
2:B:1109:LEU:HA	2:B:1120:LEU:HD21	1.86	0.58
2:B:609:CYS:SG	2:B:610:ASN:N	2.77	0.58
2:E:2022:PRO:O	2:E:2028:ARG:NH2	2.37	0.58
2:E:3889:GLN:OE1	2:E:3960:GLN:NE2	2.37	0.58
2:G:683:ARG:NH1	2:G:707:VAL:O	2.36	0.58
2:I:119:SER:H	2:I:137:LEU:HA	1.69	0.58
2:B:1092:PHE:HB3	2:B:1149:VAL:HB	1.85	0.58
2:G:1109:LEU:HA	2:G:1120:LEU:HD21	1.86	0.58
2:B:2911:LEU:HB2	2:B:2916:LYS:HE3	1.86	0.57
2:G:3955:MET:HG3	2:G:4019:LEU:HD22	1.85	0.57
2:G:717:ASP:OD1	2:G:720:HIS:ND1	2.37	0.57
2:E:2911:LEU:HB2	2:E:2916:LYS:HE3	1.86	0.57
2:G:1865:MET:SD	2:G:1865:MET:N	2.77	0.57
2:G:3889:GLN:OE1	2:G:3960:GLN:NE2	2.37	0.57
2:I:2257:LEU:HD11	2:I:2276:ALA:HB2	1.86	0.57
2:B:119:SER:H	2:B:137:LEU:HA	1.69	0.57
2:E:1109:LEU:HA	2:E:1120:LEU:HD21	1.86	0.57
2:E:1865:MET:SD	2:E:1865:MET:N	2.77	0.57
2:G:2022:PRO:O	2:G:2028:ARG:NH2	2.37	0.57
2:G:281:ARG:NH2	2:G:309:THR:OG1	2.36	0.57
2:I:1685:LEU:HA	2:I:1688:HIS:HD2	1.68	0.57
2:B:717:ASP:OD1	2:B:720:HIS:ND1	2.37	0.57
2:E:3955:MET:HG3	2:E:4019:LEU:HD22	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:4983:HIS:N	2:E:4983:HIS:CD2	2.73	0.57
2:G:2911:LEU:HB2	2:G:2916:LYS:HE3	1.86	0.57
2:I:23:GLN:HB3	2:I:201:ASN:HB2	1.86	0.57
2:I:4904:PRO:HB3	2:I:4913:ARG:HD3	1.86	0.57
2:I:717:ASP:OD1	2:I:720:HIS:ND1	2.37	0.57
2:B:1152:MET:HB2	2:B:1161:ILE:HB	1.85	0.57
2:B:1685:LEU:HA	2:B:1688:HIS:HD2	1.68	0.57
2:B:4904:PRO:HB3	2:B:4913:ARG:HD3	1.86	0.57
2:E:1247:PRO:HA	2:E:1598:GLN:HA	1.86	0.57
2:B:2257:LEU:HD11	2:B:2276:ALA:HB2	1.87	0.57
2:B:281:ARG:NH2	2:B:309:THR:OG1	2.36	0.57
2:E:1092:PHE:HB3	2:E:1149:VAL:HB	1.85	0.57
2:G:1152:MET:HB2	2:G:1161:ILE:HB	1.85	0.57
2:G:609:CYS:SG	2:G:610:ASN:N	2.77	0.57
2:I:4978:HIS:CE1	2:I:5027:CYS:SG	2.98	0.57
2:B:4582:VAL:HG11	2:I:4860:ARG:HD2	1.86	0.57
2:E:609:CYS:SG	2:E:610:ASN:N	2.77	0.57
2:B:1865:MET:SD	2:B:1865:MET:N	2.77	0.57
2:E:4978:HIS:CE1	2:E:5027:CYS:SG	2.98	0.57
2:G:4957:LYS:NZ	2:G:4957:LYS:HB2	2.20	0.57
2:I:1865:MET:SD	2:I:1865:MET:N	2.77	0.57
2:I:3973:CYS:SG	2:I:3976:ASN:ND2	2.78	0.57
2:G:1092:PHE:HB3	2:G:1149:VAL:HB	1.85	0.57
2:G:1247:PRO:HA	2:G:1598:GLN:HA	1.86	0.57
2:B:2022:PRO:O	2:B:2028:ARG:NH2	2.37	0.57
2:E:4904:PRO:HB3	2:E:4913:ARG:HD3	1.86	0.56
2:E:4957:LYS:HB2	2:E:4957:LYS:NZ	2.20	0.56
2:I:4582:VAL:HG11	2:G:4860:ARG:HD2	1.87	0.56
2:G:4983:HIS:N	2:G:4983:HIS:CD2	2.73	0.56
2:I:110:ARG:HH21	2:I:115:ARG:HB3	1.70	0.56
2:I:1109:LEU:HA	2:I:1120:LEU:HD21	1.86	0.56
2:E:4180:ARG:HH22	2:E:4981:GLU:HA	1.71	0.56
2:G:23:GLN:HB3	2:G:201:ASN:HB2	1.86	0.56
2:G:4180:ARG:HH22	2:G:4981:GLU:HA	1.71	0.56
2:I:2022:PRO:O	2:I:2028:ARG:NH2	2.37	0.56
2:I:609:CYS:SG	2:I:610:ASN:N	2.77	0.56
2:E:3973:CYS:SG	2:E:3976:ASN:ND2	2.78	0.56
1:F:55:VAL:HA	2:E:1784:ALA:HA	1.87	0.56
2:G:2748:PRO:HD2	2:G:2751:LEU:HD12	1.88	0.56
2:G:4904:PRO:HB3	2:G:4913:ARG:HD3	1.85	0.56
2:G:4978:HIS:CE1	2:G:5027:CYS:SG	2.98	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:110:ARG:HH21	2:B:115:ARG:HB3	1.70	0.56
2:E:23:GLN:HB3	2:E:201:ASN:HB2	1.86	0.56
2:E:717:ASP:OD1	2:E:720:HIS:ND1	2.37	0.56
2:G:119:SER:H	2:G:137:LEU:HA	1.69	0.56
2:G:2257:LEU:HD11	2:G:2276:ALA:HB2	1.86	0.56
2:G:3973:CYS:SG	2:G:3976:ASN:ND2	2.78	0.56
2:G:4582:VAL:HG11	2:E:4860:ARG:HD2	1.87	0.56
2:I:1247:PRO:HA	2:I:1598:GLN:HA	1.86	0.56
2:B:3973:CYS:SG	2:B:3976:ASN:ND2	2.78	0.56
2:E:119:SER:H	2:E:137:LEU:HA	1.69	0.56
2:G:4983:HIS:H	2:G:4983:HIS:CD2	2.22	0.56
2:I:4957:LYS:HB2	2:I:4957:LYS:NZ	2.20	0.56
2:B:1721:GLU:OE2	2:B:1725:ARG:NH2	2.39	0.56
2:B:4180:ARG:HH22	2:B:4981:GLU:HA	1.70	0.56
2:B:952:LYS:HB3	2:B:968:ALA:HB1	1.88	0.56
2:E:110:ARG:HH21	2:E:115:ARG:HB3	1.70	0.56
2:E:1721:GLU:OE2	2:E:1725:ARG:NH2	2.39	0.56
2:E:952:LYS:HB3	2:E:968:ALA:HB1	1.88	0.56
2:G:1721:GLU:OE2	2:G:1725:ARG:NH2	2.39	0.56
2:I:1721:GLU:OE2	2:I:1725:ARG:NH2	2.39	0.56
2:B:4978:HIS:CE1	2:B:5027:CYS:SG	2.98	0.56
2:I:2748:PRO:HD2	2:I:2751:LEU:HD12	1.87	0.56
2:B:23:GLN:HB3	2:B:201:ASN:HB2	1.86	0.56
2:E:2257:LEU:HD11	2:E:2276:ALA:HB2	1.87	0.56
2:G:4968:PHE:HZ	2:G:4978:HIS:HE1	1.54	0.56
2:I:4983:HIS:H	2:I:4983:HIS:CD2	2.22	0.56
2:G:110:ARG:HH21	2:G:115:ARG:HB3	1.71	0.56
2:I:4180:ARG:HH22	2:I:4981:GLU:HA	1.70	0.56
2:B:3932:ASP:HA	2:B:3935:TRP:HD1	1.71	0.56
2:E:2479:LEU:O	2:E:2487:UNK:N	2.39	0.56
2:E:2748:PRO:HD2	2:E:2751:LEU:HD12	1.88	0.56
2:E:1764:GLY:HA3	2:E:1859:VAL:HG11	1.88	0.55
2:E:3932:ASP:HA	2:E:3935:TRP:HD1	1.71	0.55
2:G:3762:ARG:O	2:G:3766:GLN:NE2	2.38	0.55
2:I:3910:THR:HG23	2:I:3911:THR:HG23	1.89	0.55
2:I:4968:PHE:HZ	2:I:4978:HIS:HE1	1.54	0.55
2:B:4983:HIS:H	2:B:4983:HIS:CD2	2.22	0.55
2:G:952:LYS:HB3	2:G:968:ALA:HB1	1.88	0.55
2:G:2770:LYS:HB3	2:G:2775:TRP:HB2	1.89	0.55
2:G:3932:ASP:HA	2:G:3935:TRP:HD1	1.71	0.55
2:B:3910:THR:HG23	2:B:3911:THR:HG23	1.89	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:1764:GLY:HA3	2:G:1859:VAL:HG11	1.88	0.55
2:I:2770:LYS:HB3	2:I:2775:TRP:HB2	1.89	0.55
2:I:4983:HIS:N	2:I:4983:HIS:CD2	2.73	0.55
2:B:4957:LYS:NZ	2:B:4957:LYS:HB2	2.20	0.55
2:B:606:LEU:O	2:B:617:ASN:ND2	2.40	0.55
2:E:1243:PRO:HB2	2:E:1600:LEU:HD22	1.89	0.55
2:G:1243:PRO:HB2	2:G:1600:LEU:HD22	1.89	0.55
2:B:2479:LEU:O	2:B:2487:UNK:N	2.39	0.55
2:E:2002:PRO:HA	2:E:2005:GLN:HB3	1.89	0.55
2:G:1808:ARG:NH1	2:G:1853:ILE:O	2.38	0.55
2:E:635:THR:HB	2:E:1639:LEU:HD23	1.89	0.55
2:G:4184:MET:HE1	2:G:4188:ARG:HE	1.72	0.55
2:B:2748:PRO:HD2	2:B:2751:LEU:HD12	1.88	0.55
2:B:1519:UNK:HA	2:B:1526:UNK:HA	1.89	0.54
2:B:4983:HIS:N	2:B:4983:HIS:CD2	2.73	0.54
2:I:952:LYS:HB3	2:I:968:ALA:HB1	1.88	0.54
2:G:664:PHE:HB2	2:G:746:CYS:HB2	1.89	0.54
2:I:1667:LEU:O	2:I:1671:ARG:NH1	2.41	0.54
2:I:1764:GLY:HA3	2:I:1859:VAL:HG11	1.88	0.54
2:I:3932:ASP:HA	2:I:3935:TRP:HD1	1.71	0.54
2:B:664:PHE:HB2	2:B:746:CYS:HB2	1.89	0.54
2:G:19:GLU:HB2	2:G:206:CYS:HB3	1.90	0.54
2:I:2479:LEU:O	2:I:2487:UNK:N	2.39	0.54
2:B:19:GLU:HB2	2:B:206:CYS:HB3	1.89	0.54
2:B:2770:LYS:HB3	2:B:2775:TRP:HB2	1.89	0.54
2:B:635:THR:HB	2:B:1639:LEU:HD23	1.89	0.54
2:E:1519:UNK:HA	2:E:1526:UNK:HA	1.89	0.54
2:E:19:GLU:HB2	2:E:206:CYS:HB3	1.89	0.54
2:G:2479:LEU:O	2:G:2487:UNK:N	2.39	0.54
2:B:1667:LEU:O	2:B:1671:ARG:NH1	2.41	0.54
2:E:2298:VAL:HG21	2:E:2335:LEU:HD21	1.90	0.54
2:E:606:LEU:O	2:E:617:ASN:ND2	2.40	0.54
2:G:606:LEU:O	2:G:617:ASN:ND2	2.40	0.54
2:I:19:GLU:HB2	2:I:206:CYS:HB3	1.89	0.54
2:I:4968:PHE:CE2	2:I:4978:HIS:CE1	2.96	0.54
2:B:1764:GLY:HA3	2:B:1859:VAL:HG11	1.88	0.54
2:B:2002:PRO:HA	2:B:2005:GLN:HB3	1.89	0.54
2:E:3897:ASN:O	2:E:3901:ASN:ND2	2.41	0.54
2:G:1667:LEU:O	2:G:1671:ARG:NH1	2.41	0.54
2:G:2002:PRO:HA	2:G:2005:GLN:HB3	1.89	0.54
2:G:3910:THR:HG23	2:G:3911:THR:HG23	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2002:PRO:HA	2:I:2005:GLN:HB3	1.89	0.54
2:I:3897:ASN:O	2:I:3901:ASN:ND2	2.41	0.54
2:B:2266:GLY:O	2:B:2330:ARG:NH2	2.41	0.54
2:E:1111:PRO:HD3	2:E:1605:TRP:HE1	1.73	0.54
2:I:2266:GLY:O	2:I:2330:ARG:NH2	2.41	0.54
2:I:3733:CYS:HB2	2:I:3803:SER:HB3	1.90	0.54
2:I:606:LEU:O	2:I:617:ASN:ND2	2.40	0.54
2:B:1808:ARG:NH1	2:B:1853:ILE:O	2.38	0.54
2:E:3910:THR:HG23	2:E:3911:THR:HG23	1.89	0.54
2:I:4059:LEU:O	2:I:4063:ASP:N	2.36	0.54
2:I:4957:LYS:HZ3	2:I:4957:LYS:HB2	1.72	0.54
2:E:2770:LYS:HB3	2:E:2775:TRP:HB2	1.89	0.54
2:E:3733:CYS:HB2	2:E:3803:SER:HB3	1.90	0.54
2:E:3762:ARG:O	2:E:3766:GLN:NE2	2.38	0.54
2:E:4968:PHE:CE2	2:E:4978:HIS:CE1	2.96	0.54
2:G:989:ALA:O	2:G:1035:ASN:ND2	2.41	0.54
2:B:1243:PRO:HB2	2:B:1600:LEU:HD22	1.89	0.53
2:E:2739:PRO:HB3	2:E:2884:ASN:HB3	1.91	0.53
2:I:1243:PRO:HB2	2:I:1600:LEU:HD22	1.89	0.53
2:B:3897:ASN:O	2:B:3901:ASN:ND2	2.41	0.53
2:E:3733:CYS:HA	2:E:3766:GLN:HG2	1.90	0.53
1:A:74:LEU:HB2	1:A:99:PHE:HB2	1.90	0.53
2:B:2739:PRO:HB3	2:B:2884:ASN:HB3	1.91	0.53
2:E:664:PHE:HB2	2:E:746:CYS:HB2	1.89	0.53
2:G:635:THR:HB	2:G:1639:LEU:HD23	1.89	0.53
2:G:3897:ASN:O	2:G:3901:ASN:ND2	2.41	0.53
1:H:74:LEU:HB2	1:H:99:PHE:HB2	1.90	0.53
2:I:2739:PRO:HB3	2:I:2884:ASN:HB3	1.90	0.53
1:J:55:VAL:HA	2:I:1784:ALA:HA	1.90	0.53
2:B:4137:ARG:NH1	2:B:4173:TYR:OH	2.42	0.53
2:E:4184:MET:HE1	2:E:4188:ARG:HE	1.74	0.53
2:G:3733:CYS:HA	2:G:3766:GLN:HG2	1.90	0.53
2:I:2298:VAL:HG21	2:I:2335:LEU:HD21	1.90	0.53
2:B:1111:PRO:HD3	2:B:1605:TRP:HE1	1.73	0.53
2:G:1111:PRO:HD3	2:G:1605:TRP:HE1	1.73	0.53
2:G:2298:VAL:HG21	2:G:2335:LEU:HD21	1.90	0.53
2:I:2737:PRO:O	2:I:2888:ARG:NH2	2.42	0.53
1:J:6:THR:HA	1:J:72:ALA:HA	1.91	0.53
2:B:989:ALA:O	2:B:1035:ASN:ND2	2.41	0.53
2:B:2298:VAL:HG21	2:B:2335:LEU:HD21	1.90	0.53
2:E:1667:LEU:O	2:E:1671:ARG:NH1	2.41	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:2266:GLY:O	2:E:2330:ARG:NH2	2.41	0.53
2:E:2737:PRO:O	2:E:2888:ARG:NH2	2.42	0.53
1:F:6:THR:HA	1:F:72:ALA:HA	1.91	0.53
2:G:2739:PRO:HB3	2:G:2884:ASN:HB3	1.91	0.53
2:G:3733:CYS:HB2	2:G:3803:SER:HB3	1.90	0.53
2:I:1519:UNK:HA	2:I:1526:UNK:HA	1.89	0.53
2:I:635:THR:HB	2:I:1639:LEU:HD23	1.89	0.53
2:B:4968:PHE:HZ	2:B:4978:HIS:HE1	1.54	0.53
2:G:41:GLY:O	2:G:45:ARG:NH1	2.42	0.53
1:H:6:THR:HA	1:H:72:ALA:HA	1.91	0.53
2:I:3830:GLN:HA	2:I:3833:GLN:HG2	1.91	0.53
2:I:4184:MET:HE1	2:I:4188:ARG:HE	1.73	0.53
1:A:6:THR:HA	1:A:72:ALA:HA	1.91	0.53
2:B:3830:GLN:HA	2:B:3833:GLN:HG2	1.91	0.53
2:B:4968:PHE:CE2	2:B:4978:HIS:CE1	2.96	0.53
1:F:74:LEU:HB2	1:F:99:PHE:HB2	1.90	0.53
2:G:2737:PRO:O	2:G:2888:ARG:NH2	2.42	0.53
2:I:1111:PRO:HD3	2:I:1605:TRP:HE1	1.73	0.53
2:I:266:ARG:NH2	2:I:272:SER:OG	2.42	0.53
2:B:2042:CYS:SG	2:B:2043:GLY:N	2.82	0.53
2:I:4786:ASP:OD2	2:I:4789:PHE:N	2.42	0.53
1:A:55:VAL:HA	2:B:1784:ALA:HA	1.90	0.53
2:B:3733:CYS:HB2	2:B:3803:SER:HB3	1.90	0.53
2:B:4681:LEU:HD21	2:B:4687:TYR:HD2	1.74	0.53
2:E:718:GLY:HA3	2:E:737:LEU:HA	1.91	0.53
2:G:1519:UNK:HA	2:G:1526:UNK:HA	1.90	0.53
2:G:173:SER:HB3	2:G:178:ARG:H	1.74	0.53
2:I:173:SER:HB3	2:I:178:ARG:H	1.74	0.53
2:I:647:ASN:ND2	2:I:820:ARG:O	2.42	0.53
2:I:989:ALA:O	2:I:1035:ASN:ND2	2.41	0.53
2:B:4184:MET:HE1	2:B:4188:ARG:HE	1.73	0.52
2:E:989:ALA:O	2:E:1035:ASN:ND2	2.41	0.52
2:G:2266:GLY:O	2:G:2330:ARG:NH2	2.41	0.52
2:E:4137:ARG:NH1	2:E:4173:TYR:OH	2.42	0.52
2:E:41:GLY:O	2:E:45:ARG:NH1	2.42	0.52
2:G:4968:PHE:CE2	2:G:4978:HIS:CE1	2.96	0.52
2:G:718:GLY:HA3	2:G:737:LEU:HA	1.91	0.52
2:I:3734:HIS:O	2:I:3738:GLY:N	2.43	0.52
2:I:4137:ARG:NH1	2:I:4173:TYR:OH	2.42	0.52
2:I:664:PHE:HB2	2:I:746:CYS:HB2	1.89	0.52
2:B:2737:PRO:O	2:B:2888:ARG:NH2	2.42	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:3734:HIS:O	2:E:3738:GLY:N	2.43	0.52
2:E:4231:MET:HE3	2:E:4960:ILE:HG23	1.91	0.52
2:G:3830:GLN:HA	2:G:3833:GLN:HG2	1.91	0.52
2:E:1166:GLY:HA3	2:E:1216:ILE:HD13	1.92	0.52
2:E:3830:GLN:HA	2:E:3833:GLN:HG2	1.91	0.52
2:G:1808:ARG:HD3	2:G:1853:ILE:HG22	1.91	0.52
1:J:74:LEU:HB2	1:J:99:PHE:HB2	1.90	0.52
2:B:173:SER:HB3	2:B:178:ARG:H	1.74	0.52
2:B:1808:ARG:HD3	2:B:1853:ILE:HG22	1.91	0.52
2:G:13:PHE:HA	2:G:164:ARG:HA	1.92	0.52
2:B:313:SER:HB3	2:B:351:VAL:HB	1.92	0.52
2:G:1166:GLY:HA3	2:G:1216:ILE:HD13	1.92	0.52
2:B:4786:ASP:OD2	2:B:4789:PHE:N	2.42	0.52
2:E:1649:ASP:HB3	2:E:1652:GLU:HG2	1.92	0.52
2:E:4232:GLU:OE2	2:E:5017:ARG:NH1	2.39	0.52
2:G:4137:ARG:NH1	2:G:4173:TYR:OH	2.42	0.52
2:B:266:ARG:NH2	2:B:272:SER:OG	2.42	0.52
2:E:13:PHE:HA	2:E:164:ARG:HA	1.92	0.52
2:G:2042:CYS:SG	2:G:2043:GLY:N	2.82	0.52
2:G:266:ARG:NH2	2:G:272:SER:OG	2.42	0.52
2:I:3733:CYS:HA	2:I:3766:GLN:HG2	1.90	0.52
2:I:4681:LEU:HD21	2:I:4687:TYR:HD2	1.74	0.52
2:I:718:GLY:HA3	2:I:737:LEU:HA	1.91	0.52
2:B:1166:GLY:HA3	2:B:1216:ILE:HD13	1.92	0.52
2:B:3733:CYS:HA	2:B:3766:GLN:HG2	1.90	0.52
2:B:718:GLY:HA3	2:B:737:LEU:HA	1.91	0.52
2:E:4681:LEU:HD21	2:E:4687:TYR:HD2	1.74	0.52
2:G:3734:HIS:O	2:G:3738:GLY:N	2.43	0.52
2:I:4232:GLU:OE2	2:I:5017:ARG:NH1	2.39	0.52
2:E:173:SER:HB3	2:E:178:ARG:H	1.74	0.52
2:B:41:GLY:O	2:B:45:ARG:NH1	2.42	0.51
2:E:266:ARG:NH2	2:E:272:SER:OG	2.42	0.51
2:G:111:HIS:CD2	2:G:114:SER:H	2.26	0.51
2:I:13:PHE:HA	2:I:164:ARG:HA	1.92	0.51
2:I:4833:ASN:ND2	2:I:4935:LEU:O	2.44	0.51
2:I:4958:CYS:SG	2:I:4961:CYS:N	2.84	0.51
1:A:82:TYR:O	1:A:86:GLY:N	2.44	0.51
2:E:4833:ASN:ND2	2:E:4935:LEU:O	2.44	0.51
2:E:671:VAL:HG22	2:E:740:PRO:HG3	1.92	0.51
2:G:264:PRO:HG2	2:G:270:SER:HB2	1.92	0.51
2:I:1808:ARG:HD3	2:I:1853:ILE:HG22	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:13:PHE:HA	2:B:164:ARG:HA	1.92	0.51
2:B:1649:ASP:HB3	2:B:1652:GLU:HG2	1.92	0.51
2:E:1808:ARG:HD3	2:E:1853:ILE:HG22	1.91	0.51
2:E:264:PRO:HG2	2:E:270:SER:HB2	1.92	0.51
2:E:4968:PHE:HZ	2:E:4978:HIS:HE1	1.54	0.51
2:G:313:SER:HB3	2:G:351:VAL:HB	1.92	0.51
2:G:4232:GLU:OE2	2:G:5017:ARG:NH1	2.39	0.51
2:G:671:VAL:HG22	2:G:740:PRO:HG3	1.92	0.51
2:I:1166:GLY:HA3	2:I:1216:ILE:HD13	1.92	0.51
2:I:41:GLY:O	2:I:45:ARG:NH1	2.42	0.51
2:E:111:HIS:CD2	2:E:114:SER:H	2.26	0.51
2:G:1649:ASP:HB3	2:G:1652:GLU:HG2	1.92	0.51
2:G:4681:LEU:HD21	2:G:4687:TYR:HD2	1.74	0.51
2:I:111:HIS:CD2	2:I:114:SER:H	2.26	0.51
2:E:2042:CYS:SG	2:E:2043:GLY:N	2.82	0.51
2:G:4786:ASP:OD2	2:G:4789:PHE:N	2.42	0.51
2:G:647:ASN:ND2	2:G:820:ARG:O	2.42	0.51
2:I:649:PHE:HB3	2:I:776:LEU:HD13	1.93	0.51
2:I:1808:ARG:NH1	2:I:1853:ILE:O	2.38	0.51
2:B:264:PRO:HG2	2:B:270:SER:HB2	1.92	0.51
2:B:4860:ARG:HG3	2:B:4876:CYS:HB3	1.93	0.51
2:B:4833:ASN:ND2	2:B:4935:LEU:O	2.44	0.51
1:F:82:TYR:O	1:F:86:GLY:N	2.44	0.51
2:I:1649:ASP:HB3	2:I:1652:GLU:HG2	1.92	0.51
2:I:4860:ARG:HG3	2:I:4876:CYS:HB3	1.93	0.51
2:G:4860:ARG:HG3	2:G:4876:CYS:HB3	1.93	0.51
2:G:4958:CYS:SG	2:G:4961:CYS:N	2.84	0.51
2:I:264:PRO:HG2	2:I:270:SER:HB2	1.92	0.51
2:I:4673:ARG:HH22	2:I:4698:LYS:HB2	1.76	0.51
2:B:4958:CYS:SG	2:B:4961:CYS:N	2.84	0.51
2:B:671:VAL:HG22	2:B:740:PRO:HG3	1.92	0.51
2:E:2337:PHE:HA	2:E:2340:PHE:HB2	1.93	0.51
2:E:313:SER:HB3	2:E:351:VAL:HB	1.92	0.51
2:G:649:PHE:HB3	2:G:776:LEU:HD13	1.93	0.51
1:H:82:TYR:O	1:H:86:GLY:N	2.44	0.51
2:I:313:SER:HB3	2:I:351:VAL:HB	1.92	0.51
1:J:82:TYR:O	1:J:86:GLY:N	2.44	0.51
2:B:111:HIS:CD2	2:B:114:SER:H	2.26	0.50
2:E:4673:ARG:HH22	2:E:4698:LYS:HB2	1.76	0.50
2:G:4833:ASN:ND2	2:G:4935:LEU:O	2.44	0.50
2:B:3734:HIS:O	2:B:3738:GLY:N	2.43	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3980:LEU:HD22	2:B:3985:LEU:HD22	1.92	0.50
2:E:4958:CYS:SG	2:E:4961:CYS:N	2.84	0.50
2:I:68:THR:N	2:I:110:ARG:O	2.44	0.50
2:E:1725:ARG:HA	2:E:1728:ARG:HG2	1.94	0.50
2:E:3980:LEU:HD22	2:E:3985:LEU:HD22	1.92	0.50
2:E:68:THR:N	2:E:110:ARG:O	2.44	0.50
2:G:3980:LEU:HD22	2:G:3985:LEU:HD22	1.92	0.50
2:G:4230:LYS:HG3	2:G:4959:PHE:CE2	2.44	0.50
2:G:4673:ARG:HH22	2:G:4698:LYS:HB2	1.76	0.50
2:B:68:THR:N	2:B:110:ARG:O	2.44	0.50
2:B:2337:PHE:HA	2:B:2340:PHE:HB2	1.93	0.50
2:B:4232:GLU:OE2	2:B:5017:ARG:NH1	2.39	0.50
2:E:647:ASN:ND2	2:E:820:ARG:O	2.42	0.50
1:H:76:CYS:HB2	1:H:97:LEU:HB2	1.94	0.50
2:I:2042:CYS:SG	2:I:2043:GLY:N	2.82	0.50
2:I:4182:GLU:OE2	2:I:4983:HIS:CD2	2.57	0.50
1:F:42:ARG:HG2	2:E:1691:GLN:HG2	1.93	0.50
2:E:4786:ASP:OD2	2:E:4789:PHE:N	2.42	0.50
2:B:1725:ARG:HA	2:B:1728:ARG:HG2	1.94	0.50
2:B:2927:LEU:HD23	2:B:2930:LEU:HD12	1.94	0.50
2:E:4860:ARG:HG3	2:E:4876:CYS:HB3	1.93	0.50
2:I:2337:PHE:HA	2:I:2340:PHE:HB2	1.93	0.50
1:J:76:CYS:HB2	1:J:97:LEU:HB2	1.94	0.50
2:B:3751:VAL:O	2:B:3756:LYS:NZ	2.45	0.50
2:B:978:THR:HB	2:B:980:ALA:H	1.77	0.50
2:E:2927:LEU:HD23	2:E:2930:LEU:HD12	1.94	0.50
2:G:3805:LEU:HA	2:G:3809:ASN:HD22	1.77	0.50
2:I:978:THR:HB	2:I:980:ALA:H	1.77	0.50
2:B:649:PHE:HB3	2:B:776:LEU:HD13	1.93	0.50
2:E:3751:VAL:O	2:E:3756:LYS:NZ	2.45	0.50
2:I:3751:VAL:O	2:I:3756:LYS:NZ	2.45	0.50
2:I:4978:HIS:HE1	2:I:5027:CYS:SG	2.35	0.50
2:B:3959:LYS:O	2:B:3963:ASN:ND2	2.45	0.49
2:B:647:ASN:ND2	2:B:820:ARG:O	2.42	0.49
2:B:886:ARG:HB3	2:B:891:TRP:HB2	1.94	0.49
2:E:359:TYR:HA	2:E:376:ALA:HA	1.94	0.49
2:E:886:ARG:HB3	2:E:891:TRP:HB2	1.94	0.49
2:I:671:VAL:HG22	2:I:740:PRO:HG3	1.92	0.49
2:G:221:ARG:NH2	2:G:397:GLU:OE2	2.45	0.49
2:G:3941:ASP:HA	2:G:4002:LYS:HE3	1.94	0.49
2:I:3762:ARG:O	2:I:3766:GLN:NE2	2.38	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:3980:LEU:HD22	2:I:3985:LEU:HD22	1.92	0.49
2:B:3941:ASP:HA	2:B:4002:LYS:HE3	1.94	0.49
2:B:4978:HIS:HE1	2:B:5027:CYS:SG	2.35	0.49
2:E:3941:ASP:HA	2:E:4002:LYS:HE3	1.94	0.49
2:I:3959:LYS:O	2:I:3963:ASN:ND2	2.45	0.49
1:A:76:CYS:HB2	1:A:97:LEU:HB2	1.94	0.49
2:B:4962:GLY:HA3	2:B:5025:GLY:HA2	1.95	0.49
2:E:4978:HIS:HE1	2:E:5027:CYS:SG	2.35	0.49
2:E:649:PHE:HB3	2:E:776:LEU:HD13	1.93	0.49
2:G:68:THR:N	2:G:110:ARG:O	2.44	0.49
2:I:3805:LEU:HA	2:I:3809:ASN:HD22	1.77	0.49
2:E:1808:ARG:NH1	2:E:1853:ILE:O	2.38	0.49
2:E:221:ARG:NH2	2:E:397:GLU:OE2	2.45	0.49
2:E:4230:LYS:HG3	2:E:4959:PHE:CE2	2.44	0.49
2:E:4962:GLY:HA3	2:E:5025:GLY:HA2	1.95	0.49
2:G:359:TYR:HA	2:G:376:ALA:HA	1.94	0.49
2:B:284:HIS:HB3	2:B:287:THR:HB	1.94	0.49
2:B:4059:LEU:O	2:B:4063:ASP:N	2.36	0.49
2:E:395:GLN:HG3	2:E:397:GLU:H	1.78	0.49
2:G:2337:PHE:HA	2:G:2340:PHE:HB2	1.93	0.49
2:G:3959:LYS:O	2:G:3963:ASN:ND2	2.45	0.49
2:B:485:SER:O	2:B:489:ASN:N	2.40	0.49
2:E:838:HIS:HA	2:E:1201:HIS:HB3	1.95	0.49
1:F:76:CYS:HB2	1:F:97:LEU:HB2	1.94	0.49
2:G:3751:VAL:O	2:G:3756:LYS:NZ	2.45	0.49
2:G:395:GLN:HG3	2:G:397:GLU:H	1.78	0.49
2:I:4231:MET:CE	2:I:4960:ILE:HG23	2.43	0.49
2:B:4231:MET:CE	2:B:4960:ILE:HG23	2.43	0.49
2:B:838:HIS:HA	2:B:1201:HIS:HB3	1.95	0.49
2:E:1848:LEU:HD22	2:E:1853:ILE:HG13	1.95	0.49
2:E:776:LEU:HG	2:E:848:HIS:HA	1.95	0.49
2:G:1725:ARG:HA	2:G:1728:ARG:HG2	1.94	0.49
2:G:2927:LEU:HD23	2:G:2930:LEU:HD12	1.94	0.49
2:I:1725:ARG:HA	2:I:1728:ARG:HG2	1.94	0.49
2:I:2869:ARG:HA	2:I:2872:GLN:HB3	1.95	0.49
2:I:2927:LEU:HD23	2:I:2930:LEU:HD12	1.94	0.49
2:B:972:LEU:O	2:B:1044:ARG:NH2	2.46	0.49
2:B:4673:ARG:HH22	2:B:4698:LYS:HB2	1.76	0.49
2:E:3805:LEU:HA	2:E:3809:ASN:HD22	1.77	0.49
2:I:229:GLU:HA	2:I:249:GLY:HA2	1.95	0.49
2:I:972:LEU:O	2:I:1044:ARG:NH2	2.46	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:615:ARG:NH2	2:B:1677:GLY:O	2.43	0.49
2:G:229:GLU:HA	2:G:249:GLY:HA2	1.95	0.49
1:H:23:VAL:HG22	1:H:47:LYS:HG2	1.95	0.49
2:B:4230:LYS:HG3	2:B:4959:PHE:CE2	2.44	0.48
2:E:3959:LYS:O	2:E:3963:ASN:ND2	2.45	0.48
1:F:23:VAL:HG22	1:F:47:LYS:HG2	1.95	0.48
2:G:284:HIS:HB3	2:G:287:THR:HB	1.94	0.48
2:G:4978:HIS:HE1	2:G:5027:CYS:SG	2.35	0.48
2:I:4833:ASN:HD21	2:I:4935:LEU:HG	1.78	0.48
2:B:359:TYR:HA	2:B:376:ALA:HA	1.94	0.48
2:B:43:GLY:N	2:B:447:ASP:OD2	2.43	0.48
2:B:776:LEU:HG	2:B:848:HIS:HA	1.95	0.48
2:E:867:LEU:HB3	2:E:929:LEU:HD13	1.95	0.48
2:G:978:THR:HB	2:G:980:ALA:H	1.77	0.48
2:B:4230:LYS:HD2	2:B:4959:PHE:CE2	2.48	0.48
2:B:4833:ASN:HD21	2:B:4935:LEU:HG	1.78	0.48
2:E:4962:GLY:H	2:E:5025:GLY:N	2.12	0.48
2:G:2869:ARG:HA	2:G:2872:GLN:HB3	1.95	0.48
2:G:4577:LEU:HG	2:G:4580:TYR:HE2	1.79	0.48
2:I:3941:ASP:HA	2:I:4002:LYS:HE3	1.94	0.48
2:I:4962:GLY:H	2:I:5025:GLY:N	2.12	0.48
2:B:1516:UNK:N	2:B:1529:UNK:O	2.47	0.48
2:B:1743:ARG:O	2:B:1964:ARG:NH2	2.43	0.48
2:E:2869:ARG:HA	2:E:2872:GLN:HB3	1.95	0.48
2:E:4833:ASN:HD21	2:E:4935:LEU:HG	1.78	0.48
2:G:1743:ARG:O	2:G:1964:ARG:NH2	2.43	0.48
2:I:4962:GLY:HA3	2:I:5025:GLY:HA2	1.95	0.48
2:B:1105:ALA:HB1	2:B:1109:LEU:HD21	1.96	0.48
2:E:43:GLY:N	2:E:447:ASP:OD2	2.43	0.48
2:E:972:LEU:O	2:E:1044:ARG:NH2	2.46	0.48
2:E:978:THR:HB	2:E:980:ALA:H	1.77	0.48
2:G:1516:UNK:N	2:G:1529:UNK:O	2.47	0.48
2:G:4962:GLY:HA3	2:G:5025:GLY:HA2	1.95	0.48
2:G:867:LEU:HB3	2:G:929:LEU:HD13	1.95	0.48
2:I:1660:GLN:O	2:I:1664:SER:N	2.47	0.48
2:I:1848:LEU:HD22	2:I:1853:ILE:HG13	1.94	0.48
2:I:359:TYR:HA	2:I:376:ALA:HA	1.94	0.48
2:I:4577:LEU:HG	2:I:4580:TYR:HE2	1.79	0.48
2:B:3762:ARG:O	2:B:3766:GLN:NE2	2.38	0.48
2:B:3805:LEU:HA	2:B:3809:ASN:HD22	1.77	0.48
2:E:1105:ALA:HB1	2:E:1109:LEU:HD21	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:4233:LEU:HA	2:E:4236:SER:HB3	1.95	0.48
2:G:972:LEU:O	2:G:1044:ARG:NH2	2.46	0.48
2:G:1848:LEU:HD22	2:G:1853:ILE:HG13	1.94	0.48
2:G:4231:MET:CE	2:G:4960:ILE:HG23	2.43	0.48
2:G:4962:GLY:H	2:G:5025:GLY:N	2.12	0.48
2:G:886:ARG:HB3	2:G:891:TRP:HB2	1.94	0.48
2:I:886:ARG:HB3	2:I:891:TRP:HB2	1.94	0.48
2:E:1516:UNK:N	2:E:1529:UNK:O	2.47	0.48
2:E:2285:GLU:HG3	2:E:2286:LEU:HG	1.96	0.48
2:E:284:HIS:HB3	2:E:287:THR:HB	1.94	0.48
2:E:4059:LEU:O	2:E:4063:ASP:N	2.36	0.48
2:G:838:HIS:HA	2:G:1201:HIS:HB3	1.95	0.48
2:G:4059:LEU:O	2:G:4063:ASP:N	2.36	0.48
2:G:4833:ASN:HD21	2:G:4935:LEU:HG	1.78	0.48
2:I:615:ARG:NH2	2:I:1677:GLY:O	2.43	0.48
2:I:776:LEU:HG	2:I:848:HIS:HA	1.95	0.48
2:I:838:HIS:HA	2:I:1201:HIS:HB3	1.95	0.48
1:J:23:VAL:HG22	1:J:47:LYS:HG2	1.95	0.48
2:E:4577:LEU:HG	2:E:4580:TYR:HE2	1.79	0.48
2:E:580:GLU:HG2	2:E:583:ILE:HD11	1.96	0.48
2:I:1516:UNK:N	2:I:1529:UNK:O	2.47	0.48
2:I:284:HIS:HB3	2:I:287:THR:HB	1.94	0.48
2:I:719:LEU:HD22	2:I:735:GLN:HG2	1.95	0.48
1:A:42:ARG:HG2	2:B:1691:GLN:HG2	1.94	0.48
2:B:395:GLN:HG3	2:B:397:GLU:H	1.78	0.48
2:B:867:LEU:HB3	2:B:929:LEU:HD13	1.95	0.48
2:E:3900:GLN:NE2	2:E:3967:GLU:O	2.47	0.48
2:E:4231:MET:CE	2:E:4960:ILE:HG23	2.43	0.48
2:E:4563:ARG:NH1	2:E:4815:ASP:OD1	2.47	0.48
2:E:719:LEU:HD22	2:E:735:GLN:HG2	1.95	0.48
2:I:395:GLN:HG3	2:I:397:GLU:H	1.78	0.48
2:B:2869:ARG:HA	2:B:2872:GLN:HB3	1.95	0.48
2:B:4577:LEU:HG	2:B:4580:TYR:HE2	1.79	0.48
2:G:2285:GLU:HG3	2:G:2286:LEU:HG	1.96	0.48
1:J:57:LYS:HB2	1:J:80:VAL:HB	1.96	0.48
2:B:2285:GLU:HG3	2:B:2286:LEU:HG	1.96	0.47
2:E:4230:LYS:HD2	2:E:4959:PHE:CE2	2.49	0.47
1:F:57:LYS:HB2	1:F:80:VAL:HB	1.96	0.47
2:G:719:LEU:HD22	2:G:735:GLN:HG2	1.95	0.47
2:G:776:LEU:HG	2:G:848:HIS:HA	1.95	0.47
2:I:1685:LEU:HD22	2:I:1718:ILE:HG21	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:580:GLU:HG2	2:I:583:ILE:HD11	1.96	0.47
1:A:23:VAL:HG22	1:A:47:LYS:HG2	1.95	0.47
2:B:1685:LEU:HD22	2:B:1718:ILE:HG21	1.96	0.47
2:B:4233:LEU:HA	2:B:4236:SER:HB3	1.95	0.47
2:E:983:THR:O	2:E:987:ARG:N	2.47	0.47
2:G:4563:ARG:NH1	2:G:4815:ASP:OD1	2.47	0.47
2:B:3946:GLN:OE1	2:B:3950:ASN:ND2	2.47	0.47
2:E:229:GLU:HA	2:E:249:GLY:HA2	1.95	0.47
2:G:1960:ALA:O	2:G:1964:ARG:NE	2.47	0.47
2:G:3900:GLN:NE2	2:G:3967:GLU:O	2.47	0.47
2:G:4230:LYS:HD2	2:G:4959:PHE:CE2	2.48	0.47
2:I:116:MET:HB2	2:I:137:LEU:HD12	1.96	0.47
2:I:1960:ALA:O	2:I:1964:ARG:NE	2.47	0.47
2:I:4563:ARG:NH1	2:I:4815:ASP:OD1	2.47	0.47
1:A:57:LYS:HB2	1:A:80:VAL:HB	1.96	0.47
2:B:229:GLU:HA	2:B:249:GLY:HA2	1.95	0.47
2:B:3850:GLN:HA	2:B:3853:ALA:HB3	1.97	0.47
2:E:3946:GLN:OE1	2:E:3950:ASN:ND2	2.47	0.47
2:G:116:MET:HB2	2:G:137:LEU:HD12	1.96	0.47
2:G:615:ARG:NH2	2:G:1677:GLY:O	2.43	0.47
2:G:3946:GLN:OE1	2:G:3950:ASN:ND2	2.48	0.47
2:G:1685:LEU:HD22	2:G:1718:ILE:HG21	1.96	0.47
2:I:2285:GLU:HG3	2:I:2286:LEU:HG	1.96	0.47
2:I:4231:MET:HE3	2:I:4960:ILE:HG23	1.95	0.47
2:I:4586:PRO:HB3	2:I:4628:VAL:HG21	1.97	0.47
2:I:983:THR:O	2:I:987:ARG:N	2.47	0.47
2:B:1848:LEU:HD22	2:B:1853:ILE:HG13	1.94	0.47
2:B:221:ARG:NH2	2:B:397:GLU:OE2	2.45	0.47
2:E:1685:LEU:HD22	2:E:1718:ILE:HG21	1.96	0.47
2:G:4239:GLU:OE2	2:G:5014:TYR:OH	2.30	0.47
2:G:580:GLU:HG2	2:G:583:ILE:HD11	1.96	0.47
2:G:983:THR:O	2:G:987:ARG:N	2.47	0.47
2:B:3900:GLN:NE2	2:B:3967:GLU:O	2.47	0.47
2:B:4182:GLU:OE2	2:B:4983:HIS:CD2	2.57	0.47
2:B:4822:THR:O	2:B:4825:THR:OG1	2.32	0.47
2:E:4104:THR:HG22	2:E:4106:PRO:HD2	1.97	0.47
2:I:103:TYR:HB3	2:I:152:PRO:HD3	1.97	0.47
2:B:2196:ASN:OD1	2:B:2199:ARG:NH1	2.38	0.47
2:E:3850:GLN:HA	2:E:3853:ALA:HB3	1.97	0.47
2:G:3850:GLN:HA	2:G:3853:ALA:HB3	1.97	0.47
2:G:4233:LEU:HA	2:G:4236:SER:HB3	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:3900:GLN:NE2	2:I:3967:GLU:O	2.47	0.47
2:E:4558:ASN:HB2	2:E:4561:THR:HB	1.97	0.47
2:G:1660:GLN:O	2:G:1664:SER:N	2.47	0.47
2:I:3850:GLN:HA	2:I:3853:ALA:HB3	1.97	0.47
2:I:4104:THR:HG22	2:I:4106:PRO:HD2	1.97	0.47
2:I:894:GLY:HA3	2:I:903:LEU:HD22	1.97	0.47
2:B:103:TYR:HB3	2:B:152:PRO:HD3	1.97	0.47
2:B:2024:PRO:HB2	2:B:2027:ILE:HG12	1.97	0.47
2:B:4563:ARG:NH1	2:B:4815:ASP:OD1	2.47	0.47
2:B:4586:PRO:HB3	2:B:4628:VAL:HG21	1.97	0.47
2:B:719:LEU:HD22	2:B:735:GLN:HG2	1.95	0.47
2:G:1105:ALA:HB1	2:G:1109:LEU:HD21	1.96	0.47
2:G:4586:PRO:HB3	2:G:4628:VAL:HG21	1.97	0.47
2:G:853:PRO:HB3	2:G:1024:TYR:H	1.80	0.47
1:H:57:LYS:HB2	1:H:80:VAL:HB	1.96	0.47
2:I:468:LEU:HB3	2:I:472:ARG:HH12	1.80	0.47
2:B:1960:ALA:O	2:B:1964:ARG:NE	2.47	0.47
2:B:4962:GLY:H	2:B:5025:GLY:N	2.12	0.47
2:E:2189:LYS:HA	2:E:2192:TYR:HD2	1.80	0.47
2:E:4158:PRO:HA	2:E:4161:ARG:HB2	1.97	0.47
2:I:2024:PRO:HB2	2:I:2027:ILE:HG12	1.97	0.47
2:B:853:PRO:HB3	2:B:1024:TYR:H	1.80	0.46
2:E:2751:LEU:HD11	2:E:2823:ILE:HG21	1.97	0.46
2:G:2751:LEU:HD11	2:G:2823:ILE:HG21	1.97	0.46
2:G:4158:PRO:HA	2:G:4161:ARG:HB2	1.97	0.46
2:I:4233:LEU:HA	2:I:4236:SER:HB3	1.95	0.46
2:I:488:LEU:O	2:I:492:ASP:N	2.45	0.46
2:I:867:LEU:HB3	2:I:929:LEU:HD13	1.95	0.46
2:B:580:GLU:HG2	2:B:583:ILE:HD11	1.96	0.46
2:E:1743:ARG:O	2:E:1964:ARG:NH2	2.43	0.46
2:E:468:LEU:HB3	2:E:472:ARG:HH12	1.80	0.46
2:E:853:PRO:HB3	2:E:1024:TYR:H	1.80	0.46
2:G:103:TYR:HB3	2:G:152:PRO:HD3	1.97	0.46
2:I:1105:ALA:HB1	2:I:1109:LEU:HD21	1.96	0.46
1:J:92:PRO:HD3	2:I:627:PRO:HB2	1.98	0.46
1:J:42:ARG:HG2	2:I:1691:GLN:HG2	1.97	0.46
2:E:1660:GLN:O	2:E:1664:SER:N	2.47	0.46
2:E:615:ARG:NH2	2:E:1677:GLY:O	2.43	0.46
2:G:2024:PRO:HB2	2:G:2027:ILE:HG12	1.97	0.46
2:G:3528:UNK:HA	2:E:1220:GLN:NE2	2.30	0.46
2:G:4697:VAL:O	2:G:4701:TRP:N	2.47	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:894:GLY:HA3	2:G:903:LEU:HD22	1.97	0.46
2:I:1743:ARG:O	2:I:1964:ARG:NH2	2.43	0.46
2:B:116:MET:HB2	2:B:137:LEU:HD12	1.96	0.46
2:B:4104:THR:HG22	2:B:4106:PRO:HD2	1.96	0.46
2:E:1796:ALA:HB1	2:E:1797:ARG:HH21	1.81	0.46
2:E:1960:ALA:O	2:E:1964:ARG:NE	2.47	0.46
2:G:887:ILE:HG21	2:G:959:TYR:HA	1.98	0.46
1:J:21:THR:HA	1:J:49:ARG:HA	1.98	0.46
2:B:2189:LYS:HA	2:B:2192:TYR:HD2	1.80	0.46
2:B:4558:ASN:HB2	2:B:4561:THR:HB	1.97	0.46
2:E:116:MET:HB2	2:E:137:LEU:HD12	1.96	0.46
2:E:286:THR:HA	2:E:405:HIS:HB2	1.98	0.46
2:E:4882:CYS:SG	2:E:4886:HIS:NE2	2.89	0.46
2:G:4182:GLU:OE2	2:G:4983:HIS:CD2	2.57	0.46
2:I:1931:LEU:HB3	2:I:1935:VAL:HB	1.98	0.46
2:I:2189:LYS:HA	2:I:2192:TYR:HD2	1.80	0.46
2:I:4558:ASN:HB2	2:I:4561:THR:HB	1.97	0.46
2:B:4231:MET:HE3	2:B:4960:ILE:HG23	1.97	0.46
2:B:468:LEU:HB3	2:B:472:ARG:HH12	1.80	0.46
2:B:870:ILE:HD12	2:B:873:LYS:HB2	1.98	0.46
2:E:2024:PRO:HB2	2:E:2027:ILE:HG12	1.97	0.46
2:E:4957:LYS:HG3	2:E:4964:GLY:HA3	1.96	0.46
2:E:870:ILE:HD12	2:E:873:LYS:HB2	1.98	0.46
2:G:4957:LYS:HG3	2:G:4964:GLY:HA3	1.97	0.46
1:H:21:THR:HA	1:H:49:ARG:HA	1.98	0.46
2:I:3696:ASP:O	2:I:3700:GLN:N	2.46	0.46
2:I:786:GLY:HA2	2:I:1631:GLN:HA	1.98	0.46
2:I:853:PRO:HB3	2:I:1024:TYR:H	1.80	0.46
2:I:870:ILE:HD12	2:I:873:LYS:HB2	1.98	0.46
2:B:786:GLY:HA2	2:B:1631:GLN:HA	1.98	0.46
2:B:983:THR:O	2:B:987:ARG:N	2.47	0.46
2:E:4924:VAL:HG12	2:E:4928:LEU:HD12	1.98	0.46
2:G:2189:LYS:HA	2:G:2192:TYR:HD2	1.80	0.46
2:G:286:THR:HA	2:G:405:HIS:HB2	1.98	0.46
2:G:4960:ILE:O	2:G:4960:ILE:HG22	2.16	0.46
2:G:870:ILE:HD12	2:G:873:LYS:HB2	1.98	0.46
2:I:57:ASN:HD22	2:I:308:HIS:HB2	1.81	0.46
2:E:786:GLY:HA2	2:E:1631:GLN:HA	1.98	0.46
2:E:887:ILE:HG21	2:E:959:TYR:HA	1.97	0.46
2:G:1848:LEU:HB3	2:G:1853:ILE:HB	1.98	0.46
2:G:786:GLY:HA2	2:G:1631:GLN:HA	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:3946:GLN:OE1	2:I:3950:ASN:ND2	2.47	0.46
2:I:4230:LYS:HG3	2:I:4959:PHE:CE2	2.44	0.46
2:B:2751:LEU:HD11	2:B:2823:ILE:HG21	1.97	0.46
2:B:57:ASN:HD22	2:B:308:HIS:HB2	1.81	0.46
2:B:894:GLY:HA3	2:B:903:LEU:HD22	1.97	0.46
2:E:2375:GLY:HA3	2:E:2378:ALA:HB3	1.98	0.46
2:E:4586:PRO:HB3	2:E:4628:VAL:HG21	1.97	0.46
2:I:2104:ARG:HA	2:I:2107:GLN:HB3	1.98	0.46
2:I:4697:VAL:O	2:I:4701:TRP:N	2.47	0.46
2:I:4882:CYS:SG	2:I:4886:HIS:NE2	2.89	0.46
2:B:1848:LEU:HB3	2:B:1853:ILE:HB	1.98	0.46
2:B:1931:LEU:HB3	2:B:1935:VAL:HB	1.98	0.46
2:B:4924:VAL:HG12	2:B:4928:LEU:HD12	1.98	0.46
2:E:103:TYR:HB3	2:E:152:PRO:HD3	1.97	0.46
2:E:57:ASN:HD22	2:E:308:HIS:HB2	1.81	0.46
2:E:695:TYR:OH	2:E:1073:ARG:NH1	2.48	0.46
1:F:21:THR:HA	1:F:49:ARG:HA	1.98	0.46
2:G:1796:ALA:HB1	2:G:1797:ARG:HH21	1.81	0.46
2:G:57:ASN:HD22	2:G:308:HIS:HB2	1.81	0.46
2:G:4104:THR:HG22	2:G:4106:PRO:HD2	1.96	0.46
2:I:823:LEU:HD23	2:I:1626:TRP:HB3	1.98	0.46
2:I:2517:UNK:O	2:I:2521:UNK:N	2.49	0.46
2:B:1078:GLU:HB3	2:B:1081:TYR:HD2	1.82	0.45
2:E:1848:LEU:HB3	2:E:1853:ILE:HB	1.98	0.45
2:E:1931:LEU:HB3	2:E:1935:VAL:HB	1.98	0.45
2:E:2277:ALA:HB1	2:E:2337:PHE:HD2	1.81	0.45
2:G:823:LEU:HD23	2:G:1626:TRP:HB3	1.99	0.45
2:G:4081:VAL:HB	2:G:4088:ILE:HD12	1.98	0.45
2:I:1848:LEU:HB3	2:I:1853:ILE:HB	1.98	0.45
2:I:4960:ILE:O	2:I:4960:ILE:HG22	2.16	0.45
2:I:880:GLU:OE1	2:I:968:ALA:N	2.47	0.45
2:I:887:ILE:HG21	2:I:959:TYR:HA	1.97	0.45
2:B:4158:PRO:HA	2:B:4161:ARG:HB2	1.97	0.45
2:G:2277:ALA:HB1	2:G:2337:PHE:HD2	1.81	0.45
2:G:468:LEU:HB3	2:G:472:ARG:HH12	1.80	0.45
2:I:790:ARG:HG2	2:I:1627:ALA:HA	1.98	0.45
2:I:794:GLY:H	2:I:798:GLY:HA3	1.82	0.45
2:B:2517:UNK:O	2:B:2521:UNK:N	2.49	0.45
2:B:4882:CYS:SG	2:B:4886:HIS:NE2	2.89	0.45
2:E:1078:GLU:HB3	2:E:1081:TYR:HD2	1.82	0.45
2:E:823:LEU:HD23	2:E:1626:TRP:HB3	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:2104:ARG:HA	2:G:2107:GLN:HB3	1.98	0.45
2:I:2751:LEU:HD11	2:I:2823:ILE:HG21	1.97	0.45
1:A:21:THR:HA	1:A:49:ARG:HA	1.98	0.45
2:B:823:LEU:HD23	2:B:1626:TRP:HB3	1.98	0.45
2:B:2375:GLY:HA3	2:B:2378:ALA:HB3	1.98	0.45
2:E:1148:VAL:HB	2:E:1165:ASN:HA	1.98	0.45
2:E:2517:UNK:O	2:E:2521:UNK:N	2.49	0.45
2:E:894:GLY:HA3	2:E:903:LEU:HD22	1.97	0.45
2:G:2517:UNK:O	2:G:2521:UNK:N	2.49	0.45
2:G:485:SER:HA	2:G:488:LEU:HB2	1.99	0.45
2:G:794:GLY:H	2:G:798:GLY:HA3	1.82	0.45
2:I:1148:VAL:HB	2:I:1165:ASN:HA	1.98	0.45
2:I:1718:ILE:HG13	2:I:1719:HIS:CD2	2.52	0.45
2:I:2277:ALA:HB1	2:I:2337:PHE:HD2	1.81	0.45
2:I:3943:ILE:HD11	2:I:4002:LYS:HZ3	1.81	0.45
2:I:4059:LEU:HD13	2:I:4166:LEU:HB3	1.99	0.45
2:B:1660:GLN:O	2:B:1664:SER:N	2.47	0.45
2:B:1796:ALA:HB1	2:B:1797:ARG:HH21	1.81	0.45
2:B:266:ARG:NH2	2:B:269:TRP:O	2.50	0.45
2:B:2874:MET:O	2:B:2878:LEU:N	2.42	0.45
2:E:4782:VAL:O	2:E:4785:THR:OG1	2.30	0.45
2:G:266:ARG:NH2	2:G:269:TRP:O	2.50	0.45
2:G:4059:LEU:HD13	2:G:4166:LEU:HB3	1.99	0.45
2:I:2375:GLY:HA3	2:I:2378:ALA:HB3	1.98	0.45
2:I:3994:HIS:O	2:I:3998:HIS:ND1	2.46	0.45
2:B:4957:LYS:HG3	2:B:4964:GLY:HA3	1.96	0.45
2:B:887:ILE:HG21	2:B:959:TYR:HA	1.97	0.45
2:E:4059:LEU:HD13	2:E:4166:LEU:HB3	1.99	0.45
2:I:637:LEU:HD23	2:I:1637:MET:HB3	1.99	0.45
2:I:4158:PRO:HA	2:I:4161:ARG:HB2	1.97	0.45
2:I:4957:LYS:HG3	2:I:4964:GLY:HA3	1.96	0.45
2:B:2587:UNK:O	2:B:2591:UNK:N	2.50	0.45
2:B:286:THR:HA	2:B:405:HIS:HB2	1.98	0.45
2:B:4059:LEU:HD13	2:B:4166:LEU:HB3	1.99	0.45
2:B:794:GLY:H	2:B:798:GLY:HA3	1.82	0.45
2:E:485:SER:HA	2:E:488:LEU:HB2	1.99	0.45
2:E:892:THR:N	2:E:902:ARG:O	2.48	0.45
2:G:3658:LYS:HA	2:G:3661:TRP:CE2	2.52	0.45
2:I:221:ARG:NH2	2:I:397:GLU:OE2	2.45	0.45
2:I:495:ASN:HD21	2:I:550:LYS:HE3	1.82	0.45
2:B:1718:ILE:HG13	2:B:1719:HIS:CD2	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:3658:LYS:HA	2:B:3661:TRP:CE2	2.52	0.45
2:B:3829:PHE:HA	2:B:3832:ILE:HD12	1.99	0.45
2:B:4081:VAL:HB	2:B:4088:ILE:HD12	1.98	0.45
2:B:4697:VAL:O	2:B:4701:TRP:N	2.47	0.45
2:E:637:LEU:HD23	2:E:1637:MET:HB3	1.99	0.45
2:E:4960:ILE:HG22	2:E:4960:ILE:O	2.16	0.45
2:G:1802:ILE:HG21	2:G:1807:LEU:HD22	1.99	0.45
2:G:1931:LEU:HB3	2:G:1935:VAL:HB	1.98	0.45
2:G:4687:TYR:OH	2:G:4699:GLY:O	2.34	0.45
2:G:4924:VAL:HG12	2:G:4928:LEU:HD12	1.98	0.45
2:G:495:ASN:HD21	2:G:550:LYS:HE3	1.82	0.45
2:I:1802:ILE:HG21	2:I:1807:LEU:HD22	1.99	0.45
1:A:87:HIS:HD2	1:A:90:VAL:HB	1.82	0.45
2:E:2235:PHE:HA	2:E:2238:TYR:HD2	1.82	0.45
1:F:87:HIS:HD2	1:F:90:VAL:HB	1.82	0.45
1:F:92:PRO:HD3	2:E:627:PRO:HB2	1.98	0.45
2:G:1095:VAL:HB	2:G:1199:VAL:HG23	1.99	0.45
2:G:637:LEU:HD23	2:G:1637:MET:HB3	1.99	0.45
2:I:286:THR:HA	2:I:405:HIS:HB2	1.98	0.45
2:I:3658:LYS:HA	2:I:3661:TRP:CE2	2.52	0.45
2:E:2004:GLU:HA	2:E:2007:ASN:HD22	1.82	0.45
2:E:2874:MET:O	2:E:2878:LEU:N	2.42	0.45
2:E:794:GLY:H	2:E:798:GLY:HA3	1.82	0.45
2:G:1078:GLU:HB3	2:G:1081:TYR:HD2	1.82	0.45
2:G:790:ARG:HG2	2:G:1627:ALA:HA	1.98	0.45
2:G:1718:ILE:HG13	2:G:1719:HIS:CD2	2.52	0.45
2:G:2235:PHE:HA	2:G:2238:TYR:HD2	1.82	0.45
2:G:2375:GLY:HA3	2:G:2378:ALA:HB3	1.98	0.45
2:G:4558:ASN:HB2	2:G:4561:THR:HB	1.97	0.45
2:G:652:ARG:HB2	2:G:750:LEU:HD13	1.99	0.45
2:I:43:GLY:N	2:I:447:ASP:OD2	2.43	0.45
2:I:4924:VAL:HG12	2:I:4928:LEU:HD12	1.98	0.45
2:B:2104:ARG:HA	2:B:2107:GLN:HB3	1.98	0.44
2:B:637:LEU:HD23	2:B:1637:MET:HB3	1.99	0.44
2:E:2104:ARG:HA	2:E:2107:GLN:HB3	1.98	0.44
2:G:1148:VAL:HB	2:G:1165:ASN:HA	1.98	0.44
2:G:2034:PHE:O	2:G:2038:LEU:N	2.50	0.44
2:G:4798:MET:HG3	2:G:4811:ALA:HB3	1.99	0.44
2:G:4848:VAL:O	2:G:4852:THR:N	2.50	0.44
1:H:87:HIS:HD2	1:H:90:VAL:HB	1.82	0.44
2:I:1457:UNK:N	2:I:1497:UNK:O	2.50	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1105:ALA:O	2:B:1189:LEU:N	2.51	0.44
2:B:2862:LEU:HB3	2:B:2928:LYS:HB3	1.99	0.44
2:B:4848:VAL:O	2:B:4852:THR:N	2.50	0.44
2:B:4959:PHE:O	2:B:4959:PHE:CG	2.70	0.44
2:B:4960:ILE:HG22	2:B:4960:ILE:O	2.16	0.44
2:B:495:ASN:HD21	2:B:550:LYS:HE3	1.82	0.44
2:E:2034:PHE:O	2:E:2038:LEU:N	2.50	0.44
2:G:3943:ILE:HD11	2:G:4002:LYS:HZ3	1.83	0.44
2:I:1095:VAL:HB	2:I:1199:VAL:HG23	1.99	0.44
2:I:2265:LEU:O	2:I:2330:ARG:NH1	2.51	0.44
2:I:2587:UNK:O	2:I:2591:UNK:N	2.50	0.44
2:I:695:TYR:OH	2:I:1073:ARG:NH1	2.48	0.44
2:B:2235:PHE:HA	2:B:2238:TYR:HD2	1.82	0.44
2:E:206:CYS:SG	2:E:207:SER:N	2.90	0.44
2:E:2587:UNK:O	2:E:2591:UNK:N	2.50	0.44
2:E:2862:LEU:HB3	2:E:2928:LYS:HB3	1.99	0.44
2:E:54:ASN:O	2:E:58:VAL:N	2.47	0.44
2:G:1105:ALA:N	2:G:1189:LEU:O	2.50	0.44
2:G:4959:PHE:CD2	2:G:4959:PHE:O	2.70	0.44
2:I:1796:ALA:HB1	2:I:1797:ARG:HH21	1.81	0.44
2:I:4798:MET:HG3	2:I:4811:ALA:HB3	2.00	0.44
2:I:485:SER:HA	2:I:488:LEU:HB2	1.99	0.44
2:B:1457:UNK:N	2:B:1497:UNK:O	2.50	0.44
2:B:2034:PHE:O	2:B:2038:LEU:N	2.50	0.44
2:B:2265:LEU:O	2:B:2330:ARG:NH1	2.51	0.44
2:B:290:TYR:O	2:B:302:VAL:N	2.51	0.44
2:E:790:ARG:HG2	2:E:1627:ALA:HA	1.98	0.44
2:E:266:ARG:NH2	2:E:269:TRP:O	2.49	0.44
2:E:4848:VAL:O	2:E:4852:THR:N	2.50	0.44
2:E:495:ASN:HD21	2:E:550:LYS:HE3	1.82	0.44
2:E:652:ARG:HB2	2:E:750:LEU:HD13	1.99	0.44
2:G:2265:LEU:O	2:G:2330:ARG:NH1	2.51	0.44
2:G:2862:LEU:HB3	2:G:2928:LYS:HB3	1.99	0.44
2:I:4081:VAL:HB	2:I:4088:ILE:HD12	1.98	0.44
2:I:4959:PHE:O	2:I:4959:PHE:CD2	2.70	0.44
2:B:215:THR:HG22	2:B:273:HIS:HA	2.00	0.44
2:B:4782:VAL:O	2:B:4785:THR:OG1	2.30	0.44
2:E:290:TYR:O	2:E:302:VAL:N	2.51	0.44
2:E:551:LEU:HD11	2:E:589:LEU:HD13	2.00	0.44
2:G:2004:GLU:HA	2:G:2007:ASN:HD22	1.82	0.44
2:I:206:CYS:SG	2:I:207:SER:N	2.90	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2235:PHE:HA	2:I:2238:TYR:HD2	1.82	0.44
2:I:652:ARG:HB2	2:I:750:LEU:HD13	1.99	0.44
2:B:1148:VAL:HB	2:B:1165:ASN:HA	1.98	0.44
2:B:2022:PRO:HB2	2:B:2024:PRO:HD2	1.99	0.44
2:B:2226:PRO:HA	2:B:2229:VAL:HG12	2.00	0.44
2:B:652:ARG:HB2	2:B:750:LEU:HD13	1.99	0.44
2:E:1718:ILE:HG13	2:E:1719:HIS:CD2	2.51	0.44
2:E:3658:LYS:HA	2:E:3661:TRP:CE2	2.52	0.44
2:E:4081:VAL:HB	2:E:4088:ILE:HD12	1.98	0.44
2:E:4798:MET:HG3	2:E:4811:ALA:HB3	1.99	0.44
2:E:488:LEU:O	2:E:492:ASP:N	2.45	0.44
2:E:4959:PHE:CD2	2:E:4959:PHE:O	2.70	0.44
2:E:4959:PHE:CG	2:E:4959:PHE:O	2.70	0.44
2:G:206:CYS:SG	2:G:207:SER:N	2.90	0.44
2:G:914:PRO:O	2:G:918:ARG:N	2.48	0.44
2:I:266:ARG:NH2	2:I:269:TRP:O	2.50	0.44
1:J:87:HIS:HD2	1:J:90:VAL:HB	1.82	0.44
2:B:790:ARG:HG2	2:B:1627:ALA:HA	1.98	0.44
2:E:2226:PRO:HA	2:E:2229:VAL:HG12	2.00	0.44
2:G:4959:PHE:CG	2:G:4959:PHE:O	2.70	0.44
2:I:1078:GLU:HB3	2:I:1081:TYR:HD2	1.81	0.44
2:I:2004:GLU:HA	2:I:2007:ASN:HD22	1.82	0.44
2:I:4848:VAL:O	2:I:4852:THR:N	2.51	0.44
2:I:681:HIS:O	2:I:784:SER:N	2.45	0.44
2:B:1103:GLY:HA3	2:B:1123:VAL:HA	2.00	0.44
2:B:2277:ALA:HB1	2:B:2337:PHE:HD2	1.81	0.44
2:B:485:SER:HA	2:B:488:LEU:HB2	1.99	0.44
2:B:4959:PHE:CD2	2:B:4959:PHE:O	2.70	0.44
2:E:1095:VAL:HB	2:E:1199:VAL:HG23	1.99	0.44
2:G:1973:GLN:HA	2:G:1976:ARG:HB3	2.00	0.44
2:G:43:GLY:N	2:G:447:ASP:OD2	2.43	0.44
2:G:695:TYR:OH	2:G:1073:ARG:NH1	2.48	0.44
2:I:1103:GLY:HA3	2:I:1123:VAL:HA	2.00	0.44
2:I:2034:PHE:O	2:I:2038:LEU:N	2.50	0.44
2:I:485:SER:O	2:I:489:ASN:N	2.40	0.44
2:B:1802:ILE:HG21	2:B:1807:LEU:HD22	1.99	0.44
2:E:1841:VAL:HG13	2:E:1844:LEU:HD23	2.00	0.44
2:E:3829:PHE:HA	2:E:3832:ILE:HD12	1.99	0.44
2:G:2353:VAL:O	2:G:2357:LEU:N	2.51	0.44
2:G:2587:UNK:O	2:G:2591:UNK:N	2.50	0.44
2:G:3829:PHE:HA	2:G:3832:ILE:HD12	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1841:VAL:HG13	2:I:1844:LEU:HD23	2.00	0.44
2:I:4743:MET:HB3	2:I:4746:ALA:HB3	2.00	0.44
2:I:4959:PHE:CG	2:I:4959:PHE:O	2.70	0.44
2:I:583:ILE:HA	2:I:586:ILE:HD12	2.00	0.44
2:B:4673:ARG:HH12	2:B:4698:LYS:HE3	1.83	0.43
2:E:1105:ALA:O	2:E:1189:LEU:N	2.51	0.43
2:E:1105:ALA:N	2:E:1189:LEU:O	2.50	0.43
2:E:1457:UNK:N	2:E:1497:UNK:O	2.50	0.43
2:G:215:THR:HG22	2:G:273:HIS:HA	2.00	0.43
2:G:583:ILE:HA	2:G:586:ILE:HD12	2.00	0.43
2:G:892:THR:N	2:G:902:ARG:O	2.48	0.43
2:I:2226:PRO:HA	2:I:2229:VAL:HG12	2.00	0.43
2:I:3829:PHE:HA	2:I:3832:ILE:HD12	1.99	0.43
2:I:914:PRO:O	2:I:918:ARG:N	2.48	0.43
2:B:1841:VAL:HG13	2:B:1844:LEU:HD23	2.00	0.43
2:B:206:CYS:SG	2:B:207:SER:N	2.90	0.43
2:E:1802:ILE:HG21	2:E:1807:LEU:HD22	1.99	0.43
2:E:4697:VAL:O	2:E:4701:TRP:N	2.47	0.43
2:E:575:LEU:HD22	2:E:609:CYS:HB3	2.00	0.43
2:G:2226:PRO:HA	2:G:2229:VAL:HG12	2.00	0.43
2:G:2271:THR:HG22	2:G:2273:LEU:H	1.83	0.43
2:G:488:LEU:O	2:G:492:ASP:N	2.45	0.43
2:G:551:LEU:HD11	2:G:589:LEU:HD13	2.00	0.43
2:I:2022:PRO:HB2	2:I:2024:PRO:HD2	1.99	0.43
2:I:551:LEU:HD11	2:I:589:LEU:HD13	2.00	0.43
2:B:2004:GLU:HA	2:B:2007:ASN:HD22	1.82	0.43
2:B:4798:MET:HG3	2:B:4811:ALA:HB3	1.99	0.43
2:E:1973:GLN:HA	2:E:1976:ARG:HB3	2.00	0.43
2:E:4743:MET:HB3	2:E:4746:ALA:HB3	2.00	0.43
2:E:880:GLU:OE1	2:E:968:ALA:N	2.48	0.43
2:G:1103:GLY:HA3	2:G:1123:VAL:HA	2.00	0.43
2:G:1154:ASP:O	2:G:1158:ASN:N	2.52	0.43
2:G:3805:LEU:HG	2:G:3805:LEU:H	1.74	0.43
2:B:1973:GLN:HA	2:B:1976:ARG:HB3	2.00	0.43
2:B:583:ILE:HA	2:B:586:ILE:HD12	2.00	0.43
2:E:2022:PRO:HB2	2:E:2024:PRO:HD2	1.99	0.43
2:E:4182:GLU:OE2	2:E:4983:HIS:CD2	2.57	0.43
2:G:1457:UNK:N	2:G:1497:UNK:O	2.50	0.43
1:H:87:HIS:HA	1:H:88:PRO:HD3	1.88	0.43
2:I:2271:THR:HG22	2:I:2273:LEU:H	1.83	0.43
2:B:551:LEU:HD11	2:B:589:LEU:HD13	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:215:THR:HG22	2:E:273:HIS:HA	2.00	0.43
2:G:2022:PRO:HB2	2:G:2024:PRO:HD2	1.99	0.43
2:G:485:SER:O	2:G:489:ASN:N	2.40	0.43
2:G:575:LEU:HD22	2:G:609:CYS:HB3	2.00	0.43
2:I:2862:LEU:HB3	2:I:2928:LYS:HB3	1.99	0.43
2:I:290:TYR:O	2:I:302:VAL:N	2.51	0.43
2:I:4230:LYS:HD2	2:I:4959:PHE:CE2	2.48	0.43
2:B:2353:VAL:O	2:B:2357:LEU:N	2.51	0.43
2:B:3552:UNK:O	2:B:3556:UNK:N	2.52	0.43
2:E:1154:ASP:O	2:E:1158:ASN:N	2.52	0.43
2:E:1698:LEU:N	2:E:1712:TYR:OH	2.52	0.43
2:E:2265:LEU:O	2:E:2330:ARG:NH1	2.51	0.43
2:E:4984:ASN:ND2	2:E:4986:ALA:HB3	2.33	0.43
2:G:1698:LEU:N	2:G:1712:TYR:OH	2.52	0.43
2:G:4984:ASN:ND2	2:G:4986:ALA:HB3	2.33	0.43
2:G:683:ARG:HG2	2:G:717:ASP:HB3	2.01	0.43
2:G:880:GLU:OE1	2:G:968:ALA:N	2.48	0.43
2:I:2272:PRO:HA	2:I:2275:VAL:HG12	2.01	0.43
2:B:3994:HIS:O	2:B:3998:HIS:ND1	2.46	0.43
2:B:575:LEU:HD22	2:B:609:CYS:HB3	2.00	0.43
2:E:2271:THR:HG22	2:E:2273:LEU:H	1.83	0.43
2:E:2353:VAL:O	2:E:2357:LEU:N	2.51	0.43
2:E:583:ILE:HA	2:E:586:ILE:HD12	2.00	0.43
1:F:87:HIS:HA	1:F:88:PRO:HD3	1.89	0.43
2:G:1105:ALA:O	2:G:1189:LEU:N	2.51	0.43
2:I:1269:CYS:HA	2:I:1473:UNK:HA	2.01	0.43
2:I:215:THR:HG22	2:I:273:HIS:HA	2.00	0.43
2:I:4982:GLU:HB3	2:I:4983:HIS:H	1.71	0.43
2:I:4984:ASN:ND2	2:I:4986:ALA:HB3	2.33	0.43
2:I:929:LEU:HD23	2:I:932:LEU:HD12	2.01	0.43
2:B:683:ARG:HG2	2:B:717:ASP:HB3	2.01	0.43
2:B:892:THR:N	2:B:902:ARG:O	2.48	0.43
2:E:3781:GLN:HA	2:E:3784:SER:HB3	2.01	0.43
2:E:929:LEU:HD23	2:E:932:LEU:HD12	2.01	0.43
2:G:1841:VAL:HG13	2:G:1844:LEU:HD23	2.00	0.43
2:G:290:TYR:O	2:G:302:VAL:N	2.51	0.43
2:G:4673:ARG:HH12	2:G:4698:LYS:HE3	1.84	0.43
2:I:1154:ASP:O	2:I:1158:ASN:N	2.52	0.43
2:I:3552:UNK:O	2:I:3556:UNK:N	2.52	0.43
2:B:1095:VAL:HB	2:B:1199:VAL:HG23	1.99	0.43
2:B:4743:MET:HB3	2:B:4746:ALA:HB3	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4984:ASN:ND2	2:B:4986:ALA:HB3	2.33	0.43
2:G:929:LEU:HD23	2:G:932:LEU:HD12	2.01	0.43
2:I:4673:ARG:HH12	2:I:4698:LYS:HE3	1.83	0.43
2:B:1154:ASP:O	2:B:1158:ASN:N	2.52	0.43
2:B:2271:THR:HG22	2:B:2273:LEU:H	1.83	0.43
2:B:4962:GLY:H	2:B:5025:GLY:HA2	1.84	0.43
2:B:929:LEU:HD23	2:B:932:LEU:HD12	2.01	0.43
2:E:1269:CYS:HA	2:E:1473:UNK:HA	2.01	0.43
2:E:4673:ARG:HH12	2:E:4698:LYS:HE3	1.83	0.43
2:I:1698:LEU:N	2:I:1712:TYR:OH	2.52	0.43
2:I:683:ARG:HG2	2:I:717:ASP:HB3	2.01	0.43
2:B:1731:LEU:HA	2:B:1772:ARG:HH12	1.84	0.42
2:B:695:TYR:OH	2:B:1073:ARG:NH1	2.48	0.42
2:E:2272:PRO:HA	2:E:2275:VAL:HG12	2.01	0.42
2:E:3552:UNK:O	2:E:3556:UNK:N	2.52	0.42
2:I:2874:MET:O	2:I:2878:LEU:N	2.42	0.42
2:B:1105:ALA:N	2:B:1189:LEU:O	2.50	0.42
2:B:3781:GLN:HA	2:B:3784:SER:HB3	2.01	0.42
2:E:1103:GLY:HA3	2:E:1123:VAL:HA	2.00	0.42
2:E:1691:GLN:HE22	2:E:1802:ILE:HG12	1.85	0.42
2:E:379:HIS:CD2	2:E:382:GLY:H	2.32	0.42
2:E:4962:GLY:H	2:E:5025:GLY:HA2	1.84	0.42
2:I:4962:GLY:H	2:I:5025:GLY:HA2	1.84	0.42
2:B:3703:LEU:HA	2:B:3706:SER:HB3	2.01	0.42
2:B:54:ASN:O	2:B:58:VAL:N	2.47	0.42
2:E:3817:LEU:HD13	2:E:3899:PHE:HD1	1.84	0.42
2:E:3832:ILE:O	2:E:3836:MET:N	2.50	0.42
2:E:4968:PHE:CE1	2:E:4978:HIS:ND1	2.76	0.42
2:E:683:ARG:HG2	2:E:717:ASP:HB3	2.01	0.42
2:I:1973:GLN:HA	2:I:1976:ARG:HB3	2.00	0.42
2:B:842:PRO:HD3	2:B:1073:ARG:HG3	2.02	0.42
2:B:1286:UNK:HA	2:B:1461:UNK:HA	2.02	0.42
2:G:3552:UNK:O	2:G:3556:UNK:N	2.52	0.42
2:I:2132:GLY:O	2:I:2136:ARG:N	2.51	0.42
2:I:4227:GLU:HG3	2:I:4228:ALA:H	1.84	0.42
2:B:1698:LEU:N	2:B:1712:TYR:OH	2.52	0.42
2:E:3696:ASP:O	2:E:3700:GLN:N	2.46	0.42
2:E:681:HIS:HB3	2:E:784:SER:HB3	2.02	0.42
2:E:914:PRO:O	2:E:918:ARG:N	2.48	0.42
2:G:4227:GLU:HG3	2:G:4228:ALA:H	1.84	0.42
2:G:4743:MET:HB3	2:G:4746:ALA:HB3	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:2265:LEU:HD22	2:I:2330:ARG:HB3	2.01	0.42
2:I:3703:LEU:HA	2:I:3706:SER:HB3	2.01	0.42
2:I:575:LEU:HD22	2:I:609:CYS:HB3	2.00	0.42
2:B:1164:LEU:HB3	2:B:1169:LEU:HD21	2.02	0.42
2:B:3817:LEU:HD13	2:B:3899:PHE:HD1	1.85	0.42
2:E:1164:LEU:HB3	2:E:1169:LEU:HD21	2.02	0.42
2:E:1808:ARG:HD2	2:E:1854:PHE:HA	2.02	0.42
2:E:4712:PRO:HB2	2:E:4718:LYS:HA	2.01	0.42
2:G:1808:ARG:HD2	2:G:1854:PHE:HA	2.02	0.42
2:I:842:PRO:HD3	2:I:1073:ARG:HG3	2.02	0.42
2:I:1164:LEU:HB3	2:I:1169:LEU:HD21	2.02	0.42
2:I:2810:LYS:O	2:I:2814:LYS:N	2.43	0.42
2:I:4712:PRO:HB2	2:I:4718:LYS:HA	2.01	0.42
2:I:4822:THR:O	2:I:4825:THR:OG1	2.32	0.42
1:J:7:ILE:N	1:J:71:ARG:O	2.48	0.42
2:B:1189:LEU:HD12	2:B:1190:PRO:HD2	2.02	0.42
2:B:2265:LEU:HD22	2:B:2330:ARG:HB3	2.01	0.42
2:B:4687:TYR:OH	2:B:4699:GLY:O	2.34	0.42
2:E:1668:ARG:HA	2:E:1671:ARG:HH11	1.85	0.42
2:E:3361:UNK:O	2:E:3365:UNK:N	2.53	0.42
2:G:1164:LEU:HB3	2:G:1169:LEU:HD21	2.02	0.42
2:G:1269:CYS:HA	2:G:1473:UNK:HA	2.01	0.42
2:G:3832:ILE:O	2:G:3836:MET:N	2.50	0.42
2:G:4982:GLU:HB3	2:G:4983:HIS:H	1.71	0.42
2:G:4962:GLY:H	2:G:5025:GLY:HA2	1.84	0.42
2:I:1668:ARG:HA	2:I:1671:ARG:HH11	1.85	0.42
2:I:681:HIS:HB3	2:I:784:SER:HB3	2.02	0.42
1:J:87:HIS:HA	1:J:88:PRO:HD3	1.88	0.42
2:B:1668:ARG:HA	2:B:1671:ARG:HH11	1.85	0.42
2:B:4227:GLU:HG3	2:B:4228:ALA:H	1.84	0.42
2:B:488:LEU:O	2:B:492:ASP:N	2.45	0.42
2:B:4892:ARG:HD3	2:I:4918:ILE:HD13	2.02	0.42
2:E:1728:ARG:HA	2:E:1731:LEU:HB2	2.01	0.42
2:G:1286:UNK:HA	2:G:1461:UNK:HA	2.02	0.42
2:G:1668:ARG:HA	2:G:1671:ARG:HH11	1.85	0.42
2:G:3840:SER:OG	2:G:3875:MET:O	2.34	0.42
2:I:1189:LEU:HD12	2:I:1190:PRO:HD2	2.02	0.42
2:B:2132:GLY:O	2:B:2136:ARG:N	2.51	0.42
2:B:3696:ASP:O	2:B:3700:GLN:N	2.46	0.42
2:E:2265:LEU:HD22	2:E:2330:ARG:HB3	2.01	0.42
2:E:3994:HIS:O	2:E:3998:HIS:ND1	2.46	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:4687:TYR:OH	2:E:4699:GLY:O	2.34	0.42
2:G:3361:UNK:O	2:G:3365:UNK:N	2.53	0.42
2:G:3781:GLN:HA	2:G:3784:SER:HB3	2.01	0.42
2:G:4231:MET:HE3	2:G:4960:ILE:HG23	2.02	0.42
2:G:681:HIS:HB3	2:G:784:SER:HB3	2.02	0.42
2:I:1731:LEU:HA	2:I:1772:ARG:HH12	1.84	0.42
2:I:892:THR:N	2:I:902:ARG:O	2.48	0.42
2:B:2272:PRO:HA	2:B:2275:VAL:HG12	2.01	0.42
2:B:876:GLU:O	2:B:880:GLU:N	2.51	0.42
2:E:1966:VAL:HA	2:E:1969:LEU:HB3	2.02	0.42
2:E:3703:LEU:HA	2:E:3706:SER:HB3	2.01	0.42
2:G:1697:ALA:HB1	2:G:1708:ARG:HB3	2.02	0.42
2:G:1691:GLN:HE22	2:G:1802:ILE:HG12	1.84	0.42
2:G:1966:VAL:HA	2:G:1969:LEU:HB3	2.02	0.42
2:G:2121:PHE:O	2:G:3725:TYR:OH	2.33	0.42
2:G:3817:LEU:HD13	2:G:3899:PHE:HD1	1.84	0.42
2:B:1697:ALA:HB1	2:B:1708:ARG:HB3	2.02	0.41
2:B:1966:VAL:HA	2:B:1969:LEU:HB3	2.02	0.41
2:B:3832:ILE:O	2:B:3836:MET:N	2.50	0.41
2:E:842:PRO:HD3	2:E:1073:ARG:HG3	2.02	0.41
2:E:1731:LEU:HA	2:E:1772:ARG:HH12	1.84	0.41
2:E:4227:GLU:HG3	2:E:4228:ALA:H	1.83	0.41
2:G:2265:LEU:HD22	2:G:2330:ARG:HB3	2.01	0.41
2:G:3663:LEU:H	2:G:3663:LEU:HG	1.76	0.41
1:H:7:ILE:N	1:H:71:ARG:O	2.48	0.41
2:I:599:VAL:HG23	2:I:600:LEU:HD12	2.02	0.41
2:B:3361:UNK:O	2:B:3365:UNK:N	2.53	0.41
2:B:4982:GLU:HB3	2:B:4983:HIS:H	1.71	0.41
1:A:92:PRO:HD3	2:B:627:PRO:HB2	2.01	0.41
2:G:1728:ARG:HA	2:G:1731:LEU:HB2	2.01	0.41
2:I:3781:GLN:HA	2:I:3784:SER:HB3	2.01	0.41
2:I:3817:LEU:HD13	2:I:3899:PHE:HD1	1.85	0.41
2:E:1697:ALA:HB1	2:E:1708:ARG:HB3	2.02	0.41
2:E:2196:ASN:OD1	2:E:2199:ARG:NH1	2.38	0.41
2:E:4821:LYS:HB3	2:E:4821:LYS:HE2	1.96	0.41
2:G:2272:PRO:HA	2:G:2275:VAL:HG12	2.01	0.41
2:G:3703:LEU:HA	2:G:3706:SER:HB3	2.01	0.41
2:G:842:PRO:HD3	2:G:1073:ARG:HG3	2.02	0.41
2:I:1697:ALA:HB1	2:I:1708:ARG:HB3	2.02	0.41
2:I:1728:ARG:HA	2:I:1731:LEU:HB2	2.01	0.41
2:I:1966:VAL:HA	2:I:1969:LEU:HB3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:342:GLY:HA2	2:I:389:PHE:HB2	2.03	0.41
2:I:940:GLY:O	2:I:1052:ASN:N	2.52	0.41
2:B:1728:ARG:HA	2:B:1731:LEU:HB2	2.01	0.41
2:B:1691:GLN:HE22	2:B:1802:ILE:HG12	1.85	0.41
2:B:3880:PHE:O	2:B:3884:LEU:N	2.54	0.41
2:B:3937:TYR:HB3	2:B:4002:LYS:HZ3	1.85	0.41
2:B:4712:PRO:HB2	2:B:4718:LYS:HA	2.01	0.41
2:E:1189:LEU:HD12	2:E:1190:PRO:HD2	2.02	0.41
1:F:30:LEU:HD23	1:F:33:GLY:HA3	2.03	0.41
2:G:2132:GLY:O	2:G:2136:ARG:N	2.51	0.41
2:G:599:VAL:HG23	2:G:600:LEU:HD12	2.02	0.41
2:I:1286:UNK:HA	2:I:1461:UNK:HA	2.02	0.41
2:I:15:ARG:HG2	2:I:100:THR:HA	2.03	0.41
2:I:1808:ARG:HD2	2:I:1854:PHE:HA	2.02	0.41
2:I:3361:UNK:O	2:I:3365:UNK:N	2.53	0.41
2:I:4702:ASP:OD1	2:I:4778:TRP:NE1	2.48	0.41
2:B:1808:ARG:HD2	2:B:1854:PHE:HA	2.02	0.41
2:B:914:PRO:O	2:B:918:ARG:N	2.48	0.41
1:H:30:LEU:HD23	1:H:33:GLY:HA3	2.03	0.41
2:I:1691:GLN:HE22	2:I:1802:ILE:HG12	1.85	0.41
2:I:2950:UNK:O	2:I:2954:UNK:N	2.54	0.41
2:I:4163:PHE:HA	2:I:4166:LEU:HB2	2.02	0.41
2:B:1269:CYS:HA	2:B:1473:UNK:HA	2.01	0.41
2:B:681:HIS:HB3	2:B:784:SER:HB3	2.02	0.41
2:E:4106:PRO:O	2:E:4110:PHE:N	2.53	0.41
2:G:1256:GLU:HG2	2:G:1273:ALA:HB3	2.03	0.41
2:G:2810:LYS:O	2:G:2814:LYS:N	2.42	0.41
2:G:3365:UNK:O	2:G:3369:UNK:N	2.54	0.41
2:G:3994:HIS:O	2:G:3998:HIS:ND1	2.46	0.41
2:I:1256:GLU:HG2	2:I:1273:ALA:HB3	2.03	0.41
2:I:379:HIS:CD2	2:I:382:GLY:H	2.32	0.41
2:B:342:GLY:HA2	2:B:389:PHE:HB2	2.03	0.41
2:B:599:VAL:HG23	2:B:600:LEU:HD12	2.02	0.41
2:E:2950:UNK:O	2:E:2954:UNK:N	2.54	0.41
2:E:3365:UNK:O	2:E:3369:UNK:N	2.54	0.41
2:G:123:THR:OG1	2:G:134:ASP:OD1	2.39	0.41
2:I:2353:VAL:O	2:I:2357:LEU:N	2.51	0.41
2:I:3365:UNK:O	2:I:3369:UNK:N	2.54	0.41
2:B:1130:GLN:HG2	2:B:1138:PRO:HA	2.03	0.41
2:B:379:HIS:CD2	2:B:382:GLY:H	2.32	0.41
2:E:876:GLU:O	2:E:880:GLU:N	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:1731:LEU:HA	2:G:1772:ARG:HH12	1.84	0.41
2:G:3880:PHE:O	2:G:3884:LEU:N	2.54	0.41
2:B:15:ARG:HG2	2:B:100:THR:HA	2.03	0.41
2:B:410:LEU:HD12	2:B:413:GLN:HE21	1.86	0.41
2:B:45:ARG:NH2	2:B:447:ASP:OD1	2.52	0.41
2:E:102:LEU:HB3	2:E:160:GLY:HA2	2.03	0.41
2:E:4163:PHE:HA	2:E:4166:LEU:HB2	2.02	0.41
2:G:1938:GLN:HA	2:G:1941:ASN:HD22	1.86	0.41
2:G:410:LEU:HD12	2:G:413:GLN:HE21	1.86	0.41
2:G:54:ASN:O	2:G:58:VAL:N	2.47	0.41
2:I:4782:VAL:O	2:I:4785:THR:OG1	2.30	0.41
2:I:4968:PHE:CE2	2:I:4978:HIS:ND1	2.89	0.41
2:I:734:GLY:O	2:I:736:HIS:ND1	2.54	0.41
2:I:911:HIS:O	2:I:918:ARG:NH2	2.52	0.41
2:B:102:LEU:HB3	2:B:160:GLY:HA2	2.03	0.41
2:B:123:THR:OG1	2:B:134:ASP:OD1	2.39	0.41
2:B:1256:GLU:HG2	2:B:1273:ALA:HB3	2.03	0.41
2:B:1938:GLN:HA	2:B:1941:ASN:HD22	1.86	0.41
2:B:4780:PHE:HA	2:B:4783:ILE:HD12	2.03	0.41
2:B:911:HIS:O	2:B:918:ARG:NH2	2.52	0.41
2:E:379:HIS:CD2	2:E:381:GLU:H	2.39	0.41
2:E:446:GLN:HA	2:E:449:ILE:HD12	2.03	0.41
2:G:102:LEU:HB3	2:G:160:GLY:HA2	2.03	0.41
2:G:1189:LEU:HD12	2:G:1190:PRO:HD2	2.02	0.41
2:G:2874:MET:O	2:G:2878:LEU:N	2.42	0.41
1:J:30:LEU:HD23	1:J:33:GLY:HA3	2.03	0.41
2:B:2950:UNK:O	2:B:2954:UNK:N	2.54	0.41
2:B:3365:UNK:O	2:B:3369:UNK:N	2.54	0.41
2:B:379:HIS:CD2	2:B:381:GLU:H	2.39	0.41
2:B:4237:PHE:O	2:B:4241:THR:OG1	2.33	0.41
2:E:342:GLY:HA2	2:E:389:PHE:HB2	2.03	0.41
2:E:3880:PHE:O	2:E:3884:LEU:N	2.53	0.41
2:E:4822:THR:O	2:E:4825:THR:OG1	2.32	0.41
2:E:485:SER:O	2:E:489:ASN:N	2.40	0.41
2:I:410:LEU:HD12	2:I:413:GLN:HE21	1.86	0.41
1:A:87:HIS:HA	1:A:88:PRO:HD3	1.88	0.40
2:B:1727:ARG:HH21	2:B:1775:HIS:CE1	2.39	0.40
2:B:309:THR:O	2:B:313:SER:OG	2.39	0.40
2:B:4163:PHE:HA	2:B:4166:LEU:HB2	2.02	0.40
2:B:446:GLN:HA	2:B:449:ILE:HD12	2.03	0.40
2:E:1256:GLU:HG2	2:E:1273:ALA:HB3	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1286:UNK:HA	2:E:1461:UNK:HA	2.02	0.40
2:E:410:LEU:HD12	2:E:413:GLN:HE21	1.86	0.40
2:G:1130:GLN:HG2	2:G:1138:PRO:HA	2.03	0.40
2:G:342:GLY:HA2	2:G:389:PHE:HB2	2.02	0.40
2:G:4962:GLY:H	2:G:5025:GLY:CA	2.34	0.40
2:G:742:ASP:HA	2:G:760:ASN:HD21	1.86	0.40
2:G:897:ARG:HD2	2:G:905:PRO:HG3	2.04	0.40
2:I:4106:PRO:O	2:I:4110:PHE:N	2.53	0.40
2:I:4780:PHE:HA	2:I:4783:ILE:HD12	2.03	0.40
2:I:4962:GLY:H	2:I:5025:GLY:CA	2.34	0.40
2:B:1735:ILE:HG23	2:B:1771:LEU:HD23	2.03	0.40
2:E:1141:ARG:HD2	2:E:1141:ARG:H	1.87	0.40
2:G:4712:PRO:HB2	2:G:4718:LYS:HA	2.01	0.40
2:G:940:GLY:O	2:G:1052:ASN:N	2.52	0.40
2:I:1105:ALA:O	2:I:1189:LEU:N	2.51	0.40
2:I:102:LEU:HB3	2:I:160:GLY:HA2	2.03	0.40
2:I:309:THR:O	2:I:313:SER:OG	2.39	0.40
2:I:3880:PHE:O	2:I:3884:LEU:N	2.54	0.40
2:B:4984:ASN:HD21	2:B:4986:ALA:HB3	1.86	0.40
2:E:1735:ILE:HG23	2:E:1771:LEU:HD23	2.03	0.40
2:E:184:THR:HA	2:E:189:LEU:HA	2.03	0.40
2:E:599:VAL:HG23	2:E:600:LEU:HD12	2.02	0.40
2:G:184:THR:HA	2:G:189:LEU:HA	2.03	0.40
2:G:3662:ILE:H	2:G:3662:ILE:HG13	1.79	0.40
2:G:4176:PRO:O	2:G:4202:ARG:NH2	2.55	0.40
2:G:4984:ASN:HD21	2:G:4986:ALA:HB3	1.87	0.40
2:I:123:THR:OG1	2:I:134:ASP:OD1	2.39	0.40
2:I:1727:ARG:HH21	2:I:1775:HIS:CE1	2.39	0.40
2:I:4957:LYS:NZ	2:I:4957:LYS:CB	2.83	0.40
2:I:876:GLU:O	2:I:880:GLU:N	2.51	0.40
2:B:3843:ASP:H	2:B:3874:VAL:HG13	1.87	0.40
2:B:4735:GLU:HA	2:B:4738:ALA:HB3	2.03	0.40
2:B:897:ARG:HD2	2:B:905:PRO:HG3	2.04	0.40
2:E:321:GLU:HB3	2:E:322:LYS:H	1.73	0.40
2:G:4578:LEU:O	2:E:4880:MET:HG3	2.21	0.40
2:E:4982:GLU:HB3	2:E:4983:HIS:H	1.71	0.40
2:E:897:ARG:HD2	2:E:905:PRO:HG3	2.04	0.40
2:G:2950:UNK:O	2:G:2954:UNK:N	2.54	0.40
2:I:2793:PRO:HG3	2:I:2855:TYR:CZ	2.57	0.40
2:B:4106:PRO:O	2:B:4110:PHE:N	2.53	0.40
2:E:1090:PHE:HD2	2:E:1202:LEU:HD11	1.86	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:149:THR:N	2:E:172:VAL:O	2.54	0.40
2:E:4702:ASP:OD1	2:E:4778:TRP:NE1	2.48	0.40
2:E:4962:GLY:H	2:E:5025:GLY:CA	2.34	0.40
2:G:2196:ASN:OD1	2:G:2199:ARG:NH1	2.38	0.40
2:G:446:GLN:HA	2:G:449:ILE:HD12	2.03	0.40
2:G:4968:PHE:CE2	2:G:4978:HIS:ND1	2.89	0.40
2:I:396:GLU:OE2	2:I:451:TYR:OH	2.32	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 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 EM 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	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
1	F	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
1	H	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
1	J	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
2	B	3235/4416 (73%)	2899 (90%)	332 (10%)	4 (0%)	56	90
2	E	3235/4416 (73%)	2900 (90%)	331 (10%)	4 (0%)	56	90
2	G	3235/4416 (73%)	2900 (90%)	331 (10%)	4 (0%)	56	90
2	I	3235/4416 (73%)	2900 (90%)	331 (10%)	4 (0%)	56	90
All	All	13360/18096 (74%)	11967 (90%)	1377 (10%)	16 (0%)	59	90

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG
2	I	1708	ARG
2	G	1708	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	E	1708	ARG
2	B	4641	PRO
2	I	4641	PRO
2	G	4641	PRO
2	E	4641	PRO
2	B	1932	PRO
2	I	1932	PRO
2	G	1932	PRO
2	E	1932	PRO
2	B	1840	PRO
2	I	1840	PRO
2	G	1840	PRO
2	E	1840	PRO

5.3.2 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 EM 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	88/89 (99%)	88 (100%)	0	100	100
1	F	88/89 (99%)	88 (100%)	0	100	100
1	H	88/89 (99%)	88 (100%)	0	100	100
1	J	88/89 (99%)	88 (100%)	0	100	100
2	B	2493/3022 (82%)	2471 (99%)	22 (1%)	84	93
2	E	2493/3022 (82%)	2471 (99%)	22 (1%)	84	93
2	G	2493/3022 (82%)	2471 (99%)	22 (1%)	84	93
2	I	2493/3022 (82%)	2471 (99%)	22 (1%)	84	93
All	All	10324/12444 (83%)	10236 (99%)	88 (1%)	85	93

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	131	LEU
2	B	534	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	553	ARG
2	B	1076	ARG
2	B	1141	ARG
2	B	1600	LEU
2	B	1676	LEU
2	B	1964	ARG
2	B	3787	LYS
2	B	3805	LEU
2	B	3896	ASN
2	B	4034	ASN
2	B	4085	ARG
2	B	4120	ASN
2	B	4166	LEU
2	B	4201	ASN
2	B	4796	MET
2	B	4839	MET
2	B	4957	LYS
2	B	4958	CYS
2	B	4983	HIS
2	B	4995	LEU
2	I	131	LEU
2	I	534	ARG
2	I	553	ARG
2	I	1076	ARG
2	I	1141	ARG
2	I	1600	LEU
2	I	1676	LEU
2	I	1964	ARG
2	I	3787	LYS
2	I	3805	LEU
2	I	3896	ASN
2	I	4034	ASN
2	I	4085	ARG
2	I	4120	ASN
2	I	4166	LEU
2	I	4201	ASN
2	I	4796	MET
2	I	4839	MET
2	I	4957	LYS
2	I	4958	CYS
2	I	4983	HIS
2	I	4995	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	G	131	LEU
2	G	534	ARG
2	G	553	ARG
2	G	1076	ARG
2	G	1141	ARG
2	G	1600	LEU
2	G	1676	LEU
2	G	1964	ARG
2	G	3787	LYS
2	G	3805	LEU
2	G	3896	ASN
2	G	4034	ASN
2	G	4085	ARG
2	G	4120	ASN
2	G	4166	LEU
2	G	4201	ASN
2	G	4796	MET
2	G	4839	MET
2	G	4957	LYS
2	G	4958	CYS
2	G	4983	HIS
2	G	4995	LEU
2	E	131	LEU
2	E	534	ARG
2	E	553	ARG
2	E	1076	ARG
2	E	1141	ARG
2	E	1600	LEU
2	E	1676	LEU
2	E	1964	ARG
2	E	3787	LYS
2	E	3805	LEU
2	E	3896	ASN
2	E	4034	ASN
2	E	4085	ARG
2	E	4120	ASN
2	E	4166	LEU
2	E	4201	ASN
2	E	4796	MET
2	E	4839	MET
2	E	4957	LYS
2	E	4958	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	E	4983	HIS
2	E	4995	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (134) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	43	ASN
1	F	87	HIS
1	A	43	ASN
1	A	87	HIS
1	H	43	ASN
1	H	87	HIS
1	J	43	ASN
1	J	87	HIS
2	B	57	ASN
2	B	71	GLN
2	B	105	HIS
2	B	111	HIS
2	B	273	HIS
2	B	379	HIS
2	B	413	GLN
2	B	479	GLN
2	B	1598	GLN
2	B	1660	GLN
2	B	1691	GLN
2	B	1693	GLN
2	B	1719	HIS
2	B	1775	HIS
2	B	1941	ASN
2	B	2007	ASN
2	B	2127	GLN
2	B	3809	ASN
2	B	3889	GLN
2	B	3896	ASN
2	B	3946	GLN
2	B	3950	ASN
2	B	3960	GLN
2	B	3963	ASN
2	B	3976	ASN
2	B	3994	HIS
2	B	4034	ASN
2	B	4054	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	4120	ASN
2	B	4209	GLN
2	B	4833	ASN
2	B	4978	HIS
2	I	57	ASN
2	I	71	GLN
2	I	105	HIS
2	I	111	HIS
2	I	273	HIS
2	I	379	HIS
2	I	413	GLN
2	I	479	GLN
2	I	1598	GLN
2	I	1660	GLN
2	I	1691	GLN
2	I	1693	GLN
2	I	1719	HIS
2	I	1775	HIS
2	I	1941	ASN
2	I	2007	ASN
2	I	2127	GLN
2	I	3809	ASN
2	I	3889	GLN
2	I	3896	ASN
2	I	3946	GLN
2	I	3950	ASN
2	I	3960	GLN
2	I	3963	ASN
2	I	3976	ASN
2	I	3994	HIS
2	I	4034	ASN
2	I	4054	ASN
2	I	4120	ASN
2	I	4833	ASN
2	I	4978	HIS
2	G	57	ASN
2	G	71	GLN
2	G	105	HIS
2	G	111	HIS
2	G	273	HIS
2	G	379	HIS
2	G	413	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	G	479	GLN
2	G	1598	GLN
2	G	1660	GLN
2	G	1691	GLN
2	G	1693	GLN
2	G	1719	HIS
2	G	1775	HIS
2	G	1941	ASN
2	G	2007	ASN
2	G	2127	GLN
2	G	3809	ASN
2	G	3889	GLN
2	G	3896	ASN
2	G	3946	GLN
2	G	3950	ASN
2	G	3960	GLN
2	G	3963	ASN
2	G	3976	ASN
2	G	3994	HIS
2	G	4034	ASN
2	G	4054	ASN
2	G	4120	ASN
2	G	4833	ASN
2	G	4973	HIS
2	G	4978	HIS
2	E	57	ASN
2	E	71	GLN
2	E	105	HIS
2	E	111	HIS
2	E	273	HIS
2	E	379	HIS
2	E	413	GLN
2	E	479	GLN
2	E	1598	GLN
2	E	1660	GLN
2	E	1691	GLN
2	E	1693	GLN
2	E	1719	HIS
2	E	1775	HIS
2	E	1941	ASN
2	E	2007	ASN
2	E	2127	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	E	3809	ASN
2	E	3889	GLN
2	E	3896	ASN
2	E	3946	GLN
2	E	3950	ASN
2	E	3960	GLN
2	E	3963	ASN
2	E	3976	ASN
2	E	3994	HIS
2	E	4034	ASN
2	E	4054	ASN
2	E	4120	ASN
2	E	4833	ASN
2	E	4978	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	G	14
2	B	14
2	I	14
2	E	14

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	4345:UNK	C	4540:PHE	N	74.58
1	I	4345:UNK	C	4540:PHE	N	74.58
1	G	4345:UNK	C	4540:PHE	N	74.58
1	E	4345:UNK	C	4540:PHE	N	74.58
1	B	3613:UNK	C	3639:THR	N	46.52
1	I	3613:UNK	C	3639:THR	N	46.52
1	G	3613:UNK	C	3639:THR	N	46.52
1	E	3613:UNK	C	3639:THR	N	46.52
1	B	4253:GLU	C	4320:UNK	N	29.50
1	I	4253:GLU	C	4320:UNK	N	29.50
1	G	4253:GLU	C	4320:UNK	N	29.50
1	E	4253:GLU	C	4320:UNK	N	29.50
1	B	3163:UNK	C	3170:UNK	N	16.19
1	I	3163:UNK	C	3170:UNK	N	16.19
1	G	3163:UNK	C	3170:UNK	N	16.18
1	E	3163:UNK	C	3170:UNK	N	16.18
1	B	3063:UNK	C	3134:UNK	N	14.97
1	I	3063:UNK	C	3134:UNK	N	14.97
1	G	3063:UNK	C	3134:UNK	N	14.97
1	E	3063:UNK	C	3134:UNK	N	14.97
1	B	3468:UNK	C	3511:UNK	N	14.26
1	I	3468:UNK	C	3511:UNK	N	14.26
1	G	3468:UNK	C	3511:UNK	N	14.26
1	E	3468:UNK	C	3511:UNK	N	14.26
1	B	2703:UNK	C	2734:ASN	N	13.16
1	I	2703:UNK	C	2734:ASN	N	13.16
1	G	2703:UNK	C	2734:ASN	N	13.16

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	2703:UNK	C	2734:ASN	N	13.16
1	B	3236:UNK	C	3241:UNK	N	12.69
1	I	3236:UNK	C	3241:UNK	N	12.69
1	G	3236:UNK	C	3241:UNK	N	12.69
1	E	3236:UNK	C	3241:UNK	N	12.69
1	B	2976:UNK	C	2995:UNK	N	12.19
1	I	2976:UNK	C	2995:UNK	N	12.19
1	G	2976:UNK	C	2995:UNK	N	12.19
1	E	2976:UNK	C	2995:UNK	N	12.19
1	B	1564:UNK	C	1573:MET	N	12.11
1	I	1564:UNK	C	1573:MET	N	12.11
1	G	1564:UNK	C	1573:MET	N	12.11
1	E	1564:UNK	C	1573:MET	N	12.11
1	B	3254:UNK	C	3261:UNK	N	8.68
1	I	3254:UNK	C	3261:UNK	N	8.68
1	G	3254:UNK	C	3261:UNK	N	8.68
1	E	3254:UNK	C	3261:UNK	N	8.68
1	B	1297:UNK	C	1430:UNK	N	5.91
1	I	1297:UNK	C	1430:UNK	N	5.91
1	G	1297:UNK	C	1430:UNK	N	5.91
1	E	1297:UNK	C	1430:UNK	N	5.91
1	B	2479:LEU	C	2487:UNK	N	3.40
1	I	2479:LEU	C	2487:UNK	N	3.40
1	G	2479:LEU	C	2487:UNK	N	3.40
1	E	2479:LEU	C	2487:UNK	N	3.40
1	B	2939:ARG	C	2942:UNK	N	3.21
1	I	2939:ARG	C	2942:UNK	N	3.21
1	G	2939:ARG	C	2942:UNK	N	3.21
1	E	2939:ARG	C	2942:UNK	N	3.21